Fig. 1

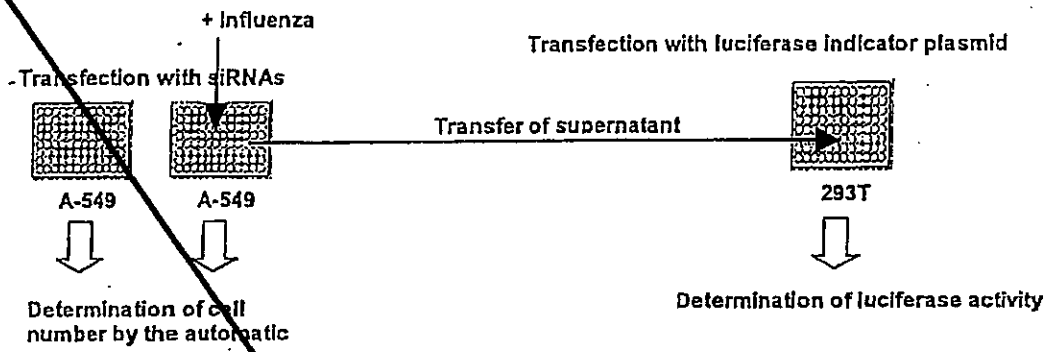

+ Influenza
Transfection with luciferase indicator plasmid
Transfection with siRNAs
Transfer of supernatant
A-549
A-549
293T
Determination of cell number by the automatic
Determination of luciferase activity

Fig. 2

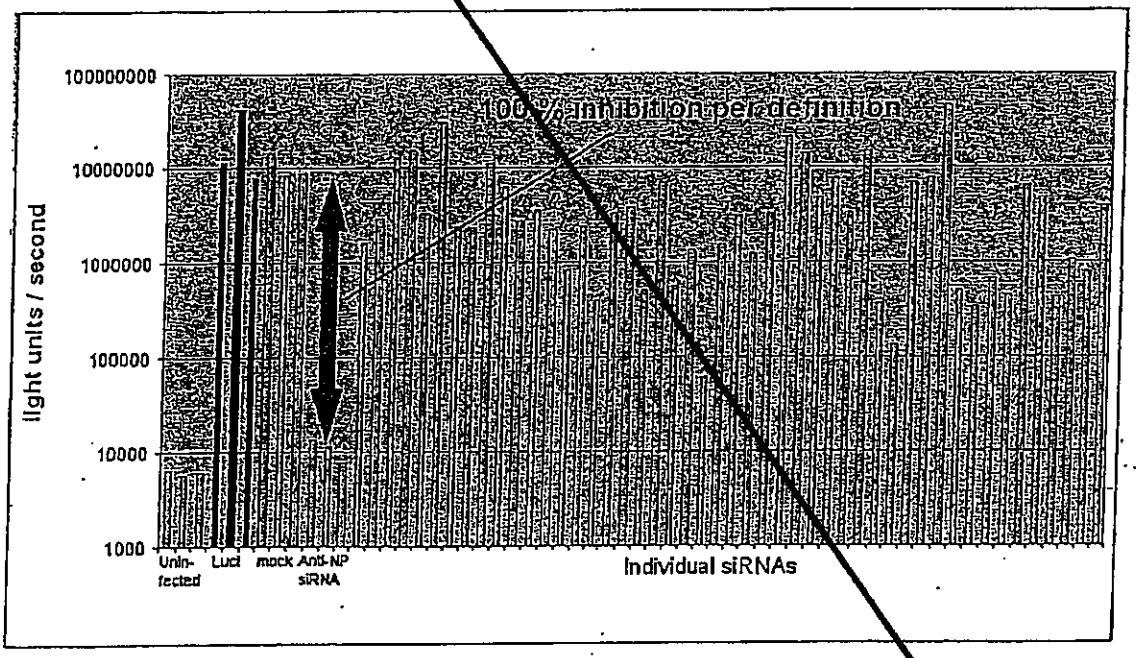

100000000
10000000
1000000
100000
10000
1000
light units / second
100 % inhibition per definition
Unin-fected
Luci
mock
Anti-NP siRNA
Individual siRNAs

Fig. 3

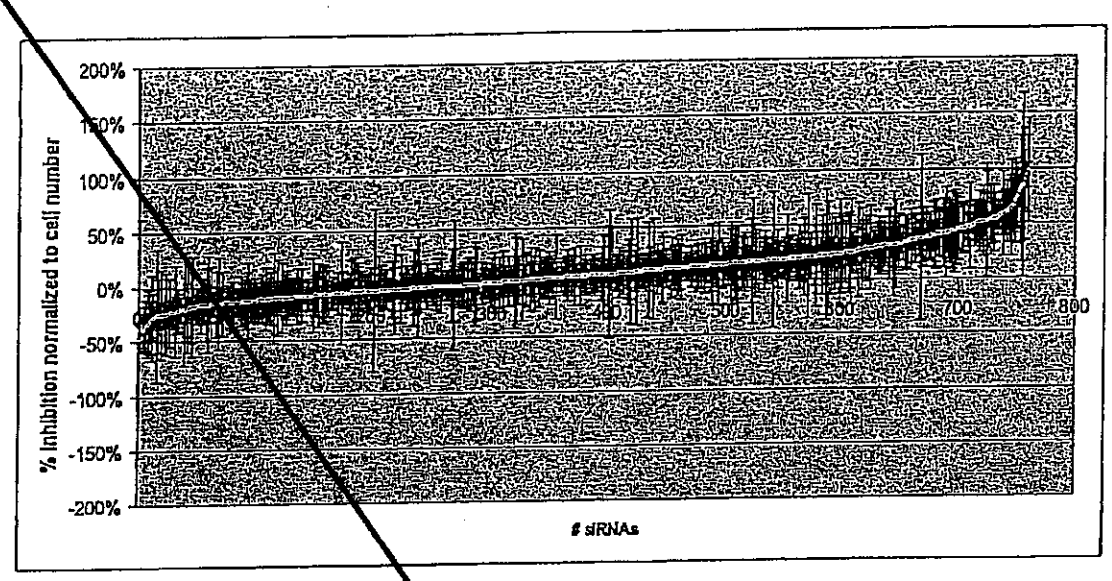

200%
150%
100%
50%
0%
-50%
-100%
-150%
-200%
% Inhibition normalized to cell number
# siRNAs

Fig. 4

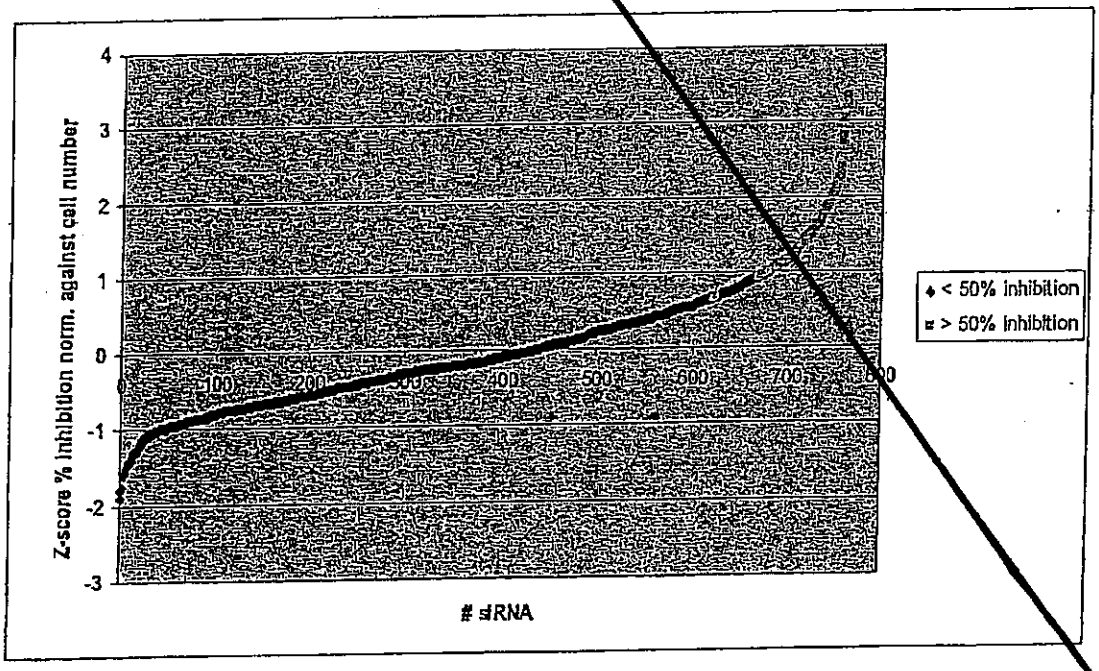

4
3
2
1
0
-1
-2
-3
Z-score % Inhibition norm. against cell number
siRNA
< 50% inhibition
> 50% inhibition

Fig. 5

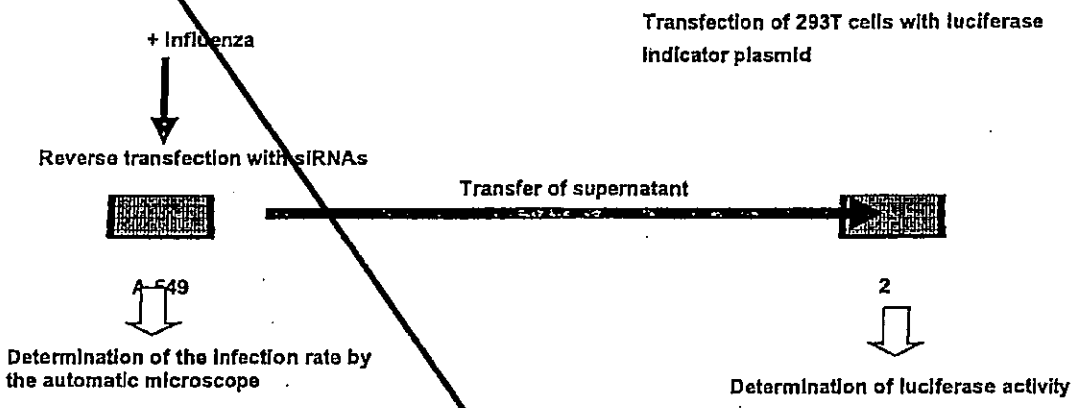

+ Influenza
Reverse transfection with siRNAs
A-549
Determination of the infection rate by the automatic microscope
Transfection of 293T cells with luciferase indicator plasmid
Transfer of supernatant
2
Determination of luciferase activity

Fig. 6

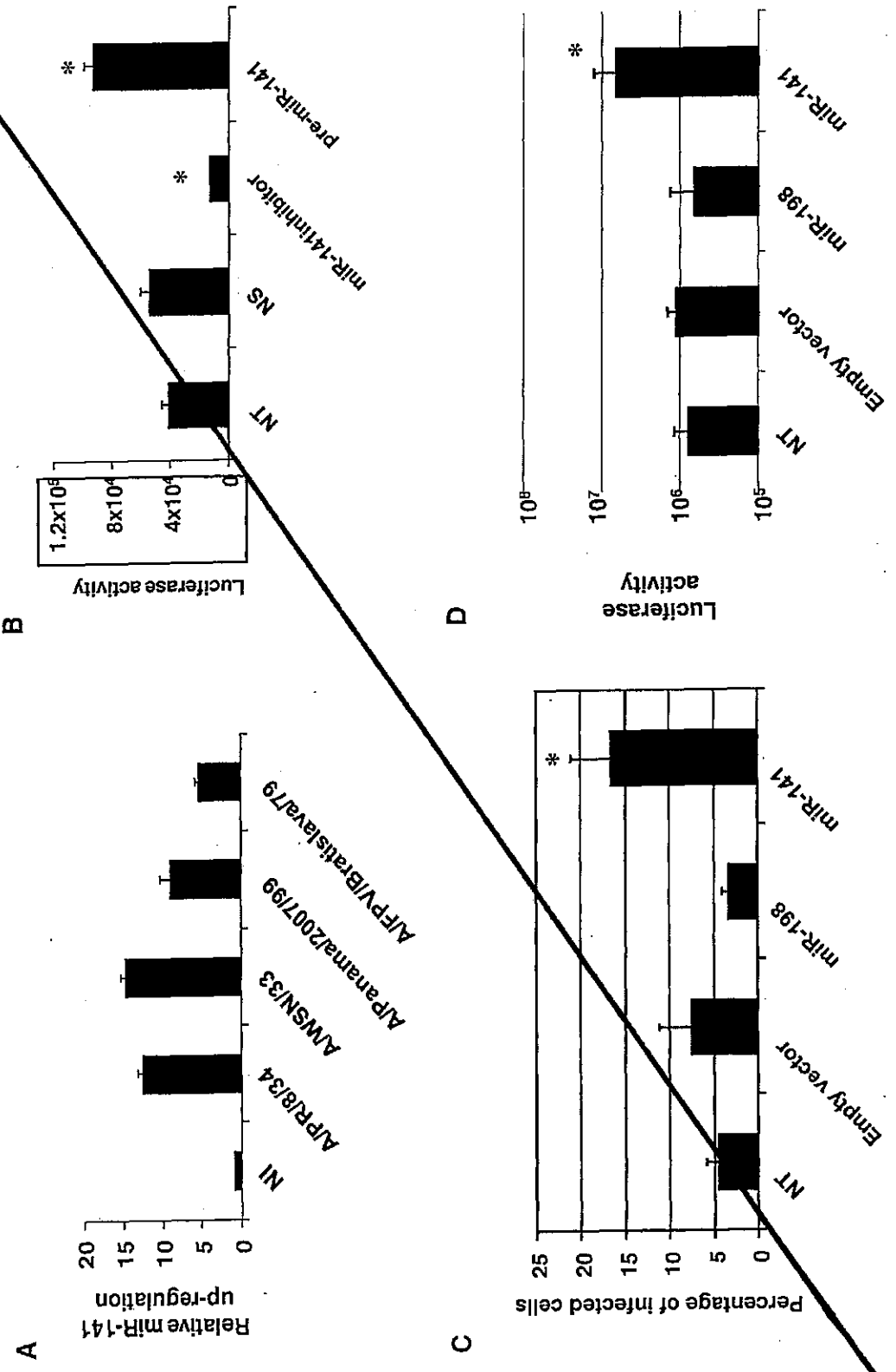
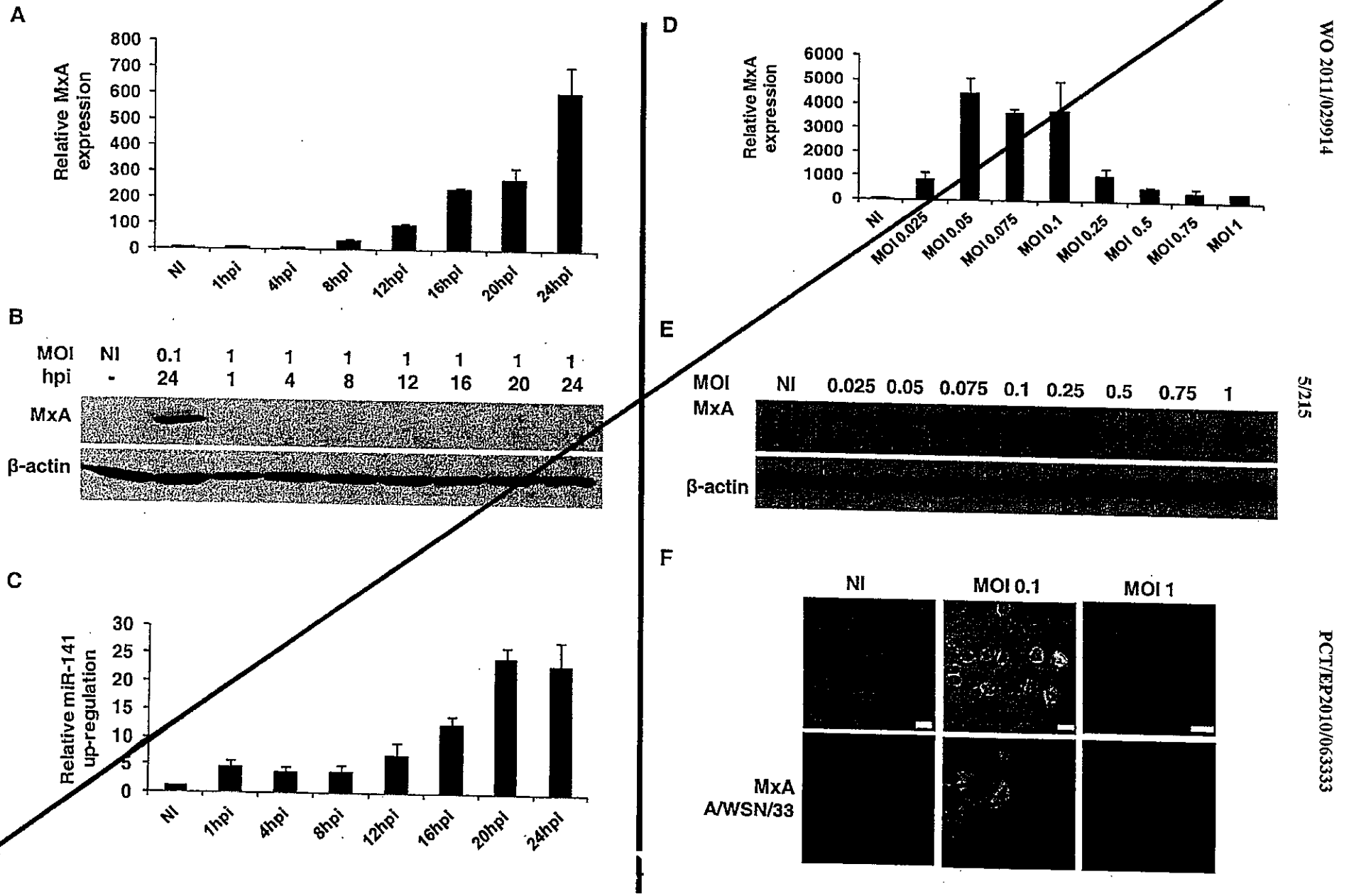

A
Relative miR-141 up-regulation
0
5
10
15
20
NI
A/PR/8/34
A/WSN/33
A/Panama/2007/99
A/FPV/Bratislava/79
B
Luciferase activity
0
4x10^4
8x10^4
1.2x10^5
NT
NS
miR-141inhibitor
Pre-miR-141
C
Percentage of infected cells
0
5
10
15
20
25
NT
Empty vector
miR-198
miR-141
D
Luciferase activity
10^5
10^6
10^7
10^8
NT
Empty vector
miR-198
miR-141

Fig. 7


A
Relative MxA expression
800
700
600
500
400
300
200
100
0
NI
1hpi
4hpi
8hpi
12hpi
16hpi
20hpi
24hpi
B
MOI NI 0.1 1 1 1 1 1 1 1
hpi - 24 1 4 8 12 16 20 24
MxA
β-actin
C
Relative miR-141 up-regulation
30
25
20
15
10
5
0
NI
1hpi
4hpi
8hpi
12hpi
16hpi
20hpi
24hpi
D
Relative MxA expression
6000
5000
4000
3000
2000
1000
0
NI
MOI 0.025
MOI 0.05
MOI 0.075
MOI 0.1
MOI 0.25
MOI 0.5
MOI 0.75
MOI 1
E
MOI NI 0.025 0.05 0.075 0.1 0.25 0.5 0.75 1
MxA
β-actin
F
NI
MOI 0.1
MOI 1
MxA
A/WSN/33

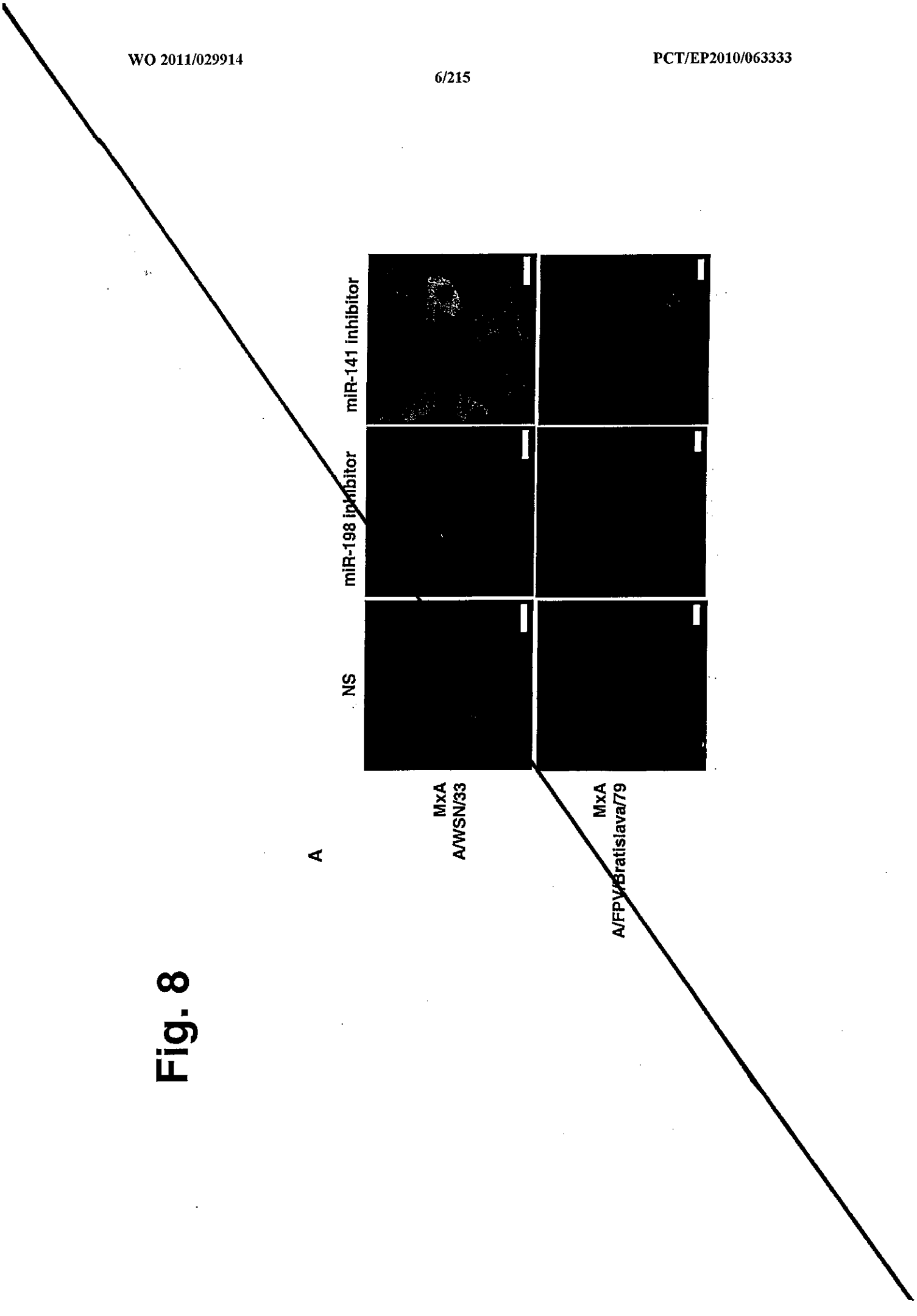

A
MxA
A/WSN/33
MxA
A/FPV/Bratislava/79
NS
miR-198 inhibitor
miR-141 inhibitor

Fig. 8

Fig. 8

B
Relative miR-141 up-regulation
0
5
10
15
20
25
NI
MOI 0.025
MOI 0.05
MOI 0.075
MOI 0.1
MOI 0.25
MOI 0.5
MOI 0.75
MOI 1
C
MOI
miR-141 inhibitor (nmol)
NS (nmol)
MxA
β-actin
1
100
-
1
200
-
1
-
200
1
-
-
0.1
-
-

Fig. 9

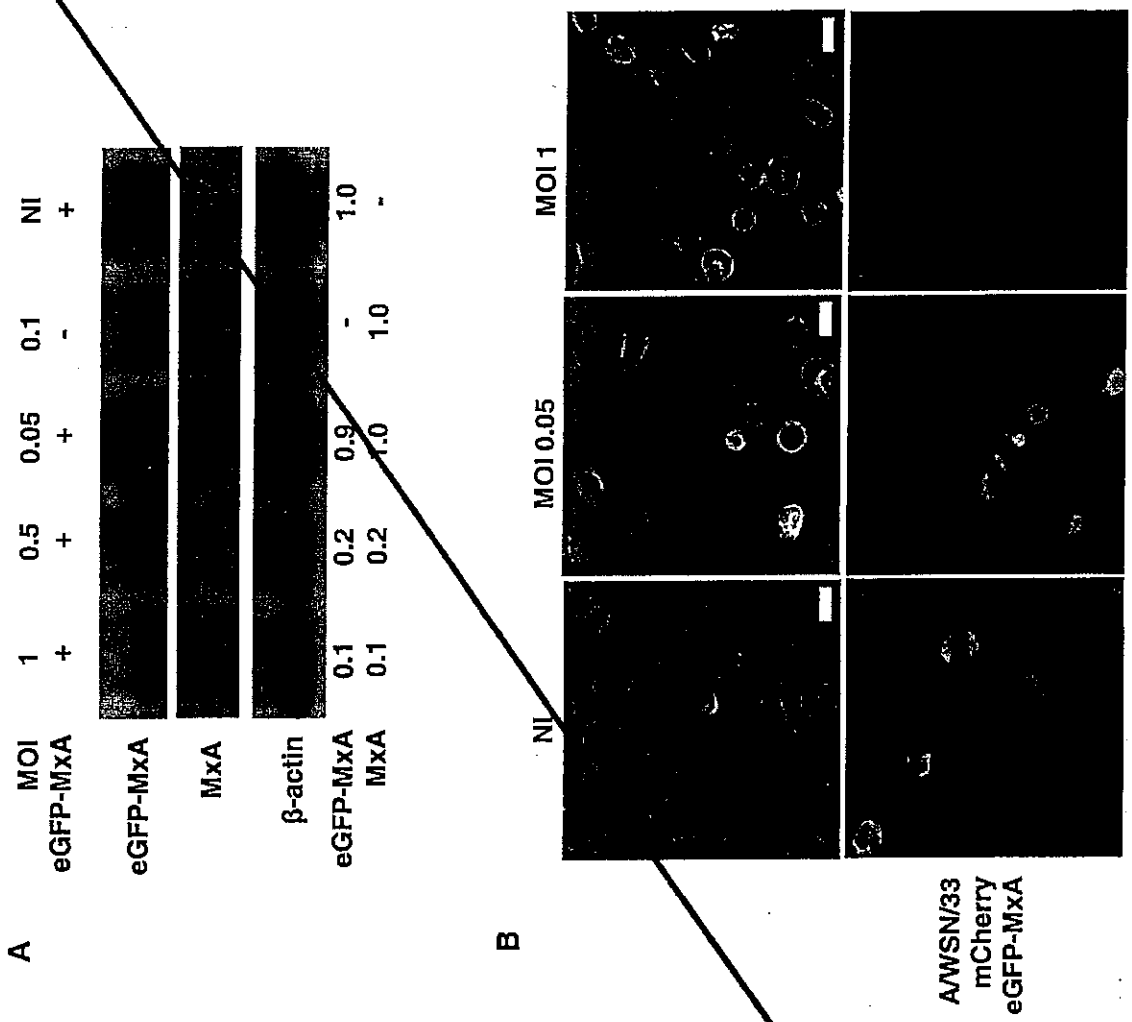

A
MOI 1 0.5 0.05 0.1 NI
eGFP-MxA + + + - +
eGFP-MxA
MxA
β-actin
eGFP-MxA 0.1 0.2 0.9 - 1.0
MxA 0.1 0.2 1.0 1.0 -
B
NI
MOI 0.05
MOI 1
A/WSN/33
mCherry
eGFP-MxA

Fig. 9

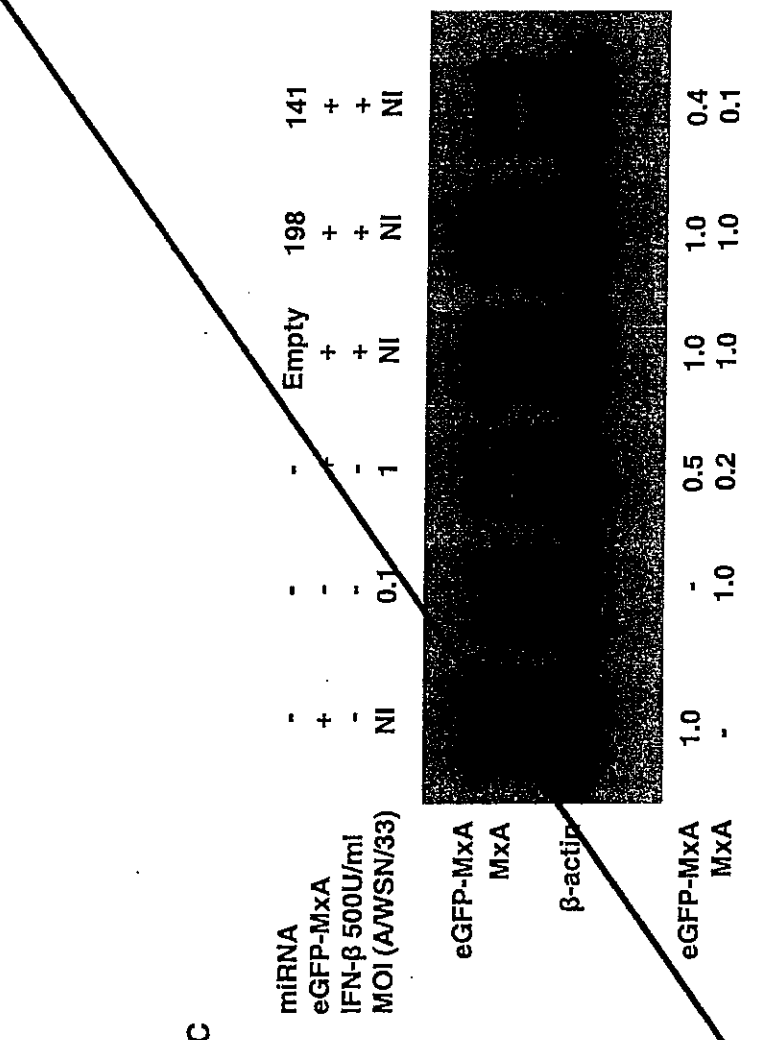

C
miRNA - - - Empty 198 141
eGFP-MxA + - + + + +
IFN-β 500U/ml - - - + + +
MOI (A/WSN/33) NI 0.1 1 NI NI NI
eGFP-MxA
MxA
β-actin
1.0 - 0.5 1.0 1.0 0.4
- 1.0 0.2 1.0 1.0 0.1
eGFP-MxA
MxA

Fig. 9

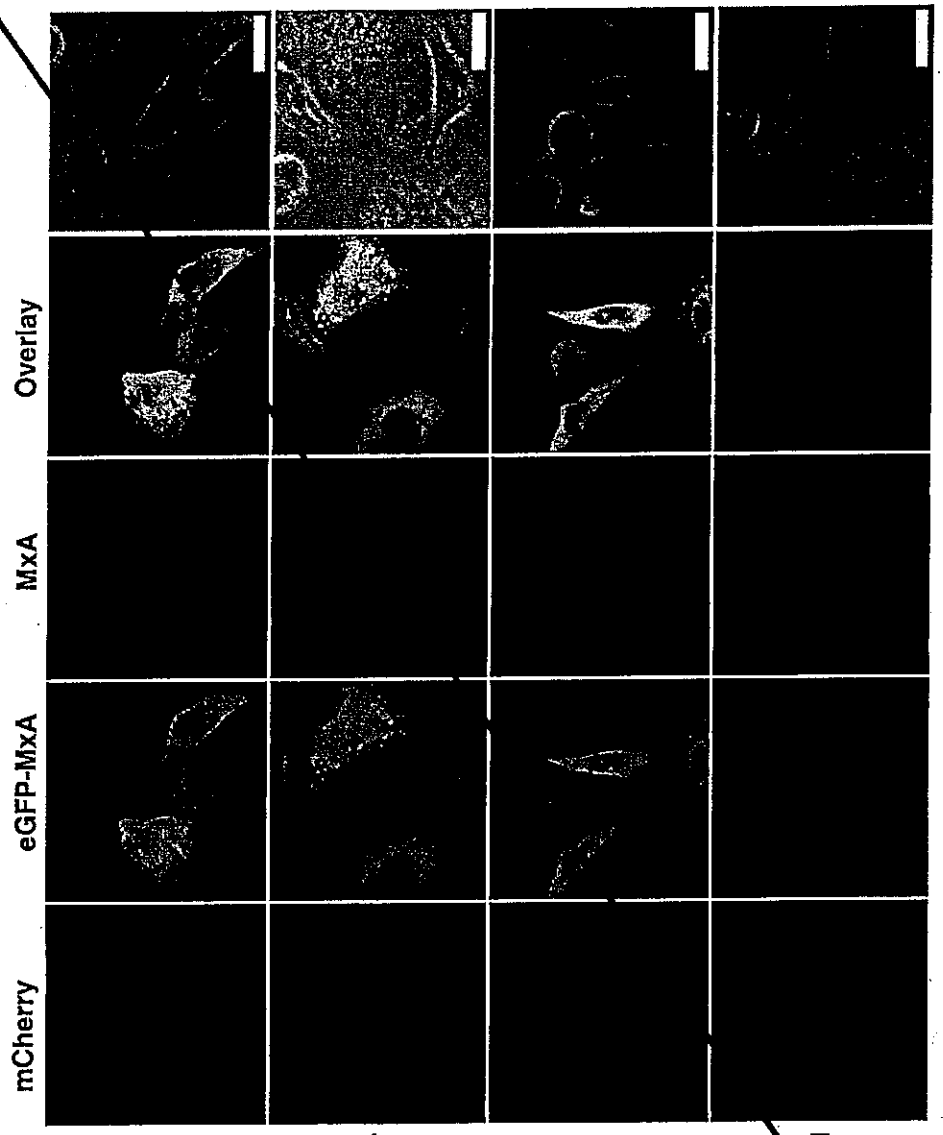

D
Control
Empty vector
miR-198
miR-141
mCherry
eGFP-MxA
MxA
Overlay

Fig. 10

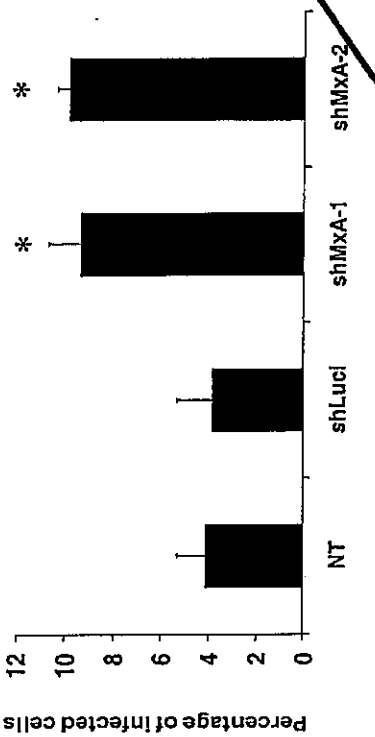
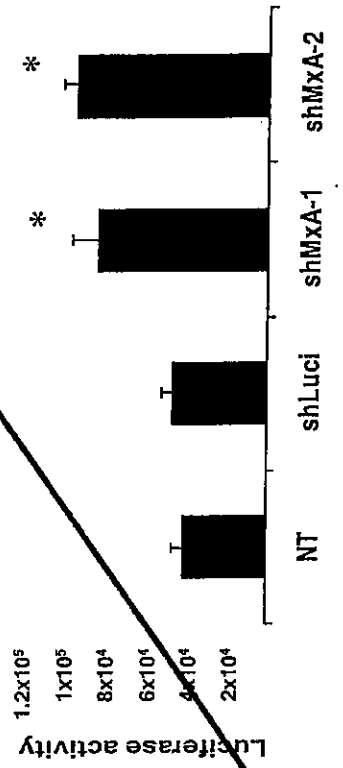

Percentage of infected cells
0
2
4
6
8
10
12
NT
shLuci
shMxA-1
shMxA-2
*
*

Fig. 11


Luciferase activity
2x10⁴
4x10⁴
6x10⁴
8x10⁴
1x10⁵
1.2x10⁵
NT
shLuci
shMxA-1
shMxA-2
*
*

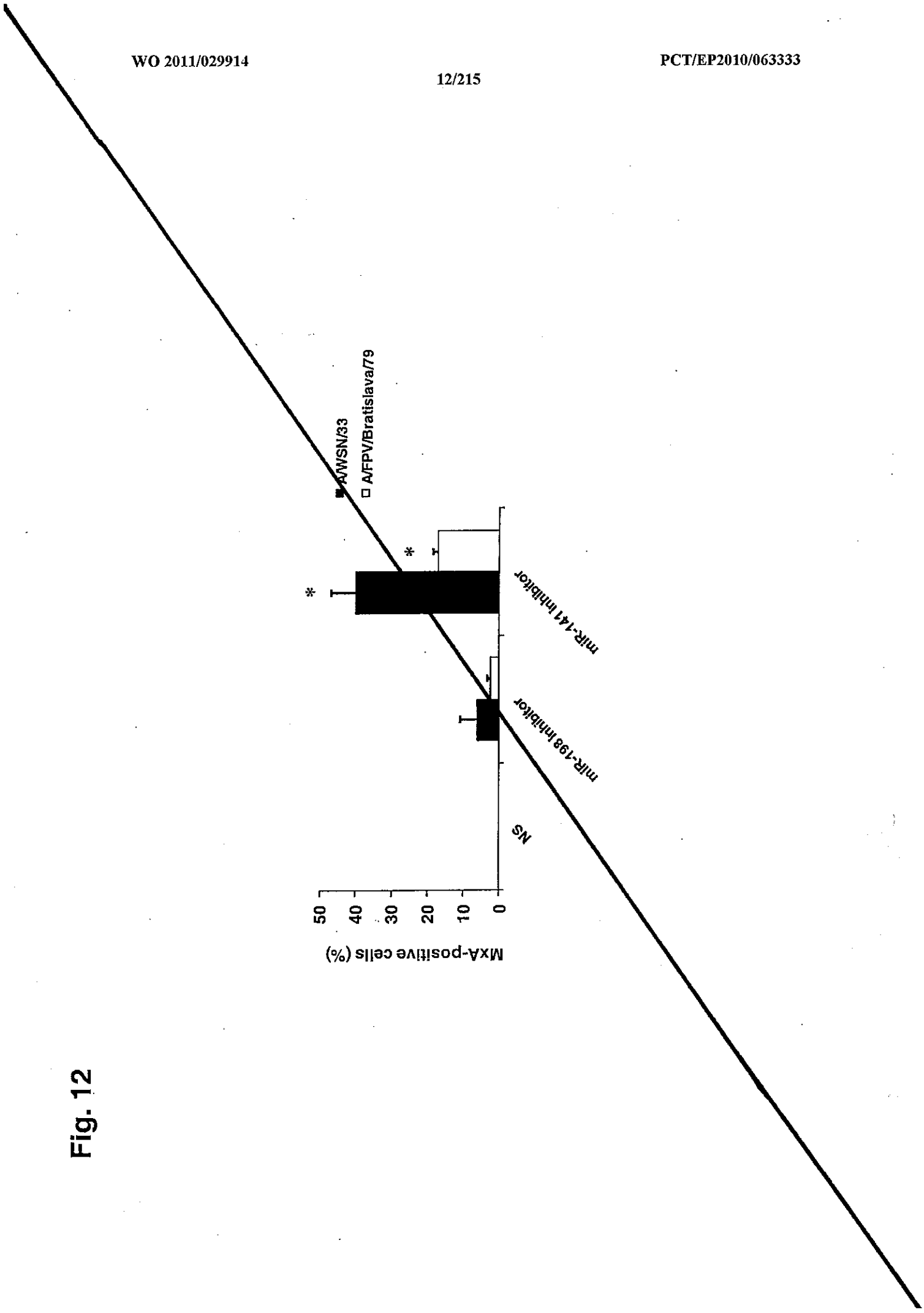
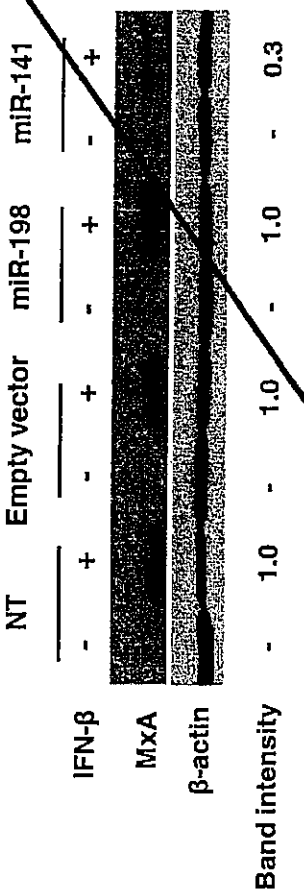

A/WSN/33
A/FPV/Bratislava/79
MxA-positive cells (%)
50
40
30
20
10
0
NS
miR-198 inhibitor
miR-141 inhibitor
*
*

Fig. 12

Fig. 13


NT
Empty vector
miR-198
miR-141
IFN-β
MxA
β-actin
Band intensity
- + - + - + - +
- 1.0 - 1.0 - 1.0 - 0.3

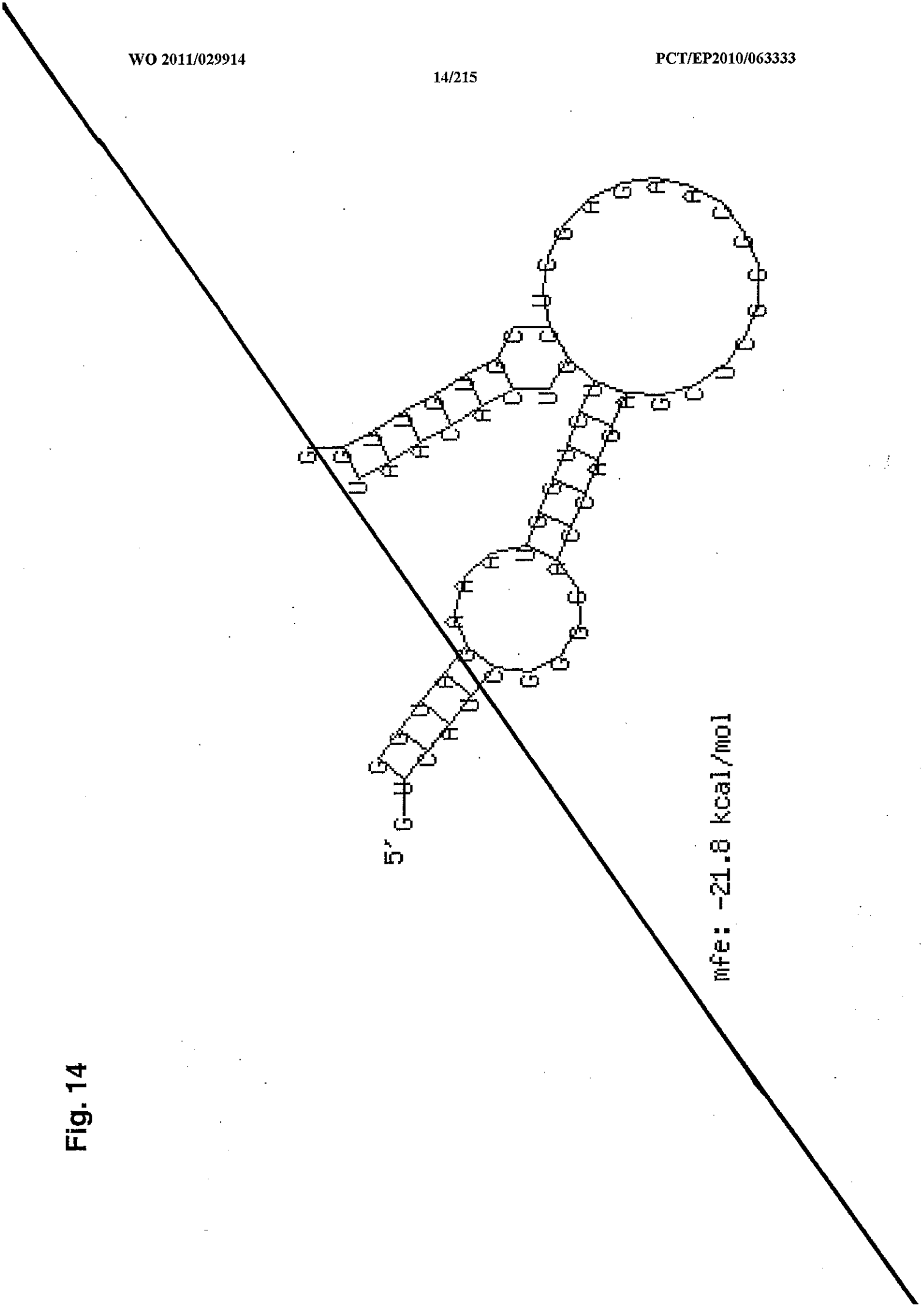


Fig. 14

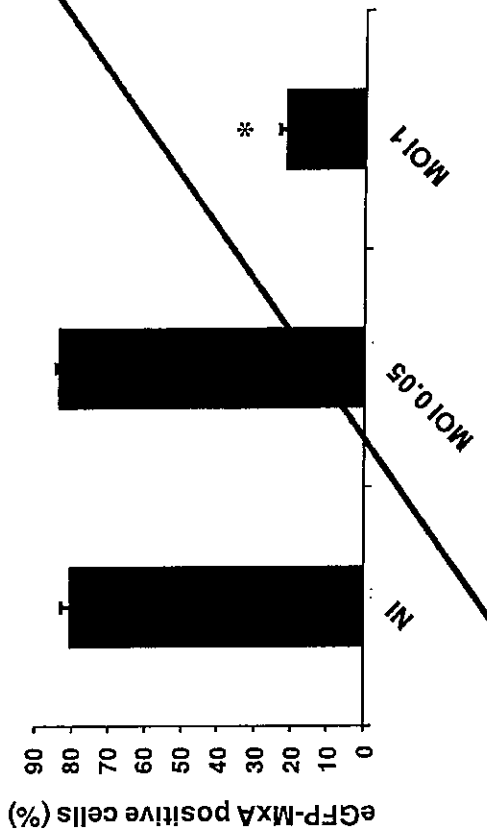

eGFP-MxA positive cells (%)
0
10
20
30
40
50
60
70
80
90
NI
MOI 0.05
MOI 1
*

Fig. 15

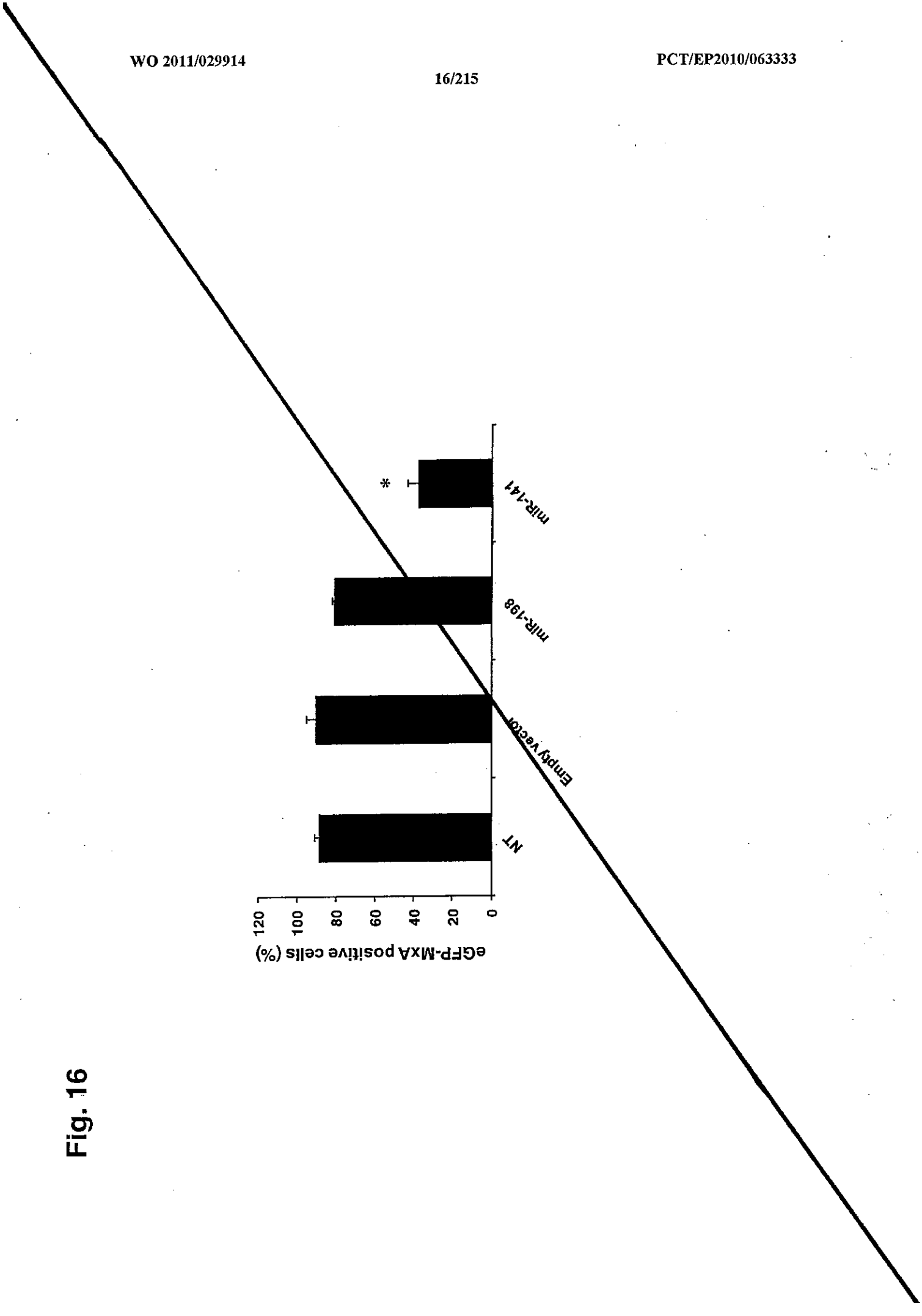

eGFP-MxA positive cells (%)
0
20
40
60
80
100
120
NT
Empty vector
miR-198
miR-141
*

Fig. 16

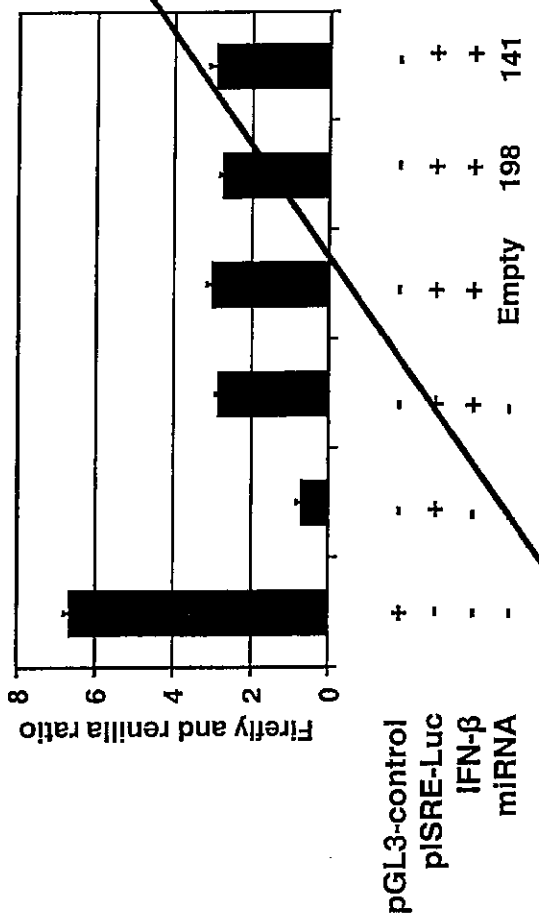

Firefly and renilla ratio
0
2
4
6
8
pGL3-control + - - - - -
pISRE-Luc - + - + + +
IFN-β - - + + + +
miRNA - - - Empty 198 141

Fig. 17

Fig. 18

miR-141/141*

precursor sequence

>hsa-mir-141 MI0000457
5'-CGGCCGGCCCUGGGUCCAUCUUCCAGUACAGUGUUGGAUGGUCUAAUUGUGAAGCUCCUAACACUGUCUGGU
AAAGAUGGCUCCCGGGUGGGUUC-3'

precursor structure

```
c    g    u   -u        --    u        -   ugg  ua
 ggcc gccc ggg  ccaucuu  ccag acaguguu gga   uc  a
 |||| |||| |||  |||||||  |||| |||||||| |||   ||  u
 uugg uggg ccc  gguagaa  gguc ugucacaa ccu   ag  u
c    g    -   uc       au    -       u   cga  ug
```

miR-141

>hsa-miR-141 MIMAT0000432
5'-(59)-UAACACUGUCUGGUAAAGAUGG-(80)-3'

miR-141*

>hsa-miR-141* MIMAT0004598
5'-(17)-CAUCUUCCAGUACAGUGUUGGA-(38)-3'

miR-200c/200c*

precursor sequence

>hsa-mir-200c MI0000650
5'-CCCUCGUCUUACCCAGCAGUGUUUGGGUGCGGUUGGGAGUCUCUAAUACUGCCGGGUAAUGAUGGAGG-3'

precursor structure

```
  cu    -      a        u   u  ggu
cc  cguc uuaccc gcaguguu ggg gc   u
||  |||| |||||| |||||||| ||| ||
gg  guag aauggg cgucauaa cuc ug   g
  ag    u      c        u   -  agg
```

miR-200c

>hsa-miR-200c MIMAT0000617
5'-(44)-UAAUACUGCCGGGUAAUGAUGGA-(66)-3'

miR-200c*

>hsa-miR-200c* MIMAT0004657
5'-(5)-CGUCUUACCCAGCAGUGUUUGG-(26)-3'

Table 1a

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
Pool 19			-47%	109%
CKM	1158	NM_001824	-46%	14%
MAP3K3	4215	NM_002401	-45%	3%
SNARK	81788	NM_030952	-39%	16%
DDR1	780	NM_001954	-38%	21%
IHPK2	51447	NM_016291	-34%	23%
MARK3	4140	NM_002376	-33%	8%
Pool 31			-33%	30%
Pool 69			-31%	30%
AK7	122481	NM_152327	-30%	17%
Pool 46			-28%	17%
ARAF1	369	NM_001654	-28%	39%
Pool 75			-27%	22%
AKAP1	8165	NM_003488	-27%	10%
Pool 56			-27%	8%
IRAK2	3656	NM_001570	-26%	60%
ERK8	225689	NM_139021	-25%	34%
PANK3	79646	NM_024594	-25%	12%
AK5	26289	NM_174858	-25%	41%
PDK2	5164	NM_002611	-25%	6%
DGUOK	1716	NM_001929	-25%	12%
HGS	9146	NM_004712	-25%	10%
Pool 114			-24%	38%
Pool 33			-24%	9%
Pool 39			-23%	8%
Pool 43			-23%	31%
Pool 55			-23%	12%
MAPK8IP2	23542	NM_012324	-23%	10%
SKP2	6502	NM_005983	-22%	15%
Pool 45			-22%	7%
STK23	26576	NM_014370	-22%	41%
SRPK2	6733	NM_182692	-21%	20%
PKIG	11142	NM_181805	-21%	20%
PRKY	5616	NM_002760	-21%	16%
TESK1	7016	NM_006285	-21%	19%
NEK2	4751	NM_002497	-20%	11%
Pool 64			-20%	12%
PSKH1	5681	NM_006742	-20%	5%
PRKAR2B	5577	NM_002736	-20%	52%
TRAD	11139	NM_007064	-20%	11%
DYRK1A	1859	NM_001396	-20%	24%
LIMK1	3984	NM_002314	-19%	41%
WEE1	7465	NM_003390	-19%	10%
Pool 37			-18%	6%
ADRBK1	156	NM_001619	-18%	33%
TPK1	27010	NM_022445	-18%	46%
PHKB	5257	NM_000293	-17%	6%

Table 1a (continued)

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
PRKWNK4	65266	NM_032387	-17%	11%
Pool 82			-17%	16%
Pool 32			-17%	17%
PIK4CA	5297	NM_002650	-17%	17%
MK-STYX	51657	NM_016086	-17%	7%
Pool 103			-17%	26%
IRAK1BP1	134728	BX537762	-17%	13%
PRKCD	5580	NM_006254	-16%	17%
KIT	3815	NM_000222	-16%	9%
IRAK1	3654	NM_001569	-16%	14%
FGFR2	2263	NM_000141	-16%	8%
Pool 106			-16%	33%
Pool 111			-16%	44%
DGKH	160851	NM_178009	-16%	17%
Pool 113			-16%	35%
DAPK1	1612	NM_004938	-15%	11%
RAGE	5891	NM_014226	-15%	9%
KSR	8844	XM_290793	-15%	12%
TAO1	9344	NM_016151	-15%	3%
TAO1	9344	NM_004783	-15%	3%
Pool 30			-15%	31%
PAK2	5062	NM_002577	-15%	16%
AURKC	6795	NM_003160	-15%	42%
MARK2	2011	NM_004954	-15%	13%
MVK	4598	NM_000431	-15%	30%
MAPKBP1	23005	XM_031706	-15%	30%
PRKCE	5581	NM_005400	-14%	5%
EKI1	55500	NM_018638	-14%	7%
EPHA7	2045	NM_004440	-14%	10%
CDK4	1019	NM_000075	-14%	16%
AKAP12	9590	NM_005100	-14%	6%
Pool 29			-14%	16%
AURKB	9212	NM_004217	-14%	9%
PIK3C3	5289	NM_002647	-14%	18%
MAP2K6	5608	NM_002758	-14%	19%
ADCK4	79934	NM_024876	-14%	14%
MAPK8IP1	9479	NM_005456	-13%	5%
Pool 65			-13%	12%
PIK3CB	5291	NM_006219	-13%	10%
PIK3R3	8503	NM_003629	-13%	12%
PDK1	5163	NM_002610	-13%	11%
HRI	27102	NM_014413	-13%	23%
CSNK1G1	53944	NM_022048	-13%	17%
BMPR1A	657	NM_004329	-13%	12%
DAPK3	1613	NM_001348	-13%	20%
SIK2	23235	AB096248	-13%	10%
PDPK1	5170	NM_002613	-12%	27%
Pool 104			-12%	35%
CAMKK1	84254	NM_032294	-12%	10%

Table 1a (continued)

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
TK1	7083	NM_003258	-12%	20%
CSNK2B	1460	NM_001320	-12%	10%
MGC4796	83931	NM_032017	-12%	16%
DGKB	1607	NM_145695	-12%	16%
MET	4233	NM_000245	-12%	5%
ERBB4	2066	NM_005235	-12%	21%
PRKCDBP	112464	NM_145040	-12%	16%
BTK	695	NM_000061	-12%	11%
RPS6KB1	6198	NM_003161	-11%	13%
AKAP11	11215	NM_016248	-11%	9%
PRKAG1	5571	NM_002733	-11%	15%
PIK3C2A	5286	NM_002645	-11%	22%
CDK11	23097	NM_015076	-11%	16%
Pool 54			-11%	14%
MKNK2	2872	NM_017572	-11%	29%
PTK9	5756	NM_002822	-11%	11%
FLT3LG	2323	BF688722	-11%	13%
CDK8	1024	NM_001260	-11%	20%
ITPKA	3706	NM_002220	-11%	24%
CDK3	1018	NM_001258	-11%	14%
CDK7	1022	NM_001799	-11%	9%
PRKACA	5566	NM_002730	-11%	41%
Pool 3			-10%	11%
LAK	80216	NM_025144	-10%	16%
ITPKB	3707	NM_002221	-10%	35%
PI4KII	55361	NM_018425	-10%	12%
PRKCBP1	23613	NM_183048	-10%	16%
SH3KBP1	30011	NM_031892	-10%	5%
BRAF	673	NM_004333	-10%	13%
Pool 34			-10%	33%
KHK	3795	NM_000221	-10%	9%
DCAMKL1	9201	NM_004734	-10%	21%
CLK3	1198	NM_001292	-10%	13%
BCR	613	NM_004327	-10%	25%
STK16	8576	NM_003691	-10%	17%
MAPKAPK3	7867	NM_004635	-10%	18%
IKBKE	9641	XM_375834	-9%	12%
ATR	545	NM_001184	-9%	15%
STK17A	9263	NM_004760	-9%	16%
MOS	4342	NM_005372	-9%	16%
MAPK3	5595	NM_002746	-9%	9%
SMG1	23049	NM_014006	-9%	26%
FER	2241	NM_005246	-9%	17%
PFKP	5214	NM_002627	-9%	12%
CSK	1445	NM_004383	-9%	13%
BUB1	699	NM_004336	-9%	24%
AK3L1	50808	NM_016282	-9%	13%
GRK7	131890	NM_139209	-9%	3%
MAP3K6	9064	NM_004672	-9%	6%

Table 1a (continued)

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
ACVR2B	93	NM_001106	-9%	6%
IRAK4	51135	NM_016123	-8%	14%
EPHA5	2044	NM_004439	-8%	15%
PRKWNK3	65267	NM_020922	-8%	4%
RIOK1	83732	NM_031480	-8%	7%
MAK	4117	NM_005906	-8%	12%
CSNK2A2	1459	NM_001896	-8%	35%
Pool 60			-8%	17%
AXL	558	NM_001699	-8%	21%
IHPK1	9807	NM_153273	-8%	15%
Pool 98			-8%	29%
JAK2	3717	NM_004972	-8%	3%
Pool 61			-8%	17%
DDR2	4921	NM_006182	-8%	26%
ADCK5	203054	NM_174922	-8%	27%
EPHA1	2041	NM_005232	-7%	14%
Pool 77			-7%	25%
GKAP42	80318	NM_025211	-7%	12%
PIK3R4	30849	NM_014602	-7%	22%
ROCK1	6093	NM_005406	-7%	3%
Pool 22			-7%	13%
LCK	3932	NM_005356	-7%	8%
RPS6KA2	6196	NM_021135	-7%	13%
KIDINS220	57498	AB033076	-7%	15%
Pool 24			-7%	10%
SNF1LK	150094	NM_173354	-7%	6%
FGFR1	2260	NM_015850	-7%	10%
Pool 53			-7%	19%
PRKCI	5584	NM_002740	-7%	9%
HSPB8	26353	NM_014365	-6%	10%
JAK1	3716	NM_002227	-6%	47%
Pool 68			-6%	20%
CLK1	1195	NM_004071	-6%	13%
SAST	22983	AB023190	-6%	8%
PDGFRB	5159	NM_002609	-6%	11%
CLK2	1196	NM_001291	-6%	9%
VRK2	7444	NM_006296	-6%	12%
LOC91807	91807	NM_182493	-6%	17%
MELK	9833	NM_014791	-5%	29%
Pool 18			-5%	11%
CCRK	23552	NM_178432	-5%	31%
PRKAG3	53632	NM_017431	-5%	21%
SPEC2	56990	NM_020240	-5%	6%
Pool 44			-5%	27%
ACVR1B	91	NM_004302	-5%	10%
CHUK	1147	NM_001278	-5%	22%
FYN	2534	NM_002037	-5%	17%
DTYMK	1841	NM_012145	-5%	8%
SRMS	6725	NM_080823	-5%	19%

Table 1a (continued)

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
MAP3K9	4293	XM_027237	-5%	6%
ALK	238	NM_004304	-5%	13%
PAK6	56924	NM_020168	-5%	10%
Pool 8			-5%	15%
ILKAP	80895	NM_176799	-5%	16%
SPHK2	56848	NM_020126	-5%	4%
CDK2	1017	NM_001798	-5%	21%
NEK3	4752	NM_152720	-5%	7%
TESK2	10420	NM_007170	-5%	9%
AKT2	208	NM_001626	-5%	74%
PRKG1	5592	NM_006258	-5%	8%
KIP2	10518	NM_006383	-5%	8%
Pool 88			-4%	32%
MAPK14	1432	NM_001315	-4%	15%
CARKL	23729	NM_013276	-4%	23%
NME4	4833	NM_005009	-4%	5%
VRK1	7443	NM_003384	-4%	17%
TAO1	9344	NM_016151	-4%	11%
TAO1	9344	NM_004783	-4%	11%
NLK	51701	NM_016231	-4%	10%
NME1	4830	NM_000269	-4%	19%
Pool 12			-4%	18%
CALM3	808	NM_005184	-4%	10%
ADRBK2	157	NM_005160	-4%	8%
Pool 21			-4%	10%
PRKWNK2	65268	NM_006648	-4%	26%
Pool 97			-4%	20%
Pool 115			-4%	41%
RAF1	5894	NM_002880	-4%	7%
PACSIN3	29763	NM_016223	-4%	6%
PGK2	5232	NM_138733	-4%	9%
MAPK10	5602	NM_002753	-3%	7%
Pool 36			-3%	32%
PRKWNK1	65125	NM_018979	-3%	13%
ITPKC	80271	NM_025194	-3%	15%
FLJ13052	65220	NM_023018	-3%	8%
RPS6KA3	6197	NM_004586	-3%	21%
MAST2	23139	NM_015112	-3%	10%
STK25	10494	NM_006374	-3%	18%
LMTK2	22853	NM_014916	-3%	11%
MAPK1	5594	NM_002745	-3%	13%
MAGI-3	260425	NM_020965	-3%	8%
PFKFB1	5207	NM_002625	-3%	20%
Pool 71			-3%	35%
GRK6	2870	NM_002082	-3%	25%
STK6	6790	NM_003600	-3%	13%
Pool 101			-3%	46%
STK11IP	114790	NM_052902	-3%	10%
DOK1	1796	NM_001381	-2%	23%

Table 1a (continued)

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
PTK9L	11344	NM_007284	-2%	9%
CNK1	10256	NM_006314	-2%	9%
FLT3	2322	NM_004119	-2%	13%
ZAP70	7535	NM_001079	-2%	13%
MAPKAP1	79109	NM_024117	-2%	20%
AK1	203	NM_000476	-2%	9%
FGFR3	2261	NM_000142	-2%	6%
TXK	7294	NM_003328	-2%	10%
CDKN1C	1028	NM_000076	-2%	14%
Pool 7			-2%	17%
MUSK	4593	NM_005592	-2%	8%
ACVR1	90	NM_001105	-2%	22%
AKAP5	9495	NM_004857	-2%	11%
MKNK1	8569	NM_003684	-2%	11%
UGP2	7360	NM_006759	-2%	10%
RYK	6259	NM_002958	-2%	5%
Pool 107			-2%	25%
ITPK1	3705	NM_014216	-1%	13%
RPS6KL1	83694	NM_031464	-1%	8%
PIM1	5292	NM_002648	-1%	6%
CAMK2D	817	NM_001221	-1%	13%
CAMK2G	818	NM_172173	-1%	8%
TYK2	7297	NM_003331	-1%	13%
LIMK2	3985	NM_005569	-1%	10%
HK2	3099	NM_000189	-1%	14%
Pool 91			-1%	33%
DYRK1B	9149	NM_004714	-1%	17%
TTBK1	84630	XM_166453	-1%	59%
Pool 58			-1%	15%
Pool 41			-1%	8%
MAP3K5	4217	NM_005923	-1%	17%
CDKL2	8999	NM_003948	-1%	10%
LOC149420	149420	NM_152835	-1%	20%
EGFR	1956	NM_005228	-1%	15%
FRK	2444	NM_002031	-1%	22%
Pool 78			-1%	21%
CDKN2C	1031	NM_001262	-1%	14%
IRAK3	11213	NM_007199	-1%	4%

Table 1b

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
AKAP8	10270	NM_005858	1%	19%
Pool 2			1%	13%
HSA250839	55351	NM_018401	1%	14%
JAK3	3718	NM_000215	1%	18%
LYK5	92335	NM_153335	1%	8%
PIK3C2G	5288	NM_004570	1%	12%
EPHB4	2050	NM_004444	1%	14%
KIAA1804	84451	NM_032435	1%	11%
STK39	27347	NM_013233	1%	22%
ABL1	25	NM_005157	1%	10%
Pool 48			1%	16%
PRKR	5610	NM_002759	1%	27%
IKBKAP	8518	NM_003640	1%	17%
PRKCB1	5579	NM_002738	1%	6%
PLK4	10733	NM_014264	1%	13%
EPHA8	2046	NM_020526	1%	24%
PFKM	5213	NM_000289	2%	11%
EPHB6	2051	NM_004445	2%	11%
Pool 110			2%	28%
Pool 62			2%	14%
DYRK4	8798	NM_003845	2%	14%
MAPK7	5598	NM_002749	2%	10%
Pool 81			2%	23%
PRKCL2	5586	NM_006256	2%	10%
PACSIN1	29993	NM_020804	2%	14%
YES1	7525	NM_005433	2%	9%
MAP3K7IP1	10454	NM_006116	2%	13%
PSKH2	85481	NM_033126	2%	22%
Pool 108			3%	43%
Pool 74			3%	39%
MYLK2	85366	NM_033118	3%	22%
Pool 73			3%	14%
RIPK3	11035	NM_006871	3%	22%
PRKCM	5587	NM_002742	3%	2%
PHKG2	5261	NM_000294	3%	9%
SGK2	10110	NM_016276	3%	38%
STK17B	9262	NM_004226	3%	13%
Pool 6			3%	23%
PRPF4B	8899	NM_176800	3%	26%
DMPK	1760	NM_004409	3%	6%
PIK3AP1	118788	NM_152309	3%	6%
BMP2K	55589	NM_017593	3%	15%
Pool 52			3%	29%
CKMT2	1160	NM_001825	4%	16%
Pool 5			4%	21%
Pool 51			4%	29%
TK2	7084	NM_004614	4%	8%
CAMK1G	57172	NM_020439	4%	6%

Table 1b (continued)

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
CALM2	805	NM_001743	4%	14%
Pool 99			4%	26%
Pool 11			4%	19%
ITK	3702	NM_005546	4%	10%
PKM2	5315	NM_182471	4%	17%
Pool 17			4%	17%
MST4	51765	NM_016542	4%	16%
ROCK2	9475	NM_004850	4%	19%
OSR1	9943	NM_005109	4%	13%
PRKAR1A	5573	NM_002734	4%	18%
MARK4	57787	NM_031417	5%	25%
DGKZ	8525	NM_003646	5%	14%
MAPK6	5597	NM_002748	5%	20%
PRKAG2	51422	NM_016203	5%	13%
CaMKIINalpha	55450	NM_018584	5%	18%
EPHA3	2042	NM_005233	5%	8%
Pool 70			5%	38%
PGK1	5230	NM_000291	5%	9%
CAMK1	8536	NM_003656	5%	5%
MAP2K2	5605	NM_030662	5%	3%
PTK2B	2185	NM_173176	5%	14%
EPHB3	2049	NM_004443	5%	8%
TBK1	29110	NM_013254	5%	17%
GUK1	2987	NM_000858	6%	14%
LOC161635	161635	BC028192	6%	18%
ACVRL1	94	NM_000020	6%	24%
MERTK	10461	NM_006343	6%	15%
DGKQ	1609	NM_001347	6%	9%
SSTK	83983	NM_032037	6%	6%
HIPK3	10114	NM_005734	6%	19%
ROR1	4919	NM_005012	6%	10%
ARK5	9891	XM_374996	6%	18%
URKL1	54963	NM_017859	6%	27%
CDK9	1025	NM_001261	6%	10%
CDKN2B	1030	NM_004936	6%	10%
KIS	127933	NM_175866	6%	4%
TGFBR2	7048	NM_003242	6%	6%
BLK	640	NM_001715	6%	28%
TTK	7272	NM_003318	6%	12%
CDKL1	8814	NM_004196	6%	11%
CLK4	57396	NM_020666	7%	15%
PRKDC	5591	NM_006904	7%	18%
STK38L	23012	NM_015000	7%	15%
AKAP4	8852	NM_003886	7%	3%
STK11	6794	NM_000455	7%	5%
MAGI1	154043	NM_173515	7%	13%
SNRK	54861	NM_017719	7%	9%
CDC42BPA	8476	NM_003607	7%	17%

Table 1b (continued)

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
CERK	64781	NM_182661	7%	13%
RBKS	64080	NM_022128	7%	14%
ATM	472	NM_000051	7%	19%
MAPK8IP3	23162	NM_015133	7%	7%
HAK	115701	NM_052947	7%	16%
RIPK2	8767	NM_003821	7%	8%
GRK5	2869	NM_005308	7%	13%
AKAP6	9472	NM_004274	7%	13%
Pool 13			7%	25%
MATK	4145	NM_002378	8%	37%
Pool 1			8%	35%
GIT1	28964	NM_014030	8%	8%
CAMK1D	57118	NM_020397	8%	13%
Pool 87			8%	43%
KSR2	283455	NM_173598	8%	58%
SGK	6446	NM_005627	8%	12%
Pool 92			8%	41%
NEK4	6787	NM_003157	8%	5%
PIK3CD	5293	NM_005026	8%	9%
ASK	10926	NM_006716	8%	17%
TIE	7075	NM_005424	8%	16%
AKAP7	9465	NM_004842	8%	17%
XYLB	9942	NM_005108	8%	23%
MARK1	4139	NM_018650	8%	11%
FN3K	64122	NM_022158	8%	13%
NEK6	10783	NM_014397	9%	12%
RPS6KC1	26750	NM_012424	9%	20%
MAPKAPK5	8550	NM_003668	9%	3%
ICK	22858	NM_014920	9%	8%
Pool 23			9%	15%
PRKAB2	5565	NM_005399	9%	30%
HK3	3101	NM_002115	9%	25%
Pool 96			9%	48%
IBTK	25998	AB037838	9%	8%
PDK3	5165	NM_005391	9%	8%
SKIP	80309	XM_051221	9%	19%
PRKAA2	5563	NM_006252	9%	14%
HCK	3055	NM_002110	9%	50%
STK29	9024	NM_003957	10%	14%
DGKA	1606	NM_001345	10%	17%
GK	2710	NM_000167	10%	8%
DAPK2	23604	NM_014326	11%	15%
STK31	56164	NM_031414	11%	10%
Pool 59			11%	16%
PI4K2B	55300	NM_018323	11%	8%
MADD	8567	NM_003682	11%	8%
PRKCQ	5588	NM_006257	11%	12%
PDK4	5166	NM_002612	11%	44%

Table 1b (continued)

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
PRKRIR	5612	NM_004705	11%	19%
PFKFB4	5210	NM_004567	11%	15%
CAMK2A	815	NM_015981	11%	10%
Pool 83			11%	46%
DGKG	1608	NM_001346	11%	8%
APEG1	10290	NM_005876	11%	16%
Pool 80			11%	23%
CKS1B	1163	NM_001826	11%	15%
DYRK2	8445	NM_003583	11%	17%
PACSIN2	11252	NM_007229	11%	17%
LYN	4067	NM_002350	11%	33%
Pool 67			12%	30%
MAP4K3	8491	NM_003618	12%	13%
PNKP	11284	NM_007254	12%	17%
PMVK	10654	NM_006556	12%	18%
Pool 4			12%	10%
LATS2	26524	NM_014572	12%	13%
CKMT1	1159	NM_020990	12%	7%
HIPK1	204851	NM_181358	12%	29%
STK10	6793	NM_005990	12%	16%
STK22D	83942	NM_032028	12%	16%
TRIO	7204	NM_007118	12%	20%
GIT2	9815	NM_014776	12%	21%
AKAP28	158798	NM_178813	12%	15%
UMP-CMP	51727	NM_016308	13%	26%
Pool 14			13%	21%
LIM	10611	NM_006457	13%	20%
PIP5K2C	79837	NM_024779	13%	30%
PRKG2	5593	NM_006259	13%	6%
PCTK1	5127	NM_006201	13%	9%
Pool 35			13%	9%
PKLR	5313	NM_181871	13%	13%
LATS1	9113	NM_004690	13%	9%
ACVR2	92	NM_001616	13%	11%
STK24	8428	NM_003576	13%	8%
NJMU-R1	64149	NM_022344	13%	18%
PANK4	55229	NM_018216	13%	19%
CDKL3	51265	NM_016508	13%	12%
PHKG1	5260	NM_006213	13%	7%
ERN1	2081	NM_001433	13%	14%
MAP3K7IP2	23118	NM_015093	13%	24%
AK2	204	NM_001625	13%	21%
GRAF	23092	NM_015071	13%	21%
PRKD2	25865	NM_016457	14%	10%
PRKAA1	5562	NM_006251	14%	21%
TTBK2	146057	NM_173500	14%	8%
Pool 50			14%	20%
KDR	3791	NM_002253	14%	25%

Table 1b (continued)

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
NME6	10201	NM_005793	14%	20%
EIF2AK3	9451	NM_004836	14%	16%
CDK6	1021	NM_001259	14%	9%
FGFR4	2264	NM_002011	15%	17%
CDK5R2	8941	NM_003936	15%	24%
SYK	6850	NM_003177	15%	37%
DCK	1633	NM_000788	15%	21%
MAP4K4	9448	NM_004834	15%	12%
BUB1B	701	NM_001211	15%	21%
CHK	1111	NM_001277	15%	21%
Pool 38			15%	38%
FLJ11149	55312	NM_018339	15%	7%
DYRK3	8444	NM_003582	15%	8%
NRGN	4900	NM_006176	15%	23%
PIK3CA	5290	NM_006218	15%	20%
PAK1	5058	NM_002576	15%	16%
TYRO3	7301	NM_006293	15%	11%
TLK2	11011	NM_006852	15%	10%
NEK9	91754	NM_033116	15%	12%
ERBB3	2065	NM_001982	16%	20%
PFKFB3	5209	NM_004566	16%	14%
NEK1	4750	NM_012224	16%	32%
PKE	282974	NM_173575	16%	38%
PRKCG	5582	NM_002739	16%	21%
CDK5	1020	NM_004935	16%	34%
PCTK2	5128	NM_002595	16%	25%
ALS2CR7	65061	NM_139158	16%	38%
Pool 76			16%	34%
HIPK2	28996	NM_022740	16%	6%
CDC42BPB	9578	NM_006035	16%	14%
EPHB1	2047	NM_004441	16%	24%
BCKDK	10295	NM_005881	16%	23%
STK22C	81629	NM_052841	17%	26%
CSNK1G3	1456	NM_004384	17%	13%
AK3	205	NM_013410	17%	28%
EPHA2	1969	NM_004431	17%	10%
ANKRD3	54101	NM_020639	17%	14%
NEK11	79858	NM_024800	17%	7%
Pool 94			17%	39%
LTK	4058	NM_002344	17%	25%
Pool 100			17%	57%
MAP3K12	7786	NM_006301	17%	8%
Pool 66			18%	34%
MAP2K7	5609	BC005365	18%	21%
NUCKS	64710	NM_022731	18%	9%
PIK3CG	5294	NM_002649	18%	29%
TYROBP	7305	NM_003332	18%	8%
ROR2	4920	NM_004560	18%	9%

Table 1b (continued)

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
PFTK1	5218	NM_012395	18%	12%
MAP3K14	9020	NM_003954	18%	17%
PRKRA	8575	NM_003690	18%	27%
pknbeta	29941	NM_013355	18%	19%
SGKL	23678	NM_013257	18%	22%
PANK2	80025	NM_024960	18%	13%
CDC2L5	8621	NM_003718	18%	16%
MAP2K3	5606	NM_002756	18%	14%
PKIB	5570	NM_181795	18%	20%
MAP3K7	6885	NM_003188	18%	63%
PFKFB2	5208	NM_006212	19%	11%
CDKN1A	1026	NM_000389	19%	12%
CSNK2A1	1457	NM_177560	19%	17%
PIP5K2A	5305	NM_005028	19%	17%
STK36	27148	NM_015690	19%	27%
CINP	51550	NM_032630	19%	17%
TEK	7010	NM_000459	19%	15%
MAP4K2	5871	NM_004579	19%	7%
EEF2K	29904	NM_013302	19%	14%
Pool 72			19%	12%
TLK1	9874	NM_012290	19%	20%
ULK1	8408	NM_003565	19%	16%
Pool 79			19%	40%
CDKN2D	1032	NM_001800	19%	19%
NRBP	29959	NM_013392	19%	21%
CDK10	8558	NM_003674	19%	17%
NEK8	284086	NM_178170	19%	13%
NYD-SP25	89882	BC033792	20%	10%
NYD-SP25	89882	NM_033516	20%	10%
MAP2K5	5607	NM_002757	20%	8%
PRKACB	5567	NM_182948	20%	13%
NTRK2	4915	NM_006180	20%	21%
MAP3K13	9175	NM_004721	20%	16%
CSNK1D	1453	NM_001893	20%	29%
MAP2K1IP1	8649	NM_021970	20%	17%
PINK1	65018	NM_032409	20%	8%
Pool 25			20%	23%
ERBB2	2064	NM_004448	21%	12%
Pool 42			21%	36%
AKAP10	11216	NM_007202	21%	17%
PANK1	53354	NM_138316	21%	10%
Pool 47			21%	57%
MAPKAPK2	9261	NM_004759	21%	17%
Pool 15			21%	21%
PRKX	5613	NM_005044	21%	21%
TOPK	55872	NM_018492	21%	9%
TNIK	23043	XM_039796	21%	8%
Pool 27			22%	27%

Table 1b (continued)

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
FES	2242	NM_002005	22%	47%
Pool 84			22%	22%
PHKA2	5256	NM_000292	22%	7%
MAP3K4	4216	NM_005922	22%	9%
ULK2	9706	NM_014683	22%	15%
MAPK13	5603	NM_002754	22%	36%
Pool 10			22%	13%
Pool 49			22%	13%
NME2	4831	NM_002512	22%	27%
Pool 116			23%	59%
BMPR2	659	NM_001204	23%	19%
CASK	8573	NM_003688	23%	28%
HSMDPKIN	55561	XM_290516	23%	48%
AKT1	207	NM_005163	23%	13%
PXK	54899	NM_017771	23%	36%
RIPK1	8737	NM_003804	23%	15%
DGKD	8527	NM_003648	23%	14%
IHPK3	117283	NM_054111	23%	33%
RPS6KA5	9252	NM_182398	23%	10%
PKIA	5569	NM_181839	24%	27%
RPS6KB2	6199	NM_003952	24%	14%
Pool 95			24%	49%
CDKL5	6792	NM_003159	24%	36%
CDC2	983	NM_001786	24%	33%
MAP4K5	11183	NM_006575	24%	5%
Pool 85			25%	29%
VRK3	51231	NM_016440	25%	8%
EPHA4	2043	NM_004438	25%	12%
IKBKG	8517	NM_003639	25%	37%
PLK2	10769	NM_006622	25%	33%
CAMK4	814	NM_001744	25%	48%
PIK3R1	5295	NM_181504	25%	17%
Pool 16			25%	17%
EPHB2	2048	NM_017449	25%	5%
MGC45419	139728	NM_198452	25%	14%
T3JAM	80342	NM_025228	26%	21%
MAP3K8	1326	NM_005204	26%	11%
Pool 112			26%	43%
PHKA1	5255	NM_002637	27%	6%
TGFBR1	7046	NM_004612	27%	18%
AKAP9	10142	NM_005751	27%	37%
PAK7	57144	NM_177990	27%	26%
MINK	50488	NM_015716	27%	13%
CSNK1A1	1452	NM_001892	28%	30%
PIM2	11040	NM_006875	28%	31%
PIP5K1A	8394	NM_003557	28%	10%
PLK1	5347	NM_005030	29%	29%
PIP5K3	200576	NM_152671	29%	39%

Table 1b (continued)

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
PRKCABP	9463	NM_012407	29%	7%
MAP3K2	10746	NM_006609	29%	18%
TEC	7006	NM_003215	29%	14%
FLT4	2324	NM_182925	29%	18%
CDKN2A	1029	NM_000077	30%	12%
EIF2AK4	27104	BX640919	30%	21%
Pool 9			30%	20%
PTK2	5747	NM_005607	30%	26%
MARCKS	4082	NM_002356	30%	23%
AKAP13	11214	NM_006738	30%	26%
Pool 63			30%	17%
UCK1	83549	NM_031432	31%	25%
STK33	65975	NM_030906	31%	20%
SRC	6714	NM_005417	31%	16%
P101-PI3K	23533	NM_014308	31%	6%
MAP3K10	4294	NM_002446	31%	32%
PIP5K1C	23396	NM_012398	31%	33%
RET	5979	NM_020975	31%	13%
TNNI3K	51086	NM_015978	31%	21%
Pool 105			31%	48%
PRKCH	5583	NM_006255	31%	24%
Pool 89			31%	41%
ADK	132	NM_001123	32%	15%
MAP2K1	5604	NM_002755	32%	28%
FLT1	2321	NM_002019	32%	15%
MGC33182	122011	NM_145203	32%	9%
Pool 26			32%	15%
SKP1A	6500	NM_006930	33%	4%
AKIP	54998	NM_017900	33%	26%
CHEK1	1111	NM_001274	33%	23%
MAP3K11	4296	NM_002419	33%	25%
RPS6KA1	6195	NM_002953	34%	25%
STK38	11329	NM_007271	34%	21%
PIP5K1B	8395	NM_003558	34%	7%
PIK3R2	5296	NM_005027	35%	28%
SLK	9748	NM_014720	36%	22%
CAMKK2	10645	NM_006549	36%	10%
AKAP3	10566	NM_006422	36%	23%
GNE	10020	NM_005476	36%	22%
KIAA1446	57596	NM_020836	37%	7%
AATK	9625	AB014541	37%	15%
ADCK2	90956	NM_052853	37%	17%
Pool 28			37%	76%
PTK6	5753	NM_005975	37%	28%
MAPK12	6300	NM_002969	37%	22%
CRK7	51755	NM_016507	38%	7%
PASK	23178	NM_015148	38%	27%
TNK1	8711	NM_003985	38%	13%

Table 1b (continued)

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
PFKL	5211	NM_002626	38%	20%
MAP4K1	11184	NM_007181	38%	23%
MAPK9	5601	NM_002752	39%	20%
FUK	197258	NM_145059	39%	13%
LOC55971	55971	NM_018842	39%	13%
ZAK	51776	NM_016653	39%	30%
NTRK3	4916	NM_002530	40%	25%
NTRK1	4914	NM_002529	40%	32%
STK35	140901	NM_080836	41%	12%
CDK5R1	8851	NM_003885	41%	21%
PAK3	5063	NM_002578	41%	22%
CAMK2B	816	NM_001220	41%	4%
NME5	8382	NM_003551	41%	22%
Pool 90			41%	31%
GAK	2580	NM_005255	41%	32%
AKT3	10000	NM_181690	42%	41%
ADCK1	57143	NM_020421	42%	19%
STK4	6789	NM_006282	43%	26%
AKAP8L	26993	NM_014371	43%	29%
MAPK11	5600	NM_002751	43%	28%
UMPK	7371	NM_012474	43%	35%
CSNK1G2	1455	NM_001319	43%	24%
PIK3C2B	5287	NM_002646	43%	38%
C21orf124	85006	NM_003681	44%	31%
CKB	1152	NM_001823	44%	33%
CIB3	117286	NM_054113	45%	28%
ILK	3611	NM_004517	45%	19%
PRKACG	5568	NM_002732	45%	20%
SRPK1	6732	NM_003137	45%	5%
AAK1	22848	NM_014911	46%	21%
PCTK3	5129	AK126879	46%	23%
NEK7	140609	NM_133494	46%	22%
LOC375449	375449	NM_198828	46%	4%
ROS1	6098	NM_002944	47%	11%
PDGFRA	5156	NM_006206	47%	19%
CIT	11113	NM_007174	48%	12%
LOC388226	10595	XM_370946	48%	39%
CDKN1B	1027	NM_004064	48%	5%
NME7	29922	NM_197972	48%	8%
RPS6KA6	27330	NM_014496	49%	16%
Pool 57			49%	20%
PIK4CB	5298	NM_002651	51%	16%
Pool 20			51%	20%
MAP2K4	6416	NM_003010	51%	14%
CHEK2	11200	NM_007194	51%	28%
ALS2CR2	55437	NM_018571	52%	18%
GRK1	6011	NM_002929	52%	17%
Pool 93			52%	32%

Table 1b (continued)

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
MAPK4	5596	NM_002747	52%	24%
STK22B	23617	NM_053006	52%	15%
Pool 109			52%	51%
NYD-SP25	89882	BC033792	53%	44%
NYD-SP25	89882	NM_033516	53%	44%
ANKK1	255239	NM_178510	53%	7%
SPHK1	8877	NM_021972	53%	33%
PLK3	1263	NM_004073	53%	19%
GRK4	2868	NM_182982	54%	23%
PIP5K2B	8396	NM_003559	54%	30%
Pool 102			55%	22%
NIPA	51530	NM_016478	55%	11%
RPS6KA4	8986	NM_003942	55%	16%
IKBKB	3551	NM_001556	56%	10%
FGR	2268	NM_005248	57%	12%
PTK7	5754	NM_152883	58%	5%
RIOK2	55781	NM_018343	59%	20%
CSNK1E	1454	NM_001894	59%	39%
PRKCL1	5585	NM_002741	60%	21%
STK3	6788	NM_006281	60%	20%
GSK3A	2931	NM_019884	60%	28%
HK1	3098	NM_033498	61%	19%
PRKCZ	5590	NM_002744	62%	16%
RIOK3	8780	NM_003831	62%	19%
CKS2	1164	NM_001827	63%	31%
FASTK	10922	NM_006712	63%	44%
MST1R	4486	NM_002447	65%	24%
BMPR1B	658	NM_001203	66%	33%
PRKAR2A	5576	NM_004157	69%	39%
CDC2L1	984	NM_001787	73%	26%
PRKAB1	5564	NM_006253	74%	30%
PKMYT1	9088	NM_182687	78%	15%
PAK4	10298	NM_005884	81%	49%
CALM1	801	NM_006888	82%	68%
BMX	660	NM_001721	84%	33%
NME3	4832	NM_002513	85%	50%
JIK	51347	NM_016281	89%	27%
ACK1	10188	NM_005781	93%	11%
HUNK	30811	NM_014586	94%	35%
MAPK8	5599	NM_002750	98%	47%
DGKE	8526	NM_003647	113%	25%

Table 2

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
AB014541	9625	AATK	apoptosis-associated tyrosine kinase	CTCCAACGTGTCAGCCAACAA	TCCGCTGAGATCAGAAGGCAA
AB023190	22983	SAST	syntrophin associated serine/threonine kinase	CAGCCTCCGTATACATATGTA	CCCGAGGTCATCCTGCGTCAA
AB033076	57498	KIDINS220	likely homolog of rat kinase D-interacting substance of 220 kDa	CAGGCGAGACTCCTTATAATA	TCCCAGATGCGCTATTATCTA
AB037838	25998	IBTK	inhibitor of Bruton agammaglobulinemia tyrosine kinase	CAGATTGAGGAGCATGCCATA	TAGAAGAGTCATTACACCATA
AB096248	23235	SIK2	salt-inducible serine/threonine kinase 2	AAGGGCAAGATTATTTGCTTA	CCGAAGGATGTTGGTCCTAGA
NM_004935	1020	CDK5	cyclin-dependent kinase 5	CCCTTTGTGGACTTTATTTAA	CCGGGAGATCTGCCTACTCAA
AK126879	5129	PCTK3	PCTAIRE protein kinase 3	AACCCGTTACTTAGCTCGTGTA	CAGGTTGGATACGGATGGCAT
BC028192	161635	LOC161635	similar to casein kinase I alpha	TCCATCGATCTGGAATTTATA	TTGGTCGTGTGAATTATTAAA
BC033792	89882	NYD-SP25	protein kinase NYD-SP25	ATCATATACTTCAGACATCAA	CACGTTAAATCAAGGAAGGAA
BF688722	2323	FLT3LG	Fms-related tyrosine kinase 3 ligand	GCGGGATTTGTTGAAGAGAAA	TAGTATAGTTGAAATAAGAAA
BX537752	134728	IRAK1BP1	interleukin-1 receptor-associated kinase 1 binding protein 1/DKFZp779F0411	AACCTGGAGTATCATATTATA	ACCAAGATACTTGAGTGATTA
BX640919	27104	EIF2AK4	eukaryotic translation initiation factor 2 alpha kinase 4	CTGGAGGAATTTAGTAACATT	TCCGATAATCTTGCAGTGCAA
NM_000020	94	ACVRL1	activin A receptor type II-like 1	CACCGAGTTCGTCAACCACTA	CAGGAAGACGCTGGAATAAGA
NM_000051	472	ATM	ataxia telangiectasia mutated (includes complementation groups A, C and D)	AACCATGAGTCTAGTACTTAA	TTGGCTTATACGCGCAGTGTA
NM_000061	695	BTK	Bruton agammaglobulinemia tyrosine kinase	CAGCTCGAAACTGTTTGGTAA	CCCTTTATGATTACATGCCAA
NM_000075	1019	CDK4	cyclin-dependent kinase 4	AAGGTAATCCGGAGTGAGCAA	CCGAACTGACCGGGAGATCAA
NM_000076	1028	CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	AAGCTTTAAGAGTCATTTATA	TACACTGGTCCCAAAGTGTAA
NM_000077	1029	CDKN2A	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	CACGCCCTAAGCGCACATTCA	CAGGTGTGCCACATTCGCTAA
NM_000141	2263	FGFR2	fibroblast growth factor receptor 2	CCGAATGAAGAACACGACCAA	CGGAGGAGCGTTGCCATTCAA
NM_000142	2261	FGFR3	fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)	ACCCTACGTTACCGTGCTCAA	CCGATGTTATTAGATGTTACA
NM_000167	2710	GK	glycerol kinase	CCACCACTTAAGTGACATAAA	CTGAGGGTAGCCCATTTATAA
NM_000189	3099	HK2	hexokinase 2	CCGGCCGTGCTACAATAGGTA	CGGCCGTGCTACAATAGGTAA
NM_000215	3718	JAK3	Janus kinase 3 (a protein tyrosine kinase, leukocyte)	CGGGAGATTCAGATCCTCAAA	TCCGGGAGGCGCAGACACTTA
NM_000221	3795	KHK	ketohexokinase (fructokinase)	TAGCCGCACCATCCTATACTA	TAGGGTGGGTAAGGCCTTATA
NM_000222	3815	KIT	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	CACGGTTGAATGTAAGGCTTA	CTCGCACCTTTCCAAAGTTAA
NM_000245	4233	MET	met proto-oncogene (hepatocyte growth factor receptor)	ACCGAGGGAATCATCATGAAA	CGCGCCGTGATGAATATCGAA
NM_000269	4830	NME1	non-metastatic cells 1, protein (NM23A) expressed in	TAGGATTCATTGAGTTGGTTA	TTCCGCCTTGTTGGTCTGAAA
NM_000289	5213	PFKM	phosphofructokinase, muscle	AACAGATCAGTGCCAATATAA	AAGGACTTTCGGGAACGAGAA
NM_000291	5230	PGK1	phosphoglycerate kinase 1	CACAATTATAGATTAGATCAA	GAGGAACGGATCAGATGTCTA
NM_000292	5256	PHKA2	phosphorylase kinase, alpha 2 (liver)	CCGCCTAACAAGGTAGATGAA	CCGGATTCTTAGTCACATATA
NM_000293	5257	PHKB	phosphorylase kinase, beta	AGGGCTGTTCGTGGTCAGTTA	TCGATGGGTCTTTGAATAGAA
NM_000294	5261	PHKG2	phosphorylase kinase, gamma 2 (testis)	CTGCATGCACTGCATATGAAA	TACGGGCACTGGGTAAAGAAA
NM_000389	1026	CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	CAGTTTGTGTGTCTTAATTAT	CTGGCATTAGAATTATTTAAA
NM_000431	4598	MVK	mevalonate kinase (mevalonic aciduria)	CCGCTTGGCGATGCCAGCCAA	GCGGTGGGCCTGGTTAAATAA
NM_000455	6794	STK11	serine/threonine kinase 11 (Peutz-Jeghers syndrome)	CAGGAGTGTGCGGTCAATATT	GAGGGCCGTCAAGATCCTCAA
NM_000459	7010	TEK	TEK tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucosal)	ACGGGCCAGATTGTAAGCTTA	TCGGTGCTACTTAACAACTTA
NM_000476	203	AK1	adenylate kinase 1	CCGGGATGCCATGGTGGCCAA	GCGGCTGGAGACCTATTACAA
NM_000788	1633	DCK	deoxycytidine kinase	AAGTTGCAAAGTGGAATTAAA	TTGGTATAAATTAATTTGTTA
NM_000858	2987	GUK1	guanylate kinase 1	CAGGGCTGACATCCTAATAAA	CCCGGCGAGGAGAACGGCAAA
NM_001079	7535	ZAP70	zeta-chain (TCR) associated protein kinase 70kDa	CCGCAACGTCCTGCTGGTTAA	GGCGTAGATCACCAGAATAAA
NM_001105	90	ACVR1	activin A receptor, type I	CGGATGGTGAGCAATGGTATA	CTGGTCTGTCTTTGGATAATA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_001106	93	ACVR2B	activin A receptor, type IIB	CAGCTCATGAATGACTTTGTA	TACGGTCATGTGGACATCCAT
NM_001123	132	ADK	adenosine kinase	AAGGGTATGGTAATGCTTGTA	TAGTTTGATAGTGCCACTTAA
NM_001184	545	ATR	ataxia telangiectasia and Rad3 related	CAGGCACTAATTGTTCTTCAA	GCCGCTAATCTTCTAACATTA
NM_001203	658	BMPR1B	bone morphogenetic protein receptor, type IB	AACGAATGTAATAAAGACCTA	ACGGATATTGTTTCACGATGA
NM_001204	659	BMPR2	bone morphogenetic protein receptor, type II (serine/threonine kinase)	AAGCACCGAAGCGAAACTTAA	CTCGTAAGTATGTAAAGGAAA
NM_001211	701	BUB1B	BUB1 budding uninhibited by benzimidazoles 1 homolog beta (yeast)	ACGAGAATACCTAATATGTGA	CAGATTTAGCACATTTACTAT
NM_001220	816	CAMK2B	calcium/calmodulin-dependent protein kinase (CaM kinase) II beta	CAAGAGTTTACTCAACAAGAA	CCGGAAGCAGGAGATCATTAA
NM_001221	817	CAMK2D	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	CCGCCTGCATAGCATATATTA	GTGCGACTTCATGATAGCATA
NM_001258	1018	CDK3	cyclin-dependent kinase 3	ATGGATATGTTCCAGAAGGTA	CAGACTGGATTTGGAGATGGA
NM_001259	1021	CDK6	cyclin-dependent kinase 6	AAGACTCAAGGTGGTCAGTAA	TCTGAAGTGTTTGACATTTAA
NM_001260	1024	CDK8	cyclin-dependent kinase 8	CCAGCTGGACAGAATATTCAA	TTCGAGAGCTTAAGCATCCAA
NM_001261	1025	CDK9	cyclin-dependent kinase 9 (CDC2-related kinase)	TAGGGACATGAAGGCTGCTAA	TGGGCACAGTTTGGTCCGTTA
NM_001262	1031	CDKN2C	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	CAGGCTTATGAATATATTTAA	TGCCTCTACTTTATCAATTAA
NM_001274	1111	CHEK1	CHK1 checkpoint homolog (S. pombe)	AAGAAAGAGATCTGTATCAAT	CCCGCACAGGTCTTTCCTTAT
NM_001277	1119	CHK	choline kinase	AGCCGGCGATTAGATACTGAA	CCGGCCCTTACCAAACCTGAT
NM_001278	1147	CHUK	conserved helix-loop-helix ubiquitous kinase	CAGGAGAAGTTCGGTTTAGTA	TTCCATAAGCTTGGTGACAAA
NM_001291	1196	CLK2	CDC-like kinase 2	CAGCTACAGACGCAACGATTA	TCGCCTGGATTGGGATGAGAA
NM_001292	1198	CLK3	CDC-like kinase 3	CACGAAGATCTCGGTCCAGAA	CTGCATTCTCTTTGAGTACTA
NM_001315	1432	MAPK14	mitogen-activated protein kinase 14	CAGAGAACTGCGGTTACTTAA	CTCAGTGATACGTACAGCCAA
NM_001319	1455	CSNK1G2	casein kinase 1, gamma 2	AAGAATCTCTATACAAATGAA	TAGGAAAGAATCTCTATACAA
NM_001320	1460	CSNK2B	casein kinase 2, beta polypeptide	CAGGTCCCTCACTACCGACAA	GTGGTGGGAATATGAAATAAA
NM_001345	1606	DGKA	diacylglycerol kinase, alpha 80kDa	ATCCATCTTCTCAACATGCAA	CACGACCAGTGTGCCATGAAA
NM_001346	1608	DGKG	diacylglycerol kinase, gamma 90kDa	ACCGCAAATGTGAATTATCAA	TAGCCACTCACATAAAGTTTA
NM_001347	1609	DGKQ	diacylglycerol kinase, theta 110kDa	CAGCGACACCAGGTTTGAGAA	CCGGAAGGTGACGCTCACCAA
NM_001348	1613	DAPK3	death-associated protein kinase 3	CCCAGAGATTGTGAACTATGA	CCGGCAGAAGGGCACGGGCAA
NM_001381	1796	DOK1	docking protein 1, 62kDa (downstream of tyrosine kinase 1)	AGGGATCAAAGAAGATGGTTA	CCGCCTGGACTGCAAAGTGAT
NM_001396	1859	DYRK1A	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A	CAAGAATGGGTTGCCATTAAA	TACGGTCGCTGACTACTTGAA
NM_001433	2081	ERN1	ER to nucleus signalling 1	CAGCACGGACGTCAAGTTTGA	CAGGACGTGAGCGACAGAATA
NM_001569	3654	IRAK1	interleukin-1 receptor-associated kinase 1	CCGGGCAATTCAGTTTCTACA	TCCCATCGCCATGCAGATCTA
NM_001570	3656	IRAK2	interleukin-1 receptor-associated kinase 2	CAGCAACGTCAAGAGCTCTAA	CCAGATCATCCTGAACTGGAA
NM_001616	92	ACVR2	activin A receptor, type II	GAGGTATTAGAGGGTGCTATA	TCCACGGTTGCTAAATTATAA
NM_001619	156	ADRBK1	adrenergic, beta, receptor kinase 1	CCGGGAGATCTTCGACTCATA	CGGCTGGAGGCTCGCAAGAAA
NM_001625	204	AK2	adenylate kinase 2	ATGGGTGGGAATGATAGGACA	CCACATGTAAAGACTTGGTTA
NM_001626	208	AKT2	v-akt murine thymoma viral oncogene homolog 2	ACGGGCTAAAGTGACCATGAA	CAAGCGTGGTGAATACATCAA
NM_001654	369	ARAF1	v-raf murine sarcoma 3611 viral oncogene homolog 1	CCGACTCATCAAGGGACGAAA	CCGGGATGGCATGAGTGTCTA
NM_001699	558	AXL	AXL receptor tyrosine kinase	CCGGTGTTCTAAGATGTGATA	TCCAAGATTCTAGATGATTAA
NM_001715	640	BLK	B lymphoid tyrosine kinase	CAGCCGTGCTGTTAAACCAAA	CTGGTAAGCGACTGTCATCAA
NM_001721	660	BMX	BMX non-receptor tyrosine kinase	CCCAATATGACAACGAATCAA	CGGAACAAAGTTTCCAGTCAA
NM_001743	805	CALM2	calmodulin 2 (phosphorylase kinase, delta)	ACAAAGGAATTGGGAACTGTA	CAAAGGAATTGGGAACTGTAA
NM_001744	814	CAMK4	calcium/calmodulin-dependent protein kinase IV	CAGAAGCCTTATGCTCTCAAA	TTGCAAGTTAACACAACGTAA
NM_001786	983	CDC2	cell division cycle 2, G1 to S and G2 to M	TCGGGAAATTTCTCTATTAAA	TTGACTAACTATGGAAGATTA
NM_001787	984	CDC2L1	cell division cycle 2-like 1 (PITSLRE proteins)	CAAGATCTACATCGTGATGAA	CAGGATAAAGCTCGCCGGGAA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_001798	1017	CDK2	cyclin-dependent kinase 2	CACGTACGGAGTTGTGTACAA	CAGGTTATATCCAATAGTAGA
NM_001799	1022	CDK7	cyclin-dependent kinase 7 (MO15 homolog, Xenopus laevis, cdk-activating kinase)	CCGGATGGCTCTGGACGTGAA	GAGGGTTTAAGGTAGCTTTAA
NM_001800	1032	CDKN2D	cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)	ACCCAAGGGCAGAGCATTTAA	ATGAGTTATGAGTTATTCATA
NM_001823	1152	CKB	creatine kinase, brain	CCAGATTGAAACTCTCTTCAA	CCGGCCTCACCCAGATTGAAA
NM_001824	1158	CKM	creatine kinase, muscle	GACGGGCGAGTTCAAAGGGAA	TCCACGCAAAGCGATAAATAA
NM_001825	1160	CKMT2	creatine kinase, mitochondrial 2 (sarcomeric)	CCTGCCTATCTTTACAATAAA	GAGGTTGAGCTTGTTCAGATA
NM_001826	1163	CKS1B	CDC28 protein kinase regulatory subunit 1B	AACATCTTTCTGATAACATTA	AAGAAATCTGTTCATGTTAAA
NM_001827	1164	CKS2	CDC28 protein kinase regulatory subunit 2	CTGTAAGATGTTTAAGATAAA	TCGGACAAGTACTTCGACGAA
NM_001892	1452	CSNK1A1	casein kinase 1, alpha 1	AGGGCTAAAGCCTGCAACAAA	CAAGAGTAACATGAAAGGTTT
NM_001893	1453	CSNK1D	casein kinase 1, delta	CCGGTCTAGGATCGAAATGTT	CTCCCTGACGATTCCACTGTA
NM_001894	1454	CSNK1E	casein kinase 1, epsilon	GAGCTTTATCGTGGTTGTTAA	GTGGTTGTTAATTTGAAGTAA
NM_001896	1459	CSNK2A2	casein kinase 2, alpha prime polypeptide	CAGCAGTACAATGTTCGTGTA	CTGGGACAACATTCACGGAAA
NM_001929	1716	DGUOK	deoxyguanosine kinase	CACCTTTGTAAAGAATCTGTA	CAGCACGATGGTCCTACACAT
NM_001954	780	DDR1	discoidin domain receptor family, member 1	ACGGTGTGAATCACACATCCA	CAGGAATGATTTCCTGAAAGA
NM_001982	2065	ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	ACCGGCGATGCTGAGAACCAA	CCAGAGCTTCAAGACTGTTTA
NM_002005	2242	FES	feline sarcoma oncogene	AAGGCCAAGTTTCTACAGGAA	CAGCCTGAGGCTGAGTACCAA
NM_002011	2264	FGFR4	fibroblast growth factor receptor 4	CACATTGACTACTATAAGAAA	CCGCCTGACCTTCGGACCCTA
NM_002019	2321	FLT1	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)	ACCGCATATGGTATCCCTCAA	CACTACAGTATTAGCAAGCAA
NM_002031	2444	FRK	fyn-related kinase	CAGGACAGTCAAGGTGATATA	CTGGGAGTACCTAGAACCCTA
NM_002037	2534	FYN	FYN oncogene related to SRC, FGR, YES	AAGAAGCAGGATGCTGATCTA	AAGACATGTGGTGTATATAAA
NM_002082	2870	GRK6	G protein-coupled receptor kinase 6	AAGGATGTTCTGGACATTGAA	AGGCATGTGGGCGGCACGTAA
NM_002093	2932	GSK3B	glycogen synthase kinase 3 beta	AACACTGGTCACGTTTGGAAA	CTGCATTTATCGTTAACCTAA
NM_002110	3055	HCK	hemopoietic cell kinase	AACGACGGGCTCTGCCAGAAA	CGGGAGCACATCAGAGGCTTA
NM_002115	3101	HK3	hexokinase 3 (white cell)	CACTCAGGTTAGCAATATATA	CCGGAATGCGATGTCTCCTTA
NM_002220	3706	ITPKA	inositol 1,4,5-trisphosphate 3-kinase A	CACCAGCGGGCTGATCCTGAA	CCGGTCTAACGTCTCACACCA
NM_002221	3707	ITPKB	inositol 1,4,5-trisphosphate 3-kinase B	AAGGCCATTCGAACCACTCTA	GACGTAAAGATTCTATGAATA
NM_002227	3716	JAK1	Janus kinase 1 (a protein tyrosine kinase)	ACCGGATGAGGTTCTATTTCA	CACGGATAACATCAGCTTCAT
NM_002253	3791	KDR	kinase insert domain receptor (a type III receptor tyrosine kinase)	AACGCTGACATGTACGGTCTA	AAGGCTAATACAACTCTTCAA
NM_002314	3984	LIMK1	LIM domain kinase 1	CTGCCTGGTCCGCGAGAACAA	GAGCATCTAGGAAGTATTAAA
NM_002344	4058	LTK	leukocyte tyrosine kinase	ACAGATCTTTGGAGTGCCTAA	CCTGCAGATGCTTCTAATAAA
NM_002350	4067	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	CCCGGACGACTTGTCTTTCAA	CGGGAAATATGGGATGTATAA
NM_002356	4082	MARCKS	myristoylated alanine-rich protein kinase C substrate	CTCCTTCAAGAAGAACAAGAA	TTGAGTTTCTTTGTTGAAGAA
NM_002376	4140	MARK3	MAP/microtubule affinity-regulating kinase 3	AACGGCGAACCGCAACATATA	CCCGGGAACGGCGAACCGCAA
NM_002378	4145	MATK	megakaryocyte-associated tyrosine kinase	ACGGATTCTAAGGACTCTAAA	GACGGATTCTAAGGACTCTAA
NM_002401	4215	MAP3K3	mitogen-activated protein kinase kinase kinase 3	CAGGAATACTCAGATCGGGAA	CCACGTGTCTGTGCACCACAA
NM_002419	4296	MAP3K11	mitogen-activated protein kinase kinase kinase 11	CCCGAGGTCTGGAGGACTCAA	CCGGAGGAGAAACGTCTTCGA
NM_002446	4294	MAP3K10	mitogen-activated protein kinase kinase kinase 10	AAGCGGCTTGAAGTCATCGAA	CAGGATGTTCACTCTATTTAT
NM_002447	4486	MST1R	macrophage stimulating 1 receptor (c-met-related tyrosine kinase)	ATGGAGCATCCTTCTCCGATA	TGCCATTAAGTTTGAGTATAT
NM_002497	4751	NEK2	NIMA (never in mitosis gene a)-related kinase 2	TACGAGGATGTTAAACTTAAA	TTACGAGGATGTTAAACTTAA
NM_002512	4831	NME2	non-metastatic cells 2, protein (NM23B) expressed in	ATAGAGCATATTTGCCAATAA	TAGAGCATATTTGCCAATAAA
NM_002513	4832	NME3	non-metastatic cells 3, protein expressed in	ACGCACCTTCCTGGCCGTGAA	CTGCATCGAGGTTGGCAAGAA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_002529	4914	NTRK1	neurotrophic tyrosine kinase, receptor, type 1	CACATCATCGAGAACCCACAA	CGAGAGCATCCTGTACCGTAA
NM_002530	4916	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	CACGGATAACTTTATCTTGTT	CTGCTTGGAGCGAATCTGCTA
NM_002576	5058	PAK1	p21/Cdc42/Rac1-activated kinase 1 (STE20 homolog, yeast)	TCCACTGATTGCTGCAGCTAA	TGGAAGAGAACTGCAACTGAA
NM_002577	5062	PAK2	p21 (CDKN1A)-activated kinase 2	CCGCGACCGGATCATACGAAA	CCGGATCATACGAAATCAATT
NM_002578	5063	PAK3	p21 (CDKN1A)-activated kinase 3	CAAGAAGGAATTAATTATTAT	TTCCAGTACTTTGTACAGGAA
NM_002595	5128	PCTK2	PCTAIRE protein kinase 2	AGGCTTAATTCTTGCGTATAA	TAGGCTTAATTCTTGCGTATA
NM_002609	5159	PDGFRB	platelet-derived growth factor receptor, beta polypeptide	CCGAGCAACTTTGATCAACGA	CTGCCGAGCAACTTTGATCAA
NM_002610	5163	PDK1	pyruvate dehydrogenase kinase, isoenzyme 1	CCCGAACTAGAAGTTGAAGAA	TCGGGTTTCTATAGGAAACTA
NM_002611	5164	PDK2	pyruvate dehydrogenase kinase, isoenzyme 2	AAGAACCTTGTTAGACCGAGA	TAGGTCTGTGATGGTCCCTAA
NM_002612	5166	PDK4	pyruvate dehydrogenase kinase, isoenzyme 4	ACCCGTCTCAATTAACATTTA	AGGCCTCTTGTTCACATCAAA
NM_002613	5170	PDPK1	3-phosphoinositide dependent protein kinase-1	AAGCCGTTAGGCTGTGAGGAA	CACGCCTAACAGGACGTATTA
NM_002625	5207	PFKFB1	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1	CTCCACAAAGCTCACACGATA	CTGCGAGACCAAGATAAATAT
NM_002626	5211	PFKL	phosphofructokinase, liver	CACGATGGCTTCGAAGGCCTA	CCGGACCTACTCGCACCTGAA
NM_002627	5214	PFKP	phosphofructokinase, platelet	CAGCACTTTATGCACGTATTA	CCGCCTGAAGGCTGCTTGCAA
NM_002637	5255	PHKA1	phosphorylase kinase, alpha 1 (muscle)	ATGGGAGTGCTTGGAACTTCA	CCCAATCGTCTGTACTATGAA
NM_002645	5286	PIK3C2A	phosphoinositide-3-kinase, class 2, alpha polypeptide	CAAGATGGTCGAATCAAGGAA	TACCCACTAATTGCATTGGAA
NM_002646	5287	PIK3C2B	phosphoinositide-3-kinase, class 2, beta polypeptide	AAGGGTTGTCTTCCTCGCCAA	CAGGGTGGTCCAGTCCGTCAA
NM_002647	5289	PIK3C3	phosphoinositide-3-kinase, class 3	AACGCGAAAGTGGAAATCGTA	TCGGTTGGTGCATCTAATGAA
NM_002648	5292	PIM1	pim-1 oncogene	AAACATCCTTATCGACCTCAA	AAAGATTGTAGTGGATCTAAT
NM_002649	5294	PIK3CG	phosphoinositide-3-kinase, catalytic, gamma polypeptide	ATCGAAGTTTGCAGAGACAAA	CACCTTTACTCTATAACTCAA
NM_002650	5297	PIK4CA	phosphatidylinositol 4-kinase, catalytic, alpha polypeptide	CATCTGGAACATGAAGACTAA	CCAGTTCATCTGGAACATGAA
NM_002651	5298	PIK4CB	phosphatidylinositol 4-kinase, catalytic, beta polypeptide	CCGAGAGTATTGATAATTCAT	TCGGCTGATAGTGGCATGATT
NM_002730	5566	PRKACA	protein kinase, cAMP-dependent, catalytic, alpha	CAAGGACAACTCAAACTTATA	CAGAAGGTGGTGAAACTGAAA
NM_002732	5568	PRKACG	protein kinase, cAMP-dependent, catalytic, gamma	AACCAGCTGGATCGCCATCTA	CTGGATCGCCATCTATGAGAA
NM_002733	5571	PRKAG1	protein kinase, AMP-activated, gamma 1 non-catalytic subunit	CCCTAAGATAATAGCACAACA	TTGGCCCTGATTCAACCCTAA
NM_002734	5573	PRKAR1A	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	CAGCTAGTGCCAAATAATTGA	CTGGACCGACCTAGATTTGAA
NM_002736	5577	PRKAR2B	protein kinase, cAMP-dependent, regulatory, type II, beta	ACGAACATGGATATTGTTGAA	CACGCCATTGGGACTGTCAAA
NM_002737	5578	PRKCA	protein kinase C, alpha	CGCAGTGGAATGAGTCCTTTA	TACAAGTTGCTTAACCAAGAA
NM_002738	5579	PRKCB1	protein kinase C, beta 1	CAAGAGCTAAGTAGATGTGTA	CCGGATGAAACTGACCGATTT
NM_002739	5582	PRKCG	protein kinase C, gamma	AACGGTGAAAGCCACGCTAAA	GACCTTTGTGTTCAACCTGAA
NM_002740	5584	PRKCI	protein kinase C, iota	CACCCAATATCTTCTCTTGTA	TACCACGTTCTATGTCTGTAA
NM_002741	5585	PRKCL1	protein kinase C-like 1	CAGGACAGTAAGACCAAGATT	CCGCAAGGAGCTGAAGCTGAA
NM_002742	5587	PRKCM	protein kinase C, mu	CAGGAAGGCGATCTTATTGAA	CCTCAGTATATTTAAACTCAA
NM_002744	5590	PRKCZ	protein kinase C, zeta	CGGAAGCATGACAGCATTAAA	GACCAAATTTACGCCATGAAA
NM_002745	5594	MAPK1	mitogen-activated protein kinase 1	AACACTTGTCAAGAAGCGTTA	ATCATGGTAGTCACTAACATA
NM_002746	5595	MAPK3	mitogen-activated protein kinase 3	CCCGTCTAATATATAAATATA	CTCCCTGACCCGTCTAATATA
NM_002747	5596	MAPK4	mitogen-activated protein kinase 4	AAGGATCGTTGATCAGCATTA	CGCCTTAAATCTAATCAGCAA
NM_002748	5597	MAPK6	mitogen-activated protein kinase 6	CAAGTTCAATTTGAAAGGAAA	CAGGCTTCCTGTTGAAATAAA
NM_002749	5598	MAPK7	mitogen-activated protein kinase 7	CAGACCCACCTTTCAGCCTTA	TACGAGATCATCGAGACCATA
NM_002750	5599	MAPK8	mitogen-activated protein kinase 8	AAGCCCAGTAATATAGTAGTA	TCGGGACTTAAAGCCCAGTAA
NM_002751	5600	MAPK11	mitogen-activated protein kinase 11	CAGGATGGAGCTGATCCAGTA	CTGAGCGACGAGCACGTTCAA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_002752	5601	MAPK9	mitogen-activated protein kinase 9	AAAGTCGATTTATGTGTATTA	ATCGTGAAGTTGTCCTCTTAA
NM_002753	5602	MAPK10	mitogen-activated protein kinase 10	CCGCATGTGTCTGTATTCATA	TCCGAGCACAATAAACTCAAA
NM_002754	5603	MAPK13	mitogen-activated protein kinase 13	CCGGAGTGGCATGAAGCTGTA	CGGCATGAGCCTCATCCGGAA
NM_002755	5604	MAP2K1	mitogen-activated protein kinase kinase 1	CTGGAAGAATTCCTGAACAAA	CTGGATCAAGTCCTGAAGAAA
NM_002756	5606	MAP2K3	mitogen-activated protein kinase kinase 3	ACGGATATCCTGCATGTCCAA	CCGGGCCACCGTGAACTCACA
NM_002757	5607	MAP2K5	mitogen-activated protein kinase kinase 5	AAGACGTATGTTGGAACAAAT	CAAGACGTATGTTGGAACAAA
NM_002758	5608	MAP2K6	mitogen-activated protein kinase kinase 6	AAGGCTTGCATTTCTATTGGA	TAGACCTATGATAAATAACCA
NM_002759	5610	PRKR	protein kinase, interferon-inducible double stranded RNA dependent	ACGGAAAGACTTACGTTATTA	CGGAAAGACTTACGTTATTAA
NM_002760	5616	PRKY	protein kinase, Y-linked	CCAGAGTTCGCCTACAGATAA	TTGGGATACAGTAAGAGAATA
NM_002822	5756	PTK9	PTK9 protein tyrosine kinase 9	ACCGGCATCGTAGCAAGTGAA	TCCAAGCAAGTGAAGATGTTA
NM_002880	5894	RAF1	v-raf-1 murine leukemia viral oncogene homolog 1	CAGATCTTAGTAAGCTATATA	TGGGAAATAGAAGCCAGTGAA
NM_002929	6011	GRK1	G protein-coupled receptor kinase 1	CCAGATGAAGGCGACCGGCAA	CTGGAAAGACATCGAGGACTA
NM_002944	6098	ROS1	v-ros UR2 sarcoma virus oncogene homolog 1 (avian)	AAGGTAATTGCTCTAACTTTA	ACCGAGAAGGGTTAAACTATA
NM_002953	6195	RPS6KA1	ribosomal protein S6 kinase, 90kDa, polypeptide 1	CCCAACATCATCACTCTGAAA	TGCCACGTACTCCGCACTCAA
NM_002958	6259	RYK	RYK receptor-like tyrosine kinase	CGGTCTTGATGCAGAACTTTA	CTGATCGGTCTTGATGCAGAA
NM_002969	6300	MAPK12	mitogen-activated protein kinase 12	CTGGACGTATTCACTCCTGAT	TGGAAGCGTGTTACTTACAAA
NM_003010	6416	MAP2K4	mitogen-activated protein kinase kinase 4	AGGGAGAATGGTGCTGTTTAA	AGGGTGTATAGTGTTCACAAA
NM_003137	6732	SRPK1	SFRS protein kinase 1	CAGACTCTTGTACACCTATAA	TACCATGTGATCCGAAAGTTA
NM_003157	6787	NEK4	NIMA (never in mitosis gene a)-related kinase 4	CACAATCAGTAGCGTAAATAT	CAGACATATATAATGGGTGAA
NM_003159	6792	CDKL5	cyclin-dependent kinase-like 5	AAGATAGACGCTTCATGTTAA	AAGGCAATAATGCTAATTACA
NM_003160	6795	AURKC	aurora kinase C	AAGATGTAAGATGCTAATTAA	CCGGGTGTACCTGATTCTGGA
NM_003161	6198	RPS6KB1	ribosomal protein S6 kinase, 70kDa, polypeptide 1	AAGAAGGGTATCCTTTCATTA	CAGAGAGTCAATGTCATTACA
NM_003177	6850	SYK	spleen tyrosine kinase	CCCGCTCTTAAAGATGAGTTA	TCCGGAATGCATCAACTACTA
NM_003188	6885	MAP3K7	mitogen-activated protein kinase kinase kinase 7	CAAGAATATATGAAAGTTCAA	CCCGTGTGAACCATCCTAATA
NM_003215	7006	TEC	tec protein tyrosine kinase	CAGTACAAAGTCGCAATCAAA	CCGCAGCTAATCAGAATCAGA
NM_003242	7048	TGFBR2	transforming growth factor, beta receptor II (70/80kDa)	CTCCAATATCCTCGTGAAGAA	TCGGTTAATAACGACATGATA
NM_003258	7083	TK1	thymidine kinase 1, soluble	CGGGCCGATGTTCTCAGGAAA	TCGGCTCTGCTACTTCAAGAA
NM_003318	7272	TTK	TTK protein kinase	CAGCAATACCTTGGATGATTA	TCCGACTTTATGATTATGAAA
NM_003328	7294	TXK	TXK tyrosine kinase	CAGCTGGGTTTAGCTACGAAA	CCCGGTGACATTCTATTTCCA
NM_003331	7297	TYK2	tyrosine kinase 2	CACCATCTGGTAATAAACTCA	CTGATGCTATATTTCCGCATA
NM_003332	7305	TYROBP	TYRO protein tyrosine kinase binding protein	CCGAATCATGACAGTCAGCAA	CTGGATCCAGCCATTCCTGAA
NM_003384	7443	VRK1	vaccinia related kinase 1	CAGGTTATACTCCTTAAGTTA	CCAGGTGTACTTGGTAGATTA
NM_003390	7465	WEE1	WEE1 homolog (S. pombe)	CAGGGTAGATTACCTCGGATA	TTGACTAATAATACTGGCTAA
NM_003488	8165	AKAP1	A kinase (PRKA) anchor protein 1	AGCGCTGAACTTGATTGGGAA	CACGCAGAGATGACAGTACAA
NM_003551	8382	NME5	non-metastatic cells 5, protein expressed in (nucleoside-diphosphate kinase)	ATGATATTAGCTAGACATAAA	CATGATATTAGCTAGACATAA
NM_003557	8394	PIP5K1A	phosphatidylinositol-4-phosphate 5-kinase, type I, alpha	CAGCCTCTTGATGTCAATCCA	CCCTGCCTTGATAATATGTTA
NM_003558	8395	PIP5K1B	phosphatidylinositol-4-phosphate 5-kinase, type I, beta	AAGGCTCAACGTATAAGCGAA	CAGGCCTACACTCTATTCAAA
NM_003559	8396	PIP5K2B	phosphatidylinositol-4-phosphate 5-kinase, type II, beta	CACGCCATACGATACAAAGAA	CCGCTTTAAGTTTAAGGAGTA
NM_003565	8408	ULK1	unc-51-like kinase 1 (C. elegans)	CGCGCGGTACCTCCAGAGCAA	TGCCCTTTGCGTTATATTGTA
NM_003576	8428	STK24	serine/threonine kinase 24 (STE20 homolog, yeast)	CCCACCGACGTTGGAAGGAAA	CTGGAGGGAGCACGAACCTAA
NM_003582	8444	DYRK3	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	AGCCAATAAGCTTAAAGCTAA	TCGACAGTACGTGGCCCTAAA
NM_003583	8445	DYRK2	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	TAGAAGCGGTATTAAAGTAAT	TGCACAGAGATTATTGTATTA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_003600	6790	STK6	serine/threonine kinase 6	CACCTTCGGCATCCTAATATT	CACGTGCTCTACCTCCATTTA
NM_003607	8476	CDC42BPA	CDC42 binding protein kinase alpha (DMPK-like)	CAGACTTTCCGTAGCAGCTTA	CAGATAATAGTCGGAAACAAA
NM_003618	8491	MAP4K3	mitogen-activated protein kinase kinase kinase kinase 3	GAGGTGGTTCTTTACAGGATA	TGGAGCTGTTGGATAAAGTAA
NM_003629	8503	PIK3R3	phosphoinositide-3-kinase, regulatory subunit, polypeptide 3 (p55, gamma)	AGGGAGGCAATAATAAGTTAA	GAGGATATCAATCGAGTACAA
NM_003639	8517	IKBKG	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma	CTCCTCTAGTTCAGAGACATA	TTCGGAAATGCCTCACATATA
NM_003640	8518	IKBKAP	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein	CAGCGGTTTACTATAGACAAA	GCGGTTTACTATAGACAAATA
NM_003646	8525	DGKZ	diacylglycerol kinase, zeta 104kDa	CAAGAGGAACGAGTTCTGTAA	CTGGAGCGAGTCAGCGACATA
NM_003647	8526	DGKE	diacylglycerol kinase, epsilon 64kDa	ATCGATGGAAAGTTCAAGTAA	CTGGAAGTCGTTGGAGTATAT
NM_003648	8527	DGKD	diacylglycerol kinase, delta 130kDa	CAGCAGATTCTCTTCTATGAA	CCGCCTCGTGACCAAGTTTAA
NM_003656	8536	CAMK1	calcium/calmodulin-dependent protein kinase I	CAGGTGCTGGATGCTGTGAAA	CTGCATGACCTGGGCATTGTA
NM_003668	8550	MAPKAPK5	mitogen-activated protein kinase-activated protein kinase 5	ACCGACCTTTCTGATTAGTAA	CCGACCTTTCTGATTAGTAAA
NM_003674	8558	CDK10	cyclin-dependent kinase (CDC2-like) 10	CCGTCTGAAGTGTATTCGTAA	CTGATGCTGAGCGAAGCTATA
NM_003681	85006	C21orf124	chromosome 21 open reading frame 124	CACAGGTTATACGAGGGACAA	GAGGCTGAACAACATGAATAA
NM_003682	8567	MADD	MAP-kinase activating death domain	CAGACCCACTACTATAGTAAA	CAGGAGGGCGTTAGTGGATCA
NM_003684	8569	MKNK1	MAP kinase-interacting serine/threonine kinase 1	CCAGCAAAGATGATACCTTAA	TAGATAGTGCTCTGTGCCTAA
NM_003688	8573	CASK	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	AACCAATGGGAATCACTTTAA	AAGGACGACAGATCTATGTAA
NM_003690	8575	PRKRA	protein kinase, interferon-inducible double stranded RNA dependent activator	ATGATTGATTGTTAAATTTCA	TAAGTATGATTGATTGTTAAA
NM_003691	8576	STK16	serine/threonine kinase 16	CACATAGTGTTCTGACTCCAA	CAGGAGAATGTGTAACAAGAA
NM_003718	8621	CDC2L5	cell division cycle 2-like 5 (cholinesterase-related cell division controller)	AACGACGTAGTTTCATTGGAA	TCAGAGTATTATCAATATGAA
NM_003804	8737	RIPK1	receptor (TNFRSF)-interacting serine-threonine kinase 1	CCGACATTTCCTGGCATTGAA	TACCACTAGTCTGACGGATAA
NM_003821	8767	RIPK2	receptor-interacting serine-threonine kinase 2	ACGTATGATCTCTCTAATAGA	CACAAGGACATCGACCTGTTA
NM_003831	8780	RIOK3	RIO kinase 3 (yeast)	ATGCGGCAGTTATATCATGAA	CTGGCTGTATTAGTACAGGAA
NM_003845	8798	DYRK4	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 4	CTCCATATGAACAAAGTGAAA	CTGCATCACGGCGGAGTTGTA
NM_003885	8851	CDK5R1	cyclin-dependent kinase 5, regulatory subunit 1 (p35)	CCGGAAGGCCACGCTGTTTGA	TGAGCTGGTTTGACTCATTAA
NM_003886	8852	AKAP4	A kinase (PRKA) anchor protein 4	GTCGGTGAACACATTCTCAAA	TACAGTGTCTATGCCGATCAA
NM_003936	8941	CDK5R2	cyclin-dependent kinase 5, regulatory subunit 2 (p39)	CAGCAAGAAGGTGACACCCAA	CCGCGAGAACCTTCTCCGCAA
NM_003942	8986	RPS6KA4	ribosomal protein S6 kinase, 90kDa, polypeptide 4	CAGGCTGTGCCTTTGACTTTA	CGCCACCTTCATGGCATTCAA
NM_003948	8999	CDKL2	cyclin-dependent kinase-like 2 (CDC2-related kinase)	ATGATGTGTTTAGGTAATCTA	TTCTACGGACTTTAAATTAAA
NM_003952	6199	RPS6KB2	ribosomal protein S6 kinase, 70kDa, polypeptide 2	ACCGCAGAGAACCGGAAGAAA	CGGGCTGAGCGGAACATTCTA
NM_003954	9020	MAP3K14	mitogen-activated protein kinase kinase kinase 14	CACATGCATGTGACTCCTCAA	TACCTAGTGCATGCTCTGCAA
NM_003957	9024	STK29	serine/threonine kinase 29	CCCGACTGCCAGAGTCTGCTA	GCGAGCTACTGTAAACTTTAA
NM_003985	8711	TNK1	tyrosine kinase, non-receptor, 1	AAGGATCTAGTCTGCCCACTA	ATCGGTCATGATGAACTTGGA
NM_004064	1027	CDKN1B	cyclin-dependent kinase inhibitor 1B (p27, Kip1)	AAAGCGTTGGATGTAGCATTA	ACCGACGATTCTTCTACTCAA
NM_004071	1195	CLK1	CDC-like kinase 1	AAAGCCGGTATCAGAACCATA	AACGTGATGAACGCACCTTAA
NM_004073	1263	PLK3	polo-like kinase 3 (Drosophila)	CAGAAAGACTGTGCACTACAA	CTGCATCAAGCAGGTTCACTA
NM_004119	2322	FLT3	fms-related tyrosine kinase 3	CCGGCTTGAGTGAATTGTGTA	TACGTTGATTTCAGAGAATAT
NM_004157	5576	PRKAR2A	protein kinase, cAMP-dependent, regulatory, type II, alpha	AACGGCATGTCTCTCCAACAA	AACTTGAAAGTCAGCACTAAA
NM_004196	8814	CDKL1	cyclin-dependent kinase-like 1 (CDC2-related kinase)	CTGGACCGAGTGACTACTATA	TCGGGAAATCCGAATGCTCAA
NM_004197	8859	STK19	serine/threonine kinase 19	CCCGGAGACCTTTGGAGTTAA	CTGTTATTACTCTGTCTTGAA
NM_004217	9212	AURKB	aurora kinase B	AACGCGGCACTTCACAATTGA	ACGCGGCACTTCACAATTGAT
NM_004226	9262	STK17B	serine/threonine kinase 17b (apoptosis-inducing)	AGCATATATGTTGTTAACTCA	CATGTTAATGAAATAATTCAA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_004274	9472	AKAP6	A kinase (PRKA) anchor protein 6	AAGCATGTGGATGTACATCTA	CACGTTTGTCACTGCCGTTTA
NM_004302	91	ACVR1B	activin A receptor, type IB	CCGTTCTTACGTCGCCATAAA	CTGTGATTACCTCTCAATCTA
NM_004304	238	ALK	anaplastic lymphoma kinase (Ki-1)	CACCTACGTATTTAAGATGAA	CTCGGCCTGTATACCGGATAA
NM_004327	613	BCR	breakpoint cluster region	ACGGCAGTCCATGACGGTGAA	CAGCATTCCGCTGACCATCAA
NM_004329	657	BMPR1A	bone morphogenetic protein receptor, type IA	CAGCTACGCCGGACAATAGAA	GCGGCAGACATTAAAGGTACA
NM_004333	673	BRAF	v-raf murine sarcoma viral oncogene homolog B1	ACACGACATGTGAATATCGTA	TTGCTTATATGTTAAATTGAA
NM_004336	699	BUB1	BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast)	CAGCTTGTGATAAAGAGTCAA	TGGCACTTACATGAAAGTGAA
NM_004383	1445	CSK	c-src tyrosine kinase	CCGGTACAGAATGTATTGCCA	TACGCGCCTCATTAAACCAAA
NM_004384	1456	CSNK1G3	casein kinase 1, gamma 3	CAACATATCTTCGTTATGTAA	TACCGCAAACTTGATATGGAA
NM_004409	1760	DMPK	dystrophia myotonica-protein kinase	AACCAGAAGTTCGCCAGTCAA	GAGCCTGAGGGCTAAATTTAA
NM_004431	1969	EPHA2	EphA2	CAGCGCCAAGTAAACAGGGTA	TCGGACAGACATATAGGATAT
NM_004438	2043	EPHA4	EphA4	CCCCCGAATGAAGTTACCTTA	CCGCCAGGACATTTCCTATAA
NM_004439	2044	EPHA5	EphA5	ACCAGTTGGATCTCCAATGAA	CCCGGCAGTATGTGTCTGTAA
NM_004440	2045	EPHA7	EphA7	ACCAGTCATGATAGTAATAGA	CAGGCTGCGAAGGAAGTACTA
NM_004441	2047	EPHB1	EphB1	ATGGCCCTGGATTATCTACTA	GCGGGATGATGTGACCTACAA
NM_004443	2049	EPHB3	EphB3	CCGCAGCTGACCGCCAGATTA	GCGGGTCTACGTGGAGCTCAA
NM_004444	2050	EPHB4	EphB4	CCCAGGCAATAGCCACTCTAA	TCGGACAAACACGGACAGTAT
NM_004445	2051	EPHB6	EphB6	AACCGCCAATCTCTAGATCAA	CTGGAGCTTTGGGATACTCAT
NM_004448	2064	ERBB2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)	AACAAAGAAATCTTAGACGAA	CACGTTTGAGTCCATGCCCAA
NM_004517	3611	ILK	integrin-linked kinase	AAGGAAGAGCAGGGACTTCAA	TAGCCGTAGTGTAATGATTGA
NM_004560	4920	ROR2	receptor tyrosine kinase-like orphan receptor 2	CCGGTTTGGGAAAGTCTACAA	CTGGTGCTTTACGCAGAATAA
NM_004566	5209	PFKFB3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	CAGGGACTTGTCGCTGATCAA	CTCCAATATCATGGAAGTTAA
NM_004567	5210	PFKFB4	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4	ACGGAGAGCGACCATCTTTAA	CAGAAAGTGTCTGGACTTGTA
NM_004570	5288	PIK3C2G	phosphoinositide-3-kinase, class 2, gamma polypeptide	CCAGATCAAGAAATTCGTAAA	CCCGTAGAAATGATAACTCCA
NM_004579	5871	MAP4K2	mitogen-activated protein kinase kinase kinase kinase 2	CTGGCTCTACTGCGTGAACAA	TCGGTCAGCCTCAGAATTCCA
NM_004586	6197	RPS6KA3	ribosomal protein S6 kinase, 90kDa, polypeptide 3	AGCGCTGAGAATGGACAGCAA	TCCAAACATTATCACTCTAAA
NM_004612	7046	TGFBR1	transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 53kDa)	TCCATTGGTGGAATTCATGAA	TGGGATTGTACTATACCAGTA
NM_004614	7084	TK2	thymidine kinase 2, mitochondrial	ATGCCAGAAGTGGACTATGTA	CGGGATCGAATATTAACTCCA
NM_004635	7867	MAPKAPK3	mitogen-activated protein kinase-activated protein kinase 3	CAGGCTTTCACTGAGAGAGAA	CCAGATAGTAATAAACACCAT
NM_004672	9064	MAP3K6	mitogen-activated protein kinase kinase kinase 6	CACCATCCAAATGCTGTTGAA	TCAGAGGAGCTGAGTAATGAA
NM_004690	9113	LATS1	LATS, large tumor suppressor, homolog 1 (Drosophila)	CCCATGAATCCTCCTAATCAA	CGCGATCTAGTATATGTTTAA
NM_004705	5612	PRKRIR	protein-kinase, interferon-inducible double stranded RNA dependent inhibitor, repressor of (P58 repressor)	AAGGTGTATGTAGACCACTTA	CTGGACAGTTACAAGAAATTA
NM_004712	9146	HGS	hepatocyte growth factor-regulated tyrosine kinase substrate	CCGGAACGAGCCCAAGTACAA	GCACGTCTTTCCAGAATTCAA
NM_004714	9149	DYRK1B	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1B	CACGGAGATGAAGTACTATAT	CCGGACCTACCGCTACAGCAA
NM_004721	9175	MAP3K13	mitogen-activated protein kinase kinase kinase 13	CAGACTCAATATGCACGGACA	GCGAATAATTTATACATGGAA
NM_004734	9201	DCAMKL1	doublecortin and CaM kinase-like 1	CAGGTTTATAACTTCGACACA	CCGGAAGTGATAACACGCAAA
NM_004759	9261	MAPKAPK2	mitogen-activated protein kinase-activated protein kinase 2	CGCCATCATCGATGACTACAA	CTACGAGCAGATCAAGATAAA
NM_004760	9263	STK17A	serine/threonine kinase 17a (apoptosis-inducing)	AACCAGGATATTTAACAGGTA	TCCATTGTAACCGAAGAGTTA
NM_004783	9344	TAO1	thousand and one amino acid protein kinase	CACGCCCAAAGCTCAGCACAA	GCCCAAGAGCCTCAAATCTAA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_004834	9448	MAP4K4	mitogen-activated protein kinase kinase kinase kinase 4	AGGCAAGATCCTACCCGGAAA	TCGGAGCTGCACCGAGGGCAA
NM_004836	9451	EIF2AK3	eukaryotic translation initiation factor 2-alpha kinase 3	CACAAACTGTATAACGGTTTA	CGGCAGGTCATTAGTAATTAT
NM_004842	9465	AKAP7	A kinase (PRKA) anchor protein 7	AACGATGGGTCTGAAGTCCAA	CCCGATGACGCTGAACTAGTA
NM_004850	9475	ROCK2	Rho-associated, coiled-coil containing protein kinase 2	AAGCTACATATGGAGCTTAAA	ATGCACTTGTATAAAGCCATA
NM_004857	9495	AKAP5	A kinase (PRKA) anchor protein 5	AGGGCTTTCATCAAGAAATTA	ATCAGGTTGATCTTTAAATAA
NM_004936	1030	CDKN2B	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	CTGCTTACTTATGCCATAGAA	GAGAGCAATTGTAACGGTTAA
NM_004938	1612	DAPK1	death-associated protein kinase 1	AAGCATGTAATGTTAATGTTA	CGGCTATTACTCTGTGGCCAA
NM_004954	2011	MARK2	MAP/microtubule affinity-regulating kinase 2	CACCTCTAATTCTTACTCTAA	CCACCTCTAATTCTTACTCTA
NM_004972	3717	JAK2	Janus kinase 2 (a protein tyrosine kinase)	AGCCATCATACGAGATCTTAA	CTGCCTTACGATGACAGAAAT
NM_005009	4833	NME4	non-metastatic cells 4, protein expressed in	ACCAACTACCTCCGTCAGCAA	CAGCACATGGGTGGTACACTA
NM_005012	4919	ROR1	receptor tyrosine kinase-like orphan receptor 1	CCCAGTGAGTAATCTCAGTAA	CCGTACTGCGATGAAACTTCA
NM_005026	5293	PIK3CD	phosphoinositide-3-kinase, catalytic, delta polypeptide	CCGGTCACGCATGAAGGCAAA	CGCCGTGATCGAGAAAGCCAA
NM_005027	5296	PIK3R2	phosphoinositide-3-kinase, regulatory subunit, polypeptide 2 (p85 beta)	CCGCGAGTATGACCAGCTTTA	TTGGTACGTGGGCAAGATCAA
NM_005028	5305	PIP5K2A	phosphatidylinositol-4-phosphate 5-kinase, type II, alpha	ATGGAATTAAGTGCCATGAAA	CTGCCCGATGGTCTTCCGTAA
NM_005030	5347	PLK1	polo-like kinase 1 (Drosophila)	CCGGATCAAGAAGAATGAATA	CGCGGGCAAGATTGTGCCTAA
NM_005044	5613	PRKX	protein kinase, X-linked	CGGATGGGATTCACTTAAGAA	TTGGAATACTCTAAGAGAATA
NM_005100	9590	AKAP12	A kinase (PRKA) anchor protein (gravin) 12	ACGGATGTAGTGTTGAAAGTA	CCCGAAATAATCGAACAGATT
NM_005108	9942	XYLB	xylulokinase homolog (H. influenzae)	CTGAAATTATTGGACGTCATA	TCAGGACTCCAGCTAAATCAA
NM_005109	9943	OSR1	oxidative-stress responsive 1	CTGGAGTAGGGACTAACTATA	TAGGGACTAACTATAGCACAA
NM_005157	25	ABL1	v-abl Abelson murine leukemia viral oncogene homolog 1	ACGCACGGACATCACCATGAA	CCAGTGGAGATAACACTCTAA
NM_005158	27	ABL2	v-abl Abelson murine leukemia viral oncogene homolog 2 (arg, Abelson-related gene)	ATCAAGCATCCTAATCTGGTA	CCCAAGTGTAATAAGCCTACA
NM_005160	157	ADRBK2	adrenergic, beta, receptor kinase 2	AAGATGTTCAGTGTTGGGTAA	CAAGTGTATGGGATTAACTAA
NM_005163	207	AKT1	v-akt murine thymoma viral oncogene homolog 1	ACGCTACTTCCTCCTCAAGAA	CACGCTTGGTCCCGAGGCCAA
NM_005184	808	CALM3	calmodulin 3 (phosphorylase kinase, delta)	CACCAATTGATTGACTGAGAA	CCGCAGAGCTGCGTCACGTAA
NM_005204	1326	MAP3K8	mitogen-activated protein kinase kinase kinase 8	AAGAAAGTGATCCATCATGAT	AGAGATTGATTTATTAATTAA
NM_005228	1956	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	CCCATCCAATTTATCAAGGAA	CCCGTCGCTATCAAGGAATTA
NM_005232	2041	EPHA1	EphA1	CAGATGGGATCCCGTATCGAA	TACCTCAGTAATCACAATTAT
NM_005233	2042	EPHA3	EphA3	TCGGATATGATTGTTTCTCAA	TTGGATAGTTTCCTACGTAAA
NM_005235	2066	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	CTACGTGTTAGTGGCTCTTAA	TCGGGATTTGGCAGCCCGTAA
NM_005246	2241	FER	fer (fps/fes related) tyrosine kinase (phosphoprotein NCP94)	CAGAACAACTTAGTAGGATAA	CAGATAGATCCTAGTACAGAA
NM_005248	2268	FGR	Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog	CACGTGGAACGGCAGCACTAA	CAGACCTTGTCTAGTTATTTA
NM_005255	2580	GAK	cyclin G associated kinase	ACGCGTGTGACATTCAAGAAA	CCCGTGGTTGTCTGTACAGAA
NM_005308	2869	GRK5	G protein-coupled receptor kinase 5	AGCGTCATAACTAGAACTGAA	CAGGAACAACGCGGTAGGCAA
NM_005356	3932	LCK	lymphocyte-specific protein tyrosine kinase	AAGGGCCAGGACTTTATCTAA	CGCCATTACACCAATGCTTCA
NM_005372	4342	MOS	v-mos Moloney murine sarcoma viral oncogene homolog	CGCGAACATCTTGATCAGTGA	CTCGGTGTACAAGGCGACTTA
NM_005391	5165	PDK3	pyruvate dehydrogenase kinase, isoenzyme 3	AACGTTGTAGGTTGAAACTGA	TTCATTAGCACTAACATCCAA
NM_005399	5565	PRKAB2	protein kinase, AMP-activated, beta 2 non-catalytic subunit	ACCCAAAGTACTACTCATTTA	TCCAATATTAGTTGGAGTTAA
NM_005400	5581	PRKCE	protein kinase C, epsilon	CACGGAAACACCCGTACCTTA	CCCGACCATGGTAGTGTTCAA
NM_005406	6093	ROCK1	Rho-associated, coiled-coil containing protein kinase 1	AACGGTTAGAACAAGAGGTAA	CAAGCTCGAATTACATCTTTA
NM_005417	6714	SRC	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	AAGCAGTGCCTGCCTATGAAA	CGGCTTGTGGGTGATGTTTGA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_005424	7075	TIE	tyrosine kinase with immunoglobulin and epidermal growth factor homology domains	CCCAGTGAGAACGTGACGTTA	GCGCTTCAAGGTCAATGTGAA
NM_005433	7525	YES1	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	CCAGCCTACATTCACTTCTAA	GAGGCTCCTGCTTATTTATAA
NM_005456	9479	MAPK8IP1	mitogen-activated protein kinase 8 interacting protein 1	CTGGAGGAGTTTGAGGATGAA	TGCCATCAGCTTACAGTGCAA
NM_005476	10020	GNE	glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase	ATGGAAATACATATCGAATGA	GCCGATCATGTTTGGCATTAA
NM_005546	3702	ITK	IL2-inducible T-cell kinase	CAGGACTTTAGTAGAGACTGA	CTGGTGAGTTAAGTAAGATTA
NM_005569	3985	LIMK2	LIM domain kinase 2	CAGGAGGAATCTGTTACTCGA	CAGGGTGAACCTGCCTGTGAA
NM_005592	4593	MUSK	muscle, skeletal, receptor tyrosine kinase	ACGGCCTGGAATGAACTGAAA	CCCACCAATGACGTCCTCAAA
NM_005607	5747	PTK2	PTK2 protein tyrosine kinase 2	CACCTGGGTACTGCTATGGAA	CCGGTCGAATGATAAGGTGTA
NM_005627	6446	SGK	serum/glucocorticoid regulated kinase	CACAGCTGAAATGTACGACAA	CTGGGCTGTGATGACGAATAT
NM_005734	10114	HIPK3	homeodomain interacting protein kinase 3	CACGTTTGCCCAGGTAGTTAA	CTCATTCTGGTTGGAGATTAA
NM_005751	10142	AKAP9	A kinase (PRKA) anchor protein (yotiao) 9	CAGCCTATCAGTGAACATCAA	CAGCTTCAAAGGGATATACAA
NM_005781	10188	ACK1	activated Cdc42-associated kinase 1	ACGCAAGTCGTGGATGAGTAA	CGGCAGTCAGATCCTGCATAA
NM_005793	10201	NME6	non-metastatic cells 6, protein expressed in (nucleoside-diphosphate kinase)	CAGACTTCTCCTAGACATCTA	CAGGATCTAGCCTTCTATCTA
NM_005813	23683	PRKCN	protein kinase C, nu	CACGATATGTCAGTACTGCAA	CGGGAGAGTGTTACCATTGAA
NM_005858	10270	AKAP8	A kinase (PRKA) anchor protein 8	CAAGGTTAGCACGCAACAGAA	GAGGCCGGTAGTGATCCTCAA
NM_005876	10290	APEG1	aortic preferentially expressed protein 1	AACACCTATTTCTTAACTCAA	CAGCTGGAATAACAAGCCCAA
NM_005881	10295	BCKDK	branched chain alpha-ketoacid dehydrogenase kinase	AACGCCCACCATGATGCTCTA	CAGAACTTGGAGAGCAGGGAA
NM_005884	10298	PAK4	p21(CDKN1A)-activated kinase 4	CGGCGCCGAGCCGATGAGTAA	CTGGACAACTTCATCAAGATT
NM_005906	4117	MAK	male germ cell-associated kinase	CACAGTGTTGATATATGGGTA	CCGGATATAATCGATCAGGTT
NM_005922	4216	MAP3K4	mitogen-activated protein kinase kinase kinase 4	CACCAATCCCTGAAAGATTAA	CTCAAGCATCGCATAGTTTAA
NM_005923	4217	MAP3K5	mitogen-activated protein kinase kinase kinase 5	CAGCGAGTAGATAATATCGAA	CCGGGAATCTATACTCAATGA
NM_005965	4638	MYLK	myosin, light polypeptide kinase	AACCTGAAATCCGCTAGCAAA	CAGCATCCATGGCTAATGAAA
NM_005975	5753	PTK6	PTK6 protein tyrosine kinase 6	CCGGGTCCAGGTGGCCATTAA	CGGGTTAGCCAGGCTTATCAA
NM_005983	6502	SKP2	S-phase kinase-associated protein 2 (p45)	AAGTGATAGTGTCATGCTAAA	ACCCTTCAACTGTTAAAGGAA
NM_005990	6793	STK10	serine/threonine kinase 10	CACGGAATTAGAGAACCTGGA	CAGCTCAAACTGATGAAGAAA
NM_006035	9578	CDC42BPB	CDC42 binding protein kinase beta (DMPK-like)	CGCCGAGATATTCCATGTATA	TAGGACCTTAAGAGAATAGTA
NM_006116	10454	MAP3K7IP1	mitogen-activated protein kinase kinase kinase 7 interacting protein 1	CACCTTGGACAAGCCACACAA	CTGCAGGTGAGAGGATTTAAA
NM_006176	4900	NRGN	neurogranin (protein kinase C substrate, RC3)	AAGCCGGACGACGACATTCTA	TGGGTTGGAATGTGAACAATA
NM_006180	4915	NTRK2	neurotrophic tyrosine kinase, receptor, type 2	ACCACGAACAGAAGTAATGAA	CTGACGAGTTTGTCTAGGAAA
NM_006182	4921	DDR2	discoidin domain receptor family, member 2	ACGCACTGTCAGTTACACCAA	CCGGTTCATTCCAGTCACCGA
NM_006201	5127	PCTK1	PCTAIRE protein kinase 1	CACCATAATCGCTGTATGAAA	CACGCCAACATCGTTACGCTA
NM_006206	5156	PDGFRA	platelet-derived growth factor receptor, alpha polypeptide	ACGCAGGAAGCCTACTATTTA	CGCAGGAAGCCTACTATTTAA
NM_006212	5208	PFKFB2	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	CCAGAGCAAGATAGTCTACTA	CCGTGACAAGCCAACTAACAA
NM_006213	5260	PHKG1	phosphorylase kinase, gamma 1 (muscle)	CAAGAGCCTGCAAGCACTTAA	CCGGGAGATCGTCATCCGAGA
NM_006218	5290	PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide	CTGAGTCAGTATAAGTATATA	TGCGAAATTCTCACACTATTA
NM_006219	5291	PIK3CB	phosphoinositide-3-kinase, catalytic, beta polypeptide	CCCTTCGATAAGATTATTGAA	TCGGGAAGCTACCATTTCTTA
NM_006251	5562	PRKAA1	protein kinase, AMP-activated, alpha 1 catalytic subunit	CCCACGATATTCTGTACACAA	TCGGGATCAGTTAGCAACTAT
NM_006252	5563	PRKAA2	protein kinase, AMP-activated, alpha 2 catalytic subunit	ACGACTAAGCCCAAATCTTTA	CCGATTTCGGATTATCTAATA
NM_006253	5564	PRKAB1	protein kinase, AMP-activated, beta 1 non-catalytic subunit	CACGTCTAGAAGTCACATGAA	CTGGCTATGGAACTAAATACA
NM_006254	5580	PRKCD	protein kinase C, delta	CCGCTTCAAGGTTCACAACTA	CCGGGACACTATATTCCAGAA
NM_006255	5583	PRKCH	protein kinase C, eta	CGCCGTGTGCTCATCACTGAA	GACCAGATTTGTGGCTTATAA
NM_006256	5586	PRKCL2	protein kinase C-like 2	AAAGTATGATATCTACGCAAA	CACGTCAAAGTATGATATCTA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_006257	5588	PRKCQ	protein kinase C, theta	CCGCAGACAAGTAATCACTAA	CGGGCAGATTGTATATCCAGAA
NM_006258	5592	PRKG1	protein kinase, cGMP-dependent, type I	CCGGTGTATATACCATACAAA	GAGGTTCGTTTGAAGATTCTA
NM_006259	5593	PRKG2	protein kinase, cGMP-dependent, type II	GACCTACAATTTGATTCTCAA	TTGAGTACTACTAACGTTTAA
NM_006281	6788	STK3	serine/threonine kinase 3 (STE20 homolog, yeast)	CCGGCGCCTAAGAGTAAACTA	CGGCGCCTAAGAGTAAACTAA
NM_006282	6789	STK4	serine/threonine kinase 4	AGGATTCATAGCATCACTATA	CACCATTTGCTGTGCGAATTA
NM_006285	7016	TESK1	testis-specific kinase 1	CAGGACCGCCCTGACACAAAA	CTGCGGTACCTGCACTCCAAA
NM_006293	7301	TYRO3	TYRO3 protein tyrosine kinase	AACGGTGACCTTTAGTGCCAA	CGGACTGACCAAATCACCCAA
NM_006296	7444	VRK2	vaccinia related kinase 2	CACACAATAGGTTAATCGAAA	CTGGAGGATTTGGATTGATAT
NM_006301	7786	MAP3K12	mitogen-activated protein kinase kinase kinase 12	CAGGGAGCACTATGAAAGGAA	CTCGTATTCCTTGTACATAGA
NM_006314	10256	CNK1	connector enhancer of KSR-like (Drosophila kinase suppressor of ras)	CCGCCGCTGGTTTGTGCTCAA	CGGACTCAGCTTAGTGCTGAA
NM_006343	10461	MERTK	c-mer proto-oncogene tyrosine kinase	CAGATGAATGTTGTTAAGGAA	TTGCCTGACGTTCGGAACCAA
NM_006374	10494	STK25	serine/threonine kinase 25 (STE20 homolog, yeast)	AAGGGCATCGATAACCACACA	CACCAAGCTATGGATCATCAT
NM_006383	10518	KIP2	DNA-dependent protein kinase catalytic subunit-interacting protein 2	CACCGAAGAGCAGCTAGACAA	CTGCACCTTCTTCAATAAGAA
NM_006422	10566	AKAP3	A kinase (PRKA) anchor protein 3	AGGGATCATGACCTATGCTAA	ATCAAGCTATCCATAATGAAA
NM_006457	10611	LIM	LIM protein (similar to rat protein kinase C-binding enigma)	CAGCAGGGAAACGAACTCCGA	TCCGATGTGCGCCCATTGTAA
NM_006549	10645	CAMKK2	calcium/calmodulin-dependent protein kinase kinase 2, beta	CCGCAAGATCTTCTCTGGGAA	CTAGCTGATTGTTGTGGTCAA
NM_006556	10654	PMVK	phosphomevalonate kinase	CCCAGTGTGGATACTAATAAA	TTGGCTGTGCTTGAAGGCGAA
NM_006575	11183	MAP4K5	mitogen-activated protein kinase kinase kinase kinase 5	CTTGCCTATTTGCATACTAAA	TCCGCTTATTAGGATCAGACA
NM_006609	10746	MAP3K2	mitogen-activated protein kinase kinase kinase 2	CACAGTAATATGATTGTCCTA	CAGAATGATGTCCGAGTCAAA
NM_006622	10769	PLK2	polo-like kinase 2 (Drosophila)	CAGATGCTCCTGAGCAATTTA	CAGATTGTGTCTGGACTGAAA
NM_006648	65268	PRKWNK2	protein kinase, lysine deficient 2	AACGTTCATCGAGCAGATGAA	ACCTATAAGTCTAGTAGCAAA
NM_006712	10922	FASTK	FAST kinase	CAGCAGCAAGGTGGTACAGAA	CTGGTGGTTCAGGAAACGCAA
NM_006716	10926	ASK	activator of S phase kinase	CAGTATCAAGTTGTTGATGAT	CATGAATCTATTGTCACTAAA
NM_006738	11214	AKAP13	A kinase (PRKA) anchor protein 13	CCGCCTGTTTGGGTTAACAAA	CTCGGTGTTTCAGGCACTAAA
NM_006742	5681	PSKH1	protein serine kinase H1	CCCGATTAGGGTCGAGTGTCA	CCGCTCCACACGCTCCAATAA
NM_006759	7360	UGP2	UDP-glucose pyrophosphorylase 2	CCCAAAGTTAGTTACTCTTAA	CGAGTTCAAGTCTGTATCAAA
NM_006852	11011	TLK2	tousled-like kinase 2	AAGGTTCATCTGTCCATGCAA	CAAGAGAATACGATTCTTAAA
NM_006871	11035	RIPK3	receptor-interacting serine-threonine kinase 3	ACCGCTCGTTAACATATACAA	CAGCCTGATGTCGTGCGTCAA
NM_006875	11040	PIM2	pim-2 oncogene	CCGGGATTGTCCAATTACTAA	CGGGATTGTCCAATTACTAAA
NM_006888	801	CALM1	calmodulin 1 (phosphorylase kinase, delta)	CGGCAACTTACACACATTGAA	CTGGTTGTATCTTATTAGCAA
NM_006904	5591	PRKDC	protein kinase, DNA-activated, catalytic polypeptide	CTCGTGTATTACAGAAGGAAA	TTCGGCTAACTCGCCAGTTTA
NM_006930	6500	SKP1A	S-phase kinase-associated protein 1A (p19A)	AGGGTACTTTAGAGCAACTTA	TAGGAAAGACTACTCAAGTTA
NM_007064	11139	TRAD	serine/threonine kinase with Dbl- and pleckstrin homology domains	CAGGACATCAATCAAGTCTTA	CCCATTGAGTATCAACGGAAA
NM_007118	7204	TRIO	triple functional domain (PTPRF interacting)	ACCGTTGTTCTTAGATGTCGA	CCGGGAATGTATGGATACGTA
NM_007170	10420	TESK2	testis-specific kinase 2	CCGGGAAGAATCGCTATCTGA	CGAGATGAGCCCTATAATGAA
NM_007174	11113	CIT	citron (rho-interacting, serine/threonine kinase 21)	ATGGAAGGCACTATTTCTCAA	CAGGATATACCGTAACACGAA
NM_007181	11184	MAP4K1	mitogen-activated protein kinase kinase kinase kinase 1	CTGACTAAGAGTCCCAAGAAA	TACGTGGGTGTACTCCATCAA
NM_007194	11200	CHEK2	CHK2 checkpoint homolog (S. pombe)	ACGCCGTCCTTTGAATAACAA	AGGACTGTCTTATAAAGATTA
NM_007199	11213	IRAK3	interleukin-1 receptor-associated kinase 3	CACATTCGAATCGGTATATTA	CTGGATGTTCGTCATATTGAA
NM_007202	11216	AKAP10	A kinase (PRKA) anchor protein 10	CAGATAAGCATAGAACTGATA	TAGCAGGACAGCCACACTTAA
NM_007229	11252	PACSIN2	protein kinase C and casein kinase substrate in neurons 2	CACCCTTAATGTCCCGAGCAA	GAAGCTTTACATAGAACCTTA
NM_007254	11284	PNKP	polynucleotide kinase 3'-phosphatase	CACGTGAACAGGGACACGCTA	CACGTGTGAGACAGCCCTGAA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_007271	11329	STK38	serine/threonine kinase 38	AACCTTATCGCTCAACATGAA	TACGTCGCCCATAAACAGCTA
NM_007284	11344	PTK9L	PTK9L protein tyrosine kinase 9-like (A6-related protein)	AAGACAGAGATCAGTGTGGAA	TTGGGATGGTTGAATGCTGTA
NM_012145	1841	DTYMK	deoxythymidylate kinase (thymidylate kinase)	ATCAGTTGGAATTCTCCTAAA	TCCCGGAAAGATCAACTGAAA
NM_012290	9874	TLK1	tousled-like kinase 1	CAGAGAGTATAGAATACACAA	GCGGAGAAGAAACAATCGGAA
NM_012324	23542	MAPK8IP2	mitogen-activated protein kinase 8 interacting protein 2	ACAGGTAATGTCGGCTTCCAA	CTGGAAGAATTTGACGACGAA
NM_012395	5218	PFTK1	PFTAIRE protein kinase 1	AAGGGACACCTTTCACAGCTA	CTGGGTCTTGTCAACATCTAA
NM_012398	23396	PIP5K1C	phosphatidylinositol-4-phosphate 5-kinase, type I, gamma	CCGCGTCGTGGTCATGTACAA	CGGCAAGACCTATTTATAATA
NM_012407	9463	PRKCABP	protein kinase C, alpha binding protein	CCGGTGTCAATGGCAGGTCAA	TCGCCTCACCATCAAGAAGTA
NM_012424	26750	RPS6KC1	ribosomal protein S6 kinase, 52kDa, polypeptide 1	CAGGATTGGTTTATATGATTA	CCGGGTTGTTTCACGAAGAAA
NM_012474	7371	UMPK	uridine monophosphate kinase	CCGGATGCCTTTGACAATGAA	TCAGTACATTACGTTCGTCAA
NM_013233	27347	STK39	serine threonine kinase 39 (STE20/SPS1 homolog, yeast)	TGGAATAGTCTCAGATCTAAA	TTGGAGTATTTGTAACTTCTA
NM_013254	29110	TBK1	TANK-binding kinase 1	CAGAACGTAGATTAGCTTATA	CTGACTTGACACGTTTGTAAA
NM_013257	23678	SGKL	serum/glucocorticoid regulated kinase-like	ACCAACTAACTTACATGCTTA	CCACAGCGAGACCCTAGTTAA
NM_013276	23729	CARKL	carbohydrate kinase-like	ATGAAACATATTGTCTCTTTA	CAGGTAGTTTATTCAAAGAGA
NM_013302	29904	EEF2K	elongation factor-2 kinase	CAGACACTACATGAACACGAA	CGGGATGGCGCTCTTCTTCTA
NM_013355	29941	pknbeta	protein kinase PKNbeta	AGGGAAATACTACGCCATCAA	CCCGGGAAGTTTCAAGTTTGA
NM_013392	29959	NRBP	nuclear receptor binding protein	CCGGTTGACTTCTCTGCTAGA	TCGGTGGAGGAGGGAGTCAAA
NM_013410	205	AK3	adenylate kinase 3	CAGGAAGATGTGGTCATTCAT	CCTGGTAACAGTGAAATTGAA
XM_375834	9641	IKBKE	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon	ACGGCGGAACAAGGAGATCAT	CCGCATCATCGAACGGCTAAA
NM_014006	23049	SMG1	PI-3-kinase-related kinase SMG-1	ATCGATGTTGCCAGACTACTA	CACCATGGTATTACAGGTTCA
NM_014030	28964	GIT1	G protein-coupled receptor kinase-interactor 1	CAGCCTTGACTTATCCGAATT	GCCGCTGAGGATGTCCCGAAA
NM_014216	3705	ITPK1	inositol 1,3,4-triphosphate 5/6 kinase	CACGCCGTCATTGACATCAAT	CCGATTAATGTCTGTACGTCA
NM_014226	5891	RAGE	renal tumor antigen	AAAGAATAAGCTGTCGTTAAA	CCGGCTGTGTGTTCTACGAGA
NM_014264	10733	PLK4	polo-like kinase 4 (Drosophila)	CACCAAATGGTCAAACAACTA	CTGGTAGTACTAGTTCACCTA
NM_014308	23533	P101-PI3K	phosphoinositide-3-kinase, regulatory subunit, polypeptide p101	ACCGGTGCTGCTGCAACTCTA	ATCGCAGATCAAAGTGGACAA
NM_014326	23604	DAPK2	death-associated protein kinase 2	CGGAATTTGTTGCTCCAGAAA	CTGGTTAAAGAGACCCGGAAA
NM_014365	26353	HSPB8	heat shock 27kDa protein 8	CCGCATGGTTTGGTTAATGAA	CGCATGGTTTGGTTAATGAAA
NM_014370	26576	STK23	serine/threonine kinase 23	AAGATGAGGCGCAAACGGAAA	AAGCGCTTTGTGGCCCTCAAA
NM_014371	26993	AKAP8L	A kinase (PRKA) anchor protein 8-like	AAGGAACACTTTAAGTACGTA	CAGGATAACACCACCAACTAT
NM_014397	10783	NEK6	NIMA (never in mitosis gene a)-related kinase 6	ACCACGGAAGTCGAGAATTAA	ACCGGAGAGGATCCATGAGAA
NM_014413	27102	HRI	heme-regulated initiation factor 2-alpha kinase	CCCGAATATGACGAATCTGAT	CTGATTAAGGGTGCAACTAAA
NM_014496	27330	RPS6KA6	ribosomal protein S6 kinase, 90kDa, polypeptide 6	CAGCGGTATACTGCTGAACAA	GGCGAGGTAAATGGTCTTAAA
NM_014572	26524	LATS2	LATS, large tumor suppressor, homolog 2 (Drosophila)	CACACTCACCTCGCCCAATAA	CAGGACCTTCACTGCATTAAA
NM_014586	30811	HUNK	hormonally upregulated Neu-associated kinase	CACGGGCAAAGTGCCCTGTAA	TCGGACCAAGATCAAACCAAA
NM_014602	30849	PIK3R4	phosphoinositide-3-kinase, regulatory subunit 4, p150	AAGCAGAATTCTAGATCAGAA	TAGAGGCAGAAGATTACTTAA
NM_014683	9706	ULK2	unc-51-like kinase 2 (C. elegans)	ACCGGGAAGTTATCAGATCAA	ATCGGTACAGTTATTCTTAAA
NM_014720	9748	SLK	SNF1 sucrose nonfermenting like kinase (yeast)	CCAGATCAGGACCGTGATAAA	TAGCATCTTGTGATCACCCAA
NM_014776	9815	GIT2	G protein-coupled receptor kinase-interactor 2	AAGCATCGTGCAATAAGTGAA	CTGCCTATGGCTGAAACTATA
NM_014791	9833	MELK	maternal embryonic leucine zipper kinase	CGGGTTGTCTTCCGTCAGATA	CTGGATCATGCAAGATTACAA
XM_374996	9891	ARK5	AMP-activated protein kinase family member 5	CTTGAGTTGATGATCAATTAA	TAGGGATTTACTGGCATGGTA
NM_014911	22848	AAK1	AP2 associated kinase 1	AACGTGAGTAGCGGTGATGTA	CCAGGTGGTAAACCTGATGAA
NM_014916	22853	LMTK2	lemur tyrosine kinase 2	CACCTCCGACTTAAATGTGAA	CAGATCAGACTAAGTATAGTA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_014920	22858	ICK	intestinal cell (MAK-like) kinase	ACCTAATGACTTGGTAAATTA	CTCAGTAATCTAGCTTATATA
NM_015000	23012	STK38L	serine/threonine kinase 38 like	AGGGAGATGTACTGTATTATA	TACAACCATGATAACCATTAT
NM_015071	23092	GRAF	GTPase regulator associated with focal adhesion kinase pp125(FAK)	ACCGTATGGCCTATAGTTTAA	AGCGAGTATACTAGTAGGTTA
NM_015076	23097	CDK11	cyclin-dependent kinase (CDC2-like) 11	CACTGTCGTCAGGAAGATATA	GAGGATTTGTTTGAGTACGAA
NM_015093	23118	MAP3K7IP2	mitogen-activated protein kinase kinase kinase 7 interacting protein 2	CAGTCAATAGCCAGACCTTAA	TGGCTGGGTATCTCAGTTTAA
NM_015112	23139	MAST2	microtubule associated serine/threonine kinase 2	CAGGAGTGTGCTGTCTGGCAA	CAGTGAAATAATAATGATGAA
NM_015133	23162	MAPK8IP3	mitogen-activated protein kinase 8 interacting protein 3	CAGCCGCAACATGGAAGTACA	GACGAGTGGTCTGATGTTCAA
NM_015148	23178	PASK	PAS domain containing serine/threonine kinase	ATCCTGGTTGCTAACGACAAA	CGCGCTGACACTGTTTGGTTA
NM_015690	27148	STK36	serine/threonine kinase 36 (fused homolog, Drosophila)	ATGGATGCTGACCTCCTTATA	CCAGTTGGTGTCAGCCCTGTA
NM_015716	50488	MINK	misshapen/NIK-related kinase	CACGTACGGGCGCATCATTAA	CGCAGACTTTGTGTTGCTGAA
NM_015850	2260	FGFR1	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome)	CAGAGATTTACCCATCGGGTA	CCGGCCTCTATGCTTGCGTAA
NM_015978	51086	TNNI3K	TNNI3 interacting kinase	CAGCATTCGGCGTATACCTAA	GGAGCTAATGTCAATATTCAA
NM_015981	815	CAMK2A	calcium/calmodulin-dependent protein kinase (CaM kinase) II alpha	CAGGAACTTCTCCGGAGGGAA	CCAGGATTTCATCTCACCATA
NM_016086	51657	MK-STYX	map kinase phosphatase-like protein MK-STYX	AAGCTTCTGCACATCCGGATA	CAAGATTCAGAAGGACTTGAA
NM_016123	51135	IRAK4	interleukin-1 receptor-associated kinase 4	ATCCTATTAGTCATATATTTA	TTGCAGGACAGTGGTTATTAA
NM_016151	9344	TAO1	thousand and one amino acid protein kinase	AACGGAAACCACCGCTCTTTA	ATCGAGCTGGCTGAACGGAAA
NM_016203	51422	PRKAG2	protein kinase, AMP-activated, gamma 2 non-catalytic subunit	AAGCACGAGCCTGAACGGTTA	CCGGAAAGCATTCCTCTCGAA
NM_016223	29763	PACSIN3	protein kinase C and casein kinase substrate in neurons 3	AAGGATATGCTGCTCACCTTA	CAGAGGACAATCAGCCGGAAA
NM_016231	51701	NLK	nemo like kinase	CCGGATAGACCTATTGGATAT	TTGGTGTTGTCTGGTCAGTAA
NM_016248	11215	AKAP11	A kinase (PRKA) anchor protein 11	ACCGGTTATCTAAATCTATTA	CTGACCGGTTATCTAAATCTA
NM_016276	10110	SGK2	serum/glucocorticoid regulated kinase 2	CAGGGCCAATGGGAACATCAA	TGGGTACGTGACTATCCCTAA
NM_016281	51347	JIK	STE20-like kinase	CAAACAGTATAAAGCACTCAA	CAGCTCCTCCGTCGTGCATAA
NM_016282	50808	AK3L1	adenylate kinase 3 like 1	CCCGTGGCACTATGTAAATAA	CCGTGGCACTATGTAAATAAA
NM_016291	51447	IHPK2	inositol hexaphosphate kinase 2	AAGCATCGGAACCAGTACAAA	TCGGAACCAGTACAAATTTAT
NM_016308	51727	UMP-CMP	UMP-CMP kinase	AAGTATTGCTAAGTACTATAA	CGCGTATATATCCCTCTAGTA
NM_016440	51231	VRK3	vaccinia related kinase 3	AACCAGGGCATTCTCTATGAA	CTCACTCAAACTGGATGCCAA
NM_016457	25865	PRKD2	protein kinase D2	CACGACCAACAGATACTATAA	TTGGGTGGTTCATTACAGCAA
NM_016478	51530	NIPA	nuclear interacting partner of anaplastic lymphoma kinase (ALK)	AGGGAGAATGGTGGAACTGAA	CCGCTTGAGGCTCTCTATGAA
NM_016507	51755	CRK7	CDC2-related protein kinase 7	ACCGGATATCGGGAAGTTCAA	ATCGGGATATTAAGTGTTCTA
NM_016508	51265	CDKL3	cyclin-dependent kinase-like 3	CAACATTATTGTCATGGACTA	TGGGCAGATAGTGGCCATTAA
NM_016542	51765	MST4	Mst3 and SOK1-related kinase	CAGCAAGTCGTTGCTATTAAA	CCAAACCTACGTCAAGATTAA
NM_016653	51776	ZAK	sterile alpha motif and leucine zipper containing kinase AZK	ACGTGGTAGTATATCACTCAA	TCGGGTAGCAACAAACTTATT
NM_017431	53632	PRKAG3	protein kinase, AMP-activated, gamma 3 non-catalytic subunit	CAGATCTATGAGATTGAACAA	TAGCCTGTTTGAAGCTGTCTA
NM_017449	2048	EPHB2	EphB2	CACGCTTTCTAGAGGACGATA	CCGAGAGGACCTCGTCTACAA
NM_017567	55577	NAGK	N-acetylglucosamine kinase	ACCTGAGTGAAAGCTACTTAA	CCCGGTCTTGTTCCAGGGCAA
NM_017572	2872	MKNK2	MAP kinase-interacting serine/threonine kinase 2	CCGCTTCTACCTGGTGTTTGA	TTGGACTTTCTGCATAACAAA
NM_017593	55589	BMP2K	BMP2 inducible kinase	AGGCATCACCTGAATATCTTA	TCCGATGTGCATTGAAGCGAA
NM_017719	54861	SNRK	SNF-1 related kinase	ACCACTGAATTGGAACGGATA	CACCACTGAATTGGAACGGAT
NM_017771	54899	PXK	PX domain containing serine/threonine kinase	CTGGCAGATTGTTAGAAGATA	TAAGATCCCTACAAAGTTAAA
NM_017859	54962	URKL1	uridine kinase-like 1	ACCCAGGACTGTTGAATACAA	TACAATGAACACGGCACGCAA
NM_017900	54998	AKIP	aurora-A kinase interacting protein	ATCCGTAGTAATAAATTCTCA	CTGCTGTGATCCGTAGTAATA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_018216	55229	PANK4	pantothenate kinase 4	CTGGGAGACGTTCATATTGGA	TCGACATAGGCGGGTCGTTAA
NM_018323	55300	PI4K2B	phosphatidylinositol 4-kinase type-II beta	ATGAACTTTGTGCAAGATTTA	CAGAGTACTGGCCTTGTTCAA
NM_018339	55312	FLJ11149	riboflavin kinase	ACGATGTAATTTAATGCTAAA	CAGGATGTAATTTAATGCTAA
NM_018343	55781	RIOK2	RIO kinase 2 (yeast)	AACGCGATTATCATAAACATA	CGCGGTTGAAATGGGCATGAA
NM_018401	55351	HSA250839	gene for serine/threonine protein kinase	CTGGGACGCGGTGTTCAAGAA	TTGGGCTGAGTTCACGAATTA
NM_018425	55361	PI4KII	phosphatidylinositol 4-kinase type II	ACGCAAATGTATGAATAAGAA	CCGCATCGGGCTACCACCAAA
NM_018492	55872	TOPK	T-LAK cell-originated protein kinase	AAGTGTGGCTTGCGTAAATAA	TCAGTAGTTATTAGACTCTAA
NM_018571	55437	ALS2CR2	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 2	CAGGAACACTGGTAACTATAA	CCAGTGGAACTCACACAGTAA
NM_018584	55450	CaMKIINalpha	calcium/calmodulin-dependent protein kinase II	AGCAAGCGGGTTGTTATTGAA	CGGGTTGTTATTGAAGATGAT
NM_018638	55500	EKI1	ethanolamine kinase	CCGTATGTCGTGGATTAGAAA	TCCGTATGTGGTGGATTAGAA
NM_018650	4139	MARK1	MAP/microtubule affinity-regulating kinase 1	CCCGGTGTAGAAACTCCATTA	CCGGCCCAGTAGTGACTTAAA
NM_018842	55971	LOC55971	insulin receptor tyrosine kinase substrate	CACCGAGAGCACCTACCGGAA	CTCAACGAGAGTCTTGATGAA
NM_018979	65125	PRKWNK1	protein kinase, lysine deficient 1	CTAGAGGATCTTGATGCTCAA	CTGCGACGACTACGAGATAAA
NM_019884	2931	GSK3A	glycogen synthase kinase 3 alpha	CAGGGAACTAGTCGCCATCAA	CCGGGTGTAAATAGATTGTTA
NM_020126	56848	SPHK2	sphingosine kinase 2	CAGGATTGCGCTCGCTTTCAT	CCGAGGGTAGTGCCTGATCAA
NM_020168	56924	PAK6	p21(CDKN1A)-activated kinase 6	CGGAAGGACCATGTTCCGCAA	CTGTGTTACCTTTCAAGTTTA
NM_020240	56990	SPEC2	non-kinase Cdc42 effector protein SPEC2	AAGGGAGGTTATGGAGGTGGA	CAGGAGACCTGTTCAGTGGAA
NM_020397	57118	CAMK1D	calcium/calmodulin-dependent protein kinase ID	CAGGCGCTTTCTATACTTAAT	CCAGGCGCTTTCTATACTTAA
NM_020421	57143	ADCK1	aarF domain containing kinase 1	TAACAAGTACTTGGACCCTAA	TACGACGGCTGTCATCAGTTA
NM_020439	57172	CAMK1G	calcium/calmodulin-dependent protein kinase IG	AACAGGCCGCCTGAAACTCAA	CAGGTCTTGTCGGCAGTGAAA
NM_020526	2046	EPHA8	EphA8	ACGGCCCACCAGGGTATGTAA	GAGCGTGTGCTTATCCGTTAA
NM_020639	54101	ANKRD3	ankyrin repeat domain 3	AAGCCTGATGACGAAGTGAAA	CACACGCAGTATGAAGATAAA
NM_020666	57396	CLK4	CDC-like kinase 4	AAGTCTGACTATGTAGTCAAA	TCGAAGAATGTTAGAATATGA
NM_020804	29993	PACSIN1	protein kinase C and casein kinase substrate in neurons 1	CAGCAGCTACATCCATGTGTA	CGCCATAGAGTTCCAGACATA
NM_020836	57596	KIAA1446	brain-enriched guanylate kinase-associated protein	CGGGCGGACCATGTCACCGTA	CTGCAGCTTCTCTGAACGCTA
NM_020922	65267	PRKWNK3	protein kinase, lysine deficient 3	AAGATTGGTGATCTAGGATTA	CCGGGTGACGCCAATAAAGAA
NM_020965	260425	MAGI-3	membrane-associated guanylate kinase-related (MAGI-3)	CCCTATGATGTTGTCTTGCAA	CGGGATGTCGAAGACGCTGAA
NM_020975	5979	RET	ret proto-oncogene (multiple endocrine neoplasia and medullary thyroid carcinoma 1, Hirschsprung disease)	CCGCTGGTGGACTGTAATAAT	TAGGCTGGTTCTCAACCGGAA
NM_020990	1159	CKMT1	creatine kinase, mitochondrial 1 (ubiquitous)	ACGGATCTAGATGCCAGTAAA	CTGGACGTTACTATAGGCTCA
NM_021135	6196	RPS6KA2	ribosomal protein S6 kinase, 90kDa, polypeptide 2	CCGAGTGAGATCGAAGATGGA	CCGGAGGTCCTGAAGCGTCAA
NM_021733	60385	TSKS	testis-specific kinase substrate	AACCAACGTCTTGAAGCAGAA	CACCAACGTGTCACTGCTCAA
NM_021970	8649	MAP2K1IP1	mitogen-activated protein kinase kinase 1 interacting protein 1	ATGCCCAGGCTTGCAGAATAA	TAGCATATAGATGTAATTTAT
NM_021972	8877	SPHK1	sphingosine kinase 1	CACGAACCAAATCCAAATAAA	CCGGCTGCTGTCACCCATGAA
NM_022048	53944	CSNK1G1	casein kinase 1, gamma 1	ATGGACCATCCTAGTAGGGAA	CCGGCAGACCAATACCTCATA
NM_022128	64080	RBKS	ribokinase	AACACAGTCATCTTACCCTTA	CAGGTGGTAATCATTACCTTA
NM_022158	64122	FN3K	fructosamine-3-kinase	CCAGCTGTTTAACTACCTGAA	CCCAGTGTTCGTCAAAGTCAA
NM_022344	64149	NJMU-R1	protein kinase Njmu-R1	TTGAGTTACACTCCTGTTGAA	TTGGCAGATACTAATCTACCA
NM_022445	27010	TPK1	thiamin pyrophosphokinase 1	AACCTGGTGCATCGAAATGTA	CAGGTTGTCTGTAGAGAATGA
NM_022731	64710	NUCKS	nuclear ubiquitous casein kinase and cyclin-dependent kinase substrate	AAGGTGTACCACGGTTGTAAA	ACCCTAGAATTTAATCAACAA
NM_022740	28996	HIPK2	homeodomain interacting protein kinase 2	AACCAGTACCCTTACATATAA	TCCCGAAGTCTCCATACTAAA
NM_023018	65220	FLJ13052	NAD kinase	AAAGAGCGTCCTTGTCATCAA	CCAGGAGAACATGATCGTGTA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_024117	79109	MAPKAP1	mitogen-activated protein kinase associated protein 1	CTAGGTATCTCTGGAGACAAA	GACCCTGTTACGAATCAGAAA
NM_024594	79646	PANK3	pantothenate kinase 3	AAGCGAGAATCTGTTAGTAAA	TCCAAAGGTGATAGCACACAA
NM_024779	79837	PIP5K2C	phosphatidylinositol-4-phosphate 5-kinase, type II, gamma	CCGGAGCAGTATGCTAAGCGA	TTGATGTGTGATAATCTCATA
NM_024800	79858	NEK11	NIMA (never in mitosis gene a)- related kinase 11	CTGCCTATGCTTGGAGTCATA	TGAGATAAGCTTATAGATCAA
NM_024876	79934	ADCK4	aarF domain containing kinase 4	CAGATGCTGAGAGTTCTTGAA	CCGGGTCCCAGCCGTGGTTAA
NM_024960	80025	PANK2	pantothenate kinase 2 (Hallervorden-Spatz syndrome)	CAGAGCGACTTTGATCACCAT	CTGTGTGTGAACTTACTGTAA
NM_025144	80216	LAK	lymphocyte alpha-kinase	CAGCCCTTGGTCCTATGTGAA	CAGGCCCTACATTTAAAGCTA
NM_025194	80271	ITPKC	inositol 1,4,5-trisphosphate 3-kinase C	CCGGAAGGACATGTATGAGAA	TCGGCCGAAGCCCGAACCGAA
NM_025211	80318	GKAP42	protein kinase anchoring protein GKAP42	AACGCTCAACATGATCTTCCA	CATGCTGTTTGTAACGCTCAA
NM_025228	80342	TJAM	TRAF3-interacting Jun N-terminal kinase (JNK)-activating modulator	CAGACTTGCCACCAACATTAA	TAGCAGGGACTTACAGATGAA
NM_030662	5605	MAP2K2	mitogen-activated protein kinase kinase 2	CAGCATTTGCATGGAACACAT	CCGGCCTGCCATGGCCATCTT
NM_030906	65975	STK33	serine/threonine kinase 33	ATGTGTCTAGTGCATCCTTAA	CAGGATGGTAATAGGTTAAGA
NM_030952	81788	SNARK	likely ortholog of rat SNF1/AMP-activated protein kinase	CGGGTGGCTGTTGATGGTGAA	CTGAACGAAGAGGATACTAAA
NM_031414	56164	STK31	serine/threonine kinase 31	CACAGTACAAGCTAAGTACAA	CCCAGTGTGGATCACTTGCTA
NM_031417	57787	MARK4	MAP/microtubule affinity-regulating kinase 4	CCGCATCATGAAGGGCCTAAA	CTGCAGCCTGTTGCCCAATAA
NM_031432	83549	UCK1	uridine-cytidine kinase 1	AACGGTGGAGGTGCCGACCTA	TGCGGTTTAAAGATCCCTCTA
NM_031464	83694	RPS6KL1	ribosomal protein S6 kinase-like 1	CGCGATGTTAGTGAGGACTAT	CTGAATTTGATTGGAAAGGAA
NM_031480	83732	RIOK1	RIO kinase 1 (yeast)	GCCCAACAAGATAATATTCTA	TACCATGTCCAGAACCAATAA
NM_031892	30011	SH3KBP1	SH3-domain kinase binding protein 1	CTCTGAGATCTCAATGCGAAA	TAGCTTATATATGACGGTATA
NM_032017	83931	MGC4796	Ser/Thr-like kinase	CAGCGCTACCTGCGGAAATAA	CCGGATGGTTAAGAAGATGAA
NM_032028	83942	STK22D	serine/threonine kinase 22D (spermiogenesis associated)	CCAGCTTTCCTTGGCCATCAA	TAGAAGCTGATTTAACACCAA
NM_032037	83963	SSTK	serine/threonine protein kinase SSTK	ATCGAGGTGTGCAACGGGAAA	CCGGTTGGAACCTGCAATAAA
NM_032294	84254	CAMKK1.	calcium/calmodulin-dependent protein kinase kinase 1, alpha	AGCGATGAGCAAACTCTATAA	CGGCGTTATCTGGAAAGTGGA
NM_032387	65266	PRKWNK4	protein kinase, lysine deficient 4	CAGCTTGTTGGGCGTTTCCAA	CAGGAGGAGCCAGCACCATTA
NM_032409	65018	PINK1	PTEN induced putative kinase 1	CCGGACGCTGTTCCTCGTTAT	GACGCTGTTCCTCGTTATGAA
NM_032435	84451	KIAA1804	mixed lineage kinase 4	ACGGACCATGTCTGATGGAAA	CGGGAACTTAACATTCTGATA
NM_032630	51550	CINP	cyclin-dependent kinase 2-interacting protein	CGGCTGATTGGCACAATTTAA	GCGGCTGATTGGCACAATTTA
NM_033116	91754	NEK9	NIMA (never in mitosis gene a)- related kinase 9	CACGAACCAGTGAAGTCTATA	TACACTTGGGTGAACATGCAA
NM_033118	85366	MYLK2	myosin light chain kinase 2, skeletal muscle	AACGCTGTAACCGACGCCTTA	CGGGATCCTCTTCATGCACAA
NM_033126	85481	PSKH2	serine/threonine kinase PSKH2	AAGGACTTTATAGACAAACTA	GAGGATCAAGTTTACATGGTA
NM_033214	2712	GK2	glycerol kinase 2	CTCGGGTGTGCCATAATAATA	TACGTTAGAAGAGCACTGTAA
XM_370946	10595	LOC388226	similar to protein kinase/ribonuclease IRE1 beta	AAGGATGAAACTGGCTTCTAT	CACCTGCATTCTTTACACATA
NM_033498	3098	HK1	hexokinase 1	CACGATGTAGTCACCTTACTA	CCGTGTCGTATGACCTAGTAA
NM_033516	89882	NYD-SP25	protein kinase NYD-SP25	ATGGACCTAACTATACATCTT	TAGACGAAATGTGCCATTATA
NM_052841	81629	STK22C	serine/threonine kinase 22C (spermiogenesis associated)	ATGGCAAGTGCTCTCCAATAA	TGGCAAGTGCTCTCCAATAAA
NM_052853	90956	ADCK2	aarF domain containing kinase 2	CAGATTGACCTGCGTTACGAA	CCGGAATGTGAAAGCCGTCAA
NM_052902	114790	STK11IP	serine/threonine kinase 11 interacting protein	AAAGTTGTTTCCAACTCATAA	CTCTGCGTTTCTTGAACCTAA
NM_052947	115701	HAK	heart alpha-kinase	AGCGAAGACCTTGGCATTTAT	CGGCCTCATGCCTGTCTTCAA
NM_053006	23617	STK22B	serine/threonine kinase 22B (spermiogenesis associated)	CAAGTTCAATGTGGCTGTCAA	GTCGGCCTTCACGTAAACTAA
NM_054111	117283	IPPK	inositol hexaphosphate kinase 3	AAGACTGGTGGACAAGTGTAA	CTGAGATACGTTACCCAATTA
NM_054113	117286	CIB3	calcium and integrin binding family member 3	CACGAGCAGCTGGAAGCGTAT	CTGGAGCAGACGGTGACCAAA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_080823	6725	SRMS	src-related kinase lacking C-terminal regulatory tyrosine and N-terminal myristylation sites	CAGACCAACCCTGGTACTTTA	CCGGGTGTCCATGGCAGCTGA
NM_080836	140901	STK35	serine/threonine kinase 35	CTCGGCTGTTAGGGATCTGAA	TTGGGTTGGTATGATACATTA
NM_133494	140609	NEK7	NIMA (never in mitosis gene a)-related kinase 7	ACGACCGGATATGGGCTATAA	CCGGATATGGGCTATAATACA
NM_138316	53354	PANK1	pantothenate kinase 1	AACGCTGGTTAAATTGGTGTA	CCGAAGGATATTACAGCCGAA
NM_138733	5232	PGK2	phosphoglycerate kinase 2	CAGCAACATGTAGTTAATATA	CAGGCCATCAGGAACTCTTAA
NM_139021	225689	ERK8	extracellular signal-regulated kinase 8	CCCACTGACTTCCTCCAATAA	CCCAGAGAACATTCCGGGAAA
NM_139158	65061	ALS2CR7	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 7	CTGGACATAAACTAAGTCTAA	CTGGCGTACATCCACCACCAA
NM_139209	131890	GRK7	G protein-coupled receptor kinase 7	ATCCATGACATCTGTGAATTA	TCGGCTGACATAATCCTCGAA
NM_145040	112464	PRKCDBP	protein kinase C, delta binding protein	AAGGAGCGAATCCTACATCCA	CACGCCCTAATAAGGAGCGAA
NM_145059	197258	FUK	fucokinase	CCGAAGGCAGTTGATTGGACA	TGGCTTAGAGTTGTAGACTTA
NM_145203	122011	MGC33182	casein kinase I alpha S-like	CAAGAATAATGTGAAAGATAA	CAGATTATCTTTAGAATTCCA
BC005365	5609	MAP2K7	mitogen-activated protein kinase kinase 7	ATGGATCTCTCTCAACAACTA	CCGGCGGAGGATCGACCTCAA
NM_145695	1607	DGKB	diacylglycerol kinase, beta 90kDa	CCCGAACTACTTCTCCTGCAA	CTCATTCTAGTCCAATGGTAA
NM_152309	118788	PIK3AP1	phosphoinositide-3-kinase adaptor protein 1	ATGCTCAAGAGTCACATTAAA	CAGCAGGGTATTTAAGTGCTA
NM_152327	122481	AK7	adenylate kinase 7	CAAGATTGTCTTGACCATTTA	GACGATCAATATATAATTAGA
NM_152671	200576	PIP5K3	na	ACCCAGTAACATAATATTTCA	TTGCCGTTACCCAGTAACATA
NM_152720	4752	NEK3	NIMA (never in mitosis gene a)-related kinase 3	ACGATAGAGGTGGTTCTGTAA	CAGAGATATCAAGTCCAAGAA
NM_152835	149420	LOC149420	casein kinase	AAGCTAGACTCTACCCTCTAA	CAGCCAAAGTACGATCTAATA
NM_152883	5754	PTK7	PTK7 protein tyrosine kinase 7	ACGGTTCGAGGTCTTCAAGAA	ATGGGACATGGTACCGTTGTA
NM_153273	9807	IHPK1	inositol hexaphosphate kinase 1	AAGGTGGATGTCCGCATGATT	CCGGCAGATGCGGAAATGCGA
NM_153335	92335	LYK5	protein kinase LYK5	CACCCAGATGCTGCTAGAGAA	CTGGTTCTAGTTCTGGTTCTA
NM_172173	818	CAMK2G	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma	CCGATGAGAAACCTCGTGTTA	GAGGAAGAGATCTATACCCTA
NM_173176	2185	PTK2B	PTK2B protein tyrosine kinase 2 beta	AAGCTGATCGGCATCATTGAA	CAGGAGAACTTAAAGCCCAAA
NM_173354	150094	SNF1LK	SNF1-like kinase	AGCGAAATAAGCAATACGTTA	CACAATTGATTCCAACACAAA
NM_173600	146057	TTBK2	tau tubulin kinase 2	ACGGCCCAGGTTAAATGGAAA	CACATTGGTCATGACATGTTA
NM_173515	154043	MAGI1	membrane associated guanylate kinase, interacting protein-like 1	CCGGAGTTGTGTTACTGCTTA	CGGAGTTGTGTTACTGCTTAA
NM_173575	282974	PKE	PKE protein kinase	CCGGGCTTCGTGCCCAACAAA	TCCGAGAATGACTATCTTCAA
NM_173598	283455	KSR2	kinase suppressor of Ras-2	ATCCGGTGACCTCGAATCCAA	TCCGTTGTGAGGGATGCCAAA
NM_174858	26289	AK5	adenylate kinase 5	CAGAGCTAGTCAGTACATGAA	CAGCATGGCAGTTGACAACAA
NM_174922	203054	ADCK5	aarF domain containing kinase 5	AAGGCCTTTGCTGAGCAGATA	CCGCTACTTCCTTATGGCTAA
NM_175866	127933	KIS	kinase interacting with leukemia-associated gene (stathmin)	AAGCAGTACTGTAGTACTGAA	CCACATATGAATGCAGGACTA
NM_176799	80895	ILKAP	integrin-linked kinase-associated serine/threonine phosphatase 2C	ATGGAGGAATTCGAGCCTCAA	TTCGGTGATCTTTGGTCTGAA
NM_176800	8899	PRPF4B	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	GAGCCGATCCTTAGAAAGAAA	TCGTCTGATGATAACCTTGAA
NM_177560	1457	CSNK2A1	casein kinase 2, alpha 1 polypeptide	ACCGTTGCTTGTGGATTTATA	CTGGTCGCTTACATCACTTTA
NM_177990	57144	PAK7	p21(CDKN1A)-activated kinase 7	ATGATCTGGATCCGTATTATA	ATGGTGTGCACGTTTCATTAA
NM_178009	160851	DGKH	diacylglycerol kinase, eta	CAGGTGGAGTATAATGACATA	CCGGATCTAGATTCCGTAGAT
NM_178170	284086	NEK8	NIMA (never in mitosis gene a)- related kinase 8	ACGGACAGTTGGGCACCAATA	CCAGAAGCTGGTGATCATCAA
NM_178432	23552	CCRK	cell cycle related kinase	AAGGAGAAGTGCAGAGAGTAA	TGGCGAGATAGTTGCCCTCAA
NM_178510	255239	ANKK1	ankyrin repeat and kinase domain containing 1	AGGAGCCGAGATGGAAATTTA	GCGGACGGAGTACGCCATCAA
NM_178813	158798	AKAP28	A-kinase anchoring protein 28	CCCATTGTCGTTTCTTATGTA	TACGAGGATGAATTGACTCAA
NM_181358	204851	HIPK1	homeodomain interacting protein kinase 1	AGGGAAGCTGTACACCACTAA	CTGAGCTATGTTTGTAATGCA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_181504	5295	PIK3R1	phosphoinositide-3-kinase, regulatory subunit, polypeptide 1 (p85 alpha)	CAGCATTAAACCAGACCTTAT	TAGCTGGTTATGAACTAGTAA
NM_181690	10000	AKT3	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	AACTGTTGGCTTTGGATTAAA	CAGCAGGCACGTTAACTCGAA
NM_181795	5570	PKIB	protein kinase (cAMP-dependent, catalytic) inhibitor beta	CAGCATGTGTATATTAGATAA	CCGGAATGCCTTACCAGACAT
NM_181805	11142	PKIG	protein kinase (cAMP-dependent, catalytic) inhibitor gamma	CCACAAGATGTTATTTATTGA	GAGCTCCATGTCCCAGATAAA
NM_181839	5569	PKIA	protein kinase (cAMP-dependent, catalytic) inhibitor alpha	ATGATTATCATTAGAAGCTAA	TCACTTGATCATATGACGAAA
NM_181871	5313	PKLR	pyruvate kinase, liver and RBC	CGGGTGCAATTTGGCATTGAA	GAGGCCTATCTGAGACTATAA
NM_182398	9252	RPS6KA5	ribosomal protein S6 kinase, 90kDa, polypeptide 5	AAGCCAGTCATTCGACATGAA	CTGGATCTCTTACGTAATTCA
NM_182471	5315	PKM2	pyruvate kinase, muscle	AACATCAAGATTATCAGCAAA	CCCGATCAGTGGAGACGTTGA
NM_182493	91807	LOC91807	myosin light chain kinase (MLCK)	ACGGAGGACAATGACCTTGCA	GACCATGAATTTCATTGTAAA
NM_182661	64781	CERK	ceramide kinase	ATGGCATTATTTGATCTGAAA	CGGCTTAAACTTTGATCTGTA
NM_182687	9088	PKMYT1	membrane-associated tyrosine- and threonine-specific cdc2-inhibitory kinase	CCGGCCAGAGTCCTTCTTCCA	CTGGGAGGAACTTACCGTCTA
NM_182692	6733	SRPK2	SFRS protein kinase 2	AACGGTGACTCTCATTCTTTA	CCGGTATCATGTTATTAGAAA
NM_182925	2324	FLT4	fms-related tyrosine kinase 4	CACCGTGTGGGCTGAGTTTAA	CACGCTCTTGGTCAACAGGAA
NM_182948	5567	PRKACB	protein kinase, cAMP-dependent, catalytic, beta	CAGCCTGTGTAGTGTGACAAA	CTGACCAATCAAGTACACTAA
NM_182982	2868	GRK4	G protein-coupled receptor kinase 4	CAGGATGTTACTCACCAAGAA	CCGGGTGTTTCAAAGACATCA
NM_183048	23613	PRKCBP1	protein kinase C binding protein 1	AGCGAACTTGTCATAGATTTA	CACCATTGAACAGTTATCCTA
NM_197972	29922	NME7	non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinase)	CCCGGCATTTACGCCCTGGAA	TTCATGTAGATCACCAGTCAA
NM_198452	139728	MGC45419	Similar to calcium/calmodulin-dependent protein kinase 1, beta	CTCGAAGATCATGGTCTCTGA	TCCGTGTGTCACAGCCCGAAA
NM_198828	375449	LOC375449	similar to microtubule associated testis specific serine/threonine protein kinase	ATGAATTGCCACCACATTAAA	GAGGAGCTTGACCACATATTA
XM_027237	4293	MAP3K9	mitogen-activated protein kinase kinase kinase 9	AGCGATGAAATTGTCGTGTAT	CAGCGATGAAATTGTCGTGTA
XM_031706	23005	MAPKBP1	likely ortholog of mouse mitogen activated protein kinase binding proten 1	CAGGACCGAAATATTCGGATA	CCCGTTTGTACTGATGTATGA
NM_001556	3551	IKBKB	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta	CAGACCGACATTGTGGACTTA	CAGGACACTGTGAGGGAACAA
XM_039796	23043	TNIK	TRAF2 and NCK interacting kinase	AAGGACCATATTGATAGAACA	CTGGAATATAAGCGCAAACAA
XM_042066	4214	MAP3K1	mitogen-activated protein kinase kinase kinase 1	CACGCATGTCAAATTCTCATA	CTCCGGGTGTTTCAACTAGAA
XM_051221	80309	SKIP	SPHK1 (sphingosine kinase type 1) interacting protein	CTGAAATTCTGGACACCTTAA	GGCAAGTATGCTACAAATTTA
XM_166453	84630	TTBK1	tau tubulin kinase 1	CAGGAACGAGAAGTTTAACTA	TGGCAGGAACGAGAAGTTTAA
XM_290516	55561	HSMDPKIN	myotonic dystrophy protein kinase like protein	CGCCGGTGGCTTTGCACTCTA	CTCGCCGCCTACCAACTTCAA
XM_290793	8844	KSR	kinase suppressor of ras	AAGGGCGAAGCTGGTCCGTTA	CTGGAAGTCAGCTGACATTAA
NM_012224	4750	NEK1	NIMA (never in mitosis gene a)-related kinase 1	ACCGTAGGAGATGTTCGTCAA	TAGGGATAGACCATCAGTCAA

Table3

Pool No.	Accession #	LocusLink	Symbol	Gene Name
1	NM_005734	10114	HIPK3	homeodomain interacting protein kinase 3
	NM_181358	204851	HIPK1	homeodomain interacting protein kinase 1
2	NM_000269	4830	NME1	non-metastatic cells 1, protein (NM23A) expressed in
	NM_002512	4831	NME2	non-metastatic cells 2, protein (NM23B) expressed in
	NM_002513	4832	NME3	non-metastatic cells 3, protein expressed in
	NM_003551	8382	NME5	non-metastatic cells 5, protein expressed in (nucleoside-diphosphate kinase)
	NM_005009	4833	NME4	non-metastatic cells 4, protein expressed in
	NM_005793	10201	NME6	non-metastatic cells 6, protein expressed in (nucleoside-diphosphate kinase)
	NM_197972	29922	NME7	non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinase)
3	NM_000291	5230	PGK1	phosphoglycerate kinase 1
	NM_138733	5232	PGK2	phosphoglycerate kinase 2
4	NM_182471	5315	PKM2	pyruvate kinase, muscle
	NM_181871	5313	PKLR	pyruvate kinase, liver and RBC
5	NM_018323	55300	PI4K2B	phosphatidylinositol 4-kinase type-II beta
	NM_018425	55361	PI4KII	phosphatidylinositol 4-kinase type II
6	NM_000289	5213	PFKM	phosphofructokinase, muscle
	NM_002626	5211	PFKL	phosphofructokinase, liver
	NM_002627	5214	PFKP	phosphofructokinase, platelet
7	NM_002733	5571	PRKAG1	protein kinase, AMP-activated, gamma 1 non-catalytic subunit
	NM_016203	51422	PRKAG2	protein kinase, AMP-activated, gamma 2 non-catalytic subunit
	NM_017431	53632	PRKAG3	protein kinase, AMP-activated, gamma 3 non-catalytic subunit
8	NM_025144	80216	LAK	lymphocyte alpha-kinase
	NM_052947	115701	HAK	heart alpha-kinase
9	NM_000189	3099	HK2	hexokinase 2
	NM_002115	3101	HK3	hexokinase 3 (white cell)
	NM_033498	3098	HK1	hexokinase 1
10	NM_002742	5587	PRKCM	protein kinase C, mu

Table3 (continued)

	NM_005813	23683	PRKCN	protein kinase C, nu
	NM_016457	25865	PRKD2	protein kinase D2
11	NM_002648	5292	PIM1	pim-1 oncogene
	NM_006875	11040	PIM2	pim-2 oncogene
12	NM_003936	8941	CDK5R2	cyclin-dependent kinase 5, regulatory subunit 2 (p39)
	NM_003885	8851	CDK5R1	cyclin-dependent kinase 5, regulatory subunit 1 (p35)
13	NM_013410	205	AK3	adenylate kinase 3
	NM_016282	50808	AK3L1	adenylate kinase 3 like 1
14	NM_000476	203	AK1	adenylate kinase 1
	NM_174858	26289	AK5	adenylate kinase 5
15	NM_004721	9175	MAP3K13	mitogen-activated protein kinase kinase kinase 13
	NM_006301	7786	MAP3K12	mitogen-activated protein kinase kinase kinase 12
16	NM_173598	283455	KSR2	kinase suppressor of Ras-2
	XM_290793	8844	KSR	kinase suppressor of ras
17	NM_002314	3984	LIMK1	LIM domain kinase 1
	NM_005569	3985	LIMK2	LIM domain kinase 2
18	NM_000142	2261	FGFR3	fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)
	NM_015850	2260	FGFR1	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndron
19	NM_004438	2043	EPHA4	EphA4
	NM_005233	2042	EPHA3	EphA3
	NM_020526	2046	EPHA8	EphA8
20	NM_004441	2047	EPHB1	EphB1
	NM_004443	2049	EPHB3	EphB3
	NM_017449	2048	EPHB2	EphB2
21	NM_002645	5286	PIK3C2A	phosphoinositide-3-kinase, class 2, alpha polypeptide
	NM_002646	5287	PIK3C2B	phosphoinositide-3-kinase, class 2, beta polypeptide
	NM_004570	5288	PIK3C2G	phosphoinositide-3-kinase, class 2, gamma polypeptide
22	NM_005026	5293	PIK3CD	phosphoinositide-3-kinase, catalytic, delta polypeptide
	NM_006219	5291	PIK3CB	phosphoinositide-3-kinase, catalytic, beta polypeptide
	NM_006218	5290	PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide

Table3 (continued)

23	NM_003629	8503	PIK3R3	phosphoinositide-3-kinase, regulatory subunit, polypeptide 3 (p55, gamma)
	NM_005027	5296	PIK3R2	phosphoinositide-3-kinase, regulatory subunit, polypeptide 2 (p85 beta)
	NM_181504	5295	PIK3R1	phosphoinositide-3-kinase, regulatory subunit, polypeptide 1 (p85 alpha)
24	NM_000167	2710	GK	glycerol kinase
	NM_033214	2712	GK2	glycerol kinase 2
25	NM_012474	7371	UMPK	uridine monophosphate kinase
	NM_017859	54963	URKL1	uridine kinase-like 1
	NM_031432	83549	UCK1	uridine-cytidine kinase 1
26	NM_005399	5565	PRKAB2	protein kinase, AMP-activated, beta 2 non-catalytic subunit
	NM_006253	5564	PRKAB1	protein kinase, AMP-activated, beta 1 non-catalytic subunit
27	NM_020421	57143	ADCK1	aarF domain containing kinase 1
	NM_024876	79934	ADCK4	aarF domain containing kinase 4
	NM_052853	90956	ADCK2	aarF domain containing kinase 2
	NM_174922	203054	ADCK5	aarF domain containing kinase 5
28	NM_000292	5256	PHKA2	phosphorylase kinase, alpha 2 (liver)
	NM_002637	5255	PHKA1	phosphorylase kinase, alpha 1 (muscle)
29	NM_007229	11252	PACSIN2	protein kinase C and casein kinase substrate in neurons 2
	NM_016223	29763	PACSIN3	protein kinase C and casein kinase substrate in neurons 3
	NM_020804	29993	PACSIN1	protein kinase C and casein kinase substrate in neurons 1
30	NM_080836	140901	STK35	serine/threonine kinase 35
	NM_152835	149420	LOC149420	casein kinase
31	NM_001184	545	ATR	ataxia telangiectasia and Rad3 related
	NM_006904	5591	PRKDC	protein kinase, DNA-activated, catalytic polypeptide
32	NM_003648	8527	DGKD	diacylglycerol kinase, delta 130kDa
	NM_178009	160851	DGKH	diacylglycerol kinase, eta
33	NM_001345	1606	DGKA	diacylglycerol kinase, alpha 80kDa
	NM_001346	1608	DGKG	diacylglycerol kinase, gamma 90kDa
	NM_145695	1607	DGKB	diacylglycerol kinase, beta 90kDa
34	NM_001258	1018	CDK3	cyclin-dependent kinase 3
	NM_001786	983	CDC2	cell division cycle 2, G1 to S and G2 to M

Table3 (continued)

35	NM_003583	8445	DYRK2	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2
	NM_003582	8444	DYRK3	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3
	NM_003845	8798	DYRK4	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 4
36	NM_001396	1859	DYRK1A	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A
	NM_004714	9149	DYRK1B	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1B
37	NM_003137	6732	SRPK1	SFRS protein kinase 1
	NM_014370	26576	STK23	serine/threonine kinase 23
	NM_182692	6733	SRPK2	SFRS protein kinase 2
38	NM_004071	1195	CLK1	CDC-like kinase 1
	NM_020666	57396	CLK4	CDC-like kinase 4
39	NM_005906	4117	MAK	male germ cell-associated kinase
	NM_014920	22858	ICK	intestinal cell (MAK-like) kinase
40	NM_002093	2932	GSK3B	glycogen synthase kinase 3 beta
	NM_019884	2931	GSK3A	glycogen synthase kinase 3 alpha
41	NM_001315	1432	MAPK14	mitogen-activated protein kinase 14
	NM_002751	5600	MAPK11	mitogen-activated protein kinase 11
	NM_002969	6300	MAPK12	mitogen-activated protein kinase 12
	NM_002754	5603	MAPK13	mitogen-activated protein kinase 13
42	NM_002752	5601	MAPK9	mitogen-activated protein kinase 9
	NM_002753	5602	MAPK10	mitogen-activated protein kinase 10
	NM_002750	5599	MAPK8	mitogen-activated protein kinase 8
43	NM_002745	5594	MAPK1	mitogen-activated protein kinase 1
	NM_002746	5595	MAPK3	mitogen-activated protein kinase 3
44	NM_003718	8621	CDC2L5	cell division cycle 2-like 5 (cholinesterase-related cell division controller)
	NM_016507	51755	CRK7	CDC2-related protein kinase 7
45	NM_000075	1019	CDK4	cyclin-dependent kinase 4
	NM_001259	1021	CDK6	cyclin-dependent kinase 6
46	NM_001260	1024	CDK8	cyclin-dependent kinase 8
	NM_015076	23097	CDK11	cyclin-dependent kinase (CDC2-like) 11
47	NM_001787	984	CDC2L1	cell division cycle 2-like 1 (PITSLRE proteins)

Table3 (continued)

	NM_003674	8558	CDK10	cyclin-dependent kinase (CDC2-like) 10
48	NM_001825	1160	CKMT2	creatine kinase, mitochondrial 2 (sarcomeric)
	NM_001823	1152	CKB	creatine kinase, brain
	NM_001824	1158	CKM	creatine kinase, muscle
	NM_020990	1159	CKMT1	creatine kinase, mitochondrial 1 (ubiquitous)
49	NM_002736	5577	PRKAR2B	protein kinase, cAMP-dependent, regulatory, type II, beta
	NM_004157	5576	PRKAR2A	protein kinase, cAMP-dependent, regulatory, type II, alpha
50	NM_003384	7443	VRK1	vaccinia related kinase 1
	NM_006296	7444	VRK2	vaccinia related kinase 2
	NM_016440	51231	VRK3	vaccinia related kinase 3
51	NM_001319	1455	CSNK1G2	casein kinase 1, gamma 2
	NM_001893	1453	CSNK1D	casein kinase 1, delta
	NM_001894	1454	CSNK1E	casein kinase 1, epsilon
	NM_001892	1452	CSNK1A1	casein kinase 1, alpha 1
	NM_004384	1456	CSNK1G3	casein kinase 1, gamma 3
	NM_022048	53944	CSNK1G1	casein kinase 1, gamma 1
	NM_145203	122011	MGC33182	casein kinase 1 alpha S-like
52	NM_002610	5163	PDK1	pyruvate dehydrogenase kinase, isoenzyme 1
	NM_002611	5164	PDK2	pyruvate dehydrogenase kinase, isoenzyme 2
	NM_002612	5166	PDK4	pyruvate dehydrogenase kinase, isoenzyme 4
	NM_005391	5165	PDK3	pyruvate dehydrogenase kinase, isoenzyme 3
53	NM_024594	79646	PANK3	pantothenate kinase 3
	NM_024960	80025	PANK2	pantothenate kinase 2 (Hallervorden-Spatz syndrome)
	NM_138316	53354	PANK1	pantothenate kinase 1
54	NM_016291	51447	IHPK2	inositol hexaphosphate kinase 2
	NM_054111	117283	IHPK3	inositol hexaphosphate kinase 3
	NM_153273	9807	IHPK1	inositol hexaphosphate kinase 1
55	NM_002220	3706	ITPKA	inositol 1,4,5-trisphosphate 3-kinase A
	NM_025194	80271	ITPKC	Inositol 1,4,5-trisphosphate 3-kinase C
56	NM_018979	65125	PRKWNK1	protein kinase, lysine deficient 1

Table3 (continued)

	NM_020922	65267	PRKWNK3	protein kinase, lysine deficient 3
	NM_032387	65266	PRKWNK4	protein kinase, lysine deficient 4
57	NM_001433	2081	ERN1	ER to nucleus signalling 1
	XM_370946	10595	LOC388226	similar to protein kinase/ribonuclease IRE1 beta
58	NM_001262	1031	CDKN2C	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)
	NM_001800	1032	CDKN2D	cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)
	NM_004936	1030	CDKN2B	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)
59	NM_020639	54101	ANKRD3	ankyrin repeat domain 3
	NM_178510	255239	ANKK1	ankyrin repeat and kinase domain containing 1
60	NM_001348	1613	DAPK3	death-associated protein kinase 3
	NM_004938	1612	DAPK1	death-associated protein kinase 1
	NM_014326	23604	DAPK2	death-associated protein kinase 2
61	NM_012290	9874	TLK1	tousled-like kinase 1
	NM_006852	11011	TLK2	tousled-like kinase 2
62	NM_004073	1263	PLK3	polo-like kinase 3 (Drosophila)
	NM_005030	5347	PLK1	polo-like kinase 1 (Drosophila)
	NM_006622	10769	PLK2	polo-like kinase 2 (Drosophila)
63	NM_000294	5261	PHKG2	phosphorylase kinase, gamma 2 (testis)
	NM_006213	5260	PHKG1	phosphorylase kinase, gamma 1 (muscle)
64	NM_004226	9262	STK17B	serine/threonine kinase 17b (apoptosis-inducing)
	NM_004760	9263	STK17A	serine/threonine kinase 17a (apoptosis-inducing)
65	NM_033118	85366	MYLK2	myosin light chain kinase 2, skeletal muscle
	NM_182493	91807	LOC91807	myosin light chain kinase (MLCK)
66	NM_003684	8569	MKNK1	MAP kinase-interacting serine/threonine kinase 1
	NM_017572	2872	MKNK2	MAP kinase-interacting serine/threonine kinase 2
67	NM_003668	8550	MAPKAPK5	mitogen-activated protein kinase-activated protein kinase 5
	NM_004635	7867	MAPKAPK3	mitogen-activated protein kinase-activated protein kinase 3
	NM_004759	9261	MAPKAPK2	mitogen-activated protein kinase-activated protein kinase 2
68	NM_001220	816	CAMK2B	calcium/calmodulin-dependent protein kinase (CaM kinase) II beta
	NM_001221	817	CAMK2D	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta

Table3 (continued)

	NM_015981	815	CAMK2A	calcium/calmodulin-dependent protein kinase (CaM kinase) II alpha
	NM_172173	818	CAMK2G	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma
69	NM_006742	5681	PSKH1	protein serine kinase H1
	NM_033126	85481	PSKH2	serine/threonine kinase PSKH2
70	NM_003656	8536	CAMK1	calcium/calmodulin-dependent protein kinase I
	NM_020397	57118	CAMK1D	calcium/calmodulin-dependent protein kinase ID
	NM_020439	57172	CAMK1G	calcium/calmodulin-dependent protein kinase IG
	NM_198452	139728	MGC45419	Similar to calcium/calmodulin-dependent protein kinase 1, beta
71	NM_003565	8408	ULK1	unc-51-like kinase 1 (C. elegans)
	NM_014683	9706	ULK2	unc-51-like kinase 2 (C. elegans)
72	NM_006549	10645	CAMKK2	calcium/calmodulin-dependent protein kinase kinase 2, beta
	NM_032294	84254	CAMKK1	calcium/calmodulin-dependent protein kinase kinase 1, alpha
73	NM_032037	83983	SSTK	serine/threonine protein kinase SSTK
	NM_052841	81629	STK22C	serine/threonine kinase 22C (spermiogenesis associated)
	NM_032028	83942	STK22D	serine/threonine kinase 22D (spermiogenesis associated)
	NM_053006	23617	STK22B	serine/threonine kinase 22B (spermiogenesis associated)
74	NM_003160	6795	AURKC	aurora kinase C
	NM_003600	6790	STK6	serine/threonine kinase 6
	NM_004217	9212	AURKB	aurora kinase B
75	XM_374996	9891	ARK5	AMP-activated protein kinase family member 5
	NM_030952	81788	SNARK	likely ortholog of rat SNF1/AMP-activated protein kinase
76	NM_004954	2011	MARK2	MAP/microtubule affinity-regulating kinase 2
	NM_018650	4139	MARK1	MAP/microtubule affinity-regulating kinase 1
	NM_031417	57787	MARK4	MAP/microtubule affinity-regulating kinase 4
77	NM_006251	5562	PRKAA1	protein kinase, AMP-activated, alpha 1 catalytic subunit
	NM_006252	5563	PRKAA2	protein kinase, AMP-activated, alpha 2 catalytic subunit
78	NM_018401	55351	HSA250839	gene for serine/threonine protein kinase
	NM_173575	282974	PKE	PKE protein kinase
79	NM_004690	9113	LATS1	LATS, large tumor suppressor, homolog 1 (Drosophila)
	NM_014572	26524	LATS2	LATS, large tumor suppressor, homolog 2 (Drosophila)

Table3 (continued)

80	NM_007271	11329	STK38	serine/threonine kinase 38
	NM_015000	23012	STK38L	serine/threonine kinase 38 like
81	NM_006258	5592	PRKG1	protein kinase, cGMP-dependent, type I
	NM_006259	5593	PRKG2	protein kinase, cGMP-dependent, type II
82	AB023190	22983	SAST	syntrophin associated serine/threonine kinase
	NM_015112	23139	MAST2	microtubule associated serine/threonine kinase 2
83	NM_001619	156	ADRBK1	adrenergic, beta, receptor kinase 1
	NM_005160	157	ADRBK2	adrenergic, beta, receptor kinase 2
84	NM_002741	5585	PRKCL1	protein kinase C-like 1
	NM_006256	5586	PRKCL2	protein kinase C-like 2
	NM_013355	29941	pknbeta	protein kinase PKNbeta
85	NM_002744	5590	PRKCZ	protein kinase C, zeta
	NM_002740	5584	PRKCI	protein kinase C, iota
86	NM_002737	5578	PRKCA	protein kinase C, alpha
	NM_002738	5579	PRKCB1	protein kinase C, beta 1
	NM_002739	5582	PRKCG	protein kinase C, gamma
	NM_005400	5581	PRKCE	protein kinase C, epsilon
	NM_006254	5580	PRKCD	protein kinase C, delta
	NM_006255	5583	PRKCH	protein kinase C, eta
	NM_006257	5588	PRKCQ	protein kinase C, theta
87	NM_002730	5566	PRKACA	protein kinase, cAMP-dependent, catalytic, alpha
	NM_002732	5568	PRKACG	protein kinase, cAMP-dependent, catalytic, gamma
	NM_002760	5616	PRKY	protein kinase, Y-linked
	NM_005044	5613	PRKX	protein kinase, X-linked
	NM_182948	5567	PRKACB	protein kinase, cAMP-dependent, catalytic, beta
88	NM_002953	6195	RPS6KA1	ribosomal protein S6 kinase, 90kDa, polypeptide 1
	NM_004586	6197	RPS6KA3	ribosomal protein S6 kinase, 90kDa, polypeptide 3
	NM_014496	27330	RPS6KA6	ribosomal protein S6 kinase, 90kDa, polypeptide 6
	NM_021135	6196	RPS6KA2	ribosomal protein S6 kinase, 90kDa, polypeptide 2
89	NM_001626	208	AKT2	v-akt murine thymoma viral oncogene homolog 2

Table3 (continued)

	NM_005163	207	AKT1	v-akt murine thymoma viral oncogene homolog 1
	NM_181690	10000	AKT3	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)
90	NM_005627	6446	SGK	serum/glucocorticoid regulated kinase
	NM_013257	23678	SGKL	serum/glucocorticoid regulated kinase-like
	NM_016276	10110	SGK2	serum/glucocorticoid regulated kinase 2
91	NM_003161	6198	RPS6KB1	ribosomal protein S6 kinase, 70kDa, polypeptide 1
	NM_003952	6199	RPS6KB2	ribosomal protein S6 kinase, 70kDa, polypeptide 2
92	NM_002082	2870	GRK6	G protein-coupled receptor kinase 6
	NM_005308	2869	GRK5	G protein-coupled receptor kinase 5
	NM_182982	2868	GRK4	G protein-coupled receptor kinase 4
93	NM_003942	8986	RPS6KA4	ribosomal protein S6 kinase, 90kDa, polypeptide 4
	NM_182398	9252	RPS6KA5	ribosomal protein S6 kinase, 90kDa, polypeptide 5
94	NM_002497	4751	NEK2	NIMA (never in mitosis gene a)-related kinase 2
	NM_003157	6787	NEK4	NIMA (never in mitosis gene a)-related kinase 4
	NM_014397	10783	NEK6	NIMA (never in mitosis gene a)-related kinase 6
	NM_024800	79858	NEK11	NIMA (never in mitosis gene a)- related kinase 11
	NM_033116	91754	NEK9	NIMA (never in mitosis gene a)- related kinase 9
	NM_133494	140609	NEK7	NIMA (never in mitosis gene a)-related kinase 7
	NM_152720	4752	NEK3	NIMA (never in mitosis gene a)-related kinase 3
	NM_178170	284086	NEK8	NIMA (never in mitosis gene a)- related kinase 8
	NM_012224	4750	NEK1	NIMA (never in mitosis gene a)-related kinase 1
95	NM_004783	9344	TAO1	thousand and one amino acid protein kinase
	NM_016151	9344	TAO1	thousand and one amino acid protein kinase
	NM_016281	51347	JIK	STE20-like kinase
96	NM_002756	5606	MAP2K3	mitogen-activated protein kinase kinase 3
	NM_002758	5608	MAP2K6	mitogen-activated protein kinase kinase 6
97	NM_002401	4215	MAP3K3	mitogen-activated protein kinase kinase kinase 3
	NM_006609	10746	MAP3K2	mitogen-activated protein kinase kinase kinase 2
98	NM_005109	9943	OSR1	oxidative-stress responsive 1
	NM_013233	27347	STK39	serine threonine kinase 39 (STE20/SPS1 homolog, yeast)

Table3 (continued)

99	NM_003618	8491	MAP4K3	mitogen-activated protein kinase kinase kinase kinase 3
	NM_006575	11183	MAP4K5	mitogen-activated protein kinase kinase kinase kinase 5
100	NM_004834	9448	MAP4K4	mitogen-activated protein kinase kinase kinase kinase 4
	NM_015716	50488	MINK	misshapen/NIK-related kinase
101	NM_002576	5058	PAK1	p21/Cdc42/Rac1-activated kinase 1 (STE20 homolog, yeast)
	NM_002577	5062	PAK2	p21 (CDKN1A)-activated kinase 2
	NM_002578	5063	PAK3	p21 (CDKN1A)-activated kinase 3
	NM_005884	10298	PAK4	p21(CDKN1A)-activated kinase 4
	NM_020168	56924	PAK6	p21(CDKN1A)-activated kinase 6
	NM_177990	57144	PAK7	p21(CDKN1A)-activated kinase 7
102	NM_006281	6788	STK3	serine/threonine kinase 3 (STE20 homolog, yeast)
	NM_006282	6789	STK4	serine/threonine kinase 4
103	NM_006374	10494	STK25	serine/threonine kinase 25 (STE20 homolog, yeast)
	NM_016542	51765	MST4	Mst3 and SOK1-related kinase
104	NM_003607	8476	CDC42BPA	CDC42 binding protein kinase alpha (DMPK-like)
	NM_006035	9578	CDC42BPB	CDC42 binding protein kinase beta (DMPK-like)
105	NM_004850	9475	ROCK2	Rho-associated, coiled-coil containing protein kinase 2
	NM_005406	6093	ROCK1	Rho-associated, coiled-coil containing protein kinase 1
106	NM_001743	805	CALM2	calmodulin 2 (phosphorylase kinase, delta)
	NM_005184	808	CALM3	calmodulin 3 (phosphorylase kinase, delta)
	NM_006888	801	CALM1	calmodulin 1 (phosphorylase kinase, delta)
107	NM_006383	10518	KIP2	DNA-dependent protein kinase catalytic subunit-interacting protein 2
	NM_054113	117286	CIB3	calcium and integrin binding family member 3
108	NM_003559	8396	PIP5K2B	phosphatidylinositol-4-phosphate 5-kinase, type II, beta
	NM_005028	5305	PIP5K2A	phosphatidylinositol-4-phosphate 5-kinase, type II, alpha
	NM_024779	79837	PIP5K2C	phosphatidylinositol-4-phosphate 5-kinase, type II, gamma
109	NM_003557	8394	PIP5K1A	phosphatidylinositol-4-phosphate 5-kinase, type I, alpha
	NM_003558	8395	PIP5K1B	phosphatidylinositol-4-phosphate 5-kinase, type I, beta
	NM_012398	23396	PIP5K1C	phosphatidylinositol-4-phosphate 5-kinase, type I, gamma
110	NM_001616	92	ACVR2	activin A receptor, type II

Table3 (continued)

	NM_001106	93	ACVR2B	activin A receptor, type IIB
111	NM_000020	94	ACVRL1	activin A receptor type II-like 1
	NM_001105	90	ACVR1	activin A receptor, type I
	NM_001203	658	BMPR1B	bone morphogenetic protein receptor, type IB
	NM_004329	657	BMPR1A	bone morphogenetic protein receptor, type IA
	NM_004302	91	ACVR1B	activin A receptor, type IB
	NM_004612	7046	TGFBR1	transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 4
112	NM_002005	2242	FES	feline sarcoma oncogene
	NM_005246	2241	FER	fer (fps/fes related) tyrosine kinase (phosphoprotein NCP94)
113	NM_000061	695	BTK	Bruton agammaglobulinemia tyrosine kinase
	NM_001721	660	BMX	BMX non-receptor tyrosine kinase
	NM_003215	7006	TEC	tec protein tyrosine kinase
	NM_003328	7294	TXK	TXK tyrosine kinase
114	NM_005157	25	ABL1	v-abl Abelson murine leukemia viral oncogene homolog 1
	NM_005158	27	ABL2	v-abl Abelson murine leukemia viral oncogene homolog 2 (arg, Abelson-related g
115	NM_001715	640	BLK	B lymphoid tyrosine kinase
	NM_002110	3055	HCK	hemopoietic cell kinase
	NM_002350	4067	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog
	NM_002037	2534	FYN	FYN oncogene related to SRC, FGR, YES
	NM_005356	3932	LCK	lymphocyte-specific protein tyrosine kinase
	NM_005433	7525	YES1	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1
	NM_005248	2268	FGR	Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog
	NM_005417	6714	SRC	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)
116	NM_002344	4058	LTK	leukocyte tyrosine kinase
	NM_004304	238	ALK	anaplastic lymphoma kinase (Ki-1)

Table 4

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
2	A2M	NM_000014	CTCAAAGATTCGTAAACCCAA	CACCAACTCAAAGATTCGTAA	CACGGAGACCGTACGAAAGTA	ACGGATGAGCATGGCCTTGTA
12	SERPINA3	NM_001085	AAGGTTCTACTTGAGCAAGAA	AAGGCTGTGCTTGATGTATTT	CCCAAGATACTCATCAGTCAA	AAGGACCATTGTGCGTTTCAA
14	AAMP	NM_001087	CAGGGAAGCCCTATCCATGTA	GAGGAAGAGATACTAGTTAAA		
20	ABCA2	NM_001606	CCGCAGAGAGATGGACAAGAT	CTGGGTCAGTCCCGTATTTAT	CAGCATGCCCACCTACCTCAA	CTGGAAGAACGTGACGCTCAA
21	ABCA3	NM_001089	CACGGAGAAATTACATGTGGA	CCAAGTTTATCTCATCCTTTA	TACGTTGTGACCATCCAGAAA	CCGCTTGAAGATTCAGTCGGA
25	ABL1	NM_005157	CTGGGCGAATGTCTTATTTAA	CCAGTGGAGATAACACTCTAA	ACGCACGGACATCACCATGAA	AACACTCTAAGCATAACTAAA
29	ABR	NM_001092	CACGGACGTGATTGAGATGAA	CAGCGAAGAGATCTACATTAA		
30	ACAA1	NM_001607	CACGCTGCTCAATGAGCTGAA	AAGGCCATGGTTAATTCTTAA		
31	ACACA	NM_000664	TCCGTAGGTGGTCTTATGAAA	TCGCATCACAATTGGCAATAA	AACGCAGGCATCAGAAGATTA	CTGGATAATCTGGTCAATGTA
34	ACADM	NM_000016	AAGGAGATGAGTATATTATTA	AAGGTACTTCACAAATTCAAA	CTGGCTGAAATGGCAATGAAA	CAACTTGACAGTAACTTTGTA
38	ACAT1	NM_000019	CGGGCTAACTGATGTCTACAA	CCAGATGTAGTGGTGAAAGAA	AAGCTGAATATTGCACGAAAT	TAGTCTGGTTGTACTAGCAAA
54	ACP5	NM_001611	CACTGGTGTGCAAGACATCAA	ACGGCGCTGCTCATCCTGCAA	CTGGTACGTGCTAGCCGGAAA	CTCGGGCAAGTCCCTCTTTAA
55	ACPP	NM_001099	ATGAACAGGTTTATATTCGAA	CTCTATTACCATTATGGATAA	CCGGACTTTGATGAGTGCTAT	ACAGATGGCGCTAGATGTTTA
56	ACRV1	NM_001612	TCCATAGATCATCAAACTTCA	ATGGAACGAGGATGCAAATTA	CCAGCAGTGCATGTTAAAGAA	CAGGCACAATATTAAATTGCT
72	ACTG2	NM_001615	CCGCTGGAATTCATGAGACAA	CAGGAAGTGCTTCTAAAGTCA		
94	ACVRL1	NM_000020	CCGGGAGACTGAGATCTATAA	CACGGACTGCTTTGAGTCCTA	CAGGAAGACGCTGGAATAAGA	CACCGAGTTCGTCAACCACTA
101	ADAM8	NM_001109	CCGGCTACACAGAGACCTATA	AGGCATCATCGTCTACCGCAA	CAAGCTATATCAGAAACTCAA	CCCAGCTTTGTGTGTGTTTAA
102	ADAM10	NM_001110	ATGGTGTTGCTGAGAGTGTTA	ACCAAACTTCACAGACTGTAA	ATGGTAAGAAGAAGTCCTTAA	ATGGGACACATGAGACGCTAA
112	ADCY6	NM_015270	AAGTGCTTAGGTAATGAGCTA	CAGCCTGAGTCTAGCATGTTT	CAGCCCGGATGCTGAATTTAA	ACCATGTATTTCAGTGAAATA
123	ADFP	NM_001122	AAGAATGTGTATAGTGCCAAT	TCCGTTGCAGTTGATCCACAA	CTGGTTCAGAAGCCAAGTTAT	CTGCAGGATAGACCAGTTAAA
125	ADH1B	NM_000668	AACCAATCCATTACAGCTTAA	AAGCCTCAATTACTAATTGTA	AAGGAGGTAGCTGTCTCCAAA	AAGACCTTAGACATAAAGTAA
126	ADH1C	NM_000669	ATGCATTAATAACAAATATTT	GGGAAATTATTTGTCAAGCAA	CTGCTCTTCAGAGATGTTAAA	ACTGGATGCATTAATAACAAA
131	ADH7	NM_000673	CACCAGTACATTTACCGAGTA	CAGATATAGCGTATAAAGATA	CTGGGAATTAGTATAATAACA	AACGATTAAGAATCATCATTA
132	ADK	NM_001123	TCCACTGATGGAAGAGCTGAA	AAGTTGTACCACAATATTCAA	TAGTTTGATAGTGCCACTTAA	AAGGGTATGGTAATGCTTGTA
133	ADM	NM_001124	AGAGGTAACTATCAATATTTA	ACCGAGTCTCTGTATAATCTA	GAGGTAACTATCAATATTTAA	CTGTATAATCTATTTACATAA
135	ADORA2A	NM_000675	CCACACCAATTCGGTTGTGAA	AAGGGCTTGGGTTCTGAGGAA	CAGGAGTGTCCTGATGATTCA	CAGCATGAGGCCCAGCAAGAA
140	ADORA3	NM_000677	CAACTGCATCATCTACTTTAA	CCCTATCGTCTATGCCTATAA	TCGGAACAAACTCAGTCTGAA	AAGCGTCAACTCGTGCAAGAA
141	ADPRH	NM_001125	CTGGTCTACCTCCTAAATATA	CAGAGTTATGTTTACGAATAA		
142	PARP1	NM_001618	CTTGAAATATGTAGTATTAAA	CCCGGTGGCTGTGGTATGAAT	CCGAGAAATCTCTTACCTCAA	ACGGTGATCGGTAGCAACAAA
147	ADRA1B	NM_000679	GGCGGTCATTCTAGTCATGTA	CAGGAGTTCCATAGCTGTCAA	GAGGGCGGACTCTAAGATGAA	CCGTGTCTATATAGTGGCCAA
150	ADRA2A	NM_000681	CCCGCTGTAAATATACACTAT	GTGGATCAAGACATAAGTAAA	CTCCCGCCGCTTAGAAATAAA	CAAGGCTTGGTGCGAGATCTA
156	ADRBK1	NM_001619	CAGGCCCTTGGTGGAATTCTA	CGGCTGGAGGCTCGCAAGAAA	CGGCTGGAGGCTCGCAAGAAA	CCGGGAGATCTTCGACTCATA
157	ADRBK2	NM_005160	AAGCTACTTGATTGCGACCAA	TGGGATTAACTAATCATTGAA	CAAGTGTATGGGATTAACTAA	AAGATGTTCAGTGTTGGGTAA
166	AES	NM_198970	TAGCTGTGCCTTTCCAATAAA	CGGCTTGAACATCGAGATGCA	CTGACATGTGAGGCAAGCTAA	CAGGCCCACCTCTCCAAGGAA
177	AGER	NM_172197	TAGCTCCTGGTGGAACCGTAA	CACGGCTGGTGTTCCCAATAA	CTGTATAATCTCTCTCCTGTA	AAGGGAGTATCTGTGAAGGAA
181	AGRP	NM_007316	CTGAAGAAGACAACTGCAGAA	CAGCCGCACCTAGCTGGCCAA	AAGCTGGGTACTGCCATGAAT	CAAGCTGGGTACTGCCATGAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
183	AGT	NM_000029	ACCGACCAGCTTGTTTGTGAA	CTGTTTGAATGCGGAACAATA	CTCCGTGTAGTGTCTGTAATA	CAGAGTCTACCCAACAGCTTA
185	AGTR1	NM_000685	ATCCAAGATGATTGTCCCAAA	CTGGATGTATTGATTCAACTA	CGCGGGTTTGATATTTGACAA	ACGCACAATGCTTGTAGCCAA
187	AGTRL1	NM_005161	CACCTGCATCAGCTACGTCAA	CACCATCATGCTGACCTGTTA	CACTGTGGTTCATCAAATAAA	CACCACTAAGGTGCAGTGCTA
189	AGXT	NM_000030	CCGAGTGCACCCGATGACCAA	CTGGAGAGACATCGTCAGCTA	CCAGGATGTACCATCACACAA	CTCCCGGGAATGTTTAATAAA
190	NR0B1	NM_000475	ACGGCAGGGCAGCATCCTCTA	ATGGATGATATGATGCTGGAA	ATCGAACTTAATAGTACCCTT	ATGCTCTGTACAAAGATATAA
197	AHSG	NM_001622	CCAGGGCTGATTTATAGACAA	CTGAAAGACCTTCCTTAATAA	AAGCTTATATGTGCCTGTTAA	CACATGCGATCTACATTAATA
199	AIF1	NM_004847	CCCAGATATCATGTCCCTGAA	CAGAGTCAACAAATTAAATAA	AAGCCAGAGTCAACAAATTAA	CACCTAGCAGTTGGTTGGCAA
207	AKT1	NM_005163	CAGGGTTTACCCAGTGGGACA	AAGGTTTAAATTTGTTATTGT	CACGCTTGGTCCCGAGGCCAA	ACGCTACTTCCTCCTCAAGAA
210	ALAD	NM_000031	CAGGGTATCGGTGATGAGCTA	AAGGGTGAGCCATCAAGCTAA	CCCAAGAACTAGAACTTTAAA	CTCCCAATAATCAACAGCAAA
215	ABCD1	NM_000033	CCGCACCTTCCTGTCGGTGTA	CCACCTCTTTCTACAGCCTAA	CTCGGAGGAGATCGCCTTCTA	CTCTTTCTACAGCCTAATTTA
217	ALDH2	NM_000690	CAGGCATACACTGAAGTGAAA	CACAGTCAAAGTGCCTCAGAA	AAGCTATTGTTTACAATTATA	CAGCCATTGATGGAAAGTTCA
219	ALDH1B1	NM_000692	CTTGGATTACTCAGCCATAAA	TTGAACTAGGTGGATACTAAA	CTCAGAGTTCTACCTATCTAA	CAGCACGTGGATGTTGACAAA
220	ALDH1A3	NM_000693	TTGGGAAAGGATTCACAGTAA	ACCAGTGTGTGTATAACGAAA	AACGGTCTGGATCAACTGCTA	AACCTTGATAGTGATACGTTA
222	ALDH3B2	NM_000695	CTCCGGCCTGGAGAAATTAAA	CACGGCCGTCTCCACCAGAAA	CAGGCCTGGATGAAGGATGAA	CCCACCCTATACCGACTGGAA
225	ABCD2	NM_005164	CAGTGACACATTGGCAATTAA	CAGCATTGATGTCGAAGGAAA	CACTCGAGAATTATAGCCAAT	TCGCCTAGTAGACCACGCCTA
226	ALDOA	NM_000034	CTGTCTCTGCTTCGAGATCAA	TCCGGCACACTGCCAAATAAA	CACGTCAACGATTCTATTTGA	GCCAAATAAACAGCTATTTAA
239	ALOX12	NM_000697	CAAGCCCAAAGCTGTGCTAAA	CCCAAAGCTGTGCTAAACCAA	CTGGCCCTATGAATATCTGAA	CTGGTATGCCTGGGTCCCTAA
248	ALPI	NM_001631	CCGGGCTACGTGTTCAACTCA	CCAGACAATAAAGGGACCAAA	TCCATTCTCCTAGGAGACAAA	CACGTCCATCCTGTACGGCAA
258	AMBN	NM_016519	CACCATCAGATAAGCCACCAA	TACCAGCATGACACTATTATA		
262	AMD1	NM_001634	CGGGAGAAGAGGTTTAATTTA	CTGGGCTTAATATTCTTTAAA	TGGGTTTATATACTAATTCTA	AAGGTGGACCTTGTTGCTAAA
265	AMELX	NM_001142	ATCCCTGAGTTTCAAACAGAA	CAAACAGAAACTTGCACTGAA	TCCCTGAGTTTCAAACAGAAA	CAGGAGTGACACAAGAACACA
268	AMH	NM_000479	CCAATAAAGACCAGCAAGCAA	CCACGTGGTGCTGCTGCTGAA	CAGGCCATCCGCGGAACTCGA	CGCGTGGCTGCTGAACTGCAA
269	AMHR2	NM_020547	CACGACCACATTGTCCGATTT	ATGGCCAATATAAACCAGGTA	CTGGCAGAATGGCCAATATAA	CAGAATGTGCTCATTCGGGAA
270	AMPD1	NM_000036	AACCTGGGCTATCACCTCAAA	CGCCATGTCACCACTAAGTAA	CACCTTCTTAGACGATATGAA	TTGCTGAGGGTCTTAAATCAA
271	AMPD2	NM_004037	CAAGTTTAATGCCAAATACAA	CGGCTTCTCGCACAAGGTAAA	CCGGAACTGCATCTCTTCTTA	CCGGACCAATGTGCCAGACAT
283	ANG	NM_001145	CCGGGATGACAGATACTGTGA	CAGCATCAAGGCCATCTGTGA	CGGGATGACAGATACTGTGAA	AACGTTGTTGTTGCTTGTGAA
287	ANK2	NM_001148	AAGCTTGGTTACACACCTTTA	CAGGACCCTTCTAAACATAAA	ATCAAGCTATTTGCAACTTAA	ACCGTGCAAACGGGTGATATA
288	ANK3	NM_001149	CAGGATTATCACGAAAGATTT	CGCATCCTTAGCTTTACGTAA	AAGGATCTTAACCTCAATTAA	CTAGTCGATTATTTAAGCATA
290	ANPEP	NM_001150	CACCACCTTGGACCAAAGTAA	CCGGGTGAACTACGACGAAGA	AACGATCTCTTCAGCACATCA	CCGAAATGCCACACTGGTCAA
291	SLC25A4	NM_001151	CTGTATCATCAAGATCTTCAA	CAGATCCATTGTGTGGTTTAA	TACAGTGAACTTGATCTACAA	CTGAATGTGAAACATCAATAA
292	SLC25A5	NM_001152	CAGGCATGTTGTATTCTATAA	CGGAAGATTGCTCGTGATGAA	CACAATCTTGAGCATTCTTGA	ATGTTGTATTCTATAACACAA
310	ANXA7	NM_001156	CAGAAATTCTTCGTAAGGCAA	CTGTGTAATAATATTGAATAA		
312	ANXA13	NM_001003954	CAGGCCAAGCTGTGTAAGTTA	CAAGAGCACATTCCAAATCAA		
317	APAF1	NM_001160	TAGGCAGAGTATAAAGTATTA	CAGTGAAGGTATGGAATATTA	CCGCATTCTGATGCTTCGCAA	AAGGGCAATGGAGATAAATTA
320	APBA1	NM_001163	CAGGATCAAGATGGCCCAGAA	CAGGAAGAGAAGAATCCACAA		
324	APC	NM_000038	CAGAGACTAATGAAAGTTCTA	CCGGTGATTGACAGTGTTTCA	TCCATCTAACATCATAATTAA	CAGACTAAGCATTGAGCATAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
327	APEH	NM_001640	CCGCCAATACCTGGTGTTCCA	CAGGAGGAACACTTTGATGCA	CTGGAAGTTGCTCACAATTGA	CAGAGGAATGTGGGCTATGTA
329	BIRC2	NM_001166	CAGGGCTTTAAGTTAGTATTA	TCCCAGGTCCCTCGTATCAAA	TCGAAACTTTATAAAGGGATA	TAGGCGTTTCTGATAACACTA
336	APOA2	NM_001643	ATCAAGAAGGCTGGAACGGAA	CCCACTCTTTGCTACAATAAA	TACAATAAATGCTGAATGAAT	AGGCCAAGTCTTACTTTGAAA
339	APOBEC1	NM_001644	CACCAATCACGTGGAAGTTAA	CACCCTGTTTAAAGATTTCAA		
345	APOC3	NM_000040	AAGACTACTGGAGCACCGTTA	CTGGAGCACCGTTAAGGACAA	CAGGAACAGAGGTGCCATGCA	CCCAATAAAGCTGGACAAGAA
350	APOH	NM_000042	ACACATGGAAATTGGACTAAA	CTGGATGGCCCGGAAGAAATA	CACATGGAAATTGGACTAAAT	CAAGTTGTAAAGCATCTTGTA
351	APP	NM_000484	CTGGTCTTCAATTACCAAGAA	ACCCAATTAAGTCCTACTTTA	CAGACTGAACATGCACATGAA	AAGGATGACTACAGACATTAA
353	APRT	NM_000485	CACACTGAACCCAATTACACA	CTGTGTTTCAGCCACACTGAA	CAGCTGGATCCCAGCGGAAATA	CAGCCACACTGAACCCAATTA
355	FAS	NM_000043	TCAGTGTATGTTAGTACAAAT	CACATTGATTAAAGATCTCAA	CAGAATTTAAATAAGGCTCTA	AAGGACATTACTAGTGACTCA
366	AQP9	NM_020980	CAGCCTCTAATTGGAACGGCA	CAACCAAACCCTAAATTGAAA	AACCGTCTTTGGCATTTACTA	ACGACTGTGCTTGTCCATTAT
367	AR	NM_000044	AAGAAACTTGGTAATCTGAAA	CACGGGAAGTTTAGAGAGCTA	CAGGAATTCCTGTGCATGAAA	AAGGAACTCGATCGTATCATT
368	ABCC6	NM_001171	CTGAGGGAATCCACACTTCAA	ACGGTTGACGTGGACATTCCA	CACCCATTGGTCACCTGCTAA	CACGTGTGCTGTGCTGAGCAA
372	ARCN1	NM_001655	AAGGCAAATTCTTTAATCAAA	CCCACTTGTGTCAATATTAAA		
375	ARF1	NM_001658	AAGCTGGAGCTGTTAAATTTA	CACGATCCTCTACAAGCTTAA		
382	ARF6	NM_001663	CTCAGTATGTTAAACAGGTAA	ATGGTTAACCTCTAACTACAA		
388	RHOB	NM_004040	CCTGCTGATCGTGTTCAGTAA	CCCAGTGGTACTTCTACTAAA	AGCTAAGATGGTGTTATTTAA	CACAATTGTTTCATTGTTTGA
389	RHOC	NM_175744	CAGGAGAGAGCTGGCCAAGAT	CCCTACTGTCTTTGAGAACTA	CCGGATCAGTGCCTTTGGCTA	CACCATGGCTGCAATCCGAAA
391	RHOG	NM_001665	CAACAGGATGGTGTCAAGGAA	CGGGCGCACAGTGAACCTGAA		
397	ARHGDIB	NM_001175	AAAGGAAACCATTGTGTTAAA	CACTGAATAAATAGATCAGAA	AAGGAAGGTTCTGAATATAGA	CACAGCTGGGTCCCTCTTCAA
401	PHOX2A	NM_005169	CCAGCAGAGCGGAGTTCTTTA	CAGAGGGATTCTCTTTCCCTA		
403	ARL3	NM_004311	CAGACCTGTAAGGACTTGCAA	ACCGATATTCTTATATATGTA	ATCTGACATGAAAGTCATTAA	AGGGAACAACACGGTTTAGAA
405	ARNT	NM_001668	AACCCGAGACTTGGCCATAAA	ACGGAACAAGATGACAGCCTA	CCCAGCCAATATACAACTGTA	CAGCCAATATACAACTGTAAA
406	ARNTL	NM_001178	TACGTTTGGACCCAAGCTTAA	TAGGCACATCGTGTTATGAAT	TCGGCACGCGATAGATGGAAA	TCGATGGTTCAGTTTCATGAA
410	ARSA	NM_000487	CTGGGTCTGCGGTATCGGAAA	CAGGGCTTCCATCGATTTCTA	CCCGGTTCGGATGGGCATGTA	TCGGCAGTCTCTCTTCTTCTA
411	ARSB	NM_000046	AAGGGTATGGTCTCTAGGCAA	CACATTTCTTACGCAAATGAA	ATGGGTGTACACTACGCATAA	AACCAACTTTATAGTACATAA
414	ARSD	NM_001669	ATGGAGGACATTTAGAGGCAA	AAGGTTCTTAATGCCATCGAA	AACAGCGAGTCTTATGCTAAA	TCGGTTGCTACGGGAACAATA
415	ARSE	NM_000047	CCGCTGGGAACTCTCAGAGAA	CACGAGTTCCTGATGCATTAT	CCCTCTTATCACTATGGAGAA	AGGGAAGATGACCCACAATAA
416	ARSF	NM_004042	CGCGTTCTTGACGGGAAGATA	CTGAACGAGCTGGATCCATTA	CAGGTATGGTTTCTAGTGGTA	ACGGAGGGCATTTGGAAGCTA
421	ARVCF	NM_001670	CACGGAGAGCCGGAACTTCAA	CCGGAAGGACACTGACAACAA		
427	ASAH1	NM_004315	CACGGATGGCACGAAAGCCAA	CACGTTCTGTTAATTTAGTAA	ATGGTATGTGGTACAAACAAA	CACGATTAACTGTGAAATGTA
430	ASCL2	NM_005170	CACGCTTTGGGCCTTACAGAA	GAGGGTTATCTATACATTTAA	AAGGAAGGAGGGCGTGAGAAA	AGGGAGCGTGAACTTTATAAA
432	ASGR1	NM_001671	CTCCTTTAATTTATTTCTTCA	TCCGAAGGTGAGGAGCTTGAA	CAGGAGCCACCTCTCCTTTAA	CAGGTTATCATTGTGAACTTT
433	ASGR2	NM_080914	CTGTAATTCATTGTAATTATT	GAGCAGAAATTCATTGTACAA	CAGACTATAGGCACAACTACA	CACGAGCTGGGTGGAAGTGAA
443	ASPA	NM_000049	AACCGGAGTATTTCTGGTTAA	CTGCGCCATTGAGGTCTATAA	TACGTTTATCTGATTGAGCAT	TACATCTTACACGGTGTCTTA
472	ATM	NM_000051	TTGGCTTATACGCGCAGTGTA	CACTTATTCATTAGTAATTTA	CACCTGTTTGTTAGTTTATTA	AACCATGAGTCTAGTACTTAA
473	RERE	NM_012102	CAAGAGAGAGTGAGAATTCAA	CAGGAAGATTATTACAGTCGA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
477	ATP1A2	NM_000702	ACCCATAGCAATGGAGATTGA	CCGATTAATTGGAGATTACTA	AACAATCAGATTAGACACTAT	CAGATTAGACACTATGTGTTA
480	ATP1A4	NM_144699	CTGGTTTATGCTGGCCCGAAT	CTCAATGAACGATGAAATGAA	AAAGGGAGACGTACTACTAAA	CCGGGCTGACTTTAAGGCTAA
483	ATP1B3	NM_001679	CCGCATTGGAATATACATTCA	CAGACTGTGGACTGTAATAAA		
486	FXYD2	NM_001680	CACCAGCCTCTCCAAGCTCAA	CCCGTTCTACTATGACTATGA	CCACCTCATGCTTATAATAAA	ATCAATGAAGATGAGCCGTAA
487	ATP2A1	NM_004320	CCCGTGTCATGTGTCTGTTTA	CCCGATAGTGACACATCTTCA	CACCAACATTGCAGCCGGCAA	TCGGAACTACCTAGAGGGATA
492	ATP2B3	NM_021949	CCCTCTTTATAAAGCATTATA	CCGGAAGACAAGCTTTACAAA	TTCCCTGATGTCCTTGTTTAA	CACAGATACGTAATAATTTAA
501	ALDH7A1	NM_001182	CGGGAGAAGATCCAAGTACTA	TCCGATTCTCTATGTCTTTAA	AAGGATGATTGGAGGACCTAT	AAGGTCTACTTGTACTATCAA
506	ATP5B	NM_001686	AACAGTATTTAAGGTTTCCAA	AAGAATTACCACTACCAAGAA	ATCTGGTGTTATCAAGTTAAA	ACCCGTGAAGGCAATGATTTA
509	ATP5C1	NM_001001973	CAGGTCTGTCATCTCCTATAA	CAGCAAGATATTTGTAAATTA		
523	ATP6V1A	NM_001690	TAAGGTAGAGTCAATTATGAA	ACCCAAATTGTGATAGCATAA	GAGCTTGAATTTGAAGGTGTA	ATGGAGGTTGATGGTAAGGTA
527	ATP6V0C	NM_001694	CTGGATGTTTATTTATAAAGA	CAGCCACAGAATATTATGTAA		
533	ATP6V0B	NM_004047	CAGCTGGAGCTGTGTCCCTTA	TCCTAGTGTTTGTGAAATAAA		
535	ATP6V0A1	NM_005177	AAGGTTCAGTTTCGTGACTTA	ACGGCCGATGTTTACTTATAA		
537	ATP6AP1	NM_001183	CACAGTGACATTCAAGTTCAT	CAGGGAAGTCCTCACAGGCAA		
538	ATP7A	NM_000052	CAGCAAGTCACTTAGATCATA	CAGCCAGTTATTCTTCCATTA	CTGGACCGGATTGTTAATTAT	TAGCAGCTTGTAGTATTGAAA
545	ATR	NM_001184	AAGGACATGTGCATTACCTTA	GCCGCTAATCTTCTAACATTA	CCGCTAATCTTCTAACATTAA	CAGGCACTAATTGTTCTTCAA
546	ATRX	NM_000489	ACCGGTGGTGAACATAAGAAA	CCGACAGAAACTAACCCTGTA	CCGGTGGTGAACATAAGAAAT	AGGCGACGTATTAAGGTTCAA
547	KIF1A	NM_004321	TCGGATCAACGACACGACCAA	CAGCCCGATCGTTTCCAAGAA	TCGGGTCATGCCACTGTCCAA	CAACTCGGAAATTAACTATAA
552	AVPR1A	NM_000706	CAGAAATACAACAGAAGTTAT	CACTTTATTAATATAACCATA	TCGCAAACATAGGGTAATAAA	ATGAACGGACTGGATAGTAAA
567	B2M	NM_004048	CAGGTTTACTCACGTCATCCA	TCCGACATTGAAGTTGACTTA	CTGGGTTTCATCCATCCGACA	AAGTGGGATCGAGACATGTAA
570	BAAT	NM_001701	TTGGCTTACCATAACTATGAA	ATGGCTATTTACCTAAAGCAA		
576	BAI2	NM_001703	CCCACTGCATATAAATATATA	CGAGGTCTTGCTCATCAACAA	CTCTCTGATTGTCACAGATAA	CCCGAACGAAAGGATACGGTA
577	BAI3	NM_001704	TTCGGGATATACCAAATACAA	GAGATCCATAATACTAATTAA	TTGGATGATAATGCAGGACTA	ATGGACTAAGGTAGAGACAAA
578	BAK1	NM_001188	CTCTGAGTGTTTGGAAATAAA	CAGGATTCAGCTATTCTGGAA	CTGGACTTAAGCGAAGTCTTT	AACCCATTCACTACAGGTGAA
580	BARD1	NM_000465	TCCGATGAATTCATTAGTCTT	GACCATCAATACAGTCGCATA	TGCAGTAATTCTTAAGGCTAA	CTGAATATTATACCAGATGAA
581	BAX	NM_004324	CCGAGTGGCAGCTGACATGTT	CAGCTCTGAGCAGATCATGAA	CAGGGTTTCATCCAGGATCGA	ATCATCAGATGTGGTCTATAA
587	BCAT2	NM_001190	CCGGCTCATCGAAGTGGACAA	CACCTGAAGTGCAATACGAAA	AACCATGAACATCTTTGTCTA	CTGAAGTGCAATACGAAATAA
594	BCKDHB	NM_000056	CAGGCCGAAGTCATACAGGAA	CTGGAAGATTATGACTAGATA		
595	CCND1	NM_053056	ATGCATGTAGTCACTTTATAA	CTCCTACGATACGCTACTATA	AGGGTTATCTTAGATGTTTCA	AAGGCCAGTATGATTTATAAA
596	BCL2	NM_000633	GTGGATGACTGAGTACCTGAA	CCGGGAGATAGTGATGAAGTA	CTGTGGCATTATTGCATTATA	CAGGCTTAAGATTTGGAATAA
598	BCL2L1	NM_001191	CAAGCTTTCCCAGAAAGGATA	AAGGCGGATTTGAATCTCTTT	CTGCTTGGGATAAAGATGCAA	AAAGTGCAGTTCAGTAATAAA
602	BCL3	NM_005178	CTCGACATCTACAACAACCTA	CACGATGTAAATTATTAAGCA	CAACGTGAACGCGCAAATGTA	ACGGATCACGATGTAAATTAT
605	BCL7A	NM_020993	TACGATGCTGATCATCATTGA	CTGCACTTCGAGAAGAATCAA	CAGCACCTTCCTACAACCCTA	TGGAATGTTCATTATCGCCAA
611	OPN1SW	NM_001708	TTGGCCTGTTTGCAACAGCTA	GCGCTACATTGTCATCTGTAA	CGCCATGTACATGGTCAACAA	CAAGAGTGCTTGCATCTACAA
613	BCR	NM_004327	CAGCCGCAACGGCAAGAGTTA	TGAACTTAACTTAGAGTCTAA	CAGCATTCCGCTGACCATCAA	ACGGCAGTCCATGACGGTGAA
622	BDH	NM_004051	TGGCTGCTTGATGAAGGACAA	CAGCAGCGAAGAGGTGGAGAA	CTCAATGTCTGCAGCAGCGAA	CAAGCAGGTGGCAGAAGTGAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
624	BDKRB2	NM_000623	ATGAGTTGATGTCTCCGGTAA	GCCCTGGGTTTCTTTAATCTA	CTGGCAGGTTAGAACCTAGAA	CTGCACGGTGGCAGAGATCTA
638	BIK	NM_001197	GAGGAGAAATGTCTGAAGTAA	TCGGCAAAGAATCTACTGGAA	CCACACTTAAGGAGAACATAA	CCGAGGAGCAGGAGTGCTCAA
640	BLK	NM_001715	AAGGTGGTTCTTTAGATCACA	CAACATGAAGGTGGCCATTAA	CTGGTAAGCGACTGTCATCAA	CAGCCGTGCTGTTAAACCAAA
641	BLM	NM_000057	GACGCTAGACAGATAAGTTTA	CTGACCATCTGTGACTATAAA	ATGCTCGGAAATAAAGCCCAA	CGGAATCTCAATGTACATAGA
643	BLR1	NM_001716	AACGCTGGAAATGGACCTCGA	ACGGAGAAAGGTGGACTGGAA	CCCGCTAACGCTGGAAATGGA	CAGCCATGAACTACCCGCTAA
644	BLVRA	NM_000712	TCCAGAAATATTGCTGTTCAA	ACCATTATCTCTATTCTTAAA		
649	BMP1	NM_001199	AAAGGGCTTCTTTGCAGTCTA	CAGCTATATTGTGTTCACCTA	CTGGCTCAAGTTCGTCTCTGA	AAGGACTATGGCCACATTCAA
651	BMP3	NM_001201	CCCAGCTGGTTTGGAGTTCAA	CCGCCATTTCTGAGCCAGAAA	CTGTCTAAAGATATCACTCAA	CAGGAGATACCTCAAGGTAGA
654	BMP6	NM_001718	CCCGGACGACCATGAGAGATA	CAGCATTTATCAAGTCTTACA	CCGGACGACCATGAGAGATAA	ACCGTGCTGTGCGCCAACTAA
656	BMP8B	NM_001720	CAGGTAGACATGTGGAGTCAA	TAGGAAAGACATGTAAGAGCA	CTGAGTGAACAGCATGATTTA	ACAGATATGATGTAAAGTGAA
657	BMPR1A	NM_004329	ACCAATTTATGTAACCAGTAT	CACTGAATGATAGTCATTTAA	GCGGCAGACATTAAAGGTACA	CAGCTACGCCGGACAATAGAA
659	BMPR2	NM_001204	CCATATGAGCATTGTAATTAA	AAGCTCTAAATTGATGTGCTA	CTGGTAAGTATGTAAAGGAAA	AAGCACCGAAGCGAAACTTAA
671	BPI	NM_001725	CCCAGGGTTAACGAGAAACTA	CAGACGTTGTCTATAAATGAA	CAGGGTTAACGAGAAACTACA	AGGAATCGTGTTTCAATTGTA
675	BRCA2	NM_000059	TACGTACTCCAGAACATTTAA	TTGGAGGAATATCGTAGGTAA	CAGCGTTTGTGTATCGGGCAA	CAGGACACAATTACAACTAAA
686	BTD	NM_000060	AACCAGAACCTTGACATCTAT	CACAAATGTCGTGTTCAGCAA	CAGATTATAGTGTTTCCAGAA	ATGCGATTGGTCTCAAGCTAA
708	C1QBP	NM_001212	CAGGCTTTGGCCAGTGAACAA	CACGGTCACTTTCAACATTAA		
710	SERPING1	NM_000062	CGCCAACTTGGAGCTCATCAA	AACCTGAAACATCGTCTTGAA	CTGGGTGGCCAAGAACACCAA	TCACCAGACTCTATAAATAAA
712	C1QA	NM_015991	ACGGTCATCACCAACCAGGAA	CCCGGGAATTAAAGGCACCAA		
713	C1QB	NM_000491	CAGAAGTGCCATGCTCAGAAA	CACCAACATGAACAACAATTA		
717	C2	NM_000063	CCGGGATATGACTGAGGTGAT	ACCCTGGCATGTCACTATTAA	CAGAGAGATCCTGAACATCAA	CCCAGTTATGAAATTAATAAA
718	C3	NM_000064	CCGAGCCGTTCTCTACAATTA	CACGGAGAAGCGAATGGACAA	CACGGTCATCGCTGTGCATTA	TAGGAACACCCTCATCATCTA
720	C4A	NM_007293	AACCCTGTACGACTACTACAA	TCCAGTGTTAGACAGGAGCAT		
721	C4B	NM_000592	AACCTGGGAAAGAATATTTGA	AACCCTGTACGACTACTACAA		
726	CAPN5	NM_004055	CCCGGGAGTCGCTGTGGCAAA	CCGCGTGATCAACACATCCCA	CCGGTACTTCACGGACATCAT	CTGGTGTTCTCCCACCTTGAA
730	C7	NM_000587	CACGCAGTTATACTTCACATA	AAGGATTAGAACACTCATTAA	ACCCTGGTAAATATATTTCAA	CCGAAGATTAATCGACCAGTA
757	C21orf4	NM_006134	AAGGGATAATACATGATCAAA	AAGCTGGGATACAGCATTTAA	CACCTGGTATGCTTACATTAA	ATGGAGTAGATTGTACATTAA
762	CA4	NM_000717	ATGCACATAGTACATGAGAAA	CTGGCTACGATAAGAAGCAAA	TGGGACTTTAGGCATGATTAA	CTGGTCCGACTTGCCATATAA
773	CACNA1A	NM_000068	CACCGTCGTACAAGTGAACAA	CCGGGTGCTACGACCTCTTAA	TCGGAACAACGTGCTGCGATA	CGGGTGCTACGACCTCTTAAA
774	CACNA1B	NM_000718	CCCAGGAACAACGCTCTGAAA	CCGGCAGTCGTTCCAGTATAA	CCCGAACACTATTGTACATAT	TCGAATTGGCTCTGACCCTTA
778	CACNA1F	NM_005183	CACCATCATGTCTTCACCAAT	CTGGCCTGCACTGCTATACAA	CACCACACTTCTGCAATTTAT	CCGGACATCCCTGAAGATCAA
780	DDR1	NM_001954	CAAGATCTGGTTAGTCTTGAT	CACTAGGCAGGTAATAATAAA	CAGGAATGATTTCCTGAAAGA	ACGGTGTGAATCACACATCCA
781	CACNA2D1	NM_000722	ATCGGGCATTATGGTAAGCAA	TTCGATAACGACAGTAAATCA	TCGGCCGTCACTATCAAATCA	CCGCCTGTTATGACCTTCTAA
784	CACNB3	NM_000725	CCGGCGTGAAGTAGAGAGCCA	CCGCTTGTTAGGTTAGGGTTA	CTGGAGAGCATCCGGCTCAAA	CTCACTGTCATCACTAATAAA
797	CALCB	NM_000728	AAGGAATGAAACTGAATGCAA	CCCACCAATGTGGGTTCCAAA	ACCTTTGTCACTTGAAAGGAA	AACCTTGGTGATGCATTACAA
801	CALM1	NM_006888	TTCCTGAACAACGAATGTAAA	CTGGTTGTATCTTATTAGCAA	CGGCAACTTACACACATTGAA	ATGCCCGTGTATGTTGGTTTA
813	CALU	NM_001219	CAGGGTTTCAGTCCTTATCAA	AAGCCTGAGATCAATAAGAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
816	CAMK2B	NM_001220	CAGGATCTCTGACATCCTGAA	CCCGGAAGCAGGAGATCATTA	CCGGAAGCAGGAGATCATTAA	CAAGAGTTTACTCAACAAGAA
823	CAPN1	NM_005186	TCCCACGGAACTGCTGTCAAA	CCGGACCATCCGCAAATGGAA	TAGGATCATCAGCAAACACAA	CAGGGACTTGTGTACTGGTTA
824	CAPN2	NM_001748	CTGGAACACTATAGACCCAGA	AACGGATGCTATGAAGCTCTA	AACATGGTATATCATGAAGTA	CCCGAGAATACTGGAACAATA
834	CASP1	NM_001223	TCGGCAGAGATTTATCCAATA	CTCATTGAACATATGCAAGAA	TACCTCTTCCCAGGACATTAA	CCCAGATATACTACAACTCAA
839	CASP6	NM_001226	ACCCAAGATATTTATCATTCA	CTCAGGAAATTAGATAAATAA	GCGCAGATAGAGACAATCTTA	CAGGAATTAAATCATCCCTTA
841	CASP8	NM_001228	GACAAAGTTTACCAAATGAAA	AAGATAATCAACGACTATGAA	CGGAGGGTCGATCATCTATTA	AAGAGTCTGTGCCCAAATCAA
845	CASQ2	NM_001232	CGGCATATTTGGGAACGAGAA	TAGCCTAAGCTGGGATCTGAA	GAGGTTGATTTGCTCTCTAAA	TAGTGTTAAGTGTGCAGTATA
857	CAV1	NM_001753	TCCAGTCTTCCTGACACTTTA	CTGGTCAACCGCGACCCTAAA	TCCTGACACTTTAATTACCAA	CAGCCGTGTCTATTCCATCTA
860	RUNX2	NM_004348	CACCTTGACCATAACCGTCTT	CAGCAGCACTCCATATCTCTA	CAGAAGCTTGATGACTCTAAA	CAGCACGCTATTAAATCCAAA
861	RUNX1	NM_001754	CAGGTCGTTCTTATCTAGAGA	CTCCCTTTCATGTTAATCAAA	TTGGCGATAGGTCTCACGCAA	CAGGAAAGTTAAGGTATCAAT
868	CBLB	NM_170662	ACGGGCAATAAGACTCTTTAA	TCGGTTGGCAAACGTCCGAAA	TCCGGTTAAGTTGCACTCGAT	CACAGCGAGTTCAAATGTCAA
871	SERPINH1	NM_001235	CTCAATCAGTATTCATATTTA	CCCAACCTCTCCCAACTATAA	CAGCCCTCTTCTGACACTAAA	CAAGAACTTATTTGTACATTT
883	CCBL1	NM_004059	CAAGTGGATGATCAAGAACAA	CACAGACATCTCAGACTTCAA		
885	CCK	NM_000729	ATCTATTTATTAAGTTCTCAA	ACCAGAATTGTGCAAATGGAA	TGGACGAATGTCCATCGTTAA	ACGAATGTCCATCGTTAAGAA
887	CCKBR	NM_176875	CACAGCGTCCCTAGCAGTGAA	CCCAAACTGTTCAAGAAATAA	CCGCCGGGTCGAGCTGAGTAA	CCCGTGTACACTGTCGTGCAA
896	CCND3	NM_001760	TGGGACAGAATTGGATACATA	GACCATCATCCTAGTGTAATA	CACAACTTTAAGAGGACATAA	CAGGAACCACACCACATCTAA
899	CCNF	NM_001761	CACAGATGGCGTCAATGTGAA	CCGGTTTATCAGTAAAGAGAT	AACCCAAGCGTTGGAACTGTA	CACGGACAACACTTACAAGTA
901	CCNG2	NM_004354	GGGACAGTGGATAATCCTTAA	CTGGAGAGAGTTGGTTTCTAA	AAGGCAGAAATAATTAGGCTA	AAGAGTGAGTATGCTCTTAAA
905	CCNT2	NM_001241	CTCGATGTAAGGGATCATTAT	AAGGGCTTTCTTGGTAATTTA	TCCACATATGATAGTGTTATA	AAGCAAGAATATACTCATAAA
910	CD1B	NM_001764	AAAGCAGATCTGCAAAGACAA	CTTGGTCTAAAGGTAACTTTA	CACAGAAATTCTGTGCACTAA	CTGAGTGTCAAGAATGCTTCA
914	CD2	NM_001767	AACCTGTATCAAGATGGGAAA	TAAGATGAGCTTTCCATGTAA	CCCAACAAATTCCAGCTTCAA	CCCGAATTAAACCTGTATCAA
915	CD3D	NM_000732	CTCACTTATTAATTCTAGTAA	CACGAGGAATATATAGGTGTA	TGGCACGATATGTTAAACCAA	CAGGCTATATATGGTATTAAA
919	CD3Z	NM_000734	CAGGAAGGCCTGTACAATGAA	CACGCTTTCAGCGAATGACAA	TTGGTTATATTTAGCTCCAAA	ACCCAACACATGGGACCTATA
923	CD6	NM_006725	CAGCACTACTGCGGCCACAAA	CTGGCGGTTCAACAACTCCAA	CCGGCAGGATGTACTACTCAT	CAGGGAGGATGCTGCCTCCAA
926	CD8B1	NM_172100	TAGCACTAAATTGGAGAAGCA	CAAATACAATAGAGCCACTAA	TAGCTGTGTTTCGGGATGCAA	ACCCGGCAACATCAGTTTAAA
928	CD9	NM_001769	CAAAGAGGTCTTCGACAATAA	ACAAATGTCTATCAACTTTAA	CCGCGAGATGGTCTAGAGTCA	AAAGAGGTCTTCGACAATAAA
929	CD14	NM_000591	CCCGAGGTGGATAACCTGACA	CTCAGAGGTTCGGAAGACTTA	CAGAATAATGAATGGACTCAA	CAGCCTAGACCTGTCTGACAA
931	MS4A1	NM_021950	GAGCAACTTTCTTACACTGAA	TTCAATCATGGACATACTTAA	CACACACCATATATTAACATA	CACCATATATTAACATATACA
939	TNFRSF7	NM_001242	AACGAAGGAAATATAGATCAA	ACCGAGTGTGATCCTCTTCCA	AGGAAATATAGATCAAACAAA	AAGGTTGGCTTGCCACCTGAA
940	CD28	NM_006139	TGGGTTAAGCATGCCAATTTA	CAGGGATGAGGTGCTATAATA	CTCGAGTGACTAGACCAAATA	ATGATGGTTCTTCAACTATAA
961	CD47	NM_198793	TACCATTCCTATAGTACTTTA	CACTACTGAAGTATACGTAAA	TACAGCTGTGTTACCGTTAAA	CACGATAAGTTTACTCCTCCA
962	CD48	NM_001778	CTGGCGAGTCTGTAAACTACA	CTGCAAGTGCTTGACCCTGTA	CACCCTTATGCCACATAATTA	CAGAAGCATGCTGCTGAATTA
965	CD58	NM_001779	TCCAATTGATTGGTAACAGAA	TAGCAGTAATTACAACATGTA	ATGCATGATACCAGAGCATTA	AGCAATGTAAACGTAACTCAA
967	CD63	NM_001780	CTGGCTATGTGTTTAGAGATA	CAGATGGAGAATTACCCGAAA	TGGGATTAATTTCAACGAGAA	CAACGAGAAGGCGATCCATAA
970	TNFSF7	NM_001252	CTGCGTCTCAGCTTCCACCAA	CAGCTACGTATCCATCGTGAT		
975	CD81	NM_004356	AAGGAACATCAGGCATGCTAA	CCGCCTGTGTATATAACGTTT	CGCCTTCAACTGTAATCACAA	CACCTTCTATGTAGGCATCTA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
983	CDC2	NM_001786	AAGCCTAGCATCCCATGTCAA	TTGACTAACTATGGAAGATTA	TCGGGAAATTTCTCTATTAAA	CAGGTTATATCTCATCTTTGA
987	LRBA	NM_006726	CACGATGGAAACAGATGATAA	CAAGGGTACATTTAAATTCAA		
988	CDC5L	NM_001253	ACGCAGATTTCAGGAAATTAA	TCGAGACAAGTTAAACATTAA		
995	CDC25C	NM_001790	GAGCTGCAATCTAGTTAACTA	CCAGGGAGCCTTAAACTTATA	CCAGAGCTATATATCCTTAAA	CAGGAAGGGCTTATGTTTAAA
1002	CDH4	NM_001794	CCAGAATATGTTCACCATCAA	CACGTCCATCATCAAAGTCAA		
1010	CDH12	NM_004061	CAAAGTCAATATACTGATTAA	CTCCACCTTCTTCTAATTCAA		
1012	CDH13	NM_001257	CAGGATATATTTAAATTTGCA	CTGGAAGATCTCCAAGATCAA		
1019	CDK4	NM_000075	CAAGGTAACCCTGGTGTTTGA	CCGAACTGACCGGGAGATCAA	ACCCTGGTGTTTGAGCATGTA	AAGGTAATCCGGAGTGAGCAA
1022	CDK7	NM_001799	CTCTTGAAATGTAGAATTGAA	TTGGACATAGATCAGAAGCTA	GAGGCTTTAAGGTAGCTTTAA	CCGGATGGCTCTGGACGTGAA
1024	CDK8	NM_001260	CAGGGCAATAACCACACTAAT	TTCGAGAGCTTAAGCATCCAA	CCAGCTGGACAGAATATTCAA	CAGAAGAAATACGTATACCAA
1025	CDK9	NM_001261	CGGCCAGAAGGTGGCTCTGAA	TGGGCACAGTTTGGTCCGTTA	TAGGCACATGAAGGCTGCTAA	AACCGCTGCAAGGGTAGTATA
1027	CDKN1B	NM_004064	CTGTAAGTAACTTCACATTAA	CACGCATTTGGTGGACCCAAA	ACCGACGATTCTTCTACTCAA	AAAGCGTTGGATGTAGCATTA
1029	CDKN2A	NM_000077	TACCGTAAATGTCCATTTATA	CAGGTGTGCCACATTCGCTAA	CAGAACCAAAGCTCAAATAAA	CACGCCCTAAGCGCACATTCA
1043	CDW52	NM_001803	GAGAATAAAGTTACCCTTGTA	CTGGTTATGGTACAGATACAA		
1046	CDX4	NM_005193	CACCGGCTTTCTCGCACTATA	CAAGGAGAGAAAGATGATCAA	GTAGTTTACACTGATCATCAA	CAGGTTATAGTCTCCGAATGA
1047	CLGN	NM_004362	CTGGATTATATTGCAGCATAT	AAGAAAGTAATCAATCAAATA		
1050	CEBPA	NM_004364	CAAGAAGTCGGTGGACAAGAA	CTCAGCCTTGTTTGTACTGTA	CCGAGTCACACCAGAAAGCTA	CAGCCGATATCAACACTTGTA
1056	CEL	NM_001807	CAGCCACATCCTGGCTGGCAA	AGCCCTGACGCTGGCCTATAA	CCCGTTATGATCTGGATCTAT	TCCCATGAGCCTTGGTATCAA
1059	CENPB	NM_001810	CCGGGAGAAGTCACGGATCAT	TTCGAGGTCTTGGACATCAAA	CACGCTGAGCACGATCCTGAA	CGCCTTGAGAAGCACAGTTTA
1069	CETN2	NM_004344	AAGCTCTTTGATGATGATGAA	GCGAATTACCCTAATTCTCAA	AAGCACATGTAACTAGATTTA	CAGAACGACTTTAGACAAGCA
1070	CETN3	NM_004365	CTGGTGACATTTAAAGAATTA	TCGAGCTATGATAGAAGAATT	TAGCTTTGTATTTATAATAGA	CAGTTACCATCTTATATTCTA
1072	CFL1	NM_005507	CAAGGTGTTCAACGACATGAA	CTGACAGGGATCAAGCATGAA	CAGTAAGGGACCTTCGATTAA	CAAGCATGAATTGCAAGCAAA
1082	CGB	NM_000737	CACCACCATCTGTGCCGGCTA	CCCACAATAAAGGCTTCTCAA	CCAGGACTCCTCTTCCTCAAA	CCCGAGGTATAAAGCCAGGTA
1084	CEACAM3	NM_001815	CAGTTCCATGTATAGCAAGAA	CAGGACAGCAGCTTCCATCTA		
1088	CEACAM8	NM_001816	TTGCTTCTTCTTCAAGATTTA	CAGGCATGCAATGCTAGATAA		
1103	CHAT	NM_020549	CAGGACGGTCCTCGTGAAAGA	CCCGAGATGTTCATGGATGAA	CCGGAAATTCAAGGCCACTTA	CACGGAGATGTTCTGCTGCTA
1109	AKR1C4	NM_001818	CTGGGAACCCAACGACATAAA	GAGGGTGTTGCACGACATCTA	ATGGACCATCCTGATTATCCA	CCAGAAAGCAAACATAATAAA
1112	CHES1	NM_005197	CTGGACTTGGTTTATATTGCA	TCGAAGGAGCCTTCACGTAAA	CACGGCCAAATTAATTTACGA	CCGGTCCTGTTTGAATAACAT
1113	CHGA	NM_001275	TACCGAGGTGATGAAATGCAT	TCCAAGGATGTTATGGAGAAA	AAGGAGTGGGAGGACTCCAAA	TATGAACTTTATCTAAAGAAA
1116	CHI3L1	NM_001276	CAGCTGCTCAATAAAGTACAA	AAGGCCGAATTTATAAAGGAA		
1119	CHKA	NM_001277	TACCACAGAGATTGTACTATA	CACAGAGATTGTACTATACAA	CCGGCCCTTACCAAACCTGAT	AGCCGGCGATTAGATACTGAA
1121	CHM	NM_000390	TCGGAGTTTGATGTGATCGTA	CCGGAGAGTTCTGCATGTTGA	CGGAGTTTGATGTGATCGTAA	CTCCAATATATTGTCATGCAT
1128	CHRM1	NM_000738	TGGCTCCGAAGTGGTGATCAA	CAGCAAGACAATGACACTGGA	TACAGTCAAGAGGCCGACTAA	CCGGCTTGGCTAGTCACATAT
1130	LYST	NM_000081	CACATCATTGTCAACACCTAA	CACGCCGACCTGATTACCTAA	TCCGAGTATGCCATAAGTTAA	CAAGGTGTTATTAAACTATTA
1135	CHRNA2	NM_000742	CAGCCTCTGTTTGACCATGAA	CACGGGCACCTACAACAGCAA	CAGGAGTGGAGCGACTACAAA	AAGGGCTTTGAACAATGTTTA
1136	CHRNA3	NM_000743	GCGGCTGTTTGAAGATTACAA	AACTGTCTTAGTACACCATAA	TACCGATAAATGAACATTTAA	CCCACCTTCTATCTAAGACAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
1138	CHRNA5	NM_000745	CTGAACCTTCTTCTATTGCAA	CTGAAGTATACATTTAGTTAA	ATCGTTCTTCCTCAACACATA	CTGAGTAACAGCTAATCTTTA
1142	CHRNB3	NM_000749	CCACCACAGGTTTCAACTCAA	CGGAGAATGGGAAATACTGAA	ACGCTGGAATCCTGATGATTA	CAGGTAGTACAAGACTGGAAA
1143	CHRNB4	NM_000750	CCCAGGGAGAAGGACAGTGAA	CAGCAAGTCATGCGTGACCAA	CAGCTACGTGGACGTGACTTA	CACATGAAGAATGACGATGAA
1144	CHRND	NM_000751	CCGGCACCTGTTTCAAGAGAA	CCGCCAGGACATCACCTTCTA	CGGCTGAAGTGGAATGCTGAA	AACAATTACAATGAGGAGAAA
1146	CHRNG	NM_005199	CACCAATGTCTGGATAGAGAT	CTGCTCTATCTCAGTCACCTA	CACCAACCTCATCTCCCTGAA	CCACCAGAAGGTGGTGTTCTA
1147	CHUK	NM_001278	CAGCGTGCCATTGATCTATAT	CAGGGCAATAGTATGATGAAT	TTCCATAAGCTTGGTGACAAA	CAGGAGAAGTTCGGTTTAGTA
1163	CKS1B	NM_001826	CCAAGAAACCAAAGAAATGAA	GCGATCATGTCGCACAAACAA	AAGAAATCTGTTCATGTTAAA	AACATCTTTCTGATAACATTA
1164	CKS2	NM_001827	TAGGTTACTGTAAGATGTTTA	TCGGACAAGTACTTCGACGAA	CTGTAAGATGTTTAAGATAAA	AAGTTTGTATGTTGCATTTAA
1173	AP2M1	NM_004068	ACGTGTGACTTCGTCCAGTTA	TGCCATCGTGTGGAAGATCAA	TTGGAGGCTTATTCATCTATA	TGGAGGCTTATTCATCTATAA
1178	CLC	NM_001828	CACCTTTGACCATAGAATCAA	CAGGATGGCCAAGAATTTGAA		
1181	CLCN2	NM_004366	ACCGGGATGAAGAGACTATTA	CCGAATCAAGAAACTGCCCTA	CAGATGGAATTCATACGGACA	CTCATTGGAATCGTTACTCTA
1184	CLCN5	NM_000084	CACCGAGAGATTACCAATAAA	AAGGATGTGTTAAAGCATATA	TAAGTGGACTCTGGTTATCAA	ATCCTTGTTCCTGTTACAATA
1185	CLCN6	NM_001286	AAGATGTGAATTCAAGTATCA	TCAGATTTACGTCTACCCTAA	CACCAGAAACATAAAGGATTA	CCGGTGAATGTTATTGGAATT
1186	CLCN7	NM_001287	AGCGTGGAGCTGGATGATGAA	CTGGCTGACCATGTTTCGAAT	CCAGATCAAGTGCTTCCTCAA	CCAGCTCATCGTTCTCCTAAA
1187	CLCNKA	NM_004070	ACTGGCCATCACATTAATGAA	CTGAGTGTGAGAAGATGGAAA	CAGCTCCATTCTTTGGCATAA	TTGGCATAACAGGCAACTCTA
1192	CLIC1	NM_001288	TTCCTGCTGTATGGCACTGAA	AAGGTGTCTCTCAGAGGAAGT	CTGGTGGTTTCCACATTGCTA	AAACCCAGCACTCAATGACAA
1193	CLIC2	NM_001289	AAGCTAGACGGTCTTCTTAAA	CACAATGCCTATGCCCGTGAA	CTGGCTGATTGTAGCTTGTTA	CCCGTGAAGAATTTACCCACA
1195	CLK1	NM_004071	CCGTATTTCCAACACACGATA	CACGATAGTAAGGAGCATTTA	AACGTGATGAACGCACCTTAA	AAAGCCGGTATCAGAACCATA
1198	CLK3	NM_001292	CTGCAAACCTCTGAAGAGTTA	ACCCAAGCTATTTATATGTTA	CTGCATTCTCTTTGAGTACTA	CACGAAGATCTCGGTCCAGAA
1212	CLTB	NM_001834	CTCGGTGCTCATGTCCCTGAA	CAGCGCCAGAGTGAACAAGTA		
1230	CCR1	NM_001295	AAGCACGGGCCATATGAATAA	CAGCGATTAATAACAGGCAAA	GACGGAAGAGTTGAGACCTAA	CTGGATCGACTACAAGTTGAA
1234	CCR5	NM_000579	AGGCAACATATAGGTTGTAAA	AAGGGACATATTCATTTGGAA	TAGGTGAGGATTGATTACCTA	AAGATGGATTATCAAGTGTCA
1238	CCBP2	NM_001296	CACCAGATTACAACAAATTTA	CTCAATTAGCGTTATTGGCAA	CTGCATGAGCCTGGACAAGTA	CTCAGTGACTGTGTTGCTAAA
1244	ABCC2	NM_000392	CTGATCCAATACAGGAGACAA	CTGGAGTACCTACAAGCAATA	CTGGTGGATAGCAACAATATT	CCGTATCAGGTTTGCCAGTTA
1258	CNGB1	NM_001297	CACAAATAGCGGCATCATCAA	CGCCATCGACGTGAACTACAA	CATGGCCTTCTTCGAGTTTAA	CAGAAGTTACTCCGGAAGAAA
1260	CNGA2	NM_005140	CAGGGCTGAGATAGCCATCAA	TGGCGAGATCAGTATCCTTAA	TAGAGGCACCTATGAGTTAAA	AGCACCGACTATAGACATTTA
1261	CNGA3	NM_001298	CCACCTGATAATGGGTATATA	AAGGTTGGAATGGTGTACTAA	CACCTGATAATGGGTATATAA	TCCCTTGGAATTGCATCCCAA
1263	PLK3	NM_004073	GTGGGTTGACTACTCCAATAA	CTGCATCAAGCAGGTTCACTA	CCCGAAATCGTAGTGCTTGTA	CAGAAAGACTGTGCACTACAA
1272	CNTN1	NM_001843	CAGCCTAGTAGCAGTCATTAA	AAGGGTGATAATTGAATGCAA		
1281	COL3A1	NM_000090	TCCGTTCTCTGCGATGACATA	ACCGATGAGATTATGACTTCA	CGCGGTGAGGCTGGTATTCCA	CTCAAGTCTGTTAATGGACAA
1284	COL4A2	NM_001846	CACACCATTCATCGAATGCAA	CACGTTGTCCCTGAGATTTAA		
1285	COL4A3	NM_031366	CTGCTTGTATCCAAGCATATA	TCCCAAGGTTACTTAATTCAA	TACATTCCCAAGGTTACTTAA	AGCGGATATAGAGCTAGCTAA
1287	COL4A5	NM_000495	AAGGGTGATGATGGAATTCCA	CCGGGTCTCAATGGAATGAAA		
1290	COL5A2	NM_000393	CCGGGTCTACGTGGTGAAAGA	TAGGTTTAAGATGACCAATGA	CCGCACGTGTGATGACCTAAA	CACACTAGTATATACCATTTA
1297	COL9A1	NM_001851	CACCGACAGATCAGCACATTA	CAGCATGATTACAATGTATTA	AACGGTTTGCCAGGAGCTATA	CACCTCCCTTGAACAAATTTA
1299	COL9A3	NM_001853	CAGGGTGACAGAGGAGACAAA	CAGGCTCTCGAAGCTCATAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
1300	COL10A1	NM_000493	TACGGAAGTCCTGGACTCCAA	AGCAATCTTAAGGCTCTTTAA	CCCAGCTGGCATAGCAACTAA	AAGCCTGTTTCTAACTATGAA
1307	COL16A1	NM_001856	AAGGGTATTTCCCTCCTTAAA	CAGGAAGGACTCAAATTGGAA		
1314	COPA	NM_004371	CTGGATTTCAACAGCTCCAAA	TCCCACTGAGTTCAAATTCAA		
1315	COPB	NM_016451	CAAGGATTGGTTATAATATAA	CAGGATCACACTATCAAGAAA		
1347	COX7A2	NM_001865	ATCAATATTTATTGACTTGTA	GACCAGTAATCTGATAAATAA		
1349	COX7B	NM_001866	CAGCTCATAATTGATGCCAAA	TGGCATTATTGAAGAAATAAA		
1352	COX10	NM_001303	ACCATAGTCCTTCTAACAATA	AAAGGGATTGTAGGTAGATAA	AAGGGTAGCCCTGGACTTAAT	TAGGTAGATAACATCCAATCA
1359	CPA3	NM_001870	CCCAATAGAATCAACAATTTA	CAGTAGCACCATAACGAAGTA	ATCCTCAAGCATACTTCCTAA	AACGAAGTAGCTTTAAGTGAA
1363	CPE	NM_001873	TACCTGGAAACTATAAACTTA	CTCGGAGTTGTGAGCACTCTA	CAGGCTATCTGGCAATAACAA	TAGTCCGTTAACACTACTTAA
1365	CLDN3	NM_001306	CACCGGCCAGATGCAGTGCAA	CACCATTATCCGGGACTTCTA	CACCACCACCACCACCACCAA	CACGGCCACCAAGGTCGTCTA
1366	CLDN7	NM_001307	GCCGTTGGTGGGAGAGACAAA	CCGCTCTTACCCTAAGTCCAA		
1369	CPN1	NM_001308	CCGCAACTTCCCTGATCTCAA	CAAGGGAATGCAAGACTTTAA	CCGGTGGATGCACTCCTTCAA	AAGACTTTAATTATCTCCATA
1378	CR1	NM_000573	CAGTCCTACGATCCCAATTAA	CTGCATGGTGAGCATACCCTA	TCGGTGTATTTCTACTAATAA	CTGGAGCCAATTGGATCATTA
1385	CREB1	NM_004379	CAGCCACAGATTGCCACATTA	CCGCATGCATAAAGTAAGTAA	CAGCCGGGTACTACCATTCTA	AGGGCAGTTGTTGCTTCTTAA
1393	CRHBP	NM_001882	CTGCAGCTTCTCCATAATTTA	CAGGAAATGGATTCAGATTAA		
1394	CRHR1	NM_004382	CAGGACTGCAGTGCAACGCAT	CCGCTACAATACGACAAACAA	GCGGGTGGCTGGTATAAATAA	CAGGTTGGTGACAGCCGCCTA
1395	CRHR2	NM_001883	CTGCAGCTCGTTGACCATGAA	AAGCTCTACTATGAGAATGAA	CACGGCCATTGTCATGACCTA	ACGGATCAGCTTCCACAGCAT
1397	CRIP2	NM_001312	CTGGCACAAGTTCTGCCTCAA	GAGCCTTGTGCTGTCAATAAA		
1398	CRK	NM_005206	TACACTATTTGGACACTACAA	CAGGATGTACCGAGCACTTTA	CTGAGTATAGTTCAACAGTTT	CAGCAGCTAACTAGAGTCCTA
1401	CRP	NM_000567	AAGCGCTGATCTTCTATTTAA	AAGGAGAAATGATGTTATAAA		
1407	CRY1	NM_004075	GAGGATCTTGATGCCAATCTA	AAGGAATGGAACATTACTAAA	CTGTTTGTGATTCGTGGACAA	ATCAGCAGCTTTCACGATATA
1409	CRYAA	NM_000394	CCCGGAGGACCTCACCGTGAA	CCGGGACAAGTTCGTCATCTT		
1421	CRYGD	NM_006891	TCCTCCTTTGTTGTTTCTTAA	TTGTTGTTTCTTAATTTGGAA	CAGCGGCTGCTGGATGCTCTA	ACCGCTTCCGCTTCAATGAAA
1427	CRYGS	NM_017541	AAGATTCAGATCTTTGAGAAA	CCAAATAGGCATCATCAATAA		
1428	CRYM	NM_001888	CACCAAGTTGCTCACCTTCTA	CTGGATGATGAGCTCATGAAA		
1436	CSF1R	NM_005211	CTGGAAGATCATCGAGAGCTA	ATGAGCCAAGTGGCAGCTAAA	ATGGAAATGGACTGACTTTAT	ACCCTCAACCTCGATCAAGTA
1441	CSF3R	NM_172313	TCCTATAACTTCAGTATTGTA	CCAGGCGATCTGCATACTTTA	CTCCTGCATCATCAAGCAGAA	CAGGCGATCTGCATACTTTAA
1444	CSHL1	NM_001318	CCTCAGGAGTACCTTCACCAA	CAGGAGTACCTTCACCAACAA		
1445	CSK	NM_004383	AGGGAACAAAGTCGCCGTCAA	CCCAACTGGTACAAAGCCAAA	TACGCGCCTCATTAAACCAAA	CCGGTACAGAATGTATTGCCA
1447	CSN2	NM_001891	CAGAGTGATGCCTGTCCTTAA	ATGGAAGTCCCTAAAGCTAAA		
1452	CSNK1A1	NM_001892	AAGAACTTAATTTCAGTATAA	CACAGTTGTGATGGTTGTTAA	CAAGAGTAACATGAAAGGTTT	AGGGCTAAAGGCTGCAACAAA
1453	CSNK1D	NM_001893	AACACGCACCTTGGAATTGAA	CGGTCTAGGATCGAAATGTTA	CTCCCTGACGATTCCACTGTA	CCGGTCTAGGATCGAAATGTT
1454	CSNK1E	NM_001894	TCCCTCCGAATTCTCAACATA	CTGGCTCTGAGTTATAAATTA	GTGGTTGTTAATTTGAAGTAA	GAGCTTTATCGTGGTTGTTAA
1455	CSNK1G2	NM_001319	ATGTAAGACTTTGGCCGAAAT	GCACACCAAGAGCCTAATCTA	TAGGAAAGAATCTCTATACAA	AAGAATCTCTATACAAATGAA
1456	CSNK1G3	NM_004384	CAGGTTGTAAGTTCTACAAAT	AAGAGCATAATCAAACAGGAA	TACCGCAAACTTGATATGGAA	CAACATATCTTCGTTATGTAA
1465	CSRP1	NM_004078	CAGGATGTTGTTTGATCTTCT	TGGGAGGATCCTAATGAAATA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
1466	CSRP2	NM_001321	CAGGCCTACAACAAATCCAAA	CAGATAATCTTTAACACTAAA		
1475	CSTA	NM_005213	CAGGAGATTGTTGATAAGGTT	CTGGAACAAATTACTACATTA		
1486	CTBS	NM_004388	CTCCCTATAATCAGACATTAA	AACGATCATGAAGCAAATAAA		
1489	CTF1	NM_001330	CCCGTTCTCTTAACTCTTGGA	CAGCAGATCTGTGGAGACAAA		
1493	CTLA4	NM_005214	AAGAAGAGAGTCCATATTTCA	AAGCATCACTTGGGATTAATA	CCCAAATTACGTGTACTACAA	CAGCATTATGATGTGGGTCAA
1495	CTNNA1	NM_001903	ACAGACTTTACCCGAGGTAAA	GCGAATTGTGGCAGAGTGTAA	CAGTCACTGTTCGTCACTCAA	CACCCTGATGTCGCAGCCTAT
1496	CTNNA2	NM_004389	CAGCATGTAAGCAGGATTTAT	TACCATTGTATTCACTAACTA	ACAGGCTTTAAGTGAATTCAA	CCCATGAATTGAACAATTTAA
1497	CTNS	NM_004937	CTCGCTAGGCGCCCTAAGCAA	CGCCATTAGCATCATAAACCA	CAGCGCCATTAGCATCATAAA	CACCTACTTGAGACTCACCAA
1511	CTSG	NM_001911	CAGACGGAATCGAAACGTGAA	CACAGTGTTGCCAGAGCCTTA	CAGCCTTTCAGGAAAGATGCA	CCACAGAGTATAAATAACCAA
1512	CTSH	NM_004390	GTCCTTCTTAACAGACTCAAA	CACCCGTGTCTATGACGCAAA	CGAGTATATCCTGTACAACAA	ATGGATGTCTAAGCACCGTAA
1513	CTSK	NM_000396	CCCGATGGAATAAATCTAGCA	AGGGCTGATGCTGTACAGGTA	CCGCAGTAATGACACCCTTTA	CACGGGACTAGTTAGCTTTAA
1520	CTSS	NM_004079	CTGCCACATGTTCAAAGTACA	TGGGATAATGTCATTAATATA	AAGGATATATTCGGATGGCAA	AGGAATCTAATTATATCGAAA
1521	CTSW	NM_001335	CCCAGCATGGGCAGAGAAATA	CGCGTTCATAACTGTCCTCAA	CGGCGCCATCTCACCCATCAA	CACCGTGACCATCAACATGAA
1524	CX3CR1	NM_001337	AACTCAGACTAGTTTAGTTAA	CAGACTAGTTTAGTTAAATGA	TCAGATGTGGTAACTGTTAAA	TAGAGTTGCAATCGTAATGTA
1525	CXADR	NM_001338	CTCCATCAATTCTGTATTCCA	CAGGTAATAGGGACTTAGCAA	TTGGTTATATCGAAATAGTTA	CAGGAACTGTACGGAATATAT
1536	CYBB	NM_000397	CACGCTGTGCCTCATATTAAT	CCAGATCATTAGGACATAATA	ACCCTTCGCATCCATTCTCAA	CAGGCTAAGGATACTAACCAA
1538	CYLC1	XM_088636	CAGGTAGAGTTCCTCCATCAA	AAGGAATTACTCACAGAATAA		
1548	CYP2A6	NM_000762	CAACACGGAGTTCTACTTGAA	CACCTTCGACTGGGTCTTCAA	CCGCTTTGACTATAAGGACAA	TCGGGATTTCTTCCTCCCTAA
1549	CYP2A7	NM_000764	ATGCAAATATTCCAAACTCTT	CCTGATGATGAGCACGTTGAA	CCCAAGCTAGGTGGCATTCAT	CAGCTTCTTCTCCAACCCTCA
1558	CYP2C8	NM_000770	CCGGCGTTTCTCCCTCACAAA	ACGAAGTTACATTAGGGAGAA	AACTCACAACAAAGTGCTTAA	AAGTCAGAATTCAATATTGAA
1572	CYP2F1	NM_000774	CAGCATAAGCACAGCCATCTT	CACCATTATCCGCCTTATCAA	CAGCGGGTACCAAGCTGTGAA	TCGCGGCTTCCTGATACCCAA
1579	CYP4A11	NM_000778	CCCTGACGCACCATAATCTAA	ATCAATTGTATCTTGAGTTAA	TCCTATATTAGTTTCCTATTA	CAGCTGTAAATTGTGTGCTTA
1584	CYP11B1	NM_000497	CTGGGACTGCATCTTCCAGTA	CAGGTGGAGACACTAACCCAA	CAGGACAGTGCTGCCCTTTGA	CACCTTCAGAGCCATCAACTA
1585	CYP11B2	NM_000498	CAGGGAGGCTGCAGTTCCCTA	CAGAGATGGCTTCCTTGTTTA	AAGGCGGAACTGTCACTAGAA	CACTAGATCATGGGATCCTAA
1586	CYP17A1	NM_000102	CAGACATGGCCATATGCATAA	CCGGAGTGACTCTATCACCAA	TGAGTTGAATGTCATACAGAA	CAGGCTGAGGGTAGCACCTAA
1591	CYP24A1	NM_000782	CTCGGACTGTTGACAAGGCAA	AAGTTAGAGATCTGTTATATA	TAGGGTAAAGATGAAGCAATA	TGCAATACTTATAAGACTTAA
1593	CYP27A1	NM_000784	CAGCGGAAGCAGCGCTCTATA	CACGCTGACATGGGCCCTGTA	CTCGAAGATATGGAGGCCCAA	CCGCATTGTCCTGGTTCCCAA
1595	CYP51A1	NM_000786	TCCGTTACAAACGAAGATCAA	TAGGGAATAATCGAACATCTA	TAGGTAATTGGCAGATTCTAA	AAGGTCCTTGGGAGTAATAAA
1600	DAB1	NM_021080	AAGGATAAGCAGTGTGAACAA	AAGGATTAAGTAGGATGTCAA		
1601	DAB2	NM_001343	TGGGAGGTTATGTTTATTTGA	TAGAGCATGAACATCCAGTAA	ACGAAGTAGAAACAAGTGCAA	AAGGTTGGCCTTAGTAGTCAA
1603	DAD1	NM_001344	CAACTTTCTAACAAACATTTA	TTGCCTGAGAATACAGATCAA	CAGCCTCTGCCTTTCATTAAA	CAGATTTGACACTTACTGCTA
1605	DAG1	NM_004393	CAAGAAGATTGCCTTGGTAAA	AAGGGTGTGCATTACATTTCA	AAGAACCATATTGACAGGGTA	CCGGTGGTGAATAACAGACTA
1608	DGKG	NM_001346	CAGCATGTACGGAGGCACCAA	CAGCCATGTTGCACGATTAAA	TAGCCACTCACATAAAGTTTA	ACCGCAAATGTGAATTATCAA
1610	DAO	NM_001917	CTGGAGGGAAAGAACTATCTA	ATGGAGGATAATTGAGGCTAA	CAAGAATTATTGGTGAACGAA	CAAGTTGTACTAACATATTAA
1611	DAP	NM_004394	CTGCTGGGAAATCTAAGGCAA	CACCAAAGAAGAGAAAGACAA		
1613	DAPK3	NM_001348	CGCAGCCAAGTTCATCAAGAA	CACCAACATCTCAGCCGTGAA	CCGGCAGAAGGGCACGGGCAA	CCCAGAGATTGTGAACTATGA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
1622	DBI	NM_020548	CTGGATTTGGTTACTGTGCCA	CCAGTTAAACCAGCTACTCAA	AAAGTGTATTTGTTACTTTAA	CAACAAAGTAGAAGAGCTAAA
1627	DBN1	NM_004395	AAAGTTGATAGGAGACTTGTA	CTCATGTCTGTTAATAAAGAA		
1629	DBT	NM_001918	ATGACTGTTCCTATACTAGTA	ACGATTTGTATCGTATGATTA	AACGATTTGTATCGTATGATT	TAGCCATATACAGACAGTATA
1630	DCC	NM_005215	CCGAGGAGTTCCAGTGATCAA	CAGCATACCAATTACCCATAA	TCACTGCAATGTCAAAGTTTA	CACCTGTGTCCAAGAACTCTA
1633	DCK	NM_000788	AGGCAGCCTGCTATAAAGTTA	TGGACTCATCTTAGTTCTGTA	TTGGTATAAATTAATTTGTTA	AAGTTGCAAAGTGGAATTAAA
1636	ACE	NM_000789	CTCCTGTTACCCGAAACGAAA	CACCACAGAGGCTATGCTAAA	CCCGAAATACGTGGAACTCAT	CAGCGACGAGCATGACATCAA
1641	DCX	NM_000555	AAGGGTTTGATGAATAGCACA	ACCCTGCACATTTGATTCTAA	ATGGACTTTAGTATTAGCCTA	CTGAATAGACAGTCCATATAA
1645	AKR1C1	NM_001353	CACGTGGGAGGCCGTGGAGAA	AATTGTTCTGGTTGCCTATAG	CTTGGTGATTTCAGCAAGCTA	AAGGTGGAATGTCATCCTTAC
1649	DDIT3	NM_004083	AGGGAGAACCAGGAAACGGAA	CAGCTTGTATATAGAGATTGT	CAGCTAGCTGAAGAGAATGAA	AAGGAAGTGTATCTTCATACA
1650	DDOST	NM_005216	CCAGTTTAAAGTGGATTACAA	CAGCCTGTCTCTCATAAAGTA		
1652	DDT	NM_001355	AACATTCCTGTGATCACATAA	TCCTCATATGAAATAAATGAA		
1653	DDX1	NM_004939	ATGAAAGTCTGTAGTCTTAAA	CCGGATGGTTACATTGTCAAA	CCGGGCAATCAAGGAACATAA	CACGGTGTTCCTTATGTTATA
1660	DHX9	NM_001357	TTGGTTGTTGAAGTAACCAAA	CTGTGGTTCATTGTAGTTTAA		
1665	DHX15	NM_001358	CCGGACATGTACAGACATCAA	AGGGACTATTATATTAATATA		
1673	DEFB4	NM_004942	TGCCTTAAGAGTGGAGCCATA	GCCCTAGAAGGTATAAACAAA	GCGACATGTAAACCAAATTAA	GACGTGCGACATGTAAACCAA
1676	DFFA	NM_004401	TGCCTTGAACTGGGACATAAA	CCGGAGCATCTCAGCAAGCAA		
1687	DFNA5	NM_004403	CTGATAAGTTACAGCTTCTAA	TAGAAAGAGTCTGACCCTTTA	AACATACTAATTCTATGTCTA	GCGGTCCTATTTGATGATGAA
1716	DGUOK	NM_001929	AAGGCTCTCCATCGAAGGCAA	CCGCCTGAAAGTACAGCTGGA	CAGCACGATGGTCCTACACAT	CACCTTTGTAAAGAATCTGTA
1723	DHODH	NM_001361	CAGGTATGGATTTAACAGTCA	CTCCCGGATTTATCAACTCAA	CAGGGCTTTGGCGGAGTCACA	CAGGAACTTGACTGTCTTTCA
1733	DIO1	NM_000792	TTGGGAGTTTATGCAAGGTAA	CCCAATCAAGACAAATTGTTA	CACAGTTAATCTGGACAGATA	AAGAGGAGAGTACTCACTTTA
1737	DLAT	NM_001931	CACAGCGATTAATGCAATCAA	TTGGTTTATCATCGATGGGAA	TACCTCATTATTACCTTTCTA	CTCCAGCATCGTCTCATGTAA
1739	DLG1	NM_004087	CGGGTCAATGACTGTATATTA	ACGGGTTATTAACATATTTCA	ATGACTGTATATTACAAGTAA	AACAGTGAAATTCAATTCTAA
1740	DLG2	NM_001364	CCGGACTAACGTGAAGAAGTA	TACGCTCGATTTGAGGCCAAA	CTCGGCTGTATGTGCGTAGAA	CTCGACTAACCCACGAAGTAA
1749	DLX5	NM_005221	ATGTAAGTTATTGCATTTCAA	CTGTATATTCTGGATAAATAA		
1756	DMD	NM_004014	CTGCTTCCAATTTGCTAATAA	CAGGAGTCTAAAGCACTTTAA		
1760	DMPK	NM_004409	CAGCGAGGTAGCGGTAGTGAA	CTGGGTGTATTCGCCTATGAA	GAGCCTGAGGGCTAAATTTAA	AACCAGAACTTCGCCAGTCAA
1761	DMRT1	NM_021951	CTGCATGATTTAAGTGCTTTA	TTGGTAAAGGGTGTAATTTAA	AAGCCATTTGTGTGCCTCTAA	ATGGAGTACTTTGTTATATAA
1774	DNASE1L1	NM_006730	AAGGAAAGTTACTGAGAACAA	CAGGGAGAAACAGACATCAAA		
1777	DNASE2	NM_001375	AAGGGCCACCACGTTAGCCAA	GACCTTGATTGTGTGCCTTAA	CAGCAGAGCTTATAAGATCTA	AAGGGCCACCACGTTAGCCAA
1778	DNCH1	NM_001376	AAGGAGGTTCTTAGCAAATTT	CAGGAGGTAATTGCAGACAAA	CCCGTGATTGATGCAGATAAA	CAGGTGGGTGTACATTACGAA
1788	DNMT3A	NM_022552	TTGATTAATTGGCGTAACTTA	CAGAACAAGCCCATGATTGAA	CTCAGTGGTGTGTGTTGAGAA	AACACCGGGATCTATGTTTAA
1791	DNTT	NM_004088	ACCGGTGGAAATGACAGGAAA	CTGGGATTGGATTATATTGAA		
1796	DOK1	NM_001381	CCGGCAGAAGGCCCAGGGAAA	AAGGATCCCAATTCTGGGTAA	CCGCCTGGACTGCAAAGTGAT	AGGGATCAAAGAAGATGGTTA
1803	DPP4	NM_001935	ACACTCTAACTGATTACTTAA	CAGTAAAGAGGCGAAGTATTA	AACAATGACATTTATGTTAAA	ATCGGGAAGTGGCGTGTTCAA
1804	DPP6	NM_001936	TACTGTCTTAATAGAAGGCAA	TCCCTACACGTTATTGGCTTA	ATGGTTAACCTGATAGAATTA	ACGCTAATGGTTAACCTGATA
1806	DPYD	NM_000110	CTGAGGATAGTAGTTAAATAA	TCGGTGAATGATGGAAAGCAA	CCCACGGAAGGTTATAGTAAA	TCGAGAGTATCCTGGCTTTAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
1807	DPYS	NM_001385	AACACCCGACTTCCTCATGAA	TGGGAAGTTTATTCCTCGAAA	CTCCCTAGGATCCTTTAGAAA	CGGCAGGAGATGGGAAGTTTA
1808	DPYSL2	NM_001386	TACCATGGAACGCCTAATAAA	CAGGCTTGCGTTATTGGCCTA	ACGGATTGCCAGATTTATGAA	CTCGTGTTTATTATTCCTTAA
1809	DPYSL3	NM_001387	CTCAGCTTATATGAAAGTCAA	AAGGATTGTAGTCATCCTGAA		
1810	DR1	NM_001938	AAGATAGTATTAAGTAATTAA	CAGCCGTATATGGAACATAAA		
1812	DRD1	NM_000794	ATCGGTCATATTGGACTATGA	CACAATTAACTCCGTTTCCAA	GACGGTGAGTATCAATAACAA	ACGGTGAGTATCAATAACAAT
1820	ARID3A	NM_005224	CAGCATGTCGGTGGAGATCAA	AAGGATATCTATATATCTATA		
1830	DSG3	NM_001944	AAGGCTCTAGATTATGAACAA	CTCACTGGTGATGATACTAAA		
1832	DSP	NM_004415	CAGAAGAATGACTATGACCAA	CCGACATGAATCAGTAAGTAA	CAGGGAGATCATGTGGATCAA	AAGGGCCACGGTATTCGCTTA
1834	DSPP	NM_014208	GAGGATGTCGCTGTTGTCCAA	CATGATAGTAGCATAGGTCAA	AACGAGGGTAATACAAGTGAA	TCGGATAGTAAAGAATATTAT
1837	DTNA	NM_001390	CAGCCATAGAATTTAGTGTAA	TGCGACCTATTCAATACATTA	CAGCATTGAAATTATATAGAA	CCCGTTGTCATAGCTATTTCA
1838	DTNB	NM_021907	CAGCTTATTGCAGAACTGGAA	CCACTTGACCTTGCACATATA		
1840	DTX1	NM_004416	CCGGGAAGAAGTTCACCGCAA	GTGGGAGTCAGCCAAGATTTA	CAGTGTGGGTGGAGAAATAAA	GACCAAGAAGAAGCACCTTAA
1844	DUSP2	NM_004418	CGCGGGAAAGACCGAAAGGAA	AAACTTAGCACTTTATATTTA	CTGGTCCACCACCATGTTGAA	CAGCCTGAGAGCTCCAAGGAA
1856	DVL2	NM_004422	CTGGCTGGTGTCCTCAGATAA	CACGCTAAACATGGAGAAGTA	CCGGATACGAGAGCTCCTCTA	CTGGGAGATTTGGGCCATGTA
1857	DVL3	NM_004423	CCCGGCTAAATGGAACTGCGA	CTCCTGGTTACTTCATCACAA	CAGCATATCATATCCATTTCA	ACCAAGTATGTTCCTCCTGAA
1869	E2F1	NM_005225	CTCACTGAATCTGACCACCAA	CAGATGGTTATGGTGATCAAA	CAGGACCTTCGTAGCATTGCA	ACGCTATGAGACCTCACTGAA
1870	E2F2	NM_004091	TCCGTGCTGTTGGCAACTTTA	TAGGGACCAGGTAGACTTTAA	ACCCATTGGGAATGAGTTTAA	TTGAGACGAGGGATTATTTCA
1874	E2F4	NM_001950	GCGGATTTACGACATTACCAA	AACGAATGGATTCCTATATAA	ACCCGGGAGATTGCTGACAAA	AGGTATCGGGCTAATCGAGAA
1893	ECM1	NM_004425	CTGAACACTCATTACACTAAA	CCGGGACATCTTGACCATTGA		
1908	EDN3	NM_000114	CTGGACGTCAGCAGTAATTCA	TAGACACAGATCATAGCTCTA	CAGAAGCATGCGACTTTCATA	TTGCAGGAAGCCGACTGTAAA
1912	PHC2	NM_004427	CTGGTTCACAAAGAGCATTAA	CCGGGTGGACTTTGCCTATAA		
1915	EEF1A1	NM_001402	CAACGTTACAACGGAAGTAAA	AAGCTGGAAGATGGCCCTAAA	CTGGGTCTTGGATAAACTGAA	CTGGTTAATGATAACAATGCA
1933	EEF1B2	NM_001959	CTGGATCATGGCATTTAAATA	ATCCTGGATCATGGCATTTAA		
1936	EEF1D	NM_001960	CTGGTTCGACAAGTTCAAATA	CCGGCTGAACGTGCTGGAGAA		
1937	EEF1G	NM_001404	CACCCTGTTGTGGCTCTATAA	ATGGCCCAGTTTGATGCTAAA		
1938	EEF2	NM_001961	TGCCGTTTCTTTCAATATTTA	CCGCGCCATCATGGACAAGAA		
1942	EFNA1	NM_004428	CACCATACATGTGCAGCTGAA	TACAATGTTCTTTGTCTCAAA	CCCGGAGAAGCTGTCTGAGAA	CACGTGTATAGTATCTGTATA
1945	EFNA4	NM_005227	CTGGAGAGACTTACTACTACA	CTGGGATTTGGTATGATCAAA		
1947	EFNB1	NM_004429	ACCGACATCATCATTCCCTTA	ACGGACTACAGAGAACAACTA	CTACATTACCTCAACATCCAA	CTCACGGTAATTAATGTCTTA
1952	CELSR2	NM_001408	CCCACTATACAGTGAATGTTA	CCGGGAGGAAGTTGATTTCTA	CACGTGGTGGTCTTCAACGTA	ACGACAACAATCCAACCTTTA
1953	EGFL3	NM_001439	CCCGTATTTATGTAAAGGTAT	CAGGACCTGCCTGGCCATTAA		
1955	EGFL5	XM_376905	TTGGAAGATGATGGCAATGAA	CCCAGGTAAATTGACCATTAA		
1956	EGFR	NM_005228	TACGAATATTAAACACTTCAA	CCCGTCGCTATCAAGGAATTA	CCCATCCAATTTATCAAGGAA	CAGGAACTGGATATTCTGAAA
1964	EIF1AX	NM_001412	CACGTAGAATGTATATTTGTA	AAGTCTGTTTGTCATATTTAA		
1969	EPHA2	NM_004431	CAGCCTTCGGACAGACATATA	TTGCAGATGATTCAAACCGAA	TCGGACAGACATATAGGATAT	CAGCGCCAAGTAAACAGGGTA
1973	EIF4A1	NM_001416	AAGGATCATGTCTGCGAGCCA	CCCGATGGGATGGAGCCCGAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
1979	EIF4EBP2	NM_004096	CAGGAATAAGCTGGATCTCCA	CACCTTAATTGAAGACTCCAA		
1993	ELAVL2	NM_004432	CTGAATGGATTGAGACTTCAA	CAAGACCAACTTAATAGTCAA		
1995	ELAVL3	NM_001420	CTGGTGCATCTTCGTGTACAA	CCCGACTTTAGCTATAGTTAA		
1996	ELAVL4	NM_021952	ATGGTCCGACATCCAATACAA	AAAGGTGATTCGTGACTTCAA	TTGGAGCAGTGAACAACGTAA	GCAGTGTTGCCTAAGTATTAA
1997	ELF1	NM_172373	CAGAACTTAAATAGAAGGCAA	CAGAGTGAATTTGTATTTAAA		
1998	ELF2	NM_006874	AAGCATCAGTTCACAGCAGTA	AACAACTGAACCCATCAATAA	CACCAGATAGCCATGAAGCAA	TACGATATCAAGTTACACTAA
2009	EML1	NM_001008707	CAGGCCGTGCTTAACAGGAAA	CAGATTGAAATTTATTGTTTA		
2012	EMP1	NM_001423	TAGTATGTTATTCCTGGTTAA	CTCTATGTTTATTCTAGTTAA		
2020	EN2	NM_001427	CCCGCTCTTTCGGATCGCTAA	TACGTTGTACATAATAGTGTA	CACCAAGTAGCTATATATGTA	CCCACGGTAAACAATATGGAA
2021	ENDOG	NM_004435	CCGCACCTACGTGATGCCCAA	CTGGAACAACCTGGAGAAATA	CTGATGGGAAATCCTACGTAA	CCCGGGCGAGCTGGCCAAGTA
2022	ENG	NM_000118	AAGGGAGAACTTGAAACAGAT	CGCCATGACCCTGGTACTAAA	ACCAATAAATCAGACCATGAA	CAGCAATGAGGCGGTGGTCAA
2027	ENO3	NM_001976	CCAGACCTGCTTCCTGAAATA	TAAGAGCTTTATCAAGAACTA		
2029	ENSA	NM_004436	TTGGGAGAAATATCAATGAAA	TCAGTATTCGAAATAAACAAA	CTAGTTGAGAACTCAACATTA	TAGTTGAGAACTCAACATTAA
2030	SLC29A1	NM_004955	CCGCCTGGAATTCTACCGCTA	CAGCCTCAGGACAGATACAAA		
2033	EP300	NM_001429	CAGGGAATGAATGTAACAAAT	CACCGATAACTCAGAGTTGAA	CCGTTTGTGGTTTAAAGCAAA	TTGGACTACCCTATCAAGTAA
2035	EPB41	NM_004437	ACCGAGCAGCTAAGAAATTAT	CACGGCCTAGTGAATGGGATA	GAGGATTTAGACAAGAGTCAA	TAGGATATCAGAATTGTTCAA
2037	EPB41L2	NM_001431	CAGGTCTTAGATAAAGAGGAA	ACGCAGTAACTTCTACATTAA		
2039	EPB49	NM_001978	CAGAAGATCTATCCCTATGAA	CCGCCCAGATTCCAACATCTA		
2040	STOM	NM_004099	CCCATTCATTACATAGTATAA	TTGGTGATTTATATAAGGTAA		
2043	EPHA4	NM_004438	AGGGTGTATATTGAGATTAAA	CCAGTACTGAATAAACTCAAA	CCGCCAGGACATTTCCTATAA	CCCGCGAATGAAGTTACCTTA
2044	EPHA5	NM_004439	ACCAGCTACACGATTATCAAA	AACGGAATGGTGCCATTGTAA	CCCGGCAGTATGTGTCTGTAA	ACCAGTTGGATCTCCAATGAA
2045	EPHA7	NM_004440	CCCAATGGAGTCATCACAGAA	TACGAGAAAGATCAAAGGGAA	CAGGCTGCGAAGGAAGTACTA	ACCAGTCATGATAGTAATAGA
2047	EPHB1	NM_004441	GAGATGTACCTTCAATTGAAA	ATGATACTGACTGATTAATTA	GCGGGATGATGTGACCTACAA	ATGGCCCTGGATTATCTACTA
2048	EPHB2	NM_017449	CCCGGATCATTCACTGTGATA	TAGGCCTCACTCAACAACCAA	CCGAGAGGACCTCGTCTACAA	CACGCTTTCTAGAGGACGATA
2051	EPHB6	NM_004445	CGCCAATCTCTAGATCAACAA	CCGGGAGACCTTCACCCTTTA	CTGGAGCTTTGGGATACTCAT	AACCGCCAATCTCTAGATCAA
2052	EPHX1	NM_000120	CCACTATGGCTTCAACTCCAA	TTCCAGGAATTCTACATTCAA	CAACAGATACCCTCACTTCAA	CAACATGGCTTTGATGATAAA
2058	EPRS	NM_004446	AAGCATGAAGAGCTAATGCTA	CAGGAGGAGACTATACAACTA	AAGGAGGTGGGCTCTCATCAA	AAGGCGATTACTCAGTGTTAA
2059	EPS8	NM_004447	CGCCATATAGATAGAAATTAT	TTGGATATTGTGAGACCTCCA	CAGGTGGATGTTAGAAGTCGA	TCGGTTCTAAAGGATGATATT
2065	ERBB3	NM_001982	AACACTGGTGCTGATCGGCAA	CTTCGTCATGTTGAACTATAA	CCAGAGCTTCAAGACTGTTTA	ACCGGCGATGCTGAGAACCAA
2066	ERBB4	NM_005235	CACCGGAATACTGTGGTGTAA	TCGGGATTTGGCAGCCCGTAA	CTGGAGAATTTACGCATTATT	CTACGTGTTAGTGGCTCTTAA
2067	ERCC1	NM_001983	CACCGTGAAGTCAGTCAACAA	CACCGTGAAGTCAGTCAACAA	CCCGGGTGACTGAATGTCTGA	ACCGTGAAGTCAGTCAACAAA
2068	ERCC2	NM_000400	CCGGGAGGATATTGCTGTGAT	CCGATTCTATGAGGAATTTGA	TCGAAAGTTGCTCAACTTCTA	CCCGCTCACCCTCCTTGCTAA
2070	EYA4	NM_004100	CTGGGTCAGTAATTACAAGTA	CAGCTTTAGCAAAGAACTCTT	AGCGTATATGACATCGAATAA	CAGTCCTATTTAGACATGTAA
2071	ERCC3	NM_000122	ACCCATGTGCATGAGTACAAA	CCGGGAATATGTGGCAATCAA	CCGGTTCACCTCCGATGCCAA	ACCGTTCTGAATAAACAGAAT
2103	ESRRB	NM_004452	CAGCTGCGGCTCCTTCATCAA	ACGCAGGTACAAGAAGCTCAA	CCGCTTCATGAAATGCCTCAA	CAGCACTTCTATAGCGTCAAA
2113	ETS1	NM_005238	CTCGGATTACTTCATTAGCTA	CCGACGAGTGATGGCACTGAA	TCGGATTACTTCATTAGCTAT	ATGCATGTCGTTCCAAACTAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
2114	ETS2	NM_005239	CCCGGTCAAGTTGGTTTCAAA	CTGTGATGAGTCAAGCCTTAA	CTCATTGTATGTGAGGTTGAA	AGGGATTTATGTAGCAGCTAT
2118	ETV4	NM_001986	ATGGGCTATGGCTATGAGAAA	CAGCAGAGCTTTAAGCAAGAA	ACCGGAGTCATTGGGAAGGAA	CCGGAGTCATTGGGAAGGAAA
2119	ETV5	NM_004454	CAGAAATTACTCAATGCTGAA	CAGGATCTCAGTCAACTTCAA		
2121	EVC	NM_014556	CAGCTAATCGATAATATGGAA	AAGAAGCAACTTGTAGTTTAA		
2122	EVI1	NM_005241	CTGAACTAGCAGATCACCAAA	CCAGTGCTATCCAGTCCATAA	GAGCTGTGAATGATTCTATAA	CAGCACTACGTCTTCCTTAAA
2123	EVI2A	NM_014210	AACCCTATAACTCCTGAAGTA	CATGGTAGACCTTGCAATTTA	ATGGCTATGCTAATTTGCTTA	GAGCTAAACTGTGTAATTTAA
2124	EVI2B	NM_006495	CAGGATTTATCTTAGATACTA	CAGGTATTGGCTAATTCTCAA		
2130	EWSR1	NM_005243	CAGAGTAGCTATGGTCAACAA	CTGCATTGACTACCAGATTTA	TCCGGGTTGTGGAAACCAGAA	CAAGAGGGCCTCTTAACTGTA
2134	EXTL1	NM_004455	CCCGACTGCATCAACCAGATA	TAGATGGATGGCAGACATTAA		
2138	EYA1	NM_000503	CCCAATGGCACCGAAGTTAAA	CAGGAAATAATTCACTCACAA	TCGGTATAAATATGTAGATAA	AACTCGGTAACTCTCATATAA
2151	F2RL2	NM_004101	TCAGTTAGGATACATCACTAA	AAGGCTAACTTGCTAATCACA	CAGTTAGGATACATCACTAAA	CAGGAGCCACGATTACTGTAA
2153	F5	NM_000130	TTGGATAATTTCTCAAACCAA	CCCATTCAAGACCCTGATCAA	TAGGAATTAGGTCATTCCGAA	CGCCATTAATGGGATGATCTA
2155	F7	NM_000131	CAGTTGAATATCCATGTGGAA	TCGAACTGTCCTGGCACCAAA	CAGGGTCTCCCAGTACATCGA	CTGGTTCTTATCCATTATCAT
2162	F13A1	NM_000129	CACGAGCGTTCACCTGTTCAA	AGCGTTGACATTCTATTGGAA	CAAGGAGAGATGGGACACTAA	TACAATGTAATAGAAGCTTAA
2177	FANCD2	NM_033084	CGGCTTCTCGGAAGTAATTTA	TTGGAGGAGATTGATGGTCTA	CAGAGTTTGCTTCACTCTCTA	ACGGGAGAGAGTCAGAATCAA
2178	FANCE	NM_021922	TCGAATCTGGATGATGCTAAA	TAGCCTGAGGATAAGGCTGA	CTGACTTGAATAATTTATCAA	AACGCCGAGGAGAGCTTGTAA
2182	ACSL4	NM_004458	ATGCATCATAGCAATTTGATA	TTGGAGCGATTTGAAATTCCA	CAGATTATAGATCGTAAGAAA	AAGGGCAGAGTTACTTGATAA
2189	FANCG	NM_004629	CCGGCTCGTTCGACAGGCCAA	CCGCGGGAACTAACTCTTCAA	CTCATTGAGGTAGAATTACTA	CCCAGGTAATCGAGACACTTA
2192	FBLN1	NM_001996	CAGGTCATGTGAAGACATCAA	CAGGATGTGTGTCGATGTCAA		
2197	FAU	NM_001997	GGCCGCATGCTTGGAGGTAAA	CCGCCGTTCAGTCGCCAATAT	ACAGGAGAAGAAGAAGAAGAA	AAGCCACTTAGTTCAGTCAAA
2204	FCAR	NM_002000	TGGAACTAAGTTATTCGGCAA	GAGCTTATTGTCGTAAGAATA		
2205	FCER1A	NM_002001	TCCATGGAATAGAATATTTAA	CACATTTCTCTTGAAGATTAA		
2212	FCGR2A	NM_021642	CCCAATGTCCAGCCTCTTTAA	AACCTCTAACAACAAATTAAA		
2214	FCGR3A	NM_000569	TTCGCTGAGTTAAGTTATGAA	CAGACTGAGAAGTCAGATGAA		
2220	FCN2	NM_004108	CAGCTTTGCAAATGGCATCAA	AAGGATACAATTATAGCTACA	CCGGGACTGGGCCACGTACAA	CTGCCATGTGTCAAACCTGAA
2232	FDXR	NM_004110	CAGGTTGGGAACATGCTGGAA	TGGGAACATGCTGGAAATAAA	CACGTGGACATCTACGAGAAA	AAGCGTGCCCTTTGACTCCAA
2235	FECH	NM_000140	CTGGAATATTAATGCTAAACA	CCGACTGGTGTGGCAATCCAA	ACCCATATCCTCAGGAGGTAA	CCCAAGGGTAATAAACGTGTA
2237	FEN1	NM_004111	CACAATGATGAGTGCAAACAT	TAAGTCCATTGTTACATGAAA	CTGACTGCCAGTGAAGCCAAA	CAAGAGCTACTTTGGCCGTAA
2239	GPC4	NM_001448	ATGGCCATTTATACATGCAAA	TACCAAATGATAGCTCATAAA	CAGATTGTATTCAAAGCATCA	TAGGTAGAGCTGAGAATACTA
2243	FGA	NM_000508	AGGGTTGATTGATGAAGTCAA	AGGGCTTTAGCTCGTGAAGTA	CAGCCAATAACCGTGATAATA	ACGCGTCGTTCATGCTCTAAA
2244	FGB	NM_005141	ACCGTATAGAGTATACTGTGA	CAGGAAATGGGATCCATATAA	TAGAGTATACTGTGACATGAA	CAGCACGTATGACAGAGACAA
2246	FGF1	NM_000800	GCCCATTTCGAAGATATACAA	GAGAATGATAGTAATAGGATA	AAAGTAGGAACTCTTAAGCAA	CTGATACTTATTTACCTATAA
2247	FGF2	NM_002006	TGCCTTGTGGATATCAAGAAA	ATGCTAAACTTTACTGATGTA	TAGCACTAGTCTTAAATTGTA	AACAATATTAGTCGTATCCAA
2248	FGF3	NM_005247	CGGGCGGTACCTGGCCATGAA	TTGTGTCATCACAACATTAAA	CAGGGTCCAGTGGGAACTGAA	TTGCTCCTGGGTGGAAATTAA
2252	FGF7	NM_002009	CACAAGAGTCTAGATCAGTTA	TAGTTTGTAGCTACAGTAGAA	AGCCTTTACATTTGTACACAA	CACCCGGAGCACTACACTATA
2253	FGF8	NM_006119	GCGCTTCGAGTTCCTCAACTA	CAAGAGCAACGGCAAAGGCAA	CACGGAGATTGTGCTGGAGAA	CTACATCTGCATGAACAAGAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
2254	FGF9	NM_002010	TTGGATATACCTCGCCTAATA	GCGATACTATGTTGCATTAAA	TACGTACTCGTCAAACCTATA	ATCGCAGTGAACTTAAAGCAA
2259	FGF14	NM_004115	CAGGAAGTAAGCTAATGCTTA	AGGGTTGTATATAGCCATGAA		
2262	GPC5	NM_004466	AAGAATTTAGTGTATCTGTAA	CAGCTTTGTGCTAATGAATTA		
2264	FGFR4	NM_002011	CAGGAGGTTCTGGGCCTCTGA	CCGCCTGACCTTCGGACCCTA	CAGGCTCTTCCGGCAAGTCAA	GACATTGACTACTATAAGAAA
2268	FGR	NM_005248	CAGCACTAAGGTGGCGGTGAA	TTGATTCTGTAAATAAGTAAA	CAGACCTTGTCTAGTTATTTA	CACGTGGAACGGCAGCACTAA
2271	FH	NM_000143	GAGATCTACGATGAACTTTAA	CAGGAATTTAGTGGTTATGTT	CCCAACGATCATGTTAATAAA	TAGGATGTGCTAGGTCTAAGA
2272	FHIT	NM_002012	TCCACTGAGAACAGTCTGTAA	TTCGCTCTTGTGAATAGGAAA		
2274	FHL2	NM_001450	ACCCTTTAGTGCTTTGTGATA	CTCCCGTTGCGTCAAGTCTAA	AAGGTAATGACCAGTTGTTAT	ATCGAGTAAGGCACACCCAAA
2281	FKBP1B	NM_004116	CACTGCCTTACCTTCACTTAA	CAGAGGGACTTGAGCCAGTTA	CACAAGGTGGTCAGACATGAA	AACAATGTCCTCTTTGAGAAA
2288	FKBP4	NM_002014	CACGCTTGTATTTGAGGTGGA	AGGGATGAGGTCTGATAAGAA	TTGAGTGAATTAGACCTTTAT	AGCAATAAAGTGGAAACAATA
2289	FKBP5	NM_004117	GCGACAGGTTCTCTACTTAAA	TCGGCTGGCAGTCTCCCTAAA	AACGCCGATGATTGGAGACAA	ACGGGTAAACAGATTGAGCAT
2296	FOXC1	NM_001453	CCGCCACAACCTCTCGCTCAA	AACGGGAATAGTAGCTGTCAA	CTCCAGTGAACGGGAATAGTA	ACGGGAATAGTAGCTGTCAAA
2298	FOXD4	NM_207305	AAGACCATCATCCCTGGACTA	TCCACCACACATGGTCTTGAA		
2301	FOXE3	NM_012186	CACCAGGGCTCCTGACTGAAA	TAGGACTTATTGGGTTATTAT		
2305	FOXM1	NM_021953	CCAAATTATCCTCTAATTATA	CCGCCGGAACATGACCATCAA		
2306	FOXD2	NM_004474	CCGAGTGAGCCTTAACATCCA	CACTGGGTGTGCATTGATTTA	CCGGCGGGTCGTGCCCTGGAA	CCCATTGGTGTCAATTGAATA
2313	FLI1	NM_002017	ACCTTTGTATTTGTTCTTTAA	CAGGACATATGTGGCCTTGAA		
2316	FLNA	NM_001456	CACAGGCAACATGGTGAAGAA	CCGCTTCACCATCGACACCAA		
2321	FLT1	NM_002019	CCCGAATCTATCTTTGACAAA	TCGCGGGAAGTTGTATGGTTA	CACTACAGTATTAGCAAGCAA	ACCGCATATGGTATCCCTCAA
2322	FLT3	NM_004119	ACCAATTCAAGTGAAGATTAT	CAGGTTTAAAGCCTACCCACA	TACGTTGATTTCAGAGAATAT	CCGGCTTGAGTGAATTGTGTA
2323	FLT3LG	BF688722	TAGTATAGTTGAAATAAGAAA	GCGGGATTTGTTGAAGAGAAA	GCGCGTGAACACGGAGATACA	CTCCTCCGACTTCGCTGTCAA
2324	FLT4	NM_002020	CCGCCGATTATTCCTTGGTAA	CGCGCTGATGTCGGAGCTCAA	CACGCTCTTGGTCAACAGGAA	CACCGTGTGGGCTGAGTTTAA
2326	FMO1	NM_002021	CAGTACTTTCATAGCCGGCAA	AGGCCTCACTGTACAAGTATA	ATCATGCAAATTACGGCTTAA	CCGAACATTCAAGGTCATCAA
2328	FMO3	NM_006894	CCGGACATCATGTGTATCCCA	AAGAATCATGTCATGATCTTA	CCCGCTGGGCAGCACAAGTAA	AACTATGTTCTTTATATCTAA
2329	FMO4	NM_002022	ACGAAGATTATGCTAATTTCA	ATCGGCCTTATCGGCCTTAAA	AAAGAAGATATTTCTATACAA	CACGATGGGTCACAAGAGTAT
2330	FMO5	NM_001461	AAGGCGGACAGGCGACACTAA	AACCAAAGGTTTGACCATGAA	CTGAGTCAGCATCCAACCTTA	CTGGGCCACTCAGGTATTTAA
2334	FMR2	NM_002025	CACGTGATAGTCATAACCCTA	CTGGGTAAGACTACTCAGTAA	TAGGAACTAATTAAACATGGA	CGGCCTTATTCTCATAATTAA
2348	FOLR1	NM_000802	CTGGACTTCAGGGTTTAACAA	CACATGTGTCTTGAGAATTAT	CCCACTGTTCTGTGCAATGAA	TAAGGATGTTTCCTACCTATA
2353	FOS	NM_005252	TAGAGGGTTCCTGTAGACCTA	TGGGTTCATTATTGGAATTAA	ATGGATTCTCAGATATTTATA	GACCAATATTATACTAAGAAA
2356	FPGS	NM_004957	CTGGAGTGAATTAAAGCCTTT	CCGCACTGTCCCAGTAGCCAA		
2357	FPR1	NM_001629	ACGACCCTAAAGAGAGGATAA	TTGCAAGGCATGTACAAAGAA	CACCGTGAGCCTGGCCAAGAA	AACCAGTGACACAGCTACCAA
2475	FRAP1	NM_004958	CCGGAGTGTTAGAATATGCCA	CCGGCACAATGCAGCCAACAA	ACCAATTATACCCGTTCTTTA	CAGGCCTATGGTCGAGATTTA
2488	FSHB	NM_000510	CAACATCACCATTGCAATAGA	TCGTTTCTGCATAAGCATCAA	AAGAATGTCGTTTCTGCATAA	CACCAGGGATCTGGTGTATAA
2515	ADAM2	NM_001464	CGGGCTGCGGATGGACAGTAA	TGCTATAATGGTGAAAGTTAA	CTGTTGGTTAGTAGACACTAA	AACCATATACTGTGAATTTAA
2516	NR5A1	NM_004959	ACGCAGGTGCATGGTCTTCAA	AAGGATAACCGAGTTTGCTAA	CAGGGAGAAGTTGAGCAGGTA	CTGGAATAAATTTCGCAATTA
2517	FUCA1	NM_000147	CCGGAAGAGGAACATCCGCTA	TACGACCTTGTTAACAGCTAT	TCCACTCTATCTACTTGATAA	TTCGCTATGTTTACAGTGATA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
2521	FUS	NM_004960	ACAGGATAATTCAGACAACAA	CAAGCAGATTGGTATTATTAA	CTGGGTGAGAATGTTACAATT	ACAGCCCATGATTAATTTGTA
2524	FUT2	NM_000511	CAGCGGCTAGCGAAGATTCAA	CACGGGCGGAGACACCATCTA	CAGTGCTAGCCTCAACATCAA	CACCATCTACCTGGCCAATTA
2531	FVT1	NM_002035	CAGGCAAAGAAAGAAATTGAA	TAGACTCAAATGCTTAGGGAA	CAGGAATGTGGCTGCAAGCAA	AAGAATTTACAGTTCCTTCAA
2532	FY	NM_002036	CTGGACACCCTTGGAAGCAAA	CACCTGTCAACCTGAATTAAA	CAGCTGGACTTCGAAGATGTA	ACCAGTGTCCTGGGTATCCTA
2535	FZD2	NM_001466	CACGGTGAGACCACCGTGTGA	CACCATGGTGTCGGTGGCCTA	CACGTACTTGGTAGACATGCA	CACGGTCTACATGATCAAATA
2537	G1P3	NM_002038	CAGCAGCGTCGTCATAGGTAA	CAGAATAAACTTCACCCAGAA		
2538	G6PC	NM_000151	TAGCAGAGCAATCACCACCAA	CTGGCTTATTCCCATGTGTGA	TGGGATCCAGTCAACACATTA	CAGCAGGTGTATACTACGTGA
2539	G6PD	NM_000402	ATCGGGTGACCTGGCCAAGAA	CACCAAGATGATGACCAAGAA	CTGCGTTATCCTCACCTTCAA	CAGCCTCTCTGCTATAAGAAA
2542	SLC37A4	NM_001467	TTGGATATAGGTGGGAAGAAA	CCGGGTGGCGCTGGAAGTTAT		
2547	G22P1	NM_001469	CAGGTTAAAGCTGAAGCTCAA	GAGGGTTAGCGTTAGCCTTAA	GAGGATCATGCTGTTCACCAA	CGCCTAGTGAGCAGTAGCCAA
2556	GABRA3	NM_000808	TACAATGAGGTTAACAATTCA	CCCGACTGAGACCAAGACCTA	CAGAGATAATCCGGTCTAGTA	CCCTCAATTCATATTTATGAA
2561	GABRB2	NM_000813	TCCTATAATGTAATACCTTTA	TACCTATTTCCTGAACGATAA	CAGAAGCACAATGCTAGCCTA	ATCCCTCAGCTTTAAGCTTAA
2563	GABRD	NM_000815	CCGCGGCACCAGAGCGATGAA	ATCGGAGGACATCGTCTACTA	CACCTTCATCGTGAACGCCAA	CACGGAGCTGATGAACTTCAA
2564	GABRE	NM_004961	CCGCATCTACAAGGATGGCAA	CAGGCATTACTCGCCATTGAT	CAGCAGACCATTTCAAATTAT	CACTCTAACCATCACAATCAA
2566	GABRG2	NM_000816	CACCATCAGATCATAAGCATA	CACCCTAAGGTTGACAATTGA	TAGGAGTGAAGCCAACGTTAA	TAGATTCATAATGCAATTAGA
2568	GABRP	NM_014211	TAGATTGGTCTTACAGTTTGA	AAGTGGCTTAGCTTAAGTAAA	GAGCCCAAGATTACAAATGTA	CAGAAATAAACCAAGGCTCTA
2569	GABRR1	NM_002042	CAGGGTTACAGTAACTGCAAT	CACCACCAAACTGGCTTTCTA	ACGTGCTCTCTTGAAATTGAA	CAGAAATAACTGTATAATGAA
2572	GAD2	NM_000818	ACGGGCGGCATCGGAAACAAA	CGCCTTGGACAAGATTTATAA	AAGTTTCGATAGATCAACCAA	CAACCTGTTCTTCCTACCAAA
2580	GAK	NM_005255	CACGCAGTACACGGTCTTCCA	AAGGCCTAACTATGCCTCGAA	CCCGTGGTTGTCTGTACAGAA	ACGCGTGTGACATTCAAGAAA
2581	GALC	NM_000153	TTCAAGGTGGTTGATGTTATA	TACACTCACGTTAACTATTAA	CAGTATTATAGGAGACTACAA	TAGGAATTTATAAGAGTCTAA
2585	GALK2	NM_002044	TCCTAGGTTACTGAAGCTAAA	CTGGAGGAACTCCGAACCCAA	TGCGCGAGTGCTCCAGTTTAA	AAAGCTCTCTATGCTTCATAA
2615	GARP	NM_005512	CTGGAGTTTGAGACTATGCAA	AACCAACAGTATAAAGCCTAA		
2622	GAS8	NM_001481	CACCGACATTAAGAACTACTA	ATGCATAAGTATATTTGTTTA		
2628	GATM	NM_001482	TAGAATGTACACACATCCAAA	CAGGTCAATTATCAAAGACTA	CCACTAATAATTAACCATCTA	ACCGAGCGTACAGGTCAATTA
2629	GBA	NM_000157	CCGGAATTACTTGCAGGGCTA	CCAGAACAGAAGTTCCAGAAA	CAGGGCTAACCTAGTGCCTAT	AAGAAGGAATCGGATATAACA
2642	GCGR	NM_000160	CCGCAATGCCATCCACGCGAA	CAGCTCCGTGCTGGTCATTGA	CTCCAACAATAAAGAGCTCAA	CAACAGAACCTTCGACAAGTA
2645	GCK	NM_000162	CTGGACAAGCATCAGATGAAA	CACGATGATCTCCTGCTACTA	CAGCTGTATGAGAAGCTCATA	CAGGACTTTGATGCATTTCCA
2661	GDF9	NM_005260	ATCAGTGGAACTGCTATTTAA	CAAGTCAGTCTTGCTGTACAA	TACCGTTGAACACTTACTCAA	CAGCTGGTATTCCCTTCACTA
2662	GDF10	NM_004962	AGCGCTCGAGGTGCTATGCAA	AACAGGATAATCGTGGTGTAA	CACGGAAAGAACTCTGTTTAA	TAGTAACGTGGGAATACTAAA
2664	GDI1	NM_001493	ATCCACTGACCAAATCCTTAA	ACCCTTATCTTGCAAAGTGAA	CTCTAGTGTATTTCACAGAAA	CCGCATCAAGTTGTACAGTGA
2668	GDNF	NM_000514	CGGGACTTTAAGATGAAGTTA	CTGGAGTTAATGTCCAACCTA	CTGGTTTACCATATTCTAAGA	CGCGCTGAGCAGTGACTCAAA
2671	GFER	NM_005262	ATGGCCCAGTTCATACATTTA	CCGGGCCTGCGTCGACTTCAA		
2677	GGCX	NM_000821	CCGCCTGCTTCCCAAGTATAA	CAGACCTTTCTTAGACGCCAA	TACGTCTATGTCAACACTACA	CAGGAAGAGGTTAGACGCAAT
2702	GJA5	NM_005266	CTCCCTCTACTCAGCCTTAAA	CTCAATGACGTTGCTCATTAA		
2705	GJB1	NM_000166	CTGCACAGACATGAGACCATA	TGCCTGAAATGTTACACATTA	TGGCATCTGCATCATCCTCAA	GCCTGAAATGTTACACATTAA
2720	GLB1	NM_000404	CCAGAGGATGTTTGAAATTGA	ACCACTGATGGAGCACATAAA	CAGAATGGAGGGCCAGTTATA	CACCAAAGTTTGCATATGGAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
2740	GLP1R	NM_002062	CAGGAACTCCAACATGAACTA	CAGACTCAAACTCAAGGTCAA	CCAGACAGAGCCGCAAATCAA	CAGGCTCGTTCGTGAATGTCA
2741	GLRA1	NM_000171	CTGGAGTTTAACAAACAGCAA	TCGGATTTCCTGGATAAGCTA	CCCATAACTCGTGGACTACAA	CCGCTTTAACTTCTCTGCCTA
2746	GLUD1	NM_005271	CAAGCCTAACCTTGACTCAAA	CCTATAGAAATAATAAATGAA	CAGTGAATGCCTATAGAAATA	CAGAATTTGCTTACCATAATT
2768	GNA12	NM_007353	TAGCTATACTGTGTACACATA	GAGGTAGTTGTGCCTCAATTA	GTCCGTTTAACTCGATAGAAA	CCGGATCGGCCAGCTGAATTA
2769	GNA15	NM_002068	CTCCGTGCGGGCTGAAATTAA	CCGGTTTGCGGACGAGAGAAA	GAGGTTCATCCTGGACATGTA	TCCGTGCGGGCTGAAATTAAA
2779	GNAT1	NM_000172	CACCGACACGCAGAACGTCAA	CAGCATCTGTTTCCCGGACTA	ACGCACAGACTCAGCAATAAA	ACGCGCCATGACCACACTCAA
2780	GNAT2	NM_005272	TAGGGAGTCTCAGTCAATGTA	AACCAATTAGAACGAATTACA	ACGGCAAATATGGGAAGTGGA	TGGGATAGCTATTGCAGCTTA
2783	GNB2	NM_005273	CGCCTGTGATGCCTCTATCAA	CGGCCATGAATCCGACATCAA		
2784	GNB3	NM_002075	CAGATTGCAGATGCCAGGAAA	TCCGGGTGCCATTCCCACTAA	CAACATGTGTTCCATCTACAA	TCCCTTAATGAGCAAGGACAA
2785	GNG3	NM_012202	CTCGGTGACCTGCTCAGACAA	GTGGAACAGCTTAAGATTGAA	CTGGAGCTACTGGGAGGGTAA	CAAGATGGTGGAACAGCTTAA
2788	GNG7	NM_052847	CAGGGCATCATTCAGTAATTA	ACGGCTAAACTCGGATTGTGA	ATGGTTGAACCCGTCGCTAAA	ACGCATCCATCTCCAAGTTAA
2794	GNL1	NM_005275	TCGGCTTTCCACTAAGGTCAA	CCAGGCTACAGTGAACAGAAA		
2798	GNRHR	NM_000406	ACCAGTATTGATGAATAACTA	CAGGTTGTCAGACCCAGTAAA	ACGGTTGCATTTGCCACTTCA	AAGCATGGATTGGATCAGTAA
2799	GNS	NM_002076	CGGCGGCATGACACCGCTAAA	AAGCAAGATGCTGGTTGCCAA	CTGGTTAATTAGGCAAGCCAA	ATCAGTCAACTTCCACATTAA
2802	GOLGA3	NM_005895	CGGAAACTTTAGAGAAGTTAA	CTGGCCGATTACAGAACTGAA		
2813	GP2	NM_001502	TTGATGGGACCTTGAAAGCAA	CCAGAACTACACGAATCCTTA	CACAGGCTTGGTATTAACAGA	CAGGACCTCAATAGTTCTGAT
2817	GPC1	NM_002081	TTGAGTCCTTGTATGAATAAA	TACAACACAGACGATATTTAA	CAGGGACACGCTCACGGCCAA	CCGCCAGATCTACGGAGCCAA
2825	GPR1	NM_005279	CCGGGACACTGTGGAGTTCAA	CTCAGTTGCTGAGATACTCAA	CCGACTCCACTTTCATAGTTA	AAGCCTTAAGTCTTAATATTA
2838	GPR15	NM_005290	CCCAGAAGAAACTTCAGTTTA	CAGCTATTCTTCAGCTTGGTA	TTGCGGCAAGAACACTATTTA	TTCAGTTTATTTGGATTATTA
2846	GPR23	NM_005296	TAGGTTGGGCCTATAAATATA	TTGGGAAACTAGGTTCTATAA	GGGCCTATAAATATAGAACAA	AGGAAGTGAGTGATCAAACAA
2848	GPR25	NM_005298	GCGCATCATCTTCGCCATCGA	CAGGGACGACAGTTCCGTGTT	CTGCGCCAACCCGCTCATCTA	CCGGAGGAACTCGCTGCGCAT
2857	GPR34	NM_005300	CTGAATAGATTCAGTCATTAT	AAGGAGGGCATAATTCCACAA	TGCGACTATTACCAAATAGAA	TCAGGCGAACCTGAACTTTAA
2859	GPR35	NM_005301	CAGGCAGATCCCAGGAAGAGAA	CAGGACCATGAATGGCACCTA	CGCCCTGTACATAACCAGCAA	CCGGCACAATTTCAACTCCAT
2868	GRK4	NM_182982	AAGCCTTTGAGGAATGTACTA	CACCGCAGATGAAGACTTCTA	CCGGGTGTTTCAAAGACATCA	CAGGATGTTACTCACCAAGAA
2870	GRK6	NM_002082	CCGGAGGTGGTGAAGAATGAA	CAGAGACTCTTCAGTCGCCAA	AGGCATGTGGGCGGCACGTAA	AAGGATGTTCTGGACATTGAA
2876	GPX1	Y00433	CAGGAGAAGCCAAGAACGAA	GAGGAACACCTTGATCTTACA	CCGGGACTACACCCAGATGAA	AACACCTTGATCTTACAGAAA
2886	GRB7	NM_005310	CGGGAGTGGATCTGAAATAAA	CCCAACAAGCTTCGAAATGGA	CGCCAAGTACGAACTGTTCAA	CACACTGGTATATCCCATGAA
2888	GRB14	NM_004490	CAGCGATTGATTATTCAGCAA	CAGAAGTGACTTATTAAACTA		
2889	RAPGEF1	NM_005312	GCAGGTCTTGTTGCCAATTTA	CAGGGTTACATTGTAATATAT	CCGGGTTTAGGACGTGGTCAA	CAGGAAAGATTTGGTGTTGTA
2890	GRIA1	NM_000827	CAGGTGCGATTTGAAGGTTTA	CAGCATCCGAAAGATTGGTTA	CTCCACGTGATTGAAATGAAA	CACCATGAAGGTGGGAGGTAA
2895	GRID2	NM_001510	AAGCAATGGATCGGAGAACAA	CACGATTACAAATGGGATCAA	AACGATGTGGACGTACAGGAA	CTGGCAGAAATTCATTATATT
2897	GRIK1	NM_000830	CCAGCATTAACAGAAACCGAA	TGGGCATATCACCTTTAATAA	ACAGGTCTAATTCGTCTACAA	ACGGATTTAGAATGTGGTAAA
2900	GRIK4	NM_014619	CCGGCAATTCCTTATCTCCAA	CGCGTTCATATGGGACGCAAA	TGGGATGGTGTCAGCCTATTA	CAGGGTGTTGAATTCCAACTA
2902	GRIN1	NM_000832	GACGCGTTCGGTCCTATTAAA	CAAGGAGGAGTTCACAGTCAA	CAGACTGAAGATTGTGACGAT	CACGCTGGACTCGTTCATGCA
2903	GRIN2A	NM_000833	TACGATAACATTGTCGACAAA	CACAGTGGCCATTGTAGTTTA	ACCAGATAGGTGAGTCCTTAA	AGGGTTGTATAGTATCTGTTA
2909	GRLF1	NM_004491	CACCACCGAAGAGGTGTTTAA	CAGGATGTTCTGGGAGAGGAA	CAAGGTTTCCATCGTGAGCAA	CAGCCTAAGGAGGAACACTAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
2912	GRM2	NM_000839	CCGCTACAACATCTTCACCTA	CTGCACGCTTTATGCCTTCAA	CTACAAGGACTTTGTGCTCAA	CACCATCGAGCTGGCCTCCTA
2913	GRM3	NM_000840	CACGGCTCCATTCAACCCAAA	TAGGTCCTTGTTGTAACTAAT	TACGGTGGCAATATTATGTAA	GTCCTTGTTGTAACTAATTTA
2917	GRM7	NM_000844	AAGGGTTTGATGCCTACTTTA	CACGCTTACAATCTCCATGAA	TCGGATTTATCGCATATTTGA	CCCAGATTAGTTATGCATCAA
2931	GSK3A	NM_019884	CGGGTGTAAATAGATTGTTAT	CAATAAATTATTGGCATGAAA	CCGGGTGTAAATAGATTGTTA	CAGGGAACTAGTCGCCATCAA
2932	GSK3B	NM_002093	CACGTTTGGAAAGAATATTAA	CTGCATTTATCGTTAACCTAA	CACTCAAGAACTGTCAAGTAA	AACACTGGTCACGTTTGGAAA
2944	GSTM1	X08020	CCACCGTATATTTGAGCCCAA	TCCAGAATTTGAGAAACTGAA	CAGACTCAAGCTATGAGGAAA	CTGCTACAATCCAGAATTTGA
2947	GSTM3	NM_000849	AACGGAAGAAGTTACCCTTAA	ATGGCTGGATGTGAAATTCAA		
2950	GSTP1	NM_000852	CCTCATCTACACCAACTATGA	TCCTTTCTCCAGGACCAATAA	GCCGCCCTACACCGTGGTCTA	CCAGATCTCCTTCGCTGACTA
2954	GSTZ1	NM_001513	TACCATCAGCTCCATCAACAA	ACGGTGCCCATCAATCTCATA	CTGAAATTTGGCGTGAATTAA	CGCGCTGAAATTTGGCGTGAA
2956	MSH6	NM_000179	CAGCAGGGCTATAATGTATGA	CCGAAGTTGTAGAGCTTCTAA	AAGCCTATTGTGTGCTTGTTA	ATCGCCATTGTTCGAGATTTA
2957	GTF2A1	NM_015859	CAGCTTCTACTGCAAGTTCAA	CAGGAACTCTTTGACACAGAA		
2959	GTF2B	NM_001514	TTGCCTGTTGTACATAGCCTA	TTGACGAATTTGGCAATTCTA	CCAGTGTGGATTTGATTACAA	ACGTCAAATTCTTGAATACAA
2965	GTF2H1	NM_005316	AAGGCAAAGATAGATTTACAA	CCCAGAGCTGATGCTATTGTA	TCGGCTGAATACAGGGTCAAA	ATGGCACAGGGTAGACCTTAA
2974	GUCY1B2	NM_004129	CAGCATCCGCAGATTTATCAA	CAGTGTGCACGCAGTCTATAA	CGCAGATTTATCAACAGTCAA	CCGATGTTCAGAGGCATCCAA
2975	GTF3C1	NM_001520	CAGGAAAGAGGATGAACTTAA	CAGGCCTATCTCAACTATAAA		
2983	GUCY1B3	NM_000857	CAGTTTCTTGTCAGAATAATA	CAAGACTTTCTTCTAGATATA	AAGGGTCAAATGATCTACTTA	ACCTAACATGGTGATCTGCAA
2986	GUCY2F	NM_001522	CAGGCAGACAGAATTCGCATA	ACCGTTGTTTGGAACCATCTA	CTGGAGTTCGATCAAGTTTCA	AAGGCAGTTGGTGAGAAACAA
2997	GYS1	NM_002103	CTGGGCGAGGAGCGTAACTAA	CCGCTATGAGTTCTCCAACAA		
3024	HIST1H1A	NM_005325	ACCCAAGAAAGCGGCACCCAA	CAGGTTTATACCACTTTATTT		
3029	HAGH	NM_005326	CTGGTCCGTGCGGGAAATTCA	ATCGGACATTCTAATGCATAT	TCAGTCTTGATTTAACCTTAA	ACAAGTATTTATTCCCATAAA
3037	HAS2	NM_005328	GTGGAAGATTGGTACAATCAA	CAGCTCGATCTAAGTGCCTTA	CCAGCTAGTAGGTCTCATAAA	AACGCAATTGGTCTTGTCCAA
3038	HAS3	NM_005329	CACCTTCTCGTGCATCATGCA	TACCAGTTCATCCACACGGAA		
3053	SERPIND1	NM_000185	CAACGCCAAGTTCGCTTTCAA	CCCAAGGAGGGTACACAACTA	TGGCATCATTTACGTAGTTTA	TGGGCTAATGTTAGGGCTTAA
3055	HCK	NM_002110	CCGGGATAGCGAGACCACTAA	CGGCAGGGAGATACCGTGAAA	CGGGAGCACATCAGAGGCTTA	AACGACGGGCTCTGCCAGAAA
3059	HCLS1	NM_005335	CAGCCAGTGATAGGTATGGAA	AAGGAGAAGTGGAGAAGCATA		
3062	HCRTR2	NM_001526	CCCGTGATGTCCGGCACCAAA	CCGGAAGTCCTTGACCACTCA	CCGGTGCAACATCGCCTGTAA	ACCGACTATGACGACGAGGAA
3066	HDAC2	NM_001527	GACCCATAACTTGCTGTTAAA	CTGGGTTGTTTCAATCTAACA	TCCCAATGAGTTGCCATATAA	ACGGTCAATAAGACCAGATAA
3067	HDC	NM_002112	TGCCGACTCCTTCACCTTTAA	CCACAATAGGATACAAACGAA	CTGGGTCAAGGACAAGTACAA	CAGCTTGTGACATGATATATA
3068	HDGF	NM_004494	CCAGCTTATAGTCATATATAT	GAGGGAGCAATTGAATTTCAA		
3074	HEXB	NM_000521	TTCGACGATATCATGGCTATA	TGGATATTATTGCAACCATAA	CCAGACATTATCTGCCAGTTA	CCGGGCACAATAGTTGAAGTA
3092	HIP1	NM_005338	CAGGTTAGGGTGCTAGAGCTA	CACAACAATGGGTATCCTTAA	CAGGAACTTGCCACAAGCCAA	ATGGCTTAGGATCGACAAGAA
3097	HIVEP2	NM_006734	CTGGGTTATCTTTGTGCTATA	ACCGTAAAGCATTAAAGTAAA		
3098	HK1	NM_000188	AACGGTGGAAATGCACAACAA	CAGATCGAGAGTGACCGATTA	CCGTGTCGTATGACCTAGTAA	CACGATGTAGTCACCTTACTA
3107	HLA-C	NM_002117	ACCGGGAGACACAGAAGTACA	AAGCGTTGATGGATTAATTAA		
3118	HLA-DQA2	NM_020056	ATGGTTATAGCAGAAATACAA	CAGGGCTGACTGAGAGCATAA		
3119	HLA-DQB1	NM_002123	CCGGAGGCCTTCGGGCAGCAA	ATCCATCACAGGAGTCAGAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
3120	HLA-DQB2	NM_182549	AAGGATTTCTTGGTCCAGTTT	CAAGAGAAGCATGACAAACAA		
3122	HLA-DRA	NM_019111	CAACCTGGAAATCATGACAAA	CTGAAGAAACTTCTGCTTTAA		
3135	HLA-G	NM_002127	ATAACTTACTTCTGTATTAAA	ATGAGGTTTCTTTGACTTCAA		
3142	HLX1	NM_021958	AAGGTTTGAGATTCAGAAGTA	CGCCTTAAATTTGTAAATAAA		
3159	HMGA1	NM_002131	CAGCCAGCCCTTGGCCTCCAA	CTGGACAAGGCTAACATCCCA	CAGCGAAGTGCCAACACCTAA	CACCACAACTCCAGGAAGGAA
3162	HMOX1	NM_002133	CACCAAGTTCAAGCAGCTCTA	CGGGCCAGCAACAAAGTGCAA	CAGGCAGAGGGTGATAGAAGA	CAGGCAATGGCCTAAACTTCA
3174	HNF4G	NM_004133	AAGCACTGACATAAACGTTAA	CACCGGATGGATTCTGATGAA	ACCGATAAGCAGCGAGTGTAA	ACCCTGTAATTTATTCGTGTA
3175	ONECUT1	NM_004498	ATGGAAGAGATCAATACCAAA	AAGGAAGAACCACAAACTAAA		
3176	HNMT	NM_006895	CGGGAAATATGTTGAATCTTT	TGCAGGCTCAACATAACATAA	TGGGACTTTATTCATATGATT	CAACATAACATAAGCTAGAAA
3187	HNRPH1	NM_005520	AAGCAGTTGAATTATGTTAAA	CAGGTATATTGAAATCTTTAA		
3198	HOXA1	NM_005522	CAGGATAATATATTTGCAGAT	TAGGATGTCTGTAATAAATAA	CAGACTGAGTTCTATCAGTTA	CAGCTCCTTTATTATAATCAA
3201	HOXA4	NM_002141	AAGCCATGTGCTAAGAATAAA	CTGGACCATAATAGACACCAA		
3225	HOXC9	NM_006897	CACGACAATGAAGACCTCCTA	CCGAAATAAATGACACATACA		
3236	HOXD10	NM_002148	GTGCATCCTTATATACCTCAA	CCCTATGAGTATATATATATA	CTCCTTCACCACCAACATTAA	CAGGGTAACTATTATTGCGCA
3240	HP	NM_005143	TGGAGTGTACACCTTAAACAA	AAGGTGTCTGTTAATGAGAGA	CAAACAGAAGGTGTCTGTTAA	CTGACCAAGACCAATGCATAA
3242	HPD	NM_002150	AGGAGGTTTGACTAAGATCAA	CCAGGAATATGTGGACTATAA	ATCCATTGTGGTGGCCAACTA	CTGGTGGACTACGACGAGAAA
3248	HPGD	NM_000860	CAGCCGGTTTATTGTGCTTCA	CAAGAGCTTCTTAGAGTAGTA	CAAGACTATGATACAACTCCA	CTGGCAGTGACTAATCAGTAA
3249	HPN	NM_002151	GTGGATCTTCCAGGCCATAAA	CAGCCAGGGAATCATTAACAA	TGGGATGCTCTTTAAATAATA	GGGATGCTCTTTAAATAATAA
3250	HPR	NM_020995	CTGCATTGCTGAGTCAATCAA	CTGACCAATACGATTGCATAA	AAGCAAGATTTCAGCCTGGAA	AAGGTGCTTGTTAATGAGAGA
3251	HPRT1	NM_000194	TCCTATTGACATCGCCAGTAA	CACTATTGAGTGAAACATTGA	AACATTGAACTCATATCTGTA	ATGGGAGGCCATCACATTGTA
3280	HES1	NM_005524	CTGGTGCTGATAACAGCGGAA	AAAGACGAAGAGCAAGAATAA	CACGACACCGGATAAACCAAA	ACCATGCACTATATTTGTATA
3292	HSD17B1	NM_000413	AACCATGGTCATGTGAGTTAT	ATCCCAGAGCTTCAAAGTGTA	CTGGACGAAACCAACACATAT	CAGCTGTGGGTGGCTAATTAA
3299	HSF4	NM_001538	AAGGGCGAGAATGGACCCTGA	CAGAGCCGTTTCGCCAAGGAA	CCGGGTCATTGGCAAGCTGAT	CCGACTATCCCTGCACATAAA
3300	DNAJB2	NM_006736	AAAGAGTTTGCTGAGAAGAAA	TTCGCTCTGTTTCTACATCTA		
3308	HSPA4	NM_198431	ATGGACATTGATTGATTCCAA	CAGGTATAAAGGTGACATATA	CCAGGTAATTTCTAATGCAAA	CAGACTATTATAAAGCTTTAA
3309	HSPA5	NM_005347	AACTGTTACAATCAAGGTCTA	TGGGATAAGGAAACACTTCTA	CAAGCCCAATACAGCCATTAA	TAGGGTGTGTGTTCACCTTCA
3313	HSPA9B	NM_004134	AACCAAGATGGAAGAATTCAA	TAGGATGAATTGATCATTATA		
3321	IGSF3	NM_001007237	CAGGGTGATTTGGCCGTCAAA	CAGGAGCGGCTCAGTCATGAA		
3324	HSPCAL3	XM_084514	ACCAGCCTTCTTCCTAGTCAT	CTGGAGATAAATCCTGATGAT		
3326	HSPCB	NM_007355	AAGCTCATGAAAGAAATCTTA	CAAGAATGATAAGGCAGTTAA	AAGGCTGAGGCCGACAAGAAT	CCGCATCTATCGCATGATCAA
3338	DNAJC4	NM_005528	TAGGGAGTGGCAGGTGCTCAA	CAGGAGGGTGGGTGAATTCCA		
3339	HSPG2	NM_005529	CGGGAAGTGCAGGCCCGTCAA	CACCCGAGCCATGGATTTCAA	ACGGTGGGAAGTTGCGATACA	ACGCCTGGACGTGGAGTTCAA
3359	HTR3A	NM_000869	CACCGTATCCATTGACGTCAT	ATCCATTGACGTCATTGTCTA	TACGTGTATATTCGGCATCAA	CAAGCTGCTATTCCACATTTA
3361	HTR5A	NM_024012	TGGATTTACCAGTGAACCTAA	TACGGCTTTCAACAAGAACTA	CTCGGTCTTCGGAGTGCTTAT	CCTGATCTATACGGCTTTCAA
3362	HTR6	NM_000871	CTGCAGCGCCTCCATCCTCAA	CAGGGCCGCTGCCGCCGTCAA	CGCCGTCAATTTCTTCAACAT	CAGGAGGCTGCAAGTCTCCTA
3363	HTR7	NM_000872	TCCAGTCATCAGCTAATACAA	ATGGCACTATGTAGTAATTAA	CTGAAGTGACCGTATATATTA	CGGCGCGATGATGGACGTTAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
3371	TNC	NM_002160	AAGGACCTTCAGGTTTCTGAA	CTGGGATGCCCTCAAACTCAA	CCGAACGTACCAGGGACTTAA	CCGGGCATCAGTCACCGGTTA
3375	IAPP	NM_000415	ACAGCTAATAATGAAGTTATT	TTAGAGGACAATGTAACTCTA	ATGCAGGGTATTGCGAAACAA	CTGGTACTAAGAGGCTATTTA
3431	SP110	NM_004509	TCCCAATCTGGTGACGATTTA	AAGGAAAGGCTGATTACGGAA	ATGGAACTTGGTTAACACCAA	CCGAGACACTTCATAGGATTA
3441	IFNA4	NM_021068	CTGGTTCAACATGGAAATGAT	ACAGAGCAAAGTCTTCAGAAA	ATCTATTTATTTAAATATTTA	TACCTAGAGGCCGAAGTTCAA
3442	IFNA5	NM_002169	ACAGGAGGACTTTGATGATAA	ATGCAGGAGGTTGGAGTGGAA	CAGGAGGACTTTGATGATAAA	ATCCTTCTCTTTATCAGCAAA
3443	IFNA6	NM_021002	CAGCAGCTGAATGACCTGGAA	ATCCTTCTCTTCATCAAGAAA	CTAGACAAACTCTATACTGAA	CATCAAGAAACTTGCAAGAAA
3444	IFNA7	NM_021057	TCCACTGAACTTTACCAGCAA	CTGGTTCATCATGGAAATGAT	CAGCAACTGAATGACCTGGAA	TAGCCTAGTGATATTTGCAAA
3446	IFNA10	NM_002171	GTCGCTTTACATTGTGGTTAA	CTGGTTCAACATGGCAATGAT	TCCACTGAACTTTACCAGCAA	CAGCAACTGAATGACCTGGAA
3455	IFNAR2	NM_000874	AGGCGAGAGCTGCAAAGTTTA	CACAGTGATGAGCAAGCAGTA	CAAGTTAATTCCAAACACGAA	AAGCACCATAGTGACACTGAA
3456	IFNB1	NM_002176	CAGGTAGTAGGCGACACTGTT	CAGAGTGGAAATCCTAAGGAA	CAAGGACAGGATGAACTTTGA	CAGGTTACCTCCGAAACTGAA
3460	IFNGR2	NM_005534	ACCAAGTGCAGTTTAAATACA	TCGGGCATTTAAGCAACATAT	AAGGCTTCTCTTAAACACTAA	AGGCTTCCCAATGGATTTCAA
3467	IFNW1	NM_002177	AGGGCCTGACTTCCTACATAA	AACCATGTGTTTCCTATTAAA	TAGATTGTTGTCATCCTCTTA	AAGACTCTTATTTCGGCTTTA
3468	IFNWP2	XM_378052	CACAGGTAGGCAGGCCAACAA	ACAGGAAAGATTGAGAAGTAA		
3479	IGF1	M27544	CCGGAGCTGAATTACCTTTCA	ATCAATAATGTTCTATAGAAA	CCAGAAGGAAGTACATTTGAA	ACGGTAATACGTGAAAGCAAA
3483	IGFALS	NM_004970	CACCAACGTGGCGGTCATGAA	CCGACTCTTCCTCAAGGACAA	CCGCCTGGAGGCATTGCCCAA	CAGCTTGAGGTGCTCACGCTA
3484	IGFBP1	NM_000596	CATACATAACTTGATATAGAA	AAGGAGGACGGTTAACTTGTA	TACATGTGTAGGGAAAGTTAA	TACACTGGATATGTTGTTAAA
3491	CYR61	NM_001554	TCCCTTCTACAGGCTGTTCAA	AAGGTATTTCGAAACTGCCAA	AGGGCACACCTAGACAAACAA	AGGCAGCTATCTGCACTCTAA
3508	IGHMBP2	NM_002180	CAGGAGAACATCTCTCTGAAA	CAGAGGATATAAATTATTTA		
3512	IGJ	NM_144646	AAGAAGTGAAGTCAAGATGAA	CAGAGCAATATCTGTGATGAA		
3547	IGSF1	NM_001555	CTGGAGGAGCTCACTGGAGAA	AAGCAAGTTCCTGCTGCTGAA		
3549	IHH	XM_050846	CTGGGTGTATTACGAGTCAAA	CGGCTTTGACTGGGTGTATTA	CCGCCTGAACTCGCTGGCTAT	CTGGGTGTATTACGAGTCAAA
3550	IK	NM_006083	AACCCGTAACAAGAAGCTTAA	CAGCGAGTATATGAACAACAA	GAGGAGGTGGATTATAGCAAA	CAGGCGCTTCAAGGAAACCAA
3551	IKBKB	NM_001556	TAGGGAGCTATTCATGTTTCA	CAGGACACTGTGAGGGAACAA	CAGACCGACATTGTGGACTTA	CACACTGGAGGTCCTCCATTA
3552	IL1A	NM_000575	TCGAGTTGAATGAACATAGAA	CTGAGGTGATTTATGCCTTAA	AAGGCAAAGCACGAAATGTTA	CACGCCTACTTAAGACAATTA
3557	IL1RN	NM_000577	AAGGAATAAATTGCTCCTTGA	CAGCGAATGAATGCTGTATAT	CTGGATACTTGCAAGGACCAA	CCAAATGTCAATTTAGAAGAA
3559	IL2RA	NM_000417	CCCGTTCACGTTGCCTAATAA	CTCCACCCTATATGTAGTATA	CAGAGAATCATACTTAGCAAA	CCACCCTATATGTAGTATAAA
3560	IL2RB	NM_000878	CCAGTTCACATGCTTCTACAA	ATGGCTGAAGAAGGTCCTGAA	TGGCTTCATCATCTTAGTGTA	CCCGGATGCCTTGGAGATAGA
3561	IL2RG	NM_000206	CACGACAATTCTGACGCCCAA	CTGAACAATCAGTGGATTATA	AAGAACTCGGATAATGATAAA	CTAGAGGATCTTGTTACTGAA
3566	IL4R	NM_000418	CCCGGCAGATTTCAGAATCTA	CCGCCTCGTGGCTATAATAAT	CAGAATCTATAACGTGACCTA	CACATACATGAGGGTCTCTTA
3577	IL8RA	NM_000634	CCGGTGCTTCAGTTAGATCAA	CAGGCAGATGTTCCTAATAAA	TCCGCCAGGCTTACCATCCAA	CCCGTTGAACGTCACATCTTT
3578	IL9	NM_000590	GAGGCAAGATATGAAGATGAA	TACCACCATGCAAACAAGATA	ATCCTATTTATTAAATTTAAA	ATCAGTTGAAGTACTAAAGAA
3581	IL9R	NM_002186	CCAGAGATAGTTGGGTGACAA	AAGGACAAGGGCCAAGGTCTA	CAGAGATAGTTGGGTGACAAA	CAGCTATGAGCTGGCCTTCAA
3596	IL13	NM_002188	CAGCATGGTATGGAGCATCAA	AACAAGTTGTTTCATTGACTA	CAGCTCTCAGCCAACGAGTAA	TTCATTGACTATCAAACTGAA
3597	IL13RA1	NM_001560	CCAAATAATGGTCAAGGATAA	CTCAGTGATGGAGATAATTTA	ACCATGTTTGTGGCTATTAAA	AACCATGTTTGTGGCTATTAA
3608	ILF2	NM_004515	CAGACAGCCTTTGGCCCTAAA	CTCCATAGAAGTGTCATTCCA	TTGAAATGTTGTGAAATGTTA	CAGGCCCTTTGTACCACATAT
3609	ILF3	NM_153464	CAAGCTGCACGTGGCCGTTAA	CTGGTTTAGCTAGAGAGTGAA	CAAGAGTTGAAGTATTGATAA	AACGATTTCACCACATCTGAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
3612	IMPA1	NM_005536	CCAGATTTGGTGACTCATCAA	TAGAAAGTTAACTGTTTGGAA	CCGGAAGAGACGAGTGCGGTA	ACGAAGAGTAATTGCTGCAAA
3614	IMPDH1	NM_183243	CCCAGGATTCATAGACTTCAT	CAGCAGCAGCCAGAAACGATA	CCGCACCGACCTGAAGAAGAA	ATGGCCTGCACTCTTACGAAA
3617	IMPG1	NM_001563	CTCCAAGTTCAAGGAACCAAA	CCGTAGAATATGAAGAATTTA	AAGGGCGAAGTTGTACTATAT	TCGGATCTTTCTGGATCGCAT
3623	INHA	NM_002191	CGGATGGAGGTTACTCTTTCA	AAGGCAGAGTTGGGAAATAGA	CAAGTATGAGACAGTGCCCAA	CAGCACTGTGCTTGTATCTAA
3624	INHBA	NM_002192	CAGGAAGACGCTGCACTTCGA	AAGGAAGATGTGGAAATCTTA	ACCCATGTCCATGTTGTACTA	CTGCAGTAGTGTGGACTAGAA
3625	INHBB	NM_002193	CAGCCTGTGGCTTTACCTGAA	CCACGTGAACTATGCAATTTA	CAGGTGGAACATGGTGGAGAA	CACGTGAACTATGCAATTTAA
3627	CXCL10	NM_001565	TTAGTTTGCAGTTACACTAAA	CAGGAAGGTAGAAATATCTGA	TGCATCAGCATTAGTAATCAA	CTGACTCTAAGTGGCATTCAA
3635	INPP5D	NM_005541	TCGGAATTGCGTTTACACTTA	CCCGGGACTGTTGACAGCCAA	TCCCATCAACATGGTGTCCAA	CAGGTGCTATGCCACATTGAA
3641	INSL4	NM_002195	AGCAGCAAGTCTCTAAAGAAA	CTGAGCCAACTCCTTAGAGAA	TAGGTACGACATCAGAATTCA	ATCCATTCTGTTGTGAAGTAA
3643	INSR	NM_000208	TCGAACGATGTTGGACTCATA	TAGGAAGACGTTTGAGGATTA	CAACGGGAGTCTGATCATCAA	ACCGCTTTACGCTTCTTCAAA
3646	EIF3S6	NM_001568	CAGGAGTCTTACACATATAAA	AAGGAATTATTACAAGGTAAA		
3656	IRAK2	NM_001570	GAGAATATGTGTTGTTATTTA	CCGGTTTACCTGAAGGACTTA	CCAGATCATCCTGAACTGGAA	CAGCAACGTCAAGAGCTCTAA
3660	IRF2	NM_002199	CCCTATCAGAACGGCCTTCTA	ACGGTGAACATCATAGTTGTA	CGGTCCTGACTTCAACTATAA	CACCTTATCTTAAAGCACTTA
3663	IRF5	NM_002200	CGGAGATAACACCATCTTCAA	CCGCATGGTGGAGCAATTCAA		
3667	IRS1	NM_005544	CCGCCTTTGCCTGACCAGCAA	CCGGTATCGTTTCGCATGGAA	ACAATAGGCCATGTTAATTAA	CCGGGTGAACCTCAGTCCTAA
3670	ISL1	NM_002202	TACGGTGGTCTTTGAATTATA	CCGGCTTAAATTGGACTCCTA		
3672	ITGA1	NM_181501	CCCTCGAAACACAACCTTTAA	CTGCATGTCGCCACCACTGAA	CCCTAGATTCACTAAGACAAA	ACTGAGGACATTGGAAATGAA
3673	ITGA2	NM_002203	TCGGAGCAATTCAATATGCAA	TCGCTAGTATTCCAACAGAAA	CCGGTTGATGGGACAGAAGTA	CCCGAGCACATCATTTATATA
3675	ITGA3	NM_002204	CAGCTACATGATTCAGCGCAA	CTGCATTGACTTTGCTGTCAA	CTCGCTTAGCATGGTAAATCA	CACCATCAACATGGAGAACAA
3679	ITGA7	NM_002206	GACCAGGGAGCTGATATGCAA	CACAGTGAAGTCCTCCATAAA	CCCTTTGATGGTGATGGGAAA	CCCAGTGATGGTATACTTGGA
3680	ITGA9	NM_002207	ACAGGTCACTGTCTACATCAA	CACATGCTAATGTGTGCTAAA	CCGAAGGTACAAAGAAATTAT	ACCGAAGATCAGGCACCTTAA
3683	ITGAL	NM_002209	AACGTGTGACCAGAACACCTA	CCCTGTTTAATGATTGACGTA	CTCGGTTGAATTGCACGCCAA	CAGGGCGTGGGACATCTAGTA
3684	ITGAM	NM_000632	CGCAATGACCTTCCAAGAGAA	CTCGTTTGACTGGTACATCAA	TCGGGTCATGCAGCATCAATA	TCAGACATCGGTTCATATTAA
3685	ITGAV	NM_002210	AGCAACTTTATTATAGATTTA	CACATACATGATACCATCCAA	TAGCATGATGTTACAGGAATA	ATGTAGTAGTTTGATGAATAA
3688	ITGB1	NM_002211	CTGCGAGTGTGATAATTTCAA	ACAGATGAAGTTAACAGTGAA	TACGTATTCAGTGAATGGGAA	AAGAGGGATAATACAAATGAA
3690	ITGB3	NM_000212	CAAGCTGAACCTAATAGCCAT	CCGCTTCAATGAGGAAGTGAA	CTCTCCTGATGTAGCACTTAA	CACGTGTGGCCTGTTCTTCTA
3692	ITGB4BP	NM_002212	CCGAGCTTCGTTCGAGAACAA	AAGCTACTGTGTCTTCAGCAA	CAGGGAGACAGAAGAAATTCT	CTGGATCTATCATTACTGCAA
3693	ITGB5	NM_002213	CTCGGTGTGATCTGAGGGCAA	CCGCTATGAAATGGCTTCAAA	ATGGGTGGACACCATCGTGAA	CAAGATTGTTTGGGATTGGAA
3700	ITIH4	NM_002218	CACATCTATGGTAGTCACCAA	ATGGATCGAAGTGACCTTCAA		
3704	ITPA	NM_033453	CAGGAGGCAGTTCGCCAGGTA	GAGGAGGTCGTTCAGATTCTA	CTGGATGAGACTTGTTTCCAA	CTGGAGAAGTTAAAGCCTGAA
3706	ITPKA	NM_002220	CTCCTGCAGCACCGACTTCAA	CCCAGCGTTCCCAGAGCCAAA	CCGGTCTAACGTCTCACACCA	CACCAGCGGGCTGATCCTGAA
3710	ITPR3	NM_002224	CAGGTGTTCCTGCGAACTACA	CCGCAGCATGCCGCTGATCTA	AAGCCGGTGAAGCGCATTCAA	TCAGTTTACCTTAATGCCTTA
3714	JAG2	NM_002226	CCAGAGGTTGTGCACTGTTTA	CTACGTTTCTTTAACCTTGTA	CACTCTGTATATTTGATTGAA	CTGCGTCGTCACCAAATCGTA
3725	JUN	NM_002228	TTCGTTAACATTGACCAAGAA	CGCGCGCGAGTCGACAAGTAA	CTGCCCAGTGTTGTTTGTAAA	AAGAAGTGTCCGAGAACTAAA
3730	KAL1	NM_000216	ATGCATGTCTATATAATTATA	AAGCGTAAATCTAATCAATAA		
3741	KCNA5	NM_002234	ACCAGGGAACCCATTTCTCTA	CAGAGGGATAACCCAAACAAA	CGCAGAGTATTTGAAGTCACA	AGGAATACTTCTGATAATTTA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
3742	KCNA6	NM_002235	TACAATGACCACGGTAGGTTA	CTGGTGTTCGGTCTACATTTA	CAGGACCAAATACCTGGACTA	CTCGATCTTGCCATAACTTTA
3744	KCNA10	NM_005549	CTAGTTATTAGTTTATGCAAA	CACCGGGAGACTGAGAATGAA	CCGGGAGGATAGGGAGCTAAA	CAGCACAGACTCTCTTAATAA
3745	KCNB1	NM_004975	CCGGAGCATTGAGATGATGGA	TCGGTATTTCATAGTACCTGA	AACCACTTGTCTCCTAACAAA	CACGCTTTCTTTACATCACTA
3753	KCNE1	NM_000219	GCCCAGGATGATCCTGTCTAA	AAGAGAAGGACAAGGCCTATG	AACCATCTGGCCATAGAACAA	AACTGGGATTCTTCGGCTTCT
3756	KCNH1	NM_002238	ATCAGCGATGTGAAACGTGAA	CTGAGATACTCAGGATATTAA	TACAGCCATCTTGGTCCCTTA	TCGGCGGTCCAATGATACTAA
3758	KCNJ1	NM_000220	CAGGGTGTTGACAGAAAGTAT	CTCCCATAGTATCCAAGACAA	CAGTCTATACTTGGAGTTATA	TACGTTTAGACAGAGGCTAAA
3759	KCNJ2	NM_000891	CAGGAGCCGCTTTGTGAAGAA	CGAGATGGTGATGTACTCTTA	AGGGTCAATGAGAGCGATAAA	CAACTCTCTTATGGTATTATA
3760	KCNJ3	NM_002239	ACCAGCCATAACTAACAGCAA	AAGGCTACTGGCATTAATTAT	ATGGACTAGATGATATTACTA	CTGTGTGAAGTTACACAATTA
3764	KCNJ8	NM_004982	CAGGACGATGTTGGCCAGAAA	AAGGTGCAATTTATGACTCCA	GAGGTGGTTCCTATTCACCAA	CCAGATCGCTGTGTTACTAAT
3765	KCNJ9	NM_004983	TGGGAAGATGGTAGCAGATAA	AGGGATAATTCAAACTGACAA	GTGAATGACCTTAGTCCGCAA	CAGGCCCGACAGAGAGATGAA
3769	KCNJ13	NM_002242	AACCTACAAACTAGACTTGTA	ATCGCCTTACTTGCCATACAA	CAAACTAGACTTGTAGATTAA	CACATGGATGGCAAACCTAAT
3770	KCNJ14	NM_013348	CGCGGTCGCTTCGTCAAGAAA	CTGGATTCACCTAAGATTCAA	CAGGGTGAGAAGCCAATGGTA	AAGACTGAAGTGACAGATTAA
3773	KCNJ16	NM_018658	CAGACTGGCACTTTATCTCAA	CCGGTAACTATTGTCCATGAA	CAGCAGCTATCATATTATCAA	AAGCTTAATATTAGAGACCCA
3776	KCNK2	NM_014217	CACGACCATTAATGTTATGAA	TCGCATCATCTCAACAATCAT	AGGGATTATACCGTTAGGAAA	AGCCTAGATATGGACCATTTA
3778	KCNMA1	NM_002247	ACCGAGAGAGCCGTATATTAA	ACGGGATGTTACGTCAACCAT	AACCATCTTAAGATCCAAGAA	TAGGCAGAGCAAGTTTATTTA
3780	KCNN1	NM_002248	CAGGGAGACGTGGCTCATCTA	ACCGTCATGTACGACCTTGTA	CACGCTTACCGACCTAGCCAA	CCGGCCTAGCCTAGAATCCTA
3785	KCNQ2	NM_004518	CAGCCAGGGCGTGTGGTTTAA	CCCGCCCTCCTGAGCTATGAA	AACGGTCACCGTGCCCATGTA	CCCATTGACACAAACCCTCAA
3788	KCNS2	NM_020697	CCCATAAAGTTAAATCCCTTA	CACCAAGTGAACTCAGTTTAA	CACCTTATGGTTATGGTGTAA	AGGGACTATTATGCCCATAAA
3792	KEL	NM_000420	CTGGTAAATGGACTTCCTTAA	CCCGACAAGAATACAACGATA	ACCCGAAGTGCTGCCATGAAA	CAGCACAGAAATATCGACCAA
3796	KIF2	NM_004520	AAGAACCAAGATTGTTCTAAA	CAGCAAGCAAATCAACCCGAA	CCAAACCAGATTGATGACTTA	ACCATATAACATGTGATTATA
3806	KIR2DS1	NM_014512	ATCATAGGTCTATATGAGAAA	AACAGCGAGGATTCTGATGAA		
3808	KIR2DS3	NM_012313	CACGTTCTGATTGGGACCTGA	CACCATGTCGCTCATGGTCAT		
3809	KIR2DS4	NM_012314	AGCGAGGATTCTGATGAACAA	CAGCTCCATCTATCCAGGGAA		
3810	KIR2DS5	NM_014513	AACAGGGAGGATTCTGATGAA	TACCTGCGGCTGGAATCTGAA		
3814	KISS1	NM_002256	CAGGACTGAGGCAAGCCTCAA	CCAGGTGGTCTCGTCACCTCA	AAGAAATGTTGCGTAACTCAA	CACCCTCTGGACATTCACCCA
3817	KLK2	NM_005551	CAGCATATAATTCTCCCTGCA	TACTTGAATAATTGACCTGAA	GACGAGTATGGAGTACTTGAA	CTGAGGTTCCCTAGAGTTCAA
3818	KLKB1	NM_000892	CAGCAAGTTCAATCAATGACA	AACGTGGAATCTGGATTCTCA	CGCTATAAAGGTGCTGAGTAA	ATGGTCTGTGCTGGCTATAAA
3827	KNG1	NM_000893	CCGCATAACTGAAGCCACTAA	CTCGGCTGTGTGCATCCTATA	TCCCTCTTCATGCTTAATGAA	ACCGGTGAATGTACAGATAAT
3832	KIF11	NM_004523	GTCGGGAAGCTGGAAATATAA	GCCGATAAGATAGAAGATCAA	CTAGATGGCTTTCTCAGTATA	ACGGAGGAGATAGAACGTTTA
3833	KIFC1	XM_371813	TCGGGAAACACAGGCCATTAA	TGGGACTTAAAGGGTCAGTTA	CAGGGCTATCAAATAAAGAAT	TCGGGAAACACAGGCCATTAA
3835	KIF22	NM_007317	CCACAGTATCCTTATTGCCAA	CAGGACATCTATGCAGGTTCA	ACAGATGGAGTCCTTCCTGAA	ATCCACATCCTGAAGAATAAA
3849	KRT2A	NM_000423	AAGCAGCACCATTTCATCAAA	CTGGTGGAAGCCGGAGATCAA		
3856	KRT8	NM_002273	CCAGGAGCTGATGAACGTCAA	CAGGGTGACCCAGAAGTCCTA	CAGGGCCGTGGTTGTGAAGAA	CAGCATCATTGCTGAGGTCAA
3860	KRT13	NM_002274	CGCCAAGAGTGCAGAGCTGAA	CTGCCTTTCTGCAAACATAAA		
3861	KRT14	NM_000526	CTGGCAATCAATACAGCTTCA	CAAGTATGAGACAGAGTTGAA		
3884	KRTHB6	NM_002279	ATGGTCTGGAAGGAGAACAAA	CCGAGGCATCACCACAAATCA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
3887	KRTHB1	NM_002281	CAATAAATTAATGTAGCCAAA	CAGCAGCTGCCGGAAATGTTA		
3891	KRTHB5	NM_002283	CAGCCCTTCACTTAACTCCTA	CAGGTCTTGCTATTCAGTGAA		
3912	LAMB1	NM_002291	CCGAAACAGCAACGCCTGTAA	TACCAAGATCCTGTTACTTTA	AGGGAATTTGTGACAGCTATA	TCCGTTCACTCCTAAAGGATA
3913	LAMB2	NM_002292	CGGGTGAACCTGACTCGTCTA	CCAGGCCACCTTTGAACGCTA	CAGGTACTTGATATTTCCTAA	GCGAGATAGGCTTGCACTTAA
3914	LAMB3	NM_000228	ACAGTTACACTTGACAGACAA	ACCGGTTGGGTCAGAGTTCCA	TTGGCATGCCATTGAAACTAA	AAGAGGGATTTGAGAGAATAA
3916	LAMP1	NM_005561	CACGTAATGCATTGCCTGTAA	CACGAGAAATGCAACACGTTA		
3920	LAMP2	NM_002294	CAGTACGCTATGAAACTACAA	CTGGAGCATTTCAGATAAATA	CTGGAACCTATTCAGTTAATA	TAAGGACTATAGTGATTTAAA
3930	LBR	NM_002296	AAGACTCAAGTATAGATTAAA	TAGCAATTAAATTCTAGTGAA	CAGAAGACAGTGTTAATATAA	TAAGGTAGCTTTAGCAATTAA
3931	LCAT	NM_000229	CTGGCTGGATCTCAACATGTT	AACCAGATGTGGTGAACTGGA	CAGCATCAAGCTGAAAGAGGA	AACAGCATCTCAACATGGTCT
3932	LCK	NM_005356	CTACGGGACATTCACCATCAA	CGCCATTACACCAATGCTTCA	AGGCATCAAGTTGACCATCAA	AAGGGCCAGGACTTTATCTAA
3939	LDHA	NM_005566	AAGGATCAGCTGATTTATAAT	CAGATTTGGCAGAGAGTATAA	CAGGTGATTTATAATCTTCTA	AAGTCCAATATGGCAACTCTA
3956	LGALS1	NM_002305	CGCCAACACCATCGTGTGCAA	CGCCAGCAACCTGAATCTCAA	GACGGTGACTTCAAGATCAAA	CACCATCGTGTGCAACAGCAA
3957	LGALS2	NM_006498	CAAGCTGAACCTGCATTTCAA	CACTGATGGCTTTGTAATTAA		
3959	LGALS3BP	NM_005567	CACGGTCATCCTGACTGCCAA	CTGAGGCTCAGCTTCAAGAAA	CAGCTTCCTCTTCCAGGACAA	CAGCTTCAAGAAATTACTGGA
3965	LGALS9	NM_002308	CTCCTTTCCCAGTGTCCTTAA	CCCACCATCAACAGAGTGGAA		
3977	LIFR	NM_002310	CAAGACCATTATCAACTCCTA	TTGGAAGCCTTTACCCATTAA	TGGGTCGATCACAATCAACAA	TGCAGATTCGATATTAGTAAA
3980	LIG3	NM_002311	CAGCTGGTTGAAGGTCAACAA	CTGGGAAGAGCTGGAAGATAA	CACCCGAATCCGAGATGATAA	CTGGAAGATAATGAGAAGGAA
3984	LIMK1	NM_002314	CAGAGGTTTCTGGGAGACCTA	GAGCATCTAGGAAGTATTAAA	CTGCCTGGTCCGCGAGAACAA	CACCATGGACTTTGGCCTCAA
3988	LIPA	NM_000235	TACCTGGTCTCGGAAACATAA	CACGTTTGCACTCATGTCATA	CTGACTTAAGCGAGGTATAAA	CCCGCTACTGTCGTTATTGAT
3990	LIPC	NM_000236	AAGTTTATCATTACCAGTTAA	CTGAAGACGATCAGAGTCAAA	AAAGGAATTGCTAGTAATAAA	CAGGAGAAACCCAGCAAAGAA
3992	FADS1	NM_013402	TCGGAATGTTACAATGGTAAA	CAGGAAGAGATTTAACACTAA		
4000	LMNA	NM_005572	AAGCGCCAGAATGGAGATGAT	CCCACCAAAGTTCACCCTGAA	CCGGCTGCGCAACAAGTCCAA	CCAGGAGCTTCTGGACATCAA
4010	LMX1B	NM_002316	CCGCTTCCTGATGCGAGTCAA	CAGCAGATCGTGGCCATGGAA		
4012	LNPEP	NM_005575	CAGGGCACAATTATACGTTGA	CCGCTTTATCAAATATGCCTA	TCCAATGGAACTCAAAGCCTA	CACGTAAATGCCAACCATCTA
4015	LOX	NM_002317	AAGCTGGCTAGTCGACATCTA	CTGCACAATTTCACCGTATTA	AACTACTACGATACTTATGAA	CTGGAACTTTAGTGAAACATA
4016	LOXL1	NM_005576	CAAGGTGGACGTGAACCCAAA	TCGCTACGTTTCTGCAACAAA		
4017	LOXL2	NM_002318	CTCGAGATTCCGGAAAGCATA	CCGGAGTTGCCTGCTCAGAAA	CAGGCAATGAGAAGTCCATTA	CCAGTCTATTATAGTCACATA
4033	LRMP	NM_006152	CTGGGAAAGTATAGCATGAAA	CAGATTATCTTTGGGATTTAA		
4034	LRCH4	NM_002319	CCGCCTGGATTTCTCCTGTAA	CAGCGTTGATAGTGGCAGCAA	TTGGCTCCATTCAGAGACCAA	GCTGGTTGTGTTGACAATAAA
4038	LRP4	XM_035037	CAGCGTGTTGACAAATACTCA	CCGCAAAGTACTGATCAACAA	CCGCGCGGTGCTCATCAACAA	CAGGAAATCATTCGCAACAAA
4041	LRP5	NM_002335	CTGGACGGACTCAGAGACCAA	CCCGTTCGGTCTGACGCAGTA	CTGGATGGGCAAGAACCTCTA	CAGGGCTGGGAGAACTTTGTA
4043	LRPAP1	NM_002337	CTGGAAGAAACTAAAGCTTGA	TACCATGCACAGAGTCCTTAA	CAAGTATGGTCTGGACGGAAA	CGGGAGTTCCTGCATCACAAA
4046	LSP1	NM_002339	CCGCTCCATAGAGAAGAGTAA	CAAGGAGAAACTGCAGGTCAA		
4049	LTA	NM_000595	CAGGTGGTCTTCTCTGGGAAA	CCGGAGCTTTCAAAGAAGGAA	CAAGGCTGACCAAGAGAGAAA	ACCCTCGATGAAGCCCAATAA
4052	LTBP1	NM_000627	CCCAATATATCTACCATTGTA	TTGATTAAATTTGGCATTTAA	CTGGGTATGAATGCTACTGTA	TACCGGGTTATAAGCGGGTTA
4054	LTBP3	NM_021070	CCGCTACTGCGTGGATGTGAA	CCGGGACAGATCTCAGCAGAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
4055	LTBR	NM_002342	TACATCTACAATGGACCAGTA	CCGGCGGGTCTATGACTATCA	AAAGGGAGTCATTAACAACTA	CCGCCACACGGTCACCTGCAA
4057	LTF	NM_002343	ACCCTTGATGGTGGTTTCATA	CAGCCACGAACTCACTATTAT	CAGAGAGAGCACAGTGTTTGA	AAGCAGTGACCCTGATCCTAA
4058	LTK	NM_002344	CAGGGATATTGCCGCCCGGAA	CCGGGCCTTGCTCCCAGTCAA	CCTGCAGATGCTTCTAATAAA	ACAGATCTTTGGAGTGCCTAA
4067	LYN	NM_002350	CTCCGAGTCACTAATGTGCAA	CCCAATAATTGCAGAACTAAA	CGGGAAATATGGGATGTATAA	CCCGGACGACTTGTCTTTCAA
4070	TACSTD2	NM_002353	TCGGCGCAAAGGAGACGTTTA	TTGCGACATTGTGAAGGCTTA	CCCGGGATCGTTTGCAAGTAA	CTCGAAATAAGTGGTACTATT
4071	TM4SF1	NM_014220	TTCACTTGTATTCATTTGTAA	TCACAGGATGTCAGTGTTTAA		
4084	MAD	NM_002357	CAGTAGCAGATCAACTCACAA	TACGTTGAGTTTATTAACAAA	CCGAATCAAGTCGACACACTA	AGCCAAATTGCACATAAAGAA
4085	MAD2L1	NM_002358	AAGAGTCGGGACCACAGTTTA	CTGAAAGTAACTCATAATCTA	TCCGCCTTCGTTCATTTACTA	ATGGATATTTGTACTGTTTAA
4086	SMAD1	NM_005900	TTGGAAGTTAAGAATTGATTA	CACACACACCTTGGTAACATA	AACCGGAATTCCACTATTGAA	CAGGACTTTGTGTACAGTTAA
4088	SMAD3	NM_005902	CCGCTGTTCCAGTGTGTCTTA	ATCAAGGGATTTCCTATGGAA	AAGAGATTCGAATGACGGTAA	AAGGAGCACCTTGACAGACTT
4093	SMAD9	NM_005905	CAGCCTCAAGGTCTTCAACAA	TTGGACTTCTTTCTAATGTAA		
4099	MAG	NM_080600	CACTCGCTGTACAGAATGATA	CCCGGTGATTGTGGAGATGAA	CTCGCTGTACAGAATGATATT	ATCGCGCAATGTGACCGTGAA
4101	MAGEA2	NM_005361	TCGACAGATGCAGTGGTTCTA	CAGGGAGTTGATGACCTTGTT		
4109	MAGEA10	NM_021048	CCCAGAAGTGAGATAGATGAA	AAGAAGATCTTCAATCCCAAA		
4118	MAL	NM_002371	TCAGATGGAAGTCTTCATAAA	ACCCTGTGAAATACTTATAA		
4123	MAN2C1	NM_006715	CACCCAGAAATTGAGCTGGAA	CTCGCTCTTGCGGGCGCCTAA	CAGCCTGTGTTCGTAGTGCAA	CAGGATGCTGGCGTTATCCAA
4125	MAN2B1	NM_000528	GCGCCTTGATTATCAAGATAA	CGCCAAGGAGCTGGTCGATTA	TCGACCCACCTGGAAACTGAA	GCGGAGTATCGGAGCCACTAA
4128	MAOA	NM_000240	TTGCATATTTGGATTACAATA	ACCCTGGTGTGAGGACATAAA	ACGCTGAACCATGAACATTAT	CAGATGTGCCTAGACACGAAA
4137	MAPT	NM_016835	CGGGAAGGTGCAGATAATTAA	TTAGGCAACATCCATCATAAA	CAGTGTGCAAATAGTCTACAA	CCGCCAGGAGTTCGAAGTGAT
4141	MARS	NM_004990	CAGCGAGGGATTCACGGCGAA	TAGGAGCTGAGGATAACTATA	CTGCATAACCCGAGACCTCAA	CTCGACATGGCAACCAATATA
4142	MAS1	NM_002377	CCCATATGCATGAGATACTAA	GAGATACTAATTAATGATGAA	ACAGTTGAGACTGTCGTCTAA	AAGTATCTCCTAAATGTGATA
4144	MAT2A	NM_005911	CAGCAGGATCCTGATGCCAAA	CAACAGTTTAATGAAGATCTA		
4148	MATN3	NM_002381	CACCACTGTGAGTGTAGCCAA	CACCTTGAATGCCGACAAGAA	AAGGTCAGCTCGTATCTTCAA	TTGGTAGGAAATAGAATGAAA
4150	MAZ	NM_002383	CCGCGACGTCTAGCACCTGAA	CGCGTCTGCCTTGGAGAAGAA		
4152	MBD1	NM_002384	AAGAGAGTTCGGGGAAACATA	CCGGGAACAGAGAATGTTTAA	CCTGAGGATAACTCAATATAA	AAGGATGATTCTGCCTCCAAA
4153	MBL2	NM_000242	TAGGGTTCCCTTATATTAATA	TACGATGTTTAGTAACCTCAA	CAAGTCAAGATTTCCATATAA	CACATTGAGTCTATCAATCAA
4155	MBP	NM_002385	CACGGCCGGACCCAAGATGAA	CAGTTAAATGAGAACATGAAA		
4157	MC1R	NM_002386	CCAGGAAAGTCTGGTAATAAA	CAGGAAAGTCTGGTAATAAAT	CACGCTCTTCATCGCCTACTA	CACCAGGGCTTTGGCCTTAAA
4161	MC5R	NM_005913	CACCATCTACCTACTCAACAA	TCGCTTCATGTCTCACTTCAA	CTGGGAGACCATCACCATCTA	CGGCATTGTCTTCATCCTGTA
4162	MCAM	NM_006500	CAGCTGGTTAAAGAAGACAAA	TACACACATTATGGCTGTAAA	CCGAACTTGTAGTTGAAGTTA	AAGACCGAACTTGTAGTTGAA
4168	MCF2	NM_005369	TAGAATGTCATCGGCAAATAA	CACGTACTAAATGAACTGATA	TGGCTATATTGGAAACTTAAA	AGGGACTATAGCTCAAGTAAA
4172	MCM3	NM_002388	CAGGGAATTTATCAGAGCAAA	CGGCAGGTATGACCAGTATAA	ATCCAGGTTGAAGGCATTCAA	CACGATTTGACTTGCTCTTCA
4193	MDM2	NM_002392	GCCCAGTATGTAGACAACCAA	CCGGATCTTGATGCTGGTGTA	CAGGCAAATGTGCAATACCAA	AACCTGAAATTTATTCACATA
4201	MEA	NM_014623	CACAGTGAGAGCTGCCTTATA	TGGGAAGATGTGGTACAGAAA		
4222	MEOX1	NM_004527	CAGGCTTGACTGGGTGGACAA	CTCAATTCACTTTGTAAGAAA		
4224	MERTA	NM_005588	AAGGACGGACCGGGATGATTA	GACACCTATGATGATAGCTTA	CCGGGATGATTATGTGAACAT	GAGGCTGAACCGAATGTACAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
4234	METTL1	NM_005371	CGCGCATGGCTGCGTCATTAA	CACGTGGATTTGGTAGAGAAA	CAGAATATGCCTACGTGCTAA	CTGGTGTATACCATAACCGAT
4239	MFAP4	NM_002404	CTGGACTGTGACGACATCTAT	CCGCGGCTGGAATGACTACAA	CAGAAGAGATTCAATGGCTCA	AACTGGCTTCATACACACAAA
4242	MFNG	NM_002405	ATGCTTATTTGTTTAAGTCAA	CTGGCTAATGTCTCTCAGTCA	CTGGCCGTTGGCCCTGGCTAA	CAAGACAATCATCCACAGCTA
4254	KITLG	NM_000899	AAGCGAGATGGTAGTACAATT	CAGAAATGTCTAAATGCTGAA	TACTGTGAAACTGGCACTGAA	CACTGAATTAATCATCTATAA
4255	MGMT	NM_002412	AAGCTGCTGAAGGTTGTGAAA	CCGGCTCTTCACCATCCCGTT	AAGGTTGTGAAATTCGGAGAA	CACCAGACAGGTGTTATGGAA
4259	MGST3	NM_004528	CAAGATGGCTGTCCTCTCTAA	CTGGTGCTGCCAGCTTTATAA	ATGGCTGTCCTCTCTAAGGAA	CCAGAACACGTTGGAAGTGTA
4283	CXCL9	NM_002416	ACCAATAAGTATTCTGTGTTA	CCACCCGAACGTCTTATCTAA	CCGGTGGAGATCCCACCCGAA	CAGGTAGACAGTATATAACTA
4284	MIP	NM_012064	CCGCTGTGCTGTATAGCGTTA	CCGAGGAAACCTAGCACTCAA	CCGGCTCAAGACTATTTCTGA	CCCGATGTCTCCAATGGACAA
4286	MITF	NM_000248	ATCGATGACATCATTAGCCTA	CAGCCTACAACTGAATAGCAA	TAGCCTAGAATCAAGTTATAA	CATGATGGTATCTATAGTCAA
4287	ATXN3	NM_004993	CAACATTGCCTGAATAACTTA	TGCGTCGGTTGTAGGACTAAA	TCGGAAGAGACGAGAAGCCTA	TACGATGGGATCATTATTTCA
4291	MLF1	NM_022443.1	GAGGGAGAGCTCATAATCGTA	CAGGAGTTCATCAATATGAAT	GACCGAGCTCATGTCATTAAA	GACCAATCTCTTGCTGTTAAA
4295	MLN	NM_002418	CAGCAAATAAAGCATGAAATA	AAGGAACGGAATAAAGGGCAA	CCAGCTGGGCTTGGAAGGAAA	CTCCAAGATGGTATCCCGTAA
4296	MAP3K11	NM_002419	CAAGGCCTCCACCTTCTCTAA	CCGGCCTTGACCGGAGGAGAA	CCGGAGGAGAAACGTCTTCGA	CCCGACGTCTGGAGGACTCAA
4301	MLLT4	NM_005936	TAGCTCTACAGTCCACTTTAA	CAGCAGTTGGGCCATATTGAA	CTCTATAATAATTCAACTCAA	ATGCCGGTATGTATTGTCCAA
4306	NR3C2	NM_000901	CCAGACCTAGTCTTTAATGAA	CAGCAATTAATTAGATCAACA	CCACGAGGAAGCAGCAATTAA	CAACATTACCTTGTCTTTCAA
4308	TRPM1	NM_002420	AACGGGAATGTATCTTTGTAA	CAAGATTATACAATCTCTTTA	TTCAGTTGCAGTAGTATCAAA	CACCATTAGGTCACTTAAGAA
4317	MMP8	NM_002424	AACGCACTAACTTGACCTACA	ATGGACCAAGACCTCCGCAAA	CCGAAGAAACATGGACCAACA	TCCCAAGGATATATCAAACTA
4319	MMP10	NM_002425	GACAGTAATCTCATTGTTAAA	CAGGATGGTGACACACATATT	GAGCCTAAGGTTGATGCTGTA	GACACACATATTAAAGAGTAA
4324	MMP15	NM_002428	CCGGAGCGCTGAGCCAGACAA	CACCAAATACTGGAAATTCGA	CTGGCTCTTTCGAGAAGCGAA	TACATTTATTTCTGTAAATAA
4326	MMP17	NM_016155	CACAAGATCGTCTTCTTTAAA	AAGGACAATAACGTAGAGGAA	CTGGGTGTTCAAGGACAATAA	ATGACAGGACTTATTTCTTTA
4328	MMPL1	NM_004142	ATCGGTGTGTAAGGTGGCCTA	CTCCATTATGAGGCCCTTCTA	CAGGCTGGAGTGCAATGACAT	CAGGGATGATGGAGAGTTCAT
4329	ALDH6A1	NM_005589	CAGGTCTTGCTCCGCTATGAA	CAGCTTTGTGGGATCCAACAA	TGCGATCATCCGGACATCAAA	AACCATCATCTCGAATGTCAA
4355	MPP2	NM_005374	CTAGCGATTGACAAGGAATAA	AACGGCCGAGTTTGTCCCTTA	ACGGCGCAGCCTGAAGAACAA	CCAGTTCTTCCAAGTGTCTAA
4357	MPST	NM_021126	CAAGACCTACGAGGACATCAA	CACCAAGAGAGTGTTTCTTCA	CAGGAATTCCGTTGACTTGTT	AACCAAGTGCTAAATCTTGTA
4361	MRE11A	NM_005590	TGCGATTCAGTTCACCGCTAA	CACATCTTTATTGAACTTGAA	CCCGACATTTCTTCATAGGTA	AAGGGTTATTTGAGCAAGTAA
4435	CITED1	NM_004143	CAGAAACTTAATAGCCAGTAT	ACCAATTCTGTTGTAAATAAA		
4436	MSH2	NM_000251	CAAGGATATGATATCATGGAA	TCCAGGCATGCTTGTGTTGAA	TTGATAAGCTATTGTCTGTAA	CCCATGGGCTATCAACTTAAT
4438	MSH4	NM_002440	AAGCATTAACATGAGATTAGA	TCGCTCATATTAATTGATGAA	ATCAATTGTCTTGGATGCCAA	ATGCAGTGAGGTCTAACATAA
4439	MSH5	NM_002441	TTGCCAGACATTAGTGGATAA	TAGGAAGACTCCCGGATTCTA	CACCTTCATGATCGACCTCAA	AAGAAAGATATTGTTTCTTTA
4482	MSRA	NM_012331	ACCCTTCTTGGTAGAAGCTAA	AAGGAAATTCTGGGTCTTGAA		
4486	MST1R	NM_002447	CAGGTCTGCGTAGATGGTGAA	AGGGAGTACTATAGTGTTCAA	TGCCATTAAGTTTGAGTATAT	ATGGAGCATCCTTCTCCGATA
4493	MT1E	NM_175617	CTGCAAGTGCAAAGAGTGCAA	CTGGGCTTTCTTTGCCCTCAT	AAATATGTGACTGACAATAAA	CTCCAGGCTTTCTGCCCTAAA
4499	MT1K	NM_176870	GCCTAGCAGTCGCTCCATTTA	CACGCCGTCCGGGTGGGCCTA		
4520	MTF1	NM_005955	CAGCACAAATAGGCAGCTTAA	ATGAAAGGTCATGATAACAAA		
4521	NUDT1	NM_002452	CCGCGAGGTGGACACGGTCTA	CCGGGTTTCATCTGGAATTAA		
4522	MTMR1D1	NM_005956	GAGGTAGAATTATATGGTGAA	ACAGGTGAATGGATTATTCTA	CAGATCACCATCCATCTTCAA	ATCGTTTGGTGCCATCAGTAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
4524	MTHFR	NM_005957	AAGCGCCGAGAGGAAGATGTA	CTCGGGAGAACCAAACCGGAA	AACCTAGTACTCTCTGCTCTA	TGCCCTGTAACTTATCTAGAA
4544	MTNR1B	NM_005959	CGGCCTCGCTGTGGCCATCAA	CTGCCTGAATGCCATTGTCTA	CACTAGCTACTTACTGGCTTA	AACCCACGGCACTGCATTCAA
4580	MTX1	NM_002455	TTGGATAGACACCAAGAACTA	CAGGGCCCGCTCCAAACATAA		
4583	MUC2	NM_002457	CCGGTTTGGCAACAACACCAA	CCCGCTGGGATTCGAAGTGAA		
4586	MUC5AC	XM_495860	CCAGTCTGTTGCATAAATACA	ACCCTTCAAGATGTGCCTCAA	CTGGACAGTGTGCAGCATCAA	CACCCGGAGGTGAACATTGAA
4587	MUC5B	XM_039877	CACCTATGATGAGAAACTCTA	CCCGATGGGTTTCCTAAATTT		
4591	TRIM37	NM_015294	TTGGACTTACTCGCAAATGAA	CTCGAAGGTGGTCCTACTACA	CTAGAGCTTAGTTGTGTTTAA	CTGTAGATTAGTGAACAGAAA
4594	MUT	NM_000255	AAGAGAGATACTATGGACTTA	CTGGGCTCACTTAATAGAGAA	CTGGAGCTGGCCTATACTTTA	AGGGAATACCTAAACTTCGAA
4595	MUTYH	NM_012222	CACATCAAGCTGACATATCAA	CAGGAGGAATTTCACACCGCA	GAGAATCCTGTTGTTAGTAAA	CAAGCTGACATATCAAGTATA
4598	MVK	NM_000431	AAGGGAAGATTTCATCCTTAA	CTGTGGCATCACACTCCTCAA	GCGGTCGGCCTGGTTAAATAA	CCGCTTGGCGATGCCAGCCAA
4599	MX1	NM_002462	TAGAGCTTACTTTGCAAAGAA	TCCGTTAGCCGTGGTGATTTA	CTGAAGAAACTTGTGAACGAA	TAAGATCAAGACACTCATCAA
4606	MYBPC2	NM_004533	CCGCCTCGAGGTCAAAGCCAA	TCCCAAGTTCCTGATAACCAA		
4607	MYBPC3	NM_000256	CAAGGTCAAGTTCGACCTCAA	TAGCACGGAGCTCTTTGTGAA	CCGCATAAAGGTGTCCCACAT	CAGGATGTCGGCAACACGGAA
4609	MYC	NM_002467	TAGCAGTTACACAGAATTTCA	CTCGGTGCAGCCGTATTTCTA	CCCAAGGTAGTTATCCTTAAA	AACGTTTATAGCAGTTACACA
4610	MYCL1	NM_005376	CAGCACTATTTCTACGACTAT	TGGCTAGTGACAAATAAATTA	CTGTGGCTAGTGACAAATAAA	CTCCAGTTGGCTTTACTTTAA
4615	MYD88	NM_002468	TCCGGCAACTGGAACAGACAA	CTCTGGCATATTGATCAAGTA	CAGAGAGTAGCTGTGTTTGAA	CATCCTGAGTTTATAATAATA
4618	MYF6	NM_002469	CTCGTGATAACGGCTAAGGAA	AAGTGGGAAAGTTGCATTTAA	TGCGAGGATCCTGGTATTGTA	TCCTGGTATTGTAATATTAAA
4619	MYH1	NM_005963	AAGCGCATCCATGAACTGGAA	CTGGGCTTTACTTCAGATGAA		
4625	MYH7	NM_000257	CAGAGAGAGATTATCACATTT	CAGACGGAGGAGGACAGGAAA		
4628	MYH10	NM_005964	CTCGTTCATCGCATCAATAAA	AAGCGGTTCAAAGCAAATCTA	CCCATGTTGCTTCTTCACATA	CAGGACTAATCTATACTTATT
4636	MYL5	NM_002477	CAAGGAGGCATTCACACTCAT	CTCATCCAATGTCTTCTCCAA		
4653	MYOC	NM_000261	CCCATTCAAGAACCGCTATAA	GGCGTAGACAATTTCATATAA	CAGCATTTATGGGATGTTTAA	CAGCATCGAATATAAGTAAGA
4654	MYOD1	NM_002478	CCGCCTGAGCAAAGTAAATGA	CCGCCTGAGCAAAGTAAATGA	CTGCACGTCGAGCAATCCAAA	TACAGGGAATTTGTACGTTTA
4656	MYOG	NM_002479	CAGGCTCAAGAAGGTGAATGA	CCCAGATGAAACCATGCCCAA	CCAACTGAGATTGTCTTCCAA	CTGCCCTGAATTGAGAGAGAA
4670	HNRPM	NM_005968	TGGCATCTTGTTGACATCGAA	CCCACCCAGTATCCTAAATAA	CCCGCAGGAATGGGAATGGAA	CCGGATGATGAATGGCATGAA
4671	BIRC1	NM_004536	ATCCTCAATCTAAGTACTTAA	CTCAATCTAAGTACTTAACTA	TCGAAATTCATGATACTACTA	CGTGGTGAACTTTGTGAATTA
4684	NCAM1	NM_000615	CCGATTCATAGTCCTGTCCAA	TCCATGTACCTTGAAGTGCAA	CCGAAACAACGTACGCCGTAA	CAGCGCGGCCTCCGAGTTCAA
4686	NCBP1	NM_002486	CAGGTATGGACTGCTGATAAA	CTGGAAGAAGCTAAAGAGAAA		
4688	NCF2	NM_000433	CAGAAGCATTAACCGAGACAA	CAAGAAGGATTACCTAGGCAA	CAAGTACACGGTAGTCATGAA	CAGTTTGGAAGTGTTAACTAT
4691	NCL	NM_005381	ACGGTGAAATTGATGGAAATA	TCCGTCTAGTTAACATTTCAA	TTGACTGGATATTCATATAAA	ATCCGTCTAGTTAACATTTCA
4692	NDN	NM_002487	CCGCGAAATCACCAAGATGCA	CAGTGCAGTATTCACGTGTAA	CCCACCGTGAGTCAACTTTAA	CCACCGTGAGTCAACTTTAAA
4696	NDUFA3	NM_004542	CAGCCTGGAGTGGCTGAAGAA	CAAGTACTCCGTCATGATCAA		
4704	NDUFA9	NM_005002	TCCGGAAGCCATTATCGTAAA	AAGAGAGGATAGATTCCTTAA		
4705	NDUFA10	NM_004544	AAGCAGGACAATCGCACTTTA	CTGGATGTTTGGAACCCTTTA		
4709	NDUFB3	NM_002491	CAGATTGAGGATGCACATATA	CAGAATATTAGTAAAGATTTA		
4716	NDUFB10	NM_004548	CAGCAGAACTGTATCAAGGAA	ATGACTGTTGCTGAAATATAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
4717	NDUFC1	NM_002494	CTCATCAAACAACACAATGAA	CACCATCTGTTGAGTTGTAAA		
4718	NDUFC2	NM_004549	CTGTAGGTATTAAGTCATTAA	CTGGTCTATATGTGATTTCAA		
4719	NDUFS1	NM_005006	CCGCAGATAATTAATGGACAA	TTGGCTTATCTTCATAAATAA		
4722	NDUFS3	NM_004551	CCGGAGAGTCTCAAGCTTGAA	TTGAGTGTCCGTGTAAATAAA		
4736	RPL10A	NM_007104	CAGCGCCTATATTAAGGCACA	CACATTTGAATAAATTCTATT		
4739	NEDD9	NM_006403	CGCTGCCGAAATGAAGTATAA	CACCCAAGAACAAGAGGTATA		
4741	NEF3	NM_005382	CCCAATCACAATATCCAGTAA	CAGCAGTACTTGCTCAATAAA		
4745	NELL1	NM_006157	TGCGAGAAAGATATTGATGAA	CTCATGTGAGTGAGAAATTAA		
4750	NEK1	NM_012224	ATGGCTCTCTCTACATAGTAA	CAGAATAAAGCTCGAGCCGAA	TAGGGATAGACCATCAGTCAA	ACCGTAGGAGATGTTCGTCAA
4760	NEUROD1	NM_002500	CACGAATTTGGTGTGGCTGTA	CAGATCGTATTAATTATCTGA	CAAGCTTGTATATACATATTA	CCCATGGTGGGTTGTCATATA
4761	NEUROD2	NM_006160	CAATGGCAACTTCTCACTCAA	CCCGCTCTGTCTCAATGGCAA	CTCGGAGAATCTCTTGTCTTA	CAAGACAATTTGTAACTAGAA
4762	NEUROG1	NM_006161	CCCAGGCTGTTGGGAACGTAA	CCGGCTGACAATACAATGAAA	CAGGGCTGGAGAGTACTTTAA	CAGACGCTTCATGTAAATAAA
4779	NFE2L1	NM_003204	AAGGGTAGAGTGAACAGGAAA	AAGGAGATTCCCAATATTCAA		
4781	NFIB	NM_005596	CTGGACAATCAGGAAGTCCAA	TACAATCACTAATTCCCTTAA	AAGGTTAAACTGTAATGACAT	ACAGAGGGCAAGTGCAATTTA
4784	NFIX	NM_002501	CTGGTGCTTCTTACATTATAA	CCGGACAATCAGATAGTTCAA		
4796	NFKBIL2	NM_013432	CCCATCCGGGTTCGAGTTCAA	CGGGAGCTCAGTGTAGCTGAA		
4804	NGFR	NM_002507	ATGGCAATTCTTTGACCTCAA	CTCCTGAAAGTTACACACAAA	ACGTTAAGTGATGAACATTAA	AACGTTAAGTGATGAACATTA
4814	NINJ1	NM_004148	CAGGACATTCCAGAAGGACAA	CACGCTCTTTGTCAGGCTCAA		
4818	NKG7	NM_005601	AACCTTGTGAGCAGAAGGCAA	CTCCTTCTCTCTGAGATTCAA		
4824	NKX3-1	NM_006167	ACGCTATAAGACTAAGCGAAA	CAGGCTATCATATATACTGTA	AACTGTGTTTATTGCCTATAA	CCGGAGTACTAGCCAGCACAA
4825	NKX6-1	NM_006168	CCCGCTGTACCCTGCCGCGTA	CTGGAGAAGACTTTCGAACAA		
4832	NME3	NM_002513	CCGGCAGATGCGCGTCAGAGA	ACGGCCGCCTTGTCAAGTATA	CTGCATCGAGGTTGGCAAGAA	ACGCACCTTCCTGGCCGTGAA
4833	NME4	NM_005009	ACGCCTTTATGCAAGTTGTAA	TTGTAAGGAGTTGAACAGTAA	CAGCACATGGGTGGTACACTA	ACCAACTACCTCCGTCAGCAA
4838	NODAL	NM_018055	GTGCTCCTAGATCACCATAAA	CTGGATGTTCTCTTTACTGAA	AAGATTAAGGATCACTGTATA	AAGGATCACTGTATAGATTAA
4849	CNOT3	NM_014516	ACGGCTGAGGGACCAAATCAA	CTCGGACACTGTGGAATTCTA		
4853	NOTCH2	NM_024408	TACCAGCATGTTATAGGGCAA	TTAGATGATAATGGACAACTA	AAGGGAAGGTAAGATGGATAA	CTGACTAAACGTAGTAAGGAA
4858	NOVA2	NM_002516	GAGGTGGTCAACATCCTTCAA	CAGGTCTGTGTGATATCTGTA		
4861	NPAS1	NM_002517	TGGCTTTGTGTTCGCCTTGAA	CGCCTTGAACCAGGAAGGAAA	CAGCGTCTTCGACTACATTCA	GCCCGTAGCCCTGAGAATTAA
4868	NPHS1	NM_004646	CAAGGCCTCATTCACCGTGAA	CAGCAGCAATCCGCCGGTCAA	TCGGACCAAACCAACATTCAA	CTGGTTAGGTGAGCTCCATAA
4879	NPPB	NM_002521	CACCTGCTTCTGATTCCACAA	CTGAGGCGGCATTAAGAGGAA	AAGATGGTTTCTTACCTTTGA	TCCACGGTGAAATAAAGTCAA
4880	NPPC	NM_024409	CAAGGGCTGCTTCGGCCTCAA	CCCAACGCGCGCAAATACAAA		
4881	NPR1	NM_000906	CCGGTACTCACTCACCAATGA	CCTGACGTTGCGCAAATTTAA	ACGCATTGAGCTGACACGAAA	AACGCATTGAGCTGACACGAA
4882	NPR2	NM_000907	CCCGGGAGGATGGACTTCGAA	ACCCAACTGAATGAAGAGCTA	CAGGACAATCGCACCCGGGAA	AAGGATGCCCTAGATGAGCTA
4885	NPTX2	NM_002523	TTCGATTAAAGTGCACTGAAA	CTGGACTGTCTTCATCAAGTA		
4889	NPY5R	NM_006174	CCCTTAGTTTGTCTTACTGTA	TAGGCATTTCAAGTTGGTGTA	TTGGGCTCTATACATTTGTAA	CACAGTCTTGTGGAACTTCAA
4899	NRF1	NM_005011	CAGGCAGATGAATGTCTTGAA	CAGAGGTGCAATCAAATGGAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
4901	NRL	NM_006177	CCGAATTTAGATGCTGGTCAT	CAAGATTTCAATATCCAACAA	ATCCAACAACTAGATAGATTA	CTAGATAGATTAGGACCTCTA
4905	NSF	NM_006178	AAGGAATGCAATAAAGAGTAA	CAGGTACACATTTACACTGAA		
4913	NTHL1	NM_002528	CAGGCTGAGGTGGACCAAGAA	GAGCAAGGTGAAATACATCAA	CTGGAGGAGCAAGGTGAAATA	CACGCTGGGCAAGCTCATCTA
4915	NTRK2	NM_006180	CTGCATAGACAAAGGCCTTAA	ATGGCTTAAGCCTGTGTATAA	CTGACGAGTTTGTCTAGGAAA	ACCACGAACAGAAGTAATGAA
4916	NTRK3	NM_002530	CGCGATGGTTTCAGACGCTGA	CAGAGAGCACGGATAACTTTA	CTGGTTGGAGCGAATCTGCTA	CACGGATAACTTTATCTTGTT
4919	ROR1	NM_005012	CAGCAATGGATGGAATTTCAA	CCCAATATTGTCTGCCTTCTA	CCGTACTGCGATGAAACTTCA	CCCAGTGAGTAATCTCAGTAA
4928	NUP98	NM_005387	CGGGATTTCTTTGTAAAGCAT	CTGGAGTTAGCACTAACATAA	CAGTGTATTACTGCTATGAAA	TGGGACTACTATTAAATTTAA
4935	GPR143	NM_000273	CTGAGGCTGGCTGTAAAGTAA	CTGGCTGTAAAGTAAGTGTAA	TCGGATATGAACGACACGGAA	CAGCTAGAGCTTCTTCCCGAA
4948	OCA2	NM_000275	CCGCGGAAGTGTAGAAACCCA	CTGGCTGTGATTGGCGATAGA	TGGAATAGACCTTGACACTAA	GACCTTGACACTAACACTCTA
4957	OGDH	NM_002541	CAGGATCAATCGTGTCACCGA	CTGCAATTGGGTTGTTGTCAA	CACTCTTTCTTTCTCCTTTAA	TTGGCTTGACCCATAAACTAA
4975	OMP	NM_006189	AAGGAGGACTCGGATGCCATA	CCGGGCAAGGTCACCATCACA	CTCGGATGCCATAGATTGGAA	CTGGAATGTCGTGCTGGACAA
4978	OPCML	NM_002545	CACGTGTAGGATAATCATTCA	ATGCATGAAACCCAACACTAA	TAGGCCAAAGTAGCAAGCTAA	CTGGGACACTATCCTACTATA
4985	OPRD1	NM_000911	CACGCTCACCATGATGAGTGT	CTCCATCGACTACTACAATAT	CGGCATCGTCCGGTACACTAA	CAGCATCTTCACGCTCACCAT
4986	OPRK1	NM_000912	CAGGGAAGACGTCGATGTCAT	ATCGATGGGATGAATAAACCA	TAGGTTTAACTCAGATCACTA	CAGATGCTTTAGTTACTACAA
4987	OPRL1	NM_000913	CTGCCTTGTCATGTACGTCAT	CAGCGGTGCAATGAAGTATCA	CTGGCTGGGTATTCTTCGTAA	ATGGGACAGGTCAAAGCATTA
4988	OPRM1	NM_000914	CCGTAGTAACACATAAAGTAA	AGGGAAGAGATTAGCATGAAA	TTCACCGTAGTAACACATAAA	TCCAGAGTGTGAATTACCTAA
4992	OR1F1	NM_012360	CCCACTCAGCTGAGAAAGACA	CTGAGAAAGAGACTATGGCTA	CAGCACCATCATTGCTGTGTA	ATGGGTGGTTGCCAACCTGAA
4993	OR2C1	NM_012368	TCAGCTATGGTGGCTGCATAA	CCCAAATGCTGATCAATTTAT	CAAGTTCATTTCCCTGTTCTA	AAGCATCATCGTGATCTCCTA
4994	OR3A1	NM_002550	CTGGGTTCAACCAAGCTTTCA	TTCAGGTATCTTTAACTATAT	CAAGCTTTCAGACAAGGATAA	AAGCTTTCAGACAAGGATAAA
4995	OR3A2	NM_002551	AGGGTGCTCTGTGGCAAATAT	ATGGACAAACTCCAAGGCAAA	CACGTGGCAGCTGCAGTTCTA	AAGAGGTATCTTCAACTACAT
5003	SLC22A1LS	NM_007105	CTGCAGCAACATAGAGTACAA	CTCAGCCAGTCTTAAAGGCAA		
5004	ORM1	NM_000607	TCGAAACGAGGAGTACAATAA	TTCCCTCACTTGCATCAATAA	CAGCACGAGAAGGAGAGGAAA	CACGATCTTTCTCAGAGAGTA
5008	OSM	NM_020530	CAAGGCCTGGATGTTCGTAAA	CGGGCTCAGGAACAACATCTA	CTGACGTAAGGTGGATATTAA	TGGAGGGACATGACTAATTTA
5009	OTC	NM_000531	AGCGGTGGAGCTTGGCATAAA	AGGGCATAGAATCGTCCTTTA	AGCATCCATCCCAATTATCAA	TACGTGCTTAACTTTGCTTAA
5025	P2RX4	NM_002560	CTCCGTTACGAGCAAGGTCAA	AGGCAGGTGCGTAGCTTTCAA	TCGTGCATTTATGATGCTAAA	CGGGACGTTGAGCACAACGTA
5030	P2RY4	NM_002565	CTGGGATGCAACGGCCACCTA	CAGAGGTGAGGGAACCCAATA	CCCAATAGTGATACCTGGTAA	CAGATAGATTGTAACACGGGA
5033	P4HA1	NM_000917	CAGAGAAGTTAGATCGGCTAA	TGGCAACAAATGGGTATCCAA	CGAAATCATCATATTGCATAA	CAGGGTGGTAATATTGGCATT
5034	P4HB	NM_000918	GAGGAAGACGATGATCAGAAA	CTATTTCACAATCGAATTGAA	CAGGACGGTCATTGATTACAA	AAGATGAACTGTAATACGCAA
5051	PAFAH2	NM_000437	CAGCGGGTAAGCGAGTGTTTA	ACGGGTGTTGAAGATCCTGCA	CCCGAGGACCTGTGTTCTTTA	GAGAAGTAGTTTGGTCAGCTA
5062	PAK2	NM_002577	TGCAGTAGTATAAATCATGAA	CCGGATCATACGAAATCAATT	CCGCGACCGGATCATACGAAA	ACGAGTAATTGTGAAGCATAA
5069	PAPPA	NM_002581	TGGGCAGTTCATGAAGCTCTA	CCGACAAGAAGTCTCCTTCAA	CTGGCCAATGCTTAAATACTA	CAGGGAGTGCTTGTTTGATAT
5101	PCDH9	NM_020403	ACGGTTCACCATCAATTTAAA	ACCGTCTAATACTTCCTTTAA	ACCGACGTGGGTTATACTTAA	AAGGCGGTATATGACAACCAA
5104	SERPINA5	NM_000624	CTCCGTTTCCTCATAGAACAA	TACACAGGTTTAGTTGACTAA	CACCAGCATGGTAGTGGCAAA	AAGGTGGAAATGGCCCATTTA
5108	PCM1	NM_006197	CGGATAAACTTCAGTGATTTA	CAGTATCACATCTGAACTAAA	ACCGTGATTCACTTAGATCAA	CAGGCTTTAACTAATTATGGA
5110	PCMT1	NM_005389	CAGGCGCTAATAGATCAGTTA	TTGGAGCAGTATGACAAGCTA	CTACAAGATGGCAGCATCAAA	TACGTGCCTTTAACAGATAAA
5111	PCNA	M15796	TGCGGATATGGGACACTTAAA	TACACTAAGGGCCGAAGATAA	ATGGATTTAGATGTTGAACAA	AAGGATCTTAGGCATTCTTAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
5121	PCP4	NM_006198	ATCATCTGTCAAGAAATTAAA	ATGGAATTGTGAGTAGCTTAA		
5129	PCTK3	NM_002596	CCGGCGGAATGAGAACTTGCA	CCGGGTATAAGGAGCAAAGGA	CAGGTTGGATACGGATGGCAT	AACCCGTTACTTAGCTGTGTA
5133	PDCD1	NM_005018	CTGGTTGGAGATGGCCTTGGA	CCCTGTGGTTCTATTATATTA	CCCATTCCTGAAATTATTTAA	ATCGGAGAGCTTCGTGCTAAA
5134	PDCD2	NM_002598	CAGATCATCTGGACCATATAA	CCAGATCATCTGGACCATATA		
5138	PDE2A	NM_002599	TCCGACGATGAGTATACCAAA	CATGAATTTCATCAACAACTA	ATCGCGGAGCTGATCTACAAA	ACCGCTTTGTACATGAGAATA
5140	PDE3B	NM_000922	TACGGAGTATTAGTAGCTTAA	TGGGATCGTAATAATGGCAAA	CACAGAGTGAACAGCAAACAA	CAGGTTATGTATACCTTATTT
5141	PDE4A	NM_006202	CAGGGCTGGCGGGCCATGTAA	CTGCTGTATTATACAACTGTA	ATGGGAAGTCGTGTCATCCTA	TTCGATCTTGTCTCCAATTAA
5146	PDE6C	NM_006204	AAGGTCGTCCTTTCTGAACAA	CTGGTGGGCCCTGACAAAGAA	CACGGTTAGATGATATCTGAA	ACGGATTGATTAAATGTGGAA
5150	PDE7A	NM_002603	CAGATAGGTGCTCTGATACTA	TCGGACGTGGGAATTAAGCAA	CCCGAACATACAGCAATATGA	CCGAACATACAGCAATATGAA
5152	PDE9A	NM_002606	ATGGACGCATTCAGAAGGTAA	CCGGAGGGAAGGAGCATTTGA	CGCGTCGAATTGGAAGGACTA	AACGGATATCCTGATCCTAAT
5156	PDGFRA	NM_006206	CTGAGCCAGATTGGCCAATTA	CGCAGGAAGCCTACTATTTAA	CCCGAGACTCCTGTAACCTTA	ACGCAGGAAGCCTACTATTTA
5157	PDGFRL	NM_006207	CCAGGAGAGAATAGAATCAAA	CTGCGTATCTGGACACCTTTA	CTGGAGGATGTTACTGGCCAA	ACGCAGTCTATCATGATGCAA
5158	PDE6B	NM_000283	GCCCACCACATTTGACATCTA	CTGAAGCCAACTGTGAATAAA	CACGCTGCTCATGACCGGCAA	CCGGGAAATTGTCTTCTACAA
5166	PDK4	NM_002612	CAGGACACTTTACGGGATCAA	CTAGACAGTGACATTTCTTAA	AGGCCTCTTGTTCACATCAAA	ACCCGTGTCAATTAACATTTA
5178	PEG3	NM_006210	AAGGATGACCCTGATGACAAA	CCGGATGTCATCATAGGAGAA		
5184	PEPD	NM_000285	CACCGTGGAGCCGGGCATCTA	CAGGCTGTGACAAGGCCTTTA	TCGGCATTTGATCAGACCAAA	CTGTCCTTTAGTAGCAAGTAA
5189	PEX1	NM_000466	CAGTAGCAAGTTTATGGACTA	CAGAGTATATCCACCAGAGAA	CTCATGGATACTATCCAGTTA	AAGGCAGATACCGGAGCCAAA
5190	PEX6	NM_000287	CCAGAGAGTTACACATCGAAA	CACACGCAAATTCAAGCTAGA	CCAGAGCTCATTAACATGTAT	CAGGATGTGTTTGTGATTGGA
5191	PEX7	NM_000288	CGGGCTGTGGAACCCTACTAA	CAGCAGGTGTATAGTGTTGAT	AAGCGTGACTCTCTTCTTGAA	TAGGTTATACGTATATAGATA
5204	PFDN5	NM_002624	ACAGGCCGTCATGGAAATGAT	CAACATGGCGCAGTCTATTAA		
5205	ATP8B1	NM_005603	CTGGATATCTTTGCAAATGAA	CTGGTTCTTGGTTGAATGAAA		
5208	PFKFB2	NM_006212	CAGAACAACAACAGCTATGAA	GCCCTTGTCACTAATCACCAA	CCGTGACAAGCCAACTAACAA	CCAGAGCAAGATAGTCTACTA
5209	PFKFB3	NM_004566	CTCCTAGTTGCTGAAAGTTAA	CTGGGATATAAAGCTATGCTA	CTCCAATATCATGGAAGTTAA	CAGGGACTTGTCGCTGATCAA
5210	PFKFB4	NM_004567	CCCACGGGAATTGACACAGAA	TACGAGGAAATTCAGGATAAT	CAGAAAGTGTCTGGACTTGTA	ACGGAGAGCGACCATCTTTAA
5214	PFKP	NM_002627	TCGGAGAACCGGTGCCCGGAAA	TGCGGGCAACCTGAACACCTA	CCGCCTGAAGGCTGCTTGCAA	CAGCACTTTATGCACGTATTA
5216	PFN1	NM_005022	TCAACAAGAAATGTTATGAAA	CCACGGTGGTTTGATCAACAA	TAGCATGGATCTTCGTACCAA	CGGGTGGAACGCCTACATCGA
5228	PGF	NM_002632	CAGGCTCTGCACAGTCAAGCA	AAGAGCTGCCTGGATGAGAAA	TGCCCTCTATTTATTAGCCAA	ACCCGGCTCGTGTATTTATTA
5236	PGM1	NM_002633	CAGGTACAGTTTACACTACAA	CAGCAAGACAATTGAAGAATA		
5243	ABCB1	NM_000927	GAGGTCGGAATGGATCTTGAA	GACAGAAAGCTTAGTACCAAA	CACGGAAGGCCTAATGCCGAA	ATCGAGTCACTGCCTAATAAA
5253	PHF2	NM_005392	CTGGATTTGTTTCTCAGGCAA	AAGATGAATCTTCAACTTTAA		
5256	PHKA2	NM_000292	CTGGTGAAATCGATCCCTTAA	CACCACATCGTTCTACACATA	CCGGATTCTTAGTCACATATA	CCGCCTAACAAGGTAGATGAA
5265	SERPINA1	NM_000295	AAGGCTGACACTCACGATGAA	TACGTGGAGAAGGGTACTCAA	CACCCACGATATCATCACCAA	CCCGAGGTCAAGTTCAACAAA
5271	SERPINB8	NM_002640	CTCAATCAAGGCGGACGTGAA	AGGGCAAACCCTATAGAGTAA	ACCACTGAGTCCTCTAACTAA	TTAGACAGTTTGAGTAATTAA
5281	PIGF	NM_002643	CACCATGAAAGATAACGATAT	AAGAAGTTCATTATCACACAA		
5283	PIGH	NM_004569	CAGGAAGAAATGTCCTACAAA	CAGGTTTACTTTGTTGATGTT		
5288	PIK3C2G	NM_004570	CTGGTGTGTGGTAACATTCAT	CCGGGCCTCTGAATCACATAA	CCCGTAGAAATGATAACTCCA	CCAGATCAAGAAATTCGTAAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
5295	PIK3R1	NM_181504	ACGGCTGAATATGAATAGATA	CACCCAGTGTAGCATCCTAAA	TAGCTGGTTATGAACTAGTAA	CAGCATTAAACCAGACCTTAT
5296	PIK3R2	NM_005027	CAGGGCCAGACTCAAGAGAAA	CGGCGTGAGGGCAACGAGAAA	TTGGTACGTGGGCAAGATCAA	CCGCGAGTATGACCAGCTTTA
5298	PIK4CB	NM_002651	TGGCGACATGTTCAACTACTA	CGACATGTTCAACTACTATAA	TCGGCTGATAGTGGCATGATT	CCGAGAGTATTGATAATTCAT
5300	PIN1	NM_006221	CGGCTACATCCAGAAGATCAA	CAGGCCGAGTGTACTACTTCA	GACCGCCAGATTCTCCCTTAA	GAGTATTTATTGTTCCCACAA
5303	PIN4	NM_006223	CACACTATTCACACAACTGAA	CAGCATTTGCCTTGCCTGTAA		
5310	PKD1	NM_000296	CCGCGTGAACAGGGCGCATTA	CCGAGCCATTTACCACCCATA	CTGGGTCTCAGCCACGTACAA	CCCGTCCATTGTGGGTAGCAA
5313	PKLR	NM_000298	CTGAAAGTCTGTGTCCAATTA	AAGCATGTCGATCCAGGAGAA	GAGGCCTATCTGAGACTATAA	CGGGTGCAATTTGGCATTGAA
5314	PKHD1	NM_170724	TTGCAGCTAGATATAAATTAT	CTGATGAGTATTGAAGTACTA	CACGAGATAGCTGTACTTTCA	CACCGGCATATTGGAAGTGTA
5315	PKM2	NM_182471	CTGGATAACGCCTACATGGAA	CCGGGTGAACTTTGCCATGAA	CCCGATCAGTGGAGACGTTGA	AACATCAAGATTATCAGCAAA
5317	PKP1	NM_000299	CAGGATGAATCTGCCAAGCAA	AAGCATAACCACAAACTGCAA	TCCCGACGGCCTTATGAGAAA	CTGGTGTTAGAGAGGAATTAA
5318	PKP2	NM_001005242	CAGGAGATACTTTACCTATAA	CAGAATGGAAATGACAAGAAA		
5324	PLAG1	NM_002655	AAGGGTCAGTTGGGACATTAA	AACCAACATAATCTTCTTAAA		
5325	PLAGL1	NM_002656	CAGCATTGTGATTAGAATGAA	CAGGAACATATTTGCATGTTA		
5326	PLAGL2	NM_002657	AAGGATATTTATGTAATAAGA	TCCAGATTATTTAAAGAGAAA		
5328	PLAU	NM_002658	CTGCCTGCCCTCGATGTATAA	CACGAGAGTCTCACACTTCTT	GAGCTGGTGTCTGATTGTTAA	CCGCATGACTTTGACTGGAAT
5330	PLCB2	NM_004573	CTCGGTGCAGTTTGTGGACTA	CCGGCCGGACAAGCAGTTCAA	CTCCATCAATCCTGTCTGGAA	GCGGCTTGCCTGGAACAGATA
5332	PLCB4	NM_000933	ACCAATAATAACTCATGGAAA	CAGGTCAATTGTTATCAGATA	CTGCAGATTCCGGATATTATA	AACCCGGTAGTCTAGAACTAA
5334	PLCL1	NM_006226	CTCGATGTAAGTGATGGTTCA	TCGAAGGATGTCGGTAGATTA	AAGGATGTCGGTAGATTACAA	CTCAGGAATATCGGTCTTAAA
5336	PLCG2	NM_002661	GACGCGGACTACCAAGATCAA	TAGGGTCTCTTTGCAGAGGAA	GACGACGGTTGTGAATGATAA	CACGTGGAAGATTGACAGCAA
5338	PLD2	NM_002663	CCACAGGTCCTTGATTCTCAA	CCGGCCTTTCGAAGATTTCAT	CAGCCTGCTGACAGACACTAA	CGGGACCTCCTGAGACACAAA
5340	PLG	NM_000301	CTGGGAGCAGGAAGTATAGAA	CTGCCGCAATCCTGACGGAAA	CACCACCACCACAGGAAAGAA	CAGGAAAGAAGTGTCAGTCTT
5341	PLEK	NM_002664	CTGGATGATGGGTTAATACAA	CTGTGACAAATCAACGGGAAA	GAGCATTTCTCTAACGTTTAT	ACCATTGACTTAGGTGCCTTA
5346	PLIN	NM_002666	ACGCCTTATTTGATTTAACTA	ACCCTAGTCTTCGAAATGTTA	GCGGGTTTCTCTAACAAATAA	TGGCTTGTTTATGAACATTAA
5347	PLK1	NM_005030	CAACGGCAGCGTGGAGATCAA	CGCGGGCAAGATTGTGCCTAA	CCGGATCAAGAAGAATGAATA	CACCATATGAATTGTACAGAA
5356	PLRG1	NM_002669	ACGGATTCATATGTTCATAAA	CGGCATTATCATGGACATTTA		
5357	PLS1	NM_002670	TAGGATGTTATTAGAGAGATA	ATAGAATATATTCATAATCAA		
5364	PLXNB1	NM_002673	ATGCTGGACCAGCTTTATAAA	ATCCTAGGTCTAAGAGTTGAA	CCGGGTGGAATTTATCCTTGA	AACGCGGACAGTTCAAGTATA
5371	PML	NM_002675	TGCGGTGAACCGGGAAAGCAA	CTCCAAGATCTAAACCGAGAA	CAGGGTTGTCCGCTCTGATTA	CAGGAGCAGGATAGTGCCTTT
5376	PMP22	NM_000304	CAGCCTCGTGTTGAGCCTTAA	TAGGCTGCTATTATTACTATA		
5407	PNLIPRP1	NM_006229	CCGCTTCCTGCTGTACACCAA	CCGGGACTTTGTGGCTTGCAA	CAAGTATTACTTGGAAAGCAT	CCCGATGGGTTTGCTGCATAT
5408	PNLIPRP2	NM_005396	CTAGTTGGAGATATAAGGTAT	TCAGGATTGCTTTGTATGGAA	CTGGAACAAACGTGGGATAAA	TGCGGCTATTGCGGTAATAAA
5412	UBL3	NM_007106	TGGGTGTATATCAAACGGCAA	CCCGGCGGATATGATAAATTT	AAGGACGATTTCTACATGGAA	CGCGTAGTATATAGAACAATA
5413	NA	NM_002688	AACAATGTTGGTGAACGTCAA	CCGGACGGTCACAGCACCCAA		
5423	POLB	NM_002690	CCGGAGCGAATGAGGCCTGTA	CCCAATAGGAGTCTTAATTTA	TACGAGTTCATCCATCAATTT	CAAGATATTGTACTAAATGAA
5426	POLE	NM_006231	CCAGATTATGATGATTTCCTA	CTGGATGGATCCATCTAACTA	CCGCCTCTCCATTGACCTGAA	CCGCATCATCCTCTGTACAAA
5428	POLG	NM_002693	CTCACTGACAATAGTGCCATA	CTCCAAGGCAGTGGAAATAAA	CAGATGCGGGTCACACCTAAA	CACGAGCAAATCTTCGGGCAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
5429	POLH	NM_006502	CAGCCAAATGCCCATTCGCAA	GAGGCAGTGTCATAAAGTAAA	CTGGTTGTGAGCATTCGTGTA	ATCCATTTAGGTGCTGAGTTA
5430	POLR2A	NM_000937	CTCGGGAAGAACAAAGCTAAA	CACCACAGTCTCCAACCTATA		
5434	POLR2E	NM_002695	CTGGAGGAGTTCAAAGCCCAA	ACGAAATAAATTTGCTTGATA		
5435	POLR2F	NM_021974	TCACTTTATATGTGTAAATAA	CACACCATACATGACCAAGTA		
5436	POLR2G	NM_002696	CTGGTGCTTCTTGTAGCTTAA	CAGGGAAGTATGGCTTTGTAA		
5437	POLR2H	NM_006232	CAGAGTTTATCTCCTGATGAA	ATGGATCTAATCTTAGATGTA		
5439	POLR2J	NM_006234	CAGCGGTGACTTCGCAAGCAA	CAGGGATGAATTCATTCTGGA		
5440	POLR2K	NM_005034	CAAGAGATTAATAATAATGTA	AACAATGATAACATACTATAA		
5441	POLR2L	NM_021128	AAGGTCTTTCAGAACCACTAA	CTGGAAGGAACCATCCAGTAA		
5452	POU2F2	NM_002698	TCCAGAAATAAGAATGTCTAA	AAGAAATGGACCAGACACTAA		
5464	PP	NM_021129	CTGGAAAGTCATTGCCATTAA	TAGCACATGCTTAAATATCAA		
5467	PPARD	NM_006238	CCCGTGGAGCAGTGATCTCTA	CAGTGATATCATTGAGCCTAA	CACAGACTGACGAAACTTTAA	ACTGACGAAACTTTAAATAAA
5468	PPARG	NM_005037	GAGGGCGATCTTGACAGGAAA	CAGACAAATCACCATTCGTTA	CCGGAGAACAATCAGATTGAA	CAGCGACTTGGCAATATTTAT
5475	PPEF1	NM_006240	CTGGGAAACCCTCTTCAATAA	ATCGAATATGCTGATGAACAA	CCCAATCGGTACAATCGTTGA	CAGCATTAGTACCTACATATT
5476	PPGB	NM_000308	CCGGAGTACAAGAACAACAAA	TGCAACTTTCTGGTAAACTTA	ATACCAGATCCTATTATATAA	CCGGCCCTGGTTAGTGAAGTA
5496	PPM1G	NM_002707	GAAGTTGTAGATTTCATTCAA	TACTCTGTGAACTTTATTTAA	CCAGAGGATGAAGTAGAACTA	CAGGACCTGAGGACTCAACTA
5498	PPOX	NM_000309	CAGCGGCTTGGCCGCCAGTTA	CACGTTATTAGTGCCATTCCA	CAGGAAGCAGCTGCTACACAA	CTGCTTGGTCCATCTACACAA
5501	PPP1CC	NM_002710	GAGGAGTAAGTGTACAATTGA	CTGCGGTGAAGTTGAGGCTTA	CTGGTTATAACAGCAAATGAA	AACATCGACAGCATTATCCAA
5509	PPP1R3D	NM_006242	TCAGGTGACTAGAGAATTTCA	AAGCATAGCTTTCTTCGGTAT	CTGAGTTAGGCAATCACTTAA	CAGGTACCCACCAACTTTATA
5511	PPP1R8	NM_002713	AACCCTGAAGCTGTAAATGAA	CTGCTGAAGTTTCTTATTTAA	TACAAATAAAGATGCCCTAAA	CAGGCCCAGGAACTGAAGAAA
5514	PPP1R10	NM_002714	CAGCAACATCTAAGCCCTTGA	CACAGGATCAGCTGCACTTAA	CCGAAGGACCGTCACTACATA	CCCAGCCTGCTGAGAAAGATA
5516	PPP2CB	NM_004156	CACCGGATACAAACTACTTAT	ATGGAATTAGATGACACTTTA	TGGGATCTGTCTTGGCATTAA	CCGACAAATTACCCAAGTATA
5519	PPP2R1B	NM_002716	TGGACCAATTCTAGATACCAA	CTGACGTTCGTTTGAATATCA	CAGGAAATAACTACTAAGCAA	CAGAAGTTAGGTCAAGATGAA
5520	PPP2R2A	NM_002717	AAGCGAGACATAACCCTAGAA	CTCGCCGTGTCTGGCACTGAA	CTGCAGATGATTTGCGGATTA	ATGGAAGGTATAGAGATCCTA
5521	PPP2R2B	NM_004576	CGGCTACAAATAACCTATATA	CCGGAAGATCCAAGCAACAGA	CAGGGACTACTTGACCGTCAA	CAGGAAATGATTGGAATAGAA
5524	PPP2R4	NM_178003	CGGATTCATCCTTACCCTCAA	CCGCTCCCTAAGGGTAACCTA	CTGAGGTGGCTGTTTACCTAA	CTCCGGGTGGATGACCAAATA
5527	PPP2R5C	NM_002719	CTGGAAATATTGGGAAGTATA	CTGCTACTTCAGTAAGAATAA	CCCATTGGAACAAGTAAGAAA	AACGAGCTGCTTTAAGTGAAA
5528	PPP2R5D	NM_006245	GAAGTTGTTTATGGAAATGAA	CAGGAGATTATTCTCACCAAA		
5532	PPP3CB	NM_021132	CAGCCCGGAAAGAAATCATAA	TAGTTTATTGTGAGTACTCAA	TAGGAGATTAGATAGATTCAA	AAGGGTTTGGATAGGATCAAT
5534	PPP3R1	NM_000945	GAGCCTCATGAAGCCAACTAA	TCCCTTTATAGTTTCTCTATA	GCCCATATAATTGGTAATGGA	ATCCTTTAGTACAGCGAGTAA
5544	PRB3	NM_006249	TCCCTCCGTAATATCAGGAAA	CCGGGAAAGCCAGAAGGACAA	CAAGAAGGTAACAAACCTCAA	AAGAAGGTGGTCATAGCTCTA
5549	PRELP	NM_002725	CAGGTCAAGAATAACACTTCA	AAAGATTATACTCTTAAGAAA		
5551	PRF1	NM_005041	GAGCACCGTGTGGGACAATAA	ACCATGTACATAGCTTGATAA	CACGGTGGAGTGCCGCTTCTA	CACCGTGTGGGACAATAACAA
5554	PRH1	NM_006250	TCAGCTCAGGATTTAAATGAA	TAACTTCAGTATACCAATAAA	CAGGAAGTGAATAAGAAGATA	TGGCATCATGCTCTAACTTCA
5562	PRKAA1	NM_006251	CAGCAATAAGCATGCATAATA	ACCAGAGTATATTTAAGTATA	TCGGGATCAGTTAGCAACTAT	CCCACGATATTCTGTACACAA
5567	PRKACB	NM_182948	ACCAATGTGTTCTATATGTAA	GGCATTAGGAGTGCTAATCTA	CTGACCAATCAAGTACACTAA	CAGCCTGTGTAGTGTGACAAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
5569	PKIA	NM_181839	CAGCAATGAATTAGCCTTGAA	CTCAAGTGTTCACCCAGTAAA	TCACTTGATCATATGACGAAA	ATGATTATCATTAGAAGCTAA
5573	PRKAR1A	NM_002734	CTGGACCGACCTAGATTTGAA	CAGCTAGTGCCAAATAATTGA	CAAATATTGGTTAGTATTTAA	ATGAAATAATTTAAATTCTTA
5576	PRKAR2A	NM_004157	AGCAGATTTAATAGACGAGTA	CTGCAGAAACCTGTTGTATAA	AACTTGAAAGTCAGCACTAAA	AACGGCATGTCTCTCCAACAA
5577	PRKAR2B	NM_002736	CTGGCCTTAATGTACAATACA	AAGGATGTTATCATAGGCTAT	CACGCCATTGGGACTGTCAAA	ACGAACATGGATATTGTTGAA
5578	PRKCA	NM_002737	TACAAGTTGCTTAACCAAGAA	CGCAGTGGAATGAGTCCTTTA	CAGCTGGTTATTGCTAACATA	CAAGACGTCTTTGGAATCCAA
5581	PRKCE	NM_005400	TACAATGACGTTAAGTCTTAA	GCCCATCATATTCATGTGTAA	CCCGACCATGGTAGTGTTCAA	CACGGAAACACCCGTACCTTA
5583	PRKCH	NM_006255	AGGGACATCTTCCAATGATTA	CAGGATGAGTTTAGAAACTTT	GACCAGATTTGTGGCTTATAA	CGCCGTGTGCTCATCACTGAA
5585	PKN1	NM_002741	CCGGAGCAGCCTCAAAGCAGA	CAGCCTCAAAGCAGAAGCCGA	CCGCAAGGAGCTGAAGCTGAA	CAGGACAGTAAGACCAAGATT
5587	PRKD1	NM_002742	AACAAAGCTGTTAAACTGTTA	TCGATTATTTCCAGTGTTCTA	CCTCAGTATATTTAAACTCAA	CAGGAAGGCGATCTTATTGAA
5589	PRKCSH	NM_002743	CAGCCTTCAAAGATGGGTAAA	CACCACCAACGAATACGTCTA	CTGCACCAACACTGGCTATAA	ACCTGTGACCTCAATACAATA
5592	PRKG1	NM_006258	AAACACTTCAATGTAGTATAA	TAGATTACTATGGTACAGAAA	GAGGTTCGTTTGAAGATTCTA	CCGGTGTATATACCATACAAA
5593	PRKG2	NM_006259	CTGGTTATAGATCGAGAAACA	CACGACGACCTGAGGATTTGA	TTGAGTACTACTAACGTTTAA	GACCTACAATTTGATTCTCAA
5599	MAPK8	NM_002750	TCGGGACTTAAAGCCCAGTAA	CTGGTAATAGATGCATCTAAA	AAGCCCAGTAATATAGTAGTA	AAGCAGTTAGATGAAAGGGAA
5603	MAPK13	NM_002754	CAGAAGGGTCCTTCTCCTTAT	TAGGGATGCTCTAACGAATTA	CGGGATGAGCCTCATCCGGAA	CCGGAGTGGCATGAAGCTGTA
5604	MAP2K1	NM_002755	AACAACGTGTATAGTGCCTAA	CTAGATGTTTAACAAATCTAA	CTGGATCAAGTCCTGAAGAAA	CTGGAAGAATTCCTGAACAAA
5605	MAP2K2	NM_030662	CACAAACCACACCTTCATCAA	TTCCAGGAGTTTGTCAATAAA	CCGGCCTGCCATGGCCATCTT	CAGCATTTGCATGGAACACAT
5606	MAP2K3	NM_002756	CTGGATGCCATCCAAGTTGTA	CTCCAATGTCCTTATCAACAA	CCGGGCCACCGTGAACTCACA	ACGGATATCCTGCATGTCCAA
5610	EIF2AK2	NM_002759	CTCCACATGATAGGAGGTTTA	TACGTGTGAGTCCCAAAGCAA	CGGAAAGACTTACGTTATTAA	ACGGAAAGACTTACGTTATTA
5617	PRL	NM_000948	CAGCGAATTCGATAAACGGTA	TGCAACGATCACGAACATGAA	CAGCATATTGCGATCCTGGAA	CCCGGAGGCTATCCTATCCAA
5619	PRM1	NM_002761	CCGAGATGTAGAAGACACTAA	CCGCCTGTCAATAAATGTTGA		
5631	PRPS1	NM_002764	CCCAAGGTCTATGCTAAATTA	CACCATCTGCTTGACTATGTA	AACATGCTTCCTGCTATGTAA	TTGATTAATTTAAGTATTTAA
5639	PRRG2	NM_000951	CCCAGTGAGGAGACAGACCAA	TTGGGAGAGCTACATCTACAA		
5653	KLK6	NM_002774	CTGACCCTGATGCTTAATAAA	CACGTTTGATTTCTTCCTGCA	CTGCAGATTTCTCACCTGTAA	CACCATGCACTCAATAAAGAA
5654	PRSS11	NM_002775	CCGGGTCAAAGTTGAGCTGAA	CGGTGAAGTGATTGGAATTAA	AGCGTATATAATTGAAGTAAT	CGACGTCATAATCAGCATCAA
5660	PSAP	NM_002778	CCGACATATGCAAGAACTATA	AAGAACTATATCAGCCAGTAT	CAAGCTGATTGACAACAACAA	CTGCCTGAATGTAACCTGCTA
5663	PSEN1	NM_000021	CTCAGGTTCCAAATTCAGTAA	CTGAGGTTGCTTTATCCTAAA	CAGGCATATCTCATTATGATT	CAGCTCTCATTTACTCCTCAA
5676	PSG7	NM_002783	CCCATGGAACCTCAAAGAGCA	ATCCTTGTACCTGATGTCTGA		
5682	PSMA1	NM_002786	CTGCCTGTGTCTCGTCTTGTA	TCCATTGGAATTGTTGGTAAA	CACAGTTGGTCTGAAATCAAA	ATGGAGTGTAATTTAAATGAA
5683	PSMA2	NM_002787	ATGCAAGAATATACTCAGTCA	ATGAGGGACGACCATATTTAT	AAGGATTACTTGGCTGCCATA	GAGATACATTATGTAAATAAA
5687	PSMA6	NM_002791	CAGGGTGGCCTTACATCAGTA	CACAGTGACTCACTTATTCAA	ACCGAAGTGGTTAGGACTCTA	CCAGGGATTGTGTTTAAAGTA
5688	PSMA7	NM_002792	AACAGATGATCTGACCATTAA	GACCATTAAGCTGGTGATCAA	ATGGATGAGTCTCGATGTGTA	CACACTGAGTGTCCTACAATA
5689	PSMB1	NM_002793	CCGGATCTGCATAGTGACCAA	ATCGGTGGACTTGATGAAGAA		
5690	PSMB2	NM_002794	CGCACTCTTGATAAATGGTTA	AAGATGCGAAATGGATATGAA	CAGCAATATTGTCCAGATGAA	GTGACTATGGATATAATTGAA
5692	PSMB4	NM_002796	TCGCATTATGCGAGTCAACAA	ATGCTTGGTGTAGCCTATGAA	ACCATTGTCTACAGAGACCAA	CACATGATCAGTGGCTTTGAA
5694	PSMB6	NM_002798	CGCCTGAATCCTGGGATTCTA	TGGGATTCTAGTATGCAATAA	CTGGGATTCTAGTATGCAATA	CTCCGGGAGCTCCTACATCTA
5698	PSMB9	NM_002800	CTGCAAATGTGGTGAGAAATA	GTGAGAAATATCAGCTATAAA	AAGGAGGTCAGGTATATGGAA	CAGCACCTTTATCTATGGTTA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
5699	PSMB10	NM_002801	CCCAGACAGTGAAGCCACTAA	CAGGCTATGGAGGTGGAGTAA	CACACGGATGGTGGCGTCCAA	CTGCGAGAAGATCCACTTCAT
5705	PSMC5	NM_002805	CAAGGTTATCATGGCTACTAA	CCGGGTGGCTCTAAGGAATGA	AAGGTACATCCTGAAGGTAAA	TTGGTCAAGGTACATCCTGAA
5706	PSMC6	NM_002806	CTGAGAAATGTTTGTACTGAA	AAGGAGTTAAGGGAACAATTA		
5707	PSMD1	NM_002807	CAGGCTGTGAGTGATATCTTA	TTGGAAGGCATCGTAAATAAA		
5708	PSMD2	NM_002808	TAGCGAACACTTTGACTCCAA	CAGGGTTCCAGACGCATACAA	CTCCGGAGGGCTGTACCTTTA	TGGGTGTGTTCCGAAAGTTTA
5718	PSMD12	NM_002816	ATGGGTTTAAATTTAACATAA	AAGGATTACATTCGAACACAA		
5723	PSPH	NM_004577	CAGAGACTCATAGCAGAGCAA	TAGGCTGAAATTCTACTTTAA	TGCCAATAGGCTGAAATTCTA	CCGGCATAAGGGAGCTGGTAA
5727	PTCH	NM_000264	ACCAAGCTTCATTAGTCTTAA	CCCGTCATTAGTGCTCTTTCA	TCGCACAGAACTCCACTCAAA	ACAGCATACCTCCTAGGTAAA
5729	PTGDR	NM_000953	AAGCATAATTTCTTACCCTAT	TCCAGTATCTGAGATAATATA	CCGGTGCAGCAATTCCACTAA	CCAGTATCTGAGATAATATAA
5733	PTGER3	NM_000957	AACAAATATCGCTAAACCTTA	CCGCTATAGAGTATTCCATAA	AAGGACCGATTTGAGCACTAA	ATCGATACCATTATTCAAATA
5739	PTGIR	NM_000960	TCGGGCGACAGGAGCCAGAAA	CAGAAAGAATGGTTCTCTCAA	CCCATCCATCTCATTGTCTAA	CCCAGGGTCCTGAATAAATAA
5743	PTGS2	NM_000963	TCGTATTGCTGCTGAATTTAA	TAGGGTAGAATCACCTGTAAA	GCCGCAGTACAGAAAGTATCA	ACGCTTTATGCTGAAGCCCTA
5745	PTHR1	NM_000316	AGGGAAGCCCAGGAAAGATAA	CTCCATTGTGCTCAACTTCAT	CGCCGTGAGCATCTTCGTCAA	CAGCATAATGGAATCAGACAA
5746	PTHR2	NM_005048	AACGCCTCTATGTAATGTATA	CTGAATACGGTTAGAGTTCTA	TGGCATGTGGGATCAATTAAA	AAGGTGTTACTTAATAATAGT
5747	PTK2	NM_005607	CCGGTCGAATGATAAGGTGTA	CCCAGGTTTACTGAAGTTAAA	CACCTGGGTACTGGTATGGAA	AACAATTTATGTTCACATTAA
5754	PTK7	NM_152883	ACGCCACAGCACAAGTGATAA	CCGAGAGAAGCCCACTATTAA	ATGGGACATGGTACCGTTGTA	ACGGTTCGAGGTCTTCAAGAA
5764	PTN	NM_002825	CTGGAGCTGAGTGCAAGCAAA	ACCGTAGGCTTTGTATTCAAA	TACCGTAGGCTTTGTATTCAA	TACATGATAAATGATAGACAA
5771	PTPN2	NM_002828	CACAAAGGAGTTACATCTTAA	TCGATTGAATTGTACTGGATA	CCGCTGTACTTGGAAATTCGA	AACTGTATTCATACATGTCAA
5774	PTPN3	NM_002829	CCGCTCATTTGCTGACTTCAA	CCGAGAAATGCTGGTCACAAA	CCGGGTATTATTGCAGGGAAA	CAGGTTATTCAGCGATAGTTA
5775	PTPN4	NM_002830	AGCACGTACCTTAGAACTCTA	CTCCGTCATCAACACAAGCTA	TCCGTCATCAACACAAGCTAA	CTCCGAACAAATAGTAAATAA
5777	PTPN6	NM_002831	CCAGTTCATTGAAACCACTAA	CCGCACCTCGTCCAAACACAA	TAGGCCCTGATGAGAACGCTA	CCGGAACAAATGCGTCCCATA
5781	PTPN11	NM_002834	GCCGCTCATGACTATACGCTA	GCGGTCCAGCATTATATTGAA	CCGCTCATGACTATACGCTAA	CAGAAGCACAGTACCGATTTA
5782	PTPN12	NM_002835	GTGGATCATGATAACACTTCA	CTGCTTGTAGACATGTTAATA	TTGCAGGTTATCAGAGATCAA	AAGCTTAATGAGGAAATATCA
5787	PTPRB	NM_002837	CCAGTATTAGTGGAGACTTAA	TCGGGTGTATCAGACTAATTA	CCGGTCGACTTTATCAAGTTA	CCCGGAGATGTGGATAACTAT
5789	PTPRD	NM_002839	ATGGCATTATCACCAAGTATA	CGCCTTGTTAATATTATGCCA	CTGGGTGTCATTGAAGCAATA	ACGGCCAGTCCCGAACAGTAA
5794	PTPRH	NM_002842	TCGAAGCACAGCACACACTAA	CAGGTACTGACATCACCCTAA	CCGGGTCATTGTATACGTGTT	CCGGGACGTTGTACAATTTCA
5795	PTPRJ	NM_002843	ACCCGTATCTTCTACAATCAA	ACGAGTCGTCATCTAACTATA	TCGGGTAGAAATAACCACCAA	TCCGAGTATGTCTACCATTTA
5796	PTPRK	NM_002844	CAGGATTTGTATCGCTGTGTA	CCGGCGAGTCAAGTTATCAAA	CTGGAGATTAGTGTATGATTA	CCGGGTTAAATGCTATAAATA
5798	PTPRN	NM_002846	CTGGTGAAGTCTGAACTGGAA	CAGGAAGGTGAACAAGTGCTA	CAGGTCTGGCTTGGCACCCAA	CACCCTTCACTGAGTTACGAA
5800	PTPRO	NM_002848	CAGCTTCAAAGTAGAGTAGAA	CCGGGAAGACTTAGCCTTAAA		
5801	PTPRR	NM_002849	AACCCTTTGTGTCTATACCAA	TAGGTTTATCACACAGCCTAA	TCGCCTCATTGGAAAGAAGAA	CGCCACCAGATTGTCAATTCA
5803	PTPRZ1	NM_002851	CAGACTAATTACACTGAGATA	CCGCCAAATTTATATCATTAA	TAGCCATATACCAATACCTAA	ACGCTGGAATTTGGTAGTGAA
5810	RAD1	NM_002853	TCGAATGTGTTACCAAGGTTA	CTGCAGCACCAATGTTATTAA	CAGTATATGATTAGAAATGAA	CAGCACCAATGTTATTAATAA
5818	PVRL1	NM_203286	CAGGTGGAGGTCAATATCACA	CAGGTGAACGACTCCATGTAT	AGGGCTGTTGTCAGAATTCTA	ACAGATCAGTCTGTCAATAAA
5819	PVRL2	NM_002856	CCCGTGACACTCAGGAGTTAA	CAGAGTCATAGCCAAGCCCAA	CTGGACGACACTGGAGTGGAA	CAGGTCATCTTTGTCCGAGAA
5830	PEX5	NM_000319	ACCGATCGCTGGTATGATGAA	CCAGTTCACAAGACCAGTAAA	TACGTCAGCTACCTATGATAA	CAGCTTCCTTGGGCAGTGTAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
5837	PYGM	NM_005609	CACACTCGTAAAGGACCGCAA	CTACCTGTCTTTAGAGTTCTA	TCGGGATGTGGCCAAAGTGAA	CAAGTTGAAGTTTGCTGCCTA
5870	RAB6A	NM_002869	CAGATGGGTCATATTCTTTAT	ATGGGTGTGATTGTCTTCCTA	TACGGTCTTCTTTGAGGTCAA	CCGACTTATTGTCACCTTGTA
5871	MAP4K2	NM_004579	ACGGTATTTAAGAGAGAACTA	GAGAACTATATTGGTATTAAA	TCGGTCAGCCTCAGAATTCCA	CTGGCTCTACTGCGTGAACAA
5876	RABGGTB	NM_004582	AAGGATGTTATTATCAAGTCA	TACGCTGTATGACAGTATTAA	ACGCTGTATGACAGTATTAAT	CCGGAGAAGTTACCAGATGTA
5878	RAB5C	NM_004583	GAACAAGATCTGTCAATTTAA	CAGCCGATCGATCGACCTCAA	CCCGACTGGAATCCACTCTAA	CACCATGATTTCTCCATATAA
5879	RAC1	NM_006908	TACATTGTACAAGGAATGAAA	GGGCATTTAATTCATCTTTAA	ACGATGTTCTGTACAACTTAA	AAGGTTGGTATTATCAGGAAA
5881	RAC3	NM_005052	GACATGCTTGCTGATCAGCTA	CAACGTGATGGTGGACGGGAA	CGCGCCCATGCAGGCCATCAA	CCGGGAGATTGGCTCTGTGAA
5892	RAD51L3	NM_002878	CCCAGTAACGCCTGCTGTTTA	CTCACTCTCTGTAAGCATATA	CTGGGTGGAAATAAGCTTATA	CTGGAAGAGGTAGCTCAGAAA
5893	RAD52	NM_002879	TCGGGTAATTAATCTGGCCAA	CAGCTGAAGGATGGTTCATAT	CAGGAGTGACTCAAGAATTAA	AAGGAAGGAAATAATCATCTA
5901	RAN	NM_006325	CAGCAGTATTCTATTTGGTTA	TAGTGTGAAGTTGATACGCAA	TTGCGAATTCTTGCTGTTAAA	ATGTGGTTTGTACATATCAAA
5902	RANBP1	NM_002882	CTCGGTGAAGGAGGAGACCAA	CGGCGCCAGACGCGGAGGGAA		
5905	RANGAP1	NM_002883	ACGGAAGATTCTGGACCCTAA	AGGCAAGAGCCTCAAACTCAA		
5908	RAP1B	NM_015646	AATGGTGTACTGTATACTTTA	TAGCATCAGTAGTTCAATAAA	GACGAGTACTGTGGATGTGAA	CAGTATAATGTCTTAGATTAA
5909	RAP1GA1	NM_002885	CCGGCTCATCGTCACCTTTGA	CCACCTTGTCTTCTCACTCAA		
5911	RAP2A	NM_021033	AAGGCATAGTCCATCGATCTA	ACCAGTGTATTCCGTCAAGTA	CCAGTGTATTCCGTCAAGTAA	CAGAGATAATTGCCTATACTA
5912	RAP2B	NM_002886	AAGGTGGTCTTAGTAATATAA	TAGAATAGAGCCAAAGCCTAA	TACGGTTCTTTCGTAGAACAA	CTCACTTAAGTTTGATATCAA
5919	RARRES2	NM_002889	CTGCCGGAAGAGGGACTGGAA	CCCAATGGGAGGAAACGGAAA	CAGGGAGAGGAACCCGTTCTA	CTGGAAGAAACCCGAGTGCAA
5924	RASGRF2	NM_006909	AAGGTGAAAGATGGCTATTTA	AAGAAGGAACACCAAACTTTA		
5926	ARID4A	NM_002892	CTCGAGATGTAAATTCTATTA	ATGGCTTATCTAAGACAGCAA	CTGGTTTGACATTGCTAAGTA	ACGATTGAAGTTGATAGTATT
5927	JARID1A	NM_005056	CGGCAAGTAAAGAATCTGCTA	GCGGACGTTTCTTAAGAAGAA	CAGATGCTTAATTGAGCTCTA	AAGGAATGGTATCACAGTCTA
5930	RBBP6	NM_006910	GACGCTATCATTCACGATCAA	CCAGGTCTAAATCTCCCTATA	ATAGTGGTTCTTCGTATTCAA	CCCAGTTAAGTCATTCCTCTA
5933	RBL1	NM_002895	CTGGATGTTTCAAATGAGTTA	CTCCAGGTTTCTGCAAACAAA	CACCAAGTGACCAACTTATAA	ACAGGCTAATGTGGAGTATAA
5935	RBM3	NM_006743	CAGGAGGAAATTAGAGAGACA	CCAAATGGCTGTATTTATAAA		
5950	RBP4	NM_006744	CTGGTACGCCATGGCCAAGAA	CCAGATGAGCGCCACAGCCAA	CCCTGCCAAGTTCAAGATGAA	CTGGATCGTCGACACAGACTA
5961	RDS	NM_000322	CAGCACCACACCATCCCTAAA	CACGGTGAAAGTGCTGCTCTA	GAGGAGCGATGTGATGAATAA	CACGGATTTAGTCCCACCCTA
5967	REG1A	NM_002909	CCCAGTCTTTGGAACCCTAAA	CAGCAATTACAACGGAGTCAA		
5968	REG1B	NM_006507	CTCCAATTACTATGAAGTCAA	CTCAGTCTCTAGAGCCCTGAA		
5971	RELB	NM_006509	CACAGATGAATTGGAGATCAT	CAGCTACGGCGTGGACAAGAA	GCGGATTTGCCGAATTAACAA	CCAGATTGCCATTGTGTTCAA
5976	RENT1	NM_002911	ATCAAGGTCCCTGATAATTAT	CACCATGAGCGTGGAGGCGTA	CATCTTATTCTGGGTAATAAA	ACGGAGCGCTGCACACCGAAA
5977	DPF2	NM_006268	ATCCATCTTGCCTCCAATTTA	CTGTATTCTAAACATTAGTAA	CTGGATGACCTCGATGATGAA	CTGGACCTGTTGAAAGAGAAA
5992	RFX4	NM_002920	CAGGCATTACCTGACAGCTTA	CTGGAGGAACGTGGACCTGAA		
6000	RGS7	NM_002924	TTGATAAAGAACTTAACTATA	TGCCTGGATGTGTAAATACAA	AAGTATATATCAATAAGTATA	ACGGATCATCTTGTAGCATGA
6003	RGS13	NM_144766	CCAGATTTCTAAAGTCAGAAA	CAGAATTTCTAGGGCAAAGAA	CACAGTGACGAGAATATTCAA	CCAGAGTGCCATCGAAGGTAA
6015	RING1	NM_002931	CCGAAAGAAGCTGGTGTCCAA	CAGGGTCAGATCAGACCACAA	CTGGAGCTGGTGAATGAGAAA	CAGCCAATAAGAGGACACAAA
6039	RNASE6	NM_005615	CCCTGTGTTCACAGCAATAAA	CACTTAGATAGTATTCTCTAA		
6041	RNASEL	NM_021133	GCCAATGTTAATTTCCAGGAA	CCCGAAATGTCCTGTCATCTA	CCAGAGTACACTAGTCCATAA	CACCTGGACATGTCAATTAAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
6051	RNPEP	NM_020216	CACGCCTGCTGTTAAATACAA	CCGAAGCATCTTAGCCGATGA	CTGGACATGAAGGCCATTGAA	CACCAGGAAGATTTCTGGAAA
6059	ABCE1	NM_002940	ACCCATAAATACATGTTGTAA	ATGGCTAGAAAGTATGGTTTA	CCAGTTGGGTTCTAAATTGTA	CTGATTGACATTTGATAAATA
6097	RORC	NM_005060	TAGGATGTGCCGGGCCTACAA	CCGGGCCTACAATGCTGACAA	AAGGAGCTCTTCAGCACTGAA	CGGGTTCATCTGAGTAAACAT
6100	RP9	NM_203288	TCTGTTGTTGAGAATAATAAA	AAGGAAGATGAGACTAAGCCA		
6103	RPGR	NM_000328	CCCGGTAAATTCTGGTTTAAA	TCCGAAGGGCAAATTGGTTTA	CACAGCTTTGATAACAGATAT	ATGAGCCTGAATTCCAATGAA
6122	RPL3	NM_000967	CGGCAAGCTGATCAAGAACAA	TGGCGTGATGTCTCACAGAAA		
6125	RPL5	NM_000969	TTCGTGTGACAAACAGAGATA	AAACTTATGAACAGCAACTAA		
6128	RPL6	NM_000970	CAGCGCAAGATTGATCAGAAA	GACCGGAAGCCGGGACCTTAA		
6129	RPL7	NM_000971	CTGGTTGGTTAATAAACAGTA	ACGCTTCAAAGAGGCAAATAA		
6130	RPL7A	NM_000972	CACCTTGGTGGAGAACAAGAA	ACAGGTGAACTCGGAAGACAA	CACCACCTTGGTGGAGAACAA	CAGGTGAACTCGGAAGACAAA
6132	RPL8	NM_000973	CTCAATAAAGTTTGTGTTTAT	CCGGGCGTACCACAAATATAA		
6133	RPL9	NM_000661	CAGGCTGATGAATAAGATCTA	CGGACTATTTGTAGTCATGTA		
6134	RPL10	NM_006013	CCCGTTGTTACCGGTATTGTA	CAGCAAAGCCTTGCAATCCCA	TGGCCTTATGTCAGTTGTCTA	CAGAAACAGGTTGACAACTCA
6136	RPL12	NM_000976	ATCCGGGTTCATCCGACACCA	AACATTTCAATAAAGGATCAT		
6144	RPL21	NM_000982	CCACATATATGCGAATCTATA	CTGGAAGAGTGTACAATGTTA		
6152	RPL24	NM_000986	AAGAGGAATCAGAAACCTGAA	AAGGCTAAGCAAGCATCTAAA		
6154	RPL26	NM_000987	CAGGTTGTACGTGGACACTAT	CAGGAATAAAGTAATCTTATA		
6156	RPL30	NM_000989	CAGGAAGATGGTGGCCGCAAA	CTGAAATAGAGTACTATGCTA		
6157	RPL27A	NM_000990	AGGGAGTTTCATTAAATGCTA	CCGGATCAACTTCGACAAATA		
6160	RPL31	NM_000993	CAGATCAAATAAAGTTATAAA	ATCGCTGATCGTCAGATCAAA		
6164	RPL34	NM_000995	AAGCACAGAGTCAGAAAGCTA	CAGTATATGATCACTAATATA		
6165	RPL35A	NM_000996	CCGAGATGAAACAGAATTCTA	GCGCTTATGTATATAAAGCAA		
6170	RPL39	NM_001000	CTGAAGGTCACGATCATGTTA	TTGGTTGGCTGGATTCAGTAA		
6173	RPL36A	NM_021029	CTGGTTGAGTTCACATCATAT	AAGCTAGAGCCATCAATACAA		
6176	RPLP1	NM_001003	CTGCATGTACTCGGCCCTCAT	AAGAAAGTGGAAGCAAAGAAA		
6181	RPLP2	NM_001004	CAGGGTGGGTATCGAGGCGGA	CAGCGCCAAGGACATCAAGAA	AAGGAGGAGTCTGAAGAGTCA	CAAGGTTATCAGTGAGCTGAA
6187	RPS2	NM_002952	CACCTTTGATGCCATTTCTAA	CCGCTTGGTCAAGGACATGAA		
6188	RPS3	NM_001005	CGGCAAGATGGCAGTGCAAAT	GAGGTTGTGGTGTCTGGGAAA		
6189	RPS3A	NM_001006	CCGGAAGAAGATGATGGAAAT	CACCTGCTATGTTCAATATAA		
6191	RPS4X	NM_001007	CAGATCTTTGTACGTAATTAA	AAGAATTGGTGTGATCACCAA		
6193	RPS5	NM_001009	CACCGATGATGTGCAGATCAA	CTCGAACTCCTATGCCATTAA		
6194	RPS6	NM_001010	ATCCAGTCAGAAATAAGATTT	TTGAGTAACAAATAAATAAGA		
6196	RPS6KA2	NM_021135	CTGGAACACGCTGTACCGGAA	CTCGATATCTGACGCAGCTAA	CCGGAGGTCCTGAAGCGTCAA	CCGAGTGAGATCGAAGATGGA
6202	RPS8	NM_001012	TTGGAGTTCTATCTTAGGAAA	TCAGAGTGTTGTACTCGTAAA		
6203	RPS9	NM_001013	ACGGCGTCTGTTCGAAGGCAA	CCCGCGGAGACCCTTCGAGAA		
6204	RPS10	NM_001014	CGCAGAGATGTTGATGCCTAA	ACCGCGCATGCTCCTTCCTTT		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
6205	RPS11	NM_001015	CCCTGCGTAATCGATAAGGAA	CGGGAAGATGGCGGACATTCA		
6206	RPS12	NM_001016	AAGGTTGATGACAACAAGAAA	AAGATTCAACTTCACCCGTAA		
6208	RPS14	NM_005617	CAGGAGGAAATAGGACCAAGA	CCGAGATGAATCCTCACCATA		
6217	RPS16	NM_001020	TACCAGAAATCCTACCGATAA	CCCTCGTCGCTGCGAGTCCAA		
6218	RPS17	NM_001021	CCGCAACAAGATAGCAGGTTA	AAGCGAATTCAGAGAGGCCCA		
6223	RPS19	NM_001022	TGGCTCCATGACCAAGATCTA	AAGAAGCATTAGAACAAACCA	CTGGGTTAATAAATTGCCTCA	AACAAGAAGCATTAGAACAAA
6227	RPS21	NM_001024	TGGAATATTTGTCATAAATAA	CGGCGAGTTCGTGGACCTGTA		
6229	RPS24	NM_001026	CGCAAGAACATTAATAAACTA	CAAGAACATTAATAAACTAAA		
6233	RPS27A	NM_002954	TTGTCTGACTACAATATTCAA	CTGGCTGTCCTGAAATATTAT	CTGACTTACTGTTTCAACAAA	AAGGTGGATGAGAATGGCAAA
6234	RPS28	NM_001031	AGCGTTTGTGTTTCAAGTTAA	CTGAGATGCTCCTTTAAATAA		
6235	RPS29	NM_001032	ATGATAATTCTTTGTATATAA	CCGGCACGGTCTGATCCGGAA		
6240	RRM1	NM_001033	CCGAGATTTCTCTTACAATTA	CTGAGAGTATATAACAACACA	AACGGATATATTGAGAATCAA	CTGGTGGGTCTCTAGAAGCAA
6272	SORT1	NM_002959	CAAGGACAGGGTACAAACTTA	CTGGGTTTGGCACAATCTTTA	CGCACGTCAGTTACACATTAA	CAGCAGAGAATTGACTAGATA
6284	S100A13	XM_371380	CTGAAGATCAGGAAGAAGTAA	ACCGCACTCTTCCCAAATAAA	CAGGAAGAAGAAAGACCTGAA	AACCGCACTCTTCCCAAATAA
6286	S100P	NM_005980	CAGGAGGAAGGTGGGTCTGAA	TAGGCTGAGCCTGCTCATGTA		
6289	SAA2	NM_030754	TAGGCATCTAATAAATGCTTA	GCCGATCAGGCTGCCAATAAA	ATGGCATATAATAGGCATCTA	AAGCTGAGATATGGCATATAA
6293	VPS52	NM_022553	TCCATTCGGGATTATATTCAA	CCGGGTCAAGGCAGTGACGAA		
6294	SAFB	NM_002967	CCGAAGATGACTCGGATACAA	AAGGTGGTAATCCTGACGAAA	CTGCCATATTGTAGCTCAATA	ACGGACTGTAGTAATGGATAA
6296	SAH	NM_005622	CCCTCAGAATTTCTCCAACTA	CAGAAGCCTGTTCCCTACAAA	CAAGCTGATTGTATCAGAGAA	ATGCTTGTACAGAATGATATA
6297	SALL2	NM_005407	TAGGAAGTAGGGAGAAATGAA	CGGCCTGAGGGTCACAATAAT	CCCGGGAATGTCTCGGCGAAA	AAGCTGGGCACTGCTTACCAA
6300	MAPK12	NM_002969	CGGCGCTAAGGTGGCCATCAA	CACAGGCAAGACGCTGTTCAA	TGGAAGCGTGTTACTTACAAA	CTGGACGTATTCACTCCTGAT
6301	SARS	NM_006513	CCAGTTTGATGAAGAACTTTA	CTGATGAAACCATGTAATAAA		
6304	SATB1	NM_002971	TGGGTACGCGATGAACTGAAA	CACTCTTATTGTTGTATGCAA	ACCGAATATACCAGGACGAAA	TCCAAGCAATTCATACTATAA
6305	SBF1	NM_002972	GACGCCTGTGTTCCACAATTA	TCCGGTCGTTACCGACCACTA	CCGCGTGGTGTGGCCCTGTTA	CAGCGCCGAGCTCTTCCGTAA
6311	ATXN2	NM_002973	ATGGATCAACTACTAAACAAA	CTGACGGATTATTATTTATAA		
6317	SERPINB3	NM_006919	AAGGTAATATTGGCAGCAATA	CTCGTGCTATCTGGAGTCCTA	TAGGATTCGGATCATCACCTA	TCGGATCATCACCTACTTCAA
6324	SCN1B	NM_001037	CCACATTGAGGTAGTGGACAA	CACATTGAGGTAGTGGACAAA	CAGAGATGATTTACTGCTACA	ACCGCCATGCATGATGGGTAA
6328	SCN3A	NM_006922	CAGCGTAATTTCAGATGTTAT	AAAGCTGATAGTCTATGTCAA	TTGGATTTATGTGAGGTCAAA	CTCCCATAATAAATTATATAA
6329	SCN4A	NM_000334	GACGCCTACATCAGTGATGAA	AACGCTGAACATGCTCATCAA	CAAGATTGCCTTGGACTGCAA	CTGGCTCAATGTCAAGGTCAA
6331	SCN5A	NM_000335	GCCGCTGTGGATGTCCATCAA	CTGGAGCACTACAACATGACA	CTGGACCAAGGTGAAAGTCAA	TCCTGTAAGAGTATTAACAAA
6332	SCN7A	NM_002976	TCCAATGAGTAAACAAACTAA	CCCAGCATTATTGAACATCAT	AGAGATGTTCATGCTACTAAA	CCGATGGTAATTAAGCTTGTA
6336	SCN10A	NM_006514	CGGGCTCTTTCTCGATTTGAA	TCCCGGGAGGTCAACATGCAA	CACAGGCGAATGTGTCATGAA	CCGCTCCATGGCACTCTCTAA
6337	SCNN1A	NM_001038	CTGCACCTTTGGCATGATGTA	CAGCCTCAACATCAACCTCAA	TACAGGTACCCGGAAATTAAA	CCCGATGTATGGAAACTGCTA
6338	SCNN1B	NM_000336	CCGGAACTTCACGTCCATCTT	CACGTCCATCTTCTACCCTCA	TCGGCCAACCCTGGAACTGAA	CTGCAATGACACCCAGTACAA
6339	SCNN1D	NM_002978	CTGCAGGGAGTCTGCATTCAA	CCGCAATGGCTGAGCACCGAA	CTGCAGGGAGGCAGAAGGCAA	CACACTTGGGCTGCTCTGAAA
6340	SCNN1G	NM_001039	CGGCGGTAGCATCATTCACAA	AAGAGTGGACACTAACCACAA	CAAGGCCGGCAAGTAAACAAA	ATCCCGGGACCTGAACTATTA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
6343	SCT	NM_021920	CAGCGAGCAGGACGCAGAGAA	CTGGCGCTGCTGCAGAAGGAA	ACCAATAAAGGAGGAATCAGA	GTGGTACTTGGCACCAATAAA
6344	SCTR	NM_002980	CACAGGATGGCTGGTCAGAAA	CAGAAAGGGACAGGGAAATAA	CTCCTTCTTCTCTGAAAGAAA	CCGGATGCTCACCAGCAGAAA
6354	CCL7	NM_006273	TTGGGATTAATACTTCAACTA	TTGGATGTATATGTCATCTCA	TGGAAGCATATTGTTATTATA	AAGATTTGCTTTAATTGTTAA
6367	CCL22	NM_002990	CTGGGTGAAGATGATTCTCAA	TACCTTTGACTTGGTATTATA	TAAGCTGGAGTTATATATGTA	CAGGTAAAGGACATAAATGTT
6368	CCL23	NM_145898	GACAGAGTTCATGATGTCAAA	TAGAGCAATTCATCTAATAAA	CAGGAAGAATTGAACTTGTCA	CTCCTGGAGAGTTACTTTGAA
6369	CCL24	NM_002991	CTGCATGTTCTTTGTTTCCAA	CAGGCCTGATGACCATAGTAA	CAGAGATATCCTGGCAACCAA	AGGAGTGATCTTCACCACCAA
6376	CX3CL1	NM_002996	CCACGGTGTGACGAAATGCAA	CAGCAAGATGACATCAAAGAT	CGGAGCTGTGGTAGTAATTCA	CACCATCAAGCCACCAACATA
6382	SDC1	NM_002997	TCCGACTGCTTTGGACCTAAA	GCCGCAAATTGTGGCTACTAA	CAGGGCCTCCTGGACAGGAAA	CAGGAGGAATTCTATGCCTGA
6383	SDC2	NM_002998	GACGCTGAATATACAGAACAA	CCGTTTAGTCATATCTATCTA	ATGAATAGACATAAATTGTAA	AAGGTACGAGTAGAGGTTTAA
6386	SDCBP	NM_005625	AGAGATTGTGATGATTCTTAA	GAGATTGTGATGATTCTTAAA	TTGACTCTTAGATTATGTAA	TGGGATGGTCTTAGAATATTT
6396	SEC13L1	NM_030673	CAGATTGATCATCTGCCTTAA	TCGGAGATGCTTTGTAATCTA		
6400	SEL1L	NM_005065	CTGCAAATTGGGCGTCGTCTA	AAGAGTGAACATGTACACAAA	CAGGATATTCACCTTGCGAAA	ACGGCACAAGGAAGCATTGAA
6401	SELE	NM_000450	CATGGTAGAATTGGAGAGTAA	ACCAGTGTGGTTTGTGTTTGA	CGGAAAGTATTTCAAGCCTAA	CAGGTTGAATGCACCACTCAA
6404	SELPLG	NM_003006	TCCATGGAACCTACTACCAAA	CAGCAATTTGTCCGTCAACTA	ATGGAGATACAGACCACTCAA	ACGGAGGCACAGACCACTCAA
6406	SEMG1	NM_003007	AGGGTAGTTATACACCATAAA	CAGGGTAGTTATACACCATAA		
6423	SFRP2	NM_003013	TAGCATGATTTCTTCAAGTAA	TACATAGTAGTTTACCTTTAA		
6425	SFRP5	NM_003015	ACGAATGTTGTTACTGGCACA	TAGGCTAAGCTATTTGGGAAA	CTGCGAGGAGTACGACTACTA	CCGCTGGGACAAGAAGAATAA
6428	SFRS3	NM_003017	CACAATATGGTTCAAATGTAA	CAGACTGATAATAAACCTCTA		
6434	SFRS10	NM_004593	TCGGGCAAATCCTGATCCTAA	CCCAATTTCACTCAAATGTTT	CGGGACTACTATAGCAGATCA	CCCGATCTGAATCTAGGTCTA
6435	SFTPA1	NM_005411	CACAGCAGGGATGAGGACAGA	ACAGATGGTGTGAGTCAGTGA		
6439	SFTPB	NM_000542	AACATGGAAGTCAACGTTTAT	CCCACCATCTCTGGTCTACAA	ACGGCTTGCACCATTCAGCTA	AAGGGACGAGATCGTTAGCTA
6441	SFTPD	NM_003019	TGCTGCCAATATCCTAATAAA	TAGGATTAGGATTGTTGTGAA	CTACCTGGAAGCAGAAATGAA	AGGAGTTTGGCCAGAAGTCAA
6443	SGCB	NM_000232	CTGCTTCGATTTAAGCAAGTA	ATGGGTGGTAATATGGAGTTA	ATGCAGATTTCTAGTGCATTA	CACTTTGAATTGTGCACATAA
6452	SH3BP2	NM_003023	CCCACGGACAATGAAGACTAT	AACCTCTAACAAAGTGAGGAA	TAGCACCTTATGTCAGGGAAA	TAGGAAGTAAACGATCTGCAA
6455	SH3GL1	NM_003025	AAGGTGCTCTTAGAAACACTA	CCGCCTGGACTTTGACTACAA	ACGGTCCAGGGCAAACTGAAA	ACGCCCTAAGCGGGAGTATAA
6468	SHFM3	NM_022039	CCGGGAAGGAGGCACAAGGAA	ACGAGTGAAGGTGTCTCAGAA	TGGGAAGATTGGCATTCATAA	CAGCACCTTCACTGTCAAGTA
6472	SHMT2	NM_005412	CAGCAAATTCAATTTGTTAAA	CCGGAGAGTTGTGGACTTTAT		
6487	SIAT6	NM_006279	CACAATATCCAGCGAGAGAAA	TCGGTTGGGCTTCCTCCTGAA		
6489	SIAT8A	NM_003034	CTGGCTTAATAATATTAATAA	CAGAAAGACATTTGTGGACAA		
6492	SIM1	NM_005068	CACAGAAAGATCGGAATCTGA	ATCCAGTTTGATCCTAGCTAA	CACACTAAACTTCTTAACGAA	TCACCTGGTATCCATTATAAA
6493	SIM2	NM_005069	CACGGGCAACAGTATTTATGA	TAGCAGCTCGTCTCCAGCTAA	CCGGCAAATGCGCACGACCTA	CCGTGATTCTTGAAAGGTGTA
6497	SKI	NM_003036	CTGGACGACGTGAAGGAGAAA	AACCAGTAAGGAGACTTGAAA	GCGAGTGTTTGTAACCATGTA	CCGACTTTATAGAGCAGTCAA
6502	SKP2	NM_005983	AGGCCAACTATTGGCAACAAA	CTCAAATTTAGTGCGACTTAA	ACCCTTCAACTGTTAAAGGAA	AAGTGATAGTGTCATGCTAAA
6503	SLA	NM_006748	AAGGAACTTCGTGACACTAAA	CTGGCTGGATCGGGTAGGTAA	CTGGATCGGGTAGGTAAGAAT	CCCGGTACTTTATTCTAAGAA
6504	SLAMF1	NM_003037	CTCCGGCAGTTGGGAAGCAAA	CAGGACCCTTGCACCACCATA	CAGAGTCTGTCCAGGAAACAA	AACAAATTCCATCACAGTCTA
6510	SLC1A5	NM_005628	CTGGATTATGAGGAATGGATA	CCGGTCCTGTACCGTCCTCAA	CAGCCTTTCGCTCATACTCTA	CACGCTGCCGCTGATGATGAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
6512	SLC1A7	NM_006671	CCGGAACATGTTCCCAGCCAA	CACGTTAAGGTCAAGACACTA		
6514	SLC2A2	NM_000340	TGGGTTATCAGTTAACATTAA	ATGGTGTGTTCCTAACATAAA	CAGACTTTAGCTTACAGTCAA	CAGGGTGCTAACGTATCTCTA
6517	SLC2A4	NM_001042	CAGGATCGGTTCTTTCATCTT	AAGGGCCATGCTGGTCAACAA	ACGCTGCTGCCTCCTATGAAA	CACCTTGGACTCCTCCCACAA
6523	SLC5A1	NM_000343	AACCATAGTGTCTGATGGCAA	TTGGGATTTCACGTATGATTA	AAGGAGACCATTGAAATAGAA	GAGGACAGTGTTGAACGTCAA
6525	SMTN	NM_006932	CACATTCACCATCGAGATCAA	CAGCACCATGATGCAAACCAA		
6528	SLC5A5	NM_000453	CGGAATTATCTGCACCTTCTA	ACCCAGGAAACTCGTGATTAT	CAGCTTCTATGCCATCTCCTA	CTGGATTGCCTTGTATGCAAA
6529	SLC6A1	NM_003042	CAGCAAGGAGGCCTACATCTA	ATCCTTAATAACTATGGTAAA	CACGTAAGGTCTCATTTGATA	CGGGCGTTATGTAAGTTTCTA
6534	SLC6A7	NM_014228	CCCGCTCTCCAAGATGAAGAA	TTGGTTCATTGTTAATAAATA	CCTGGTGTATAGCATCGTCAA	CACGTTTCACCAGAACATCTA
6541	SLC7A1	NM_003045	CAGCACCCAATAGACTATTTA	ACGGATCTGGATATACACTAT	ACGCTTATGACTCCTAATGTA	GAGGGTTGGTTTATTATCAAA
6543	SLC8A2	NM_015063	CACGGTGGATAAACTCATCAA	CTGGAATGAGACGGTGTCCAA		
6550	SLC9A3	NM_004174	CAGCACCGACAACGTGGTCAA	CCCGTTCATCTGGACCTGGAA	TGCGCAGAATTTCACCATCAA	CACCACCATCATCGTAGTGTT
6554	SLC10A1	NM_003049	ACGGAGTCAGCCGGAGAACAA	CACCATAGGGATCGTCCTCAA	AGGGATCGTCCTCAAATCCAA	CACAAGTGCTGTAGAATTAAA
6558	SLC12A2	NM_001046	CAGGATTGTCTACTTCAGCAA	AACGTTAATGACACTATCGTA	CAGGATTTACACCACTAATTT	CAGAGTATTCATTGGTGGAAA
6559	SLC12A3	NM_000339	ATCGCTGAGCTCAACACCATA	CCCGGCCACAGTGGAAGACTA	CAAGAAGACCATAGACATCTA	CAGGATGGACCAGGAGAGAAA
6560	SLC12A4	NM_005072	CCGGGAGCTGGTGCACATTAA	CCGGCATGATCTACAAATACA		
6570	SLC18A1	NM_003053	CCGGATGTATGCAACCCAGAA	CAGCATTGTCTTGCTGCCAAA		
6572	SLC18A3	NM_003055	CACGTCTGGCATAGCCATGAT	CACCATTGCCACGTGGATGAA	CTGCTTGATGAGCCACCGCAA	TACGGAGAGCGAAGACGTGAA
6573	SLC19A1	NM_003056	CAAGCGCAGCCTCTTCTTCAA	CCGCAAGCAGTTCCAGTTATA		
6578	SLCO2A1	NM_005630	AAGGAGGTCATTCATCAACAA	AACCTTTATTCTATTATATTA		
6581	SLC22A3	NM_021977	AAGGAACTTATGGGCATATTA	ATCAATTATATCCATGCTTAA		
6591	SNAI2	NM_003068	GAGGGAAAGATTAGCTTTGAA	TACCACAAATGCAATAATACA	CCGAAGCCAAATGACAAATAA	CACACTGAGTGACGCAATCAA
6601	SMARCC2	NM_003075	AAGAAGTATATACAAGCTGAA	CCGAAAGAAGATTTCAGCCAA		
6602	SMARCD1	NM_003076	AAGCACTGTGGCAATATATTA	TCCAAATATGATGCCACTAAA		
6604	SMARCD3	NM_003078	GTGGCAGTATGTGAAGACCAA	CAGGACTCCCATGACAAGGAA	CTCAAGGTGATGACAGATGTA	CAGTCGCTACTTCTACTGCAA
6610	SMPD2	NM_003080	CCGCATTGACTACGTGCTTTA	CAGGAGGTCAATGGCTTATAT		
6616	SNAP25	NM_003081	AAGATGCTGGGAAGTGGTTAA	CAGAGCTCACGTTGCATTGAA	AAGATTAAGTTATACCAGCAA	AAGGTTGTACATAGTGGTCAT
6623	SNCG	NM_003087	ACCCACCATGGATGTCTTCAA	AAGACCAAGGAGAATGTTGTA		
6624	FSCN1	NM_003088	AACTGGAAATAGCGAAATAAA	CACGGGCACCCTGGACGCCAA		
6625	SNRP70	NM_003089	CGAGAGTGAATTATGACACAA	CTCCGGAGAATGGGTATTTGA	CCGGAGAGAGTTTGAGGTGTA	AAGATTGAGCGGCGACAGCAA
6627	SNRPA1	NM_003090	TAGCCTTGTTTGTGTTAGCAA	TCCACTCACTATGCTACCAAA	CAGCATTGTTGAAATGCTTAA	AGCCTTGTTTGTGTTAGCAAA
6628	SNRPB	NM_003091	ATGAAACTGGTTTATAATAAA	CTGGTTTATAATAAACTCTTA		
6632	SNRPD1	NM_004938	AACGCTGAGTATTCGAGGAAA	ACAGTTCTATGTACTGAGAAA	TAGGCTAAACTTAACAATATA	CAGAGCTGTCTATTTAGTATA
6633	SNRPD2	NM_004597	AACGGAGAGCGTAGTGACCAT	CGCGGAGGAAACGGGAGTGAA		
6634	SNRPD3	NM_004175	CAAGAGGAAGAGGACGTGGAA	CAGCTCAGCTTTAACAACACA	ACCCATGTTAAAGAGCATGAA	AAGGACTTTGTGTTCATTTGA
6636	SNRPF	NM_003095	GCCAGTGATGGTGAAACTTAA	AAGGTGTAATAATGTCCTTTA		
6638	SNRPN	NM_003097	CAGAAAGATCAAGCCAAAGAA	TTGGATTTGGTGGAACAGCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
6640	SNTA1	NM_003098	CACCGTATTTCAAGAACTCTA	CCGGAACTTCAGCGAGGCCAA		
6641	SNTB1	NM_021021	CAGGAATTAAATAAAGCATCA	TAGACTGAATGCTATAATCAA		
6643	SNX2	NM_003100	AACCATCTAAATAAACCACTA	AGGGAAGAGATTGAAGAAGAA		
6649	SOD3	NM_003102	CTGGAATGGATGAGCACCCAA	AAGGGCTGCTATGATTGAGAA	CTCCTTCATCTCTTTAATAAT	AACCTTTGTGTTACAGATTAA
6651	SON	NM_003103	ATGATGTTGATTTATCTTTAA	CAGAATCTTCAATTACGTTAA		
6653	SORL1	NM_003105	CAAGACGGTCATTGTCAGTAA	CACGTCCTTTCTTGACCTCTA	CTGGGATTTATCGGAGCAATA	TACGGACAGGTTAGTCTGAAT
6654	SOS1	NM_005633	TACGGCATTATGAAATTACAA	CATGAACTTAGTGTAAAGTTA	TGGGTTGAATCCATCACTAAA	ACGAGTAGAATCAGATATCAA
6656	SOX1	NM_005986	CAACGTTAAGATGAAATTATA	TTGGGTTGGTTTGTTAATTTA		
6659	SOX4	NM_003107	CCGCGAGAAACTTGCATTGGA	TCCTTTCTACTTGTCGCTAAA	CACGGTCAAACTGAAATGGAT	AAGGACAGACGAAGAGTTTAA
6662	SOX9	NM_000346	ACCGAAGAAAGAGAGGACCAA	TCGTGTGATCAGTGTGCTAAA	ATGGGAGTAAACAATAGTCTA	CAGCCCACTGACAGACCTTAA
6675	UAP1	NM_003115	AAAGGTTTCTATGGTACTAAA	TTAGAGCATTATGAACATTAA		
6683	SPG4	NM_014946	CACGATGCTAGTAGACGCCTA	TGCCCTTAGTTTACTGGTTAA	AACGTTATTGATACTTGGATA	TCAGGTTAATACTATCTTAAA
6693	SPN	NM_003123	TTCAATAACAAGTGACCCTAA	ATGGTTCATATAGGACACACA	AAGGGTGTTTGTAGAGTTGTT	CCCAATGGCCTTTATCATCTA
6697	SPR	NM_003124	CAGGAAAGGCTGCTCGTGATA	CACGTGGACTTCTATGACAAA	AACTGCTGAGCTTACTGGAAA	AAGGAAAGGCTGCTCGTGATA
6699	SPRR1B	NM_003125	GAGACTTAAGATGAAAGCAAA	AAGGTCTTAGTACCAGAGCTA		
6700	SPRR2A	NM_005988	ATGATGATCCCTGACAGCAAA	ACCAAGAAAGGATAAGGATAT		
6710	SPTB	NM_000347	CTGCCGCATCACCGATCTCTA	ACGGCCCGCAAGGACAATATA	CACTCTCTGGATCAACGACAA	CAGGATGTCTCCTATGATGAA
6712	SPTBN2	NM_006946	CCGGCTCATCTCGGACATCAA	CAGCGTCAACATCCTGCTCAA		
6715	SRD5A1	NM_001047	CTCCGGAAATTTGAAGAGTAT	CGGGCATCGGTGCTTAATTTA	ATCCATTCAGATCATATCCTA	GAGGCTTATTTGAATACGTAA
6717	SRI	NM_003130	CAAAGAATACTCCACACATAA	TACATTATAAGCTTAACTATA	CAGGCTGTGAATTCAATTGCA	AGGATTCACCTTAGAAGTTTA
6718	AKR1D1	NM_005989	CAGGGTCCTCCAGCTAGATTA	ATGGCAAATGGTTATATCACA	CTGGGTAGTAGCGTTGGTAAT	TAGTGTTACTTGGATAGCTTA
6729	SRP54	NM_003136	ATGGGATTCAATAATATGTAA	ATGGATAGTATGAATGATCAA		
6732	SRPK1	NM_003137	CACCCTTGGCTTAACTCCTAA	AAGCAATAGACTAGAACTGAA	TACCATGTGATCCGAAAGTTA	CAGACTCTTGTACACCTATAA
6737	TRIM21	NM_003141	CAGCGTTGAGTTGCCCTGTAA	AGCGTTGAGTTGCCCTGTAAA	CCGGCAGCGCTTTCTGCTCAA	CAGAGCATACCTGGAAATGAA
6738	SSA2	NM_004600	CAGGATGGATATGTATGGCAA	CTGAGGGAGTATCGAAAGAAA		
6746	SSR2	NM_003145	CAGGTGCTTTCCAGACTCCAA	CCCAGTGTCTATTCTGGGTTA	CACCTCGGCAACAATTACTTA	CAAAGGGTATCTTAAATGCAA
6750	SST	NM_001048	TGCAGAGATCTGCTAACTCAA	CAGCGAGACCCTTGCATTAGA	CCCTTGCATTAGAAACTGAAA	ACGGAGAATGATGCCCTGGAA
6751	SSTR1	NM_001049	CTGGTGGTGCCTATTAATCAT	TGGGAACTCTATGGTCATCTA	CGCGCTGGTGGTGCCTATTAA	CACGAACTCATTAACAACTCA
6755	SSTR5	NM_001053	CACCGTCAACATCGTCAACCT	ACGGGCTTATGCAGACCAGCA	CGGGCTTATGCAGACCAGCAA	CGGGAACACGCTGGTCATCTA
6757	SSX2	NM_003147	CCACCTTTCATGTGTAATAAA	AGGGCAGTTCTGAGTGTTTAA	CCCGAAGATCATGCCCAAGAA	TTGGTCGATTCAGTTTGTCAA
6775	STAT4	NM_003151	TGGAATCAAGTCCAACAGTTA	TCAGAGGCCGTTGGTACTTAA	TTGGTACAACGTGTCAACCAA	CAGCCTCGATTTCAAGAGAAA
6778	STAT6	NM_003153	CACCCTTGAGAGCATATATCA	AACCAAGACAACAATGCCAAA	CAGGATGGCTCTCCACAGATA	ACGGATAGGCAGGAACATACA
6788	STK3	NM_006281	CAGACCATGATTGAACATAAT	CAGCTGCATACCAGTAATAAA	CGGCGCCTAAGAGTAAACTAA	CCGGCGCCTAAGAGTAAACTA
6790	STK6	NM_003600	TAGCATGTGTGTAAACTTTAA	GAGGGTTTAACTCCTATTTAA	CACGTGCTCTACCTCCATTTA	CACCTTCGGCATCCTAATATT
6793	STK10	NM_005990	TGCAGAATGTATATAACGCAA	CAGAATGTATATAACGCAATA	CAGCTCAAACTGATGAAGAAA	CACGGAATTAGAGAACCTGGA
6794	STK11	NM_000455	AACGTGAAGAAGGAAATTCAA	CCGCCCAAATTTGGCAATAAA	GAGGGCCGTCAAGATCCTCAA	CAGGAGTGTGCGGTCAATATT

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
6799	SULT1A2	NM_001054	CACGTCGTTCAAGGAGATGAA	AAGAGGCTCCAGAATAAAGTA		
6810	STX4A	NM_004604	AGGAAGCTGATGAGAACTATA	CAGCTCGGACGAAGAGGACAA	TCCGGACAATTCGGCAGACTA	AAGCGAGGTGTTTGTGTCCAA
6811	STX5A	NM_003164	CAGTGGAAATTGAAGAGCTAA	CAGCAAGACTGTCAGCCTCAA	AAGTCCCTCTTTGATGATAAA	ATCAATAGCCTCAACAAACAA
6829	SUPT5H	NM_003169	CCGGAAGGGCTTTCTGTTCAA	CAGAACAACATCCATGTGAAA		
6830	SUPT6H	NM_003170	TAGGAGCATCTTTGAAATGTA	CAGCACAATTCAGAAGATCAA		
6840	SVIL	NM_003174	CACATCGAAGCCATGATTTAA	ACCGGTTGTAAACAAACAGTA	CAGGACTGATGTCAAGGCATA	CCGAGTATTTATCCCGCTATA
6844	VAMP2	NM_014232	ATAGTTTACTTCAGCTCTTAA	CAGCTGTTATTTATACATATA	TCCCTTCATTTGCATCTGCTA	CCCATTAGTTCTTGTATCACA
6853	SYN1	NM_006950	CCAGATGGTTCGACTGCATAA	ATGGTTCGACTGCATAAGAAA		
6854	SYN2	NM_003178	CCAGCTGGTCGCTATCTATAA	CTCACTGGAATCCATATACAA		
6860	SYT4	NM_020783	CAGGGAGATCTTAATACCTAA	CTGCACTGTATTAAACATGTA		
6873	TAF2	NM_003184	AAGCATAAGCATGACAGTAAA	TAGAATCAAGTTGAACAGCAA		
6884	TAF13	XM_496381	TAGGGTGATATTGGTGCATGT	GCCCTTGTAAGCTATACTGTA		
6887	TAL2	NM_005421	GACCAGGAAGATCTTCACAAA	CAGAACTCTGCTTGAGAACTA	CCCACTCACCCTCCAGACAAA	AAACGCTTCGCCTGGCAATGA
6891	TAP2	NM_000544	CAGGACCAGGTGAACAACAAA	CCTGCTTTCCTTTATGATGTA	TAGCGACATTGGTAACAGCTA	CCCTATGAGGTTGGTTATTAT
6898	TAT	NM_000353	TTCGCTAGTGATGGACCCATA	CTCGGGCAAATATAATGGCTA	TCGGGCAAATATAATGGCTAT	CAAGCTATTGACCTTTGTTTA
6900	CNTN2	NM_005076	ACGATAGTTACTCACAAGTAA	CAGCCACAAACAAGTACTTTA		
6906	SERPINA7	NM_000354	CACTATGGTCTTAGTGAACTA	CACCCTATTATCCAAATTGAT	ACCCTATTATCCAAATTGATA	TAGGGAAAGTTGTGAACCCAA
6910	TBX5	NM_000192	AAGGCGGATGTTTCCCAGTTA	GCCGACGATCACAGATACAAA	CCACAAGATCACGCAATTAAA	TACCATTGTACCAAGAGGAAA
6916	TBXAS1	NM_001061	CCCAATAAGAACCGAGACGAA	CCGGAGACCTTCAACCCTGAA	ACCGCTGCAGCTAGAATCCAA	CCGCTGCAGCTAGAATCCAAA
6921	TCEB1	NM_005648	CCGAGATTCCTGAATTCCCAA	AAAGTTGAAATTTGTTTGCTA	TACCTGTAGTTCAGTTAGTAA	TGCGAACTTCTTAGATTGTTA
6924	TCEB3	NM_003198	TAGCATCTTTGTAAACTATAA	TACAATCATGTATTAATTGAA		
6926	TBX3	NM_005996	GCGAATGTTTCCTCCATTTAA	GTGCACTTTGTCGGATATAAA	TCGGGACAAGTGAACACATTA	CTGCCTATAGAGATATATTCA
6927	TCF1	NM_000545	CAGCCGAGCCATGGTTTCTAA	CAGGAGTAGCTGAGCTCACAA	CAGGACAAGCATGGTCCCACA	GCGAGTGGCACGTTTATTTAA
6928	TCF2	NM_006481	CACGGATCTTATCTGGTTTAA	CTGGGATATGCTAGTGATGTA	GCGGTGTAATAAGATCCTATA	TAAGGTTATAACTGTGGCTAA
6929	TCF3	NM_003200	CTCGGTCATCGTGAACTTGGA	CTGGATGATTGGGACTTTAAA	CCGGGCACATGTGAAAGGTAT	CCCGGATCACTCAAGCAATAA
6932	TCF7	NM_003202	TACGAACATTTCAACAGCCCA	ATGAGCTGGTTTGTCAAACAA	AACAGAAATAATCTGACACTA	CTGGGCAGCTTGAGAGGGCAA
6939	TCF15	NM_004609	AGAGAGAATTGGTGAGTTTAA	TCTGATATGGTTGGTAAAGAA	ATGGTTGGTAAAGAAATCTTA	TGGTTGGTAAAGAAATCTTAA
6943	TCF21	NM_003206	CAGATCCTGGCTAACGACAAA	CTGGTCCAAGTGCAATATGTA	CAAGTGCAATATGTAATTATA	ATCTTTCTTTATATTGCTAAA
6949	TCOF1	NM_000356	TACGTTGGTCTCAGAAACTGA	CAGCGAGGAATCGGACAGTGA	CAAGCAGTGAGGAATCAGATA	ACGGTTGAAGGTGGAGATCAA
6975	TECTB	NM_058222	CAGGGCAACCTTCCAATTCAA	TAGGTTTAAAGTGGTCTTGAA		
6988	TCTA	NM_022171	CCGGAGTCACTCATCCCTTAA	TAGGATGGTACCAAGCATTTA		
6992	PPP1R11	NM_021959	TGGCTTGAGATTGGTCACTTA	CAGAGATCAGTCAAATCCATA	CGCCCTAACTTTGCTTGCTAA	AACATGAGTAGCGAACACTTA
6993	TCTEL1	NM_006519	AACGCTTATCAACACAGCAAA	ATGTAGTAGAACAAACTTTAA		
6997	TDGF1	NM_003212	CCCGCTTCTCTTACAGTGTGA	AACCAAGTGATCAAACTACAT	CTGCCTTTCTATACAAAGCTA	TTGAATTATATGTTCAGATTA
7005	TEAD3	NM_003214	ATGGGTTATATCATAAATGCA	AACCAGCACAATAGCGTCCAA		
7006	TEC	NM_003215	CACGTGCATTTGGCCTATGTA	TCAGGTGACCTTCGCAACAAA	CCGCAGCTAATCAGAATCAGA	CAGTACAAAGTCGCAATCAAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
7010	TEK	NM_000459	CAGCACGTTGATGTGAAGATA	TGGAATGACATCAAATTTCAA	TCGGTGCTACTTAACAACTTA	ACGGGCCAGATTGTAAGCTTA
7019	TFAM	NM_003201	AAGGAATTATATATTCAGCAT	AGGACGAAACTCGTTATCATA	CACAATAAAGAAACAACGAAA	AAGATTGAGATGTGTTCACAA
7026	NR2F2	NM_021005	CTGGCCGTATATGGCAATTCA	TAGGTGAAGTCGAGCACTCTA	GTGGAATTTATTGGCAGCCAA	CCGCTTAGTTCTTGAATTGTT
7029	TFDP2	NM_006286	CTGGTACAGAGAAATCGACAA	AGGGACTACTTCTGAACTCTA	CGCTACTTCTTAAGTACTTAA	AAGGCAGAAATGAACATGAAA
7030	TFE3	NM_006521	TCCGGGATTGTTGCTGACATA	AAGGAGATTGATGATGTCATT	TCGCAGGCGATTCAACATTAA	CAGCTCCGAATTCAGGAACTA
7036	TFR2	NM_003227	CACGGAGTGGCTAGAAGGCTA	CAGGCACATCGGGAACCTCAA	GACGGTCATACTGTCGGTTAA	TGGAGTTTCAATATCAATAAA
7040	TGFB1	NM_000660	CTAGGTTATTTCCGTGGGATA	CACACTGCAAGTGGACATCAA	CAGCATATATATGTTCTTCAA	CACGTGGAGCTGTACCAGAAA
7043	TGFB3	NM_003239	CCGAGTCGGAATACTATGCCA	CCGGGTCTTGCGGGTGCCCAA	ACGCATAGACTGAGGTATAAA	AAGTATGAATATTACTCTCAA
7045	TGFBI	NM_000358	CGGGAAGGCGATCATCTCCAA	AAGGCGATCATCTCCAATAAA	CCGCACCATAATGAGATGTGA	TGGAGAAATGGCATCATTATA
7046	TGFBR1	NM_004612	CTGTAATGTTACGTCATGAAA	TGGGATTGTACTATACCAGTA	TCCATTGGTGGAATTCATGAA	CTGCCTTATTATGATCTTGTA
7048	TGFBR2	NM_003242	TACCATGACTTTATTCTGGAA	TCGGTTAATAACGACATGATA	TCGCTTTGCTGAGGTCTATAA	CTCCAATATCCTCGTGAAGAA
7049	TGFBR3	NM_003243	GACAATGGCTATAGTCCAATA	CACCTTCAACATGGAGCTATA	CCCGCAAGCTGACATGGATAA	ACCTGAAATCGTGGTGTTTAA
7050	TGIF	NM_003244	TACCACTGTGACTGCATTGAA	TACCCAGAGGACACTTGTAAA	TCCAAGAACTATAAACTTAAA	CACATACTGTCTAATTAATAA
7052	TGM2	NM_004613	CACCTTGATCCCAATCCTTAT	ATGGCCCAGCCTTGTAAATAA	CCGCAAGGAGCAAACACTGAA	CCGCGTCGTGACCAACTACAA
7058	THBS2	NM_003247	TGCATAAGCCATTATGATAAA	ATGACATAAGCTACCGATTAA	CAAGAGAGTGTCGAATGATAA	AGCGTTGGGATACTTCATTAA
7059	THBS3	NM_007112	CACGCCGTGAACCTACAGCAA	CCGCCTGGGTTTCCTGGGCAA	CTGCATGGAAGTGTACGAGTA	ATCGATGGCTACCCAGACCAA
7064	THOP1	NM_003249	CAAGTTGAAGGTCACCCTCAA	TGCGGTGATTCTGGAGCTGAA	CAAGTTCTACCTGGACCTGTA	CAGCAAGGTTGGCATGGATTA
7067	THRA	NM_003250	CAGCGAGTTTACCAAGATCAT	CTGGCCCAAGCTGCTGATGAA	CTGGATGGAATTGAAGTGAAT	CCCGATGACATTGGCCAGTCA
7072	TIA1	NM_022173	CGGAAGATAATGGGTAAGGAA	CACAACAAATTGGCCAGTATA	CTGGGCTAACAGAACAACTAA	AACGATTTGGGAGGTAGTGAA
7074	TIAM1	NM_003253	CGCCTGAAATTTCTAATAGAA	AACGGAAATGGTAGAGTTTCA	CTGGTTCTGTCTGCCCAATAA	ACGGCGAGCTTTAAGAAGAAA
7075	TIE1	NM_005424	CCAGTGAGAACGTGACGTTAA	TACTTGTATATCGCTATTGAA	GCGCTTCAAGGTCAATGTGAA	CCCAGTGAGAACGTGACGTTA
7077	TIMP2	NM_003255	CAGGCACATTATGTAAACATA	CTCAAATACCTTCACAATAAA	CTCGCTGGACGTTGGAGGAAA	CTCGACATCGAGGACCCATAA
7078	TIMP3	NM_000362	CAGGTGAAAGACTGAGATGAA	CCCTGCGGAGTCGATAAATTA	CGGCGGCATTATTCCCTATAA	CACGCTGGTCTACACCATCAA
7080	TITF1	NM_003317	CCCACTTGTCACTGACACAAA	TGGCTTAAATATAGTTCCTAA	TACCTTGTCATCAGCATGTAA	CTCCGTTACGTGTACATCCAA
7084	TK2	NM_004614	AAGGTGTTCAATTAATCTGCA	CTCCCGATAAAGAACAGGAAA	CGGGATCGAATATTAACTCCA	ATGCCAGAAGTGGACTATGTA
7087	ICAM5	NM_003259	CCGGGAGAACGTGACCATCTA	CAGGAGGAAACTTCACGTTGA		
7088	TLE1	NM_005077	AAGGTTAAACATTTGTATAAA	TCGAATTTATAGAAATAGAAA		
7089	TLE2	NM_003260	CTGCATTGATATTTCCGATTA	CAGCGAGAAGACGGAAATGCA		
7090	TLE3	NM_005078	CAGGATCAAAGACGAATTCCA	CACAGTTTATGAGGTCATCTA		
7092	TLL1	NM_012464	GAGGCGTTATTCCTTATGTTA	CAGATCGAGATAACCACGTAA	TAGAATCAATCTCGACCTATA	CAGCATTACAAGGATATTTGA
7096	TLR1	NM_003263	CACCATTTATATGTGGTATTA	CTGGTTTGGCATACAACTGTA	CCGCAAAGTTATATCTATGAA	CAGGGTCTTCATGAACACTAA
7097	TLR2	NM_003264	CTGGGCAGTCTTGAACATTTA	AACATTTAGACTTATCCTATA	CAGGTAAAGTGGAAACGTTAA	CCGCAACTCAAAGAACTTTAT
7101	NR2E1	NM_003269	CCGGTTGATGCTAACACTCTA	TACGTTATGTTGGAGCATTTA	TCCCGTTAACATAGTGCTGAA	CTCTATACTTATGGAAATGTA
7102	TM4SF2	NM_004615	CACGGACGCTATGCAGACTTA	AAGGGTTGTTATGATCTGGTA	CCGGTTCATCACGGCCAATCA	CAGGCTGCCTAAGACATGTAA
7104	TM4SF4	NM_004617	AAGGAAGAAAGCACATTTAAA	CAGGTCAGGGAGAATGTATAA		
7108	TM7SF2	NM_003273	CCGCATCATGCCCTACATCTA	CACCATGGATATCACACATGA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
7112	TMPO	NM_003276	ACCCATCAAATTACAGTATAA	GAGGAGAAGTATGCAAAGTAA		
7124	TNF	NM_000594	AACCCAAGCTTAGAACTTTAA	CAAGCTTAGAACTTTAAGCAA	TAGGGTCGGAACCCAAGCTTA	CCGACTCAGCGCTGAGATCAA
7126	TNFAIP1	NM_021137	CTCACATACGGTAAAGCCAAA	TGCCCTCTTGAGGTCCTTTAA	CAGGAGGTGAGTTCCTCTTTA	ACCCATGTCTTTCTACCCTAA
7127	TNFAIP2	NM_006291	CTGGCTGTGTAACCTAACATA	TAGGAGTTAGCGTGTTTGATA	CCGGATGTCCATGGAGCAGAA	CAGGGTGATGCTGAAGATGAT
7128	TNFAIP3	NM_006290	CTCGGCTATGACAGCCATCAT	CAGATGTATGGCTAACCGGAA	CCGAGCTGTTCCACTTGTTAA	CAGCCTTTACTCATACTATTA
7130	TNFAIP6	NM_007115	CTGGCACATTAGACTCAAGTA	CCCACTGCATAGAAATAACAA	TGGCGTCTTTACAGATCCAAA	AAGGCGGTGTGTGAATTTGAA
7139	TNNT2	NM_000364	CAGGCAGCTCCTGTTTGGAAA	CCACTCCACACCAGTAATAAA	CCGAAACAGGATCAACGATAA	CAGGATCAACGATAACCAGAA
7140	TNNT3	NM_006757	AAGCGTCAGAACAAAGACCTA	GAGGAGCAGTACGAAGAAGAA		
7142	TNP2	NM_005425	CAGAAAGAACTTGGAAGGCAA	CAGGATGGAAATCCAACTAAT		
7151	TOP1P1	M55632	CTCACAATTCACACCAATAAA	TTGGGACATCATGAAAGTTTA	TGCCTTCATATTAATATATAA	GTGGAAGTTTACTGACAGGAA
7153	TOP2A	NM_001067	CCCATTGTAAAGGTATCTAAA	CAGACTATAGGGAATACCATA	CACGTAGGCTGTTTAAAGAAA	ACGAATAACCATAGAAATGAA
7155	TOP2B	NM_001068	GTGGATTATGTGGTAGATCAA	CTGATTGAAGTAGTTAAGAAA	CAGCCGAAAGACCTAAATACA	TCGGGCTAGGAAAGAAGTAAA
7158	TP53BP1	NM_005657	AAGCAGTAACACCTCTTACAA	CTCCAGAACTACCGTAATTAT	TTGTTTGACCAGAGCAATAAA	CAGGACAGTCTTTCCACGAAT
7161	TP73	NM_005427	CCCGCTCTTGAAGAAACTCTA	CCGGGCCATGCCTGTTTACAA	CCCGGGATGCTCAACAACCAT	ATCGAGTATTTCACCTCCCAA
7164	TPD52L1	NM_001003395	CAGCTAGAAGACGAAATTACA	CAGCAATAGGATGATTTACTA		
7166	TPH1	NM_004179	AAAGACAATGTCTACCGTAAA	CGGGAGGATAATATGCCACAA	TCCATTTGGAGTGAAGTATAA	CGGAGTATTCAGATCCTGAAA
7167	TPI1	NM_000365	CCGAGGATGGCTGAAGTCCAA	ATGGAAGGCGTGGTGGGATTT		
7168	TPM1	NM_000366	CACACTGTGCTTTCTATTGTA	CTCAAGGGCACCGAAGATGAA	TGCGGAGAGGTCAGTAACTAA	AACGATATGACTTCCATGTAA
7171	TPM4	NM_003290	AGCGTTTGCTTTCGCCTGTAA	ATAGTAATTAATAGATGGTAA		
7172	TPMT	NM_000367	ACCGAAATTCCTGGAACCAAA	AGGGTTCAAGGTGGTCCCAAA	CACCGGTTGAATGGACAACTA	ACCGGTTGAATGGACAACTAA
7175	TPR	NM_003292	CTGAAGGAAGATCTAAATAAA	CAGGAGGTTTCTAGAGAACAA		
7177	TPSAB1	NM_003293	CTGAGTGCTGGACCTCATTAA	CTGCCTGGGACCGGACGTCAA	CTGGACCTCATTAAAGTGCAT	CAGGATCATCGTGCACCCACA
7187	TRAF3	NM_003300	CTGGAAGATTCGCGACTACAA	ACACTTCACTCTGAAGAATTA	TCCGATGATCGCGCTGCAGAA	AGAGAGCATCGTTAAAGATAA
7188	TRAF5	NM_004619	AAGGTAGGCTGTTCCAGTTAA	AAGCATTTCTTTAGCCCACAA	CTGGAGGGTACTTGCTATAAT	AGGGTACTTGCTATAATGGAA
7189	TRAF6	NM_004620	CAGGAAACTATTCACCAGTTA	CAGCGCTGTGCAAACTATATA	CAGGGATGAGTTTAAACCCTA	AGGGATGAGTTTAAACCCTAA
7224	TRPC5	NM_012471	CAGAGCTATCGATGAGCCTAA	GAGGCCTGTTCTCAAAGTGAA	CACACTAAGTCCATCTTACAA	ACCAGCTATCAGATAAGGCAA
7252	TSHB	NM_000549	GAGAGTGTGCTTATTGCCTAA	CCCAGGATGTTTGCACATATA	CTGCATACATGAAGCCATCAA	AAGACAAACTACTGTACCAAA
7253	TSHR	NM_000369	TCCAGAATCTACGTATCTATA	CAGAATCTACGTATCTATAGA	TACGCAGACTCTGAAGCTTAT	AGCACTGATATTCAGGTTCAA
7262	PHLDA2	NM_003311	CACTGTGCCCATTGCAAATAA	CGGCTTTGAATGAATAAATGA	CTGGTTCTTTGTAGTCACATA	CGCGCTCGGCACGACATGAAA
7266	DNAJC7	NM_003315	AAGCTTATAATTATTATACAA	AAGGAAGGAAATTACAAACTA		
7270	TTF1	NM_007344	AAGGAGATACTGAGAAGTTAA	CAGTTTGATTATATTTATATA		
7272	TTK	NM_003318	ATCCGACTTTATGATTATGAA	TTGGACTGTTATACTCTTGAA	TCCGACTTTATGATTATGAAA	CAGCAATACCTTGGATGATTA
7273	TTN	NM_003319	TGCGGCGAGTATACATGCAAA	TCGGGACGGTCAAACCTATAA	CGCATTCTAGCTCGAGTCAAA	ATCGACTATTACATCGTAGAA
7280	TUBB2	NM_001069	CAGATCAATCGTGCATCCTTA	CATGGTCTTTCTACTTGTAAA	CTGTGAAGGTATCTATACTAA	GAAGGTATCTATACTAATAAA
7297	TYK2	NM_003331	ACGAAATTCCTTGAGCTCATA	CTGATGCTATATTTCCGCATA	CGGGTCTGTGCTGAATGTGTA	CACCATCTGGTAATAAACTCA
7299	TYR	NM_000372	ACCCATGTTTAACGACATCAA	AAGGATTTGCTAGTCCACTTA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
7314	UBB	NM_018955	GAGGCTCATCTTTGCAGGCAA	CCAACTTAAGTTTAGAAATTA	ATGGCATTACTCTGCACTATA	CAGGATCCTGGTATCCGCTAA
7316	UBC	NM_021009	TTGCACTTTCCTTTCAATAAA	AACGTCAAAGCAAAGATCCAA	GAGGTTGATCTTTGCTGGGAA	GAGGTTGATCTTTGCCGGAAA
7317	UBE1	NM_003334	CCCGCTCACCTTTGATGTCAA	CTGGGATGTCACGAAGTTAAA		
7318	UBE1L	NM_003335	TTGGAGTTTGACACCAACCAA	CGGCCGGATGGTCACCTGAAA	CAGCAGAAGGAACTGAACAAA	ATGCTTGTTAAAGGAAGGCAA
7320	UBE2B	NM_003337	CTCATTAGAAAGGCTAACAAA	TTGGATTACAGTATGGCAATA	CCCAGTATTAGCAATGAATTA	ACCTCTCATTAGAAAGGCTAA
7325	UBE2E2	NM_152653	TCCGATGGAGATCAACGTGAA	CCGCTGCTAAATTGTCAACTA		
7334	UBE2N	NM_003348	ACCTTGTCTCTTGCAGTTTAA	AAGATGAAGAATTAACTATTA	TAGCCAGTCATAAATACATAA	CAGATTTGTGTTAAGATAGTA
7335	UBE2V1	NM_021988	ATCCATGCGAGTAAACATTTA	TTGGATGTAACGGCTTGGTAA	CACGGGAATTATTATTGTCAA	AAGGAAGACTTGAACCTAGAA
7343	UBTF	NM_014233	CCGGAGAAGAAGAAGATGAAA	CAGGACTTCCAGAGAGAGAAA		
7350	UCP1	NM_021833	TCCAGTGTTATTAGGTATAAA	CAGAATAATAGCAACAACCGA	TGCAATGAAAGTGTTCACTAA	AACGAGAACTGTCAAAGTCAA
7358	UGDH	NM_003359	TACAATCATGTTTGAAATTAA	ACGGTTGTTGATGTCAATGAA		
7363	UGT2B4	NM_021139	CTGGGAAACCCAATAAATGAA	CCCAATAAATGAACTCCTTTA	ATGAGGTTATATTGAAATGTA	AGGAAGCTAATAAATAATTAA
7367	UGT2B17	NM_001077	CACATTGTATTTGAACACAAA	TTGGGAATATTCTGACTATAA		
7376	NR1H2	NM_007121	CAGGGCAACAGGAGTAGTTCA	CCGGAAGAAGAAGATTCGGAA	ATCGTGGACTTCGCTAAGCAA	CTGGGCGAGCCTGTAGACCTA
7378	UPP1	NM_003364	CAGGAAACTAATTTCCTGATA	CACACTTTACACAAGAATCTA		
7380	UPK3A	NM_006953	CACGGAGTACAGGTTCAAGTA	CAGTGTGACTTTCGGCACCAA		
7384	UQCRC1	NM_003365	CCGGGAGCACACAGCTTACTA	CGCCACCGTGATGATGCTCTA	CCGGACAATGTGGCCTTGCAA	CCACAGGTGACCACCAATAAA
7385	UQCRC2	NM_003366	TACATCCAGTCTGACGACAAA	CCAGAATTTGGTCGTTGGGAA	ATCAAGGCTGCCTATAATCAA	AAGGCTGCCTATAATCAAGTA
7392	USF2	NM_003367	CCGGGAGTTGCGCCAGACCAA	CAGCAAGACGGGAGCGAGTAA	AAGACTGTAACGCAGACAACA	AAGAGCCCAGCACAACGAAGT
7399	USH2A	NM_007123	CAGGTACAATTTGACCATTGA	CAGAGGGAAACTTGACTTTAA		
7407	VARS2	NM_006295	CCGGATTTACCACCAGTTGAA	CTGTTTCACCATGGACCCTAA	CACGAGGAAGGCATCATCTAT	CCGGTTTGGATTATGTGCCTA
7414	VCL	NM_003373	CGGATTAGAACCAACCTCTTA	AAGAGAGTAATGGGTTTCATA	TAGGTGTTTGTTCATCTGTAA	CTGATATAAATGCAATATTAA
7415	VCP	NM_007126	CACAAGCAGTTTCTAAACGAA	CCCATTGATGACACAGTGGAA		
7422	VEGF	AF022375	GAGGGTTTCAATATACATCTA	CTGGAATTTGATATTCATTGA	ATAGAGAATTCTACATACTAA	AAGAAAGATAGAGCAAGACAA
7423	VEGFB	NM_003377	CAGGACAGAGTTCGAAGAGGA	CCGGATGCAGATCCTCATGAT	CAGTGTGAATGCAGACCTAAA	AAGACCCAAACCTCTGCATAA
7425	VGF	NM_003378	CCGGAGGAAGAAGCAGCTGAA	CGGCAGCCTCTTGGTCATGAA		
7434	VIPR2	NM_003382	CACCGGTTGCTGGGATACAAA	CTCCAGCATTTAGATAATCTT	CCCGCTGTTCGGCGTCCACTA	AACGGAGACCTCGGTCATCTA
7436	VLDLR	NM_003383	CCCTGAAAGAGTGTCATATAA	ATCCAACTAGTTGAACAGCTA	CAAGGTTGGTAGACATGTTAA	CAAGATCGTAGGATAGTACTA
7441	VPREB1	NM_007128	AGGCTATGTATTACTGTGCTA	CTGCTGAGATATTTCTCACAA	TCCCAGGTTCCTGCTGAGATA	AGACTGCATTAGGGAATTAAA
7442	TRPV1	NM_018727	CAAGTGGGACAGATTCGTCAA	CAGAACCACATCCCAAAGGTA	CTCAATTGCTGTGCAGGTTAA	CCCGAGGAAGTTTATCTGCGA
7447	VSNL1	NM_003385	TAAGCGTTTACCCGAATTAAA	CGGCTTAAGCGTTTACCCGAA	CAGAGACGGCTTAAGCGTTTA	AGCGTTTACCCGAATTAAATA
7450	VWF	NM_000552	AAGGGACGAGATCGTTAGCTA	AACATGGAAGTCAACGTTTAT	CCCACCATCTCTGGTCTACAA	ACGGCTTGCACCATTCAGCTA
7453	WARS	NM_004184	CAGAAGGGAAACTGAAAGAAA	AAAGAGCTAATAAACCGAATA	CAGGTTCTTGATGCCTATGAA	AGGGTTCCAAGTATACTCTTA
7455	ZAN	NM_173059	TGCGATCTTAATAAACCCTCA	CCGTGTGCTAATCAACAGCAA	CCCGGCTATGTGCTGAGTGAA	CAGCTTAAGAATGGCCAGTAT
7461	CYLN2	NM_003388	CACCTTCTGAACCTTCTTCAA	CAGGACAAAGCTCAGAAACAA		
7462	WBSCR5	NM_014146	AAGCTTGTACAGTTAACTTAT	AAGGACCATTTCCCAGAGCTA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
7472	WNT2	NM_003391	AAGGCATTTATTGCCATATTA	CTGGAGAAGAATGGCTTTCAA		
7474	WNT5A	NM_003392	CAGAGTAAATACTCTGAATAA	CCGGATAACCTTGTAACATAT	CCGGGTCTGCAGAGAATGAAA	CACACAAACTTTACACTTTAA
7480	WNT10B	NM_003394	AAACCTGAAGCGGAAATGCAA	CAGGCACTGTTTGGAGCCATA	CAGGATCGGCTGAGGGCCAAA	ACGAATGCGAATCCACAACAA
7483	WNT9A	NM_003395	CCGGCTGAAGCTGGAGCGGAA	CCGTGTGGACTTCCACAACAA		
7484	WNT9B	NM_003396	CAGCACCAAGTTTCTGAGCAA	AAGCAAAGCCTCCTCCCTTAA		
7498	XDH	NM_000379	GACAGTCTTTGCGAAGGATAA	CTGCACCATTGCTGTTCCAAA	CCGGATTGTGGTTCGAGTGAA	ACAGGTAATAACGTGAAGGAA
7499	XG	NM_175569	CAGCCAGTTATTTCAAACTAA	ACGGTGGAGATCACCATTCAA		
7511	XPNPEP1	NM_020383	AAGGAGAACCTCGTTGACAAA	ATGAGATTGCGTGGCTATTTA	CCCGACTGGAACCAAAGGTCA	CCCGACTTCTTTGGCCAGTGA
7514	XPO1	NM_003400	TACATGTTACTCCCTAATCAA	CTGTGTCAGTTTGTAATGGAA	CCCATTGTAAAGCGACTTCAA	CAGCAAAGAATGGCTCAAGAA
7516	XRCC2	NM_005431	CACGATGTATACTTCCCAAAT	AGGGTACTACGCAAGCCTTAA	TTGCAACGACACAAACTATAA	CAGGGTACTACGCAAGCCTTA
7517	XRCC3	NM_005432	AAGCCAAACTGAAATCGGTAA	CCGCTGTGAATTTGACAGCCA	GAGAGACTTAAGGGAAATTAA	CAGAATTATTGCTGCAATTAA
7520	XRCC5	NM_021141	GACGATTTATTGGACATGATA	ACCCTCATAAGTCGTCACTAA	AAGCGAGTAACCAGCTCATAA	AAGCATAACTATGAGTGTTTA
7525	YES1	NM_005433	GAGGCTCCTGCTTATTTATAA	CCAGCCTACATTCACTTCTAA	AAGTATAATGCAGTACATTAA	AACAGTCAGTATGCAATCTTA
7529	YWHAB	NM_003404	AAGGTTTAATCTGATATCAAA	CTGCCGTTGTTCGGGACTTAA	CTGGATAATACCTTTAAGAAT	CAGCAATATGTTCACTATGTT
7533	YWHAH	NM_003405	ATCAAGATGGGTGATTATGAA	ATGGGTGATTATGAAATGCCA	TTCCATCAGCTTTATAATAAA	CAGGCTACAGTTGATATTTAA
7555	ZNF9	NM_003418	CAGCAAGACAAGTGAAGTCAA	AAGAGTTGAGTCAGACCAGTA	CTGACCTCAGTAGCTATTAAA	CACATAGATGGTGATGGCAAA
7559	ZNF12	NM_006956	CAGCAATGGATTATAGTTTAA	CTCGCAGAAGTCAGCACTTAA		
7567	ZNF19	NM_006961	CAGGCTATTGTAGCTATTATA	CACCAGTGAATCCATTCTCAA		
7579	ZNF31	NM_145238	CAGGGAAGTTATCTTGGTATA	ACCAGGTAATTTGGAAGTGAA		
7592	ZNF41	NM_007130	CAGCATATCCTGGGACATAAA	CACAGTGTATATGCAATTCTA		
7593	ZNF42	NM_003422	CCGCAGGTCCAGGTAGTGTAA	CTGGCGATTACATAAGTATAA		
7596	ZNF45	NM_003425	AACGAGATGATTTGCACTATA	CACCAAGATCAATGTATACAA		
7617	ZNF66	NM_001009883	CAGGATCAAATTCTCACATAA	CAGCATATAAACAGAACCAAA		
7620	ZNF69	NM_021915	AAGAAAGTCAATGAAATTAAA	CAGGCTGAACTTCCAGGAGAA		
7629	ZNF76	NM_003427	CCGCTCCTTCACCACATCTAA	CATGGATGAATGAGTATTTAA		
7634	ZNF80	NM_007136	CAGGGTTATATGCAATGTTCA	CTGGAGGAAGATGAGCCCTAA		
7675	ZNF121	NM_001008727	CACATTTGAATTCACACTGAA	TAGGAATTTCTCATACCATAA		
7681	MKRN3	NM_005664	CCAGTGGGACTTGCTTCATTA	TCCTGTTTAGCTTGACATGAA	AAGCCAGTAATTAGCATCTAA	GAGGACTTACAAAGCACTATA
7695	ZNF136	NM_003437	ATGCTTAATCTCACAAAGAAA	ATGGAAGGACCAGAACATTAA		
7705	ZNF146	NM_007145	CACGAATGAGGTTAACTTTAA	CTGGATTCATTTCCAATTAAA		
7707	ZNF148	NM_021964	CAGGAATGAATTCTCCACTAA	TCGGATGGCATAAGTGATTAA		
7712	ZNF157	NM_003446	CCGAATGAAGATGACTCTCAA	CAGGGTGAACATGCCAGCTAA		
7730	ZNF177	NM_003451	CCTGAGTACATTTATATTTAA	CTGGGTATAAGTAAGCAAGAA		
7739	ZNF185	NM_007150	CGCAATTATAATAAATGCTAA	CTCCCTGAACTTCACACATAA		
7743	ZNF189	NM_003452	AACACTAACATTATCCGTAAA	CTGCCAAGTATTGGAAATGAA		
7748	ZNF195	NM_007152	AAGACCTTTCATGAAATATAA	CACAAGAGTATTTCTTCTGAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
7750	ZNF198	NM_003453	ACGGGCGAGATATGAACTTAA	CGCCATGAAGTCAGCTTTAAA	CACGCTGGGTATTACCATGTA	ACGCTGGGTATTACCATGTAA
7756	ZNF207	NM_003457	CAGGTACATAAAGAAACAATA	CAGGAACTATTGGACATTTAT		
7780	SLC30A2	NM_001004434	AAGGGCTGTATTTGGGCCTAA	GAGAGGCTTCTTACTAGGTAA		
7799	PRDM2	NM_015866	CTGGCACTAATTTATAACTAT	CTACACGTAAGTATAAATGAA	CCCGGGTGATTGAGATCCAAA	CAGATGTATGTCTACACGTAA
7804	LRP8	NM_017522	TTGCGGAAAGGTAACCACAAA	CTGGACTGACTCGGGCAATAA	CCGGATGGTGTATGACTGGAT	CAGTACCTTACTCATCATTTA
7809	BSND	NM_057176	CTCGGTGTTTAGGCTGAACTA	CCAGATGAAAGTCATGAGCTA	CTGGACATGGACTCCAGTGAA	TGGGATGATATGGAGGTTCAA
7818	DAP3	NM_033657	CCCGAGGAATTAGCACTTGTT	CGGCACTGTGCCTACCTCTAA	TTGGCTCTGGACCTGCATTAA	TCGCTTTGTGATGCAGGTGAA
7837	D2S448	XM_056455	TACCTGCACTTTAATCAGATA	ACGGAACAAGTTACCACTACA	AACAACCGGATTACACATTTA	CAGGAGTGGAATGTACATATT
7857	SCG2	NM_003469	ATGACTGTGTTTAATAGTATA	CTGGATGAGAATAATACTCGA		
7862	BRPF1	NM_004634	CCGAAAGGTCTACAAGAGTTA	TCCCAAGTCAGGCAAACATAA	AAGGGAGACGATCAAGGTTCA	CAGCAACTGCCTCAAGTATAA
7866	IFRD2	NM_006764	CCGGATCTACGCTGCCTTCAA	ACGCTTTGAGAAGCACCTGTA		
7874	USP7	NM_003470	ATGGAGTTGCGTGGGATTCAA	CCCAAATTATTCCGCGGCAAA	CGGGCCGACACCAGTACATAA	CGAGTATGAAGTAAATTTGAA
7879	RAB7	NM_004637	AACGTTGATTTGCATAATACA	TCCCGTTAGATCAGCATTCTA	TAGATCAGCATTCTACTACAA	CACGTAGGCCTTCAACACAAT
7884	SLBP	NM_006527	TACGATCGTTATATTAAAGAA	ATCAGTTAATTTACCATGTAA		
7903	SIAT8D	NM_005668	ACGAGATGTGTCAGTGGTCAA	CACAATGTAGAAGGTTGGAAA		
7915	ALDH5A1	NM_001080	AAGAAAGACTCCGTAATCTTA	ACCCTCTTTCAAAGACAATAA	TTCGGAAGTGGTACAATTTAA	AAGGAGACTTATCTACATATA
7917	BAT3	NM_004639	CAGCGGTTGATCAACTTGGTA	ATGATGCACATGAACATTCAA	CCGGTTGCTGGAGTTGTGTAA	CAGCTCCGGTCTGATATACAA
7919	BAT1	NM_004640	CCAGGTGGTGATCTTTGTGAA	CTCAACCTCAAACACATTAAA		
7940	LST1	NM_007161	ATGGCTCACCCTTCCACCCAA	TTCAAATTGATCATCATCAAA		
7942	TFEB	NM_007162	CAGCAGCCACCTGAATGTGTA	GAGACGAAGGTTCAACATCAA	CCGCCTGGAGATGACCAACAA	AAGCAGGAGCTGCCTAGCGAA
7979	SHFM1	NM_006304	CCGGTAGACTTAGGTCTGTTA	AAGAAGTGTTGAAGTAACCTA		
7988	ZNF212	NM_012256	CAGAAACGTGATGGAGAGTAA	TAAGTAGAAGAAATAATTTAA		
7991	TUSC3	NM_006765	ACGGATGTTCATATTCGGGTT	CACGGCTATCCTTATAGTGAT	CAGGATTGAAATAAATGACAA	ATGGTAGCATTTAGTAATCTA
7993	D8S2298E	NM_005671	CGGGTGAAGCCTGGAAATTAA	AAGGATTGCTTTCTATATATA		
7994	MYST3	NM_006766	CGGCGCTATAGTAATCCAATA	AAGTTGTTTCTTGACCACAAA	CTGGACTTCCGTAGTGACCAA	CAGCTGAATTTGCGACCTGTA
8000	PSCA	NM_005672	CCCAGCATTCTCCACCCTTAA	CCCAGTAAAGGCTGAGATGAA		
8021	NUP214	NM_005085	CCCGGAGATGATCCCAACAAA	CAGAGATATTTGTGAACTTTA		
8022	LHX3	NM_014564	CCGACAGATGTCTGTTGCCAA	CTGGCCTGTGTGTAAGTCAAA	CAGCTCTTTCCAAGACTTCAA	CTGCTATTTCTAGACATGAAA
8029	CUBN	NM_001081	CGGAACCATCTCTCACATTAA	CACCTATGTCATAGAGGCTAA	CAGCTGCAATTTGAAGATCGA	CCGGTTAGAATCCATGGACAA
8031	NCOA4	NM_005437	AAGAGAAGTGGTTATATCGAA	CCCACGTTAGTTCTACATTAT	CTGGTCAATAGTGATTACCAA	ACCGACTAAGCAAATAGGCAA
8048	CSRP3	NM_003476	ATGGGAGAGGCAATAAATAAA	AACGAGTTGCAGAGCATATAA		
8061	FOSL1	NM_005438	CTGGACAGTATCCCACATCCA	CACAATTTGCACTAAATCAGA	CCGAGTAAGGCGCGAGCGGAA	CCCACCTAGAACACTAACTCA
8065	CUL5	NM_003478	CTGGAGGACTTGATACCGGAA	CCAGCTGATTCAGTTAATATA	CAGGTTTGAATCAGTCACCTA	CAGCTGGTTATTGGAGTAAGA
8073	PTP4A2	NM_003479	AGGGACTGTGTTGCTTGTGAA	ATGCAACAATAGATTCCATTA	CAGAGAATGCTGGTAGCTTAA	AACAGCATACCTGCTAAGCTA
8085	MLL2	NM_003482	CTCGGAGTGGTTTGAGAACTA	CCCGTTGAGTCCCATAGGGAA	CGGCCGGAGTTTGTAATCAAA	CACCAGCATGTCTAAGGCATA
8111	GPR68	NM_003485	TAGAGCTTGAACCACCTTCTA	CAGGATGGCGGTGGAGAGACA	CCGCGTGTGCTTTGAGCACTA	CAGCGTGGTCATCTGGGCCAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
8131	C16orf35	NM_012075	CCCGGCGTCCCAGACAAGTAA	CAGACATGGGTTGATCACCTA		
8139	GAN	NM_022041	AACGTTGGCAATGAAAGATAT	CACCATAACATAGCTCCGAAA	ATCATGATGAATTGAAATGAA	CCGCACAGTCATGTAATTCAA
8153	ARHN	NM_005440	CAGGTTCCTCTTACTATGATA	CAGCTATTCTCACACATCTAA		
8175	SF3A2	NM_007165	CCCGGGCTACAAAGTGACCAA	CTGCCTGACACTTCACAACAA		
8178	ELL	NM_006532	CCGAAGTGCCATTGTCATCAA	AAGGAATTATGAAGCTAAGAA		
8190	MIA	NM_006533	CTCCTTGGGTTTATGCAAATA	CAGGGAGATTACTATGGAGAT		
8192	CLPP	NM_006012	CCGGGTGGCGTCATGCAGGTA	GCCCATCCACATGTACATCAA	CACGATGCAGTACATGCTCAA	GCCCAGGAGTTTGGCATCTTA
8200	GDF5	NM_000557	CACTATGGGACTGGATACAAA	CAGCTCCTTCCTGCTGAAGAA	CTGTTAGACTGTTAGATTTAA	TAGATTTAAATGTATATTGAT
8204	NRIP1	NM_003489	GCGGAGAAGAATGAGTATGAA	ATGGTTGACAGTGTCCGTAAA	AAGCGTGCTAACGATAAAGAA	AACCAACCCAATACTATATTA
8209	C21orf33	NM_004649	ACCACATTTATGGACCATGAA	CAGGAAGAAAGGGAAATTGCA		
8214	DGCR6	NM_005675	CAGAGAAATAAAGATGCCTCA	TGGCTTCTACGTGACCACCAA	CTGGCCAGAGTTCATCTTCTT	ACCCTAGGATAGTCTCATAAA
8237	USP11	NM_004651	CCCATTGAACGCAAGGTCATA	AAGGTCGAAGTGTACCCAGTA	ACCGATTCTATTGGCCTAGTA	CTGCGTCGGGTACGTGATGAA
8241	RBM10	NM_005676	CAGGACTATCGGACCGAGCAA	CCAGAAGGTGTCGATGCACTA	CTCCAACGTGCGCGTCATAAA	ACCACTCACTATCGACGGCAA
8243	SMC1L1	NM_006306	TCGGAAGTGAATGACAAGAAT	ATGGAGGAGATTCGTAAGAAA	CGGCGTATTGATGAAATCAAT	CACCATCACACTTTAATTCCA
8260	ARD1	NM_003491	CCGGGCCGCCCTGCACCTCTA	ACGAGCTTTCACAATAAATTT	CACAGAGAGCACAGATGTCAA	CCGCCCTGCACCTCTATTCCA
8266	UBL4	NM_014235	TCCCTTCTGTTCAGTAAACAA	CTGTTCAGTAAACAAACTGAA	CAGGGACACACTCGTGAGCAT	TAGGCTGTTTCTGATATCCAA
8270	DXS9879E	NM_006014	CTGGTTCTTAAATGTTTGTTA	CCGAATTTCCGTCATCAACTT		
8273	SLC10A3	NM_019848	CAGGGACAGCCCTGCCATCAA	ATCAAGAACGTGAGTGCTATA	GCGGAGAGACTTCTGCATCAA	CATGGTGTTAATGCAGGACAA
8284	SMCY	NM_004653	CTGACGATTGCTTAGCATTAA	CGCGTCCAAAGGCTAAATGAA	CCCAGAGACGTTGGATCTCAA	CAGGGTAGAAACGTTGAGAAT
8291	DYSF	NM_003494	CACCGTCAAGGTCATCGATAA	CCGGGATGAGCCCAACATGAA		
8292	COLQ	NM_005677	TCCAATGACTTTGGGAATTTA	AACAGCGTTCTTCCAATCTCA	AAGAAGCGTGGTGGCCACAAA	AAGGACAAATTCCTGCTACTA
8309	ACOX2	NM_003500	ATGGCATATATGCAACATTAA	CTGCCTATGAGGAATATATAA		
8312	AXIN1	NM_003502	CGGGAAAGGTGTTGGCATTAA	CTGGATACCTGCCGACCTTAA	CAGCATCGTTGTGGCGTACTA	CAGCTACAGATACTACTTCAA
8318	CDC45L	NM_003504	ACGGATCTCCTTTGAGTATGA	ATTGAAGAGTCTGCAAATAAA	TAGGCCAGTCAATGTCGTCAA	TACGAGCAGTATGAATATCAT
8322	FZD4	NM_012193	ATGGTGCTTAATGAATCTCCA	CTGGAGAGAGTTGCTATTCCA	TAGGTGATCGATACTTGTCAA	CAGAATGATAGTGCCTTTAAA
8339	HIST1H2BG	NM_003518	CTCCAAGTAAATGTGTGCTTA	GCCACTCAAGTCTCACATAAA		
8340	HIST1H2BL	NM_003519	TTGCCACTATTGTTTCATTAT	CAAGCTCTTGTCCAACCCAAA		
8341	HIST1H2BN	NM_003520	CAAGCCCATGGGCATCATGAA	TTCGGTCAGTCTCGGCCCACA		
8347	HIST1H2BC	NM_003526	TAACGACATATTTGAGCGCAT	CCAAGTAAACATTCCAAGTAA		
8356	HIST1H3J	NM_003535	CTGCTCTATCTTGGGTTTCTT	ATCCGTGGCGAGCGAGCATAA		
8370	HIST2H4	NM_003548	CCGCAAGGTCTTGAGAGACAA	GCGGATCTCTGGCCTCATTTA		
8379	MAD1L1	NM_003550	CAGCTGGACCTGCAACACAAA	CAGGACCAAAGTGCTGCACAT	CAGGCGACTGCTCATCTTCAA	CAGCGATTGTGAAGAACATGA
8382	NME5	NM_003551	GAGGAGATACAAGATATTATT	CTCGAAAGAACAAATCATGAA	CATGATATTAGCTAGACATAA	ATGATATTAGCTAGACATAAA
8392	OR3A3	NM_012373	CAGGTGTCTTCAGCTACATGA	TGGAATCTTCAGACAAGGATA	CTGGGTTCAGTGGAATCTTCA	CAGGGCGCTCTGTGTCAGCTA
8396	PIP5K2B	NM_003559	CACGCGTTTCCTCACCACCTA	CCCATTTGACACCCAGGTTAA	CCGCTTTAAGTTTAAGGAGTA	CACGCCATACGATACAAAGAA
8417	STX7	NM_003569	CAGCAGATTATCAGCGCAAAT	TTGCTGTAGATTGCCTAGTAA	CAGCAGTATACTAACCAGCTT	TCTGATGAAATTAGCGAATAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
8419	BFSP2	NM_003571	CAGGGTGTGAGCTGGAACAAA	CAGGCTGAGACAGAATCCTTA		
8425	LTBP4	NM_003573	AACCGGCTTTGAAAGAGTTAA	ACACGTGATCTCAGAGGCCAA	GCGGCTGGAGTGCATCGATAA	TACGAGTACGGCCCAGACTTA
8435	SOAT2	NM_003578	CAGGTTAGGTTCCTGATGAAA	CAGGTGGAATTATGTGGCCAA		
8438	RAD54L	NM_003579	CGCGCGCTTTGGGAACAGGAA	CTCGCTAAAGAAGCTTTGTAA	ATGGAGGATCTAAGGATGAAA	AAGCATTTATTCGAAGCATTT
8440	NCK2	NM_001004720	ATCTCACAATTATGTATTTAA	GACACTAATACAGATGATTAA	TAGCCGTTTGTTGACACTAAT	TCGGCTTGTTTGAATCTCACA
8446	DUSP11	NM_003584	ATGATGCAATTGAATTATTCA	CACAATAAGCCTGTTAAACAA	CCCTTATGTATTCAAGCTTAA	CAGAAACTGTTCCTTACTTAA
8448	DOC2A	NM_003586	CACGAGTGTGTTGCACGTTTA	GCGGAGTTCTATATTCACATA		
8456	FOXN1	NM_003593	TCCCGTCAGCGAGATCTACAA	CAGCGTTTGCCTGGTCTGGAA	CGGGCTCACCTTAAAGGTCAA	CACACAAATTATTCAGATGTA
8459	TPST2	NM_001008566	CAGATTTGCCATCCTCCTTAA	AAGCATATTGCTTGCTATTAA		
8460	TPST1	NM_003596	AAGATATGCCTTTAATATTTA	GAGGCTGGTGTTACTGATGAA		
8468	FKBP6	NM_003602	CAGGCTTTGATCATTGACCAA	CAGGTTTCTGTTCAAACCGAA		
8476	CDC42BPA	NM_003607	ACGGCTTTCATTACCAAATAA	TCGGAAAGATATACCCTGTAT	CAGATAATAGTCGGAAACAAA	CAGACTTTCCGTAGCAGCTTA
8481	OFD1	NM_003611	CCGCCCGGGCTGGGCACTAAA	CTCAGACAAGTTCGACATTTA	CCCAGTCTTTGGCAATAACAA	TACCATCGGAGAGTCATTAAA
8493	PPM1D	NM_003620	TACATGGAGGACGTTACTCAA	ATGGCCAAGGGTGAATTCTAA	CTCGGCGTCGTCGAAGATAAA	ACGGGTCTTCCTAGCACATCA
8498	RANBP3	NM_003624	AACGAACTATTTCCTCCAGTA	CAGAGTTAAGCTGATAAATGA		
8499	PPFIA2	NM_003625	ACCGATGAAACTAGTCAAATA	TCCAATGAACGCCTACAACTA	TACCAGCTGGATTTAGGTTAA	AACGTTTGGGTGACTCATGAA
8504	PEX3	NM_003630	GCGGGTCCAGTTAAACATAAT	CGAGACATTACCACTATTAAA	TGGGTAAATCACCTATACTTA	ATGGTGAATTCCAACAACTAT
8507	ENC1	NM_003633	AAAGGCATTGTCCAAAGTTTA	CACCTTAGTACTTTAGACTAA	CAGCGGCTCCATTAACATCTA	ACGGCATGTATCACAGATGTA
8511	MMP23A	NM_004659	CGGCCAGAAGATCCTCCACAA	CCAGAAGATCCTCCACAAGAA	CCGGGCGCTCATGCACCTGAA	CAGAAGATCCTCCACAAGAAA
8513	LIPF	NM_004190	CAGCTTTGATGAAATGGCTAA	CACAATCGACTTCATTGTAAA	CAGCAATGCCTTATTTATAAT	CAGGCTGTTAAGTCTGGGAAA
8517	IKBKG	NM_003639	GAGGAGCTTCTGCATTTCCAA	ACCATAAATAATGGCATAGTA	TTCGGAAATGCCTCACATATA	CTCCTCTAGTTCAGAGACATA
8518	IKBKAP	NM_003640	ACTGGATATTATAGAAACCAA	AGCATGGTAACTTATATTGAA	GCGGTTTACTATAGACAAATA	CAGCGGTTTACTATAGACAAA
8520	HAT1	NM_003642	CACGCTAGAAGGGTTTATGAA	AAGACTAATTAGCCCATATAA	CCCTTCTTAAACAGTATAATA	TACCGGCGTGTTATTGAACGA
8526	DGKE	NM_003647	ATCCATTAATCAGATGCGTAA	CTAGATCGATGGAAAGTTCAA	CTGGAAGTCGTTGGAGTATAT	ATCGATGGAAAGTTCAAGTAA
8532	CPZ	NM_003652	CGCGCAGAACCTGGATCTGAA	CCCGGAGACAAAGGCAATCAT	CCGGATCTCAGTCAAAGGCAT	TACGCCAAAGTCATCAAGAAA
8535	CBX4	NM_003655	CAGCCCGAGGTCATCCTGCTA	CTGCCTCACCGTTACTTTCAA	GAGGCTGGTCGCCCAAATATA	AAGCCCTTCTTTGGGAATATA
8536	CAMK1	NM_003656	CAGCCTGGATGAAGACTCCAA	CAGGAGATACAGCTCTAGATA	CTGCATGACCTGGGCATTGTA	CAGGTGCTGGATGCTGTGAAA
8539	API5	NM_006595	CTCGAGTGGCAGATATACTAA	CCGACCTAGAACAGACCTTCA	CAAGTTTGCTATTCAAATCAA	AAGAGTAATGGTCAATCTTAA
8541	PPFIA3	NM_003660	CTGGTGGACGCTCGAATGTTA	TCGAATGTTAGATCACCTTAA	CACGGGTAAAGAGAACTGTTT	ACGGCTCAACTATGACCGGAA
8542	APOL1	NM_003661	CTGGACAACCTTGCAAGACAA	CAGGTGGAGAGGGTTAATGAA		
8543	LMO4	NM_006769	ATGGTGTATTTAAATAATAAA	ATGACTGAATATGAACATTAA		
8555	CDC14B	NM_003671	CCAAATAATGTCGGCTTACAA	CAGAATTGATGTGCTGCTAAA	CCGTACAGTGATGATGACGAA	CAAGATCAGCAAGAACCCGAA
8559	PRPF18	NM_003675	AACGGATATTATTAAATTCAT	CAGAATGATCTGAAAGTTCAT		
8564	KMO	NM_003679	TAGTGTTCTGCTTATAATTAA	CAGAGTTACCCTCTAAAGATA	AAGGCTATTAATATCATACTA	TGGGTACAACATCGAATAATA
8566	PDXK	NM_003681	CCCTGTATTAAGCAAGAATTA	CCCGGGCATGTTCGTCTCTCA	TCGAGTGACTTTCTAACCCAA	CCGGAGCTTCATCTAGTGATT
8567	MAD	NM_003682	CCAGGAAATGATCGACAGGTA	CTCAACAAGTTCTATACTAAA	CAGGAGGGCGTTAGTGGATCA	CAGACCCACTACTATAGTAAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
8568	D21S2056E	NM_003683	CAGGGAATTCAGCTCCAGTAA	TCCGAGCAGTGTGGTGGTTTA		
8600	TNFSF11	NM_003701	ATCCATGCTCTTGACCTTGTA	CAGCGTCGCCCTGTTCTTCTA	CAGATGGATCCTAATAGAATA	ACGGGTTGACCTTATGAGAAA
8601	RGS20	NM_003702	TAGCATGTTGTCAGTGGCCAA	TCGGTTTGAATACGTCACTTA	CACATATTCGATGATGCTCAA	CTGCTATATATTCACCATGTA
8612	PPAP2C	NM_177543	CATGGTGTTCTTGGCGCTGTA	ACCCGCGTGTCTGATTACAAA	TCGCTCGGACTTCAACAACTA	CCGGGTCAACTGCTCGGTCTA
8620	NPFF	NM_003717	TTGGGAAGAAGTGACATGTCA	TCCGCGGAGGAAGACAGCGAA	CCCAGAGGTTTGGCAGAAATA	CAGGGATCCTGGAGGAATGAA
8635	RNASET2	NM_003730	CCGGATTACTGGACAATACAT	CAGGATGAGGAAGTACAGACA		
8638	OASL	NM_003733	GCGGGTGCTGAAGGTAGTCAA	CAAGTACTACACACTCCACAA	CAGGTGCTCCTTAGCCAAATA	CAGCTGGAATTCCAAGGCCAA
8642	DCHS1	NM_003737	CACGGTATTGCTACCACCAAA	CTGGTGTTGCTTGAACCTCTA		
8644	AKR1C3	NM_003739	TAGAATGTCATCCGTATTTCA	CCGGAGTAAATTGCTAGATTT	CTGGGATCTCAACGAGACAAA	CACCCTAATTATCCATATTCA
8649	MAP2K1IP1	NM_021970	AAGAGCTAGCATATAGATGTA	TTGCATTGAGTGAGGAACATA	TAGCATATAGATGTAATTTAT	ATGCCCAGGCTTGCAGAATAA
8651	SOCS1	NM_003745	CTGTAGGATGGTAGCACACAA	TAGGATGGTAGCACACAACCA	CCCGCCGTGCACGCAGCATTA	CTGGTTGTTGTAGCAGCTTAA
8654	PDE5A	NM_001083	TCGGTTCAATGCAGAAGTTGA	AACAACAATCATTAGAAGTAA	TCGGATGTTTACTGACCTCAA	CAGAGATGGTGTGTTCTGCAA
8659	ALDH4A1	NM_003748	CCGGAAAGAGTGGGACCTGAA	CAGGGTAAGACCGTGATCCAA	CAACTTCTACATCAACGACAA	CAGGGTAAAGTGTAACTCAGA
8661	EIF3S10	NM_003750	GAGGATCTAGATAATATTCAA	CAGGAACATGAACAAATCAAA		
8663	EIF3S8	NM_003752	ACCGTGATTTCGAGTCCCATA	GGGCGTCATTGTCAAGATCAA	AACGAATGGATGAAGAATTTA	CCGCCGACGCATGATCAGCAA
8664	EIF3S7	NM_003753	TCGGAACATGTTGCAGTTCAA	CCGCCAAGTTTCAGTGATGAA		
8665	EIF3S5	NM_003754	CGGAGTTGACCTGATCATGAA	CACAATGAGTCAGAAGATGAA	CCGCATGAGCATCAAAGCCTA	TACGCGTACTACGACACTGAA
8666	EIF3S4	NM_003755	CACGCAGAACAAGACAGGGAA	GAGGTCATCAACGGAAACATA		
8668	EIF3S2	NM_003757	CAGATTAAGTATAACCGCGAA	AAGAAATAAATTGGTTTGGTA		
8673	VAMP8	NM_003761	CTGGTGCCTTCTCTTAAGTAA	AAGACCTTTCAGTATCCCTAA		
8675	STX16	NM_001001433	CTGGGATCAGTTATAATATAT	TCCAACGTAATTGGTCAGATA	ACCATCATTGATGTTAATTAA	CCGGATTAAGCAGAAGATGAA
8685	MARCO	NM_006770	CAGGACTTTGGCCATCTATAA	CCCAGGGATGTTCAGAATCAA	CAGGATTGTCGGCAGTAGTAA	CTGAAGTTTACTACAGTGGTA
8688	KRTHA7	NM_003770	CTGCATTAAATGGTCAATAAA	CCAGTGTTTCAGAATCTCCAA		
8692	HYAL2	NM_003773	TCCCTTGCCCTAGATAGTTTA	AAGGGCTCTCTTAGGCATGTA	CTGCCAGTACCTCAAAGATTA	AAAGATGTGTATCGCCGGTTA
8697	CDC23	NM_004661	CTGCAATAGCAAGAAAGCCTA	TAGGGACAGCTTGTATAATTA	TACGAGAAACTCAATCAACTA	ACCCATCTTAATTAAGCCTTA
8698	EDG6	NM_003775	TTGAAGTTCGATCATGGTAAA	CCGGCTCATTGTTCTGCACTA	CCGGAGCTTCCACCACCGACA	CAGCCGGCTCATTGTTCTGCA
8701	DNAH11	NM_003777	CACCGTCAAATGAAAGGATAA	CAGGTGGCTGTTAACATCTTA	GAGCTTGTTAACCATAATTAA	TACGTTGTACACGCTTTGCAA
8702	B4GALT4	NM_003778	CACAGTGAACTTGGGAATGAA	TACATATTAACTAATAATAAA		
8704	B4GALT2	NM_001005417	CCCATGGATGACCGCAACCTA	CAGAGGTTTACCAAGATTCAA		
8707	B3GALT2	NM_003783	ATGGAAGTATTTACAATGAAA	AACCGTGGATTTCATATTATA		
8708	B3GALT1	NM_020981	CAGAGTTAAGAGGAAGATTTA	CACACTGGATGTGATTATTAA		
8711	TNK1	NM_003985	AAAGAGCTACTATACATCATA	CCCTATTACATACATCTTTCA	ATCGGTCATGATGAACTTGGA	AAGGATCTAGTCTGCCCACTA
8717	TRADD	NM_003789	CAGGGTCAGCCTGTAGTGAAT	CCGAATGTTAAGCAATGATAA	CCCGAATGTTAAGCAATGATA	AGCAATGATAATAAAGTATAA
8718	TNFRSF25	NM_003790	GAGAACCACCATAATTCTGAA	CACAAGAAGATTGGTCTGTTT	CACCGTCCAGTTGGTGGGTAA	CGCGGTATTAAATCTGTGAAA
8720	MBTPS1	NM_003791	CACAGGAAGAATTGTAGATAA	CAGAACGGAGACAACATTGAA	CAGAACAGACTTCAACAGTAA	CAGGGATAATTTAAGGATGAA
8721	EDF1	NM_003792	CGGACGGGCCATACCCAATAA	CTAGGGCGAAATGAACACAAA	CAGAAGGACCTGGCCACGAAA	CACGGTGACGGTGCTGCGCAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
8722	CTSF	NM_003793	CCTGTCCGTCTTTGTCAATAA	CGGACATATGAGTCAAAGGAA	CACCTTTGTTGAATTGTGGTA	CCCAATCTCCGTGGCCATCAA
8723	SNX4	NM_003794	AACATTATGCAGATCAGTTAA	TACCTAGTATACATAAACATA	CCCATCCTTTGTAGAGACAAA	CTCGTTATTTCTAATGATGTA
8724	SNX3	NM_003795	ACCCTTCACATGGAAGATTAA	CAAGATGAAATAATAGATAAA		
8725	C19orf2	NM_003796	AAAGAGGGTTTCAAAGTTTAA	CTGGAAAGAATACCACTTTAA		
8726	EED	NM_003797	AAGGAATCTTATGATTATAAT	AAGCAACAGAGTTACCTTGTA	AGGCATAATTAGGATAATAAA	CTGAACGCCCTGATACACCTA
8727	CTNNAL1	NM_003798	CTGCAGAGGGTTTAAAGCTTA	CGGATGGGTCTCAGTTACAAA	ACGCTTATTAATCATAAAGAT	AAGCTTGGGAATCCCAAATTA
8729	GBF1	NM_004193	AAGAATATTTACATCATTCAA	ACGGGAACTAATTGAAATTAA		
8731	RNMT	NM_003799	CTGGTCTTAATTAACAGGTAA	CAGGGTGACTCTCCAAAGAAA		
8736	MYOM1	NM_003803	CACCAACTAATGACACTTTAA	CAGGTCTTTCACTCATATAAA		
8739	HRK	NM_003806	AGCGAGCAACAGGTTGGTGAA	ATACAGCTCTATATATATAAA	CGAGAAGGAAGTGGAGAGTAA	AGCGATCGTAGAAACACAGAA
8747	ADAM21	NM_003813	TACCACAAACATTGTCATTAA	CAGGAATATGTCGTCCACCTA		
8767	RIPK2	NM_003821	CAGGGACTTGATCATGAAAGA	CCAGGCTTAATTGCCCTACAA	CACAAGGACATCGACCTGTTA	ACGTATGATCTCTCTAATAGA
8772	FADD	NM_003824	TCCTAAGGTAATCCTATTAAA	CAGGACGAATTGAGATAATAT	CAGCGGGATCTCGTATCTTTA	AGCGGGATCTCGTATCTTTAA
8773	SNAP23	NM_003825	AAGAGGTTGTTACCTCAGTAA	TACCACATGAATTCAGATTTA	CAGGCCTATTAACATCATACA	CTGGCAAGGCTTATAAGACAA
8775	NAPA	NM_003827	CCGGGAATGCAAGTTGATGAA	CACCGAGTCGGTGAAGGAATA		
8778	SIGLEC5	NM_003830	TTGTGGCAATGTTAACATTAA	CTCGGAGATCAAGACAAGCAA	AAAGGTTGTTGTGAACATTAA	CAGGAACGGCATAGCCCTAGA
8784	TNFRSF18	NM_004195	CAGCAGAAGTGGGTGCAGGAA	CCCTGGGAAGAAGACCCACAA	TCGGGATTCTCAGGTCATGAA	CAGGAGGGAGAGAGAGACACA
8787	RGS9	NM_003835	AAGCTATTGACCCTCAGGAAA	AACGATGGGCCTTCAACTTCA	CAAATAGGTGTTTGAACTGTA	CTGACACCAGTTTCAAATTTA
8792	TNFRSF11A	NM_003839	CCCAGTGTGTGTTCATTGTAA	TAAGTTTGTGTCGTTCCTTAA	CCCGCTAGGTGGTTAATTTAT	ACCCGCTAGGTGGTTAATTTA
8797	TNFRSF10A	NM_003844	CAGGAACTTTCCGGAATGACA	CAGGCAATGGACATAATATAT	CCGGGTCCACAAGACCTTCAA	ATCAAACTTCATGATCAATCA
8798	DYRK4	NM_003845	ACACGGCTCCTGAGAAATTTA	CAGATGCTTTCGGTAGAGAAA	CTGCATCACGGCGGAGTTGTA	CTCCATATGAACAAAGTGAAA
8802	SUCLG1	NM_003849	CAACATCTCTATGTTGATAAA	ATGGATCACGTAGACATGTAA		
8807	IL18RAP	NM_003853	AGCGGTAACCTGGTACAAGAA	ATCGTAGTGGATGAAGTTTAT	CCCAGTATCTTTGAACTACAA	CCCAGCCTAAGGAATGGTGAA
8808	IL1RL2	NM_003854	CAGGAGTCTACCAATGTGTTA	TAGGTGGTTTACCAAATTTAT	TGGGTCCAATAAAGTGGTATA	AAGGACTGTAACGAGATTAAA
8809	IL18R1	NM_003855	CGAGAAGAGATGAAACATTAA	CCGAGTCTTAATCTTCAGAAA	AAGAGTGAGATTGTCAGTGTA	TTGCTATTGCATAGTCTCTAA
8811	GALR2	NM_003857	CTGCACCTTCGTCTTCAGCTA	GACGGTTGATGTGGCCTGAAA	TACCAACCTGTTCATCCTTAA	CCCGCTCACGCGCGCCACTTA
8812	CCNK	NM_003858	CAGCCATATTGGCTCAATAAA	CTCAATAAATAGCTTCGGTAA	ATCCTGGATCTTTACTCACAA	AAGCAACTCAAAGGTGATAAA
8816	WDR22	NM_003861	CTGGTTAACTTGAGAAGCCAA	TAGAATTACTTTGGATTTGTA		
8818	DPM2	NM_003863	TAGCCTGATCATCTTCACCTA	CAGCATGTCATCCACAAGTAT		
8821	INPP4B	NM_003866	CTCCATAGATTTGAAACAGAA	ATCGATGTCAGTGACACTTGA	CCCGGAAAGTGTGAGCGGAAA	AACGATTTGCCGCAAACTGAA
8822	FGF17	NM_003867	CTGGAGGTGGCTGTCCTCAAA	CTGCTGATTCTCTGCTGTCAA		
8828	NRP2	NM_003872	CGCAAGTACTGTGGACAAGAA	CTGGTCTGTCATAAGACAGAA	CTCGTGATATTTGTAGGATAA	CAGGCTCTGAAGATTGCTCAA
8831	SYNGAP1	NM_006772	CAGAGCAGTGGTACCCTGTAA	ACGAACGAAGTCACAACCCAA	CCCGGCTGATGCAAAGCTTTA	ACGCTTGCCACTAAAGCCATA
8832	CD84	NM_003874	CTGGGACTTCAAGCTATGAAA	ACCCACAGAAATTATTATGAA	CTCAGAAATCTTCACAGTGAA	CAGAATGTGGGCTGCATATAA
8836	GGH	NM_003878	ATGCCGTAATAAAGTCATGAA	AAGCATTGATTTATCAGTTCA	TCAGTCCAATTTATACTGGAA	CTGGCTCTGATTCTTCATTAT
8848	TGFBI4	NM_006022	AACTTTCAATAAAGCATATAA	CTCACTTTGTGTAATCTGAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
8851	CDK5R1	NM_003885	CACATGCACTACTGAAATTTA	CTGGTCATCAGTATTGTGTAA	TGAGCTGGTTTGACTCATTAA	CCGGAAGGCCACGCTGTTTGA
8852	AKAP4	NM_003886	CTGCCTTATCATGGCTAAGTA	CAAGACTCTCTTGGACATGAA	TACAGTGTCTATGCCGATCAA	GTCGGTGAACACATTCTCAAA
8875	VNN2	NM_004665	TGGGCGTTTGGTAAACAAGAA	ATGGCTACTTTCAATACAATA	AGGAGCTTTGCTGTCATTTAA	CAGCAATAACTTACCTGCTAA
8881	CDC16	NM_003903	AAAGAACTTCTTGAATCACTA	TAGAATATGGTTTGACCAATA	CCCATGCACTTCGGTCACGAA	ATAGTGGAATAAAGAAGGTAA
8882	ZNF259	NM_003904	GAGGAAGATCTCAGAAATGAA	CTGGAGGACATGAACAGAGAA		
8883	APPBP1	NM_003905	CAGGTATTGGTTCGTTTACAA	ATGGATTGTGATCATAGCTAA		
8888	MCM3AP	NM_003906	CAGGAGCATTTACGGATTTAA	CTGAGTGAAGATGGTCAGATA		
8893	EIF2B5	NM_003907	CTTGTATATGTTAATATTAAA	CAAAGTGAAGATGAAAGGTTA		
8896	G10	NM_003910	ATGAGAGAAGCTGAAACAGAA	CAGCAGAGAACTCTATGAATA		
8900	CCNA1	NM_003914	CAAGCAAGGGTTTGACATCTA	AAGCAATTAGGGAGAAGTACA	TTCGAAATATGAAGAGATATA	CACCGATGATACATACACAAA
8905	AP1S2	NM_003916	ATGGCATTAGATGGCTCTATA	ATGGCACATCATATACATGTA	AAGGGAACTTTAGTTAATTAA	CAGGCAGTATACATTTATTAA
8906	AP1G2	NM_003917	CCGCCAGGTGGTGTCCATCTA	CCCACAAATAAAGCCCAATAA		
8910	SGCE	NM_003919	CAGGTAAATGGTATCCCTGAA	TAACATTTAATACAAATTTAA		
8914	TIMELESS	NM_003920	CCGGCTCATGGGATCAGTAAA	CAGCCGCATCATCAAGAACAA		
8926	SNURF	NM_005678	GAGGTGGAAGTCCAAGTCAAA	CAAGAGGTGGTTAAAGCCATA		
8932	MBD2	NM_003927	ACCCTTCAGGTGTTACTAGAA	CTCGCGAGTGTAAGTTTCATA	TGGAAAGATGATGCCTAGTAA	AAGATGATGCCTAGTAAATTA
8936	WASF1	NM_003931	TACACTCAGAAAGTACATTTA	TTGCTTGCCTATAGGAGTTAA	GCCCTATAACCGATTAATTAA	CAAGAACGTGTGGACCGTTTA
8938	BAIAP3	NM_003933	CTCGCCTGACTCCATCCAGAA	CAGCCAGAGGACCCAGGTGAA	GTCGACCTTGCTGGACATTAA	TGGGATCATGACGACGATGTA
8940	TOP3B	NM_003935	CACGGAGAAGAAAGAAGCTAA	CACGGACACAGACATCTGTAA		
8942	KYNU	NM_003937	CCACATGTAACTAACAATAAA	CAGATTTAAGATGGATAACAA		
8945	BTRC	NM_003939	CTGGTTTCAGGTGGAACTTAA	CTGGAGGCAGATGACATCTAA	CTGGGCTAGAATAAATGTAAA	CAGGATGAGCAACAACAGTAA
8972	MGAM	NM_004668	TCGGCATGATATGAATTGGAA	CTGGCCCATATTTAACAGAGA	CCCAATGGAAACGGAACTAAT	TGGGAGGAATAATATACCTAA
8976	WASL	NM_003941	ATGCTACATATGAATGTTGAA	CACATTGAGTAATATGCATAA	CAGATACGACAGGGTATCCAA	AACCTTAATGTAATTTACTTA
8986	RPS6KA4	NM_003942	CGGCCAGGAGTTCGCAGTCAA	AAGGAGATAGGTGGCTCCTAA	CGCCACCTTCATGGCATTCAA	CAGGCTGTGCCTTTGACTTTA
8989	TRPA1	NM_007332	CAGTAGACAGTTGCACATTAA	CCACGAATTCATATCTAATAA	CACGAATTCATATCTAATAAA	CTGGTTCTAACTTTCAATTTA
8992	ATP6V0E	NM_003945	AACGTTAACAGCACATTTGAA	AACCCTCTCTTTGGACCGCAA		
8993	PGLYRP1	NM_005091	CTGGTGCGACGTGGGCTACAA	CAGCTTCATGGGCAACTACAT	TGGCATCAGCTTCATGGGCAA	GAGGTCCAACTATGTGCTCAA
8996	NOL3	NM_003946	CCCAGTACCGCTGGAAGTGAA	ACCCTGGAGATCCCAAACCTA		
8999	CDKL2	NM_003948	TGCGAGAAATCAAGTTACTAA	TCAGGCATTTATAACATTAAT	TTCTACGGACTTTAAATTAAA	ATGATGTGTTTAGGTAATCTA
9002	F2RL3	NM_003950	CAGGCTGGTGCCCGCCCTCTA	ACGCGTGAAACACAGAAGAAA	CACATTCACGATACTGTGCAA	AAGGCTGTACTGGGTCGAACA
9015	TAF1A	NM_005681	AAGCAAGATCACCAAATCTTA	CCGGATGCACTAAGAATATAA		
9019	MPZL1	NM_024569	CTGGTTGCAGATAACGAACTA	CCAGTCATATATGCACAGTTA	CACCTTCTTTATAAAGCGTCA	AAGGCATTACTTAGAGATTGA
9025	RNF8	NM_003958	CAGCCTGTGATAGGCATTCAA	ATGGACAATTATGGACAACAA		
9026	HIP1R	NM_003959	CTCCGACATGCTGTACTTCAA	AAGTGTTCTGTTGGCAATAAA		
9028	RHBDL1	NM_003961	CCGCTGGTACTTCTACCGTCA	TGGGATGAGATGTCCCTACAA		
9038	PNP	NM_003967	CAGGCTCAGCAGATTACCACA	CCCACTGGTCTTTGACATCTT	CTGCCTCATTATGATCAGCTT	CACCATAGACACGATGGTCGA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
9045	RPL14	NM_003973	CAGATTGATAGTAGGATTATA	CACCAGAAGTATGTCCGACAA		
9046	DOK2	NM_201349	TGGGTGAGTCACCATCCCAAA	GACAATGTTGTACTAAAGAAA	CAGCAGACGTTTGGAAAGAAA	CAGATTTCTTGGTGGCATTAA
9048	ARTN	NM_057090	CTGGTGTTGATAGAGATGGAA	CCGGTGGGTGATGGATATCAT	CCCGAACAGGTGAAGGGACAA	CAGCATTTGAAGGACACATAT
9050	PSTPIP2	NM_024430	ACGAATAAACTTCTTCCGGAA	CTCAGTGGTGCAAGATTTAAA	CCGGCTAGTGCTTCTGTGATA	CCACGTTATGTCAGCAATGAA
9053	MAP7	NM_003980	AAGCTGTTGTACGGCGCACAA	AAGGGCTGTATCTCCATCTAA	GTGCTCCTTCTTAGCAATCAA	CAGGCATATGGTCTTTAGTAA
9056	SLC7A7	NM_003982	CCCTTCTTGCTTAAATCCATA	ATCAGATATTTGGAATATTTA	TAGAGAGACATGAAACTATCA	CAGGTGCTGGATGACAATAAA
9064	MAP3K6	NM_004672	CAGGAACTGAATGTGGATTCA	TACCAGACAAAGCGTATTAAA	TCAGAGGAGCTGAGTAATGAA	CACCATCCAAATGCTGTTGAA
9068	ANGPTL1	NM_004673	GAGGCGGGTCATACTCCTTAA	CAGAAAGTTTGGACAGCTTTA	CTCGTGTTACTCAACTCTATA	CGGGAGATAGATGTTCTGCAA
9075	CLDN2	NM_020384	AAGGCTAAGGGCTATAGACAA	CCAGACTAATTTGTGCATGAA		
9081	PRY	NM_004676	AAGGACTCAGAGAGACATGAA	AAGAAGGATCTTAAAGACTCA		
9086	EIF1AY	NM_004681	TTGGCTTTCATGAACAAGTAA	ACCATAATATTTGCTGTTAAA		
9088	PKMYT1	NM_004203	CTCCTACGGAGAGGTCTTCAA	CTGCCTGGCCGTGTCTAATAA	CTGGGAGGAACTTACCGTCTA	CCGGCCAGAGTCCTTCTTCCA
9091	PIGQ	NM_004204	ACGCTGCTGTGTGCTCCTGAA	CAGGTGTTGCTGTCACAGCTA		
9092	SART1	NM_005146	CTCAACCTTCATATTAAATAA	CCCGTGTACAGTGACCCAGAA		
9096	TBX18	XM_496819	TCGCCTGAAGATAGATAGGAA	CAGCAATGCCTTCGCCACTAA		
9101	USP8	NM_005154	CACGGAAAGAAGCACTTGTAA	AAGGCTCGTATTCATGCAGAA	CAGGTTCAGGCAAGCCATTTA	CAGGGTCAATTCAAATCTACA
9110	MTMR4	NM_004687	CCGGCTGCATATCAAATTCAA	AAGAGTGGCTCTCACGGCTAA	TTGCCATAGATGTAACCTAAA	TCGGCACTGGAGAGTACCAAA
9114	ATP6V0D1	NM_004691	CACTTTCATGTTCCTCCCTAA	CCGCGCCTTCATCATCACCAT		
9118	INA	NM_032727	CAGCTAAATAATCTTACTCTA	CAGGCTATTCCTGAACTATAA		
9126	CSPG6	NM_005445	AACCGGTTACCAATCGATAAA	TACCCAGGAACTGTAAATTTA	GAGGACTAAGTTGGAGCTTAA	ATGGAGGATATCGAACGCCAA
9132	KCNQ4	NM_004700	GACGATTACATTGACAACCAT	CTGGTACTACTATGACAGTAT	CGGGCATCTCTGAGACTCAAA	CCGCTCCATCAGGATTCTCAA
9136	RNU3IP2	NM_004704	CTGGAGGAAACTGCACAGGAA	CACTCTTATCCTCCTTATTTA		
9138	ARHGEF1	NM_004706	CAGCAGCTCTGAGAAGGGCAA	TCGGAAAGTGCTGTCCCTGAA		
9140	APG12L	NM_004707	ATGGTATGTAGTAGAAATTCAA	CAGCTTCGATTTGAATGACTA		
9141	PDCD5	NM_004708	CAGAACAAGGTTTAATAGAAA	CAAGTCTAGGACAGAAGTTAA		
9146	HGS	NM_004712	TACGAGCAGCTGAACAGGAAA	CACGTCCGGAGTAACACTACA	GCACGTCTTTCCAGAATTCAA	CCGGAACGAGCCCAAGTACAA
9149	DYRK1B	NM_004714	ACGGAGATGAAGTACTATATA	CTCGCTGAACCTGACCCGGAA	CCGGACCTACCGCTACAGCAA	CACGGAGATGAAGTACTATAT
9150	CTDP1	NM_004715	CCGAATATTATCAAGGGATGA	CCCGACAAACTTCCCGATAGA	CTGCATGGTTTGCATTATTGA	CCGGCTGTACGCACACACCAT
9156	EXO1	NM_003686	GAACGAGTGATTAGTACTAAA	AGGGTTAAATCTCCCAAGGAA	CAGATGTAGCACGTAATTCAA	ATGGATGTACTTTACCTTCTA
9159	PCSK7	NM_004716	CAAGCGCAGCGTCCACTTCAA	TAGCTATGACCTCAACTCTAA	ATGCCTTTCTATGCAGAAGAA	TCGGAGCATTGTGACCACTGA
9169	SFRS2IP	NM_004719	CACGAGGAAATGATCGGTACA	ATGGTTCTCAGCTACCTATAA	CTGGACAGGATTCTAGCCTAA	AAGGAGGTGATCCATTGGAAA
9170	EDG4	NM_004720	CTACCTGAGTCTGATTCTTTA	AAACCTTTCTTTACACTCTAA	GACCATCGGCTTCTTCTATAA	CCCGCGAGTCTGTCCACTATA
9181	ARHGEF2	NM_004723	CTGCAATGTGACTATCCACAA	CCGGCGGGACCGAGTGCTTTA	CAGCGATTGGTCAATCTCTAT	CAGCACCCTACTGCCCTTTAA
9183	ZW10	NM_004724	CTCGCCTATCAGACTTTACTA	GCCAGTGAATATATATTGCAA	TACCACGAAGTGATGAATTTA	ACCGGTGAATTTACAGACTTA
9187	SLC24A1	NM_004727	CACTGACTTACTACACCTCAA	CAGTGACATTACAGCAACCTA	CACAATGGGCATGGATCAGAA	ACTGCAGATTATGATGGTAAA
9196	KCNAB3	NM_004732	AACCCTAGGGAACATCCTCAA	AGGGAACATCCTCAAGAGCAA	CCGAGCGAGGTTTAAGCCGAA	TCGAGTAGTGATACGCATGAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
9200	PTPLA	NM_014241	AAGTGAGTTCAAGAATCTTTA	CTGGTGAACTTCTTACAATAT	CACTGTTTAATTGGAATTGTA	ACCACTTGCCATACTTCATTA
9201	DCAMKL1	NM_004734	CACCTTTAGGTTACCTATATA	CAGTGGAATGTGACCAGTCAA	CCGGAAGTGATAACACGCAAA	CAGGTTTATAACTTCGACACA
9211	LGI1	NM_005097	GCCGTGTGTACTTGTACCAAA	TCCCAGCGTCCTGTAATTTAT	AAGCAACACAATTATTCACTA	AAGATTCATTGGTGATTCCAA
9214	TOSO	NM_005449	TACCGTGGTATCCACCACCAA	CAGGTAAGCTGTAGGCATGTA	CCGAGTTACTCTGAAGCAATA	GAGGGTTGGGTCTTACACAAA
9215	LARGE	NM_004737	CACGGCCAAGAACCTACATTA	ACGGCCAAGAACCTACATTAA	AAGGGTTATCATCTTACTGCA	ACCAGCGAAAGCTGCATTTAA
9219	MTA2	NM_004739	TAGACGGATTGAGGAGCTCAA	ACGGCCTTATGCTCCTATCAA	CAGCCAAGCGTCAGAAACTAA	ACGCCAGTTCTCAGAAATAAA
9220	TIAF1	NM_004740	CAGATTCTTATGCACGCTTGA	CACGCTTGAGTCCGAGACTCA	TACCCGATGTATGGAAATAAA	AGGAGTGTCATTTGTCCCTAA
9228	DLGAP2	NM_004745	CAGGATGGAATTTCACAGGAA	CTCATTATTACTCAAAGTAAA		
9229	DLGAP1	NM_001003809	CACGAGGTAAAGATGATGAAA	CAGGAAGAAGGACCACTTTAA		
9244	CRLF1	NM_004750	CTGCTGGTCCAAGAACATGAA	CTCAAGGATTTCCTCTTTCAA	AACGCTGGATATCCTGGATGT	AACACCAACTACTCCCTCAAG
9247	GCM2	NM_004752	ATGGATTACCATTGTACTAAA	ACCCTGGTTATACAAATTCAA		
9256	BZRAP1	NM_004758	CCGCCGTCTGGTGGTCCTCAA	CAGGTCTTCCTAGCACGTTAT	CAGAGCTAAATGGCTCCTTAA	CACAGTGAGTATGTAACTTGA
9263	STK17A	NM_004760	TGCCTAAATACTAGTAACATA	TACTAGTAACATATCAGTGAA	TCCATTGTAACCGAAGAGTTA	AACCAGGATATTTAACAGGTA
9267	PSCD1	NM_004762	AAGGATGAGATAGCAGAAGTA	CAAGTTCTTGTTGGGCTTTAA		
9276	COPB2	NM_004766	CAGTACGTATTTGGCATTCAA	CCCAGTCAGGTTTCAAGGGTA	CAGGTTTCAAGGGTAGTGAAA	ACGATTCTTCAGAGTATGCAA
9278	ZNF297	NM_005453	CCCGCCCATTCTACTACTCAA	CAAGGTATTTCCAGAACTAAA		
9282	CRSP2	NM_004229	CGGGTTGGGACTTAACTTTAA	CGGGTGAAGTTTCGTGTTGAA	CACGTTTACCTGACATATGAA	CACGACAAGGTGAATGCACAA
9287	GPR58	NM_014626	CTGCCCAGTGATGTTCAACAA	CACCTTGTTTATGGCAGGTTT	CAGGATCCATATTCATCACAA	CACATGTAATCCGTTAATATA
9289	GPR56	NM_005682	AACCGACATGCTGGGAGATTA	CACCATCAAGGTGCACATGAA	TCGGCCGCCCATCATGGTTAA	GAGGGTCTGGCACATCCTTAA
9290	GPR55	NM_005683	CCGAGAGTTTGGACCCACATA	TTGATTAATCTGATTCGCCAA	CTGAGAGGACCTGATCATGTA	CCGGTTCTTGGCCATCCGTTA
9293	GPR52	NM_005684	CAGGAAGCACAAGAACCCAAA	AACGGGCTAATTCTTGCTCCA	CAGGTGTCCACGAGTCATTAA	AACCTGGCTTGCAGTAAGTAA
9294	EDG5	NM_004230	TCCAGGAACACTATAATTATA	AGGCGTGGCCTTCGTAGCCAA	CACCCTGAATTCCCTGCTCAA	ACCCACGTTTCTGGAGGGCAA
9296	ATP6V1F	NM_004231	CAGTGTCATTGTTGATGTTAA	CCGGCAATTTCTAAACCGGGA		
9311	ACCN3	NM_004769	CACCCGGATGGGAAAGTGCTA	TGGGAAAGTGCTACACATTTA	CTGGGCAGCCATCGAACCCAA	CCCAAATAAAGTCCTAATGCA
9312	KCNB2	NM_004770	CTGCGGCTTTGTCCAGTTCAA	CCCAATTATTGTGAACAATTT	CCCAGTTGACATAACTGTGAA	GCGGTTAATAATGCCTGTGAA
9319	TRIP13	NM_004237	ACCCAAATTGATCAGATTAAA	CAAGACTATTTAATGGATGTA	TTGACACAGAATTAAAGGTTA	GAGGATTCACATTAATATAAT
9322	TRIP10	NM_004240	TTGGAAGAACGCAGTCGTGAA	CACCATTGATGTACATACTCA	ACGGCTGAAATTGGAAGTGCA	ACGGCTAGACCAGGATATCAA
9329	GTF3C4	NM_012204	CAGGTCAAGCATAACAACGAA	CAGGTAGATTTAATAGACCTA		
9332	CD163	NM_004244	CCCGCCCAGAAGGAACTTGTA	CACATGGGAGATTGTCCTGTA	TCGCATTATTCTTCTTGACTA	CGCATTATTCTTCTTGACTAA
9333	TGM5	NM_004245	CAGGAGTATGTCATGAATGAT	CTGCCTGAAGCTGCTAGACAA	CTCCCAGTTCAAGGACCTCAA	CAGATCCAAGCTAATATGAGA
9337	CNOT8	NM_004779	ATGGCTTTCTTTAGGATGAAA	ATGCTTGTAAATACTATTTAT		
9343	U5-116KD	NM_004247	CTGATTGAAGGTGTTGATCAA	AACGCCTAATAAGAAGAACAA		
9349	RPL23	NM_000978	TGCGAAATTCCGGATTTCCTT	TTGCATGATTCTCCAGTATAT		
9356	SLC22A6	NM_004790	CACCAGAACCACATCATTAAA	CCGGAAGGTACTCATCTTGAA		
9360	PPIG	NM_004792	CAGGAAAGGAGTAGAAGTAAA	CTGGATAATTTGTACTGCTAA		
9361	PRSS15	NM_004793	CCCGCGCTTTATCAAGATTAT	CAGCCTTATGTCGGCGTCTTT	CCGGGACATCATTGCCTTGAA	TAGAAGCTATTTAATGATTAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
9364	RAB28	NM_004249	TTGGGAAACAGTACAAACAAA	ACCCTTCAAATTTGGGATATA	CAGGGCAGAAATAGTGAAGTA	CAGCGTATTGTCAGGGCAGAA
9368	SLC9A3R1	NM_004252	CAGGGCATCTGTTATCCTGAA	CAGAAGGAGAACAGTCGTGAA	CACCAGAAACGCAGCAGCAAA	AGCGAGGAGCTGAATTCCCAA
9369	NRXN3	NM_138970	CTGGAGGGTCATATATACAAT	CATGGCTTACTTGTTCCATAA	CAGGATTATAAAGAGATATCA	ACCAGTGTGCGTGTAACTTTA
9371	KIF3B	NM_004798	CAGAAATGCATGGGTAAGGTA	TTAGGGAAATAGCTTCTTTAA	CAGAGAATTCACCGAATCCTA	AACGCTAAGGTGGGTAGCCTA
9373	PLAA	NM_004253	TAGGTGTTGATTCTCAAATAA	AAGAGTGTGAACACAAATTTA		
9392	TGFBRAP1	NM_004257	CCGCCGATCGTCAAGAGGATA	CAGGTACATAGTAATCCAAGA	CACCCACTTAGCTGTGGTGTA	CACAGAGGTAGCAAATGGCTA
9394	HS6ST1	NM_004807	CCCGTACAACCTGGCCAACAA	CCGCGCGGCAGGACCATGGTT		
9404	LPXN	NM_004811	ATGGAAGAGTTAGATGCCTTA	CAGCTCGTGTATACTACCAAT	CTGCTTAATAGTCTTATAGAA	ATGACTAGGCTGATAATCTTA
9409	PEX16	NM_004813	CCGGACCATCCTGCTGCTCTA	CCGCGGAAGTTAAGCAACCAA		
9424	KCNK6	NM_004823	TCCGTCTGTGTCTCTCAATTA	CCGTCTGTGTCTCTCAATTAA	CTGGTTGAGCTCAAATCCCAA	ATCATCATAATACAACTTCAA
9427	ECEL1	NM_004826	CAGCATCCAGCTCTCAGTTAA	CCGGCTCAAGTACACACATGA	CAGGTGCTGACTGACAAGCAT	CTGCAAAGTCTGGTCAATAAA
9429	ABCG2	NM_004827	ACGGATTAACAGGGTCATTGA	ACCGAGCTCTATTAAGCTGAA	CTGGCGAAGAATATTTGGTAA	CTGGTCTAATTTATTAATCTA
9435	CHST2	NM_004267	ATCGTAGTGTGTTTAAATAAA	CCCTGTGGTGATACCTATAAA		
9436	NCR2	NM_004828	CAGGCTCTCAGGCACAATCCA	CAGGACATTACTGGTGTAGAA	CACGGGCAGTCTCTACGAGAA	ACACACTTTGTGAATAATAAA
9437	NCR1	NM_004829	TCGGTTCATCCTGGACCCGAA	CTGGATCTGGTGGTAACAGAA	ATGGTTGTATATTCCTAATAA	AAGCATGTTCTTACTGCTCAA
9440	CRSP6	NM_004268	TCAGTTCGTAATGGACCTGAA	GTCCAAATTCCTAGTGATTTA	CAGGTACATGCAGTTCAGCAA	CAGCCTACTCTAAATTATTGA
9443	CRSP9	NM_004270	TTGGAAAGTCAGGGCATCGAA	TAGCATCATATATTAGTTCAT	ATCAAGGAATATACGGATGAA	AGGCAGTAATTTCGCTGTATA
9446	GSTO1	NM_004832	GCCCTGCTTACTAGTGAGAAA	CAGGCATGAAGTCATCAATAT	CAGGAGTCAGCAATAAAGCTA	CAGCAATAAAGCTATGTCTGA
9448	MAP4K4	NM_004834	TCGGAGCTGCACCGAGGGCAA	CAGGACTTTAGTTAGAATTAA	AGGCAAGATCCTACCCGGAAA	AACCATTAATGTTTAATTTAA
9453	GGPS1	NM_004837	AGGGATGATTATGCTAATCTA	TACACTCGTAATACCCTTAAA		
9455	HOMER2	NM_004839	CGGAGCCAAGGTGATCATAAA	CAGCACAATCACACCGAATAT	CAGAACTAGGTCTACCTTCAA	ACCGAATATGACCTTCACCAA
9468	PCYT1B	NM_004845	AAGAGCCATGATCTAATTCAA	CACCATAATACTCCTCTGAAA		
9469	CHST3	NM_004273	CAGGTTGACTTAATTTATTTA	CAGCTGTATATTCTAGTCCAA		
9472	AKAP6	NM_004274	CTGCGGATGATTGCAAGTCAA	CCGGGAGACTTGCAATCTGAA	CACGTTTGTCACTGCCGTTTA	AAGCATGTGGATGTACATCTA
9479	MAPK8IP1	NM_005456	ATGCAGTTTATTGTAATATAT	CCGGCTCACCGTGCACTTTAA	TGGCATCAGCTTACAGTGCAA	CTGGAGGAGTTTGAGGATGAA
9493	KIF23	NM_004856	CAGAATAAACTCTGGGTTAAA	CACCTTTGCCGTCATGCGAAA	CAGAAGTTGAAGTGAAATCTA	AAGGCTGAAGATTATGAAGAA
9498	SLC4A8	NM_004858	TGGGAGCAGTACAATTCTCAA	AAGCATCATCATCAGAATGAA	AGCCGTCATTATTAACAGGAA	GACGGCTATCTTAAAGTTTAT
9508	ADAMTS3	NM_014243	CAGGAAGCTTGGGTACCTTAA	CCGCTCTAGCCTGACATATAA	AACAATGTGATACGTAAATTA	TAGGCAAATTCCAGATAGTAA
9509	ADAMTS2	NM_014244	GACAGGCAAGTTCATCTTAAA	CCGGGTCTCACTGACGTACAA	CCGCCGGAGGCTGGACCACAA	CAGGCGAATGGGAGCCATGTA
9510	ADAMTS1	NM_006988	CGGCAGTGGTCTAAAGCATTA	TAGGATAGTTAGTGAGGATTA	CTGAGCAGTGATATAGCATAA	CAGCAACGTGAAATAACGCAA
9516	LITAF	NM_004862	CAAGGTCGTAAATGCATGCTA	CTGGGCCTGAACATAATTTCA	TGCCAATGTAGTCTCACTTAA	GCCAATGTAGTCTCACTTAAA
9520	NPEPPS	NM_006310	CAGACCAATGGGTGAAGTTAA	CATGGTGATGGCACTACTTTA	GAGGGATTTGCAGTTGATAAA	CTGGGAATGGTTAAACACAAA
9522	SCAMP1	NM_004866	AACACTGTTGTTAACATCTAA	CACCACATTTCTTATATTAAA		
9524	GPSN2	NM_004868	GTGGATGGCCTATTACATCAA	CTGGATCGGTTTCGCCATCAT		
9542	NRG2	NM_013982	TTGTCTTATAATACTAGCTAA	AGGGAAACTATTTATATGTAA	CCGAGACATTCGCATCAAATA	ACCCGTGGTGGTGGAGGGCAA
9554	SEC22L1	NM_004892	TAGGACATTCTCAAATTTCAA	CCACAATTTGCTAACATTTAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
9555	H2AFY	NM_004893	CTGGCTGTGGCCAATGATGAA	AAGGCTTTGGTTTCCAGTTTA		
9559	VPS26	NM_004896	CTGCATAATGTTGATTATAAA	CACCAAGGAATTAGAATTGAA		
9562	MINPP1	NM_004897	ATGAAATTCTTCCTACTTATA	AAGTCGGAAAGTACAATGAAA	CCGAGTGCAGATGTTATTAAA	CACGGTCAAACAGATCCGCAA
9570	GOSR2	NM_004287	TTGGGAGTGATTGTGGTCTAA	CAGGACAAGTACTTTATGATA	CAGCATTCCCACAGCCTGCAA	AACGAAATCCAAGCAAGCATA
9575	CLOCK	NM_004898	AAGGAGCCATCTACCTATGAA	GACACGCATGATAGAAGCAAA	ATCGGCAACAAGAAGAACTAA	ATCCAGCAACTTGCACCTATA
9580	SOX13	NM_005686	AAGGAACTCTATGGAAGCCAA	CACCATCAAGTCAGAGGAGAA		
9586	CREB5	NM_004904	TAGCTTTAAATACATCATTAA	CAGCAATAAACTTACAAGTAA		
9589	WTAP	NM_004906	AAGGTTCGATTGAGTGAAACA	GGGCAAGTACACAGATCTTAA	CAGACTAAAGACAAACTGGAA	ATGCAAGAGTGTACTACTCAA
9598	CSAG2	NM_004909	CAGCTGTGTGGTCAAACAGTA	CTACCACAAGACTAACATAAA		
9605	C16orf7	NM_004913	CTGGGTGTATCTCAGAGATAA	CGCCGTGTATACTCCGATGAA		
9609	RAB36	NM_004914	AAGACAGTACAAAGCATATAA	GTGGCCATTCTTGTAGTTATA	CAGCTCAGCGATTGCCAAATA	AGGCACTGTGGTGATCCCATA
9611	NCOR1	NM_006311	CCCGGTGGTTTCCTAGAAACA	CCCGCTCACCAGGGAGTATAA	AGGCAATTCAGTGGACTATAA	ACCGCAGTATTGTCCAAATTA
9620	CELSR1	NM_014246	CACCATGATGGAGCTGGACTA	TGGCGTTTCCTAAGTACGAAA	CGGGATCCTGGATGTGATCAA	CGCCAACAGTGTGATTACCTA
9625	AATK	AB014541	CCGGTTCCGCTGAGATCAGAA	CTGACTCAGCTAGACCCGTAA	TCCGCTGAGATCAGAAGGCAA	CTCCAACGTGTCAGCCAACAA
9629	CLCA3	NM_004921	CAGAGTACTTTCGGTTCTGAA	CCCAGCGAAGAAATGGATAAA	GAGAGCTACATTATAAGAATA	TAGGCCCGAAATGACTAGCAA
9636	G1P2	NM_005101	CAGGATCAAGGGCCGGAAATA	CCGGAAATAAAGGCTGTTGTA	AAGCACCGTGTTCATGAATCT	AATGCGACGAACCTCTGAGCA
9638	FEZ1	NM_005103	CACAGATAAACTCATCCTGAA	ATGGAGGACCTCGTAAATGAA		
9640	ZNF592	NM_014630	TCAGACTATATTTCAAATAAA	CCCACTAAAGAGAGTTCTAAA		
9648	GCC2	NM_014635	ACGGGAAGACTTAGAGTTTAA	ATGGATAATTTCCATAAGAAA		
9673	KIAA0446	NM_014655	AGGGTGATGTGTGTATAATTA	CCCGTGGTGGGCACAGTTCTA	CAGCATGGAGGACAAACGCAA	CCGGAAGTTTGTAGCTGACTA
9674	KIAA0040	NM_014656	ACCCTGTGAATCATAATTTAA	CCGAGTGATCTTCTCTTCTAA		
9679	FAM53B	NM_014661	ATGGCGAGACCTGGACAGGAA	GACAAGAAGGTCGGTGTTAAA	CGGGAGATGCTTCCTTCTGTA	TACTTGTACTGTGTAAATAAA
9688	NUP93	NM_014669	TCGAAGTTTCCTGAACATTAA	AGGGATGAGAAAGATAGTCAA		
9706	ULK2	NM_014683	CAGCCTGAGATACGTGCCTTA	TAGGATAATCGGTACAGTTAT	ATCGGTACAGTTATTCTTAAA	ACCGGGAAGTTATCAGATCAA
9716	AQR	NM_014691	ACGATTGGAATTAGAATTAAA	CAGGATGGATTTAGCCGACTA		
9717	KIAA0420	XM_032693	ACGGTCCACCCTGAGAATGAA	CAGGCGGAAGTTCCTCATCTA		
9719	ADAMTSL2	NM_014694	CCAGGAGTTCTTCTCGGCTAA	CACCCTCAATGAGACTGTGAA		
9720	KIAA0565	XM_113947	TAGTCTTGTAGTATGTTTGAA	TAGCGTTACAATAGAATAGTA		
9722	CAPON	NM_014697	ACGGTATGAGTTTAAAGCCAA	CAGCAATATCTTCAGGTGTAA		
9726	ZNF646	NM_014699	AACAATTTATTTAAGTTTAAA	CGGGAGCTAGAAGACAATGAA		
9727	RAB11FIP3	NM_014700	CACATGAAATATATATATATA	CCCGTCCATCCTGGAGGTCAA		
9728	KIAA0256	NM_014701	AAGGATGAGAATATTCAACAA	CCACATAAGTTTATAATTTAA		
9730	VprBP	NM_014703	CAGAGTGAACTCAACAACCAA	CAGGGTGTTACTCCTCACCAA		
9733	SART3	NM_014706	CAGCAGCTGGAGAAATATAAA	ATGGAGTTGATCATCAAGTAA		
9735	KNTC1	NM_014708	CAGCACATTAAAGCTCACGAA	CAGGCAGTATATCCAGTTAGA	TGCTCTTAATTTCGAAATTAA	TCCCGTGGATCTAGAATATCA
9737	GPRASP1	NM_014710	TGGGTCTATAGATGTAATTAA	GGGTCTATAGATGTAATTAAA	CTAGCAGTAAATCCAGACCAA	ACGCCCTAAGAGTAAGGCCAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
9744	CENTB1	NM_014716	CACCGTGAGCCTGAACCACAA	ACGGGCCAGCAACGCATTTAA		
9746	CLSTN3	NM_014718	CCCAGTCAAGTTCCTCTGGAA	CAGGTGAAGCCCACCTGTAAA		
9748	SLK	NM_014720	GACCATTAACTGAGTCCCAAA	TCGAATGGCCATGTTTAAGAA	TAGCATCTTGTGATCACCCAA	CCAGATCAGGACCGTGATAAA
9751	SNPH	NM_014723	CACGATGTTCATCCAGGCCAA	ATGAGGGTTCCTAAACCTTAA		
9761	KIAA0152	NM_014730	AAAGATATAATTAACGATCAA	CAGGATTGTGCTGGCAGCCAA		
9767	PHF16	NM_014735	TCGGTGGGCCTTAGTCTGCAA	CACGCTAGCTGTGGACTTTAT	CACCAATAGGTGGGTGAAGAA	ACCATGATTATCAGACACTAA
9775	DDX48	NM_014740	CCGGAAGGGTGTGGCCATTAA	CCCATAAACTCTATACTTCTA	CCGCATCTTGGTGAAACGTGA	AAAGAGCAGATTTACGATGTA
9780	FAM38A	NM_014745	CTGCGTCATCATCGTGTGTAA	CAGCCTTGTATGCACCGTCAA		
9781	RNF144	NM_014746	TGCGATGACCACAACAAGGTA	AAGGATTAGAAACCGCAATTA	GTGGAGAAAGTGTATTCTTTA	CAGGAATAACTGTCCAAATTA
9783	RIMS3	NM_014747	CTCCAGTATCCTGACATGTAA	CAGGGAAGAATCATCTCCAAA		
9784	SNX17	NM_014748	ACGGAAGTTGCAAGAGTTTGA	CTCCGCCTACGTGGCCTATAA	CAGCGAGACTTTCAACAGTTT	CTGGCCCTCGATGCCAAATTA
9797	TATDN2	XM_376203	ACAGTTCTAAAGGGCTTTATA	CAGCCATGTGTGGATCTTGAA		
9806	SPOCK2	NM_014767	CACATGCATAAAGGAAATCAA	CACGTTTGTGTGTCCTTGTAA		
9810	RNF40	NM_014771	CAGCTTAACTCTGGCTACTAT	CACGCTGGCCCAGGTAGGCAA	GCGCATCGAGTTTGAGCAGAA	AAGCGGAAGCTTCGAGAAGTA
9811	KIAA0427	NM_014772	CCCGGATTAGTGGGAGATCAA	CAGAACGAGACTGGCAAATTA		
9815	GIT2	NM_014776	CCCGTTGATTATGCAAGGCAA	CAGCGTTGAGAGTCAAGACAA	CTGCCTATGGCTGAAACTATA	AAGCATCGTGCAATAAGTGAA
9818	NUPL1	NM_001008564	AAGGTACAAGAAGATATTAAA	AAGCAAATAATTCACATATAA		
9819	KIAA0669	NM_014779	CAGGATTGCATTTAATAGATA	CTGGCATATTTCTAACACTAA		
9825	SPATA2	NM_006038	CACAATGTTAAGGGATTTATA	CCCAGTTCAATGGATACTAAA		
9826	ARHGEF11	NM_014784	CACTTGTATCTCCTTAGTTAA	AAGCGATTCAATCCTGATCAA	CTGGAGGATCAGCAAGGATAA	CACAACGACTCTCGACCGGAA
9830	TRIM14	NM_014788	CACCGAGAAGCTCAAGGCTAA	GCGCCTCACCTTAGCATTCAA	CAGGTGCCTATCACTGAGTAA	AAGCAGAGCTGCGTAAAGTTA
9832	KIAA0555	NM_014790	CTGCATTTAATGAAACATGTA	CACCTGCTTGAAAGAAATTAA		
9833	MELK	NM_014791	CACCTCGATGATGATTGCGTA	AAGACTAAAGCTTCACTATAA	CTGGATCATGCAAGATTACAA	CGGGTTGTCTTCCGTCAGATA
9834	KIAA0125	NM_014792	CAGCATGGTGACTTAGTTAA	CAGGAACAGTTCTGAAGTCAA		
9836	LCMT2	NM_014793	TAGATTTATAAGTGTCAATAA	ATGGCCATTAATGTTACACAA	ACCCACTAAAGTAGACAATAA	CAGAGGCATTTCCTCGCGTAA
9837	KIAA0186	XM_375911	ACAATTGAATGTTGAACTTGTA	TTGGGAGAATTGACATCTTAA		
9842	PLEKHM1	NM_014798	CCCATTCATATTTCAACAGAA	CAGGCAGCCTCTGGAACTCAA		
9846	GAB2	NM_012296	CAGACCAGACGTTTCATTCTA	CACTAAGGACACAAGAATCAA	CACCAATTCTGAAGACAACTA	AACCTCAAACCTGATCGGAAA
9848	MFAP3L	NM_001009554	CCGAAACTGCAGAACCTTCTA	CACCATCGTCATGGTCCTCAA		
9851	KIAA0753	NM_014804	CAGAGAAAGGAAGAAACTTAA	CTGGCTCAGTTTGGTGATGAA		
9853	RUSC2	NM_014806	ATGTATTTATTTATTTATTTA	CCCGATCAAGACCTAGGACAA		
9854	TMEM24	NM_014807	TAAAGTCAAATTGGAGTTTAA	CACAATTGAGGAACTGATCAA		
9855	FARP2	NM_014808	CAGGAACATGCGCCAGTTAAA	CAGGTTTGGACACAACTACAA		
9860	LRIG2	NM_014813	AGGGATGTCATTGTAAATATA	CTGGAATATACTAGTATCTTA		
9863	AIP1	NM_012301	AACCCATTCATCGTAAACAAA	CAGACCTAAACTGATCCTAAA	TTGGATGTCATCCAAACTTTA	ACGCAGTGACTACGCAACCTA
9871	SEC24D	NM_014822	CAGCTGCTTAATTAATTGAAA	AAGGTACAATTGTACCATAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
9877	KIAA0663	NM_014827	AAGATTGATAGTGAAATTAAA	CAGCTAATGATTACAGTTTAA		
9880	KIAA0352	NM_014830	AAGCTTAACATCAGAATGAAA	CTGGGTGGTCTGTGTACTTAA		
9890	LPPR4	NM_014839	AAGGAGTTGTTTACAGATGAA	CACATTGTTAAGGACATATAA		
9894	KIAA0683	NM_016111	CCAGTTTGTGATGACCCAGAA	CCGGGAGACGCTGCTGGGCAA		
9896	KIAA0274	NM_014845	GAGGGTGATGTTGCAAATGAA	AAGAAATTCCACAAATATGAA		
9899	SV2B	NM_014848	CTGGTTGATTTGAGAGATAAA	AAGATGGATCTTGTAAATTTA		
9901	SRGAP3	NM_014850	AACCAGCAAGTTGTTCATTTA	AACCTAGTTAGTAGTCTTCAA		
9908	G3BP2	NM_012297	ACCAGCGTGTGTACACATAAA	CAGCCAAGAGTCGAAGCTAAA	TTCAGTGAATGTCATACTAAA	CCGAGTGGCTCCTGAATTTAA
9914	KIAA0703	NM_014861	ACGGACCTCTTGGTGGATGAA	CAGGCTGAAGAGACACCTAAA	ATGGACTTAAGTGATATTAAA	CCGAGAGTTGGCGTGAAGGAA
9915	ARNT2	NM_014862	CAGAATAACCACCATGAGGAA	TAGCTTTAGCCGAGAAAGAAA	CCGGAACAGCTCTAGGAATAA	GTGGACAGTTTAAGTACTTAA
9921	RNF10	NM_014868	TCCAAGCGTTATAATCGCAAA	CCGGGTAGTTCTGGAGGAGAA	TTCGATGAAGAAACCACGGAA	CAGGATTGAGATAGAGGAGAA
9936	DCL-1	NM_014880	CAGAATTATGTGCATACCAAT	ATGGCGTATTATGTGAACTAA	GAGGCTATTTAAGTAAATTTA	TAGCTAGTAATAACAATATAA
9940	DLEC1	NM_005106	ACAGCCTGACATGGAATTTAA	CAGGTTCTGCATTATGCCCAA		
9941	ENDOGL1	NM_005107	CTCGGGCAAGATGGCTATCAA	CAGAGGCAAGGTGTTACACTA	AAGAAGCTAGAAGAACTCAAA	AACAGTGGAATCCTAAATTTA
9949	AMMECR1	NM_015365	CCCACTGTTTGTAACATGGAA	CACACTTACCAGTGCGCTTAA	CTGACCAGGTATCGTAGTGAA	CGCCAGCATCATCATTTCCAA
9950	GOLGA5	NM_005113	CTGGACCTAAATCTACGTATA	AAGCAGGAGTTCCACTATATA	AAGAAGATCTTTATCGAACAA	CACGACCAACCATATGGCAAA
9951	HS3ST4	NM_006040	CCGTGTTGTTATAAAGCTTAA	CAGAGGATAAATAGTTGTCAA		
9958	USP15	NM_006313	ATGAATAATGTTGTAACTCGA	GACACAATAGATACAATTGAA	AAGATGATACCAGGCATATAA	TATGTCGGAATTCTTAATTAA
9965	FGF19	NM_005117	TTGTCTGATCATAACATTGTA	AAGAAACATCTAGAAGTTGTA	CAACATGATATTTATGAGTAA	CCGTAAGGCGCTACTATATAA
9970	NR1I3	NM_005122	AAGCCACAGGCTACCACTTTA	TTGAACAGTTTGTGCAGTTTA	CACACACTTCGCAGACATCAA	AACACTTTCATGGTACTGCAA
9976	CLECSF2	NM_005127	AAGCAGTAATGTCCTAAAGAA	CCCAGTTGAGAAAGTAAGAAA	CAGCTAGATGTTACACCGAAA	ACGTGTCAGGCTACACATAAA
9978	RBX1	NM_014248	CACATTATGGATCTTTGCATA	TTGCATAGAATGTCAAGCTAA	CTGCTGTTACCTAATTACAAA	AAGAAGCGCTTTGAAGTGAAA
9985	REC8L1	NM_005132	CCGGAGAAATTCCAGGAACAA	CAGAGGGACAATGTTCTACTA		
9988	DMTF1	NM_021145	ATGGATAAGCATAGTAACAAA	CAGATTATTGTTCATGCTTTA		
9989	PPP4R1	NM_005134	CAGCTAGTAATGAGAATGATA	AACCTGGTAACTACAAATCTA	TGGGAGTGCTGCAGTCTTTAA	CAGGCGTTGTTAGATCAGTAT
9993	DGCR2	NM_005137	TCGCTGGGAGGTGGCATTCAA	CTCCCTCAATACTGTGGTGTA	AAGCCCAGTTGTGAATATCAA	GAGGTGGGATTTGATACTGTA
9994	CASP8AP2	NM_012115	CAGCTGATGTGCGGAAGTCAA	CAGTATTCAAATAGTCAGAAA	CAGTCTGATCTCAATAAGGAA	AACGAAGTTTCGAGATTCTTA
10001	MED6	NM_005466	TCCCACTAGCTGATTACTATA	CACCCAAATTTGTGCAGCTAA	AAGGGTATTGGTGGCACTTCA	ACCCAAATTTGTGCAGCTAAA
10002	NR2E3	NM_014249	CAGGCAAGACTAATTGACAAT	AGGGAATACTCCAATGGAGAA	CACGGAGTTTGCCTGCATGAA	CACAAATGTATTCATACGTAA
10003	NAALAD2	NM_005467	CAGCAAGTATCTATAATCTAT	TCGATTGTGGATGAACATGAA	AAGAAACATGATCAACAATTA	ACGGTGGAAACTGGTATCCGA
10004	NAALADL1	NM_005468	CACAGAAGAGTTCTTCAACAA	ACGCATATCAACACTGCAGAA	TCCCTTTACTCCGGTGCTTTA	CTCCGGTGCTTTATATTTACA
10019	LNK	NM_005475	CAGCTTTACAGTGATAGTTAA	CAGCACATTGTGATAACATAA		
10020	GNE	NM_005476	CTGCTTACTAATGTATTAATA	ATGAAGGTTTCTACAACATAT	CCCGATCATGTTTGGCATTAA	ATGGAAATACATATCGAATGA
10025	THRAP5	NM_005481	CACCCGGATCCTGGCCATGAA	CAAGGTCATGATCAACCTCAA	TGGGAAGGACAGGTCCAATAA	CACGTGCAGCCCAGTATGGTA
10039	PARP3	NM_005485	CCAGACCAACATCGAGAACAA	CCCAGTGAGGACTGTGACTAA	CACGCAGAAGCTCATCACTAA	CAGCAAGGAGATGTTCAAGAA
10044	SH2D3C	NM_005489	CCAGAGAAACTCCACAAGGAA	CAACCAGGCCTTGCACTTCAA	CAGGCGAGAGCTACACACACA	CCACACCAATGCTGAAGTCAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
10046	CXorf6	NM_005491	AAGAATAAATTTGCAGGTCAA	CCGTCTAACATTACTCATGTA		
10048	RANBP9	NM_005493	CAGTGCAATATTAGAAACCCA	ACGGTGTGGTTATGACCTTTA	CAGGTTGGGATAAGCATTCAT	AAGCAATGAGTGAACAGCTAA
10050	SLC17A4	NM_005495	ACGCTAGTTATTTAACTGCAA	GAGCAAGATAGTACACTTTAA		
10053	AP1M2	NM_005498	CTCCGAGGGTATCAAGTATAA	CTGGATTGAGTCTGTCATTGA		
10054	UBA2	NM_005499	AAGAGTAGATTTGATATCAAA	CTGGGTATCTTGGACAAGTAA		
10055	SAE1	NM_005500	TACCAAGTCTTTGGATGTTAA	TCCAGGGATGTCATAGTTAAA		
10060	ABCC9	NM_005691	AACAGAGGACATTGCAATAAA	CAGCCAGATATTGACTTATTA	CTGCATCTATAGCATCCATTA	CCCAAATTTGTTCGCCCACAA
10062	NR1H3	NM_005693	CCCACAGAGATCCGTCCACAA	CAGGAGTGTCGGCTTCGCAAA	GAGATAGTTGACTTTGCTAAA	CATGAATGAGCTGCAACTCAA
10063	COX17	NM_005694	CTGAAGAATGAAGAAGATTAA	AAGGAATGCATGAGAGCCCTA		
10068	IL18BP	NM_005699	CTGCTTCGGATCCACACTGTA	TCCCATGTCTCTGCTCATTTA	CAGGATGTGGACGGACTGGTA	ACCGATCAAGTCAACTCAGTA
10077	PHEMX	NM_005705	CAGCAATGGTGCATTGAGCAA	TCAAATATACATCACATCAAA		
10086	HHLA1	NM_005712	CCCAAGTGGGCTACATTTGAA	CTGGAGGGTCTCTCTGGGAAA	AAGCATGTTAATGTTACCATT	CTCCAGCTAGATCATCAGTTA
10092	ARPC5	NM_005717	CAGCCTCTGAATGAAATGCTA	CAGGGTAGTTGGGATCTCAAA		
10094	ARPC3	NM_005719	GCGCTTAATAAGAATAAGTAA	CTCATGGATCCTGATACCAAA		
10095	ARPC1B	NM_005720	AAGCACTATGCTGGTCATGAA	TCGTGTGATCTCCATCTGTTA		
10102	TSFM	NM_005726	CAGGAAGGAAACACAACTGTA	CAGCAAGGAGCTGCTCATGAA		
10105	PPIF	NM_005729	CTGTGTGTTAAAGAAATTCAA	ATGGATTTGTGTTCACCTTAA		
10107	TRIM10	NM_006778	ACGGACATCAGAAGCACTCTA	TTAGTTTGTGTTAACTATGAA	TCCAATAATGTTAGAGTTCAT	CAGTTGTATGACTTTAAACAA
10111	RAD50	NM_005732	TAAGATTGAATTGAATCGTAA	CACGAGTAAGATTAAGAGCAA	CAGGAACAGATTCAACATCTA	CAGAAAGTGTATAATAAGAAA
10131	TRAP1	NM_016292	CCCGGTCCCTGTACTCAGAAA	AAGGATGTCGGTGAGTGGCAA	CCGCTACACCCTGCACTATAA	CGCGCTCATCAAGAAGCTGAA
10134	BCAP31	NM_005745	CTGCACGTTGACTGTGGGAAA	CACCTTCTTTGTGGTTCTCAT	CAAGAAGTACATGGAGGAGAA	AAAGGTGAACCTCCAGAACAA
10136	ELA3A	NM_005747	CACATCCTGAATAAAGAATAA	TGGCTGCAACTTCATCTGGAA	CTGGCTTTGGCTGCAACTTCA	AAGAATAAAGATCTCTCGGAA
10139	ARFRP1	NM_003224	CCGATTTAACAAGAACTACAA	CACCACCACCGTGGGCCTAAA		
10140	TOB1	NM_005749	CAGCCTGTTATGGCTAACTAA	AGCCTGTTATGGCTAACTAAA	CCAGCCTGTTATGGCTAACTA	CAGATATGGCCTCTTACAGTA
10142	AKAP9	NM_005751	CAGGTTCGTGAATATATGGAA	ACAGATTATATCACTCGGCTA	CAGCTTCAAAGGGATATACAA	CAGCCTATCAGTGAACATCAA
10154	PLXNC1	NM_005761	TTGGTGAGAATTTGACTTCAA	CCCAACCAGAGCAACCTACAA	TCGAGGGAAGCACAAGTTCAA	GACGTCGTACATATTTGGAAA
10158	MAP17	NM_005764	CCCTAATTTCTGTGAAATAAA	CCGGCCCTACCCGCCCTTGAA		
10165	SLC25A13	NM_014251	CAGACCAAAGATGGATTAATA	CTCAGAAATTTGGTCAGGTTA	TAGCAGATTTATATGAGCCAA	CAGTATCTACCTCAAAGGCTA
10166	SLC25A15	NM_014252	AGCCTTATGCACCTAATTCAA	CACCAGCAGGGTATCTCCCAA	ATAGGCCTGGATCGAAGTAAA	AGGCCGTCCATTAGAGATTTA
10168	ZNF197	NM_006991	TCAGGCCTAATTATACATCTA	CACCAATGAGTCCAAGATTGA	TCCCAACTTTCAAGTCTACAA	CACCTACACTTTAGACAATTA
10178	ODZ1	NM_014253	CCCAGTCATATCAACCATAAT	CCGACCTGCCTTTACCTTTAA	AAGGCTATAATCCGGCCTTAA	CTCTATGATTTCCTTACTAAA
10180	RBM6	NM_005777	CAAGCAAGAATTAATAACCTA	CAGACTGGTCTTCAGATACAA		
10188	TNK2	NM_005781	TGGCCTTACCATGGACTTGAA	CAGGATCTTGTGCCTGGAAAT	CGGCAGTCAGATCCTGCATAA	ACGCAAGTCGTGGATGAGTAA
10189	THOC4	NM_005782	CAGGAACTCTTTGCTGAATTT	CCAGTTAAACAGACCAGCAAA		
10194	SDCCAG3	NM_005786	CACGGGCAAGGTCAACATCAA	ACCGCGGAACATTGCACTAAA		
10202	DHR52	NM_005794	CAGCACCGGGATAGACAGGAA	CTGGAAGAACTTCAAGGAACA	TAGATTTGGCTGATCCAATTA	CTCTCTGTAATTTGTGCTTTA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
10206	RFP2	NM_001007278	CAGAATTTGTGTGCAAATATA	AAGGAGATCATAAGAAATTAA		
10208	C13orf22	NM_005800	CAGCCTCAGTTTCACAGTTAA	CTGAATGAAGTTAGAGATGAA		
10213	PSMD14	NM_005805	TAGGACATGAACCAAGACAAA	CAGGCATTAATTCATGGACTA	AGAGACATTATTACTCCATTA	TTGGATACTGTCGTATTTAAA
10218	ANGPTL7	NM_021146	TCGGGCTTGGAAGGAAAGCTA	CCGCATCTCTGGAGTGTATAA	ACCGCCTGGGTGAGCACAATA	CTGAAGGTAGATGGTGTTATA
10220	GDF11	NM_005811	AAGGTGATGTTCACAAAGGTA	TTGGCAGAGCATCGACTTCAA	CAGAGCATCGACTTCAAGCAA	CTGAAATGGAGTAATAAATGA
10228	STX6	NM_005819	CAGGCTGAAGCTAAATAGAGA	TCCCAGGTTTCTTAAGAATAA	CTGAAGCTAAATAGAGAACAA	AACCTAGTCATTAATGAGTAA
10231	DSCR1L1	NM_005822	ATGGATTACTTTAGATGCAAA	CTCAAAGAGCTTAGACTTCAA		
10234	LRRC17	NM_005824	AGCGTAATAATTACTATAGTA	ATGCAGGGTAATCCAGCTAAA	AAGGAACAATTGGACCCGAAA	CCCGTGTGACGTGTACACATA
10244	RAB9P40	NM_005833	TAGGTGAAGAAACTAATGCAA	AAAGAGGATTCAGCTGACAAA	ATTGATATAAGTGACATGAAA	AAGCAACATGGTACACCTTGA
10245	TIMM17B	NM_005834	CAGCACTTCCTCCAGCTCCAA	GGCACCCTGATGAGTATTTAA		
10250	SRRM1	NM_005839	CAGAATAAATTTCTAAATTTA	TAGGTTGAAGTTCAACATGTA		
10257	ABCC4	NM_005845	TTGGCTATACTGCATCACTTA	TACAACCAATAGGAACAACAA	CTCCTAGTACTTAGAAATACA	GAGGTTAAAGACAGTCATATA
10261	IGSF6	NM_005849	CAGAATGTAAGGAAACTATAA	CAGGAAATTGCTCAAGAACTA		
10262	SF3B4	NM_005850	CTGGATGAGAAGGTTAGTGAA	CACAGGCAACTCCAAAGGTTA		
10267	RAMP1	NM_005855	CACCTGGCACATGGCGGAGAA	CCCGCCCGGCAGCATCCTCTA	CAGGTTCTTCCTGGCAGTGCA	CAGGGACGTGACCTTGACTTA
10276	NET1	NM_005863	ACGGAAAGAGACTTTGGTGTA	GAGCATCATAGGGTTACTTTA	TCGGTGTGGATTGATTGGAAA	CTGGAGGATGCTATATTGATA
10279	PRSS16	NM_005865	TCCGAGTATAATGACGTGGTA	ACGTGGTATCCCGAAGCCTAA	CAGAGAGTTATGGAAATATAA	CTGTTCTTTCCTAAAGATCAA
10280	OPRS1	NM_005866	CAGCGTCTTCCATTCCAGAAA	TGGGAACAAATGAGACACATA	CCGGCTTGAGCTCACCACCTA	AGGGATATCCATGCTTATGTA
10282	BET1	NM_005868	TCAGATTAAATAGCATTATAA	ATCATTTATTGGATTATTAAA	CAGAATAAATTATTAGCTGAA	CACTGATGTCGTGGCGCTTTA
10284	SAP18	NM_005870	AAGCCACGGGATTGTATGAAA	TCGCTTTAGTTTGTTACAGTA	AACGGCCTATAGGATTGTTAA	AGCCACGGGATTGTATGAAAT
10290	APEG1	NM_005876	CCCGAGGACACCACCACCGAA	CAAGTGTATCATCACTGCCAA	CAGCTGGAATAACAAGCCCAA	AACACCTATTTCTTAACTCAA
10291	SF3A1	NM_005877	CAGGTGTGTTACCGAGTGGAA	CGCAAGGATTATGATCCCAAA	CAGGATAAGACGGAATGGAAA	CAGCATGTAGGTAGCGTCCTA
10293	TRIP	NM_005879	CCGGCTCAGGAGCAAGATGAA	AAGGAAATCATGAGCCTGAAA	CGGGACCAGCCTGAGGTGTAA	CCGTGATGATATTGATCTCAA
10300	KATNB1	NM_005886	CTGCTGTAATTTATAAGGCAA	CAGGGAGGAGAGGCTGCATAA		
10322	SMYD5	NM_006062	CTCGAGGAGCTGGGCTAGATA	TTGGATGCTATGGGAATTACA	CTGGCCTTATGGAGTATGGAA	AACATTGAAGTCTTCCAGAAA
10328	NOC4	NM_006067	CTGGACAAACCCAGAGATCAA	TGCAAGATTGTTCCTATTAAA		
10329	TMEM5	NM_014254	CAGCCTCAGGAAACAAATGAA	TCCCTTTATCTTTATCAAGAA		
10344	CCL26	NM_006072	AACAATTGTGACTCAGCTGAA	TCCCAGAGTTACTTTAATAAA	AAGCTATGAATTCACCAGTAA	CAGGGCCGTCTCAGTCTCATA
10352	WARS2	NM_015836	CCGGCATTCAACCTACAGGAA	CTACCTCGATTACAACATTTA	GCCAATGGATGCGAACTTAAA	AAGGTAGATCTATCAAGCCAA
10360	NPM3	NM_006993	TTGGATAAAGGTTGAAATAAA	CACCCGCTCCTTCACCTTTAA		
10361	NPM2	NM_182795	CAGGAACGTTATGAAGCATCA	CAGGCGAGCGTGGCTAAGAAA		
10363	HMG20A	NM_018200	AAGGAAGATAACGGACTGTAA	CAGGAATGCATGAGATTTCAA		
10369	CACNG2	NM_006078	CCGTGTGATCTTTATAATTTA	ATACATATATCCATTATATTA	ATCCATTATATTAGTAGTGGA	TCGGTTGGGTGTTTATATAAT
10370	CITED2	NM_006079	TGGAAACAAAGTAAACTATAA	CTCCCTTATGTAGTTGAAATA	CAGATTTACGAGTGAAAGGAA	TGGAATGTCGTCAGTGGCAAA
10381	TUBB3	NM_006086	CACGGTGGTGGAGCCCTACAA	CCAGCAGATGTTCGATGCCAA	GCGGATCAGCGTCTACTACAA	TTGCTGTCAGATACCCTTAAA
10385	BTN2A2	NM_006995	AACTCCAAACATCGCGATTAA	CTCATTGAAATCAAGGCCCAA	TACGTCAGCATTCAGGTTCAA	AACGATTAATGTTTCATTATT

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
10395	DLC1	NM_006094	CAGCTTGATCAGGACATAGAA	AAGGTATTTCAGAGAAGGAAA		
10396	ATP8A1	NM_006095	GAGGATAAATTACAAGATCAA	ATGCAATGTAATGCAGTTTAA		
10398	MYL9	NM_006097	GAGGCACCCATTGATAAGAAA	ACCCATTGATAAGAAAGGCAA		
10403	KNTC2	NM_006101	CACAATTAGCAGAGTATCACA	TCCAAAGGTTATGACTTTGAA	TCCCTGGGTCGTGTCAGGAAA	CCGAGACCACTTAATGACAAA
10407	SPAG11	NM_016512	ATGGCAGATCTGGGATCTAAA	TTGAATGAATTTAGCACCAAA		
10412	TINP1	NM_014886	AAGAGATTTATTAAATTGTAA	AAGGCTAAGCTTTACCATAAA		
10423	CDIPT	NM_006319	CACCATGTGCCTGTTGGTCAA	CCGGATTGTCTTCGCCATCAT		
10424	PGRMC2	NM_006320	CCCTAAATCAAATCAATATTA	CACATCAATTTGAGTTGTTCA	CCGGCGGGTCCATATGGAATA	CAAGATAAATTAATCTCACTA
10426	TUBGCP3	NM_006322	TCGCATGGACTTTAACTGCAA	CCACTACCTAAGAGTATTTAA	TACGACTTTGTATCAGCATAA	TACCGCGAATGCATCAGCTAA
10431	TIMM23	NM_006327	CAGGCATGTTGTATAAATGTA	CCCGCTGTTATTGAGGAGTAA		
10436	C2F	NM_006331	CAGAAGAATGTTCTGATTGAA	AAGGTAATTAAGAATCCAGTA		
10450	PPIE	NM_006112	CAGATTCCTCTGGATTATGAA	AAGACGCTTGAAGAGAATAAA		
10454	MAP3K7IP1	NM_006116	ACGCCTTGGCTGAGAAGGCAA	CACGAGGACATGACCCTGCTA	CTGCAGGTGAGAGGATTTAAA	CACCTTGGACAAGCCACACAA
10457	GPNMB	NM_002510	CCGTGAGAATTCAGCATGGAA	ATCGAAATTCATCCGACGAAA	CTACTATTGATTAGAGCCTAA	TCCATGTAACTGTATGCATAA
10458	BAIAP2	NM_006340	AAGAAATACCAGACTGAGCAA	CACGGGCAACCTCCTGGACAA	CAGCAAGAATCCTCAGAAGTA	CTGCTTCTCCTGCCTAATAAA
10460	TACC3	NM_006342	CAGGAAGTTCTGAGAACCAAA	AAGGAACTTTCCAAAGCTGAA		
10465	PPIH	NM_006347	CAGGGTCATAAAGGATTTCAT	CCGCATGAAGATCGAGCTCTT		
10469	TIMM44	NM_006351	AAGAAATGAAAGAAAGTATAA	CTAGATAATGTCAAACAAGAA		
10474	TADA3L	NM_006354	ACCGACTGGCAGGATAAGAAA	CTGACCGAACTGGACACTAAA		
10478	SLC25A17	NM_006358	CTCCTGGAGATCATTAAAGAA	CTCATTGCTGTTGGTCTTCAA	CTGGACCTGTTGTCACCTTAA	ACCCAAATGATTCTCTTATAA
10480	GA17	NM_006360	ATGGATAAGAATACTCCTGTA	TTCGTGCTTATCTGAAATCTA		
10482	NXF1	NM_006362	CAGAACAAGTAGAACAGCTAA	AACGCGTTAATTTCCCTCAAA		
10489	MUF1	NM_006369	CCCAGGCTTTAGAGAAGTATA	CCGGCGTAAGAGTGAAGCCAA		
10490	VTI1B	NM_006370	AAGCAACAGGAAGCAAATGAA	ATGATATACCAAGGTAATAAA	AAGGTAATAAATGCTGTTTAT	CAGTATGATATACCAAGGTAA
10491	CRTAP	NM_006371	CAGCATGTCAGTGGCATTTAA	CAGGGAGATCAAGGACTTCAA		
10494	STK25	NM_006374	CCGGCCGAGTCCACACAGCAA	AAGACCTGACTTGGAGACAAA	CACCAAGCTATGGATCATCAT	AAGGGCATCGATAACCACACA
10499	NCOA2	NM_006540	CAGTCTAGTGCCAAAGATTAA	CCAGGAATGATGGGTAATCAA	AAGGATTGGCATTCAGTCAAA	AGGGCTGTTAACATTAGCAAA
10500	SEMA6C	NM_030913	CGCCCTGGAACCCAAATTCAA	CCGCGTAGCCCGAGTATGTAA		
10516	FBLN5	NM_006329	CAGATCTGCATCAATACTGAA	CAGATGGATGAAAGCAACCAA		
10517	FBXW10	NM_031456	CCGGTGTATATCCGAAATGAA	AAGGAAGGTCTTGAATTTCAA		
10521	DDX17	NM_006386	CACGTAAATGAAACCACTCAA	CTGGGACATTGTAATCATAAA		
10522	DEAF1	NM_021008	CAAGTCATTAACACACTTTAA	CAGCGGCACTCTGTACAAGAA		
10525	HYOU1	NM_006389	ACGCAAAGTCATCACCTTTAA	CAGCAAAGCCTTTAAAGTGAA		
10536	LEPREL2	NM_014262	GAGGCTGATGCTTTAAATGAA	CAGGAGTGGATAGAAGCCAAA		
10537	UBD	NM_006398	AAAGCATTCTTTGTCTATTAA	CTGGACAAACACAGCAATCCA	ATGGGATTTAATGACCTTTGA	AACCCATATGACAGCGTGAAA
10539	TXNL2	NM_006541	AACGAAGTTATGGCAGAGTTA	AGCGCTAATGAACATCTTAAA	TTCGATATATTGGAGGATGAA	TACCCTCAGCTGTATGTGAAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
10561	IFI44	NM_006417	CTGGGATATCTGAGAAGTATA	TCAGATGATAGTAAAGATCAA		
10562	OLFM4	NM_006418	CTCATTGTCCACCTTACTAAA	CGGGAATATTGCCAGAGTTAA	TAGGGATTCTTTGTACAGGAA	CAGAGTTAACCTGACCACCAA
10563	CXCL13	NM_006419	CTGAATGGATACAAAGAATGA	CGCTTCATTGATCGAATTCAA	AAGGGTGATGTACACATGTAT	ACCGAGGAGAATTAAGTCCTA
10569	SLU7	NM_006425	CTGGCTTTAATAAATATTTCA	CAGGCAGATCCTACAAAGCTA		
10571	SMA3	NM_006780	AAACTCATTCAAGGAGGTGAA	CAGCCGGGATGCACTAGGCAA		
10573	MRPL28	NM_006428	CAAGTTTGGGATGGACCTGAA	CAGTGAGATCCTGGACAAGAA		
10575	CCT4	NM_006430	CTCGATAATCTGGATAACTGA	TTGCCTGAAGTTGTATTGAAA	TTGCTCATATTGACCAATTTA	TAGAGTTGGCCCTACGATTAA
10577	NPC2	NM_006432	CCCGAGCTTGGAACTTCGTTA	GTGGATGGAGTTATAAAGGAA	AAGGACAGTCTTACAGCGTCA	CAGATCGTTTCTCATCTCTAA
10578	GNLY	NM_006433	CAGAAATTTCATGAGGAGGTA	CAGGGTGACCTGTTGACCAAA		
10580	SORBS1	NM_006434	TCCGGAACACTGAGAGATCAA	CTGAACAGAGATGATGATTCA	CAGGATTCCAGTCCTCTACTA	ACCCGGCAACACGAAAGCAAA
10581	IFITM2	NM_006435	ACCATGAACCACATTGTGCAA	CCAGGACCTCCACACCATTAA		
10594	PRPF8	NM_006445	ACGGGCATGTATCGATACAAA	CAACGTCGTCATCAACTATAA	CGGAAAGTCATATAAGATGAA	ATGGCTTGTCATCCTGAATAA
10595	ERN2	NM_033266	CAGCCACTCGACGACCCTGAA	CAGGGATTAATGAAACTGCCA	CACCTGCATTCTTTACACATA	AAGGATGAAACTGGCTTCTAT
10606	PAICS	NM_006452	CACGTGGAAATCTCCGTTATT	GCCCAAGGACTTCTAACAATA	CTCGACTAACAGGGACTATAA	CCCAAGGACTTCTAACAATAA
10613	SPFH1	NM_006459	CACTGGAATGTTAAACACTAA	CCCGGAATATCTGGAGCTCAA		
10615	SPAG5	NM_006461	TCGACATGACTTGGAAGATAA	CCCGAGTAGCATGAATGGTTT	TCCCGACAACTCACAGAGAAA	CCAAATTAGCTCTACTCCTAA
10623	POLR3C	NM_006468	CAGCTTGATAGGGAAAGGTAA	CCCACACTTGTCATTAATGAA		
10628	TXNIP	NM_006472	TAGAGGGCAGGTGTTCATAAA	TAGAGCTGATTTGATGGACAA	AAGAATACCTTAATTCCTTAA	AAGAGCCAATTTAACAAACTA
10630	T1A-2	NM_001006624	CGGGAAGGTACTCGCCCTAAA	CTCAAGTGTGTTTGAAACCAA	CAGGAAGTCGATAGTCTCAAA	ATCGAGGATCTGCCAACTTCA
10631	POSTN	NM_006475	ACGGATCTTGTGGCCCAATTA	CAGGAGAAGAACGAATCATTA	ACCAGATTCATTACAATTCAA	CTGCTTATTGTTAACCCTATA
10634	GAS2L1	NM_006478	CTGGGACACGCTGGAGCATTA	CAGCAGAGCCTCTGACAGTAA		
10651	MTX2	NM_001006635	CTGCAGAACCTTGGCCTGAAA	AACCTCAAATTATATAATGTA		
10653	SPINT2	NM_021102	CAGCGATATGTTCAACTATGA	AAGGAGGAGTGCCTCAAGAAA		
10658	CUGBP1	NM_006560	TTCTAGAACTTCATAAGATAA	CGGCTTAAAGTGCAGCTCAAA	CGGGAACTCTTCGAACAGTAT	CAGGGTCCTCACCTAGCTCTA
10659	CUGBP2	NM_006561	CTGAAATTTATTATTAGACAA	CAGGAGAAAGGTTACTGTAAA		
10663	CXCR6	NM_006564	CTGCTATTCAGTCATAATCAA	CACCAGCATGTTCCAGTTATA	TCGTTTCATTGTAGTGGTTAA	CAGGTCATGTGCAAGAGCCTA
10668	CGRRF1	NM_006568	CTGATAGGACTTATAAACTAT	TCCATCTGTGTTGATACATAA	CGGGAAATTTATGATATTATT	CCGGGAAATTTATGATATTAT
10670	RRAGA	NM_006570	CCGGTTTGAGAAGATCAGCAA	TTGGTATGGTGTAACACTAAA		
10673	TNFSF13B	NM_006573	CACGCAGGACATCAACAAACA	CAGACAGTGAAACACCAACTA	CGGAGGGTAAATGCCAGCAAA	CACGCCTTACTTCTTGCCTTA
10683	DLL3	NM_016941	CCCGGTGAATGCCGATGCCTA	CCGGATGCACTCAACAACCTA	CCTGAAGATGTAGACCCTCAA	AAGGCTATTATTGTGATCAAA
10692	RRH	NM_006583	CTGGAAGAATCTGAAATAAGA	CACTGTACTGATGACCTTTAA	CAGACATGGATCATTGTCCTA	CACAAATGCAATTATTATTAA
10693	CCT6B	NM_006584	CAGGAGATGGTACTACTTCAA	TAGAACATCATTACAAACTAA		
10694	CCT8	NM_006585	AACCTTCGAGATATTGATGAA	CTGGACTTGAACAGTATGCTA	GAGGCTGTGTATAGAAACATA	AAGGCTGTATTTGTAGTAGTA
10713	USP39	NM_006590	GTGGCTGATGATGGTAAATAA	AAGAGGCGAGATAATGATGAA		
10716	TBR1	NM_006593	TCCCATTATCTCGACCACTGA	CTGGTTTGTGACGCCGGCCAA	ATGGCCGTCTGCAGCGAATAA	AAGTCTCGGCCTCCACATTAA
10717	AP4B1	NM_006594	TGGAACAATTGAAGAAATAAA	GAGGAAATTCTGAAACAGGAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
10724	MGEA5	NM_012215	CTGGTACAAATCAAACATGAA	CAGGGAGAGAGTCTTCAATAA		
10726	NUDC	NM_006600	TGGCCTACTGTTACACATTAA	CACCAAGAAGATTAACCCTGA		
10730	YME1L1	NM_014263	TTCCAGATTGACCATGAATAA	GAGGCATTAGATAATGCCTTA	TGGGCATTTATGGACTTCTAA	TCCGTTGATCCAGAAATTATA
10735	STAG2	NM_006603	CAGAAATATATTGAAAGTTTA	TTGCTTGTCCTTTAAGATAAA		
10748	KLRA1	NM_006611	CTGGAATTAATTCTACAATAA	TCGGATTATCATATGATGAAA		
10749	KIF1C	NM_006612	ACCTCCATCATCAATCCTAAA	CCGGCTGATTAGAGAGCTGCA	CACGGTCCAGACCATTGTCAA	CTGGAGAATCAGTACCGGAAA
10753	CAPN9	NM_006615	CCCGAGAACTTCTATGAGATT	AAGGAGTTCATTCATCTCAAT	GAGGAGTGTAGTTTCCTTGTA	GAGAACTTCTATGAGATTCTA
10761	PLAC1	NM_021796	CCGGTTCAGGACAAAGTCCAA	AAGGATTTGTATAAAGAGTGA		
10765	JARID1B	NM_006618	TAGGGTTGTGTGATTAATCAT	CAGGAATGTAGTAAGCCACAA	ACGCACCAAGCCGAAAGTAAA	TCGTCCTAACATAACACTAAA
10768	AHCYL1	NM_006621	CAGGGTGGTAAAGCTAAATGA	AAACAGTTGTATCGTATGCAA	CTGATAGAACTCTATAATGCA	CCCACTTGGATTTATAGTATA
10771	ZMYND11	NM_006624	CCGGATGAAGTCGGACCACAA	ACCAGTGGGTATATGATTGAA	CACCTCATGTATCGTAAGTTA	TAGGAATGGATCGATAGTTGA
10773	ZNF482	NM_006626	AACGTTTGTATTATTCTATTA	TACAGGGTTAATAATCCTTAA		
10776	ARPP-19	NM_006628	CACATGAAAGATTAATCTGAA	CACTCTGTCATTGTTAATCTA	CGGCATGTTTGTAGCATACAA	CCCGGCCGGCTTATGATTTAA
10780	ZNF234	NM_006630	AAGGGTTTCATTTACAGTTCA	CAGGACTATATACAACTCACA		
10781	ZNF266	NM_006631	CTCGCCTTAGTGAACATACAA	TTGCTATTTCTTCAAATCTTA		
10783	NEK6	NM_014397	AAGGGATAAAGTGGAAATCAT	ATGCAAGTTAGCTAATACAAA	ACCGGAGAGGATCCATGAGAA	ACCACGGAAGTCGAGAATTAA
10785	WDR4	NM_018669	CAACGTGACCTCCTACCTGAA	CAGCTTCAGCAGTCTCTACAA		
10791	VAMP5	NM_006634	CTGCAGCAGCGTTCAGACCAA	GACGGAAATTATGCGTAACAA		
10797	MTHFD2	NM_006636	AGCGAGAAGTGCTGAAGTCTA	AGCCATTAACCTAGTGATTAA	TAGGATTATTCCTTGCTATTA	CTCGCGGCAGTTCGAAATGAA
10803	CCR9	NM_006641	TTGGAAGAAATGAGAAATACA	CGCACTTTATTCTGAGGAATA	CAGTCTTGTTATCCTTGTCTA	AAGGGATGAATCTGAACTATA
10811	NOXA1	NM_006647	CAGGTGGAGCAAGTTGGCAAA	CAGCAGGGAGATCAGCCCTAA		
10815	CPLX1	NM_006651	AGCCATAACGTTAGACTGCAA	CCGTGTTCACTTCTAAACTAA	AACGTTAGACTGCAATACTAA	CACGGCCGTGTTCACTTCTAA
10844	TUBGCP2	NM_006659	CCCGGTGGCTAAAGAGATCAT	AAAGAGATCATCTACACGTTA	CCAGGAGGATTACAACGACAA	CAGCGTCTGGATCAGCAACAA
10846	PDE10A	NM_006661	ATGCAGGGAGTTGTATATGAA	AACCCTTTGCATAAAGAACAA	TAGACTCTCATTCACAATGAA	CAGTATTACTATACAATGTAA
10849	ASE-1	NM_012099	CCGGGAAACTGAGGAACTAAA	AAGGAGCTGTTTCCTGGGTAA		
10858	CYP46A1	NM_006668	CACGAGTCCTGAGTCGGTTAA	CCTGATGTCAACCAAGTACAA	AGGCTTGGTGTCCGAATGCAA	GCGGATGGACACATACTTTGA
10859	LILRB1	NM_006669	CAGAAAGTGCATTAAACTGAA	ATGAATGAATTAGGAAAGAAA		
10863	ADAM28	NM_014265	TCGGATAATTTGCCCTGGAAA	CACCTAAGGACTCAAATCCAA	AAGAAATATCTCCGAAGTTAA	CACACTAATCTTGGAGGAATA
10869	USP19	XM_496642	CGGCCTTAGCTAGAAGTCGAA	GACCCGCATTATAAACATTAT	CCGGGCTGTGGAGAAGGATAA	ACCCGCATTATAAACATTATA
10874	NMU	NM_006681	CCAATATTACCTCAAGGATTA	CAAAGTCCCTTTGCAAGTCAA	CAGAGTGGACGAAGAATTCCA	GAGCAATGCTATGGAATACAA
10881	ACTL7A	NM_006687	CTGCTCGGAGATGTTCTTCAA	CACAAGAACCTACTGAATCAA		
10886	GPR74	NM_004885	CAGCTTGTCCAGGAATCTACA	CTACTACGCATTATATATTTA	CTGGCCATAAGTGATTTACTA	CCGGGAAGACTGGCCAAATCA
10890	RAB10	NM_016131	AAGGGACAAACTAGTAGGTTT	AAGCACTGATGTAACTTGCTA	CTGATGTAACTTGCTAGGTAA	CAAATTCGGTTTCATATTCTA
10897	YIF1	NM_020470	CACGAAGGCCTTCATTACTTA	CTGGCCTACAGTGGCTACAAA		
10901	DHRS4	NM_021004	CAGGATGCTCTGGATGGACAA	AACCCTTTCTTTGGAAGCATA	AAGGAGCAGAGTTGCAAATTA	TTGCGCGGCTTTGAATCCAAA
10906	FLNB	NM_006700	TACTGTTATAATAATTATTAA	CAGGAAAGGAATAGAGGCCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
10907	TXNL4A	NM_006701	TGGCAACAACAACAAGATTAA	CAGCATCGCCGAGAAGGTTAA	TGGCCTAATCTTAACTAATTA	AAGGTTTACTCTGGTTATAAA
10908	NTE	NM_006702	CCGGCGGTCTACAGACCTTAA	ACGCATGAGGAAGAAACTGAA		
10933	MORF4L1	NM_006791	CAGAAACAGCGAGAACTTCAA	TCCGGAGAGCAGAGTACTCAA		
10934	MORF4	NM_006792	GGGCACCCAGCTACTCAACAA	GCCGAAATTCTTGCAGATTGT		
10936	GPR75	NM_006794	CTCGGATTGAACCTTACTACA	ATGCATTATCACACCACTAAT	CCAGCTCGTATCAGCCATCAA	ATGGACTTTATTCTAACTTGA
10939	AFG3L2	NM_006796	CCGGCACCAATCGACCAGATA	GAGCGAGTGATTGGTGGCTTA	CATGGTATTGGAGAAACCTTA	ATGATGAAGTACGAATACTTA
10945	KDELR1	NM_006801	CCGCACGCTCTATCTCTTCAA	TAGCAAGTTCAAAGCTACTTA	CCACTGGTTGCCAAACACTAA	CACGTGTATGAAGGTGGTCTA
10946	SF3A3	NM_006802	AAGGAAGAATGCAGAGTATAA	CAGAGACTATTCAGTACCAAA		
10947	AP3M2	NM_006803	CCCAGTGTATGTCAAACATAA	CACAATTAACCTGCAGTTTAA		
10956	OS-9	NM_006812	ACCCACCATGTTCTTGAACAA	AACAATCAGGTTTCTAAATAA		
10957	PNRC1	NM_006813	TTGTATATATACAATGGATAA	TTGCCTTGTTGCAACATACAA	TACAGTTGTATGAGCAACCAA	CAGATTTCAGTATGTGTGTAA
10966	RAB40B	NM_006822	AACGGTGATATTGGAGTGATT	ACGGTGATATTGGAGTGATTA	TCGGCGAATGCTGCTTGCGAA	CCGTCGGACTTCGAATTTCTA
10982	MAPRE2	NM_014268	AACGCAGGTCATACAGCTTAA	TCCCAATATCTTCTAGAATAA	GACCTTATTAATAGGAGCATA	CAGCAGGTGCAGCTAAATCAA
10983	CCNI	NM_006835	AAGGCTGTAGAAGGAAATATA	CAGCGTTATTTAAGCACATAA		
10985	GCN1L1	NM_006836	CTGGAAGATTGTTGTCTCCAA	CAGGTTCAGCTGGAATGTGAA		
11001	SLC27A2	NM_003645	CAGCCACTTGATATAATCCAA	CTGAGAGATGTCTTTAAGAAA		
11012	KLK11	NM_006853	CCAGGAGACGATGAAGAACAA	ACAGGAGATGGTGTCACTTAA	ATGCTGTCACTTAATAATCAA	CAGCTCCTGGCCATATATCAA
11016	ATF7	NM_006856	CGGGCTGTGGACAGAGATTTA	CAGCTACTGTTAGCTCATAAA		
11017	RY1	NM_006857	ATGACTTGCCATTATAATTAA	ATGGTTCTCTCCGCAAGTATA		
11027	LILRA2	NM_006866	CAGGCTGAGGAGTACCATCTA	GAGGCTCTGGAGGACAATCTA		
11031	RAB31	NM_006868	CGGGCACATTAGGCAGTTGAA	CACACACTGATTCATACTAAT	CAGGATTCACATAAACATTGT	AAGGAATACGCTGAATCCATA
11033	CENTA1	NM_006869	CACCCGTAACATCTTCATCTA	CGCAGTGGAGGCGCACTTCAA	CCGGAAGTTTGTGCTGACAGA	GAGGCGCACTTCAAGCATAAA
11035	RIPK3	NM_006871	ATGGCAAGTCTGGATAAGGAA	CACAGGGTTGGTATAATCATA	CAGCCTGATGTCGTGCGTCAA	ACCGCTCGTTAACATATACAA
11041	B3GNT6	NM_006876	ACCGATGACAATGTGTAAATA	AAGTCTGAATACTTAATGAAA		
11045	UPK1A	NM_007000	AAGCATATACTAGATAGTCAA	CAAGCAGATGCTGACCTTCTA		
11054	OGFR	NM_007346	CACGGTGGGCCGAGCACAGAA	CAGGAGTGAACTGGCATGCCA	CACGCCAAACCTGAGTTTCTA	CAGAATGACAGGGTCCAGAAA
11068	CYB561D2	NM_007022	CACAAAGAGCAGCTTGGCAAA	CAGCTCATACTTGTACTGTAT	CAGGTGAGCAATGCCTACCTA	CACCAGCTTGGTCATTATGAA
11072	DUSP14	NM_007026	TAGCTGTTAAGTAACTATAAT	CCCAGGATTATATTAGCATTA	ACCCTTATTATTTAGCTGTTA	AAGGGAATGCATACATTGCTA
11073	TOPBP1	NM_007027	CAGCAATATTTCCAACATAAA	AACGAAGTTTGGAAACAGAAA		
11079	RER1	NM_007033	CACGATGAAGAGGCAAATCAA	CGGAATTATAAATATATATTA		
11092	C9orf9	NM_018986	CAGCATCGAGCAGAAGTACAA	CAGGTGCAGAGCTACATGGAA		
11098	PRSS23	NM_007173	ATGGTAGTCTTTGAACAGTAA	CACATATTAAACTATACCTTA	AACAGTTGTGGCCACACTAAA	CTGCATTGTAGCAATTTGTAA
11099	PTPN21	NM_007039	CCCACCGCAGTTGCACTATAA	AAGCACCTCCTTACCGGGCAA	GTGCATAGATTTCTATCTTAA	GAGGAGACCATTCAATTTCAA
11113	CIT	NM_007174	CCGGAAGCTCCAAGAAATCAA	AGGAATTTAGTCGGCGTCTTA	CAGGATATACCGTAACACGAA	ATGGAAGGCACTATTTCTCAA
11119	BTN3A1	NM_194441	TCAGCCTATAATGAATGGAAA	CTGGAGGAACTCAGATGGAGA	CAGATGGAGAAGTATCCAGTA	AAGACTCAGTTCAGAAAGAAA
11126	CD160	NM_007053	CTCAGTTGATGTTCACCATAA	ATGACCTCTTGTCATAGTTAA	AAGGAACGCGACTAAACTTAA	AAGAGATGCTAAATATACCAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
11127	KIF3A	NM_007054	GCCGATCAATAAATCAGAGAA	CCCAATTCATTTGCTCACATA	CTGGTTCAGAAAGACAGGCAA	GTGCCTTATCGTAACTCTAAA
11128	POLR3A	NM_007055	ACCAAGAAAGTCAGCATGTAA	ACGGCTGTAAAGACAGCTGAA		
11131	CAPN11	NM_007058	CAGGATGGCCATCAAATTCAA	CCCAAGAATACTGGCCATATT	CACATTCTTTCTAACCATGGA	ATGCGCCTGGTTATTGAGAAA
11132	CAPN10	NM_023083	CAGCAGGAACTTTGCCTCATA	CAGGATTGACAGGCCATCCAT	CTCCGTCATGGCAGTGATGAA	CAGATCTTCTTTATAACTATT
11135	CDC42EP1	NM_007061	GCCCAGCACAGTGCAAGCAAA	CTGGGAGAGACGAGCCATGAA		
11141	IL1RAPL1	NM_014271	GCGGGATACTTGTGAAATATA	ATCGGGCACTTTGAGAACTAA	ACGCATTGTGATGACCAGCAA	ATGCAACAAGTTGAACTCCAA
11146	GLMN	NM_007070	TAGCTATGCTTCAGCTGTATA	TAGCATCGAAACTAGGAGAAA	GAGGAACTTCAGTCTATAATA	AAGGCATATTCAATTGGATTA
11154	AP4S1	NM_007077	ATGCTCTTTCATTGAATATAA	CTGGTCCTTATCAGGAACCAA		
11157	LSM6	NM_007080	CTGGATGGCTACATGAATATA	CTGACATGTGAGTAAGATAAA		
11163	NUDT4	NM_019094	CAAATTCATGTTAGTGAAGTA	ATGAAACTGGTACCAATTTAA	CAGGTACTATTTGTCACATAA	AACATTTGTTCTACAAATTAA
11166	SOX21	NM_007084	CCGGTTTGTATGTACATAGAA	TTGAGCGAATATCAAAGTTAA		
11176	BAZ2A	NM_013449	CACTGAGAAGGCTAAGACTAA	CACCACTACAGAGATATCATA	CCCGCAGTGACGGCCAGTAAA	CTCGGTAGCTTTGAATCTTAA
11177	BAZ1A	NM_013448	CAGCTAGACCAGCTTATTGAA	AACGAGGAAGACCACAAGTTA	CACAAGTTAGATTGCCAGTTA	AACCCTCGTAACACAAGTGAA
11181	TREH	NM_007180	CAGGCCTGAGTCCTACAGCAA	CTCGCAGAAGTCAGCCATGTA		
11194	ABCB8	NM_007188	CACGATGCTGGTGCATTTATT	CACCTTCTTTGACGCCAATAA	AGGAATTTAAGTCATCCTTCA	AAGCTGGAAGCTTCCGATGAA
11197	WIF1	NM_007191	CACAAGGCATCAGTTGTTCAA	CCCTGTCGAAATGGAGGTAAA	TTGCATTGGCTTGAAGCAATA	AAGCAATATAATATATTGTAA
11211	FZD10	NM_007197	CAGGTGTGCAGCCGTAGGTTA	ACCTCACATTTGTGAACTCAA	CCCGATTATGGAGCAGTTCAA	CAGCCGTAGGTTAAAGAAGAA
11212	PROSC	NM_007198	AAGGTTCTCCTGAAAGGTTAA	ATGGCTCAGGTTAATTCTCAA		
11218	DDX20	NM_007204	CAGGGCATGGCAAGAATATTA	CCAGATGAAGACAAGACTTAA	CTGGACTATCAGTCAAATCAA	GGGCTCGATTTAATTGTTCAA
11221	DUSP10	NM_007207	CCGAAGATACTACACACTTTA	CAGGGCAGCTTAAGTGGTCTA	CAGGTTCATAGACCGAAGATA	ATGAGAATACAGGCTCTCTAA
11222	MRPL3	NM_007208	GCCGCCGAAACAGACAGTTAA	AGGGCATAAATATATCATTCA	CCGCCGAAACAGACAGTTAAA	CACATTAAATATATGAGTTAA
11224	RPL35	NM_007209	CGAGGAGAACCTGAAGACCAA	CAGGAAATTCTACAAGGGCAA	TGCAGCAATGGCCAAGATCAA	CCGTGTTCTCACAGTTATTAA
11226	GALNT6	NM_007210	CAGCGTGATCATTGTGTTCCA	CACCTTCTATGGTGCCATCAA		
11232	POLG2	NM_007215	CAGATACGAAATGGTGTTAAA	AAGGAACAAACTTTACTACAA		
11240	PADI2	NM_007365	CAGCAAGCGAAATCACCATCAA	CAGCCTTGACTCATTTGGAAA		
11243	PMF1	NM_007221	AAGGATCTGCACAGTGTTATA	GAGGAAATCTCTGACATCAAA		
11248	NXPH3	NM_007225	CAGCGTCCACTTCCAACACAA	CGACTTCTACTCCAACATCAA		
11259	DOC1	NM_014890	AAGACTGAAACTGAAGCTAAA	GAGGATTTAACTAAACTGAAA		
11279	KLF8	NM_007250	GTCAGTCAGTCTGCCAAATAA	CTGAGATAGAATACAGAAGTA		
11283	CYP4F8	NM_007253	CAAGGACATAGTCTTCTACAA	TGCCCTTGTAGTGAAACGGAA	AGGGAATGTCTGTAACATCAA	CAGAGTCTAAGTAAAGACTTT
11284	PNKP	NM_007254	CAAGCTGGTGATCTTCACCAA	CGGGAAGTCCACCTTTCTCAA	CACGTGTGAGACAGCCCTGAA	CACGTGAACAGGGACACGCTA
11316	COPE	NM_007263	CAGAGCTGTCAGGACCATGAA	CCGGAAGGAGCTGAAGAGAAT		
11317	RBPSUHL	NM_014276	TCCCTTGTCCTTACACATACA	CTCAAAGGTCTCCCTCTTCAA	CCCATGATCATCCGTAAAGTA	CAGGTCCTTCCTGGAATATTA
11326	VSIG4	NM_007268	CAGACTCCTGATGGCAACCAA	CTGGTGCTCAATAAATATCTA		
11328	FKBP9	NM_007270	CAGCGGCGACTTCGTGCGCTA	AAGCTTGCCTACGGAAATGAA	TCGAGTCACAATCGCATGAAA	CTGGTGTTTGATGTTGCATTA
11329	STK38	NM_007271	AAGGCGTTGACTGGGAACATA	CCATAGTACTAAGGAAATAAA	TACGTCGGCCATAAACAGCTA	AACCTTATCGCTCAACATGAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
11331	PHB2	NM_007273	TCGCCACATCACAGAATCGTA	CAGAATCGTATCTATCTCACA	CACAGCTGCTGTAGAAGCCAA	AACCCAGGAATTCTCAATAAA
11334	TUSC2	NM_007275	AAGGCTGGTGCCAGTAGTTAT	CCAGTAGTTATGAGTAGCCTA	CCGCGGCTCTATGTTCTATGA	CAAGCTGAGGCGAGTGCATAA
11336	SEC6L1	NM_007277	CTGGAGCAACATCTGAATGAA	CACGCTCACTTCAAACATCAT		
11340	EXOSC8	NM_181503	CAGGAGATTTCTGAAAGAGAA	CAGAATTTGCAGCACCATCAA		
11343	MGLL	NM_007283	CCCGATTTGCCTGGTTCTGAT	AAGACAGAGGTCGACATTTAT	CTGGACCTACCTTAATGGTTA	TCAGAGCTTGATGCTACTGTA
11344	PTK9L	NM_007284	AAGGAATTCTTTGCCAAGGCA	CCAGATGAAGCTGGACCTAGA	TTGGGATGGTTGAATGCTGTA	AAGACAGAGATCAGTGTGGAA
22795	NID2	NM_007361	CCCACAGAAAGTAAAGTATCA	CTGGAATAGAGAAGCTCCTAA	AAAGCACATGTGATCAATATA	CACGTATAATGCTGCCAACAA
22803	XRN2	NM_012255	ATGGATTACATTAGAAGGCAA	AAGGAGGTTCAGGGCATCAAA		
22818	COPZ1	NM_016057	AGCGATTTAAATTGTATTGAA	TTGGCTGTGGATGAAATTGTA		
22820	COPG	NM_016128	CAGGAAAGGGACATTGTAAAT	AGGCCCGTGTATTTAATGAAA	CACCGACTCCACTATGTTGAA	CCGAGCCACCTTCTACCTAAA
22827	SIAHBP1	NM_014281	CTGGGACTCCGTCACCATGAA	CTCCGTCACCATGAAGCACAA		
22828	RBM16	NM_014892	CACGGTCGTATTCAAGTGAAA	CAGAATGATCCTGAACTTTAT		
22838	RNF44	NM_014901	CAGAGGGATATTCACTAATAA	CAGGTGACGTTTCTATATTTA		
22841	RAB11FIP2	NM_014904	TTGGAAGTATTTAATATGCAA	CTCGTTATAAACACTACTAAA		
22843	PPM1E	NM_014906	CCGCCTAATCATGTGTTTATA	TTGGTTCTATAAACTAGATAA	GAGGCGGTTTATAGTCAGAAA	CCCATTTAGGTCTGTACTAAA
22848	AAK1	NM_014911	CTCCTCGGACCTCTCAACAAA	CCCGAGAAGCTTGGAGGCTCA	CCAGGTGGTAAACCTGATGAA	AACGTGAGTAGCGGTGATGTA
22850	KIAA0863	NM_014913	AAGCAATTTCTTAAAGATTAT	CAGGAGAGAAATACTTTCATA		
22853	LMTK2	NM_014916	AGCGACTATTATATCCAGTTA	ACGGCTCTTAGCTGCGTTCAA	CAGATCAGACTAAGTATAGTA	CACCTCCGACTTAAATGTGAA
22871	NLGN1	NM_014932	CCGCCTCAACACAATGCCTTA	CGGAGGTATATTCTACCATTA	GAGGAATATTATGTGAATATA	AAGAAACATGACTGTCTCAAA
22882	ZHX2	NM_014943	ACGGCAGATCTTCCAAATCAA	CAGTACTATTGTGACATTAAA		
22888	UBOX5	NM_014948	CAGACAGTAACTTTGGTGTAA	TCCCTACAACTTGGTACTCTA	CCGGCACATTCCTTTCCTTTA	TCCGGTGTGCTTGTGTTCTTA
22901	KIAA1001	NM_014960	TCGCAATGGAGTCACACGCAA	CACAGGGTGATGGACCATCAA	AAGGACAAAGTTGACCACACA	CTGGAAGACGATACCGCAGAA
22902	RIPX	NM_014961	TTGGTATAAGTTCCTAATTAA	AACATTGTAAATAATCCTATA		
22913	RALY	NM_007367	CGGGCAGACCCTGGACATCAA	CTCAGCCAAGATCAAGTTAAA		
22915	MMRN1	NM_007351	CACAACTTACTTAGAAATGAA	TCCCTGTATATAAATATATAA		
22920	KIFAP3	NM_014970	TCGAGTTAGCTACAAACATAA	CCACATCTTGATGCTAAGTAA	CACAAGAGACGTCATAATCAA	CAGCATGATGGACCAACTAAA
22925	PLA2R1	NM_001007267	ATGCGTGGAAATATTATGCTA	ACGGTGTAAATACATCTGATA	AAGGTTTGGCTCATAGAGAAA	AAGGAGGTACGCTGTTAAGTA
22927	HABP4	NM_014282	AAGCGAGAATTTGAAAGATAT	CAGACCAAAGCCTGAGTTTAA		
22936	ELL2	NM_012081	CTGGGATTTATACAAGATAAA	CAGAAAGATGGTGTCAATCAA		
22937	SCAP	NM_012235	CCCGGTAGACCTGGAGGTGAA	CACCTGCTTAATTGACACCAA	CCTGACTGTAATAATATTAAA	CTGGCCGACGCTCTTCAGCTA
22938	SKIIP	NM_012245	CACAGGTCTCTCCAAAGTGAA	TCGGATGGTAGAAATGCAGAA	CTGGATATGGGACGAAAGAAA	CCCGATGAAGAAGCTATTAAA
22943	DKK1	NM_012242	CAGTAAATTACTGTATTGTAA	CCCTGTGATTGCAGTAAATTA	CACACTTGTCAGAGACACTAA	ATGTACTATCTTAATGCTTAA
22947	DUX4	NM_033178	GAGCTCTGCGGCACCCGGAAA	AGAGAGGAACGGGAGAGACTA		
22949	LTB4DH	NM_012212	CGCGCCGGAGGGAATAGGAAA	CACTGTTATCGGCCAGATGAA	CCGCATTTATGGGAATGCTGA	GGCCATTTAGATGATTAGTTA
22954	TRIM32	NM_012210	CTGGGTAGTTCTAGAACTTTA	CAGCAGGAATTTGACCCTCTA		
22977	AKR7A3	NM_012067	CTGGGCAGAGATGTACAGGAA	AAGGCTCTTCTGTAACATCTT	AACTGGAAGGAGCACCACTTT	AAGCGACTGCAGAGTGAAAAT

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
22979	KIAA0953	XM_039733	CTCAAGGATATCAGAAGCCAA	CAGCATTTGCGGAATTAACAA		
22980	KIAA1049	NM_014972	CCGGTCACTGTTGCCAAACTA	CCGCTTCGAGCTGATAAACAT		
22986	SORCS3	NM_014978	CAGGCTATTCTGAGCTCAGAA	ATGGAGGAGGGTGATCTACAA	AAGGCAGTCAGTGGATCTTAA	CACAACTTCCTTAAAGTCAAA
22987	SV2C	XM_043493	CCAGATTTAGCTGGAGATTAA	CTGCTCCTAATTTAACATTAA		
22992	FBXL11	NM_012308	AAGCCAGACTGAATCAACAAA	AGCGCTATGTGTACTGCATAA	CTCACTGGAGTTCCTATAGTA	ACCCATTTCGTTGCTACCCAA
23001	WDFY3	NM_014991	CGGCATTAATACTTTAATTTA	AACATGAAACTTCAAACTAAA		
23015	GOLGIN-67	NM_015003	CTGAAAGACAAGAGCATTTAA	ACCGGTCATCGTACAAAGAAA		
23030	JMJD2B	NM_015015	CCCGGCCACATTACCCTCCAA	CAAATTGAAGATGGAGATCAA	AAGCAATGTTTATATTATAAA	CACCTGACAAATCCTAGCGAA
23032	USP33	NM_015017	AAGAATTCCTTCGATGTTTAA	AAGAAGATCCGCAAACCATAA	CTGCAAGTAGTGGACACTATA	CCGGTTGTTCATGTTGATCCA
23033	KIAA1117	NM_015018	AAGGAGGGATATGTCTCTGAA	AACGAGAGATCTCCATATAAA	CCGGATTTCTGTTATGGGCAA	CCGGAGTTCTATGTACATAGA
23040	MYT1L	NM_015025	ACGGAAATGTATACAAATCAA	CAGGACTGAGTCAGAAATGAA		
23043	TNIK	XM_039796	CCGGAATATTGCTACATACTA	ATGGCGTTATTTCTAATTTAA	CTGGAATATAAGCGCAAACAA	AAGGACCATATTGATAGAACA
23045	KIAA0826	XM_093839	ATGCAAATTAATAGACATCAA	ACGCATTGGTACCAAATTTAA		
23049	SMG1	NM_014006	TTCGTTTGCATCACAGTTTAA	ATGGGTCAGGTTCGAAGTCAA	CACCATGGTATTACAGGTTCA	ATCGATGTTGCCAGACTACTA
23052	KIAA0830	XM_290546	AAGATCTATATGTTAAGCTAA	CAGCCAAACTATTATTTGATA	CCGCCCAGGATCAATCAGAAA	AACGAATGGTACAATCTCAAA
23053	KIAA0913	NM_015037	CTGGTATTTATTTGGCATTTA	CACGGGCAAGAGACTCCAATA		
23063	KIAA0261	NM_015045	CTGGATCATATTGTAGATAAA	AAGGAGATAAATCAAAGGAAA		
23081	JMJD2C	NM_015061	CAGATATTAATGGGAGCATAT	TCCCAGAAGTTCGATTCACTA	CCCAGAAGTTCGATTCACTAA	AGCGGGTAGGGCGATAATTTA
23082	PPRC1	NM_015062	AAGGAGCGTGCAATAGAAGAA	CAGGCTTTCATCAGTGAGATT	CAGACTAATAAACATCAACTA	AAGGGTGGTCTTCATTGGAAA
23085	RAB6IP2	NM_015064	CTGAAGTTATATAGCCTTGAA	AACGGGCTTTAACATGTTTAA	TAGAAGTAAATTAAAGTTGTA	CAGGAACTTAACCCAAATCTA
23086	SLAC2-B	NM_015065	AAGGAAGATTATGGAAACCAA	CAGGAGAATAAGAGATATGAA		
23090	ZNF423	NM_015069	CAGCAAGAAGTATAACTGTAA	CAGAGAGAAATGCTTAGTCAA		
23091	KIAA0853	NM_015070	CTGGCATATAGTAATAGCCAA	AAGAAGCGCTATAGAAATGAA		
23098	SARM1	NM_015077	CTGGTGGTTAAGGGTAGCAAA	CAGGATCGGGATTACAGGCAA	CTGCTATTAAATCCACATTAA	AGCGGTGTTGGCGACTAACAA
23108	GARNL4	NM_015085	CACATTGTATTTGTTAATGTA	CAGGGAGTTTCTGCTCACCAA		
23116	KIAA0423	NM_015091	AAGGCGTATTTGGAAGTTTAA	CTGGAGCTATTTCACAGTATA		
23118	MAP3K7IP2	NM_015093	ATCCTAGGTAATTAAACCATA	CTGGGTAAACTATCTTTGTAA	TGGCTGGGTATCTCAGTTTAA	CAGTCAATAGCCAGACCTTAA
23126	POGZ	NM_015100	CAGGGATTTCCTGTAAGGAAT	CCGGGTGTAAGGTCCCTTTAA		
23129	PLXND1	NM_015103	CAGCCGCACTGCACAAGTGTA	CATGACAGTCATGGTCTATAA	CACGAGTACCGGGTCAAGATA	CACGCTCTGCAAGGTTCTCAA
23144	ZC3HDC3	NM_015117	AACGTGGTCATCAAAGTTAAA	CAGCGACTTCCTCAAAGGCTA		
23148	KIAA0363	XM_166871	CCGGGTGAGGCTGGAGTGCAA	ACGATCAGATCTGTCCTGCGA		
23149	FCHO1	NM_015122	CAGGAAGTTTGCAGAGAGTAA	CAAGTTCTATGTGCACATCAA		
23158	KIAA0882	NM_015130	CTGCAAGATAATGTAACTGAA	CTGAATGGATGTGGAAATGAA		
23163	GGA3	NM_014001	CTGGAGTCCTGGCTCAATAAA	AAGGAATAAATCCAAGAGCTT	CACGTTAGAGGAAGTTAACAA	CAGGGTGTCTGAGAAAGTGAA
23165	NUP205	NM_015135	CTGCGTCAGTTTAAATTTCAA	CTGACAGGAATTATAAGTAAA		
23166	STAB1	NM_015136	CACCTCGTGCGCGGCCATCAA	CACGAAATACTCCTACAAGTA	CACGCCAACTGTAGCCAGGTA	TAGGAACAATGGTCACTTGTA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
23170	KIAA0153	NM_015140	CGGCCACATCTTCAAGGTCTA	ACCCAGAACCTTCACCAGCAA		
23177	KIAA0582	NM_015147	CGGCAATTTAAGAAAGATATA	CACCCTCAAATCACCTACTAA		
23180	RAFTLIN	NM_015150	CAGGCAGATGAGGAAATCAAA	CTGAAATTCGTTGGTGTTATA		
23191	CYFIP1	NM_014608	TCGAAAGGTTATAGAAATAAA	CCAGCCAAATTTCAACACTAA		
23203	PMPCA	NM_015160	CAGAATAAGTTTGGACAGTTT	CAGGATCGAGATATGAAGCGA	CTCACCGAGATGATTCATGAA	TCGAGAAATGGTAGAAATCAT
23213	SULF1	NM_015170	AGCATGGATTTGATTATGCAA	AAGAGGCAAATTTCTACGTAA	TCCGTCGAATTTGAAGGTGAA	CTGGTGTTTGCGTACAGTTAA
23218	KIAA0540	XM_291064	CTCGGGAGAGACGGAATACAA	CACACAGAATGTATACTTCTA		
23231	KIAA0746	NM_015187	TAGAAGATTCTTAGTACTTAA	CCGGGAGGATTTCCATTATAA		
23235	SNF1LK2	NM_015191	CGGGTATGTCCTGGTGAATTA	ATCTACCGAGAAGTACAAATA	CCGAAGGATGTTGGTCCTAGA	AAGGGCAAGATTATTTGCTTA
23236	PLCB1	NM_015192	AAGCGAGTTGAAACTGCTTTA	CACACTACCAAGTATAATGAA	CAGAGATGATCCGGTCATATA	TCGAGATTACATGGATGTTAA
23258	RAB6IP1	NM_015213	CCGATTTGTCACTGCAATCAA	ACCATTGAGAAGAACATTCAA		
23259	DDHD2	NM_015214	CAGGATGAGTATGGACCTTAA	AAGAAAGAAGATATTAAACTA		
23268	DNMBP	NM_015221	TCCGAGGTTCCTCAAAGTTAA	CCAGCTCTTCACAAACTTTAA		
23277	KIAA0664	NM_015229	CAGCCCGACCTTCAAGAAGAA	CCGAGAAAGGGCCATATTCAA	AAGGGCCATATTCAAGGTGCA	CTCGGCCAAGCACATCTTCAA
23283	CSTF2T	NM_015235	CAGGATAAGGTTACACTTGTA	CAGCCATTTAGTCCTAATATA		
23284	LPHN3	NM_015236	CAAGCGTACAATGACAGGTTA	AAGTATGGGAGTAAAGCTAAA	CAGGAACTATAGGTGTATCAA	AAGCTAAACATTGCATATCAA
23303	KIF13B	NM_015254	AAGGTTATTCTTAATCCTGTA	ACGGGAAGCATTAGCAAGAAT	CCCACTAATGTCTTAACCTAA	ATGTCTTAACCTAAACCATAA
23304	UBR2	NM_015255	ATGGATCCAATTACACGTCAA	CCAGATTTATTACTACCATAA	CAGAACAATACTCTAATAGAA	CAGGTAAATGCTACAGATGAA
23309	SIN3B	NM_015260	CACATTAAAGTTAATAATTGA	CAGCTATGTGAATAAGATTAA		
23313	C22orf9	NM_001009880	CTCGCCCTTTGTAATAACCTA	AAGAATGTACCTGCACTCAAA		
23315	SLC9A8	NM_015266	CACCCTGGTTGTCACGACGAA	CTGGATGCCTATTTAGAAATA	CAGAGTCGCCTTAGTCCAGAA	TTGGCTCACCTTGGTAACAAA
23316	CUTL2	NM_015267	AACATTCTCATAAACATTTAA	AGGGAGGAACTCAACCATCAA		
23324	MAN2B2	NM_015274	GTCCAATATCAGAACTATTAA	CCGGACGTTCTTTATTCACTT	CACGGGTTTCTCTATGAAACA	CGGGCTTTCTTTGGAAGATGA
23326	USP22	XM_042698	AAGGTGAATTTCATAAATGTA	CTGAGTTTATACAGAAATTTA		
23332	CLASP1	NM_015282	CAGGATTAGAAACACACTTAA	AAGCGTAATGTTACACTTTAA		
23347	KIAA0650	XM_113962	AAGGATCTTAACAGTCAATTA	CAGGGATAAAGTAATTCCTAA	AGGACCAATTATCTCAGTCTA	CCCGTTCGTCTCAATGTTAAA
23352	RBAF600	NM_020765	CTGCGTGAAGGTGAAAGTCAA	CAGCAGGGTTATGCCCTTAAA		
23367	LARP	NM_015315	CAGGCTGAAGTGATTCATTCA	CACCTAATCCACAGAAAGTAA		
23378	KIAA0409	NM_015324	AAGGGTAGTACTACAAATGAT	AAGGGAAGAAGAAATGTCAAA		
23379	KIAA0947	XM_029101	CTGGCAGTTTATTGCTCTTAA	CCGCATCATTCAGAACATAAA		
23385	NCSTN	NM_015331	CCCGAATGGCTGAGCCCTGAA	CAGTGCCAGGATCCAAGTAAA	AAGGTTTAATGTCAGGGTCAA	TCAGATTGGGATTAACATAAA
23386	KIAA1068	NM_015332	AGGCAGGAACTTGAAGAGAAA	CCCTGCTTTAATAAACAGCAA		
23396	PIP5K1C	NM_012398	CGGCGAAACCACCTACAAGAA	GACGGCGAGAGCGACACATAA	CGGCAAGACCTATTTATAATA	CCGCGTCGTGGTCATGAACAA
23398	KIAA0073	NM_015342	AAGGTTGATGCTGTAAGATTA	ATGGGAGACATTCACACCAAA		
23403	FBXO46	XM_371179	CAAGATCACATGTGACTTATA	CCCGCCTTCTGCGGCCCTCAA	CAGCGATAGCTCCAAGGCCAA	CTAGATGGTTTGCCTATTAAA
23404	EXOSC2	NM_014285	CTGGTAAAGTTGGAAGAATAA	CTCCATTCCTATATCCTTTAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
23411	SIRT1	NM_012238	CAAGCGATGTTTGATATTGAA	TTGGGTCTTCCCTCAAAGTAA	CAGGATTATTGTATTTACGTT	ATAGCTGTTCTTTATGCATAA
23413	FREQ	NM_014286	CTGCGTGGCTAGGATGATTAA	CCCGGGCTGGTTGGTCTTGAA	GCGGAATAAACCCAATGGTTA	CGGAATAAACCCAATGGTTAA
23416	KCNH3	NM_012284	CCGGCGGGAGCAGGTGGTAAA	AGGGTAGTAGATGGCATTGAA	CCGTACCACATTCGTGTCCAA	CAAGGACATCAGCGAAACCAA
23417	MLYCD	NM_012213	CCCGGGTTCCTGAACCTAGAA	CAAGGTGTGTGTAGTAAGTTA	AAGTTGGATAATAGGCTTTAA	TAGGCTTTAAATGATCAGGGA
23428	SLC7A8	NM_012244	CTCCCAATATATTTACACGAA	TGGTGAGAAATTGTAAACAAA	CAGGCGGTTGAGGAACATATT	CCCGAATTCTGTCTGCTTAAA
23451	SF3B1	NM_001005526	AAGACTCACGAAGATATTGAA	CAGGTTATTATGACCAGGAAA		
23456	ABCB10	NM_012089	ACCCTGCTTCTGGAACTATTA	CCCAGTGTGGCTGAGATCCAA	CTAGGTATTATTAAGAATGAA	TAGACCCTAAGAAGTAATTAA
23457	ABCB9	NM_019624	CTCCCTAGCCTCCTAAGCAAA	TTGAGAGAACCCGGTCAATAA	CTGCGTGACCACGGCCATCTA	CCCGGTCAATAAAGTGTACTA
23463	ICMT	NM_012405	CAGAAATATGACTTATTTCTA	CAGAGTGTAAGTAAAGGATAA		
23468	CBX5	NM_012117	CAGGGAGAAGTCAGAAAGTAA	GCCGATGACATCAAATCTAAA		
23471	TRAM1	NM_014294	CCGGAACAATTGTGTGCTTTA	CTGGCATTATACTGAACTATA	ATGGTGTGAATGGAACATTAA	CAGGGTAACATGGAAATACTA
23474	ETHE1	NM_014297	TCCCTGGAGCTCCCTAAATAA	CAGCTGTGAGGAGTTTGTCAA		
23480	SEC61G	NM_014302	CAGCAATAGGATTTGCTATAA	CTAAATTAAAGTAATTTCAAA		
23484	LEPROTL1	NM_015344	TCCCAATGTTATGCAGACATA	CACAGTCATCTTTGCAACTAT	CAGAGACTTGCTGAAGGATTA	CAGACGGTTGGCATACGTTAT
23495	TNFRSF13B	NM_012452	CTGTAGGTCGTCATCACCTAA	CAGCGGAGTGGAGAAGTTGAA	AAAGGAGCAAGGCAAGTTCTA	AACCCTAAGCAATGTGCATAC
23506	KIAA0240	NM_015349	TTGGATATAGTCAACATATAA	CCCAATTAATATACAGCCAAA		
23507	TA-LRRP	NM_015350	AAGCATATTGGATTTATTTAA	CAGATCAACGTCAATAATGAA		
23511	NUP188	XM_497078	AACAATGTTATTCGGCTGAAA	AACAACCTCATTGCTGTTCTA		
23513	SCRIB	NM_015356	CTGGGAGGCAACGATCTGGAA	CAGGATGAAGTCATTGGAACA		
23524	SRRM2	NM_016333	CCCACTTGGTACAGAAATGAA	CTGGGTCATCTCCAGAAACAA		
23531	MMD	NM_012329	CGCCATTTGGAAATACCTTTA	ACGGACTTTATGCGGCATTTA	AACCATTTATGTATTTCTCTA	AACCACTAATATGTATGTAAA
23532	PRAME	NM_006115	AAGGAAGGTGCCTGTGATGAA	CAGGATGTGCATGCATCTTGA		
23533	PIK3R5	NM_014308	CAGGATCTATAAACTCTTCAA	TAGGATCCTTTCTAGAAGGAA	ATCGCAGATCAAAGTGGACAA	ACCGGTGCTGCTGCAACTCTA
23543	RBM9	NM_014309	TAAGAAGATGGTCACACCATA	TCCGTTTGGTTTATGGAGAAA	ACGGCTGCTTTGAAAGGTTTA	AACGGTATAAAGAGAGATCAA
23548	OSRF	NM_012382	CAGGAAGATACTATTGGTGTA	CCGCTTTATGTTAAAGATCTT		
23549	DNPEP	NM_012100	CACGAGGGTGATGAAGGCCTA	CAAGTACTTCATGACCAGGAA	GAGCTGAAGCTGGATTATTAA	AAGTGGATTGTCACTCAGAAA
23550	PSD4	NM_012455	CTGCCAGGAATTCATAACCAA	CACGGCCAAGGTGAAGCGCAA		
23551	RASD2	NM_014310	CTGGGAGGGATCCGACAGAAA	CTCCGTGTACACTATCAATAA	TCCGTGTACACTATCAATAAA	ATGGATCTCCGTGTACACTAT
23562	CLDN14	NM_012130	AACAAGTTTAATATAAAGTGA	ACGGCCGTGTCCTACCTGAAA	CGGGTACAGGCTGAACGACTA	CACGGCCGTGTCCTACCTGAA
23563	CHST5	NM_012126	CAGGGAGTAAGTTACTGCTAA	AGGGAGTAAGTTACTGCTAAA		
23564	DDAH2	NM_013974	CTGGATCTGGCCAAAGCTCAA	TAGGATAGTATAGGAAGTAGA		
23567	ZNF346	NM_012279	ATGGGCCAGACTACAACTTAA	GGGCCTCATGAAGGTCTTTAA	CGCAAAGAACTTAAAGCTGAA	ACGCAAAGAACTTAAAGCTGA
23584	VSIG2	NM_014312	CTGCCTGGTCAGGTTCCAGAA	CAGCACCGTGACGACCACCAA	CCCACCAGATTTCTACACCAA	ATCCAACTGGTTCTAAGTCAA
23586	DDX58	NM_014314	AAGGATAATACTGAACTGTAA	CAGGAATGTGAAGAAATTCTA		
23589	CARHSP1	NM_014316	CACCATCTGAAGAGCATTAAA	CTGCACATCTCTGATGTGGAA		
23590	TERT	NM_014317	CTGGCACGAATTGGAAATACA	CAGAGTGATGGTGTGCAACAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
23604	DAPK2	NM_014326	ACGCCGGTGGACAACCAGCAA	AACCCTTGGTACCACAGAATA	CTGGTTAAAGAGACCCGGAAA	CGGAATTTGTTGCTCCAGAAA
23613	PRKCBP1	NM_183048	TTGACGCAAATAGCGAAAGTA	ATCGACACGTTCCGATCACAA	CACCATTGAACAGTTATCCTA	AGCGAACTTGTCATAGATTTA
23616	SH3BP1	NM_018957	CCCTGGAGACATCAACTTCAA	CAGCCCAGTCTCTTTGAGTAA		
23620	NTSR2	NM_012344	CAGCTTCGTGTGGTTCCACTA	CAGAGCCATCGTGGTCATGTA	TCGTATGGAAGAAGACCTTTA	CCGGACCTGAATGTAATGCAA
23624	CBLC	NM_012116	CAGACCATCCCTGCCAACAAA	CAAGATCTGTGCTGAGAGCAA	CTGGGAGGCCGTGAGTATCTA	CAGCCGAAAGTGAGACTCCTA
23626	SPO11	NM_012444	TACCTTCTACGATACAACTAA	ACAACTAATGTTAACGCATAA	TACATATATTATCTACATCAA	CAGAGTGTACTTACCTAACAA
23632	CA14	NM_012113	GTGGGTGAGACTAAGAATATA	TTGCATGAAGTCAGGCATAAA	AAGCAGGATCCTCGTATACCA	CGGGATCTCTCCTTAGGATAA
23633	KPNA6	NM_012316	CAGGTACTTATTATTGGCCAT	ACGCTTGGATTGAGTTATTTA	CTGGGTGGATTACATATGATA	AACCATTCTCTTACAGTTTAA
23636	NUP62	NM_016553	CTGGAGAGCCTGATCAACAAA	CCGCGAGGTGGAGAAGGTGAA	CGGCTTTGCCTTGAATTTAAA	ACCGGCTTTGCCTTGAATTTA
23645	PPP1R15A	NM_014330	CAGGATCAGCCGAGGATGAAA	GTGGGTTTATATAAGGAATAA	TGGGTTTATATAAGGAATAAA	CCAGTTGTTGATCTTATGCAA
23650	TRIM29	NM_012101	CTCCATGTACCTGACACCCAA	CCGGCCATTCTACGTCAACAA		
23673	STX12	NM_177424	AAGAATTTGATGAGCCAGCTA	CTATATTTAATTGGAAGGTAA	TCCTTCTGTTATTATACTTAA	CTGGGTTTAAAGTTTACTTCA
23678	SGKL	NM_013257	CCGAGATGTTGCTGAAATGTA	CATGGTATGATCGAAATGTAA	CCACAGCGAGACCCTAGTTAA	ACCAACTAACTTACATGCTTA
23682	RAB38	NM_022337	ACGAGGGTCTATTACCGAGAA	CAGCAAAGGCCTCAAGTCTTA	CTCCAAGTTAAGTCTCCCTAA	ATGATTTGGACTCCAAGTTAA
23683	PRKD3	NM_005813	CAGGCGGGAAACTGAATAATA	CTGAGCCTATTTCTAGTATAA	CGGGAGAGTGTTACCATTGAA	CACGATATGTCAGTACTGCAA
23704	KCNE4	NM_080671	CTCGGAGAACATCCATCAGAA	TCGGAGAACATCCATCAGAAT	CCCAGCCCATTTGCACACTAA	CCAGCCCATTTGCACACTAAA
23760	PITPNB	NM_012399	AACAAAGTAAATGAAATTTAA	CAGGATAAAGACTGATGTTTA		
23761	PISD	NM_014338	TTCCTTCTGCCTACAAATAAA	CAGCTTCGTGACGCACACCAA		
23765	IL17R	NM_014339	CAGGTTTGAGTTTCTGTCCAA	CAGGAAGGTCTGGATCATCTA	CGGCACCTACGTAGTCTGCTA	CAGCGGTCTGGTTATCGTCTA
23770	FKBP8	NM_012181	CTCCTACGACCTCGCCATCAA	CTGCCAGGAACTGACCACCTA	AAGACAACATCAAGGCTCTCT	AATCCCATGGAAGTGGCTGTT
23786	BCL2L13	NM_015367	CAGGCATTTCGGGAATGTACA	CTGGATGGTCCCTGTCTATAA	TTGGGCTTATAGAGCCAGTTA	CCGTGTCTTTCCAGCCCTAAA
24139	EML2	NM_012155	CAGCAGCTGCTTTGTCACCAA	CTGCGGGAAATCTCACATCTA		
24142	NAT6	NM_012191	CTGCTGGAGACACAATATCAA	CCGCCTGTCACGGGTGCTGAA		
25764	HYPK	NM_016400	CAGCAGAGTTACTGTACTCAA	CTGGATTAATTTATGGCAATA		
25776	PGEA1	NM_001002880	CGGCTGAAAGTGGACATCTTA	CTGGAAGAGAGTATCATATAA		
25777	UNC84B	NM_015374	CTGGGAGTGTGTATATATGTA	AAGGAGGATTTCCGCAGGGAA		
25778	RIPK5	NM_015375	CTGGTCCATTAGATTCCGAAA	CACCGCTTTATCGCCAGCTAA	TTGCTTCATCGTAAACCTAAA	TAGAGCTTGTTTGATGTTAAA
25788	RAD54B	NM_012415	CACGAACTTCGACCTACTGAA	CAAAGGCAGATCAGTAAGCAA	CTGGATCAAATTAAGAATATA	ACCCAAGAAATTATAAATAAA
25793	FBXO7	NM_012179	CCGATTTACAATTACATTGAA	CAGGATGAACAACCAAGTGAT	GACAATACTGTCAGAGTTCAA	CACAGATTGGAAAGAACTGTA
25796	PGLS	NM_012088	AAGCCAGGTGATCACCATTAA	CAGCGTGTGACCCTCACACTA		
25804	LSM4	NM_012321	ACGGATCTGCTCAGAAAGGAA	CGACAACTGGATGAACATTAA		
25822	DNAJB5	NM_012266	AACGAGGATGAGATCAAGAAA	CCGGAAGATGGCCTTGAAGTA		
25824	PRDX5	NM_012094	ATGGTGGTACAGGATGGCATA	CAGCCAGGAGGCGGAGTGGAA	CTGAGTGTTAATGATGCCTTT	CACCTGCAGCCTGGCACCCAA
25828	TXN2	NM_012473	CCCGGACAATATACACCACGA	CAGGATGGACCTGACTTTCAA	CGGGAAGGTGGTGATGGCCAA	CCCAAACTAGTGAGAGTAATA
25830	SULT4A1	NM_014351	AAGCAGATGCTTAATAGTAAA	CCGGAGGTTTATGAATGATAA		
25832	DJ328E19.2.1	NM_015383	AACGATGACGATGAAGATGTT	AACGAGAGCTGACCCAGTTAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
25839	COG4	NM_015386	CAGGGATGTTCTGTGTAATAA	CAGGAGCTAATTGGCTTATAT		
25847	ANAPC13	NM_015391	CTGGAATTATTTGCCTGTTAA	ACGGTTTGTTTCAGTCTCCAA		
25853	WDR40A	NM_015397	CAGCATCAATGTGATTAGTAA	AACACTGATAATAGGAAGTAA		
25859	PART1	NM_016590	ATGAGATATTCTACACATTAA	AAGAAAGTCACTCATGAGTAA		
25865	PRKD2	NM_016457	CCGGCAGGGCCTGCAATGCAA	CAGCGGCACCTTCCCTTTCAA	TTGGGTGGTTCATTACAGCAA	CACGACCAACAGATACTATAA
25873	RPL36	NM_015414	CGGGAGGAGCTGAGCAACGTA	AAAGAACAGCTTGACAGGAAA	GCCCTCAAATTTATCAAGAAA	CTGCCCTCTCCCTGAAATAAA
25874	DKFZP564B167	NM_015415	AAGCTAAAGCACACAAATAAA	CAGGGTTTATTTGGTCAAGAT		
25886	DKFZP434C245	NM_015426	CCGGGCTCACACACAAATGAT	TAGAAATTGATTGCACATTGA	CTCCAGTGACTCAACCCTGAA	CCGGGAATGTGTCCACTCGTA
25903	OLFML2B	NM_015441	CAGGCTGCTGTTCGAGAATGA	TCGAGAATGAGTATTCCTATA	TTGTATAATATTGCAAATGTA	GCGGATTTACGTAACCAACTA
25911	DPCD	NM_015448	ATGGTCATATTTCCTGAGTAA	AAGGAAATGGCTGAAGAATAT		
25913	POT1	NM_015450	CAGGCTGAAGATTCAAGTATA	CAGGGTCTTGCCAGAAAGTAA		
25917	THUMPD3	NM_015453	AAGAGGATGTATCAACATTAA	CAGGAGAGAAACATTGCTTTA		
25926	DKFZP586L0724	NM_015462	CAGGACAGTCATCCTCTATAA	TTCGGGAGCTACAGAAATTAA		
25927	C2orf32	NM_015463	AAGGATGGTAACAAACTAGAA	CAAGGTTGAGGTGAAGATTAA		
25932	CLIC4	NM_013943	CACGAACATGCAGTTATTGAA	CTGGATATGTACTAAGGAATA	TAGCAGTACAATGATTAGTAA	CAGGGAAGTTAGTCAAATGAA
25937	WWTR1	NM_015472	AGACATGAGATCCATCACTAA	CTGGCTGTAATCACTACCATT	CTGCGTTCTTGTGACAGATTA	ACAGTAGTACCAAATGCTTTA
25938	C14orf125	XM_113763	TCGATTTATGAGAAAGATGTA	TAGGTTCATATCTACATTGTA	CAGCCTTACAGTGCAACATAA	CTAGGCATAATATTAGCTAAA
25942	SIN3A	NM_015477	CAGAGGATATATGCTGATAAA	CAGATCCGCAGACATCCTACA	GAGCGTGTAAGCAAGCGTCTA	CTGGTCACTCGAGCACATCTA
25943	C20orf194	XM_045421	ACCGGGAAATTGAGAAGTATA	AAGGTAATTATCAGCATTGTA		
25959	ANKRD25	NM_015493	CAGGTTCATTAAAGAAGGCAA	AAGCTGATTGGAAACAATTAA		
25963	DKFZP564G202	NM_015497	AAGATTGTCATCAACACCATA	CAGAAGTTGTAGCTTATACAA	AGCGCTGATTGTTACAATGAA	CTGGCTTAATTTAAACAGTTA
25972	UNC50	NM_014044	CCGGCTGAAACTGCTTTCTTA	AAGAAAGAGCATTTAGTATAA		
25977	NECAP1	NM_015509	CGGGAACATTACAAACAAGAA	TAGCTTCTCCATCACATTCAA		
25979	DKFZp566O084	NM_015510	GAGGATGAAGTTGATTGACTA	CCGAGATGGAACAGTATGAAA	TTGCATTTGTTGAGACTTTAA	CAGATGTTATGTCACCTGAAA
25980	C20orf4	NM_015511	CAAGAGCATAATGTACATTAA	TAGGAGCTTAGGAAACAAGAA		
25981	XLHSRF-1	NM_015512	CAGGATGTACATCACCACCAA	CAGCCGTACATCGATAATGAA		
25988	MIZF	NM_015517	CCCAAGGACTTTCATGATTAT	CAGGGCATTATTCTAGAAACA		
25992	SNED1	XM_059482	AAAGCTGTTCTTAGACTCCAA	CTCAGTGAAGCGAAACAGTAA	CAGGTAGTAAACACGATCTTA	CACCTAGGCTTCAGCCTTAAA
25998	IBTK	AB037838	AAGCATGGTGTTAGTCTGTAT	GAGGATTTAAATTATCCTAAA	TAGAAGAGTCATTACACCATA	CAGATTGAGGAGCATGCCATA
26009	ZZZ3	NM_015534	CAGCCTGATGGGAACACTAAA	TAGGAATTTACCTGAATATAA		
26015	RPAP1	NM_015540	AAGGAGGATAGCTGAAGCCAA	CAGCAACATCTGGTAAGAGAA		
26020	LRP10	NM_014045	TACAGAGAATCCTAATGATAA	CAGGGTGCCATCCCACCTGTA	ACCCTATGTAGCTGCTATAAA	CACCGGAATGCCAATTAACTA
26030	PLEKHG3	NM_015549	AGGAATGAAGCCAATAATTTA	CCGGTCTTCCTGCAAGAAGAA		
26031	OSBPL3	NM_015550	CTGCATTGTACTAATCTGTTA	AAGAACCAAGGTAGAATTTAA		
26033	ATRNL1	NM_207303	CAGGTTATTATGGAGATCCAA	CAGGGTGACAAGATATGTATA	CAGCTTTCCGCCTAACTAGAA	TTGGTCGTAGGTAAAGGTCAA
26038	CHD9	NM_015557	CCCACGGTACATGATCCTCAA	CAGCTACAAGATTGATTACAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
26040	SETBP1	NM_015559	ATGGAATGCCTTACACATCAA	CAGAGGGAAGTCTGAAGCTAA		
26043	KIAA0794	XM_087353	CAGCTTGAAAGGAGTGTTTAA	CAGCACGTGCATATTCATTTA		
26050	SLITRK5	NM_015567	TTGCATCTAAACAATAATAAA	CAGGCTAAACCTGAGGAGTAA		
26063	DECR2	NM_020664	CAGAATCGACATTCTCATTAA	CTGCACCACCTGTTTGCATAA	AAGATAATCTATTTACTGTAA	AAGAAAGAGGATTAAAGAGAA
26088	GGA1	NM_001001560	CAGAGGCCTACCAGATGCTAA	TCGGACATCGGAGAAGGTGAA	TCGGTGTGTCTCCTTCATTCA	CCGAAGAATGTGATCTTTGAA
26091	HERC4	NM_015601	TACGTTAGCGCTAAATGACAA	CAGAGTACCCAGAAATATTAA	TAGAAATACTACATAGGGTAA	GAGGGAATTATTGGATCCTAA
26127	FGFR1OP2	NM_015633	CCCGCCGGTGATGGCGTTGAA	TACGCTAAATTTCATCCTTAT	TAGACATATTTAGTAGGTTAA	ACGGAGGATTTGTACGCTAAA
26145	IRF2BP1	NM_015649	CTCCGATTTCGAGAAAGAGAA	CCCGTTCAATGTGCGCTTCAA	TTCAAGTACCTCGAATATGAA	ACCGCTGCCGCGGATAAATTA
26148	C10orf12	NM_015652	CAGAGGATTTATAATTATAAA	CAGGATTTAGAGGCAAATGAA		
26154	ABCA12	NM_015657	CACTCAGTTAATACCGATCAT	TTGCGACTCTTAATCAACGAA	AAGCCTAATGATCCGACTTTA	CAGGTGACTCCGATAATATAA
26155	DKFZP564C186	NM_015658	AAGGATGAGGACAGGAAGCAA	CACGGACAGTGCTGCATTCAA		
26165	C9orf36	NM_015667	GGGAAGAGAAAGAGTCCAGTA	CTCAGAAGCTCTCAGATCCTA		
26166	DKFZP434I092	NM_015668	CCCAGACTATATAAACTTCAA	TCGGACCAAATTGCTTATAAA		
26175	C14orf109	XM_058628	CAACATAGTGATGATTCAGAA	CTGGCCTTGGAACACATTCAA		
26190	FBXW2	NM_012164	CAGAGTGTATGCACTTTACTA	ACGGAATGGGTCACCAAGGTA	CCAGTGGGACTTTGCCAGTTA	CACGCAGTGCACAATCATTTA
26212	OR2B6	NM_012367	CCACAAATGCTAGTAAATTTA	CAGCATCATACAGGAGTTTAT		
26226	SHFM3P1	NM_012165	CCGGGAAGAGTACAAGGACAA	ACCGCTGGCTGTGGCACTTCA	CTGGCTGTGGCACTTCACCAA	CCCAGTGAAGGTGTCTCAGAA
26227	PHGDH	NM_006623	CTCGAGAATACTGCCCAGTTA	TGGGATGAAGACTATAGGGTA	CACGACAGGCTTGCTGAATGA	CAGCAATAACCGTCTAATAAA
26228	BRDG1	NM_012108	GAGGCTTCATTCTTACAGTAA	CACCTGAACACCAGAATTAGA	AAGGAACCAACTGAAGATTAT	CACCAGAATTAGAATTAAACA
26232	FBXO2	NM_012168	CACAAAGTGGGCTCTCAATAA	TCGAGGGTAGATAGGCCTTAA	AAGCTCACCGTTAAGCTACTG	AACGATGAGAGCGTCAAGAAG
26233	FBXL6	NM_012162	CCGGCTGACTCTAGCCAAGGA	CCCGGGCCTGCTCTACCTCAA		
26235	FBXL4	NM_012160	CACCGGTCTTTCCCATGTTAA	TTGGCTGGTGTACCAAATGTA	TCCGAATTAGTACGCCTTGAA	AACGACTTGTTCTCTATCGAA
26254	OPTC	NM_014359	CACCTGCAGAATAACCTGATA	CAGGGACAGCTTCTCTCCCAA		
26256	CABYR	NM_012189	ACCAGTGTAATGTATCAATAA	CCAGTGTAATGTATCAATAAA		
26261	FBXO24	NM_012172	CCACCACTCAATGACCTTCAA	CCGAATCTTCATGCAAGGAAA	CCCAAGGTGTGACACAGTTTA	CAGGCGAGTGACTGTCAAGAA
26273	FBXO3	NM_012175	CTGACGATTATCGATGTTCAT	CTGCCAGAACTTAGCTCTGTA	GTCGGGTATATGAATACACAA	TCGCTAAGACCTTGACTTTAA
26275	HIBCH	NM_014362	CAACTTAGGTATACAATATAA	CACGGGAGTCATAACACTAAA		
26276	VPS33B	NM_018668	CCGGAGAGGCATGGACATTAA	CAGCGTTGGATCAACACTGTA		
26292	MYCBP	NM_012333	AAGCAGGAGAATCCAAAGTAA	CAGGACAGAGGCAATATACAA		
26298	EHF	NM_012153	CAGCAATAATATGCAAATGAA	CTGGAAGTAAGAAGAATTAAA		
26330	GAPDS	NM_014364	CAGGCCAATGATAACCTTATA	CCCGGAATACATGGTGTACAT	CTCCATGAACATTGTGAGCAA	CCGAGACAAGTGAAACGGGAA
26338	OR5L2	XM_372387	CCGCTTTGTGGCCATCTGTAA	TTCACTCGTCCTTAGCTCTTA	CACCACTATCCTGAAGATACA	AACAGTGGAGATGTTGACAAA
26469	PTPN18	NM_014369	CCGGGTGTAAGTCTAACGCCA	GTGGGCCTGGATCAAAGTTAA	CCCAATGACTGTAGCATTCAA	CAGGCAGACATCAGTCCACAT
26507	CNNM1	NM_020348	CAGGTCTTAAGTGCAAATCAA	CAGGTGCAATTCCAAGCATAA		
26515	FXC1	NM_012192	CACCGAGAAGCTGAAACGGAA	CAAGTATTTGTTGGTTCATAA		
26523	EIF2C1	NM_012199	CCAGACCTCGACCATGATAAA	CAGCTACAACTTAGATCCCTA	CTCCAAGAATTGTGCAAGTAA	TAGGCTTAACATAAAGCCGAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
26533	OR10G3	NM_001005465	CTGCGTTTATCCTGACAGGAA	CTCATGATGAACTTCACTTTA		
26538	OR10H2	NM_013939	AGAACTGAAGGTTGCCATGAA	TGCCTCTGTCATCTACCTCAA	TTGGCCTGTGGAAATAATGTA	CACCCTGATGGCCACCACCTA
26539	OR10H1	NM_013940	CACCTTGATGGGCATCACCTA	TTCAGTAAACTCTACCCAGAA	GACCTTCTTCAGTAAACTCTA	AAGAAGACCTTCTTCAGTAAA
26578	OSTF1	NM_012383	CAGATGCAGTTCGAACATTAA	GAGGACTATCTCGATGATGAA		
26583	DUX2	NM_012147	AGCCAAAGCAAGGCCCTACAA	CTGAGGCAGCACTGGCATTAA		
26610	ELP4	NM_019040	AAGGAATTTGATGAAGATGTA	TTGGACCAGTATCATCTTCAA		
26658	OR7C2	NM_012377	CTGTGGAATCCTATTCTCTTA	CGCAGAGGACTCTGACATGCA	CTGGTGAATATCCAAACACAA	CTGCAGTTACACCACCTTCTA
26659	OR7A5	NM_017506	AAGATAATTTATTGGCTATAA	AACTGGTCTTGTAGAATTTAA	ACAGTCAGAGATGACCTTAAA	AAGCTTAGTGCCCATATATAA
26716	OR2H1	NM_030883	CTGCTAGACAACGTTTGATCA	TACGTAGGTCATGTAAGCAAA	TAGCTCCATAAGGCACACAAA	CCACATTAAAGTTGCAAATAA
26762	HAVCR1	NM_012206	AACGCTGATCCCATAATGCAT	TCGGAAGGACACACGCTATAA	GGCCTTTGGAATAACAATCAA	CACCATTGTACTCTTACACAA
26873	OPLAH	NM_017570	CTGCCTCATCATCGACAGTAA	CTGCTGCACATTGGCACCCAA		
26985	AP3M1	NM_012095	ACGGTCTTCCTGCATATTTAA	CTGGATTATGTAGAAGATTTA		
26993	AKAP8L	NM_014371	TAGCTCTGACACAAATGCAAA	CCGGCCAATGGCCTCAGGCTA	CAGGATAACACCACCAACTAT	AAGGAACACTTTAAGTACGTA
26995	TRUB2	NM_015679	AAGCTGTAACAGAAAGGTCAA	CTGCGGAAGTTGGTTCATGAA		
26998	FETUB	NM_014375	ACCGCTCAAGTCTGCCTTAAA	CAGCAGTATATATGTCCTGAA		
27012	KCNV1	NM_014379	CCGATATGTCCTGCACTACTA	AAGCTATGTACAATTAACTAA	CTGACACATTTGAGTGTCCAA	CTGTATCCCATTATTACTATA
27013	C2orf24	NM_015680	CTCCATGATGGTGGCCAGTAA	CTGGCTCTGGTGTACATTGAA		
27018	NGFRAP1	NM_014380	CTGCCATTTATCATGAGATTA	TGCCATTTATCATGAGATTAA	CTGGGAAAGAATCCCGGGAAA	ATGGCAAATATTCACCAGGAA
27020	SDFR1	NM_012428	TACATAAAGATGAGTAATATA	ACAGGTATATACAGCATATAA	CTGGTACATAAAGATGAGTAA	CAGGTATATACAGCATATAAA
27032	ATP2C1	NM_014382	AAGGTGCTTACGAACAAGTAA	AAGGGCAGACCTTGACACTTA	TAGGGTAACAGTGTCCATAAT	TACGTATTAAATGCACGTTAA
27034	ACAD8	NM_014384	CTGAATGTAAATCATGATAAA	AAGCTCTTTGCTACAGATGAA		
27036	SIGLEC7	NM_014385	CCGAATATAGTGAGATTGTAA	CAGGGAATGATATAAGCTGGA	TAGTGAGATTGTAACGTGAAA	CTGGAGGAGTCTGACCCTGTA
27040	LAT	NM_014387	CTACTCTGTGTAATAGAATAA	CCTCAGATAGTTTGTATCCAA	CCTCTTGTGGTTCTCAATAAA	CCCGTAACTTATTATCACTTT
27071	DAPP1	NM_014395	TCGGTCGTTCATCTTTAAATA	CTGGAAATTGGTCAAGGACAA	TAGGTAGTATAATAAAGGTAA	CTGGGCCTTATTAAAGAGCAA
27086	FOXP1	NM_032682	CAGGCGGTACTCAGACAAATA	CAAGACCTCCTTAATAATGAA		
27089	QP-C	NM_014402	CTGAAAGACTTTCTCTGGAA	CCGCACGTCTTCACTAAAGGA		
27092	CACNG4	NM_014405	GACGACGAACAATGAACTAAA	CTAGGTGGTTACAAATCATAA	CAGGAGAGCAACTTACCTTCA	CCCTGTGTGTTTCGCCAGTTA
27098	CLUL1	NM_014410	CAGGTTGGTCAATGTATCCAA	CAGGAAAGTATGTTAGCTATA		
27099	NAG8	NM_014411	CAGGTTGTTATCTGTCTATTA	AGCCAGTATATTTAAAGGTAA		
27104	EIF2AK4	BX640919	CACCCATTATATTTCATTGAA	CAGGTATAATTACTAATTATA	TCCGATAATCTTGCAGTGCAA	CTGCAGGAATTTAGTAACATT
27120	DKKL1	NM_014419	CCGGGCTGTGGTCTAGCATAA	CAAGCACCATATGGAAATAAA		
27124	PIBSPA	NM_014422	ATGGGAATACCTACCAGGTAA	CTGGAGGTCATCCATTAGGAA	CTGGGACTGGATCGGCTTATA	CAGGTAACATTCAGTGAGGAA
27129	HSPB7	NM_014424	CAGGTGGACCATCCTCCCAAA	CAGAGGGAAGGTCACAGGCAA		
27148	STK36	NM_015690	CTCACCAGTTCTAGCGAGTAA	CTGGTCATGTCACCATAATAA	CCAGTTGGTGTCAGCCCTGTA	ATGGATGCTGACCTCCTTATA
27154	BRPF3	XM_166450	CCAGATTACCTGGAATTCATA	CCAGGATATCACCGAATGCAA	TACCAACTGCATGAAGTATAA	CCGGCTTGAGAAAGAGTCATA
27156	RTDR1	NM_014433	CTGCAGAGCTTCATTTGGAAA	CAGCATATCTCGAGAGGGCAA	CACAGTGATCACTGAAGGGAA	CAACAGTATGGTGCGCATAAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
27163	ASAHL	NM_014435	CCGGAGAACATCTGCCATCAA	CAGTGGATGTGCAATTCTTAA		
27177	IL1F8	NM_014438	CTGAGTGGAAATTCTTTAATA	CAAGCCTACTTTGCAGCTTAA	TTGGAATTCACACATGCATAA	AACGCTCTGTTTAGTATGTAT
27179	IL1F6	NM_014440	CCAGCCCACACTGCAGCTGAA	TCCAGTCACTATTGCCTTAAT	CTGGGCCTGAATGGACTCAAT	AAACGATATAATGGATTTGTA
27190	IL17B	NM_014443	CGGAATGGACTGGCCTCACAA	TTGCACCTTTGTGCCAAGAAA	CTGCTGTTTCTTCTTACCATT	CCAGAGAAAGTGTGAGGTCAA
27199	OXGR1	NM_080818	TACATCGTTTCTAGACCATTA	CTCAATGGAACTCCTGGTAAA	CCGCTACTGTGTGATCATTCA	CACCAGTTCGGATGAACTCAA
27202	GPR77	NM_018485	TCGGGCCTGCCTGGTGGTCTA	TAGAGATATAGCAGTGACCAA	CAGCAAGAAATCCACCAGCCA	CACGTGCTGGACAAATCTTAA
27229	76P	NM_014444	CTGGATGTTACCACCAAGTAA	CAGGATCACCATCCATCTCAA		
27232	GNMT	NM_018960	AGGGAAGAACATCTACTATAA	AACATCAGTGCTGATAGTGAA	CAGACGGAAGGGTAAACAATA	GACGGAAGGGTAAACAATATA
27235	CL640	NM_015697	CTGGAGTTATGTGGACACTAA	TTGGAATAAATTTATCTCCAA		
27237	ARHGEF16	NM_014448	TACATTAAAGTTATTTCTTAA	CACCATTGTGGTCAAGAGCTA		
27239	GRCA	NM_014449	CCCGCCCAGTATGAAAGCTGA	TTGGACTTCCTTTGGGACTAA	CCGAGTATGACTGGAACGAGA	ATCAATTGCAGGGATGCTTAA
27240	SIT	NM_014450	CAGACTGGAGTGGACCTGGAA	CCGGAGCTCTATGCCTCAGTA		
27247	HIRIP5	NM_001002755	CAGGTTATGGATGATGAATCA	AAGAAGCAAACTCACCTTAAA		
27254	PIPPIN	NM_014460	CAGGAGGTAGGTGGAGGGCAA	CACGTCAAACTCTCTTCCCAA		
27255	CNTN6	NM_014461	GTGGGTGTGTATAATAATGAA	CTGCAAAGGATTCATCTGTAA		
27257	LSM1	NM_014462	CAGCAAGTATCCATTGAAGAA	CCGCTGTGCATTGGAGCATTA		
27286	SRPX2	NM_014467	CCACTCGTTCTAGGAATGTTA	CTGGCTACTATCCGGATGAAA	CCCGATGGTGTTATACATTAA	GAAGATTAACGTCAACGTCAA
27291	C10orf28	NM_014472	AAGGAGCATAATTGTAGAGAA	CCCACATGTCATTGAAATTTA		
27292	HSA9761	NM_014473	CAGGTGTGCTATACTTATGTT	TTGGCACGTGTGGACCATCTA	TGGGATGGTCTAGTAAGGATA	CTGGTCCAATCTATTCATAAT
27295	PDLIM3	NM_014476	CGGGAACTACTTTGAACACAA	CAGGATTACACCAGGAAGCAA		
27302	BMP10	NM_014482	AAGGATGAGTTTCTTAAGACA	AGAGTACATGTTGGAACTCTA	TACGATGGAGTAGACCGGAAA	CCCGCTCTACATCGACTTCAA
27303	RBMS3	NM_001003792	CCGACAGCTGTTTCTATTGAA	ACCGTACAGTATTGCAACCAA		
27314	RAB30	NM_014488	CTGCGGGAGATAGAACAATAT	TAGGGCTTCGGTGGTAATCAT	TCGGTCCATTACCCAGAGTTA	AAGAGAGATTTCGGTCCATTA
27329	ANGPTL3	NM_014495	CAGTTGGGACATGGTCTTAAA	CTCAGAAGGACTAGTATTCAA	CAGGTAGTCCATGGACATTAA	ACCGTGGAAGACCAATATAAA
27330	RPS6KA6	NM_014496	TTGGATCATCTGGACCAATTA	CGGGAGGCTAGTGATATACTA	GGCGAGGTAAATGGTCTTAAA	CAGCGGTATACTGCTGAACAA
27334	P2RY10	NM_014499	CTGACGTGCATCAGTCTTCAA	TCAGAGTTTCGTGACCAACTA	CTCCCTATCATATTAACTTTA	AAGTTGAATAGTTTACCTTAA
27335	EIF3S12	NM_013234	AGCCAAGAAGAGAGCATTAAA	AAAGATGTGTTGACTCAGAAA		
27338	UBE2S	NM_014501	CCGCCTGCTCTTGGAGAACTA	CCGGCCGGCCGCAGCCATGAA	TCCCTCCAACTCTGTCTCTAA	CCCGATGGCATCAAGGTCTTT
27342	RABGEF1	NM_014504	ACGGAATTCTTTATCAATAAA	CAGGAAGAAGATGAGCCTTAA		
27345	KCNMB4	NM_014505	CCCGCGCTGCAGGATCTGCAA	AAGGAGGCTTGTAGAAAGCAA	CTGGAAGACTTGGAACCTCAA	ACCCTCAGTTTCCACTATTAA
27350	APOBEC3C	NM_014508	CAGCATAACCAAATCTTACTA	ACGCTGTAAGCAGGAAGAGAA		
27434	POLM	NM_013284	CTGAATGTCTCCAAGCAAATA	TAGGAGCTGGGAGGAAGATAA	CGGGAAGGACTGCGAACCTTA	CCCAGAATGCCCAGAAGAGAA
27436	EML4	NM_019063	CAGATGCAAATACCATAATTA	CGGCAATTCACTAACAAGAAA	CAGGAATCGATCGGATTGTAA	TCGGATTGTAAGGACATTGAT
28231	SLCO4A1	NM_016354	CTGCAGGGAAATGCACTTCAA	TGGATTGTAGTTAGAATACTA		
28232	SLCO3A1	NM_013272	TAGGACAAAGTTTATCTATAA	TCGGATGGCCATGCTCGTCAA		
28234	SLCO1B3	NM_019844	ATGGATAAGTCTATGCATCTA	CTAGAATATAAGGGAGGTAAA	TAGCTATGCCTTTATGGTTAA	TTCATCTATGTTGCAATTCAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
28951	TRIB2	NM_021643	TCGAAGAGTTGTCGTCTATAA	TACCCTTTCCATGACATTGAA	CAGGTTGTCCCACATGTATAA	CACGTGGAGTCTAGTATGTAA
28952	CXorf37	NM_014008	CAGGAAGGAGGAGGTCTATAA	CAGAAGGAAATCAACTCCCTA		
28955	DEXI	NM_014015	ATGAGTGTTGTGCCTACTTAA	AAGCAATACTTAGGAGGCTTA		
28956	MAPBPIP	NM_014017	TAGAAGAACCTTCTTAGACAA	CACCGCTGCCATAGCCAGTAA		
28959	LR8	NM_014020	CCGGGCAAACTTGCTGGCTAT	CACAATGCTGATTAAACATAA	CTGATTAAACATAATAAACAA	GAGGAAGTTGTTCACAGCAAT
28964	GIT1	NM_014030	ATGGCTGACAGCCTTGACTTA	CACCTTGATCATCGACATTCT	GCCGCTGAGGATGTCCCGAAA	CAGCCTTGACTTATCCGAATT
28965	SLC27A6	NM_014031	TAGACAGATTTGGAAATATAA	AGGGAACTTTATGATCAAATA		
28977	MRPL42	NM_014050	CAGTAATATATAGTAAAGTAA	TAGCTTATGTATGATCCTTAA		
28988	DBNL	NM_014063	TGGGCTCTCTTTACCTATGAA	ATCCGTGTCTCTGAAGAACAA		
28989	AD-003	NM_014064	AAGGCCCGAACAAGACAGGAA	GAGGTGGATATGGTCGACATA	ACGGAGGACTTCCTGGTTCAA	CTCCAGCAGCATCGACATCAA
28990	HT001	NM_014065	AAGCAACTTTATGAATATCTA	GTGGAAGATCATAGTAATGAA		
28996	HIPK2	NM_022740	CCGAGTCAGTATCCAGCCCAA	ACGGGTCGGGACACCAGTGAA	TCCCGAAGTCTCCATACTAAA	AACCAGTACCCTTACATATAA
28998	MRPL13	NM_014078	CAGGTGGATTTAGACAAGTAA	CAGGAAGGTATAGTCCTTCAA		
29028	ATAD2	NM_014109	CTGGTACTTAGGCACCATAAA	AAGAATAATTAGCAGCGTTAA	CCGGATAAAGAAGAACGGACA	AAGGCATTTATAAAGATCGAA
29068	HSPC063	NM_014155	CAGGAAATGCTTGGAAAGCTA	CCGCAGGACATTTCTGATTTA		
29085	PHPT1	NM_014172	TAGCCTGGCCACAGAATTAAA	CCGATTCCACGTTTCCTTTAA	TCGGGCGACATGCAGAAGCAA	CACGCCATTTCAACTGAGAAA
29087	THY28	NM_014174	TCAGTTGATCCTAATTAGCAA	AGCAAATTACTTCATCATCTA		
29095	ORMDL2	NM_014182	TCCGGCTATATGGGCAACAAA	TCAGCTATAGCTGCAGTTTAA		
29097	HSPC163	NM_014184	CTGGTTCATCTTCCTTCTCAA	CTGCTTCTTCATGTATCTTTA		
29109	FHOD1	NM_013241	CACGGTCACCCTCATCAACAA	CAGCGAGAGGAGCATCTACAA		
29110	TBK1	NM_013254	CAGGATATCGACAGCAGATTA	CCCAATTTATCCAAGTTCTAA	CTGACTTGACACGTTTGTAAA	CAGAACGTAGATTAGCTTATA
29113	C6orf15	NM_014070	ATCGGTGTTGTGGAGGAGAAA	CTAGAGCACGATAGAGGGAAA		
29114	TAGLN3	NM_001008272	CTCTGTTTGATTATTTATTTA	ACCCAAGATCTCAGAGTCAAA		
29115	HCNGP	NM_013260	CTGGTCTGGATTCCACTTAAA	CAGCTCATTGTTTACAGGCAA		
29116	MYLIP	NM_013262	CCCAATTAATAGGATAGCTTA	TGCACTATTATAAACTATTAA	AAGTAAGTGCTTAAGTATTAA	ATCGGGTGCAATACTAGCTAA
29121	OCIL	NM_001004419	TCAGATATCTTGAGACAAGAA	CTCATAGAAACTGGAGGCAAA	TAGAAGCATATTGGAACTGAT	CAGGAGAGTGTGCCTATTTGA
29122	TSP50	NM_013270	CAAGCTCAAGCAGGAACTCAA	CACTCTGGTTCAGATCATCAA	CAGGGAGAAGTTCTGCTATGA	GAGGTGCTCAATTAAACATTA
29124	LGALS13	NM_013268	TACGTACATTACAATGAGTAT	TGGCAATCATGTGGTCATGAA		
29127	RACGAP1	NM_013277	CAGGTGGATGTAGAGATCAAA	CACCACAGACACCAGATATTA	CTGGTAGATAGAAGAGCTAAA	CTGAATGTATCTCCTAGCTAT
29775	CARD10	NM_014550	CACAGGGAGTGTGACACTTAA	CTGCACATTATGGAGCATTAA		
29798	C2orf27	NM_013310	ATGCTTCAGATTCAAGTGCTT	ATGATAGCAGAGTACCTTCAA		
29799	YPEL1	NM_013313	CAGGGTCTCTTTAGATAGCAA	CTGTCAGATATTAGAATTGAA		
29802	VPREB3	NM_013378	CTGCTGGTCTTCCCAGGCCAA	AATATTCAACATGTCAACAAA	TGGGTTAATAATATTCAACAT	AAATGGGTTAATAATATTCAA
29841	TFCP2L2	NM_014552	AGGGATGAAGAACGAAAGCAA	CTGCACTGTTTAACAAATGAA		
29851	ICOS	NM_012092	TGGGATTATGTTGTAGTTTAA	CCGGAATTGAAAGCAAATTTA		
29881	NPC1L1	NM_013389	AAGCACCTTGGTCATGGATTA	CAGCTTTGAAGGTTCTATCAA	AAGCCTCATGACACTCTCCAA	CCGAGTGATGGTGGACTCCAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
29882	ANAPC2	NM_013366	CAGCGGTGCAGTCCCGCCAAA	GAGAGTCTATATGCAGAGTAA	CTCACTGGATCGTATCTACAA	AAGGTTCTTCTACCGCATCTA
29894	CPSF1	NM_013291	CCGCGGCTTCCTGTACTTCAA	CAAGATGGTCATCTCCCTCAA		
29922	NME7	NM_013330	CGGCAAACACTGCTAAATTTA	CAGGTTGGGACATTTAGACAA	TTCATGTAGATCACCAGTCAA	CCCGGCATTTACGCCCTGGAA
29924	EPN1	NM_013333	AACTTTGGGAATAAATGGCAA	TCCCGCGACGCTCACCCTGAA		
29927	SEC61A1	NM_013336	CCGAGTGGACCTGCCAATCAA	AAGGTGAATAAGTGACAAATA		
29930	PCDHB1	NM_013340	CGCGCTGAGAACCATGGATTA	ACGTTTCAGATTGACCCTCAA	ACCAAGCATTCTAGAAAGGTA	CTCGGCCTTGTCCATATGAAA
29933	GPR132	NM_013345	CAGGATTGCCGGGTACTACTA	TACCAATTTCTCGTTCCTGAA	CTGGGTCACCATCGAGATCAA	ACGGACCATTCCCGCCAAGAA
29945	ANAPC4	NM_013367	TGGCTCGGAGTCTTTATTATA	CTGAGCTAGACTCCTAATCTA	CAAGGCTAGATGAACAGTGTA	CAAGCTGGTGCTGCCGCTTTA
29946	SERTAD3	NM_013368	CAGCCTGATCCAGTCTTCTTA	CAGGCATGTCCTCATCCATAA		
29947	DNMT3L	NM_013369	CCACTGCAAACCGGCACTGAA	AACTCACTTCCTCTTTATAAA	AAGCATGTGGTTGATGTCACA	AAGGCTAACCAGCGAAATATA
29948	OKL38	NM_013370	CCCGGTCATCATTGTGGGTAA	CAGAAGCAGGTCCCAAATAAA		
29953	TRHDE	NM_013381	CTGGAGATTATTAATTGATCA	CAGGAACAGAATACCACTAAA	CCGAATCTATAGAATAAAGTA	CACCACTGAATTCATGTAATA
29954	POMT2	NM_013382	ACCAACCATCATTAATGTTAA	AACCTGTGGATTATCAAGAAA		
29956	LASS2	NM_013384	AACGAAGAGAGTCTTTCTTAA	TTGGAGTAGAATGGCAACTAA		
29959	NRBP	NM_013392	AGGCGAGAAGAGGTGAATCAA	AACATGGATACTAGTGCCGTA	TCGGTGGAGGAGGGAGTCAAA	CCGGTTGACTTCTCTGCTAGA
29965	C16orf5	NM_013399	CACGTAGGACAGGGTCACAAA	CTGCCTCATCAATGACTTCAA		
29982	NRBF2	NM_030759	TTCGGTTTCTCCTGATACAAA	TTATGTGTAATTTATCTATAA	CACACTTTGCACTACTCATAA	CAAAGGGATAGCCATATGAAA
29984	RHOD	NM_014578	CCGGTGGTACCCAGAAGTGAA	AACCTGCAAGTGAAAGGCAAA		
29997	GLTSCR2	NM_015710	TCGAGAGAGAGCCAAGTTCAA	CAAGTTCAAACGCAAGTACAA	CTGACAAAGAAGAGAACCAAA	CCGGAGCTTCCTACAATCCAT
29998	GLTSCR1	NM_015711	CCCGCAGAACCTGACGTTCAT	CAGGCCATGCTCAATAAATAT	CGGGCTCAAGCTCAAGATCAA	CCGCATCGGGCTCAAGCTCAA
30000	TNPO2	NM_013433	CCCGAGCATCTCTCTCTGTAA	ATCGTGCAGGATAAACTCAAA		
30008	EFEMP2	NM_016938	CCTGGAGATGGTCACCATGAA	CCGCTCCTGTGTTGATGTGAA	CCGCTCCGCTGCCGTCATCAA	CACGGAATGCACAGATGGCTA
30009	TBX21	NM_013351	CCGCGTGAGGACTACGCGCTA	ACCTGTTGTGGTCCAAGTTTA	CCGCCTGGACCCAACTGTCAA	AACAAATACACGTATGTTATA
30010	NXPH1	NM_152745	AAGCAGCAAATCCACACTAAA	TAGGAGTATCTGCTTGTTAAA		
30062	RAX	NM_013435	CCGCACGACTTTGACCACGTA	CCGCGAGGAGCTGGCCGGCAA	CAGGCTGAAGCTCCTAAACTT	CCAGATAACCATAACAGGGAA
30811	HUNK	NM_014586	AACTAAGTACGTTGCAAATAA	TACGTTGCAAATAATAGTACA	TCGGACCAAGATCAAACCAAA	CACGGGCAAAGTGCCCTGTAA
30814	PLA2G2E	NM_014589	AAGCTGGGCTGTGAGCCCAAA	CTGGGCACCTACAACCGCAAA	CAAGTCCGCCCTGCAGTACAA	AACCGCAAATATGCCCATTAT
30817	EMR2	NM_013447	TAGGTCAGTGTAAGAATTAAA	TTGCTTGATATAGACTGCTAA	ACGGGTTTGATTATTTAGTCA	AAGCATGGTGATGATATAGGA
30818	CSEN	NM_013434	CGCGGCTGACCAACATTCAAA	TCCAGGAACATTCCCACATAA	CAGGAACATTCCCACATAATA	CCCACATAATACATTCCATCA
30836	ERBP	NM_014597	ACCACTGTGTTCCACCATATA	CCACTGGGAAGCAAAGTTTAA	CACGAACAGGCCAATGTTGAA	AAGAAGAAATTTCGCAATTAA
30837	SOCS7	NM_014598	CAGCTTTGAAGAACCAAATTA	CCCAAGTTGACAAGAACTCAA	CCGAAAGTTCTACTACTATGA	ACCAAATTAAGCTACCATGAA
30845	EHD3	NM_014600	CACTTTATATACATTATTCTA	CTGGTGGTGGATCCCAAGAAA		
30850	HUMPPA	NM_014603	CAGCGTCACCTTTGAAGTATA	CAGGCTGGTGCTGGAGAGTAA		
43849	KLK12	NM_019598	TCCCGGGAGAATCACGAGCAA	TCCCTGGAGTCTACACCTATA	TGGGAACTTCTTGGAACTTTA	TGCAATAGTCTGGAATAAATA
49861	CLDN20	NM_001001346	TACAAAGAAAGTAGAATGTAA	CTGCAGGAATCTCTAGTTTAA		
50484	RRM2B	NM_015713	AAGGGCTTATGGACTGAGAAA	AAGGAGCAGGCCATAACTTTA	GAGCAGTTCAGTGGTACATAA	AACCAGGAGGTTATCATGGTA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
50485	SMARCAL1	NM_014140	CCCGCAGAGCTGAGAAGTTAT	CAGAACAGCATCAGAGGACTA	TTGAGTTATGAGTTAGGTCAA	CAGCTTTGACCTTCTTAGCAA
50488	MINK1	NM_015716	CACATGTCTCATCAAGACTTA	CCGGAACAAGATTCTGCACAA	CGCAGACTTTGTGTTGCTGAA	CACGTACGGGCGCATCATTAA
50489	CD207	NM_015717	CTCGGTGACCTCAGAGAGTGA	CCAGGATGACTTTGCACGTTA	ACCCTGGATTCTGAAATTAAA	CAGGATGACTTTGCACGTTAA
50515	CHST11	NM_018413	CAGCATAGTGAGAATTATTTA	CCGCAACAAGTTCACCCAGAA		
50613	UBQLN3	NM_017481	CGAGGAGTCAGTAGCAATCAA	CTCCATATGCTGCAAGATTTA	CAAGATTTAGTTAGTACAAAT	TTGAGATGCAATTACACCCAA
50614	GALNT9	NM_021808	CCCGGAGATGAGGGTCTACAA	CACCAGGAAGCCCTACAACAA		
50615	IL21R	NM_021798	CCCGGTCATCTTTCAGACCCA	CTGCAAGAAGTCCATATTGTT	CCAGAGCAGACCCTCAATAAA	ACCTGTTGAAATGTGAATTAA
50616	IL22	NM_020525	CTGATAGGTTCCAGCCTTATA	CCTGCGTTAGTTACAAAGGAA	AAGGTAGACTTTCTAAGCATA	AACATGTTTATTTGACCTCAA
50628	GEMIN4	NM_015721	CCGCCATATGGAAGTGTGCTA	CAGCCAGAACGCGACGCTCTA	CACCGCAAGTTAGAACAGCTA	CAGCCTGGACTTTACAGTTAT
50649	ARHGEF4	NM_015320	AAGGTTGGCCTTGGCTCATAA	CAAGCCAGAAACCACATTTAA	CCGCGACGTGTTGTACTACAA	CACATTTAATTTCATAAATAA
50700	RDH8	NM_015725	CAGGGTGTCATCTTCAACGAT	AAGGATGAACAGACTCTTCAT	CAGCTGTCTCTGGGAAAGCAA	CACACCAGCAATGTATGTATA
50717	WDR42A	NM_015726	GAGGAATAAGTCATTAATCTA	CAGCTGAATTCTTGCCCTTAA		
50835	TAS2R9	NM_023917	CTCCCTAGTTAGACACACCAA	CCAGGTACTTTCAAACAGTTA	TGGATTCATTGTACTAGTTAA	CTGGCTGAAGCTAAAGATCAA
50846	DHH	NM_021044	ATGGCTCTCCTGACCAATCTA	TCGGTCAAAGCTGATAACTCA	ACCGAGTGGCCTCCACGCAAA	CCCAGGCATAGAAACCTCGAA
50852	TCRIM	NM_016388	AAGGTTGAGATGACAATGTTT	ATCAGTATTTCAAATAACTTA	AAGCATGAATGCGTTCTGGAA	AAGGATGGAGATGAGCAACTA
50861	STMN3	NM_015894	CACGTAGTAAAGTGAACTTAA	TTCAATCAAATGAACAATTAA		
50862	RNF141	NM_016422	ATCACGGATCATGAATTTATA	TTGGTGAGTAACACACATATA	CACTGATAAATTGTGCAATAA	CTCGATTTCCTTATATCTAAT
50939	IMPG2	NM_016247	GAGGATGGAGTCACAAGTATA	AAGGTTGGTAGTTATGTGGAA	TCAGGCATTCATCTAAATAAA	AAGGAAATTCGTGTACTTGAA
51015	CGI-111	NM_016048	TACCAACATCTTGAATATATA	AGGGATTCTAATATTTATTTA		
51020	C6orf74	NM_016063	AAGGCTAGGTTCATTGAATAA	CCAGATGAAATTGCTGCCTTA		
51031	C17orf25	NM_016080	CTGATGTAATTTAGAAATGAA	AACGATTTCTTCAGCCTGAAA		
51043	ZFP67	NM_015872	CAGAGGGTTCTGGAAGATGAA	CCCGGAAAGCTTTCCTGCAAA		
51056	LAP3	NM_015907	CCCAGTCTTCTTGGAAATTCA	ATGGGAGGAGCTGCAACTATA	AAAGCTTAATTTGCCCATTAA	AAGCTTAATTTGCCCATTAAT
51060	TLP19	NM_015913	CTACGTGATCTGCACCTTTAA	AAGGGAATATTGAGGAATCAT	AACAATTAAGCCGACCAGGAA	AAGTGTAAATCAGTTATTCTA
51062	SPG3A	NM_015915	ACGCCTCAAGGTCTCAGGGAA	TCCCGAGAGCCTAGATATTAA	CCCGAGAGCCTAGATATTAAA	ACAGCAGAAGCTAACAATTTA
51068	CGI-07	NM_015938	CAGCATGAAGATAATGGCTAA	CAGAATACACTTCGTATCAAA		
51070	NOSIP	NM_015953	CAGGATGACGCGGCATGGCAA	CCCGTGCACTTCACACCGCTA		
51076	CUTC	NM_015960	CAGGATGAAGGTAGAACTATA	CAGAATATTCCCTAAAGGTAA		
51077	C14orf111	NM_015962	AACCATAGATACAACATTGAA	AAGGAAGTATGCGACCATGAA		
51084	CRYL1	NM_015974	CAGCTTGATTGCATTTGACTA	CAGCCAGTGATTGTAGTTTCA		
51095	TRNT1	NM_016000	ACGCAGAGATCTCACTATAAA	AAGGATTTGGGTGGAACTGAA		
51097	CGI-49	NM_016002	CAGCTTATAAGTTGCTATCAA	AAGAAATGTATCAAATCTGAA		
51099	ABHD5	NM_016006	AAGGCCTGATTTCAAACGAAA	TACGTCTATATCACACCTTAA		
51101	CGI-62	NM_016010	CCAGGTGTGCTTACAAACAAA	CAGGTAAAGTGTCTTCAAGTA		
51105	PHF20L1	NM_016018	ATGGCTAAGTGGATAATTTAA	TCCGTTGATCTTAGTGGTGAA	CAGCTGAAGATTGGAATACTA	ACGGAAATTTAGGGTATTTAA
51112	TTC15	NM_016030	CAGGCTGGCACTACTAGTGAA	ATCCAGGGAGATGCAGTTAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
51116	MRPS2	NM_016034	CACGACATCATCGACCTGGAA	CACGCTCAACAACATCTTTGA		
51121	RPL26L1	NM_016093	AAAGAAGAACTTATTGAGAAA	GAGGGTCACCATGAAGTTCAA		
51130	ASB3	NM_016115	AACGCTTGGATTCTACAGCAA	ACCCATCTTTGTCGTTTGGAA	TACGGTCTGACAGTTATATTA	CTGAGGATGTATGAAGTTCCA
51131	PHF11	NM_016119	CACCGTGGGATGTGATTTAAA	ATGGAGTTCGAGGAATTTATA	GAGATCTTATGTCAAGTTCTA	ACAGCCCATGATAGCCTCTTA
51135	IRAK4	NM_016123	GTCCATTATTAGATTATGTTA	CAGCTTAGAAGAGTACTCCAA	TTGCAGGACAGTGGTTATTAA	ATCCTATTAGTCATATATTTA
51138	COPS4	NM_016129	CAGGAAGTACAAGCATTTAAA	CAGAATGAATCAACCAATGAA		
51162	EGFL7	NM_016215	AGGAGTGGACAGTGCAATGAA	CAGCACCTACCGAACCATCTA		
51167	NCB5OR	NM_016230	CAAGCTATGATTGGTTCCAAA	TTAAGGATTGTTTATATCTTA	AGGCTTCACACCAATGGTTAA	TCGATCATGTTTCCATGCAAA
51168	MYO15A	NM_016239	CAAGATTAGATTTGAACGGAA	CAGGATCGTGTTTCAGGCCAA		
51179	HAO2	NM_001005783	CCGGTCGGTCGCTGAGATCAA	CAGGAGGATCACAAACTCACA		
51182	HSPA14	NM_016299	CGCGAGCCATGATGAAATTAA	ATCCCTATTGGTGCAGCTATA	AATGGATTACGTGATATATTA	CTCTATTGAGATAGCATCTTA
51184	MGC14560	NM_016301	TTGGACCTAGATAACAAGTAA	CAGCCTCATGCCTGAATCAAA		
51187	C15orf15	NM_016304	CAGCATTTGTATAGTAACTAA	CCCTTTGTTAATGTTATAGAA		
51191	HERC5	NM_016323	CCGGACGCCGAAATGCATTAA	ACCATTTGAGTATGACAACTA	GAGGAGAATGGTAATGTTCAA	TGGAAGTAGCATAACTGTCAA
51194	IPO11	NM_016338	CAGCTACAACTTTGAAGTTAA	GAGGAGATTCTTGGAAATATA		
51195	RAPGEFL1	NM_016339	ACGGAGAAACTTCAATATTCA	CCCATTGCTCCTTCAAGCCAA	ACGGTGGAACTAAAGATTCCA	ACCCAAAGCTCTGGAATTGTA
51199	NIN	NM_016350	CTGGAAGAATATCGTGCACAA	CTGGAAGACCTAAGAAATGTA		
51205	ACP6	NM_016361	GAGGCCAAACTTGAAATACAA	GTGCCTTTATACAATGCCAAA	CCCGCTGGACATGTTCTTGAA	CCATGTCAGTTTATACCTTAA
51207	DUSP13	NM_016364	CAGGTGGACACAGGTGCCAAA	ACCCAATTCAGAGATTCTTTA	TCAGTCCATCTCTATAATAAA	ACCCTGAGATGTAAACAGCAA
51208	CLDN18	NM_001002026	AAGGATGAGCAGACAAGTCAA	CCGAACTTGGCTAGTAATAAA		
51214	IGF2AS	NM_016412	CAGGCGGTGGACGCTGCTGAA	CTCAATCTGCCCAAAGCCAAA		
51222	ZNF219	NM_016423	CCCAATAAACAGGTGTCTTAA	CAAGGGAGTCACAGTGCCTTA		
51234	LOC51234	NM_016454	CACAAAGAAACTATACCATAA	ATGGTTGAGAACAATGCATAA		
51237	PACAP	NM_016459	CAGGACTACGGAGTTCGAGAA	AAGGCAGAGACCAAACTTCAT		
51239	MGC41816	NM_016466	TGGACAGATGATCATATTCTA	CTGGGCCGAGTGAAGCATTTA		
51256	TBC1D7	NM_016495	CCGGGTGTGTTTGCACTACTA	ACGCTTTGTGAACCAATTAAA		
51258	MRPL51	NM_016497	AAGGGCGATGTTCGGAGTGTA	GACCTGCACAACCTTAATAAA		
51260	CXorf26	NM_016500	AAGGACATCTTTCTAGTCTAA	AACCGGGAAGGCTATAACAAA		
51265	CDKL3	NM_016508	CTAAAGCAATTTCATCACGAA	AGCTCCCGAATTAGTATTAAA	TGGGCAGATAGTGGCCATTAA	CAACATTATTGTCATGGACTA
51266	CLEC2	NM_016509	AAGGTGGACCAACTACCTTAA	ATACATCACCTTAAATATTAA	CTGACAGATACTGAAATTGTA	AGGGCTTTATTGTACAATAAA
51275	FLJ39616	NM_016534	CAGGATTGTATAGAATATATA	AGGATTGTATAGAATATATAA	GAGCATAAGTTAAGTAAGTAA	CTCCACCGATAACCTATCAAA
51276	ZNF571	NM_016536	CAGGGATTTCTGAATAATGTA	CTGAATTATATCCTTTATTAA		
51295	SITPEC	NM_016581	TACGAGTTTGACATCAATGAA	CCGCAACAAGTGTGTGTATTA		
51296	SLC15A3	NM_016582	CAGGAAGGGTAGGGCAAGAAA	CAAGGACTTTGGGAACATCAA		
51298	THEG	NM_016585	CCGGATCATCTCCCTGGCCAA	AAGGATGAGGAGGACAATAAT		
51301	C2GNT3	NM_016591	AAGGATGAAGTCAGGTATGAA	CAGCTTAGTTCCAGAGAGAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
51307	FAM53C	NM_016605	CAGGATGTTGGGTTTGCTCAA	CAGGTGCTGAGTGAAAGCGAA		
51312	MSCP	NM_016612	CACCAAGGAAACAGCCACCTA	CCGGACGGTGTACCAGCTCAA		
51317	BHC80	NM_016621	TACGGAAGAACCTGATAGTAA	ACGGAAGAACCTGATAGTAAA	ACCGGACAAGTTCCAAATACA	ACCATGCCAAGTGAAATAATA
51321	LOC51321	NM_016627	GACAACTATTATATTCCAGAA	ACCCATGAGATCGGACACATA	CAGCATTGTAGAAAGATACAA	CCCGTGGAAGCCTTTAAGGAA
51330	TNFRSF12A	NM_016639	CGCCCACTCATCATTCATTCA	CTCAGATGTCCTGAAATTCCA	CAGCTGACACTGACTAAGGAA	GAGGGAGAATTTATTAATAAA
51332	SPTBN5	NM_016642	CCGGCGTATGTTAGAAGAGCA	ACGGGCCACATTCGCAAGCTA		
51334	LOC51334	NM_016644	CCGGGAAAGATTCCTCACCAA	CTCAGCTATATATGTAATAAA		
51335	NEUGRIN	NM_016645	CTGGGCAAGTATTAATGTATA	CCCGGTTGCCCTTGCGATCAA		
51339	DACT1	NM_016651	CACAGAGACATTCACTATTAA	CCGCAGGAGAACAAAGTTGTA		
51343	FZR1	NM_016263	TCGCCAGATCGTCATCCAGAA	CAGGATTAACGAGAATGAGAA	TGCAGTGACGCTGTCATTAAA	CGGGTCGATCTTCCACATTCA
51347	TAOK3	NM_016281	CAGAGACTGTACTACGACAAA	ACGCAGCGAGAGAATAAAGAA	CAGCTCCTCCGTCGTGCATAA	CAAACAGTATAAAGCACTCAA
51352	WIT-1	NM_015855	CCCGGCCTCGAAGGTGCATAA	GCCTCTATTATTATACCGTAA	TAGGCCCATGAAATTGATGAA	CAGTCTGAGGTTACAATTAGA
51364	ZMYND10	NM_015896	CTGCAGGGAGTGCCAAGTCAA	CTGCAGGGTGGAGGACTTCAA		
51368	TEX264	NM_015926	CAGGACCCAGAATAAAGCCAA	CCGGGCCAGAGGAGAGCCATA		
51373	MRPS17	NM_015969	TGACATGTTTATGTTATGGAA	CTCTGTGGTGTTTATGAAATA	TCCCTATTTATTAAAGTATTT	CAGGCTTGTTCTGGATCCCTA
51374	C2orf28	NM_016085	ACCTCTTATATAGACAACCAA	AACCAAATCTGTCAAGGGCAA	CTGGAATACTATCACCTCTTA	AAGCCAAGACTTCATGAACTA
51382	ATP6V1D	NM_015994	AAAGAAGATAATAGAGACTAA	ATGGATGAAAGAGATCTGTAA		
51389	RWDD1	NM_001007464	AAGGGCCACGATGACAGATTA	CAGGAGAATATTCTTCTGATA		
51390	AIG1	NM_016108	CAGAGAGATGATATACCCGAA	CAGATGTTTCTCATTGCATAA		
51393	TRPV2	NM_016113	TCAGATAAGAGTCAACCTCAA	CTGGCTGAACCTGCTTTACTA	CAGAGGATCTTTCCAACCACA	CCAGTGAATTCTGGTGGCAAA
51400	PME-1	NM_016147	ACGGCAGCGATTATTAGTAGA	AGGAAGGAAGTGAGTCTATAA	AGGCGATACATCTGAGTTCAA	AACATCGAGCTCTGTTGTAAA
51409	HEMK1	NM_016173	CAGGGTGGCAACCAACTATAT	CAGTAAAGTATTGAGAGACTA	CAGGGATTGATTAGTCCTCCA	ATCCACGTTCATTTAACTGAA
51411	BIN2	NM_016293	CAGGGAAATGAGCAAGCTGAA	AACGATTTGAACAAAGCGCTA		
51412	ACTL6B	NM_016188	CACCTACAGCAAAGACGTCAA	CACGGCCATTCCAGTACATGA	CTGGCATAACTACATGTGTAA	CAACAGCACCATGGAGCGCAA
51421	AMOTL2	NM_016201	AAGCATATTGCTTCCAATTCAA	AAGGGTGTTAGTCTTGGAGAA		
51422	PRKAG2	NM_016203	AAGCGCGGTTATGGACACCAA	CGCGGTTATGGACACCAAGAA	CCGGAAAGCATTCCTCTCGAA	AAGCACGAGCCTGAACGGTTA
51426	POLK	NM_016218	AAGGATAAACCCATTGCTGTA	CAAGGATTTACCCATTAGAAA	TAGGATGGGACTTAATGATAA	CCGGGTGACGACGGGTAGAAA
51429	SNX9	NM_016224	ACAGATCTCAATGATGCAATA	CAGCCGCTTTCCAGTGATGTA	CCCATCATTGTTGGAGATTAT	TACCCAGTGTCAGATAATTAA
51435	SCARA3	NM_016240	CCCTGAGAAGTTCAACATTTA	ATAGTATTACTGACTCAGTAA	CCAGAGGAAGAGACCATGAAA	CACCATCTTCACCAACATCAA
51442	VGLL1	NM_016267	CTGCATATTGTTCCAGATAAA	CAGGTGATGGTCCAGAATTAA		
51449	PCYOX1	NM_016297	AAGCATCCAAATGGTAATTAA	CAGGATGGCTTATATGAGAAA		
51466	EVL	NM_016337	CACACAGTAATAAACGGTTTA	CGGCTTAAACTTTGCAAGTAA	CAGGTTGTGATCAATTATTCA	CCGGATCAACATCTACCACAA
51475	CABP2	NM_016366	CAGAAGCTGGAGGCAGCATAA	CAGCATGTTCCTTGAAGCCCA		
51490	C9orf114	NM_016390	AACGCTGCTAGGAGAATCGAA	TCGCAGGACCCTCGCACCAAA	TCGGGTGACTGTGCGACTGAA	CCGGCACACCTGAAAGTTCTA
51491	HSPC111	NM_016391	ACGAATAAATTGAGCCTTGTA	CAGGGTGGGTGATGTAAATAT	TCGGAGTAAGATCAACGTCTA	CGGGACCTCATTGACTATGTA
51496	HSPC129	NM_016396	CTCAGTTACAATCAATTTAAA	AAGTACAGTATTGGAAATTAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
51497	TH1L	NM_016397	CAGGAGGATGATTCTGGAGAA	AAGCGAGTGAGCATCAATAAA		
51513	ETV7	NM_016135	CAGATGTGAAGCTCAAATTAA	TGCGCCACTATTATAAGCTTA	GCGCCACTATTATAAGCTTAA	CCCGATATGAGCCCTACATCA
51524	HSPC196	NM_016464	CTAGCTGTGTTCAGCATTCAA	TAGAGAATAAATTGAATTCTT		
51526	C20orf111	NM_016470	CACAATGAAATCCGAAGCCAA	AAGGCTTGTCAAAGAGATTTA		
51531	C9orf156	NM_016481	CAGACTTTAATTTACAGAATA	AAGGTAGAAGGTGGAGCTATA		
51535	PPHLN1	NM_016488	CAGAATGAAGGAAATCCTGAA	AGGGACGATATGAATATGAAA		
51548	SIRT6	NM_016539	GTCGAGGATGTCGGTGAATTA	CACGGGAACATGTTTGTGGAA	CCGGCTCTGCACCGTGGCTAA	CTCCCTGGTCTCCAGCTTAAA
51550	CINP	NM_032630	ACGGATATCTGTGGACCTTAT	CAAGGGAATTTGTGAACTAGA	GCGGCTGATTGGCACAATTTA	CGGCTGATTGGCACAATTTAA
51552	RAB14	NM_016322	AGGAATCGAACTAACAATACA	AACGGTTCACGTCTAGCCAAA	TCCATTGATCGCGTATCTTAA	CACGTTAATAGAGGTAGTACA
51554	CCRL1	NM_016557	AACCCACTATGCTATAAGTTA	AAGAACGATTTCCCTGCATAA	TTCCATGGTAGTGGCAATTTA	CGCCGTGGTTGCAACTTATAA
51560	RAB6B	NM_016577	ATGGCCAGAGTGGGTCGTCAA	ATCCATGTTCTTAGAGCCTCA	CGGCTGTTACTTAAACAACTA	CAGGGATCACATCACTCTTAA
51561	IL23A	NM_016584	CGCGCTGAACAGAGAGAATCA	AACAGAGAGAATCAGGCTCAA	CCAGATTTGAGAAGAAGGCAA	CAGATTTGAGAAGAAGGCAAA
51574	HDCMA18P	NM_016648	TCAGGTGATTTAGTAAATAAA	CAGGAGAAAGTTAATGCAACA		
51582	OAZIN	NM_015878	CCGGATTTGCTTGTTCCAGTA	CGGATTTGCTTGTTCCAGTAA	CAGGTTAAGCTTGTCTGGTCA	ATCATAGTATTTGTTGACCTA
51592	TRIM33	NM_015906	CGCCAAGAATGCAGACAGATA	AAGGGTGCAATTGAGAATCTA	CTGGGCAAAGAATGTAGTCAA	TCCCGTAGTATCGGTACACAA
51596	C6orf82	NM_015921	TGAGGTGCTGATGATGATTAA	ACGTGTGGCCTTTCAGATCAA		
51599	LISCH7	NM_015925	CACGTCGTTTACGCTCATTAA	ACGTCGTTTACGCTCATTAAA	GAGGATTACCATCACCGGAAA	CGGGACGACCTCTATGACCAA
51606	ATP6V1H	NM_015941	CAAGAGATGCTTCAAACTGAA	CAGCAGAAGTACGATGATGAA		
51616	TAF9L	NM_015975	TAGGCTGAAGTCCTTAATTAA	ATCACTGATAGTAGCATTTAA		
51637	C14orf166	NM_016039	CTGGCATGTTTGGAAATCAAA	AAGATTCAAGATCGACAAGAA		
51639	SF3B14	NM_016047	TCGGATATTGTATATAAGAAA	TACATTCGACTTCCACCTGAA		
51645	PPIL1	NM_016059	CAGCTTCTAGATGACATAGAA	AAGGAAGTTAATACCTATGTA		
51659	Pfs2	NM_016095	CTGGGACATTCTTCAATTCCA	AAGCCTTAGGTAAATAAGTCA	CTGGCGATTAACCTGAAACAA	CTCCTGTTAAATCATGCTTCA
51660	BRP44L	NM_016098	CTGTAACTTAATGGCTATAAA	CAGTAATATGTATATCATCTA		
51661	FKBP7	NM_016105	CTGGCTAAAGACGGCTCGAAA	ACGGAGCATTGAGACATTTAA	CGGAGCATTGAGACATTTAAA	CACGATGAACTATAGCATATT
51667	NYREN18	NM_016118	AAGCAGTACTCTGACAGACTA	ACCGTACTTAGACATAGCTAA	TAGAGGCTTATGAGTATCTTA	ATCCTCAGATGTGGTGGTTAA
51676	ASB2	NM_016150	CCGAGAGACACCGCTCTACAA	CAAGTACGGTGCTGACATCAA	CGGCGCGAACATCGACGCCTA	CCCAGGCAGGCTGATTAGATA
51678	MPP6	NM_016447	TTGGTTGGTATACTCAAAGAA	ACGGATTCAGAGAGCATACAA	CTGATGATTCAGTAAGGTTAA	TGGAAGGTGTACTAATATATA
51684	SUFU	NM_016169	ATGGACGGCACTTTACATATA	TGGGACTGTTACAATACTTCA	GAGCGTACATCTGAAATTCAA	CCAGGTTACCGCTATCGTCAA
51700	CYB5R2	NM_016229	CCCTTGATTGAGAAAGAGAAA	CAGAGGCTTTGTGGACCTAAT	TCAGTATTTGGAGAACATGAA	CCAGGGAATCTTGGAATCAGA
51702	PADI3	NM_016233	TCGCTAATAAATCAACAGAAA	CACAGAAATGTTTGAGGTCTA		
51704	GPRC5B	NM_016235	CGCAAACTAAAGCAAAGCTAA	CTGCAGATACTCTAATCACTA	TCCGTTTAGAAGCAACGTGTA	CTCGCCCTGTTCCTACACTTA
51710	ZNF44	NM_016264	CACGCTGAATAGAAACTATAA	CAGGGATAGTCTACAAATGTA		
51715	RAB23	NM_016277	ATGATAAACTCTAGACATATA	TTCATTATTTGTACTAAACAA	CAGAATTTATATTGTTTATTA	AAGGTTAAAGTTAAGATTCTA
51716	CES4	NM_016280	CCACAGCAGAATCTAAAGAAA	CAAGCTTCTTGCTATAATGTA	ATGGAGGATTTCGGTAGATTT	ATCGATAGGAATCCAGACCTA
51720	RAP80	NM_016290	CAGATTGCTTAGTGGACTTTA	ACGACATGCCATGTACTGCAA	CACGTCGTGACTTAAATGAAT	CAGTATTGACTCGGAGACAAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
51727	UMP-CMPK	NM_016308	TCCGAGGTTCTTAATATGAGA	TACAGAGGTGGTTTAATCAAA	CGCGTATATATCCCTCTAGTA	AAGTATTGCTAAGTACTATAA
51738	GHRL	NM_016362	CACGACTGTTGTACAAGCTCA	CCGACAAGTGATCGCCCACAA	CAGGAGGCGAATAAATGTTCA	CGCCCGGAAGATGGAGGTCAA
51755	CRK7	NM_016507	CCGCTTGGTATCGAAGCACAA	AACGGCGACGTCAGCGACAAA	ATCGGGATATTAAGTGTTCTA	ACCGGATATCGGGAAGTTCAA
51759	C9orf78	NM_016482	ACGGTGTGATAATACTCTTTA	CAGGATGAGATCAGAAGGATA		
51760	LOC51760	NM_016524	CAGCTGGTGCATGGACTCAAA	CCGGAACGCAGGGAAAGGCAA		
51761	ATP8A2	NM_016529	CAGGAAGAAATAAGACATGAA	ATGCAATATCATGAACTTTAA		
51763	SKIP	NM_016532	ACGGTCGGAGTCCGGAAGAAA	CACGTTCGACTTGGAGCTGAA	CTGGAATTAGCCGCTTAAATA	CAGCCAAGTGTCGTCCACATA
51773	HBXAP	NM_016578	CCGGACGTCGGCAACGGAGAA	CAGCCAATTGGTCGAGACAAA	CACCGAGTCGTGTACCATGAA	ACGCACAAAGATTGAGTCCAA
51780	JMJD1B	NM_016604	AAGGAACTTTGTCACATCTAA	ACCCTGCATCAAAGAAATTAA		
51802	ACCN5	NM_017419	CAGTCTGATCACGATCATAGA	CACGATCATAGAAATTATTGA	ATCATAGAAATTATTGAATAT	AGGAGTGTTAATGGTCACTTA
51805	COQ3	NM_017421	CTCGGCGGTTTATGTGAAGAA	TCAGTGGGACTCTACAGATAA	AACGATATGGTTCAAATCCTA	CTGGAATCAAATGGTCTGTCA
53340	SPA17	NM_017425	ACCCTTGGATTTAGAATTATA	ATCCATCAACCTTCTTATTAA		
53342	IL17D	NM_138284	CTGGGCCTACAGAATCTCCTA	CAGCATCAACTCCAGCATCGA	TGGCTGGAAGCTGATGGGAAA	TGGGTGCTTGCCAAAGAGATA
53343	NUDT9	NM_024047	TTCGATTTAAGCATGGCTTAA	AAGATTAGTGCCACACTGAAA	ATGGATAATCTTATGCTAGAA	CACGCTGCAGATCCCATTATA
53347	UBASH3A	NM_001001895	CCCGCAGACGTCATCCGGGAA	CTGGGTGATTGGGATCTCACA	ACGGCCAAACTCATCCTGGAA	AACAGGTGTAATAGTCAATAA
53353	LRP1B	NM_018557	AACGTTTATACTGGACAGATA	CTGGATGGTGGTAATTTAGAA	CCCTACTATACTCGTTAGCAA	TAGATGATTCATGTAAGTTAA
53373	TPCN1	NM_017901	CGCACACAACTGGGAGATGAA	CCGAATGAAGTACAGCCGCAA	TAACACAATAGTATTACTCTA	CGAGCTGTATTTCATCATGAA
53635	PTOV1	NM_017432	CCCAGTCCAGATCGTCAACAA	CAGATCGTCAACAACAAGTTT	CCGGCGTGTCATTGCCAACCA	CTGGAGCAGGAGCAACAGCAA
53826	FXYD6	NM_022003	CCCAGAAAGCAGAGAACTGAA	CAGGTGCAAGTGCAGTTTCAA		
53827	FXYD5	NM_014164	CACCAGAGGACAGACGTTGAA	CCCGGTTATGCCGGAATCGTT	GAGGACAGACGTTGAAAGATA	CTCAACTATCATGGACATTCA
53829	P2RY13	NM_023914	CAGGATGTTAATATGCTATAA	AAGGAGTAGTTAAGCTCTGTA	CAACTGTTTATTGCTAAAGAA	AAGACTGACTGTAGACTGCAA
53905	DUOX1	NM_017434	CCAACTAATCTTAGAAGGTAA	CCCGGGCAGATCCGTGTGGTA	TCGGCGGAGGTTTGGCAAGAA	CCAGTCTAACACCACAACTAA
53916	RAB4B	NM_016154	CTACATAAGAGTTATCTGTTA	AAGAGTTATCTGTTACTGTTA	CCGCACTATCCTCAACAAGAT	CAGGAGCTATAGTGGAGTGAA
53918	PELO	NM_015946	CATATTTGATTTAGAGGGTAA	AAGCAGTGGGATAGTGTGGTA	CTGAAGAGGATTAATGATTGA	ACGTACTACCATCTTGATTAA
53947	A4GALT	NM_017436	CAGGATCGCACTCATGTGGAA	CACGGACTTCATTGTTCTCAA	CACGTGCTGGTCCTGATGAAA	AGGAGAATAATCAATAGAATA
53981	CPSF2	NM_017437	CACATTTGGTTCAGAAATTAA	CTGCTTGACCTTTCTAAGAAA		
54039	PCBP3	NM_020528	CCGGCATGCAGTGGTAATTAT	ATGGATCTGCTCTAAACCTTA		
54058	C21orf58	NM_058180	CAAAGTCTAATTTAATAACTA	TAGGTGGAACTTGGGAAACTA		
54067	C21orf49	NM_001006116	TAGGTAATGTGTAGTTCTCAA	CACAGAAATGCTAGTTGGAAA		
54102	CLIC6	NM_053277	CCGAATCTAATTCCGCAGGAA	CACGCATATTCAGATGTTGCA	ACACACAATTTCATTCATATA	TGGTATGTGTTTGATGCTATA
54107	POLE3	NM_017443	AAGCTTTAGGAAACTACTAAA	AGGGATGAGGACAATGATGAA		
54112	GPR88	NM_022049	GGCGTTGAGTGTTATAGTGAA	CTCCTAGATGCTAGAACTTAT	TACCACGACATTTAACATCAA	ACCAGTATGAGTTGCCATTAA
54207	KCNK10	NM_021161	CGGGAGTCAGTCCAATAGGAA	TTGGCTGGAATTGGAGACCAA	CAGCGTGGAGATCCACGATAA	CTGGAATTTGTTGGAAGCAGA
54209	TREM2	NM_018965	CAGGGCTGAGAGACACGTGAA	AACACTTACAAATAAATCCAA	AAGGAAGATGATGGGAGGAAA	ATCCAAGACTGTCATATTTAA
54212	SNTG1	NM_018967	CTCACAAAGCACAATATTAAA	GAGGATTTGGATTAAGCATAA		
54329	GPR85	NM_018970	CTGTATGTCACTACATATGAA	TTGGAGCATAGTACCATAGAA	CAAGGGAACCTTACTGTGTTA	AAGCACAAACTAGGAAGACTA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
54332	GDAP1	NM_018972	ACGCATTCCTTCAGCTCTCAA	ACCCAGGTTAATGCCTGATAA	TCCCGGCTTATGCAACTACAA	CGAGCGTGTCTTGAAGAGAAA
54344	DPM3	NM_018973	CCCATTAAAGAGCCAGTTTAT	TCCCATTAAAGAGCCAGTTTA		
54361	WNT4	NM_030761	CAGGGAAGGCCGATAATTTAA	TTGGGTCCTCATGTTATTTAT	CTCATGTTATTTATTGCCGAA	CAGACCTAAGGTGGAGTAACA
54429	TAS2R5	NM_018980	TCAGCTCAATTCAGGAAGTTA	CCAAATTGGCTTAACATTCTA	TCGGTTTAATTGGAAATGGAA	GCCGTTGGCTTCGCTATCTTA
54431	DNAJC10	NM_018981	CTGGAGAACTGTGGTTTGTAA	CAGGGCCTATCCAACTGTTAA	CAGCTTAAGTTTGGTACACTA	CTCGACGGACTTATAATGTTT
54433	NOLA1	NM_018983	CTGCATGATCTGTTTCTACTA	ACCAGTTGACTTCTGCATTAA		
54439	RBM27	XM_291128	CAGGGAAAGATCGAAGTTTAA	AAGCAAGGAAATAACAATCAA		
54443	ANLN	NM_018685	CTCAATCTAAAGACAAATCTA	AAGGTTTCACTGAATGCGAAA	CTGATGCTTGCTACAAACCTA	CACCGTTTCCATCGTCTCGTA
54457	TAF7L	NM_024885	CTCCATAAGATTCAGAATAAA	CTGGTTGTTATTCACCAACTA		
54458	DKFZp564J157	NM_001005354	GAGCGGCCACATAATTACCAA	CGGCCACATAATTACCAATTA		
54461	FBXW5	NM_018998	CACCCAGTTCTCCCAGTTCAA	CTGGACCACGTCATAGACATA	CACGAGGATGTGGTCAACTCA	CCCGTTCAGGGCCCTGAATAA
54462	KIAA1128	NM_018999	GAGCATAATTATCTCAGGTAA	ACGAGTTGGCCTTATCCTTAA	ACCGTATATTTATGAAGCATA	CCGTATATTTATGAAGCATAA
54475	FLJ10458	NM_018096	ATGACCAAATAAGTAACTTAA	CAGCAGTGACAGCACACTGAA	AAGGACAAATGCCTCCGGATA	CCCAGGTTCTATGACCAAATA
54495	TXNDC10	NM_019022	TTCGAGGTTATCCAACAATTA	CAGATTGAAGTCAATTATTGA	ATGCTGTTAATTTAACAAGTA	TAGGATATTAAGACTATCAAT
54498	SMOX	NM_019025	CCAGTCAATGCTGAAAGTCAA	CACGTCATCCAGCTAGGGAAA	ACCGACAAGATCTTTCTGGAA	CCGGCACGATAAACCAGTCAA
54499	LOC54499	NM_019026	TTGGGTATGATTAGAGTGAAA	AAGAATAACAACAGAGATCTA		
54503	ZDHHC13	NM_001001483	TGGATACATATTGGACTTCAA	CAGCTCATTATTCATATGCTA		
54508	FLJ11235	XM_496773	CCGTAGCACAGTAGAAATGAA	CAGGATCAGCATAACCGCCAA		
54510	PCDH18	NM_019035	CTGAGTATAGTTTGACTGTAA	CCCGAAGCAACTGGTAAGCAA	CTGCGCCATAGTAGCAGGTAA	CCGGAGAATATTTCTCTCACA
54512	EXOSC4	NM_019037	CCCTAGTGAACTGTCAATATA	CAGGCAGATGGTGGGACCTAT		
54514	DDX4	NM_019039	CTGAATAACAACATTGCTAAA	AAGGTTTAAATGAAGAAGTAA		
54518	APBB1IP	NM_019043	AAGATTTAAATGAGTCCTTAA	CAGCATCTCTACAAGCATCAA		
54538	ROBO4	NM_019055	CCGGGCCTGTGAGTTACGAAA	CCGGGAGGATTTCCAGATCCA	CACCTCAGGAAGTGACTCTAA	CTCCTGTAGATTACTCCTGAA
54540	FLJ10404	NM_019057	CCGAGAGGTGGAGTACTTTAA	CAGAAACTCAGAGCAACTAAA		
54554	WDR5B	NM_019069	AAGACTGTCCAGAAACTTTAA	AACCGTAACCTCACACATTAA	TAGCACAATAATTTAACTGAA	ATCAGAGTTACTAGTAGGGTA
54556	ING3	NM_019071	GAGGCGATGTTTGGAATTAGA	CGGCACTTATGACAACATTAA	AACCAAGATTGCCCTATAGAA	CTAGAGTACCTGGGTACATAA
54558	SPATA6	NM_019073	CAGGCTCATCAAAGACATTTA	CAGGATAAATTTATTTACCAT		
54575	UGT1A10	NM_019075	AAGCACAGGCACAAAGTATAT	CTGGAAGATCAGAACCGGGAA		
54579	UGT1A5	NM_019078	CACACTCAATCGTTCTTTGAA	CACCCTGGAGGTGAATATGTA		
54581	SCAND2	NM_022050	CTCCAAATAGTTAAACTGGAA	TAGAGTTAACTTTGTAATGTA		
54584	GNB1L	NM_053004	CCCGTCATGGACCTTGACTTT	CACGATCCGGCCAGATCGCAA	CAGCCTTGGCCTGAAACCTCA	CAGGTGCGTGGGACTCATGAA
54585	LZTFL1	NM_020347	AAGACGTATATTCAACATAAA	AAGCATTAAGATAAACAAATA		
54620	FBXL19	NM_019085	CCGCTGGATCGAGGATGTTAA	CACTCTTTCATCGTCATGGAA	CCGGGTCTGTACAATACGGTT	TACAATACGGTTTGCTATAAA
54658	UGT1A1	NM_000463	AAGGGAAGCTTTGTACCTTTA	CTGATGTTTCCTACAACTAAA	ATGGTTGCAATTGATCCTTAA	TTCCCACTTACTGCACAACAA
54662	TBC1D13	NM_018201	CCGGTGGAACACGTACTTCAA	CACAGAAATCTTGGAAACCAA		
54663	FLJ10489	NM_018093	AAGGTTTATCTCAAGTCTCAA	CACCGAGACTGGGATCTTGAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
54716	SLC6A20	NM_020208	CGAGATGTTCCCGCAAATCAA	TGAGATGTTGTTAGCCTATAA	CCCGTGGATTCAATCTTCTTA	TCCAATTATATGGAAGAGTTA
54734	RAB39	NM_017516	TCAGTTCAGGATAAATACCAA	AAGGTTACAAACCCACACCAA	TAGCTTCACAACGTCAAGTTA	CAGGAGCGGTTCAGATCAATA
54737	HSMPP8	NM_017520	AAGGGTGAAATAAGAGATTTA	CTGGTGAACTTCTGTGCTTAA		
54741	LEPROT	NM_017526	ATGGCGTTTACTGGCCCTTAT	CTGGCCCTTATTCGTCCTGAT	CGGCCTTGTGTTGGCAGGCAA	AAGCATCATCATAGAGAAGTA
54752	DKFZp434H2215	NM_017559	ACGGGTGTCATCCCGAACAAA	GAGGATGATACCATCAACCTA		
54754	DKFZp434I1117	XM_030729	CCGGCCGGACGACTCCTGTAA	CCGCAGGAAGAGGACGGGATA		
54763	ROPN1	NM_017578	CTGGGATGGTGTGGTGAGCAA	CACACTAAGGATAGCAATTTA	AGGATAGCAATTTATGTCAAA	TACACACTAATAAACAATTAA
54790	FLJ20032	NM_017628	AAGGCCTTTCATATAAATTTA	CAGCTGTAGACTAACAATATA		
54795	TRPM4	NM_017636	CTGCACGACGTTCATAGTTGA	CAAGATCGTCATCGTGAGCAA	CGGGTTTACGTTTCTAAGGAA	AACGTGGGAATCGGTGCATAA
54801	FAM29A	NM_017645	CCGGAAGAAGTTGGTCATCTA	AAGGAACACTGTCAAACTATA		
54820	NDE1	NM_017668	ACGCAGCTGCAACAAATTGAA	CGCGCAGACCAAAGCCATTAA		
54828	BCAS3	NM_017679	CAGATTTAAATGATACATCAA	CTGGAAGAGATTGAACAAGAA		
54831	VMD2L1	NM_017682	CCGCGACAACAGCGCCCTTAA	TCGAGTTGTCATGAGGATGAA		
54836	BSPRY	NM_017688	CAGCTGATTCAGAAGGAGCAA	GTCGGAAATGTTAAACTTTAA	CTGGATGGTGAATGTCCAGAA	CCAGAACAGTTGTGCCTATAA
54841	BIVM	NM_017693	CTGCTGGAAATAATTCATCAA	GAGGTGGTTTAGACAAATTAA		
54843	SYTL2	NM_032379	AAGGGATTTAAATATAACAAA	CCGGTGGAATCTGATCTTGAA		
54847	SIDT1	NM_017699	CCGGACCAAGATGTTCCTTTA	CACATTCCTCTTAACAAGTAA		
54850	FBXL12	NM_017703	CTGGTGGATGTAACTACTCCA	CACCTTGAAGAGGGCAGATAA	TCGCGATTCAATGATCGATAT	AATGATCGATATGCTCATAAA
54855	FAM46C	NM_017709	TTGGAACATATTCCAATTCAA	CTGGTCATTCATGACCTTAAA		
54866	PPP1R14D	NM_017726	GAGCCTGAGATTGACCTGGAA	CAGGCCTGCCCTGAAACTCCA	CCGCCTGACAGTGAAGTATGA	CAGGAGCTCTTCCAGGATCAA
54873	PALMD	NM_017734	CTGGGTATTGGTGTAAATGAA	TAGGTTAAGGAAGGAGATAAA		
54901	CDKAL1	NM_017774	TAGCACATCCTTCAAATTAAA	CAGCGTACTCATGGAAATGAA		
54913	RPP25	NM_017793	TGGAGTCTTGTTTCCAATAAA	GACAGGTAGCATGGACCTTAA		
54918	CKLFSF6	NM_017801	AAGAATTATAAGAGAAATGAA	ATGGGAATTTAACATATTTAA		
54919	FLJ20397	NM_017802	CTGCAGCTGATTTGAAATTAA	GCCAAAGTGATTAGAAAGAAA		
54935	DUSP23	NM_017823	CAGGAGATGCCATTGCTGAAA	TTGGCTGAAGACACTGAAGTA	GAAGTGGACTAAAGTATTAAA	CAGTTCTACCAGCGAACGAAA
54937	FLJ20449	NM_017826	CAGAAACTATTTGCAAACATA	CTGAATTGTTCTTATATGTAA		
54938	SARS2	NM_017827	CACCTGGAAATTGGCGAGAAA	CTGGATATGCCCACCCAAGAA		
54939	COMMD4	NM_017828	ACCCTGGATGTTACATATAAA	AAGGAACCTATCGAAGAATAA		
54941	RNF125	NM_017831	CAGAAGTACATAGATAAGTAT	CTGGATCATTGTATTACTCAT	CTCGGTTTGCAAATTAGATAA	ATGGTTAGGCACGATAACTAA
54946	SLC41A3	NM_001008485	ACCCATCGTGAAGATCCTGAA	AAACCTCTATTTAGATTTCAA		
54955	FLJ20508	NM_017850	CAGGATATTGAGAGACATTAT	CCAGATAACTATTATTAATAA		
54957	TXNL4B	NM_017853	AAGGAAGTAGACCAGGCGATA	CCACCACTCTATTCAGGTAAA	CTCGTGGTGGTTATTGAAACA	TCGATATGCTAAGAAGAACAA
54958	FLJ20512	NM_017854	ATGGGTCGGGAAGCAGCATAT	CCCGAGGACTGGGACATTAAA		
54962	FLJ20516	NM_017858	ATGCTATTGCCAATACTTTAA	CAACAGCAACTTGATGCTACA	CTGAGTTAAGTAGAAGCCTAA	AAGCTTGGCGTTACTATGTAT
54973	FLJ20842	NM_017871	CCGCAAGATCGCCGTAGACAA	GAGGAACATGTTTGAGTTCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
54988	FLJ20581	NM_017888	TAAGATGATCACACAGCATTA	AAGAATATCATTGGCCCTGAT		
54989	FLJ20582	NM_014106	CAGGTAATAATGTTAACTATA	CAGGAGAATCACATGCTTTAA		
54998	AKIP	NM_017900	AAGCAGATCAAGTTCGAGAAA	CTCAGAGGACTCAGCCTTTAA	CTGCTGTGATCCGTAGTAATA	ATCCGTAGTAATAAATTCTCA
55002	C13orf11	NM_017905	CACGTGCAGATCACCACTTTA	CGGGCTCTTCATGGCCGTCAT	GAGGAGCAGCCAGTACATCAA	TAGTCAAATATTTGTTATTAA
55006	FLJ20628	NM_017910	CGGCGCCTTCGCGAAACACTA	CTGGCTAAGAAGAATTACAAA	GGCGTGATTCATGGAAATTAA	CAGGAGCAACCGAAGACATAA
55010	FLJ20641	NM_017915	TCCCAATTTGCTTGTACTTAT	ACAGAATAGATTGTACGGCAA	CCCAATTTGCTTGTACTTATA	CAGAATAGATTGTACGGCAAA
55011	FLJ20643	NM_017916	CAGGGAGGGCCTTGAGGACAA	TCCGGAATGGCGCATGATGAA	CCCGCTGCAGATCAAGTCTCA	ACCGGAAGAGAAAGCAATTAA
55014	STX17	NM_017919	TTGAGGTTTGTTAGTGAGGAA	TTGCAATTTGGTCCAACTATA	CTCCTATAACCTCTAGGTAAA	ACCCTGAATTGGAGACCTTAA
55016	MARCH-I	NM_017923	TACCTTAACCAAGATGCCAAA	ACCAAGATGCCAAATTATCTA	AAGAACTTCTCATGTAATGTA	TAGGCAGTAATCAAAGATTAA
55049	FLJ20850	NM_017967	CCGCTCTTGTAGGGTAATTAA	CAGCTTCGCGGCAGCAGCTAA		
55066	PDPR	NM_017990	TTGGAGCAAGTATGTACTTAA	TAGCTACAAGATTCAGCTTTA	ATCTCTTATCTCCTTGATATA	ACCACATAGCCCAGTGATTAA
55072	RNF31	NM_017999	CTGGCGTGGTGTCAAGTTTAA	CCGAGATGTGCTGCGATTATA	ACGCATGAACGACCCAGAATA	CAGGACAATAACGTCATGTTT
55082	FLJ10154	NM_018011	CAGATTGTAGATGACAATATA	AAGGATGAAATTGAACGAGAA		
55083	FLJ10157	XM_371354	CAGCAAACACATTCCATACAA	CAAGCTCATAAACGAACGCAA	ATCAGTATTGCTTATGAATAA	AAGCACTTTGAGGAACCTTAA
55089	SLC38A4	NM_018018	CAGGACTGGATAAATAATTAA	ACCCAAATACTTTGTATTCAA		
55102	C14orf103	NM_018036	CTCCAACATGTTGACAGTGAA	CTGGGTGGCATGAGAAACCAA		
55104	FLJ10246	NM_018038	CAGGTTCATCTTTGACTTCAA	CAGGTTGTATCTCCAGATAAT		
55111	PLEKHJ1	NM_018049	CAGGGTGCTTGTTCTGTTCAA	CCCGTGCTGAATGAATGTACA		
55117	SLC6A15	NM_182767	TGGAATTACATAAGCCCTAAA	CACGCCTATTGTGGACACTTT	CCAGCAGATATTACTACTATA	CCCAATGGACGGTATGGAATA
55118	CRTAC1	NM_018058	CACCAGTCACTTAACTTGTTA	CCAGGACATCGCCTCACCCAA		
55122	C6orf166	NM_018064	CTGCAGCATCCTCACCATTAA	TTCACTGGTTGTGTAAATAAA		
55124	PIWIL2	NM_018068	AAGGATGTACATAAGATTGAA	AAGAAGCAAGTTTCTGAGTAA		
55128	TRIM68	NM_018073	TTCATGTATGTAGGAGTTAAA	ACGCATTCTGTCCACCATGAA	TAGGCCAAACTGGAGAAATAA	AAGAGAGATCCTGAAGACTTA
55129	FLJ10375	NM_018075	CAGACCCTTTATCAACATAAA	TAGACCATTGTTAAATAAATA		
55139	FLJ10415	NM_018089	CCGAAGGTTCATGGAGAAGAA	CAGGAGGAGCGTGAACGAGAA		
55148	C14orf130	NM_018108	AAGCCTCAAGGCAGAATCAAA	CAAGGTTGCACTATTAGTATA	CACAATAGTACCGATCAGTTA	ATCAGTTAACTCAGCGCTGAA
55154	FLJ10504	NM_018116	AAGGAGCTAGTTTGCAATAAA	CTGATCCTTAGTAACATGTTA		
55166	C6orf139	NM_018132	TTGGATATTCTTCATAATTCA	ATGGAAGATTTAACTAATGTA		
55167	FLJ10546	NM_018133	CTGGCACGGGATATAATAGAA	CAAGGCGTTTACTGAGATTAA	CAGTGTCTTATGAAACATGTA	AGGGCCTTGATTGTTATGTAA
55170	HRMT1L6	NM_018137	CCGCCTGGGTATCCTTCGGAA	CCGCAGCGCTTTGCTCAGCTA	CACACCTTATCTAAGTCTGAA	ATAGCCTAACATTTATTGTAA
55174	FLJ10569	NM_018142	CTGGTTCTTCTTGAAGATGTA	CCAGTGTGAAATGTTACTAAA		
55180	WINS1	NM_018148	AACCCGGATATTGTCTGTCAA	AAGAAACTTCTTAGAGATTCA		
55182	FLJ10597	NM_018150	CAGGCAGCTCGCGAACACAAA	ACGGCAAGTCTTAGGAGGGAA	CCCAATCAGTATGCTGAATCA	CTCGGTGTTCAGTGGTGTATA
55183	RIF1	NM_018151	CTCATGGAAATTACAATTAAA	AAGGAAATGCATGTAAAGTAA		
55192	FLJ10634	NM_018163	ACCCAGAAACTTGATGAGAAA	AAGGAAGAAAGTGAAGCTTGA		
55193	PB1	NM_018165	CAAGGATGCAAATTCAATTAA	TCCCAGGTTTATAATGATGCA	CCGGAGTCTTTGATCTACAAA	CAGGCTTACATCGCACATACA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
55194	FLJ10647	NM_018166	CTCCGTTTACTTGATCTGCGA	GAGGTGAAGTGACCAAATGAA		
55200	FLJ10665	NM_018173	AAGGCAGAGGAGTATGTTCAA	CCCACAGAAAGTTGTGCATAA		
55206	SBNO1	NM_018183	CAGGTTCAACTTTGATAATAA	CTGGATGAACTTATCGATGAA		
55218	C14orf114	NM_018199	CAGAATCTCAGCAGAAGCCAA	GTGGGTAAATTTGGAAGGCAA		
55219	FLJ10747	NM_018202	ATCCTCTTTGTTTATATTGAA	CAGGCTGGAACAAGACATTAA		
55228	FLJ10781	NM_018215	CAGGTGTATGGTAGTAAGTAA	CACCATGACTAGTAAATGTAA		
55234	SMU1	NM_018225	CAGAATGTTCAAATACCTTTA	CAGGTTGTTCTGGAATTGATA		
55239	FLJ10826	NM_018233	CCGGATTGCCTTCATCCTGTA	TTGCCTGACAGTGTTCTTAAA		
55243	KIRREL	NM_018240	CTGGGAGGAAAGAGAGATAAA	CCGGGTCATGAAGGCCATCTA		
55247	FLJ10858	NM_018248	TCGGATATACAGCATATTCCA	AAGGATTATGCGACACAATAA	CCTGGATATTCTAACAGTGAA	ACGGATTCATTTCGGAATGAA
55256	MTCBP-1	NM_018269	AAGCCTTAAATGTTTAAGTAA	AACAGGAGTATTAGTACATAA		
55257	C20orf20	NM_018270	CTCGGATTAGCAAGCAATAAA	TCGTGTGACTGCGAACATTAA		
55265	KIF24	AK001795	AAGGTTATCAAATTCACTTAA	AAGGGCATGTAGTTTAATTAA	AACAAGTAATCCCTAGTACTA	TAGCGTAACATGATACATCTA
55274	PHF10	NM_018288	ACGAATTACAGACCATTATAA	CGGACAGTTCCAGGAATATTA	TCCAGGGAAGACAGAAATCAA	ATGGCAGTGTATGGAATGTAA
55275	FLJ10979	NM_018289	AAGGAGATTTAGATCAACCAA	ACCCGTGATATTAAGCAATTA		
55283	MCOLN3	NM_018298	TCAGTTAATCTTCGCAGTAAA	CAGACAGTTCGTCATCAAGAA	ATGACTTTACTCTGACTATAA	CTGATACATACGAAACAATTA
55284	FLJ11011	NM_001001481	AAGGTTAACAGCATGAATTAA	CTGGTTATAGTGGGAATATAA		
55295	FLJ11078	NM_018316	AAGAATTAACCTCCTATCTTA	CACGGGCATCGTACAGGTGTA		
55304	C20orf38	NM_018327	AAGCATCATATTTGAAGGAAA	CAGAGGTTCTTTAAAGCATAA		
55308	DDX19L	NM_018332	ATCAAGGAAGAGAAAGTCAAA	GGGAATTATGCTGTTCATTTA		
55314	FLJ11155	NM_018342	TAGGTTATCAGTAACAATTTA	ATCCTTTGTTTCATAAAGTAA		
55317	C20orf29	NM_018347	CACCGGAGTAAGAAACTACAA	CCCACAGTCATCGAAACACAA		
55324	ABCF3	NM_018358	CAGGGAAATAGCCAGGTGCTA	CCCAAGTGGCTGCTATGTAAA	TCGGTTGGAATCATCTGGCAA	CGAGGCTCGACTTAAGGCAAA
55342	STRBP	NM_018387	AAGGATGTATAGAGTCTCAAA	CTGGAAATTCTACAACTGAAA		
55359	STYK1	NM_018423	GCCCAAGAGTGTTATTCTCAA	CCGATTAGACTAAGGAGACTA	TTCACCTTAGGTATAGATAAA	CTGGGCTGCAAGATATCAATA
55361	PI4KII	NM_018425	TCCAAAGATATCGGACCCTAA	TCCGCACACAATCATAGAGAA	CCGCATCGGGCTACCACCAAA	ACGCAAATGTATGAATAACAA
55364	IMPACT	NM_018439	CAGGATGGATTCTGAAATATA	AAGAAGAGGAATGAACATTAA		
55366	LGR4	NM_018490	CACACTTGGGCCAATAACTAA	TCCAGCTAGATTGCAGTTTAA	TAGGTGTAGTAGAGCAATATA	TAGGATTTCATAGTAATTCTA
55437	ALS2CR2	NM_018571	CAGGATTTACATGGGTATAAT	ATGCTGTTACAGAAACTGAAA	CCAGTGGAACTCACACAGTAA	CAGGAACACTGGTAACTATAA
55503	TRPV6	NM_018646	CAGCAGAAGCTACTTCAGGAA	CAGGCCTGCATTACTCCTTCA	GAGGAGTAGCATGAACGCCAA	CTGCATGTCAGAGCACTTTAA
55511	SAGE1	NM_018686	AAGGGAGCTGTTTAAATTTAA	CTGGTATTTCATGCAGAAGTA		
55520	ELAC1	NM_018696	ATGAGTGGAATTACTAGGTAA	ATGAATTGGCTCAGTATTTAA		
55530	DKFZp761H039	NM_018711	CCCATGAAAGCCAGAGCTAAA	CCCGGCCAAACCCTCAGTGAA		
55534	MAML3	NM_018717	CTGACTTATGGCAACACTAAA	CAGCAGCTTTGGAGACACAAA		
55561	CDC42BPG	XM_290516	CACAGTCATTATATTGTTATT	CCGGCCCGTGTACACACTCAA	CTCGCCGCCTACCAACTTCAA	CGCCGGTGGCTTTGCACTCTA
55572	H17	NM_017547	CCCGCTAGTTGTCAACATGTA	CAGCTTTCTACGGAACATCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
55578	FAM48A	NM_017569	CTGAAGTTAAGCAGAAATTAA	AAAGATGATTATGTATTTGAA		
55600	ITLN1	NM_017625	CTCAGACAAGATTACAATGAA	CCCGGTGATCCCTGTGGTCTA	CTGCGGGATTTGTTCAGTTCA	ACCCAGTAGCTAGAATGTTAA
55601	FLJ20035	NM_017631	CCCAGTGTCAGTATTTATAAA	AAGGGTATTTGCTACCTTTAA		
55611	OTUB1	NM_017670	CAGCAGGACCGAATTCAGCAA	CAGGGCTTCACTGAATTCACA		
55621	FLJ20244	NM_017722	AAGGATCGTCTCTGTGGCTAA	CCAGGAGAGAAGGACACGCAA	ACGCCGGAATGTCCAGCTCAA	CAGCATCAGCGCTGACTTCTA
55622	FLJ20272	NM_017735	AAGCCATATTCTTAAATTCAA	CCGCAGGTGTATTTACGGTAA		
55626	FLJ20294	NM_017749	TGCGTAGAATTTAGAGTTATA	CTCCTAATGAATGCTAAATAA		
55627	FLJ20297	NM_017751	TAGGCTGTCGTCTGCCATCAA	CAGTGGTACTTAAGTATTCAA		
55629	PNRC2	NM_017761	CTGAAGGTTTAGTATATTAGA	AAGATGTAAACTCTTGCATAA	ACAAGTTTATGTAGTACTTAA	CCCAATGGCCCTGTTTATTAA
55632	KIAA1333	NM_017769	AACGACATTAAGTGATAAATA	CTCATTACATTGGACATTAAA	AAGGAATATTATAGCCACTTA	TAGATTAATCTGTATGGTCAA
55636	CHD7	NM_017780	CAGGGATTAGTTAACAATACA	TACCATTGGTATTATAATAAA		
55640	C14orf58	NM_017791	ATCAGATATTCTAAACTTAAA	AAAGGTATTAACAAATGTTTA		
55643	BTBD2	NM_017797	CCGCATCAGGTTCTCAGTCAA	CACGCTATACACCGCCAAGAA		
55644	OSGEP	NM_017807	CTGGACCACGGGAAAGAGATA	CTGGAGGGACTAATAAGATCA	TAGCAAAGCTATAGACTCCAA	CCAGGATGACTCAGCAATAAA
55652	FLJ20489	NM_017842	CTGGAGCTTCATTTCCTTCAA	GTGAGGAATCTTTGTACTTAA		
55662	HIF1AN	NM_017902	CACTGTGAACTTCTGGTATAA	CACCCACAAGTTCTTGTACTA	CAAGCTCAAGCCATACATAAA	AACACATAGGCTTGCGTCTTA
55663	FLJ20626	NM_017908	CCCAATGTCGATGGACAGGAA	AAATTCCACTTTCATAATAAA		
55667	C9orf55	NM_017925	CAGCACAATAATGTTCTTAAA	CAGCTTGAGATGGAAATTCAA		
55669	MFN1	NM_017927	ACCCAGCAAGAAATTATTGAA	AAGGCTTGTTATAGTCACTTA		
55680	RUFY2	NM_017987	AAGAATTATGTTGAAGAATTA	CAGGATGTAGAGAATGAGCTA		
55683	FLJ10081	NM_017991	CCGGATGCTTGTGTCATCCAA	CCGACCTGCCTTTATGATAAA		
55687	TRMT1	NM_001008568	CTGACAGAGATGGATCTGCTA	AACGAAAGAGTTTGTAAAGAA		
55690	PACS1	NM_018026	CCCGGAGGAAACTAACGTCAA	CCCGGTGCAGATGAACCTGTA		
55699	FLJ10326	NM_018060	CAGTCGTTCAATATATGTAAA	ACCGAATTATACAAACAATAT	ACCACTGAGCATATTGTTAAA	AAGAGTCTTCCTATAAAGTAA
55702	FLJ10374	NM_018074	CTGGAGCAGCTTCCAACACTA	TGCGAGGTGATCAGAAGGCAA		
55711	MLSTD1	NM_018099	CAGGTTGGCTTGATAATATAA	CAGGATGACAAAGCTCATGAA		
55718	POLR3E	NM_018119	CAGGAGGTGGATAAAGTACTA	CCGCGGAGAGATCGAGCTGAA		
55732	FLJ10706	NM_018186	CAGGATTTCTAAAGCACACCA	CAGGTAGCAGATCAACCTTAT	CAGCCTGGCTTTCAATGGAAA	CTGGGTTTGATGCTTTGTCAA
55734	ZFP64	NM_018197	AAGGACATGGAGCGGCATTTA	CAGCAGTTTAACAACCTGGAT		
55743	CHFR	NM_018223	AACAGTGATTAACAAGCTGAA	TCACCACGCCATGAAATTCAA	TCCCGTGGAGCGGATCTGTAA	AACCAGAGGTTTGACATGGAA
55754	TMEM30A	NM_018247	ATCGATGGCGATGAACTATAA	ACCGGATAACACGGCCTTCAA	CTCGAGATGATAGTCAACTAA	AACGATTTAAAGGTACAACAA
55760	DHX32	NM_018180	ATGGATCAGGTAACTACTTAA	ACGCCTTATCTTTGAAATTCA		
55769	ZNF83	NM_018300	ACGCAATTTAAATGTGATATA	AAGGAGAGTAATACAGGAGAA		
55779	FLJ11142	NM_018338	CTGAGATTAATAGAAATTGAA	AACTATCACTTTCAACATTAA		
55781	RIOK2	NM_018343	CTCATAAATGGTTATCCACTA	GAGCTATGAATCAGTATAGAA	CGCGGTTGAAATGGGCATGAA	AACGCGATTATCATAAACATA
55793	FLJ11280	NM_018379	TCCAGTTGTTTCAGAGCTTAA	TAGCACCATGACTAAGCATAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
55794	DDX28	NM_018380	CAGGGCAATGAGGAACAACTA	CACGTACTTGATCACTTTGTA		
55795	FLJ11305	NM_018386	AAGGATGATTCTGATCTATTT	AAAGCGTATTCTGAATTTATA		
55801	IL26	NM_018402	AACTTAATTTAAAGTATGTAA	AAGCAGCATGGCTCAAAGCAA	CAAGTACATTGTGTCAACTTA	CAGTGTGAACTTAGTACTTAA
55802	DCP1A	NM_018403	CAGGATACATTAATACATCTA	CTGGAGCAGAATAAGTCTAAA		
55805	DKFZp761O0113	NM_018409	CTCAAAGATCTTAATGAGTAA	CCGCTAAACACTATTATTCTA		
55813	HCA66	NM_018428	CACGCATTGGATATTCATTTA	CTGGCCATTTATGAAGATGAA		
55814	BDP1	NM_018429	CAGAGCAAGGATAGAAATTAA	AAGGTTCTTAATGAATGTCTA		
55815	TSNAXIP1	NM_018430	CCGCACGCAGATGGAACTCAA	CAGGAGGGACTTTGAAATGCA		
55819	RNF130	NM_018434	CAGAATGATGTCGTCCGAATT	CTGTCCTATGTGCAAACTTAA	CAAGCTGTTAACCGAAGATCA	TCCGAGAACAGGAGAAATCAA
55829	SELS	NM_018445	AAGGAGATTTATGGACTTCAA	CTGGCGGATGAGGCTAAGAAT	AACCCTTAACCCTCGATTCAA	AGGCCTCTAGATGATTAGCAA
55830	GLT8D1	NM_018446	TACCGAGATCTCAAACATAAA	CAGACAGACTATAGACTATAA		
55836	C6orf35	NM_018452	TAGGCTCTAATTAGTCAGCAA	CTGCCTTTCATTTGTAACTAA		
55837	C14orf11	NM_018453	CCGGAGAAAGTGAATCATCTA	ATGAATTGTTCTATTAACAAA		
55844	PPP2R2D	BC047379	CCGCTCCATTAAGAACAGTGA	TTCATCCATATCCGATGTTAA	TAGGTGGTTACCACAACAGAA	CAGAGACTACCTGTCGGTGAA
55848	C9orf46	NM_018465	CTGCTTGGCTTCCACCTTTAA	AAAGGAGTTCATGCTTATGAA		
55850	MDS032	NM_018467	TCGAATCATGCCTAAACTCAA	ACCGGCCTCTGAGGTGATCAA		
55851	PEN2	NM_172341	CTCCCAGGACAGGCTCCTTAA	ACAGAACAGAGCCAAATCAAA	CTCGCCCAAAGAAGACTACAA	CACAGAACAGAGCCAAATCAA
55870	ASH1L	NM_018489	CAGGCTGTCGTATCAATGCAA	CCGAGATGATGGGAATATCAA	TCGACTGTTATCTCACATTAA	ACGGTAGTTCTTGCAATTATT
55872	PBK	NM_018492	AACGCTGTAAACTGTAACATT	TCAGTAGTTATTAGACTCTAA	CTCATTCTCCTTGGGCTGTAA	AAGTGTGGCTTGCGTAAATAA
55884	WSB2	NM_018639	CACGTTAATTCGGAAGCTAGA	CGGAAGCTAGAGGGCCATCAA	CACGGCTTCTTACGATACCAA	AAAGATGTCTTAATTGTGTAA
55889	GOLGA6	NM_018652	CAGGAGAGACTGTGTGAACAA	CGGACGGGACGGAGCAGTGGA		
55894	DEFB103A	NM_018661	TACCATTGGGTTCCTAATTAA	CAGGTCATGGAGGAATCATAA		
55897	MESP1	NM_018670	ACCCATAGGGCTAGACACTTT	CACGAGCTGCGCCGCTTTCTA	CTGCCTAATGTGAATTTATTT	GTGAATTTATTTATTTGTGAA
55908	LOC55908	NM_018687	CCGAGAATTTGAGGTCTTAAA	ACGGCTGACAAAGGCCAGGAA		
55914	ERBB2IP	NM_001006600	CTGCAGTAAGTCGAAGTACAA	CAAGTTTGATTCAAATCATAA	CAAGATGTTATCAATTGGTTA	CCCGAAGAGCCAAATATAATA
55915	LANCL2	NM_018697	AAGGAAAGAATTTGAAGTCCA	CAGATGGGTTATTGCAGATTA	CTGGCAGTTCCAGAACATTTA	ACCCAGGTATATGTTACTAAA
55922	NKRF	NM_017544	TCGCTTATTTCTGGAATGTAA	CAAGATGTCAATTGAATACAA		
55929	DMAP1	NM_019100	GCGGATGTACGGGACATTCTA	CAGCTTTATCTCCACGATGAT		
55959	SULF2	NM_018837	CTCCATGGAGACGATTTACAA	TCGGTGCTACATCCTAGAGAA	TCGAAAGTGGCCAGAAATGAA	ATGACAGATTCTGGAGGATAA
55968	NSFL1C	NM_016143	CAGTAAATGCTTGACAAGTAA	CACCAGCATGTTGTACGGAAA		
55969	C20orf24	NM_018840	TGGATTCAGATGAAACATTAA	CTGGATTCAGATGAAACATTA		
55997	CFC1	NM_032545	CTGGAGTAAAGACACCTTCAA	TTCCTGGAAACTGATCTTCAA		
55998	NXF5	NM_032946	CAGGAAGCTAGTGAAATGACA	AAAGTATACTCTACCATTAAA		
56000	NXF3	NM_022052	CTGAATTTGATTCAGAATGAA	CCAGTTGAGTTTCACTATGAA		
56107	PCDHGA9	NM_018921	CAACGGATTTACCGAGTTAAA	ACGGAATAGAAATAGAAGTAA		
56108	PCDHGA7	NM_018920	AACATCCTGATGGAAGATAAA	AAGGATTAGATTATGAAGAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
56110	PCDHGA5	NM_018918	TCAGATTATAATATCACTTTA	CAGATTATAATATCACTTTAA		
56124	PCDHB12	NM_018932	AAGCTACACAATAAATCCGAA	CTCCAGGTCAAATAAGTTCAA		
56132	PCDHB3	NM_018937	CCGGAACTAGTACTGGATAAA	ATGGACACAAATATAGACTAA		
56143	PCDHA5	NM_018908	CACAATTGAGATACAGGTTAA	AAAGTCCAAATTTATAATTAA		
56156	TEX13B	NM_031273	CAGGAGAGACTCCGAACTCCA	CGGAGCTATTGTAGCAGGCAA		
56171	DNAH7	NM_018897	CAGGATAAATCGGCCAGCAAA	TTGGAGAGTTATGCTAAGCAA	TCGGAAGGCAATATATTAGAA	CGGGCTAATATCATTCGATCA
56172	ANKH	NM_054027	CACGCTCTGTTTCGTGATGTT	CACGGAGTTCGAAACCATCTA	ATCAATGAACATTGTACCTTA	TTGAATGTAAGGCTCAGTAAA
56204	FLJ10980	NM_019600	CAGCACCATAACCCAAATGAA	CACATTGTTGTGGAAGAATAA		
56241	SUSD2	NM_019601	CGGCACCAACTTCACATTCAA	CAGCCTGACCTGGCATGTCAA		
56255	DJ971N18.2	NM_021156	CTCCAATAACAGCCAGGTTTA	CAAGGTAGTCTTGTGAAGAAA	CTGGGTCTTGAACTACTTTAA	CTCCAGTACCTGAAAGTGAAA
56256	SERTAD4	NM_019605	AGGGAGTTATTTGGTAAGCAA	ATCCAAGATCACATACTTTAA		
56259	CTNNBL1	NM_030877	CAGGCATATCATCAAGGAGTA	TCGATTTGCTTCAGGAATTAA		
56265	CPXM	NM_019609	CCGGATTCGAGTCATCAAGAA	CTGGAGGACGGCGATCTATAT	CAACCAGAGCATCGATCTTAA	GAGCATCGATCTTAACCATAA
56270	WDR45L	NM_019613	AAGACTGTTATTGAAATAGAA	GCCGGTTTCTTTAGTTCTTTA		
56271	BEXL1	XM_043653	CTAATGGAAATTAGAATTCTA	AGGGCAGATGATGGAAATCAA		
56301	SLC7A10	NM_019849	TGGCTGGAACTTCCTCAACTA	CCCACTGGTGACGTTCGTGTA	CACGTTCACCAACATTGCCTA	CAGCTTCATCTCAGAGCCTAT
56311	ANKRD7	NM_019644	CCGGTTAAGTGAACTATGATA	AAGGATGGGTATACTCCACTA		
56341	HRMT1L4	NM_019854	CAGGCTCTTATGGGCATGAAA	CAACATCATCACCATATTTAA	CGCGTGTGCCTAGAATATATA	CAGATGTTAAGCAGCTATGAA
56479	KCNQ5	NM_019842	CGGGTTGCTGTTGTCGATATA	CAGAGTATTAAGAGCCGACAA	AAGGGCAAATCACATCAGATA	TCCAAGGTGCATCGACATTAA
56606	SLC2A9	NM_001001290	CACGTTGGACAATTATGTCAA	ACCCATTATTGGGAAGCTTAA		
56649	TMPRSS4	NM_019894	CAGGATCCTGACAGTGATCAA	CAAGGTGATTCTGGATAAATA	CAGGATCTGGATGTTGTTGAA	CTGGATGTTGTTGAAATCACA
56650	C3orf4	NM_019895	ACCGGAAAGAGTACACCTTAA	ACGGTGTATCACCATACCCAA		
56652	PEO1	NM_021830	CAGGCACCTAAGGCATTTCAA	CAGGATCGCAGCTCAAGACTA	TAGGATAGGCTGGAGCATAAA	CTGGCAGGCTAGTGTAGATAA
56659	KCNK13	NM_022054	ATCCTTATTCTTTAAGTCTAA	CCAGGCTTCCTTCAAAGCATA	TAACTAAAGAACATAGCTTAA	TGCAAAGATGATGACTATTTA
56660	KCNK12	NM_022055	TGGGACCATCCTGTTCTTCAA	CTGCATTTACTCGCTCTTCAA	CGCGCTGGGCATCATGAACAA	CTGGCGCTTTCTTAATCTTTA
56729	RETN	NM_020415	CAGCATTGCCCTGGAGTGCCA	CAGGAGGTCGCCGGCTCCCTA	CTCCATGGAAGAAGCCATCAA	CCCTAATATTTAGGGCAATAA
56848	SPHK2	NM_020126	CACGCTTTGCCCTCACCCTTA	CAGGTGGAGTATGGGCCGCTA	CCGAGGGTAGTGCCTGATCAA	CAGGATTGCGCTCGCTTTCAT
56851	C15orf24	NM_020154	TACATTATGTATATTAATTAA	CAGGTCCACCTTCTTACTTTA		
56888	KCMF1	NM_020122	GTCCTAATACTCCACATTCAA	CAAGAACATGTTACTTCTGAA		
56889	SMBP	NM_020123	CACGTCTTTCTGGGCATATAA	CAGATGTACATAGATGATTTA		
56893	UBQLN4	NM_020131	CACATGCTCAATAACCCTGAA	AGAGATGCTAATGGAATTTAA	CACACTGGCCTTTGTAAATAA	CCAGAGGAAATTCGTGTGAAA
56897	WRNIP1	NM_020135	ATGAATTAATGTTATAAGGAA	CGCCATGTTCATAGAGGATAA		
56900	AD-020	NM_020141	CTGGAAATTCTATTTACTTTA	AAGGTAATTTACAGCCAGAAA		
56904	SH3GLB2	NM_020145	CACCAAGAACTGGACAGAGAA	CAGACAGAGTTTGACCGGCAA		
56911	C21orf7	NM_020152	CTGAGAATTGTTGTAAAGTAA	AAGGTGTGGAATAACCCTTAA		
56915	EXOSC5	NM_020158	CCCAGCAAGGATAACATTCAA	ATGGAATGGATGAATCAATAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
56919	DHX33	NM_020162	ACGGTTCCTCTTAGCTATTTA	CTGGGTGAAGGTTGATTTGTA		
56922	MCCC1	NM_020166	CAACATTGACTTCTTACTCAA	TAGCATGCAGATTGAAGATAA	CATGGTTATGATCGCCATGAA	ATGCATTTGGGTCACTAATTA
56928	SPPL2B	NM_020172	CACGGTGAGGGCGGCGCTGTA	CAGGTTTGACATCCAGGTACA		
56930	LOC56930	XM_373790	CACCAACCCAGTTCTCAGTTA	TTGCCACGTGTTTCCTGTTAA		
56935	FN5	NM_020179	AAAGGAGATAATAGCCTTAAA	CTGGTCTTTGACTTGATTAAA		
56943	e(y)2	NM_020189	CGCGGTGATGGTGGTTAGCAA	AAGGAGCTCCTACAAAGAATA		
56949	XAB2	NM_020196	CCGGACCTTGTCTTCGAGGAA	CAGCTACGTTTGTACATCAAA	CCGCGTGTACAAGTGACTGAA	CACGTACAACACGCAGGTCAA
56950	SMYD2	NM_020197	AAGATAGAAATGACCGGTTAA	ACCGGTTAAGAGATTCTTATT	CCGGAGGGCCAAGCACTATAA	GAGGTTAGTCTGAATCTTGAA
56951	C5orf15	NM_020199	AAGGATATTTGTGTACAATTA	TAGGATAATGATATTGCTCAA		
56952	PRTFDC1	NM_020200	CAGGGTATGACTTGAATTTAT	TACCGGGAATGCAGCTATTAA	CCGGGAATGCAGCTATTAATA	CTCGAAACTAAGCAAGTATAA
56956	LHX9	NM_020204	CCGGCACTGCGACCACTTTAA	CAAAGTGTATTTGGATTTAAA	AACCAGATAATTAATTAGTTA	CCGGGCGTGTGTATATGGAAA
56961	SHD	NM_020209	CCAGGGCTTCCTGCATCTGAA	TCCGGAGACCTCCGCCCAGAA		
56967	C14orf132	NM_020215	CGCCATAAATTCTGAAATAAA	CAGCATGAAAGTGATGAGCTA		
56970	ATXN7L3	XM_375456	CAGCATCTATGATGACATCAA	CCACAAGAGTTTACAAATGAA		
56974	DKFZp547K054	XM_498167	CGGGTCGATGTGCAAATCCAA	CCGCATTAATGTCCTGTGGAA		
56981	PRDM11	NM_020229	CTGGCTGATTGTGGACAAGAA	CTGGATGAGGTAGGTGGTCAT	CAGGTTCTGGATAACCCAGAA	ACGCCTACAGTCAGTGTGCAA
56988	C8orf17	NM_020237	AAGAGCAATAATACAATTCAA	ATCAAATTTCTTTATCTATAA		
56990	CDC42SE2	NM_020240	ACGGCGGATTGACAGAAGTAT	CCCACAAACTTTGTGCATACA	CAGGAGACCTGTTCAGTGGAA	AAGGGAGGTTATGGAGGTGGA
56992	KNSL7	NM_020242	CTCTATACACTCAGAATTCTA	CAGGATTCCTATGACAACTTA	TTGAGATTGACCAACTTTCAA	ACGCAATAACAAATTATCATT
56995	TULP4	NM_020245	CCGTTTCTTGATCACCACTTA	CTCGGTGCAGTAATCTATAAA	CACACTGTGTTGGACCAACAA	ATGCATTACTGTAAACATGAT
56996	SLC12A9	NM_020246	CAGCAGTACCCTGAAGGACAA	CACGATCGTCGCCGTCGCCTA	CCCACTGGTGTTGATCGGAAT	CTGGTGTTGATCGGAATCTAT
56998	CTNNBIP1	NM_020248	TCCCTTCAGACTGGCCCTTAA	CAGTATCGTTTGTTTATGAAA	TGCGTTTATAATTGGCTTAAA	CACCTGTTTGCCTGAAGTTAA
57007	CMKOR1	NM_020311	CACGCTCTCCTTCATTTACAT	CTGGGTGAATATCCAGGCCAA	CCGGAAGATCATCTTCTCCTA	CACTATTGGTGTACCTTATAA
57018	CCNL1	NM_020307	TTGGATATAAGGGATCTTGTA	CAGTGTGATGTATGGACTCAA	CTCCAAGAAGACACTATAATA	CCCTAGCAGTATCTAATTAAA
57019	CIAPIN1	NM_020313	CAGGTTGAACATGATGATCAA	CAAAGTGAAGACAGCATCTAA		
57026	PDXP	NM_020315	CAGGTTTCAGTCAGTAAATAA	CCAGTTTAGGTTCCTAAGTAA		
57048	PLSCR3	NM_020360	TAGCATCTGCTTGGCCAATTA	TACATTCATATAAACTTTGTA		
57060	PCBP4	NM_020418	AACGGCGAGACTGTAAAGCGA	ACAGGAGTTCTTGGTTCCCAA		
57085	AGTRAP	NM_020350	TTGGGTCTTCTCAGGACCGTA	AACCTGAAGGTGATTCTCCTA	CTGCTTCGTCTACCACATGTA	CAGGGATTGCCTGAACCAAGA
57093	TRIM49	NM_020358	CAGGATCTCACATTTGCTTAA	TACGTATTGGTTCTTTATTAA	CAGGCCTTGTTTCTACCTCAA	ATGATATCTTTCTGTATGAAA
57105	CYSLTR2	NM_020377	CAGATTATGCCAGGCACTTTA	AAGGGTGGAGGTGATATGGCA	TGGGATCATATGGATCCTTAT	CAGGCTTTCTAAATTCTTCAA
57113	TRPC7	NM_020389	AACGGTGATGTGAACTTCCAA	CCGGATCAAACTCGCCATTAA	CGGATCAAACTCGCCATTAAA	CAGGCTTACGTCAACAGTCTA
57115	PGLYRP4	NM_020393	CCAGTGAATGTCCTTGTTATA	CAGGATGACTCTCCCAGCGAA	CAGCGAAGTATGGCATCATTA	TCAGCAGTGTCTGAAATTTAA
57117	LOC57117	NM_020395	CCAAGTTGTACTGAACGCCAA	AACCTGCTACTTCGTCAGCTA	TACGCCCACTGTACCTTTAAA	CAGGACCTAGTGGAAGTACTA
57118	CAMK1D	NM_020397	CTGAGAAAGATTAAGCATGAA	ATGGAGAAGGACCCGAATAAA	CCAGGCGCTTTCTATACTTAA	CAGGCGCTTTCTATACTTAAT
57122	NUP107	NM_020401	CAGCTTTAAGTGGGAATCTTA	CAGGTGAATATACTGAGTAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
57124	CD164L1	NM_020404	CAAGCGCATCACTGACTGCTA	CCAGCAGATGTGTGTCAACTA	CCCTATGATCTCAACCAAATA	CACGCTGGCTGTCGACGGCTA
57130	ATP13A1	NM_020410	CAGGAGCTGCACTTCATTGAA	CACCTTCGCCATCAATTACAA		
57140	RNPEPL1	NM_018226	CACCTACTCTGCCGTCGTCAA	CCTGATGAACCTGTTCACCTA	CCGAGCCTATGTGGAGAAGTA	CCGGGCAGGGCTGGAATTCGA
57144	PAK7	NM_177990	ACGCCTCTAGTAGCAAACCAT	AAGGTGGATTACGATCGAGCA	ATGGTGTGCACGTTTCATTAA	ATGATCTGGATCCGTATTATA
57146	LOC57146	NM_020422	AAGGTGTAGTTTCCACTGTAA	CAGATGGATGAAGACCACTAA		
57147	PACE-1	NM_020423	TGAGGAGTATTCAGTCAATAA	CAGGAGGTGGAATCACTGCTA	CAGGACAATTCCGGAAGTAAA	AAGCTCTATTATGAAATACAA
57148	KIAA1219	NM_020336	CCGGTACTTTGTCTTGGATAA	CCGGGCTGTTACTGTGAATAA		
57151	LYZL6	NM_020426	AAGCAAGTTCAACATATCAAA	CAGCAGCTTTCTTGCCCTAAA		
57152	SLURP1	NM_020427	CTGCTTCCGAGACCTCTGCAA	CAGCTCCTGTGTGGCCACCGA	CAGGGCGGAAGGTGCTCCTCA	CAGGACCATTACCCGCTGCAA
57153	CTL2	NM_020428	CCGGGACTTTGAGTACTATAA	CACAGTGAACACCCACGTTTA		
57161	PELI2	NM_021255	CAGAACTGTTTGGTTGATTAA	CAGGGTTAGGGTTTAAAGAAA	CACGTGATATAACTGGTTATA	CTCGGGTACAATGGTGCTTTA
57162	PELI1	NM_020651	CAGGACTACATTATAAATTTA	CAGGCTATATATTGTAGCTTA		
57167	SALL4	NM_020436	CCGAACCAACACATCCATTAA	CGCGGTGGATGTCAAACCCAA		
57172	CAMK1G	NM_020439	CTGGAAGAAACAGACCACCAA	TAGAAAGAAGTTCATGAGTAA	CAGGTCTTGTCGGCAGTGAAA	AACAGGCCGCCTGAAACTCAA
57176	VARS2L	XM_373419	CCGGAGGAACCGTGAAGCCAA	TAGTATTGTATGAAATCCCTA	CATGCAGGAATTGCTACACAA	CGCTTTATCCTCAATGCTTTA
57238	KIAA0492	XM_378914	CTGTGTTATAATGATACTTAA	TAGCAATTGAATAAACATAAA		
57325	CSRP2BP	NM_020536	CTGGAAGGAAGTGGACGTCAA	CAGGCGTGATTATGAAACAAA		
57404	CYP20A1	NM_020674	TAGAGAGACCCTCGTCCTTTA	ATCCTAGAAGACAGTATGATA	CAGAGTTGAGGTTTGCATATA	CCAGGGATTACTCCAACTGAA
57405	Spc25	NM_020675	CGGGACTAAGAGATACCTACA	ACGGTTTATAATTAACATACA	CTCGTCATTTCATTAGGTATA	CCACGGTTTATAATTAACATA
57407	HSCARG	NM_020677	CACCTTCATCGTGACCAATTA	AGGCACCAACATCTGAATAAA		
57413	AD026	NM_020683	CAGAGGAGCTATGATAGACCA	TGGGAAAGACCTATCAGGCAA	CTCGCGTGTCCTGACTCCAAA	CACGGCTTCTGCCATCTGCAA
57452	GALNTL1	XM_031104	AAGGATCCACATACCCATAGA	AGCAGCTAGGCGCGAGCGAAA		
57462	KIAA1161	NM_020702	CGCGGCCGCCATCAAAGTCAA	AGGACTCTCGTAGGAAATAAA	CAGGCCAGACTTCGTGCCTTA	CACCTCTATACCACCCATTAA
57472	KIAA1194	NM_015455	CCAGGATATATTGAACCTTTA	CAGAGGCAACTTATTCATGAA		
57484	RNF150	XM_371709	TCCAGAGGTTTCGATATGCAA	AACCCGGAACTTGCAGAAATA	CCGGAACGCGTTCCTGCAGAA	CAGAAGGACTGTTGCCTTGTA
57504	MTA3	NM_020744	AAGAAGGATAGAAGAACTCAA	ACGGCCGTTTGTTGCTATTAA		
57508	KIAA1287	NM_020748	CAGGTAAACCCTAATCATTAA	ATGAGTGTTAGTGGAATTTAA		
57510	XPO5	NM_020750	ATGGTACAGGCTACTGCTAAA	CACGGTTTGCTGTGTTTCAAA	CCAGATGTTTCGAACACTAAA	CTGTCTCGAATTGTAGTGGAA
57514	CDGAP	NM_020754	CAGGATGTCACCATAGATAAA	CTGGATCAGACTCCAAATCAA		
57520	HECW2	XM_038999	CTCCATCACTTGAGAAGTATA	ACGGTCTACTATCATCAGTAA	AAGGCTCTTCTCAGAATTCTA	CAGGATTGGTGCGCCTTTCAA
57529	RGAG1	NM_020789	CACCATCTCACTACATTCTTA	AAGCAATATCCTCACTGATAA	CAGGGCATATATGACTCCCTA	AAGGCCCATACCAACAAGTAA
57533	TBC1D14	NM_020773	CAGCAGGACTGTGTTCATGAA	AACACTGGAGTTGGCCTTAAA		
57538	ALPK3	NM_020778	CAGGTGGATGCTGGGACACAA	CAGGCAGATGGGAAGATACAA		
57558	USP35	XM_290527	GTGGATCATTGCACTGCTGAA	ATCGAGGTTTCGCTCACCAAA	CCCTTCTAACTTCTAACCGAA	ACCCATGTTCATAAATAAATA
57560	KIAA1374	NM_020800	AAGGAATGAAATTCTGATAAA	CCCAAAGTTATTACCACATAA		
57565	KLHL14	NM_020805	CCAAATTTAATCCATAATAAA	AAGCATTTATGAGAATTATAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
57572	DOCK6	NM_020812	CACGGTGAAGATGAAGGAACA	AAGACCAAGGATGAAATGGAA		
57579	KIAA1411	NM_020819	CAGCAATTACATTAAATTCAA	AAGGTGCTGAATAGCATTAAA		
57582	KCNT1	XM_029962	CTGGCTCTTTCCAAACTAGAA	AGCGCTGGAAACTTCTATTAA	CAGGTCATCGTGGCCATAATA	ACGAGGACGTAGCAAATTTAA
57585	CRAMP1L	NM_020825	CTGCATAATGATCCCATTTCA	CAGATCGTCAGTGGGATTGAA	CCCGACAACCTTGCCACCCAA	AAGGGCCACCACTGTACGTTA
57592	KIAA1441	NM_020832	CCGCCTGGTCTTCTTCAACAA	CAGGCTCTCAGGAATCCTTTA		
57593	KIAA1442	XM_044921	CAGGGAGAAGTGACCTGGAAA	CAAGTTCTTCCTCAAATGCAA		
57599	WDR48	NM_020839	CAAGTTTGTCATATAAAGTAA	AAGGGAGATCATAGTGAGTTA		
57605	PITPNM2	NM_020845	CTCCAAGATGATTATAAAGGA	CTCGTGCAAGCAGGAGAGAAA	CTCGAGTTTCTCAACTGTTCA	ACGGGAAGGCTTGGACTCCAA
57608	KIAA1462	XM_166132	CTGGAAGTAACTTTACTTATA	AAGGTAAATAATAGCCTATAA		
57609	KIAA1463	NM_173602	CCGGCATACATTGAGTATAAA	ATGGAATTAATTTACACGTAA		
57613	KIAA1467	XM_370682	GTGAATCTCTTAAGTATTTAA	CGGCGCAGTGATGGATGTTAA	CATCGTGTATTTGCAAACTAA	TTGGTTTAGTATAGAATTTGA
57617	VPS18	NM_020857	CCCGATTATCTCGCTGCATAA	ATGGAGGTGGAGAGCATTAAA		
57621	ZBTB2	NM_020861	AACGTTTAATTAAATGAGTAA	CAGGAGTACCTTTCACATCTA		
57633	LRRN1	NM_020873	AAGATTGATAACCCTCACATA	AACCTCTTCAATCCCACTTAA	CTGGTTTGATTCTACACCCAA	AAGACTTTGCTTGAATGTTTA
57636	ARHGAP23	XM_290799	CTCCTTCATCTCGGCCGTCAA	CTGGCTGAAAGCAGGCACTGAA		
57642	KIAA1510	NM_020882	CCCGACCTTCACGCTCTTCAA	CTGGGAAGAGAGCAAGTTCAA		
57646	USP28	NM_020886	CTGGAACAGTTTGCAGATAAA	AAGGATTAGGTGGGCACATAA		
57647	DHX37	NM_032656	CCCAGTGACTGTGCATTTCAA	CCAGATCAACTTGGATCATTA		
57650	KIAA1524	NM_020890	ACCACTCTTATAGAACAACAA	CAGCTAGTAGACAGAGAACAT	CGGCACAATCTTTCTGTTCAA	CAGAAAGAGCGCAGAGTGATA
57654	KIAA1530	NM_020894	CACGGTGATCTCGAACTCCTA	ATCCAAGATCACAGAGATTTA		
57657	HCN3	NM_020897	CTGAGTGGGAACATACTTCTA	AGGGACAAGAGTAGTCCTTTA	CAGCTTTCTGCCAACATGTAA	CCCGCCTTGGATCGTCTTCAA
57661	KIAA1542	XM_290536	CACACGAACCATCTCCATGAA	CGAGCTCAATTTGGTGGTAAA	CGCGTCCTTGATAAATCTCTA	CCGGATCAATATTCCTGGAAA
57665	RDH14	NM_020905	TATAGTAAGTATAATGAATAA	ACAAGTCTTACTTGGAATAAA	CTGCCTGGTGTGTGCACACAA	CAAGCATGGATGACATATTAA
57666	KIAA1545	XM_495939	CCGAAGTTACAGATTATATTA	TAGTCTGTTGATATAAATATA		
57693	ZNF317	NM_020933	CCGCTGGAAGTCCAACTTTAA	CAGCTTGGCATTTAATGTCAA		
57703	KIAA1604	NM_020943	CAGGAACAGATTACAGATAAA	CAGCAAACAAATGATAGGAAA		
57707	KIAA1609	NM_020947	CAGGCAGTGCACTTAGAGAAA	CGCGTTGCAAACTATTATAAA		
57711	ZNF529	NM_020951	ATGGATTTAATAGGTAATCAA	AACCTTGTATACAGACATTAA		
57716	PRX	NM_020956	CAGGCTACTTCGAACCAGGAA	CCCGCTGCTCCTGAAGTTGTA	AGGGATGGAATTTGGCTTCAA	CCCGCCGTGGAAATTGAGGAA
57717	PCDHB16	NM_020957	ACAGCATTAAACAGTCAATAA	AACCTGATTTATAGTCCTGTA	AAGCAAGAGCTGAATATAATA	AACGGGTACGGTGATAATTAA
57722	NOPE	NM_020962	CCGGCTCAAGAAGAAAGTGAA	CCAGCCTATGATAACACTAAA		
57729	KIAA1639	XM_290923	TCGGAAGCACTGCTCAGTGAA	CACACAGAGGACCTACACATA	CACAAAGACCTTCGCATTCCA	CCGCACGGCATGTGTCAGCAA
57733	GBA3	NM_020973	AACCATGATTTGCAACTGTAA	CAGATAGACCTGGAAACATAA		
57758	SCUBE2	NM_020974	CAGGACAAGTGTAACCTTTAA	CAGGAACTCATTGAAGACATA		
57763	ANKRA2	NM_023039	CACAGTGTGATTGTTTACAAA	CTCGATTTGTGAAGTCCTTAA		
57787	MARK4	NM_031417	TAGGAGTTAGTTAGGCATTGA	CAGTAGGGCCTTGAAGGTTAT	CTGCAGCCTGTTGCCCAATAA	CCGCATCATGAAGGGCCTAAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
57801	HES4	NM_021170	CCGCCACTCGAAGCTGGAGAA	TGCCGAGACTGTAGCAGAGAA	CTCCAAGCCGGTCATGGAGAA	AAACGTATTTATTATTCCAAA
57804	POLD4	NM_021173	TTCACTAATGCTTATCAATAA	GAGGCTCAACTCCTCCATCTA		
57805	KIAA1967	NM_021174	CCACTTAACAACTAAATACAA	CCGGTTCCACTTAACAACTAA		
57820	CCNB1IP1	NM_021178	AAGATAATTTAGCTAACTTTA	TAGCAGGGCCTTCAAAGTAAA		
57823	SLAMF7	NM_021181	ATGTATTAATTGGCTCTATAA	CACCATGGGTCTGCAGAGCAA	AACAGATATTGTGAGATTCAA	CACTAATAGAACAATCCTAAA
57864	TSCOT	NM_033051	AAGGAAGAGGAGGTACATTAA	CACCTTGTACAACAAGATCTA		
58189	WFDC1	NM_021197	CCGGATGTGCTGAGGCCTAAA	CTCAAATGTTCCCAAGATAAA		
58190	CTDSP1	NM_021198	CAGCTCCTTCAAGCCAGTGAA	CTCCTTCAAGCCAGTGAACAA		
58475	MS4A7	NM_021201	TCGGAGTACTATTATCCAATA	CAGGAAGGATTTGACTATCAT	CACACTCATATTGCTTAAATA	CACGGTCTTGGATATAAGTAA
58480	RHOU	NM_021205	CACCTCTAATCTGGATGTTAA	TACCCAGTTACTTATGATTTA	CCCAGGTATTACACAAGCCAA	ACCCAGTTACTTATGATTTAA
58484	CARD12	NM_021209	AAGGTTCAAGCCAAAGTATAA	CCGGGATTTCAGCAAGTTGAA		
58490	C20orf77	NM_021215	AAGCTTAAATTTGTATATTAA	ATGGTTGGAAATAACCTTCTA		
58493	C9orf80	NM_021218	AAGTGACTTTGTAATATCAAA	TGCGTTTATAGTCAACATGTA		
58496	LY6G5B	NM_021221	CCGCATGTACTTGTTCCTCAA	CACCATCTATTATGATGTCAA		
58497	PRUNE	NM_021222	CTGGTATACTGTTCTCATAAA	ATGGCTGAATTTCTATTCTTA		
58499	ZNF462	NM_021224	CCCGGGATCCTTAAATTATAA	AAGAAGGGCAAGAATAATTAA		
58508	MLL3	NM_021230	ATCAGAGTTCACGACCATTAA	ACCAGTGATCAGTTTACTAAA	CTAGAACAGATTCGTAAACAA	CCCAGTGAGCTTCCTCAACAA
58510	PRODH2	NM_021232	CAGGAGCTGCTCAGCCAAGAA	CAGGATGCTCCGGACCTGTTA		
58513	EPS15L1	NM_021235	AGCCTTGTTATTTAGCAACAA	CCGGATCCTTTCCAGACAGAA	AACCATCATCAAGTCCCTGAA	CAGAACCTTCTAGCACACATA
58533	SNX6	NM_021249	CCGAAACTTCCCAACAATTAT	GCCACTCTTATTTACCTTTAA	TCGCCAGTAGTTATATTACAA	CCGCGGACTTAAAGCAATAAA
58538	MPP4	NM_033066	CAGGCCACTAGTATCCTACTA	CAGGTGTTATCCTATGAGGTA	TCGAGGCACAATCATGTTCAA	TACGGTCAGAAGTTCTTTATA
59082	ICEBERG	NM_021571	CAGTGGGTGCAGGCACAATAA	AGCCAGGAAGACATGAACAAA	CCAAGTCTTGCTGCAAATTTA	AAGATATTCTCGTGAAAGAAA
59283	CACNG8	NM_031895	CACGCGCGCCCTCATCTGCAA	AGGCGTCTGCGTGAAGATCAA	CTGCGTGAAGATCAATCATTT	CACCAACACGCTCAACAGGAA
59286	UBL5	NM_024292	AACCTGGAGCTTTATTATCAA	TTGGAACAAGATTGTCCTGAA		
59341	TRPV4	NM_147204	CACCAAGTTTGTTACCAAGAT	CCCGGGCAAGAATGAGACCTA	CTGGAGTGAATTCTCTCTTCA	CTGGGATTTGCCGGTGCTCAA
59343	SENP2	NM_021627	ATGGTCGGAATCAGATTTGAA	CAGATTATATTTCTAGGGACA	CCACACAAGAACAAACGCTAA	AAGAACAAACGCTAACTAATA
59345	GNB4	NM_021629	TACCTTATATTTGCAGGTGAA	AAAGTAGGTAATAGCATATAA	TACGATGACTTTAATTGTAAT	CTGCTCTATATATAACTTAAA
59350	LGR7	NM_021634	CTGCAGTTACCTGCTTTGGAA	CAGGAGATGCCACCTGAGTTA	ACAGACTAGAATGGCTGATAA	AAAGGATGTTTAGACCTCTTA
60385	TSKS	NM_021733	CTGGAAGATGCTGAAATCAAA	AAGCTGTTCACCGGCATCGAA	CACCAACGTGTCACTGCTCAA	AACCAACGTCTTGAAGCAGAA
60386	SLC25A19	NM_021734	CTCCCTGTGATCAGTTACCAA	CTCGTATGAATTCTTCTGTAA	AACCTATTTAATAGACATTAA	ACCTATTTAATAGACATTAAA
60437	CDH26	NM_021810	CACAAGTTACACTTTCTTAAA	CACACTATTAGTTTGAATTAA		
60468	BACH2	NM_021813	CCGGGAAGATAACTCTAGCAA	CTGATGCAAGTGCACCTCTAA	CAGGTGATAATTATGTAGGAA	CACGAGGCATTGTGTGTTGAA
60490	MDS018	NM_021823	CCCGTATAACATGGTGGTTAA	ATGAAATAAACTATAACTAAA		
60526	FLJ21820	NM_021925	TTCGATATGTTCTCTATGTTA	AGGAGCATTTATGTAAGCTTA	CTGCACTAGACAGAGAATAAA	GAGATACTCACTGATACTAAA
60529	ALX4	NM_021926	CAGGTTCCCTGCTACGCTAAA	CAGCAGCTACCTGAGTGTCAA	CCGGACCACCTTCACCAGCTA	CAGCCTCAGCCCAGGCCTCAA
60592	SCOC	NM_032547	TAGGATTAGTAAGATATACAA	CTGGATGAGAACAGTTACAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
60673	FLJ11773	NM_021934	CACAGGCAAGTTCCACTACAA	CGGGAGAAGGTGGGTGAGAAA		
60675	PROK2	NM_021935	CAAGGCTCTTACCTTACTTTA	TCGCTCTGGAGTAGAAACCAA	TAGCCACATCTTACCTGTAAA	CGGTATTAAGTTGTAATTTAA
63027	C6orf85	NM_021945	ACGGAGTGAAATGTACATGAA	AAGGATATGCTAAGTGATGAA		
63891	RNF123	NM_022064	CACATGCGTGTACAAAGGGAA	CCGCAAGTTTCTGCTTAGCAA	CTGCGCTACTATTGGGATGAA	CAGGGCCACAGTGAGCATTAA
63892	THADA	NM_022065	CAGACTTCTATTGATGCTAAA	CACCTTGAGTTCACAGATTAA		
63925	ZNF335	NM_022095	CTGGAGGAGGATAGCGACTAT	CGGGCAGCGTTTCAACCGTAA	CAGGCGCTTCCTAGGCAAGAA	TGGCCTGTCAGTCTCAATAAA
63939	C20orf177	NM_022106	AAGCAAGATATTCTATACATA	AAGGGAAGTGTCTTTCAATAA		
63940	GPSM3	NM_022107	TTGGTTGTGTGAATAAATATA	CGGGCTGTGAATGGACCTTCA		
63971	KIF13A	NM_022113	CCGGCAGGCCGTCACAGTCAA	AACCTATGAAATAGTATCCAA	CCGCAACAAGTTGGTAGGAAA	CTGGCGGGTAGCGAAAGAGTA
64061	TSPYL2	NM_022117	CAGACATATCTCCATGGGCTA	CAGCGAGAATCCTGACCACAA	CCAGAGGTTAGTTGACCCGAA	CACAAACATGGTGATTGTCAA
64072	CDH23	NM_022124	CCGGCTGCCCTTCTTCACCAA	CAGCGGAGTGCTGACCTTGAA		
64083	GOLPH3	NM_022130	CACCATTGGTTTCATAATGTA	CACAGTAAATACTTAATATAA		
64087	MCCC2	NM_022132	CCCGAGCACTTCACATATCAA	AACAATTACGGGCCCAAGAAA	ACCCTTACTATTCCAGCGCAA	CCCATAAAGCGGAGACAGTAA
64090	GAL3ST2	NM_022134	CACCAACATCATGTTCCTGAA	CACAGTCACCGAAGAAATGAA		
64100	ELSPBP1	NM_022142	AAGCTTAAATAACCACCTTTA	CAGCTGGTCCTTTGTGAAGAA		
64101	LRRC4	NM_022143	ACCACTATCTCTGAACCTTAT	AAGCCACAAGTTAACTTGCTA	CAGAAGGGATTTCTGGTATAA	AAGCTGTGAGATCCACAGTTA
64102	TNMD	NM_022144	CAGATTAAAGTGATTCCTGAA	TTGGAAGTACACGACTTTAAA		
64106	GPR147	NM_022146	CTACGGCTACTTCAACGAGAA	CACCAACATGTTCATCCTCAA	CTGTTTCATCGTGCTCAAGAA	CTGGTGGCCATTGCTGTGGAA
64109	CRLF2	NM_022148	AACCGTGCAGGTGACATGGAA	ACACAGCACTGTCAAAGTCAA	CACATGAGTCTCTGTGTTCAA	CAGGATCCACGTTGACATTTA
64127	CARD15	NM_022162	CTGCCACATGCAAGAAGTATA	CAACATGGCCGTGAACTTTAT	TAGGCCGTTCCTTCAAAGCAA	CAGTTATGGATTGAAAGTTTA
64129	LCN7	NM_022164	AACGTACTGGGACAACTGTAA	CCCATCTTCCTCGGTCATGAA	CCGGCCTGGGATCCAGGCTAA	CAGCCCTGTATTCTTATTCTT
64131	XYLT1	NM_022166	CAGGGTGCTGACGAAATCCAA	CAGCAGGATCTCAACGGGAAA		
64132	XYLT2	NM_022167	CCGGGACAAGAATTTCCTCAA	CACACCCATTTCAGCCATCAA		
64145	ZFYVE20	NM_022340	CAGGATGGCAGCATCATTAAA	ATGGAGAAAGTTGACCAGAAA		
64146	PDF	NM_022341	CCGGTGGAGCGGGCGCAGCTA	CTGGTGCTGGGTCCTCCCGAA		
64147	KIF9	NM_182902	CCCGGACCTTATCAGAGGAAA	CACGCTCTGAAGGACTCGTTA	AACAGACAGACTGGTCGTTTA	CAGGACTTGGTTTATGAGACA
64149	NJMU-R1	NM_022344	AACTGTGGTAGTGGAGATATA	CACTGAGTCCTAGATAGATAA	TTGGCAGATACTAATCTACCA	TTGAGTTACACTCCTGTTGAA
64170	CARD9	NM_052813.1	CAGGGACAACACCGACACTGA	ATGCACTGTATTAGTGTTAGA	CCGCGTCTTCTCCATGATCAT	ACGTAAGGACTCCAAGATGTA
64174	DPEP2	NM_022355	CTCCATCTTACGTACCTTCTA	CTGGGCATGATGGTAGACTTA	CAAGGCTGTCATTGGATCCAA	CAGGCACAAATATTTCTTGAA
64211	LHX5	NM_022363	CAGGTACAAGCTAATACTCAA	GCCAATTTAGATATGCTATAA	TTAGATATGCTATAAATTTAA	AAGCAGCCTCCTGAAACCAAA
64223	GBL	NM_022372	CCAGGTGAACGCACCCATTAA	CAGCTACATGGCAGCTGTCAA		
64232	MS4A5	NM_023945	TAGACTGAAGTACCAACTAAA	CAGCATTATTGAATTATTCAT	AAGAACATGGTCTAGACTGAA	GAGGATTGTGATTGTGAACAA
64236	PDLIM2	NM_021630	AGACATAATCGTGGCCATCAA	CTGAGAGTCAGTCCTCCTTAA		
64328	XPO4	NM_022459	CAGAACTTTATGCTTAATTTA	AAGGAATGCCTTGGTAAGTAA		
64332	NFKBIZ	NM_001005474	ACCATTAAGTGCCTAATTCAA	TAGCTGCTGCTTATCATGTAA	CACTAAGTCTTTGTAGATAAA	TCCGACGTATCCTGAAGGGAA
64344	HIF3A	NM_022462	CAGACTCTTCACCTCCGGGAA	CTGTCGGAGAATGTCAGCAAA	CGGGCGCACCCTCAACCTCAA	ACCAATCTCTATACACCATAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
64359	NXN	NM_022463	AAGCTCAAACTTTGGAACAAA	CCGGGTCCTGGTGGAATCCTA	AACCGGCTGTACGGAATCCAA	AAGGTAATGGTTCATATCATA
64374	SIL1	NM_022464	CCGAAATAATTTGAAAGGCAA	AAGGCTGGATATCAACACCAA		
64375	ZNFN1A4	NM_022465	CAGACCATCACTGCACTTTAA	TTCCTTGAGATTCAAACCAAA		
64377	CHST8	NM_022467	TTGGATTAAGGTTCCAAATAA	CAGGAATAAAGTTCAACATCA		
64393	WIG1	NM_022470	CAGGCTCATTATCAGGGTAAA	CAGCATTTAGAGAGCAAGCAA		
64400	FTS	NM_022476	CTGCACTGTCTTACTGATTTA	AAGGTGAAGAGAAGACATTAA		
64409	WBSCR17	NM_022479	CTGGTTAGGGTGCACATATAA	CAGAAATGAGAAGATACAATA		
64419	FLJ22405	NM_022485	CAGCGTGATTCCAAACACGAA	CACGTTTGAGAGTACCGTACA	CTGCCCAGTAATCCTGTTCAA	AAGGTGAAGTTTGGCATGAAT
64421	DCLRE1C	NM_022487	AAGAAACGAATTATATCTATT	CCCAGTGGGAAGTATTCTTTA	CAGGTTCATGTGAATAAGCTA	AAGTACGGAGCCAAAGTATAA
64423	C14orf173	NM_022489	CAAGATCAGCACATTGCTGAA	CAGCGATGTCCTAACCACTGA	CCTGATTCTGATGATAATAAA	CCCGGCCTTGATGCTACAACA
64429	ZDHHC6	NM_022494	TAGAAGGTGTTTCAAGAATAA	TACGTTCTGTTCGGTTATCAA		
64446	DNAI2	NM_023036	CAGGGTAATGCTTAGCATATA	CCGGAAGAAAGTGGAGAAAGA		
64478	CSMD1	NM_033225	ACGGGCGAGCGCAATAGGATA	CCGGTTCAGTATGAAGATAAT	CAGGAAGTCGAATTCACCTAA	CAGGACTGATTCATAGCCATA
64582	GPR135	NM_022571	AAGACAATGTCCCTTCTTCAA	ACCAAGCATTGTGAACTGCTA	CAACAGGATGTCCTCTTCCAA	ACCAAACAGCCTAAATCCGAA
64601	VPS16	NM_022575	CTGCATGAAACAACATAACAA	CCGCACGGAGCTGGCCATCAA	CAGCATGGACTGGGACCTGAA	GAGGCCAGTGCTCGATATATA
64648	SPANXD	NM_032417	AAGCCTGCCGCTGACATTGAA	AACCTTGGGCAATGACAATAA		
64710	NUCKS	NM_022731	TACCACGGTTGTAAAGCAATA	CCCGACCTTATTTGAGGGTAT	ACCCTAGAATTTAATCAACAA	AAGGTGTACCACGGTTGTAAA
64711	HS3ST6	NM_001009606	CCGGCGCCTGCAGGAGTTCTA	TCGCCTGGTACCGGAGTCTGA		
64714	PDIP	NM_006849	CACTGTGGTTCTCTTCAAGAA	GCGCCTGGTCACGGAGTTCAA	CTGCGCTTGGTCAACCTTGAA	GAGCTGTGCATTGTGAATAAA
64747	FLJ14153	NM_022736	CAGGTGAAGTTATTAAATTAA	AACCTGGTGTTTGGACTTCAA		
64748	LPPR2	NM_022737	CCGCGTGGCCGAGTACCGAAA	CTGCGTTGTGCATAACTTTCA	CCGGGACAACTTCAGCCCTTA	CCCGTGTCTAAGCATGTGCAA
64759	TENS1	NM_022748	AAGGCGGATATTTCAAGAGAA	ACGGTCTCTACCCATGTTTAA	CGGTGTGATTGTGGACTACAA	CAGGACCTCGATATTATCGAT
64768	C9orf12	NM_022755	CACGCATGAGATGAAGCATAA	CAGCTTTGTTTAAAGATACAA		
64772	FLJ21865	NM_022759	CAGGCAATTAATTAGGAGTAA	CGGCTTCTTCACTAACTATAA		
64779	FLJ12998	NM_022764	CAGCCTTACATTTGCTCATTA	CAGGTCGTGGACATCCCTGAA		
64782	FLJ12484	NM_022767	AGGGTTGTAATGAGCACTAAA	AACCATTTGTTCTAGAATAAA		
64783	RBM15	NM_022768	AAGGTGATAGTTGGGCATATA	TTCGGTGATGTAAGTGTGAAA		
64785	FLJ13912	NM_022770	TAGGAGCTGGTTGACCTTGTA	AAGAATCACTGCCATATAATA		
64805	P2RY12	NM_022788	TCGGTCTAGTCTGGCATGAAA	TAGTCTGGCATGAAATAGTAA	CCGGAGTAAATCAAACTTTAT	CAGGGTCAGATTACAAGAGCA
64838	FNDC4	NM_022823	CTGGGACGTCCCAGAAGGCAA	CCAGGTGACATCACAGTGGAA		
64839	FBXL17	NM_022824	CTGTCTGAACTGGATCATAAA	AGGCATGATCGTCATAGCTAA	ACGAAAGTTAATTATACATTA	ACGAGAGGGTAGTCACATTAA
64840	PORCN	NM_022825	ACAGATGATTGTGGCCATGAA	CTGGATATCCTTCCACAGCTA		
64850	AGXT2L1	NM_031279	CACGACAACATTGTTGAGTAT	ACCAACTTGATAGGATTCTAA	CAGAATAAACCAAGTGATAAT	ATGTGTCAAATTAGAGAGCAA
64853	FLJ12806	NM_022831	CAGGTCATTAGCTTACTATAA	AAAGAATATTCTTACATATAA		
64854	USP46	NM_022832	CCGGGAGAATGTGTTGGCATA	CAGCACGGCATTGTTCCTTAT	TAGGGAAATGTTTGTACTATA	CAGTTATTTAATCGAAGTAAT
64856	WARP	NM_022834	CGGGACCGCACTGACAGGAAA	CACTAACATCCCAGACTTTAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
64924	SLC30A5	NM_022902	CTCACTCTTTGTGGACCACTA	TCGAATCATATGATCTCCTAA		
64926	FLJ21438	XM_029084	CACAACCTAACAAGCAATGAA	CAGTATGAAGTTGCCCAGTAA		
64943	FLJ12442	NM_022908	CCGCGTGGACTTCACCTTCTA	TAGGTCTTCAATCAAGGTTTA		
64951	MRPS24	NM_032014	CTCAAAGGTTGTGTATAAGTA	CAGTGAAACTTTGCTGTCCTA		
64965	MRPS9	NM_182640	AACAGTCATACTATTCATTAA	CCGCAGAAAGTTTACGTGGAA		
65009	NDRG4	NM_020465	AAGGGTCAGGTAGAAGAGAAA	CCGCAGAGACCTGGACATTAA		
65055	C2orf23	NM_022912	CTGAGCCGAAATATAAGAATA	CACCAATACCTAAATCTGTTA	AAGCCTGTAAGTGTAGATGTA	CCCAGAATTATCAGAAACGAA
65083	NOL6	NM_022917	CACTACAGACCTGACAGTCAA	CACGCACACGGATGTCCTTAA	CCGGCCGCCCTTGGACATTTA	CAGGAGATCCATCCACCTATT
65084	FLJ22104	NM_022918	AAGATGTTGCTTAATAATTAA	AAGGTGTATTTCTACAATTTA		
65109	UPF3B	NM_023010	AAGGTGGTAATTCGAAGATTA	CAGAGCATACATCAACTTTAA		
65121	LOC65121	NM_023013	GACGGTTAGTTGCCAAATTCA	CCCACAGCACTCATTCCTGAA		
65123	FLJ21919	NM_023015	CTGCCTGATGATGGACATGAA	AAGGATAGCATTATGAACATA		
65217	PCDH15	NM_033056	ACCATAGTTGCTATTGATGAA	ACACGAGTCAATCTTAATGAA	ATCGCTATGTTCAGGAACAAA	ATGGATTTAGTAGTATGCTTA
65220	FLJ13052	NM_023018	CCAGACCATCATGCACATTCA	CACGCACCTCATGGAGGAGAA	CCAGGAGAACATGATCGTGTA	AAAGAGCGTCCTTGTCATCAA
65250	FLJ13231	NM_023073	AAGGCTCATCTTAAATTTGTA	ACCAGAGAATTCCATAATTAA		
65266	WNK4	NM_032387	CAAGGTCACTTCGGGCAGAAA	CACTAGTGTCTCAGACCAGAA	CAGGAGGAGCCAGCACCATTA	CAGCTTGTTGGGCGTTTCCAA
65268	WNK2	NM_006648	GACGCTGAAGACATACCTGAA	CACGTATATGGTGGAGCATGA	ACCTATAAGTCTAGTAGCAAA	AACGTTCATCGAGCAGATGAA
65975	STK33	NM_030906	TCCATAAGTGACTGTGCTAAA	CAGTGGTTAACAGGCAATAAA	CAGGATGGTAATAGGTTAAGA	ATGTGTCTAGTGCATCCTTAA
65977	PLEKHA3	NM_019091	CAGGGTGTATTGTAGCTTATA	CAGGAATTTGTTCACCATGAT		
65981	C1QDC1	NM_001002259	AAGCTTCGAACTATACTTCAA	CAGTACAGTATTGACAATAAA		
65983	NS3TP2	NM_023927	CTCGGTAACCCTAATAAAGAA	CAGGTTTGCTTCAAACAAGTA		
65987	KCTD14	NM_023930	CTGCCTGGAGATGGACATTAA	CAAGGTATTCTCCAAGTTCTA		
65989	EGFL9	NM_023932	AAGTTCTGTGACAAAGATGAA	CAGCCTCACACCAGAAATATT	AACCTGCCTTGACGGCATAAA	AAGACCTGTGAGCTTGTCTTA
65990	MGC2494	NM_023933	CTGAGTATTAGACACGATAAA	CAGGATCGTGCTGGCGGCCCA		
65999	MGC3036	NM_023942	CTGCAACTTAGTGGAAGGAAT	AAGGGCTGTGAGCAGGTGTAA		
66000	MGC3040	NM_023943	CAGGGAGATCCAGTCCCTTGA	CAGGACCAGATGATACCATGA	CACTGGGATGGTCCTTGTTAA	CCCTCTATTGCCAACTGTTAA
66002	CYP4F12	NM_023944	GTCCTATATAACGATCTTCAA	ACCTGCCTCATCGATATTATA	CCGCAGGAAGCTGGAATTGAT	TTGCAGATTGTCATGAATAAA
66036	MTMR9	NM_015458	TACGTTGGAATAGATCCTCTA	ATGCCTGAACCTGTTATCTAA	CAGGTCTAAGGATTAACTATA	CAGACCTAGTATTCTAAGTTA
78989	COLEC11	NM_024027	CCCAGAATTGCTCTTCCATAA	CCCAATGTCATTATGTAATTA		
78990	OTUB2	NM_023112	CAGGGAGATCTTCAAGTTCAA	CAGCCGATAAACATTGATTAA		
78994	MGC3121	NM_024031	ACCAATCAGGTTGAACAAGAA	CAGCCTCTGACTCGAGCATTA		
79000	MGC2603	NM_024037	CAAGACTAAATTGGAAAGAAA	CAGGAGGATGGGCCAACTCAA		
79012	MGC8407	NM_024046	TCGGAGGTGACTGACAGATAT	CTCGTGCTGCAAAGAGTGATA	AAGGTAGGGCAGTATGTTTAA	CTGCATGGCAATAACTCATAA
79016	PCIA1	NM_024050	CAGGAGCAAGTGGAGCTGGAA	CTGCGCTACCTGCATCAGCAA		
79018	C17orf39	NM_024052	GAGGGCAATACTAAACTTAAA	CTCCTCAATCCTGAAATTCAA		
79027	ZNF655	NM_024061	GTGCAGGACACCGACATGGAA	AGGAAGCAGCAGGGTCACCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
79048	SECISBP2	NM_024077	CTAGATTTGTTTGATAATCAA	CTGGAAATTGATCAGCATTAA		
79054	TRPM8	NM_024080	TCGAATGTTCTCACCTATTAA	CCGGGACGAGATGGACATAGA	CAGAATGTTATCATACTACAT	AAGGTTAGATTCCAATAAATA
79066	MGC3329	NM_024086	AAGGAGGAGCTTCGCATACAA	ATGGATGCTCTTAAAGAAGAA		
79068	FTO	XM_051200	AAGGAGATGTTAATAATTAAA	CAGGGTCATTACAGAGATTAA		
79073	MGC5508	NM_024092	CAGGTTTGATGTGGAATCACA	CACCGCCAGTGTCATACCAAA		
79075	DCC1	NM_024094	TTGGTTTAGATCAAAGTTCAA	AACGAGTTTATAATCCTATAA		
79080	MGC2574	NM_024098	CAGCCAGAGTACAGTCCTGAA	AGCGTCCAAGAAGTTGAATAA	CTCGGAGTTGGCCCAGAATAA	CCGAAAGGCCGCCGAAGACAA
79092	CARD14	NM_024110	ACGGACGGTTATAAGAGGCTA	ACCAGTGTGTTTACTTGTAAA	CCGCATCGTCAGTATGGACAA	CACCTGGATTATGAGCTCCTA
79094	MGC4504	NM_024111	TCCCATACTGTTACCCATAAA	CTGCTTGACACTGACTTACTA		
79095	C9orf16	NM_024112	CTGGCTTAGACACCTTCTCAA	GGCCTTGAGTGTCCACATTAA		
79097	TRIM48	NM_024114	CAGGCCCTGTTTCTACCTCAA	CTGGGAGAAGCTGTTAAAGAA	TTGCATTCTAATGTTATTAAA	AAGAATCAGAATGGCAATATA
79143	LENG4	NM_024298	AAGCATAAGCTTCCCATTTCA	TCCCAATAAAGTGTTGCACAA		
79153	MGC4171	NM_024307	CAGAGTGGTGGTGGTGTCACA	GACGCTATGACCGTAATGAAA	CCGGACCTCCTAAGTCCAGAA	ACCCATGAGCGTAGAGATCAA
79155	TNIP2	NM_024309	CCGGAAGTTAAAGCACACTTA	CGGGCTCAAAGTAGGATTCAA		
79169	C1orf35	NM_024319	TTGACTCTTTGTATTTCAATA	CTGGGAGGACGTGAAGACTGA		
79171	MGC10433	NM_024321	CCGCCCAATTATCGCGACCAA	CCGCTTCCCATCCTTCCTTAA		
79176	FBXL15	XM_370575	CAGCCTCTCTCTGGCCGTCAA	CTGAGGAAGAAGAGATAGCAA	CTGAGCTGTAGGGAAACTGAA	CACCCTGGAGCTTCAAATAAA
79178	THTPA	NM_024328	CAGGCTTTGCATCCTTGGGAA	ACGGAGTATAAGGAACTCACA		
79184	CXorf53	NM_024332	CAGCATTTGCAGGAATTACAA	CAGATTGAGATGAATTTGCAA	TACGATGTTGATTATAACATT	ATGGACCTACATACACACAAA
79187	FSD1	NM_024333	CAGAGGTACTCCATCTCCCAA	TCCGGCTATCATTGAAAGCGA	CACGGCCAAGCACGCCAACAA	AGGTCTCAAGTTTGACATGAA
79258	MELL1	NM_033467	CTCCCGAGAGTACTACTTCAA	CTGGACCGCATTGGTAGCCTA	CACGCACGGCTTTGACGACAA	TGGCCGGAACTTCGACAAGAA
79369	B3GNT4	NM_030765	CACCCTGTTAGCTCTGATTAA	CAGGAACACTAAGGTCAAATA		
79442	LRRC2	NM_024512	CAGGAGAGACTTGTAGGTACA	CCGCAAGATATAGACAGGCTA	AAGACCAAATACTGAAGTTAA	CTGGAGCTATATATAAATCTT
79573	TTC13	NM_024525	CAGGGTGATTTCTATAAATCA	TCCGATTATGAAGCAGTTTAA		
79574	EPS8L3	NM_024526	CAGCTTAGACACCTCCAAGAA	CAGGAAGAAGAAATTTGGGAA	AGCCATTTACTTGCACCGGAA	CCGGAAGGAGTACTCCCAGAA
79585	CORO7	NM_024535	CAGCCACATCACCAACCTCAA	CTGCAGCTTGATCGCCTTCAA		
79603	LASS4	NM_024552	CAGGTTCTGGTTACCACCCAA	AAGGACATTCGTAGTGATGTA		
79607	FLJ21103	NM_024556	CAGACAGTGTTTAACAAGTAA	CAGGAGGAAAGCAGTGACAAA		
79629	FLJ22709	NM_024578	TCCCAGTGAAATAAACATGTA	ATCCAGAAATTCGATGACCAA		
79631	EFTUD1	NM_024580	CACCAAATGAAAGAAGATCAA	CCCAACATACTAGTCAATAAA		
79635	FLJ13646	NM_024584	CTGGAATACCTGACTAACAAA	TCCCATTTAGTATAACTATAA		
79640	FLJ23584	NM_024588	CAGGGTCAGTTAGGAAATGAA	CAGAAACAATTAAGTCATGAA		
79642	FLJ23548	NM_024590	CTGATCTAACTTCTAGCTAAA	AGGCATATTGTTCATGTTTAA	CAGATTGATGAGGACATTCAA	CCGATCCATTATCAACATAAA
79654	FLJ21156	NM_024602	ACGGATCTACATCTACCCAGA	ACCACTGTACTGAGTGACCAA	TCGGGACATGTATGTACCCAA	CCCGAGGTATTTCACCTCTTA
79660	PPP1R3B	NM_024607	CTAGGATGACATGATGTTATA	CAGACAGTACTTTAAATGTTA	CCCGCTAGATATGCCATTCAA	CACCCAAGTTCTTATACGTTA
79671	NOD9	NM_024618	ACCTGACTTGCTGCTATTAAA	CTGCGGTTTCTCTGATACCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
79673	FLJ12586	NM_024620	CGGGAAATCCTTCAACAGAAA	TACCTGTGAATGAACAATGAA		
79679	B7-H4	NM_024626	ATCGTTCAAGAGAATGATTAA	CTCCAATATGAACAAGATAAA		
79684	FLJ23342	NM_024631	TACAGTTGTGTTGCCATTTAA	CTGGAAAGATGTTTACTACAA		
79686	C14orf139	NM_024633	AAGGAGGAATTTGTTTCTAAA	CAGGATGTTCAGGGCCTTAAA		
79692	ZNF322A	NM_024639	AGGGTTGGAAATACCAAGTAA	TACATATAATATGTATGAGAA		
79696	C14orf140	NM_024643	CAGGAGCAGAGTTAAAGGTAA	CTGGTAGCAAGCAATAATAAA		
79697	C14orf169	NM_024644	GAGGTCCAGGAAGATACGAAA	CAGATTCTAAGGATCCGCGAA	ACCCAAGTGCTTGGAAATATA	CTGCTTGAGACAGATATTAGA
79703	FLJ22531	NM_024650	CAGCTAGTGATTTCCATAGAA	CAGCATTATGTGAGACCAAAT		
79706	PRKRIP1	NM_024653	AACGATGATGATGAACACAGA	CAGCTGTGATTTCATCCCGAA		
79707	FLJ23323	NM_024654	CAGATTAAACCTGAATATTTA	ATGGAGTTTCATGGCCATGAA		
79714	FLJ12436	NM_024661	AAGGTTCATTTACATTAATTA	CAGCTTAGTCATTCCAGGCAA		
79718	TBL1XR1	NM_024665	TAGATACTAGATTGTATTGAA	AAGGAGCTATCTGTTTATGTA	ATCACAAATGATCATACTTAA	AAGCAAGATAACGGCATATAA
79724	FLJ23436	NM_024671	AGCCCAGAATTTGAAGCTCAA	AGGGAGCTAGAGGAACCTTTA		
79728	FLJ21816	NM_024675	CAGGAGGATTACCTATACAAA	CTCCTTGTAAATAAAGCTATA		
79733	FLJ23311	NM_024680	CGAGCAGATTATGATGATCAA	AAGACAAGTCTTTAAGGGTAA	CAGAGGATGTCCATTAATCAA	CACGTGGGAAACCAAACTTTA
79741	C10orf68	NM_024688	AAGCAATTTATAGAACATATA	ACCAAGAAACTTCTAGCTAAA		
79742	CXorf36	NM_024689	CTGGTTTGAAATGAAACCTTA	AACACCTAGATTAGCATTCAA		
79770	C5orf14	NM_024715	TACTATAAGGGTTATAGTAAA	AACTAGTATTGCAATAAGCAA	CTGCATGAACGTAATCCAGTA	CCGGCAGAATAGTGAGTAGAA
79784	MYH14	NM_024729	TCCCAGAATCGGGAAAGTGAA	CGCGGGCAAGGTCGACTACAA		
79794	FLJ21415	NM_024738	CCCGTGGAAAGTGCAGTTTAA	AACGTTGAGGCAATTCCTAAA		
79797	ZNF408	NM_024741	CAGCCTGGTGCTAATCCATAA	CCGAGACATCCTCGCTTTAAA		
79807	FLJ13273	NM_024751	CCAACTATACCTGTAGAAATA	TTGGTAATTATCAGCAGGAAA	AAGACTCAGAATCTTAAGGAA	GAGGTTTATAGGTTTAAGTAA
79811	FLJ13213	NM_024755	CAGCTTCGTTATGAACAAGAA	CAGAAGGTACTGTTACATTAA		
79815	FLJ13955	NM_024759	CACCTTTCAAGTACTAAGTTA	CTGCACAAGGCTGACACATAA		
79816	TLE6	NM_024760	CTGAATTATCAGGGCATTCTA	CACGATCTAGTCTGTGGTGTA		
79823	FLJ23451	NM_024766	CAGCCTTGTTGATGCAATAAA	CACGCCGAGGGAATACTTTAA		
79829	FLJ13848	NM_024771	CTGGATGTTGCTGCATTCTAA	AACGAATATGCAAACCATGTA		
79830	ZMYM1	NM_024772	CACCACTAATTTGAAGATAAA	CAGGAGTTGGTAAATAAACTA		
79836	RNF127	NM_024778	ATGGAGGAGCTCATAGCTAAA	CAGCGGGATGGCTACAACACA	TTCGCTCAAATTATCCCTAAA	CAGAGAGAAATTGAGTAGAAA
79837	PIP5K2C	NM_024779	TAGGATTCATTCTCCATGTAA	CTGTCCTGTCTTATACTGCAA	TTGATGTGTGATAATCTCATA	CCGGAGCAGTATGCTAAGCGA
79838	TMC5	NM_024780	CCGGGCTTATCGGAGATCCAA	TAGGGACACAGTGATGTACTA	CAGGAATGATTGGTTCTTAGA	CGCGATTATTGCTAATTGGAA
79841	FLJ23598	NM_024783	CAGCCTACCATCCAGAAGTAA	CAGCTTTGGAAACGCACCTAA	CCAATAGATATTCTCTCTAAA	CATGTATTACCCAGAATTTAA
79846	FLJ21062	NM_024788	CTGAAGTTAATTGTACTATAA	TTGGAGAAATATGGAATGAAA		
79852	ABHD9	NM_024794	ATGTATGTTAATTGAAATGAA	CTGGCATTTCTCCATCTACTA		
79864	FLJ23554	NM_024806	CAGGGCGCCAATAACAGGCAA	AAGACTTACATCGGATTTCAA		
79872	CBLL1	NM_024814	CGCGAACTCAAAGAACTATAA	CTCGATCGGTCAGTCAGGAAA	CCGCCTCAACATGGTGGTCCA	ACCATTATAATCCTAACTCAT

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
79875	FLJ13710	NM_024817	CAGAAGAGAGAGAATCTTGTA	ATGAATATTGTGCTTTATTTA		
79884	FLJ21159	NM_024826	ATGGAATATCTTAAAGAGAAA	AAGGATGGACTAGAAGATAAA		
79896	THNSL1	NM_024838	CAGGATGTTGGTAATGAGCAA	CAGGCTTTAAAGATTAAAGAA		
79897	RPP21	NM_024839	CAAGCAGATTCCAAACCACTA	CTCAATGATCCCGGGCATTTA		
79908	BTNL8	NM_024850	GTGGACGGAGGACACAATAAA	CACGGGATATGTTGATAGAGA	CACAGTATCAAGGCAGGACAA	CAGGATTAGTTCCCAGTCTTA
79912	FLJ22028	NM_024854	CAGCGAGTTCAGGAGACTCTA	CTAGATCCAAATATTGATATA	TAGCAATATCTCGTTTGGTAA	AAGAATAATGATCATAGGGAA
79923	NANOG	NM_024865	ACCGAGTGTTTCGATGAGTAA	TTGGTTTAAGTTCAAATGAAT		
79924	ADM2	NM_024866	AAGGGCTCCTTCTGCTATTTA	CACTGAGCATTTAATTTACAA	CTGGTACGTCAAGGAGCCTAA	TAGCGAACACTGAGCATTTAA
79943	FLJ14129	NM_030895	CAGGCCTTTGTAAGTTGTCAA	CAGGTGCTAAAGAGAGCAGTA		
79953	C20orf39	NM_024893	CACCGCATTAGCAATATACAA	CCGGCCCAACATCATCCTCTA		
79958	FAM31C	NM_024898	CAGCTCAAACACACCAATAAA	TACCTTGGAGACGACCTTTAA		
79960	PHF17	NM_024900	ACTGACCAATGAAGAATTTAA	AAGCGGGAGCAGGATGTCTTA	CGCCCAGAGCAAGAAATGATA	ACCGATTAAATTCATTAGTGT
79962	FLJ13236	NM_024902	CAGGTGATAGTTGGCATCTAT	CAGCTTGAGGGTCTAAGGATA		
79963	FLJ14297	NM_024903	CACGAAGTAGAGGAACTCATA	CCCTAGGTGTCTGGAAATGAA		
79968	FLJ12973	NM_024908	AAGGGATTATCTAGCATTAAA	CAGGATGGAGACAGTGATGAA		
80006	FLJ13611	NM_024941	AAGCTTAGGCTGTTAAATAAA	CAAGAGCATATTTGCAACCAA		
80013	C10orf97	NM_024948	TCGCTCTCCTTCACTAAATTA	ATCACAGTTAGTATTGATAAA	TTGAATGATTCCGGCTTGTAA	ACGTTATTTATTATGATCCTA
80028	FBXL18	NM_024963	CAGCACAGATCTGATTCTGAA	CCTGCAGCACATGAAATTCAA	CCGCGCGGCTTTGGCAAGAAA	CAGCCAGTTTCTGTTGTTTGA
80036	TRPM3	NM_020952	CAGACTAGAGGAATTGTACAA	ACGGGCTGAAACTCTTCATAA	ATCATCGTGTATAGACATCTA	CAAGGTAACAGTCATAGTTCA
80045	GPR157	NM_024980	CTAGATGATCTTGACTTTCCA	AAGACCTTACTTTGCGATTCA	CACCTGGGTGTCACACGGCAA	AAGGGCTTCTTTGATAAAGAA
80069	C6orf208	NM_025002	TTGGAGGTTGGCAGAATTCTA	CAGCAGGTGGATGAGACACAA		
80086	TUBA4	NM_025019	CCCAACCTACACCAACCTCAA	AAGGAGTTCATCGACCTGCTA	AGGCTTTAAGGTTGATATCAA	CTGTGTGTCTGTCCTACATAA
80094	FLJ14107	NM_025026	CACAAATTCCATTATTGTCAA	CCGCCACACCTTCCTCCATAA		
80099	FLJ21075	NM_025031	AAAGATAAATACGGTCCTGAA	TTCCACTTAATTTCACTATTA		
80110	ZNF614	NM_025040	CTGAGCTTAATTGTACATTAA	CACCACAAAGTCAGTACTCAA		
80115	FLJ22582	NM_025045	CAGGTCCAGCATGGCCATCTA	TTGTAAATGATGAGAAATAAA		
80118	FLJ22684	NM_025048	AAAGAAATATTTAGTAAATTA	CTGGCCTAGGACCTTAAATAT	ATGGGCTAATTAGAATTATCA	AAAGCATATGAAAGAATTCAA
80122	FLJ23074	NM_025052	GTGGTACATCGCGATATCAAA	CGCGATATCAAAGGAAATAAT	CTGACCAGGTAAGAAACTGAA	ATGTCTAATTGGAGATTTCAA
80127	C14orf45	NM_025057	CACAAGCTGCTTTCAATTTAA	CAGGAGTGATGCATCCAGAAA		
80129	C6orf97	NM_025059	CCGATCCAAGATGCTTTCTAA	CACCAATGAACTGAAGATTAA	AAGCTCTAGCATGAAATTAAA	CAACCGTTCGTGAGTCATCAA
80139	FLJ14299	NM_025069	ACCGGACTGTGTATTTATTTA	CTGGGAATATAAGTGCATTAA		
80145	NIF3L1BP1	NM_025075	CAGACAGGCATGAGACATTAA	AAGCATGGAATCAGATCCTAA		
80146	UXS1	NM_025076	TAGAATTTGCTCAGTTAATTA	CTGGAGGAAGGTTTAAACAAA		
80161	CXYorf2	NM_025091	CACACTGGAAATCGTGCAGAA	TGCACTGATGATAACTTCAAA		
80167	FLJ21106	NM_025097	CAAGTGAATATTGAACCTTAA	ATGGATGAATGTACTCATGTA		
80184	Cep290	NM_025114	CCGGAAGAAATGAAGAATTAA	AACGATCATTATCAACTTCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
80194	FLJ21749	NM_025124	CTGCTCTGTGCCTTAACTTAT	CAGCATTGATGATGCCTTCGA		
80195	C10orf57	NM_025125	TAGAGGAGGTGCAGTAATTTA	CCAGTTGTTACTTAAGAAAGA	ACCCTGAAAGATTATGAACTA	AACCATAGAGTTAGGCATCAT
80207	OPA3	NM_025136	CCTGATCAGTGTTAACCTTTA	CTGAATCAATGTGTTATTGTT		
80209	C13orf23	NM_025138	CACCTGGGAAAGCGCCTTCAA	ACGGTGCAAGAGAATACTTGA	AAGGAAGACCTAGCCGCATAA	TACAAGTAAGACTTAGGATAA
80210	FLJ12584	NM_025139	CCAGATAGAATTCATCATCAA	TCGGATCTTCTTGGCCATGAA		
80213	BLP2	NM_025141	CTCAGCTTCAGTCATGTGTAA	TCGGGCGGTGAAAGTACTGAA	CTGAACTATGCTAATCTGGAA	CAGAATGTTTATGTCTAGTTA
80216	ALPK1	NM_025144	CACCCAATTCATCGTAATCAT	CCGCAGGTGGTTATTCGCCAA	CAGGCCCTACATTTAAAGCTA	CAGCCCTTGGTCCTATCTGAA
80217	C10orf79	NM_025145	AAGGACCAAATTGAAAGGCAA	CAGACTGAAGTTGAAAGATTA		
80222	TARSL1	NM_025150	CAGGCCGAACAGGTCCTTAAA	TCGCCAGTTGTTCAAGGATAA		
80223	RAB11FIP1	NM_001002233	ACAGAAGGAAACGATAAGCAA	AGGGCTTAATGTAGTTAATAA	CAGGTTAATGATTACAATTAA	CACAGAGTTCGGAATTCACAA
80233	FLJ22175	NM_025161	TAGGAGCAGAACGCTCATGAA	AAGCCTCAACGAGGCCATGAA		
80274	SCUBE1	NM_173050	CAAGCTCTGGATCCAGTTCAA	CAGGTGCTACAGGACAGCAAA	CACGTGTGGTTGCCACCAGAA	CCCGGCTTTGACCTTGCCCAA
80309	SKIP	XM_051221	CACCAACATGTTAATTCATGA	AAGAAGATGAGTCATATTGTA	GGCAAGTATGCTACAAATTTA	CTGAAATTCTGGACACCTTAA
80313	LRRC27	NM_030626	CTCCGGTACAATAGAATTAAA	CTGCTTTCTGATAGTGATCAA		
80318	GKAP1	NM_025211	CTGCAAGTTGATGAATCACAA	TAGCTCCCTAATGGTCTATAA	CATGCTGTTTGTAACGCTCAA	AACGCTCAACATGATCTTCCA
80329	ULBP1	NM_025218	AACCTGTATATGTACCTTGTA	ACCCTACAATTAAACACTGTA	TATGATGATAATTGTATAATA	TCGGGATATACCCACAGGAAA
80341	BPIL1	NM_025227	CTGCACATTGGGAGCCTTATA	CTGGTGCAGAAGCACATTAAA	CAGGCGAATTTCTCATTTCAA	ACCATACTTAGTCATCACCAA
80342	T3JAM	NM_025228	ACCCAGGACCTACAAGATCAA	CAGGACCTACAAGATCAACTA	TAGCAGGGACTTACAGATGAA	CAGACTTGGCACCAACATTAA
80343	C20orf50	XM_046437	AACGAAATCAAACAATATTTA	CAGGATTACTACAAAGCATTA		
80346	C8orf20	NM_025232	TCGGTTCCGTGCAACTTTCAA	CGCGTACATCGTGCAGGCCAA	CCCTTTCTACTATGAGATCAA	CAGGGATGCACCCACAATGTA
80347	COASY	NM_025233	CCGGGTGTTTGGGAATAAGAA	TCCGATTATGGGATAGGAGAA		
80381	B7H3	NM_025240	AAGAAGATGATGGACAAGAAA	CTGGCAGCTGACAGATACCAA	CTGAAACACTCTGACAGCAAA	CAGCATGACCCTGGAGCCCAA
80723	TMEM22	NM_025246	CAGGACTACCAGGAAATACTA	CTGATTATTATTGTCTCATTA		
80725	SNIP	NM_025248	CCGCAGTATTATCAAGATCTA	CTGGCCCAGATCCGAAGGCAA		
80736	C6orf29	NM_025257	CCCGGACAACAAGAAGAGGAA	CCGGGTCATCTTGGAGTATAT		
80740	LY6G6C	NM_025261	CAGGACAGCAATGCCTGACAA	TAAGCTGGGTCTGACATATAA		
80742	PRR3	NM_025263	ACCCATGACATGTCTTATAAA	AAGCTGGTCTCTTATCAAGAA		
80755	MGC2744	NM_025267	ACGGCAGTTGCTGACCATCTA	CTGGCTCATGTGGAACATTAT		
80759	C6orf148	NM_030568	CTCCTTCATTCCTACCGTCAA	TTGGCAAAGCAATCCAATAAA		
80761	UPK3B	NM_030570	CTCCTTCATGGGCAAGCGCTA	CTGGTTTCTCTCCCTCTCCAA		
80762	NDFIP1	NM_030571	TAGGATACAAATGAAGCTTAA	AAGTCTTTAATTGGTAAATAA		
80776	MGC4093	NM_030578	TCGCGGAAGTATCGCGGCTTA	CCAGCGGTTTCTCGGAAAGTA		
80789	KIAA1698	NM_030628	ACCCAGTTATATGCAGGGCTA	TCAGCAGGAAGTGATCTATAA	CTGGGTAATATGCATGAAGTA	CACGCGTACATTAATGGACAT
80824	DUSP16	NM_030640	AACCCAGTTGTTACTCTCTTA	CAGGACAAAGTGTTAATTACA	CCGGCCATTTGTGGAATACAA	AAGGTTGTAGTTTACGATCAA
80831	APOL5	NM_030642	GAGGAATAAATTGGTCTGAAA	TGGGAGAAGGTTGTAAAGAAA		
80832	APOL4	NM_030643	TTGCTCATATATAGTAGACAA	CAGCAATTGTTCAGGGAATAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
80834	TAS1R2	NM_152232	CACAATTTGCATCTCCTGTAT	GGCATTTATCACGGTACTCAA	CAGCGTGTACTCTGCGGTCTA	CACACTGAAGATGAATATGAA
80835	TAS1R1	NM_138697	CACTGTGGCGTTTAATGACAA	CTCCGGGCTGCCAATAAAGAA	CTCCATGAGTTCTGCCTACAA	CAAGGACACTGTGGCGTTTAA
80864	EGFL8	NM_030652	CAGCACTTACAGGACCATGTA	TCCCTCAGAGAGAGTCAGGGA		
81061	OR11H1	NM_001005239	CAACATATGCACTGACTATAA	ATCCTATACTCTTGTCCTGAA		
81127	OR4K15	NM_001005486	CAGCAGTTACTCAGTTGACAA	CCAGTTGGCATTCACTGTTAA		
81282	OR51G2	NM_001005238	CCCAGTTCTCTCACATTCTTA	CCGGGCAACTGCACAATTCTT		
81285	OR51E2	NM_030774	ATGGTTAGCTGTCACATACAA	ATGAGAGATAACCTTGCCCTA	TGGCTGGAATAGTAAACTAAA	ACGGGTGCTGGCTATGTTCAA
81300	OR4P4	NM_001004124	CACAACATTCTCAGAAGATAA	CCACTTGTAGTTCTCATGTAA		
81488	GRINL1A	NM_015532	CAGGGAGATACCGAGAAGTAA	CAGCAATTTGATTATGTATTA	CCGGGACTTAATTAAATACAA	ATATTTGAATATTGTGTTTAA
81494	CFHL5	NM_030787	AAGAATTTAATCATAATTCTA	AAGGGAAATTTGAATATCCTA		
81502	HM13	NM_030789	CAACCTCCTGCTGTCCATGTA	ATGCTTCAGACATGCCTGAAA		
81544	PP1665	NM_030792	CCGGGACGTCAGCATCATGAA	CAGGCCTGCCTCCATGCTTAA		
81553	FAM49A	NM_030797	CACCTAGACATTGAGAATGAA	AACAACATCTATAACGATAAA		
81554	WBSCR16	NM_030798	CTGGTGTTAAGGGTCACGCAA	CACAGGAGCCGGAAAGATAAA		
81557	MAGED4	NM_030801	AAGGATGTCATCAGAGAATAT	CCAGATGTTAGTCACCAGTAA		
81563	C1orf21	NM_030806	CACGTTCTTTATGAAAGGCAA	CCACGTGTATCTGAACATTAA		
81565	NDEL1	NM_030808	CAGGCTGAACAAAGAAATAGA	AAGACTTTGAACAAAGGCTAA		
81566	C12orf22	NM_030809	CTCCATCTTGATGATATATAA	CTGCGTAGTGCTGAACATTAA		
81577	MGC11335	NM_030819	CTGAGAAATGTTAATAAATAA	CACAGTGACACTCAACTTCAA		
81607	PVRL4	NM_030916	CTGCTTTGAATCCTTTACGAA	CTGCTTGACCTTTACCTCCAA	CCCTGATAGTCTCAAGGACAA	CAGAGCAGTATTAATGATGCA
81608	FIP1L1	NM_030917	ACCTGTAAATCTTAACATCAA	CAGGGAAGAACTGGAAACTCA		
81617	CAB39L	NM_030925	CTGAGAGATCCCAGAAGGTAA	GCCAATGTCTTTGGACTGTAA		
81620	CDT1	NM_030928	CCGGGCCAGAAGATAAAGAAA	CACCTGGTGGATTCACATTAA		
81622	UNC93B1	NM_030930	CTGCCCGACATCGACAGCAAA	CACCAGGATGGCGCAGAAGTA		
81693	AMN	NM_030943	CGCATTTGACCTGGAGCGGTA	CCAGGTGGTGCTGGTGGAGAA	CAGCCACAGTTACTTCGTCAA	CAGGGTGGCCTTACTCAGTAA
81706	PPP1R14C	NM_030949	CCGCAGAAGAAGAGTGTATGA	AACCCTTAATTTGAAGAACTA	TAAAGTTGTATGAACCCTTAA	AAGAGCTGCTTTCTCGGATAA
81787	DKFZP547L112	XM_375153	CAGGGCTGTACCCTGGACTGA	CTGCCAGGCCCTAGACCAAGA		
81792	ADAMTS12	NM_030955	CCCGGAGTGATCTATGATGTT	CCAGTGGAACGGGAACTATAA	CCGGAGAGTTCTGAAACCAAA	CAGGAAAGACGGCAAACCGTA
81794	ADAMTS10	NM_030957	CGGGCACACATTCGGCATGAA	CAGGACTTTGTGTACCCGACA	ACGGATTAATGCATCTCTCAT	CCGGAAGTTATTTATTGGGAA
81797	OR12D3	NM_030959	CCGGATAATGGCCATCATGTA	TACATTACTGTCCCTGCATTA	CCCAAATAACCAAACGCGTAA	CACAATCAAGCTAAACCTACA
81833	SPACA1	NM_030960	CTGGATAATAATGAAATAGTA	ATGAATGATGTTTGAATGATA		
81844	TRIM56	NM_030961	TTGGCTAAGATTAAGTATTAA	CAGCGACTTCCTGGCCTGTAA		
81858	Sharpin	NM_030974	CAGGAGGGCCTGGAACCCTCA	CCCGGAAGCCTCCACACTCAA	CAGGCTGCAGGTCACACTTGA	AGGCTGCAGGTCACACTTGAA
81875	FLJ12671	NM_030980	CAGGGCATACTGGGAAATGTA	CAGACTTAATACCCATTGAAA		
81930	KIF18A	NM_031217	CACATGAAGAGAAGTATTCAA	ATCCGTCTACAGTAACCTTAA	CAGGTGGAACTAATCTGGTTA	CAGGAGGACTTGGACTCTACA
81932	HDHD3	NM_031219	ATCGCTGAACAGCTTTATAAA	CAGTGTTATTACCTCCAGTAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
83259	PCDH11Y	NM_032971	CAGGAGATTATTTCACCTCAA	CAGGCAGATGATAATGATGAA		
83394	PITPNM3	NM_031220	CAGCAGTGGTCGCATCACATA	CTCGCGCATGATCCTGCGCAA	CACGAAGGACATCTCTGTCTA	CCGGGAGAAGTGGCTTCGTAA
83401	ELOVL3	NM_152310	CTGGGTCTTTCTTCTCAGCAA	ATCGATAATTCCACAGTCAAA		
83445	GSG1	NM_031289	AAGAGCAGTGTTAGGAGTTAA	CAGGATGGTGCTGGAGTTCAA		
83446	DKFZP434K1172	NM_031290	CCAGAAGAAACTAATGCACAA	CCGGCTGATAAGGAAGATGTT		
83449	PMFBP1	NM_031293	CAGGATGATCTCATTCAAGAA	AAGGGTGATCATTCAAAGGTA		
83468	GLT8D2	NM_031302	CCCGATGGTCCTCAAAGGGAA	CTGAGAGAAATAAACTTTAAA		
83479	DKFZP564B1023	NM_031306	AAGGTCAAACTAGGCCTTAAA	CAGGCCCATTATTGACTTTGA		
83482	SCRT1	NM_031309	TCGAATAATAATGACACATAT	CCCGGCTTTCTCCCAGCAATA		
83539	CHST9	NM_031422	CAGAATCTATGTAGAAGATAA	AAGGCATTATGTGATTTACAA		
83549	UCK1	NM_031432	TCCCTCTAGGTCACTGAGAAA	AAGGCTGGTTGTGGCCTACAA	TGCCGTTTAAAGATCCCTCTA	AACGGTGGAGGTGCCGACCTA
83552	MFRP	NM_031433	CAGGGAGTTTGTGGTCAGCGA	CGGACACAGCATAGAACTACA	CAGCATAGAACTACAGTTCCA	CTGCTCCTTCCTGTCCCTTTA
83650	AMAC1L2	NM_054028	CCGCACTCCAATGAGGTCACA	CAGGAGAGTTCCAGGGAAGAA		
83660	TLN2	NM_015059	CTCCTTGAATAACTGCGTAAA	CCAAGTGATAGGGAACCTCAA	CAGATGTTGTATGCAGCCAAA	CTGCATGATCGTGATGTCACA
83690	LOC83690	NM_031461	CTGGTGGATTTACATATTAAA	CTGCTGGTGGATAAAGATTAA		
83698	CALN1	NM_031468	CCGGATGACCTTTGTAAGTTA	CAGACTCAGGTCATAAATCAA		
83706	URP2	NM_031471	CCAGCGAAAGTTCAAGGCCAA	CGGCCAGAAGTTCTGCATTAA		
83707	MGC11134	NM_031472	AAGGAGGAGGATCCAACAATA	CTGGCCATCCATCCTACTCAA		
83729	INHBE	NM_031479	AAGGGTTAGGGTGATGGTCCA	TGGCTTATACTTTCTTAATAA	AGGGCTGTTGAGGTACCTTAA	TAGGGTGATGGTCCAGAGCAA
83733	SLC25A18	NM_031481	CCCACTGTTTGCCAACCTTAA	CAGCACCTAGTTTGAGACCAA		
83743	GRWD1	NM_031485	TCCCAGGAGTTTCCAGGGTAA	GCGGATCTCATTAGGCGGAAA		
83844	USP26	NM_031907	TACCTATAATATAGAAATCAA	AAAGATTTGTATGAAGATAAA		
83849	SYT15	NM_031912	GCGGCGCTTCCTCCAATCCAA	CAGCCGCATGCTAGGACCCAA		
83855	KLF16	NM_031918	CTGCCTGGCCTCATCCTTGTA	TTGTATTTAATTAATTAAACA	TGGCCTCATCCTTGTATTTAA	TCCTTGTATTTAATTAATTAA
83861	RSHL2	NM_031924	CAGCGTGAGTATGAAGAACTA	AAGGCTATATTGTAATTCTAA		
83862	TMPIT	NM_031925	CTGGTGGGTGTTCCATCACTA	CTCGCCCTGAAGAAATGCAAA		
83872	FIBL-6	NM_031935	CTGCAGATTCTGAATACTCAA	CCGCCTGACATTACATGGCAT	TAGACTCTAAGCAATTGCCAA	CCGAGTATATGTTCCGCCAAA
83873	GPR61	NM_031936	TGGATTTATGAGGAAACTGAA	TACCCAGAACTGGGACTACAA	GTGGGATAGTCTCCCATTTAA	CCCATTTAAGCAGCTAATAAA
83876	MRO	NM_031939	CGGGATAACAATAGTAGGTAA	ATGGATGGTTAGAAATGTTAA		
83877	BLP1	NM_031940	TTGGTGGTTTGTTGACCTTAT	ATGGCCGTGGATTGTAATACA	CACTACTTCATAACCACTTTA	TGGATTGTAATACACACTGAA
83879	CDCA7	NM_031942	CAGAGTAAAGAAGAACTTAAA	CACAATAATAGTATTAACTAA		
83884	SLC25A2	NM_031947	TACAATTTGGTCTGTCGTGAA	GTCGTGAAGGGTATCCTTAAA	TACCCTAAATCTTAACTTTAT	CCCTATGTACCTAATCTGAAA
83886	MPN	NM_031948	ACCAGTGCCCTTCACCAATTA	CCCACCAGACTCATTTGTAAA	AACCCAAAACCATCAAGAATG	AAGTGCCCTTCACCAATTACA
83893	NYD-SP12	NM_031955	CAGGTAGAAATCACACTTGAA	CAGAATTGCTGCAGTCACTAA		
83899	KRTAP9-2	NM_031961	CCCTGGTAGCAGAAATCCTTA	ATCGATGATCTTTGCAATCTT		
83903	GSG2	NM_031965	TTCGGGCAGATGGGAAGAATA	CAGGCTCATGAAGAAGGAGAA	ACAGTCTGTTTAAGTAAGCTA	CAGTCTGTTTAAGTAAGCTAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
83933	HDAC10	NM_032019	CGGGTTCTGTGTGTTCAACAA	CCGTTAGTAAACATCGCTCAA	CGCCCTTGCGCCGTTAGTAAA	CAGGTGAACAGTGGTATAGCA
83938	C10orf11	NM_032024	CAGAAAGTAACCAGACAAGAA	TTGCCTTGAAATGAATGGAAA		
83941	BBP	NM_032027	ACGCTACGCAAGAACCAGTTA	AGCACCCAACATAACTTGTAA	AAGTAGTTACATTATAGATTA	ACGCAATTATATCCATAAATA.
83954	FKSG83	NM_032030	TGGGCATGGCTCAAACTCAAA	AACGTGTGTCTTTCCACTTAT	AAGACTGTTTATATACTACCA	ACGTGTGTCTTTCCACTTATA
83956	FKSG42	NM_032032	AAGGAAACGAACTCCAATTTA	CAGATTTGGGAGCAAAGGCAA	CAGGTGGATGCAGACATCCAA	AAGGAAGGAAACGAACTCCAA
83959	SLC4A11	NM_032034	CCGAAAGTACCTGAAGTTAAA	CCGGGAAATCGAGATGAGCAA		
83983	SSTK	NM_032037	CGCAGTCACTTCACAAGGCAA	CAAGGGTACCGTGGCCATCAA	CCGGTTGGAACCTGCAATAAA	ATCGAGGTGTGCAACGGGAAA
83990	BRIP1	NM_032043	TAGCATGGCAACAATCTCTTA	CAGGCCCTTGGTAGATGTATT	AAGATAAACAGTCCACTTCAA	CCTGAACTTTACGATCCTGAA
84000	MSP	NM_032046	CTCAGTTGTTTCAGAAACATA	CAGCAACTGGAATGACTCCTA	CTGGAAATTACCTGGAGACAA	ACGGGAATGCATCTCCAGCAA
84034	EMILIN2	NM_032048	ACGGGTCATGATGGAATTAAA	CACCTGAAGGACAAAGTTCAA		
84058	FLJ12953	NM_032118	CCCTGTGGTATTCATAAAGTA	CAGGGCCAGAATTCACATTAT		
84062	DTNBP1	NM_032122	CTGCTGGATTAGAATTACTTA	CAACTGGAGAATTACAAGAAA	CACCCAGCAAATGAAGCTGAA	TTGGCTGTATGCGGAATTCCA
84066	DKFZP564J047	NM_032126	CTGAGGGAAGGTGAAGCTTAA	CCAGCTTGAAATGAGAGTAAA		
84083	ZRANB3	NM_032143	TTGCCAGTGTATGACACCTTA	TGCCAGTGTATGACACCTTAA	CCGGATTCACATCTATACTAA	TGGATAGTTCTATAGAATTAA
84106	PRAM-1	NM_032152	CCGGAAGAAGTTCAAGTTTGA	CCGAAGCCTGAGTTTGGTAAA	CCGCAAGTTCTCACAGCCTGA	CCGGAGCATCAAAGCAAAGTT
84108	PCGF6	NM_032154	TAGGAGAATTTGAGAAGTTTA	AAAGATTTCCATGAAATGTAA		
84109	GPR103	NM_198179	ATGCTTATTCTGTACAGTAAA	TTGTTATTGCATAGTAAATAA	ATGGAAATTCAGGAATTACAA	AGGAATTACAATGATGCGGAA
84132	USP42	XM_374396	CAGCCCGTGATGAATGGCAAA	CAGGACCAGGCGAAAGCCCAA	TTGGAGGATACCTAAGATCTA	CACGACAGAACTGCACTTGTA
84152	PPP1R1B	NM_181505	CTGAGTCTCACCTGCAGTCTA	CAGGGATTTGCCCTTCACAAT	CAGCTTGTTTGAAGCCCTTGA	ATAAATCTTTGTAAATAACAA
84162	KIAA1109	XM_371706	AAGGATGCAGCTTGACTTTAA	CAGGTGTGGAGTATAGATGAA	CTCGAAGAGATTCACTTTCAA	CACCTCTTAAGCGAATGGAAA
84168	ANTXR1	NM_018153	CAGCAGTGTTTGATACCGTAT	CTCCCATTATAGGGCAAACAA	CTGACAGAAGACAGAGAACAA	CCGAGGAACAACCTTAATGAA
84171	LOXL4	NM_032211	CCGGGTGGAAGTGCTCATGAA	CAGAGTCAGATTTCTCCAACA	CAGGATTGGTCTAAACTTCAA	CTCATTATGGACTGCTACAAA
84174	SLA2	NM_032214	CTCGTTGAGACCACCAGCATA	TCGGACAGTCTAGGTCCTCAA	CATCAACAGGTTCTCAATTAA	CAGGTTCTCAATTAAAGATTT
84186	ZCCHC7	NM_032226	CAGGGAATTGAGCTTCAGCAA	ACAGATTTCCTAAACAAGTAA		
84196	USP48	NM_032236	CACAGTCTGGTGAATGGTATA	ATGGCTGAGATGCGTAAGCAA	CCGAAGTATGCGACATAGAAA	ACCAGATGCGTTGGTCCATAA
84197	FLJ23356	NM_032237	AACACTATGCTTACTGAATAT	ACGGGTCATGTGCGACTCCAA	CACGATGATCTCATGCCCTCA	AAGGTCTTGGATACACTTAGA
84203	TXNDC2	NM_032243	TAGCTTCTCATGTGTAAACTA	CACCTTGAAGCTCTCAAATAT	AGCAGTCATTGCAGAATTAAA	CAGAATTAAAGTAAACATGTA
84217	ZMYND12	NM_032257	CAGCATATTAAGGGAATATAA	CAGCTTGATGTCCATGAGCAA		
84220	RANBP2L1	NM_005054	CAGCATGAAATAAACACTCTA	CAGGCGTTCAGTGGAATTAAA	CAGCATGGTAATAATGTTCAA	CAGAATTATGATAATAAGCAA
84229	DKFZp434I099	NM_032269	CAGGACAATGACAGAGTACTA	CACACTGACCATCTCCATCTA		
84231	TRAF7	NM_032271	AAGGAGTGCGAGCACATCAAA	TCGGAGAAGATCGACCAGCTA	GCGGGACGCATCCATGTTAAA	CACGCTGGTCTCCTCACACAA
84233	DKFZp586C1924	NM_032273	CAGGTGATTTGGATTGTGAAA	ATCGGTTTATGTTGGATTAAA		
84259	MGC2714	NM_032299	AACATTTATTTCAGAACAATA	TCCCACGTGTATACAAGCTAA		
84263	HSDL2	NM_032303	AGGCACCTACCTTGCATCTAA	AAAGAGGTGACTTAAGTTCAA	ACCCAGTTCATGAATCGCTAA	CAGTTCATGAATCGCTAATAA
84265	MGC3200	NM_032305	AAGGGAGAAAGGAGAATTGAA	ATAGAGGATGATGACAGTTTA		
84266	SPATA11	NM_032306	CGGGACTCTGAGGGAAGTCAA	CAGGCGGGAGGTGGCGCCCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
84270	C9orf89	NM_032310	CAGGATCATCCTCCAGCTGAA	CAAGGTGCTGACCATATTAAA		
84279	C2orf7	NM_032319	CATGATTATTTGTACTTTCAA	CTGGCTAGAACCCGAAACAAA		
84284	MGC13186	NM_032324	AAAGATTTCTTGTTTATTTAA	AAAGATCAAATTAGCCTTAAT		
84288	MGC12458	NM_032328	AAAGATGATCGTAACACTTTA	AACGAGTAGCAGTGTAATGAA		
84289	ING5	NM_032329	CTGCGTGGACCTTACCACGAA	CCGGATCCGAGGAGCAAGTTA	AACCGTGAGGGATGTTAATTA	ACCGTGAGGGATGTTAATTAT
84291	MGC2408	NM_032331	CAGACACTATGCCCAAGCCTA	CAGCTCCAACTAGATCCAGAA	CTGGAGGCCGGTTTATCTCAA	TCCGGAGTTACCGGAGCGGAA
84292	MGC4238	NM_032332	CCGGCTCTATTGATTCCAGTA	ACGATTTAATGTGGATGGCAA		
84296	SLD5	NM_032336	CAGCACTTGATCCGATACAAA	TCGCCTCATGAAGATAGAGAA		
84298	MGC14817	NM_032338	CAAGCTCTACTGATACTTTAA	ATGAAAGATGTTCAAGAGATA		
84299	C17orf37	NM_032339	TGCCTTTGAGATAGAGATAAA	CCCAGGGTAAGTGCCCACGAA		
84302	C9orf125	NM_032342	CAGGGTTTAGCTGGCCTGTAA	CTGCAGGTATTTCACTGTTTA		
84310	MGC11257	NM_032350	CAGAGCGTGGATGCTCTGGAA	TGGCCTCACTTTCCATCATAA		
84311	MRPL45	NM_032351	AAGAAATAATTTATCCCTTAA	CACGCATATCATCTCTTTCAA		
84312	BRMS1L	NM_032352	CACAGCATTGATATTACCTCA	TAGGTAGTACTCTAAATAGAT	CCGCTGGCAACTTTACAGGAA	ATGCAAATTCGTACAAAGGTA
84318	MGC13183	NM_032358	AGGCTTTAAGACAGATATTAA	CACCAGAGAAATCAGAACAAA		
84321	THOC3	NM_032361	CAGCGTCTTCTTGCTGGAGAA	ACCAGCTTTGTTGGCATCCAA		
84324	CIP29	NM_033082	CAGGCATATCTTGAAGAACAT	CTCCTTCTTCTTGGTCACATA		
84327	ZBED3	NM_032367	CCTGGTGACTTTGAAAGGATA	CCCAGAATCCTTGGGAAATTA		
84329	MGC15619	NM_032369	CCCGGCCTTCTCCTTTAAGTA	TGGGAGCTCACTAAGAACAAA	CAGGTTCCAGGCCATCAGTAA	CAGCCCGACAAGAATAACTAT
84330	MGC15716	NM_032370	CACAGCAAACTGCACTACAAA	CACACAGTCCCTGGAAGGCAA		
84334	C14orf153	NM_032374	AAGGATTTGGAACAAGCTTAA	TCACAAATAAATTGTAATTAA		
84337	MGC4549	NM_032377	CCCGTGGATGTGTACAGTGAT	CTGGACAAGGGAAGCCCACTA		
84366	PRAC	NM_032391	CTGTCTCTATTTATACAATAA	TAGGCCGATGCTTGCTTGCAA		
84376	HOOK3	NM_032410	CTGCCAATAATTGATATACAA	CAGCATGAGAATAAGATGTTA		
84433	CARD11	NM_032415	CTGGATGATGACAGTCACGAA	CCCGTTGGACACATGCACCAA	CACAGTACTCGCAGTGCTTAA	CAACTCGAGATCGATCAGCTA
84435	GPR123	NM_032422	CCGACTTTCCTAGGCAACAAA	AAGCCGTGTTCTGATTATCAA	CTGCCCAAGGGTAAATTGCTA	CACTGTAAAGCTCTTCACCTA
84436	ZNF528	NM_032423	TAGGATTTACACAAGAAGTAA	AACGCAGATAATCCTTACAAA		
84439	KIAA1822	NM_032425	CAACAAGAACCTCAACTCAAA	GAGGATAATCCTGGAGGTCAA	CAGGAACACTTGATGAATAAA	GCGCATCGACGTGGACCGTAA
84441	MAML2	NM_032427	CCAGTCGAAAGTAATGGCTAA	CTCCAAATAAACAATGGACAA	CAGAGTTCAATTTCAGCTCAA	CAGGATACAGTATCCAATTTA
84450	ZNF512	NM_032434	CAGCACAGTTCCAGAAAGTAA	CAGCCAGGAAGTACTACATAA		
84465	MEGF11	NM_032445	AAGCAGCTATGTAGAAATGAA	CAGCAAGTTTACACTGCTTAA		
84498	KIAA1838	NM_032448	AACCCTGAAATTAAACAAGAA	CTGAAGTAAAGCAACAAGTAA		
84504	NKX6-2	NM_177400	CTCGGACGCCGAGAAGCTGAA	CGGCTGCTCAAGAAGCACAAA		
84520	C14orf142	NM_032490	CTGATTTATCATGTACCTTAA	AACAATCTGCATTGATTACAA		
84536	C21orf67	NM_058188	CAGAGGAAGATCAAAGATCAA	CAGAAGGACCACAGTAGAGAA		
84614	ZBTB37	NM_032522	CAGGGTTACACCAAATCTCAA	ATGCAGCATATTATAGACAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
84630	TTBK1	XM_166453	TGGCAGGAACGAGAAGTTTAA	AACGAGAAGTTTAACTATGTA	TGGCAGGAACGAGAAGTTTAA	CAGGAACGAGAAGTTTAACTA
84639	IL1F10	NM_032556	CCGGATAGCCTCAGTCAGGGA	CCATGGCAAGATACTACATAA	GCAAGATACTACATAATTAAA	AAGGCTCTATACACAAGAGAT
84641	FLJ14753	NM_032558	CACCAGTAAATGGACCATTAA	ACGAGTGAAGTTTATATCCAA		
84643	LOC84643	NM_032559	CACGGTAGAGTGGGTGGAGAA	AAGAGTCTTCTAGCCCTCAAA	CAGAGGGATGAATTTATTAAA	CTGGTGGAGTACACCATGATA
84645	C22orf23	NM_032561	AAGGGTCTTGCCACCACTTAA	CCGCCTTAGGCAAGTATTCAA		
84651	ECG2	NM_032566	CTCCATGGACATAGAGAGAAA	ATGGAGAAAGTTTCTGTGCTA		
84658	EMR3	NM_032571	CTCCGGGATGTGGAATCGAAA	AAGGAACGTGTCTCTCTCCAA	GTGGTTTAGAGAGATCGTAAA	AACGATAGTGTAGCTATTGAA
84659	RNASE7	NM_032572	CCACTTCATATTTGTATAGAA	CAGCACGAAGACCAAGCGCAA		
84675	TRIM55	NM_033058	TACAATCATATCACACATTAA	CAGAACATAAGTGTAACTTTA		
84676	TRIM63	NM_032588	AAGGAAGAGGACACCAGTAA	AAGGAGCACGAAGATGAGAAA		
84678	FBXL10	NM_032590	CCGGCAAGACCGGGAAACAAA	CAGATCTAACAAAGTAGGCTA	TAGGAGTGGACTAGAAGTTTA	AGGAGTGGACTAGAAGTTTAA
84680	PHACS	NM_032592	CTGGGTTGACTTGAGAAAGTA	CAGCAGGTGCTTGCAGGCAAA		
84687	PPP1R9B	NM_032595	CCGGGAGGTGCGCAAGATTAA	CACTGAGGAATTCCAATTCTA	CCCGGGAGGTGCGCAAGATTA	CAACTCGAAGCTGGTCAGCAA
84691	NYD-SP18	NM_032599	CAGGTATGTGACCACTATGAA	CTGAGAAGATTTATTACCTAA		
84692	NYD-SP17	NM_032600	ACGGCTTTATTTGTTCCTTAA	CTGAAGAAACGTAACCATCAA		
84699	CREB3L3	NM_032607	CCCGAGAAGAGTCTCCAGGAA	ACGATGCAATCTCACCGTGAA		
84701	COX4I2	NM_032609	CTGGAGCTTGGTGCTGAGGAA	CCGGTGGGACTATGAGAAGAA		
84708	LNX	NM_032622	ATCATCCTCGATAGTACTCAA	CACGGTGCTTGTATAACTGTA	CTCGCTCAGAGAATTAATTAT	CACAGCTAACACAGCTCTTTA
84720	PIGO	NM_032634	CAGGTACTGGATGATCTGCAA	TAGGACTTCATTATTCTATAA		
84733	MGC10561	NM_032647	CACCTGCGGGTGCACCTTAAA	GCCGGCTGGATGTGACTCAAA		
84749	USP30	NM_032663	CAGAAATAACTCCCAAACAAA	CACACCAGTATTTATGCTTAA		
84750	FUT10	NM_032664	CAGCGCGAGAGTAGAAGTGAA	TAGGATCATTGCACAGTATAA		
84775	ZNF607	NM_032689	TAGGTTCATTTCTGTACTTAA	TAGGCTCAATTCATCCCTTAA		
84787	SUV420H2	NM_032701	AACCTTGTTATAAGCAGCAAA	CCGGCGCTATGGGCTGCCTTA	AAGAAGAATGAGCACTGTGAA	AATGACTTCAGCATCATGTAC
84816	RTN4IP1	NM_032730	TTCGAGCATTTCATATGCGAA	ATCATACACTATCCAAATGAA	CAGGAGGAAAGACTGTAATTA	ACGAGGAAAGACTGTAATTAA
84833	USMG5	NM_032747	CAGCTGTGAAAGCAACATAAA	TACCAGTTCACTGGTATTAAA		
84836	MGC15429	NM_032750	CAGGTTACACACTAAAGTAAA	CTCAGGAATCAAGGAACATAA		
84844	PHF5A	NM_032758	ATGGCTAAACATCATCCTGAT	CTGGCACACCATATCGGAGAA		
84864	MINA	NM_032778	TTGGCTCGAATGTGTACATAA	CTGTTGCTACAAGACGATTAA	TACCTGCGTATCTACTAACAA	AACCAGTATTTAAGTCTATAA
84868	HAVCR2	NM_032782	AACCATCAGAATAGGCATCTA	CAGGCATAATGAATGATGAAA	CTGATATAAATCTAACACAAA	TTGACAGAGAGTGGTCCCTAA
84870	THSD2	NM_032784	ATGGAACTCGATATCCAGATA	ATGGAATACATCGGCAGCCAA	AAGGGAAGCATTACTGGGTTA	CTCGATATCCAGATATAAATA
84872	FLJ14451	NM_032786	CACCAAGAGTGGCAAGATAAA	CTGCCATGACTTCCAGAACAA		
84873	GPR128	NM_032787	CTCGATCAAAGTGCTGTGGAA	AAGAAGATTGTTAGCACATTA	CACAGCTCTATTACCTTCTAA	AGGCGAGTGGTTGGACAGATA
84875	PARP10	NM_032789	CAGGCAGATCATGAACTACAT	TTGAATAAACGTGAACGTGAA		
84888	SPPL2A	NM_032802	CAGCAATAATATTATGTGGAA	TGGGCTGTGTTTCGAAATGAA		
84893	FBXO18	NM_032807	CCCGCTGTTCATTCCTTGGAA	CTGCATAGCCGTGCTTCTCTA	TAGGGCGGAAGTACCAGTCAA	CACCGTCCTTACCATGAAGAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
84894	LRRN6A	NM_032808	CAGCGAGAACAAGATCGTTAT	CCGCTGGCGGCTCAACTTCAA	AAGGACTTCCCTGATGTGCTA	CAAGGGCAACACAAAGCACAA
84896	ATAD1	NM_032810	CTGGATTAATTTATCTGATAA	CAGGTGAACAATGGATAACAA		
84898	PLXDC2	NM_032812	TCCAGTGGATTTGATCGTCAT	CCAAGATAGCACTACATCTAA	CACAGTACATAGCACCTTTAA	ACAGACCACAATTACTATATA
84904	C9orf100	NM_032818	CTGGATTGTGGGAGAACTAAA	CCCAACTAAACCTCAAATGAA		
84918	LRP11	NM_032832	TACGTATTTCTAGACCATAAA	CAGAAACTTAGTTGAAGGCAA		
84925	DIRC2	NM_032839	ACAGATTATCACATTAATTTA	CACAGACTTGAAGGAGTTTAA		
84926	FLJ14800	NM_032840	CAGACCAGAGATGTTTATACA	CCCTACGATGTATGAAATGTA	CCAGTTTGGGTCAAAGTGCAA	CCGGTTTGTTCTCATGAACAA
84934	FLJ14827	NM_032848	ACCAAGGAAGAAGAACAAATA	CAGCTTTATAGGTGTGACCTA		
84938	APG4C	NM_032852	CACGTAATTGCAGGAAATGTA	ACAGATGAAGTTGACAAGCTA		
84948	TIGD5	NM_032862	CACAATCATCTCAGTGGCGAA	CCGCAAGGCCTACTCCATCAA		
84950	FLJ14936	NM_032284	AACCTGGATGTGAGGCATTAA	TCCGACGGAAATAGAATTGAA		
84959	STS-1	NM_032873	AAGAGAGTTGTTCTTAGGTTA	AACCAAATCATCAGTTATCAA	CCGGCTTATTTGAGTGGACAA	CCGCTTAAGGATGCTAACATT
84961	FBXL20	NM_032875	ATGGCAGTAACTGGCAGCGAA	CAGGACCCATTTACCCAATAT	GACCCATTTACCCAATATTAA	CTTGGCGAACTGAGTATTTAA
84972	MGC15912	NM_032886	ATGGATGAGGTCATCATGAAA	CTCGCTGGGTTTATATTTGAA		
84991	RBM17	NM_032905	TCCGCTGACTGAAATACTTAA	ATGGAGTATGTGGGTATAGAA		
85013	MGC13159	NM_032927	CAGCTTTAGTAATTACTATAA	TTGCATATGCATAAATTATTA		
85014	MGC14141	NM_032928	ATGGCTTATCCTTCTCTCCAA	CTGCATCTCCAACAAGTCCAA		
85015	USP45	XM_371838	AAGCATATATAATGTTATCAA	CAGAGAAAGCATGTTAAATTA	CGGGTGAAAGATCCAACTAAA	CAGGAAATTATCGGAACATAA
85236	HIST1H2BK	NM_080593	AAGAGAATCATTTACAAGTTA	AAGGAGGGACTTTCTCTGGAA		
85285	KRTAP4-10	NM_033060	AAGGGCATCCATCTACATTTA	TAGATATTAACTGTTCTTCAA		
85300	ATCAY	NM_033064	CAGCGTCAAGTTCATCAACAA	CTCGCCTTTGTTTGCCAGTAA		
85315	C6orf33	NM_133367	TAGGAATTTAAGTCCATAGAA	AAAGCTAGAATTGCTTATCAA	AGGAAGCTTATTCTCATATAA	CTAGAATTGCTTATCAATCAA
85317	BAGE4	NM_181704	CCGAGGCAAGTCAAAGCTGAA	GAAGATCAAATTGAAGATAAA	CTGCAGATATTTCATCAAATA	ATGGCTGGAAATGCAAATGAA
85320	ABCC11	NM_032583	CCGGTGTATTTGAATAAACCA	CCGCTCATGATCCAAAGCTTA	CTCCTCCAGTTGGATCATCAA	AGGCTACTTGATGGCTCTCAA
85358	SHANK3	XM_037493	CAGGGATGTCCGCAACTACAA	CCGCAAGTTCATCGCCGTGAA		
85359	DGCR6L	NM_033257	AACCCTAGGATAGTCTCATAA	CCGCGCTCGGGATGTCGTGAA		
85360	7h3	NM_033025	CTCCATCTTTGTGGATAATAA	GCGCCTCTCCATAAAGATGAA		
85409	NKD2	NM_033120	CTCGTCTGTGTAACCCATAAA	CACGCTCTATGACTTTGACAA	CAGCCTCATGCACACCATCTA	CACGGAGCGCAGAAACCACTA
85411	C6orf114	NM_033069	TGGAATCAGAATTCAACTTAA	AACCTCCAATGTGGACATTTA		
85414	PCANAP6	NM_033102	CACAGGCATTTAAATATTTAA	CAGGCTCAGGGTTAACAGCTA		
85417	CCNB3	NM_033031	GTGCAGGATGTCAATATGGAA	TAAGGAGTCGTTAGCCTTTAA	AGGGCTAAGCATGCATGTTAA	AAGGCTGTGTATTACAAGTAT
85439	STN2	NM_033104	CAGATGTACCTTATAATTCAA	AAGCTGGATATTTCCTCTTTA		
85443	DCAMKL3	XM_047355	GAGGAAACTGTTTAACCTCAA	CTCGAGAATCACAGAGCGGAA	TCGAAGGAGCTCAGAGTTCAA	CCAGCTAATGAAGATAAACTA
85452	KIAA1751	XM_372193	CACCTTCAAGCCGATGATAAA	CAGGACTTTGATATTGGCAAA		
85455	DISP2	NM_033510	CCGGAACAGTCCGGACTACAA	CAAGAACTTCAGTGAGACTAA		
85459	KIAA1731	XM_374922	CAGCAGATACAGAAACATGAA	CAGCATGAACTTAGTGCTATA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
85464	SSH2	NM_033389	GAGGGTTTGCCTGGAAGTTAA	CAGGAGTCTTTGAGTATCATA	TTGAGGATGAATTAAACTTAA	CAGATTTAGTCTAGCATGAAA
85465	SELI	NM_033505	CAGGCATAGTTTCCACTTTAA	CACCACTGTGTTGATATGTAA		
85480	TSLP	NM_033035	GAGAAATTTCTTTGTCTATTA	TTGGTGGACTAGTATAGTATA	AGCACCTAAACTTACATTTAA	CTGGAACAAGTGTCACAATTA
85865	LOC85865	NM_033107	CAGCTTGGTGACTGTAATTAA	AAGCCTGAACTTGGAAAGATA		
89765	TSGA2	NM_080860	AACATGGTGAATATCGTTTAA	CCGAGAGGAGATCGTATCATA		
89777	SERPINB12	NM_080474	TAGGCAAAGATGATCGTCATA	TACGATCTTGGGTGGAGTTTA	ACGATCTTGGGTGGAGTTTAA	TTGGGTGGAGTTTAATGCCAA
89780	WNT3A	NM_033131	CAGGAACTACGTGGAGATCAT	GCCGCGCTACACCTACTTCAA	CCCGACTGTGCTGCTCGCGAA	ACCGCCATCCTCTGCCTCAAA
89792	GAL3ST3	NM_033036	CAGCCGCAAGGTGGACATTAT	CTCGAACTACCTGTTGCGCAA		
89796	NAV1	NM_020443	CGGGATCATCTAAGAAATGTA	TAGGTTGTCATTCAGACTTTA		
89797	NAV2	NM_145117	CACCTTTAACGTGGACCATAA	CAGCAAGAATGTGGACCTCAA		
89822	KCNK17	NM_031460	CCGGGATGTCGTCCAAGCATA	ATGGCTGGCCTTGATCATCAA	CAGCTCTAAGGAAGACTTCAA	CTGGGTGCAGCTATATGATTA
89832	CHRFAM7A	NM_139320	AACATTAAGATTACAAGTGGA	TCCATACAAATGCACAACATA	CACCGCAACATTAAGATTACA	ATCGGTTAAATTTGATGCAAA
89845	ABCC10	NM_033450	AGGAAGGGAGTTGATTCCTTA	ACGGCTGTGGAGGGCCTTGTA	CTGCTGGTACCCGTCAACAAA	AGCCCAGATTGTGGTAGATTA
89853	C9orf28	NM_001011703	AAGCCTTGCCAGAAACGTCAA	CTGGAAAGACGGCTTATTTAA		
89858	SIGLEC12	NM_033329	CAACAGGACATCAGAACTTAT	CAGGAAATGGAACTACATATA	CCGAGACTGATTCCTTTAGAA	ATGGAACTACATATATGACAA
89869	PLCZ1	NM_033123	CAGAAATACGAGCCTATCGAA	ATGGATTCACGTGAATGTCTA	CAGCAGACTCGTGTAATTAAA	TTAGCTATGCATCGCAATAAA
89870	TRIM15	NM_033229	CAGGAGTAAAGAACTGGCTTA	GAGGGATGAATATATCACAAA	CCGGCTTGGAGCCCAGGTCAA	ATCCGTGATTTCCACAGGAAA
89882	NYD-SP25	BC033792	AACAGGTATAGCCAAATTCAA	TAGACGAAATGTGCCATTATA	CACGTTAAATCAAGGAAGGAA	TTGAATGGACCTAACTATACA
89884	LHX4	NM_033343	CCGGACCACCATCACAGCCAA	CAGAACTTGGCCACACCAATA	CACCAATAGGATTTATGGCAA	TCGAAAGTACGCCAATGTGAA
89886	SLAMF9	NM_033438	CTGGCAATAAAGTCAAATTAA	CAGGCATGGATATGACCTACA	TCAGGGCTTTACCAAGCTCAA	CTGGCTGGCAATAAAGTCAAA
89890	KBTBD6	NM_152903	CAGTATTTATTTGATTATTTA	TAGGTTTGTATTGTTGATCTA		
89894	LOC89894	NM_138341	CTCGTGTTACCTTGATGGATA	CAGGGTCTACTCAACTGTGGA	ATGGCTACTCTGAGTGTTATA	CACCGTCAATTACATCTGGTA
89953	KNSL8	NM_201521	GACCAGAATAAGTATAAGGAA	CAGCTTCGCCGTTCTATGGAA	CAGCGGCTACAGCGCAGTGAA	AAGGTTGCGGACGTTGCACAA
90007	MIDN	XM_028067	CTGTCTTGGATACCTATTTAA	CCCTTTATGTGTTGAAAGTTA	ACCGGCTTCGGCAGACAGAAA	ACCGTTGTTCTCGTAGGTGAA
90024	LOC90024	XM_028217	TACGGTCGGAAGGAAAGTAGA	CCGACCAACTGCAGCACCCAA		
90025	C6orf157	NM_198920	ATGAATGATTATCAAATTAAA	CTGCGGTGAAGTCATAATAAA		
90102	PHLDB2	NM_145753	AAGCATCAAACTAAATTGAAA	CAGAATAACTTTATCACCCAA		
90133	LOC90133	XM_029323	TACCAGCGAATTCCCACCCTA	TACAAAGACTCAGATCTCCAA		
90231	MGC33867	NM_138346	CAGCCCAGGAGTGGAAATGAA	CCAGATGGAGTCGACGCTCAA		
90249	UNC5A	NM_133369	CACACCCATTGCCCACACTTA	CCGCATAGCCTATTTGCGCAA	CCGCATTAATGTCTCAAGGCA	CACCATGGAGGTCCGCATTAA
90316	TGIF2LX	NM_138980	AGGGCCCAGTGGTCCAGACAA	AAGGTCAAGGTTTCTGTCACA		
90378	SAMD1	NM_138352	CAGCTTTCCAAGAGCAGGAAA	CTCCATGGCAGCCATGAACAA		
90379	LOC90379	XM_373433	CTGCGTGGACATGGTCATGAA	CCGGGTGTGCGTGTCCCTCAA		
90390	THRAP6	NM_080651	ATGAAAGATTATTGTAATAAA	CTACAGGATAATCTTCGCCAA	CTGAGATTGGTATATGACAAA	CAGGAAGCTGAGATTGGTATA
90427	BMF	AK024472	GAGGTCTTCAGTACTATTGAA	CCAGAGGAACTCAGTTAAGAA	GACGCTAGAAACTAAATTATA	CAGACGCTAGAAACTAAATTA
90441	ZNF622	NM_033414	CAGGCACATATGAATGACAAA	CTCCTTGATGAGATACTACAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
90485	BC37295_3	NM_001005850	CTCGCTTATAGAGCACCAGAA	AACGCGATGAATTCAGCCGAA		
90507	SCRN2	NM_138355	CACAGGGTTACTGGAGCACTA	CAGGCTTATGCGTAAGCTTCA		
90529	LOC90529	NM_178122	AAGCTTTATGAAAGCTCTCAA	ACCCAGGTGATTCCAATGATA		
90594	ZNF439	NM_152262	TTGCTTTATGGAAGAAAGTAA	CTAGGATTCTTTGAATACAAA		
90637	LOC90637	NM_182491	GAGGGAGATGGTACTATAATA	CAAGATTTCTGTAAAGATCAT		
90736	CXorf44	NM_138362	TCCTGGATGAATAATATTGAA	CTGGGCTTCCTGGGTCAAGTA		
90737	PAGE-5	NM_130467	ATGCTGGAAATTTGACTGCTA	AACCAAGAATATTGTTCTTAT		
90780	PYGO2	NM_138300	AACATGAACTTTCCCAGCCAA	TCGGAGTGAGGTGAACGATGA	ACGTATCTTCTTCATACCAAA	CAGCCCATCTGTTGCACATTA
90835	LOC90835	XM_373675	CCCAGTCTCTCTCACATTCAT	CTGGAACATTCTGGAAACTTT		
90874	MGC45731	XM_371286	CACCAGGACTCAGAAGACAAA	CTGGCCTTGGTTTCTATGTAA		
90952	ESAM	NM_138961	CTGAAATTAGCTACTCACCAA	CAGAGGATAGGGAATCTCTTA	TCAGGTGTTGTCCTACATCAA	ATACATAATGTTTGTATGAAA
90987	ZNF251	XM_291262	CAGACTCGTGTTGGAGAGAAA	AAGCATAATTTATAAACAATA		
91050	DKFZp761B107	NM_173463	CAGGCTAATCTTGCACAACTA	AAGAAACTAATTATACTACAA		
91074	ANKRD30A	NM_052997	CTGCAGATATATGTGGAGTAA	AAGGCTAACTGCGGAATGAAA	CAGGAGATGCTTGTTTGCAAA	AACCGTATATATCAATATGAA
91151	TIGD7	NM_033208	CAGACGGAACTCATAAATTAA	AAGGTTCTAAGTAGAATTGAA		
91181	NUP210L	NM_207308	AAGGAGTACTTTGAAGAGCAA	CAGGATGAAGTACAGATTGAA		
91227	GGTL4	NM_080839	GAGGACAAGGCTGACAAGCAA	CACCAGCACCATCAACCTCTA		
91304	C19orf6	NM_033420	GCCCGATGACATGAACAACAA	CGAGTTGTTCGTGCTGCTCAA		
91316	LOC91316	XM_498877	CTGCTGTGGTCTCTGCTTCTA	ATCGTGGTATCCCAAGGGTTA		
91319	DERL3	NM_001002862	CACGGCCGACTTCGTCTTCAT	CTGGGAAGAGTCCCATGCTAA		
91351	FLJ31033	XM_037817	CTGGGTATTCCAGCATATTAA	TAAGAATAAGATAGTCATTAA		
91355	DKFZp434O0213	NM_182492	TTGGCTCTGTGCATCCTTGAA	AGCACTATAATATTTATTGTA	CACGTGCAGCCTATATGGGAA	CTGGAACAAATCAGTGAACAA
91368	MGC13017	NM_080656	CCCAGGAGTTATCACTGTAAA	TCCTGGTATTACCAACATAAA		
91369	MGC15396	NM_052855	CTGGGTGTTAATCCAGATCAA	AAGGATGTTGCTCGACTCCAA		
91404	SESTD1	NM_178123	CGCCAACAAATTGACTCGTTA	TCGGTTGATCCTGAAACAGTT	CAGCGTCGATTTAATGGCTCA	ATCCCGCATGTTGTCAACATA
91409	DKFZp434E2321	NM_207310	AAGCTCATAATGAATCAGACA	CTCCAAGAAATGCCTGCTTCT		
91445	FLJ38628	NM_152267	ACAGCCAAGGATGGCAAGCAA	CCTGAGTTTAATATTACAGAA	ACCACCATCCTCAGAAGCCAA	CTGAATCTTATTGAGGGACTA
91452	ACBD5	NM_145698	CAAAGTGATAATGATAAGAAA	ACCGTTAATGGTAAAGCTGAA		
91464	LOC91464	NM_001008494	ACGGGATACAGAGATAAACAA	CTGGATGAAAGGAGAAGGCTA		
91522	COL23A1	NM_173465	CAGGATCTTGGATGCCCTCAA	CAGGAAGGAGATGAAGGTAGA		
91561	LOC91561	XM_039218	CAGGGCCGCAGAGCTCGCGGA	CGGCTTCTCTCAAGGATGAGA		
91574	FLJ38663	NM_152269	CAGCATTATTATAGTGCTTCA	TTGGATGAGAATGAACTCGAA		
91584	DKFZp434G0625	NM_181775	CCGCATCGTCCAGACCTGCAA	CTGGCCTTTGTGGGCACCAAA	TACCTGGGAATTCTTCCTAAA	CAGCCGGAAACTGACCAAGAA
91607	FLJ34922	NM_152270	CCCGATAACCTTCACACTCAA	CAGATACAACTCAGCATTAAA		
91608	RASL10B	NM_033315	ACCAATTTAGAAATAACAATA	CAGGGCAAGCAGAGGCAGCAA		
91647	ATP4F2	NM_145691	CTCCGAGAGCACCACAGTCAA	GAGACATTAGTGGAACTTCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
91662	NALP12	NM_033297	CTCATGCAGATTGAGATCAAA	CCAGACCTTGACCGACCTTTA		
91664	LOC91664	XM_039908	AAGTATGATGATTGCAGCAAA	CGCTGCGAGTGTGGTGTTTAA	AACCTGGTGTCAAGATACAAA	ACCGCCGCTATTCTCCAGATA
91754	NEK9	NM_033116	CAGGTGTCATGTGGTGATGAT	TCGGGAATTATCAACCATGAA	TACACTTGGGTGAACATGCAA	CACGAACCAGTGAAGTCTATA
91833	WDR20	NM_144574	TGGGAACATGTACTTATATAA	CACGAGGAACCCTCTCCTTAA		
91860	CALML4	NM_033429	CACGGTGCTCTTAGCATTCAA	ATGGAATTTATGGTAACTTTA		
91862	MARVELD3	NM_052858	ACGAGAGGAGGTGGAATATTA	CTGGAATGCCACAAATGCAAA	CTGGGAGAGCCTGCTGCCAAA	CAGGCGCTGTACCAAAGCAAA
91942	LOC91942	NM_174889	CCAGTTCAAACTCAAATTAAA	CCCGCAGTACAAGAACTGGAG		
91966	CXorf40	NM_178124	ATACATTAGGTTAAATCTGAA	AGGGCCAGGTAAAGAAGCTAA		
91977	MYOZ3	NM_133371	CACTAAGGATATAACAGTTAA	CTCCAGGTGATTCCAGCATAA		
91978	C19orf20	NM_033513	GAGGGCCGCCTTCAACAACAA	CGGAGGTTACACCCTCAGCAA		
92002	MGC29729	NM_152274	CAGATTTGTAGGGAGAATGAA	TACAGGCATGACATCAATGAA		
92017	LOC92017	NM_001009607	CAGCGTCATGAACAAAGTCAT	ACGGAGAAAGCAGCTCCAGAA		
92106	MGC15763	NM_138381	ATCGTCTGCTTTAACGCCTTA	AACCAGCATAATGAAATCCAA	TACCAGCGAACTCCTGTTTAA	ATGCAGTTTGCATGTTACAAA
92181	DC-UbP	NM_152277	CTGCTCTAAATTCCCTATGAA	CAGGCTTTGAGACTCATGTAA	AAGGCAGTTAAGAAATAGATA	AGGCAGTTAAGAAATAGATAA
92211	PCDH21	NM_033100	AGGGCTGAGAATTGACGAGAA	AACCTGCTATCAGGAAATCTA	CAGGTTGGTAGCAAAGATCTT	CAGGTACAACTTCTATGTGAA
92235	LOC92235	XM_043739	ACCGTCTGTTGCAAGCATGAA	AAAGCTGGCCTCAGACAACAA	TCCGATATTCTTCCCGCAGTA	CAGAACTGGATTGCCAATGTA
92249	LOC92249	XM_499179	CTGCACTAAATTCCTTCATTA	AAGTTCCTATCTAATATTATA		
92255	DKFZp434H222(	NM_001007527	AAGGACTTTAAGAAAGATCAA	AAGATTAAGATTATACTTCAA		
92312	LOC92312	XM_044166	CCGCTCCAGGGCTTCTCTAAA	CAGGCCCAAATCGCCACCTCA	CAGGCAAGGCTGCAAGATTAA	ATCCTCGAGTACAACAATGAA
92369	SSB4	NM_080862	CTCGCTCAACGTCTTCGTCAA	CATGGCTGTCACAAAGCTTTA	AAGCTTTATTTGAGCAAATTA	ATGAAGAGCGTTTCTAATAAA
92454	MGC20460	NM_053043	CCCGGTGTAACCATTTATGAA	ATCGAGATCAATGAACCTTTA		
92579	G6PC3	NM_138387	CTGGGAAATGGCCAGAAGATA	CACATGTTCAGTGCCCAGGAA	GTGGCTCAACCTCATCTTCAA	CAGGTGCTGGCTGGCCTAATA
92609	TIMM50	NM_001001563	CCGGACATACAAATATTTCAA	CACCCTGGTCTCGGAATCTAA		
92610	TIFA	NM_052864	TAGGATTATTTACTTACCAAA	CAGAATAATGATTTCTCCTAA		
92714	ARRDC1	NM_152285	CACCAAGAAGTTCTCCTACAA	CCGGTCTTCATTGGCAATATT		
92715	C9orf112	NM_138778	CAGCCTTTCATACTTGTTTAA	CAAGGGTGGAATGGAAGTTAA		
92736	OTOP2	NM_178160	CAGGCAGGCCCTGGTCATCTA	AACGCTCTGGATCCTCTTCTA		
92799	SHKBP1	NM_138392	CAGGGCCTCCTTGGAATAAAT	CCAGCTAGTGTTCATCCAGAA		
92806	MGC16385	NM_145039	AAGCGAGTTCACAAATAGCTA	CGCCTTTAGACTTATCTTAAA	AAGGTGTAATCTCGACCTTGA	CTCGGTTGACTCGCCATCGAA
92815	HIST3H2A	NM_033445	CGGAAATGTCCGGTCGTGGTA	CCGCGGTGCTCGAGTACTTGA		
92822	ZFP276	NM_152287	CGGCATGAAGAAGCACATCAA	CAGGTTAGAAGACATACAGAA		
92999	ZNF651	NM_145166	CCCGAGTGATCTGAGGATTTA	GAGGCTAGCACTAATAGGAAA		
93010	B3GNT7	NM_145236	CAGGAAAGACAACAAATACTA	CTGGGACGTGACCACCACTAA		
93034	NT5C1B	NM_001002006	TTGGATGTTTGTAGATAACAA	TAGGATAAGTTTAGAACTTGA		
93082	LOC93082	NM_138397	CACGTGTATAATGGAAATGAT	CAGAGAGACCATGCATCTGAA		
93107	KCNG4	NM_172347	CCCGCTGAGCCGCCTGAGCAA	CAGCCAGGAGTTCTTCTTCGA	ATGAACGATGTCAATGACCTA	TTGCCTATCATGCACATGTAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
93134	ZNF561	NM_152289	CAGGCTGTGGACCGCAAATAA	CACGCCTAAGTAGACATGAAA		
93145	OLFM2	NM_058164	CGGAATAAACAGGACCTTTGA	CAACGGCTCCCTGTTCTATAA	CACGGACGTGCCCTTCCACAA	CAGGACCTTTGACATTTGAAA
93185	IGSF8	NM_052868	TGGGCCCAGATTGCAGAGAAA	CCGGCATTTATGAGTGCCACA		
94033	FTMT	NM_177478	CAGGTGAAGTCTATCAAAGAA	CCGGGATGACGTGGCCTTGAA		
94086	HSPB9	NM_033194	CAGAGACGGTTTCCAAATGAA	CCCGGAGGAACTGGTGGTGCA		
94097	SFXN5	NM_144579	CCCGCTCGCTGCGGTTGATTA	TAGGCCAGAGGTGAACATTCA	CAGCCGGACAGTGGTGTACAA	CAGGCTGGTAAATTTAGGATA
94104	C21orf66	NM_013329	CATGTTAAGGATACAAATCAA	CAGCATGAGAAACATCTGCAA		
94122	SYTL5	NM_138780	CAGAATTCAATGAAACACTAA	ATGGATTTGGCTGCTATTGAA		
94134	ARHGAP12	NM_018287	CACCATTGTATTGGACACTAA	CAGGGCGTTGCTATTACTATA		
94137	RP1L1	NM_178857	CCGGAGGATACTGCTGATTAA	TTGGATAAAGTTTGTTCTCAA		
94234	FOXQ1	NM_033260	CTCCATCAAACGTGCCTTAAA	CCGATGCTTCACTGTGCCAAA		
94235	GNG8	NM_033258	CTGGCTTTCTGCGAGACGCAT	CAAGATTGCCGAGGCCCGCAA	CAAGACGGTGGAACAGCTGAA	ACAGCTGAAGCTGGAGGTGAA
94241	TP53INP1	NM_033285	CAGAACGATGTTGACCTGTTA	AAGGGACATTTGGTTAGGTTA	CTGGGAGACACTAGTAGTATA	CCGCGTCAGTACAATTACTAA
96764	NCOA6IP	NM_024831	AAGGATCATAGTGAAATACTT	CCGGCCAAAGTGAACCAGGTA	TCGCAATAATGCAGAAGTTTA	ATGGAAACTTACAGGACTTAA
112398	EGLN2	NM_017555	CCCTGTAGACAGAGAAACCAA	CCGCATGGCAGACAGCTTAAA	CAGGGAATTGTGTCTGCAGAA	CTGGCTAGGGTTACCCAGCAA
112479	MGC16943	NM_080663	TAGGTGCTTTCTAGAATCAAA	CCCAATATGAGTAAACAGGAA		
112597	MGC4677	NM_052871	CACCAGCCTCTCCTTGAATAA	AAGTTTCAAATTGACATTCCA		
112609	C6orf117	NM_138409	AAGCTGCACACTGGTATTAAA	ACCTATTGTTCTGGAAACTAA		
112616	CKLFSF7	NM_138410	CAGGCTGGTGGGCACCAGGAA	AAGCATATGGCTGTCCTATAA		
112724	RDH13	NM_138412	CCGCTTAAGGAAGGAAGGAAA	CTGGCAGACGAGGAAGTATAA	ACGAGGAAGTATAACACCAAA	AAGTACTTCGATGGACTCAAA
112770	MGC31963	NM_144580	CTGCAGAACCTGCTTCATATA	CAGCACTCCATCGACGATGAA		
112858	TP53RK	NM_033550	TTGGCTCGAATGCACGATGAA	CTAAGTAAAGGTGTTAAGATA	TAAGTTTATACCGCTAAACAA	AAGTATTGGCGTATAACATTA
112939	BTBD14B	NM_052876	CCGGCAGATCTGCAACATGTA	CCAAGTGAGATTGCACATTTA		
113026	PLCD3	NM_133373	GCGGATGAACTCAGCCAACTA	CCGGTTTGTGGTGGAAGATTA	AAGCAAGGGTACCGCCACATA	TAGGTTTGTAACTGTTTCATA
113177	C19orf36	NM_052878	CCCGAGGAGGTGGAACCTCAA	CCGCCACCATGTGAACTTCAA		
113178	SCAMP4	NM_079834	ACCCGTCAAATCTGTGCCTTA	CCGAGCCGACAGCTCCTTTAA		
113230	LOC113230	XM_053966	CCGCAGAAAGGTCTCGGAGAA	CAGGAGGAGCGCAAACCTTGA		
113246	GRCC10	NM_138425	CAGGAGGTTATCAAAGCCTAT	TCCGCTGAACCTAGAGCTTCA		
113451	ODC-p	NM_052998	TAAGCAAATTGCACAGATCAA	AAAGTTTGGAGTGTCACTGAA	CACCTCCAAGACCATCGTGTA	TAGTTCAAGTATGCAACATAA
113510	HEL308	NM_133636	TCGGTATGAGTGCAACATTAA	CAGCATTACTACCATAGGCAA		
113540	CKLFSF1	NM_052959	CCAGCCTAAATGTGACCATAA	CAGCCTAAATGTGACCATAAA		
113612	CYP2U1	NM_183075	CAGCGCTTTGATTACACTAAT	CAAGGGTATACCATTCCTAAA	CCGGAGGATTTCTACCCTAAT	CGGGTGTGTATGGGAGAACAA
113675	SDSL	NM_138432	TCCGACAACTCCGGCCAATAA	CTGCCAGGAGATGGCCAAGAA		
114026	ZIM3	NM_052882	CAGGAACTCTTAAACACTGAA	ATCAATCAACTTGCTAATTTA		
114041	C21orf88	NM_153754	CAGCCTTAATTCTACCTGCAA	TCCCGTCTCTTCCATTCTCTA		
114049	WBSCR22	NM_017528	CTGAGTGGAAGTTATCTGTCA	CCGAGCTGTCCTGCAGCTGTA	CCCTAACAGTGCCAAAGCAAA	CAGGGAGTCTGTGTTCACCAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
114131	UCN3	NM_053049	CCACAAGTTCTACAAAGCCAA	CAGAGGCACCCGGTACAGATA		
114294	LACTB	NM_032857	AAGCCAAATGCCGGAATTCAA	CTGGATCTTGATATTCCAGTA		
114548	CIAS1	NM_004895	AAGGCAGACCATGTGGATCTA	AAGCCAAGAATCCACAGTGTA	TTGATAATTTATATCTCTCAA	ACAGAACTAGTTGACTATATA
114625	ERMAP	NM_018538	AACTAGGTACAGCGACTTTAA	CACAAGACCATTGTACTGCAA	TTGGGAAAGGCTGATGAGTAA	TTGGAGAGTATTGATTTCAAA
114659	LOC114659	NM_052888	CTGAAGAAAGATCTAGCTGAA	TGGGTTCAAACTACAGATCTA		
114769	COPI	NM_052889	CAAACTGGAACTCATAAATTA	AAGGATCTCTATATCCTAGAA		
114771	PGLYRP3	NM_052891	CAGCCACTTCTTCTGAAAGAA	CTGCCAGACTGTCGTCCGAAA	CAGGATGGTGGCGTGTATGAA	CAGACTGTCGTCCGAAACATA
114783	LMTK3	XM_055866	GCCGCCTTTCTCGGAACTGAA	CCGGATGGGTAGACAACACGA	CCGGGAGACAGGACCCAGGAA	GCGGGAGGATGTGACAAGGAA
114788	CSMD3	NM_052900	CTGGTACACCCTTATATGGAA	CTGGCATTCCTCAATATGGTA	CAGGTGTATGATGGACCAAAT	CACGGTTTGCACAATGGTATA
114789	SLC25A25	NM_052901	CACGGTTGCACTTCCATTCCA	CAGGCCTGACTTCCCAACCTA	CAGAGTTATGTCCTAACTATT	GACGTTAGAAGTTGTCATTTA
114793	FMNL2	NM_001004417	CCGGTTTGTGAAAGCATATAA	ATGCAGTTTATTAATATTGTA		
114799	ESCO1	NM_052911	AAGCTACATGATAGAAATATA	TAGGCTGTTAACAAATCTCAA		
114804	RNF157	XM_290732	CAGGACGATCTCGCCTCTTGA	AAGCCTGGTCAATATCCGAAA	AAGCGTGAAAGCACTGGACAA	TCGGGTAGCCATCACCATCTA
114818	KBTBD9	XM_496546	CAGGACAGAATGGGAATTCAA	CCGGTTTGAGTTGTTATATAA		
114823	LENG8	NM_052925	TTGGAGAAGGGTGACCATGAA	CAACGTCTTCATGAAGGACAA		
114836	SLAMF6	NM_052931	CTCCAGTCCTTCGGACTTAAA	CTCCATTGTTTGAGCCAAGAA	CAGGGAATGTAGTTTCACAAA	CACAATTTACTCCACAATTAA
114881	OSBPL7	NM_017731	CGCATTGACCTTGACACTGAA	CTGGCAAGATATGAAGTGGAA		
114882	OSBPL8	NM_001003712	CAGAACTATAATGTGATTCAA	ATGGTTTAAATTAGTTAATTA		
114904	C1QTNF6	NM_031910	CAGCAACAAGTTAGTATTGCA	CAGGAAGACCTGTGCTATAAA		
114971	PLIP	XM_374879	CAGGAGTGGAAGAGACTAGGA	AAGCTCCAGAAGGGAGTCCAA	CACCTTGGACAACCTCCAGAA	CAGCTGCGGCTCAGCACAGTA
115330	GPR146	NM_138445	CAGCATTCAGTTTGTCAATGA	CTGGTGTTAAATGGAGCTATT	CAGGGTTCTGAGAACATTTCA	AGCATTCAGTTTGTCAATGAA
115426	UHRF2	NM_152306	CACATACATAGTGTTACTAGA	AAGCGGTACTCTAGAAATGAA	CAGATATGATGGCATTTATAA	CACTATATTCCCTAAAGTATA
115548	FCHO2	XM_291142	AAACATATTAATAAAGTATAA	CGGGCGGGCGCGGACGCGGAA		
115557	GEFT	NM_133483	CAGGACCATATGAGAACTGGA	CTGGATATGTATACAAGAACA		
115650	TNFRSF13C	NM_052945	CCCATGGAGTTTGGTGTGCTT	ACGGCCGGCCCTGAGCAACAA	CTCCTGTTCCTGTGCCTTCAA	CCGGGAATCTCTGATGCCACA
115708	C14orf172	NM_152307	CACCATGAGGTTCGTGGCATA	CACGGTGGAGTTCCACCAGCA	CCGCAGCGGCACGCCCATGAA	CCAAGTGTGAGTGATGAGCAA
115827	RAB3C	NM_138453	AAGGACATTTGCCAACAATGA	GTGGCAAATATGTGATCTTAA	TACAAGATTGGTCAACTCAAA	ATGCAGTACAAGATTGGTCAA
115861	TXNL6	NM_138454	CCGCATCCTGATCCGCAACAA	CCGGCTGGTGCTGCTGTTCTT	AGCCCAGAGGTTCGAGATCAA	CTCAAGGACATGCCAAAGAAA
116068	LOC116068	XM_371760	TAGCAATTAGCTCATAATCAA	AAGGAGATACATTAAATGCAA		
116093	DIRC1	NM_052952	TTCGTTTGTACTCATACTCAA	CAGAGTTTCTCTTGCCCTTAA		
116115	ZNF526	NM_133444	CACGGAAGACTGAAGCAGAAA	CAGAGATGATGGAGATGTCAA		
116143	LOC116143	NM_138458	CACCGGCGTCATTCAGCTGTA	AAGGAGCACCTGAAATTGTGA	AAGGTGTGGGACCCAAGGCAA	ACGGTGGGAGACAAACATCAA
116166	LOC116166	XM_007651	ACCCATGATGCCATACCTACA	AAGCCGAAGCTCAGAGAGGAA		
116173	CKLFSF5	NM_138460	CTAAGTCATTCCCAAATTAAA	CAGGATGTGGCTTCTCATGAA		
116225	ZMYND19	NM_138462	ATGGGAAGGGTAGAAATTACA	ATCATTTGCTGTAATCCTTAA	CACGGGAGTTGTGTCCACAAA	CAGGACGGTTCTCATTATTTA
116285	BUCS1	NM_052956	CCGGAGGAATTTAACTTTGCA	AACATTGGCATCAGAATCAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
116362	RBP7	NM_052960	CAGGCTCACCTGTATCCAGAA	CAGCGACAACTTCGAGGGCTA		
116441	LOC116441	NM_138786	CTGGAGAATAATAACAACTAT	CAGCAATAAACTCACCAACTA		
116443	GRIN3A	NM_133445	CTGAAGAACGATCCAGAGAAA	CAGAGATTACACAGAGCAATA	ACCGACGGAAATACATCTTTA	CACCCAGGGAATAACAACTTA
116447	TOP1MT	NM_052963	AAGCCGGTGTACAAGAACTTA	AGCAGCTAAGATCTTATCCTA	CCAGACGAAGATCCAGGCAAA	GTGGAGAAGATCTACAGCAAA
116511	MAS1L	NM_052967	CCAACGGGCGTTAGCAGATAA	CAGGGTCGATGTGGAAACATA	CACGAATCCCTACATGGTATA	AGGGTCGATGTGGAAACATAA
116541	MRPL54	NM_172251	CAGGCCCTGGAGGCCAATAAA	CCGGATGCTGAGTACCCTGAA		
116841	IMAGE3451454	NM_053052	CTCCAGCATAGTTGAGATCAA	CAGCGGTTTATTGGAAAGCCA		
116844	LRG1	NM_052972	ACGGCTACATCTAGAAGGCAA	ACACCCTGGTATTGAAAGAAA		
117065	PRRXL1	XM_060970	CAGAGAAGAGCTCGCCATGAA	CCGGACGACGTTCACTCTTCA		
117194	MRGX2	NM_054030	CTGGTTAATGTTTAAGTTAAA	TACCAGATTTGAGTCACTAAA	CCGAAGAACTCGGAGCATTTA	ATCAATGTCAACACATATTTA
117248	GALNTL2	NM_054110	CTGGGAAATGATTATTACATA	CTCCAGGATACATAAATTCAA		
117283	IHPK3	NM_054111	CTGAGATACGTTACCCAATTA	AAGACTGGTGGACAAGTGTAA		
117285	DEFB118	NM_054112	CACCAATATGTAATTCTATTA	CAGCTGTGTAAAGAAGTCTAA		
117286	CIB3	NM_054113	TGGCAGCATGCCCGAGCTGAA	ACTCTGGTTTCTGAGAATAAA	CTGGAGCAGACGGTGACCAAA	CACGAGCAGCTGGAAGCGTAT
117289	TAGAP	NM_054114	CAGGAGAGCAGCCAACGAGAA	CTCACTATTCTATGCCTTAAA		
117579	RLN3	NM_080864	CAGGTACATGCTGCTGCTGCT	CCGGTGGAGACGATCAGACAT	CCCGGTGGAGACGATCAGACA	CCGGATGCAGATGCTGATGAA
117584	RFFL	NM_057178	TCGCAACTTTGTCAACTACAA	CCGGCTATACAAGGATCAGAA	ATCGGTTTCTTCAGTGCCTTA	TTGGTGAGAAATGAAATACAA
117854	TRIM6	NM_001003818	TTGAGATGTGCTCAATGTATA	CAGCTGTTGAGTGAGCTGCTA	CTACACTTTCTCTAAATATTA	TAGGAAGTTCTGATCTGTTAA
118425	GDEP	NM_058168	AAGAACTTAATGTGTAATTAA	AGCGATGTGCTGTGAAATCTA		
118426	LOH12CR1	NM_058169	CCCGATGTCATCAAGTTGCAA	ATGGATGATATTGTGGTTGTA		
118430	LOC118430	NM_058173	CTGCAATTGGTCACAACTATT	TCCTGTGATTTCATCCAACTA		
118442	GPR62	NM_080865	TAGGCTCCATTCTGCCATCTA	ATGGGCAGGTGTCACAAAGAA	CTGGACCAGTTTGGTATTAGA	CCCTAAGGGCTCACAACCAAA
118472	ZNF511	NM_145806	CCGGTTTGATAAGCCAAAGAA	CACGGAAATGTTTGCTCCTTT		
118670	FAM24A	XM_058332	CAAAGTAGCTAAGGCACTAAA	ATGAGCAATATTTCTTTCTTA		
118738	ZNF488	NM_153034	TGGCATATTGTTGGTGCATAA	CACATTGTGAGTATATGAATA		
118788	PIK3AP1	NM_152309	AAGTACGAGTGTAGTTATCTA	TCCCATGGGATTATTCTCTAT	CAGCAGGGTATTTAAGTGCTA	ATGCTCAAGAGTCACATTAAA
118812	C10orf83	NM_178832	CAGCTGATAAGTATTGGGTAA	CAGGCTGTCTTCTTTCATCAA	CAGATTGTGGTGGAAGTTATA	AAAGGTGTTTATAAAGAATAA
118856	MMP21	NM_147191	ATGGTGAGATTTAGCACATAT	AAGGATCAGGCCCTCACAGAA	CCGCTTATTACTCCTATGCAT	CACACTGAACATGTAATAAGA
118945	LOC118945	XM_497242	ATCCATATGAAGGAAAGGTTA	ATGGACCAAGTGGAAGGCAAA	CAGGAATACAGCCAAGGGAAA	CAGCTTCACAATGGCCATGAA
119016	CTGLF1	NM_133446	CAGCATAGCCTCGGCCTAGGA	CAGCGGGAGTGCGTGGCCAAA		
119391	GSTO2	NM_183239	ACGGCTTGTCTTGGGAACCAA	CAGGAATTCAGCAACCTGGAA		
119764	OR4X2	NM_001004727	CAGGTGTGTACTGTCCTTGTA	CTGGCTGAAAGGAAAGTCATA		
119775	OR52P2P	XM_061677	ACCACCTTACTTGGCCATGAA	CTGCATGCTATCCACCATTGA	CGGCACATCCACATCCTTCTA	AAGCAGCTGTCTTATGGCATA
120105	LOC120105	XM_061864	GAAGATCTGTTTATAAACTAA	CACCCACAACATACTCTGTTA	TACGATGTGAGCATAAGTGAA	CCGATAGATGTGGAATACAAA
120114	FAT3	XM_061871	CACCATGCTCGGAACCTGTAA	TGCAAACTAAAGGAAACTTTA		
120318	LOC120318	XM_497316	GAGGCTAAAGAGAAGCATCAA	AACAGTGGGAACGACAAACAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
120793	OR56A4	NM_001005179	CACACTCTACTACGTCTAGAA	ATCCATTGAGATACCCGTCTA		
120796	OR56A1	NM_001001917	CTGTGATAATTTCACCCTTAA	AAGAGCTGTGCTTAGATTCAA		
120824	LOC120824	XM_062300	AGGGATTCAGAGTTTATCTTA	AAACCTGAATATGGCAACCAA		
120863	DEPDC4	NM_152317	CAGGATATGAAATGATTTCAA	CAGCATCTCTCTGAAACGAAA		
120872	LOC120872	XM_497349	GAGGAGTTAGCTGCATTTAAA	CAGGCTTATTAGAATGAACTA		
120939	FLJ31166	NM_153022	CAGCACAGCCATCGACATTAA	CCGCAGCACAGTGCTAATCTA		
121275	OR10AD1	NM_001004134	CTGGTTCTTTGGGCTGATCAA	CTCAGTTTAGTCTGTGGGCAA	CTGGTTCTTTGGGCTGATCAA	AGCTATGTTCTCTTACATGAA
121278	TPH2	NM_173353	AACGTGAAGCTGCTACCGAAA	ATGAAGTTGGTGGATTGGTAA	CTCAGTATACTTCAATCCCTA	CTGAAATAACGTATTATGTTT
121504	HIST4H4	NM_175054	CAGAATGTCTGGGCGAGGTAA	CAGCTTCTCTACAGACTCCAA		
121506	FLJ32115	NM_152321	AACAACCTGCATAATAAATAA	CTGGTGGACAGTGGTATGAAA		
121512	FGD4	NM_139241	CCGGTATGAGATGCTCCTTAA	CAGAGTCATTCTACCGATAAA		
121793	MGC35169	NM_152324	CAGCAGCAAGTTAGGGCTGAA	ATGATGTAACAGGGACAATAA		
122585	LOC122585	XM_063202	CACATATGTGTTCAGGGTGGA	CTGCGACTCGAGGCCACCCAA		
122664	C14orf8	NM_173846	CTGCGTTTGGAGAATCATCAA	ACGGGAAGAGATGACTGACAA		
122773	KLHDC1	NM_172193	CAGGCTTTATTTAAAGGATAA	CAAGTTATCTCTGAAATTTAA		
123624	FLJ32310	NM_152336	CCAGGTGATGTTATAAATAAA	AAGGAGGATCTTCTTGGCAAA		
123688	LOC123688	XM_058719	AAGACACTGCAGAGATTCCAT	CAGTAAAGATGTGTTGAATAA		
123803	NTAN1	NM_173474	TGGCATTGCTGTCAACATTAA	CAAGAAGATGACATTCACTTA		
123876	LOC123876	NM_001010845	TCCAGCATGACTAGAATATAA	CACCGTTAATCTGGGTAGGAA		
123879	MGC48972	NM_173475	CAGGAGTTATTTATTATCTTT	TAGGTTGAATTAACATTACAA		
124044	MGC26885	NM_152339	CAGGAAATGACCTGACCTCAA	AACACTCAGAGGGACGGTCAA		
124274	GPR139	XM_064062.4	CTCCATCTTCTTCATCTTGAA	CCGCATCATCATGATTCTTTA	ACCGTTAACCATTGACAGGTA	AAGAATTGTCGTGCACCTCAA
124402	LOC124402	NM_145253	AAGAACGAATTCCAAAGCAAA	CACCATGTTCTCCCGTCTCAA		
124446	LOC124446	XM_378175	AGCCCTAGAATGGGTGAGGAA	TTTCTCAGGTGTGAATCAACT	TGAAGGCCTTGTGCTGACCAA	GGACAACTGGTCCTTATCACA
124460	SLIC1	NM_153337	CAGTACTGGCAGAACCAGAAA	CTGGCTGCATGGGACCCATAA		
124512	LOC124512	XM_497558	TCGGCAAAGCTGCCAAATGAA	CAGGAAGACATACAGTTGAAA		
124535	FLJ40311	XM_064190	TAGAAATATTACAGAGATCTA	TAGGAATATGAAACTAATTAA		
124538	OR4D2	NM_001004707	CCCGCTGGTTTGAGAGTGACA	CTCACCAATTTGCTTAAATTA	CTGGATGGCGTTATGATTTCA	ACCAATTTGCTTAAATTAGTA
124602	FLJ37300	NM_153209	CGGCCGGGCCAAGAACATTAA	CACCGAAGTCTCCACCATCAA	CCGGGAGAAGTCCTACCTGTT	CCGGGTCAAGAACATCTTGCA
124637	FLJ32499	NM_144607	CCGGAGCATCCGCATCATTAA	CAGGAAGATGGGATTTACAAA		
124641	OVCA2	NM_080822	CAAGGCCTTAATGGACATTGA	ACGATGGTGACTGCCACATAA		
124783	FLJ25414	NM_152343	CCGGAGTTTCACGGAGGAGAA	AACGAGGAGTCTGACTTTGAA		
124808	FLJ31795	NM_144609	AAGGAGCAGAAACATAATCAA	ACCACATTAAATTGTAAATAA		
124817	FLJ40137	NM_173478	CAGCAACATTACAGTCTTGAA	CAGCAAGTGCTTTCATCCAAA		
124930	FLJ25555	NM_152345	CCCAAGTAGACTGGACACAAA	CACCAAGACACAGAAGTTCAA		
124935	SLC47A2	NM_152346	TCGGTGCTAATTCCTTTGTAA	CCCGCTCTACCTGATCTGCTA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
125058	TBC1D16	NM_019020	CAGGGACATCTTTGCAAGCCA	GACGATAGAAACCTAAGGAAA		
125111	GJC1	NM_152219	CACAGCATCCTTGACAGCTAA	CCCGGTGCTGTTCGTCGTCTA		
125206	SLC5A10	NM_152351	ATGGGTGTTCGTGCCCATCTA	CAGCGGGCAACTCTTCATCTA		
125476	C18orf37	NM_194281	AAGGTGTTTGACAAGAAGATA	CTGGAAGAACCTGAAACAAAT		
125875	MGC33839	NM_152353	CACCGTGAAGAATGCGTGGAA	AAGTCTCAAGGTCTCCAGTAA		
125950	RAVER1	NM_133452	ACGGACCTTTGCTGAATTAAA	CCAGCACTCCATGAAGATAAA		
125958	OR7D4	NM_001005191	CTGTGTGGTCTCCTTGTTCTA	CTCAGATTGTCTCCTCCTTAA	CTGCTCTAACACCCTCCTCAA	ACAGATCGTGTAGAAGAGAAA
125963	OR1M1	NM_001004456	CAGGAAGCTGGTCAACAGAAA	CAGCGTCATAATCGCCATGAT		
125972	CALR3	NM_145046	CACGAACATTACTTCAATCAA	CTGGAACTTAACATCACTCAA		
126014	OSCAR	NM_130771	AAGGAGTAGCTGAAAGGAAGA	CCCGCTGTGCCCTGTGCTGTA	CCCAGCTTCATACCACCCTAA	AAGGTAGTAGTGAGACGTGAA
126037	LOC126037	XM_058967	AAGGCCAAGAAGCCTGCATTA	CTAGAAGGCCCTTTCATCAAT		
126074	FLJ35119	NM_175871	CCCAATCAATATGTTGTTTAT	CAGGGACATATGCAGATCCAA		
126119	SBBI54	NM_138334	CTACTACAACCTGGACTCCAA	ACCGGCAACTATGATGTCAAT	CTGGGAAAGGCCAGCACTTCA	CTGCCGCTGCTGCCTCAATAA
126133	MGC10204	NM_153329	AAGCCTGAACACAGAAATTCA	CAGGAGTCTGTGTGGGATGAA	CCGGCTGTCCTGCCTCTCCAA	CCCAATAAACTCTCTGACCAA
126205	NALP8	NM_176811	CAGGAAATGGGTGTTAGGTAA	CTGAGATACTTGGAAATACAA		
126353	C19orf21	NM_173481	CCCAAACTGCCCTGAAATAAA	TTCCGTTTCTATCTTCCTTTA		
126374	WTIP	XM_059037	CACCGTGGACGTGGAGAACAA	AAGGACAAGATTTGACTTAAA		
126402	FLJ40365	NM_173482	CACCTTGGTAGAAATGGCAAA	TTGGAGCTGAAGGAAAGATTA		
126410	FLJ39501	NM_173483	CGGGAGCTGGCCCTAAAGCAA	AAGGACCTGAGTGCAAGTAAT	CTGGACAACATGCACCATGTA	CAAGAGAAGATGAGTGATTAT
126526	FLJ36888	NM_178830	CTGGATCTCAATAAGGAGATA	CGAGGTCAAGGTCACCATTAA		
126537	LOC126537	XM_497611	CTGGTTCATGACTTCACAGAA	AAGGAGTTGTCTGATGAGGAA	CTCAGCCACCATTGCACCAAA	AAGCCGGAGGTCATAATGTAT
126626	MGC29891	NM_144618	AAGGAAATATACAGAAGACAA	CACCAATATATATGCCTTTAA		
126661	LOC126661	XM_059061	TTGGCAGTTGGAAGCTGTTAA	CCGCTAGGAGAGCAAGCACAA		
126792	B3GALT6	NM_080605	CCCGTCTCTCACGTACTTTAA	CCCGCTGCTGCCCGTGTTTAA		
126823	KARCA1	NM_001007255	ATGGAAGCATCTACACATTAA	CAAATGCTTATTAAATTTCAA		
126859	DKFZp686H1423	NM_144696	CCGGAGGAGTATTTCAAATTA	CTCAAGATTATTAAACATTTA		
126868	FLJ38716	NM_152367	AACCAAGACATTAGATTTCAA	AAGGCATTGGATCAACACAAA		
127059	OR2M5	NM_001004690	CTCTATGGATGCAATCATTGA	ACTCAGGAAAGTGTTAGGAAA		
127247	ASB17	NM_080868	AACAATGAGTAAATCTACTAA	AACCTCGACTTCACTGAAATA	CTACTGCAATATGGAATCTTA	ACCATCAGGAATCAACTATTA
127281	MGC26818	NM_152371	CACCATTGCAGTGGCCATTTA	CCGGCAGCAACGAGCCATTAA		
127385	OR10J5	NM_001004469	AGGCCTGATATTTATCTCCTA	ATCAATGAGATAATAAATTAT		
127602	LOC127602	XM_059166	CAGGCTCATTTGGGAATTTAT	CCCAATTTAAACATAGAACAA		
127623	OR2B11	NM_001004492	CAGGTGGTCCTGACGGTGCAA	CCCAAGAGCAGGGCAAATTTA	ACCGCTGTGAATGACACCATA	AAGCCTTATCCTCGGAAGTAA
127670	HE9	NM_172000	ATGGATCATGGTTATGTTTAA	TTGGCTTCATTTCAAACTTTA		
127733	UBXD3	NM_152376	CACCAGGACTTGAGCACATAA	CTGGTAAATAACCACAGTGTA		
128077	MGC46719	NM_153713	CCGATTCATGCTGGAATCCAA	AGCCATTTCAGTAGCACTAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
128136	LOC128136	XM_497739	TTGAGCCAAATGCAACTTTAA	TGGGATAATGCTGCAATCCAA		
128239	IQGAP3	NM_178229	CACACGGACCTGAGCAAGCTA	ATGGTAGGACATGGACCTTGA	GAGCACTAAGACCACCTTCTA	CTCCGTGGTTCCGTTGAAGAA
128312	HIST3H2BB	NM_175055	GCGCCCAAGAAGGGTTCTAAA	TTGGAGAGACTCAGCCATCAT		
128322	LOC128322	XM_060943	AAGAACATCAACGATGGCTTT	CAGGTTTGCCCTGCACAATTT		
128414	C20orf58	NM_152864	CAGCGTCAAGAGAGTTTGTAA	AAGTTGGTAAATAAACAGGAA		
128486	C20orf142	XM_371399	CTGGTAAGACTTGACCTTTAT	AAGCAAGATAGTTACAAGAAA		
128497	C20orf165	NM_080608	ACGGAAGGAATACAGCCGAAA	CTGCTTGTAGATGGATGAAAT		
128853	DUSP15	NM_177991	CCGAAATAAGATCACACACAT	CTGGAGGGTATTAAAGAGACA	CACCACGATTGTGACAGCGTA	ACGGGCCTGGAGGGTATTAAA
128859	BPIL3	NM_174897	CCCGGACTTTCTGGCCATGAA	CTGTAGCTTATCCCAAGTCAA	CCTGGTCAATGTGAAGACTAA	CTGGCTGAGCTGGACATAGTA
128939	LOC128939	XM_066243	CAGCAGGTGTTTGTTGGGCCA	CAACGAGTGCATGGATGGAAA		
128989	DKFZp761P1121	NM_152906	CTGGATGTGCTCAACAATAAA	CAGGAGTAGGCTTGTATTTAA		
129049	RUTBC2	XM_059318	ACGGACTTTGCTTAAATCCTA	CAGGTGAGAATTCTTGAGCAA		
129285	LOC129285	NM_152994	AAGGAAGTTCATGTCAATAAA	AAGGCTAAACTAGAAGTGAAA		
129530	LOC129530	NM_174898	CTCAAATGTTACACAGATAAA	CAGGTTTCCCAGACAACTGAA		
130063	LOC130063	XM_059396	CATGACTTTATTGTCTTTCAA	CAGCAGAACTGTGGACAGCAA		
130162	FLJ31438	NM_152385	CAGAATGGCTTTGACAAATTA	ACGGTTAGATTTAGTTACCAA		
130399	ACVR1C	NM_145259	AAGTGTGAAACTTGTGCCATA	CAGCAAATAGATATTCCTCTA	CACAGAGTAATGAATATTTAA	TACTTTGGTAAACGAGATTTA
130576	LOC130576	NM_177964	CACATTGGACCTCAAGGCGAA	CAGGTCAAACCCTCTTGTTTA	AAGACAAATGGTGTCCACAAA	AACGGTGAACTTTGGAGTGAA
130940	LOC130940	NM_138803	CTGAATGAAGTCAGATGTAAA	CACGAGAAATATTGTGACCAA		
131034	CPNE4	NM_130808	CCGAACTGAGGTTGTGATGAA	CAGCGTCAGAGGAAACTAACA	CACCAAGGAGGCATCGCAATA	AATGTTGATAGACGAAATATA
131096	KCNH8	NM_144633	TCGCACGTTATTTGCCATGTA	TTGGAGCAAATCTATCAATTA	CAGACTTTGGTAACAATCCAA	CAAGACTATCAAACAAATCTA
131118	TIM14	NM_145261	ATCAATGAAGCTAAAGATTTA	TAGAATTTATACACTAATAAA		
131601	GPR175	NM_016372	TACCCTGATGCCCATCTCTCA	CACCATGGTGGATGGACTGAA	TCGGAGGAGCTTCTACGTGTA	CAAGATCCTCTTCTCCTACAA
131616	TMEM42	NM_144638	AAAGCCAGTCATGTAACTCTA	ACGGACCAGCTGGAAAGATCA		
131973	LOC131973	XM_497912	CAGGAAGGTATCCTCCATGAA	CTCGGCCTGCTGCATGCACAA	CCCATCAGAGGCAGCACTCAA	CCGGAGTCCGCGGTTACTCAA
132001	MGC16471	NM_138807	CTGGAGTTTACTACAATTCAT	ATGGTGGTTGGAGAAGATAAA		
132320	FLJ30655	NM_144643	CAGCTGGAAATGGCAAATGAA	AAGGTTGCACAGTGAATTAAA		
132332	FLJ30834	NM_152399	AAGAATGGTATTTGGAATTAA	CAAGATTGTCTGAGAAATGTA		
132671	LOC132671	NM_145263	CAGCTTTGAGATAAATGTTAA	AAGGCTAAGTGTAGAAGATAA		
132789	GNPDA2	NM_138335	AAGCGTGTAATAAATAAGTTA	CTGGCTATTTATTATAAAGTA		
132946	ARL9	NM_206819	CTGGAGATTGGTGGCAGTAAA	CTGGGTAATAGTCAACTAATA		
133308	LOC133308	NM_178833	ACGTACAAAGACTGAGACAAA	GGGCTGTAGTTTGGTCAATTA	CAACGATAATGTGCAGATCAA	CTGCAGAAAGTTGAACATCAA
133396	IL31RA	NM_139017	CTGGACGATCCAGCAAGATAA	TTGGGTGTCTATGATTTCTTA	AAGAATAACGATCCCAGATAA	CGGGACCAGCATAAATTTCAA
133688	FLJ34658	NM_152404	CACACTGACACTTACAATGAA	CTCAATGTAGTTATTTGCTAA		
133746	JMY	NM_152405	TTGGATAACATTAGATCCAAA	ATGGCTGTACTGTCTATTCAA		
134145	LOC134145	NM_199133	CCAACTGTTTGTAGTATCCTA	CACATCTTTAACTAAACTTAT	CTGGGATAATGGTACACATAA	CACCTAGTCTTTGGTCCATAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
134391	GPR151	NM_194251	TGGAAATGGATGATAACCAAA	AGGGAAGGCTTGAAAGGTGTA	CTCCTTCACAATGCTTGGAAA	CCGAGCTACGGCGTACTCCAA
134466	LOC134466	XM_376436	CAGGGTCAGTTCAAGCCTTAA	CAGGCAAGTTGTAGTCATCAA		
134505	LOC134505	XM_068889	CCCAGCAGATCTTCATCTGTA	CCAGGGTATCAACAGGAACAA		
134860	TRAR3	NM_175057	CTGGCAGCGTTTGGAAACTTA	AAGCATCAGGCTAGGAAGATA	TAAGGACTGATTCGTCAACAA	CATGGTGTTTATATACAGTAA
135112	NCOA7	NM_181782	ATGGATATTGACTATATGTAA	CTCCATAGCACTGAAATTTAA	AACAATTATTATACTCCTTAA	CCGGAAATCGGCATCACTAGA
135295	SRrp35	NM_080743	CACAGTCAAGTTCACCTCAAA	AACTCTCATTATGTTAAATAA		
136242	LOC136242	XM_059830	CAGGAATTCCTTATGTGTGAA	ACGGTACTGAACAGACAATTA	ACCAATGTTTACAAATATGTA	CACCATGAAATATGTCTTCTA
136306	LOC136306	NM_174959	CCGCTGGAAGGTTAATCATAA	CGGGCCCTCCAGCAAATTAAA		
136371	ASB10	NM_080871	AGGGCTTGAGTGAAAGGAGAA	ATGGAGGGATTTCCGCTTCAA	CAGCGCCAAGACCATGGACTA	CCGGGTGATGTCTGATGAAGA
137075	CLDN23	NM_194284	TAGCTACATATCATTGCATAA	CAGCAGCTTAATGGATTTCAT		
137362	MGC33309	NM_152413	CAGCTTGTTAAAGACCTACAA	CAGCTGTATCAATGCCAACAA		
138050	FLJ32731	XM_372038	ATGGATGTCTTTGGAACTTCA	CTGGACCAACTTGACCGTCTA		
138162	C9orf116	NM_144654	CTGCCATTTCACATCTAATAA	CTCCGTGTACAGGACCAGTAA		
138199	C9orf41	NM_152420	CCGGAAATGCATTGATCATAA	CACAATGTAATTGATTATATT		
138240	C9orf57	XM_059954	TACTGCATTAATTTAATTTAA	CACATTCAAGGTGGCATTCAA		
138428	C9orf115	NM_001002913	ACGGCGGCTTATGAACGCCAA	CCAGGCTGCCTGCGGATTAAA		
138429	PIP5KL1	NM_173492	ATGCTGGAACCAGGACTCAAA	ATCAAGATCATTCAGCAATAA	AAGATGGAACTGGATACCACC	AACGTCTCCACGAGGATGAGA
138639	PTPDC1	NM_152422	AACAGAGGGTTTCAAAGCATA	AGGCTATACATAAGTATTGTA	TACGTAGATACCAGAGGCCAA	CGGAATGTTGAGTGCCTTCAA
138724	MGC41945	NM_203299	CAGGAGAACCCTCAAACTCTA	CAGAAGCTACATGGAAGGATA		
138805	OR13F1	NM_001004485	CCGCTGTAGATTCACAGGAAA	TCAGTGGAAGGTCGAAGTAAA		
138864	LOC138864	XM_498304	TACCTGAGAATAAACCATCTA	TTGGGAGAGCATATCCCGAAA		
138883	OR1N1	NM_012363	CAGGAGTATTGTTTCCTCTTA	CTGCGTTGTTTGTGTGTTCTA		
139105	CXorf20	NM_153346	CAGCGAATTATCCAACTTTAA	AAGGTAGAGAAAGAAATTCAA		
139135	PASD1	NM_173493	ATGTTTGTAATTGTTTGTTAA	CAGCCTGTTTCTTGGAAGTTA		
139231	CXorf39	NM_207318	CAGGTGGAATATATTGAGTAT	TTGGTTATTAATAGAGCTCTA		
139411	PTCHD1	NM_173495	TCCGTGGAGTTTGGAGTGATA	CCCGTGTGGTTGACCAAATTA	AAGGATTTCACAAGAACTAAA	TCCCGGTTTGAGAGCTATTTA
139562	HSHIN6	NM_207320	CAAGACGACAGTAGCATTGAA	TGCGTATAACTTCACCACAAA		
139604	LOC139604	XM_498354	TGGGATCATGATGAAGGACAA	ACCCTTTGACACTGAAATAAA		
139760	GPR119	NM_178471	CAGTCTCTGCTTCACCTTGAA	CGGGCTGTGGTTAGTGTCTTA	CAGGAGTGTCACCTCTACCTA	CTCCCTCATCATTGCTACTAA
140432	ZNF183L1	NM_178861	ATCCCATGCCTGAGTATGTAA	CACTGCAGTATTATTTGCAAA	AACGGGAAGGAAATCCTCTTA	AAGGATCACATGCTACAACTA
140469	MYO3B	NM_138995	ATGGCCGTACACAGACTTCAA	CACCCATTTATTAAAGGAGTA	ACCCTGGTTGATAAATTTGAA	AACCAGTTAAATGGAACTCTA
140545	RNF32	NM_030936	CAGTATCAAACCCGAGTGATA	TGGGTTAAGTACTACAATGTA	CCGCTAATAGTCTGTCCTAAA	TTCAGTGGTATTCAACATCAA
140576	S100A16	NM_080388	CAGGGAGATGTCAGACTGCTA	CACCTGTTCAGTCTCATCTAA		
140609	NEK7	NM_133494	CGGACAATTTAGTGAAGTTTA	CCCATTTATGTCTGGTGTTAA	CCGGATATGGGCTATAATACA	ACGACCGGATATGGGCTATAA
140612	ZFP28	NM_020828	AAGGAAATTATTAAACTATAT	CCGGGCTTGGTGACTATCAAA		
140628	GATA5	NM_080473	CTGGGTTGGATGATACCTTAA	AAGGGCCTTGTTCTAGCTGAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
140706	C20orf160	NM_080625	CACCATGGAATATGAAGTCAA	ACCATACTAAACAGTGTAGAA	CTGAGGGTTAAGACCTTAGAA	CACCCGATAAGAGCTCAATAA
140730	RIMS4	NM_182970	GTAGCTCATGTTGAAATTAAA	CAGAGTGGACAGAAAGCATTA		
140766	ADAMTS14	NM_080722	CAGCACCGACTTCTTCATTGA	CACCGGCAGCTTCATCCTCAA	CAGGAGTGTGTGTACACTGGA	CCGCTTGATCATGGTTGGCTA
140803	TRPM6	NM_017662	CACGAGCCTATTGCTCACTTA	AACCTGAAGTCAAACAATCAA	GAGCAGAATCCTGCACATTAA	TTGCCCAATTGCCAAACTAAA
140809	C20orf139	NM_080725	CACCTTCTATCAGAAAGTAAA	ATGGGTATTTATTTGGATAAA		
140823	C20orf52	NM_080748	AACCATGGTTGCCAACTACAT	CTGATGGGCGGCATTGGGAAA		
140862	C20orf82	XM_097736	CCGAGTCACTTCGGTTTCTAA	AAGCGAGTTCTTAAAGAAGTA		
140870	WFDC6	NM_080827	CAGCCTTACTTTATACCATAA	CAGGATTTGGCTCATAATCCA		
140873	C20orf173	NM_080828	CAGGAGGAAATTGTAAGATCA	TTGGATCAGAATAGCAAGGAA		
140876	C20orf175	NM_080829	CACGGAGTTGGGTACCATCAA	CAGGAAGGGCTCCTTGTACAA		
140880	CST11	NM_080830	TAGGCAATAAATGTTTGTCAA	CAGGATCTTCCGAGTCCTTAA		
140883	SUHW2	NM_080764	TCAAATGTTTAAGAAGCCTAA	CAGTGGATGTAGCATCCATAA	TAGCCGTTAGTGGAGAATGAA	CCCAACTTGAATCGAGATCAA
140885	PTPNS1	NM_080792	CCCGAGAAGAATGCCAGAGAA	ACGCCTGTAAATTACTGAGAA	CTCGCTGTGGACGCCTGTAAA	CGCCTGTAAATTACTGAGAAA
140901	STK35	NM_080836	CTACGTGTGAACAACTTTATA	GACTGAGGCTTTGTAAATTAA	TTGGGTTGGTATGATACATTA	CTCGGCTGTTAGGGATCTGAA
142679	DUSP19	NM_080876	AAGGTCATATATACTATACAA	TACGGTCCTCTTTCTCACATA	CAGAGTTAACCTAATGAGTCA	ATGGTCAGTATCACTGGATAA
142686	ASB14	NM_130387	CCGGTTAACTGCCTCCAGATA	AAGGCTGGACATGTACAGTTA	ACGACCTTTATGGACAAGGAA	CTCACTATATATTATAGTAAA
143187	VTI1A	NM_145206	TCCCATAAGAAGATAATTAAA	CAGAGCTTTATGATTCTGTAA		
143379	C10orf82	NM_144661	TTGCATGTCATTAATGATAAA	TCCCAAGGAGGTGAACTTTAA		
143458	LOC143458	NM_174902	CAGCACCTCTAGTTAGAGTTA	CTGCTGGGTAGTTACCTTATA	AAGGGACTATTTATATGTGTA	AACCTGTTTGACGCTAATTAA
143503	OR51E1	NM_152430	CTGGTTCAATTCCACTACCAT	GCCCTAGGTGTCAGTGATCAA	CTCATATCTGCTTATTCTTAA	CAGTTTGATGCTTGTCTGCTA
143872	FLJ32810	XM_370651	GTGGATCTATTCAAAGCTTAA	ACCGGAAATGTTTAAATTAAA		
144106	FAM10A5	NM_153291	CTCTAATTTGAGTGAAATAAA	ATAAAGCCCTGCTGAAGGAAA		
144195	SLC2A14	NM_153449	AGGGAGTCAATTCCTAGGATA	CAGAGAGATGGACAACAGACA		
144203	OVOS2	XM_495917	ATCCAGTGAGATCCAGTTTAA	TAGGCCTGATATTAATAGCAA		
144348	ZFOC1	NM_152437	AAGGAATGTTTAGAAGACCAA	CAGCGCATAAAGGAGATTTAA		
144360	FLJ32894	NM_144667	ACAGGATTTCATACTTATTAA	CTGCAGTAGCTAAGACTATAA		
144631	LOC144631	XM_096642	TTGGAGGCTAAAGGAAGTAAA	CAGCAGTTATTTGGGTGTGAA		
144742	LOC144742	XM_378388	TACGTTGTTGTGGGAGATTTA	CAGGGAATTCACAGCAAACTA		
144809	FLJ40919	NM_182508	CAGCATTATGAGGATTTACAA	CACAATGTCAATATACATTAT		
144962	LOC144962	XM_084990	TTGCAATATTATTAGATTAAA	CAGCAAGGGTATATTTATAAA		
145173	B3GTL	NM_194318	AACCATATTATTGATGATGAA	AAGGAATAATACTGTACATAA		
145389	SLC38A6	NM_153811	CCCATATACTGTGAACTTCAA	AAGGTTATAGTAAATACTTAT		
145414	LOC145414	XM_085138	CTTGGGATTTACAGCAATTAA	CTGCATGATGTCTCACAGAAA		
145501	THSD3	NM_182509	CAGCACCGACTTCTCACCTAA	CAAGAGCGACTTCCTAATCAA		
145645	MGC33951	NM_152448	TGGATGGTTTCTAATAATAAA	CAGAGCCTTGATTACATAGAA		
145660	LOC145660	XM_085200	CCAGCTCATTTGGTCACATAA	CCGGCTGAGGTGTTCAATAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
145773	MGC26690	NM_152450	CAGGAATACTTTAACAATTAA	TCCCAGTAGATTAGACTTCAA		
145790	UNC13C	XM_496070	ATGCAGTAGGAGAACAATGTA	CACTGCAAGCTAAATACATAA	ATGGGAATGTTTAGTTCACTA	CAAGCTGATCTAATACGTTAA
145846	LOC145846	XM_096883	AAGAAATTCATCAGCCTTCTA	CAGATCAGTGGCAATCATTTA		
145853	LOC145853	XM_096885	CCGCTTCTTCACGGCGCTCAA	AACCTCGGTATTCCAACTTTA		
145946	SPATA8	NM_173499	CCCACTGATTCAGAAGATAAA	ATGGTGTATTCTGGATGTCTA		
145978	FLJ31461	NM_152454	CCAGTAATGAATAATCATTAA	CACATGTGTCTTCACATTCAA		
146057	TTBK2	NM_173500	AGGCATCACCTCAAGATGAAA	AAGAGTAAGCCAGCCAGTAAA	CACATTGGTCATGACATGTTA	ACGGCCCAGGTTAAATGGAAA
146059	CDAN1	NM_138477	CAGCATGAGCCCAATGATGAA	CCGGAGGATGGTGACTGCCAA		
146110	LOC146110	XM_018432	CAGGGACTCAGTATGAACCTA	CAGCATTCTATGTGCAAGATA	CAGTATGAAGCTACTGTCAAA	CTGCAGTCGTTCCGACACAAA
146167	LOC146167	XM_085347	CGGGCTGGTCATCCTGGGCTA	CGCTGTCTTCATCCTCATGAA		
146310	RNF151	XM_370927	CCGCCTGGAAGTCAAGTGCAA	CAGGGCCAACATACCTTGTAA	AAGGTTGTCCACATGAATAAA	TCCGGTGGCTAGCCAGACAAA
146378	FLJ25404	XM_375333	CCAGTTCTGCACCCACATAAA	GCCCAGTTTATTGGAGAGAAA		
146723	FLJ31882	NM_152460	CAGCACAATTTGCGATTGAAA	TCCAATCATAGTTGAGAACAA		
146849	FLJ32734	NM_144681	CCGCGCCATGAAGAAAGCCAA	CTGGGCGTTAAGGAAGCCCAA		
146880	MGC40489	XM_373742	CCGGAGCTGGCAGGTCTACAA	CTCACTGGTTATAGTGCTATA		
147011	PROCA1	NM_152465	CAGGACGACGCTCACAATTGA	CACAATTGAAAGATGGACTAA	CAGACGTGAGCCGATCATTAA	CAGGGTGGTCAGGGTGCAGAA
147179	WIRE	NM_133264	AAGCTTGGCAGGTATATTATA	CAGAGGATATATCCCAGCAAA	CAGGTATATTATATTTCATCA	CCCGCCTACAACAGAGAGAAA
147199	SCGB1C1	NM_145651	CACATGGAAATGTATCCTCAA	ATGGACTTCCTGCAAACACTA		
147339	C18orf25	NM_001008239	AAGAATCAGAATGTACCATAA	CAGTTTATTCTTGGCAATCAA		
147381	CBLN2	NM_182511	AAGGTCTTAAGGAGAAATGAA	CTGAATCATATAAGTTGGTAA		
147687	MGC34079	NM_152475	AACGTCATTCATCCACATTAA	CAAGAACTTTATGTTATCCAA		
147808	LOC147808	NM_203374	CCCATTGTGGTCCGTCCTTAA	TTCAGTTCTGTTCCTATTAAA		
147945	NALP4	NM_134444	AACAACAAGCTTGGAACATAA	AAGAAGCTAACTTTCATATTA		
147968	CAPN12	NM_144691	CACGCCCTGGGAAGAAAGCTA	GACAGACACAGGAGAAATAAA	CAAACCATCAATTAATATTAA	CAGGGCAGGGTTGCTGAGCAA
148003	LOC148003	XM_086001	TACGTGTGTCTCAATGAGTAT	AAGGTAAATGGTGAATACATT		
148022	TRIF	NM_014261	TACCACCTCTCCAAATACCAA	ATCGGAACAGAAATTCTATAA	CTCCCAGATCTTCGCCAGGAA	ATCATCGGAACAGAAATTCTA
148066	ZNRF4	NM_181710	CACGCGGTCATTCCAACTCAA	ACGGGCCGTGCTGGAAGACAA	CAGCTTTGACTCCACCACCTA	AAGAATAAAGTGGGTTTGAAA
148103	ZNF599	NM_001007247	AAGATTCATACCAGAGTTTAA	AAGAATTATATTAAAGATTCA		
148223	C19orf25	NM_152482	CAGGGTGTCCTGAGTCTCATA	CAGCACATAGACAGCGATGAA		
148252	DIRAS1	NM_145173	CTCGGCCAAGATGAACTACAA	CAGGGTTGTGTCCAACATACA		
148430	LOC148430	XM_042500	CCCTGGAGATCGCGGAGGCAA	CTCCGTGCTGGTGCACCTTAT		
148479	PHF13	NM_153812	CCCTGCCATTTAGGTGCCTAA	CAGCCTGTTAATGAACAGCCA	CAGCTGGTGGTTCTTAGGTTT	ATGGCCCGTGTTCATAACTCA
148523	LOC148523	NM_144697	CAGCTAGGACATCTAGCTTTA	CAGAAGTGTAAAGAACTCCAA		
148545	FLJ32833	NM_152488	ACCGCTGAGAGTGGACAAGCA	CAAGTGTGAAGAGTACAGGAA		
148870	FLJ32828	NM_152492	CAGAATGGAAACCGCACCAAA	CAGGAAGACGAGTGAACCCAA		
148898	LOC148898	NM_001008896	CCCTCCTTGTATATCCTTAAA	ACCCTCCTTGTATATCCTTAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
149041	KIAA2025	XM_086409	CAGCACCTTATCAGCAGGGTA	CTCCATATTCACCTCATCAAA	CTGCAAGCAATTCAGATTAAA	CAGCAAACTTGAACCGACTAA
149095	FLJ32785	NM_152494	AACAGACTCATGGACATTAAA	CACCGTGGAGCTGCAGATCAA	CAGAGACAGTGATGGAATCAA	TACAATGACCTATTGAAGAAA
149466	MGC52423	NM_182517	CCCGGCCAGCTTCTTAATGAA	CAGGCTCTGCACAGTACCCAA		
149478	LOC149478	XM_378860	CACCACAGGCTCGGCGAGAAA	CCCATTGACCTCCAGGACAAA		
149483	FLJ33084	NM_152500	CAGGAGATTCGAGAACTACAA	CCGGCGAGAGGCAGAACTTTA		
149620	LOC149620	XM_086604	AACATTCATAAGTAGGAAATA	CTGCAGAGTACAAGTTGCAAA		
149685	SMAF1	NM_174906	TAGCCACACATGCGCCATGAA	AGGGTGTGGGTCCATATTAAA		
149708	WFDC5	NM_145652	CCAGAGGCTAATTCTGATTTA	CAGAATGAATATTCTTGCAGA		
149709	LOC149709	XM_086637	CAAGAAGTGTTGCTACTACAA	CTGAGCTCTTCTAACACTAAA		
150051	LOC150051	XM_097792	CTGGGATGTATGTTCCTTACA	ACGCTGTGGAAGATAAACCTA		
150142	C21orf121	NM_198078	CCAGATCTCCGTGAAATTAAA	CCCACTGATGGTGGTTCACAA		
150147	C21orf128	NM_152507	CAGGCAAATGTTGGGAAGCAA	CACAAGTGAGTTAACATTTCA		
150159	LOC150159	NM_139173	CCTAATAATACTGCACATGAA	CATGCATACCACAGAATCAAA	TAAGAGGAGTATTGAATGTAA	CTCATTGATCCTAATAATACT
150209	FLJ30473	NM_144704	AACTAAGAAGGTCGTGTTCAA	CCGGGTGAAGTTCTACATGCA	CAGAAGATGCTCAACCCTCAA	AACATGTTAGACATTACCGTA
150244	FLJ31568	NM_152509	TCGCAGCCTGTCCTACAATAA	CTGGCATTTCTTTGATAACAT		
150248	C22orf15	NM_182520	CTGGCTGAGGATGGCAACCTA	CACCAACTCCACGCACATATA		
150291	FLJ35801	NM_153044	CACAGTGATACAAAGAATGAA	CAGGTTAGTGGTACAAAGTCA		
150353	DNAJB7	NM_145174	CCAAACATGTATCTCAATATA	CTGCGGACAATTAGTATTCAA	CAGGTTCAGACTACACAATTA	ACGACAGTCCGGGTAACATAA
150383	LOC150383	NM_001008917	CCGGGAGAACATCAATGCTTT	ATGCAGTTTATTCTACTCCAA		
150696	PROM2	NM_144707	CAGCATCATCTTTGCCGTCAA	CTGCATCTTATAAACCAGCAA		
150709	FLJ25415	XM_371586	ACGGGTATTGTGTATAGGAAA	CTCAATTACATGAACAATTTA		
151011	NA	NM_144710	CTCCAGGAAAGTAATGTTCAA	AAGGTGGATGTGAAACATGAA		
151121	LOC151121	XM_379133	TTGAATGAGTACAGTAATGAA	AAGCAACACATCTAACTTATA		
151242	PPP1R1C	XM_087137	AATGAGTTTAATTGACTTCAA	TAGGATTTATGTTATAGATAA	TTGGAACTGGTTAGTACCTAA	CTCGATCTGGAATTACAGCTA
151306	GPBAR1	NM_170699	CTACCTGTACCTCGAAGTCTA	TCGACCTGGACTTGAACTAAA	CAGGACCAAGATGACGCCCAA	AAGCCTCATCATCACCGCGAA
151313	DKFZp434N062	NM_199336	CCCGACATAGGATGAGGGCAT	CTAACAAGACGCAATGGGAAA		
151443	LOC151443	XM_087200	AAGCAAGGATTCTACATCAAA	ACGGCTTCTAATAGAGCTATA		
151449	GDF7	NM_182828	CCGGCCCTGGTCTCCACTCTA	CCACTTCATGATGTCGCTTTA	GCCGTTGCACGTGGACTTCAA	AACAACGTTGTCTACAAGCAA
151516	FLJ25084	NM_152792	TAGGAGCTCAGTACATGTAAA	AAGGTGGCCAATGGTGCTGAA	CAGGAGCTATCCCACTGAGAA	CAAGCTGCTGTTGATGACAAA
151531	UPP2	NM_173355	CAGAATAGGATTCGAGATTTA	CTCACACTAAATTAAATTCAA		
151636	DTX3L	NM_138287	CAGAGGGATATTTGCCTCCTA	AAGAGACAAGTCCTTACTATA	TGGAATGATATTCACCACAAA	TGGGCAAGCATTGGTAATAAA
151742	PPM1L	NM_139245	CTGTAGAGTCACATATATGAA	AAGCGTGAACCCATATTGATA	CTGGTGGTCTTAGGTCTATAA	CAGGACTACGAGAAAGACAAA
151760	LOC151760	XM_098117	CACCTTCAACACCACCACAAA	CCCACAGTAAACGCAAAGTAA		
151887	URB	NM_199511	TCCAGTAATATTGGCCACAAA	AAGGACCTTATTTGGCATATA		
151963	LOC151963	NM_178496	CTGCAAAGCCATCATCATTAA	AAGGGTAAGAAGGACAATGAA		
152028	MGC34923	NM_144717	CAGAATAATCCTTGAGAGAAA	CACCCAGCACTTGCAAGGCTA	CACGGACAAGGGATGAGAGAA	CTGGAGAAACAGTGTACTATT

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
152118	LOC152118	XM_098163	CAGAGAGAAGTGTAAATGACA	TAGTTGTTTGGTCACAAATAA		
152138	LOC152138	XM_093644	TTCTGCAGAGCTGGACTTCAA	CAGAACAATCTCCCTGGGAAA		
152404	IGSF11	NM_152538	CAAGAGCAGAATAGTACTTAA	AACCATTTCAGTATTGATAAA		
152485	LOC152485	NM_178835	AAGGAGAACACTGGTATGGAA	AACACAGATGGTGAAGATTAA		
152519	LOC152519	NM_207330	CAGAATTTCTACAAACTTTGA	CAGAAAGGTATAATCATGTAA		
152579	SCFD2	NM_152540	TACAAGTTCATTAGTTCTAAA	CAGGCTGTCTTTCACAATCCA		
153297	LOC153297	XM_098350	TCGGTCCTATTAAATAACATA	CTCATTTATAATAGTGCCAAA		
153571	CEI	NM_178569	CCCTGAGATTTGTGTTGTCAA	AACGGCATCGAGGCATTTCAA		
153745	MGC26988	NM_130899	ACGGAGATGATCGTCTTTGAA	AACGAAGAGAACCATGAGCAA		
154092	LOC154092	XM_379434	CCGGGTGTGCCCAGAAGTCAA	AAGCACTTAATCATACTTAAA		
154141	OACT1	XM_371801	TCGACTTGCTATCAAAGTGAA	CCGAATATACATCTTCCACTA		
154197	PNLDC1	NM_173516	AAGCAGAATATCCACAGCCTA	AAGGAGAGGCAAACAAGTATA		
154386	C6orf195	NM_152554	CACGGCCGACTTAGTAATTCA	CAGAGGGAGATTAGCAATGAA		
154810	AMOTL1	NM_130847	TAGGTTTGCAAACAAAGTTAA	CAGGAATGATTTGAACTGATA		
157724	SLC7A13	NM_138817	TACCATTGGTAAAGTCTCCAA	CCCAATCTATCTATACCTTAT	CGGGTTCATTATGGTCTATAT	AAGGTTAAACATATGATAGAA
157813	LOC157813	XM_098828	ACCCGCCATAGCAGTGACCAA	CCGAGAAGCCCTGGAGATAAA		
157869	RPESP	NM_153225	CACGGTGTGTGTGGATTGTCA	CAGAGGATGGTGGATACTGTA		
157983	C9orf66	NM_152569	CTGAGACACTAAATAAATATA	CGGCCTCAAACTCAAGATAAA		
158038	FLJ31810	NM_152570	CAGTAGGAGGATAATTAACAA	TGCGGGAATTATCATGATCAA	AAGGCGTTTCATCACCACCAA	ACCCAGGAGGTTCAACATGAA
158056	AEGP	NM_206920	ACGGCGCTGGCTGCAGAAGAA	CACGACCACACCACAGGCCAA	CAGGCTGCAGGTCTCAGGATA	CTCCACCTGGCTTATTATTTA
158228	C9orf122	XM_379636	CAGACCGAGTGAGCCCAGCTA	CACGCTCAGCCGAGCTCATCA		
158248	TTC16	NM_144965	CTGGTGGACTTCTATGCCTTA	CAGGACCTCACCTACTATGAA		
158399	ZNF483	NM_001007169	TAGAGTTGATTTCCCAGCTAA	CAGGATTTGGGTAAAGTCACA		
158511	CSAG1	NM_153478	CCGAACCAGGAAGTCAATCAA	CAGCCAGTAATTCCCAGGCAA		
158835	DGAT2L4	NM_001002254	CAGCGATTATTTCCCTCTCAA	TTGGATGTGATTGAACTTTAT		
158880	USP51	NM_201286	AGGCCTGAGAGGGCTAATCAA	CCAGAGACTAGGAAACGTAAA	GAGGACTTACTCTACAGTGAA	CCCAGAGACTAGGAAACGTAA
159163	RBMY1F	NM_152585	TAGATGTAATATCTACCTTAA	CAGGCTCTTTGTCCTACTAAA		
159371	TMEM20	NM_153226	CTCCATTATTCTCTAAATGAA	ACGCTTTATGTTATACATTAA		
159491	C10orf64	NM_173524	CTGGGACATGCTGGAAAGGAA	AAGGCTGAAGACAGAAATGAA		
160065	PATE	NM_138294	CTGGATCACTTTCAATGAGAA	CTCCATCTTCTGCACACGAAA	AAGGAGGAAAGGGTAGTTTAA	AAGCCTGGAAAGAGTGATGAA
160287	LDHAL6A	NM_144972	AAGAATGTGTTTACTGTGTTA	CAGAAGGAGCTCAAGCTTTAA		
160760	TA-PP2C	NM_139283	CTCAATTCTCAGGGACTTTAA	CCCTCAAAGCCTAGAAATTTA	CACAAATTGTACGTAATGATA	AAAGGGATGGTACAAGTCTAA
160851	DGKH	NM_152910	TGGGAGTTCGATTATCAACAA	CTCCTAGTGCTTAGTGGTCAA	CCGGATCTAGATTCCGTAGAT	CAGGTGGAGTATAATGACATA
160897	ITR	NM_180989	CTCCCATTTAACTGAGTATAA	TCAGTTGACAATGACCATGAA	CCCAATCATAATTAAGCCGTA	ATGCCTCATCTTAATAGCTAA
161003	STOML3	NM_145286	CTCCAGATAATTTATAAGTAA	AAGGCATAGAATATAAATGAA		
161725	C15orf16	NM_130901	CTGGTTCTGGCCTATGATCAA	CAGGACGACATTGCCCAAGAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
161823	LOC161823	XM_091156	CAGCTTACTAGTAGCCCTGAA	TCGAAGTTTCTCATCAGGAAA	TAGGTATTTGATAGCAGTTGA	TAAGATAGTTCTGAAAGGTAA
162073	LOC162073	XM_091331	TTCCTTGAAGGTGAACCGTAA	ACCCAAGAATTGGTTCAAATA		
162333	FLJ35757	NM_152598	AAGAGAGAGGTTGTCAAGAAA	AAGCAGAAGATACTACTTTAA		
162394	MGC19764	NM_144975	CAGAGTTAATTCACTATTAAA	TCCATTTAATTTAATAATCAA		
162466	PHOSPHO1	NM_178500	CCGTCCCTATCTATTCAGTTA	TACAACTATAAAGGAGGTGAA	TCGGGTCCGGACAGCCAGTAA	CGCCAACATGTGCAAGCACAA
162494	RHBDL4	NM_138328	CAAGTGGTACTATGACAGCTA	AGGCATGAAGTGCCAGTTCAA		
162605	KRT25D	NM_181535	CTGGGAATTCATCTAAAGATT	AAGACAGTGGTTGAAGAGCTA		
162835	LOC162835	XM_091830	CTGGAACACCTCATCATGCCT	CGCAAGGTGGTTGGCGCTGTA		
162993	LOC162993	XM_091914	CAGCACTTGCTAAACATCTAA	CAGGTATTCCACATACCTTAA		
162998	OR7D2	NM_175883	CCCATGCGTATACATTGTTTA	AACAATTAATCTCCAAGTAAT	ACCAATTACCTGAATAGTGAA	CAGCACGTTGATATACTTTAT
163259	FLJ37099	NM_198459	GTGGGTCTAGATATAAATGAA	AAGGAATAGACTCATCACATA		
163479	FLJ35838	NM_173532	CAGCACTTATCCCAAGACAAA	CAGGGCAACCTGAGATAACAA		
164091	MPRA	NM_178422	CCAGGGAGAGGGAAAGAGTTA	TGGCCTGGATGCAATAAAGTA	TCCTTGGAAGTCCAAACTCTA	CTGAATGGTCTTTGCTAAGAA
164118	LOC164118	XM_089384	CCCTAGCATCTTGGTACCCAA	CAGGCTGGCCAGAACCATGAA		
164153	LOC164153	NM_203412	CAGACCAAGAATAGCAGGAAA	CCCGATGTTCCTCAGAGTCAA	GAGGCAGCAGCTGATCAGTAA	CTGCTTGTGCTTCCAGCTTAA
164395	LOC164395	NM_001008409	CTGCATGTTGTGGACATGGAA	CACAGGTTTATTTCAAGGCAA		
164656	TMPRSS6	NM_153609	CCGCCTGATGTTGTTACTCTT	CCGCCTGGGAACTTACTACAA	CACGCTGGGTTGTTACCGCTA	CACGGCCGGGATCACCATCAA
165140	OXER1	NM_148962	CAGGGCGAGGTCTCTCTGGAA	GTCCCTTCCAATATTAATAAA	CCGGGTGGAGGAGACAGGCAA	CCAGCTGATAGTGCCAATCAT
165257	C1QL2	NM_182528	AAGGCCACTCTCGATTCATAA	CCGCATGATCTGGGAACCTTA		
166614	DCAMKL2	NM_152619	CCGCACTATCTACACCATCGA	TACGTGTGTGCATCCAATGAA	CTGAGCTTGACCGTTGCATAA	ACAGATGCTCTGAATCATCAA
166647	GPR125	XM_291111.1	CAGCCTTACTTTGCTCTTATA	CAGGCTTGTATTTAATATAAT	CAGCTTGATAATAGTCTGACA	ATGGATTTGACGGGATCTGAA
166752	FREM3	XM_094074	AAGGAAGGGCTTTATGAGTAA	CTGGCTGATCGTTATGATGAA		
166979	FLJ37927	NM_152623	ACCGCTGAAAGTCATAACCCA	CACTGCTAGGTTGAACATCTA	CAAGGACAACCTATTACCAAA	AAGGAGATTGCAACTGGTCAA
167227	DCP2	NM_152624	TTGGAAATTGTCAAACATTTA	CTGGGTTATCAGAGTAATGAA		
167681	PRSS35	NM_153362	CCGAACCTTAACCAGGGTGAA	AAGGGAGTATCTGTTAGGAGA	TACGGCTAACAGAGACCTGAA	CCGTAGTGAGATCACTTCATA
167838	C6orf198	XM_371849	AAAGACTTCCACTGCAATATA	TGGGTTTCTCTCTCCCTTGTA		
168433	RNF133	NM_139175	CAGTGGAGTGATCATCTATAA	GTGGTTATGATTGGTAACTTA	ACCGGAGATGGCAGCGATTAA	AACGCTATAAGCCTAATGACA
168451	THAP5	NM_182529	TTGGAAGATGAGAAAGAAGTA	CACCATTTAAGATACGTGAAA		
168507	PKD1L1	NM_138295	CACCCTTATGGCATCATGGAA	CACGAATACAGGATGCATTAA	AACGAGTTTCATGGAACCGAA	CAGGTTGACCTCAAAGGTGTA
168544	ZNF467	NM_207336	GTGGATGATTCGGAAGGTGAA	CACCAGCTCATTCACGGCGAA	CCCGCTCTTCTTCTGAGCCTA	CAGGAAAGAGTGGTTATTTAT
169270	ZNF596	NM_178539	CCGCTCGGATTTGTCTTCTTA	CAGCTGTAGCGTTAACACTAA	TACCACTTTGCTCAACCTAAA	CAGCACTTCTATAATAGATCA
169436	C9orf96	NM_153710	CTCGGATCGAATAACGATAAA	CTGCCTGGTGATGGAGTTCAA		
169522	KCNV2	NM_133497	CACGTGATCCATCCTCCTAGA	ACGGAGAATGAGGGCAGCCAA	TACGAGGAGCAGACAGACGAA	CTGGACAGAGGGCAACTATAA
170082	MGC17403	XM_372198	CGGGAGCAAAGAGATGATTAA	CTGACCCATAATGGACATTAA		
170302	ARX	NM_139058	ACCACTCAAGACCAAATGGAA	GACGCCTGATATTGAAGTAAA		
170463	SSBP4	NM_032627	AAACATGTACACTATCATGAA	CCGCGAGAAGTTGGCGCTGTA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
170626	GAGED4	NM_130776	ACAGGCAACCACAGGTTTAAA	CCAGAAGGAGGTGACAGGCAA		
170692	ADAMTS18	NM_139054	AACCAGCATAAAGCAAATGAA	CAGGTTTAATAAGGACACGAA		
171568	POLR3H	NM_138338	CTGGTTCTGTTTGTTTCTCAA	CTGCACATTCATGATCAGAAA		
192669	EIF2C3	NM_024852	AAGGCTGTACAGATTCACCAA	CGGGATGAAATGGCTCATGTA	CTCCTATAGGAAGTATCGCAA	CTGACTGATTCTCATCGGGTA
196051	PPAPDC1	XM_113641	ATCCTTGAATTTGCAAGTGAA	AACAGACAAGACTGAAATTAA		
196264	LOC196264	NM_198275	CACAGTATCAATATTTCATTA	AACCACTTATTTATTGAATAA		
196335	OR56B4	NM_001005181	TACCATTTGCTGGGCATATTA	AGGGTTCATCATGCTCAGGAA	CTCATCATAATCACCATTCAA	ATGGCAGTAGACAGATACATA
196337	LOC196337	XM_113696	CCCATCTTTGATACCTTCATA	CACCTTCATCCTCTCAGATTA	AAGACACAATACGGACACTAA	CAGCTTATTTAAGATCCAGAA
196403	DTX3	NM_178502	TCAGATACAGTTCTCCCTTAA	CACCGTGTGTCTATCCTCATA	CGGCACCATTGTCATCCAGTA	ACCGAATGTCATCACCTGGAA
196463	LOC196463	NM_173542	CAGGCTGATGAGGTACAATGA	CTGGATGAACACGGTGGTGAA		
196743	PAOX	NM_207126	CTGGACACATAAAGCAAGTTA	CACGGAGATGCTGGACACATA	CCGGACTTGAGTCTGAGTTCA	CGGAGATGCTGGACACATAAA
196792	FAM24B	NM_152644	CTGGAGCAGAGGAGCCATTAT	TTGAATAAATGTACACTATTA		
196883	ADCY4	NM_139247	CCCGCCTTCAAATACTATGAA	CCGGCGCAACGAGGATCTCTA	CCCGTAGTAGCTGGAGTTATT	CTCGCCTTCTAAGAACCTCAA
197131	UBR1	NM_174916	CACGTCATATACAGCCTACAA	ATGCAGTAATATGTGACCTAA	AACCCACAATATGGACAGAAA	CAGGAATATTGGGATACTGTA
197187	MGC23284	XM_378628	AAGGCTTTGTGACTAACTCAA	CCCGCCCAGATATAAATATAA		
197258	FUK	NM_145059	CAGAATCATGGCGTCTACCTA	TCCCTATGGCTTAGAGTTGTA	TGGCTTAGAGTTGTAGACTTA	CCGAAGGGAGTTGATTGGACA
197322	LOC197322	NM_174917	CTGGCCTCCCTTAAACCTGAA	CCGGACCTCAGTGGACATCAT		
197358	NOD3	NM_178844	CTGGCTGGGAAGGGCAGTCAA	CAGCTTAGATTTACAGGAGAA	CTCCGGAGACTCAATCTTCAA	CAGGATGATCTCAGAGGCCAT
199692	ZNF627	NM_145295	ACGGTCTAATTTGTGTAGTAA	AACCATGTGCATACAACTTAA		
199897	LOC199897	XM_117152	CAGGACTACTTCATGAGCCAA	CCCACTGGGTTGTGAAATGAA		
199953	RP13-15M17.2	NM_001010866	CAGCAGTGGGTGAGCAGCCAA	CAGCCTCAGTTTGCCATCTAT		
199990	FLJ31031	NM_182533	ATGGATGTGCAAGACCTTGAA	ATCCTTCACTTTAATTTATAA		
200081	DKFZp451J0118	NM_175852	CGCGAGGAGCATATCGACAAA	CACATACTGTGTGGACAATAA	CTGGTGTATCCTTCACATCTA	CCGGACCTATGTGGCAAGGAA
200172	FLJ23878	NM_144990	ACCCATCTGTGTAGCCAAGAA	CTGGAACTTGTGACTGTCAAA		
200186	TORC2	NM_181715	CAGGACTTCATTCACCTCTCA	CCGGCCAATGAGTGACTTCAA		
200213	LOC200213	XM_114156	CCGCTTTAAGCAGGCCACCAA	CAGGGTTATTCTATGGAGTAT		
200312	LOC200312	XM_117224	ACCCACGAAAGTACAAGATCA	CCGCATCTGAAGTTACCCAAA		
200315	APOBEC3A	NM_145699	AAGCAGTATGCTCCCGATCAA	CAATGTATTAATGAAATGAAA		
200350	FOXD4L1	NM_012184	TAGCGTTCCTGCTTCTTGCAA	CCGGACGTTGTTGCAAAGGAG		
200407	CREG2	NM_153836	CAGCAAATCTCTAGAAATTTA	AAGGAGTAGCTTTGACATTAA		
200424	MGC22014	XM_371501	CCGGATCGAGAAGGTCATCTA	CCGGCTCTATGAAACCTTCAA		
200491	LOC200491	XM_117239	AAGACATGCAGTCTCATTGAA	TCCCTGGAGCTCAGAAGCCAA		
200539	ANKRD23	NM_144994	AAGAAGAAACTTGAAAGATTT	CCGGGAGAAGCTGAAATTGGA		
200624	LOC200624	XM_117257	AGCCACCATGCTGACAAGTAA	CAGGTAGTCTGTGGAGCATTA		
200728	TMEM19	NM_198276	ACCATGTTTCTTGACATGGAA	AAACAGTATATTAACCCTAAA		
201163	FLCN	NM_144606	CTCCTTTGCCTGGCTCCTGAA	CGGTCTTTGCTCCTTTACAAA	CAGGCCTGTTGCAGTCTCCAA	CCGGGATATATCAGCCATGAT

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
201175	LOC201175	XM_371057	AAGGGAGTTCCTTACTTACTA	AAGGGAGTTCCTTACTTACTA		
201516	ZSCAN4	NM_152677	AACCAATAAATTTCTGTTGAA	AAGGGATTTCTGAGTTCTCAA		
202018	FLJ90013	NM_153365	AGGGTACTTCCTTGAACATAA	TACCACCAGAATAACCCTTAA	CAGTGTTAACTTTAAGGTATA	TCCGCTTGAATTATTCTGTTA
202020	FLJ39653	NM_152684	CCGCATATAAATGGGCCTTGA	CGGAACCTTATTATTTATGAA		
203054	ADCK5	NM_174922	CTGGGTCCTCCAGGACCTGAA	CTGGGAGATGCTCAAGTTTGA	CCGCTACTTCCTTATGGCTAA	AAGGCCTTTGCTGAGCAGATA
203074	UNQ9391	NM_198464	CAGACCAATGCTGCTGACAAA	TAGCCCATCCATGGAAATAAA	CACCTCGTTGGTGAACTACAA	AGGGAAGAACTCGGTATTCCA
203076	LOC203076	XM_114621	CAGGTGGTCAAGTTCACAGAA	AAGGAAAGAAAGCGAAGGCAA		
203100	HTRA4	NM_153692	TACCTGAAACAATCAATTAAA	ACGATGTAATTGTCAACATAA	CCCGCTCAGGAGGAATTACAA	TAGGCAGTTCTTGGCAGAATA
203859	TMEM16E	NM_213599	TACGTTGATGACGTAAAGAAA	CAGGATCATGCTTGAACTTTA		
204219	LASS3	NM_178842	AACAGTAATGACTACAATAAA	CTGGAGATACCTGGAAATGAA		
204801	NALP11	NM_145007	CAACATAAGATTCGAGTTAAA	CAGCGATATCTGTCAATATAT	GCCAGGTTCAATAATACCTAA	CAGCCATGAGAACGTCAAATA
204851	HIPK1	NM_152696	CGGGCAGTGCTGCTACATCAA	CAGGAGTTCTCACGCAGGGAA	CTGAGCTATGTTTGTAATGCA	AGGGAAGCTGTACACCACTAA
205147	FLJ38377	NM_152698	TCCCAAGTGTTGAGAATCCAA	CAGGAGAGCCTAGGACTCAAA		
205564	SENP5	NM_152699	CACGATTGTGGTCACCTTGAA	CAAGGTTTGCAAGCTAAGAAA	GTGCCTGATTGCCACACTAAA	CAGAACATCGTTCTAATACCA
205655	LOC205655	XM_497917	CTGGTGCTCAGTTGTATGCAA	AATGATGAAGTTGGAAATGAA		
205860	FLJ25801	NM_173553	CACATGGTGTGTGGGATACAA	CAGGTGGCAAGTGGGCATATA	CAGCATGTTCAGAGTACTCCA	CGGGCAGATATCATTCTACAA
206426	MGC26597	NM_152700	AAAGTTGAGGTTATCCTGTAA	CTCTTAGTTTGTAATTTAATA	AGGGTACCACTTATTCTTCAA	ACGGACCCATATACTTTATAA
219402	MTIF3	NM_152912	GAGGAGATATTTCATCAAATA	AAGGCATATAAAGAAACTCAA		
219414	LOC219414	XM_169434	CTGAGTGGATTTGGAAACTGA	AAGGAGCTCGTTGAAATATCA		
219429	OR4C11	NM_001004700	CCGCTTGCACGTCTCACATAA	CTGGATAGGGTCTTTAATACA	CCCTATTTGATTGATCATTAT	TAGGGTCTTTAATACACTCTA
219445	OR7ESP	NM_153024	TTCAAAGTTGTTTACTTATAA	CAGTGACATCAATAACATATA	TAGCGTAAACATCACGACTGA	AACGTTGATGAGGAATAAATT
219464	OR5T2	NM_001004746	CAAGTTTGTTCTAGATTTCAA	CAGGTTATCAATAAAGTATAT		
219469	OR8H1	NM_001005199	CAGATGGCCCTCTTTATACTA	TACGACATTGAAATCATGATA		
219487	OR5M11	NM_001005245	CACCATCGTCTTGGTGTCCTA	AAGACTGTTGAGGAATCTAAA		
219537	CHASM	XM_166203	AAGGAGAAGGCTACTGATGAA	CAGGAGATGACTGGCAGGAAA		
219770	CX40.1	NM_153368	CAGGGTGTCAGGGCACACGAA	CAGGAGGATCGTTTGAGAATA		
219927	MRPL21	NM_181512	AAGGATCTTGTTCGAGTAGAA	CTGATCTTAATTGGAAATGAA		
219928	MRGPRF	NM_145015	GGCGGTGTTCTCCATCCTGAA	AAGGCATTATCAGTGAGCAAA	TAAGGCATTATCAGTGAGCAA	CAGGAGAAGAAAGATCTGTTT
219972	MPEG1	XM_166227	ATGGACGAAGTTGGAGTTCAA	CACCGTGAACTTCAAATTTGA		
219995	MGC35295	NM_152717	CAAGGCTACCACAGAAGGTTA	CCGGAATCCTCCAGAATGGAA	AAGGACAAGGCTACCACAGAA	CGCCTTCAGCGCAGACTTCAA
220001	FLJ32009	NM_152718	AAGCTGCTTGTTCCCACCCAA	CACAGGCAGAATCTTCTATAA		
220032	LOC220032	NM_182833	ATGGCTGAATACTCCAAATAA	AAGGAGTGACTGTGCATATAA		
220081	FLJ32682	XM_495949	CAGATGGAAACTGGTAATTAT	AGGCAAGTTATTCATCACAAA		
220158	GTSCR1	XM_496277	CAGGATAGAAAGACATCACTA	CTGGTTTATTGCTCCTATTTA		
220164	DOK6	NM_152721	ATCGTATGAACAGTTATTTAA	TACGCCAAACCTGGATATTTA	AACCATAATTTGGTGCATTAA	CTGAGCAACATGAAAGATTAA
220416	LOC220416	XM_166971	CCAGTAGAAGTTCAGAAGTTA	CTGACTGTTGATGGGAATGAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
220441	RNF152	NM_173557	TAGGTTAGATATAGACACTAA	TAGGATTTATTTGGTATTAAT		
220717	LOC220717	XM_165448	AAACAAGGAAATAAAGGCTTA	CGGGAAGGTCGTGGTGCTGAT		
220972	MIR	NM_145021	CTGCTAGAGTCTACAGAAGTA	TCCAGCGGGATTGACACTCAA	TGGGAATTAGTGGATGCTAAA	TGGATGCTAAATGGCAATTAA
221044	C10orf49	NM_145314	TTGCTTATGGCTTACAAATAA	TACGAGGAACAAAGGAATGAA		
221060	C10orf111	NM_153244	AAGTACCTATGTAGAACCTAA	CAGGGAATCTTGAGCCCGAAA		
221078	NSUN6	NM_182543	CACCACGGATTCAGTTACTAA	CAAGACACTCGTCACTATTAA	CTCGTCACTATTAATTCGGAA	CAGAAGCAGTTTAATGGATTA
221120	DEPC-1	NM_139178	AAGAATCACTATGGAACCAAA	CACGCACATTTGAGATGAGAA	CAGAGAGGATATAACTTATCA	ATCGCTATCATCTTTAGGCAA
221178	SPATA13	NM_153023	CAGGGACATGCTGTACTACAA	CACGGTGATTACAGCAACATA		
221188	GPR114	NM_153837	CGGGCGTGTCTACAACATCTA	AAGCGGCTTTGTTTCAGCCTA	AGGCATGGGTCTCGAATCTTA	AGCGGCTTTGTTTCAGCCTAA
221223	FLJ31547	NM_145024	CTCAAGGTGCATTACCCGAAA	TTCCATTATCGGAGTCAATAA	CCCGGAATCATTAGCTTCTTT	CAACAAGATTTCTTCAATAAA
221241	C18orf20	NM_152728	CTCCTATTAAACATTTGTTTA	CTGGTTTATCAGCCACACTTA		
221261	C6orf184	XM_168053	ATGGAGGACCATTCCCAGTTA	CCCAGATACCCTAGAATATAA		
221357	GSTA5	NM_153699	CACAGAAGGTATAGTAGATTT	CACGACAGTGACAGAGTTTAA		
221391	OPN5	NM_181744	CAGCCTTTCACCATACTGGAA	CAGCCTTTCACCATACTGGAA	CACCGTAACCACAGTCAGGAA	CGCTGAAATAATGACTATCAA
221393	GPR115	NM_153838	CAGGTAAATGGTCTGGTGCTA	AGGCTCTCACTTTAACATTAA	TAGGCTCTCACTTTAACATTA	TAGGAGAATGTTCCCACTATA
221458	C6orf102	NM_145027	CAGCGTTACCATCGATGACAA	AGCGAGAAAGCTACAAATTTA	AAGATTGTCAAGAACCATTAA	ACGGTCCCAACTCCTCTCTAA
221527	ZBTB12	NM_181842	CGGCAAGTGCTTCACACAGAA	CAGCCAGTTCATTGAGCCCAA		
221656	AOF1	XM_173173	AACCTATTTCATCACTCTAAA	TTGGGTGATAGGACACTTTAA	AGGGACTAAATATGACTTTAA	ATCGATGCGGTATGAAACCAA
221662	RBM24	NM_153020	TAGTAGCTAATAAGAGAGTTA	TAGGAGCGTGGCAGTGGGTAA	AAGGTTAATGATAATGTGGTT	AACGATATATTGCTAGTTTCA
221785	ZNF498	NM_145115	AAGGTAAATGGTAATGACTAA	AAGGGTTTCATTTCTGTTTAA		
221830	TWISTNB	NM_001002926	CACATTCATCTTAACATTGAA	CTGGTTGAAGCTGGTAATCAA		
221895	JAZF1	NM_175061	ACGACCTATTAGAGTAATCTA	CAACAGCTAAACAGTCATAAA	ACGCAACTAGTTGGTGCATAA	ATGAGCCTTATTGACAATTAA
222171	LOC222171	NM_175887	CTGGTGGAAATCGCTCACCAA	CCCGAATCACTTGGCAAATAA		
222183	FLJ37078	NM_153043	TACATTTGACCCTGAGGTTAA	CAACATGGAATTTGCAAGTAA		
222229	DKFZp434K1815	NM_152892	AAGGACCAGGGACACAGCTAA	ATGGCAAGGATGCGTCCTCAA	CACAGCTAACTAACTTATTCA	GACGGTCAATGACAACCTGAA
222255	ATXN7L4	NM_152749	CAGGGAGGTTATGAGGCTTAA	CACGCAGAAGTCAGAATCAAA		
222389	C10orf30	NM_152751	CAGGTTGTACTCCATGAGAAT	AGGAAATTAATGCAAATTCAA		
222546	RFXDC1	NM_173560	CACGCAGATTGTGAAGGATAA	ACCCAGTTTAATAATGACAAA		
222584	C6orf143	XM_294139	CAGAATTATGGGTATGATGTA	TAAGATTAACTTGAAGTTCTA		
222642	BZRPL1	NM_001010873	AAGCACTTGGAGGAAGGCCTA	CAGCACTGATCTGGCATCCCA	CCCATTCTACAAAGTCTTATT	CAGAGGAGTGCTGTGGAGAAA
222658	C6orf69	NM_173562	CGGATGCTCATTAGAGGTTAA	AACATTCGCATTGGAATTGAA	TAGCATCACTGTGGAAATTAA	CCGGTCTGAAGTCATCTATAA
222698	C6orf194	NM_001007531	AAGCAGCAGTTCAGATTCCAA	AAAGAGAAAGATGACAAGTAA		
222699	LOC222699	XM_498063	CAGATGCTCTTTCTCCTCGGA	GGAGCTGGACATGAAGATCAA		
222967	LOC222967	NM_173565	CAGAACGAAGATGCCAGCCAA	CCGGACGGCAGCATGTATGAA	ACCGAGAACATTCGTCCAAAT	CTGGATGCTGAAAGACTTTAA
245934	DEFB121	NM_001011878	AAGAAAGTGAAGTATACTATA	CAGGTGCAGAACAACATGTAA		
246176	GAS2L2	NM_139285	CACAGTGTACCTCGTCAGGAA	CCCGTCCATCTACAAGCTGAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
246181	AFAR3	NM_201252	AAGACGTGTTAAGTTAAAGAA	CAGACTATTATTCGGCCATTA	CACGTTGTATGATTTCGTTTA	CCCGCTTTGTCTAATTTAGAA
246721	POLR2J2	NM_032958	CACCATTAACAAGGACACCAA	TCCGGAAGAGGCCTCTTATTA		
246777	SPESP1	NM_145658	CAGGTGAAACTGCGATAGAAA	CAGAGGAACCTTATATTGAAA		
252839	TMEM9	NM_016456	CAAGGTCATCATTGTCATCTA	CCGGATGCATATACTGAGCAA		
252884	ZNF396	NM_145756	AGGGAAGAGACTCATAGTAAA	ATGGATGATCATCTTAATATA		
252983	STXBP4	NM_178509	AAGAACTGAACTATTATTAAA	CAGCAATTTATTGAACACTAA		
253143	MGC50372	NM_173566	CAGGCATGGAAGCTACATATA	AAGAAGGAGTTTAGTTTAGAA		
253150	MGC14276	NM_153248	AAGGAAATCGAGCTTAATGAA	CACCCAATTCAACTTAATAAA		
253558	LYCAT	NM_001002257	CAGATTAGATATAGCCCTAAA	CAGAATATTATTAAACAATCA		
253582	C6orf191	NM_001010876	CAGAAATAATGTTAAATAGAA	ATGGCTCAACATAAACTATAA		
253650	FLJ35740	NM_147195	ACGGAGAAACAGCGGATGAAA	TAGGTGCTCAAGGGAAGTTTA		
253738	DKFZp667B021C	NM_001005463	CACGTTTAGTATATTAAGACA	CCGGGTGATCCCGAAAGGTTA		
253769	MGC43690	NM_182552	ACAGAATTTGGTAAAGTTAAA	CTGGATGAATGTAGAGAGAAA		
253832	FLJ25952	NM_153251	CAGCATTGACTTAGAGCTACA	CAGAATGATGCCTTAATCTTA		
253962	LOC253962	XM_172968	CTGGCACAGCCGATTCCCAAA	CTGCGAGAAGAGGAAGCCTTA		
254102	EHBP1L1	XM_170658	CAGGGTTAGAAGCTGATACAA	ACCCGTAAGACAGAAATTATA		
254263	CNIH2	NM_182553	CGCGGGCACGCGAGCGTTTAA	CTGGTGCAAACTTGCCTTCTA		
254439	LOC254439	XM_170659	ACGGAGCTTGATGAAGCCAGA	CACGGTGTCCTGATGAAGGAA		
254786	OR6C3	NM_054104	CACATCCATCATGAACAGGAA	CAGGAATAAGACTATTTCCTA		
254950	KRTAP15-1	NM_181623	TTGGATCTCTTGGTTGTGGAA	CCCGCCAGACTAACTACATAA		
255061	TAC4	NM_170685	AAGCCAGTTCTTTGGGCTGAT	CTGGGTAATTGTGGCCTTGGA		
255187	LOC255187	XM_173160	TAGGATTGAGATACACAGTTT	CAGGCACCTTATATCCTCAAA		
255239	ANKK1	NM_178510	CAACATGATGATGATTATTAT	CTGAGTGTCATCAACCTCCTA	GCGGACGGAGTACGCCATCAA	AGGAGCCGAGATGGAAATTTA
255275	LOC255275	XM_171855	CACTGGAACATCATAAGGGAA	CAGCAGGATCCTGAAGCCCAT		
255324	LOC255324	XM_171078	CACCTAGATGGGCCTCTCTAA	CACAATGAAATGAGAAGATAA		
255620	LOC255620	XM_173132	GCCTTAGTTTACCACTTCTTA	CTGGGCTGTTCTGGACTTCAA		
255714	MGC87693	NM_207341	CAGGATCACACTGGCCAACAT	CCCAATAAACAATCATTTCAA		
255738	PCSK9	NM_174936	TCCCTGATTAATGGAGGCTTA	CAGGTCTGGAATGCAAAGTCA		
255743	LOC255743	NM_198278	CAGGCAAATAGTGTCATCGAT	ACGGCAGAATATATGGCTGTA	CTCATGTATATTGGAGGCAAA	CTGGCTTAGACTAGAGTATAA
255967	PAN3	NM_175854	ATGGCTAAAGACCTTAACCAA	AAGGCAAGTTTACATCACAAA	CCGGATACAGAAATCAAGTAA	TACCTATACTTTGATACTGAA
256006	ANKRD31	XM_293911	TCGGCATGTCATAGAGATTTA	CCCAGTAATCGGCAAATTAAA		
256051	ZNF549	NM_153263	AAGCCTTATGTGTGCAATATA	CAGAAGGTACATATAACAGAA		
256076	FLJ35880	NM_153264	AACAGTATACACCAAATGAAA	CAGCTTGGGAGAATACATAAA		
256112	ZNF37B	XM_497219	ATGGGAAATCTTATGCATGTA	CACCTGTGAAGCCAACTATAA		
256130	MGC42090	NM_152774	CAGAAACATTCTAGTACAATA	CTGCTTTGATGTATAGTTAAA		
256144	OR4C3	NM_001004702	CTCCTTGTCTTTATAGGCAAT	TGCAATTAGTTCTATTACTTA	CTGCTACATTGTCATCCTGTA	CTCAGTGACCTTGGAATCTAT

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
256236	NAPSB	XR_000169	CCCGCTGGATGTACTGGTGGA	TGGGACCAAGTTTGCCATTCA	CGGGTGCTCAGAAATCCCAAA	CAGGATTACGTCATCCAGTTT
256309	MGC33607	NM_152775	AAGCAAGTATTTATAAGAATA	AACGAGAATATTTAAGTTTAA		
256356	MGC40579	NM_152776	TCCCTGGATATGACCAGAATA	AACAGTGTTAGGGCAACTTAA	TACCATCTTGTACGAGCAATA	CAGCCAATGGGTGTAATTTCA
256453	LOC256453	XM_172917	ACCTCTTGCCTTTCATTTCAA	CAGGCAAATTCCACAAACATT		
256472	MGC33486	NM_153266	CAGGAGAAGAAGCTTCCAGAA	TTGGAGGAAGTGGAAGCCTAA		
256892	OR51F1	NM_001004752	CAGCGTGATCCTGTTTGTCAT	CACGTGAAATCAGTCTATATA		
257039	LOC257039	XM_172230	TCGACCTACAGTTGAGATAAA	AGGAATCAACAGAGAATGAAA		
257169	C9orf43	NM_152786	AAGAAAGAACTCGGCAGTGAA	CACGGAGAGACCAAAGATGAA		
257177	LOC257177	XM_170909	CCGGATCACTTCCATCGCTGA	CACCTTGTGTCAAGAAGGCAA		
257202	GPX6	NM_182701	AGGGCTAGCGACTGACAGAAA	AACGGCGAGGAGTACATCCAA	CAGACTATCCTGTGTCCCTAA	CCCGAGAAGTTGTGACATCTA
259249	MRGX1	NM_147199	CAGGAACGCCTTCTCCATCTA	CTGATTCTGCTTGGTGTCAAA	CGCCTTATATATTCCCTGTTA	CACGTGGACAGGGAAGTCTTA
259285	TAS2R39	NM_176881	AACATACTTGTCTGAGATCAA	ATGGCTATACATGCAGCTGAA		
260293	CYP4X1	NM_178033	AAGCCGAGTGTTGAATCAGTA	TGGGATGTATTTGCACCTGAA	CACCAATAGACTTTCATATAT	ATAGATGTGATCATTCCTATA
267012	DAOA	NM_172370	CAAGGAAATAACTTCTACCAA	TTGCAACTCTCTGGTCAGTAA	AGGCATTTACAGAGATCATTA	AAGAGAGACGGTAACAAGGAA
280636	C11orf31	NM_170746	AAGTATTTGAGTAATAGAGTA	CTGGTGATGTTGGAACATTAA		
282617	IL28B	NM_172139	CCGGGCCTGTATCCAGCCTCA	AGGGCCAAAGATGCCTTAGAA	CTGCCACATAGCCCAGTTCAA	CAGGCCTTTAAGAGGGCCAAA
282969	C10orf125	NM_198472	ACGGAGTACGAGTCCATCCTA	CTGCAGGGAACGGCCCTCTA		
282973	C10orf39	NM_194303	CAGCAGAGAATTAAAGAGTTA	CAGCAGAATTCAAGTATTTAA		
283008	FAM22A	NM_001009610	CCCTATGAATGGAATATACAA	CAGATTTACATTGGTTTCTAA		
283092	OR4C13	NM_001001955	AAACAAGACTATCTTATTCAA	CAGCATGTTTGTAGCCTGCTA		
283117	LOC283117	XM_210184	CACCCTGCGAGTCTTCCAGAA	ATAGTTATTGATTCTGACAAA		
283130	LOC283130	NM_182556	TCCCGCCAGGGTTAAACATTA	CACGCCCTTAGACGTGATCAA	CCCGGCTGCCTTCACCTCTTA	GCGCTTCTTCAGAGTCATTAA
283135	FLJ90834	NM_173578	CCCGATTGTATGCTCCATCTA	CAGATGATCAATAAATACTAA		
283140	LOC283140	XM_498528	CGGCACCATCTAACACATTAA	CAGGCAGTCAGCACAAATTTA		
283149	BCL9L	NM_182557	CACCTACTTCTATCAAAGAA	CAACATGAACATGAACATGAA		
283150	FOXR1	NM_181721	CCCTTCCTCTTTGATCTTTAA	CTGGATGTGGGTAAATCCCAA		
283155	LOC283155	XM_208545	CTCCTTTACAACCATACTTTA	CTGCATTTGATAGCAATGTAA	AAGAAATGTTATAAAGTAGAA	TTGGAACGGATGAAGCATTTA
283162	OR8B4	NM_001005196	CTGAATGACTTTGTTTCAGAA	CAGGGACATTCACCTACTTAA		
283177	LOC283177	XM_378327	CAGGAGCAAGGGTGTCATTTA	AAGGCGCTGTTTCTTAACCAA		
283189	OR9G4	NM_001005264	ACCCATTGCTTTATTCAGGTA	CACAGACTATACAACCACAAA		
283197	MGC39681	NM_174939	CACATTGTGTTGAAAGAAGAA	ATGGATGAATTTAAACAGTTT		
283202	LOC283202	XM_208563	CAGATCACTTGTCCTCCTCAA	AGGCTGTAAGGTCATCGTATA		
283209	PGM2L1	NM_173582	AAGGATTAATGCCAAACTAAA	CAGGTATTAATTTACAAATTA		
283212	FLJ33790	NM_173583	ATGGCTGATGCTAATAATAAT	CAGGGATAGTTTCCAGCTCAA		
283237	MGC29649	NM_173810	ATCCATCTGTTTATTTCTATA	CTGGGCATGTTTGGTTAACAA		
283238	MGC34821	NM_173586	CACCGTTGACTTATCAGGAAA	CACAATAAATTTATCTACATA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
283259	LOC283259	XM_208061	TTGAATTGCATTCTAATGTTA	CAGGCCCTGTTTCTACCTCAA	TTGCATTCTAATGTTATTAAA	ACGAATCAGAATGGCAATATA
283297	OR10A4	XM_208604.1	CACCTCTGTGTTTGAACTGGA	CACCATGGCATATGACCGCTA	CTCAAGGAATAAAGAAGTGAA	ACCATTTACTTGGTTACTTTA
283377	LOC283377	NM_207344	CAGGCCTTTCTCAGACTGTAT	CAGCTTTGTTTGAATTTATTA	AAAGCTAGGCATACAGCCAAA	TACCAGATGGCTGAAGAGTAA
283383	GPR133	NM_198827	TCCGGATGAGATCGCCATGTA	CAAGGAGGGCCTGAAAGTCTA	CAGCATGCACTACTACCTGAA	CAAGCACAGATTGACACGTAA
283389	LOC283389	XM_211009	TGGCAAAGGTTTGGTGAAATA	ATCAGGTTGCTCAGCAATGAA		
283440	LOC283440	XM_211040	TACAATGTTCAAGATAGAGAA	CCGGTACTCATAAACCTTCTA		
283455	KSR2	NM_173598	CAGGCTTACCGTGGACGCCTA	AAGGAAATCCATTACTTCAAA	TCCGTTGTGAGGGATGCCAAA	ATCCGGTGACCTCGAATCCAA
283483	LOC283483	XM_378431	CACACAAAGCTTTCTCTTAAA	AAGGTGGATTTGGAAGAACAA		
283551	LOC283551	XM_378455	CACCTTTGTCTTACAGTTTAT	CCAAATAAATACATAATACAA		
283553	LOC283553	XM_211086	CTCACTGGAGTTGACCATCAA	AAGCAGGAACTTAATTTAGAA		
283579	FLJ25976	NM_174943	CCGCAAGATGCTCACGCGAAA	CCGGAGGGTATGGGAAGAGAA		
283600	C14orf68	NM_207117	ACGCTGCACCTGCCACTTAAA	CAGGATCCAGACGGAGCCAAA	TTGGGAACTGTTGTCAATAAA	CACGGTGAAGGTCAGGATCCA
283601	C14orf70	NM_001007560	AAGGATGTGACTCTCCTAGAA	CCCAGGCAGATGAAAGCTTAA		
283659	FLJ25756	XM_370866	TAGGAAATGAAGAATCTTTAA	CAACAGTAAATTGGTAATTAA		
283677	LOC283677	XM_208778	CCCAGGGCAACTGAAAGTCAA	CTGGCGGGTTTGAGAAATTAA		
283685	FLJ36144	NM_182561	CACTGTGTGAATATAGTCTGA	TCCCTCCAAAGTTCTTTGTAA		
283694	OR4N4	NM_001005241	ATGTGCACCACTCGTGTCATT	CACCACTCGTGTCATTATTAT	TAAGCTGGCTTAAGAGATCAA	AAAGATGCTAACGGTAGCATA
283761	LOC283761	XM_378542	CCCACAGGGTTTGAACTGTAA	CCCAGTCAAGTTGACCTGTAA		
283777	FLJ39743	NM_182562	AAGGGTCCAATTGACTAGAAA	TAGGATGAATATGGACTTTGA		
283848	FLJ37464	NM_173815	CCCACTGAAAGTGGCCAAGAA	CCGTATGATGGACATAGTTCA	AAGAGTGGGCATGAAGCTCAA	CAGGTTGTGACATGGAGCAAA
283902	LOC283902	XM_211251	CCCATGCTAGTTGCAGAGAAA	CAGGACATTATCTCACCATAA		
283933	MGC46336	XM_290712	ACCGCATCTCTGTGAAATAAA	CTCCTTTCCCTTATACATTAA		
284029	FLJ34790	NM_173621	CCGCCCGTTATTGCTGCTCAA	CAGCGACACCATGATGATTTA		
284040	FLJ36674	NM_173622	TAAGAAATCAGTAAATATTAA	CAGGAAGGGAATACAAAGGTA		
284058	LOC284058	NM_015443	CAGAAGAATTGGAGAGATTTA	CAGGTTGAGAGGCATATACAA		
284067	LOC284067	XM_208990	ATCCAATATATCAATGATGAA	ATGCATGTGAATATACAATTA		
284069	MGC34829	XM_208993	CCGCCCTGGCTTCCTCACCAA	CCCGCAGGAGATCCTGATCAA		
284076	FLJ35808	NM_173623	CCAGTTGGTCTTCATCTCCAA	CTGGGAGAGTCCGAACACAAA		
284086	NEK8	NM_178170	CCAGTCGGGTGTGACCATCAA	CAGGAAGCTCAGCGAGTTGTA	CCAGAAGCTGGTGATCATCAA	ACGGACAGTTGGGCACCAATA
284111	SLC13A5	NM_177550	CAGGAGTCATAATGAACATAA	CAGACTGAGGAAGAAAGGAAA		
284114	FLJ36878	NM_178518	CACCCTTACTGCTTCCCATAA	CTGGACGGCACTGAACTGCAA		
284119	PTRF	NM_012232	CAACTTTAAAGTCATGATCTA	GAGGAAAGATTGAATCCTAAA		
284121	LOC284121	NM_001007533	CACGATGGACTGAGCCAGCTT	CGGGACCGGATACATTATTAA		
284131	FLJ35220	NM_173627	TTGGCCAAGGTTAGCGATTAT	TGGGTCTAGGATTCTCAGTAA	ATGGGTGAGAGTTGAAATGAA	AAGAGAGAGATTGGTGTTAAT
284134	LOC284134	XM_211345	TCCATCTGGACTAGCAATAAA	AAAGGTATTGAATGAATTGAA		
284185	FLJ39421	NM_178519	AGGGAGGGAGATGGACTCGAA	AAGGGCTATGGATCTAAATAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
284186	FLJ38792	NM_178520	CACACAAGAGTTCCCTTTCAA	CCCTGCGGGAATTCTATTAAA		
284207	METRNL	NM_001004431	AGGCCTGACCCTGGTACCGAA	AACAGGTGCTCTCATCGTTAA		
284222	C18orf58	XM_290817	GTGTCTTGCAGCAGACTTAAA	AAGTCTGCCAGTGCCTATTAA		
284230	LOC284230	XM_208185	AAGAGAATGCTGGCTATTAAA	CCCACCAGACTTTCTGTAAGA		
284266	CD33L3	NM_213602	CCCAGGAGTCCAATTATGAAA	ACGCATTAGCTTGAGCGTGAA		
284269	LOC284269	XM_209097	CAGGTTTGTGGTGGGAGAGAT	CAGCAGCTCTTCACAGTCTCA		
284273	ZADH2	NM_175907	ACCCGTAGGTACCGTCCTTAA	AACGCTTACATTCAATTCTTT	ACGCTTACATTCAATTCTTTA	TACGATGGTCTCAACACCTTT
284293	LOC284293	XM_209104	AAATGGCACATTTGCATTAAA	GTGGCAAATTCTACCAAGCAA	CAGCTAGACTTTGTGAATGAT	AACAACTATGCAAACATTAAA
284296	LOC284296	NM_175908	CAGGATTTCATTCAAACATGT	CAGAGACATCCTCTACTGAAA		
284312	ZSCAN1	NM_182572	CACACCAAAGGTGGTACCCAA	CCCTTGGAACCTAACAGATAA		
284352	LOC284352	XM_113978	CGCCACGGCCCTGAAGATGAA	CTCGACTGTCTGGACCTGAAA		
284353	NKPD1	NM_198478	AGCCGTGGACATAGCTTCCAA	CAGGGTATACATGCAATAAAT		
284361	LOC284361	NM_175063	CCGGGATGTGGCAGCCCTGAA	CTCCCTGTAAGTCTATTTAAA		
284393	LOC284393	XM_209178	CCGAATTTGTGCCAATAAGTA	ACCAAGTTCAATGCTGAAGAA	CCGCACCAAGCTGCAGAACAA	CCCGTTGTTACCGGTATTGTA
284397	LOC284397	XM_209180	CAGGAGGATTAATAGGTGGAA	TCCCATGAGTATGTAGCCATA		
284427	MGC34725	NM_173637	AAGAATTACTTCTGTGGAATA	CTGGGTCAGAAGATTCCTGAA	ATGCATGACAACAACCTTGAA	AATGGTGAACATGTCACACAA
284475	LOC284475	XM_378886	TGGGATTTGGTGAGAATCTTA	AAGGGCAAACTTGAAACATAA		
284485	FLJ36032	XM_371311	AAGAAGTAGAGTGGCTCATAA	CAGACTGGGATTGCTAACGAA		
284498	DKFZp434E141C	XM_209234	CTGGCTTTACAGCAGAAACAA	CTGAGCTTTCTTATCTTTATA		
284593	FAM41C	XM_496333	GAGGACCTTGTGCATGAATAA	TGGAATGAAATGAATTCTCTA		
284610	KFZp434D177-like	XM_371388	CAGCTGAAATGGCACATTCTA	CAGGGCTGTCATCAGCATCAA		
284672	LOC284672	XM_208234	GCGGCAGTTGTGATAAATAAA	AAGCATTTAAATGAAATTGAT	CTGGAGAGAAGTGGACTCCAT	CAGCTTAGGGAAAGAGAGCTA
284988	LOC284988	XM_209429	CAGGGTCCCATTCGACCTCTT	TTCCGGTTAATTGTTCTGGTA		
284992	FLJ39660	NM_173646	TACACTGAACTTTCACATAAA	AGGATTGTTGTTAATAATATA		
285033	LOC285033	XM_379111	ATGCCACATGATGAATACATA	CAGGTTTCAGATCCCAAGCTA		
285095	LOC285095	XM_211764	CCGGAGGGTCATGGAGAAGGA	CACAGGATCTTCATCATGGAA		
285188	LOC285188	XM_209505	CTGACTGAACCTCGACTCCAA	AAGGAGCAACTGGACCAGGAA		
285189	PRGA	XM_376111	TGGAGGTTTCTTGAAGACCTA	AAGACCTAGAACATAGAAGAA	CAGAGAAGAATGTGCAGCAAA	ATGAAGATACGTGAAATTCAA
285195	SLC9A9	NM_173653	TACGATATGCTACAGCACCAA	TCGGCTCTTCAGAATGTGGTA	AAGGGAATGCCCAGCTATTTA	CCACTGTTTGTTAGGCCTTAA
285220	EPHA6	XM_114073	CACTGTTTATGTACTCATGTA	CACGTGAATTACACCTTTGAA	AAGGGTTATTTCCGAGCTGAA	CAGGTATGTAATGTAATGGAA
285248	LOC285248	XM_371816	CTCGCAGAAGTTATGGAGAAA	CAGGAAGTATTTATTGTGAAA		
285267	ZNF619	NM_173656	AAGGGAGGAGATAGCCAGGAA	CAGCTAAACATTTCTAAAGAA		
285268	ZNF621	NM_198484	CAGGCTGAACTGTCACTTTAA	CAGCATAAACTCTATGGTTAA		
285296	LOC285296	XM_208312	TGTGGGCAGCTCCCTGAACAA	CTGGGCTGTTCCGGACTTCAA		
285307	LOC285307	XM_211837	TGCCATCTAATCTAACTTCAA	CACGGAATCAAAGAGAACTAA		
285313	MYSF10	NM_178822	CACCAACAAACTATTATTAGA	AAGCAGAATCACAGTCCATAA	ACGCATCAATTTAGGATACAA	CAGGCGTATATCACTGTATAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
285326	LOC285326	XM_211843	CACAAGGACCAAACATATGAA	CAGATGGGATCTCAAAGCCAA		
285335	SLC9A10	NM_183061	AAGCCTCATCAGTTTAATTAA	AAGTTTGTTCCTAAACATAAA		
285362	SUMF1	NM_182760	TTGAGTGATACTAATCATGTA	CAAGTGAAGACCAATATTCAA		
285386	FLJ41238	NM_198485	AACAATGGGATAAGCATTTAA	AAGGATGACTTCCAAATTTAT		
285412	LOC285412	XM_208319	CAGCTGCTACTGTTGCTTCTA	AAGCAGAAATACCAGTGGTAA		
285453	LOC285453	XM_209616	CAGCTGCTTCAGACTACCAAA	ATGGATGAGGATGAATTGGAA	TGGCAGCTACTGCAAGGTTAA	GACATTCTTAATTACAGGTAA
285521	FLJ38991	NM_173827	AAGTATTAGAATAGAACCAAA	CTGGCAATTCCTAGTTAATAA		
285643	LOC285643	XM_209695	CTGCCTGGATCTATAAATGCA	CTGAGTGAGCACCGCCACAAA	AAGGAAGGTATTGCAGCTCGA	GCGGTAGAAGAAGAAGCTCAA
285671	LOC285671	NM_178532	CTGGATCATATGGTAAGTATA	AAGCAAGGAATTGATAACTAA		
285676	ZNF454	NM_182594	CAGGGATTTCAACCTAGCAAA	AAGAGTTCAACTCTTAATAAA		
285692	LOC285692	XM_498992	CAGGAACTCCTTCATAGATGA	CCCAGCCAAGTCAGCATATAA		
285703	LOC285703	XM_209728	ATGAGAGTGAATTCTGAAGAA	CTGGTTGAGCACTCTATACAT		
285733	LOC285733	XM_379432	CTGCACTTGATTACAATGAAA	CTGCAGCATCTTACTACATAA		
285741	LOC285741	XM_209741	CTGCGCTTGCTGCAAGCTTCA	CATGTTATGTATGTTGTCGAA		
285759	FLJ34503	NM_173673	ATTGATTGAATTAATGTTTAA	CAGACTATATTTCATCAGCAA		
285761	DCBLD1	NM_173674	CACAATGACATCTAAGAATTA	ACCGATTAATCTAGAGATAAA		
285770	LOC285770	XM_209753	AAGGTATTGGTGCCTATGAAA	CTCCTGCTATCTTTAAATCAA		
285830	FLJ35429	NM_001003807	ATCTATCATATTAGAAATCAA	AAGGAGAAGAATGACTATTTA		
285940	LOC285940	XM_376585	CTGCATCATCTTTGAGTACTA	CCCGGATGATCCGAAAGACAA	TACAGTCTTTGTGAAATGAAA	GTGAATATGTGAAACAGTAAA
285966	FLJ40722	NM_173678	CTCCTAATAAGTGTTCCATAA	CCCTGGTAACATCATCCTCAA		
285973	NOS3AS	NM_173681	CAGCTCTGGCACAGTCAAGAA	CAGCCTCACCTTTGCTCTCAA		
286094	LOC286094	XM_212170	AAGAATGGACTCTTCTATTAA	CAAGCTGTTTATAAACTATAA		
286122	FLJ37131	NM_173687	AACCATACTGTTAGTGTATTA	CTGGCTTTCCATGACTACCAA		
286183	FLJ39630	NM_173688	CACCGATCTAATGACATTCAA	CAAGTAGTTATTGAACTTCTA		
286187	LOC286187	XM_209936	AAGCATTCTGTTTCTGGAGAA	AAGCAATTCACTCATAAGTAA		
286204	CRB2	NM_173689	ACCGGAGGAGAGACTCATCTA	CAGGGTCAGTTTACTAAGTTA		
286207	C9orf117	XM_209941	CGGGACCAGCTTCCTTAGCAA	CAAGGAGATGAAGGAGTTCTA		
286238	LOC286238	XM_379684	CTCAATGAATATAGAAGGGAA	CAGCCAGGATTCAAACTATAA		
286262	C9orf75	NM_173691	CACAGTGGTGCCCAAGAGGAA	CTCCTCAAGAAAGAAGATGAA		
286327	LOC286327	XM_497054	ATCATTCTCATGAGTCGCAAA	CTGTATATCTGGAATGTTTAA		
286336	C9orf59	NM_033387	CAGCAGAATCCTTATTTATAA	AACCGCATAATTATTCATTAA		
286423	LOC286423	XM_210042	TAGGCAGATCTCCGTGAAGTT	TTGTACCAACGCAATGAACAA		
286453	dJ341D10.1	NM_001007535	TACAAAGACCAGTGAATTATA	TTGAATTCTATTAGTATGTAA		
286561	LOC286561	XM_210515	CTGGGCCAATGTTGTATCCTT	GAGGGAGGAGGCAACCTTGAA		
286749	SALF	NM_172311	TTGCTACAACATCCAGCCTAA	CAGTCTAGGTTCTACATCTTA		
286753	TUSC5	NM_172367	CAGCATTACCCTCATCATCAT	CAGGGAGAGGACAGAAATGAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
286826	LIN9	NM_173083	TTCCTTTAGATGTCTCATAAA	TAGGCTTCCAACACCAAATAA	ACGAGTGGTTCTATTCAAATA	CCAGTAGATTTTCTTATCCAA
286828	CSN1S2A	XM_379270	CCCATTTAGAAGAACATGTAA	CAAGAAGAAACTGCAAATAAA		
317702	VN1R3	NM_174980	TAGCACAAAGACAAATGATTA	CCGATTTATGTGGATTGTCTT	CTGGCAAGTGGAACAGCATAA	CTCAGTGATATTGGATGCAAA
317781	DDX51	NM_175066	CAGGAGAGCCTCGTCCAGAAA	CTGGAGGAGTCTGTCAAGGAA		
326340	ZAR1	NM_175619	CAGCACTTTCAGCTTCAAATA	CACGATTTATACATTGCATAA		
337867	PHGDHL1	NM_177967	TCCGTTGTCCATCACAAACAA	CACGCTGGACATCCAGAGACA	TGCCATTACATTAGCATCTAT	GAGGGTAATGTTACTTCACAA
337976	KRTAP20-2	NM_181616	TACTATGGTGGTCTGCGTTAT	GTGCTACTACAGCAACTACTA		
338328	LOC338328	NM_178172	CTGCAGCTTCCTGCAGAGGAA	CCAGATGACTACGACGAGGAA	AAGTACAGAGTGAGACTTAAA	CACCAGTTCAACACTCCATTA
338382	RAB7B	NM_177403	CAAGGCTGGTGTAGAGAGAAA	AACGAGCAGACTAAGGAGTAA	TCGAGGTAGCAGAGCATCTTA	CAGCATCCTCTCCAAGATTAT
338398	TAS2R60	NM_177437	AACTATTTAAGGAACCATCTA	TGGCGATAGCATACGGAGCTA	TCCGATGGCCTTCCCATACAA	CAGGCTGAGAGCTGTGCTGAA
338440	TP53I5	XM_374860	CACGGTGGTGTTCGCCATCTT	CTGCCTCAAGGGCTACGTCAA	GACCATCATCATCATGACCAA	CGGGAGCAGCCAGTTGATGAA
338611	LOC338611	XM_291745	CACAGCCATGTGCAGCCTATT	TCCAAGCAGTATATGAAGCTA		
338645	LOC338645	NM_001009909	CAGACCAATTATGATCCTTAA	AAGGAAATCTTTAATCAATAA		
338657	DLNB14	NM_198489	ATCATTGTCTTTCTTAGGAAA	CAGGACCATCTCTGACATTCA		
338661	LOC338661	XM_290501	AACATTTGTTGTTAATATAAT	AAGTATCCAGGATGAACCTGAA		
338692	LOC338692	NM_207354	CACCGTGTTTGAAGTGCCCAA	CCGGAGGAGCTTCATCTTCAA		
338751	OR52L1	NM_001005173	CTGGTAGGGATTCCAGGTTTA	CACCGCTTTAGGTCATCATGTA		
338879	RNASE10	XM_292225	AACGCTGGTGCTTAGCAACAA	CTGAATGTGGAGAGTGATCAA		
338949	LOC338949	XM_294751	AACAATGTTTAGAGTCATGAA	CAGAAATGGAATAAATATCAA		
339005	LOC339005	XM_370838	CAAAGTCACATCTTTGTGGCA	CCGAAGTTAGAGCCTAGTGTA		
339022	LOC339022	XM_294775	ATGGATTTATAGAGAACATCA	AGAGAATACATTTAAATTAAA		
339059	FLJ40448	NM_182605	AGGAGAATCACTTTCACTTAA	CACCATCTGGTTGCCTGGCAA		
339065	LOC339065	XM_294794	AAGCTACGATAGAGTTAGATA	CAGGGTAGTGATGACCTCACA		
339145	FLJ44299	NM_198491	CAGCTGAGTAGGACAAATGAA	CAGAGTGGCTTAGAACAGTAA		
339201	DKFZp762C2414	NM_178542	CCCGGCTGATTGGATTCGTTA	CTCCATGAGGCTGGTCCTGAA		
339210	LOC339210	XM_378687	CTAATAAACATTGGTATTAAA	CTGCAAAGAAATACTTGATAA		
339324	LOC339324	XM_290838	AAACATCACAATATTCATACA	AAACATAATATGGAACAATTA		
339390	LSECtin	NM_198492	CTCCTGGAGCTGATTGCCAAA	AATAAATATTTGAGAAATGAA	CAGCCTGAGGAAGCATCAATA	CTGAGGAAGCATCAATAAATA
339398	LRRN6D	NM_001004432	CACCTTGAGGCTGTCTGGCAA	ATCATTAAACCTGCTGTCAAA	CACGGCTATAAGATTATTTCA	AGCGCTAGTCAGCTAGTCTAA
339403	RLN3R2	NM_181896	CCCGGGAGAGCCGCCCTTCTA	TTCAGACACCTTCGTCTTCAA	CAGGCGGTGGGTCGCAAGCAA	CCGATGCCTGTCAAATTCCTA
339451	KLHL17	NM_198317	CACGCTTGATGGGAACCTGTA	CAGCCTCAACTCCATCGAGAA		
339457	LOC339457	NM_001003808	CAGGCGAAGTTTGACACATTT	CAGGGTGTGGTCAGCCGCAAA		
339483	LOC339483	NM_178546	GCCGCTGACTGTAACATGTAA	TAGGGAGGTCTCAATAATAAA		
339488	TFAP2E	NM_178548	TATGTTGTAATTAAATTTGAA	CTCAAGGAACAAAGAAGATAA		
339512	MGC48986	NM_178550	CAGGGTGAAATGAGCCTTGAA	AAGGGATAATTTATACTTCAA		
339559	ZNF642	NM_198494	CCAGGAATTGTTGACTTTCAA	CAAGTGTAAATTGGTGATTTA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
339669	MGC35206	NM_178552	CTCCGTCTTCTCAGACTACTA	TAGAGGTGTCTTCTACTCAAA		
339766	LOC339766	XM_291007	CAGGATCTTCTTCGACAACGA	CCGGAGGAGATGAACCTGCAA		
339778	LOC339778	XM_496547	AAGGACTTTCTGTCCATCTAA	CACCATCATCCTTACTGATAA		
339788	LOC339788	XM_379074	TTGGTAGAATTTACCTTATAA	CTGAATGTTTGTACCCTCTAA		
339799	LOC339799	XM_290345	CGGAGTTGAGCTGATCATGAA	CACAATGAGTCAGAAGATGAA	TACGCATACTATGACACTGAA	CCGCATGAGCATCAAAGCCTA
339843	LOC339843	XM_290351	CTGGGTTGTGAGCTCCTTGAA	TACCATGGAATGGGTCAGAAA		
339862	LOC339862	XM_376212	CAGCTAAATAATTGCTAAATA	TAGGTTCAACTTCAGCATATA		
339879	LOC339879	XM_291054	CTGGGCGGCACGCACTCTCCA	TAGGCTGGTGACACGTCTCCA		
339983	FLJ37478	NM_178557	CAGCCTGAAACCAACACATTT	CACATTCAGCTTAGAAGTGGA		
339997	LOC339997	XM_295126	TACAGTACATTAGACATTCAA	CAGAGCCTATGTCAATGGCAA		
340024	SLC6A19	NM_001003841	CCAGAAGATCTCCTACCCGAA	CACGAACATCCTGACCCTCAT	CTCGGTGATTGTGTCCATCAT	CAGGTTCAATAAGGACATCGA
340074	LOC340074	XM_379355	CCGGCATACAGTCACCACCAA	ATGCATCTTAATCATTTACAA		
340094	LOC340094	XM_295155	AGGCAATAAACTTAAACAATA	AAAGGCCATTACAATATTTAA		
340096	LOC340096	XM_293943	CTCCGTGGAGAGGGTGCCGGA	CCTGGGAAACCTTGCAGTCTA		
340113	LOC340113	XM_379324	CAGATGTTTGTTTCTGCTCTA	AAGGAGCAGAACATCTGTTAA		
340146	SLC35D3	NM_001008783	CAGGTATATGAAGAAGGATTA	CTGGAATATAATTCAGAATTA		
340156	LOC340156	XM_373109	ATCGGGATGCTAAGCAAATAA	AAGCTTCTGGGTAAACACATA	AAGAATAAACATGGACCTTAT	TTGGTGTTGATAAGAAATTAA
340168	LOC340168	XM_291161	AGAGCTAGAGTGATTCCTTAA	ACCAGTTTCCAGCCAATGCAA		
340265	GRID2IP	XM_294249	CAGGACTGTCCGAGTCTACAA	GCCCAGGACTGTCCGAGTCTA		
340267	LOC340267	XM_295195	CTGGTAGGTTGTGCTCAACTT	TACAGGATATCTTATTTGAAA		
340348	MGC50844	NM_178562	GCGGACATACTTAGATCCTAA	CAGCATTGTGCCAGAGTGATA		
340359	LOC340359	XM_294387	AAGGTATGACAGCATCTGCAA	CCGGGAGAAGAGTGAAGCCAA		
340393	LOC340393	XM_291270	CTGCCTGACTCAGATGCCTAA	CCGGAAACTCAACATCAACTA		
340485	ASAH3L	NM_001010887	TTGGGTCAGATGCTTGATGAA	CAACAAGAAATCATCAGTCAA		
340515	LOC340515	XM_379650	ACCAATGTATATGCACTTGTA	TAGGAAGAAGTGGTAAGCTAA		
340526	RGAG4	XM_291322	AAGGATGAAGAAGATGAAGAT	TGGGCAGTCGCTGTCGCATTT		
340542	LOC340542	XM_291335	AACATTGATATGATAGATGGA	AAAGTTAATAAAGCAATTTAA		
340595	FLJ46608	NM_001004308	CTGATTTATAACCTGCATTAA	CTGCAGTAGTTTCTAACTCTA		
340654	LIPL3	XM_291663	CAGCTTTACCACTCTGATGAA	CAGGCAGTGAATTCTGGTGAA	CAGGATACTCCCTCAAATCAA	CAGGACTAAATTGGCTGTTAA
340665	CYP26C1	NM_183374	GCGCTATGGGACAGTGTTCAA	CCGGGTGATGCCCTCGACCTA	CACCTTCGAGCTCGACGGCTA	CTGGAGCGTGATGTATAGCAT
340900	LOC340900	XM_291767	AACCTGGTATTGGAGATGTTA	CTGATTTATTAATTAGCTATA		
340913	LOC340913	XM_291770	AACAGCCATGTGGAAGTAATA	CTGAGTCATGTTTCTACCTAA		
341032	MGC50104	NM_198498	AAGGAGTGAGAGTGAAGCATA	CCGGGCAGACAAGTAACTCAA		
341356	LOC341356	XM_292023	AGGGTGGTGAGAAGAATTACA	ATGGAGTTGGTTTCAAGAAGA		
341418	OR6C4	NM_001005494	ATCCCTTCATATATACTTTAA	CAGCATGACAACAGGAAATAA		
341457	LOC341457	XM_292085	CAGGGAGAAATTTGATGACAA	CACCGTGTTCTTTGACACGGA		

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Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
341511	LOC341511	XM_292109	TAAGGACGTTAAAGCCAACAA	CAACATGCTTGTGTTCATTAA		
341784	LOC341784	XM_497370	ACCAACGTTCATGCTGAGGTA	CGGGATCATGAGGGAGTTTCA		
341883	FLJ46156	NM_198499	CTGAACCACAATACAATTAAA	CCGGTTGTTTGTAATATTTCA		
342346	LOC342346	XM_296817	CAGGAGTGCCCTGGCAGGCAA	AAGGACGTGAACACCAAGTTA		
342372	PKD1L3	NM_181536	CCGGTAGAAGACATCCTGGAA	CACCAGTTCTCGGAAATCAAA	ACGGAGATGCCCATTATGAAA	CAGCTGGATGATTTCAATTAT
342538	MGC71999	NM_199290	GAAGCTGTCGGAAACATTCAA	ACAGCATCTGATAGTGGTGAA		
342600	LOC342600	XM_292624	CCCGCTAGGCTTCCTGGGAAA	CTGGATTCTCTGAACACCCAA		
342618	LOC342618	XM_496207	AAGGACTTGTTTCACTGCAAA	CAGGAAGAGGTACAATTTAAA		
342669	LOC342669	XM_292674	CCAAGTGAACCTATCCGCAAA	CAGGGCATCTGCACTGGAGAA		
342853	LOC342853	XM_497574	CAGCATGTGGCACAAGAGACA	CATCAAGATCGCGGAGATCAA		
342931	LOC342931	XM_292796	GGCGCTGGTTTCCATCATCAA	AACGTTGTACTCTCTTCAGAA	GAC[illegible]GAAATACCAGTGCTTTA	AACGATCTCATCGTTTCTGAA
342933	LOC342933	XM_292723	AGCCGGGAAGGAGAAACTCAA	ACGTGTGCAATAAATCATTTA		
342934	LOC342934	XM_292724	CTGAATCTGAGAGGTCTCAAA	AAGGAATATCTTATGCAGGAA		
342945	HKR2	NM_181846	CCCGAGCAACCTCTCCAGTTA	CTCAGTATCTACAACACAGAA	TAACCTAAAGCTTATCTGTAA	CAGGGTATAAGTATGCTGAGA
342969	LOC342969	XM_292824	CACTCATTCCTCACACCTAAA	ATCGGTTAAGATCGAAGGCAA		
342970	LOC342970	XM_292810	AACATTGAAGATCAGTACAAA	CAGGAGGAGAAA[illegible]CCTATGAA		
342977	NANOS3	XM_292819	ACGCCTGTGCTCTTTCTGCAA	CACCCGAAA[illegible]CGGCAGGCAA		
342979	LOC342979	XM_292820	ACCACTGGGCATAGAGAGAAA	ACGGAG[illegible]GAGATCTGAATCTA		
343035	C1orf36	NM_183059	TTGAGGGAAGGAAATAATTTA	AAGA[illegible]TTGATTGGCTTATTAA		
343169	OR6F1	NM_001005286	CACCTTTGTCTCCTATGTGTA	C[illegible]GGGCTTTCCTGGTTCTCAA		
343295	LOC343295	XM_497684	ATGATTGTAAGGGAACAGCAA	CCCATGGAATATGAGCATGAA	TGCCACATTGGTGATCCTCTA	ATGTATAACGATGACCTAGAA
343406	OR10R2	XM_372798	CCCAAGATGCTTATCAACTTA	ATGGAAGGTAGGGATAATGTA	TACAGGTAATTAGATGATTTA	CACAACTGTTATTCTGCCCAA
343413	LOC343413	NM_001004310	CAGGGATGGAAGAATTCACCA	CACCAGAAAGGGAAAGATGAA	CAGACATTCACACAAACTTCA	CAGAGAGAGGAGTGAGCCCAA
343472	BARHL2	NM_020063	CACACAGAGTGC[illegible]ACCAGTAA	CGCCTTATTTCTATCACCCAA		
343505	LOC343505	XM_291607	ACCAAGGAG[illegible]TGATAAAGTA	TTGGCACTAGTTGAACAGAAA		
343563	OR2T29	NM_001004694	AACTGTG[illegible]GATTCGTCCTTTA	AACCCTTTAATCTATAGTCTT		
343629	LOC343629	XM_293121	CAGA[illegible]CTGCATTCATATACAT	CAGAGGTTGAACATACCCTAA		
343990	MGC42367	NM_207362	AT[illegible]GAACTTGCCAGAAAGAAA	CACAAGGGTGATGGACATTAA		
344018	FIGLA	NM_001004311	CAGCAAAGTTGATATCCTTAA	TACCTTCTAGAGACAAATAAA		
344065	LOC344065	XM_292[illegible]	AAGCTCTTAGTGAGCATTTAA	AAGGATATTTCTGAAGAAGAA		
344165	LOC344165	XM_2[illegible]957	AAGCCAGAGGATTGCAACCAA	CACGAAGACTGGAATCTGTAA		
344172	LOC344172	XM_[illegible]497885	ACGGAACCAGTCGGTCAGGAA	CTGAATTCGAATCACTGTTTA		
344328	LOC344328	XM_497894	AAGAGTTAAGAAGGCATGAGA	CAGGATCCGAGCAAAGCTAAA		
344561	GPR148	NM_207364	GAGGATCTATGCAGAGGCCAA	CGCCATTGTGCTGCACACCTA	CCACTTATGACTAACTTCTTA	CAGCACAATATAATAGTGGAA
344709	LOC344[illegible]89	XM_298233	CAGGACCAACTTCGCAGATCA	AAAGATTCACATGATGAATAA		
344805	TMP[illegible]SS7	XM_293599	TAACTATTCAATAACCAAGAA	CCCAGCGTTGTGATGGAGTAA	CCCGAGCTACTATCCTCCAAA	TCGGATTACTCGTCAACCATA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
344807	CD200R2	NM_001008784	AAGGATAGAAGCCACTCAGTA	CCAAGTCTGTTGATTGATTTA	CTGATCATTCTTTATGTGAAA	AGCGTTGTCCTTACTGATCAT
344838	PAQR9	NM_198504	AAGGCGTGTGTCATGATACAA	ATGCATGGAATGTGAACACAA	CAGGGCTTAACCTGCTAGAAA	CACACTCTTCGTGCACTTCTA
344892	RTP2	NM_001004312	CAGCGCTGCCTCTGAAGCCTA	CACATGATGTGGAGAATGCTA	CGGAATGAGAGGATTGCATTA	TAGGGTGTCGTACTTACCATA
345051	LOC345051	XM_293680	CAGAGGCTGGGCGATGTTGAA	CAGGATGATCCCAGCTTTGAT	CCAGCTTTGATTCACTGGAAA	CAGCTTCTTACCTCAGTCAAA
345079	LOC345079	XM_293687	AAGGCCAAGAGCAAGGAAATA	AAGCTGCTGAGAGTTGGTAAA		
345275	SCDR9	NM_178135	AAGAAAGAAGTGGGTGATGTA	TACCAAGACATTTGAGGTCAA	TCCATCGATGATGGAGAGAAA	CTCCCACTACATCAAGACTAA
345378	LOC345378	XM_293802	CTGCTGTTCTGTCTGAATTAA	ACCCTAGTAAATCATCTGCTA		
345537	LOC345537	XM_293868	TAGAATTTAGGTCCCTTGTTA	CTGGATGAGAGATCTTCCTAA		
346007	EGFL11	NM_198283	AACGATCCTGAAGATAATAAT	ATGTGGTAAATTGGACACTAA	GAGGAATAATGCTACATGTAA	AAGCTTGGAGCAAGACATATA
346305	LOC346305	XM_498257	CAGGGAGGCTTCTCAGACCTA	CACGGTGGAGACCATATTGTT		
346517	OR6V1	NM_001001667	CAGGATGCTCTCAGACCTGTT	CAGTAGTACCATCTTTCTGTA		
346702	LOC346702	XM_498271	CAGAAGGTCATTATTCACAAA	AGGCACCAATGGTATCTTCAA	AAGAGCCCTGCTCAAAGTTTA	CTCGTCATGGTTACCATTTCA
347051	SLC10A5	XM_376781	TAGAAATATCCTAATGCTTAT	CAGTGGGATTAGTGTTCTTAA	ATGCCTGTCAATTCTTATATA	ATCAATTGGAATAGTCATCAA
347088	GPR144	NM_182611	CAGCGAGTGGGCCAAGGCCAA	CTGCTGCAAATCTATGAAGTA	CCGAGTCAATGCCTTGGCCAA	CTGGCTCAATGTGCACACAAA
347292	LOC347292	XM_294581	TATGGCCATGGGCCTCTTCAA	AAGCGGCGTGCCATGGAGCTA		
347376	LOC347376	XM_293312	CTGAGTGTTGTGGGTGGGCTA	AACGTGTTTCAGTATACACCA		
347527	LOC347527	XM_293401	CACCGCTGGCTCAGGATCAAA	AAGCTCATTATGTGACTCCTA	GACGTTGGAATTGCATCCTTA	CAGCCATAAGAGAGCATCGTA
347549	LOC347549	XM_293416	CAAGAGGTGGCTGGGAAAGTT	CGCCATGGGCAGAGTGAGGAA		
347689	SOX2OT	XR_000282	CAGGACTTATCAGCTGGGATA	AGGAAGGTTGATTGGAAATAA	CAGGTGTAGATCACCTATTAT	TCCGGGTTCCCAAGAACTAAA
347731	LRRTM3	NM_178011	AAGGCTTGATTTATCAGGCAA	GAGAAATAATACATTAACCAA		
347732	CATSPER3	NM_178019	CCCAATGGTCTTGGATGATTT	CAGACAATGGTGACCATGATA	GCCCAACATTCAAGAAATTTA	CCGTTTCTTTAAGATAATTAT
347734	SLC35B2	NM_178148	CTCGCAGTTCCTGGTGCTAAT	CCCTGTCATGCTGATGGGAAA	CCCGATGTGGCAGGCCCTGAA	CAGCTTTATGGTACCTGGCTA
347918	FLJ33915	NM_182613	CTGGAGATGTGAATTCCATAA	AAGCATCTAAGAGGCAATGAA		
348035	MGC40069	NM_182615	CAACAGATGTTCATATTTCTA	TACCTTTGATAAGATGGCTAA	AACGGGATTATTCAGTAGGAA	CCCAGTCACCTGACAAATCTA
348094	LOC348094	NM_182703	CACACTGATGCCAGATGTTAA	ATGGACTTTAGTTAATAGTAA		
348174	LOC348174	NM_182619	GACACGGCCATCGGTCACTAA	CACTAATCTGCAGCACCGGAA		
348303	SELV	NM_182704	CAGCAATTTCCGAATCACCTA	ATCGATGAGGAAATCAAGAAA		
348327	ZNF530	NM_020880	CAGGTATCTGTCCTCATTCAA	CTGGATGAGTTCAAACCTTCA		
348487	FLJ36766	NM_182623	CTGTGTCATTGGCAAGGACAA	CCGGGCCCGCGGAGACATGAA		
349136	LOC349136	NM_198285	CAGCACAGATGGCACAGCCAA	CAGGATCCTGGTTGCCAACAA		
349236	LOC349236	NM_182635	ATGCATGACTGGGACAAGAAA	AAGGTGAGACTCCACATGGAA		
349565	NMNAT3	NM_178177	AAGGTCTAAATCACAAGGATA	AAGGGATAAATAATAAATTGA		
350383	GPR142	NM_181790	ATGGTGTCCCATGCACAGAAA	CAGGAGGCCCTCCTACTACTA	AACACTGGACGAGGTCCTCAA	CCGGGTCTTCGTCATGCTCTA
353145	LCE3E	NM_178435	CTGACGCATGCCTTCCCATAT	AGCGATCTTTGGAGGAAACAA		
353299	RGSL1	NM_181572	CAGGTCATTAGCCAGAATAAA	CCCGCTCTTACTTACAGTATA		
353376	TIGAM2	NM_021649	CAGGAAGTATTTCTCATTTAG	CTCCGTTAACAGGCAGCATAA	TCGGGTACTATCACCCAGAAA	TTGCCTGAGATGAAACATATA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
353514	LIR9	NM_021250	ACGGCTGAGATTCGACAGGTT	CAGGAATACCGTCTGGTTAAA		
359948	IRF2BP2	NM_182972	CCTGATCTTAGTAGCAGACAA	CTCCGTCCTCTATGAACCAAA	CCCAATGATTACCCTTAATTA	CTGGTTGAATTGTATATATAT
360023	FRBZ1	NM_194314	AAGGCAGATAGTATATATATA	AAGCCTAATGTCTGTAATTAA		
360132	FKBP9L	NM_182827	GAGGACCGTGTATGAGAGAAA	CTGGAATATTCTGTCATAAGA		
373856	USP41	XM_036729	ATGCAAGCTACTGTGAATTAA	CAGCAGGATGACTATCCTTGA		
373863	DND1	NM_194249	GAGGGTGAATCCAGAGAACAA	CAGCCCTGTGTTCCTCACCAA		
374355	C10orf96	XM_495849	AAAGAGTGAATTGATACAAGA	AAACAGTACAGTGAAATTACA		
374383	)KFZp686O2416	NM_001009913	CTGGATCAAGTGGGCATGAAA	TAGGTTGTTAATACTCGTGAA		
374387	)KFZp779M065	XM_374877	CCAGGAAAGATGAACATCCAA	ACCCTGGAAGGTAGCACATAA		
374618	TEX9	NM_198524	GAGGATGAAATTCAGAATTTA	ACGAAGATGATTACAGTTTAA		
374654	KIF7	NM_198525	TCCGTTACCCTTGACCTGGAA	AAAGAACTGGACCCTCATTTA	TAGCCTCACTGGGATCAACAA	TTGGCCAAGAATCATCACGAA
374860	ANKRD30B	XM_371111	CACTTTGAGCCTGCCACTGAA	CAAGAGCTTGGCGATACAGAA		
374890	LOC374890	XM_373798	ATCCAGTTCTATGTCCTATAA	CCAGGCAGGACTGACAATAAA		
374920	LOC374920	NM_199341	CCCGCTGGAGTTCGCCTACTA	ACGGGTAGAGACGAAATGCAA		
374955	LOC374955	NM_198546	CTGGATATTCCTGAAATGCAT	TAGGAGAATACTGTTTACAAA		
375035	LOC375035	NM_199344	CTGAATTCCCATGAATACAAA	AAGCAACAATAGATTCTCGAA		
375108	LOC375108	NM_198996	ATGCACTTGCTTGTGAATTAA	TCCAATGGTTAGGCATTCAA	AAGGATTCCTTCAGAGATTTA	ACCATATAGCAGATTAGATTA
375189	PFN4	NM_199346	AAGAATGAATTAAGGGAGCAA	AAGGAGTGTATTTCAAGGGAA		
375295	LOC375295	XM_374020	CCCGCTCAGTTCAATATTTCA	CAGGTTAGACCTGGCAGTAAA		
375298	CERKL	NM_201548	ACACTTGATCTTATTAATTTA	CAGCAGAGAAGTGGTACTTTA		
375318	AQP12	NM_198998	CTCCCAGTGGGCGCCTATGAA	CAGGCCGATGGCAGGTCTTAA		
375341	FLJ43654	NM_198562	AAGGATCTGCTTGATATGATT	ACCAAGTGAAGTATAGTATAA		
375347	FLJ44290	NM_198564	CTGGGTGGTATGGGAAGTGTA	AAGGATTCAACTATATTTATA		
375444	FLJ32363	NM_198566	CTGGTAATTTGTGAAACTGAA	CAACATATTATTAAAGTTTAA		
375484	FLJ44216	NM_198567	CACCAATATTATGTCATTCAA	CCGAAAGGACTTAATAATCAA		
375757	C9orf119	XM_372143	CTGCACCTTGACATTCAGAAA	CAGAAGGGTGTGGACATGATA		
376267	RAB15	NM_198686	CTGCACCAACCTCAACATTAA	AAGGACTATATTTGTACTGTA		
377630	DUB3	NM_201402	TCCGATGTCACAGGCAACAAA	CTGCTGGAGATCTCAAATCAA		
377677	CA13	NM_198584	AAGGGCAATGGGATAAAGCTA	ATGCACTATAAGTTAATATAA	CTCAGTGATGTTAGATGGAAA	CAGAGGGACACTAAGCATTAA
377841	UNQ2492	NM_198585	CACAGTTGAAGGGACAGGCAA	CAGCGTCTACACTCACAGCTA		
378832	C21orf123	NM_199175	CCGTGAAAGGATGGAAACAAA	CTGCAGGAGTGAGCAATTTAA		
379025	FLJ31306	XM_495990	CAGAGCTGTCAGAAAGAATAA	ATGAAACATACTCAAGATTTA		
386678	KRTAP10-11	NM_198692	GTCCAGCTGCTGAGTGCTCAA	AAGCAGGATTCTCCAGTCTCA		
387032	ZNF307	NM_019110	TTGGAAGAAGTCATTTGATAA	CGGAATAGAAGTCTTATTGAA		
387054	FOXD4L3	NM_199358	AAGCACCTGCTCCTCCATGAA	AAGATTAAGCCTAGTTATATA		
387082	SUMO4	NM_001002255	TCCGGTGTTCACCATGGCCAA	TCCGATTTGGTGGGCAACCAA		

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Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
387332	TBPL2	NM_199047	CAGAATATAGTTTCCACTGTA	TACAAGTACGTTACTTATTAA		
387357	C6orf190	NM_001010923	TACGCAGATAATGATCATTAA	AAGCCTGTTTATGAAATTCAA		
387509	GPR153	NM_207370	ACGGGCCTCGTGACCACCATA	CAGGACGTCGGGAGCAGGGAA	GACCACCATAGTCTTCATCTA	CAGCGTTGGCGCCAAGCAGAA
387601	LOC387601	NM_199352	AACGTCATAGTATACCATCAA	CTGCTAGTATTGGACATATAA		
387643	LOC387643	XM_370537	TTGAGTTGTCATGTAGATTAA	CAGGCAGTTTGTGAATATTAA		
387710	LOC387710	XM_373474	CCGGCTCTACTGAACTTCAGA	CTGCTCAGATGTGAGAAGTAA		
387715	LOC387715	XM_373477	CCGGGTGATAGGCATTAACTA	CAGCATCAATGTGAAGCCAAA		
387717	LOC387717	XM_373478	GAGGCAGGCCTCGCCATTTAA	CCCGGCTGGAATCCAGCTCAA		
387720	LOC387720	XM_370584	AACACAATGATTTGACAGGAA	AACAACTAATTTATGGAACAA		
387723	LOC387723	XM_370586	AAAGATAGACTTCTTCTTAAA	CTGAAGAATGAGGAACATAAA		
387748	OR56B1	NM_001005180	CACCAGTTCCTTAATCTTAAA	CACAGCGTGATTATTGCTCCA	ACCCTCTTCGCTATCCATCAA	AAGTCTTATTATACTGTCATA
387750	LOC387750	XM_370607	CAGCAGGCACTGAATATACAA	CAGGCCCATTTCTTTCATCTA		
387753	LOC387753	XM_370611	AAGAAAGACGCCAAAGAGAAA	AACCTATTTCCTATGAATTCA		
387758	LOC387758	NM_203371	AAGAAGATTAATGATCACTTA	CAGGTCTACATTATTTAATTA		
387763	LOC387763	XM_373497	ATGGCTGAAGGCATTTATTTA	AGGGAGAGACTTATACTTTAA		
387781	LOC387781	XM_370634	CACCTACTAAATACAAATAGA	CAGCCAGATATTTGTGGACAA		
387804	LOC387804	XM_370648	CAGCCTCATGTGGGTTTGTAA	CAGGGCCGTGCTGACACATAA		
387820	LOC387820	XM_370665	AACAGAAATGTTAAACTATAA	AAACAGGACATCTATGACAAA		
387823	LOC387823	XM_373519	CCGTGTGATCCTAAACATGTT	ACAGCTCTTCCCATCATTTAA		
387825	LOC387825	XM_370668	CAAGGTTGTTAGAGACTTCAA	CAGAAACATGTTGCATGTTAA		
387836	UNQ5792	NM_207375	CAGAAATTGGACAGCCAGTAA	AAGGAGATTCTTGGAAATGGA		
387849	REP15	XM_370686	AAGGAGTACCTTGGATTTGAA	AAGAGAGATAATAAAGTCACA		
387851	AK3L2	NM_001002921	AAGCAGTTGCTGCCAGGCTAA	AAAGCCAGTCATTGAATTATA		
387856	LOC387856	XM_370691	AACCCGTGAATTGTGTAAATA	AACAATTTACCTGGAAATTAA		
387871	LOC387871	XM_373539	TAGGTATTTAATGTATTAATA	AAGGTACTTGAGAAACATTAA		
387873	LOC387873	XM_373541	CTGGGATTACAGAAAGAAGAA	CCCGGCCAAATGAGCTATTTA		
387880	LOC387880	XM_370704	GAGGGAATCATGGCAAGCCAA	CTCAATGGTGAACACCCGAAA		
387882	LOC387882	NM_207376	CACGACAATCTCATCATATTA	ACCAATGTATTTCAACAATTA		
387887	LOC387887	XM_373549	CACAGAGTCTTTCCAACTCAA	AACGCTGTTTCTAGTGCTTAA		
387895	LOC387895	XM_373583	ATGGACAATGAGAAACATGTA	CTCAGTAACAATAACAAGAAA		
387898	LOC387898	XM_373556	CGCGCAGATAATCTGGCATAA	CTCTTGGGACTCAGAAATCAA		
387911	LOC387911	NM_001007537	AAAGGCATCAAAGGTGATCAA	AAAGGAGATCGAGGAGAGAAA		
387917	LOC387917	XM_373562	ACAGGTGAAGAAACCCTTTAA	AAGGATGCTCTTGACGCCAAA		
387923	C13orf21	XM_370724	AAGGAACTGGCTGGCCCTGAA	ACCGGCAACTGAGATGTTTAA		
387930	LOC387930	XM_370727	CAACATTTCTGGCAATTTCTA	AGGCATCAACATTTCTGGCAA		
387937	LOC387937	XM_373569	CTGGACATCATTTAGCATATA	CAGGAAAGAGATTACTTGGAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
387950	LOC387950	XM_373578	CCGGGCATTGGTGTTTGCAAA	AAGGAGGAAACGGATCACCAA		
387974	LOC387974	XM_373583	ATCGGATTCATCTGACATTTA	CTGGTTTAAATGCCACCTTTA		
387991	LOC387991	XM_370763	CCCAGAAACAAGGCAAATGAA	CAGATACATCAAATAAAGTTA		
387992	LOC387992	XM_373594	TAACAGATCTTTGAACACTAA	CACTTAAAGAAGAGAATTTAA		
388007	SERPINA13	NM_207378	CAACATAGACTTTGCCTTCAA	CCAAATGCTTTCTATCTCTTA	TCCGTGCATGATTGCTTTGAA	AAGGATAGTAATGGTGATCAA
388019	LOC388019	XM_373611	CAGCAATACAGTCACATTCCA	CAGGGTGTGTTTGCTGGATTA		
388021	FLJ42486	NM_207379	CTCAAATGAGAATCAGCTTAA	CACGCTCTTCTTCCTATGCAA		
388022	LOC388022	XM_370779	CTCCACAGAACTGCCAGTAAA	ACACGCTAAGTTTATGTTTAA		
388069	LOC388069	XM_370829	TTACAATGCAGTAAACTTTAA	AAGGAACCATGGAAATAACAA		
388076	LOC388076	XM_370833	AAGAAATATCATGAAAGGAAA	AACGATCATCGATGTTGTCTA		
388116	LOC388116	XM_370856	CAAAGCAGAAACGGAATTACA	CACCTGGTGAATGAAATCAAT		
388129	LOC388129	XM_373631	ACGGAGACCCAGGAAAGATAA	CAGCCGAGGGCGAGAAATGAA		
388142	LOC388142	XM_373638	CAGCCCTCACTAGACTACAAA	ACCATAAACCATGCAATACAA		
388143	LOC388143	XM_370879	TCCCTGCGCCATCTTCCAGTA	AACAGGTGTTAATAAATAAAT		
388159	FAM42B	XM_370893	ACAGTTGATCGCAAACTAGTA	CAGATTGACTATCCAGTTTAT		
388166	LOC388166	XM_370898	AAGAGGTTTCAGGCTGCCTTA	CTCCCTTAACATAGACATTGA		
388174	LOC388174	XM_370905	CAGCAATCTCTGCATGCCTTT	CCCAAGAGGTTGTGTATCTTT		
388177	LOC388177	XM_370909	AAGCCCTCTCAAAGACACTAA	ATGGGTGATAGTGGCTTTAAA		
388180	LOC388180	XM_373650	TGCAATCAGACTAGAAGGAAA	CCGGGCATGATTCTCAACTTT		
388205	LOC388205	XM_370930	CAGAACCGATTTGGATTTGGA	AGCCAGGATTCCAGTACAGAA		
388214	LOC388214	XM_373666	GCGGCTGGATCTGTAATGAAA	TAGGCTGATGTTAATAAATAA		
388227	LOC388227	XM_373670	TCCGATGACTTCTGTCCGTAA	CCCGCTGTTGGGAGTCCTTTA		
388231	LOC388231	XM_373671	CAGGAAGAACCTCATACCCAA	CAGCATGTTTCTGATCATATA		
388248	LOC388248	XM_370968	CAGGGATGGAAGTGAAGTGAT	CCAGGTCTTTAGGAGAAGAAA		
388255	LOC388255	XM_370973	CAGCATCTGAATTACACTTAT	CAGAGTTGTGTTCACGAAGAA		
388276	LOC388276	XM_373685	CAGAATGCCAAGCTCCAGTAA	CAGAAGGAGCTTGGGAATACA		
388295	LOC388295	XM_373693	CAGGAAGAATTAGTGACCGAT	CCCAATAAGGCTGCTGACTCA		
388298	LOC388298	XM_370992	CAGCAGGCTAGTGATGGTTAA	CTGGGTGTTTGAAAGAATCAA		
388300	LOC388300	XM_373695	TTGGGATTCATGCTAGATCAA	TTGGCTGTTTCTAGAAAGATA		
388325	UNQ5783	NM_207108	CTCACTGGTAAATAAAGTTAA	ATGGTTCTGAGTGATATTAAA		
388344	LOC388344	XM_371023	ACCGGTCATGCCCATCCGGAA	AAGGGAGACAGTTCTGCTGAA		
388364	UNQ9372	NM_206832	CAAGAGTAGATCTGAGTTTAA	CACCTGATTGTTAAAGATAAA		
388387	FLJ31222	NM_207388	CAGCCTCCAAATTTCTTTAAA	CCGGCTGAAATTGTATACTTT		
388394	LOC388394	NM_203400	CCGGCGCCGCGCGGCGATGAA	TGGAAAGAAATCTTGTAATAA		
388419	LOC388419	XM_371078	CAAGTTCATCAGGTACCTGTA	CGCCAAGTTCTTCGACGTCAA		
388420	LOC388420	XM_373749	TAGCCTTGTTTGGGATACAAA	CAGCTATTTGGCACATTTCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
388428	FLJ44861	NM_207389	CGGGTCCTTCAACTACCTCAA	CAGGTACATCCTGTCCATCAT		
388429	LOC388429	XM_373756	CTGGTGGAAGCTGCAGGAACA	ATGGGCGTCTCCTAACCGTAA		
388489	LOC388489	XM_373786	CACGGTCAGCGTGGCGAAGTA	TCAGATCATCTTCATGTTGAA	CAGGCTGTGCAGGTCCTGGAA	TACCGTGTTCACCGAGTGGAA
388491	LOC388491	XM_371125	ATGCAGGCACTTGACATTTAT	CACCTTGAACATAACAGGAAA		
388494	LOC388494	XM_373788	CAGGAAGTATTTATCCAATGA	CAGAATCACAAGTGAAATAAA		
388514	LOC388514	XM_371145	ACCCTATATAAAGATCTTCAA	ATCTGCATCATCAACATTATA	CGGGACCCAGTTTATGCGAAA	CGCCTTCAGTACTTTCCACAA
388524	LOC388524	NM_001005472	ATGGAACAGTACATCTATAAA	AAGGAGGAATTTCAGGGTGAA	CACGGAGGCATCTTATGTTAA	CCCGTCGTAACTTAAAGGGAA
388531	FLJ45744	NM_207391	CAGGAGCTTTATTCCCTATTA	CAGCTTTAACTTGGGATTTAA		
388532	LOC388532	XM_371160	CTCACAAGTGTCACCATGGTA	CTGGGATAGCTTCCTGAAATA		
388533	UNQ467	NM_207392	CTGGGTGGTCCTGAGGAAGAA	CTGATTCTCAACCTACCATAA		
388536	MGC62100	NM_206894	CTGGTGGACTTGGAATGTTAA	CAGCGATCACATCTTATTAAA		
388538	LOC388538	XM_371165	AACCTTGGAGTGTACACTGAA	AAGGGCAGACATGGAGAAGAA		
388551	LOC388551	XM_371177	CCGCACAGGCTGCACCATCAA	CAGGCCCTAAAGAACGGCCAA		
388554	LOC388554	XM_371182	CTGGAGTGGGTCCAATATGAA	CACGGCCTTTGTGAAAGCCAA		
388564	LOC388564	XM_371196	CTCCCTCCTCACTTGGATAAA	CAGCGAGTGAGGCCCAGACAA		
388565	LOC388565	XM_371197	CAGCGCTTCGAGCCCATGGAA	CAGGGAGAGTCTGAAGCGCCA		
388566	FLJ26175	NM_001001668	AAGGCTTTCACTGATCACATA	AAGCATAGAGAGGATAAGTAA		
388579	LOC388579	XM_371207	AACAAATGTTCAACATTCAAA	ATGAGGGAGGTGGATGAACAA	CTGGTGTCTGAATATCAGCAA	CCAGCAGATGTTTGATGCTAA
388587	LOC388587	XM_373822	CCGGTTAGAAATGGCCGCGGA	CTGAGTGGATGTAGATGAGAA		
388605	HS6ST1P	XM_371230	CAGAGGTAGCTGCGTCCTGAA	ACCCATCTGTAGCTCCCTCAA		
388616	LOC388616	XM_373837	TACCATGGGATGGTTACTGTA	CCGTGTTATTTGGGAAACTCA		
388621	LOC388621	XM_371243	AAGCCGAGATAGCTTCCTGAA	AAAGAAAGAAGCCAAAGAGAA		
388624	LOC388624	XM_371244	CTGGCACTACTTCTCTCTCAA	AAGGATGTTACCAGTGCCTTA		
388630	LOC388630	XM_371250	AAGGGAGTGGATGTTAGGGAA	CAGGACATCCATGGCCAAATA		
388633	LOC388633	XM_371253	AAGCTTGTATAACACTGACAA	CACATCATTTCTGAATAGGAA		
388648	LOC388648	XM_373852	CCGCCAGCAGCCGGATTACAA	CAGGGATGTGCGGGTTCTCAA		
388652	LOC388652	XM_373854	CTGGCATTGTTTACTGGAGAA	AAGGGAAGTCGACGAAATAAA		
388662	SLC6A17	XM_371280	CACCCTCTCCGTGTCCTACAA	CAGCTACAATAAGCAGGACAA	GTGGTCGAGAATGCTGAGAAA	CTGGATTTATGGAACCAAGAA
388714	LOC388714	XM_371326	CAGGAATATATAAAGACATAT	CCGGATGATTACCCAAACTAT		
388720	LOC388720	XM_371330	CTGACTTACTGTTTCAACAAA	CGGATACAATAGATAATGTAA	AAGGTGGATGAGAATGGCAAA	TCGGATACAATAGATAATGTA
388730	LOC388730	NM_203376	TTGGTGGTGACTACACCTAAA	CTCCCACTTTGTGAAGTTTAA		
388818	LOC388818	NM_203405	CAGCTTCTTTGTTCCAGTGAA	CACCTTCTAGGGATAAATAAA		
388830	LOC388830	XM_371418	CAGGAGGGAAAGTCTAATGAA	AAGAATTGTGTTGGTCATGAA		
388882	LOC388882	NM_001006606	CACCTTGGTGAGAATCAGGAA	CCACAGATACAGATTATTAAA		
388885	LOC388885	XM_373949	ACCGTCAGCCACCTCAGTAGA	AGGCTACTACGTGAAGGAACA		
388900	LOC388900	XM_371466	CAGAGAAGAATTAATGTTGTA	CAGGAAGATGGAGGTCATCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
388903	LOC388903	XM_373962	CGGGAAGCACTTAACCAATGA	CAGCCAATCCTAGCTCGTTAA		
388907	LOC388907	XM_371470	CAGACAATAAACTTAGGGCCA	TTCGTGTAACTGACAGAGATA		
388917	LOC388917	XM_373970	CCATATGAAATTTGCAGTTAA	AGGGAGAATCTCAGACTACAA		
388922	LOC388922	XM_371476	AAGGATAGCAAGACAAATGAA	AAGGAAGTTGAAGGAAATCAA		
388927	LOC388927	XM_371478	CAGCTCCTTTCTCAAGCTTTA	CAGGGCTTTCAAGGTAATGAA		
388929	LOC388929	XM_371480	CCAGATTTATTACAACATAAA	CGCCATAATGTGATAAATAAA		
388931	LOC388931	XM_371481	CACGTTCTTCCAGGTGCCCTA	ACCCAATGTTCACACAAGTAA		
388939	LOC388939	XM_371488	AACCTCTTCATCCCAGCTGAA	AAAGAACAGCTGATTAAACTA		
388942	LOC388942	XM_373981	CAGGTTGACATCACATATGTA	CAGGACGAAGTCACACACTAA		
388954	LOC388954	XM_371495	ATGGAACAGTACATCTATAAA	AGGAGGAATTTCAGGACGGGA		
389002	ANKRD20B	XM_371535	AGAAGTAGTCACCGCCATGAA	GTTATTATTCATATTAATTTA		
389033	LOC389033	XM_374010	GCCAGGCAGCACCCTCTGATA	TCGGACTGAGAGCATTTCCTT		
389055	LOC389055	XM_374016	TAGCAGTGTGTGACACCATAA	CGGGAGTGCTCTGCAACTGAA		
389058	SP5	NM_001003845	CAGGGCGGTTCCAAACTCTAA	CAGCATGATATGTCTCTGTAA		
389067	LOC389067	XM_374021	CAACATTATTGTGACTATCAA	AAGAGTTATAATTACATTTCA		
389070	LOC389070	XM_374022	CAAGTTTCAGTGCTCAATATA	AAGAGATCAGTGATTACAATA		
389075	RESP18	NM_001007089	TAAGGAAGAAATTATCTATAA	CAGATTTGAATCATTAAAGTA		
389077	LOC389077	XM_374025	CACCTTACAGGCTGACCTTAA	TCCCACAAAGTTAGAAGCAAA		
389089	LOC389089	XM_374029	TACAGCATTCTCGACCTGTGA	TGGAAGGCTTGTGTTGAGTTA		
389090	OR6B2	NM_001005853	CCTGAGGAACAAGGAATTTAA	CACCGTGGTCACCGTCTTCTA	CACGCCAATAATTAACCCTTT	TTGGGTCAAACTTCACACTAA
389108	LOC389108	XM_374038	CAGGTTTCTGCCCGCCAAGAA	CACGTAGTTGCGAGAGCCCAA		
389118	LOC389118	NM_001007540	CAGCCTGCCCTGCTTTATTAA	CAGGCACAGCCTGAAGAGGAA		
389123	IQCF2	NM_203424	AAGCATTGAATGGAAGACATT	CAGGGCTAATGAACCATCTAA		
389127	LOC389127	XM_371645	CCCTGGAGACTCATTCCTACA	TCCCGAGGCTACAACACAGAA		
389145	LOC389145	XM_374048	GTGCATATTCCTGATCCTAGT	AGGCATGCCTGCCATCTTCAT		
389147	LOC389147	XM_371663	AAGGCCAGTAAGACCAGGGAA	CAGCACTGGCAAGGCCAGTAA	CACACAGTATTTGTTTCTTCA	AAGGAACAACTGTATCTTATA
389151	LOC389151	XM_371665	AAGGTATATTCTAGACCTCAT	AAATGTTAGTTTATTACTGTA		
389153	LOC389153	XM_374053	CCGGTCCTCTCTTGCCCACTA	TCGGGCTTGGATTTGGAGAAA		
389189	LOC389189	XM_374071	CCGGCTCTGGCTCCAAACAAA	CCGAGTGTGGTTTGCTATCAA		
389197	FLJ46481	NM_207408	CCGGGCTTCCCTTGATGTTAA	ACCGCTGGAGTTAGAAATGTA		
389233	LOC389233	XM_374091	CAGAAAGTCTGAGAAAGGATA	CAGGTTGTCATTGGAAGTCCA		
389239	LOC389239	XM_371714	AAGGATATCTGTCACAGATAT	CACAACTAAATGAAAGCCTAA		
389246	LOC389246	XM_371718	AGACATGAAATATGACATATA	CAGATTGGCTCAGAAACCATA	AAGCAACAGGAAGCAAATGAA	CACCAAGAGTAGACTGATAAA
389247	LOC389247	XM_374099	CAGGATAGAAATTGGAGGCTA	AGGGAATGATTTAGCAATAAA		
389253	LOC389253	XM_374104	CCGGGCAGCTGTCTCCCTCTA	CAGGCGGAATCCATCCAAGTA		
389288	LOC389288	XM_374120	TGGCACCTGAAGAAAGCATTA	AACGCCATTCATTTCTCTAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
389290	LOC389290	XM_374121	AAGGAACTAAGAGTTGCAGAA	CAGCTGAGAATACATACCAAA		
389293	LOC389293	XM_371741	TCCCAGAATAGCCCACATTAA	CACGGGAGAACTCATAATGAA		
389305	LOC389305	XM_371757	AAGAATGAACTAAGGTGTCTA	AACCTTTGTGAAGCTCAACAA		
389308	LOC389308	XM_371758	CAGAATGTCCGGCCTTATATA	CAGCGCCTATATTTGAATAAA		
389321	LOC389321	XM_371769	CAGAATCGAGGCATCTGTTGA	CAGCATCGAGAACAAGCTAAT		
389332	LOC389332	XM_374141	CGCGCTCAGAGCCGCCAGAAA	CGGGCTGTTGTAAAGCCGAAA		
389333	LOC389333	XM_374142	CCGGGACGCCTCACAGCCCAA	CAGGAAGCTCAGAATGGGTTA		
389338	LOC389338	XM_374145	CTCTCCGAATTGAAACACTAA	TAAGAAGATTGGCGAAATTTA		
389342	LOC389342	XM_371781	ACCAAGTTCAATGCTGATGAA	CCAATAAATTCTACTAACTCT		
389345	LOC389345	XM_374150	CACAGAGGCTACAACTAGAAA	CAGGCATTATCGGGACTATAA		
389352	LOC389352	XM_371791	CTGGGAGACAAGAGTCCGGAA	CCGGATGTCCAGAATGATGAA		
389383	UNQ3045	NM_207409	CAGCTTAGTATCTGCACATAA	CAGGGATTGCATCATATTCAT		
389389	LOC389389	XM_371820	TCCAACAAACTGTGTCTTTAA	TAGGATGGGAAACAAGGTTAA		
389390	LOC389390	XM_374167	TTGTTCCAGTTCAATGATTAA	ATGGAATCTGTCTCTCCTTAA		
389398	LOC389398	XM_374170	CAGCTATGATACTCAGAGAAA	CAGGAATATTTCACCCAAGTA		
389413	LOC389413	XM_374175	CTGCATCAACTGCCTCCCTTA	CTCACCTTACTTTCACCTTAA		
389415	LOC389415	XM_374177	CCAGCCCTTTGGAAGAGAGTA	CCAGGCCTTTGCCCTGAGCTA		
389425	LOC389425	XM_371843	AAGACTGATCTTTGCTGGAAA	CTGGCTGTCCTGAAATATTAT	CTGATCTTTGCTGGAAAGCAA	AAGGTGGATGAGAATGGCAAA
389427	LOC389427	XM_371845	GAGGATCAAATTATAGTTTCA	GCGGTTGAATCCAGTCATAAA		
389435	LOC389435	XM_371853	AAGAGCTGAGGAGAAGATTAA	CAAGCAGGCTGTCACCGTGCA		
389458	LOC389458	NM_203393	CCGGATGCTAACACCCAGGAA	CCCAGATGCATTTATTAGAAA		
389469	LOC389469	XM_374203	CAGGATAGTCAAGGACCTCTA	AAGAGAGAATGTAATACACAA		
389533	LOC389533	XM_374226	CCACCTTATATTATAGTCAAA	CAGGCACTCCTTGATGAAATA		
389541	LOC389541	NM_001008395	CGGCTGCACCGCCGGCATGAAT	CTGTCTGTGGTCTTTGGAGAA		
389599	LOC389599	XM_372002	CGGGAACGCTGGTAACTACAA	CAGGATTTACATGGCTGGGTA		
389618	LOC389618	XM_372019	CTGGAATGCCTTTGTACATAT	CTTGCCTGAACTTCCCAAGAA		
389634	LOC389634	XM_374252	CAGGGATGGCAGTCCCAGGAT	CCCGCCGCTACCGGGCAGGAA		
389641	LOC389641	XM_374260	TTCAATCTATCTGAAGCTTTA	AAGAGTCTTGAAAGTCCTTAA		
389643	HMFN0672	XM_372035	AAGAGTCATCTTCAATACCTA	TAGAAAGAAATGAAATGATAA		
389674	LOC389674	XM_372058	AAGAATTGGATGCAGCTATGA	AAGCTTGTGTATCATCCATTA		
389676	LOC389676	XM_374276	GAGGATTTAGAGGGCAAGCAA	CAGGACTTTGACAGCATTCAT		
389727	LOC389727	XM_372092	CTGGCGGTGAATGACTTTGAA	CCGGGAGAAGTTCTATGCCAA	CCACGCAGAGATGACAGCCAA	CACGTACACACGGGAGCGCAA
389734	LOC389734	XM_372097	TAGCATTTACATGATGTTTAT	AAGGATTGGAATTAACTTTAT		
389753	LOC389753	XM_372112	CCCAATCTCCTTTGGATATAA	CTGATTTGTGGTCTTCATTTA		
389756	LOC389756	XM_497059	CCCGAGGTGGATGAGGGTGCT	CTGCCTCTTGCCTGCAGCGAT		
389757	LOC389757	XM_372114	CAAGTCCATCTTTGAACAATA	CGGGACCGAGGTGCAGCAGTT		

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Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
389773	LOC389773	XM_374297	AAGAAATTGTAGCGCCAGTAA	AACCTAAATTTAATTAATAAA		
389777	LOC389777	XM_374300	AAGATGCTATGAATCCAGAAA	TCGCATCTGGATAATCCTTCA		
389792	IER5L	NM_203434	TCGAGCCATTGTCGCCTTCTA	CAGAAACAGCAGAAGCGTTAA		
389813	LOC389813	XM_372159	CAACGCCTGCCTCTACTTCAA	GACCGTGTACCAGGACATCAA		
389832	LOC389832	XM_372190	CAGGAGAACGCCAGCCCTTAT	CTACCATAACACTGAAATAAA		
389840	FLJ16518	XM_372199	ATCCCTCTATTCGGGAATTAA	CTGGATGTTCGCGATGGACAA	CTGATTGTTGCTGGACACAA	GCCGATCAGCATAACATTAAA
389844	LOC389844	XM_372202	GTCCTTGATTCCAATCATGAA	CAGCTGCGAGGTCGCCATCAA		
389846	LOC389846	XM_374325	CAGGATTGGGTGGATAAATAT	CTGGATGCCAATCGAGATTTA		
389848	LOC389848	XM_372204	AAGGAGGAATTTCAGGGTGAA	TCCGGGAATACTGGCCAGGGA		
389878	CXorf35	XM_374333	ATGGGTGGCGATGTTGAAGAA	CAGCACCATACTGGAACTTCA		
389907	LOC389907	XM_372274	CCGCCTGCCAACCGCCTTCAA	CACGCTGGTCACCGTGGGTGA		
389932	tAKR	XM_372302	CAACGGCACTGTGAAGAGAAA	CTCAGCTTATACACACCTGAA	AGATATATTCTATACCACAA	AAGGTTGCTATGAGTAATGTA
389950	LOC389950	XM_372307	TTGGTGTGTGATGTGGCTTAA	CTGGGTAGTCTGGACAATGAA		
389953	LOC389953	XM_372310	CAGCTAAGGAACACTGTGTAA	CAGGAATGGATTCTCCACATA		
389988	LOC389988	XM_372323	TACATCCAAAGTTGCCCATAA	CTCACTGAGACTGCAGTCGAA	CAGCCAGAGACAAGAAGAGTA	AAGGTTGTTATCTTTATTGAT
390003	LOC390003	XM_497249	CACAACTTATGATGTTTATAA	ATCCGTTACGTTGGTGACCAA	CTCAATGACGTGTACAGTTTA	CAGCATGAGATACACCAACAA
390020	LOC390020	XM_372337	TTCCAACATCATCACCATCAA	ACCCACCTACTTTGAAATATA		
390036	OR52K1	NM_001005171	CCCAGTGATTGCCCATTGCTA	CCCATCGTCAATCCTATCATA		
390054	OR52A5	NM_001005160	CACAGGTTTGGTTCACACATA	TTAGTTATAATCAAATATGAA		
390058	OR51B6	NM_001004750	TCGGAGTGACATTGACCACAA	ACCCATTTATCTATAGCATTA		
390059	OR51M1	NM_001004756	CACAGATACCACCTTCAATAA	CCCAATCATATACAGCATTAA		
390063	OR51I1	NM_001005288	ATCCATGTTAACAACATTTAT	CAGGCATTCCTGGGATACAAA		
390067	OR52H1	NM_001005289	TCCCAAGATGCCTGCCAGAAA	TCCCAGGATGCCTTACACAAA	CAGATCAGAGATAAGGTTATA	TACCACCATCTTGACTCCCAA
390072	OR52N4	NM_001005175	ACCAGCTTCATTCATTCTGAA	TCCCTTTACTTTCCTCACCAA		
390083	OR56A3	NM_001003443	CCCAAGAAATTAAGCAGGGAA	CTGCGATGATGTCACCATCAA		
390144	OR5D16	NM_001005496	CTCCCTGATATCACTCTCTTA	TAGGCATTGGTATCCATTTAA		
390158	LOC390158	XM_372396	GCCCAAGACAGAAGTTATGAA	CTGGATGATAGTTCATGTAAT		
390167	OR5M10	NM_001004741	CAAGAACATTTGCATCTCTCT	TTACATGTATGGCTTCCTTAA		
390183	LOC390183	XM_495875	TTCCCAGCTTAACAGACTTAA	CAGGAGGGAATTTCTGTCTGA		
390190	OR5B2	NM_001005366	TGGGACAGTAATCTTCATCTA	AAGAAAGTGTTGAGAAGGCAA		
390205	LOC390205	XM_372416	CGGCCTCTGGCTCTACGGCAA	CTGCCTCTGGATCGAGGGCAA		
390212	GPR152	NM_206997	CCAGCCACAGGCAGACACTAA	CAGCTAGATTCTGAGGGTCCA	CAAATGGACACTACCATGGAA	CAGGACCATTCTGTCAGCCTA
390221	LOC390221	XM_497309	CCCACTGCTCTGTGCAGTGAA	CTGGACCTCAGGGTCTAACAA	CTCCTACACCTGCAAGAGCAA	CTGCCTGCAAACGGCACTTTA
390226	LOC390226	XM_495887	TACCAGGAGGCTGGCATTCCA	ACCAGGTTACCATATACTTCA		
390231	LOC390231	XM_372423	CTGGACAAAGAGGAATGACAT	AAGACTCTTGTAATTGGGTTA		
390233	LOC390233	XM_372424	AAGGAAGAGGATAATCACTAT	CTGAGCGAAGCAGACATGGAA	ACCCAGACTATGTGTCATTAA	CACTCTGATTACTCAATCTTA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
390234	LOC390234	XM_372425	AAGCTGAACCTCAACCAAATA	CAAGAGATTTGTTCAATGAAA		
390260	OR6X1	NM_001005188	CACAGTAATCACAGAATTCAT	AAGACTGGTCATGCAAAGTAA		
390264	OR10G4	NM_001004462	ATGGATGCCATGGATGGAGTT	GCACATCCTCAGAGGAAATAA		
390281	LOC390281	XM_497327	AAGCACCTATATGCCCTTCTA	CTGGAAGGACAGGTTGTTAAA		
390282	LOC390282	XM_372447	AAGCTGTTGAGAGAAAGGAAA	AAGGAAAGTTAAGGCCACCAA	CGAGATCATGCTCAACGGTAA	AACGTCAGAGTGAAATATGTA
390284	LOC390284	XM_372448	CCAGACAAACTCAGAGCTTCA	CTGGTGGTGGTCATCGAAGAA		
390335	LOC390335	XM_372466	AAGAAAGAAGCTGCCCAGAAA	CAGCTCTCATCTTGCAGTACA		
390349	LOC390349	XM_372472	CAGGTGTGCAGAGATACTTGA	CAGCACCAATGAAGACAGGAA		
390377	LOC390377	XM_372486	CACCCACCGTTTCATCACCAA	CAGAAGAGCTGGCGTCATGAA		
390387	LOC390387	XM_372490	CAGGGTCTCCATGGCCTGTCA	ATGACTCTGATTCCACATTAA		
390407	LOC390407	XM_497376	AGGTAGATGGTTTGACCTTAA	TCGAGACATCAGGACCTTCTA		
390421	LOC390421	XM_497382	CTGCCTGCATTTGTTCCTAAA	CAGGAGTGAGATCCCACCCAA		
390429	OR4N2	NM_001004723	AACAGTGATAAGAGAATTCAT	AAGGTGTTTAATAAGCACATA		
390442	OR11H4	NM_001004479	TTGGATTCCTTGGATACCCAA	TGGGACAGTCATGGTAATGTA		
390443	RNASE9	NM_001001673	AACGTATTCCTCATACTATAA	AAGGAGTGTATTGTAATTTAA		
390445	OR5AU1	NM_001004731	CAAGAGGAAAGTGATCTCTTA	CTCCTACTTCTTAATTCTCAA		
390529	LOC390529	XM_372542	GACCCTGGAGGAAGAAGCAAA	CAGGCGTTTGCTGCCTCCTTA		
390550	LOC390550	XM_374354	CCCACTCTCATGGATGCCTTA	ACACTCAGTATTGGTAGATAA		
390551	LOC390551	XM_372556	CTGAGGTGGGTCTGACTCAGA	AAGCAGGTAGGTGCGAATGAA		
390560	DNM1DN4-1	XM_497444	AGCAGTGTTTCTTCTCTATCA	CAGCTTCATCATCCTGGTTCA		
390564	LOC390564	XM_372562	ACCGATGGGTACAGAGGCCCA	CTCCCTACTCTTTGCGAGGAA	CAGGGTCAGCCGAATGCCAGA	ATGGACGACCTTCTGAACAAA
390570	LOC390570	XM_372566	CTGTCTCACCGAAGATGTTAA	CACGAATGTACCAGTGAACAA		
390577	LOC390577	XM_372569	CCGAGCTGGGTCGGAGCATGA	TGGCCCGGAGTTAGAGGCCAA		
390641	LOC390641	XM_497469	CAGGTGGACATGTAAAGAAGA	CAGCAGCTGAAGGACAGATAA		
390667	LOC390667	XM_372607	TTGCTCGTGGAGGAAGACCTT	CTGGAGGAACAGTTCCGGAGA		
390736	LOC390736	XM_372641	CGGCTCGATGTCTGCAGGCAA	GTGGAGGAAGATGGACAACTA		
390801	LOC390801	XM_372676	CACAGTGAACTTCCAGAACTT	CACCACTGTGGACAACAACTA		
390842	LOC390842	XM_497583	CTGAGGAACCTGCAAGACTCA	ACCAATGACAGTATCCAGTAT		
390919	LOC390919	XM_497622	AAGGGCTTTCCTGCAGCGCAA	CAGAGAAAGTCTATACATCTA		
390975	LOC390975	XM_372748	CTGGTCCACGCAGATGTCAAA	CTGGTCACCCATCGTCAGAAA	CCCGGCAAACAGTCTGAGGAA	ATGAACTAGATCCAAATCCAA
390988	LOC390988	XM_372755	CCGCCTGGAGGAGACCCACAA	GACGGCCATGTTCGACTTCAA		
391039	LOC391039	XM_497673	CACCCTCTATGACACAACCTA	CAAGGACATGAAGATGCATAA		
391053	LOC391053	XM_497689	ATGATGGATAGTGACACCATA	ATGAACAACTCTACAACATAA		
391059	LOC391059	XM_372784	CACCTTTACATGACCCAAGAA	TCCTATAATTTCACAACCAAA	CAGATTGAAGTTACTTTGTCA	CTGAAGGTTCATGGTGCCTTA
391105	LOC391105	XM_497715	CAGCTCTGCTAAGGACTTGAA	TTCATCTGAGTTTGAGATTAA	CAGTTTCATTTGACTCCTCAA	CTGGATTTAACGGAAGTAATT
391109	OR10K1	NM_001004473	CACCCTAATATCTGTGTCATA	CCAAGACTAATTACACTTCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
391123	LOC391123	XM_372802	AAGGTCATTGTCACTGTCCAA	ATGAGGCTAGGTGGGAAGGAA		
391126	LOC391126	XM_497721	GTGACTTCCAACCAAATCAAA	CCACATTCACAGGAAGATTAT		
391137	LOC391137	XM_372805	TTCCTGCTTCACCACCCTCAA	AGGATTCTGCTCAGCCAGTAA		
391142	LOC391142	XM_496426	CCAGCAGAGACACTACAATCA	CAAGAGGGCACGGGAGGCCAA		
391192	OR2L3	NM_001004687	CTCCATATTCCTTATTGCCAA	CACCCTCACTCCAATGCTCAA	ATGGCTCTAATTGGAAACCCA	TAGGATTCTTCCCACCATCAA
391205	LOC391205	XM_372838	CTGGAGGAGCAGCGTCACGCA	CGACATCGTCTCTGCTCTGAA		
391209	LOC391209	XM_372840	CTGGTCGATCGCACTTGTACA	CACGGGCTGTGCTGAATGACA		
391253	C20orf137	XM_372869	CCGAAATAAAGACACAAGAAA	CCGGCTGTAATGGCAACCTTA		
391265	LOC391265	XM_497576	CCCAAGAAGGGCAGAGGAACA	CGGGACCAAGTCTGTCACTAA		
391340	LOC391340	XM_372908	ATCCCTATATTGAGGAGCAAA	CTGCCCATCATCTGTATCCTA		
391347	LOC391347	XM_372913	CAGGCCCTGCTGAGCTAGCAA	CAGATATGTGTTGTCCTGTTA		
391370	LOC391370	XM_372926	CAAAGGCTTTGGTGTGTTCAA	AAGATTGGGCTTCACCCATAA		
391429	LOC391429	XM_372954	CAGATGGCATAGAGCATCCAA	AAGATGGGATAGAGCATCCAA		
391599	LOC391599	XM_497949	CAGGGACTTCATCAGCTGCTA	CAGGACCTGTTTGGAGACCGA	CAGGAGATATTTAGGTACCAA	TCGGACAAGGATGGAAACTTT
391634	LOC391634	XM_496686	CCACATCTACTGCATGATCAA	AAGATTGGATGTTATTTATTA		
391711	LOC391711	XM_373037	AAGAGAAGGATGATAAAGAAA	AAGAATTATAAGAACATTTCA		
391717	LOC391717	XM_496725	ATCAGGTGAGAGCGTGTGAAA	CTGGTGAATTTGAGAAGTGTA		
391722	LOC391722	XM_373042	CACCAGAACAGTGGTCATCTT	ACAGACAAATGTGAATAAGAA		
391730	LOC391730	XM_497990	CTGGATGGAATTCCTTCCCAA	AAGAACTTGCTCCATCATTAA		
391733	LOC391733	XM_373053	GTCAGAGACGGAGAAAGATAA	GACCATCACGGCACACTCCAT		
391769	LOC391769	XM_373079	CACGCAGCTGCTCCTGCGCAA	CTCCGCAGAGAGGGTCCTTAA		
391773	LOC391773	XM_497999	CTCATCAACAATTACGGCCCA	CAGCGTCATGATAACGTGAAC		
391804	LOC391804	XM_498008	CACACTTTCTAGCCCGTACAA	CCGAAGGGCGTAGTCACAGAA		
391819	LOC391819	XM_498013	CTCAGTTTGGAGCAAATTGGAA	CCAGGACATGGCGGTCAACAA		
391827	LOC391827	XM_498018	TGGGTTGATGGTGGAGGTAGA	CCCTGGAATCTCTACACTAAA		
391833	LOC391833	XM_498020	CCGGACCTCGCTGCTCCCGAA	CAGGCCAGCAGCATCCTTATA		
392169	LOC392169	XM_499232	ACGCGCGCGGTCAGTGCCTGA	ACGGTGAAGACCTGAGATTTA		
392222	LOC392222	XM_373253	AGGCACCAGTTTCTTGCTTTA	CTGAGTGATGAGGAAATGAAA		
392238	LOC392238	XM_374372	AAGGGAAGAATTACACAGGAA	CAGGTACACGTAAGAAAGAAA		
392262	LOC392262	XM_373[illegible]	CACCTATGACACAAATGTCAA	CTGCTGAAGAATCAAGTATAA		
392267	LOC392267	XM_496992	CACCTCAGCCCTTACCTGGAA	TGCCATGGTGTATTACGTCAA		
392281	LOC392281	XM_497005	TGGACCCAAATTGCTTACGAT	CAGGTACATTACTCCTCAGCA		
392309	OR13J1	NM_001004487	CAAGATCCTGGCAGTGCTGAA	CCCTCTGTGCTCAGCCATGTA		
392376	OR13C2	NM_001004481	AAGGGACTTTCTGGTCACCCA	AAGGATGTGAAAGAGGCAGTA		
392392	OR1[illegible]	NM_080859	CCGTGTGGCCACTGTCATGTA	TGGGACAGTCATTGCAGTCTA		
392395	LOC392395	XM_373319	CAGCCAGGCCATCGCCAACTA	TGGGACAAAGAAAGAGACCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
392459	LOC392459	XM_373344	ATGGAGCACCATTTCCATGAA	CAGGCTAGCAACAAAGGTGAA		
392517	NCBP2L	XM_373362	CAGGCCTGTGATTAAGAGCAA	CCCAAGTGTTGTAGCCTTAAA		
392546	LOC392546	XM_373372	GCGGTCCGCATTACTCACATA	CACCCTCTTAACGATGATGGA		
392556	LOC392556	XM_498396	CACTCTATGGAGCCAATCTAA	CACGATTATAATGGAGGGCAA		
392583	LOC392583	XM_374379	CCGCCTTGTGAGCCAGAGCCA	CCAGCGGAGGTCCTCAGGAAA		
392702	LOC392702	XM_374730	CTCCTGGGCAGCGGAAACAAA	CTCCCGGAATCTGGTGGACAA		
392758	LOC392758	XM_374498	TCCAGTGGTCTTTGGAGAACA	CGGCTGCACCGCGGGCATGAA		
392895	LOC392895	XM_499284	AAGGTGCACCAGGTAAGATGA	CAGTGGGAAGAGGAATTTGAA		
399665	EEIG1	NM_203305	CAGGAAGGTTGGAGCAAGCAA	TGGAATCTTCTTGAAAGTTTA		
399668	MGC39606	NM_203306	CAGCGTGAAGGGCCTGAACAA	CAGGTCCTGAATGAAGCTGTA		
399671	MGC48595	NM_203309	CACTATGTTTATAAAGAGAAA	CTGCTTGGATATGAAACATAA		
399706	RP11-529L18.1	XM_378200	AAGAGCTTCGTGTTAGAGAAA	AAGACAAATGAGACAGAGCTA		
399708	LOC399708	XM_378203	CAGGGTATCAAGAGTCAGTAA	AAGGATAGAATTATCCATCTA		
399715	LOC399715	XM_374766	ACCCAATAGCATAAGTATTAA	CAGCCTCAGTACTGTAAGAAA		
399763	LOC399763	XM_374803	CGGTATATAAATAGAATTAAA	CAGGTGTTTCTGAAAGATTAA		
399833	FLJ44653	NM_001001678	AACCCTAAGCCTAAACCTTAA	ACCCTTAACCATAACCCTTAA		
399851	LOC399851	NM_207427	TGGCTTGAACCCAGAGGTGAA	CAGAGTCACACTGGATTTACA		
399919	LOC399919	XM_378299	CTCGCTCAGGTGAGCATTCAA	TAGAGAGGTAATTAAGTTAAA		
399921	LOC399921	XM_374904	CCCATCCAGGAAGGTTATATA	CAGGGTCAAAGTTCTGAGCAT		
399937	LOC399937	XM_374917	AAGAGACAGAATGACAAGATA	CTGAAGCAAATGTACCATAAA	CAGCAACTCAATGAAAGCCAA	CAGAGTGTGAGTGATACTTTA
399940	LOC399940	XM_374920	AAGAGACAGAATGACAAGATA	CTGAAGCAAATGTACCATAAA	CCGGCCCTGTTTCTACCTCAA	CAGCAACTCAATGAAAGCCAA
399961	LOC399961	XM_378317	CTGAGAAATGAAAGTGTGAAA	ATGGTGCTTCCTATAATCCAA		
400047	LOC400047	XM_378363	TTGGACTTGACCCTACTGTAA	AAGGAGTCTTCAGGAATCAAA		
400083	FLJ43808	NM_207438	TACATTTAATATGCCAATTAA	AAGGATGAAATTTGACGAATA		
400099	LOC400099	XM_378399	AAGGTCTGACAGAAACTTTAA	CAGGTTCATGTCCCAATGAAA		
400156	LOC400156	XM_375035	CAAGCTGTATGTGAAGCTACA	AAGGACAACGCCATTAAGAAA		
400201	LOC400201	XM_378449	ATGGAGCTATGAAATGGCAAA	AAGGATATTACCAACAATGGA		
400224	LOC400224	XM_375090	AGGGTGGGTGATGACCTTCTA	AAGAGCTTTGAAACCAATAAA		
400238	LOC400238	XM_378473	CAGGTCAACTGTGGAATTTGA	CACCATTTAGAGGACAATGAA		
400263	LOC400263	XM_378491	AAGAGCCATCATGGTGATCAA	ACGGAGCAACGTCCAGTTTAA		
400353	LOC400353	XM_375183	CAGGCATAACTGAAGGTGAAA	CAGGCAGGAGAATCACCTAAA		
400400	LOC400400	XM_378529	CAGGGTCTCACCTTACAGCAA	CACATCTAGCATGGCATATAA		
400446	LOC400446	XM_496093	AAGGCTTTCTTAGGTGTGAAA	CTGGTTAAGTTGTGTACTAAA		
400475	LOC400475	XM_378553	TTGCAGAGTCTCAATACCCAA	TAGCTATAAATTATCATATAT		
400481	LOC400481	XM_375284	CAGCAGCAACAACAACAACTA	CCCGACCTACCTCCTGTTCAA	AGGCACCTTTCTAGAGATTAA	CAGGGTGAAGAGAATCTTCTA
400496	LOC400496	XM_378562	ACCAATTTAGGTGTAATTTAA	AACGCTTTGCTTTATCATTAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
400523	LOC400523	XM_378582	AACGCAGGATATTGCATCATA	CTCGTGGGTCTTCATACCTAA		
400552	LOC400552	XM_378623	CCAGAGTGTATTGCTTATAAA	ACCGTGTTTGGCAGACATTAA		
400569	MGC88387	NM_001001683	CGCGCTCTGGAAGACATTGAA	CAGAGTGATAATGGCTACCTA		
400586	LOC400586	XM_375424	CCCGCAGAATGGAGGAGATAA	CTGGAGAAACATCATCCTTAT		
400591	FLJ44815	NM_207454	CAGGATTTCATATATAGCAAA	CAGGAGAATGTCAGCAGTGAA		
400619	LOC400619	XM_378703	CTGGAGTAACTATTCCACTAA	CTGAGTCTTCTCTTTCTTCAA		
400623	LOC400623	XM_378708	CTGCGACATTTAGTCCTTTAA	ACCAGTGTGTTTGAGCATTAA		
400624	FLJ45079	NM_001001685	CAGGGTCTGAACTAAGAGCAA	CTGGGTCTGCGTGAAGATAAA		
400642	LOC400642	XM_378735	CACATCTTCCATATACTTTAA	CCAGAGTTTCTTATCAAGTAA		
400651	LOC400651	XM_378747	CAGGCTGAATTTGACGTTAAT	AAGGACATACATGCAAATGAA		
400658	FLJ44313	NM_207460	TCCGCGAGTCCTCAAATGTAA	CAGGGCATTGTCTGTCTACAA		
400664	LOC400664	XM_375549	CTGGTGATTTCCAGTAGGTGA	CGCCCACTAATTCTACATTAT		
400668	PRSSL1	NM_214710	CACACCCATTCCACATGCAAA	CGCCCTGATGCTGCCCGT[illegible]AA		
400673	VMAC	XM_375560	TTCGAAAGTGCTGCAGTTATA	CTGTCTGTGCTCAAG[illegible]TAAA		
400679	FLJ46230	NM_207463	CCCGGAAGGAAAGGAAAGGAA	CTGGACTTTGGTC[illegible]AGTACTA		
400681	LOC400681	XM_375589	GACCCTATATTTGGAATTTAA	TAGATTAAATT[illegible]GCTAATTAA		
400684	LOC400684	XM_378793	CCACTGTTTATTTCAGCATAA	CACGAAA[illegible]CTCCCATCTCAA		
400685	LOC400685	XM_378795	TAGAGTAATACTGGCCTTATA	CTGC[illegible]GTGGTGGAAACATAA		
400709	SIGLECP16	XM_375634	CTCCGTGTGGCCTCCCTGGAA	AA[illegible]GGCAGCATTGGGCATGGA		
400721	LOC400721	XM_375664	CACACTGGTCACACCACCTTA	[illegible]TGGGAAATCATTTAGTTCAA		
400729	LOC400729	XM_378824	CGGCTCCTGTCTGACCAG[illegible]A	ATGATGTACTAGATCCCTTAA		
400764	LOC400764	XM_378880	CAGGGAGCAGAAGAC[illegible]TAAT	AAGGGCTATGAAGAAACATAT		
400790	LOC400790	XM_375814	CAGGAGCTCCTGC[illegible]CATAAA	AAGGAACATATTTCCACATAA		
400800	LOC400800	XM_378925	AAGGTACAAAT[illegible]CAGATATA	AAGGAAATGATTTAACTTCAA		
400842	LOC400842	XM_375914	CCCATGAA[illegible]ATGAAGCACAA	CCGAGCGATCGCAGAGACCTA	TTCATACAGAATGGCACTAAA	CTGGGATTATTGATTACAACA
400846	LOC400846	XM_378981	CACGT[illegible]TTTCTGAATCTAAA	CACAAAGATGTGAGCAATAAA		
400850	FLJ44790	NM_001001691	CCC[illegible]GCGTTCCTGGAAGCCAA	CCCGCAGCAAGTTAAATCTAA		
400865	LOC400865	XM_379006	[illegible]GGCAAACCATAGCCATTAA	AAGAATTTGCATCATAATTAA		
400876	LOC400876	XM_379023	CAGCTCGGACAGCATCCATAA	CTGTCTGAAATTGAATGTTTA		
400888	LOC400888	XM_375[illegible]5	CAGGCATCACCTTGCCTGGAA	CCGGTGATTGATGATACTACA		
400890	LOC400890	XM_[illegible]79036	AACCAGAATAATCAGCCCTAA	ACGCAGAGATGCACACATTAA		
400916	C22orf16	NM_213720	CCCAGATAGCTGGGATTGGAA	CACAGATAACCCAAGACACAA		
400921	LOC400921	XM_376001	CTGGCTGACGTGCTCCATCCA	CATTGTGGACTTGGACATTTA	CTGACACTAAGCTCGGCTTCA	GCCCTCTACTCAGCATGGATA
400931	FLJ27365	NM_207477	CTGGGTAAGTCTAGCCCAGAA	CAGGTGATGCCTGAAGCTCAA		
400932	FLJ46[illegible]57	NM_001001693	ATGCATTCGTTTATCAATCAA	CCGGGAAGTGTTCACAAATAT		
400934	FL[illegible]44385	NM_207478	AAGAAGGAAACTGGACACATA	CAGGACAATTATTAAGTTCCA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
400937	LOC400937	XM_379068	CAGGATCTACGTTATAATTAT	CACAATTATGAAATAATGTAA		
400944	LOC400944	XM_379077	CACCAACTCCTTGTATTGCAA	CTGGGATGGAATCCTAATGAA		
400945	LOC400945	XM_379078	CAGGTTTATAATATGCATTCA	CAGCAATTTAATAATAATGCA		
400964	LOC400964	XM_379106	CTGGGATTACACAGTCGGTAA	CAGGTTAATGGAAATAATTAA		
400997	FLJ44006	NM_001001696	ATGGAGATATACAATTGTTAA	AAGGTCTTAATGAGAATGAAA		
401025	LOC401025	XM_379149	CCCATCCTGAGTGACTACTAA	CCAGCATGTCTTTCCACTATA		
401034	LOC401034	XM_376179	CCACCGGAGACTCAAGATGAA	CACACTCACAGTTACCAGCTA		
401037	LOC401037	XM_379161	CCAGTGCAGCTAGAAATGTAA	TCCCTCAGAATTTACATCTAA		
401050	LOC401050	XM_379173	TTAGATAATAATGGAACTGAA	CCCAGTTTAGTTTATATATAA		
401054	LOC401054	XM_376207	TTGGCTGGACACAATCCTGAA	CAGGTTGACCTTGGTGAACTA		
401056	LOC401056	XM_379180	TAGGACTCTGGAGAAGATCAA	TGGAAGCTCTTTGGAAACCAA		
401058	LOC401058	XM_379182	AAGAATACATAAGAAGTCAAA	TACAATATATTCTTAATTTGA		
401059	LOC401059	XM_379184	TACATTCTGAGTTGAAGGAAA	TCCAAGTATGATTGGAAATTA	TAGATATTTATTATCCAGGTA	ACGAAATTCATTGGCAGATTA
401078	LOC401078	XM_379200	CTGCGTGGTGGCAGTTGTTGA	CGGGTTTGTAGTTACCTATAA		
401081	LOC401081	XM_379206	AAGCAGGTATTTGTATTAGAA	CTGATAGAAGAAGAGATTAAA		
401087	LOC401087	XM_376267	AACAAGTACGAATTTGCCAAA	CTCCTTGTGTTTCATTGGCTA	ACGAATTTGCCAAATGGACAA	ACGGTCTATGGTGGCACAAGA
401089	LOC401089	XM_376269	CACGTTCCAGATACACTTTAA	TTGGATTTCTATCACCATAAA		
401097	LOC401097	XM_376281	CGCCAACTGCCTCAGACCTTA	GCGGGGTGCCTCTGACATTTA		
401101	LOC401101	XM_379234	AACGATCTGCGATGAAGATAA	CAGCTGTGACTTGATAAACAA		
401103	LOC401103	XM_379235	CAGGACCTCTGAATCCTATAA	ATGTAGTAATATACTCAATAA		
401114	FLJ35816	NM_207489	CTGACTTTACTCTGAGATCAA	AAAGGTAATGACCAAGATAAA		
401123	FLJ45721	NM_207490	TAGGAAGTAATTACTAATAAT	AACCATGTAGCTCATAAGTAA		
401149	LOC401149	XM_379273	CCGGGACAACAGGCTCTCCAA	CTGGCTGTAGATCCCAATGAA		
401165	LOC401165	XM_379299	TAGGGTTAATGCTACATGGAA	AAGGCAAATTCTATCTTCAAA		
401172	FLJ33360	NM_001001702	CAGGCTTTGCTTCTCTCCCAA	AGGAACCTTACTGATAATTTA		
401176	LOC401176	XM_379318	AACCAAGAGTTATAAACTATA	AACGTAAATATTATTACGTTA		
401180	LOC401180	XM_379325	CACGTCCTCCTTACTCCCGAA	CAGAAACTAAACCGACACCAA		
401206	LOC401206	XM_376420	AACCAGCTGTACATTTGGAAA	GACGAGAAGAAGGACGCTGGA		
401207	LOC401207	XM_376423	AAGGGAGAGACAGACAATAAA	AAGATACAACTTAACTTTAAA		
401210	LOC401210	XM_379369	CCGGTCCACTGTGGAAGGCAA	CAGCCAGAATCTCGCATGTAA		
401215	LOC401215	XM_379368	AAGCTCAGGCTGTGAAATTAA	AACGATAATTTGTGAAAGTAA		
401217	FLJ40453	NM_001007542	AAGAGATTGCTTTGTCCTGAA	CACGATGTCTATTAAACAGAT		
401220	LOC401220	XM_379378	AAGAAATTAGGTGAAGAATTA	AACAATCACTATAGTAAGATA		
401224	AACSL	XM_376454	CTGGTTGACCTTGCAAATTGA	AAGCAGATGCTTGTAAGCTAA		
401236	LOC401236	XM_376469	ATCAATCTATATTATCTTAAA	AAGGTTAGTTGAGTAAATTAA		
401254	LOC401254	XM_379406	CCAAATGGGACTGAACTTTAA	CAGGAGAACCATCACAAGCTA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
401262	CRIP3	NM_206922	ATGCCTGAAGTATGGCATGTA	AAGTGATGTCATTAAGCAGAA		
401278	FLJ44955	NM_207500	CCCATTTCATCTAGAAAGTAA	TAGAGGTTTGTTAATCTAATA		
401281	FLJ27255	NM_207501	CAGCTAGGTAAGATCATGTAA	GACCATGATACTAACAATAAA		
401308	LOC401308	XM_376576	TGCCCAGTTTGAAGAATTGAA	ATCCTCTATTGTTCTGACAAA		
401328	LOC401328	XM_379485	AACGTTTAACACAGACATTAA	AACCTAATAGTCTTAGCCAAA		
401400	LOC401400	XM_379518	CTGGAATTCTACAGCCATGAT	CTGCTGGGAGAAAGAATGGAA		
401431	LOC401431	NM_001008745	ATGACTTTGATTTCTGCATAA	CAGGGAATTATTCACATGGCA		
401470	LOC401470	XM_376787	AAGGGCAAGGCCATTAAGAAA	CCGCCACCACGCGCAGCCTAT		
401472	FLJ45248	NM_207505	AGGGTATTTCCTAGCAAGAAA	TAGGAAGAATTTCCTGACAAA		
401476	LOC401476	XM_379603	AAGCAATTTGCTCAAGATAAT	ACCCATCAAGAGATTAAGTAA		
401477	LOC401477	XM_379605	CAGGATGCTGTCACAATTACA	TCAGGAGTAATTGTTAACTAA		
401480	LOC401480	XM_379608	CAGCTTTGAGGTCCTAGGAAA	CAGAGTTTCCTTCCCAGCTAA		
401495	LOC401495	XM_379625	TACCAGGAAACTTGAGACCAA	CACACCCTTACCAGACTTCAA		
401497	LOC401497	XM_376822	CACAACAACAGTATAACATAA	TTCAATAAAGTTATCAATAAA		
401499	LOC401499	XM_379628	AACGGGAAAGCTCTTGGAACA	TTGAGCCAGTTTACAAAGAAA		
401508	FLJ45202	NM_207507	CTCAAAGGCTGTCCACAAGAA	AACCCTGTCTGTCCTACTAA		
401537	LOC401537	XM_376888	CCAGATGAAACAGTACATCTA	CACCTACATCCCAAATCTGAA	CACGGAGGCATCTTATGTTAA	CAGACTGGTTTGAAGGAAGAA
401539	LOC401539	XM_379648	AAGACGTAATAGAGATTTCAA	CTCGTAGTCAGTGACAAGTAA		
401550	C9orf148	XM_379667	AAGAAGAATCCTAACCTCAAA	AAGGCTCGTGGTGAGAATCAA		
401584	LOC401584	XM_376986	ACCAAGTACTCCAGATTAATA	CAGCTTGAACTGTTGCCTTAA		
401607	LOC401607	XM_379717	ATTGATCAGCCAGCAGTCAAA	CACTCGCCAATTAGAGATTGA		
401679	LOC401679	XM_377185	CTGCAAGGCGTGCCACCTGAA	CCGGTGCTCCTGCCTTGTGAA		
401704	LOC401704	XM_377231	CTACTGGATGATGACAATGAA	AAGCAGTAGATATGAATAATA		
401713	LOC401713	XM_377259	TGCCAATATGGTCTACAGGAA	TCACAAGACCTTCAATTTAAA		
401855	LOC401855	XM_497509	CTGGCCTACAAGAACACATAA	AAAGTGGGTCACCAAATGCTA	CCAGGCCGCTTTGGAAGCGAA	CCCTCGAGAGTTGGAAGTCAA
401876	LOC401876	XM_497534	CATGGTATCAAGGGAAATATA	CCCACTTGAATTGCTCAACAA		
401891	LOC401891	XM_377488	CTGCTGGTAATGGATCAACAA	CAGATTTAACTGCAATAGATA		
401895	LOC401895	XM_377500	AAGTGACCTTCCGCAACTTCA	CAGCAAGACGGCAGAGGTACA		
401896	LOC401896	XM_377511	ACCAAGTTCAATGCTGATGAA	ACGCTCGGAAGGGTTGACATT		
401921	LOC401921	XM_497639	CAGGTCTTCGGTGGCAAGAAA	CCCGGTCACTACACTATGAAA		
401943	LOC401943	XM_497659	TGGGAGGACGAGAAGAGCCAA	AAGCCCTTGGAGAATGAACTA		
401945	LOC401945	XM_377579	ACCGGATATGCAGCTCTGAAA	CCGGAGAAATCTGCAGGTAAA		
401980	LOC401980	XM_497729	CTGAGTGACGTTAATCACTCA	CGGGAAGCTGCTGGTGATCAA		
402011	LOC402011	XM_497758	CACAATATTGGTGGTATCAAT	TACCATCAACTTGTCCAACTA		
402036	LOC402036	XM_377696	CACGGTGCTCTGGACCGTCTT	CCTCATCAACATTGACTTTCA	CTGGAGAATGACAGCCACACA	CACGGAGGTGAGAGAGAGCAA
402037	LOC402037	XM_497793	CTGGGCCTGCCTGGACCATAA	AAGGATGAGAGGGAAGCAGAA	CAGACGCTGAGGATTCTTGTA	CCCGAAAGATGTGGGCATTAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
402055	LOC402055	XM_377713	CCAGGATTGAAGGAAGGGAAA	CAGGAGTTTGCTAGTGGGACA		
402057	LOC402057	XM_377716	AAGAAGCTCCGCAACAAGATA	CACGCATCTGATGAAATGGAT		
402072	LOC402072	XM_377741	CTGGTACTTCTTATGACACTA	AACATGGTCTATAATGTGTAA		
402094	LOC402094	XM_377755	CCGGGCATCTGCATTCCGGAA	CAGAAGGAAGAGAAAGTGCTA		
402095	LOC402095	XM_377756	TGCCATGGAAATGGTCCAATA	CAGGTTTAACCACCAGTTTAA		
402112	LOC402112	XM_496610	CTGTCTCAGGAGATTCTCAAA	CACCCAAGAGATTATCCTGAA		
402146	LOC402146	XM_497943	AAGCCTGAGCCCATGGAGAAA	ACGGTTATGTATGTAGCAAGA		
402184	LOC402184	XM_497977	GACAAGAAACTAGAGCAATAA	CCAGCATGTGGAATTCTTGAA		
402196	LOC402196	XM_497991	CTCCTTGTGGCCCACAGCCCA	AAGCCATTCCTCATGCCAGAA		
402199	LOC402199	XM_377875	CCGCTGCAGCCCAAGCATTTA	CTGCAGAAGAATCATGTTCTA		
402200	LOC402200	XM_377877	TGCCATGGCTGGAATAGCCAA	CCGCTGCAGCCCAAGCATTTA		
402253	LOC402253	XM_377935	TCGCCTCAGATCTGACCAGAA	TCAGAGTGTTTCAAATGTGTA		
402330	LOC402330	XM_378015	GAACTACGATAAGTTCTCATA	GAGAACTACGATAAGTTCTCA		
402353	LOC402353	XM_378043	ACGGGACGGCTGCCCAATGAA	CGCGGATAATCGAGACTGCAA		
402367	LOC402367	XM_378064	CAGGCACATGCTCCTGCTTCA	CCCAAGCATTCCCGACAGGAA		
402388	LOC402388	XM_378103	CAGATGTGCATTGGAGACTCT	GACGTGGGCATTGGAGACTGA		
402397	LOC402397	XM_497102	TCTGGAAGTATGTATCTACCA	CAGGATTTGATGGTGCTAGTA		
402485	LOC402485	XM_380104	CTCATTGACAAGATTAACATA	AACGTTTAACACAGACATTAA		
402504	LOC402504	XM_380107	CAGAGCTGGATCTACCATGAA	AAAGATGACTGAAGAATGGCA		
402522	LOC402522	XM_379849	CGCCGAGGATTTCAGAAGATA	CAGGAGGGTTGGACACGGCAA		
402523	LOC402523	XM_380114	AAGGGCATACATGGTAATTAT	AACGTGCTAAGTATCAGTAAA		
402532	LOC402532	XM_380117	CGGAGAAAGACTGGTCTTGAA	CAGACTTGGTGTTATGGTAAA		
402563	LOC402563	XM_380128	GCCGGGAGGTTGAGTAGAGAA	CAGAAGGAGTGGAGACATTGA		
402604	LOC402604	XM_379939	CAGGAATTCCTTATGTGTGAA	ACGGTACTGAACAGACAATTA	ACCAATGTTTACAAATATGTA	CACCATGAAATATGTCTTCTA
402634	LOC402634	XM_379987	CAGAAGGTGGAGAGGTCATCA	CCGGCGATGCTGCGTTGCCAA		
402641	LOC402641	XM_379995	AAGACATGAGGGAATCATTAA	ACAGCTGGATATAAACCTGAA	CAGAAGAAGTCTTGTCATCAA	TTCCAGGTTATTGATAAGAAA
402669	LOC402669	XM_380011	AGGGACCACTCTGAAGACAAA	CAGGTGGTGTCTATGATGCAA		
402716	LOC402716	XM_380072	AACACTGGTTATGGGAACAAA	CAGGGTTTGGAGAACATTCAA		
403282	OR6C65	NM_001005518	CCCGTGATTATGGGCCTCCAA	CTCCTACACACTCATCCTTAA		
404033	FLJ34077	XM_495846	AAGGGAAACAAGAGCATAAAT	CAGCCTGATGATGCAGTAGAA		
404550	MGC17624	NM_206967	CCCAGATGATGGAGAAATCGA	CCGCAGTGAGCCCACCAAGAA		
404552	SCGB1D4	NM_206998	AAGAAACGACTCTCATTGAAA	CTCCAAGTTGCCAAACTTAAT		
404785	POTE14	NM_001005356	CAGAAGCAACTTTCTGAAGAA	CAGGAAGAAATTGTCATGCTA		
407835	LOC407835	NR_002144	CAGGGAGATCAGCATCTGCAT	CAGCCCGTGGTCGACAGGGAA	CTGCTGGACTATATTGTGAAA	TTCCAGGAGTTTGTCAATAAA
408263	MGC27121	NM_001001343	AAACAAGATAATATTAAATAA	CAGCCTTATATTACTCCATAA		
414153	SMRPEL1	XM_034623	AACCTCATCTTCAGATACTTA	TTGCAAGTGTGCTCTTTGTGA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
414918	MGC33692	NM_001001794	CCGCGACAAGGCGCTGCTCAA	CACCATTGTCTCAGCAGTAAA		
415116	PIM3	NM_001001852	CACCGCGACATTAAGGACGAA	GAGCGTTTAATTTATTCAGTA	CTGTCAGAAGATGAACATGTA	ATGAACATGTATAGTGGCTAA
439919	LOC439919	XM_498448	TGGGTATTAATTCTCACTGTA	CTGTATAAGTGAAGACATTAA		
439928	LOC439928	XM_498427	AACCAGCAGAACAAATACAAA	TTCTTACTTTGATGGGAACAA		
439952	LOC439952	XM_495799	ATGCTGAAACATCGAAGTCCA	CCGAGAAATCAACGACCTATA		
439957	LOC439957	XM_495805	TACCCTTACCATCAATGCCAA	CCGGGAGACAGCCAGACTCAA		
439959	LOC439959	XM_495806	CACCAAGACTATCAATTTGAT	AGGGAAATTCATCTATTTATA	AAGATGCAGGATGATGGCCAA	TAGGTATTCAATAGCATTAGA
439982	LOC439982	XM_495828	CAGAATCAGATGTTCCAGCTT	ACGGGCTTATTGAGACCCTCA		
439985	LOC439985	XM_495832	AAAGCGATACATTGTCTATTA	AAAGATAAGAAGAAGAAGTAA		
439994	LOC439994	XM_498491	CAATGTCTTTCTTGTATTAAA	TACAGATAGGATTACACTAAA		
440000	LOC440000	XM_498494	CCGGCTGCTCGTCACCGCGAA	GACAATTTACTTGACTGGAAA		
440004	LOC440004	XM_498497	ATGGTATTTCTGGTTATTAAA	CCGGAGTGGTTCTGACTTTAA		
440021	KRTAP5-2	NM_001004325	CTCTCATGTCTGTAAATCAAA	AATGAATTTCCTTGCAATAAA		
440042	LOC440042	XM_498516	ATAGTAGATTCTATCAATCAA	CAGGTGAACAGAAGTTCTCAA		
440050	LOC440050	XM_498520	AGGGTCCATTCCTCACTATAA	AGGAGAGTCCACGCTAATTAA		
440055	LOC440055	XM_495885	CAAGATTCAGGTTCACCCGTA	CAGGTTCACCAGTAACCCACT		
440058	LOC440058	XM_498524	TTGGAAGAATTGTGTTATATA	AAGGGTAGACTGAGTCTTGAA		
440066	LOC440066	XM_495897	TAGGGTCAAATCAGTCACTCA	CACCTGCATTGTGCAAGGAAA		
440071	LOC440071	XM_498531	CCGGAGAGGCCGAGTGATCTA	CACAATTCTCTCTCTCCTTAA		
440077	FLJ16353	NM_001004328	CAGCACATAGTTAGTGCTCCA	TTGACAAATCAATATATTAAA		
440079	LOC440079	XM_498535	TGCAAGGTACTTGACACGCAA	AAGAGAGAATAGATAACTTCA		
440083	LOC440083	XM_498536	AAGAAGATGAGAGTGAATCAA	AAGGAGACAACAAGTCCCGAA		
440093	LOC440093	XM_495919	ATGCATGTTTCTGTTGTTAA	ACCAAGCAGACTGCTCGTAAA		
440098	LOC440098	XM_498543	ATCGGGTAAAGGAGTCGATAA	CTGGAGACAAGTGGACCCTAA		
440101	LOC440101	XM_498545	CAGAAGTTAATTTCTCACTTA	CACATAGATTACACTAAATAA		
440102	LOC440102	XM_498546	GAGAAAGTTGCTGCCACTCAA	AAAGAAAGGAATATCATTATA		
440106	LOC440106	XM_495929	AAGAGGGTCCATCGCCATCAT	AGGGCTGGAAGTAGGCCTGAA		
440112	LOC440112	XM_498548	AAGATGTTGTTTCAACCTGTA	AAGCTTTAAGTTGCAAATGAA		
440134	LOC440134	XM_498562	CCACTCCATAGTGAATGGTTA	TTGATTGTCTTTCATCGGAAA		
440138	LOC440138	NM_001004127	AACGGTCAACAGATACTAGAA	CTCATTGTATGTGGAACTTTA		
440142	LOC440142	XM_495960	ATCCAGTTCATCTCACTTCAA	AAGCCTTTGAGAAGCATGAAA		
440151	LOC440151	XM_498568	CACCAGCATTCCAGAGTCCAA	CTGGAAATAAATAATTCATAA		
440153	LOC440153	XM_495967	CAACATATGCACTGACTATAA	CTCACTCTTTACTACAACATA	CAGCAACTTCACAACCCAGTA	CAGGCCTCAGATAGACGCCAA
440155	LOC440155	XM_498569	TACAAATGGAGACACAGGAAA	CCGGCTGCTGCTTACACCTTT		
440157	LOC440157	XM_495969	AAGGGAAGCCAGGCTGAGATA	CAGAGTCTGCCTCCATGAGAA		
440186	LOC440186	XM_498579	AGCCTCGGAAATTTCCTTTAA	CCCGGAAAGCAGGGCATTCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
440190	LOC440190	XM_498580	AAGGAACTTTGGGAAGATGAT	CCGGGCCTCCTTGAAGGTTGA		
440191	LOC440191	XM_498582	TAGCATAAGATGCTTCCTTAA	TACTTAATAAATAAACATTTA		
440228	LOC440228	XM_496031	CTCCTGGGTAGATGCATATAA	CAGCCCAAGGACAGCCAATTA		
440232	LOC440232	XM_496036	CTGTGCCTGGCCTGTATTGTA	AAGCAGGTGGATGCAAATGAA		
440233	LOC440233	XM_496037	CAAGAAGGCAAAGACAATAAA	CACCTGGAAGCTGCCATCTAA		
440242	LOC440242	XM_496040	TGCAGAGATCCAGGATACAAA	ATACAACAGCTTCTTAGGTAA		
440243	LOC440243	XM_496041	CACCTGGAAGCTGCCATCTAA	GTGCATCCTCACGTAAGTGCA		
440245	LOC440245	XM_496042	CCCAAACGAGGTGATCGACTT	CTCCTTTCGGTGCATGAACAA		
440252	LOC440252	XM_496049	AACAAGAAACAGAAAGCCAAA	AGAGATGAGTATTCTGAACAT		
440254	LOC440254	XM_498602	CAGCTGCTGCGGCGCCATGAT	TTGCAAATAATGAGAAGCCGA		
440266	LOC440266	XM_496062	CTGCAGCAAAGCACATACAGA	GATGAGTGTGCTGAACATATA		
440274	LOC440274	XM_498608	CTTGAGAATTATGTAGAATAA	CAGAGGTCATCTTTAAGTAAA		
440277	LOC440277	XM_498610	AACATTGGCCAGGGAAGTTAA	CAGGATGGTGACTTGTCTTTA		
440284	LOC440284	XM_498614	ACGGAAAGCCTTTATAATGTA	CAGAATGTTATTAATCTTTAA		
440298	LOC440298	XM_496086	CCGGGACCCTGCAGAAATGAA	ACCCGGGATCCTCAAATAGAA		
440301	LOC440301	XM_498620	ATAAATTCTCACACACACATA	CTGCCCTGTTCTATAGCTATA		
440303	DNM1DN11-13	XM_498621	TTGACCGTTGCTGAAACTTGT	CTGAGCATTCATCTGAACTAT		
440307	LOC440307	XM_496092	ACGCAGATCACTGGCCATCAA	ATCGAGGACATCATCATCAAA		
440317	LOC440317	XM_496097	AACCCTAGTGTTGGTACAGCA	CAGAGCGTTTCAGGCAATGAA		
440329	LOC440329	XM_498628	TCCCAAGTCAAAGACACTCCA	CGGCTTGAAGGAACAGGGCTA		
440334	LOC440334	XM_498631	TTGTAACTACTTGAAGTTAAA	ACGGTCTTTCTTTGCCAACTA		
440344	LOC440344	XM_496123	CACGGGAGGTGACATGAGCAA	GAAGGAGAAATTCCAAAGAAA	CAAAGAAATGTAGTTTATTTA	CTGGCTGTGAAGGACCCTTTA
440361	LOC440361	XM_496145	AGGGAGCAGTGAGGACACCAA	CACAACGATGTGCTTAGTAAA		
440370	LOC440370	XM_496158	CTCCTTGTATGTTCAAATGAA	ATGGTATACTTTATTAAGAAA		
440372	LOC440372	XM_496161	GCCGATGGAGATGCCTATGAA	CACGGAGAATGACCAGCTCAA	ATGGACAAGAAGAAAGAGTAA	CGCGGGCGTCTAGGCAAGAAA
440374	LOC440374	XM_370980	ACCTATTTATGAATATACAAA	AAACCATTAAACAGATTTCTA		
440380	LOC440380	XM_498645	AAGCCAAGAGAAAGTCAGAAA	ATGGAGGAATGAGGAGTTCAA		
440387	LOC440387	XM_496169	TACCACCACGCCCGCTGTGTA	CTGCCTTAAGATTTCCCATTA		
440391	LOC440391	XM_498650	ATGGTATTGGTGTAACATGTA	AAGGATCGCATGGCAGAACTA		
440414	LOC440414	XM_496194	CGCGGATAGTGTGCAGGCATA	CCTGGTGTTGTCAATCATGAA		
440426	LOC440426	XM_498662	TCCCAAGTGGCTAAGACTTAA	CAGGATTAGCTTGTGGTTTAT		
440432	LOC440432	XM_498666	CCGGGCATACTTAGTATCTTT	CTGGTTGGTAAAGAACATTAA		
440434	LOC440434	XM_496214	GCCGCAGGCGTTATTCCTAAA	CAGCCGAAAGAGCAACTCATA		
440435	GPR158LY	NM_001004334	AACCAAGGAAATGGCCGCAAA	CAGGTGTGTATAAATCTGACA	ACAGAAGAATTCACTACTGAA	CACCATCATACTCAAGCTTTA
440447	LOC440447	XM_496231	TCCCAGGGTCTCTACAGATTT	AAGGAGTTGCAGGAAGCATTT		
440449	LOC440449	XM_498675	CTAGATGAAGAGTTATCTTAA	CTGGAGTTCCTTGACTAGGAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
440455	LOC440455	XM_498678	CCCGAGGCTCCACGTACTCAA	CGCGCTTGTCAGGGAACAGAA		
440461	LOC440461	XM_498680	CTTGTGATGTGTGGAGATCAA	CTCCCTGGTTATACTGTTATA		
440462	LOC440462	XM_498681	CCGGGCCTTGTGAACCTGCAA	CACCCTGGTCTTCTCCTGTAA		
440472	LOC440472	XM_496255	ATGGCTATAACAACAAACTAA	CAGACTCTTCTTAGAAGTCTA		
440484	LOC440484	XM_496268	CAGGATCATCCATACCCTAAA	CACTGTAACATAATCCATTAA		
440493	LOC440493	XM_498698	GCGGCTCAGTTTCACTAACAA	CCCGACTTTCCGTGCAATAAA		
440495	LOC440495	XM_498700	GGCGACATATACTAACAACAA	CTGGTGTTACATTATCAACAT		
440498	LOC440498	XM_498704	ATGGTGCAAGCTGGCATTGAA	CTGGTAGATTATCATGGAGTA		
440501	LOC440501	XM_498706	CGGAGCAGAGTTCTCCTCAGA	CAGATTTCAGTGGTACTGCGA		
440508	LOC440508	XM_496285	CAGGGCTACTCCCACTGGTTA	CTCCATAAGCCTCAGAATGAA		
440526	LOC440526	XM_498718	CAGCAACCACGCCACCATGAA	CTGAACAGGGTTCTAACCAAA		
440536	LOC440536	XM_498721	CAGGCATCACATCCAGACTCA	AGCCTTTGTAGGAACGAGAAA		
440546	LOC440546	XM_496328	AAGCAGAGAAATGCAAACTAA	TTGCTTCAAATAGGGCCAGTA		
440551	LOC440551	XM_496331	GAGGGAGATGCGCTCCCTGGA	CCCGCCTCTCGTGGTGGTCTA		
440552	LOC440552	XM_496332	CTCCAAATATCTCATCAACAA	AACCAACACACTAAGCATATA		
440554	LOC440554	XM_498731	AAGCACAGTTTCCTATGACAA	CACGTCACTCAGAAAGTTGAA		
440563	LOC440563	XM_496344	TCGAAACACCAGCGCATATCA	ACCAGCTTCATTTGATCAAGA		
440567	LOC440567	XM_496348	GAGCTCTATGATGAGCATGTA	CTGCTGATGTTAAATCTAGAA		
440568	LOC440568	XM_496349	AAGGTCTTAAGTGCAGCAGGA	AAGATCTTTGTTGGAGAAGGA		
440572	LOC440572	XM_498736	CCGTTTAATATCAGAGAGAAA	ACCATATTTATGAAAGTAAA		
440583	LOC440583	XM_498743	CCGGGATGACCTAAGGAACAA	CAGAGAGTGATGACTGCTTAA		
440586	LOC440586	XM_496361	TCAGGTTATGTTGGAGCTAAA	AAGCGAATTTATGATCTGAAA		
440587	LOC440587	XM_496362	CAGGCAGTCATGTGCCCGAA	CCCAAACATCTTATTGATACT		
440596	LOC440596	XM_498746	TTGGGTTTCCTTGAGTCTCAA	GTGGGTGAAGTGGAAGAACAA		
440606	LOC440606	XM_496385	CTGGAACATTTAGGCCTTGTA	TAGCTACAGCATATTATTTAA		
440607	LOC440607	NM_001004340	ACTGTGATAGGCCTCCAGTTA	CAGCAGGAATATCACAATACA		
440609	LOC440609	XM_498754	AAGCCTTGTTAACTTGCTGAA	CACATCGTGTTTGGGATCAAA		
440665	LOC440665	XM_498809	GTCCAAGAAGTTTCTGACAAT	GAGAATGTTCCTCTTCAGTAA		
440667	LOC440667	XM_498810	CAGCAGCTGTTGCCAAATGAA	CACGCGGGTTCTGCCCTCAAA		
440678	LOC440678	XM_496401	AAGGATGTCATCAAAGTAGTT	TAGGAGATCTTTCACTTGTAA		
440683	LOC440683	XM_496404	GAACATAAGTTTCTATTTCAA	CAGAGGCGCTTCAGGAAGCAA	AGGAATGAACATAAGTTTCTA	GTGCAATTCGTCAGAACTTAA
440684	LOC440684	XM_496405	CTCCTTGTCAGGAGCACCTAA	AGGGATTATTACTCACTGCAA	CTGCAACTTAGCCTAGCATTA	TAGCATTAAGTTGCTTGACTA
440692	LOC440692	XM_498820	AAGCAGATCAGTGCTCAAGTA	TAGGAGTTGTAGAGCAGAGAA		
440696	LOC440696	XM_496420	AAGCCAATTGATGACATATAT	AAGCGTAAAGCTTGAAATATA		
440705	LOC440705	XM_496427	CACCTTCATGCTCAGCATTCA	TCCGAATTTCTTGATCAAGAA		
440707	LOC440707	XM_498827	CCGAGACTCAGACTTACCCAA	CTGCATCTTCTCATCCCATAT		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
440722	LOC440722	XM_498831	AGGCATCACGTCCACATGCAA	CAGTGTGGCATGGGCATGTAA		
440724	LOC440724	XM_498833	AAGGGAAAGGGTGACCACATA	CACTGTGAAGAATATATTAAA		
440725	LOC440725	XM_498834	TTGCATCAAATGGGACCTTAA	ACGAGACTTACAAATAATAAA		
440730	TRIM67	NM_001004342	CTGGCTTTAATAGTGATTCAT	TACCTAAGTTCTGGTATCTAA	CCGGGAAGTGTACGTCGGTAA	CACAACTATCTCAGGCCTTAA
440747	LOC440747	XM_380170	ATCCAATTCTCTACACCATAA	ATGCAGAATCAACAACAACAA		
440752	LOC440752	XM_498844	CTGCTTGAAGCTGGCATTTGA	ATGGCTGGTTACTGTGCTAAA		
440757	MGC44328	NM_001004344	ACAAGTGTTAATCCCAATAAA	CAGGGAAGACACAGTCACTAA		
440764	LOC440764	XM_496476	CACGGTGCTCCTGGAGGCCTA	CACGCTCACGGTCAAGTATGA		
440765	LOC440765	XM_498851	CAGCAGTAACTTATTAAATCT	CACAGCCGAGTTGCTAGCTAA		
440766	LOC440766	XM_498852	ACCCATGAACATGTACAATTA	ATGGCTAATAATCACATGATA		
440771	LOC440771	XM_498856	CCGGTAGCCAGTCAGAATTTA	CACGGTCAAGACGGAAGCAAA		
440772	LOC440772	XM_498857	AAGCAAATGGCTCATTTCCAA	AACCTCTAAGATTTGAATGAA		
440773	LOC440773	XM_496481	CAGGTAGATGATAAGGAGATT	AAAGAAGAATCTGAAGTGAAA		
440786	LOC440786	XM_496488	CTGGCGTTAAAGAGGTCCATA	TAGAATATGGAGGCCCTGAAA		
440787	LOC440787	XM_496489	TAGACTCAGAGAGATGGCAAA	CAGAACAAACATAGTACGGCA		
440788	LOC440788	XM_496490	ACGGAGCATTACATTCCCAGA	CCCGGAATCAATGGGAATGAA		
440790	LOC440790	XM_498869	AACATTCTTCATTATGCATAA	CAGCAGGTGTTGCTTAGTGAA		
440793	LOC440793	XM_496494	AAGGTCTTCTCAAATATTGTA	CTGCAGCGGAGCCATGGCCCA		
440804	LOC440804	XM_036936	AACAGAGATCCTGGATACCAA	CTGGAGGAAGACAGCTTATTA		
440815	LOC440815	XM_498875	GCAGATGGCGAGCATGGCAAA	AAGGGAGACCAAAGTTGGAAA		
440824	LOC440824	XM_496523	CAGATCCATGCTGATCCCGCA	CAGGGCGCTGAGTACCATGTA		
440839	LOC440839	XM_496539	TTGAGGGATTTCAGACTTCAA	AAGTCTTATTTAAGAAATATA		
440843	LOC440843	XM_498885	TTGAATTTGTGTTCAAAGTAA	CTGGGAAGAAAGCAACACAAA		
440854	CAPN14	XM_496548	CTGGAGTGACAGTTCAAGTAA	CAGGATGAATTCTTCACCAAA		
440855	LOC440855	XM_498894	CTGGACATATTTCTTCTGGAA	CCGGAACAGAGATTTACTCAA		
440856	LOC440856	XM_498895	ACGAACGTAATTTGTTTCTGA	AAGGGAGAGAAGAGAGTTGAA		
440857	LOC440857	XM_498896	TCCAGTCTGTTTACTATACAT	GGGACTCAAAGTATTAGCTAA		
440859	LOC440859	XM_498898	CCGGGAAGCCTGGCTCCGAAA	CACATTACAGTTAATCTGTAA		
440866	LOC440866	XM_496551	CAGAAAGTTTGTGAAGATCTT	ATGGTCTGACTTTCACAGAAA	CCGGTTCATCTAATACAGACA	CAGATTTGTCAAGGTTTGAAA
440867	FLJ16124	NM_001004345	AAGGAAGGAATTTATCTACCA	CACGAGAAATATTACGTTGTA		
440872	LOC440872	XM_496559	AAAGAGATACGTATGTACTTA	CAGTGGCTGTGAAGAATATAA		
440900	LOC440900	XM_498909	ATCCGTCACACTAGATGCATA	CCGGAGCCGTTTACAGTTTGA		
440923	LOC440923	XM_498916	AACAGTGAATAAGCACCATAA	TAGGAGGAAGGCCACAACTAA		
440925	LOC440925	XM_496609	CAGAGGTTAGCCTAACTACAA	ATAGGTTTAAGAGTTAATATA		
440927	LOC440927	XM_496612	AAGATCAATGCCCTCATTAAA	AAGAAAGTGGAAGCAAAGAAA		
440930	LOC440930	XM_498918	CCGCTAGGTGTAGGACCGCTA	TTGGCAGAATACTCAGGTCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
440937	LOC440937	XM_498922	ACCTGAGAATTCAATGATGTA	CCCAACCTACAGGAAGCATAA		
440940	LOC440940	XM_498923	CAGGGCGACAGTGTAGGGCCA	AGCCTGCGTCTCAGCAGCAAA		
440954	LOC440954	XM_498932	CTCATTTACCTTCCACATAAA	AAGGAACAGATGTACAGTAAA		
440959	LOC440959	XM_498934	CTGCACCAATTCGCTCATTTA	CAGCCAGTTCATAGACACCAA		
440960	LOC440960	XM_498935	CGGGAGAATATGCAGCAATAA	CCGGCTCAGGTATTTATTGAA		
440965	LOC440965	XM_498938	CGGCAGACACACCACGTTCCA	TAGGTCTATCAGTGCTTTGGA		
440970	LOC440970	XM_496650	AAGGAAGAGAGTGATTATATA	CAACATCTTATTGCTATTTAA		
440971	LOC440971	XM_496651	ATGGAGTAAACTACAGCTTAA	TAGGATATATTTGTCCCTTAA		
440978	LOC440978	XM_496659	CAGGGTAATCACGGAATCCCA	AAGGGAGAGATTGGTGATGTA		
440990	LOC440990	XM_498952	GAGGATGTATGTGATGAGTAA	CTGCTGTAAACCAATGTTAAA		
440992	LOC440992	XM_496668	TTCGCTCTCGCCGCCGAGGAA	AAGGAGGAGTTCGAATGCCTT		
440995	LOC440995	XM_498955	CCAGAACTGGCAGCCCTTAAA	TAGCGTGCCGTGGCCATTGAA		
440997	LOC440997	XM_498957	AAGGTTCATAGTTGTGTTGTA	TAGGCTATTTCAAGAAATTAA		
440998	LOC440998	XM_498958	TGCAGAATTCATTATAATAAA	CAGGTGAGACTTCACCGTGAA		
441022	LOC441022	XM_496700	CACCCTATGGATGAACAGGAT	CACAAGCATCTGATGAAGCAA		
441023	LOC441023	XM_498970	TCCCTCCATCCTTGCCCTAAA	ACCATGAGTTGTCACATCTAA		
441027	LOC441027	XM_496707	CGGAATGACCTTACTTGGTAA	TACCATTAAATTCAGCTGAAA		
441030	LOC441030	XM_498973	AAGAATCTTTACAAAGCTGAA	AAGGATGAGAGTGGATGTCAA		
441035	LOC441035	XM_496713	CAACTTGGTAAGAACACATAA	GTGAGAAATAATACTCATAAA		
441042	LOC441042	XM_498981	AAGGTTTGCTCTAACCTAGAA	TAGCAGGAATTCTTATATCAA		
441050	LOC441050	XM_496721	CTGGAGTAAGAAATATTTCAT	CTGGCTTAGTATGGACTTCAA		
441053	LOC441053	XM_496723	ACCATTTGCAATGAAGAGGAA	AGGAAAGGAATTTGACATTAA		
441059	LOC441059	XM_498991	AACTCCCAATTTGGAAAGTAA	CTGCTAAAGAATAAATGTAAA		
441068	LOC441068	XM_496743	CTACAAGAATTCGAAGAGAAA	CACCAAGGAAATGAAAGTTCA		
441069	LOC441069	XM_498996	CGGGAGCTGAACCGAGAGCAA	CAGGGTTCCATCAGGAAGGAA		
441071	LOC441071	XM_498997	CAGCTTGAACAACTCAGCTAA	CCCATGGATATTGAAAGGATA		
441073	LOC441073	XM_496746	AAGAGCTGAGACAGAAGTACA	AAACTGGACAAAGACTGTGAA		
441077	LOC441077	XM_496748	AGGGTTCAACCTCCAACCTTA	CCTGAGATCGATAAAGCTTAA		
441093	LOC441093	XM_499007	AAGATGGAGTTTGGAAGGATA	CTGGAAGATTCTGTTCATGTA		
441099	LOC441099	XM_496770	AAGCCTCAGAGTATTTCGAAA	AACATTTCACTTTACATCTAA		
441113	LOC441113	XM_496782	AACCACAGATCTCGTAGGAAA	CACGATGTATTTATTTGATTT		
441117	LOC441117	XM_496786	GTGGAAGAATTCATATATGAA	AAGGATCTTAGCTTTGAGAAA		
441118	LOC441118	XM_496787	CTGGAAGAGTAGAAACAGAGA	CAGGTGGTGTTTGGGTGCATA		
441128	LOC441128	XM_496793	AAGCCCAAATAGAGAACAGTA	AAGAGGCACCTAATTCCTTAA		
441129	LOC441129	XM_499026	CCCACTCACCGCACACCATCA	CAGGGCGCCTCTAGTCCCTCA		
441140	FLJ45422	NM_001004349	TTGGGAGGTGATGTCATATAA	CAGACGGTACATACACTCTAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
441141	LOC441141	XM_499031	CAGAATGACTACCCATGCAAA	AAGACAGGTACTGGAAGATAA		
441157	LOC441157	XM_499037	CCGGGATTCAGAATTGATCCA	CTGCACGTCACGGCTACTCAA		
441162	LOC441162	XM_499039	ATGGGACATGCATATAAACTA	TACCTAATACACTGCAATATA		
441165	LOC441165	XM_496820	CACCCTTAAACTACAAAGAGA	AAAGAAGACATCACCCTTAAA	CACCTGCTACTCAGAAAGCTA	TTGGAAGAGATTCTTATTAAA
441167	LOC441167	XM_499042	CAGGCAAGCTTTCAACTATAA	CTGAAGGTAATCAGAGATTAA		
441171	LOC441171	XM_499044	CCCAGAAACACTGTACTTTAT	ATGATGAATCACCAACACTAA		
441173	FLJ39824	XM_496827	CAGGACCATTTGACTATTTCA	TAAGTTATTTATACTCATTTA		
441189	LOC441189	XM_496843	CCGGGCCTCAGTTTCCCGGAA	CCCGGAGGAGATCGCGCGCAA		
441199	LOC441199	XM_496855	AAGGATACTTGTTAACCTTAA	TCCAGCTTTGTTGGTATTCAA		
441209	LOC441209	XM_496859	CTGGCTGTCAATTTATCAGTA	AGGAAGATTGTTGGTGATGAA		
441215	LOC441215	XM_496862	TTGCAAAGAGAAGAAGATCAA	CAGGGTGTATGAGGAGAGAAA		
441220	LOC441220	XM_496867	CAGCATGTCTTCAGCCAGGAA	CTGGTGGTTGTACTCAGATAA		
441221	LOC441221	XM_496868	CTGAGAAATGGAATAATCGTA	CAGGATGAACGGCGCCAGGTA		
441235	LOC441235	XM_496880	CAGGTCATATCCTGAGATCAA	CACTGTCCTGATTATAAATAA		
441243	LOC441243	XM_376622	AGGCCAAAGCTTTGTATTTCA	ACAGAGTGGTGTGGAGAATAA		
441268	LOC441268	XM_496908	TTGCTCCATACAGACCTCCCA	CTGCTGATTTGTTCACTTGCT		
441307	LOC441307	XM_499093	AAGGATGTTTGGAGGCTTCAA	CCGGCCTTCGTTTCCATTCAA		
441309	LOC441309	XM_496942	CTGAATGATATTTAAGCTGAA	GGCGACCTTGCTGCAGGACAA		
441313	LOC441313	XM_496945	GACGTTGTAGTTGGCGTGGTT	CTGGAATGCCTTTGTACATAT		
441328	LOC441328	XM_496957	ACCAAAGAGCGTGGAAGGAAA	TCCGGATCAGAAGGAGCAGGA		
441333	LOC441333	XM_496962	TAGGGAAGGGTGGTTCTGGAA	CACCTTGGATCTAGGAGACAA		
441336	LOC441336	XM_499101	CACCAGGACCTGAAATGTTAT	CCAGCTGGATATCACGGGAAA		
441377	LOC441377	XM_496991	AAGGAACAACGGTGACACCAA	CCCACCTTGATTTAGACCTGT		
441386	GD:PTPRD	XM_497007	CCCAAGCTGTATGTGAAGCTA	AAGGACAAGGCCATTAAGAAA		
441395	LOC441395	XM_497014	ACAGATCCTGGTCAGAGTAAA	CAGGTGCTGGTTATGCTTTAT		
441401	LOC441401	XM_499136	CAGCCGGTCAAAGCAGCAGAA	ATGACAGATTATGAGAATGAA		
441421	LOC441421	XM_497042	AAGCGCGTGCTGTCGCCTGCAA	AAGAGGTTTCTGGGTCATCTA		
441424	LOC441424	XM_497044	AACACCCATAAGAATTCCTAT	CAGAAGGAACAAGCACAATAT		
441432	LOC441432	XM_376852	CAGGAAATATGATGCGAGGAA	CAGGGTGTACCATGGCATGAA		
441447	LOC441447	XM_497061	AAGGAGGAATTTCAGGGTGAA	TAGCACGATTTCCTATGACCA		
441450	LOC441450	XM_499151	CTGGGTTCTGCTGACATGTGA	TAGGACGAATTTCTTGCTCCA		
441454	LOC441454	XM_499153	CAGCTCTGAAATCATTGCCAA	TTGGTTTATATGATCTAGTTA		
441455	LOC441455	XM_497068	AACTGCTGTGGAAACCAAGAA	GTGCCTCTCCATGGAGATTCA		
441458	LOC441458	XM_499155	CTAAGTGGAGTGGACCATAAA	ATGATAATAGCTTACCACAAA		
441460	LOC441460	XM_499156	TGGGAACAATAAAGCACTTCA	CTGCACCTATTGTCACAGCAA		
441464	LOC441464	XM_499160	CTGGGATTAAGACACAAACAA	CAGGGACAACTTGGATCTTCA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
441467	LOC441467	XM_499164	CTGCTTGGCGGTAGACCTTAA	CAGGATCCTAACGAAGACCAA		
441468	LOC441468	XM_499165	AAGCAAGGTCTCGCTGTGTTA	TAGGACTTTCTTTGCATTCAT		
441471	LOC441471	XM_351854	AAGCGTCTTCGTCTTGCTCAT	CTGCACCTCACTGGAGCGGAA		
441474	LOC441474	XM_499168	CGCCGCCTGCTTCACTTCTTA	CCCAGGAGATAGAACCTTCTA		
441483	LOC441483	XM_497093	GGCCCTGATAAGGCCACCCAA	CCACGCTGGGTTTAAGTGACA		
441490	LOC441490	XM_497100	ATGGAATCAGCGACCACACTA	TTTGACCATTGTTAACAATAA		
441491	LOC441491	XM_499175	CCCAGTGGAGCACGTCCTCAA	CTCCAGAAACATGAGCACAAA		
441494	LOC441494	XM_499177	CAGAGGCATGAAGCTAGAATA	CAGGTTCATCTCATTAGTGGA		
441515	LOC441515	XM_497146	CTCACTAAAGCTCTAGTGCAA	CAGCACATTCAGTTAATGTTA		
441525	SPANX-N4	NM_001009613	CTGGAGAATAACCAGCCTACA	CAGAGTTTGAAAGAGACAGAA		
441528	LOC441528	XM_497181	CTGGCCCAGCATTTAAACTTA	CTGAATATTGTGCGCATGAAA		
441529	LOC441529	XM_497182	CTGGAGGAATCACCCAGTGAA	CAGGCCACTCAGGATATC[illegible]A		
441531	LOC441531	XM_497185	AAGCCATTCCTCATACCAATA	AAAGTATAGTATATATT[illegible]ATA		
441540	LOC441540	XM_351948	CTGGCACCCTTCAGATCCTTT	CCTTACGGATTTC[illegible]GGTTTA		
441542	LOC441542	XM_497201	CAGCATTCTGACGCTGAAGTA	CAGGACATATC[illegible]GACTTATTA		
441551	LOC441551	XM_497216	TCGACCAATTTGCCAACGTTA	CTGGGAAT[illegible]GGCTCCTGAAA		
441560	LOC441560	XM_497230	GCGGATGAGCACCAACCCTGA	CAGAC[illegible]CTTGTATCTCGCAA		
441561	LOC441561	XM_497231	ATGGACCAAGTGGAAGGCAAA	CA[illegible]AGATTATATGACATGAA		
441569	LOC441569	XM_499192	ATCAGAAGACATAGCCAGAAA	[illegible]TGCAAGAAAGGCCTCAACAA		
441599	LOC441599	XM_497281	ATGGGTGACTCTTAAAGGTT[illegible]	CTGAATCTAGAGCTCATTAAA		
441631	LOC441631	XM_497334	ATGGTCCATTATAAGAC[illegible]AA	CAGCATGATGCCATTGCTGAA		
441634	LOC441634	XM_497338	CTGGAGCTCACTCG[illegible]ATTCAT	CGGGAGTTGAAGGACTTGGAA		
441636	LOC441636	XM_497341	CAGGAACAACTG[illegible]ACCATCAA	ATCCATATTGATGACAATAAA		
441663	LOC441663	XM_497381	TAGCAACAA[illegible]ATGAAGACCCA	TAGCCGCAAACTAGACCCAAA		
441665	LOC441665	XM_497385	CCGGGA[illegible]CTGTGACCCACTCA	CACCTGAGACCTGTCCTGTGA		
441682	LOC441682	XM_497406	CAC[illegible]TCCAAGGTATCGTGTA	CAGGCCTAGCATAGTCCTTTA		
441696	LOC441696	XM_499197	[illegible]CAGACATGCCTCCGCGTAA	CACAAAGAGTTTGTTACTGTT		
441706	LOC441706	XM_497431	TGGGATGACAGATGCATTCAA	CCAGGATATCTAATTCGCTAA		
441709	LOC441709	XM_497[illegible]4	TCTGGTATTTATTACTAGAAA	CACCCTAAGTCTGCACTTCAA		
441740	LOC441740	XM_[illegible]477	ACAGCTGTACATATTATACTA	CAGGAAACTGCCAGAAAGTAA		
441754	LOC441754	XM_497493	TTGGAACATCGGCAACACAAA	CAGGATGAAGCTCATGCCTCA		
441755	LOC441755	XM_497494	CAGGCAATGGAAGATGCATAT	TAGATGAAACTTACAATATAA		
441759	LOC441759	XM_497498	CTGGCCGAGTTGCACCCTTGA	ACGGACGATGGAGGTCTGTGA		
441790	LOC441790	XM_497536	TCCAAACAGATTCCTTGGGAA	CAGCTTGTGATTGAGGACCTA		
441798	LOC441798	XM_497553	TCCGCGGTCTTTACCCTGGAA	CAGGAGCATGCAGGCCTACAA		
441816	LOC441816	XM_497584	CAGCAGGTGTGGGAAATCCTA	ATGGACTTGGTCAACATCAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
441821	LOC441821	XM_497592	AAAGATTGCTCCAAAGATTAA	CAGCAATATCCCATCCACAAA		
441826	LOC441826	XM_499202	CTGGGAATTCTGGATGTTCCA	CTGGGTATTCTGGGCATTCCA		
441827	LOC441827	XM_499203	AAGCCTATCTAGATCTACTAA	CAGCCTATCTAGACCTACTAA		
441833	LOC441833	XM_497603	CTCTCGGACATTAGTCACCAA	TCCCGAGAATGTGACATCTAA		
441842	LOC441842	XM_497614	AAGCTTCTAACGGGTTCTCAA	CTGAATGTGAGATAATTTATA		
441847	LOC441847	XM_497623	ACCCACCTTGTTAGGCATAAA	TCCAACCTCATTAAATATAAA		
441848	LOC441848	XM_497624	CAGTTGAAGATCAATAAGAAA	ATGCATCGAGTTCACACTAAA		
441866	LOC441866	XM_497645	ACCCTGATTTGTCCTGATAAA	TCCTGATAAAGAGAAGGCATA		
441874	LOC441874	XM_497654	CACGTCAATTACCGCGAGGAA	CAGTTCTGTATCAGTCTTGAA		
441898	LOC441898	XM_497698	AAGCTCCTTCTCCTATTATTA	TAGGCAGAATCCCGTCAAGAA		
441915	LOC441915	XM_497724	CCAGTTACATCTGGTGATCAA	AACGCTTATGGTATGAAGAAA		
441916	LOC441916	XM_497726	ATCCAGAGTATGGAGAAGTAA	CAAATCCAATATATTAAGAAA		
441922	LOC441922	XM_497733	CAGGAGAGACAGGACCCATTA	CAGGAGAGACAGGAGCTATTA		
441925	LOC441925	XM_497740	CAAGTTCATGCTTATAAATTT	CAGGGACTACAGTGCCTTGAA		
441928	LOC441928	XM_497743	TGGGAAATATGAGGTCATGAA	CTGGAGGTAGCTGCAGCGGAA		
441955	LOC441955	XM_497773	AGGGATGAGGTAGCAGAGAAA	AAGGCTATGAGAATACACCAA		
441959	LOC441959	XM_497777	CAGACCATGACAACAACATCA	TGAGCAGATCGCGGAGATCAA		
441994	LOC441994	XM_497814	TCGACAGACCCTGGAGGTGTA	CAGCACCATATCCGACATCAT		
442008	LOC442008	XM_497828	GACGACAAGAACTTTAGCAAA	CAGAATCAAATGATCCTGCAA		
442011	LOC442011	XM_497831	AAGCTTATTGATGGCATTCAT	ACGGCTTCATTTAACAGTGAA		
442016	LOC442016	XM_497838	CAGATAGATCTGTTTCAAGAA	AAGGGAAATGCTTGATGGTTA		
442020	LOC442020	XM_497844	CAGCATCATGAGCCAGTTTCA	CAGGCTGACTCGGTACGCAAA		
442022	LOC442022	XM_497846	CGAGCAACTCTCTGGGAACTA	TGAGGTGGTGTCCTTCCGTAA		
442044	LOC442044	XM_497872	CCAGGTGTCAAGGACAGCAAA	CAGCTCCATTGTCTCCCATAA		
442081	LOC442081	XM_497923	CCGCCAGACATTCCAATTGGA	CACGGGCTACATGACCTGTGA		
442093	LOC442093	XM_497939	ATCGTCATTGTTAATGAGCTA	AAGGCTGATTACGAGAGCAAA		
442099	LOC442099	XM_497951	TCGGACAGACCTCCACTTCAA	AACCCTCAGCTTCCATTTAAA		
442108	LOC442108	XM_497964	AAGGGACATGTGGAAGTAATA	CAGATTAGTCAAGAAGATGAA		
442119	LOC442119	XM_497984	CAGGATTTGAAGGAAGCCACA	AACGACATCTTTGGCACCAAA		
442121	LOC442121	XM_497986	CAGAATAGCTTTGCACATACA	CAGCTGGACTTTAAGAATGTA		
442124	LOC442124	XM_497989	CCCGCCTTCGTTATCATTTGT	CACCTTCTACCTCTTATTCCA		
442140	LOC442140	XM_498021	CTCATGGCTCTTGGAAGGAAA	CACCCTGGAAGAAACCATCAA		
442141	LOC442141	XM_498022	CTCAAGGAGCCTCATATGGAA	CCGGAGCATGGCAGAACTCCA		
442145	LOC442145	XM_498027	CCGGGTCCTAAACTCTGGATA	TAGGCTCTGGGTATAAGCTTT		
442158	LOC442158	XM_498040	TGCCAGCAAAGTCCATGTAAA	AGGAACAATAATTGTGCCAAA		
442174	LOC442174	XM_498056	CTGGCTCTGTGAATTCGAATA	CTGGTGGGAGTGAGAATTGAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
442208	LOC442208	XM_498091	GCGGATCAGGTTCAAAGTGAT	CAGGACCAACATCCTCTCCAT		
442209	LOC442209	XM_498092	AACAATAAAGGCGAGATGAAA	CAGATCAAGGGATCAAGGGAT		
442228	LOC442228	XM_498111	ACGGAAGTACTTGGCATATAA	CACCATGTAGTTGTAATTCAA		
442243	LOC442243	XM_498127	CTGACACCTCAGGGTCAGAAA	CAGAGGCACCTATACCACCAA		
442272	LOC442272	XM_498157	AAGCAGAAGGACACAGATGTA	CCGAACCAGATGAAACCCAAA		
442339	LOC442339	XM_498230	GTGACTTTGAAGATAGCTTCA	CCGGTGAGTGGCAAACAACGA		
442350	LOC442350	XM_498243	CAGAAACAGGGAAATCCTGAA	CGGAATGGAAATACTTTCTAA		
442375	LOC442375	XM_498266	ATGGCTTTGCAAAGGAGCCAA	TGGCATCATCTCAGGAAGAAA		
442397	LOC442397	XM_498297	CCCGTAACAGATTTCCATGAA	CAGGTAGTAGTGACACATATT		
442398	LOC442398	XM_499238	GTGCGAGATGAGAAATCTCAA	CCGGGACAACTGCACCAGTGA		
442400	LOC442400	XM_498299	AACGACAACATGAAGTTCGAA	CAGGGACGCTTTAGCACTCGA		
442401	LOC442401	XM_378044	CCGCCTCTTTGGGCACCTTAA	CAGCGAGATGACCAAGACGAA		
442410	LOC442410	XM_498312	CGGTGTGAGCATGGCAGAGAA	CAGGGCCATTTCCATTGTCAA		
442429	LOC442429	XM_498335	CTGGCCAAGAAGCCATTCACA	CAGAGCCTGCGCAGTGTGGTA		
442451	LOC442451	XM_498366	CATGATGAACACAGTGTGAAA	CAGCTGAAAGTCAGCATAGTA		
442454	LOC442454	XM_498369	TGCATTGGACCTGACCATGAA	TACCTTGAACTGCATGTGCAA		
442481	LOC442481	XM_498410	CAGGATGGAGGCTACGAAGGT	CCGACCCAGAGGCTCCAGTAA		
442524	LOC442524	XM_499272	CAGACTTGAGGGCCCAGACAA	CTCGAAGATGCCAGTATTTCA		
442535	LOC442535	XM_499279	TACTATGACGTCTCCAACTCA	ACTGTTTGTCATAGTGCCGTA		
442562	LOC442562	XM_499306	CAGTCACAATGAGTAATTTAA	CCCGTCGAACACAGCCACCTA		
442573	LOC442573	XM_499315	ATCGGGTATTGAGTCCATGGA	AAGGGTGGAGCACAACGTCAA		
442578	LOC442578	XM_499318	TGGAATTGGCAGCGTGGCAAA	TCCACCTTACATGCAGTTGTA		
442606	LOC442606	XM_499352	GAACAACATCATGGAGTATTA	CCGTGCCTTCTTCCACTACAA		
442608	LOC442608	XM_499354	CTTCCACTTCCTGCCAGGAA	TGCAGTCCAGGAGGATTTGAA		
442616	LOC442616	XM_499536	TTGGACATGCTATTCCCAAA	CCCGGCGGTTATTCCGTTTAA		
442622	LOC442622	XM_499365	CAAGGAGAAACTGGACTAATA	CTGGAGGGCCTTTGACTTCAA		
442625	LOC442625	XM_499368	AAGCAGGAGATTAGTAATGGA	AAGGAGAAATTGAGCGATGTA		
442696	LOC442696	XM_499441	CAGTTACATGTTCTCATTTCA	CTCAAGCGGTACTACACATAA		
442699	LOC442699	XM_499444	AAGCTCCACAATTGCCAGGAA	AGCTGTGACCTTAATAATTTA		
442708	LOC442708	XM_49945	AAGAATTTGACAAGAAGGATA	CTGCCTTGTCAAGGCCATTAA		
442709	LOC442709	XM_499455	ACAGATCACATTGCATGCAAA	TAGGAACAATGTGGCCTTCAA		
442711	LOC442711	XM_499457	CAGGAACATCAGCTTAACCAT	CTGGTGCATTTAGGCCACCTA		
442721	LOC442721	XM_499467	CACCACAGAAGTCAATTTGAA	AAAGTCAAATAGAGAACATAA		
445328	FLJ43692	NM_001003702	ATGTGTTTCATCAGCACTCAA	CTGGATGATTACTATCTCTTT		
445449	HBM	NM_001003938	TTGGTCTGTGCCTGTCAATAA	CAGGACGAGTTCACCGTGCAA		
474338	LOC474338	NR_002190	CAGAGAATTGCTGATAATCAT	CTCATTATTCATTATTGTTTA	AAGGAAGGTGAATATATTAAA	CAGGCTTGTGGTGATAAATAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
474343	SPIN-2	NM_001006681	CAGCAGGGAGGCGGAGGGCTA	CAAACTTGTGTGTACATGAAA		
474344	GIMAP6	NM_001007224	AGCGATCAATTTCCCATTGAA	CCCATTGAACTGAACATGCAA		
494143	LOC494143	NM_001008708	CAGAACCTCAATTGCATATAA	CTGGAAGACATTGCTGAACAA		
497049	FLJ25758	NM_001011541	CAGGCTGTTCCTAGTCATGGA	CACCCTCGAATTCTTCTTGAA		
503497	MS4A13	NM_001012417	CTGCAGTAACTCTAACAATAA	CTGGAATTATAAGTACTTTAA		

Table 5

Gene_ID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
19	ABCA1	NM_005502	CCGGAACATGCTACAATACCA	CACCGACAATAAGCTGAATAA	CTGGATGTACAACGAACAGTA	CTCAGTGGCTGTGATCATCAA
1537	CYC1	NM_001916	CCCATCATGGGAATAAATTAA	TACCATGTCCCAGATAGCCAA	CAGCATGGACTTCGTGGCCTA	GCGGGAAGGTCTCTACTTCAA
5270	SERPINE2	NM_006216	CAGGATGGCTGGAACACTGTA	CACCAGACTGGTCCTCGTCAA	CTGGGAGGTATTGGAGGGAAA	AACGCCGTGTTTGTTAAGAAT
6183	MRPS12	NM_021107	CAGGACCACTATTAAGCCATA	CTGCTGGGACAAGACACTGTA	TTCCATCAGGACCACTATTAA	CACGTTTACCCGCAAGCCGAA
9493	KIF23	NM_004856	AAGGCTGAAGATTATGAAGAA	CACCTTTGCCGTCATGCGAAA	CAGAAGTTGAAGTGAAATCTA	CAGAATAAACTCTGGGTTAAA
9994	CASP8AP2	NM_012115	AACGAAGTTTCGAGATTCTTA	CAGTATTCAAATAGTCAGAAA	CAGTCTGATCTCAATAAGGAA	CAGCTGATGTGCGGAAGTCAA
84056	KATNAL1	NM_032116	AAGGAAATTAATATTAGTAAA	AAGGAAATTAATATTAGTAAA	TAGGTTATATTTGGTAATAAA	TAGGTTATATTTGGTAATAAA
3384	ICAM2	NM_000873	CCCGAAGATGTTGGAGATCTA	CAGGTCATCCTGACACTGCAA		
10036	CHAF1A	NM_005483	CACAATAAACTAAATTCTGAA	AAGGAAGAAGAGAAACGGTTA		
10336	PCGF3	NM_006315	CACGTTGTACGTGAATGTTTA	ACGGTTTGAGTTACTCAGTTA		
23151	KIAA0767	XM_027105	AAAGAGGAACAAAGTCATCAA	AAACTTTGTTTGTTTAAAGAA		
26064	RAI14	NM_015577	TAGGATGATAGATGAACTCAA	ATGGATGAAGATGTCCAGAAA		
26073	POLDIP2	NM_015584	CACGTGAGGTTTGATCAGTAA	TAGGTATGGATTGATGACTAA		
50804	MYEF2	NM_016132	AACATTTATTTAATAATTATA	AACCTGCTATTAAATAGTAAA		
51186	WBP5	NM_001006612	CAGGAGTTTAAAGAAGATATA	CACATTATTATTGCTAGAATA		
55004	FLJ20625	NM_017907	AAGGAAGTATATTCATCCAAA	CTGCTACTAATCACAGAGAAA		
55707	FLJ10420	NM_018090	CCGGGCATGTTTGGCAGTAAA	CTGGTTTATAAGAAATCTGAA		
57194	ATP10A	NM_024490	CAGGAAATGATAACAACCCAA	CACCTGGGCATTGAAACCAAA		
57479	KIAA1205	XM_046306	CTGAATGAGCACAAGAAGAAA	ACGCCAGGACACGGTCATCAA		
57591	MKL1	NM_020831	CCGCATTTCATGAGCAGAGAA	TTGGTGTAGTGTAACCATTTA		
58506	SR-A1	NM_021228	AACGGTTTCTCCACAGTCGAA	CTGGGCTCCATTGGCGTCAAA		
60677	BRUNOL6	NM_052840	ATGCAGGTAATTAGAACGTTA	CAGGAGTTTGGTGATGCGGAA		
121053	MGC40397	NM_152318	ATGGGACAGGTTGCTCATCAA	CCTGGTCGTTTCAATATTGAA		
127703	FLJ36984	NM_152374	TAGGAGAATGGGAATTCTAAA	ACGCCGGAAGGTGGTGACTAA		
146850	C17orf38	NM_001010855	CAGGAGGTGGAAGCAATCAAA	ACCCATCTATTTCCAGATCTA		
221491	C6orf1	NM_001008703	CAGATGTATAGTATTCAGTAT	CCAGATGTATAGTATTCAGTA		

Fig. 1

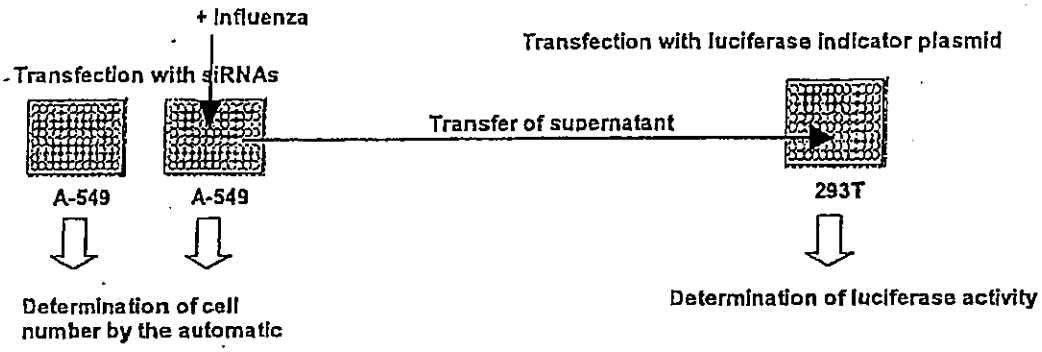

+ Influenza
Transfection with siRNAs
Transfection with luciferase indicator plasmid
Transfer of supernatant
A-549
A-549
293T
Determination of cell number by the automatic
Determination of luciferase activity

Fig. 2

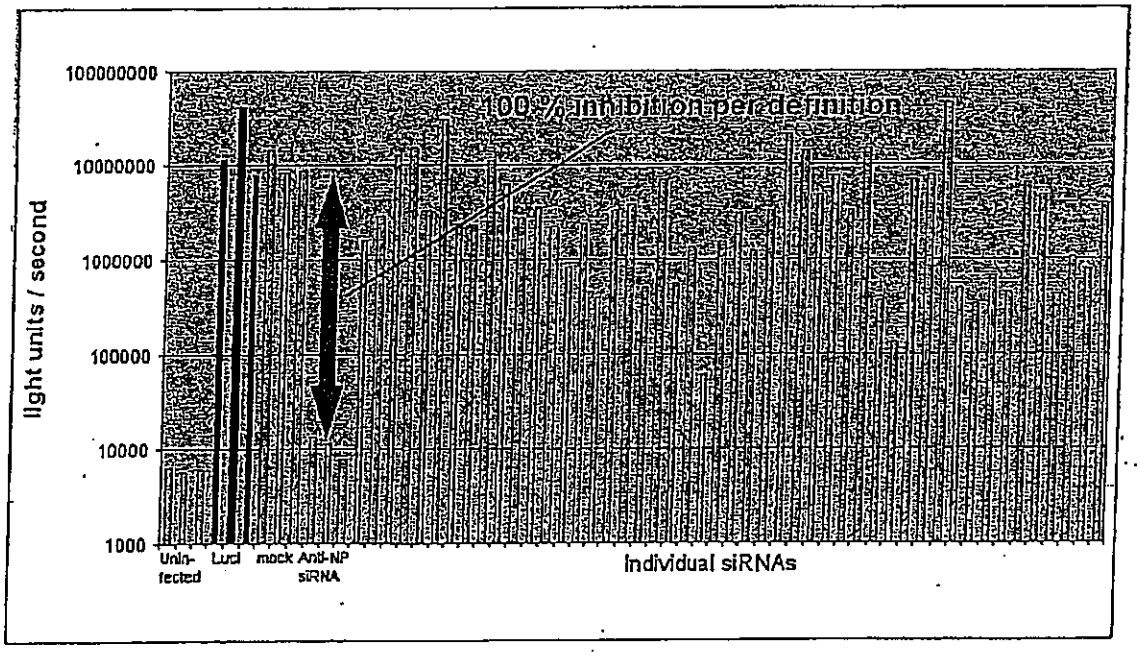

100000000
10000000
1000000
100000
10000
1000
light units / second
100 % inhibition per definition
Unin-fected
Luci
mock
Anti-NP siRNA
Individual siRNAs

Fig. 3

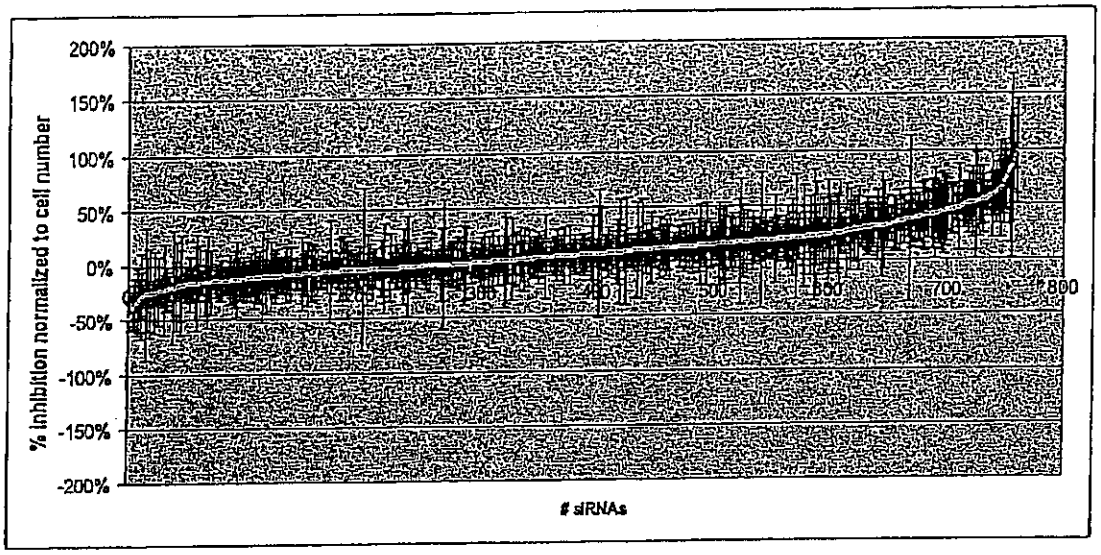

200%
150%
100%
50%
0%
-50%
-100%
-150%
-200%
% inhibition normalized to cell number
# siRNAs

Fig. 4

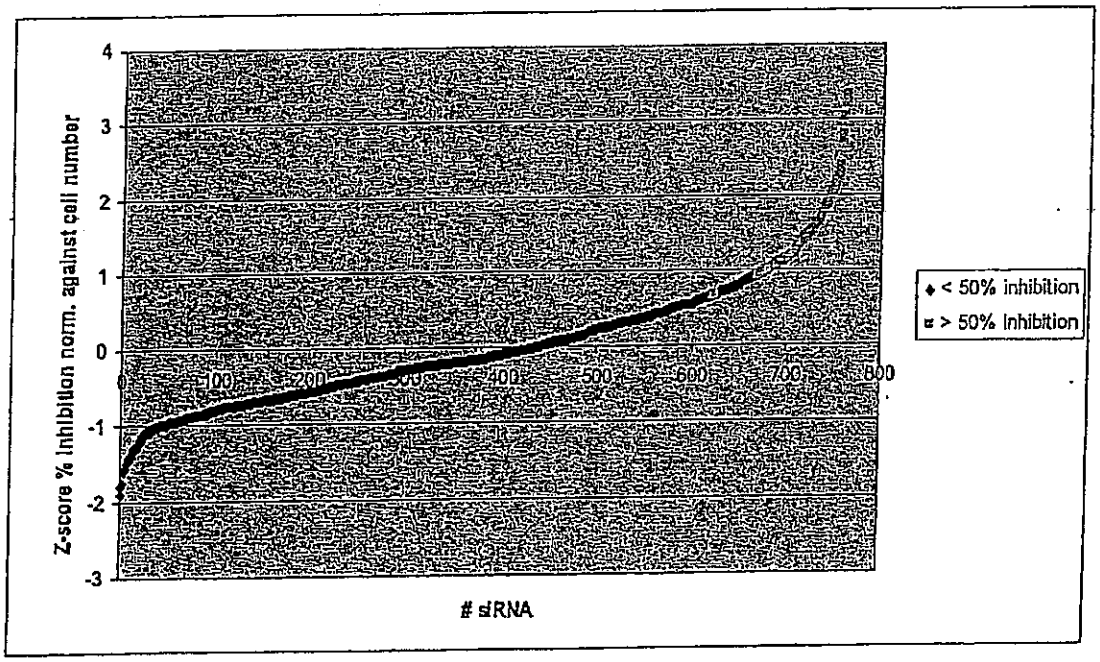

4
3
2
1
0
-1
-2
-3
Z-score % inhibition norm. against cell number
siRNA
< 50% inhibition
> 50% inhibition

Fig. 5

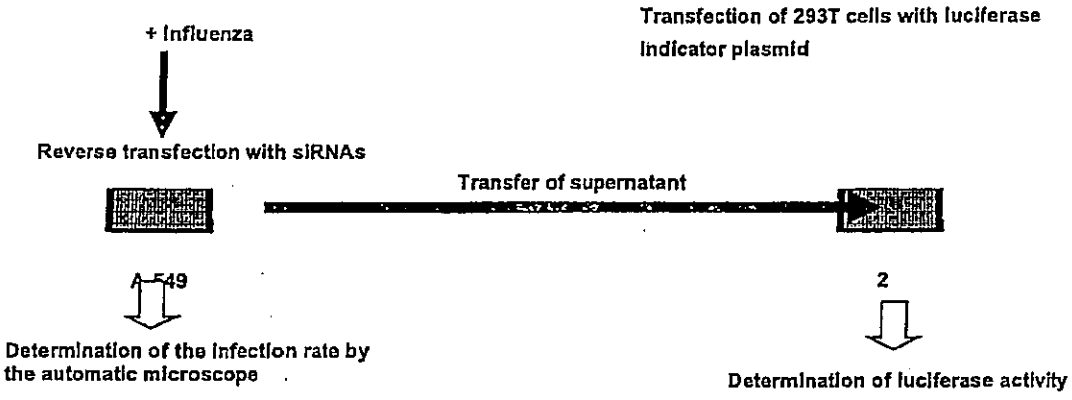

+ Influenza
Reverse transfection with siRNAs
Transfection of 293T cells with luciferase indicator plasmid
Transfer of supernatant
A-549
2
Determination of the infection rate by the automatic microscope
Determination of luciferase activity

Table 1a

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
Pool 19			-47%	109%
CKM	1158	NM_001824	-46%	14%
MAP3K3	4215	NM_002401	-45%	3%
SNARK	81788	NM_030952	-39%	16%
DDR1	780	NM_001954	-38%	21%
IHPK2	51447	NM_016291	-34%	23%
MARK3	4140	NM_002376	-33%	8%
Pool 31			-33%	30%
Pool 69			-31%	30%
AK7	122481	NM_152327	-30%	17%
Pool 46			-28%	17%
ARAF1	369	NM_001654	-28%	39%
Pool 75			-27%	22%
AKAP1	8165	NM_003488	-27%	10%
Pool 56			-27%	8%
IRAK2	3656	NM_001570	-26%	60%
ERK8	225689	NM_139021	-25%	34%
PANK3	79646	NM_024594	-25%	12%
AK5	26289	NM_174858	-25%	41%
PDK2	5164	NM_002611	-25%	6%
DGUOK	1716	NM_001929	-25%	12%
HGS	9146	NM_004712	-25%	10%
Pool 114			-24%	38%
Pool 33			-24%	9%
Pool 39			-23%	8%
Pool 43			-23%	31%
Pool 55			-23%	12%
MAPK8IP2	23542	NM_012324	-23%	10%
SKP2	6502	NM_005983	-22%	15%
Pool 45			-22%	7%
STK23	26576	NM_014370	-22%	41%
SRPK2	6733	NM_182692	-21%	20%
PKIG	11142	NM_181805	-21%	20%
PRKY	5616	NM_002760	-21%	16%
TESK1	7016	NM_006285	-21%	19%
NEK2	4751	NM_002497	-20%	11%
Pool 64			-20%	12%
PSKH1	5681	NM_006742	-20%	5%
PRKAR2B	5577	NM_002736	-20%	52%
TRAD	11139	NM_007064	-20%	11%
DYRK1A	1859	NM_001396	-20%	24%
LIMK1	3984	NM_002314	-19%	41%
WEE1	7465	NM_003390	-19%	10%
Pool 37			-18%	6%
ADRBK1	156	NM_001619	-18%	33%
TPK1	27010	NM_022445	-18%	46%
PHKB	5257	NM_000293	-17%	6%

Table 1a (continued)

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
PRKWNK4	65266	NM_032387	-17%	11%
Pool 82			-17%	16%
Pool 32			-17%	17%
PIK4CA	5297	NM_002650	-17%	17%
MK-STYX	51657	NM_016086	-17%	7%
Pool 103			-17%	26%
IRAK1BP1	134728	BX537762	-17%	13%
PRKCD	5580	NM_006254	-16%	17%
KIT	3815	NM_000222	-16%	9%
IRAK1	3654	NM_001569	-16%	14%
FGFR2	2263	NM_000141	-16%	8%
Pool 106			-16%	33%
Pool 111			-16%	44%
DGKH	160851	NM_178009	-16%	17%
Pool 113			-16%	35%
DAPK1	1612	NM_004938	-15%	11%
RAGE	5891	NM_014226	-15%	9%
KSR	8844	XM_290793	-15%	12%
TAO1	9344	NM_016151	-15%	3%
TAO1	9344	NM_004783	-15%	3%
Pool 30			-15%	31%
PAK2	5062	NM_002577	-15%	16%
AURKC	6795	NM_003160	-15%	42%
MARK2	2011	NM_004954	-15%	13%
MVK	4598	NM_000431	-15%	30%
MAPKBP1	23005	XM_031706	-15%	30%
PRKCE	5581	NM_005400	-14%	5%
EKI1	55500	NM_018638	-14%	7%
EPHA7	2045	NM_004440	-14%	10%
CDK4	1019	NM_000075	-14%	16%
AKAP12	9590	NM_005100	-14%	6%
Pool 29			-14%	16%
AURKB	9212	NM_004217	-14%	9%
PIK3C3	5289	NM_002647	-14%	18%
MAP2K6	5608	NM_002758	-14%	19%
ADCK4	79934	NM_024876	-14%	14%
MAPK8IP1	9479	NM_005456	-13%	5%
Pool 65			-13%	12%
PIK3CB	5291	NM_006219	-13%	10%
PIK3R3	8503	NM_003629	-13%	12%
PDK1	5163	NM_002610	-13%	11%
HRI	27102	NM_014413	-13%	23%
CSNK1G1	53944	NM_022048	-13%	17%
BMPR1A	657	NM_004329	-13%	12%
DAPK3	1613	NM_001348	-13%	20%
SIK2	23235	AB096248	-13%	10%
PDPK1	5170	NM_002613	-12%	27%
Pool 104			-12%	35%
CAMKK1	84254	NM_032294	-12%	10%

Table 1a (continued)

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
TK1	7083	NM_003258	-12%	20%
CSNK2B	1460	NM_001320	-12%	10%
MGC4796	83931	NM_032017	-12%	16%
DGKB	1607	NM_145695	-12%	16%
MET	4233	NM_000245	-12%	5%
ERBB4	2066	NM_005235	-12%	21%
PRKCDBP	112464	NM_145040	-12%	16%
BTK	695	NM_000061	-12%	11%
RPS6KB1	6198	NM_003161	-11%	13%
AKAP11	11215	NM_016248	-11%	9%
PRKAG1	5571	NM_002733	-11%	15%
PIK3C2A	5286	NM_002645	-11%	22%
CDK11	23097	NM_015076	-11%	16%
Pool 54			-11%	14%
MKNK2	2872	NM_017572	-11%	29%
PTK9	5756	NM_002822	-11%	11%
FLT3LG	2323	BF688722	-11%	13%
CDK8	1024	NM_001260	-11%	20%
ITPKA	3706	NM_002220	-11%	24%
CDK3	1018	NM_001258	-11%	14%
CDK7	1022	NM_001799	-11%	9%
PRKACA	5566	NM_002730	-11%	41%
Pool 3			-10%	11%
LAK	80216	NM_025144	-10%	16%
ITPKB	3707	NM_002221	-10%	35%
PI4KII	55361	NM_018425	-10%	12%
PRKCBP1	23613	NM_183048	-10%	16%
SH3KBP1	30011	NM_031892	-10%	5%
BRAF	673	NM_004333	-10%	13%
Pool 34			-10%	33%
KHK	3795	NM_000221	-10%	9%
DCAMKL1	9201	NM_004734	-10%	21%
CLK3	1198	NM_001292	-10%	13%
BCR	613	NM_004327	-10%	25%
STK16	8576	NM_003691	-10%	17%
MAPKAPK3	7867	NM_004635	-10%	18%
IKBKE	9641	XM_375834	-9%	12%
ATR	545	NM_001184	-9%	15%
STK17A	9263	NM_004760	-9%	16%
MOS	4342	NM_005372	-9%	16%
MAPK3	5595	NM_002746	-9%	9%
SMG1	23049	NM_014006	-9%	26%
FER	2241	NM_005246	-9%	17%
PFKP	5214	NM_002627	-9%	12%
CSK	1445	NM_004383	-9%	13%
BUB1	699	NM_004336	-9%	24%
AK3L1	50808	NM_016282	-9%	13%
GRK7	131890	NM_139209	-9%	3%
MAP3K6	9064	NM_004672	-9%	6%

Table 1a (continued)

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
ACVR2B	93	NM_001106	-9%	6%
IRAK4	51135	NM_016123	-8%	14%
EPHA5	2044	NM_004439	-8%	15%
PRKWNK3	65267	NM_020922	-8%	4%
RIOK1	83732	NM_031480	-8%	7%
MAK	4117	NM_005906	-8%	12%
CSNK2A2	1459	NM_001896	-8%	35%
Pool 60			-8%	17%
AXL	558	NM_001699	-8%	21%
IHPK1	9807	NM_153273	-8%	15%
Pool 98			-8%	29%
JAK2	3717	NM_004972	-8%	3%
Pool 61			-8%	17%
DDR2	4921	NM_006182	-8%	26%
ADCK5	203054	NM_174922	-8%	27%
EPHA1	2041	NM_005232	-7%	14%
Pool 77			-7%	25%
GKAP42	80318	NM_025211	-7%	12%
PIK3R4	30849	NM_014602	-7%	22%
ROCK1	6093	NM_005406	-7%	3%
Pool 22			-7%	13%
LCK	3932	NM_005356	-7%	8%
RPS6KA2	6196	NM_021135	-7%	13%
KIDINS220	57498	AB033076	-7%	15%
Pool 24			-7%	10%
SNF1LK	150094	NM_173354	-7%	6%
FGFR1	2260	NM_015850	-7%	10%
Pool 53			-7%	19%
PRKCI	5584	NM_002740	-7%	9%
HSPB8	26353	NM_014365	-6%	10%
JAK1	3716	NM_002227	-6%	47%
Pool 68			-6%	20%
CLK1	1195	NM_004071	-6%	13%
SAST	22983	AB023190	-6%	8%
PDGFRB	5159	NM_002609	-6%	11%
CLK2	1196	NM_001291	-6%	9%
VRK2	7444	NM_006296	-6%	12%
LOC91807	91807	NM_182493	-6%	17%
MELK	9833	NM_014791	-5%	29%
Pool 18			-5%	11%
CCRK	23552	NM_178432	-5%	31%
PRKAG3	53632	NM_017431	-5%	21%
SPEC2	56990	NM_020240	-5%	6%
Pool 44			-5%	27%
ACVR1B	91	NM_004302	-5%	10%
CHUK	1147	NM_001278	-5%	22%
FYN	2534	NM_002037	-5%	17%
DTYMK	1841	NM_012145	-5%	8%
SRMS	6725	NM_080823	-5%	19%

Table 1a (continued)

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
MAP3K9	4293	XM_027237	-5%	6%
ALK	238	NM_004304	-5%	13%
PAK6	56924	NM_020168	-5%	10%
Pool 8			-5%	15%
ILKAP	80895	NM_176799	-5%	16%
SPHK2	56848	NM_020126	-5%	4%
CDK2	1017	NM_001798	-5%	21%
NEK3	4752	NM_152720	-5%	7%
TESK2	10420	NM_007170	-5%	9%
AKT2	208	NM_001626	-5%	74%
PRKG1	5592	NM_006258	-5%	8%
KIP2	10518	NM_006383	-5%	8%
Pool 88			-4%	32%
MAPK14	1432	NM_001315	-4%	15%
CARKL	23729	NM_013276	-4%	23%
NME4	4833	NM_005009	-4%	5%
VRK1	7443	NM_003384	-4%	17%
TAO1	9344	NM_016151	-4%	11%
TAO1	9344	NM_004783	-4%	11%
NLK	51701	NM_016231	-4%	10%
NME1	4830	NM_000269	-4%	19%
Pool 12			-4%	18%
CALM3	808	NM_005184	-4%	10%
ADRBK2	157	NM_005160	-4%	8%
Pool 21			-4%	10%
PRKWNK2	65268	NM_006648	-4%	26%
Pool 97			-4%	20%
Pool 115			-4%	41%
RAF1	5894	NM_002880	-4%	7%
PACSIN3	29763	NM_016223	-4%	6%
PGK2	5232	NM_138733	-4%	9%
MAPK10	5602	NM_002753	-3%	7%
Pool 36			-3%	32%
PRKWNK1	65125	NM_018979	-3%	13%
ITPKC	80271	NM_025194	-3%	15%
FLJ13052	65220	NM_023018	-3%	8%
RPS6KA3	6197	NM_004586	-3%	21%
MAST2	23139	NM_015112	-3%	10%
STK25	10494	NM_006374	-3%	18%
LMTK2	22853	NM_014916	-3%	11%
MAPK1	5594	NM_002745	-3%	13%
MAGI-3	260425	NM_020965	-3%	8%
PFKFB1	5207	NM_002625	-3%	20%
Pool 71			-3%	35%
GRK6	2870	NM_002082	-3%	25%
STK6	6790	NM_003600	-3%	13%
Pool 101			-3%	46%
STK11IP	114790	NM_052902	-3%	10%
DOK1	1796	NM_001381	-2%	23%

Table 1a (continued)

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
PTK9L	11344	NM_007284	-2%	9%
CNK1	10256	NM_006314	-2%	9%
FLT3	2322	NM_004119	-2%	13%
ZAP70	7535	NM_001079	-2%	13%
MAPKAP1	79109	NM_024117	-2%	20%
AK1	203	NM_000476	-2%	9%
FGFR3	2261	NM_000142	-2%	6%
TXK	7294	NM_003328	-2%	10%
CDKN1C	1028	NM_000076	-2%	14%
Pool 7			-2%	17%
MUSK	4593	NM_005592	-2%	8%
ACVR1	90	NM_001105	-2%	22%
AKAP5	9495	NM_004857	-2%	11%
MKNK1	8569	NM_003684	-2%	11%
UGP2	7360	NM_006759	-2%	10%
RYK	6259	NM_002958	-2%	5%
Pool 107			-2%	25%
ITPK1	3705	NM_014216	-1%	13%
RPS6KL1	83694	NM_031464	-1%	8%
PIM1	5292	NM_002648	-1%	6%
CAMK2D	817	NM_001221	-1%	13%
CAMK2G	818	NM_172173	-1%	8%
TYK2	7297	NM_003331	-1%	13%
LIMK2	3985	NM_005569	-1%	10%
HK2	3099	NM_000189	-1%	14%
Pool 91			-1%	33%
DYRK1B	9149	NM_004714	-1%	17%
TTBK1	84630	XM_166453	-1%	59%
Pool 58			-1%	15%
Pool 41			-1%	8%
MAP3K5	4217	NM_005923	-1%	17%
CDKL2	8999	NM_003948	-1%	10%
LOC149420	149420	NM_152835	-1%	20%
EGFR	1956	NM_005228	-1%	15%
FRK	2444	NM_002031	-1%	22%
Pool 78			-1%	21%
CDKN2C	1031	NM_001262	-1%	14%
IRAK3	11213	NM_007199	-1%	4%

Table 1b

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
AKAP8	10270	NM_005858	1%	19%
Pool 2			1%	13%
HSA250839	55351	NM_018401	1%	14%
JAK3	3718	NM_000215	1%	18%
LYK5	92335	NM_153335	1%	8%
PIK3C2G	5288	NM_004570	1%	12%
EPHB4	2050	NM_004444	1%	14%
KIAA1804	84451	NM_032435	1%	11%
STK39	27347	NM_013233	1%	22%
ABL1	25	NM_005157	1%	10%
Pool 48			1%	16%
PRKR	5610	NM_002759	1%	27%
IKBKAP	8518	NM_003640	1%	17%
PRKCB1	5579	NM_002738	1%	6%
PLK4	10733	NM_014264	1%	13%
EPHA8	2046	NM_020526	1%	24%
PFKM	5213	NM_000289	2%	11%
EPHB6	2051	NM_004445	2%	11%
Pool 110			2%	28%
Pool 62			2%	14%
DYRK4	8798	NM_003845	2%	14%
MAPK7	5598	NM_002749	2%	10%
Pool 81			2%	23%
PRKCL2	5586	NM_006256	2%	10%
PACSIN1	29993	NM_020804	2%	14%
YES1	7525	NM_005433	2%	9%
MAP3K7IP1	10454	NM_006116	2%	13%
PSKH2	85481	NM_033126	2%	22%
Pool 108			3%	43%
Pool 74			3%	39%
MYLK2	85366	NM_033118	3%	22%
Pool 73			3%	14%
RIPK3	11035	NM_006871	3%	22%
PRKCM	5587	NM_002742	3%	2%
PHKG2	5261	NM_000294	3%	9%
SGK2	10110	NM_016276	3%	38%
STK17B	9262	NM_004226	3%	13%
Pool 6			3%	23%
PRPF4B	8899	NM_176800	3%	26%
DMPK	1760	NM_004409	3%	6%
PIK3AP1	118788	NM_152309	3%	6%
BMP2K	55589	NM_017593	3%	15%
Pool 52			3%	29%
CKMT2	1160	NM_001825	4%	16%
Pool 5			4%	21%
Pool 51			4%	29%
TK2	7084	NM_004614	4%	8%
CAMK1G	57172	NM_020439	4%	6%

Table 1b (continued)

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
CALM2	805	NM_001743	4%	14%
Pool 99			4%	26%
Pool 11			4%	19%
ITK	3702	NM_005546	4%	10%
PKM2	5315	NM_182471	4%	17%
Pool 17			4%	17%
MST4	51765	NM_016542	4%	16%
ROCK2	9475	NM_004850	4%	19%
OSR1	9943	NM_005109	4%	13%
PRKAR1A	5573	NM_002734	4%	18%
MARK4	57787	NM_031417	5%	25%
DGKZ	8525	NM_003646	5%	14%
MAPK6	5597	NM_002748	5%	20%
PRKAG2	51422	NM_016203	5%	13%
CaMKIINalpha	55450	NM_018584	5%	18%
EPHA3	2042	NM_005233	5%	8%
Pool 70			5%	38%
PGK1	5230	NM_000291	5%	9%
CAMK1	8536	NM_003656	5%	5%
MAP2K2	5605	NM_030662	5%	3%
PTK2B	2185	NM_173176	5%	14%
EPHB3	2049	NM_004443	5%	8%
TBK1	29110	NM_013254	5%	17%
GUK1	2987	NM_000858	6%	14%
LOC161635	161635	BC028192	6%	18%
ACVRL1	94	NM_000020	6%	24%
MERTK	10461	NM_006343	6%	15%
DGKQ	1609	NM_001347	6%	9%
SSTK	83983	NM_032037	6%	6%
HIPK3	10114	NM_005734	6%	19%
ROR1	4919	NM_005012	6%	10%
ARK5	9891	XM_374996	6%	18%
URKL1	54963	NM_017859	6%	27%
CDK9	1025	NM_001261	6%	10%
CDKN2B	1030	NM_004936	6%	10%
KIS	127933	NM_175866	6%	4%
TGFBR2	7048	NM_003242	6%	6%
BLK	640	NM_001715	6%	28%
TTK	7272	NM_003318	6%	12%
CDKL1	8814	NM_004196	6%	11%
CLK4	57396	NM_020666	7%	15%
PRKDC	5591	NM_006904	7%	18%
STK38L	23012	NM_015000	7%	15%
AKAP4	8852	NM_003886	7%	3%
STK11	6794	NM_000455	7%	5%
MAGI1	154043	NM_173515	7%	13%
SNRK	54861	NM_017719	7%	9%
CDC42BPA	8476	NM_003607	7%	17%

Table 1b (continued)

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
CERK	64781	NM_182661	7%	13%
RBKS	64080	NM_022128	7%	14%
ATM	472	NM_000051	7%	19%
MAPK8IP3	23162	NM_015133	7%	7%
HAK	115701	NM_052947	7%	16%
RIPK2	8767	NM_003821	7%	8%
GRK5	2869	NM_005308	7%	13%
AKAP6	9472	NM_004274	7%	13%
Pool 13			7%	25%
MATK	4145	NM_002378	8%	37%
Pool 1			8%	35%
GIT1	28964	NM_014030	8%	8%
CAMK1D	57118	NM_020397	8%	13%
Pool 87			8%	43%
KSR2	283455	NM_173598	8%	58%
SGK	6446	NM_005627	8%	12%
Pool 92			8%	41%
NEK4	6787	NM_003157	8%	5%
PIK3CD	5293	NM_005026	8%	9%
ASK	10926	NM_006716	8%	17%
TIE	7075	NM_005424	8%	16%
AKAP7	9465	NM_004842	8%	17%
XYLB	9942	NM_005108	8%	23%
MARK1	4139	NM_018650	8%	11%
FN3K	64122	NM_022158	8%	13%
NEK6	10783	NM_014397	9%	12%
RPS6KC1	26750	NM_012424	9%	20%
MAPKAPK5	8550	NM_003668	9%	3%
ICK	22858	NM_014920	9%	8%
Pool 23			9%	15%
PRKAB2	5565	NM_005399	9%	30%
HK3	3101	NM_002115	9%	25%
Pool 96			9%	48%
IBTK	25998	AB037838	9%	8%
PDK3	5165	NM_005391	9%	8%
SKIP	80309	XM_051221	9%	19%
PRKAA2	5563	NM_006252	9%	14%
HCK	3055	NM_002110	9%	50%
STK29	9024	NM_003957	10%	14%
DGKA	1606	NM_001345	10%	17%
GK	2710	NM_000167	10%	8%
DAPK2	23604	NM_014326	11%	15%
STK31	56164	NM_031414	11%	10%
Pool 59			11%	16%
PI4K2B	55300	NM_018323	11%	8%
MADD	8567	NM_003682	11%	8%
PRKCQ	5588	NM_006257	11%	12%
PDK4	5166	NM_002612	11%	44%

Table 1b (continued)

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
PRKRIR	5612	NM_004705	11%	19%
PFKFB4	5210	NM_004567	11%	15%
CAMK2A	815	NM_015981	11%	10%
Pool 83			11%	46%
DGKG	1608	NM_001346	11%	8%
APEG1	10290	NM_005876	11%	16%
Pool 80			11%	23%
CKS1B	1163	NM_001826	11%	15%
DYRK2	8445	NM_003583	11%	17%
PACSIN2	11252	NM_007229	11%	17%
LYN	4067	NM_002350	11%	33%
Pool 67			12%	30%
MAP4K3	8491	NM_003618	12%	13%
PNKP	11284	NM_007254	12%	17%
PMVK	10654	NM_006556	12%	18%
Pool 4			12%	10%
LATS2	26524	NM_014572	12%	13%
CKMT1	1159	NM_020990	12%	7%
HIPK1	204851	NM_181358	12%	29%
STK10	6793	NM_005990	12%	16%
STK22D	83942	NM_032028	12%	16%
TRIO	7204	NM_007118	12%	20%
GIT2	9815	NM_014776	12%	21%
AKAP28	158798	NM_178813	12%	15%
UMP-CMP	51727	NM_016308	13%	26%
Pool 14			13%	21%
LIM	10611	NM_006457	13%	20%
PIP5K2C	79837	NM_024779	13%	30%
PRKG2	5593	NM_006259	13%	6%
PCTK1	5127	NM_006201	13%	9%
Pool 35			13%	9%
PKLR	5313	NM_181871	13%	13%
LATS1	9113	NM_004690	13%	9%
ACVR2	92	NM_001616	13%	11%
STK24	8428	NM_003576	13%	8%
NJMU-R1	64149	NM_022344	13%	18%
PANK4	55229	NM_018216	13%	19%
CDKL3	51265	NM_016508	13%	12%
PHKG1	5260	NM_006213	13%	7%
ERN1	2081	NM_001433	13%	14%
MAP3K7IP2	23118	NM_015093	13%	24%
AK2	204	NM_001625	13%	21%
GRAF	23092	NM_015071	13%	21%
PRKD2	25865	NM_016457	14%	10%
PRKAA1	5562	NM_006251	14%	21%
TTBK2	146057	NM_173500	14%	8%
Pool 50			14%	20%
KDR	3791	NM_002253	14%	25%

Table 1b (continued)

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
NME6	10201	NM_005793	14%	20%
EIF2AK3	9451	NM_004836	14%	16%
CDK6	1021	NM_001259	14%	9%
FGFR4	2264	NM_002011	15%	17%
CDK5R2	8941	NM_003936	15%	24%
SYK	6850	NM_003177	15%	37%
DCK	1633	NM_000788	15%	21%
MAP4K4	9448	NM_004834	15%	12%
BUB1B	701	NM_001211	15%	21%
CHK	1119	NM_001277	15%	21%
Pool 38			15%	38%
FLJ11149	55312	NM_018339	15%	7%
DYRK3	8444	NM_003582	15%	8%
NRGN	4900	NM_006176	15%	23%
PIK3CA	5290	NM_006218	15%	20%
PAK1	5058	NM_002576	15%	16%
TYRO3	7301	NM_006293	15%	11%
TLK2	11011	NM_006852	15%	10%
NEK9	91754	NM_033116	15%	12%
ERBB3	2065	NM_001982	16%	20%
PFKFB3	5209	NM_004566	16%	14%
NEK1	4750	NM_012224	16%	32%
PKE	282974	NM_173575	16%	38%
PRKCG	5582	NM_002739	16%	21%
CDK5	1020	NM_004935	16%	34%
PCTK2	5128	NM_002595	16%	25%
ALS2CR7	65061	NM_139158	16%	38%
Pool 76			16%	34%
HIPK2	28996	NM_022740	16%	6%
CDC42BPB	9578	NM_006035	16%	14%
EPHB1	2047	NM_004441	16%	24%
BCKDK	10295	NM_005881	16%	23%
STK22C	81629	NM_052841	17%	26%
CSNK1G3	1456	NM_004384	17%	13%
AK3	205	NM_013410	17%	23%
EPHA2	1969	NM_004431	17%	10%
ANKRD3	54101	NM_020639	17%	14%
NEK11	79858	NM_024800	17%	7%
Pool 94			17%	39%
LTK	4058	NM_002344	17%	25%
Pool 100			17%	57%
MAP3K12	7786	NM_006301	17%	8%
Pool 66			18%	34%
MAP2K7	5609	BC005365	18%	21%
NUCKS	64710	NM_022731	18%	9%
PIK3CG	5294	NM_002649	18%	29%
TYROBP	7305	NM_003332	18%	8%
ROR2	4920	NM_004560	18%	9%

Table 1b (continued)

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
PFTK1	5218	NM_012395	18%	12%
MAP3K14	9020	NM_003954	18%	17%
PRKRA	8575	NM_003690	18%	27%
pknbeta	29941	NM_013355	18%	19%
SGKL	23678	NM_013257	18%	22%
PANK2	80025	NM_024960	18%	13%
CDC2L5	8621	NM_003718	18%	16%
MAP2K3	5606	NM_002756	18%	14%
PKIB	5570	NM_181795	18%	20%
MAP3K7	6885	NM_003188	18%	63%
PFKFB2	5208	NM_006212	19%	11%
CDKN1A	1026	NM_000389	19%	12%
CSNK2A1	1457	NM_177560	19%	17%
PIP5K2A	5305	NM_005028	19%	17%
STK36	27148	NM_015690	19%	27%
CINP	51550	NM_032630	19%	17%
TEK	7010	NM_000459	19%	15%
MAP4K2	5871	NM_004579	19%	7%
EEF2K	29904	NM_013302	19%	14%
Pool 72			19%	12%
TLK1	9874	NM_012290	19%	20%
ULK1	8408	NM_003565	19%	16%
Pool 79			19%	40%
CDKN2D	1032	NM_001800	19%	19%
NRBP	29959	NM_013392	19%	21%
CDK10	8558	NM_003674	19%	17%
NEK8	284086	NM_178170	19%	13%
NYD-SP25	89882	BC033792	20%	10%
NYD-SP25	89882	NM_033516	20%	10%
MAP2K5	5607	NM_002757	20%	8%
PRKACB	5567	NM_182948	20%	13%
NTRK2	4915	NM_006180	20%	21%
MAP3K13	9175	NM_004721	20%	16%
CSNK1D	1453	NM_001893	20%	29%
MAP2K1IP1	8649	NM_021970	20%	17%
PINK1	65018	NM_032409	20%	8%
Pool 25			20%	23%
ERBB2	2064	NM_004448	21%	12%
Pool 42			21%	36%
AKAP10	11216	NM_007202	21%	17%
PANK1	53354	NM_138316	21%	10%
Pool 47			21%	57%
MAPKAPK2	9261	NM_004759	21%	17%
Pool 15			21%	21%
PRKX	5613	NM_005044	21%	21%
TOPK	55872	NM_018492	21%	9%
TNIK	23043	XM_039796	21%	8%
Pool 27			22%	27%

Table 1b (continued)

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
FES	2242	NM_002005	22%	47%
Pool 84			22%	22%
PHKA2	5256	NM_000292	22%	7%
MAP3K4	4216	NM_005922	22%	9%
ULK2	9706	NM_014683	22%	15%
MAPK13	5603	NM_002754	22%	36%
Pool 10			22%	13%
Pool 49			22%	13%
NME2	4831	NM_002512	22%	27%
Pool 116			23%	59%
BMPR2	659	NM_001204	23%	19%
CASK	8573	NM_003688	23%	28%
HSMDPKIN	55561	XM_290516	23%	48%
AKT1	207	NM_005163	23%	13%
PXK	54899	NM_017771	23%	36%
RIPK1	8737	NM_003804	23%	15%
DGKD	8527	NM_003648	23%	14%
IHPK3	117283	NM_054111	23%	33%
RPS6KA5	9252	NM_182398	23%	10%
PKIA	5569	NM_181839	24%	27%
RPS6KB2	6199	NM_003952	24%	14%
Pool 95			24%	49%
CDKL5	6792	NM_003159	24%	36%
CDC2	983	NM_001786	24%	33%
MAP4K5	11183	NM_006575	24%	5%
Pool 85			25%	29%
VRK3	51231	NM_016440	25%	8%
EPHA4	2043	NM_004438	25%	12%
IKBKG	8517	NM_003639	25%	37%
PLK2	10769	NM_006622	25%	33%
CAMK4	814	NM_001744	25%	48%
PIK3R1	5295	NM_181504	25%	17%
Pool 16			25%	17%
EPHB2	2048	NM_017449	25%	5%
MGC45419	139728	NM_198452	25%	14%
T3JAM	80342	NM_025228	26%	21%
MAP3K8	1326	NM_005204	26%	11%
Pool 112			26%	43%
PHKA1	5255	NM_002637	27%	6%
TGFBR1	7046	NM_004612	27%	18%
AKAP9	10142	NM_005751	27%	37%
PAK7	57144	NM_177990	27%	26%
MINK	50488	NM_015716	27%	13%
CSNK1A1	1452	NM_001892	28%	30%
PIM2	11040	NM_006875	28%	31%
PIP5K1A	8394	NM_003557	28%	10%
PLK1	5347	NM_005030	29%	29%
PIP5K3	200576	NM_152671	29%	39%

Table 1b (continued)

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
PRKCABP	9463	NM_012407	29%	7%
MAP3K2	10746	NM_006609	29%	18%
TEC	7006	NM_003215	29%	14%
FLT4	2324	NM_182925	29%	18%
CDKN2A	1029	NM_000077	30%	12%
EIF2AK4	27104	BX640919	30%	21%
Pool 9			30%	20%
PTK2	5747	NM_005607	30%	26%
MARCKS	4082	NM_002356	30%	23%
AKAP13	11214	NM_006738	30%	26%
Pool 63			30%	17%
UCK1	83549	NM_031432	31%	25%
STK33	65975	NM_030906	31%	20%
SRC	6714	NM_005417	31%	16%
P101-PI3K	23533	NM_014308	31%	6%
MAP3K10	4294	NM_002446	31%	32%
PIP5K1C	23396	NM_012398	31%	33%
RET	5979	NM_020975	31%	13%
TNNI3K	51086	NM_015978	31%	21%
Pool 105			31%	48%
PRKCH	5583	NM_006255	31%	24%
Pool 89			31%	41%
ADK	132	NM_001123	32%	15%
MAP2K1	5604	NM_002755	32%	28%
FLT1	2321	NM_002019	32%	15%
MGC33182	122011	NM_145203	32%	9%
Pool 26			32%	15%
SKP1A	6500	NM_006930	33%	4%
AKIP	54998	NM_017900	33%	26%
CHEK1	1111	NM_001274	33%	23%
MAP3K11	4296	NM_002419	33%	25%
RPS6KA1	6195	NM_002953	34%	25%
STK38	11329	NM_007271	34%	21%
PIP5K1B	8395	NM_003558	34%	7%
PIK3R2	5296	NM_005027	35%	28%
SLK	9748	NM_014720	36%	22%
CAMKK2	10645	NM_006549	36%	10%
AKAP3	10566	NM_006422	36%	23%
GNE	10020	NM_005476	36%	22%
KIAA1446	57596	NM_020836	37%	7%
AATK	9625	AB014541	37%	15%
ADCK2	90956	NM_052853	37%	17%
Pool 28			37%	76%
PTK6	5753	NM_005975	37%	28%
MAPK12	6300	NM_002969	37%	22%
CRK7	51755	NM_016507	38%	7%
PASK	23178	NM_015148	38%	27%
TNK1	8711	NM_003985	38%	13%

Table 1b (continued)

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
PFKL	5211	NM_002626	38%	20%
MAP4K1	11184	NM_007181	38%	23%
MAPK9	5601	NM_002752	39%	20%
FUK	197258	NM_145059	39%	13%
LOC55971	55971	NM_018842	39%	13%
ZAK	51776	NM_016653	39%	30%
NTRK3	4916	NM_002530	40%	25%
NTRK1	4914	NM_002529	40%	32%
STK35	140901	NM_080836	41%	12%
CDK5R1	8851	NM_003885	41%	21%
PAK3	5063	NM_002578	41%	22%
CAMK2B	816	NM_001220	41%	4%
NME5	8382	NM_003551	41%	22%
Pool 90			41%	31%
GAK	2580	NM_005255	41%	32%
AKT3	10000	NM_181690	42%	41%
ADCK1	57143	NM_020421	42%	19%
STK4	6789	NM_006282	43%	26%
AKAP8L	26993	NM_014371	43%	29%
MAPK11	5600	NM_002751	43%	28%
UMPK	7371	NM_012474	43%	35%
CSNK1G2	1455	NM_001319	43%	24%
PIK3C2B	5287	NM_002646	43%	38%
C21orf124	85006	NM_003681	44%	31%
CKB	1152	NM_001823	44%	33%
CIB3	117286	NM_054113	45%	28%
ILK	3611	NM_004517	45%	19%
PRKACG	5568	NM_002732	45%	20%
SRPK1	6732	NM_003137	45%	5%
AAK1	22848	NM_014911	46%	21%
PCTK3	5129	AK126879	46%	23%
NEK7	140609	NM_133494	46%	22%
LOC375449	375449	NM_198828	46%	4%
ROS1	6098	NM_002944	47%	11%
PDGFRA	5156	NM_006206	47%	19%
CIT	11113	NM_007174	48%	12%
LOC388226	10595	XM_370946	48%	39%
CDKN1B	1027	NM_004064	48%	5%
NME7	29922	NM_197972	48%	8%
RPS6KA6	27330	NM_014496	49%	16%
Pool 57			49%	20%
PIK4CB	5298	NM_002651	51%	16%
Pool 20			51%	20%
MAP2K4	6416	NM_003010	51%	14%
CHEK2	11200	NM_007194	51%	28%
ALS2CR2	55437	NM_018571	52%	18%
GRK1	6011	NM_002929	52%	17%
Pool 93			52%	32%

Table 1b (continued)

Gene name	GeneID	Accession Number	% Inhibition	Standard Deviation
MAPK4	5596	NM_002747	52%	24%
STK22B	23617	NM_053006	52%	15%
Pool 109			52%	51%
NYD-SP25	89882	BC033792	53%	44%
NYD-SP25	89882	NM_033516	53%	44%
ANKK1	255239	NM_178510	53%	7%
SPHK1	8877	NM_021972	53%	33%
PLK3	1263	NM_004073	53%	19%
GRK4	2868	NM_182982	54%	23%
PIP5K2B	8396	NM_003559	54%	30%
Pool 102			55%	22%
NIPA	51530	NM_016478	55%	11%
RPS6KA4	8986	NM_003942	55%	16%
IKBKB	3551	NM_001556	56%	10%
FGR	2268	NM_005248	57%	12%
PTK7	5754	NM_152883	58%	5%
RIOK2	55781	NM_018343	59%	20%
CSNK1E	1454	NM_001894	59%	39%
PRKCL1	5585	NM_002741	60%	21%
STK3	6788	NM_006281	60%	20%
GSK3A	2931	NM_019884	60%	28%
HK1	3098	NM_033498	61%	19%
PRKCZ	5590	NM_002744	62%	16%
RIOK3	8780	NM_003831	62%	19%
CKS2	1164	NM_001827	63%	31%
FASTK	10922	NM_006712	63%	44%
MST1R	4486	NM_002447	65%	24%
BMPR1B	658	NM_001203	66%	33%
PRKAR2A	5576	NM_004157	69%	39%
CDC2L1	984	NM_001787	73%	26%
PRKAB1	5564	NM_006253	74%	30%
PKMYT1	9088	NM_182687	78%	15%
PAK4	10298	NM_005884	81%	49%
CALM1	801	NM_006888	82%	68%
BMX	660	NM_001721	84%	83%
NME3	4832	NM_002513	85%	50%
JIK	51347	NM_016281	89%	27%
ACK1	10188	NM_005781	93%	11%
HUNK	30811	NM_014586	94%	35%
MAPK8	5599	NM_002750	98%	47%
DGKE	8526	NM_003647	113%	25%

Table 2

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
AB014541	9625	AATK	apoptosis-associated tyrosine kinase	CTCCAACGTGTCAGCCAACAA	TCCGCTGAGATCAGAAGGCAA
AB023190	22983	SAST	syntrophin associated serine/threonine kinase	CAGCCTCCGTATACATATGTA	CCCGAGGTCATCCTGCGTCAA
AB033076	57498	KIDINS220	likely homolog of rat kinase D-interacting substance of 220 kDa	CAGGCGAGACTCCTTATAATA	TCGCAGATGCGCTATTATCTA
AB037838	25998	IBTK	inhibitor of Bruton agammaglobulinemia tyrosine kinase	CAGATTGAGGAGCATGCCATA	TAGAAGAGTCATTACACCATA
AB096218	23235	SIK2	salt-inducible serine/threonine kinase 2	AAGGGCAAGATTATTTGCTTA	CCGAAGGATGTTGGTCCTAGA
NM_004935	1020	CDK5	cyclin-dependent kinase 5	CCCTTTGTGGACTTTATTTAA	CCGGGAGATCTGCCTACTCAA
AK126879	5129	PCTK3	PCTAIRE protein kinase 3	AACCCGTTACTTAGCTGTGTA	CAGGTTGGATACGGATGGCAT
BC028192	161635	LOC161635	similar to casein kinase I alpha	TCCATCGATCTGGAATTTATA	TTGGTCGTGTGAATTATTAAA
BC033792	89882	NYD-SP25	protein kinase NYD-SP25	ATCATATACTTCAGACATCAA	CACGTTAAATCAAGGAAGGAA
BF688722	2323	FLT3LG	Fms-related tyrosine kinase 3 ligand	GCGGGATTTGTTGAAGAGAAA	TAGTATAGTTGAAATAAGAAA
BX537762	134728	IRAK1BP1	interleukin-1 receptor-associated kinase 1 binding protein 1/DKFZp779F0411	AACCTGGAGTATCATATTATA	ACCAAGATACTTGAGTGATTA
BX640919	27104	EIF2AK4	eukaryotic translation initiation factor 2 alpha kinase 4	CTGCAGGAATTTAGTAACATT	TCCGATAATCTTGCAGTGCAA
NM_000020	94	ACVRL1	activin A receptor type II-like 1	CACCGAGTTCGTCAACCACTA	CAGGAAGACGCTGGAATAAGA
NM_000051	472	ATM	ataxia telangiectasia mutated (includes complementation groups A, C and D)	AACCATGAGTCTAGTACTTAA	TTGGCTTATACGCGCAGTGTA
NM_000061	695	BTK	Bruton agammaglobulinemia tyrosine kinase	CAGCTCGAAACTGTTTGGTAA	CCCTTTATGATTACATGCCAA
NM_000075	1019	CDK4	cyclin-dependent kinase 4	AAGGTAATCCGGAGTGAGCAA	CCGAACTGACCGGGAGATCAA
NM_000076	1028	CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	AAGCTTTAAGAGTCATTTATA	TACACTGGTCCCAAAGTGTAA
NM_000077	1029	CDKN2A	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	CACGCCCTAAGCGCACATTCA	CAGGTGTGCCACATTCGCTAA
NM_000141	2263	FGFR2	fibroblast growth factor receptor 2	CCGAATGAAGAACACGACCAA	CGGAGGAGCGTTGCCATTCAA
NM_000142	2261	FGFR3	fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)	ACCCTACGTTACCGTGCTCAA	CCGATGTTATTAGATGTTACA
NM_000167	2710	GK	glycerol kinase	CCACCACTTAAGTGACATAAA	CTGAGGGTAGCCCATTTATAA
NM_000189	3099	HK2	hexokinase 2	CCGGCCGTGCTACAATAGGTA	CGGCCGTGCTACAATAGGTAA
NM_000215	3718	JAK3	Janus kinase 3 (a protein tyrosine kinase, leukocyte)	CGGGAGATTCAGATCCTCAAA	TCCGGGAGGCGCAGACACTTA
NM_000221	3795	KHK	ketohexokinase (fructokinase)	TAGCCGCACCATCCTATACTA	TAGGGTGGGTAAGGCCTTATA
NM_000222	3815	KIT	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	CACGGTTGAATGTAAGGCTTA	CTCGCACCTTTCCAAAGTTAA
NM_000245	4233	MET	met proto-oncogene (hepatocyte growth factor receptor)	ACCGAGGGAATCATCATGAAA	CGCGCCGTGATGAATATCGAA
NM_000269	4830	NME1	non-metastatic cells 1, protein (NM23A) expressed in	TAGGATTCATTGAGTTGGTTA	TTCCGCCTTGTTGGTCTGAAA
NM_000289	5213	PFKM	phosphofructokinase, muscle	AACAGATCAGTGCCAATATAA	AAGGACTTTCGGGAACGAGAA
NM_000291	5230	PGK1	phosphoglycerate kinase 1	CACAATTATAGATTAGATCAA	GAGGAACGGATCAGATGTCTA
NM_000292	5256	PHKA2	phosphorylase kinase, alpha 2 (liver)	CCGCCTAACAAGGTAGATGAA	CCGGATTCTTAGTCACATATA
NM_000293	5257	PHKB	phosphorylase kinase, beta	AGGGCTGTTCGTGGTCAGTTA	TCGATGGGTCTTTGAATAGAA
NM_000294	5261	PHKG2	phosphorylase kinase, gamma 2 (testis)	CTGCATGCACTGCATATGAAA	TACGGGCACTGGGTAAAGAAA
NM_000389	1026	CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	CAGTTTGTGTGTCTTAATTAT	CTGGCATTAGAATTATTTAAA
NM_000431	4598	MVK	mevalonate kinase (mevalonic aciduria)	CCGCTTGGCGATGCCAGCCAA	GCGGTGGGCCTGGTTAAATAA
NM_000455	6794	STK11	serine/threonine kinase 11 (Peutz-Jeghers syndrome)	CAGGAGTGTGCGGTCAATATT	GAGGGCCGTCAAGATCCTCAA
NM_000459	7010	TEK	TEK tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucosal)	ACGGGCCAGATTGTAAGCTTA	TCGGTGCTACTTAACAACTTA
NM_000476	203	AK1	adenylate kinase 1	CCGGGATGCCATGGTGGCCAA	GCGGCTGGAGACCTATTACAA
NM_000788	1633	DCK	deoxycytidine kinase	AAGTTGCAAAGTGGAATTAAA	TTGGTATAAATTAATTTGTTA
NM_000858	2987	GUK1	guanylate kinase 1	CAGGGCTGACATCCTAATAAA	CCCGGCGAGGAGAACGGCAAA
NM_001079	7535	ZAP70	zeta-chain (TCR) associated protein kinase 70kDa	CCGCAACGTCCTGCTGGTTAA	GGCGTAGATCACCAGAATAAA
NM_001105	90	ACVR1	activin A receptor, type I	CGGATGGTGAGCAATGGTATA	CTGGTCTGTCTTTGGATAATA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_001106	93	ACVR2B	activin A receptor, type IIB	CAGCTCATGAATGACTTTGTA	TACGGTCATGTGGACATCCAT
NM_001123	132	ADK	adenosine kinase	AAGGGTATGGTAATGCTTGTA	TAGTTTGATAGTGCCACTTAA
NM_001184	545	ATR	ataxia telangiectasia and Rad3 related	CAGGCACTAATTGTTCTTCAA	GCCGCTAATCTTCTAACATTA
NM_001203	658	BMPR1B	bone morphogenetic protein receptor, type IB	AACGAATGTAATAAAGACCTA	ACGGATATTGTTTCACGATGA
NM_001204	659	BMPR2	bone morphogenetic protein receptor, type II (serine/threonine kinase)	AAGCACCGAAGCGAAACTTAA	CTCGTAAGTATGTAAAGGAAA
NM_001211	701	BUB1B	BUB1 budding uninhibited by benzimidazoles 1 homolog beta (yeast)	ACGAGAATACCTAATATGTGA	CAGATTTAGCACATTTACTAT
NM_001220	816	CAMK2B	calcium/calmodulin-dependent protein kinase (CaM kinase) II beta	CAAGAGTTTACTCAACAAGAA	CCGGAAGCAGGAGATCATTAA
NM_001221	817	CAMK2D	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	CCGCCTGCATAGCATATATTA	GTGCGACTTCATGATAGCATA
NM_001258	1018	CDK3	cyclin-dependent kinase 3	ATGGATATGTTCCAGAAGGTA	CAGACTGGATTTGGAGATGGA
NM_001259	1021	CDK6	cyclin-dependent kinase 6	AAGACTCAAGGTGGTCAGTAA	TCTGAAGTGTTTGACATTTAA
NM_001260	1024	CDK8	cyclin-dependent kinase 8	CCAGCTGGACAGAATATTCAA	TTCGAGAGCTTAAGCATCCAA
NM_001261	1025	CDK9	cyclin-dependent kinase 9 (CDC2-related kinase)	TAGGGACATGAAGGCTGCTAA	TGGGCACAGTTTGGTCCGTTA
NM_001262	1031	CDKN2C	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	CAGGCTTATGAATATATTTAA	TGCCTCTACTTTATCAATTAA
NM_001274	1111	CHEK1	CHK1 checkpoint homolog (S. pombe)	AAGAAAGAGATCTGTATCAAT	CCCGCACAGGTCTTTCCTTAT
NM_001277	1119	CHK	choline kinase	AGCCGGCGATTAGATACTGAA	CCGGCCCTTACCAAACCTGAT
NM_001278	1147	CHUK	conserved helix-loop-helix ubiquitous kinase	CAGGAGAAGTTCGGTTTAGTA	TTCCATAAGCTTGGTGACAAA
NM_001291	1196	CLK2	CDC-like kinase 2	CAGCTACAGACGCAACGATTA	TCGCCTGGATTGGGATGAGAA
NM_001292	1198	CLK3	CDC-like kinase 3	CACGAAGATCTCGGTCCAGAA	CTGCATTCTCTTTGAGTACTA
NM_001315	1432	MAPK14	mitogen-activated protein kinase 14	CAGAGAACTGCGGTTACTTAA	CTCAGTGATACGTACAGCCAA
NM_001319	1455	CSNK1G2	casein kinase 1, gamma 2	AAGAATCTCTATACAAATGAA	TAGGAAAGAATCTCTATACAA
NM_001320	1460	CSNK2B	casein kinase 2, beta polypeptide	CAGGTCCCTCACTACCGACAA	GTGGTGGGAATATGAAATAAA
NM_001345	1606	DGKA	diacylglycerol kinase, alpha 80kDa	ATCCATCTTCTCAACATGCAA	CACGACCAGTGTGCCATGAAA
NM_001346	1608	DGKG	diacylglycerol kinase, gamma 90kDa	ACCGCAAATGTGAATTATCAA	TAGCCACTCACATAAAGTTTA
NM_001347	1609	DGKQ	diacylglycerol kinase, theta 110kDa	CAGCGACACCAGGTTTGAGAA	CCGGAAGGTGACGCTCACCAA
NM_001348	1613	DAPK3	death-associated protein kinase 3	CCCAGAGATTGTGAACTATGA	CCGGCAGAAGGGCACGGGCAA
NM_001381	1796	DOK1	docking protein 1, 62kDa (downstream of tyrosine kinase 1)	AGGGATCAAAGAAGATGGTTA	CCGCCTGGACTGCAAAGTGAT
NM_001396	1859	DYRK1A	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A	CAAGAATGGGTTGCCATTAAA	TACGGTCGCTGACTACTTGAA
NM_001433	2081	ERN1	ER to nucleus signalling 1	CAGCACGGACGTCAAGTTTGA	CAGGACGTGAGCGACAGAATA
NM_001569	3654	IRAK1	interleukin-1 receptor-associated kinase 1	CCGGGCAATTCAGTTTCTACA	TCCCATCGCCATGCAGATCTA
NM_001570	3656	IRAK2	interleukin-1 receptor-associated kinase 2	CAGCAACGTCAAGAGCTCTAA	CCAGATCATCCTGAACTGGAA
NM_001616	92	ACVR2	activin A receptor, type II	GAGGTATTAGAGGGTGCTATA	TCCACGGTTGCTAAATTATAA
NM_001619	156	ADRBK1	adrenergic, beta, receptor kinase 1	CCGGGAGATCTTCGACTCATA	CGGCTGGAGGCTGGCAAGAAA
NM_001625	204	AK2	adenylate kinase 2	ATGGGTGGGAATGATAGGACA	CCACATGTAAAGACTTGGTTA
NM_001626	208	AKT2	v-akt murine thymoma viral oncogene homolog 2	ACGGGCTAAAGTGACCATGAA	CAAGCGTGGTGAATACATCAA
NM_001654	369	ARAF1	v-raf murine sarcoma 3611 viral oncogene homolog 1	CCGACTCATCAAGGGACGAAA	CCGGGATGGCATGAGTGTCTA
NM_001699	558	AXL	AXL receptor tyrosine kinase	CCGGTGTTCTAAGATGTGATA	TCCAAGATTCTAGATGATTAA
NM_001715	640	BLK	B lymphoid tyrosine kinase	CAGCCGTGCTGTTAAACCAAA	CTGGTAAGCGACTGTCATCAA
NM_001721	660	BMX	BMX non-receptor tyrosine kinase	CCCAATATGACAACGAATCAA	CGGAACAAAGTTTCCAGTCAA
NM_001743	805	CALM2	calmodulin 2 (phosphorylase kinase, delta)	ACAAAGGAATTGGGAACTGTA	CAAAGGAATTGGGAACTGTAA
NM_001744	814	CAMK4	calcium/calmodulin-dependent protein kinase IV	CAGAAGCCTTATGCTCTCAAA	TTGCAAGTTAACACAACGTAA
NM_001786	983	CDC2	cell division cycle 2, G1 to S and G2 to M	TCGGGAAATTTCTCTATTAAA	TTGACTAACTATGGAAGATTA
NM_001787	984	CDC2L1	cell division cycle 2-like 1 (PITSLRE proteins)	CAAGATCTACATCGTGATGAA	CAGGATAAAGCTCGCCGGGAA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_001798	1017	CDK2	cyclin-dependent kinase 2	CACGTACGGAGTTGTGTACAA	CAGGTTATATCCAATAGTAGA
NM_001799	1022	CDK7	cyclin-dependent kinase 7 (MO15 homolog, Xenopus laevis, cdk-activating kinase)	CCGGATGGCTCTGGACGTGAA	GAGGCTTTAAGGTAGCTTTAA
NM_001800	1032	CDKN2D	cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)	ACCCAAGGGCAGAGCATTTAA	ATGAGTTATGAGTTATTCATA
NM_001823	1152	CKB	creatine kinase, brain	CCAGATTGAAACTCTCTTCAA	CCGGCCTCACCCAGATTGAAA
NM_001824	1158	CKM	creatine kinase, muscle	GACGGGCGAGTTCAAAGGGAA	TCCACGCAAAGCGATAAATAA
NM_001825	1160	CKMT2	creatine kinase, mitochondrial 2 (sarcomeric)	CCTGCCTATCTTTACAATAAA	GAGGTTGAGCTTGTTCAGATA
NM_001826	1163	CKS1B	CDC28 protein kinase regulatory subunit 1B	AACATCTTTCTGATAACATTA	AAGAAATCTGTTCATGTTAAA
NM_001827	1164	CKS2	CDC28 protein kinase regulatory subunit 2	CTGTAAGATGTTTAAGATAAA	TCGGACAAGTACTTCGACGAA
NM_001892	1452	CSNK1A1	casein kinase 1, alpha 1	AGGGCTAAAGGCTGCAACAAA	CAAGAGTAACATGAAAGGTTT
NM_001893	1453	CSNK1D	casein kinase 1, delta	CCGGTCTAGGATCGAAATGTT	CTCCCTGACGATTCCACTGTA
NM_001894	1454	CSNK1E	casein kinase 1, epsilon	GAGCTTTATCGTGGTTGTTAA	GTGGTTGTTAATTTGAAGTAA
NM_001896	1459	CSNK2A2	casein kinase 2, alpha prime polypeptide	CAGGAGTACAATGTTCGTGTA	CTGGGACAACATTCACGGAAA
NM_001929	1716	DGUOK	deoxyguanosine kinase	CACCTTTGTAAAGAATCTGTA	CAGCACGATGGTCCTACACAT
NM_001954	780	DDR1	discoidin domain receptor family, member 1	ACGGTGTGAATCACACATCCA	CAGGAATGATTTCCTGAAAGA
NM_001982	2065	ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	ACCGGCGATGCTGAGAACCAA	CCAGAGCTTCAAGACTGTTTA
NM_002005	2242	FES	feline sarcoma oncogene	AAGGCCAAGTTTCTACAGGAA	CAGCCTGAGGCTGAGTACCAA
NM_002011	2264	FGFR4	fibroblast growth factor receptor 4	CACATTGACTACTATAAGAAA	CCGCCTGACCTTCGGACCCTA
NM_002019	2321	FLT1	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)	ACCGCATATGGTATCCCTCAA	CACTACAGTATTAGCAAGCAA
NM_002031	2444	FRK	fyn-related kinase	CAGGACAGTCAAGGTGATATA	CTGGGAGTACCTAGAACCCTA
NM_002037	2534	FYN	FYN oncogene related to SRC, FGR, YES	AAGAAGCAGGATGCTGATCTA	AAGACATGTGGTGTATATAAA
NM_002082	2870	GRK6	G protein-coupled receptor kinase 6	AAGGATGTTCTGGACATTGAA	AGGCATGTGGGCGGCACGTAA
NM_002093	2932	GSK3B	glycogen synthase kinase 3 beta	AACACTGGTCACGTTTGGAAA	CTGCATTTATCGTTAACCTAA
NM_002110	3055	HCK	hemopoietic cell kinase	AACGACGGGCTCTGCCAGAAA	CGGGAGCACATCAGAGGCTTA
NM_002115	3101	HK3	hexokinase 3 (white cell)	CACTCAGGTTAGCAATATATA	CCGGAATGCGATGTCTCCTTA
NM_002220	3706	ITPKA	inositol 1,4,5-trisphosphate 3-kinase A	CACCAGCGGGCTGATCCTGAA	CCGGTCTAACGTCTCACACCA
NM_002221	3707	ITPKB	inositol 1,4,5-trisphosphate 3-kinase B	AAGGCCATTCGAACCACTCTA	GACGTAAAGATTCTATGAATA
NM_002227	3716	JAK1	Janus kinase 1 (a protein tyrosine kinase)	ACCGGATGAGGTTCTATTTCA	CACGGATAACATCAGCTTCAT
NM_002253	3791	KDR	kinase insert domain receptor (a type III receptor tyrosine kinase)	AACGCTGACATGTACGGTCTA	AAGGCTAATACAACTCTTCAA
NM_002314	3984	LIMK1	LIM domain kinase 1	CTGCCTGGTCCGCGAGAACAA	GAGCATCTAGGAAGTATTAAA
NM_002344	4058	LTK	leukocyte tyrosine kinase	ACAGATCTTTGGAGTGCCTAA	CCTGCAGATGCTTCTAATAAA
NM_002350	4067	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	CCCGGACGACTTGTCTTTCAA	CGGGAAATATGGGATGTATAA
NM_002356	4082	MARCKS	myristoylated alanine-rich protein kinase C substrate	CTCCTTCAAGAAGAACAAGAA	TTGAGTTTCTTTGTTGAAGAA
NM_002376	4140	MARK3	MAP/microtubule affinity-regulating kinase 3	AACGGCGAACCGCAACATATA	CCCGGGAACGGCGAACCGCAA
NM_002378	4145	MATK	megakaryocyte-associated tyrosine kinase	ACGGATTCTAAGGACTCTAAA	GACGGATTCTAAGGACTCTAA
NM_002401	4215	MAP3K3	mitogen-activated protein kinase kinase kinase 3	CAGGAATACTCAGATCGGGAA	CCACGTGTCTGTGCACCACAA
NM_002419	4296	MAP3K11	mitogen-activated protein kinase kinase kinase 11	CCCGAGGTCTGGAGGACTCAA	CCGGAGGAGAAACGTCTTCGA
NM_002446	4294	MAP3K10	mitogen-activated protein kinase kinase kinase 10	AAGCGGCTTGAAGTCATCGAA	CAGGATGTTCACTCTATTTAT
NM_002447	4486	MST1R	macrophage stimulating 1 receptor (c-met-related tyrosine kinase)	ATGGAGCATCCTTCTCCGATA	TGCCATTAAGTTTGAGTATAT
NM_002497	4751	NEK2	NIMA (never in mitosis gene a)-related kinase 2	TACGAGGATGTTAAACTTAAA	TTACGAGGATGTTAAACTTAA
NM_002512	4831	NME2	non-metastatic cells 2, protein (NM23B) expressed in	ATAGAGCATATTTGCCAATAA	TAGAGCATATTTGCCAATAAA
NM_002513	4832	NME3	non-metastatic cells 3, protein expressed in	ACGCACCTTCCTGGCCGTGAA	CTGCATCGAGGTTGGCAAGAA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_002529	4914	NTRK1	neurotrophic tyrosine kinase, receptor, type 1	CACATCATCGAGAACCCACAA	CGAGAGCATCCTGTACCGTAA
NM_002530	4916	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	CACGGATAACTTTATCTTGTT	CTGGTTGGAGCGAATCTGCTA
NM_002576	5058	PAK1	p21/Cdc42/Rac1-activated kinase 1 (STE20 homolog, yeast)	TCCACTGATTGCTGCAGCTAA	TTGAAGAGAACTGCAACTGAA
NM_002577	5062	PAK2	p21 (CDKN1A)-activated kinase 2	CCGCGACCGGATCATACGAAA	CCGGATCATACGAAATCAATT
NM_002578	5063	PAK3	p21 (CDKN1A)-activated kinase 3	CAAGAAGGAATTAATTATTAA	TTCCAGTACTTTGTACAGGAA
NM_002595	5128	PCTK2	PCTAIRE protein kinase 2	AGGCTTAATTCTTGCGTATAA	TAGGCTTAATTCTTGCGTATA
NM_002609	5159	PDGFRB	platelet-derived growth factor receptor, beta polypeptide	CCGAGCAACTTTGATCAACGA	CTGCCGAGCAACTTTGATCAA
NM_002610	5163	PDK1	pyruvate dehydrogenase kinase, isoenzyme 1	CCCGAACTAGAACTTGAAGAA	TCGGGTTTCTATAGGAAACTA
NM_002611	5164	PDK2	pyruvate dehydrogenase kinase, isoenzyme 2	AAGAACCTTGTTAGACCGAGA	TAGGTCTGTGATGGTCCCTAA
NM_002612	5166	PDK4	pyruvate dehydrogenase kinase, isoenzyme 4	ACCCGTGTCAATTAACATTTA	AGGCCTCTTGTTCACATCAAA
NM_002613	5170	PDPK1	3-phosphoinositide dependent protein kinase-1	AAGCGGTTAGGCTGTGAGGAA	CACGCCTAACAGGACGTATTA
NM_002625	5207	PFKFB1	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1	CTCCACAAAGCTCACACGATA	CTGCGAGACCAAGATAAATAT
NM_002626	5211	PFKL	phosphofructokinase, liver	CACGATGGCTTCGAAGGCCTA	CCGGACCTACTCGCACCTGAA
NM_002627	5214	PFKP	phosphofructokinase, platelet	CAGCACTTTATGCACGTATTA	CCGCCTGAAGGCTGCTTGCAA
NM_002637	5255	PHKA1	phosphorylase kinase, alpha 1 (muscle)	ATGGGAGTGCTTGGAACTTCA	CCCAATCGTCTGTACTATGAA
NM_002645	5286	PIK3C2A	phosphoinositide-3-kinase, class 2, alpha polypeptide	CAAGATGGTCGAATCAAGGAA	TACCCACTAATTGCATTGGAA
NM_002646	5287	PIK3C2B	phosphoinositide-3-kinase, class 2, beta polypeptide	AAGGGTTGTCTTCCTCGCCAA	CAGGGTGGTCCAGTCCGTCAA
NM_002647	5289	PIK3C3	phosphoinositide-3-kinase, class 3	AACGCGAAAGTGGAAATCGTA	TCGGTTGGTGCATCTAATGAA
NM_002648	5292	PIM1	pim-1 oncogene	AAACATCCTTATCGACCTCAA	AAAGATTGTAGTGGATCTAAT
NM_002649	5294	PIK3CG	phosphoinositide-3-kinase, catalytic, gamma polypeptide	ATCGAAGTTTGCAGAGACAAA	CACCTTTACTCTATAACTCAA
NM_002650	5297	PIK4CA	phosphatidylinositol 4-kinase, catalytic, alpha polypeptide	CATCTGGAACATGAAGACTAA	CCAGTTCATCTGGAACATGAA
NM_002651	5298	PIK4CB	phosphatidylinositol 4-kinase, catalytic, beta polypeptide	CCGAGAGTATTGATAATTCAT	TCGGCTGATAGTGGCATGATT
NM_002730	5566	PRKACA	protein kinase, cAMP-dependent, catalytic, alpha	CAAGGACAACTCAAACTTATA	CAGAAGGTGGTGAAACTGAAA
NM_002732	5568	PRKACG	protein kinase, cAMP-dependent, catalytic, gamma	AACCAGCTGGATCGCCATCTA	CTGGATCGCCATCTATGAGAA
NM_002733	5571	PRKAG1	protein kinase, AMP-activated, gamma 1 non-catalytic subunit	CCCTAAGATAATAGCACAACA	TTGGCCCTGATTCAACCCTAA
NM_002734	5573	PRKAR1A	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	CAGCTAGTGCCAAATAATTGA	CTGGACCGACCTAGATTTGAA
NM_002736	5577	PRKAR2B	protein kinase, cAMP-dependent, regulatory, type II, beta	ACGAACATGGATATTGTTGAA	CACGCCATTGGGACTGTCAAA
NM_002737	5578	PRKCA	protein kinase C, alpha	CGCAGTGGAATGAGTCCTTTA	TACAAGTTGCTTAACCAAGAA
NM_002738	5579	PRKCB1	protein kinase C, beta 1	CAAGAGCTAAGTAGATGTGTA	CCGGATGAAACTGACCGATTT
NM_002739	5582	PRKCG	protein kinase C, gamma	AACGGTGAAAGCCACGCTAAA	GACCTTTGTGTTCAACCTGAA
NM_002740	5584	PRKCI	protein kinase C, iota	CACCCAATATCTTCTCTTGTA	TACCACGTTCTATGTCTGTAA
NM_002741	5585	PRKCL1	protein kinase C-like 1	CAGGACAGTAAGACCAAGATT	CCGCAAGGAGCTGAAGCTGAA
NM_002742	5587	PRKCM	protein kinase C, mu	CAGGAAGGCGATCTTATTGAA	CCTCAGTATATTTAAACTCAA
NM_002744	5590	PRKCZ	protein kinase C, zeta	CGGAAGCATGACAGCATTAAA	GACCAAATTTACGCCATGAAA
NM_002745	5594	MAPK1	mitogen-activated protein kinase 1	AACACTTGTCAAGAAGCGTTA	ATCATGGTAGTCACTAACATA
NM_002746	5595	MAPK3	mitogen-activated protein kinase 3	CCCGTCTAATATATAAATATA	CTCCCTGACCCGTCTAATATA
NM_002747	5596	MAPK4	mitogen-activated protein kinase 4	AAGGATCGTTGATCAGCATTA	CGCCTTAAATCTAATCAGCAA
NM_002748	5597	MAPK6	mitogen-activated protein kinase 6	CAAGTTCAATTTGAAAGGAAA	CAGGCTTCCTGTTGAAATAAA
NM_002749	5598	MAPK7	mitogen-activated protein kinase 7	CAGACCCACCTTTCAGCCTTA	TACGAGATCATCGAGACCATA
NM_002750	5599	MAPK8	mitogen-activated protein kinase 8	AAGCCCAGTAATATAGTAGTA	TCGGGACTTAAAGCCCAGTAA
NM_002751	5600	MAPK11	mitogen-activated protein kinase 11	CAGGATGGAGCTGATCCAGTA	CTGAGCGACGAGCACGTTCAA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_002752	5601	MAPK9	mitogen-activated protein kinase 9	AAAGTCGATTTATGTGTATTA	ATCGTGAACTTGTCCTCTTAA
NM_002753	5602	MAPK10	mitogen-activated protein kinase 10	CCGCATGTGTCTGTATTCATA	TCCGAGCACAATAAACTCAAA
NM_002754	5603	MAPK13	mitogen-activated protein kinase 13	CCGGAGTGGCATGAAGCTGTA	CGGGATGAGCCTCATCCGGAA
NM_002755	5604	MAP2K1	mitogen-activated protein kinase kinase 1	CTGGAAGAATTCCTGAACAAA	CTGGATCAAGTCCTGAAGAAA
NM_002756	5606	MAP2K3	mitogen-activated protein kinase kinase 3	ACGGATATCCTGCATGTCCAA	CCGGGCCACCGTGAACTCACA
NM_002757	5607	MAP2K5	mitogen-activated protein kinase kinase 5	AAGACGTATGTTGGAACAAAT	CAAGACGTATGTTGGAACAAA
NM_002758	5608	MAP2K6	mitogen-activated protein kinase kinase 6	AAGGCTTGCATTTCTATTGGA	TAGACCTATGATAAATAACCA
NM_002759	5610	PRKR	protein kinase, interferon-inducible double stranded RNA dependent	ACGGAAAGACTTACGTTATTA	CGGAAAGACTTACGTTATTAA
NM_002760	5616	PRKY	protein kinase, Y-linked	CCAGAGTTCGCCTACAGATAA	TTGGGATACAGTAAGAGAATA
NM_002822	5756	PTK9	PTK9 protein tyrosine kinase 9	ACCGGCATCCAAGCAAGTGAA	TCCAAGCAAGTGAAGATGTTA
NM_002880	5894	RAF1	v-raf-1 murine leukemia viral oncogene homolog 1	CAGATCTTAGTAAGCTATATA	TGGGAAATAGAAGCCAGTGAA
NM_002929	6011	GRK1	G protein-coupled receptor kinase 1	CCAGATGAAGGCGACCGGCAA	CTGGAAAGACATCGAGGACTA
NM_002944	6098	ROS1	v-ros UR2 sarcoma virus oncogene homolog 1 (avian)	AAGGTAATTGCTCTAACTTTA	ACCGAGAAGGGTTAAACTATA
NM_002953	6195	RPS6KA1	ribosomal protein S6 kinase, 90kDa, polypeptide 1	CCCAACATCATCACTCTGAAA	TGCCACGTACTCCGCACTCAA
NM_002958	6259	RYK	RYK receptor-like tyrosine kinase	CGGTCTTGATGCAGAACTTTA	CTGATCGGTCTTGATGCAGAA
NM_002969	6300	MAPK12	mitogen-activated protein kinase 12	CTGGACGTATTCACTCCTGAT	TGGAAGCGTGTTACTTACAAA
NM_003010	6416	MAP2K4	mitogen-activated protein kinase kinase 4	AGGGAGAATGGTGCTGTTTAA	AGGGTGTATAGTGTTCACAAA
NM_003137	6732	SRPK1	SFRS protein kinase 1	CAGACTCTTGTACACCTATAA	TACCATGTGATCCGAAAGTTA
NM_003157	6787	NEK4	NIMA (never in mitosis gene a)-related kinase 4	CACAATCAGTAGCGTAAATAT	CAGACATATATAATGGGTGAA
NM_003159	6792	CDKL5	cyclin-dependent kinase-like 5	AAGATAGACGCTTCATGTTAA	AAGGCAATAATGCTAATTACA
NM_003160	6795	AURKC	aurora kinase C	AAGATGTAAGATGCTAATTAA	CCGGGTGTACCTGATTCTGGA
NM_003161	6198	RPS6KB1	ribosomal protein S6 kinase, 70kDa, polypeptide 1	AAGAAGGGTATCCTTTCATTA	CAGAGAGTCAATGTCATTACA
NM_003177	6850	SYK	spleen tyrosine kinase	CCCGCTCTTAAAGATGAGTTA	TCCGGAATGCATCAACTACTA
NM_003188	6885	MAP3K7	mitogen-activated protein kinase kinase kinase 7	CAAGAATATATGAAAGTTCAA	CCCGTGTGAACCATCCTAATA
NM_003215	7006	TEC	tec protein tyrosine kinase	CAGTACAAAGTCGCAATCAAA	CCGCAGCTAATCAGAATCAGA
NM_003242	7048	TGFBR2	transforming growth factor, beta receptor II (70/80kDa)	CTCCAATATCCTCGTGAAGAA	TCGGTTAATAACGACATGATA
NM_003258	7083	TK1	thymidine kinase 1, soluble	CGGGCCGATGTTCTCAGGAAA	TCGGCTCTGCTACTTCAAGAA
NM_003318	7272	TTK	TTK protein kinase	CAGCAATACCTTGGATGATTA	TCCGACTTTATGATTATGAAA
NM_003328	7294	TXK	TXK tyrosine kinase	CAGCTGGGTTTAGCTACGAAA	CCCGGTGACATTCTATTTCCA
NM_003331	7297	TYK2	tyrosine kinase 2	CACCATCTGGTAATAAACTCA	CTGATGCTATATTTCCGCATA
NM_003332	7305	TYROBP	TYRO protein tyrosine kinase binding protein	CCGAATCATGACAGTCAGCAA	CTGGATCCAGCCATTCCTGAA
NM_003384	7443	VRK1	vaccinia related kinase 1	CAGGTTATACTCCTTAAGTTA	CCAGGTGTACTTGGTAGATTA
NM_003390	7465	WEE1	WEE1 homolog (S. pombe)	CAGGGTAGATTACCTCGGATA	TTGACTAATAATACTGGCTAA
NM_003488	8165	AKAP1	A kinase (PRKA) anchor protein 1	AGCGCTGAACTTGATTGGGAA	CACGCAGAGATGACAGTACAA
NM_003551	8382	NME5	non-metastatic cells 5, protein expressed in (nucleoside-diphosphate kinase)	ATGATATTAGCTAGACATAAA	CATGATATTAGCTAGACATAA
NM_003557	8394	PIP5K1A	phosphatidylinositol-4-phosphate 5-kinase, type I, alpha	CAGCCTCTTGATGTCAATCCA	CCCTGCCTTGATAATATGTTA
NM_003558	8395	PIP5K1B	phosphatidylinositol-4-phosphate 5-kinase, type I, beta	AAGGCTCAACGTATAAGCGAA	CAGGCCTACACTCTATTCAAA
NM_003559	8396	PIP5K2B	phosphatidylinositol-4-phosphate 5-kinase, type II, beta	CACGCCATACGATACAAAGAA	CCGCTTTAAGTTTAAGGAGTA
NM_003565	8408	ULK1	unc-51-like kinase 1 (C. elegans)	CGCGCGGTACCTCCAGAGCAA	TGCCCTTTGCGTTATATTGTA
NM_003576	8428	STK24	serine/threonine kinase 24 (STE20 homolog, yeast)	CCCACCGACGTTGGAAGGAAA	CTGGAGGGAGCACGAACCTAA
NM_003582	8444	DYRK3	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	AGCCAATAAGCTTAAAGCTAA	TCGACAGTACGTGGCCCTAAA
NM_003583	8445	DYRK2	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	TAGAAGCGGTATTAAAGTAAT	TGCACAGAGATTATTGTATTA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_003600	6790	STK6	serine/threonine kinase 6	CACCTTCGGCATCCTAATATT	CACGTGCTCTACCTCCATTTA
NM_003607	8476	CDC42BPA	CDC42 binding protein kinase alpha (DMPK-like)	CAGACTTTCCGTAGCAGCTTA	CAGATAATAGTCGGAAACAAA
NM_003618	8491	MAP4K3	mitogen-activated protein kinase kinase kinase kinase 3	GAGGTGGTTCTTTACAGGATA	TCGAGCTGTTGGATAAAGTAA
NM_003629	8503	PIK3R3	phosphoinositide-3-kinase, regulatory subunit, polypeptide 3 (p55, gamma)	AGGGAGGCAATAATAAGTTAA	GAGGATATCAATCGAGTACAA
NM_003639	8517	IKBKG	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma	CTCCTCTAGTTCAGAGACATA	TTCGGAAATGCCTCACATATA
NM_003640	8518	IKBKAP	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein	CAGCGGTTTACTATAGACAAA	GCGGTTTACTATAGACAAATA
NM_003646	8525	DGKZ	diacylglycerol kinase, zeta 104kDa	CAAGAGGAACGACTTCTGTAA	CTGGAGCGAGTCAGCGACATA
NM_003647	8526	DGKE	diacylglycerol kinase, epsilon 64kDa	ATCGATGGAAAGTTCAAGTAA	CTGGAAGTCGTTGGAGTATAT
NM_003648	8527	DGKD	diacylglycerol kinase, delta 130kDa	CAGCAGATTCTCTTCTATGAA	CCGCCTCGTGACCAAGTTTAA
NM_003656	8536	CAMK1	calcium/calmodulin-dependent protein kinase I	CAGGTGCTGGATGCTGTGAAA	CTGCATGACCTGGGCATTGTA
NM_003668	8550	MAPKAPK5	mitogen-activated protein kinase-activated protein kinase 5	ACCGACCTTTCTGATTAGTAA	CCGACCTTTCTGATTAGTAAA
NM_003674	8558	CDK10	cyclin-dependent kinase (CDC2-like) 10	CCGTCTGAAGTGTATTCGTAA	CTGATGCTGAGCGAAGCTATA
NM_003681	85006	C21orf124	chromosome 21 open reading frame 124	CACAGGTTATACGAGGGACAA	GAGGCTGAACAACATGAATAA
NM_003682	8567	MADD	MAP-kinase activating death domain	CAGACCCACTACTATAGTAAA	CAGGAGGGCGTTAGTGGATCA
NM_003684	8569	MKNK1	MAP kinase-interacting serine/threonine kinase 1	CCAGCAAAGATGATACCTTAA	TAGATAGTGCTCTGTGCCTAA
NM_003688	8573	CASK	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	AACCAATGGGAATCACTTTAA	AAGGACGACAGATCTATGTAA
NM_003690	8575	PRKRA	protein kinase, interferon-inducible double stranded RNA dependent activator	ATGATTGATTGTTAAATTTCA	TAAGTATGATTGATTGTTAAA
NM_003691	8576	STK16	serine/threonine kinase 16	CACATAGTGTTCTGACTCCAA	CAGGAGAATGTGTAACAAGAA
NM_003718	8621	CDC2L5	cell division cycle 2-like 5 (cholinesterase-related cell division controller)	AACGACGTAGTTTCATTGGAA	TCAGAGTATTATCAATATGAA
NM_003804	8737	RIPK1	receptor (TNFRSF)-interacting serine-threonine kinase 1	CCGACATTTCCTGGCATTGAA	TACCACTAGTCTGACGGATAA
NM_003821	8767	RIPK2	receptor-interacting serine-threonine kinase 2	ACGTATGATCTCTCTAATAGA	CACAAGGACATCGACCTGTTA
NM_003831	8780	RIOK3	RIO kinase 3 (yeast)	ATGCGGCAGTTATATCATGAA	CTGGCTGTATTAGTACAGGAA
NM_003845	8798	DYRK4	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 4	CTCCATATGAACAAAGTGAAA	CTGCATCACGGCGGAGTTGTA
NM_003885	8851	CDK5R1	cyclin-dependent kinase 5, regulatory subunit 1 (p35)	CCGGAAGGCCACGCTGTTTGA	TGAGCTGGTTTGACTCATTAA
NM_003886	8852	AKAP4	A kinase (PRKA) anchor protein 4	GTCGGTGAACACATTCTCAAA	TACAGTGTCTATGCCGATCAA
NM_003936	8941	CDK5R2	cyclin-dependent kinase 5, regulatory subunit 2 (p39)	CAGCAAGAAGGTGACACCCAA	CCGCGAGAACCTTCTCCGCAA
NM_003942	8986	RPS6KA4	ribosomal protein S6 kinase, 90kDa, polypeptide 4	CAGGCTGTGCCTTTGACTTTA	CGCCACCTTCATGGCATTCAA
NM_003948	8999	CDKL2	cyclin-dependent kinase-like 2 (CDC2-related kinase)	ATGATGTGTTTAGGTAATCTA	TTCTACGGACTTTAAATTAAA
NM_003952	6199	RPS6KB2	ribosomal protein S6 kinase, 70kDa, polypeptide 2	ACCGCAGAGAACCGGAAGAAA	CGGGCTGAGCGGAACATTCTA
NM_003954	9020	MAP3K14	mitogen-activated protein kinase kinase kinase 14	CACATGCATGTGACTCCTCAA	TACCTAGTGCATGCTCTGCAA
NM_003957	9024	STK29	serine/threonine kinase 29	CCCGACTGCCAGAGTCTGCTA	GCGAGCTACTGTAAACTTTAA
NM_003985	8711	TNK1	tyrosine kinase, non-receptor, 1	AAGGATCTAGTCTGCCCACTA	ATCGGTCATGATGAACTTGGA
NM_004064	1027	CDKN1B	cyclin-dependent kinase inhibitor 1B (p27, Kip1)	AAAGCGTTGGATGTAGCATTA	ACCGACGATTCTTCTACTCAA
NM_004071	1195	CLK1	CDC-like kinase 1	AAAGCCGGTATCAGAACCATA	AACGTGATGAACGCACCTTAA
NM_004073	1263	PLK3	polo-like kinase 3 (Drosophila)	CAGAAAGACTGTGCACTACAA	CTGCATCAAGCAGGTTCACTA
NM_004119	2322	FLT3	fms-related tyrosine kinase 3	CCGGCTTGAGTGAATTGTGTA	TACGTTGATTTCAGAGAATAT
NM_004157	5576	PRKAR2A	protein kinase, cAMP-dependent, regulatory, type II, alpha	AACGGCATGTCTCTCCAACAA	AACTTGAAAGTCAGCACTAAA
NM_004196	8814	CDKL1	cyclin-dependent kinase-like 1 (CDC2-related kinase)	CTGGACCGAGTGACTACTATA	TCGGGAAATCCGAATGCTCAA
NM_004197	8859	STK19	serine/threonine kinase 19	CCCGGAGACCTTTGGAGTTAA	CTGTTATTACTCTGTCTTGAA
NM_004217	9212	AURKB	aurora kinase B	AACGCGGCACTTCACAATTGA	ACGCGGCACTTCACAATTGAT
NM_004226	9262	STK17B	serine/threonine kinase 17b (apoptosis-inducing)	AGCATATATGTTGTTAACTCA	CATGTTAATGAAATAATTCAA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_004274	9472	AKAP6	A kinase (PRKA) anchor protein 6	AAGCATGTGGATGTACATCTA	CACGTTTGTCACTGCCGTTTA
NM_004302	91	ACVR1B	activin A receptor, type IB	CCGTTCTTACGTCGCCATAAA	CTGTGATTACCTCTCAATCTA
NM_004304	238	ALK	anaplastic lymphoma kinase (Ki-1)	CACCTACGTATTTAAGATGAA	CTGGGCCTGTATACCGGATAA
NM_004327	613	BCR	breakpoint cluster region	ACGGCAGTCCATGACGGTGAA	CAGCATTCCGCTGACCATCAA
NM_004329	657	BMPR1A	bone morphogenetic protein receptor, type IA	CAGCTACGCCGGACAATAGAA	GCGGCAGACATTAAAGGTACA
NM_004333	673	BRAF	v-raf murine sarcoma viral oncogene homolog B1	ACACGACATGTGAATATCCTA	TTGCTTATATGTTAAATTGAA
NM_004336	699	BUB1	BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast)	CAGCTTGTGATAAAGAGTCAA	TGGCACTTACATGAAAGTGAA
NM_004383	1445	CSK	c-src tyrosine kinase	CCGGTACAGAATGTATTGCCA	TACGCGCCTCATTAAACCAAA
NM_004384	1456	CSNK1G3	casein kinase 1, gamma 3	CAACATATCTTCGTTATGTAA	TACCGCAAACTTGATATGGAA
NM_004409	1760	DMPK	dystrophia myotonica-protein kinase	AACCAGAACTTCGCCAGTCAA	GAGCCTGAGGGCTAAATTTAA
NM_004431	1969	EPHA2	EphA2	CAGCGCCAAGTAAACAGGGTA	TCGGACAGACATATAGGATAT
NM_004438	2043	EPHA4	EphA4	CCCGCGAATGAAGTTACCTTA	CCGCCAGGACATTTCCTATAA
NM_004439	2044	EPHA5	EphA5	ACCAGTTGGATCTCCAATGAA	CCCGGCAGTATGTGTCTGTAA
NM_004440	2045	EPHA7	EphA7	ACCAGTCATGATAGTAATAGA	CAGGCTGCGAAGGAAGTACTA
NM_004441	2047	EPHB1	EphB1	ATGGCCCTGGATTATCTACTA	GCGGGATGATGTGACCTACAA
NM_004443	2049	EPHB3	EphB3	CCGCAGCTGACCGCCAGATTA	GCGGGTCTACGTGGAGCTCAA
NM_004444	2050	EPHB4	EphB4	CCCAGGCAATAGCCACTCTAA	TCGGACAAACACGGACAGTAT
NM_004445	2051	EPHB6	EphB6	AACCGGCAATCTCTAGATCAA	CTGGAGCTTTGGGATACTCAT
NM_004448	2064	ERBB2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)	AACAAAGAAATCTTAGACGAA	CACGTTTGAGTCCATGCCCAA
NM_004517	3611	ILK	integrin-linked kinase	AAGGAAGAGCAGGGACTTCAA	TAGCCGTAGTGTAATGATTGA
NM_004560	4920	ROR2	receptor tyrosine kinase-like orphan receptor 2	CCGGTTTGGGAAAGTCTACAA	CTGGTGCTTTACGCAGAATAA
NM_004566	5209	PFKFB3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	CAGGGACTTGTCGCTGATCAA	CTCCAATATCATGGAAGTTAA
NM_004567	5210	PFKFB4	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4	ACGGAGAGCGACCATCTTTAA	CAGAAAGTGTCTGGACTTGTA
NM_004570	5288	PIK3C2G	phosphoinositide-3-kinase, class 2, gamma polypeptide	CCAGATCAAGAAATTCGTAAA	CCCGTAGAAATGATAACTCCA
NM_004579	5871	MAP4K2	mitogen-activated protein kinase kinase kinase kinase 2	CTGGCTCTACTGCGTGAACAA	TCGGTCAGCCTCAGAATTCCA
NM_004586	6197	RPS6KA3	ribosomal protein S6 kinase, 90kDa, polypeptide 3	AGCGCTGAGAATGGACAGCAA	TCCAAACATTATCACTCTAAA
NM_004612	7046	TGFBR1	transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 53kDa)	TCCATTGGTGGAATTCATGAA	TGGGATTGTACTATACCAGTA
NM_004614	7084	TK2	thymidine kinase 2, mitochondrial	ATGCCAGAAGTGGACTATGTA	CGGGATCGAATATTAACTCCA
NM_004635	7867	MAPKAPK3	mitogen-activated protein kinase-activated protein kinase 3	CAGGCTTTCACTGAGAGAGAA	CCAGATAGTAATAAACACCAT
NM_004672	9064	MAP3K6	mitogen-activated protein kinase kinase kinase 6	CACCATCCAAATGCTGTTGAA	TCAGAGGAGCTGAGTAATGAA
NM_004690	9113	LATS1	LATS, large tumor suppressor, homolog 1 (Drosophila)	CCCATGAATCCTCCTAATCAA	CGCGATCTAGTATATGTTTAA
NM_004705	5612	PRKRIR	protein-kinase, interferon-inducible double stranded RNA dependent inhibitor, repressor of (P58 repressor)	AAGGTGTATGTAGACCACTTA	CTGGACAGTTACAAGAAATTA
NM_004712	9146	HGS	hepatocyte growth factor-regulated tyrosine kinase substrate	CCGGAACGAGCCCAAGTACAA	GCACGTCTTTCCAGAATTCAA
NM_004714	9149	DYRK1B	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1B	CACGGAGATGAAGTACTATAT	CCGGACCTACCGCTACAGCAA
NM_004721	9175	MAP3K13	mitogen-activated protein kinase kinase kinase 13	CAGACTCAATATGCACGGACA	GCGAATAATTTATACATGGAA
NM_004734	9201	DCAMKL1	doublecortin and CaM kinase-like 1	CAGGTTTATAACTTCGACACA	CCGGAAGTGATAACACGCAAA
NM_004759	9261	MAPKAPK2	mitogen-activated protein kinase-activated protein kinase 2	CGCCATCATCGATGACTACAA	CTACGAGCAGATCAAGATAAA
NM_004760	9263	STK17A	serine/threonine kinase 17a (apoptosis-inducing)	AACCAGGATATTTAACAGGTA	TCCATTGTAACCGAAGAGTTA
NM_004783	9344	TAO1	thousand and one amino acid protein kinase	CACGCCCAAAGCTCAGCACAA	GCCCAAGAGCCTCAAATCTAA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_004834	9448	MAP4K4	mitogen-activated protein kinase kinase kinase kinase 4	AGGCAAGATCCTACCCGGAAA	TCGGAGCTGCACCGAGGGCAA
NM_004836	9451	EIF2AK3	eukaryotic translation initiation factor 2-alpha kinase 3	CACAAACTGTATAACGGTTTA	CGGCAGGTCATTAGTAATTAT
NM_004842	9465	AKAP7	A kinase (PRKA) anchor protein 7	AACGATGGGTCTGAAGTCCAA	CCCGATGACGCTGAACTAGTA
NM_004850	9475	ROCK2	Rho-associated, coiled-coil containing protein kinase 2	AAGCTACATATGGAGCTTAAA	ATGCACTTGTATAAAGCCATA
NM_004857	9495	AKAP5	A kinase (PRKA) anchor protein 5	AGGGCTTTCATCAAGAAATTA	ATCAGGTTGATCTTTAAATAA
NM_004936	1030	CDKN2B	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	CTGCTTACTTATGCCATAGAA	GAGAGCAATTGTAACGGTTAA
NM_004938	1612	DAPK1	death-associated protein kinase 1	AAGCATGTAATGTTAATGTTA	CGGCTATTACTCTGTGGCCAA
NM_004954	2011	MARK2	MAP/microtubule affinity-regulating kinase 2	CACCTCTAATTCTTACTCTAA	CCACCTCTAATTCTTACTCTA
NM_004972	3717	JAK2	Janus kinase 2 (a protein tyrosine kinase)	AGCCATCATACGAGATCTTAA	CTGCCTTACGATGACAGAAAT
NM_005009	4833	NME4	non-metastatic cells 4, protein expressed in	ACCAACTACCTCCGTCAGCAA	CAGCACATGGGTGGTACACTA
NM_005012	4919	ROR1	receptor tyrosine kinase-like orphan receptor 1	CCCAGTGAGTAATCTCAGTAA	CCGTACTGCGATGAAACTTCA
NM_005026	5293	PIK3CD	phosphoinositide-3-kinase, catalytic, delta polypeptide	CCGGTCACGCATGAAGGCAAA	CGCCGTGATCGAGAAAGCCAA
NM_005027	5296	PIK3R2	phosphoinositide-3-kinase, regulatory subunit, polypeptide 2 (p85 beta)	CCGCGAGTATGACCAGCTTTA	TTGGTACGTGGGCAAGATCAA
NM_005028	5305	PIP5K2A	phosphatidylinositol-4-phosphate 5-kinase, type II, alpha	ATGGAATTAAGTGCCATGAAA	CTGCCCGATGGTCTTCCGTAA
NM_005030	5347	PLK1	polo-like kinase 1 (Drosophila)	CCGGATCAAGAAGAATGAATA	CGCGGGCAAGATTGTGCCTAA
NM_005044	5613	PRKX	protein kinase, X-linked	CGGATGGGATTCACTTAAGAA	TTGGAATACTCTAAGAGAATA
NM_005100	9590	AKAP12	A kinase (PRKA) anchor protein (gravin) 12	ACGGATGTAGTGTTGAAAGTA	CCCGAAATAATCGAACAGATT
NM_005108	9942	XYLB	xylulokinase homolog (H. influenzae)	CTGAAATTATTGGACGTCATA	TCAGGACTCCAGCTAAATCAA
NM_005109	9943	OSR1	oxidative-stress responsive 1	CTGGAGTAGGGACTAACTATA	TAGGGACTAACTATAGCACAA
NM_005157	25	ABL1	v-abl Abelson murine leukemia viral oncogene homolog 1	ACGCACGGACATCACCATGAA	CCAGTGGAGATAACACTCTAA
NM_005158	27	ABL2	v-abl Abelson murine leukemia viral oncogene homolog 2 (arg, Abelson-related gene)	ATCAAGCATCCTAATCTGGTA	CCCAAGTGTAATAAGCCTACA
NM_005160	157	ADRBK2	adrenergic, beta, receptor kinase 2.	AAGATGTTCAGTGTTGGGTAA	CAAGTGTATGGGATTAACTAA
NM_005163	207	AKT1	v-akt murine thymoma viral oncogene homolog 1	ACGCTACTTCCTCCTCAAGAA	CACGCTTGGTCCCGAGGCCAA
NM_005184	808	CALM3	calmodulin 3 (phosphorylase kinase, delta)	CACCAATTGATTGACTGAGAA	CCGCAGAGCTGCGTCACGTAA
NM_005204	1326	MAP3K8	mitogen-activated protein kinase kinase kinase 8	AAGAAAGTGATCCATCATGAT	AGAGATTGATTTATTAATTAA
NM_005228	1956	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	CCCATCCAATTTATCAAGGAA	CCCGTCGCTATCAAGGAATTA
NM_005232	2041	EPHA1	EphA1	CAGATGGGATCCCGTATCGAA	TACCTCAGTAATCACAATTAT
NM_005233	2042	EPHA3	EphA3	TCGGATATGATTGTTTCTCAA	TTGGATAGTTTCCTACGTAAA
NM_005235	2066	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	CTACGTGTTAGTGGCTCTTAA	TCGGGATTTGGCAGCCCGTAA
NM_005246	2241	FER	fer (fps/fes related) tyrosine kinase (phosphoprotein NCP94)	CAGAACAACTTAGTAGGATAA	CAGATAGATCCTAGTACAGAA
NM_005248	2268	FGR	Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog	CACGTGGAACGGCAGCACTAA	CAGACCTTGTCTAGTTATTTA
NM_005255	2580	GAK	cyclin G associated kinase	ACGCGTGTGACATTCAAGAAA	CCCGTGGTTGTCTGTACAGAA
NM_005308	2869	GRK5	G protein-coupled receptor kinase 5	AGCGTCATAACTAGAACTGAA	CAGGAACAACGCGGTAGGCAA
NM_005356	3932	LCK	lymphocyte-specific protein tyrosine kinase	AAGGGCCAGGACTTTATCTAA	CGCCATTACACCAATGCTTCA
NM_005372	4342	MOS	v-mos Moloney murine sarcoma viral oncogene homolog	CGCGAACATCTTGATCAGTGA	CTCGGTGTACAAGGCGACTTA
NM_005391	5165	PDK3	pyruvate dehydrogenase kinase, isoenzyme 3	AACGTTGTAGGTTGAAACTGA	TTCATTAGCACTAACATCCAA
NM_005399	5565	PRKAB2	protein kinase, AMP-activated, beta 2 non-catalytic subunit	ACCCAAAGTACTACTCATTTA	TCCAATATTAGTTGGAGTTAA
NM_005400	5581	PRKCE	protein kinase C, epsilon	CACGGAAACACCCGTACCTTA	CCCGACCATGGTAGTGTTCAA
NM_005406	6093	ROCK1	Rho-associated, coiled-coil containing protein kinase 1	AACGGTTAGAACAAGAGGTAA	CAAGCTCGAATTACATCTTTA
NM_005417	6714	SRC	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	AAGCAGTGCCTGCCTATGAAA	CGGCTTGTGGGTGATGTTTGA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_005424	7075	TIE	tyrosine kinase with immunoglobulin and epidermal growth factor homology domains	CCCAGTGAGAACGTGACGTTA	GCGCTTCAAGGTCAATGTGAA
NM_005433	7525	YES1	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	CCAGCCTACATTCACTTCTAA	GAGGCTCCTGCTTATTTATAA
NM_005456	9479	MAPK8IP1	mitogen-activated protein kinase 8 interacting protein 1	CTGGAGGAGTTTGAGGATGAA	TGGCATCAGCTTACAGTGCAA
NM_005476	10020	GNE	glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase	ATGGAAATACATATCGAATGA	CCCGATCATGTTTGGCATTAA
NM_005546	3702	ITK	IL2-inducible T-cell kinase	CAGGACTTTAGTAGAGACTGA	CTGGTGAGTTAAGTAAGATTA
NM_005569	3985	LIMK2	LIM domain kinase 2	CAGGAGGAATCTGTTACTCGA	CAGGGTGAACCTGCCTGTGAA
NM_005592	4593	MUSK	muscle, skeletal, receptor tyrosine kinase	ACGGCCTGGAATGAACTGAAA	CCCACCAATGACGTCCTCAAA
NM_005607	5747	PTK2	PTK2 protein tyrosine kinase 2	CACCTGGGTACTGGTATGGAA	CCGGTCGAATGATAAGGTGTA
NM_005627	6446	SGK	serum/glucocorticoid regulated kinase	CACAGCTGAAATGTACGACAA	CTGGGCTGTGATGACGAATAT
NM_005734	10114	HIPK3	homeodomain interacting protein kinase 3	CACGTTTGGCCAGGTAGTTAA	CTCATTCTGGTTGGAGATTAA
NM_005751	10142	AKAP9	A kinase (PRKA) anchor protein (yotiao) 9	CAGCCTATCAGTGAACATCAA	CAGCTTCAAAGGGATATACAA
NM_005781	10188	ACK1	activated Cdc42-associated kinase 1	ACGCAAGTCGTGGATGAGTAA	CGGCAGTCAGATCCTGCATAA
NM_005793	10201	NME6	non-metastatic cells 6, protein expressed in (nucleoside-diphosphate kinase)	CAGACTTCTCCTAGACATCTA	CAGGATCTAGCCTTCTATCTA
NM_005813	23683	PRKCN	protein kinase C, nu	CACGATATGTCAGTACTGCAA	CGGGAGAGTGTTACCATTGAA
NM_005858	10270	AKAP8	A kinase (PRKA) anchor protein 8	CAAGGTTAGCACGCAACAGAA	GAGGCCGGTAGTGATCCTCAA
NM_005876	10290	APEG1	aortic preferentially expressed protein 1	AACACCTATTTCTTAACTCAA	CAGCTGGAATAACAAGCCCAA
NM_005881	10295	BCKDK	branched chain alpha-ketoacid dehydrogenase kinase	AACGCCCACCATGATGCTCTA	CAGAACTTGGAGAGCAGGGAA
NM_005884	10298	PAK4	p21(CDKN1A)-activated kinase 4	CGGCGCCGAGCCGATGAGTAA	CTGGACAACTTCATCAAGATT
NM_005906	4117	MAK	male germ cell-associated kinase	CACAGTGTTGATATATGGGTA	CCGGATATAATCGATCAGGTT
NM_005922	4216	MAP3K4	mitogen-activated protein kinase kinase kinase 4	CACCAATCCCTGAAAGATTAA	CTCAAGCATCGCATAGTTTAA
NM_005923	4217	MAP3K5	mitogen-activated protein kinase kinase kinase 5	CAGCGAGTAGATAATATCGAA	CCGGGAATCTATACTCAATGA
NM_005965	4638	MYLK	myosin, light polypeptide kinase	AACCTGAAATCCGCTAGCAAA	CAGCATCCATGGCTAATGAAA
NM_005975	5753	PTK6	PTK6 protein tyrosine kinase 6	CCGGGTCCAGGTGGCCATTAA	CGGGTTAGCCAGGCTTATCAA
NM_005983	6502	SKP2	S-phase kinase-associated protein 2 (p45)	AAGTGATAGTGTCATGCTAAA	ACCCTTCAACTGTTAAAGGAA
NM_005990	6793	STK10	serine/threonine kinase 10	CACGGAATTAGAGAACCTGGA	CAGCTCAAACTGATGAAGAAA
NM_006035	9578	CDC42BPB	CDC42 binding protein kinase beta (DMPK-like)	CGCCGAGATATTCCATGTATA	TAGGACCTTAAGAGAATAGTA
NM_006116	10454	MAP3K7IP1	mitogen-activated protein kinase kinase kinase 7 interacting protein 1	CACCTTGGACAAGCCACACAA	CTGCAGGTGAGAGGATTTAAA
NM_006176	4900	NRGN	neurogranin (protein kinase C substrate, RC3)	AAGCCGGACGACGACATTCTA	TGGGTTGGAATGTGAACAATA
NM_006180	4915	NTRK2	neurotrophic tyrosine kinase, receptor, type 2	ACCACGAACAGAAGTAATGAA	CTGACGAGTTTGTCTAGGAAA
NM_006182	4921	DDR2	discoidin domain receptor family, member 2	ACGCACTGTCAGTTACACCAA	CCGGTTCATTCCAGTCACCGA
NM_006201	5127	PCTK1	PCTAIRE protein kinase 1	CACCATAATCGCTGTATGAAA	CACGCCAACATCGTTACGCTA
NM_006206	5156	PDGFRA	platelet-derived growth factor receptor, alpha polypeptide	ACGCAGGAAGCCTACTATTTA	CGCAGGAAGCCTACTATTTAA
NM_006212	5208	PFKFB2	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	CCAGAGCAAGATAGTCTACTA	CCGTGACAAGCCAACTAACAA
NM_006213	5260	PHKG1	phosphorylase kinase, gamma 1 (muscle)	CAAGAGCCTGCAAGCACTTAA	CCGGGAGATCGTCATCCGAGA
NM_006218	5290	PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide	CTGAGTCAGTATAAGTATATA	TGCGAAATTCTCACACTATTA
NM_006219	5291	PIK3CB	phosphoinositide-3-kinase, catalytic, beta polypeptide	CCCTTCGATAAGATTATTGAA	TCGGGAAGCTACCATTTCTTA
NM_006251	5562	PRKAA1	protein kinase, AMP-activated, alpha 1 catalytic subunit	CCCACGATATTCTGTACACAA	TCGGGATCAGTTAGCAACTAT
NM_006252	5563	PRKAA2	protein kinase, AMP-activated, alpha 2 catalytic subunit	ACGACTAAGCCCAAATCTTTA	CCGATTTCGGATTATCTAATA
NM_006253	5564	PRKAB1	protein kinase, AMP-activated, beta 1 non-catalytic subunit	CACGTCTAGAAGTCACATGAA	CTGGCTATGGAACTAAATACA
NM_006254	5580	PRKCD	protein kinase C, delta	CCGCTTCAAGGTTCACAACTA	CCGGGACACTATATTCCAGAA
NM_006255	5583	PRKCH	protein kinase C, eta	CGCCGTGTGCTCATCACTGAA	GACCAGATTTGTGGCTTATAA
NM_006256	5586	PRKCL2	protein kinase C-like 2	AAAGTATGATATCTACGCAAA	CACGTCAAAGTATGATATCTA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_006257	5588	PRKCQ	protein kinase C, theta	CCGCAGACAAGTAATCACTAA	CGGGCAGATGTATATCCAGAA
NM_006258	5592	PRKG1	protein kinase, cGMP-dependent, type I	CCGGTGTATATACCATACAAA	GAGGTTCGTTTGAAGATTCTA
NM_006259	5593	PRKG2	protein kinase, cGMP-dependent, type II	GACCTACAATTTGATTCTCAA	TTGAGTACTACTAACGTTTAA
NM_006281	6788	STK3	serine/threonine kinase 3 (STE20 homolog, yeast)	CCGGCGCCTAAGAGTAAACTA	CGGCGCCTAAGAGTAAACTAA
NM_006282	6789	STK4	serine/threonine kinase 4	AGGATTCATAGCATCACTATA	CACCATTTGCTGTGCGAATTA
NM_006285	7016	TESK1	testis-specific kinase 1	CAGGACCGCCCTGACACACAA	CTGCGGTACCTGCACTCCAAA
NM_006293	7301	TYRO3	TYRO3 protein tyrosine kinase	AACGGTGACCTTTAGTGCCAA	CGGACTGACCAAATCACCCAA
NM_006296	7444	VRK2	vaccinia related kinase 2	CACACAATAGGTTAATCGAAA	CTGGAGGATTTGGATTGATAT
NM_006301	7786	MAP3K12	mitogen-activated protein kinase kinase kinase 12	CAGGGAGCACTATGAAAGGAA	CTCGTATTCCTTGTACATAGA
NM_006314	10256	CNK1	connector enhancer of KSR-like (Drosophila kinase suppressor of ras)	CCGCCGCTGGTTTGTGCTCAA	CGGACTCAGCTTAGTGCTGAA
NM_006343	10461	MERTK	c-mer proto-oncogene tyrosine kinase	CAGATGAATGTTGTTAAGGAA	TTGCCTGACGTTCGGAACCAA
NM_006374	10494	STK25	serine/threonine kinase 25 (STE20 homolog, yeast)	AAGGGCATCGATAACCACACA	CACCAAGCTATGGATCATCAT
NM_006383	10518	KIP2	DNA-dependent protein kinase catalytic subunit-interacting protein 2	CACCGAAGAGCAGCTAGACAA	CTGCACCTTCTTCAATAAGAA
NM_006422	10566	AKAP3	A kinase (PRKA) anchor protein 3	AGGGATCATGACCTATGCTAA	ATCAAGCTATCCATAATGAAA
NM_006457	10611	LIM	LIM protein (similar to rat protein kinase C-binding enigma)	CAGCAGGGAAACGAACTCCGA	TCCGATGTGCGCCCATTGTAA
NM_006549	10645	CAMKK2	calcium/calmodulin-dependent protein kinase kinase 2, beta	CCGCAAGATCTTCTCTGGGAA	CTAGCTGATTGTTGTGGTCAA
NM_006556	10654	PMVK	phosphomevalonate kinase	CCCAGTGTGGATACTAATAAA	TTGGCTGTGCTTGAAGGCGAA
NM_006575	11183	MAP4K5	mitogen-activated protein kinase kinase kinase kinase 5	CTTGCCTATTTGCATACTAAA	TCCGCTTATTAGGATCAGACA
NM_006609	10746	MAP3K2	mitogen-activated protein kinase kinase kinase 2	CACAGTAATATGATTGTCCTA	CAGAATGATGTCCGAGTCAAA
NM_006622	10769	PLK2	polo-like kinase 2 (Drosophila)	CAGATGCTCCTGAGCAATTTA	CAGATTGTGTCTGGACTGAAA
NM_006648	65268	PRKWNK2	protein kinase, lysine deficient 2	AACGTTCATCGAGCAGATGAA	ACCTATAAGTCTAGTAGCAAA
NM_006712	10922	FASTK	FAST kinase	CAGCAGCAAGGTGGTACAGAA	CTGGTGGTTCAGGAAACGCAA
NM_006716	10926	ASK	activator of S phase kinase	CAGTATCAAGTTGTTGATGAT	CATGAATCTATTGTCACTAAA
NM_006738	11214	AKAP13	A kinase (PRKA) anchor protein 13	CCGCCTGTTTGGGTTAACAAA	CTCGGTGTTTCAGGCACTAAA
NM_006742	5681	PSKH1	protein serine kinase H1	CCCGATTAGGGTCGAGTGTCA	CCGCTCCACACGCTCCAATAA
NM_006759	7360	UGP2	UDP-glucose pyrophosphorylase 2	CCCAAAGTTAGTTACTCTTAA	CGAGTTCAAGTCTGTATCAAA
NM_006852	11011	TLK2	tousled-like kinase 2	AAGGTTCATCTGTCCATGCAA	CAAGAGAATACGATTCTTAAA
NM_006871	11035	RIPK3	receptor-interacting serine-threonine kinase 3	ACCGCTCGTTAACATATACAA	CAGCCTGATGTCGTGCGTCAA
NM_006875	11040	PIM2	pim-2 oncogene	CCGGGATTGTCCAATTACTAA	CGGGATTGTCCAATTACTAAA
NM_006888	801	CALM1	calmodulin 1 (phosphorylase kinase, delta)	CGGCAACTTACACACATTGAA	CTGGTTGTATCTTATTAGCAA
NM_006904	5591	PRKDC	protein kinase, DNA-activated, catalytic polypeptide	CTCGTGTATTACAGAAGGAAA	TTCGGCTAACTCGCCAGTTTA
NM_006930	6500	SKP1A	S-phase kinase-associated protein 1A (p19A)	AGGGTACTTTAGAGCAACTTA	TAGGAAAGACTACTCAAGTTA
NM_007064	11139	TRAD	serine/threonine kinase with Dbl- and pleckstrin homology domains	CAGGACATCAATCAAGTCTTA	CCCATTGAGTATCAACGGAAA
NM_007118	7204	TRIO	triple functional domain (PTPRF interacting)	ACCGTTGTTCTTAGATGTCGA	CCGGGAATGTATGGATACGTA
NM_007170	10420	TESK2	testis-specific kinase 2	CCGGGAAGAATCGCTATCTGA	CGAGATGAGCCCTATAATGAA
NM_007174	11113	CIT	citron (rho-interacting, serine/threonine kinase 21)	ATGGAAGGCACTATTTCTCAA	CAGGATATACCGTAACACGAA
NM_007181	11184	MAP4K1	mitogen-activated protein kinase kinase kinase kinase 1	CTGACTAAGAGTCCCAAGAAA	TACGTGGGTGTACTCCATCAA
NM_007194	11200	CHEK2	CHK2 checkpoint homolog (S. pombe)	ACGCCGTCCTTTGAATAACAA	AGGACTGTCTTATAAAGATTA
NM_007199	11213	IRAK3	interleukin-1 receptor-associated kinase 3	CACATTCGAATCGGTATATTA	CTGGATGTTCGTCATATTGAA
NM_007202	11216	AKAP10	A kinase (PRKA) anchor protein 10	CAGATAAGCATAGAACTGATA	TAGCAGGACAGCCACACTTAA
NM_007229	11252	PACSIN2	protein kinase C and casein kinase substrate in neurons 2	CACCCTTAATGTCCCGAGCAA	GAAGCTTTACATAGAACCTTA
NM_007254	11284	PNKP	polynucleotide kinase 3'-phosphatase	CACGTGAACAGGGACACGCTA	CACGTGTGAGACAGCCCTGAA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_007271	11329	STK38	serine/threonine kinase 38	AACCTTATCGCTCAACATGAA	TACGTCGGCCATAAACAGCTA
NM_007284	11344	PTK9L	PTK9L protein tyrosine kinase 9-like (A6-related protein)	AAGACAGAGATCAGTGTGGAA	TTGGGATGGTTGAATGCTGTA
NM_012145	1841	DTYMK	deoxythymidylate kinase (thymidylate kinase)	ATCAGTTGGAATTCTCCTAAA	TCCCGGAAAGATCAACTGAAA
NM_012290	9874	TLK1	tousled-like kinase 1	CAGAGAGTATAGAATACACAA	CCGGAGAAGAAACAATCGGAA
NM_012324	23542	MAPK8IP2	mitogen-activated protein kinase 8 interacting protein 2	ACAGGTAATGTCGGCTTCCAA	CTGGAAGAATTTGACGACGAA
NM_012395	5218	PFTK1	PFTAIRE protein kinase 1	AAGGGACACCTTTCACAGCTA	CTGGGTCTTGTCAACATCTAA
NM_012398	23396	PIP5K1C	phosphatidylinositol-4-phosphate 5-kinase, type I, gamma	CCGCGTCGTGGTCATGAACAA	CGGCAAGACCTATTTATAATA
NM_012407	9463	PRKCABP	protein kinase C, alpha binding protein	CCGGTGTCAATGGCAGGTCAA	TCGCCTCACCATCAAGAAGTA
NM_012424	26750	RPS6KC1	ribosomal protein S6 kinase, 52kDa, polypeptide 1	CAGGATTGGTTTATATGATTA	CCGGGTTGTTTCACGAAGAAA
NM_012474	7371	UMPK	uridine monophosphate kinase	CCGGATGCCTTTGACAATGAA	TCAGTACATTACGTTCGTCAA
NM_013233	27347	STK39	serine threonine kinase 39 (STE20/SPS1 homolog, yeast)	TGGAATAGTCTCAGATCTAAA	TTGGAGTATTTGTAACTTCTA
NM_013254	29110	TBK1	TANK-binding kinase 1	CAGAACGTAGATTAGCTTATA	CTGACTTGACACGTTTGTAAA
NM_013257	23678	SGKL	serum/glucocorticoid regulated kinase-like	ACCAACTAACTTACATGCTTA	CCACAGCGAGACCCTAGTTAA
NM_013276	23729	CARKL	carbohydrate kinase-like	ATGAAACATATTGTCTCTTTA	CAGGTAGTTTATTCAAAGAGA
NM_013302	29904	EEF2K	elongation factor-2 kinase	CAGACACTACATGAACACGAA	CGGGATGGCGCTCTTCTTCTA
NM_013355	29941	pknbeta	protein kinase PKNbeta	AGGGAAATACTACGCCATCAA	CCCGGGAAGTTTCAAGTTTGA
NM_013392	29959	NRBP	nuclear receptor binding protein	CCGGTTGACTTCTCTGCTAGA	TCGGTGGAGGAGGGAGTCAAA
NM_013410	205	AK3	adenylate kinase 3	CAGGAAGATGTGGTCATTCAT	CCTGGTAACAGTGAAATTGAA
XM_375834	9641	IKBKE	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon	ACGGCGGAACAAGGAGATCAT	CCGCATCATCGAACGGCTAAA
NM_014006	23049	SMG1	PI-3-kinase-related kinase SMG-1	ATCGATGTTGCCAGACTACTA	CACCATGGTATTACAGGTTCA
NM_014030	28964	GIT1	G protein-coupled receptor kinase-interactor 1	CAGCCTTGACTTATCCGAATT	GCCGCTGAGGATGTCCCGAAA
NM_014216	3705	ITPK1	inositol 1,3,4-triphosphate 5/6 kinase	CACGCCGTCATTGACATCAAT	CCGATTAATGTCTGTACGTCA
NM_014226	5891	RAGE	renal tumor antigen	AAAGAATAAGCTGTCGTTAAA	CCGGCTGTGTGTTCTACGAGA
NM_014264	10733	PLK4	polo-like kinase 4 (Drosophila)	CACCAAATGGTCAAACAACTA	CTGGTAGTACTAGTTCACCTA
NM_014308	23533	P101-PI3K	phosphoinositide-3-kinase, regulatory subunit, polypeptide p101	ACCGGTGCTGCTGCAACTCTA	ATCGCAGATCAAAGTGGACAA
NM_014326	23604	DAPK2	death-associated protein kinase 2	CGGAATTTGTTGCTCCAGAAA	CTGGTTAAAGAGACCCGGAAA
NM_014365	26353	HSPB8	heat shock 27kDa protein 8	CCGCATGGTTTGGTTAATGAA	CGCATGGTTTGGTTAATGAAA
NM_014370	26576	STK23	serine/threonine kinase 23	AAGATGAGGCGCAAACGGAAA	AAGCGCTTTGTGGCCCTCAAA
NM_014371	26993	AKAP8L	A kinase (PRKA) anchor protein 8-like	AAGGAACACTTTAAGTACGTA	CAGGATAACACCACCAACTAT
NM_014397	10783	NEK6	NIMA (never in mitosis gene a)-related kinase 6	ACCACGGAAGTCGAGAATTAA	ACCGGAGAGGATCCATGAGAA
NM_014413	27102	HRI	heme-regulated initiation factor 2-alpha kinase	CCCGAATATGACGAATCTGAT	CTGATTAAGGGTGCAACTAAA
NM_014496	27330	RPS6KA6	ribosomal protein S6 kinase, 90kDa, polypeptide 6	CAGCGGTATACTGCTGAACAA	GGCGAGGTAAATGGTCTTAAA
NM_014572	26524	LATS2	LATS, large tumor suppressor, homolog 2 (Drosophila)	CACACTCACCTCGCCCAATAA	CAGGACCTTCACTGCATTAAA
NM_014586	30811	HUNK	hormonally upregulated Neu-associated kinase	CACGGGCAAAGTGCCCTGTAA	TCGGACCAAGATCAAACCAAA
NM_014602	30849	PIK3R4	phosphoinositide-3-kinase, regulatory subunit 4, p150	AAGCAGAATTCTAGATCAGAA	TAGAGGCAGAAGATTACTTAA
NM_014683	9706	ULK2	unc-51-like kinase 2 (C. elegans)	ACCGGGAAGTTATCAGATCAA	ATCGGTACAGTTATTCTTAAA
NM_014720	9748	SLK	SNF1 sucrose nonfermenting like kinase (yeast)	CCAGATCAGGACCGTGATAAA	TAGCATCTTGTGATCACCCAA
NM_014776	9815	GIT2	G protein-coupled receptor kinase-interactor 2	AAGCATCGTGCAATAAGTGAA	CTGCCTATGGCTGAAACTATA
NM_014791	9833	MELK	maternal embryonic leucine zipper kinase	CGGGTTGTCTTCCGTCAGATA	CTGGATCATGCAAGATTACAA
XM_374996	9891	ARK5	AMP-activated protein kinase family member 5	CTTGAGTTGATGATCAATTAA	TAGGGATTTACTGGCATGGTA
NM_014911	22848	AAK1	AP2 associated kinase 1	AACGTGAGTAGCGGTGATGTA	CCAGGTGGTAAACCTGATGAA
NM_014916	22853	LMTK2	lemur tyrosine kinase 2	CACCTCCGACTTAAATGTGAA	CAGATCAGACTAAGTATAGTA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_014920	22858	ICK	intestinal cell (MAK-like) kinase	ACCTAATGACTTGGTAAATTA	CTCAGTAATCTAGCTTATATA
NM_015000	23012	STK38L	serine/threonine kinase 38 like	AGGGAGATGTACTGTATTATA	TACAACCATGATAACCATTAT
NM_015071	23092	GRAF	GTPase regulator associated with focal adhesion kinase pp125(FAK)	ACCGTATGGCCTATAGTTTAA	AGGGAGTATACTAGTAGGTTA
NM_015076	23097	CDK11	cyclin-dependent kinase (CDC2-like) 11	CACTGTCGTCAGGAAGATATA	GAGGATTTGTTTGAGTACGAA
NM_015093	23118	MAP3K7IP2	mitogen-activated protein kinase kinase kinase 7 interacting protein 2	CAGTCAATAGCCAGACCTTAA	TGGCTGGGTATCTCAGTTTAA
NM_015112	23139	MAST2	microtubule associated serine/threonine kinase 2	CAGGAGTGTGCTGTCTGGCAA	CAGTGAAATAATAATGATGAA
NM_015133	23162	MAPK8IP3	mitogen-activated protein kinase 8 interacting protein 3	CAGCCGCAACATGGAAGTACA	GACGAGTGGTCTGATGTTCAA
NM_015148	23178	PASK	PAS domain containing serine/threonine kinase	ATCCTGGTTGCTAACGACAAA	CGCGCTGACACTGTTTGGTTA
NM_015690	27148	STK36	serine/threonine kinase 36 (fused homolog, Drosophila)	ATGGATGCTGACCTCCTTATA	CCAGTTGGTGTCAGCCCTGTA
NM_015716	50488	MINK	misshapen/NIK-related kinase	CACGTACGGGCGCATCATTAA	CGCAGACTTTGTGTTGCTGAA
NM_015850	2260	FGFR1	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome)	CAGAGATTTACCCATCGGGTA	CCGGCCTCTATGCTTGCGTAA
NM_015978	51086	TNNI3K	TNNI3 interacting kinase	CAGCATTCGGCGTATACCTAA	GGAGCTAATGTCAATATTCAA
NM_015981	815	CAMK2A	calcium/calmodulin-dependent protein kinase (CaM kinase) II alpha	CAGGAACTTCTCCGGAGGGAA	CCAGGATTTCATCTCACCATA
NM_016086	51657	MK-STYX	map kinase phosphatase-like protein MK-STYX	AAGCTTCTGCACATCCGGATA	CAAGATTCAGAAGGACTTGAA
NM_016123	51135	IRAK4	interleukin-1 receptor-associated kinase 4	ATCCTATTAGTCATATATTTA	TTGCAGGACAGTGGTTATTAA
NM_016151	9344	TAO1	thousand and one amino acid protein kinase	AACGGAAACCACCGCTCTTTA	ATCGAGCTGGCTGAACGGAAA
NM_016203	51422	PRKAG2	protein kinase, AMP-activated, gamma 2 non-catalytic subunit	AAGCACGAGCCTGAACGGTTA	CCGGAAAGCATTCCTCTCGAA
NM_016223	29763	PACSIN3	protein kinase C and casein kinase substrate in neurons 3	AAGGATATGCTGCTCACCTTA	CAGAGGACAATCAGCCGGAAA
NM_016231	51701	NLK	nemo like kinase	CCGGATAGACCTATTGGATAT	TTGGTGTTGTCTGGTCAGTAA
NM_016248	11215	AKAP11	A kinase (PRKA) anchor protein 11	ACCGGTTATCTAAATCTATTA	CTGACCGGTTATCTAAATCTA
NM_016276	10110	SGK2	serum/glucocorticoid regulated kinase 2	CAGGGCCAATGGGAACATCAA	TGGGTACGTGACTATCCCTAA
NM_016281	51347	JIK	STE20-like kinase	CAAACAGTATAAAGCACTCAA	CAGCTCCTCCGTCGTGCATAA
NM_016282	50808	AK3L1	adenylate kinase 3 like 1	CCCGTGGCACTATGTAAATAA	CCGTGGCACTATGTAAATAAA
NM_016291	51447	IHPK2	inositol hexaphosphate kinase 2	AAGCATCGGAACCAGTACAAA	TCGGAACCAGTACAAATTTAT
NM_016308	51727	UMP-CMP	UMP-CMP kinase	AAGTATTGCTAAGTACTATAA	CGCGTATATATCCCTCTAGTA
NM_016440	51231	VRK3	vaccinia related kinase 3	AACCAGGGCATTCTCTATGAA	CTCACTCAAACTGGATGCCAA
NM_016457	25865	PRKD2	protein kinase D2	CACGACCAACAGATACTATAA	TTGGGTGGTTCATTACAGCAA
NM_016478	51530	NIPA	nuclear interacting partner of anaplastic lymphoma kinase (ALK)	AGGGAGAATGGTGGAACTGAA	CCGCTTGAGGCTCTCTATGAA
NM_016507	51755	CRK7	CDC2-related protein kinase 7	ACCGGATATCGGGAAGTTCAA	ATCGGGATATTAAGTGTTCTA
NM_016508	51265	CDKL3	cyclin-dependent kinase-like 3	CAACATTATTGTCATGGACTA	TGGGCAGATAGTGGCCATTAA
NM_016542	51765	MST4	Mst3 and SOK1-related kinase	CAGCAAGTCGTTGCTATTAAA	CCAAACCTACGTCAAGATTAA
NM_016653	51776	ZAK	sterile alpha motif and leucine zipper containing kinase AZK	ACGTGGTAGTATATCACTCAA	TCGGGTAGCAACAAACTTATT
NM_017431	53632	PRKAG3	protein kinase, AMP-activated, gamma 3 non-catalytic subunit	CAGATCTATGAGATTGAACAA	TAGCCTGTTTGAAGCTGTCTA
NM_017449	2048	EPHB2	EphB2	CACGCTTTCTAGAGGACGATA	CCGAGAGGACCTCGTCTACAA
NM_017567	55577	NAGK	N-acetylglucosamine kinase	ACCTGAGTGAAAGCTACTTAA	CCCGGTCTTGTTCCAGGGCAA
NM_017572	2872	MKNK2	MAP kinase-interacting serine/threonine kinase 2	CCGCTTCTACCTGGTGTTTGA	TTGGACTTTCTGCATAACAAA
NM_017593	55589	BMP2K	BMP2 inducible kinase	AGGCATCACCTGAATATCTTA	TCCGATGTGCATTGAAGCGAA
NM_017719	54861	SNRK	SNF-1 related kinase	ACCACTGAATTGGAACGGATA	CACCACTGAATTGGAACGGAT
NM_017771	54899	PXK	PX domain containing serine/threonine kinase	CTGGCAGATTGTTAGAAGATA	TAAGATCCCTACAAAGTTAAA
NM_017859	54963	URKL1	uridine kinase-like 1	ACCCAGGACTGTTGAATACAA	TACAATGAACACGGCACGCAA
NM_017900	54998	AKIP	aurora-A kinase interacting protein	ATCCGTAGTAATAAATTCTCA	CTGCTGTGATCCGTAGTAATA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_018216	55229	PANK4	pantothenate kinase 4	CTGGGAGACGTTCATATTGGA	TCGACATAGGCGGGTCGTTAA
NM_018323	55300	PI4K2B	phosphatidylinositol 4-kinase type-II beta	ATGAACTTTGTGCAAGATTTA	CAGAGTACTGGCCTTGTTCAA
NM_018339	55312	FLJ11149	riboflavin kinase	ACGATGTAATTTAATGCTAAA	CACGATGTAATTTAATGCTAA
NM_018343	55781	RIOK2	RIO kinase 2 (yeast)	AACGCGATTATCATAAACATA	CGCGGTTGAAATGGGCATGAA
NM_018401	55351	HSA250839	gene for serine/threonine protein kinase	CTGGGACGCGGTGTTCAAGAA	TTGGGCTGAGTTCACGAATTA
NM_018425	55361	PI4KII	phosphatidylinositol 4-kinase type II	ACGCAAATGTATGAATAACAA	CCGCATCGGGCTACCACCAAA
NM_018492	55872	TOPK	T-LAK cell-originated protein kinase	AAGTGTGGCTTGCGTAAATAA	TCAGTAGTTATTAGACTCTAA
NM_018571	55437	ALS2CR2	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 2	CAGGAACACTGGTAACTATAA	CCAGTGGAACTCACACAGTAA
NM_018584	55450	CaMKIINalpha	calcium/calmodulin-dependent protein kinase II	AGCAAGCGGGTTGTTATTGAA	CGGGTTGTTATTGAAGATGAT
NM_018638	55500	EKI1	ethanolamine kinase	CCGTATGTGGTGGATTAGAAA	TCCGTATGTGGTGGATTAGAA
NM_018650	4139	MARK1	MAP/microtubule affinity-regulating kinase 1	CCCGGTGTAGAAACTCCATTA	CCGGCCCAGTAGTGACTTAAA
NM_018842	55971	LOC55971	insulin receptor tyrosine kinase substrate	CACGGAGAGCACCTACCGGAA	CTCAACGAGAGTCTTGATGAA
NM_018979	65125	PRKWNK1	protein kinase, lysine deficient 1	CTAGAGGATCTTGATGCTCAA	CTGCGACGACTACGAGATAAA
NM_019884	2931	GSK3A	glycogen synthase kinase 3 alpha	CAGGGAACTAGTCGCCATCAA	CCGGGTGTAAATAGATTGTTA
NM_020126	56848	SPHK2	sphingosine kinase 2	CAGGATTGCGCTCGCTTTCAT	CCGAGGGTAGTGCCTGATCAA
NM_020168	56924	PAK6	p21(CDKN1A)-activated kinase 6	CGGAAGGACCATGTTCCGCAA	CTGTGTTACCTTTCAAGTTTA
NM_020240	56990	SPEC2	non-kinase Cdc42 effector protein SPEC2	AAGGGAGGTTATGGAGGTGGA	CAGGAGACCTGTTCAGTGGAA
NM_020397	57118	CAMK1D	calcium/calmodulin-dependent protein kinase ID	CAGGCGCTTTCTATACTTAAT	CCAGGCGCTTTCTATACTTAA
NM_020421	57143	ADCK1	aarF domain containing kinase 1	TAACAAGTACTTGGACCCTAA	TACGACGGCTGTCATCAGTTA
NM_020439	57172	CAMK1G	calcium/calmodulin-dependent protein kinase IG	AACAGGCCGCCTGAAACTCAA	CAGGTCTTGTCGGCAGTGAAA
NM_020526	2046	EPHA8	EphA8	ACGGCCCACCAGGGTATGTAA	GAGCGTGTGCTTATCCGTTAA
NM_020639	54101	ANKRD3	ankyrin repeat domain 3	AAGCCTGATGACGAAGTGAAA	CACACGCAGTATGAAGATAAA
NM_020666	57396	CLK4	CDC-like kinase 4	AAGTCTGACTATGTAGTCAAA	TCGAAGAATGTTAGAATATGA
NM_020804	29993	PACSIN1	protein kinase C and casein kinase substrate in neurons 1	CAGCAGCTACATCCATGTGTA	CGCCATAGAGTTCCAGACATA
NM_020836	57596	KIAA1446	brain-enriched guanylate kinase-associated protein	CGGGCGGACCATGTCACCGTA	CTGCAGCTTCTCTGAACGCTA
NM_020922	65267	PRKWNK3	protein kinase, lysine deficient 3	AAGATTGGTGATCTAGGATTA	CCGGGTGACGCCAATAAAGAA
NM_020965	260425	MAGI-3	membrane-associated guanylate kinase-related (MAGI-3)	CCCTATGATGTTGTCTTGCAA	CGGGATGTCGAAGACGCTGAA
NM_020975	5979	RET	ret proto-oncogene (multiple endocrine neoplasia and medullary thyroid carcinoma 1, Hirschsprung disease)	CCGCTGGTGGACTGTAATAAT	TAGGCTGGTTCTCAACCGGAA
NM_020990	1159	CKMT1	creatine kinase, mitochondrial 1 (ubiquitous)	ACGGATCTAGATGCCAGTAAA	CTGGACGTTACTATAGGCTCA
NM_021135	6196	RPS6KA2	ribosomal protein S6 kinase, 90kDa, polypeptide 2	CCGAGTGAGATCGAAGATGGA	CCGGAGGTCCTGAAGCGTCAA
NM_021733	60385	TSKS	testis-specific kinase substrate	AACCAACGTCTTGAAGCAGAA	CACCAACGTGTCACTGCTCAA
NM_021970	8649	MAP2K1IP1	mitogen-activated protein kinase kinase 1 interacting protein 1	ATGCCCAGGCTTGCAGAATAA	TAGCATATAGATGTAATTTAT
NM_021972	8877	SPHK1	sphingosine kinase 1	CACGAACCAAATCCAAATAAA	CCGGCTGCTGTCACCCATGAA
NM_022048	53944	CSNK1G1	casein kinase 1, gamma 1	ATGGACCATCCTAGTAGGGAA	CCGGCAGACCAATACCTCATA
NM_022128	64080	RBKS	ribokinase	AACACAGTCATCTTACCCTTA	CAGGTGGTAATCATTACCTTA
NM_022158	64122	FN3K	fructosamine-3-kinase	CCAGCTGTTTAACTACCTGAA	CCCAGTGTTCGTCAAAGTCAA
NM_022344	64149	NJMU-R1	protein kinase Njmu-R1	TTGAGTTACACTCCTGTTGAA	TTGGCAGATACTAATCTACCA
NM_022445	27010	TPK1	thiamin pyrophosphokinase 1	AACCTGGTGCATCGAAATGTA	CAGGTTGTCTGTAGAGAATGA
NM_022731	64710	NUCKS	nuclear ubiquitous casein kinase and cyclin-dependent kinase substrate	AAGGTGTACCACGGTTGTAAA	ACCCTAGAATTTAATCAACAA
NM_022740	28996	HIPK2	homeodomain interacting protein kinase 2	AACCAGTACCCTTACATATAA	TCCCGAAGTCTCCATACTAAA
NM_023018	65220	FLJ13052	NAD kinase	AAAGAGCGTCCTTGTCATCAA	CCAGGAGAACATGATCGTGTA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_024117	79109	MAPKAP1	mitogen-activated protein kinase associated protein 1	CTAGGTATCTCTGGAGACAAA	GACCCTGTTACGAATCAGAAA
NM_024594	79646	PANK3	pantothenate kinase 3	AAGCGAGAATCTGTTAGTAAA	TCCAAAGGTGATAGCACACAA
NM_024779	79837	PIP5K2C	phosphatidylinositol-4-phosphate 5-kinase, type II, gamma	CCGGAGCAGTATGCTAAGCGA	TTGATGTGTGATAATCTCATA
NM_024800	79858	NEK11	NIMA (never in mitosis gene a)- related kinase 11	CTGCCTATGCTTGGAGTCATA	TGAGATAAGCTTATAGATCAA
NM_024876	79934	ADCK4	aarF domain containing kinase 4	CAGATGCTGAGAGTTCTTGAA	CCGGGTCCCAGCCGTGGTTAA
NM_024960	80025	PANK2	pantothenate kinase 2 (Hallervorden-Spatz syndrome)	CAGAGCGACTTTGATCACCAT	CTGTGTGTGAACTTACTGTAA
NM_025144	80216	LAK	lymphocyte alpha-kinase	CAGCCCTTGGTCCTATCTGAA	CAGGCCCTACATTTAAAGCTA
NM_025194	80271	ITPKC	inositol 1,4,5-trisphosphate 3-kinase C	CCGGAAGGACATGTATGAGAA	TCGGCCGAAGCCCGAACCGAA
NM_025211	80318	GKAP42	protein kinase anchoring protein GKAP42	AACGCTCAACATGATCTTCCA	CATGCTGTTTGTAACGCTCAA
NM_025228	80342	T3JAM	TRAF3-interacting Jun N-terminal kinase (JNK)-activating modulator	CAGACTTGGCACCAACATTAA	TAGCAGGGACTTACAGATGAA
NM_030662	5605	MAP2K2	mitogen-activated protein kinase kinase 2	CAGCATTTGCATGGAACACAT	CCGGCCTGCCATGGCCATCTT
NM_030906	65975	STK33	serine/threonine kinase 33	ATGTGTCTAGTGCATCCTTAA	CAGGATGGTAATAGGTTAAGA
NM_030952	81788	SNARK	likely ortholog of rat SNF1/AMP-activated protein kinase	CCGGTGGCTGTTGATGGTGAA	CTGAACGAAGAGGATACTAAA
NM_031414	56164	STK31	serine/threonine kinase 31	CACAGTACAAGCTAAGTACAA	CCCAGTGTGGATCACTTGCTA
NM_031417	57787	MARK4	MAP/microtubule affinity-regulating kinase 4	CCGCATCATGAAGGGCCTAAA	CTGCAGCCTGTTGCCCAATAA
NM_031432	83549	UCK1	uridine-cytidine kinase 1	AACGGTGGAGGTGCCGACCTA	TGCGGTTTAAAGATCCCTCTA
NM_031464	83694	RPS6KL1	ribosomal protein S6 kinase-like 1	CGCGATGTTAGTGAGGACTAT	CTGAATTTGATTGGAAAGGAA
NM_031480	83732	RIOK1	RIO kinase 1 (yeast)	GCCCAACAAGATAATATTCTA	TACCATGTCCAGAACCAATAA
NM_031892	30011	SH3KBP1	SH3-domain kinase binding protein 1	CTCTGAGATCTCAATGCGAAA	TAGCTTATATATGACGGTATA
NM_032017	83931	MGC4796	Ser/Thr-like kinase	CAGCGCTACCTGCGGAAATAA	CCGGATGGTTAAGAAGATGAA
NM_032028	83942	STK22D	serine/threonine kinase 22D (spermiogenesis associated)	CCAGCTTTCCTTGGCCATCAA	TAGAAGCTGATTTAACACCAA
NM_032037	83983	SSTK	serine/threonine protein kinase SSTK	ATCGAGGTGTGCAACGGGAAA	CCGGTTGGAACCTGCAATAAA
NM_032294	84254	CAMKK1.	calcium/calmodulin-dependent protein kinase kinase 1, alpha	AGCGATGAGCAAACTCTATAA	CGGCGTTATCTGGAAAGTGGA
NM_032387	65266	PRKWNK4	protein kinase, lysine deficient 4	CAGCTTGTTGGGCGTTTCCAA	CAGGAGGAGCCAGCACCATTA
NM_032409	65018	PINK1	PTEN induced putative kinase 1	CCGGACGCTGTTCCTCGTTAT	GACGCTGTTCCTCGTTATGAA
NM_032435	84451	KIAA1804	mixed lineage kinase 4	ACGGACCATGTCTGATGGAAA	CGGGAACTTAACATTCTGATA
NM_032630	51550	CINP	cyclin-dependent kinase 2-interacting protein	CGGCTGATTGGCACAATTTAA	GCGGCTGATTGGCACAATTTA
NM_033116	91754	NEK9	NIMA (never in mitosis gene a)- related kinase 9	CACGAACCAGTGAAGTCTATA	TACACTTGGGTGAACATGCAA
NM_033118	85366	MYLK2	myosin light chain kinase 2, skeletal muscle	AACGCTGTAACCGACGCCTTA	CGGGATCCTCTTCATGCACAA
NM_033126	85481	PSKH2	serine/threonine kinase PSKH2	AAGGACTTTATAGACAAACTA	GAGGATCAAGTTTACATGGTA
NM_033214	2712	GK2	glycerol kinase 2	CTCGGGTGTGCCATAATAATA	TACGTTAGAAGAGCACTGTAA
XM_370946	10595	LOC388226	similar to protein kinase/ribonuclease IRE1 beta	AAGGATGAAACTGGCTTCTAT	CACCTGCATTCTTTACACATA
NM_033498	3098	HK1	hexokinase 1	CACGATGTAGTCACCTTACTA	CCGTGTCGTATGACCTAGTAA
NM_033516	89882	NYD-SP25	protein kinase NYD-SP25	ATGGACCTAACTATACATCTT	TAGACGAAATGTGCCATTATA
NM_052841	81629	STK22C	serine/threonine kinase 22C (spermiogenesis associated)	ATGGCAAGTGCTCTCCAATAA	TGGCAAGTGCTCTCCAATAAA
NM_052853	90956	ADCK2	aarF domain containing kinase 2	CAGATTGACCTGCGTTACGAA	CCGGAATGTGAAAGCCGTCAA
NM_052902	114790	STK11IP	serine/threonine kinase 11 interacting protein	AAAGTTGTTTCCAACTCATAA	CTCTGCGTTTCTTGAACCTAA
NM_052947	115701	HAK	heart alpha-kinase	AGCGAAGACCTTGGCATTTAT	CGGCCTCATGCCTGTCTTCAA
NM_053006	23617	STK22B	serine/threonine kinase 22B (spermiogenesis associated)	CAAGTTCAATGTGGCTGTCAA	GTCGGCCTTCACGTAAACTAA
NM_054111	117283	IHPK3	inositol hexaphosphate kinase 3	AAGACTGGTGGACAAGTGTAA	CTGAGATACGTTACCCAATTA
NM_054113	117286	CIB3	calcium and integrin binding family member 3	CACGAGCAGCTGGAAGCGTAT	CTGGAGCAGACGGTGACCAAA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_080823	6725	SRMS	src-related kinase lacking C-terminal regulatory tyrosine and N-terminal myristylation sites	CAGACCAACCCTGGTACTTTA	CCGGGTCTCCATGGCAGCTGA
NM_080836	140901	STK35	serine/threonine kinase 35	CTCGGCTGTTAGGCATCTGAA	TTGGGTTGGTATGATACATTA
NM_133494	140609	NEK7	NIMA (never in mitosis gene a)-related kinase 7	ACGACCGGATATGGGCTATAA	CCGGATATGGGCTATAATACA
NM_138316	53354	PANK1	pantothenate kinase 1	AACGCTGGTTAAATTGGTGTA	CCGAAGGATATTACAGCCGAA
NM_138733	5232	PGK2	phosphoglycerate kinase 2	CAGCAACATGTAGTTAATATA	CAGGCCATCAGGAACTCTTAA
NM_139021	225689	ERK8	extracellular signal-regulated kinase 8	CCCACTGACTTCCTCCAATAA	CCCAGAGAACATTCCGGGAAA
NM_139158	65061	ALS2CR7	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 7	CTGGACATAAACTAAGTCTAA	CTGGCGTACATCCACCACCAA
NM_139209	131890	GRK7	G protein-coupled receptor kinase 7	ATCCATGACATCTGTGAATTA	TCGGCTGACATAATCCTCGAA
NM_145040	112464	PRKCDBP	protein kinase C, delta binding protein	AAGGAGCGAATCCTACATCCA	CACGCCCTAATAAGGAGCGAA
NM_145059	197258	FUK	fucokinase	CCGAAGGGAGTTGATTGGACA	TGGCTTAGAGTTGTAGACTTA
NM_145203	122011	MGC33182	casein kinase I alpha S-like	CAAGAATAATGTGAAAGATAA	CAGATTATCTTTAGAATTCCA
BC005365	5609	MAP2K7	mitogen-activated protein kinase kinase 7	ATGGATCTCTCTCAACAACTA	CCGGCGGAGGATCGACCTCAA
NM_145695	1607	DGKB	diacylglycerol kinase, beta 90kDa	CCCGAACTACTTCTCCTGCAA	CTCATTCTAGTCCAATGGTAA
NM_152309	118788	PIK3AP1	phosphoinositide-3-kinase adaptor protein 1	ATGCTCAAGAGTCACATTAAA	CAGCAGGGTATTTAAGTGCTA
NM_152327	122481	AK7	adenylate kinase 7	CAAGATTGTCTTGACCATTTA	GACGATCAATATATAATTAGA
NM_152671	200576	PIP5K3	na	ACCCAGTAACATAATATTTCA	TTGCCGTTACCCAGTAACATA
NM_152720	4752	NEK3	NIMA (never in mitosis gene a)-related kinase 3	ACGATAGAGGTGGTTCTGTAA	CAGAGATATCAAGTCCAAGAA
NM_152835	149420	LOC149420	casein kinase	AAGCTAGACTCTACCCTCTAA	CAGCCAAAGTACGATCTAATA
NM_152883	5754	PTK7	PTK7 protein tyrosine kinase 7	ACGGTTCGAGGTCTTCAAGAA	ATGGGACATGGTACCGTTGTA
NM_153273	9807	IHPK1	inositol hexaphosphate kinase 1	AAGGTGGATGTCCGCATGATT	CCGGCAGATGCGGAAATGCGA
NM_153835	92335	LYK5	protein kinase LYK5	CACCCAGATGCTGCTAGAGAA	CTGGTTCTAGTTCTGGTTCTA
NM_172173	818	CAMK2G	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma	CCGATGAGAAACCTCGTGTTA	GAGGAAGAGATCTATACCCTA
NM_173176	2185	PTK2B	PTK2B protein tyrosine kinase 2 beta	AAGCTGATCGGCATCATTGAA	CAGGAGAACTTAAAGCCCAAA
NM_173354	150094	SNF1LK	SNF1-like kinase	AGCGAAATAAGCAATACGTTA	CACAATTGATTCCAACACAAA
NM_173500	146057	TTBK2	tau tubulin kinase 2	ACGGCCCAGGTTAAATGGAAA	CACATTGGTCATGACATGTTA
NM_173515	154043	MAGI1	membrane associated guanylate kinase interacting protein-like 1	CCGGAGTTGTGTTACTGCTTA	CGGAGTTGTGTTACTGCTTAA
NM_173575	282974	PKE	PKE protein kinase	CCGGGCTTCGTGCCCAACAAA	TCCGAGAATGACTATCTTCAA
NM_173598	283455	KSR2	kinase suppressor of Ras-2	ATCCGGTGACCTCGAATCCAA	TCCGTTGTGAGGGATGCCAAA
NM_174858	26289	AK5	adenylate kinase 5	CAGAGCTAGTCAGTACATGAA	CAGCATGGCAGTTGACAACAA
NM_174922	203054	ADCK5	aarF domain containing kinase 5	AAGGCCTTTGCTGAGCAGATA	CCGCTACTTCCTTATGGCTAA
NM_175866	127933	KIS	kinase interacting with leukemia-associated gene (stathmin)	AAGCAGTACTGTAGTACTGAA	CCACATATGAATGCAGGACTA
NM_176799	80895	ILKAP	integrin-linked kinase-associated serine/threonine phosphatase 2C	ATGGAGGAATTCGAGCCTCAA	TTCGGTGATCTTTGGTCTGAA
NM_176800	8899	PRPF4B	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	GAGCCGATCCTTAGAAAGAAA	TCGTCTGATGATAACCTTGAA
NM_177560	1457	CSNK2A1	casein kinase 2, alpha 1 polypeptide	ACCGTTGCTTGTGGATTTATA	CTGGTCGCTTACATCACTTTA
NM_177990	57144	PAK7	p21(CDKN1A)-activated kinase 7	ATGATCTGGATCCGTATTATA	ATGGTGTGCACGTTTCATTAA
NM_178009	160851	DGKH	diacylglycerol kinase, eta	CAGGTGGAGTATAATGACATA	CCGGATCTAGATTCCGTAGAT
NM_178170	284086	NEK8	NIMA (never in mitosis gene a)- related kinase 8	ACGGACAGTTGGGCACCAATA	CCAGAAGCTGGTGATCATCAA
NM_178432	23552	CCRK	cell cycle related kinase	AAGGAGAAGTGCAGAGAGTAA	TGGCGAGATAGTTGCCCTCAA
NM_178510	255239	ANKK1	ankyrin repeat and kinase domain containing 1	AGGAGCCGAGATGGAAATTTA	GCGGACGGAGTACGCCATCAA
NM_178813	158798	AKAP28	A-kinase anchoring protein 28	CCCATTGTCGTTTCTTATGTA	TACGAGGATGAATTGACTCAA
NM_181358	204851	HIPK1	homeodomain interacting protein kinase 1	AGGGAAGCTGTACACCACTAA	CTGAGCTATGTTTGTAATGCA

Table 2 (continued):

Accession #	Locus Link	Symbol	Gene Name	Target 1	Target 2
NM_181504	5295	PIK3R1	phosphoinositide-3-kinase, regulatory subunit, polypeptide 1 (p85 alpha)	CAGCATTAAACCAGACCTTAT	TAGCTGGTTATGAACTAGTAA
NM_181690	10000	AKT3	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	AACTGTTGGCTTTGGATTAAA	CAGCAGGCACGTTAACTCGAA
NM_181795	5570	PKIB	protein kinase (cAMP-dependent, catalytic) inhibitor beta	CAGCATGTGTATATTAGATAA	CCGGAATGCCTTACCAGACAT
NM_181805	11142	PKIG	protein kinase (cAMP-dependent, catalytic) inhibitor gamma	CCACAAGATGTTATTTATTGA	GAGCTCCATGTCCCAGATAAA
NM_181839	5569	PKIA	protein kinase (cAMP-dependent, catalytic) inhibitor alpha	ATGATTATCATTAGAAGCTAA	TCACTTGATCATATGACGAAA
NM_181871	5313	PKLR	pyruvate kinase, liver and RBC	CGGGTGCAATTTGGCATTGAA	GAGGCCTATCTGAGACTATAA
NM_182398	9252	RPS6KA5	ribosomal protein S6 kinase, 90kDa, polypeptide 5	AAGCCAGTCATTCGAGATGAA	CTGGATCTCTTACGTAATTCA
NM_182471	5315	PKM2	pyruvate kinase, muscle	AACATCAAGATTATCAGCAAA	CCCGATCAGTGGAGACGTTGA
NM_182493	91807	LOC91807	myosin light chain kinase (MLCK)	ACGGAGGACAATGACCTTGCA	GACCATGAATTTCATTGTAAA
NM_182561	64781	CERK	ceramide kinase	ATGGCATTATTTGATCTGAAA	CGGCTTAAACTTTGATCTGTA
NM_182687	9088	PKMYT1	membrane-associated tyrosine- and threonine-specific cdc2-inhibitory kinase	CCGGCCAGAGTCCTTCTTCCA	CTGGGAGGAACTTACCGTCTA
NM_182592	6733	SRPK2	SFRS protein kinase 2	AACGGTGACTCTCATTCTTTA	CCGGTATCATGTTATTAGAAA
NM_182925	2324	FLT4	fms-related tyrosine kinase 4	CACCGTGTGGGCTGAGTTTAA	CACGCTCTTGGTCAACAGGAA
NM_182948	5567	PRKACB	protein kinase, cAMP-dependent, catalytic, beta	CAGCCTGTGTAGTGTGACAAA	CTGACCAATCAAGTACACTAA
NM_182982	2868	GRK4	G protein-coupled receptor kinase 4	CAGGATGTTACTCACCAAGAA	CCGGGTGTTTCAAAGACATCA
NM_183048	23613	PRKCBP1	protein kinase C binding protein 1	AGCGAACTTGTCATAGATTTA	CACCATTGAACAGTTATCCTA
NM_197972	29922	NME7	non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinase)	CCCGGCATTTACGCCCTGGAA	TTCATGTAGATCACCAGTCAA
NM_198452	139728	MGC45419	Similar to calcium/calmodulin-dependent protein kinase 1, beta	CTCGAAGATCATGGTCTCTGA	TCCGTGTGTCACAGCCCGAAA
NM_198828	375449	LOC375449	similar to microtubule associated testis specific serine/threonine protein kinase	ATGAATTGCCACCACATTAAA	GAGGAGCTTGACCACATATTA
XM_027237	4293	MAP3K9	mitogen-activated protein kinase kinase kinase 9	AGCGATGAAATTGTCGTGTAT	CAGCGATGAAATTGTCGTGTA
XM_031706	23005	MAPKBP1	likely ortholog of mouse mitogen activated protein kinase binding proten 1	CAGGACCGAAATATTCGGATA	CCCGTTTGTACTGATGTATGA
NM_001556	3551	IKBKB	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta	CAGACCGACATTGTGGACTTA	CAGGACACTGTGAGGGAACAA
XM_039796	23043	TNIK	TRAF2 and NCK interacting kinase	AAGGACCATATTGATAGAACA	CTGGAATATAAGCGCAAACAA
XM_042066	4214	MAP3K1	mitogen-activated protein kinase kinase kinase 1	CACGCATGTCAAATTCTCATA	CTCCGGGTGTTTCAACTAGAA
XM_051221	80309	SKIP	SPHK1 (sphingosine kinase type 1) interacting protein	CTGAAATTCTGGACACCTTAA	GGCAAGTATGCTACAAATTTA
XM_166453	84630	TTBK1	tau tubulin kinase 1	CAGGAACGAGAAGTTTAACTA	TGGCAGGAACGAGAAGTTTAA
XM_290516	55561	HSMDPKIN	myotonic dystrophy protein kinase like protein	CGCCGGTGGCTTTGCACTCTA	CTCGCCGCCTACCAACTTCAA
XM_290793	8844	KSR	kinase suppressor of ras	AAGGGCGAAGCTGGTCCGTTA	CTGGAAGTCAGCTGACATTAA
NM_012224	4750	NEK1	NIMA (never in mitosis gene a)-related kinase 1	ACCGTAGGAGATGTTCGTCAA	TAGGGATAGACCATCAGTCAA

Table3

Pool No.	Accession #	LocusLink	Symbol	Gene Name
1	NM_005734	10114	HIPK3	homeodomain interacting protein kinase 3
	NM_181358	204851	HIPK1	homeodomain interacting protein kinase 1
2	NM_000269	4830	NME1	non-metastatic cells 1, protein (NM23A) expressed in
	NM_002512	4831	NME2	non-metastatic cells 2, protein (NM23B) expressed in
	NM_002513	4832	NME3	non-metastatic cells 3, protein expressed in
	NM_003551	8382	NME5	non-metastatic cells 5, protein expressed in (nucleoside-diphosphate kinase)
	NM_005009	4833	NME4	non-metastatic cells 4, protein expressed in
	NM_005793	10201	NME6	non-metastatic cells 6, protein expressed in (nucleoside-diphosphate kinase)
	NM_197972	29922	NME7	non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinase)
3	NM_000291	5230	PGK1	phosphoglycerate kinase 1
	NM_138733	5232	PGK2	phosphoglycerate kinase 2
4	NM_182471	5315	PKM2	pyruvate kinase, muscle
	NM_181871	5313	PKLR	pyruvate kinase, liver and RBC
5	NM_018323	55300	PI4K2B	phosphatidylinositol 4-kinase type-II beta
	NM_018425	55361	PI4KII	phosphatidylinositol 4-kinase type II
6	NM_000289	5213	PFKM	phosphofructokinase, muscle
	NM_002626	5211	PFKL	phosphofructokinase, liver
	NM_002627	5214	PFKP	phosphofructokinase, platelet
7	NM_002733	5571	PRKAG1	protein kinase, AMP-activated, gamma 1 non-catalytic subunit
	NM_016203	51422	PRKAG2	protein kinase, AMP-activated, gamma 2 non-catalytic subunit
	NM_017431	53632	PRKAG3	protein kinase, AMP-activated, gamma 3 non-catalytic subunit
8	NM_025144	80216	LAK	lymphocyte alpha-kinase
	NM_052947	115701	HAK	heart alpha-kinase
9	NM_000189	3099	HK2	hexokinase 2
	NM_002115	3101	HK3	hexokinase 3 (white cell)
	NM_033498	3098	HK1	hexokinase 1
10	NM_002742	5587	PRKCM	protein kinase C, mu

Table3 (continued)

	NM_005813	23683	PRKCN	protein kinase C, nu
	NM_016457	25865	PRKD2	protein kinase D2
11	NM_002648	5292	PIM1	pim-1 oncogene
	NM_006875	11040	PIM2	pim-2 oncogene
12	NM_003936	8941	CDK5R2	cyclin-dependent kinase 5, regulatory subunit 2 (p39)
	NM_003885	8851	CDK5R1	cyclin-dependent kinase 5, regulatory subunit 1 (p35)
13	NM_013410	205	AK3	adenylate kinase 3
	NM_016282	50808	AK3L1	adenylate kinase 3 like 1
14	NM_000476	203	AK1	adenylate kinase 1
	NM_174858	26289	AK5	adenylate kinase 5
15	NM_004721	9175	MAP3K13	mitogen-activated protein kinase kinase kinase 13
	NM_006301	7786	MAP3K12	mitogen-activated protein kinase kinase kinase 12
16	NM_173598	283455	KSR2	kinase suppressor of Ras-2
	XM_290793	8844	KSR	kinase suppressor of ras
17	NM_002314	3984	LIMK1	LIM domain kinase 1
	NM_005569	3985	LIMK2	LIM domain kinase 2
18	NM_000142	2261	FGFR3	fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)
	NM_015850	2260	FGFR1	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndron
19	NM_004438	2043	EPHA4	EphA4
	NM_005233	2042	EPHA3	EphA3
	NM_020526	2046	EPHA8	EphA8
20	NM_004441	2047	EPHB1	EphB1
	NM_004443	2049	EPHB3	EphB3
	NM_017449	2048	EPHB2	EphB2
21	NM_002645	5286	PIK3C2A	phosphoinositide-3-kinase, class 2, alpha polypeptide
	NM_002646	5287	PIK3C2B	phosphoinositide-3-kinase, class 2, beta polypeptide
	NM_004570	5288	PIK3C2G	phosphoinositide-3-kinase, class 2, gamma polypeptide
22	NM_005026	5293	PIK3CD	phosphoinositide-3-kinase, catalytic, delta polypeptide
	NM_006219	5291	PIK3CB	phosphoinositide-3-kinase, catalytic, beta polypeptide
	NM_006218	5290	PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide

Table3 (continued)

23	NM_003629	8503	PIK3R3	phosphoinositide-3-kinase, regulatory subunit, polypeptide 3 (p55, gamma)
	NM_005027	5296	PIK3R2	phosphoinositide-3-kinase, regulatory subunit, polypeptide 2 (p85 beta)
	NM_181504	5295	PIK3R1	phosphoinositide-3-kinase, regulatory subunit, polypeptide 1 (p85 alpha)
24	NM_000167	2710	GK	glycerol kinase
	NM_033214	2712	GK2	glycerol kinase 2
25	NM_012474	7371	UMPK	uridine monophosphate kinase
	NM_017859	54963	URKL1	uridine kinase-like 1
	NM_031432	83549	UCK1	uridine-cytidine kinase 1
26	NM_005399	5565	PRKAB2	protein kinase, AMP-activated, beta 2 non-catalytic subunit
	NM_006253	5564	PRKAB1	protein kinase, AMP-activated, beta 1 non-catalytic subunit
27	NM_020421	57143	ADCK1	aarF domain containing kinase 1
	NM_024876	79934	ADCK4	aarF domain containing kinase 4
	NM_052853	90956	ADCK2	aarF domain containing kinase 2
	NM_174922	203054	ADCK5	aarF domain containing kinase 5
28	NM_000292	5256	PHKA2	phosphorylase kinase, alpha 2 (liver)
	NM_002637	5255	PHKA1	phosphorylase kinase, alpha 1 (muscle)
29	NM_007229	11252	PACSIN2	protein kinase C and casein kinase substrate in neurons 2
	NM_016223	29763	PACSIN3	protein kinase C and casein kinase substrate in neurons 3
	NM_020804	29993	PACSIN1	protein kinase C and casein kinase substrate in neurons 1
30	NM_080836	140901	STK35	serine/threonine kinase 35
	NM_152835	149420	LOC149420	casein kinase
31	NM_001184	545	ATR	ataxia telangiectasia and Rad3 related
	NM_006904	5591	PRKDC	protein kinase, DNA-activated, catalytic polypeptide
32	NM_003648	8527	DGKD	diacylglycerol kinase, delta 130kDa
	NM_178009	160851	DGKH	diacylglycerol kinase, eta
33	NM_001345	1606	DGKA	diacylglycerol kinase, alpha 80kDa
	NM_001346	1608	DGKG	diacylglycerol kinase, gamma 90kDa
	NM_145695	1607	DGKB	diacylglycerol kinase, beta 90kDa
34	NM_001258	1018	CDK3	cyclin-dependent kinase 3
	NM_001786	983	CDC2	cell division cycle 2, G1 to S and G2 to M

Table3 (continued)

35	NM_003583	8445	DYRK2	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2
	NM_003582	8444	DYRK3	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3
	NM_003845	8798	DYRK4	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 4
36	NM_001396	1859	DYRK1A	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A
	NM_004714	9149	DYRK1B	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1B
37	NM_003137	6732	SRPK1	SFRS protein kinase 1
	NM_014370	26576	STK23	serine/threonine kinase 23
	NM_182692	6733	SRPK2	SFRS protein kinase 2
38	NM_004071	1195	CLK1	CDC-like kinase 1
	NM_020666	57396	CLK4	CDC-like kinase 4
39	NM_005906	4117	MAK	male germ cell-associated kinase
	NM_014920	22858	ICK	intestinal cell (MAK-like) kinase
40	NM_002093	2932	GSK3B	glycogen synthase kinase 3 beta
	NM_019884	2931	GSK3A	glycogen synthase kinase 3 alpha
41	NM_001315	1432	MAPK14	mitogen-activated protein kinase 14
	NM_002751	5600	MAPK11	mitogen-activated protein kinase 11
	NM_002969	6300	MAPK12	mitogen-activated protein kinase 12
	NM_002754	5603	MAPK13	mitogen-activated protein kinase 13
42	NM_002752	5601	MAPK9	mitogen-activated protein kinase 9
	NM_002753	5602	MAPK10	mitogen-activated protein kinase 10
	NM_002750	5599	MAPK8	mitogen-activated protein kinase 8
43	NM_002745	5594	MAPK1	mitogen-activated protein kinase 1
	NM_002746	5595	MAPK3	mitogen-activated protein kinase 3
44	NM_003718	8621	CDC2L5	cell division cycle 2-like 5 (cholinesterase-related cell division controller)
	NM_016507	51755	CRK7	CDC2-related protein kinase 7
45	NM_000075	1019	CDK4	cyclin-dependent kinase 4
	NM_001259	1021	CDK6	cyclin-dependent kinase 6
46	NM_001260	1024	CDK8	cyclin-dependent kinase 8
	NM_015076	23097	CDK11	cyclin-dependent kinase (CDC2-like) 11
47	NM_001787	984	CDC2L1	cell division cycle 2-like 1 (PITSLRE proteins)

Table3 (continued)

	NM_003674	8558	CDK10	cyclin-dependent kinase (CDC2-like) 10
48	NM_001825	1160	CKMT2	creatine kinase, mitochondrial 2 (sarcomeric)
	NM_001823	1152	CKB	creatine kinase, brain
	NM_001824	1158	CKM	creatine kinase, muscle
	NM_020990	1159	CKMT1	creatine kinase, mitochondrial 1 (ubiquitous)
49	NM_002736	5577	PRKAR2B	protein kinase, cAMP-dependent, regulatory, type II, beta
	NM_004157	5576	PRKAR2A	protein kinase, cAMP-dependent, regulatory, type II, alpha
50	NM_003384	7443	VRK1	vaccinia related kinase 1
	NM_006296	7444	VRK2	vaccinia related kinase 2
	NM_016440	51231	VRK3	vaccinia related kinase 3
51	NM_001319	1455	CSNK1G2	casein kinase 1, gamma 2
	NM_001893	1453	CSNK1D	casein kinase 1, delta
	NM_001894	1454	CSNK1E	casein kinase 1, epsilon
	NM_001892	1452	CSNK1A1	casein kinase 1, alpha 1
	NM_004384	1456	CSNK1G3	casein kinase 1, gamma 3
	NM_022048	53944	CSNK1G1	casein kinase 1, gamma 1
	NM_145203	122011	MGC33182	casein kinase I alpha S-like
52	NM_002610	5163	PDK1	pyruvate dehydrogenase kinase, isoenzyme 1
	NM_002611	5164	PDK2	pyruvate dehydrogenase kinase, isoenzyme 2
	NM_002612	5166	PDK4	pyruvate dehydrogenase kinase, isoenzyme 4
	NM_005391	5165	PDK3	pyruvate dehydrogenase kinase, isoenzyme 3
53	NM_024594	79646	PANK3	pantothenate kinase 3
	NM_024960	80025	PANK2	pantothenate kinase 2 (Hallervorden-Spatz syndrome)
	NM_138316	53354	PANK1	pantothenate kinase 1
54	NM_016291	51447	IHPK2	inositol hexaphosphate kinase 2
	NM_054111	117283	IHPK3	inositol hexaphosphate kinase 3
	NM_153273	9807	IHPK1	inositol hexaphosphate kinase 1
55	NM_002220	3706	ITPKA	inositol 1,4,5-trisphosphate 3-kinase A
	NM_025194	80271	ITPKC	Inositol 1,4,5-trisphosphate 3-kinase C
56	NM_018979	65125	PRKWNK1	protein kinase, lysine deficient 1

Table3 (continued)

	NM_020922	65267	PRKWNK3	protein kinase, lysine deficient 3
	NM_032387	65266	PRKWNK4	protein kinase, lysine deficient 4
57	NM_001433	2081	ERN1	ER to nucleus signalling 1
	XM_370946	10595	LOC388226	similar to protein kinase/ribonuclease IRE1 beta
58	NM_001262	1031	CDKN2C	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)
	NM_001800	1032	CDKN2D	cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)
	NM_004936	1030	CDKN2B	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)
59	NM_020639	54101	ANKRD3	ankyrin repeat domain 3
	NM_178510	255239	ANKK1	ankyrin repeat and kinase domain containing 1
60	NM_001348	1613	DAPK3	death-associated protein kinase 3
	NM_004938	1612	DAPK1	death-associated protein kinase 1
	NM_014326	23604	DAPK2	death-associated protein kinase 2
61	NM_012290	9874	TLK1	tousled-like kinase 1
	NM_006852	11011	TLK2	tousled-like kinase 2
62	NM_004073	1263	PLK3	polo-like kinase 3 (Drosophila)
	NM_005030	5347	PLK1	polo-like kinase 1 (Drosophila)
	NM_006622	10769	PLK2	polo-like kinase 2 (Drosophila)
63	NM_000294	5261	PHKG2	phosphorylase kinase, gamma 2 (testis)
	NM_006213	5260	PHKG1	phosphorylase kinase, gamma 1 (muscle)
64	NM_004226	9262	STK17B	serine/threonine kinase 17b (apoptosis-inducing)
	NM_004760	9263	STK17A	serine/threonine kinase 17a (apoptosis-inducing)
65	NM_033118	85366	MYLK2	myosin light chain kinase 2, skeletal muscle
	NM_182493	91807	LOC91807	myosin light chain kinase (MLCK)
66	NM_003684	8569	MKNK1	MAP kinase-interacting serine/threonine kinase 1
	NM_017572	2872	MKNK2	MAP kinase-interacting serine/threonine kinase 2
67	NM_003668	8550	MAPKAPK5	mitogen-activated protein kinase-activated protein kinase 5
	NM_004635	7867	MAPKAPK3	mitogen-activated protein kinase-activated protein kinase 3
	NM_004759	9261	MAPKAPK2	mitogen-activated protein kinase-activated protein kinase 2
68	NM_001220	816	CAMK2B	calcium/calmodulin-dependent protein kinase (CaM kinase) II beta
	NM_001221	817	CAMK2D	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta

Table3 (continued)

	NM_015981	815	CAMK2A	calcium/calmodulin-dependent protein kinase (CaM kinase) II alpha
	NM_172173	818	CAMK2G	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma
69	NM_006742	5681	PSKH1	protein serine kinase H1
	NM_033126	85481	PSKH2	serine/threonine kinase PSKH2
70	NM_003656	8536	CAMK1	calcium/calmodulin-dependent protein kinase I
	NM_020397	57118	CAMK1D	calcium/calmodulin-dependent protein kinase ID
	NM_020439	57172	CAMK1G	calcium/calmodulin-dependent protein kinase IG
	NM_198452	139728	MGC45419	Similar to calcium/calmodulin-dependent protein kinase 1, beta
71	NM_003565	8408	ULK1	unc-51-like kinase 1 (C. elegans)
	NM_014683	9706	ULK2	unc-51-like kinase 2 (C. elegans)
72	NM_006549	10645	CAMKK2	calcium/calmodulin-dependent protein kinase kinase 2, beta
	NM_032294	84254	CAMKK1	calcium/calmodulin-dependent protein kinase kinase 1, alpha
73	NM_032037	83983	SSTK	serine/threonine protein kinase SSTK
	NM_052841	81629	STK22C	serine/threonine kinase 22C (spermiogenesis associated)
	NM_032028	83942	STK22D	serine/threonine kinase 22D (spermiogenesis associated)
	NM_053006	23617	STK22B	serine/threonine kinase 22B (spermiogenesis associated)
74	NM_003160	6795	AURKC	aurora kinase C
	NM_003600	6790	STK6	serine/threonine kinase 6
	NM_004217	9212	AURKB	aurora kinase B
75	XM_374996	9891	ARK5	AMP-activated protein kinase family member 5
	NM_030952	81788	SNARK	likely ortholog of rat SNF1/AMP-activated protein kinase
76	NM_004954	2011	MARK2	MAP/microtubule affinity-regulating kinase 2
	NM_018650	4139	MARK1	MAP/microtubule affinity-regulating kinase 1
	NM_031417	57787	MARK4	MAP/microtubule affinity-regulating kinase 4
77	NM_006251	5562	PRKAA1	protein kinase, AMP-activated, alpha 1 catalytic subunit
	NM_006252	5563	PRKAA2	protein kinase, AMP-activated, alpha 2 catalytic subunit
78	NM_018401	55351	HSA250839	gene for serine/threonine protein kinase
	NM_173575	282974	PKE	PKE protein kinase
79	NM_004690	9113	LATS1	LATS, large tumor suppressor, homolog 1 (Drosophila)
	NM_014572	26524	LATS2	LATS, large tumor suppressor, homolog 2 (Drosophila)

Table3 (continued)

80	NM_007271	11329	STK38	serine/threonine kinase 38
	NM_015000	23012	STK38L	serine/threonine kinase 38 like
81	NM_006258	5592	PRKG1	protein kinase, cGMP-dependent, type I
	NM_006259	5593	PRKG2	protein kinase, cGMP-dependent, type II
82	AB023190	22983	SAST	syntrophin associated serine/threonine kinase
	NM_015112	23139	MAST2	microtubule associated serine/threonine kinase 2
83	NM_001619	156	ADRBK1	adrenergic, beta, receptor kinase 1
	NM_005160	157	ADRBK2	adrenergic, beta, receptor kinase 2
84	NM_002741	5585	PRKCL1	protein kinase C-like 1
	NM_006256	5586	PRKCL2	protein kinase C-like 2
	NM_013355	29941	pknbeta	protein kinase PKNbeta
85	NM_002744	5590	PRKCZ	protein kinase C, zeta
	NM_002740	5584	PRKCI	protein kinase C, iota
86	NM_002737	5578	PRKCA	protein kinase C, alpha
	NM_002738	5579	PRKCB1	protein kinase C, beta 1
	NM_002739	5582	PRKCG	protein kinase C, gamma
	NM_005400	5581	PRKCE	protein kinase C, epsilon
	NM_006254	5580	PRKCD	protein kinase C, delta
	NM_006255	5583	PRKCH	protein kinase C, eta
	NM_006257	5588	PRKCQ	protein kinase C, theta
87	NM_002730	5566	PRKACA	protein kinase, cAMP-dependent, catalytic, alpha
	NM_002732	5568	PRKACG	protein kinase, cAMP-dependent, catalytic, gamma
	NM_002760	5616	PRKY	protein kinase, Y-linked
	NM_005044	5613	PRKX	protein kinase, X-linked
	NM_182948	5567	PRKACB	protein kinase, cAMP-dependent, catalytic, beta
88	NM_002953	6195	RPS6KA1	ribosomal protein S6 kinase, 90kDa, polypeptide 1
	NM_004586	6197	RPS6KA3	ribosomal protein S6 kinase, 90kDa, polypeptide 3
	NM_014496	27330	RPS6KA6	ribosomal protein S6 kinase, 90kDa, polypeptide 6
	NM_021135	6196	RPS6KA2	ribosomal protein S6 kinase, 90kDa, polypeptide 2
89	NM_001626	208	AKT2	v-akt murine thymoma viral oncogene homolog 2

Table3 (continued)

	NM_005163	207	AKT1	v-akt murine thymoma viral oncogene homolog 1
	NM_181690	10000	AKT3	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)
90	NM_005627	6446	SGK	serum/glucocorticoid regulated kinase
	NM_013257	23678	SGKL	serum/glucocorticoid regulated kinase-like
	NM_016276	10110	SGK2	serum/glucocorticoid regulated kinase 2
91	NM_003161	6198	RPS6KB1	ribosomal protein S6 kinase, 70kDa, polypeptide 1
	NM_003952	6199	RPS6KB2	ribosomal protein S6 kinase, 70kDa, polypeptide 2
92	NM_002082	2870	GRK6	G protein-coupled receptor kinase 6
	NM_005308	2869	GRK5	G protein-coupled receptor kinase 5
	NM_182982	2868	GRK4	G protein-coupled receptor kinase 4
93	NM_003942	8986	RPS6KA4	ribosomal protein S6 kinase, 90kDa, polypeptide 4
	NM_182398	9252	RPS6KA5	ribosomal protein S6 kinase, 90kDa, polypeptide 5
94	NM_002497	4751	NEK2	NIMA (never in mitosis gene a)-related kinase 2
	NM_003157	6787	NEK4	NIMA (never in mitosis gene a)-related kinase 4
	NM_014397	10783	NEK6	NIMA (never in mitosis gene a)-related kinase 6
	NM_024800	79858	NEK11	NIMA (never in mitosis gene a)- related kinase 11
	NM_033116	91754	NEK9	NIMA (never in mitosis gene a)- related kinase 9
	NM_133494	140609	NEK7	NIMA (never in mitosis gene a)-related kinase 7
	NM_152720	4752	NEK3	NIMA (never in mitosis gene a)-related kinase 3
	NM_178170	284086	NEK8	NIMA (never in mitosis gene a)- related kinase 8
	NM_012224	4750	NEK1	NIMA (never in mitosis gene a)-related kinase 1
95	NM_004783	9344	TAO1	thousand and one amino acid protein kinase
	NM_016151	9344	TAO1	thousand and one amino acid protein kinase
	NM_016281	51347	JIK	STE20-like kinase
96	NM_002756	5606	MAP2K3	mitogen-activated protein kinase kinase 3
	NM_002758	5608	MAP2K6	mitogen-activated protein kinase kinase 6
97	NM_002401	4215	MAP3K3	mitogen-activated protein kinase kinase kinase 3
	NM_006609	10746	MAP3K2	mitogen-activated protein kinase kinase kinase 2
98	NM_005109	9943	OSR1	oxidative-stress responsive 1
	NM_013233	27347	STK39	serine threonine kinase 39 (STE20/SPS1 homolog, yeast)

Table3 (continued)

99	NM_003618	8491	MAP4K3	mitogen-activated protein kinase kinase kinase kinase 3
	NM_006575	11183	MAP4K5	mitogen-activated protein kinase kinase kinase kinase 5
100	NM_004834	9448	MAP4K4	mitogen-activated protein kinase kinase kinase kinase 4
	NM_015716	50488	MINK	misshapen/NIK-related kinase
101	NM_002576	5058	PAK1	p21/Cdc42/Rac1-activated kinase 1 (STE20 homolog, yeast)
	NM_002577	5062	PAK2	p21 (CDKN1A)-activated kinase 2
	NM_002578	5063	PAK3	p21 (CDKN1A)-activated kinase 3
	NM_005884	10298	PAK4	p21(CDKN1A)-activated kinase 4
	NM_020168	56924	PAK6	p21(CDKN1A)-activated kinase 6
	NM_177990	57144	PAK7	p21(CDKN1A)-activated kinase 7
102	NM_006281	6788	STK3	serine/threonine kinase 3 (STE20 homolog, yeast)
	NM_006282	6789	STK4	serine/threonine kinase 4
103	NM_006374	10494	STK25	serine/threonine kinase 25 (STE20 homolog, yeast)
	NM_016542	51765	MST4	Mst3 and SOK1-related kinase
104	NM_003607	8476	CDC42BPA	CDC42 binding protein kinase alpha (DMPK-like)
	NM_006035	9578	CDC42BPB	CDC42 binding protein kinase beta (DMPK-like)
105	NM_004850	9475	ROCK2	Rho-associated, coiled-coil containing protein kinase 2
	NM_005406	6093	ROCK1	Rho-associated, coiled-coil containing protein kinase 1
106	NM_001743	805	CALM2	calmodulin 2 (phosphorylase kinase, delta)
	NM_005184	808	CALM3	calmodulin 3 (phosphorylase kinase, delta)
	NM_006888	801	CALM1	calmodulin 1 (phosphorylase kinase, delta)
107	NM_006383	10518	KIP2	DNA-dependent protein kinase catalytic subunit-interacting protein 2
	NM_054113	117286	CIB3	calcium and integrin binding family member 3
108	NM_003559	8396	PIP5K2B	phosphatidylinositol-4-phosphate 5-kinase, type II, beta
	NM_005028	5305	PIP5K2A	phosphatidylinositol-4-phosphate 5-kinase, type II, alpha
	NM_024779	79837	PIP5K2C	phosphatidylinositol-4-phosphate 5-kinase, type II, gamma
109	NM_003557	8394	PIP5K1A	phosphatidylinositol-4-phosphate 5-kinase, type I, alpha
	NM_003558	8395	PIP5K1B	phosphatidylinositol-4-phosphate 5-kinase, type I, beta
	NM_012398	23396	PIP5K1C	phosphatidylinositol-4-phosphate 5-kinase, type I, gamma
110	NM_001616	92	ACVR2	activin A receptor, type II

Table3 (continued)

	NM_001106	93	ACVR2B	activin A receptor, type IIB
111	NM_000020	94	ACVRL1	activin A receptor type II-like 1
	NM_001105	90	ACVR1	activin A receptor, type I
	NM_001203	658	BMPR1B	bone morphogenetic protein receptor, type IB
	NM_004329	657	BMPR1A	bone morphogenetic protein receptor, type IA
	NM_004302	91	ACVR1B	activin A receptor, type IB
	NM_004612	7046	TGFBR1	transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 5
112	NM_002005	2242	FES	feline sarcoma oncogene
	NM_005246	2241	FER	fer (fps/fes related) tyrosine kinase (phosphoprotein NCP94)
113	NM_000061	695	BTK	Bruton agammaglobulinemia tyrosine kinase
	NM_001721	660	BMX	BMX non-receptor tyrosine kinase
	NM_003215	7006	TEC	tec protein tyrosine kinase
	NM_003328	7294	TXK	TXK tyrosine kinase
114	NM_005157	25	ABL1	v-abl Abelson murine leukemia viral oncogene homolog 1
	NM_005158	27	ABL2	v-abl Abelson murine leukemia viral oncogene homolog 2 (arg, Abelson-related g
115	NM_001715	640	BLK	B lymphoid tyrosine kinase
	NM_002110	3055	HCK	hemopoietic cell kinase
	NM_002350	4067	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog
	NM_002037	2534	FYN	FYN oncogene related to SRC, FGR, YES
	NM_005356	3932	LCK	lymphocyte-specific protein tyrosine kinase
	NM_005433	7525	YES1	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1
	NM_005248	2268	FGR	Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog
	NM_005417	6714	SRC	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)
116	NM_002344	4058	LTK	leukocyte tyrosine kinase
	NM_004304	238	ALK	anaplastic lymphoma kinase (Ki-1)

Table 4

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
2	A2M	NM_000014	CTCAAAGATTCGTAAACCCAA	CACCAACTCAAAGATTCGTAA	CACGGAGACCGTACGAAAGTA	ACGGATGAGCATGGCCTTGTA
12	SERPINA3	NM_001085	AAGGTTCTACTTGAGCAAGAA	AAGGCTGTGCTTGATGTATTT	CCCAAGATACTCATCAGTCAA	AAGGACCATTGTGCGTTTCAA
14	AAMP	NM_001087	CAGGGAAGCCCTATCCATGTA	GAGGAAGAGATACTAGTTAAA		
20	ABCA2	NM_001606	CCGCAGAGAGATGGACAAGAT	CTGGGTCAGTCCCGTATTTAT	CAGCATGCCCACCTACCTCAA	CTGGAAGAACGTGACGCTCAA
21	ABCA3	NM_001089	CACGGAGAAATTACATGTGGA	CCAAGTTTATCTCATCCTTTA	TACGTTGTGACCATCCAGAAA	CCGCTTGAAGATTCAGTCGGA
25	ABL1	NM_005157	CTGGGCGAATGTCTTATTTAA	CCAGTGGAGATAACACTCTAA	ACGCACGGACATCACCATGAA	AACACTCTAAGCATAACTAAA
29	ABR	NM_001092	CACGGACGTGATTGAGATGAA	CAGCGAAGAGATCTACATTAA		
30	ACAA1	NM_001607	CACGCTGCTCAATGAGCTGAA	AAGGCCATGGTTAATTCTTAA		
31	ACACA	NM_000664	TCCGTAGGTGGTCTTATGAAA	TCGCATCACAATTGGCAATAA	AACGCAGGCATCAGAAGATTA	CTGGATAATCTGGTCAATGTA
34	ACADM	NM_000016	AAGGAGATGAGTATATTATTA	AAGGTACTTCACAAATTCAAA	CTGGCTGAAATGGCAATGAAA	CAACTTGACAGTAACTTTGTA
38	ACAT1	NM_000019	CGGGCTAACTGATGTCTACAA	CCAGATGTAGTGGTGAAAGAA	AAGCTGAATATTGCACGAAAT	TAGTCTGGTTGTACTAGCAAA
54	ACP5	NM_001611	CACTGGTGTGCAAGACATCAA	ACGGCGCTGCTCATCCTGCAA	CTGGTACGTGCTAGCCGGAAA	CTCGGGCAAGTCCCTCTTTAA
55	ACPP	NM_001099	ATGAACAGGTTTATATTCGAA	CTCTATTACCATTATGGATAA	CCGGACTTTGATGAGTGCTAT	ACAGATGGCGCTAGATGTTTA
56	ACRV1	NM_001612	TCCATAGATCATCAAACTTCA	ATGGAACGAGGATGCAAATTA	CCAGCAGTGCATGTTAAAGAA	CAGGCACAATATTAAATTGCT
72	ACTG2	NM_001615	CCGCTGGAATTCATGAGACAA	CAGGAAGTGCTTCTAAAGTCA		
94	ACVRL1	NM_000020	CCGGGAGACTGAGATCTATAA	CACGGACTGCTTTGAGTCCTA	CAGGAAGACGCTGGAATAAGA	CACCGAGTTCGTCAACCACTA
101	ADAM8	NM_001109	CCGGCTACACAGAGACCTATA	AGGCATCATCGTCTACCGCAA	CAAGCTATATCAGAAACTCAA	CCCAGCTTTGTGTGTGTTTAA
102	ADAM10	NM_001110	ATGGTGTTGCTGAGAGTGTTA	ACCAAACTTCACAGACTGTAA	ATGGTAAGAAGAAGTCCTTAA	ATGGGACACATGAGACGCTAA
112	ADCY6	NM_015270	AAGTGCTTAGGTAATGAGCTA	CAGCCTGAGTCTAGCATGTTT	CAGCCCGGATGCTGAATTTAA	ACCATGTATTTCAGTGAAATA
123	ADFP	NM_001122	AAGAATGTGTATAGTGCCAAT	TCCGTTGCAGTTGATCCACAA	CTGGTTCAGAAGCCAAGTTAT	CTGCAGGATAGACCAGTTAAA
125	ADH1B	NM_000668	AACCAATCCATTACAGCTTAA	AAGCCTCAATTACTAATTGTA	AAGGAGGTAGCTGTCTCCAAA	AAGACCTTAGACATAAAGTAA
126	ADH1C	NM_000669	ATGCATTAATAACAAATATTT	GGGAAATTATTTGTCAAGCAA	CTGCTCTTCAGAGATGTTAAA	ACTGGATGCATTAATAACAAA
131	ADH7	NM_000673	CACCAGTACATTTACCGAGTA	CAGATATAGCGTATAAAGATA	CTGGGAATTAGTATAATAACA	AACGATTAAGAATCATCATTA
132	ADK	NM_001123	TCCACTGATGGAAGAGCTGAA	AAGTTGTACCACAATATTCAA	TAGTTTGATAGTGCCACTTAA	AAGGGTATGGTAATGCTTGTA
133	ADM	NM_001124	AGAGGTAACTATCAATATTTA	ACCGAGTCTCTGTATAATCTA	GAGGTAACTATCAATATTTAA	CTGTATAATCTATTTACATAA
135	ADORA2A	NM_000675	CCACACCAATTCGGTTGTGAA	AAGGGCTTGGGTTCTGAGGAA	CAGGAGTGTCCTGATGATTCA	CAGCATGAGGCCCAGCAAGAA
140	ADORA3	NM_000677	CAACTGCATCATCTACTTTAA	CCCTATCGTCTATGCCTATAA	TCGGAACAAACTCAGTCTGAA	AAGCGTCAACTCGTGCAAGAA
141	ADPRH	NM_001125	CTGGTCTACCTCCTAAATATA	CAGAGTTATGTTTACGAATAA		
142	PARP1	NM_001618	CTTGAAATATGTAGTATTAAA	CCCGGTGGCTGTGGTATGAAT	CCGAGAAATCTCTTACCTCAA	ACGGTGATCGGTAGCAACAAA
147	ADRA1B	NM_000679	GGCGGTCATTCTAGTCATGTA	CAGGAGTTCCATAGCTGTCAA	GAGGGCGGACTCTAAGATGAA	CCGTGTCTATATAGTGGCCAA
150	ADRA2A	NM_000681	CCCGCTGTAAATATACACTAT	GTGGATCAAGACATAAGTAAA	CTCCCGCCGCTTAGAAATAAA	CAAGGCTTGGTGCGAGATCTA
156	ADRBK1	NM_001619	CAGGCCCTTGGTGGAATTCTA	CGGCTGGAGGCTCGCAAGAAA	CGGCTGGAGGCTCGCAAGAAA	CCGGGAGATCTTCGACTCATA
157	ADRBK2	NM_005160	AAGCTACTTGATTGCGACCAA	TGGGATTAACTAATCATTGAA	CAAGTGTATGGGATTAACTAA	AAGATGTTCAGTGTTGGGTAA
166	AES	NM_198970	TAGCTGTGCCTTTCCAATAAA	CGGCTTGAACATCGAGATGCA	CTGACATGTGAGGCAAGCTAA	CAGGCCCACCTCTCCAAGGAA
177	AGER	NM_172197	TAGCTCCTGGTGGAACCGTAA	CACGGCTGGTGTTCCCAATAA	CTGTATAATCTCTCTCCTGTA	AAGGGAGTATCTGTGAAGGAA
181	AGRP	NM_007316	CTGAAGAAGACAACTGCAGAA	CAGCCGCACCTAGCTGGCCAA	AAGCTGGGTACTGCCATGAAT	CAAGCTGGGTACTGCCATGAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
183	AGT	NM_000029	ACCGACCAGCTTGTTTGTGAA	CTGTTTGAATGCGGAACAATA	CTCCGTGTAGTGTCTGTAATA	CAGAGTCTACCCAACAGCTTA
185	AGTR1	NM_000685	ATCCAAGATGATTGTCCCAAA	CTGGATGTATTGATTCAACTA	CGCGGGTTTGATATTTGACAA	ACGCACAATGCTTGTAGCCAA
187	AGTRL1	NM_005161	CACCTGCATCAGCTACGTCAA	CACCATCATGCTGACCTGTTA	CACTGTGGTTCATCAAATAAA	CACCACTAAGGTGCAGTGCTA
189	AGXT	NM_000030	CCGAGTGCACCCGATGACCAA	CTGGAGAGACATCGTCAGCTA	CCAGGATGTACCATCACACAA	CTCCCGGGAATGTTTAATAAA
190	NR0B1	NM_000475	ACGGCAGGGCAGCATCCTCTA	ATGGATGATATGATGCTGGAA	ATCGAACTTAATAGTACCCTT	ATGCTCTGTACAAAGATATAA
197	AHSG	NM_001622	CCAGGGCTGATTTATAGACAA	CTGAAAGACCTTCCTTAATAA	AAGCTTATATGTGCCTGTTAA	CACATGCGATCTACATTAATA
199	AIF1	NM_004847	CCCAGATATCATGTCCCTGAA	CAGAGTCAACAAATTAAATAA	AAGCCAGAGTCAACAAATTAA	CACCTAGCAGTTGGTTGGCAA
207	AKT1	NM_005163	CAGGGTTTACCCAGTGGGACA	AAGGTTTAAATTTGTTATTGT	CACGCTTGGTCCCGAGGCCAA	ACGCTACTTCCTCCTCAAGAA
210	ALAD	NM_000031	CAGGGTATCGGTGATGAGCTA	AAGGGTGAGCCATCAAGCTAA	CCCAAGAACTAGAACTTTAAA	CTCCCAATAATCAACAGCAAA
215	ABCD1	NM_000033	CCGCACCTTCCTGTCGGTGTA	CCACCTCTTTCTACAGCCTAA	CTCGGAGGAGATCGCCTTCTA	CTCTTTCTACAGCCTAATTTA
217	ALDH2	NM_000690	CAGGCATACACTGAAGTGAAA	CACAGTCAAAGTGCCTCAGAA	AAGCTATTGTTTACAATTATA	CAGCCATTGATGGAAAGTTCA
219	ALDH1B1	NM_000692	CTTGGATTACTCAGCCATAAA	TTGAACTAGGTGGATACTAAA	CTCAGAGTTCTACCTATCTAA	CAGCACGTGGATGTTGACAAA
220	ALDH1A3	NM_000693	TTGGGAAAGGATTCACAGTAA	ACCAGTGTGTGTATAACGAAA	AACGGTCTGGATCAACTGCTA	AACCTTGATAGTGATACGTTA
222	ALDH3B2	NM_000695	CTCCGGCCTGGAGAAATTAAA	CACGGCCGTCTCCACCAGAAA	CAGGCCTGGATGAAGGATGAA	CCCACCCTATACCGACTGGAA
225	ABCD2	NM_005164	CAGTGACACATTGGCAATTAA	CAGCATTGATGTCGAAGGAAA	CACTCGAGAATTATAGCCAAT	TCGCCTAGTAGACCACGCCTA
226	ALDOA	NM_000034	CTGTCTCTGCTTCGAGATCAA	TCCGGCACACTGCCAAATAAA	CACGTCAACGATTCTATTTGA	GCCAAATAAACAGCTATTTAA
239	ALOX12	NM_000697	CAAGCCCAAAGCTGTGCTAAA	CCCAAAGCTGTGCTAAACCAA	CTGGCCCTATGAATATCTGAA	CTGGTATGCCTGGGTCCCTAA
248	ALPI	NM_001631	CCGGGCTACGTGTTCAACTCA	CCAGACAATAAAGGGACCAAA	TCCATTCTCCTAGGAGACAAA	CACGTCCATCCTGTACGGCAA
258	AMBN	NM_016519	CACCATCAGATAAGCCACCAA	TACCAGCATGACACTATTATA		
262	AMD1	NM_001634	CGGGAGAAGAGGTTTAATTTA	CTGGGCTTAATATTCTTTAAA	TGGGTTTATATACTAATTCTA	AAGGTGGACCTTGTTGCTAAA
265	AMELX	NM_001142	ATCCCTGAGTTTCAAACAGAA	CAAACAGAAACTTGCACTGAA	TCCCTGAGTTTCAAACAGAAA	CAGGAGTGACACAAGAACACA
268	AMH	NM_000479	CCAATAAAGACCAGCAAGCAA	CCACGTGGTGCTGCTGCTGAA	CAGGCCATCCGCGGAACTCGA	CGCGTGGCTGCTGAACTGCAA
269	AMHR2	NM_020547	CACGACCACATTGTCCGATTT	ATGGCCAATATAAACCAGGTA	CTGGCAGAATGGCCAATATAA	CAGAATGTGCTCATTCGGGAA
270	AMPD1	NM_000036	AACCTGGGCTATCACCTCAAA	CGCCATGTCACCACTAAGTAA	CACCTTCTTAGACGATATGAA	TTGCTGAGGGTCTTAAATCAA
271	AMPD2	NM_004037	CAAGTTTAATGCCAAATACAA	CGGCTTCTCGCACAAGGTAAA	CCGGAACTGCATCTCTTCTTA	CCGGACCAATGTGCCAGACAT
283	ANG	NM_001145	CCGGGATGACAGATACTGTGA	CAGCATCAAGGCCATCTGTGA	CGGGATGACAGATACTGTGAA	AACGTTGTTGTTGCTTGTGAA
287	ANK2	NM_001148	AAGCTTGGTTACACACCTTTA	CAGGACCCTTCTAAACATAAA	ATCAAGCTATTTGCAACTTAA	ACCGTGCAAACGGGTGATATA
288	ANK3	NM_001149	CAGGATTATCACGAAAGATTT	CGCATCCTTAGCTTTACGTAA	AAGGATCTTAACCTCAATTAA	CTAGTCGATTATTTAAGCATA
290	ANPEP	NM_001150	CACCACCTTGGACCAAAGTAA	CCGGGTGAACTACGACGAAGA	AACGATCTCTTCAGCACATCA	CCGAAATGCCACACTGGTCAA
291	SLC25A4	NM_001151	CTGTATCATCAAGATCTTCAA	CAGATCCATTGTGTGGTTTAA	TACAGTGAACTTGATCTACAA	CTGAATGTGAAACATCAATAA
292	SLC25A5	NM_001152	CAGGCATGTTGTATTCTATAA	CGGAAGATTGCTCGTGATGAA	CACAATCTTGAGCATTCTTGA	ATGTTGTATTCTATAACACAA
310	ANXA7	NM_001156	CAGAAATTCTTCGTAAGGCAA	CTGTGTAATAATATTGAATAA		
312	ANXA13	NM_001003954	CAGGCCAAGCTGTGTAAGTTA	CAAGAGCACATTCCAAATCAA		
317	APAF1	NM_001160	TAGGCAGAGTATAAAGTATTA	CAGTGAAGGTATGGAATATTA	CCGCATTCTGATGCTTCGCAA	AAGGGCAATGGAGATAAATTA
320	APBA1	NM_001163	CAGGATCAAGATGGCCCAGAA	CAGGAAGAGAAGAATCCACAA		
324	APC	NM_000038	CAGAGACTAATGAAAGTTCTA	CCGGTGATTGACAGTGTTTCA	TCCATCTAACATCATAATTAA	CAGACTAAGCATTGAGCATAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
327	APEH	NM_001640	CCGCCAATACCTGGTGTTCCA	CAGGAGGAACACTTTGATGCA	CTGGAAGTTGCTCACAATTGA	CAGAGGAATGTGGGCTATGTA
329	BIRC2	NM_001166	CAGGGCTTTAAGTTAGTATTA	TCCCAGGTCCCTCGTATCAAA	TCGAAACTTTATAAAGGGATA	TAGGCGTTTCTGATAACACTA
336	APOA2	NM_001643	ATCAAGAAGGCTGGAACGGAA	CCCACTCTTTGCTACAATAAA	TACAATAAATGCTGAATGAAT	AGGCCAAGTCTTACTTTGAAA
339	APOBEC1	NM_001644	CACCAATCACGTGGAAGTTAA	CACCCTGTTTAAAGATTTCAA		
345	APOC3	NM_000040	AAGACTACTGGAGCACCGTTA	CTGGAGCACCGTTAAGGACAA	CAGGAACAGAGGTGCCATGCA	CCCAATAAAGCTGGACAAGAA
350	APOH	NM_000042	ACACATGGAAATTGGACTAAA	CTGGATGGCCCGGAAGAAATA	CACATGGAAATTGGACTAAAT	CAAGTTGTAAAGCATCTTGTA
351	APP	NM_000484	CTGGTCTTCAATTACCAAGAA	ACCCAATTAAGTCCTACTTTA	CAGACTGAACATGCACATGAA	AAGGATGACTACAGACATTAA
353	APRT	NM_000485	CACACTGAACCCAATTACACA	CTGTGTTTCAGCCACACTGAA	CAGCTGGATCCCAGGGAAATA	CAGCCACACTGAACCCAATTA
355	FAS	NM_000043	TCAGTGTATGTTAGTACAAAT	CACATTGATTAAAGATCTCAA	CAGAATTTAAATAAGGCTCTA	AAGGACATTACTAGTGACTCA
366	AQP9	NM_020980	CAGCCTCTAATTGGAACGGCA	CAACCAAACCCTAAATTGAAA	AACCGTCTTTGGCATTTACTA	ACGACTGTGCTTGTCCATTAT
367	AR	NM_000044	AAGAAACTTGGTAATCTGAAA	CACGGGAAGTTTAGAGAGCTA	CAGGAATTCCTGTGCATGAAA	AAGGAACTCGATCGTATCATT
368	ABCC6	NM_001171	CTGAGGGAATCCACACTTCAA	ACGGTTGACGTGGACATTCCA	CACCCATTGGTCACCTGCTAA	CACGTGTGCTGTGCTGAGCAA
372	ARCN1	NM_001655	AAGGCAAATTCTTTAATCAAA	CCCACTTGTGTCAATATTAAA		
375	ARF1	NM_001658	AAGCTGGAGCTGTTAAATTTA	CACGATCCTCTACAAGCTTAA		
382	ARF6	NM_001663	CTCAGTATGTTAAACAGGTAA	ATGGTTAACCTCTAACTACAA		
388	RHOB	NM_004040	CCTGCTGATCGTGTTCAGTAA	CCCAGTGGTACTTCTACTAAA	AGCTAAGATGGTGTTATTTAA	CACAATTGTTTCATTGTTTGA
389	RHOC	NM_175744	CAGGAGAGAGCTGGCCAAGAT	CCCTACTGTCTTTGAGAACTA	CCGGATCAGTGCCTTTGGCTA	CACCATGGCTGCAATCCGAAA
391	RHOG	NM_001665	CAACAGGATGGTGTCAAGGAA	CGGGCGCACAGTGAACCTGAA		
397	ARHGDIB	NM_001175	AAAGGAAACCATTGTGTTAAA	CACTGAATAAATAGATCAGAA	AAGGAAGGTTCTGAATATAGA	CACAGCTGGGTCCCTCTTCAA
401	PHOX2A	NM_005169	CCAGCAGAGCGGAGTTCTTTA	CAGAGGGATTCTCTTTCCCTA		
403	ARL3	NM_004311	CAGACCTGTAAGGACTTGCAA	ACCGATATTCTTATATATGTA	ATCTGACATGAAAGTCATTAA	AGGGAACAACACGGTTTAGAA
405	ARNT	NM_001668	AACCCGAGACTTGGCCATAAA	ACGGAACAAGATGACAGCCTA	CCCAGCCAATATACAACTGTA	CAGCCAATATACAACTGTAAA
406	ARNTL	NM_001178	TACGTTTGGACCCAAGCTTAA	TAGGCACATCGTGTTATGAAT	TCGGCACGCGATAGATGGAAA	TCGATGGTTCAGTTTCATGAA
410	ARSA	NM_000487	CTGGGTCTGCGGTATCGGAAA	CAGGGCTTCCATCGATTTCTA	CCCGGTTCGGATGGGCATGTA	TCGGCAGTCTCTCTTCTTCTA
411	ARSB	NM_000046	AAGGGTATGGTCTCTAGGCAA	CACATTTCTTACGCAAATGAA	ATGGGTGTACACTACGCATAA	AACCAACTTTATAGTACATAA
414	ARSD	NM_001669	ATGGAGGACATTTAGAGGCAA	AAGGTTCTTAATGCCATCGAA	AACAGCGAGTCTTATGCTAAA	TCGGTTGCTACGGGAACAATA
415	ARSE	NM_000047	CCGCTGGGAACTCTCAGAGAA	CACGAGTTCCTGATGCATTAT	CCCTCTTATCACTATGGAGAA	AGGGAAGATGACCCACAATAA
416	ARSF	NM_004042	CGCGTTCTTGACGGGAAGATA	CTGAACGAGCTGGATCCATTA	CAGGTATGGTTTCTAGTGGTA	ACGGAGGGCATTTGGAAGCTA
421	ARVCF	NM_001670	CACGGAGAGCCGGAACTTCAA	CCGGAAGGACACTGACAACAA		
427	ASAH1	NM_004315	CACGGATGGCACGAAAGCCAA	CACGTTCTGTTAATTTAGTAA	ATGGTATGTGGTACAAACAAA	CACGATTAACTGTGAAATGTA
430	ASCL2	NM_005170	CACGCTTTGGGCCTTACAGAA	GAGGGTTATCTATACATTTAA	AAGGAAGGAGGGCGTGAGAAA	AGGGAGCGTGAACTTTATAAA
432	ASGR1	NM_001671	CTCCTTTAATTTATTTCTTCA	TCCGAAGGTGAGGAGCTTGAA	CAGGAGCCACCTCTCCTTTAA	CAGGTTATCATTGTGAACTTT
433	ASGR2	NM_080914	CTGTAATTCATTGTAATTATT	GAGCAGAAATTCATTGTACAA	CAGACTATAGGCACAACTACA	CACGAGCTGGGTGGAAGTGAA
443	ASPA	NM_000049	AACCGGAGTATTTCTGGTTAA	CTGCGCCATTGAGGTCTATAA	TACGTTTATCTGATTGAGCAT	TACATCTTACACGGTGTCTTA
472	ATM	NM_000051	TTGGCTTATACGCGCAGTGTA	CACTTATTCATTAGTAATTTA	CACCTGTTTGTTAGTTTATTA	AACCATGAGTCTAGTACTTAA
473	RERE	NM_012102	CAAGAGAGAGTGAGAATTCAA	CAGGAAGATTATTACAGTCGA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
477	ATP1A2	NM_000702	ACCCATAGCAATGGAGATTGA	CCGATTAATTGGAGATTACTA	AACAATCAGATTAGACACTAT	CAGATTAGACACTATGTGTTA
480	ATP1A4	NM_144699	CTGGTTTATGCTGGCCCGAAT	CTCAATGAACGATGAAATGAA	AAAGGGAGACGTACTACTAAA	CCGGGCTGACTTTAAGGCTAA
483	ATP1B3	NM_001679	CCGCATTGGAATATACATTCA	CAGACTGTGGACTGTAATAAA		
486	FXYD2	NM_001680	CACCAGCCTCTCCAAGCTCAA	CCCGTTCTACTATGACTATGA	CCACCTCATGCTTATAATAAA	ATCAATGAAGATGAGCCGTAA
487	ATP2A1	NM_004320	CCCGTGTCATGTGTCTGTTTA	CCCGATAGTGACACATCTTCA	CACCAACATTGCAGCCGGCAA	TCGGAACTACCTAGAGGGATA
492	ATP2B3	NM_021949	CCCTCTTTATAAAGCATTATA	CCGGAAGACAAGCTTTACAAA	TTCCCTGATGTCCTTGTTTAA	CACAGATACGTAATAATTTAA
501	ALDH7A1	NM_001182	CGGGAGAAGATCCAAGTACTA	TCCGATTCTCTATGTCTTTAA	AAGGATGATTGGAGGACCTAT	AAGGTCTACTTGTACTATCAA
506	ATP5B	NM_001686	AACAGTATTTAAGGTTTCCAA	AAGAATTACCACTACCAAGAA	ATCTGGTGTTATCAACTTAAA	ACCCGTGAAGGCAATGATTTA
509	ATP5C1	NM_001001973	CAGGTCTGTCATCTCCTATAA	CAGCAAGATATTTGTAAATTA		
523	ATP6V1A	NM_001690	TAAGGTAGAGTCAATTATGAA	ACCCAAATTGTGATAGCATAA	GAGCTTGAATTTGAAGGTGTA	ATGGAGGTTGATGGTAAGGTA
527	ATP6V0C	NM_001694	CTGGATGTTTATTTATAAAGA	CAGCCACAGAATATTATGTAA		
533	ATP6V0B	NM_004047	CAGCTGGAGCTGTGTCCCTTA	TCCTAGTGTTTGTGAAATAAA		
535	ATP6V0A1	NM_005177	AAGGTTCAGTTTCGTGACTTA	ACGGCCGATGTTTACTTATAA		
537	ATP6AP1	NM_001183	CACAGTGACATTCAAGTTCAT	CAGGGAAGTCCTCACAGGCAA		
538	ATP7A	NM_000052	CAGCAAGTCACTTAGATCATA	CAGCCAGTTATTCTTCCATTA	CTGGACCGGATTGTTAATTAT	TAGCAGCTTGTAGTATTGAAA
545	ATR	NM_001184	AAGGACATGTGCATTACCTTA	GCCGCTAATCTTCTAACATTA	CCGCTAATCTTCTAACATTAA	CAGGCACTAATTGTTCTTCAA
546	ATRX	NM_000489	ACCGGTGGTGAACATAAGAAA	CCGACAGAAACTAACCCTGTA	CCGGTGGTGAACATAAGAAAT	AGGCGACGTATTAAGGTTCAA
547	KIF1A	NM_004321	TCGGATCAACGACACGACCAA	CAGCCCGATCGTTTCCAAGAA	TCGGGTCATGCCACTGTCCAA	CAACTCGGAAATTAACTATAA
552	AVPR1A	NM_000706	CAGAAATACAACAGAAGTTAT	CACTTTATTAATATAACCATA	TCGCAAACATAGGGTAATAAA	ATGAACGGACTGGATAGTAAA
567	B2M	NM_004048	CAGGTTTACTCACGTCATCCA	TCCGACATTGAAGTTGACTTA	CTGGGTTTCATCCATCCGACA	AAGTGGGATCGAGACATGTAA
570	BAAT	NM_001701	TTGGCTTACCATAACTATGAA	ATGGCTATTTACCTAAAGCAA		
576	BAI2	NM_001703	CCCACTGCATATAAATATATA	CGAGGTCTTGCTCATCAACAA	CTCTCTGATTGTCACAGATAA	CCCGAACGAAAGGATACGGTA
577	BAI3	NM_001704	TTCGGGATATACCAAATACAA	GAGATCCATAATACTAATTAA	TTGGATGATAATGCAGGACTA	ATGGACTAAGGTAGAGACAAA
578	BAK1	NM_001188	CTCTGAGTGTTTGGAAATAAA	CAGGATTCAGCTATTCTGGAA	CTGGACTTAAGCGAAGTCTTT	AACCCATTCACTACAGGTGAA
580	BARD1	NM_000465	TCCGATGAATTCATTAGTCTT	GACCATCAATACAGTCGCATA	TGCAGTAATTCTTAAGGCTAA	CTGAATATTATACCAGATGAA
581	BAX	NM_004324	CCGAGTGGCAGCTGACATGTT	CAGCTCTGAGCAGATCATGAA	CAGGGTTTCATCCAGGATCGA	ATCATCAGATGTGGTCTATAA
587	BCAT2	NM_001190	CCGGCTCATCGAAGTGGACAA	CACCTGAAGTGCAATACGAAA	AACCATGAACATCTTTGTCTA	CTGAAGTGCAATACGAAATAA
594	BCKDHB	NM_000056	CAGGCCGAAGTCATACAGGAA	CTGGAAGATTATGACTAGATA		
595	CCND1	NM_053056	ATGCATGTAGTCACTTTATAA	CTCCTACGATACGCTACTATA	AGGGTTATCTTAGATGTTTCA	AAGGCCAGTATGATTTATAAA
596	BCL2	NM_000633	GTGGATGACTGAGTACCTGAA	CCGGGAGATAGTGATGAAGTA	CTGTGGCATTATTGCATTATA	CAGGCTTAAGATTTGGAATAA
598	BCL2L1	NM_001191	CAAGCTTTCCCAGAAAGGATA	AAGGCGGATTTGAATCTCTTT	CTGCTTGGGATAAAGATGCAA	AAAGTGCAGTTCAGTAATAAA
602	BCL3	NM_005178	CTCGACATCTACAACAACCTA	CACGATGTAAATTATTAAGCA	CAACGTGAACGCGCAAATGTA	ACGGATCACGATGTAAATTAT
605	BCL7A	NM_020993	TACGATGCTGATCATCATTGA	CTGCACTTCGAGAAGAATCAA	CAGCACCTTCCTACAACCCTA	TGGAATGTTCATTATCGCCAA
611	OPN1SW	NM_001708	TTGGCCTGTTTGCAACAGCTA	GCGCTACATTGTCATCTGTAA	CGCCATGTACATGGTCAACAA	CAAGAGTGCTTGCATCTACAA
613	BCR	NM_004327	CAGCCGCAACGGCAAGAGTTA	TGAACTTAACTTAGAGTCTAA	CAGCATTCCGCTGACCATCAA	ACGGCAGTCCATGACGGTGAA
622	BDH	NM_004051	TGGCTGCTTGATGAAGGACAA	CAGCAGCGAAGAGGTGGAGAA	CTCAATGTCTGCAGCAGCGAA	CAAGCAGGTGGCAGAAGTGAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
624	BDKRB2	NM_000623	ATGAGTTGATGTCTCCGGTAA	GCCCTGGGTTTCTTTAATCTA	CTGGCAGGTTAGAACCTAGAA	CTGCACGGTGGCAGAGATCTA
638	BIK	NM_001197	GAGGAGAAATGTCTGAAGTAA	TCGGCAAAGAATCTACTGGAA	CCACACTTAAGGAGAACATAA	CCGAGGAGCAGGAGTGCTCAA
640	BLK	NM_001715	AAGGTGGTTCTTTAGATCACA	CAACATGAAGGTGGCCATTAA	CTGGTAAGCGACTGTCATCAA	CAGCCGTGCTGTTAAACCAAA
641	BLM	NM_000057	GACGCTAGACAGATAAGTTTA	CTGACCATCTGTGACTATAAA	ATGCTCGGAAATAAAGCCCAA	CCGAATCTCAATGTACATAGA
643	BLR1	NM_001716	AACGCTGGAAATGGACCTCGA	ACGGAGAAAGGTGGACTGGAA	CCCGCTAACGCTGGAAATGGA	CAGCCATGAACTACCCGCTAA
644	BLVRA	NM_000712	TCCAGAAATATTGCTGTTCAA	ACCATTATCTCTATTCTTAAA		
649	BMP1	NM_001199	AAAGGGCTTCTTTGCAGTCTA	CAGCTATATTGTGTTCACCTA	CTGGCTCAAGTTCGTCTCTGA	AAGGACTATGGCCACATTCAA
651	BMP3	NM_001201	CCCAGCTGGTTTGGAGTTCAA	CCGCCATTTCTGAGCCAGAAA	CTGTCTAAAGATATCACTCAA	CAGGAGATACCTCAAGGTAGA
654	BMP6	NM_001718	CCCGGACGACCATGAGAGATA	CAGCATTTATCAAGTCTTACA	CCGGACGACCATGAGAGATAA	ACCGTGCTGTGCGCCAACTAA
656	BMP8B	NM_001720	CAGGTAGACATGTGGAGTCAA	TAGGAAAGACATGTAAGAGCA	CTGAGTGAACAGCATGATTTA	ACAGATATGATGTAAAGTGAA
657	BMPR1A	NM_004329	ACCAATTTATGTAACCAGTAT	CACTGAATGATAGTCATTTAA	GCGGCAGACATTAAAGGTACA	CAGCTACGCCGGACAATAGAA
659	BMPR2	NM_001204	CCATATGAGCATTGTAATTAA	AAGCTCTAAATTGATGTGCTA	CTCGTAAGTATGTAAAGGAAA	AAGCACCGAAGCGAAACTTAA
671	BPI	NM_001725	CCCAGGGTTAACGAGAAACTA	CAGACGTTGTCTATAAATGAA	CAGGGTTAACGAGAAACTACA	AGGAATCGTGTTTCAATTGTA
675	BRCA2	NM_000059	TACGTACTCCAGAACATTTAA	TTGGAGGAATATCGTAGGTAA	CAGCGTTTGTGTATCGGGCAA	CAGGACACAATTACAACTAAA
686	BTD	NM_000060	AACCAGAACCTTGACATCTAT	CACAAATGTCGTGTTCAGCAA	CAGATTATAGTGTTTCCAGAA	ATGCGATTGGTCTCAAGCTAA
708	C1QBP	NM_001212	CAGGCTTTGGCCAGTGAACAA	CACGGTCACTTTCAACATTAA		
710	SERPING1	NM_000062	CGCCAACTTGGAGCTCATCAA	AACCTGAAACATCGTCTTGAA	CTGGGTGGCCAAGAACACCAA	TCACCAGACTCTATAAATAAA
712	C1QA	NM_015991	ACGGTCATCACCAACCAGGAA	CCCGGGAATTAAAGGCACCAA		
713	C1QB	NM_000491	CAGAAGTGCCATGCTCAGAAA	CACCAACATGAACAACAATTA		
717	C2	NM_000063	CCGGGATATGACTGAGGTGAT	ACCCTGGCATGTCACTATTAA	CAGAGAGATCCTGAACATCAA	CCCAGTTATGAAATTAATAAA
718	C3	NM_000064	CCGAGCCGTTCTCTACAATTA	CACGGAGAAGCGAATGGACAA	CACGGTCATCGCTGTGCATTA	TAGGAACACCCTCATCATCTA
720	C4A	NM_007293	AACCCTGTACGACTACTACAA	TCCAGTGTTAGACAGGAGCAT		
721	C4B	NM_000592	AACCTGGGAAAGAATATTTGA	AACCCTGTACGACTACTACAA		
726	CAPN5	NM_004055	CCCGGGAGTCGCTGTGGCAAA	CCGCGTGATCAACACATCCCA	CCGGTACTTCACGGACATCAT	CTGGTGTTCTCCCACCTTGAA
730	C7	NM_000587	CACGCAGTTATACTTCACATA	AAGGATTAGAACACTCATTAA	ACCCTGGTAAATATATTTCAA	CCGAAGATTAATCGACCAGTA
757	C21orf4	NM_006134	AAGGGATAATACATGATCAAA	AAGCTGGGATACAGCATTTAA	CACCTGGTATGCTTACATTAA	ATGGAGTAGATTGTACATTAA
762	CA4	NM_000717	ATGCACATAGTACATGAGAAA	CTGGCTACGATAAGAAGCAAA	TGGGACTTTAGGCATGATTAA	CTGGTCCGACTTGCCATATAA
773	CACNA1A	NM_000068	CACCGTCGTACAAGTGAACAA	CCGGGTGCTACGACCTCTTAA	TCGGAACAACGTGCTGCGATA	CGGGTGCTACGACCTCTTAAA
774	CACNA1B	NM_000718	CCCAGGAACAACGCTCTGAAA	CCGGCAGTCGTTCCAGTATAA	CCCGAACACTATTGTACATAT	TCGAATTGGCTCTGACCCTTA
778	CACNA1F	NM_005183	CACCATCATGTCTTCACCAAT	CTGGCCTGCACTGCTATACAA	CACCACACTTCTGCAATTTAT	CCGGACATCCCTGAAGATCAA
780	DDR1	NM_001954	CAAGATCTGGTTAGTCTTGAT	CACTAGGCAGGTAATAATAAA	CAGGAATGATTTCCTGAAAGA	ACGGTGTGAATCACACATCCA
781	CACNA2D1	NM_000722	ATCGGGCATTATGGTAAGCAA	TTCGATAACGACAGTAAATCA	TCGGCCGTCACTATCAAATCA	CCGCCTGTTATGACCTTCTAA
784	CACNB3	NM_000725	CCGGCGTGAAGTAGAGAGCCA	CCGCTTGTTAGGTTAGGGTTA	CTGGAGAGCATCCGGCTCAAA	CTCACTGTCATCACTAATAAA
797	CALCB	NM_000728	AAGGAATGAAACTGAATGCAA	CCCACCAATGTGGGTTCCAAA	ACCTTTGTCACTTGAAAGGAA	AACCTTGGTGATGCATTACAA
801	CALM1	NM_006888	TTCCTGAACAACGAATGTAAA	CTGGTTGTATCTTATTAGCAA	CGGCAACTTACACACATTGAA	ATGCCCGTGTATGTTGGTTTA
813	CALU	NM_001219	CAGGGTTTCAGTCCTTATCAA	AAGCCTGAGATCAATAAGAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
816	CAMK2B	NM_001220	CAGGATCTCTGACATCCTGAA	CCCGGAAGCAGGAGATCATTA	CCGGAAGCAGGAGATCATTAA	CAAGAGTTTACTCAACAAGAA
823	CAPN1	NM_005186	TCCCACGGAACTGCTGTCAAA	CCGGACCATCCGCAAATGGAA	TAGGATCATCAGCAAACACAA	CAGGGACTTGTGTACTGGTTA
824	CAPN2	NM_001748	CTGGAACACTATAGACCCAGA	AACGGATGCTATGAAGCTCTA	AACATGGTATATCATGAAGTA	CCCGAGAATACTGGAACAATA
834	CASP1	NM_001223	TCGGCAGAGATTTATCCAATA	CTCATTGAACATATGCAAGAA	TACCTCTTCCCAGGACATTAA	CCCAGATATACTACAACTCAA
839	CASP6	NM_001226	ACCCAAGATATTTATCATTCA	CTCAGGAAATTAGATAAATAA	GCGCAGATAGAGACAATCTTA	CAGGAATTAAATCATCCCTTA
841	CASP8	NM_001228	GACAAAGTTTACCAAATGAAA	AAGATAATCAACGACTATGAA	CGGAGGGTCGATCATCTATTA	AAGAGTCTGTGCCCAAATCAA
845	CASQ2	NM_001232	CGGCATATTTGGGAACGAGAA	TAGCCTAAGCTGGGATCTGAA	GAGGTTGATTTGCTCTCTAAA	TAGTGTTAAGTGTGCAGTATA
857	CAV1	NM_001753	TCCAGTCTTCCTGACACTTTA	CTGGTCAACCGCGACCCTAAA	TCCTGACACTTTAATTACCAA	CAGCCGTGTCTATTCCATCTA
860	RUNX2	NM_004348	CACCTTGACCATAACCGTCTT	CAGCAGCACTCCATATCTCTA	CAGAAGCTTGATGACTCTAAA	CAGCACGCTATTAAATCCAAA
861	RUNX1	NM_001754	CAGGTCGTTCTTATCTAGAGA	CTCCCTTTCATGTTAATCAAA	TTGGCGATAGGTCTCACGCAA	CAGGAAAGTTAAGGTATCAAT
868	CBLB	NM_170662	ACGGGCAATAAGACTCTTTAA	TCGGTTGGCAAACGTCCGAAA	TCCGGTTAAGTTGCACTCGAT	CACAGCGAGTTCAAATGTCAA
871	SERPINH1	NM_001235	CTCAATCAGTATTCATATTTA	CCCAACCTCTCCCAACTATAA	CAGCCCTCTTCTGACACTAAA	CAAGAACTTATTTGTACATTT
883	CCBL1	NM_004059	CAAGTGGATGATCAAGAACAA	CACAGACATCTCAGACTTCAA		
885	CCK	NM_000729	ATCTATTTATTAAGTTCTCAA	ACCAGAATTGTGCAAATGGAA	TGGACGAATGTCCATCGTTAA	ACGAATGTCCATCGTTAAGAA
887	CCKBR	NM_176875	CACAGCGTCCCTAGCAGTGAA	CCCAAACTGTTCAAGAAATAA	CCGCCGGGTCGAGCTGAGTAA	CCCGTGTACACTGTCGTGCAA
896	CCND3	NM_001760	TGGGACAGAATTGGATACATA	GACCATCATCCTACTGTAATA	CACAACTTTAAGAGGACATAA	CAGGAACCACACCACATCTAA
899	CCNF	NM_001761	CACAGATGGCGTCAATGTGAA	CCGGTTTATCAGTAAAGAGAT	AACCCAAGCGTTGGAACTGTA	CACGGACAACACTTACAAGTA
901	CCNG2	NM_004354	GGGACAGTGGATAATCCTTAA	CTGGAGAGAGTTGGTTTCTAA	AAGGCAGAAATAATTAGGCTA	AAGAGTGAGTATGCTCTTAAA
905	CCNT2	NM_001241	CTCGATGTAAGGGATCATTAT	AAGGGCTTTCTTGGTAATTTA	TCCACATATGATAGTGTTATA	AAGCAAGAATATACTCATAAA
910	CD1B	NM_001764	AAAGCAGATCTGCAAAGACAA	CTTGGTCTAAAGGTAACTTTA	CACAGAAATTCTGTGCACTAA	CTGAGTGTCAAGAATGCTTCA
914	CD2	NM_001767	AACCTGTATCAAGATGGGAAA	TAAGATGAGCTTTCCATGTAA	CCCAACAAATTCCAGCTTCAA	CCCGAATTAAACCTGTATCAA
915	CD3D	NM_000732	CTCACTTATTAATTCTAGTAA	CACGAGGAATATATAGGTGTA	TGGCACGATATGTTAAACCAA	CAGGCTATATATGGTATTAAA
919	CD3Z	NM_000734	CAGGAAGGCCTGTACAATGAA	CACGCTTTCAGCGAATGACAA	TTGGTTATATTTAGCTCCAAA	ACCCAACACATGGGACCTATA
923	CD6	NM_006725	CAGCACTACTGCGGCCACAAA	CTGGCGGTTCAACAACTCCAA	CCGGCAGGATGTACTACTCAT	CAGGGAGGATGCTGCCTCCAA
926	CD8B1	NM_172100	TAGCACTAAATTCGAGAAGCA	CAAATACAATAGAGCCACTAA	TAGCTGTGTTTCGGGATGCAA	ACCCGGCAACATCAGTTTAAA
928	CD9	NM_001769	CAAAGAGGTCTTCGACAATAA	ACAAATGTCTATCAACTTTAA	CCGCGAGATGGTCTAGAGTCA	AAAGAGGTCTTCGACAATAAA
929	CD14	NM_000591	CCCGAGGTGGATAACCTGACA	CTCAGAGGTTCGGAAGACTTA	CAGAATAATGAATGGACTCAA	CAGCCTAGACCTGTCTGACAA
931	MS4A1	NM_021950	GAGCAACTTTCTTACACTGAA	TTCAATCATGGACATACTTAA	CACACACCATATATTAACATA	CACCATATATTAACATATACA
939	TNFRSF7	NM_001242	AACGAAGGAAATATAGATCAA	ACCGAGTGTGATCCTCTTCCA	AGGAAATATAGATCAAACAAA	AAGGTTGGCTTGCCACCTGAA
940	CD28	NM_006139	TGGGTTAAGCATGCCAATTTA	CAGGGATGAGGTGCTATAATA	CTCGAGTGACTAGACCAAATA	ATGATGGTTCTTCAACTATAA
961	CD47	NM_198793	TACCATTCCTATAGTACTTTA	CACTACTGAAGTATACGTAAA	TACAGCTGTGTTACCGTTAAA	CACGATAAGTTTACTCCTCCA
962	CD48	NM_001778	CTGGCGAGTCTGTAAACTACA	CTGCAAGTGCTTGACCCTGTA	CACCCTTATGCCACATAATTA	CAGAAGCATGCTGCTGAATTA
965	CD58	NM_001779	TCCAATTGATTGGTAACAGAA	TAGCAGTAATTACAACATGTA	ATGCATGATACCAGAGCATTA	AGCAATGTAAACGTAACTCAA
967	CD63	NM_001780	CTGGCTATGTGTTTAGAGATA	CAGATGGAGAATTACCCGAAA	TGGGATTAATTTCAACGAGAA	CAACGAGAAGGCGATCCATAA
970	TNFSF7	NM_001252	CTGCGTCTCAGCTTCCACCAA	CAGCTACGTATCCATCGTGAT		
975	CD81	NM_004356	AAGGAACATCAGGCATGCTAA	CCGCCTGTGTATATAACGTTT	CGCCTTCAACTGTAATCACAA	CACCTTCTATGTAGGCATCTA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
983	CDC2	NM_001786	AAGCCTAGCATCCCATGTCAA	TTGACTAACTATGGAAGATTA	TCGGGAAATTTCTCTATTAAA	CAGGTTATATCTCATCTTTGA
987	LRBA	NM_006726	CACGATGGAAACAGATGATAA	CAAGGGTACATTTAAATTCAA		
988	CDC5L	NM_001253	ACGCAGATTTCAGGAAATTAA	TCGAGACAAGTTAAACATTAA		
995	CDC25C	NM_001790	GAGCTGCAATCTAGTTAACTA	CCAGGGAGCCTTAAACTTATA	CCAGAGCTATATATCCTTAAA	CAGGAAGGGCTTATGTTTAAA
1002	CDH4	NM_001794	CCAGAATATGTTCACCATCAA	CACGTCCATCATCAAAGTCAA		
1010	CDH12	NM_004061	CAAAGTCAATATACTGATTAA	CTCCACCTTCTTCTAATTCAA		
1012	CDH13	NM_001257	CAGGATATATTTAAATTTGCA	CTGGAAGATCTCCAAGATCAA		
1019	CDK4	NM_000075	CAAGGTAACCCTGGTGTTTGA	CCGAACTGACCGGGAGATCAA	ACCCTGGTGTTTGAGCATGTA	AAGGTAATCCGGAGTGAGCAA
1022	CDK7	NM_001799	CTCTTGAAATGTAGAATTGAA	TTGGACATAGATCAGAAGCTA	GAGGCTTTAAGGTAGCTTTAA	CCGGATGGCTCTGGACGTGAA
1024	CDK8	NM_001260	CAGGGCAATAACCACACTAAT	TTCGAGAGCTTAAGCATCCAA	CCAGCTGGACAGAATATTCAA	CAGAAGAAATACGTATACCAA
1025	CDK9	NM_001261	CGGCCAGAAGGTGGCTCTGAA	TGGGCACAGTTTGGTCCGTTA	TAGGGACATGAAGGCTGCTAA	AACCGCTGCAAGGGTAGTATA
1027	CDKN1B	NM_004064	CTGTAAGTAACTTCACATTAA	CACGCATTTGGTGGACCCAAA	ACCGACGATTCTTCTACTCAA	AAAGCGTTGGATGTAGCATTA
1029	CDKN2A	NM_000077	TACCGTAAATGTCCATTTATA	CAGGTGTGCCACATTCGCTAA	CAGAACCAAAGCTCAAATAAA	CACGCCCTAAGCGCACATTCA
1043	CDW52	NM_001803	GAGAATAAAGTTACCCTTGTA	CTGGTTATGGTACAGATACAA		
1046	CDX4	NM_005193	CACCGGCTTTCTCGCACTATA	CAAGGAGAGAAAGATGATCAA	GTAGTTTACACTGATCATCAA	CAGGTTATAGTCTCCGAATGA
1047	CLGN	NM_004362	CTGGATTATATTGCAGCATAT	AAGAAAGTAATCAATCAAATA		
1050	CEBPA	NM_004364	CAAGAAGTCGGTGGACAAGAA	CTCAGCCTTGTTTGTACTGTA	CCGAGTCACACCAGAAAGCTA	CAGCCGATATCAACACTTGTA
1056	CEL	NM_001807	CAGCCACATCCTGGCTGGCAA	AGCCCTGACGCTGGCCTATAA	CCCGTTATGATCTGGATCTAT	TCCCATGAGCCTTGGTATCAA
1059	CENPB	NM_001810	CCGGGAGAAGTCACGGATCAT	TTCGAGGTCTTGGACATCAAA	CACGCTGAGCACGATCCTGAA	CGCCTTGAGAAGCACAGTTTA
1069	CETN2	NM_004344	AAGCTCTTTGATGATGATGAA	GCGAATTACCCTAATTCTCAA	AAGCACATGTAACTAGATTTA	CAGAACGACTTTAGACAAGCA
1070	CETN3	NM_004365	CTGGTGACATTTAAAGAATTA	TCGAGCTATGATAGAAGAATT	TAGCTTTGTATTTATAATAGA	CAGTTACCATCTTATATTCTA
1072	CFL1	NM_005507	CAAGGTGTTCAACGACATGAA	CTGACAGGGATCAAGCATGAA	CAGTAAGGGACCTTCGATTAA	CAAGCATGAATTGCAAGCAAA
1082	CGB	NM_000737	CACCACCATCTGTGCCGGCTA	CCCACAATAAAGGCTTCTCAA	CCAGGACTCCTCTTCCTCAAA	CCCGAGGTATAAAGCCAGGTA
1084	CEACAM3	NM_001815	CAGTTCCATGTATACCAAGAA	CAGGACAGCAGCTTCCATCTA		
1088	CEACAM8	NM_001816	TTGCTTCTTCTTCAAGATTTA	CAGGCATGCAATGCTAGATAA		
1103	CHAT	NM_020549	CAGGACGGTCCTCGTGAAAGA	CCCGAGATGTTCATGGATGAA	CCGGAAATTCAAGGCCACTTA	CACGGAGATGTTCTGCTGCTA
1109	AKR1C4	NM_001818	CTGGGAACCCAACGACATAAA	GAGGGTGTTGCACGACATCTA	ATGGACCATCCTGATTATCCA	CCAGAAAGCAAACATAATAAA
1112	CHES1	NM_005197	CTGGACTTGGTTTATATTGCA	TCGAAGGAGCCTTCACGTAAA	CACGGCCAAATTAATTTACGA	CCGGTCCTGTTTGAATAACAT
1113	CHGA	NM_001275	TACCGAGGTGATGAAATGCAT	TCCAAGGATGTTATGGAGAAA	AAGGAGTGGGAGGACTCCAAA	TATGAACTTTATCTAAAGAAA
1116	CHI3L1	NM_001276	CAGCTGCTCAATAAAGTACAA	AAGGCCGAATTTATAAAGGAA		
1119	CHKA	NM_001277	TACCACAGAGATTGTACTATA	CACAGAGATTGTACTATACAA	CCGGCCCTTACCAAACCTGAT	AGCCGGCGATTAGATACTGAA
1121	CHM	NM_000390	TCGGAGTTTGATGTGATCGTA	CCGGAGAGTTCTGCATGTTGA	CGGAGTTTGATGTGATCGTAA	CTCCAATATATTGTCATGCAT
1128	CHRM1	NM_000738	TGGCTCCGAAGTGGTGATCAA	CAGCAAGACAATGACACTGGA	TACAGTCAAGAGGCCGACTAA	CCGGCTTGGCTAGTCACATAT
1130	LYST	NM_000081	CACATCATTGTCAACACCTAA	CACGCCGACCTGATTACCTAA	TCCGAGTATGCCATAAGTTAA	CAAGGTGTTATTAAACTATTA
1135	CHRNA2	NM_000742	CAGCCTCTGTTTGACCATGAA	CACGGGCACCTACAACAGCAA	CAGGAGTGGAGCGACTACAAA	AAGGGCTTTGAACAATGTTTA
1136	CHRNA3	NM_000743	GCGGCTGTTTGAAGATTACAA	AACTGTCTTAGTACACCATAA	TACCGATAAATGAACATTTAA	CCCACCTTCTATCTAAGACAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
1138	CHRNA5	NM_000745	CTGAACCTTCTTCTATTGCAA	CTGAAGTATACATTTAGTTAA	ATCGTTCTTCCTCAACACATA	CTGAGTAACAGCTAATCTTTA
1142	CHRNB3	NM_000749	CCACCACAGGTTTCAACTCAA	CGGAGAATGGGAAATACTGAA	ACGCTGGAATCCTGATGATTA	CAGGTAGTACAAGACTGGAAA
1143	CHRNB4	NM_000750	CCCAGGGAGAAGGACAGTGAA	CAGCAAGTCATGCGTGACCAA	CAGCTACGTGGACGTGACTTA	CACATGAAGAATGACGATGAA
1144	CHRND	NM_000751	CCGGCACCTGTTTCAAGAGAA	CCGCCAGGACATCACCTTCTA	CGGCTGAAGTGGAATGCTGAA	AACAATTACAATGAGGAGAAA
1146	CHRNG	NM_005199	CACCAATGTCTGGATAGAGAT	CTGCTCTATCTCAGTCACCTA	CACCAACCTCATCTCCCTGAA	CCACCAGAAGGTGGTGTTCTA
1147	CHUK	NM_001278	CAGCGTGCCATTGATCTATAT	CAGGGCAATAGTATGATGAAT	TTCCATAAGCTTGGTGACAAA	CAGGAGAAGTTCGGTTTAGTA
1163	CKS1B	NM_001826	CCAAGAAACCAAAGAAATGAA	GCGATCATGTCGCACAAACAA	AAGAAATCTGTTCATGTTAAA	AACATCTTTCTGATAACATTA
1164	CKS2	NM_001827	TAGGTTACTGTAAGATGTTTA	TCGGACAAGTACTTCGACGAA	CTGTAAGATGTTTAAGATAAA	AAGTTTGTATGTTGCATTTAA
1173	AP2M1	NM_004068	ACGTGTGACTTCGTCCAGTTA	TGCCATCGTGTGGAAGATCAA	TTGGAGGCTTATTCATCTATA	TGGAGGCTTATTCATCTATAA
1178	CLC	NM_001828	CACCTTTGACCATAGAATCAA	CAGGATGGCCAAGAATTTGAA		
1181	CLCN2	NM_004366	ACCGGGATGAAGAGACTATTA	CCGAATCAAGAAACTGCCCTA	CAGATGGAATTCATACGGACA	CTCATTGGAATCGTTACTCTA
1184	CLCN5	NM_000084	CACCGAGAGATTACCAATAAA	AAGGATGTGTTAAAGCATATA	TAAGTGGACTCTGGTTATCAA	ATCCTTGTTCCTGTTACAATA
1185	CLCN6	NM_001286	AAGATGTGAATTCAAGTATCA	TCAGATTTACGTCTACCCTAA	CACCAGAAACATAAAGGATTA	CCGGTGAATGTTATTGGAATT
1186	CLCN7	NM_001287	AGCGTGGAGCTGGATGATGAA	CTGGCTGACCATGTTTCGAAT	CCAGATCAAGTGCTTCCTCAA	CCAGCTCATCGTTCTCCTAAA
1187	CLCNKA	NM_004070	ACTGGCCATCACATTAATGAA	CTGAGTGTGAGAAGATGGAAA	CAGCTCCATTCTTTGGCATAA	TTGGCATAACAGGCAACTCTA
1192	CLIC1	NM_001288	TTCCTGCTGTATGGCACTGAA	AAGGTGTCTCTCAGAGGAAGT	CTGGTGGTTTCCACATTGCTA	AAACCCAGCACTCAATGACAA
1193	CLIC2	NM_001289	AAGCTAGACGGTCTTCTTAAA	CACAATGCCTATGCCCGTGAA	CTGGCTGATTGTAGCTTGTTA	CCCGTGAAGAATTTACCCACA
1195	CLK1	NM_004071	CCGTATTTCCAACACACGATA	CACGATAGTAAGGAGCATTTA	AACGTGATGAACGCACCTTAA	AAAGCCGGTATCAGAACCATA
1198	CLK3	NM_001292	CTGCAAACCTCTGAAGAGTTA	ACCCAAGCTATTTATATGTTA	CTGCATTCTCTTTGAGTACTA	CACGAAGATCTCGGTCCAGAA
1212	CLTB	NM_001834	CTCGGTGCTCATGTCCCTGAA	CAGCGCCAGAGTGAACAAGTA		
1230	CCR1	NM_001295	AAGCACGGGCCATATGAATAA	CAGCGATTAATAACAGGCAAA	GACGGAAGAGTTGAGACCTAA	CTGGATCGACTACAAGTTGAA
1234	CCR5	NM_000579	AGGCAACATATAGGTTGTAAA	AAGGGACATATTCATTTGGAA	TAGGTGAGGATTGATTACCTA	AAGATGGATTATCAAGTGTCA
1238	CCBP2	NM_001296	CACCAGATTACAACAAATTTA	CTCAATTAGCGTTATTGGCAA	CTGCATGAGCCTGGACAAGTA	CTCAGTGACTGTGTTGCTAAA
1244	ABCC2	NM_000392	CTGATCCAATACAGCAGACAA	CTGGAGTACCTACAAGCAATA	CTGGTGGATAGCAACAATATT	CCGTATCAGGTTTGCCAGTTA
1258	CNGB1	NM_001297	CACAAATAGCGCCATCATCAA	CGCCATCGACGTGAACTACAA	CATGGCCTTCTTCGAGTTTAA	CAGAAGTTACTCCGGAAGAAA
1260	CNGA2	NM_005140	CAGGGCTGAGATAGCCATCAA	TGGCGAGATCAGTATCCTTAA	TAGAGGCACCTATGAGTTAAA	AGCACCGACTATAGACATTTA
1261	CNGA3	NM_001298	CCACCTGATAATGGGTATATA	AAGGTTGGAATGGTGTACTAA	CACCTGATAATGGGTATATAA	TCCCTTGGAATTGCATCCCAA
1263	PLK3	NM_004073	GTGGGTTGACTACTCCAATAA	CTGCATCAAGCAGGTTCACTA	CCCGAAATCGTAGTGCTTGTA	CAGAAAGACTGTGCACTACAA
1272	CNTN1	NM_001843	CAGCCTAGTAGCAGTCATTAA	AAGGGTGATAATTGAATGCAA		
1281	COL3A1	NM_000090	TCCGTTCTCTGCGATGACATA	ACCGATGAGATTATGACTTCA	CGCGGTGAGGCTGGTATTCCA	CTCAAGTCTGTTAATGGACAA
1284	COL4A2	NM_001846	CACACCATTCATCGAATGCAA	CACGTTGTCCCTGAGATTTAA		
1285	COL4A3	NM_031366	CTGCTTGTATCCAAGCATATA	TCCCAAGGTTACTTAATTCAA	TACATTCCCAAGGTTACTTAA	AGCGGATATAGAGCTAGCTAA
1287	COL4A5	NM_000495	AAGGGTGATGATGGAATTCCA	CCGGGTCTCAATGGAATGAAA		
1290	COL5A2	NM_000393	CCGGGTCTACGTGGTGAAAGA	TAGGTTTAAGATGACCAATGA	CCGCACGTGTGATGACCTAAA	CACACTAGTATATACCATTTA
1297	COL9A1	NM_001851	CACCGACAGATCAGCACATTA	CAGCATGATTACAATGTATTA	AACGGTTTGCCAGGAGCTATA	CACCTCCCTTGAACAAATTTA
1299	COL9A3	NM_001853	CAGGGTGACAGAGGAGACAAA	CAGGCTCTCGAAGCTCATAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
1300	COL10A1	NM_000493	TACGGAAGTCCTGGACTCCAA	AGCAATCTTAAGGCTCTTTAA	CCCAGCTGGCATAGCAACTAA	AAGCCTGTTTCTAACTATGAA
1307	COL16A1	NM_001856	AAGGGTATTTCCCTCCTTAAA	CAGGAAGGACTCAAATTGGAA		
1314	COPA	NM_004371	CTGGATTTCAACAGCTCCAAA	TCCCACTGAGTTCAAATTCAA		
1315	COPB	NM_016451	CAAGGATTGGTTATAATATAA	CAGGATCACACTATCAAGAAA		
1347	COX7A2	NM_001865	ATCAATATTTATTGACTTGTA	GACCAGTAATCTGATAAATAA		
1349	COX7B	NM_001866	CAGCTCATAATTGATGCCAAA	TGGCATTATTGAAGAAATAAA		
1352	COX10	NM_001303	ACCATAGTCCTTCTAACAATA	AAAGGGATTGTAGGTAGATAA	AAGGGTAGCCCTGGACTTAAT	TAGGTAGATAACATCCAATCA
1359	CPA3	NM_001870	CCCAATAGAATCAACAATTTA	CAGTAGCACCATAACGAAGTA	ATCCTCAAGCATACTTCCTAA	AACGAAGTAGCTTTAAGTGAA
1363	CPE	NM_001873	TACCTGGAAACTATAAACTTA	CTCGGAGTTGTGAGCACTCTA	CAGGCTATCTGGCAATAACAA	TAGTCCGTTAACACTACTTAA
1365	CLDN3	NM_001306	CACCGGCCAGATGCAGTGCAA	CACCATTATCCGGGACTTCTA	CACCACCACCACCACCACCAA	CACGGCCACCAAGGTCGTCTA
1366	CLDN7	NM_001307	GCCGTTGGTGGGAGAGACAAA	CCGCTCTTACCCTAAGTCCAA		
1369	CPN1	NM_001308	CCGCAACTTCCCTGATCTCAA	CAAGGGAATGCAAGACTTTAA	CCGGTGGATGCACTCCTTCAA	AAGACTTTAATTATCTCCATA
1378	CR1	NM_000573	CAGTCCTACGATCCCAATTAA	CTGCATGGTGAGCATACCCTA	TCGGTGTATTTCTACTAATAA	CTGGAGCCAATTGGATCATTA
1385	CREB1	NM_004379	CAGCCACAGATTGCCACATTA	CCGCATGCATAAAGTAAGTAA	CAGCCGGGTACTACCATTCTA	AGGGCAGTTGTTGCTTCTTAA
1393	CRHBP	NM_001882	CTGCAGCTTCTCCATAATTTA	CAGGAAATGGATTCACATTAA		
1394	CRHR1	NM_004382	CAGGACTGCAGTGCAACGCAT	CCGCTACAATACCACAAACAA	GCGGGTGGCTGGTATAAATAA	CAGGTTGGTGACAGCCGCCTA
1395	CRHR2	NM_001883	CTGCAGCTCGTTGACCATGAA	AAGCTCTACTATGAGAATGAA	CACGGCCATTGTCATGACCTA	ACGGATCAGCTTCCACAGCAT
1397	CRIP2	NM_001312	CTGGCACAAGTTCTGCCTCAA	GAGCCTTGTGCTGTCAATAAA		
1398	CRK	NM_005206	TACACTATTTGGACACTACAA	CAGGATGTACCGAGCACTTTA	CTGAGTATAGTTCAACAGTTT	CAGCAGCTAACTAGAGTCCTA
1401	CRP	NM_000567	AAGCGCTGATCTTCTATTTAA	AAGGAGAAATGATGTTATAAA		
1407	CRY1	NM_004075	GAGGATCTTGATGCCAATCTA	AAGGAATGGAACATTACTAAA	CTGTTTGTGATTCGTGGACAA	ATCAGCAGCTTTCACGATATA
1409	CRYAA	NM_000394	CCCGGAGGACCTCACCGTGAA	CCGGGACAAGTTCGTCATCTT		
1421	CRYGD	NM_006891	TCCTCCTTTGTTGTTTCTTAA	TTGTTGTTTCTTAATTTGGAA	CAGCGGCTGCTGGATGCTCTA	ACCGCTTCCGCTTCAATGAAA
1427	CRYGS	NM_017541	AAGATTCAGATCTTTGAGAAA	CCAAATAGGCATCATCAATAA		
1428	CRYM	NM_001888	CACCAAGTTGGTCACCTTCTA	CTGGATGATGAGCTCATGAAA		
1436	CSF1R	NM_005211	CTGGAAGATCATCGAGAGCTA	ATGAGCCAAGTGGCAGCTAAA	ATGGAAATGGACTGACTTTAT	ACCCTCAACCTCGATCAAGTA
1441	CSF3R	NM_172313	TCCTATAACTTCAGTATTGTA	CCAGGCGATCTGCATACTTTA	CTCCTGCATCATCAAGCAGAA	CAGGCGATCTGCATACTTTAA
1444	CSHL1	NM_001318	CCTCAGGAGTACCTTCACCAA	CAGGAGTACCTTCACCAACAA		
1445	CSK	NM_004383	AGGGAACAAAGTCGCCGTCAA	CCCAACTGGTACAAAGCCAAA	TACGCGCCTCATTAAACCAAA	CCGGTACAGAATGTATTGCCA
1447	CSN2	NM_001891	CAGAGTGATGCCTGTCCTTAA	ATGGAAGTCCCTAAAGCTAAA		
1452	CSNK1A1	NM_001892	AAGAACTTAATTTCAGTATAA	CACAGTTGTGATGGTTGTTAA	CAAGAGTAACATGAAAGGTTT	AGGGCTAAAGGCTGCAACAAA
1453	CSNK1D	NM_001893	AACACGCACCTTGGAATTGAA	CGGTCTAGGATCGAAATGTTA	CTCCCTGACGATTCCACTGTA	CCGGTCTAGGATCGAAATGTT
1454	CSNK1E	NM_001894	TCCCTCCGAATTCTCAACATA	CTGGCTCTGAGTTATAAATTA	GTGGTTGTTAATTTGAAGTAA	GAGCTTTATCGTGGTTGTTAA
1455	CSNK1G2	NM_001319	ATGTAAGACTTTGGCCGAAAT	GCACACCAAGAGCCTAATCTA	TAGGAAAGAATCTCTATACAA	AAGAATCTCTATACAAATGAA
1456	CSNK1G3	NM_004384	CAGGTTGTAAGTTCTACAAAT	AAGAGCATAATCAAACAGGAA	TACCGCAAACTTGATATGGAA	CAACATATCTTCGTTATGTAA
1465	CSRP1	NM_004078	CAGGATGTTGTTTGATCTTCT	TGGGAGGATCCTAATGAAATA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
1466	CSRP2	NM_001321	CAGGCCTACAACAAATCCAAA	CAGATAATCTTTAACACTAAA		
1475	CSTA	NM_005213	CAGGAGATTGTTGATAAGGTT	CTGGAACAAATTACTACATTA		
1486	CTBS	NM_004388	CTCCCTATAATCAGACATTAA	AACGATCATGAAGCAAATAAA		
1489	CTF1	NM_001330	CCCGTTCTCTTAACTCTTGGA	CAGCAGATCTGTGGAGACAAA		
1493	CTLA4	NM_005214	AAGAAGAGAGTCCATATTTCA	AAGCATCACTTGGGATTAATA	CCCAAATTACGTGTACTACAA	CAGCATTATGATGTGGGTCAA
1495	CTNNA1	NM_001903	ACAGACTTTACCCGAGGTAAA	GCGAATTGTGGCAGAGTGTAA	CAGTCACTGTTCGTCACTCAA	CACCCTGATGTCGCAGCCTAT
1496	CTNNA2	NM_004389	CAGCATGTAAGCAGGATTTAT	TACCATTGTATTCACTAACTA	ACAGGCTTTAAGTGAATTCAA	CCCATGAATTGAACAATTTAA
1497	CTNS	NM_004937	CTCGCTAGGCGCCCTAAGCAA	CGCCATTAGCATCATAAACCA	CAGCGCCATTAGCATCATAAA	CACCTACTTGAGACTCACCAA
1511	CTSG	NM_001911	CAGACGGAATCGAAACGTGAA	CACAGTGTTGCCAGAGCCTTA	CAGCCTTTCAGGAAAGATGCA	CCACAGAGTATAAATAACCAA
1512	CTSH	NM_004390	GTCCTTCTTAACAGACTCAAA	CACCCGTGTCTATGACGCAAA	CGAGTATATCCTGTACAACAA	ATGGATGTCTAAGCACCGTAA
1513	CTSK	NM_000396	CCCGATGGAATAAATCTAGCA	AGGGCTGATGCTGTACAGGTA	CCGCAGTAATGACACCCTTTA	CACGGGACTAGTTAGCTTTAA
1520	CTSS	NM_004079	CTGCCACATGTTCAAAGTACA	TGGGATAATGTCATTAATATA	AAGGATATATTCGGATGGCAA	AGGAATCTAATTATATCGAAA
1521	CTSW	NM_001335	CCCAGCATGGGCAGAGAAATA	CGCGTTCATAACTGTCCTCAA	CGGCGCCATCTCACCCATCAA	CACCGTGACCATCAACATGAA
1524	CX3CR1	NM_001337	AACTCAGACTAGTTTAGTTAA	CAGACTAGTTTAGTTAAATGA	TCAGATGTGGTAACTGTTAAA	TAGAGTTGCAATCGTAATGTA
1525	CXADR	NM_001338	CTCCATCAATTCTGTATTCCA	CAGGTAATAGGGACTTAGCAA	TTGGTTATATCGAAATAGTTA	CAGGAACTGTACGGAATATAT
1536	CYBB	NM_000397	CACGCTGTGCCTCATATTAAT	CCAGATCATTAGGACATAATA	ACCCTTCGCATCCATTCTCAA	CAGGCTAAGGATACTAACCAA
1538	CYLC1	XM_088636	CAGGTAGAGTTCCTCCATCAA	AAGGAATTACTCACAGAATAA		
1548	CYP2A6	NM_000762	CAACACGGAGTTCTACTTGAA	CACCTTCGACTGGGTCTTCAA	CCGCTTTGACTATAAGGACAA	TCGGGATTTCTTCCTCCCTAA
1549	CYP2A7	NM_000764	ATGCAAATATTCCAAACTCTT	CCTGATGATGAGCACGTTGAA	CCCAAGCTAGGTGGCATTCAT	CAGCTTCTTCTCCAACCCTCA
1558	CYP2C8	NM_000770	CCGGCGTTTCTCCCTCACAAA	ACGAAGTTACATTAGGGAGAA	AACTCACAACAAAGTGCTTAA	AAGTCAGAATTCAATATTGAA
1572	CYP2F1	NM_000774	CAGCATAAGCACAGCCATCTT	CACCATTATCCGCCTTATCAA	CAGCGGGTACCAAGCTGTGAA	TCGCGGCTTCCTGATACCCAA
1579	CYP4A11	NM_000778	CCCTGACGCACCATAATCTAA	ATCAATTGTATCTTGAGTTAA	TCCTATATTAGTTTCCTATTA	CAGCTGTAAATTGTGTGCTTA
1584	CYP11B1	NM_000497	CTGGGACTGCATCTTCCAGTA	CAGGTGGAGACACTAACCCAA	CAGGACAGTGCTGCCCTTTGA	CACCTTCAGAGCCATCAACTA
1585	CYP11B2	NM_000498	CAGGGAGGCTGCAGTTCCCTA	CAGAGATGGCTTCCTTGTTTA	AAGGCGGAACTGTCACTAGAA	CACTAGATCATGGGATCCTAA
1586	CYP17A1	NM_000102	CAGACATGGCCATATGCATAA	CCGGAGTGACTCTATCACCAA	TGAGTTGAATGTCATACAGAA	CAGGCTGAGGGTAGCACCTAA
1591	CYP24A1	NM_000782	CTCGGACTCTTGACAAGGCAA	AAGTTAGAGATCTGTTATATA	TAGGGTAAAGATGAAGCAATA	TGCAATACTTATAAGACTTAA
1593	CYP27A1	NM_000784	CAGCGGAAGCAGCGCTCTATA	CACGCTGACATGGGCCCTGTA	CTCGAAGATATGGAGGCCCAA	CCGCATTGTCCTGGTTCCCAA
1595	CYP51A1	NM_000786	TCCGTTACAAACGAAGATCAA	TAGGGAATAATCGAACATCTA	TAGGTAATTGGCAGATTCTAA	AAGGTCCTTGGGAGTAATAAA
1600	DAB1	NM_021080	AAGGATAAGCAGTGTGAACAA	AAGGATTAAGTAGGATGTCAA		
1601	DAB2	NM_001343	TGGGAGGTTATGTTTATTTGA	TAGAGCATGAACATCCAGTAA	ACGAAGTAGAAACAAGTGCAA	AAGGTTGGCCTTAGTAGTCAA
1603	DAD1	NM_001344	CAACTTTCTAACAAACATTTA	TTGCCTGAGAATACAGATCAA	CAGCCTCTGCCTTTCATTAAA	CAGATTTGACACTTACTGCTA
1605	DAG1	NM_004393	CAAGAAGATTGCCTTGGTAAA	AAGGGTGTGCATTACATTTCA	AAGAACCATATTGACAGGGTA	CCGGTGGTGAATAACAGACTA
1608	DGKG	NM_001346	CAGCATGTACGGAGGCACCAA	CAGCCATGTTGCACGATTAAA	TAGCCACTCACATAAAGTTTA	ACCGCAAATGTGAATTATCAA
1610	DAO	NM_001917	CTGGAGGGAAAGAACTATCTA	ATGGAGGATAATTGAGGCTAA	CAAGAATTATTGGTGAACGAA	CAAGTTGTACTAACATATTAA
1611	DAP	NM_004394	CTGCTGGGAAATCTAAGGCAA	CACCAAAGAAGAGAAAGACAA		
1613	DAPK3	NM_001348	CGCAGCCAAGTTCATCAAGAA	CACCAACATCTCAGCCGTGAA	CCGGCAGAAGGGCACGGGCAA	CCCAGAGATTGTGAACTATGA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
1622	DBI	NM_020548	CTGGATTTGGTTACTGTGCCA	CCAGTTAAACCAGCTACTCAA	AAAGTGTATTTGTTACTTTAA	CAACAAAGTAGAAGAGCTAAA
1627	DBN1	NM_004395	AAAGTTGATAGGAGACTTGTA	CTCATGTCTGTTAATAAAGAA		
1629	DBT	NM_001918	ATGACTGTTCCTATACTAGTA	ACGATTTGTATCGTATGATTA	AACGATTTGTATCGTATGATT	TAGCCATATACAGACAGTATA
1630	DCC	NM_005215	CCGAGGAGTTCCAGTGATCAA	CAGCATACCAATTACCCATAA	TCACTGCAATGTCAAAGTTTA	CACCTGTGTCCAAGAACTCTA
1633	DCK	NM_000788	AGGCAGCCTGCTATAAAGTTA	TGGACTCATCTTAGTTCTGTA	TTGGTATAAATTAATTTGTTA	AAGTTGCAAAGTGGAATTAAA
1636	ACE	NM_000789	CTCCTGTTACCCGAAACGAAA	CACCACAGAGGCTATGCTAAA	CCCGAAATACGTGGAACTCAT	CAGCGACGAGCATGACATCAA
1641	DCX	NM_000555	AAGGGTTTGATGAATAGCACA	ACCCTGCACATTTGATTCTAA	ATGGACTTTAGTATTAGCCTA	CTGAATAGACAGTCCATATAA
1645	AKR1C1	NM_001353	CACGTGGGAGGCCGTGGAGAA	AATTGTTCTGGTTGCCTATAG	CTTGGTGATTTCAGCAAGCTA	AAGGTGGAATGTCATCCTTAC
1649	DDIT3	NM_004083	AGGGAGAACCAGGAAACGGAA	CAGCTTGTATATAGAGATTGT	CAGCTAGCTGAAGAGAATGAA	AAGGAAGTGTATCTTCATACA
1650	DDOST	NM_005216	CCAGTTTAAAGTGGATTACAA	CAGCCTGTCTCTCATAAAGTA		
1652	DDT	NM_001355	AACATTCCTGTGATCACATAA	TCCTCATATGAAATAAATGAA		
1653	DDX1	NM_004939	ATGAAAGTCTGTAGTCTTAAA	CCGGATGGTTACATTGTCAAA	CCGGGCAATCAAGGAACATAA	CACGGTGTTCCTTATGTTATA
1660	DHX9	NM_001357	TTGGTTGTTGAAGTAACCAAA	CTGTGGTTCATTGTAGTTTAA		
1665	DHX15	NM_001358	CCGGACATGTACAGACATCAA	AGGGACTATTATATTAATATA		
1673	DEFB4	NM_004942	TGCCTTAAGAGTGGAGCCATA	GCCCTAGAAGGTATAAACAAA	GCGACATGTAAACCAAATTAA	GACGTGCGACATGTAAACCAA
1676	DFFA	NM_004401	TGCCTTGAACTGGGACATAAA	CCGGAGCATCTCAGCAAGCAA		
1687	DFNA5	NM_004403	CTGATAAGTTACAGCTTCTAA	TAGAAAGAGTCTGACCCTTTA	AACATACTAATTCTATGTCTA	GCGGTCCTATTTGATGATGAA
1716	DGUOK	NM_001929	AAGGCTCTCCATCGAAGGCAA	CCGCCTGAAAGTACAGCTGGA	CAGCACGATGGTCCTACACAT	CACCTTTGTAAAGAATCTGTA
1723	DHODH	NM_001361	CAGGTATGGATTTAACAGTCA	CTCCGGGATTTATCAACTCAA	CAGGGCTTTGGCGGAGTCACA	CAGGAACTTGACTGTCTTTCA
1733	DIO1	NM_000792	TTGGGAGTTTATGCAAGGTAA	CCCAATCAAGACAAATTGTTA	CACAGTTAATCTGGACAGATA	AAGAGGAGAGTACTCACTTTA
1737	DLAT	NM_001931	CACAGCGATTAATGCAATCAA	TTGGTTTATCATCGATGGGAA	TACCTCATTATTACCTTTCTA	CTCCAGCATCGTCTCATGTAA
1739	DLG1	NM_004087	CGGGTCAATGACTGTATATTA	ACGGGTTATTAACATATTTCA	ATGACTGTATATTACAAGTAA	AACAGTGAAATTCAATTCTAA
1740	DLG2	NM_001364	CCGGACTAACGTGAAGAAGTA	TACGCTCGATTTGAGGCCAAA	CTCGGCTGTATGTGCGTAGAA	CTCGACTAACCCACGAAGTAA
1749	DLX5	NM_005221	ATGTAAGTTATTGCATTTCAA	CTGTATATTCTGGATAAATAA		
1756	DMD	NM_004014	CTGCTTCCAATTTGCTAATAA	CAGGAGTCTAAAGCACTTTAA		
1760	DMPK	NM_004409	CAGCGAGGTAGCGGTAGTGAA	CTGGGTGTATTCGCCTATGAA	GAGCCTGAGGGCTAAATTTAA	AACCAGAACTTCGCCAGTCAA
1761	DMRT1	NM_021951	CTGCATGATTTAAGTGCTTTA	TTGGTAAAGGGTGTAATTTAA	AAGCGATTTGTGTGCCTCTAA	ATGGAGTACTTTGTTATATAA
1774	DNASE1L1	NM_006730	AAGGAAAGTTACTGAGAACAA	CAGGGAGAAACAGACATCAAA		
1777	DNASE2	NM_001375	AAGGGCCACCACGTTAGCCAA	GACCTTGATTGTGTGCCTTAA	CAGCAGAGCTTATAAGATCTA	AAGGGCCACCACGTTAGCCAA
1778	DNCH1	NM_001376	AAGGAGGTTCTTAGCAAATTT	CAGGAGGTAATTGCAGACAAA	CCCGTGATTGATGCAGATAAA	CAGGTGGGTGTACATTACGAA
1788	DNMT3A	NM_022552	TTGATTAATTGGCGTAACTTA	CAGAACAAGCCCATGATTGAA	CTCAGTGGTGTGTGTTGAGAA	AACACCGGGATCTATGTTTAA
1791	DNTT	NM_004088	ACCGGTGGAAATGACAGGAAA	CTGGGATTGGATTATATTGAA		
1796	DOK1	NM_001381	CCGGCAGAAGGCCCAGGGAAA	AAGGATCCCAATTCTGGGTAA	CCGCCTGGACTGCAAAGTGAT	AGGGATCAAAGAAGATGGTTA
1803	DPP4	NM_001935	ACACTCTAACTGATTACTTAA	CAGTAAAGAGGCGAAGTATTA	AACAATGACATTTATGTTAAA	ATCGGGAAGTGGCGTGTTCAA
1804	DPP6	NM_001936	TACTGTCTTAATAGAAGGCAA	TCCCTACACGTTATTGGCTTA	ATGGTTAACCTGATAGAATTA	ACGCTAATGGTTAACCTGATA
1806	DPYD	NM_000110	CTGAGGATAGTAGTTAAATAA	TCGGTGAATGATGGAAAGCAA	CCCACGGAAGGTTATAGTAAA	TCGAGAGTATCCTGGCTTTAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
1807	DPYS	NM_001385	AACACCCGACTTCCTCATGAA	TGGGAAGTTTATTCCTCGAAA	CTCCCTAGGATCCTTTAGAAA	CGGCAGGAGATGGGAAGTTTA
1808	DPYSL2	NM_001386	TACCATGGAACGCCTAATAAA	CAGGCTTGCGTTATTGGCCTA	ACGGATTGCCAGATTTATGAA	CTCGTGTTTATTATTCCTTAA
1809	DPYSL3	NM_001387	CTCAGCTTATATGAAAGTCAA	AAGGATTGTAGTCATCCTGAA		
1810	DR1	NM_001938	AAGATAGTATTAAGTAATTAA	CAGCCGTATATGGAACATAAA		
1812	DRD1	NM_000794	ATCGGTCATATTGGACTATGA	CACAATTAACTCCGTTTCCAA	GACGGTGAGTATCAATAACAA	ACGGTGAGTATCAATAACAAT
1820	ARID3A	NM_005224	CAGCATGTCGGTGGAGATCAA	AAGGATATCTATATATCTATA		
1830	DSG3	NM_001944	AAGGCTCTAGATTATGAACAA	CTCACTGGTGATGATACTAAA		
1832	DSP	NM_004415	CAGAAGAATGACTATGACCAA	CCGACATGAATCAGTAAGTAA	CAGGGAGATCATGTGGATCAA	AAGGGCCACGGTATTCGCTTA
1834	DSPP	NM_014208	GAGGATGTCGCTGTTGTCCAA	CATGATAGTAGCATAGGTCAA	AACGAGGGTAATACAAGTGAA	TCGGATAGTAAAGAATATTAT
1837	DTNA	NM_001390	CAGCCATAGAATTTAGTGTAA	TGCGACCTATTCAATACATTA	CAGCATTCAAATTATATAGAA	CCCGTTGTCATAGCTATTTCA
1838	DTNB	NM_021907	CAGCTTATTGCAGAACTGGAA	CCACTTGACCTTGCACATATA		
1840	DTX1	NM_004416	CCGGGAAGAAGTTCACCGCAA	GTGGGAGTCAGCCAAGATTTA	CACTGTGGGTGGAGAAATAAA	GACCAAGAAGAAGCACCTTAA
1844	DUSP2	NM_004418	CGCGGGAAAGACCGAAAGGAA	AAACTTAGCACTTTATATTTA	CTGGTCCACCACCATGTTGAA	CAGCCTGAGAGCTCCAAGGAA
1856	DVL2	NM_004422	CTGGCTGGTGTCCTCAGATAA	CACGCTAAACATGGAGAAGTA	CCGGATACGAGAGCTCCTCTA	CTGGGAGATTTGGGCCATGTA
1857	DVL3	NM_004423	CCCGGCTAAATGGAACTGCGA	CTCCTGGTTACTTCATCACAA	CAGCATATCATATCCATTTCA	ACCAAGTATGTTCCTCCTGAA
1869	E2F1	NM_005225	CTCACTGAATCTGACCACCAA	CAGATGGTTATGGTGATCAAA	CAGGACCTTCGTAGCATTGCA	ACGCTATGAGACCTCACTGAA
1870	E2F2	NM_004091	TCCGTGCTGTTGGCAACTTTA	TAGGGACCAGGTAGACTTTAA	ACCCATTGGGAATGAGTTTAA	TTGAGACGAGGGATTATTTCA
1874	E2F4	NM_001950	GCGGATTTACGACATTACCAA	AACGAATGGATTCCTATATAA	ACCCGGGAGATTGCTGACAAA	AGGTATCGGGCTAATCGAGAA
1893	ECM1	NM_004425	CTGAACACTCATTACACTAAA	CCGGGACATCTTGACCATTGA		
1908	EDN3	NM_000114	CTGGACGTCAGCAGTAATTCA	TAGACACAGATCATAGCTCTA	CAGAAGCATGCGACTTTCATA	TTGCAGGAAGCCGACTGTAAA
1912	PHC2	NM_004427	CTGGTTCACAAAGAGCATTAA	CCGGGTGGACTTTGCCTATAA		
1915	EEF1A1	NM_001402	CAACGTTACAACGGAAGTAAA	AAGCTGGAAGATGGCCCTAAA	CTGGGTCTTGGATAAACTGAA	CTGGTTAATGATAACAATGCA
1933	EEF1B2	NM_001959	CTGGATCATGGCATTTAAATA	ATCCTGGATCATGGCATTTAA		
1936	EEF1D	NM_001960	CTGGTTCGACAAGTTCAAATA	CCGGCTGAACGTGCTGGAGAA		
1937	EEF1G	NM_001404	CACCCTGTTGTGGCTCTATAA	ATGGCCCAGTTTGATGCTAAA		
1938	EEF2	NM_001961	TGCCGTTTCTTTCAATATTTA	CCGCGCCATCATGGACAAGAA		
1942	EFNA1	NM_004428	CACCATACATGTGCAGCTGAA	TACAATGTTCTTTGTCTCAAA	CCCGGAGAAGCTGTCTGAGAA	CACGTGTATAGTATCTGTATA
1945	EFNA4	NM_005227	CTGGAGAGACTTACTACTACA	CTGGGATTTGGTATGATCAAA		
1947	EFNB1	NM_004429	AGCGACATCATCATTCCCTTA	ACGGACTACAGAGAACAACTA	CTACATTACCTCAACATCCAA	CTCACGGTAATTAATGTCTTA
1952	CELSR2	NM_001408	CCCACTATACAGTGAATGTTA	CCGGGAGGAAGTTGATTTCTA	CACGTGGTGGTCTTCAACGTA	ACGACAACAATCCAACCTTTA
1953	EGFL3	NM_001409	CCCGTATTTATGTAAAGGTAT	CAGGACCTGCCTGGCCATTAA		
1955	EGFL5	XM_376905	TTGGAAGATGATGGCAATGAA	CCCAGGTAAATTGACCATTAA		
1956	EGFR	NM_005228	TACGAATATTAAACACTTCAA	CCCGTCGCTATCAAGGAATTA	CCCATCCAATTTATCAAGGAA	CAGGAACTGGATATTCTGAAA
1964	EIF1AX	NM_001412	CACGTAGAATGTATATTTGTA	AAGTCTGTTTGTCATATTTAA		
1969	EPHA2	NM_004431	CAGCCTTCGGACAGACATATA	TTGCAGATGATTCAAACCGAA	TCGGACAGACATATAGGATAT	CAGCGCCAAGTAAACAGGGTA
1973	EIF4A1	NM_001416	AAGGATCATGTCTGCGAGCCA	CCCGATGGGATGGAGCCCGAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
1979	EIF4EBP2	NM_004096	CAGGAATAAGCTGGATCTCCA	CACCTTAATTGAAGACTCCAA		
1993	ELAVL2	NM_004432	CTGAATGGATTGAGACTTCAA	CAAGACCAACTTAATAGTCAA		
1995	ELAVL3	NM_001420	CTGGTGCATCTTCGTGTACAA	CCCGACTTTAGCTATAGTTAA		
1996	ELAVL4	NM_021952	ATGGTCCGACATCCAATACAA	AAAGGTGATTCGTGACTTCAA	TTGGAGCAGTGAACAACGTAA	CCAGTGTTGCCTAAGTATTAA
1997	ELF1	NM_172373	CAGAACTTAAATAGAAGGCAA	CAGAGTGAATTTGTATTTAAA		
1998	ELF2	NM_006874	AAGCATCAGTTCACAGCAGTA	AACAACTGAACCCATCAATAA	CACCAGATAGCCATGAACCAA	TACGATATCAAGTTACACTAA
2009	EML1	NM_001008707	CAGGCCGTGCTTAACAGGAAA	CAGATTGAAATTTATTGTTTA		
2012	EMP1	NM_001423	TAGTATGTTATTCCTGGTTAA	CTCTATGTTTATTCTAGTTAA		
2020	EN2	NM_001427	CCCGCTCTTTCGGATCGCTAA	TACGTTGTACATAATAGTGTA	CACCAAGTACCTATATATGTA	CCCACGGTAAACAATATGGAA
2021	ENDOG	NM_004435	CCGCACCTACGTGATGCCCAA	CTGGAACAACCTGGAGAAATA	CTGATGGGAAATCCTACGTAA	CCCGGGCGAGCTGGCCAAGTA
2022	ENG	NM_000118	AAGGGAGAACTTGAAACAGAT	CGCCATGACCCTGGTACTAAA	ACCAATAAATCAGACCATGAA	CAGCAATGAGGCGGTGGTCAA
2027	ENO3	NM_001976	CCAGACCTGCTTCCTGAAATA	TAAGAGCTTTATCAAGAACTA		
2029	ENSA	NM_004436	TTGGGAGAAATATCAATGAAA	TCAGTATTCGAAATAAACAAA	CTAGTTGAGAACTCAACATTA	TAGTTGAGAACTCAACATTAA
2030	SLC29A1	NM_004955	CCGCCTGGAATTCTACCGCTA	CAGCCTCAGGACAGATACAAA		
2033	EP300	NM_001429	CAGGGAATGAATGTAACAAAT	CACCGATAACTCAGACTTGAA	CCGTTTGTGGTTTAAAGCAAA	TTGGACTACCCTATCAAGTAA
2035	EPB41	NM_004437	ACCGAGCAGCTAAGAAATTAT	CACGGCCTAGTGAATGGGATA	GAGGATTTAGACAAGAGTCAA	TAGGATATCAGAATTGTTCAA
2037	EPB41L2	NM_001431	CAGGTCTTAGATAAAGAGGAA	ACGCAGTAACTTCTACATTAA		
2039	EPB49	NM_001978	CAGAAGATCTATCCCTATGAA	CCGCCCAGATTCCAACATCTA		
2040	STOM	NM_004099	CCCATTCATTACATAGTATAA	TTGGTGATTTATATAAGGTAA		
2043	EPHA4	NM_004438	AGGGTGTATATTGAGATTAAA	CCAGTACTGAATAAACTCAAA	CCGCCAGGACATTTCCTATAA	CCCGCGAATGAAGTTACCTTA
2044	EPHA5	NM_004439	ACCAGCTACACGATTATCAAA	AACGGAATGGTGCCATTGTAA	CCCGGCAGTATGTGTCTGTAA	ACCAGTTGGATCTCCAATGAA
2045	EPHA7	NM_004440	CCCAATGGAGTCATCACAGAA	TACGAGAAAGATCAAAGGGAA	CAGGCTGCGAAGGAAGTACTA	ACCAGTCATGATAGTAATAGA
2047	EPHB1	NM_004441	GAGATGTACCTTCAATTGAAA	ATGATACTGACTGATTAATTA	GCGGGATGATGTGACCTACAA	ATGGCCCTGGATTATCTACTA
2048	EPHB2	NM_017449	CCCGGATCATTCACTGTGATA	TAGGCCTCACTCAACAACCAA	CCGAGAGGACCTCGTCTACAA	CACGCTTTCTAGAGGACGATA
2051	EPHB6	NM_004445	CGCCAATCTCTAGATCAACAA	CCGGGAGACCTTCACCCTTTA	CTGGAGCTTTGGGATACTCAT	AACCGCCAATCTCTAGATCAA
2052	EPHX1	NM_000120	CCACTATGGCTTCAACTCCAA	TTCCAGGAATTCTACATTCAA	CAACAGATACCCTCACTTCAA	CAACATGGCTTTGATGATAAA
2058	EPRS	NM_004446	AAGCATGAAGAGCTAATGCTA	CAGGAGGAGACTATACAACTA	AAGGAGGTGGGCTCTCATCAA	AAGGCGATTACTCAGTGTTAA
2059	EPS8	NM_004447	CGCCATATAGATAGAAATTAT	TTGGATATTGTGAGACCTCCA	CAGGTGGATGTTAGAAGTCGA	TCGGTTCTAAAGGATGATATT
2065	ERBB3	NM_001982	AACACTGGTGCTGATCGGCAA	CTTCGTCATGTTGAACTATAA	CCAGAGCTTCAAGACTGTTTA	ACCGGCGATGCTGAGAACCAA
2066	ERBB4	NM_005235	CACCGGAATACTGTGGTGTAA	TCGGGATTTGGCAGCCCGTAA	CTGGAGAATTTACGCATTATT	CTACGTGTTAGTGGCTCTTAA
2067	ERCC1	NM_001983	CACCGTGAAGTCAGTCAACAA	CACCGTGAAGTCAGTCAACAA	CCCGGGTGACTGAATGTCTGA	ACCGTGAAGTCAGTCAACAAA
2068	ERCC2	NM_000400	CCGGGAGGATATTGCTGTGAT	CCGATTCTATGAGGAATTTGA	TCGAAAGTTGCTCAACTTCTA	CCCGCTCACCCTCCTTGCTAA
2070	EYA4	NM_004100	CTGGGTCAGTAATTACAAGTA	CAGCTTTAGCAAAGAACTCTT	AGCGTATATGACATCGAATAA	CAGTCCTATTTAGACATGTAA
2071	ERCC3	NM_000122	ACCCATGTGCATGAGTACAAA	CCGGGAATATGTGGCAATCAA	CCGGTTCACCTCCGATGCCAA	ACCGTTCTGAATAAACAGAAT
2103	ESRRB	NM_004452	CAGCTGCGGCTCCTTCATCAA	ACGCAGGTACAAGAAGCTCAA	CCGCTTCATGAAATGCCTCAA	CAGCACTTCTATAGCGTCAAA
2113	ETS1	NM_005238	CTCGGATTACTTCATTAGCTA	CCGACGAGTGATGGCACTGAA	TCGGATTACTTCATTAGCTAT	ATGCATGTCGTTCCAAACTAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
2114	ETS2	NM_005239	CCCGGTCAAGTTGGTTTCAAA	CTGTGATGAGTCAAGCCTTAA	CTCATTGTATGTGAGGTTGAA	AGGGATTTATGTAGCAGCTAT
2118	ETV4	NM_001986	ATGGGCTATGGCTATGAGAAA	CAGCAGAGCTTTAAGCAAGAA	ACCGGAGTCATTGGGAAGGAA	CCGGAGTCATTGGGAAGGAAA
2119	ETV5	NM_004454	CAGAAATTACTCAATGCTGAA	CAGGATCTCAGTCAACTTCAA		
2121	EVC	NM_014556	CAGCTAATCGATAATATGGAA	AAGAAGCAACTTGTAGTTTAA		
2122	EVI1	NM_005241	CTGAACTAGCAGATCACCAAA	CCAGTGCTATCCAGTCCATAA	GAGCTGTGAATGATTCTATAA	CAGCACTACGTCTTCCTTAAA
2123	EVI2A	NM_014210	AACCCTATAACTCCTGAAGTA	CATGGTAGACCTTGCAATTTA	ATGGCTATGCTAATTTGCTTA	GAGCTAAACTGTGTAATTTAA
2124	EVI2B	NM_006495	CAGGATTTATCTTAGATACTA	CAGGTATTGGCTAATTCTCAA		
2130	EWSR1	NM_005243	CAGAGTAGCTATGGTCAACAA	CTGCATTGACTACCAGATTTA	TCCGGGTTGTGGAAACCAGAA	CAAGAGGGCCTCTTAACTGTA
2134	EXTL1	NM_004455	CCCGACTGCATCAACCAGATA	TAGATGGATGGCAGACATTAA		
2138	EYA1	NM_000503	CCCAATGGCACCGAAGTTAAA	CAGGAAATAATTCACTCACAA	TCGGTATAAATATGTAGATAA	AACTCGGTAACTCTCATATAA
2151	F2RL2	NM_004101	TCAGTTAGGATACATCACTAA	AAGGCTAACTTGCTAATCACA	CAGTTAGGATACATCACTAAA	CAGGAGCCACGATTACTGTAA
2153	F5	NM_000130	TTGGATAATTTCTCAAACCAA	CCCATTCAAGACCCTGATCAA	TAGGAATTAGGTCATTCCGAA	CGCCATTAATGGGATGATCTA
2155	F7	NM_000131	CAGTTGAATATCCATGTGGAA	TCGAACTGTCCTGGCACCAAA	CAGGGTCTCCCAGTACATCGA	CTGGTTCTTATCCATTATCAT
2162	F13A1	NM_000129	CACGAGCGTTCACCTGTTCAA	AGCGTTGACATTCTATTGGAA	CAAGGAGAGATGGGACACTAA	TACAATGTAATAGAAGCTTAA
2177	FANCD2	NM_033084	CGGCTTCTCGGAAGTAATTTA	TTGGAGGAGATTGATGGTCTA	CAGAGTTTGCTTCACTCTCTA	ACGGGAGAGAGTCAGAATCAA
2178	FANCE	NM_021922	TCGAATCTGGATGATGCTAAA	TAGCCTGAGGATAAAGGCTGA	CTGACTTGAATAATTTATCAA	AACGCCGAGGAGAGCTTGTAA
2182	ACSL4	NM_004458	ATGCATCATAGCAATTTGATA	TTGGAGCGATTTGAAATTCCA	CAGATTATAGATCGTAAGAAA	AAGGGCAGAGTTACTTGATAA
2189	FANCG	NM_004629	CCGGCTCGTTCGACAGGCCAA	CCGCGGGAACTAACTCTTCAA	CTCATTGAGGTAGAATTACTA	CCCAGGTAATCGAGACACTTA
2192	FBLN1	NM_001996	CAGGTCATGTGAAGACATCAA	CAGGATGTGTGTCGATGTCAA		
2197	FAU	NM_001997	GGCCGCATGCTTGGAGGTAAA	CCGCCGTTCAGTCGCCAATAT	ACAGGAGAAGAAGAAGAAGAA	AAGCCACTTAGTTCAGTCAAA
2204	FCAR	NM_002000	TGGAACTAAGTTATTCGGCAA	GAGCTTATTGTCGTAAGAATA		
2205	FCER1A	NM_002001	TCCATGGAATAGAATATTTAA	CACATTTCTCTTGAAGATTAA		
2212	FCGR2A	NM_021642	CCCAATGTCCAGCCTCTTTAA	AACCTCTAACAACAAATTAAA		
2214	FCGR3A	NM_000569	TTCGCTGAGTTAAGTTATGAA	CAGACTGAGAAGTCAGATGAA		
2220	FCN2	NM_004108	CAGCTTTGCAAATGGCATCAA	AAGGATACAATTATAGCTACA	CCGGGACTGGGCCACGTACAA	CTGCCATGTGTCAAACCTGAA
2232	FDXR	NM_004110	CAGGTTGGGAACATGCTGGAA	TGGGAACATGCTGGAAATAAA	CACGTGGACATCTACGAGAAA	AAGCGTGCCCTTTGACTCCAA
2235	FECH	NM_000140	CTGGAATATTAATGCTAAACA	CCGACTGGTGTGGCAATCCAA	ACCCATATCCTCAGGAGGTAA	CCCAAGGGTAATAAACGTGTA
2237	FEN1	NM_004111	CACAATGATGAGTGCAAACAT	TAAGTCCATTGTTACATGAAA	CTGACTGCCAGTGAAGCCAAA	CAAGAGCTACTTTGGCCGTAA
2239	GPC4	NM_001448	ATGGCCATTTATACATGCAAA	TACCAAATGATAGCTCATAAA	CAGATTGTATTCAAAGCATCA	TAGGTAGAGCTGAGAATACTA
2243	FGA	NM_000508	AGGGTTGATTGATGAAGTCAA	AGGGCTTTAGCTCGTGAAGTA	CAGCCAATAACCGTGATAATA	ACGCGTCGTTCATGCTCTAAA
2244	FGB	NM_005141	ACCGTATAGAGTATACTGTGA	CAGGAAATGGGATCCATATAA	TAGAGTATACTGTGACATGAA	CAGCACGTATGACAGAGACAA
2246	FGF1	NM_000800	GCCCATTTCGAAGATATACAA	GAGAATGATAGTAATAGGATA	AAAGTAGGAACTCTTAAGCAA	CTGATACTTATTTACCTATAA
2247	FGF2	NM_002006	TGCCTTGTGGATATCAAGAAA	ATGCTAAACTTTACTGATGTA	TAGCACTAGTCTTAAATTGTA	AACAATATTAGTCGTATCCAA
2248	FGF3	NM_005247	CGGGCGGTACCTGGCCATGAA	TTGTGTCATCACAACATTAAA	CAGGGTCCAGTGGGAACTGAA	TTGCTCCTGGGTGGAAATTAA
2252	FGF7	NM_002009	CACAAGAGTCTAGATCAGTTA	TAGTTTGTAGCTACAGTAGAA	AGCCTTTACATTTGTACACAA	CACCCGGAGCACTACACTATA
2253	FGF8	NM_006119	GCGCTTCGAGTTCCTCAACTA	CAAGAGCAACGGCAAAGGCAA	CACGGAGATTGTGCTGGAGAA	CTACATCTGCATGAACAAGAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
2254	FGF9	NM_002010	TTGGATATACCTCGCCTAATA	GCGATACTATGTTGCATTAAA	TACGTACTCGTCAAACCTATA	ATCGCAGTGAACTTAAAGCAA
2259	FGF14	NM_004115	CAGGAAGTAAGCTAATGCTTA	AGGGTTGTATATAGCCATGAA		
2262	GPC5	NM_004466	AAGAATTTAGTGTATCTGTAA	CAGCTTTGTGCTAATGAATTA		
2264	FGFR4	NM_002011	CAGGAGGTTCTGGGCCTCTGA	CCGCCTGACCTTCGGACCCTA	CAGGCTCTTCCGGCAAGTCAA	CACATTGACTACTATAAGAAA
2268	FGR	NM_005248	CAGCACTAAGGTGGCGGTGAA	TTGATTCTGTAAATAAGTAAA	CAGAGCTTGTCTAGTTATTTA	CACGTGGAACGGCAGCACTAA
2271	FH	NM_000143	GAGATCTACGATGAACTTTAA	CAGGAATTTAGTGGTTATGTT	CCCAACGATCATGTTAATAAA	TAGGATGTGCTAGGTCTAAGA
2272	FHIT	NM_002012	TCCACTGAGAACAGTCTGTAA	TTCGCTCTTGTGAATAGGAAA		
2274	FHL2	NM_001450	ACCCTTTAGTGCTTTGTGATA	CTCCCGTTGCGTCAAGTCTAA	AAGGTAATGACCAGTTGTTAT	ATCGAGTAAGGCACACCCAAA
2281	FKBP1B	NM_004116	CACTGCCTTACCTTCACTTAA	CAGAGGGACTTGAGCCAGTTA	CACAAGGTGCTCAGACATGAA	AACAATGTCCTCTTTGAGAAA
2288	FKBP4	NM_002014	CACGCTTGTATTTGAGGTGGA	AGGGATGAGGTCTGATAAGAA	TTGAGTGAATTAGACCTTTAT	AGCAATAAAGTGGAAACAATA
2289	FKBP5	NM_004117	GCGACAGGTTCTCTACTTAAA	TCGGCTGGCAGTCTCCCTAAA	AACGCCGATGATTGGAGACAA	ACGGGTAAACAGATTGAGCAT
2296	FOXC1	NM_001453	CCGCCACAACCTCTCGCTCAA	AACGGGAATAGTAGCTGTCAA	CTCCAGTGAACGGGAATAGTA	ACGGGAATAGTAGCTGTCAAA
2298	FOXD4	NM_207305	AAGACCATCATCCCTGGACTA	TCCACCACACATGGTCTTGAA		
2301	FOXE3	NM_012186	CACCAGGGCTCCTGACTGAAA	TAGGACTTATTGGGTTATTAT		
2305	FOXM1	NM_021953	CCAAATTATCCTCTAATTATA	CCGCCGGAACATGACCATCAA		
2306	FOXD2	NM_004474	CCGAGTGAGCCTTAACATCCA	CACTGGGTGTGCATTGATTTA	CCGGCGGGTCGTGCCCTGGAA	CCCATTGGTGTCAATTGAATA
2313	FLI1	NM_002017	ACCTTTGTATTTGTTCTTTAA	CAGGACATATGTGGCCTTGAA		
2316	FLNA	NM_001456	CACAGGCAACATGGTGAAGAA	CCGCTTCACCATCGACACCAA		
2321	FLT1	NM_002019	CCCGAATCTATCTTTGACAAA	TCGCCGGAAGTTGTATGGTTA	CACTACAGTATTAGCAAGCAA	ACCGCATATGGTATCCCTCAA
2322	FLT3	NM_004119	ACCAATTCAAGTGAAGATTAT	CAGGTTTAAAGCCTACCCACA	TACGTTGATTTCAGAGAATAT	CCGGCTTGAGTGAATTGTGTA
2323	FLT3LG	BF688722	TAGTATAGTTGAAATAAGAAA	GCGGGATTTGTTGAAGAGAAA	GCGCGTGAACACGGAGATACA	CTCCTCCGACTTCGCTGTCAA
2324	FLT4	NM_002020	CCGCCGATTATTCCTTGGTAA	CGCGCTGATGTCGGAGCTCAA	CACGCTCTTGGTCAACAGGAA	CACCGTGTGGGCTGAGTTTAA
2326	FMO1	NM_002021	CAGTACTTTCATAGCCGGCAA	AGGCCTCACTGTACAAGTATA	ATCATGCAAATTACGGCTTAA	CCGAACATTCAAGGTCATCAA
2328	FMO3	NM_006894	CCGGACATCATGTGTATCCCA	AAGAATCATGTCATGATCTTA	CCCGCTGGGCAGCACAAGTAA	AACTATGTTCTTTATATCTAA
2329	FMO4	NM_002022	ACGAAGATTATCCTAATTTCA	ATCGGCCTTATCGGCCTTAAA	AAAGAAGATATTTCTATACAA	CACGATGGGTCACAAGAGTAT
2330	FMO5	NM_001461	AAGGCGGACAGGCGACACTAA	AACCAAAGGTTTGACCATGAA	CTGAGTCAGCATCCAACCTTA	CTGGGCCACTCAGGTATTTAA
2334	FMR2	NM_002025	CACGTGATAGTCATAACCCTA	CTGGGTAAGACTACTCAGTAA	TAGGAACTAATTAAACATGGA	CGGCCTTATTCTCATAATTAA
2348	FOLR1	NM_000802	CTGGACTTCAGGGTTTAACAA	CACATGTGTCTTGAGAATTAT	CCCACTGTTCTGTGCAATGAA	TAAGGATGTTTCCTACCTATA
2353	FOS	NM_005252	TAGAGGGTTCCTGTAGACCTA	TGGGTTCATTATTGGAATTAA	ATGGATTCTCAGATATTTATA	GACCAATATTATACTAAGAAA
2356	FPGS	NM_004957	CTGGAGTGAATTAAAGCCTTT	CCGCACTGTCCCAGTAGCCAA		
2357	FPR1	NM_002029	ACGACCCTAAAGAGAGGATAA	TTGCAAGGCATGTACAAAGAA	CACCGTGAGCCTGGCCAAGAA	AACCAGTGACACAGCTACCAA
2475	FRAP1	NM_004958	CCGGAGTGTTAGAATATGCCA	CCGGCACAATGCAGCCAACAA	ACCAATTATACCCGTTCTTTA	CAGGCCTATGGTCGAGATTTA
2488	FSHB	NM_000510	CAACATCACCATTGCAATAGA	TCGTTTCTGCATAAGCATCAA	AAGAATGTCGTTTCTGCATAA	CACCAGGGATCTGGTGTATAA
2515	ADAM2	NM_001464	CGGGCTGCGGATGGACAGTAA	TGCTATAATGGTGAAAGTTAA	CTGTTGGTTAGTAGACACTAA	AACCATATACTGTGAATTTAA
2516	NR5A1	NM_004959	ACGCAGGTGCATGGTCTTCAA	AAGGATAACCGAGTTTGCTAA	CAGGGAGAAGTTGAGCAGGTA	CTGGAATAAATTTCGCAATTA
2517	FUCA1	NM_000147	CCGGAAGAGGAACATCCGCTA	TACGACCTTGTTAACAGCTAT	TCCACTCTATCTACTTGATAA	TTCGCTATGTTTACAGTGATA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
2521	FUS	NM_004960	ACAGGATAATTCAGACAACAA	CAAGCAGATTGGTATTATTAA	CTGGGTGAGAATGTTACAATT	ACAGCCCATGATTAATTTGTA
2524	FUT2	NM_000511	CAGCGGCTAGCGAAGATTCAA	CACGGGCGGAGACACCATCTA	CAGTGCTAGCCTCAACATCAA	CACCATCTACCTGGCCAATTA
2531	FVT1	NM_002035	CAGGCAAAGAAAGAAATTGAA	TAGACTCAAATGCTTAGGGAA	CAGGAATGTGGCTGCAAGCAA	AAGAATTTACAGTTCCTTCAA
2532	FY	NM_002036	CTGGACACCCTTGGAAGCAAA	CACCTGTCAACCTGAATTAAA	CAGCTGGACTTCGAAGATGTA	ACCAGTGTCCTGGGTATCCTA
2535	FZD2	NM_001466	CACGGTGAGACCACCGTGTGA	CACCATGGTGTCGGTGGCCTA	CACGTACTTGGTAGACATGCA	CACGGTCTACATGATCAAATA
2537	G1P3	NM_002038	CAGCAGCGTCGTCATAGGTAA	CAGAATAAACTTCACCCAGAA		
2538	G6PC	NM_000151	TAGCAGAGCAATCACCACCAA	CTGGCTTATTCCCATGTGTGA	TGGGATCCAGTCAACACATTA	CAGCAGGTGTATACTACGTGA
2539	G6PD	NM_000402	ATCGGGTGACCTGGCCAAGAA	CACCAAGATGATGACCAAGAA	CTGCGTTATCCTCACCTTCAA	CAGCCTCTCTGCTATAAGAAA
2542	SLC37A4	NM_001467	TTGGATATAGGTGGGAAGAAA	CCGGGTGGCGCTGGAAGTTAT		
2547	G22P1	NM_001469	CAGGTTAAAGCTGAAGCTCAA	GAGGGTTAGCGTTAGCCTTAA	GAGGATCATGCTGTTCACCAA	CGCCTAGTGAGCAGTAGCCAA
2556	GABRA3	NM_000808	TACAATGAGGTTAACAATTCA	CCCGACTGAGACCAAGACCTA	CAGAGATAATCCGGTCTAGTA	CCCTCAATTCATATTTATGAA
2561	GABRB2	NM_000813	TCCTATAATGTAATACCTTTA	TACCTATTTCCTGAACGATAA	CAGAAGCACAATGCTAGCCTA	ATCCCTCAGCTTTAAGCTTAA
2563	GABRD	NM_000815	CCGCGGCACCAGAGCGATGAA	ATCGGAGGACATCGTCTACTA	CACCTTCATCGTGAACGCCAA	CACGGAGCTGATGAACTTCAA
2564	GABRE	NM_004961	CCGCATCTACAAGGATGGCAA	CAGGCATTACTCGCCATTGAT	CAGCAGACCATTTCAAATTAT	CACTCTAACCATCACAATCAA
2566	GABRG2	NM_000816	CACCATCAGATCATAAGCATA	CACCCTAAGGTTGACAATTGA	TAGGAGTGAAGCCAACGTTAA	TAGATTCATAATGCAATTAGA
2568	GABRP	NM_014211	TAGATTGGTCTTACAGTTTGA	AAGTGGCTTAGCTTAAGTAAA	GAGCCCAAGATTACAAATGTA	CAGAAATAAACCAAGGCTCTA
2569	GABRR1	NM_002042	CAGGGTTACAGTAACTGCAAT	CACCACCAAACTGGCTTTCTA	ACGTGCTCTCTTGAAATTGAA	CAGAAATAACTGTATAATGAA
2572	GAD2	NM_000818	ACGGGCGGCATCGGAAACAAA	CGCCTTGGACAAGATTTATAA	AAGTTTCGATAGATCAACCAA	CAACCTGTTCTTCCTACCAAA
2580	GAK	NM_005255	CACGCAGTACACGGTCTTCCA	AAGGCCTAACTATGCCTCGAA	CCCGTGGTTGTCTGTACAGAA	ACGCGTGTGACATTCAAGAAA
2581	GALC	NM_000153	TTCAAGGTGGTTGATGTTATA	TACACTCACGTTAACTATTAA	CAGTATTATAGGAGACTACAA	TAGGAATTTATAAGAGTCTAA
2585	GALK2	NM_002044	TCCTAGGTTACTGAAGCTAAA	CTGGAGGAACTCCGAACCCAA	TGCGCGAGTGCTCCAGTTTAA	AAAGCTCTCTATGCTTCATAA
2615	GARP	NM_005512	CTGGAGTTTGAGACTATGGAA	AACCAACAGTATAAAGCCTAA		
2622	GAS8	NM_001481	CACCGACATTAAGAACTACTA	ATGCATAAGTATATTTGTTTA		
2628	GATM	NM_001482	TAGAATGTACACAGATCCAAA	CAGGTCAATTATCAAAGACTA	CCACTAATAATTAACCATCTA	ACCGAGCGTACAGGTCAATTA
2629	GBA	NM_000157	CCGGAATTACTTGCAGGGCTA	CCAGAACAGAAGTTCCAGAAA	CAGGGCTAACCTAGTGCCTAT	AAGAAGGAATCGGATATAACA
2642	GCGR	NM_000160	CCGCAATGCCATCCACGCGAA	CAGCTCCGTGCTGGTCATTGA	CTCCAACAATAAAGAGCTCAA	CAACAGAACCTTCGACAAGTA
2645	GCK	NM_000162	CTGGACAAGCATCAGATGAAA	CACGATGATCTCCTGCTACTA	CAGCTGTATGAGAAGCTCATA	CAGGACTTTGATGCATTTCCA
2651	GDF9	NM_005260	ATCAGTGGAACTGCTATTTAA	CAAGTCAGTCTTGCTGTACAA	TACCGTTGAACACTTACTCAA	CAGCTGGTATTCCCTTCACTA
2652	GDF10	NM_004962	AGCGCTCGAGGTGCTATGCAA	AACAGGATAATCGTGGTGTAA	CACGGAAAGAACTCTGTTTAA	TAGTAACGTGGGAATACTAAA
2664	GDI1	NM_001493	ATCCACTGACCAAATCCTTAA	ACCCTTATCTTGCAAAGTGAA	CTCTAGTGTATTTCACAGAAA	CCGCATCAAGTTGTACAGTGA
2668	GDNF	NM_000514	CGGGACTTTAAGATGAAGTTA	CTGGAGTTAATGTCCAACCTA	CTGGTTTACCATATTCTAAGA	CGCGCTGAGCAGTGACTCAAA
2671	GFER	NM_005262	ATGGCCCAGTTCATACATTTA	CCGGGCCTGCGTCGACTTCAA		
2677	GGCX	NM_000821	CCGCCTGCTTCCCAAGTATAA	CAGACCTTTCTTAGACGCCAA	TACGTCTATGTCAACACTACA	CAGGAAGAGGTTAGACGCAAT
2702	GJA5	NM_005266	CTCCCTCTACTCAGCCTTAAA	CTCAATGACGTTGCTCATTAA		
2705	GJB1	NM_000166	CTGCACAGACATGAGACCATA	TGCCTGAAATGTTACACATTA	TGGCATCTGCATCATCCTCAA	GCCTGAAATGTTACACATTAA
2720	GLB1	NM_000404	CCAGAGGATGTTTGAAATTGA	ACCACTGATGGAGCACATAAA	CAGAATGGAGGGCCAGTTATA	CACCAAAGTTTGCATATGGAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
2740	GLP1R	NM_002062	CAGGAACTCCAACATGAACTA	CAGACTCAAACTCAAGGTCAA	CCAGACAGAGCCGCAAATCAA	CAGGCTCGTTCGTGAATGTCA
2741	GLRA1	NM_000171	CTGGAGTTTAACAAACAGCAA	TCGGATTTCCTGGATAAGCTA	CCCATAACTCGTGGACTACAA	CCGCTTTAACTTCTCTGCCTA
2746	GLUD1	NM_005271	CAAGCCTAACCTTGACTCAAA	CCTATAGAAATAATAAATGAA	CAGTGAATGCCTATAGAAATA	CAGAATTTGCTTACCATAATT
2768	GNA12	NM_007353	TAGCTATACTGTGTACACATA	GAGGTAGTTGTGCCTCAATTA	GTCCGTTTAACTCGATAGAAA	CCGGATCGGCCAGCTGAATTA
2769	GNA15	NM_002068	CTCCGTGCGGGCTGAAATTAA	CCGGTTTGCGGACGAGAGAAA	GAGGTTCATCCTGGACATGTA	TCCGTGCGGGCTGAAATTAAA
2779	GNAT1	NM_000172	CACCGACACGCAGAACGTCAA	CAGCATCTGTTTCCCGGACTA	ACGCACAGACTCAGCAATAAA	ACGCGCCATGACCACACTCAA
2780	GNAT2	NM_005272	TAGGGAGTCTCAGTCAATGTA	AACCAATTAGAACGAATTACA	ACGGCAAATATGGGAAGTGGA	TGGGATAGCTATTGCAGCTTA
2783	GNB2	NM_005273	CGCCTGTGATGCCTCTATCAA	CGGCCATGAATCCGACATCAA		
2784	GNB3	NM_002075	CAGATTGCAGATGCCAGGAAA	TCCGGGTGCCATTCCCACTAA	CAACATGTGTTCCATCTACAA	TCCCTTAATGAGCAAGGACAA
2785	GNG3	NM_012202	CTCGGTGACCTGCTCAGACAA	GTGGAACAGCTTAAGATTGAA	CTGGAGCTACTGGGAGGGTAA	CAAGATGGTGGAACAGCTTAA
2788	GNG7	NM_052847	CAGGGCATCATTCAGTAATTA	ACGGCTAAACTCGGATTGTGA	ATGGTTGAACCCGTCGCTAAA	ACGCATCCATCTCCAAGTTAA
2794	GNL1	NM_005275	TCGGCTTTCCACTAAGGTCAA	CCAGGCTACAGTGAACAGAAA		
2798	GNRHR	NM_000406	ACCAGTATTGATGAATAACTA	CAGGTTGTCAGACCCAGTAAA	ACGGTTGCATTTGCCACTTCA	AAGCATGGATTGGATCAGTAA
2799	GNS	NM_002076	CGGCGGCATGACACCGCTAAA	AAGCAAGATGCTGGTTGCCAA	CTGGTTAATTAGGCAAGCCAA	ATCAGTCAACTTCCACATTAA
2802	GOLGA3	NM_005895	CGGAAACTTTAGAGAAGTTAA	CTGGCCGATTACAGAACTGAA		
2813	GP2	NM_001502	TTGATGGGACCTTGAAAGCAA	CCAGAACTACACGAATCCTTA	CACAGGCTTGGTATTAACAGA	CAGGACCTCAATAGTTCTGAT
2817	GPC1	NM_002081	TTGAGTCCTTGTATGAATAAA	TACAACACAGACGATATTTAA	CAGGGACACGCTCACGGCCAA	CCGCCAGATCTACGGAGCCAA
2825	GPR1	NM_005279	CCGGGACACTGTGGAGTTCAA	CTCAGTTGCTGAGATACTCAA	CCGAGTCCACTTTCATAGTTA	AAGCCTTAAGTCTTAATATTA
2838	GPR15	NM_005290	CCCAGAAGAAACTTCAGTTTA	CAGCTATTCTTCAGCTTGGTA	TTGCGGCAAGAACACTATTTA	TTCAGTTTATTTGGATTATTA
2846	GPR23	NM_005296	TAGGTTGGGCCTATAAATATA	TTGGGAAACTAGGTTCTATAA	GGGCCTATAAATATAGAACAA	AGGAAGTGAGTGATCAAACAA
2848	GPR25	NM_005298	GCGCATCATCTTCGCCATCGA	CAGGGACGACAGTTCCGTGTT	CTGCGCCAACCCGCTCATCTA	CCGGAGGAACTCGCTGCGCAT
2857	GPR34	NM_005300	CTGAATAGATTCAGTCATTAT	AAGGAGGGCATAATTCCACAA	TGCGACTATTACCAAATAGAA	TCAGGCGAACCTGAACTTTAA
2859	GPR35	NM_005301	CAGGCAGATCCCAGGAGAGAA	CAGGACCATGAATGGCACCTA	CGCCCTGTACATAACCAGCAA	CCGGCACAATTTCAACTCCAT
2868	GRK4	NM_182982	AAGCCTTTGAGGAATGTACTA	CACCGCAGATGAAGACTTCTA	CCGGGTGTTTCAAAGACATCA	CAGGATGTTACTCACCAAGAA
2870	GRK6	NM_002082	CCGGAGGTGGTGAAGAATGAA	CAGAGACTCTTCAGTCGCCAA	AGGCATGTGGGCGGCACGTAA	AAGGATGTTCTGGACATTGAA
2876	GPX1	Y00433	CAGGAGAACGCCAAGAACGAA	GAGGAACACCTTGATCTTACA	CCGGGACTACACCCAGATGAA	AACACCTTGATCTTACAGAAA
2886	GRB7	NM_005310	CGGGAGTGGATCTGAAATAAA	CCCAACAAGCTTCGAAATGGA	CGCCAAGTACGAACTGTTCAA	CACACTGGTATATCCCATGAA
2888	GRB14	NM_004490	CAGCGATTGATTATTCAGCAA	CAGAAGTGACTTATTAAACTA		
2889	RAPGEF1	NM_005312	GCAGGTCTTGTTGCCAATTTA	CAGGGTTACATTGTAATATAT	CCGGGTTTAGGACGTGGTCAA	CAGGAAAGATTTGGTGTTGTA
2890	GRIA1	NM_000827	CAGGTGCGATTTGAAGGTTTA	CAGCATCCGAAAGATTGGTTA	CTCCACGTGATTGAAATGAAA	CACCATGAAGGTGGGAGGTAA
2895	GRID2	NM_001510	AAGCAATGGATCGGAGAACAA	CACGATTACAAATGGGATCAA	AACGATGTGGACGTACAGGAA	CTGGCAGAAATTCATTATATT
2897	GRIK1	NM_000830	CCAGCATTAACAGAAACCGAA	TGGGCATATCACCTTTAATAA	ACAGGTCTAATTCGTCTACAA	ACGGATTTAGAATGTGGTAAA
2900	GRIK4	NM_014619	CCGGCAATTCCTTATCTCCAA	CGCGTTCATATGGGACGCAAA	TGGGATGGTGTCAGCCTATTA	CAGGGTGTTGAATTCCAACTA
2902	GRIN1	NM_000832	GACGCGTTCGGTCCTATTAAA	CAAGGAGGAGTTCACAGTCAA	CAGACTGAAGATTGTGACGAT	CACGCTGGACTCGTTCATGCA
2903	GRIN2A	NM_000833	TACGATAACATTGTCGACAAA	CACAGTGGCCATTGTAGTTTA	ACCAGATAGGTGAGTCCTTAA	AGGGTTGTATAGTATCTGTTA
2909	GRLF1	NM_004491	CACCACCGAAGAGGTGTTTAA	CAGGATGTTCTGGGAGAGGAA	CAAGGTTTCCATCGTGAGCAA	CAGCCTAAGGAGGAACACTAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
2912	GRM2	NM_000839	CCGCTACAACATCTTCACCTA	CTGCACGCTTTATGCCTTCAA	CTACAAGGACTTTGTGCTCAA	CACCATCGAGCTGGCCTCCTA
2913	GRM3	NM_000840	CACGGCTCCATTCAACCCAAA	TAGGTCCTTGTTGTAACTAAT	TACGGTGGCAATATTATGTAA	GTCCTTGTTGTAACTAATTTA
2917	GRM7	NM_000844	AAGGGTTTGATGCCTACTTTA	CACGCTTACAATCTCCATGAA	TCGGATTTATCGCATATTTGA	CCCAGATTAGTTATGCATCAA
2931	GSK3A	NM_019884	CGGGTGTAAATAGATTGTTAT	CAATAAATTATTGGCATGAAA	CCGGGTGTAAATAGATTGTTA	CAGGGAACTAGTCGCCATCAA
2932	GSK3B	NM_002093	CACGTTTGGAAAGAATATTAA	CTGCATTTATCGTTAACCTAA	CACTCAAGAACTGTCAAGTAA	AACACTGGTCACGTTTGGAAA
2944	GSTM1	X08020	CCACCGTATATTTGAGCCCAA	TCCAGAATTTGAGAAACTGAA	CAGACTCAAGCTATGAGGAAA	CTGCTACAATCCAGAATTTGA
2947	GSTM3	NM_000849	AACGGAAGAAGTTACCCTTAA	ATGGCTGGATGTGAAATTCAA		
2950	GSTP1	NM_000852	CCTCATCTACACCAACTATGA	TCCTTTCTCCAGGACCAATAA	GCCGCCCTACACCGTGGTCTA	CCAGATCTCCTTCGCTGACTA
2954	GSTZ1	NM_001513	TACCATCAGCTCCATCAACAA	ACGGTGCCCATCAATCTCATA	CTGAAATTTGGCGTGAATTAA	CGCGCTGAAATTTGGCGTGAA
2956	MSH6	NM_000179	CAGCAGGGCTATAATGTATGA	CCGAAGTTGTAGAGCTTCTAA	AAGCCTATTGTGTGCTTGTTA	ATCGCCATTGTTCGAGATTTA
2957	GTF2A1	NM_015859	CAGCTTCTACTGCAAGTTCAA	CAGGAACTCTTTGACACAGAA		
2959	GTF2B	NM_001514	TTGCCTGTTGTACATAGCCTA	TTGACGAATTTGGCAATTCTA	CCAGTGTGGATTTGATTACAA	ACGTCAAATTCTTGAATACAA
2965	GTF2H1	NM_005316	AAGGCAAAGATAGATTTACAA	CCCAGAGCTGATGCTATTGTA	TCGGCTGAATACAGGGTCAAA	ATGGCACAGGGTAGACCTTAA
2974	GUCY1B2	NM_004129	CAGCATCCGCAGATTTATCAA	CAGTGTGCACGCAGTCTATAA	CGCAGATTTATCAACAGTCAA	CCGATGTTCAGAGGCATCCAA
2975	GTF3C1	NM_001520	CAGGAAAGAGGATGAACTTAA	CAGGCCTATCTCAACTATAAA		
2983	GUCY1B3	NM_000857	CAGTTTCTTGTCAGAATAATA	CAAGACTTTCTTCTAGATATA	AAGGGTCAAATGATCTACTTA	ACCTAACATGGTGATCTGCAA
2986	GUCY2F	NM_001522	CAGGCAGACAGAATTCGCATA	ACCGTTGTTTGGAACCATCTA	CTGGAGTTCGATCAAGTTTCA	AAGGCAGTTGGTGAGAAACAA
2997	GYS1	NM_002103	CTGGGCGAGGAGCGTAACTAA	CCGCTATGAGTTCTCCAACAA		
3024	HIST1H1A	NM_005325	ACCCAAGAAAGCGGCACCCAA	CAGGTTTATACCACTTTATTT		
3029	HAGH	NM_005326	CTGGTCCGTGCGGGAAATTCA	ATCGGACATTCTAATGCATAT	TCAGTCTTGATTTAACCTTAA	ACAAGTATTTATTCCCATAAA
3037	HAS2	NM_005328	GTGGAAGATTGGTACAATCAA	CAGCTCGATCTAAGTGCCTTA	CCAGCTAGTAGGTCTCATAAA	AACGCAATTGGTCTTGTCCAA
3038	HAS3	NM_005329	CACCTTCTCGTGCATCATGCA	TACCAGTTCATCCACACGGAA		
3053	SERPIND1	NM_000185	CAACGCCAAGTTCGCTTTCAA	CCCAAGGAGGGTACACAACTA	TGGCATCATTTACGTAGTTTA	TGGGCTAATGTTAGGGCTTAA
3055	HCK	NM_002110	CCGGGATAGCGAGACCACTAA	CGGCAGGGAGATACCGTGAAA	CGGGAGCACATCAGAGGCTTA	AACGACGGGCTCTGCCAGAAA
3059	HCLS1	NM_005335	CAGCCAGTGATAGCTATGGAA	AAGGAGAAGTGGAGAAGCATA		
3062	HCRTR2	NM_001526	CCCGTGATGTCCGGCACCAAA	CCGGAAGTCCTTGACCACTCA	CCGGTGCAACATCGCCTGTAA	ACCGACTATGACGACGAGGAA
3066	HDAC2	NM_001527	GACCCATAACTTGCTGTTAAA	CTGGGTTGTTTCAATCTAACA	TCCCAATGAGTTGCCATATAA	ACGGTCAATAAGACCAGATAA
3067	HDC	NM_002112	TGCCGACTCCTTCACCTTTAA	CCACAATAGGATACAAACGAA	CTGGGTCAAGGACAAGTACAA	CAGCTTGTGACATGATATATA
3068	HDGF	NM_004494	CCAGCTTATAGTCATATATAT	GAGGGAGCAATTGAATTTCAA		
3074	HEXB	NM_000521	TTCGACGATATCATGGCTATA	TGGATATTATTGCAACCATAA	CCAGACATTATCTGCCAGTTA	CCGGGCACAATAGTTGAAGTA
3092	HIP1	NM_005338	CAGGTTAGGGTGCTAGAGCTA	CACAACAATGGGTATCCTTAA	CAGGAACTTGCCACAAGCCAA	ATGGCTTAGGATCGACAAGAA
3097	HIVEP2	NM_006734	CTGGGTTATCTTTGTGCTATA	ACCGTAAAGCATTAAAGTAAA		
3098	HK1	NM_000188	AACGGTGGAAATGCACAACAA	CAGATCGAGAGTGACCGATTA	CCGTGTCGTATGACCTAGTAA	CACGATGTAGTCACCTTACTA
3107	HLA-C	NM_002117	ACCGGGAGACACAGAAGTACA	AAGCGTTGATGGATTAATTAA		
3118	HLA-DQA2	NM_020056	ATGGTTATAGCAGAAATACAA	CAGGGCTGACTGAGAGCATAA		
3119	HLA-DQB1	NM_002123	CCGGAGGCCTTCGGGCAGCAA	ATCCATCACAGGAGTCAGAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
3120	HLA-DQB2	NM_182549	AAGGATTTCTTGGTCCAGTTT	CAAGAGAAGCATGACAAACAA		
3122	HLA-DRA	NM_019111	CAACCTGGAAATCATGACAAA	CTGAAGAAACTTCTGCTTTAA		
3135	HLA-G	NM_002127	ATAACTTACTTCTGTATTAAA	ATGAGGTTTCTTTGACTTCAA		
3142	HLX1	NM_021958	AAGGTTTGAGATTCAGAAGTA	CGCCTTAAATTTGTAAATAAA		
3159	HMGA1	NM_002131	CAGCCAGCCCTTGGCCTCCAA	CTGGACAAGGCTAACATCCCA	CAGCGAAGTGCCAACACCTAA	CACCACAACTCCAGGAAGGAA
3162	HMOX1	NM_002133	CACCAAGTTCAAGCAGCTCTA	CGGGCCAGCAACAAAGTGCAA	CAGGCAGAGGGTGATAGAAGA	CAGGCAATGGCCTAAACTTCA
3174	HNF4G	NM_004133	AAGCACTGACATAAACGTTAA	CACCGGATGGATTCTGATGAA	ACCGATAAGCAGCGAGTGTAA	ACCCTGTAATTTATTCGTGTA
3175	ONECUT1	NM_004498	ATGGAAGAGATCAATACCAAA	AAGGAAGAACCACAAACTAAA		
3176	HNMT	NM_006895	CGGGAAATATGTTGAATCTTT	TGCAGGCTCAACATAACATAA	TGGGACTTTATTCATATGATT	CAACATAACATAAGCTAGAAA
3187	HNRPH1	NM_005520	AAGCAGTTGAATTATGTTAAA	CAGGTATATTGAAATCTTTAA		
3198	HOXA1	NM_005522	CAGGATAATATATTTGCAGAT	TAGGATGTCTGTAATAAATAA	CACACTGAGTTCTATCAGTTA	CAGCTCCTTTATTATAATCAA
3201	HOXA4	NM_002141	AAGCCATGTGCTAAGAATAAA	CTGGACCATAATAGACACCAA		
3225	HOXC9	NM_006897	CACGACAATGAAGACCTCCTA	CCGAAATAAATGACACATACA		
3236	HOXD10	NM_002148	GTGCATCCTTATATACCTCAA	CCCTATGAGTATATATATATA	CTCCTTCACCACCAACATTAA	CAGGGTAACTATTATTGCGCA
3240	HP	NM_005143	TGGAGTGTACACCTTAAACAA	AAGGTGTCTGTTAATGAGAGA	CAAACAGAAGGTGTCTGTTAA	CTGACCAAGACCAATGCATAA
3242	HPD	NM_002150	AGGAGGTTTGACTAAGATCAA	CCAGGAATATGTGGACTATAA	ATCCATTGTGGTGGCCAACTA	CTGGTGGACTACGACGAGAAA
3248	HPGD	NM_000860	CAGCCGGTTTATTGTGCTTCA	CAAGAGCTTCTTAGAGTAGTA	CAAGACTATGATACAACTCCA	CTGGCAGTGACTAATCAGTAA
3249	HPN	NM_002151	GTGGATCTTCCAGGCCATAAA	CAGCCAGGGAATCATTAACAA	TGGGATGCTCTTTAAATAATA	GGGATGCTCTTTAAATAATAA
3250	HPR	NM_020995	CTGCATTGCTGAGTCAATCAA	CTGACCAATACGATTGCATAA	AAGCAAGATTTCAGCCTGGAA	AAGGTGCTTGTTAATGAGAGA
3251	HPRT1	NM_000194	TCCTATTGACATCGCCAGTAA	CACTATTGAGTGAAACATTGA	AACATTGAACTCATATCTGTA	ATGGGAGGCCATCACATTGTA
3280	HES1	NM_005524	CTGGTGCTGATAACAGCGGAA	AAAGACGAAGAGCAAGAATAA	CACGACACCGGATAAACCAAA	ACCATGCACTATATTTGTATA
3292	HSD17B1	NM_000413	AACCATGGTCATGTGAGTTAT	ATCCCAGAGCTTCAAAGTGTA	CTGGACGAAACCAACACATAT	CAGCTGTGGGTGGCTAATTAA
3299	HSF4	NM_001538	AAGGGCGAGAATGGACCCTGA	CAGAGCCGTTTCGCCAAGGAA	CCGGGTCATTGGCAAGCTGAT	CCGACTATCCCTGCACATAAA
3300	DNAJB2	NM_006736	AAAGAGTTTGCTGAGAAGAAA	TTCGCTCTGTTTCTACATCTA		
3308	HSPA4	NM_198431	ATGGACATTGATTGATTCCAA	CAGGTATAAAGGTGACATATA	CCAGGTAATTTCTAATGCAAA	CAGACTATTATAAAGCTTTAA
3309	HSPA5	NM_005347	AACTGTTACAATCAAGGTCTA	TGGGATAAGGAAACACTTCTA	CAAGCCCAATACAGCCATTAA	TAGGGTGTGTGTTCACCTTCA
3313	HSPA9B	NM_004134	AACCAAGATGGAAGAATTCAA	TAGGATGAATTGATCATTATA		
3321	IGSF3	NM_001007237	CAGGGTGATTTGGCCGTCAAA	CAGGAGCGGCTCAGTCATGAA		
3324	HSPCAL3	XM_084514	ACCAGCCTTCTTCCTAGTCAT	CTGGAGATAAATCCTGATGAT		
3326	HSPCB	NM_007355	AAGCTCATGAAAGAAATCTTA	CAAGAATGATAAGGCAGTTAA	AAGGCTGAGGCCGACAAGAAT	CCGCATCTATCGCATGATCAA
3338	DNAJC4	NM_005528	TAGGGAGTGGCAGGTGCTCAA	CAGGAGGGTGGGTGAATTCCA		
3339	HSPG2	NM_005529	CGGGAAGTGCAGGCCCGTCAA	CACCCGAGCCATGGATTTCAA	ACGGTGGGAAGTTGCGATACA	ACGCCTGGACGTGGAGTTCAA
3359	HTR3A	NM_000869	CACCGTATCCATTGACGTCAT	ATCCATTGACGTCATTGTCTA	TACGTGTATATTCGGCATCAA	CAAGCTGCTATTCCACATTTA
3361	HTR5A	NM_024012	TGGATTTACCAGTGAACCTAA	TACGGCTTTCAACAAGAACTA	CTCGGTCTTCGGAGTGCTTAT	CCTGATCTATACGGCTTTCAA
3362	HTR6	NM_000871	CTGCAGCGCCTCCATCCTCAA	CAGGGCCGCTGCCGCCGTCAA	CGCCGTCAATTTCTTCAACAT	CAGGAGGCTGCAAGTCTCCTA
3363	HTR7	NM_000872	TCCAGTCATCAGCTAATACAA	ATGGCACTATGTAGTAATTAA	CTGAAGTGACCGTATATATTA	CGGCGCGATGATGGACGTTAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
3371	TNC	NM_002160	AAGGACCTTCAGGTTTCTGAA	CTGGGATGCCCTCAAACTCAA	CCGAACGTACCAGGGACTTAA	CCGGGCATCAGTCACCGGTTA
3375	IAPP	NM_000415	ACAGCTAATAATGAAGTTATT	TTAGAGGACAATGTAACTCTA	ATGCAGGGTATTGCGAAACAA	CTGGTACTAAGAGGCTATTTA
3431	SP110	NM_004509	TCCCAATCTGGTGACGATTTA	AAGGAAAGGCTGATTACGGAA	ATGGAACTTGGTTAACACCAA	CCCAGACACTTCATAGGATTA
3441	IFNA4	NM_021068	CTGGTTCAACATGGAAATGAT	ACAGAGCAAAGTCTTCAGAAA	ATCTATTTATTTAAATATTTA	AACCTAGAGGCCGAAGTTCAA
3442	IFNA5	NM_002169	ACAGGAGGACTTTGATGATAA	ATGCAGGAGGTTGGAGTGGAA	CAGGAGGACTTTGATGATAAT	ATCCTTCTCTTTATCAGCAAA.
3443	IFNA6	NM_021002	CAGCAGCTGAATGACCTGGAA	ATCCTTCTCTTCATCAAGAAA	CTAGACAAACTCTATACTGAA	CATCAAGAAACTTGCAAGAAA
3444	IFNA7	NM_021057	TCCACTGAACTTTACCAGCAA	CTGGTTCATCATGGAAATGAT	CAGCAACTGAATGACCTGGAA	TAGCCTAGTGATATTTGCAAA
3446	IFNA10	NM_002171	GTCGCTTTACATTGTGGTTAA	CTGGTTCAACATGGCAATGAT	TCCACTGAACTTTACCAGCAA	CAGCAACTGAATGACCTGGAA
3455	IFNAR2	NM_000874	AGGCGAGAGCTGCAAAGTTTA	CACAGTGATGAGCAAGCAGTA	CAAGTTAATTCCAAACACGAA	AAGCACCATAGTGACACTGAA
3456	IFNB1	NM_002176	CAGGTAGTAGGCGACACTGTT	CAGAGTGGAAATCCTAAGGAA	CAAGGACAGGATGAACTTTGA	CAGGTTACCTCCGAAACTGAA
3460	IFNGR2	NM_005534	ACCAAGTGCAGTTTAAATACA	TCGGGCATTTAAGCAACATAT	AAGGCTTCTCTTAAACACTAA	AGGCTTCCCAATGGATTTCAA
3467	IFNW1	NM_002177	AGGGCCTGACTTCCTACATAA	AACCATGTGTTTCCTATTAAA	TAGATTGTTGTCATCCTCTTA	AAGACTCTTATTTCGGCTTTA
3468	IFNWP2	XM_378052	CACAGGTAGGCAGGCCAACAA	ACAGGAAAGATTGAGAAGTAA		
3479	IGF1	M27544	CCGGAGCTGAATTACCTTTCA	ATCAATAATGTTCTATAGAAA	CCAGAAGGAAGTACATTTGAA	ACGGTAATACGTGAAAGCAAA
3483	IGFALS	NM_004970	CACCAACGTGGCGGTCATGAA	CCGACTCTTCCTCAAGGACAA	CCGCCTGGAGGCATTGCCCAA	CAGCTTGAGGTGCTCACGCTA
3484	IGFBP1	NM_000596	CATACATAACTTGATATAGAA	AAGGAGGACGGTTAACTTGTA	TACATGTGTAGGGAAAGTTAA	TACACTGGATATGTTGTTAAA
3491	CYR61	NM_001554	TCCCTTCTACAGGCTGTTCAA	AAGGTATTTCGAAACTGCCAA	AGGGCACACCTAGACAAACAA	AGGCAGCTATCTGCACTCTAA
3508	IGHMBP2	NM_002180	CAGGAGAACATCTCTCTGAAA	CAGAGGGATATAAATTATTTA		
3512	IGJ	NM_144646	AAGAAGTGAAGTCAAGATGAA	CAGAGCAATATCTGTGATGAA		
3547	IGSF1	NM_001555	CTGGAGGAGCTCACTGGAGAA	AAGCAAGTTCCTGCTGCTGAA		
3549	IHH	XM_050846	CTGGGTGTATTACGAGTCAAA	CGGCTTTGACTGGGTGTATTA	CCGCCTGAACTCGCTGGCTAT	CTGGGTGTATTACGAGTCAAA
3550	IK	NM_006083	AACCCGTAACAAGAAGCTTAA	CAGCGAGTATATGAACAACAA	GAGGAGGTGGATTATAGCAAA	CAGGCGCTTCAAGGAAACCAA
3551	IKBKB	NM_001556	TAGGGAGCTATTCATGTTTCA	CAGGACACTGTGAGGGAACAA	CAGACCGACATTGTGGACTTA	CACACTGGAGGTCCTCCATTA
3552	IL1A	NM_000575	TCGAGTTGAATGAACATAGAA	CTGAGGTGATTTATGCCTTAA	AAGGCAAAGCACGAAATGTTA	CACGCCTACTTAAGACAATTA
3557	IL1RN	NM_000577	AAGGAATAAATTGCTCCTTGA	CAGCGAATGAATGCTGTATAT	CTGGATACTTGCAAGGACCAA	CCAAATGTCAATTTAGAAGAA
3559	IL2RA	NM_000417	CCCGTTCACGTTGCCTAATAA	CTCCACCCTATATGTAGTATA	CAGAGAATCATACTTAGCAAA	CCACCCTATATGTAGTATAAA
3560	IL2RB	NM_000878	CCAGTTCACATGCTTCTACAA	ATGGCTGAAGAAGGTCCTGAA	TGGCTTCATCATCTTAGTGTA	CCCGGATGCCTTGGAGATAGA
3561	IL2RG	NM_000206	CACGACAATTCTGACGCCCAA	CTGAACAATCAGTGGATTATA	AAGAACTCGGATAATGATAAA	CTAGAGGATCTTGTTACTGAA
3566	IL4R	NM_000418	CCCGGCAGATTTCAGAATCTA	CCGCCTCGTGGCTATAATAAT	CAGAATCTATAACGTGACCTA	CACATACATGAGGGTCTCTTA
3577	IL8RA	NM_000634	CCGGTGCTTCAGTTAGATCAA	CAGGCAGATGTTCCTAATAAA	TCCGCCAGGCTTACCATCCAA	CCCGTTGAACGTCACATCTTT
3578	IL9	NM_000590	GAGGCAAGATATGAAGATGAA	TACCACCATGCAAACAAGATA	ATCCTATTTATTAAATTTAAA	ATCAGTTGAAGTACTAAAGAA
3581	IL9R	NM_002186	CCAGAGATAGTTGGGTGACAA	AAGGACAAGGGCCAAGGTCTA	CAGAGATAGTTGGGTGACAAA	CAGCTATGAGCTGGCCTTCAA
3596	IL13	NM_002188	CAGCATGGTATGGAGCATCAA	AACAAGTTGTTTCATTGACTA	CAGCTGTCAGCCAACGAGTAA	TTCATTGACTATCAAACTGAA
3597	IL13RA1	NM_001560	CCAAATAATGGTCAAGGATAA	CTCAGTGATGGAGATAATTTA	ACCATGTTTGTGGCTATTAAA	AACCATGTTTGTGGCTATTAA
3608	ILF2	NM_004515	CAGACAGCCTTTGGCCCTAAA	CTCCATAGAAGTGTCATTCCA	TTGAAATGTTGTGAAATGTTA	CAGGCCCTTTGTACCACATAT
3609	ILF3	NM_153464	CAAGCTGCACGTGGCCGTTAA	CTGGTTTAGCTAGAGAGTGAA	CAAGAGTTGAAGTATTGATAA	AACGATTTCACCACATCTGAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
3612	IMPA1	NM_005536	CCAGATTTGGTGACTCATCAA	TAGAAAGTTAACTGTTTGGAA	CCGGAAGAGACGAGTGCGGTA	ACGAAGAGTAATTGCTGCAAA
3614	IMPDH1	NM_183243	CCCAGGATTCATAGACTTCAT	CAGCAGCAGCCAGAAACGATA	CCGCACCGACCTGAAGAAGAA	ATGGCCTGCACTCTTACGAAA
3617	IMPG1	NM_001563	CTCCAAGTTCAAGGAACCAAA	CCGTAGAATATGAAGAATTTA	AAGGGCGAAGTTGTACTATAT	TCGGATCTTTCTGGATCGCAT
3623	INHA	NM_002191	CGGATGGAGGTTACTCTTTCA	AAGGCAGAGTTGGGAAATAGA	CAAGTATGAGACAGTGCCCAA	CAGCACTGTGCTTGTATCTAA
3624	INHBA	NM_002192	CAGGAAGACGCTGCACTTCGA	AAGGAAGATGTGGAAATCTTA	ACCCATGTCCATGTTGTACTA	CTGCAGTAGTGTGGACTAGAA
3625	INHBB	NM_002193	CAGCCTGTGGCTTTACCTGAA	CCACGTGAACTATGCAATTTA	CAGGTGGAACATGGTGGAGAA	CACGTGAACTATGCAATTTAA
3627	CXCL10	NM_001565	TTAGTTTGCAGTTACACTAAA	CAGGAAGGTAGAAATATCTGA	TGCATCAGCATTAGTAATCAA	CTGACTCTAAGTGGCATTCAA
3635	INPP5D	NM_005541	TCGGAATTGCGTTTACACTTA	CCCGGGACTGTTGACAGCCAA	TCCCATCAACATGGTGTCCAA	CAGGTGCTATGCCACATTGAA
3641	INSL4	NM_002195	AGCAGCAAGTCTCTAAAGAAA	CTGAGCCAACTCCTTAGAGAA	TAGGTACGACATCAGAATTCA	ATCCATTCTGTTGTGAAGTAA
3643	INSR	NM_000208	TCGAACGATGTTGGACTCATA	TAGGAAGACGTTTGAGGATTA	CAACGGGAGTCTGATCATCAA	ACCGCTTTACGCTTCTTCAAA
3646	EIF3S6	NM_001568	CAGGAGTCTTACACATATAAA	AAGGAATTATTACAAGGTAAA		
3656	IRAK2	NM_001570	GAGAATATGTGTTGTTATTTA	CCGGTTTACCTGAAGGACTTA	CCAGATCATCCTGAACTGGAA	CAGCAACGTCAAGAGCTCTAA
3660	IRF2	NM_002199	CCCTATCAGAACGGCCTTCTA	ACGGTGAACATCATAGTTGTA	CGGTCCTGACTTCAACTATAA	CACCTTATCTTAAAGCACTTA
3663	IRF5	NM_002200	CGGAGATAACACCATCTTCAA	CCGCATGGTGGAGCAATTCAA		
3667	IRS1	NM_005544	CCGCCTTTGCCTGACCAGCAA	CCGGTATCGTTTCGCATGGAA	ACAATAGGCCATGTTAATTAA	CCGGGTGAACCTCAGTCCTAA
3670	ISL1	NM_002202	TACGGTGGTCTTTGAATTATA	CCGGCTTAAATTGGACTCCTA		
3672	ITGA1	NM_181501	CCCTCGAAACACAACCTTTAA	CTGCATGTCGCCACCACTGAA	CCCTAGATTCACTAAGACAAA	ACTGAGGACATTGGAAATGAA
3673	ITGA2	NM_002203	TCGGAGCAATTCAATATGCAA	TCGCTAGTATTCCAACAGAAA	CCGGTTGATGGGACAGAAGTA	CCCGAGCACATCATTTATATA
3675	ITGA3	NM_002204	CAGCTACATGATTCAGCGCAA	CTGGATTGACTTTGCTGTCAA	CTCGCTTAGCATGGTAAATCA	CACCATCAACATGGAGAACAA
3679	ITGA7	NM_002206	GACCAGGGAGCTGATATGCAA	CACAGTGAAGTCCTCCATAAA	CCCTTTGATGGTGATGGGAAA	CCCAGTGATGGTATACTTGGA
3680	ITGA9	NM_002207	ACAGGTCACTGTCTACATCAA	CACATGCTAATGTGTGCTAAA	CCGAAGGTACAAAGAAATTAT	ACCGAAGATCAGGCACCTTAA
3683	ITGAL	NM_002209	AACGTGTGACCAGAACACCTA	CCCTGTTTAATGATTGACGTA	CTCGGTTGAATTGCACGCCAA	CAGGGCGTGGGACATCTAGTA
3684	ITGAM	NM_000632	CGCAATGACCTTCCAAGAGAA	CTCGTTTGACTGGTACATCAA	TCGGGTCATGCAGCATCAATA	TCAGACATCGGTTCATATTAA
3685	ITGAV	NM_002210	AGCAACTTTATTATAGATTTA	CACATACATGATACCATCCAA	TAGCATGATGTTACAGGAATA	ATGTAGTAGTTTGATGAATAA
3688	ITGB1	NM_002211	CTGCGAGTGTGATAATTTCAA	ACAGATGAAGTTAACAGTGAA	TACGTATTCAGTGAATGGGAA	AAGAGGGATAATACAAATGAA
3690	ITGB3	NM_000212	CAAGCTGAACCTAATAGCCAT	CCGCTTCAATGAGGAAGTGAA	CTCTCCTGATGTAGCACTTAA	CACGTGTGGCCTGTTCTTCTA
3692	ITGB4BP	NM_002212	CCGAGCTTCGTTCGAGAACAA	AAGCTACTGTGTCTTCAGCAA	CAGGGAGACAGAAGAAATTCT	CTGGATCTATCATTACTGCAA
3693	ITGB5	NM_002213	CTCGGTGTGATCTGAGGGCAA	CCGCTATGAAATGGCTTCAAA	ATGGGTGGACACCATCGTGAA	CAAGATTGTTTGGGATTGGAA
3700	ITIH4	NM_002218	CACATCTATGGTAGTCACCAA	ATGGATCGAAGTGACCTTCAA		
3704	ITPA	NM_033453	CAGGAGGCAGTTCGCCAGGTA	GAGGAGGTCGTTCAGATTCTA	CTGGATGAGACTTGTTTCCAA	CTGGAGAAGTTAAAGCCTGAA
3706	ITPKA	NM_002220	CTCCTGCAGCACCGACTTCAA	CCCAGCGTTCCCAGAGCCAAA	CCGGTCTAACGTCTCACACCA	CACCAGCGGGCTGATCCTGAA
3710	ITPR3	NM_002224	CAGGTGTTCCTGCGAACTACA	CCGCAGCATGCCGCTGATCTA	AAGCCGGTGAAGCGCATTCAA	TCAGTTTACCTTAATGCCTTA
3714	JAG2	NM_002226	CCAGAGGTTGTGCACTGTTTA	CTACGTTTCTTTAACCTTGTA	CACTCTGTATATTTGATTGAA	CTGCGTCGTCACCAAATCGTA
3725	JUN	NM_002228	TTCGTTAACATTGACCAAGAA	CGCGCGCGAGTCGACAAGTAA	CTGCCCAGTGTTGTTTGTAAA	AAGAAGTGTCCGAGAACTAAA
3730	KAL1	NM_000216	ATGCATGTCTATATAATTATA	AAGCGTAAATCTAATCAATAA		
3741	KCNA5	NM_002234	ACCAGGGAACCCATTTCTCTA	CAGAGGGATAACCCAAACAAA	CGCAGAGTATTTGAAGTCACA	AGGAATACTTCTGATAATTTA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
3742	KCNA6	NM_002235	TACAATGACCACGGTAGGTTA	CTGGTGTTCGGTCTACATTTA	CAGGACCAAATACCTGGACTA	CTCGATCTTGCCATAACTTTA
3744	KCNA10	NM_005549	CTAGTTATTAGTTTATGCAAA	CACCGGGAGACTGAGAATGAA	CCGGGAGGATAGGGAGCTAAA	CAGCACAGACTCTCTTAATAA
3745	KCNB1	NM_004975	CCGGAGCATTGAGATGATGGA	TCGGTATTTCATAGTACCTGA	AACCACTTGTCTCCTAACAAA	CACGCTTTCTTTACATCACTA
3753	KCNE1	NM_000219	GCCCAGGATGATCCTGTCTAA	AAGAGAAGGACAAGGCCTATG	AACCATCTGGCCATAGAACAA	AACTGGGATTCTTCGGCTTCT
3756	KCNH1	NM_002238	ATCAGCGATGTGAAACGTGAA	CTGAGATACTCAGGATATTAA	TACAGCCATCTTGGTCCCTTA	TCGGCGGTCCAATGATACTAA
3758	KCNJ1	NM_000220	CAGGGTGTTGACAGAAAGTAT	CTCCCATAGTATCCAAGACAA	CAGTCTATACTTGGAGTTATA	TACGTTTAGACAGAGGCTAAA
3759	KCNJ2	NM_000891	CAGGAGCCGCTTTGTGAAGAA	CGAGATGGTGATGTACTCTTA	AGGGTCAATGAGAGCCATAAA	CAACTCTCTTATGGTATTATA
3760	KCNJ3	NM_002239	ACCAGCCATAACTAACAGCAA	AAGGCTACTGGCATTAATTAT	ATGGACTAGATGATATTACTA	CTGTGTGAAGTTACACAATTA
3764	KCNJ8	NM_004982	CAGGACGATGTTGGCCAGAAA	AAGGTGCAATTTATGACTCCA	GAGGTGGTTCCTATTCACCAA	CCAGATCGCTGTGTTACTAAT
3765	KCNJ9	NM_004983	TGGGAAGATGGTAGCAGATAA	AGGGATAATTCAAACTGACAA	GTGAATGACCTTAGTCCGCAA	CAGGCCCGACAGAGAGATGAA
3769	KCNJ13	NM_002242	AACCTACAAACTAGACTTGTA	ATCGCCTTACTTGCCATACAA	CAAACTAGACTTGTAGATTAA	CACATGGATGGCAAACCTAAT
3770	KCNJ14	NM_013348	CGCGGTCGCTTCGTCAAGAAA	CTGGATTCACCTAAGATTCAA	CAGGGTGAGAAGCCAATGGTA	AAGACTGAAGTGACAGATTAA
3773	KCNJ16	NM_018658	CAGACTGGCACTTTATCTCAA	CCGGTAACTATTGTCCATGAA	CAGCAGCTATCATATTATCAA	AAGCTTAATATTAGAGACCCA
3776	KCNK2	NM_014217	CACGACCATTAATGTTATGAA	TCGCATCATCTCAACAATCAT	AGGGATTATACCGTTAGGAAA	AGCCTAGATATGGACCATTTA
3778	KCNMA1	NM_002247	ACCGAGAGAGCCGTATATTAA	ACGGGATGTTACGTCAACCAT	AACCATCTTAAGATCCAAGAA	TAGGCAGAGCAAGTTTATTTA
3780	KCNN1	NM_002248	CAGGGAGACGTGGCTCATCTA	ACCGTCATGTACGACCTTGTA	CACGCTTACCGACCTAGCCAA	CCGGCCTAGCCTAGAATCCTA
3785	KCNQ2	NM_004518	CAGCCAGGGCGTGTGGTTTAA	CCCGCCCTCCTGAGCTATGAA	AACGGTCACCGTGCCCATGTA	CCCATTGACACAAACCCTCAA
3788	KCNS2	NM_020697	CCCATAAAGTTAAATCCCTTA	CACCAAGTGAACTCAGTTTAA	CACCTTATGGTTATGGTGTAA	AGGGACTATTATGCCCATAAA
3792	KEL	NM_000420	CTGGTAAATGGACTTCCTTAA	CCCGACAAGAATACAACGATA	ACCCGAAGTGCTGCCATGAAA	CAGCACAGAAATATCGACCAA
3796	KIF2	NM_004520	AAGAACCAAGATTGTTCTAAA	CAGCAAGCAAATCAACCCGAA	CCAAACCAGATTGATGACTTA	ACCATATAACATGTGATTATA
3806	KIR2DS1	NM_014512	ATCATAGGTCTATATGAGAAA	AACAGCGAGGATTCTGATGAA		
3808	KIR2DS3	NM_012313	CACGTTCTGATTGGGACCTCA	CACCATGTCGCTCATGGTCAT		
3809	KIR2DS4	NM_012314	AGCGAGGATTCTGATGAACAA	CAGCTCCATCTATCCAGGGAA		
3810	KIR2DS5	NM_014513	AACAGGGAGGATTCTGATGAA	TACCTGCGGCTGGAATCTGAA		
3814	KISS1	NM_002256	CAGGACTGAGGCAAGCCTCAA	CCAGGTGGTCTCGTCACCTCA	AAGAAATGTTGCGTAACTCAA	CACCCTCTGGACATTCACCCA
3817	KLK2	NM_005551	CAGCATATAATTCTCCCTGCA	TACTTGAATAATTGACCTGAA	GACGAGTATGGAGTACTTGAA	CTGAGGTTCCCTAGAGTTCAA
3818	KLKB1	NM_000892	CAGCAAGTTCAATCAATGACA	AACGTGGAATCTGGATTCTCA	CGCTATAAAGGTGCTGAGTAA	ATGGTCTGTGCTGGCTATAAA
3827	KNG1	NM_000893	CCGCATAACTGAAGCCACTAA	CTCGGCTGTGTGCATCCTATA	TCCCTCTTCATGCTTAATGAA	ACCGGTGAATGTACAGATAAT
3832	KIF11	NM_004523	CTCGGGAAGCTGGAAATATAA	GCCGATAAGATAGAAGATCAA	CTAGATGGCTTTCTCAGTATA	ACGGAGGAGATAGAACGTTTA
3833	KIFC1	XM_371813	TCGGGAAACACAGGCCATTAA	TGGGACTTAAAGGGTCAGTTA	CAGGGCTATCAAATAAAGAAT	TCGGGAAACACAGGCCATTAA
3835	KIF22	NM_007317	CCACAGTATCCTTATTGCCAA	CAGGACATCTATGCAGGTTCA	ACAGATGGAGTCCTTCCTGAA	ATCCACATCCTGAAGAATAAA
3849	KRT2A	NM_000423	AAGCAGCACCATTTCATCAAA	CTGGTGGAAGCCGGAGATCAA		
3856	KRT8	NM_002273	CCAGGAGCTGATGAACGTCAA	CAGGGTGACCCAGAAGTCCTA	CAGGGCCGTGGTTGTGAAGAA	CAGCATCATTGCTGAGGTCAA
3860	KRT13	NM_002274	CGCCAAGAGTGCAGAGCTGAA	CTGCCTTTCTGCAAACATAAA		
3861	KRT14	NM_000526	CTGGCAATCAATACAGCTTCA	CAAGTATGAGACAGAGTTGAA		
3884	KRTHA3B	NM_002279	ATGGTCTGGAAGGAGAACAAA	CCGAGGCATCACCACAAATCA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
3887	KRTHB1	NM_002281	CAATAAATTAATGTAGCCAAA	CAGCAGCTGCCGGAAATGTTA		
3891	KRTHB5	NM_002283	CAGCCCTTCACTTAACTCCTA	CAGGTCTTGCTATTCAGTGAA		
3912	LAMB1	NM_002291	CCGAAACAGCAACGCCTGTAA	TACCAAGATCCTGTTACTTTA	AGGGAATTTGTGACAGCTATA	TCCGTTCACTCCTAAAGGATA
3913	LAMB2	NM_002292	CGGGTGAACCTGACTCGTCTA	CCAGGCCACCTTTGAACGCTA	CAGGTACTTGATATTTCCTAA	GCGAGATAGGCTTGCACTTAA
3914	LAMB3	NM_000228	ACAGTTACACTTGACAGACAA	ACCGGTTGGGTCAGAGTTCCA	TTGGCATGCCATTGAAACTAA	AAGAGGGATTTGAGAGAATAA
3916	LAMP1	NM_005561	CACGTAATGCATTGCCTGTAA	CACGAGAAATGCAACACGTTA		
3920	LAMP2	NM_002294	CAGTACGCTATGAAACTACAA	CTGGAGCATTTCAGATAAATA	CTGGAACCTATTCAGTTAATA	TAAGGACTATAGTGATTTAAA
3930	LBR	NM_002296	AAGACTCAAGTATAGATTAAA	TAGCAATTAAATTCTAGTGAA	CAGAAGACAGTCTTAATATAA	TAAGGTAGCTTTAGCAATTAA
3931	LCAT	NM_000229	CTGGCTGGATCTCAACATGTT	AACCAGATGTGGTGAACTGGA	CAGCATCAAGCTGAAAGAGGA	AACAGCATCTCAACATGGTCT
3932	LCK	NM_005356	CTACGGGACATTCACCATCAA	CGCCATTACACCAATGCTTCA	AGGCATCAAGTTGACCATCAA	AAGGGCCAGGACTTTATCTAA
3939	LDHA	NM_005566	AAGGATCAGCTGATTTATAAT	CAGATTTGGCAGAGAGTATAA	CAGCTGATTTATAATCTTCTA	AAGTCCAATATGGCAACTCTA
3956	LGALS1	NM_002305	CGCCAACACCATCGTGTGCAA	CGCCAGCAACCTGAATCTCAA	GACGGTGACTTCAAGATCAAA	CACCATCGTGTGCAACAGCAA
3957	LGALS2	NM_006498	CAAGCTGAACCTGCATTTCAA	CACTGATGGCTTTGTAATTAA		
3959	LGALS3BP	NM_005567	CACGGTCATCCTGACTGCCAA	CTGAGGCTCAGCTTCAAGAAA	CAGCTTCCTCTTCCAGGACAA	CAGCTTCAAGAAATTACTGGA
3965	LGALS9	NM_002308	CTCCTTTCCCAGTGTCCTTAA	CCCACCATCAACAGACTGGAA		
3977	LIFR	NM_002310	CAAGACCATTATCAACTCCTA	TTGGAAGCCTTTACCCATTAA	TGGGTCGATCACAATCAACAA	TGCAGATTCGATATTAGTAAA
3980	LIG3	NM_002311	CAGCTGGTTGAAGGTCAACAA	CTGGGAAGAGCTGGAAGATAA	CACCCGAATCCGAGATGATAA	CTGGAAGATAATGAGAAGGAA
3984	LIMK1	NM_002314	CAGAGGTTTCTGGGAGACCTA	GAGCATCTAGGAAGTATTAAA	CTGCCTGGTCCGCGAGAACAA	CACCATGGACTTTGGCCTCAA
3988	LIPA	NM_000235	TACCTGGTCTCGGAAACATAA	CACGTTTGCACTCATGTCATA	CTGACTTAAGCGAGGTATAAA	CCCGCTACTGTCGTTATTGAT
3990	LIPC	NM_000236	AAGTTTATCATTACCAGTTAA	CTGAAGACGATCAGAGTCAAA	AAAGGAATTGCTAGTAATAAA	CAGGAGAAACCCAGCAAAGAA
3992	FADS1	NM_013402	TCGGAATGTTACAATGGTAAA	CAGGAAGAGATTTAACACTAA		
4000	LMNA	NM_005572	AAGCGCCAGAATGGAGATGAT	CCCACCAAAGTTCACCCTGAA	CCGGCTGCGCAACAAGTCCAA	CCAGGAGCTTCTGGACATCAA
4010	LMX1B	NM_002316	CCGCTTCCTGATGCGAGTCAA	CAGCAGATCGTGGCCATGGAA		
4012	LNPEP	NM_005575	CAGGGCACAATTATACGTTGA	CCGCTTTATCAAATATGCCTA	TCCAATGGAACTCAAAGCCTA	CACGTAAATGCCAACCATCTA
4015	LOX	NM_002317	AAGCTGGCTACTCGACATCTA	CTGCACAATTTCACCGTATTA	AACTACTACGATACTTATGAA	CTGGAACTTTAGTGAAACATA
4016	LOXL1	NM_005576	CAAGGTGCACGTGAACCCAAA	TCGCTACGTTTCTGCAACAAA		
4017	LOXL2	NM_002318	CTCGAGATTCCGGAAAGCATA	CCGGAGTTGCCTGCTCAGAAA	CAGGCAATGAGAAGTCCATTA	CCAGTCTATTATAGTCACATA
4033	LRMP	NM_006152	CTGGGAAAGTATAGCATGAAA	CAGATTATCTTTGGGATTTAA		
4034	LRCH4	NM_002319	CCGCCTGGATTTCTCCTGTAA	CAGCGTTGATAGTGGCAGCAA	TTGGCTCCATTCAGAGACCAA	GCTGGTTGTGTTGACAATAAA
4038	LRP4	XM_035037	CAGCGTGTTGACAAATACTCA	CCGCAAAGTACTGATCAACAA	CCGCGCGGTGCTCATCAACAA	CAGGAAATCATTCGCAACAAA
4041	LRP5	NM_002335	CTGGACGGACTCAGAGACCAA	CCCGTTCGGTCTGACGCAGTA	CTGGATGGGCAAGAACCTCTA	CAGGGCTGGGAGAACTTTGTA
4043	LRPAP1	NM_002337	CTGGAAGAAACTAAAGCTTGA	TACCATGCACAGAGTCCTTAA	CAAGTATGGTCTGGACGGAAA	CGGGAGTTCCTGCATCACAAA
4046	LSP1	NM_002339	CCGCTCCATAGAGAAGAGTAA	CAAGGAGAAACTGCAGGTCAA		
4049	LTA	NM_000595	CAGGTGGTCTTCTCTGGGAAA	CCGGAGCTTTCAAAGAAGGAA	CAAGGCTGACCAAGAGAGAAA	ACCCTCGATGAAGCCCAATAA
4052	LTBP1	NM_000627	CCCAATATATCTACCATTGTA	TTGATTAAATTTGGCATTTAA	CTGGGTATGAATGCTACTGTA	TACCGGGTTATAAGCGGGTTA
4054	LTBP3	NM_021070	CCGCTACTGCGTGGATGTGAA	CCGGGACAGATCTCAGCAGAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
4055	LTBR	NM_002342	TACATCTACAATGGACCAGTA	CCGGCGGGTCTATGACTATCA	AAAGGGAGTCATTAACAACTA	CCGCCACACGGTCACCTGCAA
4057	LTF	NM_002343	ACCCTTGATGGTGGTTTCATA	CAGCCACGAACTCACTATTAT	CAGAGAGAGCACAGTGTTTGA	AAGCAGTGACCCTGATCCTAA
4058	LTK	NM_002344	CAGGGATATTGCCGCCCGGAA	CCGGGCCTTGCTCCCAGTCAA	CCTGCAGATGCTTCTAATAAA	ACAGATCTTTGGAGTGCCTAA
4067	LYN	NM_002350	CTCCGAGTCACTAATGTGCAA	CCCAATAATTGCAGAACTAAA	CGGGAAATATGGGATGTATAA	CCCGGACGACTTGTCTTTCAA
4070	TACSTD2	NM_002353	TCGGCGCAAAGGAGACGTTTA	TTGCGACATTGTGAAGGCTTA	CCCGGGATCGTTTGCAAGTAA	CTCGAAATAAGTGGTACTATT
4071	TM4SF1	NM_014220	TTCACTTGTATTCATTTGTAA	TCACAGGATGTCAGTGTTTAA		
4084	MAD	NM_002357	CAGTAGCAGATCAACTCACAA	TACGTTGAGTTTATTAACAAA	CCGAATCAAGTCGACACACTA	AGCCAAATTGCACATAAAGAA
4085	MAD2L1	NM_002358	AAGAGTCGGGACCACAGTTTA	CTGAAAGTAACTCATAATCTA	TCCGCCTTCGTTCATTTACTA	ATGGATATTTGTACTGTTTAA
4086	SMAD1	NM_005900	TTGGAAGTTAAGAATTGATTA	CACACACACCTTGGTAACATA	AACCGGAATTCCACTATTGAA	CAGGACTTTGTGTACAGTTAA
4088	SMAD3	NM_005902	CCGCTGTTCCAGTGTGTCTTA	ATCAAGGGATTTCCTATGGAA	AAGAGATTCGAATGACGGTAA	AAGGAGCACCTTGACAGACTT
4093	SMAD9	NM_005905	CAGCCTCAAGGTCTTCAACAA	TTGGACTTCTTTCTAATGTAA		
4099	MAG	NM_080600	CACTCGCTGTACAGAATGATA	CCCGGTGATTGTGGAGATGAA	CTCGCTGTACAGAATGATATT	ATCGCGCAATGTGACCGTGAA
4101	MAGEA2	NM_005361	TCGACAGATGCAGTGGTTCTA	CAGGGAGTTGATGACCTTGTT		
4109	MAGEA10	NM_021048	CCCAGAAGTGAGATAGATGAA	AAGAAGATCTTCAATCCCAAA		
4118	MAL	NM_002371	TCAGATGGAAGTCTTCATAAA	ACCCTGTGAAATACTTTATAA		
4123	MAN2C1	NM_006715	CACCCAGAAATTGAGCTGGAA	CTCGCTCTTGCGGGCGCCTAA	CAGCCTGTGTTCGTAGTGCAA	CAGGATGCTGGCGTTATCCAA
4125	MAN2B1	NM_000528	GCGCCTTGATTATCAAGATAA	CGCCAAGGAGCTGGTCGATTA	TCGACCCACCTGGAAACTGAA	GCGGAGTATCGGAGCCACTAA
4128	MAOA	NM_000240	TTGCATATTTGGATTACAATA	ACCCTGGTGTGAGGACATAAA	ACGCTGAACCATGAACATTAT	CAGATGTGCCTAGACACGAAA
4137	MAPT	NM_016835	CGGGAAGGTGCAGATAATTAA	TTAGGCAACATCCATCATAAA	CAGTGTGCAAATAGTCTACAA	CCGCCAGGAGTTCGAAGTGAT
4141	MARS	NM_004990	CAGCGAGGGATTCACGGCGAA	TAGGAGCTGAGGATAACTATA	CTGCATAACCCGAGACCTCAA	CTCGACATGGCAACCAATATA
4142	MAS1	NM_002377	CCCATATGCATGAGATACTAA	GAGATACTAATTAATGATGAA	ACAGTTGAGACTGTCGTCTAA	AAGTATCTCCTAAATGTGATA
4144	MAT2A	NM_005911	CAGCAGGATCCTGATGCCAAA	CAACAGTTTAATGAAGATCTA		
4148	MATN3	NM_002381	CACCACTGTGAGTGTAGCCAA	CACCTTGAATGCCGACAAGAA	AAGGTCAGCTCGTATCTTCAA	TTGGTAGGAAATAGAATGAAA
4150	MAZ	NM_002383	CCGCGACGTCTACCACCTGAA	CGCGTCTGCCTTGGAGAAGAA		
4152	MBD1	NM_002384	AAGAGAGTTCCGGGAAACATA	CCGGGAACAGAGAATGTTTAA	CCTGAGGATAACTCAATATAA	AAGGATGATTCTGCCTCCAAA
4153	MBL2	NM_000242	TAGGGTTCCCTTATATTAATA	TACGATGTTTAGTAACCTCAA	CAAGTCAAGATTTCCATATAA	CACATTGAGTCTATCAATCAA
4155	MBP	NM_002385	CACGGCCGGACCCAAGATGAA	CAGTTAAATGAGAACATGAAA		
4157	MC1R	NM_002386	CCAGGAAAGTCTGGTAATAAA	CAGGAAAGTCTGGTAATAAAT	CACGCTCTTCATCGCCTACTA	CACCAGGGCTTTGGCCTTAAA
4161	MC5R	NM_005913	CACCATCTACCTACTCAACAA	TCGCTTCATGTCTCACTTCAA	CTGGGAGACCATCACCATCTA	CGGCATTGTCTTCATCCTGTA
4162	MCAM	NM_006500	CAGCTGGTTAAAGAAGACAAA	TACACACATTATGGCTGTAAA	CCGAACTTGTAGTTGAAGTTA	AAGACCGAACTTGTAGTTGAA
4168	MCF2	NM_005369	TAGAATGTCATCGGCAAATAA	CACGTACTAAATGAACTGATA	TGGCTATATTGGAAACTTAAA	AGGGACTATAGCTCAAGTAAA
4172	MCM3	NM_002388	CAGGGAATTTATCAGAGCAAA	CGGCAGGTATGACCAGTATAA	ATCCAGGTTGAAGGCATTCAA	CACGATTTGACTTGCTCTTCA
4193	MDM2	NM_002392	GCCCAGTATGTAGACAACCAA	CCGGATCTTGATGCTGGTGTA	CAGGCAAATGTGCAATACCAA	AACCTGAAATTTATTCACATA
4201	MEA	NM_014623	CACAGTGAGAGCTGCCTTATA	TGGGAAGATGTGGTACAGAAA		
4222	MEOX1	NM_004527	CAGGCTTGACTGGGTGGACAA	CTCAATTCACTTTGTAAGAAA		
4224	MEP1A	NM_005588	AAGGACGGACCGGGATGATTA	GACACCTATGATGATAGCTTA	CCGGGATGATTATGTGAACAT	GAGGCTGAACCGAATGTACAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
4234	METTL1	NM_005371	CGCGCATGGCTGCGTCATTAA	CACGTGGATTTGGTAGAGAAA	CAGAATATGCCTACGTGCTAA	CTGGTGTATACCATAACCGAT
4239	MFAP4	NM_002404	CTGGACTGTGACGACATCTAT	CCGCGGCTGGAATGACTACAA	CAGAAGAGATTCAATGGCTCA	AACTGGCTTCATACACACAAA
4242	MFNG	NM_002405	ATGCTTATTTGTTTAAGTCAA	CTGGCTAATGTCTCTCAGTCA	CTGGCCGTTGGCCCTGGCTAA	CAAGACAATCATCCACAGCTA
4254	KITLG	NM_000899	AAGCGAGATGGTAGTACAATT	CAGAAATGTCTAAATGCTGAA	TACTGTGAAACTGGCACTGAA	CACTGAATTAATCATCTATAA
4255	MGMT	NM_002412	AAGCTGCTGAAGGTTGTGAAA	CCGGCTCTTCACCATCCCGTT	AAGGTTGTGAAATTCGGAGAA	CACCAGACAGGTGTTATGGAA
4259	MGST3	NM_004528	CAAGATGGCTGTCCTCTCTAA	CTGGTGCTGCCAGCTTTATAA	ATGGCTGTCCTCTCTAAGGAA	CCAGAACACGTTGGAAGTGTA
4283	CXCL9	NM_002416	ACCAATAAGTATTCTGTGTTA	CCACCCGAACGTCTTATCTAA	CCGGTGGAGATCCCACCCGAA	CAGGTAGACAGTATATAACTA
4284	MIP	NM_012064	CCGCTGTGCTGTATAGCGTTA	CCGAGGAAACCTAGCACTCAA	CCGGCTCAAGAGTATTTCTGA	CCCGATGTCTCCAATGGACAA
4286	MITF	NM_000248	ATCGATGACATCATTAGCCTA	CAGCCTACAACTGAATAGCAA	TAGCCTAGAATCAAGTTATAA	CATGATGGTATCTATAGTCAA
4287	ATXN3	NM_004993	CAACATTGCCTGAATAACTTA	TGCGTCGGTTGTAGGACTAAA	TCGGAAGAGACGAGAAGCCTA	TACGATGGGATCATTATTTCA
4291	MLF1	NM_022443.1	GAGGGAGAGCTCATAATCGTA	CAGGAGTTCATCAATATGAAT	GACCGAGCTCATGTCATTAAA	GACCAATCTCTTGCTGTTAAA
4295	MLN	NM_002418	CAGCAAATAAAGCATGAAATA	AAGGAACGGAATAAAGGGCAA	CCAGCTGGGCTTGGAAGGAAA	CTCCAAGATGGTATCCCGTAA
4296	MAP3K11	NM_002419	CAAGGCCTCCACCTTCTCTAA	CCGGCCTTGACCGGAGGAGAA	CCGGAGGAGAAACGTCTTCGA	CCCGACGTCTGGAGGACTCAA
4301	MLLT4	NM_005936	TAGCTCTACAGTCCACTTTAA	CAGCAGTTGGGCCATATTGAA	CTCTATAATAATTCAACTCAA	ATGCCGGTATGTATTGTCCAA
4306	NR3C2	NM_000901	CCAGACCTAGTCTTTAATGAA	CAGCAATTAATTAGATCAACA	CCACGAGGAAGCAGCAATTAA	CAACATTACCTTGTCTTTCAA
4308	TRPM1	NM_002420	AACGGGAATGTATCTTTGTAA	CAAGATTATACAATCTCTTTA	TTCAGTTGCAGTAGTATCAAA	CACCATTAGGTCACTTAAGAA
4317	MMP8	NM_002424	AACGCACTAACTTGACCTACA	ATGGACCAACACCTCCGCAAA	CCGAAGAAACATGGACCAACA	TCCCAAGGATATATCAAACTA
4319	MMP10	NM_002425	GACAGTAATCTCATTGTTAAA	CAGGATGGTGACACACATATT	GAGCCTAAGGTTGATGCTGTA	GACACACATATTAAAGAGTAA
4324	MMP15	NM_002428	CCGGAGCGCTGAGCCAGACAA	CACCAAATACTGGAAATTCGA	CTGGCTCTTTCGAGAAGCGAA	TACATTTATTTCTGTAAATAA
4326	MMP17	NM_016155	CACAAGATCGTCTTCTTTAAA	AAGGACAATAACGTAGAGGAA	CTGGGTGTTCAAGGACAATAA	ATGACAGGACTTATTTCTTTA
4328	MMPL1	NM_004142	ATCGGTGTGTAAGGTGGCCTA	CTCCATTATGAGGCCCTTCTA	CAGGCTGGAGTGCAATGACAT	CAGGGATGATGGAGAGTTCAT
4329	ALDH6A1	NM_005589	CAGGTCTTGCTCCGCTATCAA	CAGCTTTGTGGGATCCAACAA	TGCGATCATCCGGACATCAAA	AACCATCATCTCGAATGTCAA
4355	MPP2	NM_005374	CTAGCGATTGACAAGCAATAA	AACGGCCGAGTTTGTCCCTTA	ACGGCGCAGCCTGAAGAACAA	CCAGTTCTTCCAAGTGTCTAA
4357	MPST	NM_021126	CAAGACCTACGAGGACATCAA	CACCAAGAGAGTGTTTCTTCA	CAGGAATTCCGTTGACTTGTT	AACCAAGTGCTAAATCTTGTA
4361	MRE11A	NM_005590	TGCGATTCAGTTCACCGCTAA	CACATCTTTATTGAACTTGAA	CCCGACATTTCTTCATAGGTA	AAGGGTTATTTGAGCAAGTAA
4435	CITED1	NM_004143	CAGAAACTTAATAGCCAGTAT	ACCAATTCTGTTGTAAATAAA		
4436	MSH2	NM_000251	CAAGGATATGATATCATGGAA	TCCAGGCATGCTTGTGTTGAA	TTGATAAGCTATTGTCTGTAA	CCCATGGGCTATCAACTTAAT
4438	MSH4	NM_002440	AACCATTAACATGAGATTAGA	TCGCTCATATTAATTGATGAA	ATCAATTGTCTTGGATGCCAA	ATGCAGTGAGGTCTAACATAA
4439	MSH5	NM_002441	TTGCCAGACATTAGTGGATAA	TAGGAAGACTCCCGGATTCTA	CACCTTCATGATCGACCTCAA	AAGAAAGATATTGTTTCTTTA
4482	MSRA	NM_012331	ACCCTTCTTGGTAGAAGCTAA	AAGGAAATTCTGGGTCTTGAA		
4486	MST1R	NM_002447	CAGGTCTGCGTAGATGGTGAA	AGGGAGTACTATAGTGTTCAA	TGCCATTAAGTTTGAGTATAT	ATGGAGCATCCTTCTCCGATA
4493	MT1E	NM_175617	CTGCAAGTGCAAAGAGTGCAA	CTGGGCTTTCTTTGCCCTCAT	AAATATGTGACTGACAATAAA	CTCCAGGCTTTCTGCCCTAAA
4499	MT1K	NM_176870	GCCTAGCAGTCGCTCCATTTA	CACGCCGTCCGGGTGGGCCTA		
4520	MTF1	NM_005955	CAGCACAAATAGGCAGCTTAA	ATGAAAGGTCATGATAACAAA		
4521	NUDT1	NM_002452	CCGCGAGGTGGACACGGTCTA	CCGGGTTTCATCTGGAATTAA		
4522	MTHFD1	NM_005956	GAGGTAGAATTATATGGTGAA	ACAGGTGAATGGATTATTCTA	CAGATCACCATCCATCTTCAA	ATCGTTTGGTGCCATCAGTAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
4524	MTHFR	NM_005957	AAGCGCCGAGAGGAAGATGTA	CTCGGGAGAACCAAACCGGAA	AACCTAGTACTCTCTGCTCTA	TGCCCTGTAACTTATCTAGAA
4544	MTNR1B	NM_005959	CGGCCTCGCTGTGGCCATCAA	CTGCCTGAATGCCATTGTCTA	CACTAGCTACTTACTGGCTTA	AACCCACGGCACTGCATTCAA
4580	MTX1	NM_002455	TTGGATAGACACCAAGAACTA	CAGGGCCCGCTCCAAACATAA		
4583	MUC2	NM_002457	CCGGTTTGGCAACAACACCAA	CCCGCTGGGATTCGAAGTGAA		
4586	MUC5AC	XM_495860	CCAGTCTGTTGCATAAATACA	ACCCTTCAAGATGTGCCTCAA	CTGGACAGTGTGCAGCATCAA	CACCCGGAGGTGAACATTGAA
4587	MUC5B	XM_039877	CACCTATGATGAGAAACTCTA	CCCGATGGGTTTCCTAAATTT		
4591	TRIM37	NM_015294	TTGGACTTACTCGCAAATGAA	CTCGAAGGTGGTCCTACTACA	CTAGAGCTTAGTTGTGTTTAA	CTGTAGATTAGTGAACAGAAA
4594	MUT	NM_000255	AAGAGAGATACTATGGACTTA	CTGGGCTCACTTAATAGAGAA	CTGGAGCTGGCCTATACTTTA	AGGGAATACCTAAACTTCGAA
4595	MUTYH	NM_012222	CACATCAAGCTGACATATCAA	CAGGAGGAATTTCACACCGCA	GAGAATCCTGTTGTTAGTAAA	CAAGCTGACATATCAAGTATA
4598	MVK	NM_000431	AAGGGAAGATTTCATCCTTAA	CTGTGGCATCACACTCCTCAA	GCGGTGGGCCTGGTTAAATAA	CCGCTTGGCGATGCCAGCCAA
4599	MX1	NM_002462	TAGAGCTTACTTTGCAAAGAA	TCCGTTAGCCGTGGTGATTTA	CTGAAGAAACTTGTGAACGAA	TAAGATCAAGACACTCATCAA
4606	MYBPC2	NM_004533	CCGCCTCGAGGTCAAAGCCAA	TCCCAAGTTCCTGATAACCAA		
4607	MYBPC3	NM_000256	CAAGGTCAAGTTCGACCTCAA	TAGCACGGAGCTCTTTGTGAA	CCGCATAAAGGTGTCCCACAT	CAGGATGTCGGCAACACGGAA
4609	MYC	NM_002467	TAGCAGTTACACAGAATTTCA	CTCGGTGCAGCCGTATTTCTA	CCCAAGGTAGTTATCCTTAAA	AACGTTTATAGCAGTTACACA
4610	MYCL1	NM_005376	CAGCACTATTTCTACGACTAT	TGGCTAGTGACAAATAAATTA	CTGTGGCTAGTGACAAATAAA	CTCCAGTTGGCTTTACTTTAA
4615	MYD88	NM_002468	TCCGGCAACTGGAACAGACAA	CTCTGGCATATTCATCAAGTA	CAGAGAGTAGCTGTGTTTGAA	CATCCTGAGTTTATAATAATA
4618	MYF6	NM_002469	CTCGTGATAACGGCTAAGGAA	AAGTGGGAAAGTTGCATTTAA	TGCGAGGATCCTGGTATTGTA	TCCTGGTATTGTAATATTAAA
4619	MYH1	NM_005963	AAGCGCATCCATGAACTGGAA	CTGGGCTTTACTTCAGATGAA		
4625	MYH7	NM_000257	CAGAGAGAGATTATCACATTT	CAGACGGAGGAGGACAGGAAA		
4628	MYH10	NM_005964	CTCGTTCATCGCATCAATAAA	AAGCGGTTCAAAGCAAATCTA	CCCATGTTGCTTCTTCACATA	CAGGACTAATCTATACTTATT
4636	MYL5	NM_002477	CAAGGAGGCATTCACACTCAT	CTCATCCAATGTCTTCTCCAA		
4653	MYOC	NM_000261	CCCATTCAAGAACCGCTATAA	GGCGTAGACAATTTCATATAA	CAGCATTTATGGGATGTTTAA	CAGCATCGAATATAAGTAAGA
4654	MYOD1	NM_002478	CCGCCTGAGCAAAGTAAATGA	CCGCCTGAGCAAAGTAAATGA	CTGCACGTCGAGCAATCCAAA	TACAGGGAATTTGTACGTTTA
4656	MYOG	NM_002479	CAGGCTCAAGAAGGTGAATGA	CCCAGATGAAACCATGCCCAA	CCAACTGAGATTGTCTTCCAA	CTGCCCTGAATTGAGAGAGAA
4670	HNRPM	NM_005968	TGGCATCTTGTTGACATCGAA	CCCACCCAGTATCCTAAATAA	CCCGCAGGAATGGGAATGGAA	CCGGATGATGAATGGCATGAA
4671	BIRC1	NM_004536	ATCCTCAATCTAAGTACTTAA	CTCAATCTAAGTACTTAACTA	TCGAAATTCATGATACTACTA	CGTGGTGAACTTTGTGAATTA
4684	NCAM1	NM_000615	CCGATTCATAGTCCTGTCCAA	TCCATGTACCTTGAAGTGCAA	CCGAAACAACGTACGCCGTAA	CAGCGCGGCCTCCGAGTTCAA
4686	NCBP1	NM_002486	CAGGTATGGACTGCTGATAAA	CTGGAAGAAGCTAAAGAGAAA		
4688	NCF2	NM_000433	CAGAAGCATTAACCGAGACAA	CAAGAAGGATTACCTAGGCAA	CAAGTACACGGTAGTCATGAA	CAGTTTGGAAGTGTTAACTAT
4691	NCL	NM_005381	ACGGTGAAATTGATGGAAATA	TCCGTCTAGTTAACATTTCAA	TTGACTGGATATTCATATAAA	ATCCGTCTAGTTAACATTTCA
4692	NDN	NM_002487	CCGCGAAATCACCAAGATGCA	CAGTGCAGTATTCACGTGTAA	CCCACCGTGAGTCAACTTTAA	CCACCGTGAGTCAACTTTAAA
4696	NDUFA3	NM_004542	CAGCCTGGAGTGGCTGAAGAA	CAAGTACTCCGTCATGATCAA		
4704	NDUFA9	NM_005002	TCCGGAAGCCATTATCGTAAA	AAGAGAGGATAGATTCCTTAA		
4705	NDUFA10	NM_004544	AAGCAGGACAATCGCACTTTA	CTGGATGTTTGGAACCCTTTA		
4709	NDUFB3	NM_002491	CAGATTGAGGATGCACATATA	CAGAATATTAGTAAAGATTTA		
4716	NDUFB10	NM_004548	CAGCAGAACTGTATCAAGGAA	ATGACTGTTGCTGAAATATAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
4717	NDUFC1	NM_002494	CTCATCAAACAACACAATGAA	CACCATCTGTTGAGTTGTAAA		
4718	NDUFC2	NM_004549	CTGTAGGTATTAAGTCATTAA	CTGGTCTATATGTGATTTCAA		
4719	NDUFS1	NM_005006	CCGCAGATAATTAATGGACAA	TTGGCTTATCTTCATAAATAA		
4722	NDUFS3	NM_004551	CCGGAGAGTCTCAAGCTTGAA	TTGAGTGTCCGTGTAAATAAA		
4736	RPL10A	NM_007104	CAGCGCCTATATTAAGGCACA	CACATTTGAATAAATTCTATT		
4739	NEDD9	NM_006403	CGCTGCCGAAATGAAGTATAA	CACCCAAGAACAAGAGGTATA		
4741	NEF3	NM_005382	CCCAATCACAATATCCAGTAA	CAGCAGTACTTGCTCAATAAA		
4745	NELL1	NM_006157	TGCGAGAAAGATATTGATGAA	CTCATGTGAGTGAGAAATTAA		
4750	NEK1	NM_012224	ATGGCTCTCTCTACATAGTAA	CAGAATAAAGCTCGAGCCGAA	TAGGGATAGACCATCAGTCAA	ACCGTAGGAGATGTTCGTCAA
4760	NEUROD1	NM_002500	CACGAATTTGGTGTGGCTGTA	CAGATCGTATTAATTATCTGA	CAAGCTTGTATATACATATTA	CCCATGGTGGGTTGTCATATA
4761	NEUROD2	NM_006160	CAATGGCAACTTCTCACTCAA	CCCGCTCTGTCTCAATGGCAA	CTCGGAGAATCTCTTGTCTTA	CAAGACAATTTGTAACTAGAA
4762	NEUROG1	NM_006161	CCCAGGCTGTTGGGAACGTAA	CCGGCTGACAATACAATGAAA	CAGGGCTGGAGAGTACTTTAA	CAGACGCTTCATGTAAATAAA
4779	NFE2L1	NM_003204	AAGGGTAGAGTGAACAGGAAA	AAGGAGATTCCCAATATTCAA		
4781	NFIB	NM_005596	CTGGACAATCAGGAAGTCCAA	TACAATCACTAATTCCCTTAA	AAGGTTAAACTGTAATGACAT	ACAGAGGGCAAGTGCAATTTA
4784	NFIX	NM_002501	CTGGTGCTTCTTACATTATAA	CCGGACAATCAGATAGTTCAA		
4796	NFKBIL2	NM_013432	CCCATCCGGGTTCGAGTTCAA	CGGGAGCTCAGTGTAGCTGAA		
4804	NGFR	NM_002507	ATGGCAATTCTTTGACCTCAA	CTCCTGAAACTTACACACAAA	ACGTTAAGTGATGAACATTAA	AACGTTAAGTGATGAACATTA
4814	NINJ1	NM_004148	CAGGACATTCCAGAAGGACAA	CACGCTCTTTGTCAGGCTCAA		
4818	NKG7	NM_005601	AACCTTGTGAGCAGAAGGCAA	CTCCTTCTCTCTGAGATTCAA		
4824	NKX3-1	NM_006167	ACGCTATAAGACTAAGCGAAA	CAGGCTATCATATATACTGTA	AACTGTGTTTATTGCCTATAA	CCGGAGTACTAGCCAGCACAA
4825	NKX6-1	NM_006168	CCCGCTGTACCCTGCCGCGTA	CTGGAGAAGACTTTCGAACAA		
4832	NME3	NM_002513	CCGGCAGATGCGCGTCACAGA	ACGGCCGCCTTGTCAAGTATA	CTGCATCGAGGTTGGCAAGAA	ACGCACCTTCCTGGCCGTGAA
4833	NME4	NM_005009	ACGCCTTTATGCAAGTTGTAA	TTGTAAGGAGTTGAACAGTAA	CAGCACATGGGTGGTACACTA	ACCAACTACCTCCGTCAGCAA
4838	NODAL	NM_018055	GTGCTCCTAGATCACCATAAA	CTGGATGTTCTCTTTACTGAA	AAGATTAAGGATCACTGTATA	AAGGATCACTGTATAGATTAA
4849	CNOT3	NM_014516	ACGGCTGAGGGACCAAATCAA	CTCGGACACTGTGGAATTCTA		
4853	NOTCH2	NM_024408	TACCAGCATGTTATAGGGCAA	TTAGATGATAATGGACAACTA	AAGGGAAGGTAAGATGGATAA	CTGACTAAACGTAGTAAGGAA
4858	NOVA2	NM_002516	GAGGTGGTCAACATCCTTCAA	CAGGTCTGTGTGATATCTGTA		
4861	NPAS1	NM_002517	TGGCTTTGTGTTCGCCTTGAA	CGCCTTGAACCAGGAAGGAAA	CAGCGTCTTCGACTACATTCA	GCCCGTAGCCCTGAGAATTAA
4868	NPHS1	NM_004646	CAAGGCCTCATTCACCGTGAA	CAGCAGCAATCCGCCGGTCAA	TCGGACCAAACCAACATTCAA	CTGGTTAGGTGAGCTCCATAA
4879	NPPB	NM_002521	CACCTGCTTCTGATTCCACAA	CTGAGGCGGCATTAAGAGGAA	AAGATGGTTTCTTACCTTTGA	TCCACGGTGAAATAAAGTCAA
4880	NPPC	NM_024409	CAAGGGCTGCTTCGGCCTCAA	CCCAACGCGCGCAAATACAAA		
4881	NPR1	NM_000906	CCGGTACTCACTCACCAATGA	CCTGACGTTGCGCAAATTTAA	ACGCATTGAGCTGACACGAAA	AACGCATTGAGCTGACACGAA
4882	NPR2	NM_000907	CCCGGGAGGATGGACTTCGAA	ACCCAACTGAATGAAGAGCTA	CAGGACAATCGCACCCGGGAA	AAGGATGCCCTAGATGAGCTA
4885	NPTX2	NM_002523	TTCGATTAAAGTGCACTGAAA	CTGGACTGTCTTCATCAAGTA		
4889	NPY5R	NM_006174	CCCTTAGTTTGTCTTACTGTA	TAGGCATTTCAAGTTGGTGTA	TTGGGCTCTATACATTTGTAA	CACAGTCTTGTGGAACTTCAA
4899	NRF1	NM_005011	CAGGCAGATGAATGTCTTGAA	CAGAGGTGCAATCAAATGGAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
4901	NRL	NM_006177	CCGAATTTAGATGCTGGTCAT	CAAGATTTCAATATCCAACAA	ATCCAACAACTAGATAGATTA	CTAGATAGATTAGGACCTCTA
4905	NSF	NM_006178	AAGGAATGCAATAAAGAGTAA	CAGGTACACATTTACACTGAA		
4913	NTHL1	NM_002528	CAGGCTGAGGTGGACCAAGAA	GAGCAAGGTGAAATACATCAA	CTGGAGGAGCAAGGTGAAATA	CACGCTGGGCAAGCTCATCTA
4915	NTRK2	NM_006180	CTGCATAGACAAAGGCCTTAA	ATGGCTTAAGCCTGTGTATAA	CTGACGAGTTTGTCTAGGAAA	ACCACGAACAGAAGTAATGAA
4916	NTRK3	NM_002530	CGCGATGGTTTCAGACGCTGA	CAGAGAGCACGGATAACTTTA	CTGGTTGGAGCGAATCTGCTA	CACGGATAACTTTATCTTGTT
4919	ROR1	NM_005012	CAGCAATGGATGGAATTTCAA	CCCAATATTGTCTGCCTTCTA	CCGTACTGCGATGAAACTTCA	CCCAGTGAGTAATCTCAGTAA
4928	NUP98	NM_005387	CGGGATTTCTTTGTAAAGCAT	CTGGAGTTAGCACTAACATAA	CAGTGTATTACTGCTATGAAA	TGGGACTACTATTAAATTTAA
4935	GPR143	NM_000273	CTGAGGCTGGCTGTAAAGTAA	CTGGCTGTAAAGTAAGTGTAA	TCGGATATGAACCACACGGAA	CAGCTAGAGCTTCTTCCCGAA
4948	OCA2	NM_000275	CCGCGGAAGTGTAGAAACCCA	CTGGCTGTGATTGGCGATAGA	TGGAATAGACCTTGACACTAA	GACCTTGACACTAACACTCTA
4967	OGDH	NM_002541	CAGGATCAATCGTGTCACCGA	CTGCAATTGGGTTGTTGTCAA	CACTCTTTCTTTCTCCTTTAA	TTGGCTTGACCCATAAACTAA
4975	OMP	NM_006189	AAGGAGGACTCGGATGCCATA	CCGGGCAAGGTCACCATCACA	CTCGGATGCCATAGATTGGAA	CTGGAATGTCGTGCTGGACAA
4978	OPCML	NM_002545	CACGTGTAGGATAATCATTCA	ATGCATGAAACCCAACACTAA	TAGGCCAAAGTAGCAAGCTAA	CTGGGACACTATCCTACTATA
4985	OPRD1	NM_000911	CACGCTCACCATGATGAGTGT	CTCCATCGACTACTACAATAT	CGGCATCGTCCGGTACACTAA	CAGCATCTTCACGCTCACCAT
4986	OPRK1	NM_000912	CAGGGAAGACGTCGATGTCAT	ATCGATGGGATGAATAAACCA	TAGGTTTAACTCAGATCACTA	CAGATGCTTTAGTTACTACAA
4987	OPRL1	NM_000913	CTGCCTTGTCATGTACGTCAT	CAGCGGTGCAATGAACTATCA	CTGGCTGGGTATTCTTCGTAA	ATGGGACAGGTCAAAGCATTA
4988	OPRM1	NM_000914	CCGTAGTAACACATAAAGTAA	AGGGAAGAGATTAGCATGAAA	TTCACCGTAGTAACACATAAA	TCCAGAGTGTGAATTACCTAA
4992	OR1F1	NM_012360	CCCACTCAGCTGAGAAAGACA	CTGAGAAAGACACTATGGCTA	CAGCACCATCATTGCTGTGTA	ATGGGTGGTTGCCAACCTGAA
4993	OR2C1	NM_012368	TCAGCTATGGTGGCTGCATAA	CCCAAATGCTGATCAATTTAT	CAAGTTCATTTCCCTGTTCTA	AAGCATCATCGTGATCTCCTA
4994	OR3A1	NM_002550	CTGGGTTCAACCAAGCTTTCA	TTCAGGTATCTTTAACTATAT	CAAGCTTTCAGACAAGGATAA	AAGCTTTCAGACAAGGATAAA
4995	OR3A2	NM_002551	AGGGTGCTCTGTGGCAAATAT	ATGGACAAACTCCAAGGCAAA	CACGTGGCAGCTGCAGTTCTA	AAGAGGTATCTTCAACTACAT
5003	SLC22A1LS	NM_007105	CTGCAGCAACATAGAGTACAA	CTCAGCCAGTCTTAAAGGCAA		
5004	ORM1	NM_000607	TCGAAACGAGGAGTACAATAA	TTCCCTCACTTGCATCAATAA	CAGCACGAGAAGGAGAGGAAA	CACGATCTTTCTCAGAGAGTA
5008	OSM	NM_020530	CAAGGCCTGGATGTTCCTAAA	CGGGCTCAGGAACAACATCTA	CTGACGTAAGGTGGATATTAA	TGGAGGGACATGACTAATTTA
5009	OTC	NM_000531	AGCGGTGGAGCTTGGCATAAA	AGGGCATAGAATCGTCCTTTA	AGCATCCATCCCAATTATCAA	TACGTGCTTAACTTTGCTTAA
5025	P2RX4	NM_002560	CTCCGTTACGACCAAGGTCAA	AGGCAGGTGCGTAGCTTTCAA	TCGTGCATTTATGATGCTAAA	CGGGACGTTGAGCACAACGTA
5030	P2RY4	NM_002565	CTGGGATGCAACGGCCACCTA	CAGAGGTGAGGGAACCCAATA	CCCAATAGTGATACCTGGTAA	CAGATAGATTGTAACACGGGA
5033	P4HA1	NM_000917	CAGAGAAGTTAGATCGGCTAA	TGGCAACAAATGGGTATCCAA	CGAAATCATCATATTGCATAA	CAGGGTGGTAATATTGGCATT
5034	P4HB	NM_000918	GAGGAAGACGATGATCAGAAA	CTATTTCACAATCGAATTGAA	CAGGACGGTCATTGATTACAA	AAGATGAACTGTAATACGCAA
5051	PAFAH2	NM_000437	CAGCGGGTAAGCGAGTGTTTA	ACGGGTGTTGAAGATCCTGCA	CCCGAGGACCTGTGTTCTTTA	GAGAAGTAGTTTGGTCAGCTA
5062	PAK2	NM_002577	TGCAGTAGTATAAATCATGAA	CCGGATCATACGAAATCAATT	CCGCGACCGGATCATACGAAA	ACGAGTAATTGTGAAGCATAA
5069	PAPPA	NM_002581	TGGGCAGTTCATGAAGCTCTA	CCGACAAGAAGTCTCCTTCAA	CTGGCCAATGCTTAAATACTA	CAGGGAGTGCTTGTTTGATAT
5101	PCDH9	NM_020403	ACGGTTCACCATCAATTTAAA	ACCGTCTAATACTTCCTTTAA	ACCGACGTGGGTTATACTTAA	AAGGCGGTATATGACAACCAA
5104	SERPINA5	NM_000624	CTCCGTTTCCTCATAGAACAA	TACACAGGTTTAGTTGACTAA	CACCAGCATGGTAGTGGCAAA	AAGGTGGAAATGGCCCATTTA
5108	PCM1	NM_006197	CGGATAAACTTCAGTGATTTA	CAGTATCACATCTGAACTAAA	ACCGTGATTCACTTAGATCAA	CAGGCTTTAACTAATTATGGA
5110	PCMT1	NM_005389	CAGGCGCTAATAGATCAGTTA	TTGGAGCAGTATGACAAGCTA	CTACAAGATGGCAGCATCAAA	TACGTGCCTTTAACAGATAAA
5111	PCNA	M15796	TGCGGATATGGGACACTTAAA	TACACTAAGGGCCGAAGATAA	ATGGATTTAGATGTTGAACAA	AAGGATCTTAGGCATTCTTAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
5121	PCP4	NM_006198	ATCATCTGTCAAGAAATTAAA	ATGGAATTGTGAGTAGCTTAA		
5129	PCTK3	NM_002596	CCGGCGGAATGAGAACTTGCA	CCGGGTATAAGGAGCAAAGGA	CAGGTTGGATACGGATGGCAT	AACCCGTTACTTAGCTGTGTA
5133	PDCD1	NM_005018	CTGGTTGGAGATGGCCTTGGA	CCCTGTGGTTCTATTATATTA	CCCATTCCTGAAATTATTTAA	ATCGGAGAGCTTCGTGCTAAA
5134	PDCD2	NM_002598	CAGATCATCTGGACCATATAA	CCAGATCATCTGGACCATATA		
5138	PDE2A	NM_002599	TCCGACGATGAGTATACCAAA	CATGAATTTCATCAACAACTA	ATCGCGGAGCTGATCTACAAA	ACCGCTTTGTACATGAGAATA
5140	PDE3B	NM_000922	TACGGAGTATTAGTAGCTTAA	TGGGATCGTAATAATGGCAAA	CACAGAGTGAACAGCAAACAA	CAGGTTATGTATACCTTATTT
5141	PDE4A	NM_006202	CAGGGCTGGCGGGCCATGTAA	CTGCTGTATTATACAACTGTA	ATGGGAAGTCGTGTCATCCTA	TTCGATCTTGTCTCCAATTAA
5146	PDE6C	NM_006204	AAGGTCGTCCTTTCTGAACAA	CTGGTGGGCCCTGACAAAGAA	CACGGTTAGATCATATCTGAA	ACGGATTGATTAAATGTGGAA
5150	PDE7A	NM_002603	CAGATAGGTGCTCTGATACTA	TCGGACGTGGGAATTAAGCAA	CCCGAACATACAGCAATATGA	CCGAACATACAGCAATATGAA
5152	PDE9A	NM_002606	ATGGACGCATTCAGAAGGTAA	CCGGAGGGAAGGAGCATTTGA	CGCGTGGAATTGGAAGGACTA	AACGGATATCCTGATCCTAAT
5156	PDGFRA	NM_006206	CTGAGCCAGATTGGCCAATTA	CGCAGGAAGCCTACTATTTAA	CCCGAGACTCCTGTAACCTTA	ACGCAGGAAGCCTACTATTTA
5157	PDGFRL	NM_006207	CCAGGAGAGAATAGAATCAAA	CTGCGTATCTGGACACCTTTA	CTGGAGGATGTTACTGGCCAA	ACGCAGTCTATCATGATGCAA
5158	PDE6B	NM_000283	GCCCACCACATTTGACATCTA	CTGAAGCCAACTGTGAATAAA	CACGCTGCTCATGACCGGCAA	CCGGGAAATTGTCTTCTACAA
5166	PDK4	NM_002612	CAGGACACTTTACGGGATCAA	CTAGACAGTGACATTTCTTAA	AGGCCTCTTGTTCACATCAAA	ACCCGTGTCAATTAACATTTA
5178	PEG3	NM_006210	AAGGATGACCCTGATGACAAA	CCGGATGTCATCATAGGAGAA		
5184	PEPD	NM_000285	CACCGTGGAGCCGGGCATCTA	CAGGCTGTGACAAGGCCTTTA	TCGGCATTTGATCAGACCAAA	CTGTCCTTTAGTAGCAAGTAA
5189	PEX1	NM_000466	CAGTAGCAAGTTTATGGACTA	CAGAGTATATCCACCAGAGAA	CTCATGGATACTATCCAGTTA	AAGGCAGATACCGGAGCCAAA
5190	PEX6	NM_000287	CCAGAGAGTTACACATCGAAA	CACACGCAAATTCAAGCTAGA	CCAGAGCTCATTAACATGTAT	CAGGATGTGTTTGTGATTGGA
5191	PEX7	NM_000288	CGGGCTGTGGAACCCTACTAA	CAGGAGGTGTATAGTGTTGAT	AAGCCTGACTCTCTTCTTGAA	TAGGTTATACGTATATAGATA
5204	PFDN5	NM_002624	ACAGGCCGTCATGGAAATGAT	CAACATGGCGCAGTCTATTAA		
5205	ATP8B1	NM_005603	CTGGATATCTTTGCAAATGAA	CTGGTTCTTGGTTGAATGAAA		
5208	PFKFB2	NM_006212	CAGAACAACAACAGCTATGAA	GCCCTTGTCACTAATCACCAA	CCGTGACAAGCCAACTAACAA	CCAGAGCAAGATAGTCTACTA
5209	PFKFB3	NM_004566	CTCCTAGTTGCTGAAAGTTAA	CTGGGATATAAAGCTATGCTA	CTCCAATATCATGGAAGTTAA	CAGGGACTTGTCGCTGATCAA
5210	PFKFB4	NM_004567	CCCACGGGAATTGACACAGAA	TACGAGGAAATTCAGGATAAT	CAGAAAGTGTCTGGACTTGTA	ACGGAGAGCGACCATCTTTAA
5214	PFKP	NM_002627	TCGGAGAACCGTGCCCGGAAA	TGCGGGCAACCTGAACACCTA	CCGCCTGAAGGCTGCTTGCAA	CAGCACTTTATGCACGTATTA
5216	PFN1	NM_005022	TCAACAAGAAATGTTATGAAA	CCACGGTGGTTTGATCAACAA	TAGCATGGATCTTCGTACCAA	CGGGTGGAACGCCTACATCGA
5228	PGF	NM_002632	CAGGCTCTGCACAGTCAAGCA	AAGAGCTGCCTGGATGAGAAA	TGCCCTCTATTTATTAGCCAA	ACCCGGCTCGTGTATTTATTA
5236	PGM1	NM_002633	CAGGTACAGTTTACACTACAA	CAGCAAGACAATTGAAGAATA		
5243	ABCB1	NM_000927	GAGGTCGGAATGGATCTTGAA	GACAGAAAGCTTAGTACCAAA	CACGGAAGGCCTAATGCCGAA	ATCGAGTCACTGCCTAATAAA
5253	PHF2	NM_005392	CTGGATTTGTTTCTCAGGCAA	AAGATGAATCTTCAACTTTAA		
5256	PHKA2	NM_000292	CTGGTGAAATCGATCCCTTAA	CACCACATCGTTCTACACATA	CCGGATTCTTAGTCACATATA	CCGCCTAACAAGGTAGATGAA
5265	SERPINA1	NM_000295	AAGGCTGACACTCACGATGAA	TACGTGGAGAAGGGTACTCAA	CACCCACGATATCATCACCAA	CCCGAGGTCAAGTTCAACAAA
5271	SERPINB8	NM_002640	CTCAATCAAGGCGGACGTGAA	AGGGCAAACCCTATAGAGTAA	ACCACTGAGTCCTCTAACTAA	TTAGACAGTTTGAGTAATTAA
5281	PIGF	NM_002643	CACCATGAAAGATAACGATAT	AAGAAGTTCATTATCACACAA		
5283	PIGH	NM_004569	CAGGAAGAAATGTCCTACAAA	CAGGTTTACTTTGTTGATGTT		
5288	PIK3C2G	NM_004570	CTGGTGTGTGGTAACATTCAT	CCGGGCCTCTGAATCACATAA	CCCGTAGAAATGATAACTCCA	CCAGATCAAGAAATTCGTAAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
5295	PIK3R1	NM_181504	ACGGCTGAATATGAATAGATA	CACCCAGTGTAGCATCCTAAA	TAGCTGGTTATGAACTAGTAA	CAGCATTAAACCAGACCTTAT
5296	PIK3R2	NM_005027	CAGGGCCAGACTCAAGAGAAA	CGGCGTGAGGGCAACGAGAAA	TTGGTACGTGGGCAAGATCAA	CCGCGAGTATGACCAGCTTTA
5298	PIK4CB	NM_002651	TGGCGACATGTTCAACTACTA	CGACATGTTCAACTACTATAA	TCGGCTGATAGTGGCATGATT	CCGAGAGTATTGATAATTCAT
5300	PIN1	NM_006221	CGGCTACATCCAGAAGATCAA	CAGGCCGAGTGTACTACTTCA	GACCGCCAGATTCTCCCTTAA	CAGTATTTATTGTTCCCACAA
5303	PIN4	NM_006223	CACACTATTCACACAACTGAA	CAGCATTTGCCTTGCCTGTAA		
5310	PKD1	NM_000296	CCGCGTGAACAGGGCGCATTA	CCGAGCCATTTACCACCCATA	CTGGGTCTCAGCCACGTACAA	CCCGTCCATTGTGGGTAGCAA
5313	PKLR	NM_000298	CTGAAAGTCTGTGTCCAATTA	AAGCATGTCGATCCAGGAGAA	GAGGCCTATCTGAGACTATAA	CGGGTGCAATTTGGCATTGAA
5314	PKHD1	NM_170724	TTGCAGCTAGATATAAATTAT	CTGATGAGTATTGAAGTACTA	CACGAGATAGCTGTACTTTCA	CACCGGCATATTGGAAGTGTA
5315	PKM2	NM_182471	CTGGATAACGCCTACATGGAA	CCGGGTGAACTTTGCCATGAA	CCCGATCAGTGGAGACGTTGA	AACATCAAGATTATCAGCAAA
5317	PKP1	NM_000299	CAGGATGAATCTGCCAAGCAA	AAGCATAACCACAAACTGCAA	TCCCGAGGGCCTTATGAGAAA	CTGGTGTTAGAGAGGAATTAA
5318	PKP2	NM_001005242	CAGGAGATACTTTACCTATAA	CAGAATGGAAATGACAAGAAA		
5324	PLAG1	NM_002655	AAGGGTCAGTTGGGACATTAA	AACCAACATAATCTTCTTAAA		
5325	PLAGL1	NM_002656	CAGCATTGTGATTAGAATGAA	CAGGAACATATTTGCATGTTA		
5326	PLAGL2	NM_002657	AAGGATATTTATGTAATAAGA	TCCAGATTATTTAAAGAGAAA		
5328	PLAU	NM_002658	CTGCCTGCCCTCGATGTATAA	CACGAGAGTCTCACACTTCTT	GAGCTGGTGTCTGATTGTTAA	CCGCATGACTTTGACTGGAAT
5330	PLCB2	NM_004573	CTCGGTGCAGTTTGTGGACTA	CCGGCCGGACAAGCAGTTCAA	CTCCATCAATCCTGTCTGGAA	GCGGCTTGCCTGGAACAGATA
5332	PLCB4	NM_000933	ACCAATAATAACTCATGGAAA	CAGGTCAATTCTTATCAGATA	CTGCAGATTCCGGATATTATA	AACCCGGTAGTCTAGAACTAA
5334	PLCL1	NM_006226	CTCGATGTAAGTGATGGTTCA	TCGAAGGATGTCGGTAGATTA	AAGGATGTCGGTAGATTACAA	CTCAGGAATATCGGTCTTAAA
5336	PLCG2	NM_002661	GACGCGGACTACCAAGATCAA	TAGGGTCTCTTTGCAGAGGAA	GACGACGGTTGTGAATGATAA	CACGTGGAAGATTGACAGCAA
5338	PLD2	NM_002663	CCACAGGTCCTTGATTCTCAA	CCGGCCTTTCGAAGATTTCAT	CAGCCTGCTGACAGACACTAA	CGGGACCTCCTGAGACACAAA
5340	PLG	NM_000301	CTGGGAGCAGGAAGTATAGAA	CTGCCGCAATCCTGACGGAAA	CACCACCACCACAGGAAAGAA	CAGGAAAGAAGTGTCAGTCTT
5341	PLEK	NM_002664	CTGGATGATGGGTTAATACAA	CTGTGACAAATCAACGGGAAA	GAGCATTTCTCTAACGTTTAT	ACCATTGACTTAGGTGCCTTA
5346	PLIN	NM_002666	ACGCCTTATTTGATTTAACTA	ACCCTAGTCTTCGAAATGTTA	GCGGGTTTCTCTAACAAATAA	TGGCTTGTTTATGAACATTAA
5347	PLK1	NM_005030	CAACGGCAGCGTGCAGATCAA	CGCGGGCAAGATTGTGCCTAA	CCGGATCAAGAAGAATGAATA	CACCATATGAATTGTACAGAA
5356	PLRG1	NM_002669	ACGGATTCATATGTTCATAAA	CGGCATTATCATGGACATTTA		
5357	PLS1	NM_002670	TAGGATGTTATTAGAGAGATA	ATAGAATATATTCATAATCAA		
5364	PLXNB1	NM_002673	ATGCTGGACCAGCTTTATAAA	ATCCTAGGTCTAAGAGTTGAA	CCGGGTGGAATTTATCCTTGA	AACGCGGACAGTTCAAGTATA
5371	PML	NM_002675	TGCGGTGAACCGGGAAAGCAA	CTCCAAGATCTAAACCGAGAA	CAGGGTTGTCCGCTCTGATTA	CAGGAGCAGGATAGTGCCTTT
5376	PMP22	NM_000304	CAGCCTCGTGTTGAGCCTTAA	TAGGCTGCTATTATTACTATA		
5407	PNLIPRP1	NM_006229	CCGCTTCCTGCTGTACACCAA	CCGGGACTTTGTGGCTTGCAA	CAAGTATTACTTGGAAAGCAT	CCCGATGGGTTTGCTGCATAT
5408	PNLIPRP2	NM_005396	CTAGTTGGAGATATAAGGTAT	TCAGGATTGCTTTGTATGGAA	CTGGAACAAACGTGGGATAAA	TGCGGCTATTGCGGTAATAAA
5412	UBL3	NM_007106	TGGGTGTATATCAAACGGCAA	CCCGGCGGATATGATAAATTT	AAGGACGATTTCTACATGGAA	CGCGTAGTATATAGAACAATA
5413	NA	NM_002688	AACAATGTTGGTGAACGTCAA	CCGGACGGTCACAGCACCCAA		
5423	POLB	NM_002690	CCGGAGCGAATGAGGCCTGTA	CCCAATAGGAGTCTTAATTTA	TACGAGTTCATCCATCAATTT	CAAGATATTGTACTAAATGAA
5426	POLE	NM_006231	CCAGATTATGATGATTTCCTA	CTGGATGGATCCATCTAACTA	CCGCCTCTCCATTGACCTGAA	CCGCATCATCCTCTGTACAAA
5428	POLG	NM_002693	CTCACTGACAATAGTGCCATA	CTCCAAGGCAGTGGAAATAAA	CAGATCCGGGTCACACCTAAA	CACGAGCAAATCTTCGGGCAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
5429	POLH	NM_006502	CAGCCAAATGCCCATTCGCAA	GAGGCAGTGTCATAAAGTAAA	CTGGTTGTGAGCATTCGTGTA	ATCCATTTAGGTGCTGAGTTA
5430	POLR2A	NM_000937	CTCGGGAAGAACAAAGCTAAA	CACCACAGTCTCCAACCTATA		
5434	POLR2E	NM_002695	CTGGAGGAGTTCAAAGCCCAA	ACGAAATAAATTTGCTTGATA		
5435	POLR2F	NM_021974	TCACTTTATATGTGTAAATAA	CACACCATACATGACCAAGTA		
5436	POLR2G	NM_002696	CTGGTGCTTCTTGTAGCTTAA	CAGGGAAGTATGGCTTTGTAA		
5437	POLR2H	NM_006232	CAGAGTTTATCTCCTGATGAA	ATGGATCTAATCTTAGATGTA		
5439	POLR2J	NM_006234	CAGCGGTGACTTCGCAAGCAA	CAGGGATGAATTCATTCTGGA		
5440	POLR2K	NM_005034	CAAGAGATTAATAATAATGTA	AACAATGATAACATACTATAA		
5441	POLR2L	NM_021128	AAGGTCTTTCAGAACCACTAA	CTGGAAGGAACCATCCAGTAA		
5452	POU2F2	NM_002698	TCCAGAAATAAGAATGTCTAA	AAGAAATGGACCAGACACTAA		
5464	PP	NM_021129	CTGGAAAGTCATTGCCATTAA	TAGCACATGCTTAAATATCAA		
5467	PPARD	NM_006238	CCCGTGGAGCAGTGATCTCTA	CAGTGATATCATTGAGCCTAA	CACAGACTGACGAAACTTTAA	ACTGACGAAACTTTAAATAAA
5468	PPARG	NM_005037	GAGGGCGATCTTGACAGGAAA	CAGACAAATCACCATTCGTTA	CCGGAGAACAATCAGATTGAA	CAGCGACTTGGCAATATTTAT
5475	PPEF1	NM_006240	CTGGGAAACCCTCTTCAATAA	ATCGAATATGCTGATGAACAA	CCCAATCGGTACAATCGTTGA	CAGCATTAGTACCTACATATT
5476	PPGB	NM_000308	CCGGAGTACAAGAACAACAAA	TGCAACTTTCTGGTAAACTTA	ATACCAGATCCTATTATATAA	CCGGCCCTGGTTAGTGAAGTA
5496	PPM1G	NM_002707	GAAGTTGTAGATTTCATTCAA	TACTCTGTGAACTTTATTTAA	CCAGAGGATGAAGTAGAACTA	CAGGACCTGAGGACTCAACTA
5498	PPOX	NM_000309	CAGCGGCTTGGCCGCCAGTTA	CACGTTATTAGTGCCATTCCA	CAGGAAGCAGCTGCTACACAA	CTGCTTGGTCCATCTACACAA
5501	PPP1CC	NM_002710	GAGGAGTAAGTGTACAATTGA	CTGCGGTGAAGTTGAGGCTTA	CTGGTTATAACAGCAAATGAA	AACATCGACAGCATTATCCAA
5509	PPP1R3D	NM_006242	TCAGGTGACTAGAGAATTTCA	AAGGATAGCTTTCTTCGGTAT	CTGAGTTAGGCAATCACTTAA	CAGGTACCCACCAACTTTATA
5511	PPP1R8	NM_002713	AACCCTGAAGCTGTAAATGAA	CTGCTGAAGTTTCTTATTTAA	TACAAATAAAGATGCCCTAAA	CAGGCCCAGGAACTGAAGAAA
5514	PPP1R10	NM_002714	CAGCAACATCTAAGCCCTTGA	CACAGGATCAGCTGCACTTAA	CCGAAGGACCGTCACTACATA	CCCAGCCTGCTGAGAAAGATA
5516	PPP2CB	NM_004156	CACCGGATACAAACTACTTAT	ATGGAATTAGATGACACTTTA	TGGGATCTGTCTTGGCATTAA	CCGACAAATTACCCAAGTATA
5519	PPP2R1B	NM_002716	TGGACCAATTCTAGATACCAA	CTGACGTTCGTTTGAATATCA	CAGGAAATAACTACTAAGCAA	CAGAAGTTAGGTCAAGATGAA
5520	PPP2R2A	NM_002717	AAGCGAGACATAACCCTAGAA	CTCGCCGTGTCTGGCACTGAA	CTGCAGATGATTTGCGGATTA	ATGGAAGGTATAGAGATCCTA
5521	PPP2R2B	NM_004576	CGGCTACAAATAACCTATATA	CCGGAAGATCCAAGCAACAGA	CAGGGACTACTTGACCGTCAA	CAGGAAATGATTGGAATAGAA
5524	PPP2R4	NM_178003	CGGATTCATCCTTACCCTCAA	CCGCTCCCTAAGGGTAACCTA	CTGAGGTGGCTGTTTACCTAA	CTCCGGGTGGATGACCAAATA
5527	PPP2R5C	NM_002719	CTGGAAATATTGGGAAGTATA	CTGCTACTTCAGTAAGAATAA	CCCATTGGAACAAGTAAGAAA	AACGAGCTGCTTTAAGTGAAA
5528	PPP2R5D	NM_006245	GAAGTTGTTTATGGAAATGAA	CAGGAGATTATTCTCACCAAA		
5532	PPP3CB	NM_021132	CAGCCCGGAAAGAAATCATAA	TAGTTTATTGTGAGTACTCAA	TAGGAGATTAGATAGATTCAA	AAGGGTTTGGATAGGATCAAT
5534	PPP3R1	NM_000945	GAGCCTCATGAAGCCAACTAA	TCCCTTTATAGTTTCTCTATA	GCCCATATAATTGGTAATGGA	ATCCTTTAGTACAGCGAGTAA
5544	PRB3	NM_006249	TCCCTCCGTAATATCAGGAAA	CCGGGAAAGCCAGAAGGACAA	CAAGAAGGTAACAAACCTCAA	AAGAAGGTGGTCATAGCTCTA
5549	PRELP	NM_002725	CAGGTCAAGAATAACACTTCA	AAAGATTATACTCTTAAGAAA		
5551	PRF1	NM_005041	GAGCACCGTGTGGGACAATAA	ACCATGTACATAGCTTGATAA	CACGGTGGAGTGCCGCTTCTA	CACCGTGTGGGACAATAACAA
5554	PRH1	NM_006250	TCAGCTCAGGATTTAAATGAA	TAACTTCAGTATACCAATAAA	CAGGAAGTGAATAAGAAGATA	TGGCATCATGCTCTAACTTCA
5562	PRKAA1	NM_006251	CAGCAATAAGCATGCATAATA	ACCAGAGTATATTTAAGTATA	TCGGGATCAGTTAGCAACTAT	CCCACGATATTCTGTACACAA
5567	PRKACB	NM_182948	ACCAATGTGTTCTATATGTAA	GGCATTAGGAGTGCTAATCTA	CTGACCAATCAAGTACACTAA	CAGCCTGTGTAGTGTGACAAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
5569	PKIA	NM_181839	CAGCAATGAATTAGCCTTGAA	CTCAAGTGTTCACCCAGTAAA	TCACTTGATCATATGACGAAA	ATGATTATCATTAGAAGCTAA
5573	PRKAR1A	NM_002734	CTGGACCGACCTAGATTTGAA	CAGCTAGTGCCAAATAATTGA	CAAATATTGGTTAGTATTTAA	ATGAAATAATTTAAATTCTTA
5576	PRKAR2A	NM_004157	AGCAGATTTAATAGACGAGTA	CTGCAGAAACCTGTTGTATAA	AACTTGAAAGTCAGCACTAAA	AACGGCATGTCTCTCCAACAA
5577	PRKAR2B	NM_002736	CTGGCCTTAATGTACAATACA	AAGGATGTTATCATAGGCTAT	CACGCCATTGGGACTGTCAAA	ACGAACATGGATATTGTTGAA
5578	PRKCA	NM_002737	TACAAGTTGCTTAACCAAGAA	CGCAGTGGAATGAGTCCTTTA	CAGCTGGTTATTGCTAACATA	CAAGACGTCTTTGGAATCCAA
5581	PRKCE	NM_005400	TACAATGACGTTAAGTCTTAA	GCCCATCATATTCATGTGTAA	CCCGACCATGGTAGTGTTCAA	CACGGAAACACCCGTACCTTA
5583	PRKCH	NM_006255	AGGGACATCTTCCAATGATTA	CAGGATGAGTTTAGAAACTTT	GACCAGATTTGTGGCTTATAA	CGCCGTGTGCTCATCACTGAA
5585	PKN1	NM_002741	CCGGAGCAGCCTCAAAGCAGA	CAGCCTCAAAGCAGAAGCCGA	CCGCAAGGAGCTGAAGCTGAA	CAGGACAGTAAGACCAAGATT
5587	PRKD1	NM_002742	AACAAAGCTGTTAAACTGTTA	TCGATTATTTCCAGTGTTCTA	CCTCAGTATATTTAAACTCAA	CAGGAAGGCGATCTTATTGAA
5589	PRKCSH	NM_002743	CAGCCTTCAAAGATGGGTAAA	CACCACCAACGAATACGTCTA	CTGCACCAACACTGGCTATAA	ACCTGTGACCTCAATACAATA
5592	PRKG1	NM_006258	AAACACTTCAATGTAGTATAA	TAGATTACTATGGTACAGAAA	GAGGTTCGTTTGAAGATTCTA	CCGGTGTATATACCATACAAA
5593	PRKG2	NM_006259	CTGGTTATAGATCGAGAAACA	CACGACGACCTGAGGATTTGA	TTGAGTACTACTAACGTTTAA	GACCTACAATTTGATTCTCAA
5599	MAPK8	NM_002750	TCGGGACTTAAAGCCCAGTAA	CTGGTAATAGATGCATCTAAA	AAGCCCAGTAATATAGTAGTA	AAGCAGTTAGATGAAAGGGAA
5603	MAPK13	NM_002754	CAGAAGGGTCCTTCTCCTTAT	TAGGGATGCTCTAACGAATTA	CGGGATGAGCCTCATCCGGAA	CCGGAGTGGCATGAAGCTGTA
5604	MAP2K1	NM_002755	AACAACGTGTATAGTGCCTAA	CTAGATGTTTAACAAATCTAA	CTGGATCAAGTCCTGAAGAAA	CTGGAAGAATTCCTGAACAAA
5605	MAP2K2	NM_030662	CACAAACCACACCTTCATCAA	TTCCAGGAGTTTGTCAATAAA	CCGGCCTGCCATGGCCATCTT	CAGCATTTGCATGGAACACAT
5606	MAP2K3	NM_002756	CTGGATGCCATCCAAGTTGTA	CTCCAATGTCCTTATCAACAA	CCGGGCCACCGTGAACTCACA	ACGGATATCCTGCATGTCCAA
5610	EIF2AK2	NM_002759	CTCCACATGATAGGAGGTTTA	TACGTGTGAGTCCCAAAGCAA	CGGAAAGACTTACGTTATTAA	ACGGAAAGACTTACGTTATTA
5617	PRL	NM_000948	CAGCGAATTCGATAAACGGTA	TGCAACGATCACGAACATGAA	CAGCATATTGCGATCCTGGAA	CCCGGAGGCTATCCTATCCAA
5619	PRM1	NM_002761	CCGAGATGTAGAAGACACTAA	CCGCCTGTCAATAAATGTTGA		
5631	PRPS1	NM_002764	CCCAAGGTCTATGCTAAATTA	CACCATCTGCTTGACTATGTA	AACATGCTTCCTGCTATGTAA	TTGATTAATTTAAGTATTTAA
5639	PRRG2	NM_000951	CCCAGTGAGGAGACAGACCAA	TTGGGAGAGCTACATCTACAA		
5653	KLK6	NM_002774	CTGACCCTGATGCTTAATAAA	CACGTTTGATTTCTTCCTGCA	CTGCAGATTTCTCACCTGTAA	CACCATGCACTCAATAAAGAA
5654	PRSS11	NM_002775	CCGGGTCAAAGTTGAGCTGAA	CGGTGAAGTGATTGGAATTAA	AGCGTATATAATTGAAGTAAT	CGACGTCATAATCAGCATCAA
5660	PSAP	NM_002778	CCGACATATGCAAGAACTATA	AAGAACTATATCAGCCAGTAT	CAAGCTGATTGACAACAACAA	CTGCCTGAATGTAACCTGCTA
5663	PSEN1	NM_000021	CTCAGGTTCCAAATTCAGTAA	CTGAGGTTGCTTTATCCTAAA	CAGGCATATCTCATTATGATT	CAGCTCTCATTTACTCCTCAA
5676	PSG7	NM_002783	CCCATGGAACCTCAAAGAGCA	ATCCTTGTACCTGATGTCTGA		
5682	PSMA1	NM_002786	CTGCCTGTGTCTCGTCTTGTA	TCCATTGGAATTGTTGGTAAA	CACAGTTGGTCTGAAATCAAA	ATGGAGTGTAATTTAAATGAA
5683	PSMA2	NM_002787	ATGCAAGAATATACTCAGTCA	ATGAGGGACGACCATATTTAT	AAGGATTACTTGGCTGCCATA	GAGATACATTATGTAAATAAA
5687	PSMA6	NM_002791	CAGGGTGGCCTTACATCAGTA	CACAGTGACTCACTTATTCAA	ACCGAAGTGGTTAGGACTCTA	CCAGGGATTGTGTTTAAAGTA
5688	PSMA7	NM_002792	AACAGATGATCTGACCATTAA	GACCATTAAGCTGGTGATCAA	ATGGATGAGTCTCGATGTGTA	CACACTGAGTGTCCTACAATA
5689	PSMB1	NM_002793	CCGGATCTGCATAGTGACCAA	ATCGGTGGACTTGATGAAGAA		
5690	PSMB2	NM_002794	CGCACTCTTGATAAATGGTTA	AAGATGCGAAATGGATATGAA	CAGCAATATTGTCCAGATGAA	GTGACTATGGATATAATTGAA
5692	PSMB4	NM_002796	TCGCATTATGCGAGTCAACAA	ATGCTTGGTGTAGCCTATGAA	ACCATTGTCTACAGAGACCAA	CACATGATCAGTGGCTTTGAA
5694	PSMB6	NM_002798	CGCCTGAATCCTGGGATTCTA	TGGGATTCTAGTATGCAATAA	CTGGGATTCTAGTATGCAATA	CTCCGGGAGCTCCTACATCTA
5698	PSMB9	NM_002800	CTGCAAATGTGGTGAGAAATA	GTGAGAAATATCAGCTATAAA	AAGGAGGTCAGGTATATGGAA	CAGCACCTTTATCTATGGTTA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
5699	PSMB10	NM_002801	CCCAGACAGTGAAGCCACTAA	CAGGCTATGGAGGTGGAGTAA	CACACGGATGGTGGCGTCCAA	CTGCGAGAAGATCCACTTCAT
5705	PSMC5	NM_002805	CAAGGTTATCATGGCTACTAA	CCGGGTGGCTCTAAGGAATGA	AAGGTACATCCTGAAGGTAAA	TTGGTCAAGGTACATCCTGAA
5706	PSMC6	NM_002806	CTGAGAAATGTTTGTACTGAA	AAGGAGTTAAGGGAACAATTA		
5707	PSMD1	NM_002807	CAGGCTGTGAGTGATATCTTA	TTGGAAGGCATCGTAAATAAA		
5708	PSMD2	NM_002808	TAGCGAACACTTTGACTCCAA	CAGGGTTCCAGACGCATACAA	CTCCGGAGGGCTGTACCTTTA	TGGGTGTGTTCCGAAAGTTTA
5718	PSMD12	NM_002816	ATGGGTTTAAATTTAACATAA	AAGGATTACATTCGAACACAA		
5723	PSPH	NM_004577	CAGAGACTCATAGCAGAGCAA	TAGGCTGAAATTCTACTTTAA	TGCCAATAGGCTGAAATTCTA	CCGGCATAAGGGAGCTGGTAA
5727	PTCH	NM_000264	ACCAAGCTTCATTAGTCTTAA	CCCGTCATTAGTGCTCTTTCA	TCGCACAGAACTCCACTCAAA	ACAGCATACCTCCTAGGTAAA
5729	PTGDR	NM_000953	AAGCATAATTTCTTACCCTAT	TCCAGTATCTGAGATAATATA	CCGGTGCAGCAATTCCACTAA	CCAGTATCTGAGATAATATAA
5733	PTGER3	NM_000957	AACAAATATCGCTAAACCTTA	CCGCTATAGAGTATTCCATAA	AAGGACCGATTTGAGCACTAA	ATCGATACCATTATTCAAATA
5739	PTGIR	NM_000960	TCGGGCGACAGGAGCCAGAAA	CAGAAAGAATGGTTCTCTCAA	CCCATCCATCTCATTGTCTAA	CCCAGGGTCCTGAATAAATAA
5743	PTGS2	NM_000963	TCGTATTGCTGCTGAATTTAA	TAGGGTAGAATCACCTGTAAA	CCCGCAGTACAGAAAGTATCA	ACGCTTTATGCTGAAGCCCTA
5745	PTHR1	NM_000316	AGGGAAGCCCAGGAAAGATAA	CTCCATTGTGCTCAACTTCAT	CGCCGTGAGCATCTTCGTCAA	CAGCATAATGGAATCAGACAA
5746	PTHR2	NM_005048	AACGCCTCTATGTAATGTATA	CTGAATACGGTTAGAGTTCTA	TGGCATGTGGGATCAATTAAA	AAGGTGTTACTTAATAATAGT
5747	PTK2	NM_005607	CCGGTCGAATGATAAGGTGTA	CCCAGGTTTACTGAACTTAAA	CACCTGGGTACTGGTATGGAA	AACAATTTATGTTCACATTAA
5754	PTK7	NM_152883	ACGCCACAGCACAAGTGATAA	CCGAGAGAAGCCCACTATTAA	ATGGGACATGGTACCGTTGTA	ACGGTTCGAGGTCTTCAAGAA
5764	PTN	NM_002825	CTGGAGCTGAGTGCAAGCAAA	ACCGTAGGCTTTGTATTCAAA	TACCGTAGGCTTTGTATTCAA	TACATGATAAATGATAGACAA
5771	PTPN2	NM_002828	CACAAAGGAGTTACATCTTAA	TCGATTGAATTGTACTGGATA	CCGCTGTACTTGGAAATTCGA	AACTGTATTCATACATGTCAA
5774	PTPN3	NM_002829	CCGCTCATTTGCTGACTTCAA	CCGAGAAATGCTGGTCACAAA	CCGGGTATTATTGCAGGGAAA	CAGGTTATTCAGCGATAGTTA
5775	PTPN4	NM_002830	AGCACGTACCTTAGAACTCTA	CTCCGTCATCAACACAAGCTA	TCCGTCATCAACACAAGCTAA	CTCCGAACAAATAGTAAATAA
5777	PTPN6	NM_002831	CCAGTTCATTGAAACCACTAA	CCGCACCTCGTCCAAACACAA	TAGGCCCTGATGAGAACGCTA	CCGGAACAAATGCGTCCCATA
5781	PTPN11	NM_002834	GCCGCTCATGACTATACGCTA	GCGGTCCAGCATTATATTGAA	CCGCTCATGACTATACGCTAA	CAGAAGCACAGTACCGATTTA
5782	PTPN12	NM_002835	GTGGATCATGATAACACTTCA	CTGCTTGTAGACATGTTAATA	TTGCAGGTTATCAGAGATCAA	AAGCTTAATGAGGAAATATCA
5787	PTPRB	NM_002837	CCAGTATTAGTGGAGACTTAA	TCGGGTGTATCAGACTAATTA	CCGGTCGACTTTATCAAGTTA	CCCGGAGATGTGGATAACTAT
5789	PTPRD	NM_002839	ATGGCATTATCACCAAGTATA	CGCCTTGTTAATATTATGCCA	CTGGGTGTCATTGAAGCAATA	ACGGCCAGTCCCGAACAGTAA
5794	PTPRH	NM_002842	TCGAAGCACAGCACACACTAA	CAGGTACTGACATCACCCTAA	CCGGGTCATTGTATACGTGTT	CCGGGACGTTGTACAATTTCA
5795	PTPRJ	NM_002843	ACCCGTATCTTCTACAATCAA	ACGAGTCGTCATCTAACTATA	TCGGGTAGAAATAACCACCAA	TCCGAGTATGTCTACCATTTA
5796	PTPRK	NM_002844	CAGGATTTGTATCGCTGTGTA	CCGGCGAGTCAAGTTATCAAA	CTGGAGATTAGTGTATGATTA	CCGGGTTAAATGCTATAAATA
5798	PTPRN	NM_002846	CTGGTGAAGTCTGAACTGGAA	CAGGAAGGTGAACAAGTGCTA	CAGGTCTGGCTTGGCACCCAA	CACCCTTCACTGAGTTACGAA
5800	PTPRO	NM_002848	CAGCTTCAAAGTAGAGTAGAA	CCGGGAAGACTTAGCCTTAAA		
5801	PTPRR	NM_002849	AACCCTTTGTGTCTATACCAA	TAGGTTTATCACACAGCCTAA	TCGCCTCATTGGAAAGAAGAA	CGCCACCAGATTGTCAATTCA
5803	PTPRZ1	NM_002851	CAGACTAATTACACTGAGATA	CCGCCAAATTTATATCATTAA	TAGCCATATACCAATACCTAA	ACGCTGGAATTTGGTAGTGAA
5810	RAD1	NM_002853	TCGAATGTGTTACCAAGGTTA	CTGCAGCACCAATGTTATTAA	CAGTATATGATTAGAAATGAA	CAGCACCAATGTTATTAATAA
5818	PVRL1	NM_203286	CAGGTGGAGGTCAATATCACA	CAGGTGAACGACTCCATGTAT	AGGGCTGTTGTCAGAATTCTA	ACAGATCAGTCTGTCAATAAA
5819	PVRL2	NM_002856	CCCGTGACACTCAGGAGTTAA	CAGAGTCATAGCCAAGCCCAA	CTGGACGACACTGGAGTGGAA	CAGGTCATCTTTGTCCGAGAA
5830	PEX5	NM_000319	ACCGATCGCTGGTATGATGAA	CCAGTTCACAAGACCAGTAAA	TACGTCAGCTACCTATGATAA	CAGCTTCCTTGGGCAGTGTAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
5837	PYGM	NM_005609	CACACTCGTAAAGGACCGCAA	CTACCTGTCTTTAGAGTTCTA	TCGGGATGTGGCCAAAGTGAA	CAAGTTGAAGTTTGCTGCCTA
5870	RAB6A	NM_002869	CAGATGGGTCATATTCTTTAT	ATGGGTGTGATTGTCTTCCTA	TACGGTCTTCTTTGAGGTCAA	CCCACTTATTGTCACCTTGTA
5871	MAP4K2	NM_004579	ACGGTATTTAAGAGAGAACTA	GAGAACTATATTGGTATTAAA	TCGGTCAGCCTCAGAATTCCA	CTGGCTCTACTGCGTGAACAA
5876	RABGGTB	NM_004582	AAGGATGTTATTATCAAGTCA	TACGCTGTATGACAGTATTAA	ACGCTGTATGACAGTATTAAT	CCGGAGAAGTTACCAGATGTA
5878	RAB5C	NM_004583	GAACAAGATCTGTCAATTTAA	CAGCCGATCGATCGACCTCAA	CCCGACTGGAATCCACTCTAA	CACCATGATTTCTCCATATAA
5879	RAC1	NM_006908	TACATTGTACAAGGAATGAAA	GGGCATTTAATTCATCTTTAA	ACGATGTTCTGTACAACTTAA	AAGGTTGGTATTATCAGGAAA
5881	RAC3	NM_005052	GACATGCTTGCTGATCAGCTA	CAACGTGATGGTGGACGGGAA	CGCGCCCATGCAGGCCATCAA	CCGGGAGATTGGCTCTGTGAA
5892	RAD51L3	NM_002878	CCCAGTAACGCCTGCTGTTTA	CTCACTCTCTGTAAGCATATA	CTGGGTGGAAATAAGCTTATA	CTGGAAGAGGTAGCTCAGAAA
5893	RAD52	NM_002879	TCGGGTAATTAATCTGGCCAA	CAGCTGAAGGATGGTTCATAT	CAGGAGTGACTCAAGAATTAA	AAGGAAGGAAATAATCATCTA
5901	RAN	NM_006325	CAGCAGTATTCTATTTGGTTA	TAGTGTGAAGTTGATACGCAA	TTGGGAATTCTTGCTGTTAAA	ATGTGGTTTGTACATATCAAA
5902	RANBP1	NM_002882	CTCGGTGAAGGAGGAGACCAA	CGGCGCCAGACGCGGAGGGAA		
5905	RANGAP1	NM_002883	ACGGAAGATTCTGGACCCTAA	AGGCAAGAGCCTCAAACTCAA		
5908	RAP1B	NM_015646	AATGGTGTACTGTATACTTTA	TAGCATCAGTAGTTCAATAAA	GACGAGTACTGTGGATGTGAA	CAGTATAATGTCTTAGATTAA
5909	RAP1GA1	NM_002885	CCGGCTCATCGTCACCTTTGA	CCACCTTGTCTTCTCACTCAA		
5911	RAP2A	NM_021033	AAGGCATAGTCCATCGATCTA	ACCAGTGTATTCCGTCAAGTA	CCAGTGTATTCCGTCAAGTAA	CAGAGATAATTGCCTATACTA
5912	RAP2B	NM_002886	AAGGTGGTCTTAGTAATATAA	TAGAATAGAGGCAAAGCCTAA	TACGGTTCTTTCGTAGAACAA	CTCACTTAAGTTTGATATCAA
5919	RARRES2	NM_002889	CTGCCGGAAGAGGGACTGGAA	CCCAATGGGAGGAAACGGAAA	CAGGGAGAGGAACCCGTTCTA	CTGGAAGAAACCCGAGTGCAA
5924	RASGRF2	NM_006909	AAGGTGAAAGATGGCTATTTA	AAGAAGGAACACCAAACTTTA		
5926	ARID4A	NM_002892	CTCGAGATGTAAATTCTATTA	ATGGCTTATCTAAGACAGCAA	CTGGTTTGACATTGCTAAGTA	ACGATTGAAGTTGATAGTATT
5927	JARID1A	NM_005056	CGGCAAGTAAAGAATCTGCTA	GCGGACGTTTCTTAAGAAGAA	CAGATGCTTAATTGAGCTCTA	AAGGAATGGTATCACAGTCTA
5930	RBBP6	NM_006910	GACGCTATCATTCACGATCAA	CCAGGTCTAAATCTCCCTATA	ATAGTGGTTCTTCGTATTCAA	CCCAGTTAAGTCATTCCTCTA
5933	RBL1	NM_002895	CTGGATGTTTCAAATGAGTTA	CTCCAGGTTTCTGCAAACAAA	CACCAAGTGACCAACTTATAA	ACAGGCTAATGTGGAGTATAA
5935	RBM3	NM_006743	CAGGAGGAAATTACAGAGACA	CCAAATGGCTGTATTTATAAA		
5950	RBP4	NM_006744	CTGGTACGCCATGGCCAAGAA	CCAGATGAGCGCCACAGCCAA	CCCTGCCAAGTTCAAGATGAA	CTGGATCGTCGACACAGACTA
5961	RDS	NM_000322	CAGCACCACACCATCCCTAAA	CACGGTGAAAGTGCTGCTCTA	GAGGAGCGATGTGATGAATAA	CACGGATTTAGTCCCACCCTA
5967	REG1A	NM_002909	CCCAGTCTTTGGAACCCTAAA	CAGCAATTACAACGGAGTCAA		
5968	REG1B	NM_006507	CTGCAATTACTATGAAGTCAA	CTCAGTCTCTAGAGCCCTGAA		
5971	RELB	NM_006509	CACAGATGAATTGGAGATCAT	CAGCTACGGCGTGGACAAGAA	GCGGATTTGCCGAATTAACAA	CCAGATTGCCATTGTGTTCAA
5976	RENT1	NM_002911	ATCAAGGTCCCTGATAATTAT	CACCATGAGCGTGGAGGCGTA	CATCTTATTCTGGGTAATAAA	ACGGAGCGCTGCACACCGAAA
5977	DPF2	NM_006268	ATCCATCTTGCCTCCAATTTA	CTGTATTCTAAACATTAGTAA	CTGGATGACCTCGATGATGAA	CTGGACCTGTTGAAAGAGAAA
5992	RFX4	NM_002920	CAGGCATTACCTGACAGCTTA	CTGGAGGAACGTGGACCTGAA		
6000	RGS7	NM_002924	TTGATAAAGAACTTAACTATA	TGCCTGGATGTGTAAATACAA	AAGTATATATCAATAAGTATA	ACGGATCATCTTGTAGCATGA
6003	RGS13	NM_144766	CCAGATTTCTAAAGTCAGAAA	CAGAATTTCTAGGGCAAAGAA	CACAGTGACGAGAATATTCAA	CCAGAGTGCCATCGAAGGTAA
6015	RING1	NM_002931	CCGAAAGAAGCTGGTGTCCAA	CAGGGTCAGATCAGACCACAA	CTGGAGCTGGTGAATGAGAAA	CAGCCAATAAGAGGACACAAA
6039	RNASE6	NM_005615	CCCTGTGTTCACAGCAATAAA	CACTTAGATAGTATTCTCTAA		
6041	RNASEL	NM_021133	GCCAATGTTAATTTCCAGGAA	CCCGAAATGTCCTGTCATCTA	CCAGACTACACTAGTCCATAA	CACCTGGACATGTCAATTAAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
6051	RNPEP	NM_020216	CACGCCTGCTGTTAAATACAA	CCGAAGCATCTTAGCCGATGA	CTGGACATGAAGGCCATTGAA	CACCAGGAAGATTTCTGGAAA
6059	ABCE1	NM_002940	ACCCATAAATACATGTTGTAA	ATGGCTAGAAAGTATGGTTTA	CCAGTTGGGTTCTAAATTGTA	CTGATTGACATTTGATAAATA
6097	RORC	NM_005060	TAGGATGTGCCGGGCCTACAA	CCGGGCCTACAATGCTGACAA	AAGGAGCTCTTCAGCACTGAA	CGGGTTCATCTGAGTAAACAT
6100	RP9	NM_203288	TCTGTTGTTGAGAATAATAAA	AAGGAAGATGAGACTAAGCCA		
6103	RPGR	NM_000328	CCCGGTAAATTCTGGTTTAAA	TCCGAAGGGCAAATTGGTTTA	CACAGCTTTGATAACAGATAT	ATGAGCCTGAATTCCAATGAA
6122	RPL3	NM_000967	CGGCAAGCTGATCAAGAACAA	TGGCGTGATGTCTCACAGAAA		
6125	RPL5	NM_000969	TTCGTGTGACAAACAGAGATA	AAACTTATGAACAGCAACTAA		
6128	RPL6	NM_000970	CAGCGCAAGATTGATCAGAAA	GACCGGAAGCCGGGACCTTAA		
6129	RPL7	NM_000971	CTGGTTGGTTAATAAACAGTA	ACGCTTCAAAGAGGCAAATAA		
6130	RPL7A	NM_000972	CACCTTGGTGGAGAACAAGAA	ACAGGTGAACTCGGAAGACAA	CACCACCTTGGTGGAGAACAA	CAGGTGAACTCGGAAGACAAA
6132	RPL8	NM_000973	CTCAATAAAGTTTGTGTTTAT	CCGGGCGTACCACAAATATAA		
6133	RPL9	NM_000661	CAGGCTGATGAATAAGATCTA	CGGACTATTTGTAGTCATGTA		
6134	RPL10	NM_006013	CCCGTTGTTACCGGTATTGTA	CAGCAAAGCCTTGCAATCCCA	TGGCCTTATGTCAGTTGTCTA	CAGAAACAGGTTGACAACTCA
6136	RPL12	NM_000976	ATCCGGGTTCATCCGACACCA	AACATTTCAATAAAGGATCAT		
6144	RPL21	NM_000982	CCACATATATGCGAATCTATA	CTGGAAGAGTCTACAATGTTA		
6152	RPL24	NM_000986	AAGAGGAATCAGAAACCTGAA	AAGGCTAAGCAAGCATCTAAA		
6154	RPL26	NM_000987	CAGGTTGTACGTGGACACTAT.	CAGGAATAAAGTAATCTTATA		
6156	RPL30	NM_000989	CAGGAAGATGGTGGCCGCAAA	CTGAAATAGAGTACTATGCTA		
6157	RPL27A	NM_000990	AGGGAGTTTCATTAAATGCTA	CCGGATCAACTTCGACAAATA		
6160	RPL31	NM_000993	CAGATCAAATAAAGTTATAAA	ATCGCTGATCGTCAGATCAAA		
6164	RPL34	NM_000995	AAGCACAGAGTCAGAAAGCTA	CAGTATATGATCACTAATATA		
6165	RPL35A	NM_000996	CCGAGATGAAACAGAATTCTA	GCGCTTATGTATATAAAGCAA		
6170	RPL39	NM_001000	CTGAAGGTCACGATCATGTTA	TTGGTTGGCTGGATTCAGTAA		
6173	RPL36A	NM_021029	CTGGTTGAGTTCACATCATAT	AAGCTAGAGCCATCAATACAA		
6176	RPLP1	NM_001003	CTGCATCTACTCGGCCCTCAT	AAGAAAGTGGAAGCAAAGAAA		
6181	RPLP2	NM_001004	CAGCGTGGGTATCGAGGCGGA	CAGCGCCAAGGACATCAAGAA	AAGGAGGAGTCTGAAGAGTCA	CAAGGTTATCAGTGAGCTGAA
6187	RPS2	NM_002952	CACCTTTGATGCCATTTCTAA	CCGCTTGGTCAAGGACATGAA		
6188	RPS3	NM_001005	CGGCAAGATGGCAGTGCAAAT	GAGGTTGTGGTGTCTGGGAAA		
6189	RPS3A	NM_001006	CCGGAAGAAGATGATGGAAAT	CACCTGCTATGTTCAATATAA		
6191	RPS4X	NM_001007	CAGATCTTTGTACGTAATTAA	AAGAATTGGTGTGATCACCAA		
6193	RPS5	NM_001009	CACCGATGATGTGCAGATCAA	CTCGAACTCCTATGCCATTAA		
6194	RPS6	NM_001010	ATCCAGTCAGAAATAAGATTT	TTGAGTAACAAATAAATAAGA		
6196	RPS6KA2	NM_021135	CTGGAACACGCTGTACCGGAA	CTCGATATCTGACGCAGCTAA	CCGGAGGTCCTGAAGCGTCAA	CCGAGTGAGATCGAAGATGGA
6202	RPS8	NM_001012	TTGGAGTTCTATCTTAGGAAA	TCAGAGTGTTGTACTCGTAAA		
6203	RPS9	NM_001013	ACGGCGTCTGTTCGAAGGCAA	CCCGCGGAGACCCTTCGAGAA		
6204	RPS10	NM_001014	CGCAGAGATGTTGATGCCTAA	ACCGCGCATGCTCCTTCCTTT		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
6205	RPS11	NM_001015	CCCTGCGTAATCGATAAGGAA	CGGGAAGATGGCGGACATTCA		
6206	RPS12	NM_001016	AAGGTTGATGACAACAAGAAA	AAGATTCAACTTCACCCGTAA		
6208	RPS14	NM_005617	CAGGAGGAAATAGGACCAAGA	CCGAGATGAATCCTCACCATA		
6217	RPS16	NM_001020	TACCAGAAATCCTACCGATAA	CCCTCGTCGCTGCGAGTCCAA		
6218	RPS17	NM_001021	CCGCAACAAGATAGCAGGTTA	AAGCGAATTCAGAGAGGCCCA		
6223	RPS19	NM_001022	TGGCTCCATGACCAAGATCTA	AAGAAGCATTAGAACAAACCA	CTGGGTTAATAAATTGCCTCA	AACAAGAAGCATTAGAACAAA
6227	RPS21	NM_001024	TGGAATATTTGTCATAAATAA	CGGCGAGTTCGTGGACCTGTA		
6229	RPS24	NM_001026	CGCAAGAACATTAATAAACTA	CAAGAACATTAATAAACTAAA		
6233	RPS27A	NM_002954	TTGTCTGACTACAATATTCAA	CTGGCTGTCCTGAAATATTAT	CTGACTTACTGTTTCAACAAA	AAGGTGGATGAGAATGGCAAA
6234	RPS28	NM_001031	AGCGTTTGTGTTTCAAGTTAA	CTGAGATGCTCCTTTAAATAA		
6235	RPS29	NM_001032	ATGATAATTCTTTGTATATAA	CCGGCACGGTCTGATCCGGAA		
6240	RRM1	NM_001033	CCGAGATTTCTCTTACAATTA	CTGAGAGTATATAACAACACA	AACGGATATATTGAGAATCAA	CTGGTGGGTCTCTAGAAGCAA
6272	SORT1	NM_002959	CAAGGACAGGGTACAAACTTA	CTGGGTTTGGCACAATCTTTA	CCCACGTCAGTTACACATTAA	CAGCAGAGAATTGACTAGATA
6284	S100A13	XM_371380	CTGAAGATCAGGAAGAAGTAA	ACCGCACTCTTCCCAAATAAA	CAGGAAGAAGAAAGACCTGAA	AACCGCACTCTTCCCAAATAA
6286	S100P	NM_005980	CAGGAGGAAGGTGGGTCTGAA	TAGGCTGAGCCTGCTCATGTA		
6289	SAA2	NM_030754	TAGGCATCTAATAAATGCTTA	GCCGATCAGGCTGCCAATAAA	ATGGCATATAATAGGCATCTA	AAGCTGAGATATGGCATATAA
6293	VPS52	NM_022553	TCCATTCGGGATTATATTCAA	CCGGGTCAAGGCAGTGACGAA		
6294	SAFB	NM_002967	CCGAAGATGACTCGGATACAA	AAGGTGGTAATCCTGACGAAA	CTGCCATATTGTAGCTCAATA	ACGGACTGTAGTAATGGATAA
6296	SAH	NM_005622	CCCTCAGAATTTCTCCAACTA	CAGAAGCCTGTTCCCTACAAA	CAAGCTGATTGTATCAGAGAA	ATGCTTGTACAGAATGATATA
6297	SALL2	NM_005407	TAGGAAGTAGGGAGAAATGAA	CGGCCTGAGGGTCACAATAAT	CCCGGGAATGTCTCGGCGAAA	AAGCTGGGCACTGCTTACCAA
6300	MAPK12	NM_002969	CGGCGCTAAGGTGGCCATCAA	CACAGGCAAGACGCTGTTCAA	TGGAAGCGTGTTACTTACAAA	CTGGACGTATTCACTCCTGAT
6301	SARS	NM_006513	CCAGTTTGATGAAGAACTTTA	CTGATGAAACCATGTAATAAA		
6304	SATB1	NM_002971	TGGGTACGCGATGAACTGAAA	CACTCTTATTGTTGTATGCAA	ACCGAATATACCAGGACGAAA	TCCAAGCAATTCATACTATAA
6305	SBF1	NM_002972	GACGCCTGTGTTCCACAATTA	TCCGGTCGTTACCGACCACTA	CCGCGTGGTGTGGCCCTGTTA	CAGCGCCGAGCTCTTCCGTAA
6311	ATXN2	NM_002973	ATGGATCAACTACTAAACAAA	CTGACGGATTATTATTTATAA		
6317	SERPINB3	NM_006919	AAGGTAATATTGGCAGCAATA	CTCGTGCTATCTGGAGTCCTA	TAGGATTCGGATCATCACCTA	TCGGATCATCACCTACTTCAA
6324	SCN1B	NM_001037	CCACATTGAGGTAGTGGACAA	CACATTGAGGTAGTGGACAAA	CAGAGATGATTTACTGCTACA	ACCGCCATGCATGATGGGTAA
6328	SCN3A	NM_006922	CAGCGTAATTTCAGATGTTAT	AAAGCTGATAGTCTATGTCAA	TTGGATTTATGTGAGGTCAAA	CTCCCATAATAAATTATATAA
6329	SCN4A	NM_000334	GACGCCTACATCAGTGATGAA	AACGCTGAACATGCTCATCAA	CAAGATTGCCTTGGACTGCAA	CTGGCTCAATGTCAAGGTCAA
6331	SCN5A	NM_000335	CCCGCTGTGGATGTCCATCAA	CTGGAGCACTACAACATGACA	CTGGACCAAGGTGAAAGTCAA	TCCTGTAAGAGTATTAACAAA
6332	SCN7A	NM_002976	TCCAATGAGTAAACAAACTAA	CCCAGCATTATTGAACATCAT	AGAGATGTTCATGCTACTAAA	CCGATGGTAATTAAGCTTGTA
6336	SCN10A	NM_006514	CGGGCTCTTTCTCGATTTGAA	TCCCGGGAGGTCAACATGCAA	CACAGGCGAATGTGTCATGAA	CCGCTCCATGGCACTCTCTAA
6337	SCNN1A	NM_001038	CTGCACCTTTGGCATGATGTA	CAGCCTCAACATCAACCTCAA	TACAGGTACCCGGAAATTAAA	CCCGATGTATGGAAACTGCTA
6338	SCNN1B	NM_000336	CCGGAACTTCACGTCCATCTT	CACGTCCATCTTCTACCCTCA	TCGGCCAACCCTGGAACTGAA	CTGCAATGACACCCAGTACAA
6339	SCNN1D	NM_002978	CTGCAGGGAGTCTGCATTCAA	CCGCAATGGCTGAGCACCGAA	CTGCAGGGAGGCAGAAGGCAA	CACACTTGGGCTGCTCTGAAA
6340	SCNN1G	NM_001039	CGGCGGTAGCATCATTCACAA	AAGAGTGGACACTAACCACAA	CAAGGCCGGCAAGTAAACAAA	ATCCCGGGACCTGAACTATTA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
6343	SCT	NM_021920	CAGCGAGCAGGACGCAGAGAA	CTGGCGCTGCTGCAGAAGGAA	ACCAATAAAGGAGGAATCAGA	GTGGTACTTGGCACCAATAAA
6344	SCTR	NM_002980	CACAGGATGGCTGGTCAGAAA	CAGAAAGGGACAGGGAAATAA	CTCCTTCTTCTCTGAAAGAAA	CCGGATGCTCACCAGCAGAAA
6354	CCL7	NM_006273	TTGGGATTAATACTTCAACTA	TTGGATGTATATGTCATCTCA	TGGAAGCATATTGTTATTATA	AAGATTTGCTTTAATTGTTAA
6367	CCL22	NM_002990	CTGGGTGAAGATGATTCTCAA	TACCTTTGACTTGGTATTATA	TAAGCTGGAGTTATATATGTA	CAGGTAAAGGACATAAATGTT
6368	CCL23	NM_145898	GACAGAGTTCATGATGTCAAA	TAGAGCAATTCATCTAATAAA	CAGGAAGAATTGAACTTGTCA	CTCCTGGAGAGTTACTTTGAA
6369	CCL24	NM_002991	CTGCATGTTCTTTGTTTCCAA	CAGGCCTGATGACCATAGTAA	CAGAGATATCCTGGCAACCAA	AGGAGTGATCTTCACCACCAA
6376	CX3CL1	NM_002996	CCACGGTGTGACGAAATGCAA	CAGCAAGATGACATCAAAGAT	CGGAGCTGTGGTAGTAATTCA	CACCATCAAGCCACCAACATA
6382	SDC1	NM_002997	TCCGACTGCTTTGGACCTAAA	GCCGCAAATTGTGGCTACTAA	CAGGGCCTCCTGGACAGGAAA	CAGGAGGAATTCTATGCCTGA
6383	SDC2	NM_002998	GACGCTGAATATACAGAACAA	CCGTTTAGTCATATCTATCTA	ATGAATAGACATAAATTGTAA	AAGGTACGAGTAGAGGTTTAA
6386	SDCBP	NM_005625	AGAGATTGTGATGATTCTTAA	GAGATTGTGATGATTCTTAAA	TTGACTCTTAAGATTATGTAA	TGGGATGGTCTTAGAATATTT
6396	SEC13L1	NM_030673	CAGATTGATCATCTGCCTTAA	TCGGAGATGCTTTGTAATCTA		
6400	SEL1L	NM_005065	CTGCAAATTGGGCGTCGTCTA	AAGAGTGAACATGTACACAAA	CAGGATATTCACCTTGCGAAA	ACGGCACAAGGAAGCATTGAA
6401	SELE	NM_000450	CATGGTAGAATTGGAGAGTAA	ACCAGTGTGGTTTGTGTTTGA	CGGAAAGTATTTCAAGCCTAA	CAGGTTGAATGCACCACTCAA
6404	SELPLG	NM_003006	TCCATGGAACCTACTACCAAA	CAGCAATTTGTCCGTCAACTA	ATGGAGATACAGACCACTCAA	ACGGAGGCACAGACCACTCAA
6406	SEMG1	NM_003007	AGGGTAGTTATACACCATAAA	CAGGGTAGTTATACACCATAA		
6423	SFRP2	NM_003013	TAGCATGATTTCTTCAAGTAA	TACATAGTAGTTTACCTTTAA		
6425	SFRP5	NM_003015	ACGAATGTTGTTACTGGCACA	TAGGCTAAGCTATTTGGGAAA	CTGCGAGGAGTACGACTACTA	CCGCTGGGACAAGAAGAATAA
6428	SFRS3	NM_003017	CACAATATGGTTCAAATGTAA	CAGACTGATAATAAACCTCTA		
6434	SFRS10	NM_004593	TCGGGCAAATCCTGATCCTAA	CCCAATTTCACTCAAATGTTT	CGGGACTACTATAGCAGATCA	CCCGATCTGAATCTAGGTCTA
6435	SFTPA1	NM_005411	CACAGCAGGGATGAGGACAGA	ACAGATGGTGTGAGTCAGTGA		
6439	SFTPB	NM_000542	AACATGGAAGTCAACGTTTAT	CCCACCATCTCTGGTCTACAA	ACGGCTTGCACCATTCAGCTA	AAGGGACGAGATCGTTAGCTA
6441	SFTPD	NM_003019	TGCTGCCAATATCCTAATAAA	TAGGATTAGGATTGTTGTGAA	CTACCTGGAAGCAGAAATGAA	AGGAGTTTGGCCAGAAGTCAA
6443	SGCB	NM_000232	CTGCTTCGATTTAAGCAAGTA	ATGGGTGGTAATATGGAGTTA	ATGCAGATTTCTAGTGCATTA	CACTTTGAATTGTGCACATAA
6452	SH3BP2	NM_003023	CCCACGGACAATGAAGACTAT	AACCTCTAACAAAGTGAGGAA	TAGCACCTTATGTCAGGGAAA	TAGGAAGTAAACGATCTGCAA
6455	SH3GL1	NM_003025	AAGGTGCTCTTAGAAACACTA	CCGCCTGGACTTTGACTACAA	ACGGTCCAGGGCAAACTGAAA	ACGCCCTAAGCGGGAGTATAA
6468	SHFM3	NM_022039	CCGGGAAGGAGGCACAAGGAA	ACGAGTGAAGGTGTCTCAGAA	TGGGAAGATTGGCATTCATAA	CAGCACCTTCACTGTCAAGTA
6472	SHMT2	NM_005412	CAGCAAATTCAATTTGTTAAA	CCGGAGAGTTGTGGACTTTAT		
6487	SIAT6	NM_006279	CACAATATCCAGCGAGAGAAA	TCGGTTGGGCTTCCTCCTGAA		
6489	SIAT8A	NM_003034	CTGGCTTAATAATATTAATAA	CAGAAAGACATTTGTGGACAA		
6492	SIM1	NM_005068	CACAGAAAGATCGGAATCTGA	ATCCAGTTTGATCCTAGCTAA	CACACTAAACTTCTTAACGAA	TCACCTGGTATCCATTATAAA
6493	SIM2	NM_005069	CACGGGCAACAGTATTTATGA	TAGCAGCTCGTCTCCAGCTAA	CCGGCAAATGCGCACGACCTA	CCGTGATTCTTGAAAGGTGTA
6497	SKI	NM_003036	CTGGACGACGTGAAGGAGAAA	AACCAGTAAGGAGACTTGAAA	GCGAGTGTTTGTAACCATGTA	CCGACTTTATAGAGCAGTCAA
6502	SKP2	NM_005983	AGGCCAACTATTGGCAACAAA	CTCAAATTTAGTGCGACTTAA	ACCCTTCAACTGTTAAAGGAA	AAGTGATAGTGTCATGCTAAA
6503	SLA	NM_006748	AAGGAACTTCGTGACACTAAA	CTGGCTGGATCGGGTAGGTAA	CTGGATCGGGTAGGTAAGAAT	CCCGGTACTTTATTCTAAGAA
6504	SLAMF1	NM_003037	CTCCGGCAGTTGGGAAGCAAA	CAGGACCCTTGCACCACCATA	CAGAGTCTGTCCAGGAAACAA	AACAAATTCCATCACAGTCTA
6510	SLC1A5	NM_005628	CTGGATTATGAGGAATGGATA	CCGGTCCTGTACCGTCCTCAA	CAGCCTTTCGCTCATACTCTA	CACGCTGCCGCTGATGATGAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
6512	SLC1A7	NM_006671	CCGGAACATGTTCCCAGCCAA	CACGTTAAGGTCAAGACACTA		
6514	SLC2A2	NM_000340	TGGGTTATCAGTTAACATTAA	ATGGTGTGTTCCTAACATAAA	CAGACTTTAGCTTACAGTCAA	CAGGGTGCTAACGTATCTCTA
6517	SLC2A4	NM_001042	CAGGATCGGTTCTTTCATCTT	AAGGGCCATGCTGGTCAACAA	ACGCTGCTGCCTCCTATGAAA	CACCTTGGACTCCTCCCACAA
6523	SLC5A1	NM_000343	AACCATAGTGTCTGATGGCAA	TTGGGATTTCACGTATGATTA	AAGGAGACCATTGAAATAGAA	GAGGACAGTGTTGAACGTCAA
6525	SMTN	NM_006932	CACATTCACCATCGAGATCAA	CAGCACCATGATGCAAACCAA		
6528	SLC5A5	NM_000453	CGGAATTATCTGCACCTTCTA	ACCCAGGAAACTCGTGATTAT	CAGCTTCTATGCCATCTCCTA	CTGGATTGCCTTGTATGCAAA
6529	SLC6A1	NM_003042	CAGCAAGGAGGCCTACATCTA	ATCCTTAATAACTATGGTAAA	CACGTAAGGTCTCATTTGATA	CGGGCGTTATGTAAGTTTCTA
6534	SLC6A7	NM_014228	CCCGCTCTCCAAGATGAAGAA	TTGGTTCATTGTTAATAAATA	CCTGGTGTATAGCATCGTCAA	CACGTTTCACCAGAACATCTA
6541	SLC7A1	NM_003045	CAGCACCCAATAGACTATTTA	ACGGATCTGGATATACACTAT	ACGCTTATGACTCCTAATGTA	GAGGGTTGGTTTATTATCAAA
6543	SLC8A2	NM_015063	CACGGTGGATAAACTCATCAA	CTGGAATGAGACGGTGTCCAA		
6550	SLC9A3	NM_004174	CAGCACCGACAACGTGGTCAA	CCCGTTCATCTGGACCTGGAA	TGCGCAGAATTTCACCATCAA	CACCACCATCATCGTAGTGTT
6554	SLC10A1	NM_003049	ACGGAGTCAGCCGGAGAACAA	CACCATAGGGATCGTCCTCAA	AGGGATCGTCCTCAAATCCAA	CACAAGTGCTGTAGAATTAAA
6558	SLC12A2	NM_001046	CAGGATTGTCTACTTCAGCAA	AACGTTAATGACACTATCGTA	CAGGATTTACACCACTAATTT	CAGAGTATTCATTGGTGGAAA
6559	SLC12A3	NM_000339	ATCGCTGAGCTCAACACCATA	CCCGGCCACAGTGGAAGACTA	CAAGAAGACCATAGACATCTA	CAGGATGGACCAGGAGAGAAA
6560	SLC12A4	NM_005072	CCGGGAGCTGGTGCACATTAA	CCGGCATGATCTACAAATACA		
6570	SLC18A1	NM_003053	CCGGATGTATGCAACCCAGAA	CAGCATTGTCTTGCTGCCAAA		
6572	SLC18A3	NM_003055	CACGTCTGGCATAGCCATGAT	CACCATTGCCACGTGGATGAA	CTGCTTGATGAGCCACCGCAA	TACGGAGAGCGAAGACGTGAA
6573	SLC19A1	NM_003056	CAAGCGCAGCCTCTTCTTCAA	CCGCAAGCAGTTCCAGTTATA		
6578	SLCO2A1	NM_005630	AAGGAGGTCATTCATCAACAA	AACCTTTATTCTATTATATTA		
6581	SLC22A3	NM_021977	AAGGAACTTATGGGCATATTA	ATCAATTATATCCATGCTTAA		
6591	SNAI2	NM_003068	GAGGGAAAGATTAGCTTTGAA	TACCACAAATGCAATAATACA	CCGAAGCCAAATGACAAATAA	CACACTGAGTGACGCAATCAA
6601	SMARCC2	NM_003075	AAGAAGTATATACAAGCTGAA	CCGAAAGAAGATTTCAGCCAA		
6602	SMARCD1	NM_003076	AAGCACTGTGGCAATATATTA	TCCAAATATGATGCCACTAAA		
6604	SMARCD3	NM_003078	GTGGCAGTATGTGAAGACCAA	CAGGACTCCCATGACAAGGAA	CTCAAGGTGATGACAGATGTA	CAGTCGCTACTTCTACTGCAA
6610	SMPD2	NM_003080	CCGCATTGACTACGTGCTTTA	CAGGAGGTCAATGGCTTATAT		
6616	SNAP25	NM_003081	AAGATGCTGGGAAGTGGTTAA	CAGAGCTCACGTTGCATTGAA	AAGATTAAGTTATACCAGCAA	AAGGTTGTACATAGTGGTCAT
6623	SNCG	NM_003087	ACCCACCATGGATGTCTTCAA	AAGACCAAGGAGAATGTTGTA		
6624	FSCN1	NM_003088	AACTGGAAATAGCGAAATAAA	CACGGGCACCCTGGACGCCAA		
6625	SNRP70	NM_003089	CGAGAGTGAATTATGACACAA	CTCCGGAGAATGGGTATTTGA	CCGGAGAGAGTTTGAGGTGTA	AAGATTGAGCGGCGACAGCAA
6627	SNRPA1	NM_003090	TAGCCTTGTTTGTGTTAGCAA	TCCACTCACTATGCTACCAAA	CAGCATTGTTGAAATGCTTAA	AGCCTTGTTTGTGTTAGCAAA
6628	SNRPB	NM_003091	ATGAAACTGGTTTATAATAAA	CTGGTTTATAATAAACTCTTA		
6632	SNRPD1	NM_006938	AACGCTGAGTATTCGAGGAAA	ACAGTTCTATGTACTGAGAAA	TAGGCTAAACTTAACAATATA	CAGAGCTGTCTATTTAGTATA
6633	SNRPD2	NM_004597	AACGGAGAGCGTAGTGACCAT	CGCGGAGGAAACGGGAGTGAA		
6634	SNRPD3	NM_004175	CAAGAGGAAGAGGACGTGGAA	CAGCTCAGCTTTAACAACACA	ACCCATGTTAAAGAGCATGAA	AAGGACTTTGTGTTCATTTGA
6636	SNRPF	NM_003095	GCCAGTGATGGTGAAACTTAA	AAGGTGTAATAATGTCCTTTA		
6638	SNRPN	NM_003097	CAGAAAGATCAAGCCAAAGAA	TTGGATTTGGTGGAACAGCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
6640	SNTA1	NM_003098	CACCGTATTTCAAGAACTCTA	CCGGAACTTCAGCGAGGCCAA		
6641	SNTB1	NM_021021	CAGGAATTAAATAAAGCATCA	TAGACTGAATGCTATAATCAA		
6643	SNX2	NM_003100	AACCATCTAAATAAACCACTA	AGGGAAGAGATTGAAGAAGAA		
6649	SOD3	NM_003102	CTGGAATGGATGAGCACCCAA	AAGGGCTGCTATGATTGAGAA	CTCCTTCATCTCTTTAATAAT	AACCTTTGTGTTACAGATTAA
6651	SON	NM_003103	ATGATGTTGATTTATCTTTAA	CAGAATCTTCAATTACGTTAA		
6653	SORL1	NM_003105	CAAGACGGTCATTGTCAGTAA	CACGTCCTTTCTTGACCTCTA	CTGGGATTTATCGGAGCAATA	TACGGACAGGTTAGTCTGAAT
6654	SOS1	NM_005633	TACGGCATTATGAAATTACAA	CATGAACTTAGTGTAAAGTTA	TGGGTTGAATCCATCACTAAA	ACGAGTAGAATCAGATATCAA
6656	SOX1	NM_005986	CAACGTTAAGATGAAATTATA	TTGGGTTGGTTTGTTAATTTA		
6659	SOX4	NM_003107	CCGCGAGAAACTTGCATTGGA	TCCTTTCTACTTGTCGCTAAA	CACGGTCAAACTGAAATGGAT	AAGGACAGACGAAGAGTTTAA
6662	SOX9	NM_000346	ACCGAAGAAAGAGAGGACCAA	TCGTGTGATCAGTGTGCTAAA	ATGGGAGTAAACAATAGTCTA	CAGCCCACTGACAGACCTTAA
6675	UAP1	NM_003115	AAAGGTTTCTATGGTACTAAA	TTAGAGCATTATGAACATTAA		
6683	SPG4	NM_014946	CACGATGCTAGTAGACGCCTA	TGCCCTTAGTTTACTGGTTAA	AACGTTATTGATACTTGGATA	TCAGGTTAATACTATCTTAAA
6693	SPN	NM_003123	TTCAATAACAAGTGACCCTAA	ATGGTTCATATAGGACACACA	AAGGGTGTTTGTAGAGTTGTT	CCCAATGGCCTTTATCATCTA
6697	SPR	NM_003124	CAGGAAAGGCTGCTCGTGATA	CACGTGGACTTCTATGACAAA	AACTGCTGAGCTTACTGGAAA	AAGGAAAGGCTGCTCGTGATA
6699	SPRR1B	NM_003125	GAGACTTAAGATGAAAGCAAA	AAGGTCTTAGTACCAGAGCTA		
6700	SPRR2A	NM_005988	ATGATGATCCCTGACAGCAAA	ACCAAGAAAGGATAAGGATAT		
6710	SPTB	NM_000347	CTGCCGCATCACCGATCTCTA	ACGGCCCGCAAGGACAATATA	CACTCTCTGGATCAACGACAA	CAGGATGTCTCCTATGATGAA
6712	SPTBN2	NM_006946	CCGGCTCATCTCGGACATCAA	CAGCGTCAACATCCTGCTCAA		
6715	SRD5A1	NM_001047	CTCCGGAAATTTGAAGAGTAT	CGGGCATCGGTGCTTAATTTA	ATCCATTCAGATCATATCCTA	GAGGCTTATTTGAATACGTAA
6717	SRI	NM_003130	CAAAGAATACTCCACACATAA	TACATTATAAGCTTAACTATA	CAGGCTGTGAATTCAATTGCA	AGGATTCACCTTAGAAGTTTA
6718	AKR1D1	NM_005989	CAGGGTCCTCCAGCTAGATTA	ATGGCAAATGGTTATATCACA	CTGGGTAGTAGCGTTGGTAAT	TAGTGTTACTTGGATAGCTTA
6729	SRP54	NM_003136	ATGGGATTCAATAATATGTAA	ATGGATAGTATGAATGATCAA		
6732	SRPK1	NM_003137	CACCCTTGGCTTAACTCCTAA	AAGCAATAGACTAGAACTGAA	TACCATGTGATCCGAAAGTTA	CAGACTCTTGTACACCTATAA
6737	TRIM21	NM_003141	CAGCGTTGAGTTGCCCTGTAA	AGCGTTGAGTTGCCCTGTAAA	CCGGGAGCGCTTTCTGCTCAA	CAGAGCATACCTGGAAATGAA
6738	SSA2	NM_004600	CAGGATGGATATGTATGGCAA	CTGAGGGAGTATCGAAAGAAA		
6746	SSR2	NM_003145	CAGGTGCTTTCCAGACTCCAA	CCCAGTGTCTATTCTGGGTTA	CACCTCGGCAACAATTACTTA	CAAAGGGTATCTTAAATGCAA
6750	SST	NM_001048	TGCAGAGATCTGCTAACTCAA	CAGCGAGACCCTTGCATTAGA	CCCTTGCATTAGAAACTGAAA	ACGGAGAATGATGCCCTGGAA
6751	SSTR1	NM_001049	CTGGTGGTGCCTATTAATCAT	TGGGAACTCTATGGTCATCTA	CGCGCTGGTGGTGCCTATTAA	CACGAACTCATTAACAACTCA
6755	SSTR5	NM_001053	CACCGTCAACATCGTCAACCT	ACGGGCTTATGCAGACCAGCA	CGGGCTTATGCAGACCAGCAA	CGGGAACACGCTGGTCATCTA
6757	SSX2	NM_003147	CCACCTTTCATGTGTAATAAA	AGGGCAGTTCTGAGTGTTTAA	CCCGAAGATCATGCCCAAGAA	TTGGTCGATTCAGTTTGTCAA
6775	STAT4	NM_003151	TGGAATCAAGTCCAACAGTTA	TCAGAGGCCGTTGGTACTTAA	TTGGTACAACGTGTCAACCAA	CAGCCTCGATTTCAAGAGAAA
6778	STAT6	NM_003153	CACCCTTGAGAGCATATATCA	AACCAAGACAACAATGCCAAA	CAGGATGGCTCTCCACAGATA	ACGGATAGGCAGGAACATACA
6788	STK3	NM_006281	CAGACCATGATTGAACATAAT	CAGCTGCATACCAGTAATAAA	CGGCGCCTAAGAGTAAACTAA	CCGGCGCCTAAGAGTAAACTA
6790	STK6	NM_003600	TAGCATGTGTGTAAACTTTAA	GAGGGTTTAACTCCTATTTAA	CACGTGCTCTACCTCCATTTA	CACCTTCGGCATCCTAATATT
6793	STK10	NM_005990	TGCAGAATGTATATAACGCAA	CAGAATGTATATAACGCAATA	CAGCTCAAACTGATGAAGAAA	CACGGAATTAGAGAACCTGGA
6794	STK11	NM_000455	AACGTGAAGAAGGAAATTCAA	CCGCCCAAATTTGGCAATAAA	GAGGGCCGTCAAGATCCTCAA	CAGGAGTGTGCGGTCAATATT

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
6799	SULT1A2	NM_001054	CACGTCGTTCAAGGAGATGAA	AAGAGGCTCCAGAATAAAGTA		
6810	STX4A	NM_004604	AGGAAGCTGATGAGAACTATA	CAGCTCGGACGAAGAGGACAA	TCCGGACAATTCGGCAGACTA	AAGCGAGGTGTTTGTGTCCAA
6811	STX5A	NM_003164	CAGTGGAAATTGAAGAGCTAA	CAGCAAGACTGTCAGCCTCAA	AAGTCCCTCTTTGATGATAAA	ATCAATAGCCTCAACAAACAA
6829	SUPT5H	NM_003169	CCGGAAGGGCTTTCTGTTCAA	CAGAACAACATCCATGTGAAA		
6830	SUPT6H	NM_003170	TAGGAGCATCTTTGAAATGTA	CAGCACAATTCAGAAGATCAA		
6840	SVIL	NM_003174	CACATCGAAGCCATGATTTAA	ACCGGTTGTAAACAAACAGTA	CAGGACTGATGTCAAGGCATA	CCGAGTATTTATCCCGCTATA
6844	VAMP2	NM_014232	ATAGTTTACTTCAGCTCTTAA	CAGCTGTTATTTATACATATA	TCCCTTCATTTGCATCTGCTA	CCCATTAGTTCTTGTATCACA
6853	SYN1	NM_006950	CCAGATGGTTCGACTGCATAA	ATGGTTCGACTGCATAAGAAA		
6854	SYN2	NM_003178	CCAGCTGGTCGCTATCTATAA	CTCACTGGAATCCATATACAA		
6860	SYT4	NM_020783	CAGGGAGATCTTAATACCTAA	CTGCACTGTATTAAACATGTA		
6873	TAF2	NM_003184	AAGCATAAGCATGACAGTAAA	TAGAATCAAGTTGAACAGCAA		
6884	TAF13	XM_496381	TAGGGTGATATTGGTGCATGT	GCCCTTGTAAGCTATACTGTA		
6887	TAL2	NM_005421	GACCAGGAAGATCTTCACAAA	CAGAACTCTGCTTGAGAACTA	CCCACTCACCCTCCAGACAAA	AAACGCTTCGCCTGGCAATGA
6891	TAP2	NM_000544	CAGGACCAGGTGAACAACAAA	CCTGCTTTCCTTTATGATCTA	TAGCGACATTGGTAACAGCTA	CCCTATGAGGTTGGTTATTAT
6898	TAT	NM_000353	TTCGCTAGTGATGGACCCATA	CTCGGGCAAATATAATGGCTA	TCGGGCAAATATAATGGCTAT	CAAGCTATTGACCTTTGTTTA
6900	CNTN2	NM_005076	ACGATAGTTACTCACAAGTAA	CAGCCACAAACAAGTACTTTA		
6906	SERPINA7	NM_000354	CACTATGGTCTTAGTGAACTA	CACCCTATTATCCAAATTGAT	ACCCTATTATCCAAATTGATA	TAGGGAAAGTTGTGAACCCAA
6910	TBX5	NM_000192	AAGGCGGATGTTTCCCAGTTA	GCCGACGATCACAGATACAAA	CCACAAGATCACGCAATTAAA	TACCATTGTACCAAGAGGAAA
6916	TBXAS1	NM_001061	CCCAATAAGAACCGAGACGAA	CCGGAGACCTTCAACCCTGAA	ACCGCTGCAGCTAGAATCCAA	CCGCTGCAGCTAGAATCCAAA
6921	TCEB1	NM_005648	CCGAGATTCCTGAATTCCCAA	AAAGTTGAAATTTGTTTGCTA	TACCTGTAGTTCAGTTAGTAA	TGCGAACTTCTTAGATTGTTA
6924	TCEB3	NM_003198	TAGCATCTTTGTAAACTATAA	TACAATCATGTATTAATTGAA		
6926	TBX3	NM_005996	GCGAATGTTTCCTCCATTTAA	GTGCACTTTGTCGGATATAAA	TCGGGACAAGTGAACACATTA	CTGCCTATAGAGATATATTCA
6927	TCF1	NM_000545	CAGCCGAGCCATGGTTTCTAA	CAGGAGTAGCTGAGCTCACAA	CAGGACAAGCATGGTCCCACA	GCGAGTGGCACGTTTATTTAA
6928	TCF2	NM_006481	CACGGATCTTATCTGGTTTAA	CTGGGATATGCTAGTGATGTA	GCGGTGTAATAAGATCCTATA	TAAGGTTATAACTGTGGCTAA
6929	TCF3	NM_003200	CTCGGTCATCCTGAACTTGGA	CTGGATGATTGGGACTTTAAA	CCGGGCACATGTGAAAGGTAT	CCCGGATCACTCAAGCAATAA
6932	TCF7	NM_003202	TACGAACATTTCAACAGCCCA	ATGAGCTGGTTTGTCAAACAA	AACAGAAATAATCTGACACTA	CTGGGCAGCTTGAGAGGGCAA
6939	TCF15	NM_004609	AGAGAGAATTGGTGAGTTTAA	TCTGATATGGTTGGTAAAGAA	ATGGTTGGTAAAGAAATCTTA	TGGTTGGTAAAGAAATCTTAA
6943	TCF21	NM_003206	CAGATCCTGGCTAACGACAAA	CTGGTCCAAGTGCAATATGTA	CAAGTGCAATATGTAATTATA	ATCTTTCTTTATATTGCTAAA
6949	TCOF1	NM_000356	TACGTTGGTCTCAGAAACTGA	CAGCGAGGAATCGGACAGTGA	CAAGCAGTGAGGAATCAGATA	ACGGTTGAAGGTGGAGATCAA
6975	TECTB	NM_058222	CAGGGCAACCTTCCAATTCAA	TAGGTTTAAAGTGGTCTTGAA		
6988	TCTA	NM_022171	CCGGAGTCACTCATCCCTTAA	TAGGATGGTACCAAGCATTTA		
6992	PPP1R11	NM_021959	TGGCTTGAGATTGGTCACTTA	CAGAGATCAGTCAAATCCATA	CGCCCTAACTTTGCTTGCTAA	AACATGAGTAGCGAACACTTA
6993	TCTEL1	NM_006519	AACGCTTATCAACACAGCAAA	ATGTAGTAGAACAAACTTTAA		
6997	TDGF1	NM_003212	CCCGCTTCTCTTACAGTGTGA	AACCAAGTGATCAAACTACAT	CTGCCTTTCTATACAAAGCTA	TTGAATTATATGTTCAGATTA
7005	TEAD3	NM_003214	ATGGGTTATATCATAAATGCA	AACCAGCACAATAGCGTCCAA		
7006	TEC	NM_003215	CACGTGCATTTGGCCTATGTA	TCAGGTGACCTTCGCAACAAA	CCGCAGCTAATCAGAATCAGA	CAGTACAAAGTCGCAATCAAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
7010	TEK	NM_000459	CAGCACGTTGATGTGAAGATA	TGGAATGACATCAAATTTCAA	TCGGTGCTACTTAACAACTTA	ACGGGCCAGATTGTAAGCTTA
7019	TFAM	NM_003201	AAGGAATTATATATTCAGCAT	AGGACGAAACTCGTTATCATA	CACAATAAAGAAACAACGAAA	AAGATTGAGATGTGTTCACAA
7026	NR2F2	NM_021005	CTGGCCGTATATGGCAATTCA	TAGGTGAAGTCGAGCACTCTA	GTGGAATTTATTGGCAGCCAA	CCGCTTAGTTCTTGAATTGTT
7029	TFDP2	NM_006286	CTGGTACAGAGAAATCGACAA	AGGGACTACTTCTGAACTCTA	CGCTACTTCTTAAGTACTTAA	AAGGCAGAAATGAACATGAAA
7030	TFE3	NM_006521	TCCGGGATTGTTGCTGACATA	AAGGAGATTGATGATGTCATT	TCGCAGGCGATTCAACATTAA	CAGCTCCGAATTCAGGAACTA
7036	TFR2	NM_003227	CACGGAGTGGCTAGAAGGCTA	CAGGCACATCGGGAACCTCAA	GACGGTCATACTGTCGGTTAA	TGGAGTTTCAATATCAATAAA
7040	TGFB1	NM_000660	CTAGGTTATTTCCGTGGGATA	CACACTGCAAGTGGACATCAA	CAGCATATATATGTTCTTCAA	CACGTGGAGCTGTACCAGAAA
7043	TGFB3	NM_003239	CCGAGTCGGAATACTATGCCA	CCGGGTCTTGCGGGTGCCCAA	ACGCATAGACTGAGGTATAAA	AAGTATGAATATTACTCTCAA
7045	TGFBI	NM_000358	CGGGAAGGCGATCATCTCCAA	AAGGCGATCATCTCCAATAAA	CCGCACCATAATGAGATGTGA	TGGAGAAATGGCATCATTATA
7046	TGFBR1	NM_004612	CTGTAATGTTACGTCATGAAA	TGGGATTGTACTATACCAGTA	TCCATTGGTGGAATTCATGAA	CTGCCTTATTATGATCTTGTA
7048	TGFBR2	NM_003242	TACCATGACTTTATTCTGGAA	TCGGTTAATAACGACATGATA	TCGCTTTGCTGAGGTCTATAA	CTCCAATATCCTCGTGAAGAA
7049	TGFBR3	NM_003243	GACAATGGCTATAGTCCAATA	CACCTTCAACATGGAGCTATA	CCCGCAAGCTGACATGGATAA	ACCTGAAATCGTGGTGTTTAA
7050	TGIF	NM_003244	TACCACTGTGACTGCATTGAA	TACCCAGAGGACACTTGTAAA	TCCAAGAACTATAAACTTAAA	CACATACTGTCTAATTAATAA
7052	TGM2	NM_004613	CACCTTGATCCCAATCCTTAT	ATGGCCCAGCCTTGTAAATAA	CCGCAAGGAGCAAACACTGAA	CCGCGTCGTGACCAACTACAA
7058	THBS2	NM_003247	TGCATAAGCCATTATGATAAA	ATGACATAAGCTACCGATTAA	CAAGAGAGTGTCGAATGATAA	AGCGTTGGGATACTTCATTAA
7059	THBS3	NM_007112	CACGCCGTGAACCTACAGCAA	CCGCCTGGGTTTCCTGGGCAA	CTGCATGGAAGTGTACGAGTA	ATCGATGGCTACCCAGACCAA
7064	THOP1	NM_003249	CAAGTTGAAGGTCACCCTCAA	TGCGGTGATTCTGGAGCTGAA	CAAGTTCTACCTGGACCTGTA	CAGCAAGGTTGGCATGGATTA
7067	THRA	NM_003250	CAGCGAGTTTACCAAGATCAT	CTGGCCCAAGCTGCTGATGAA	CTGGATGGAATTGAAGTGAAT	CCCGATGACATTGGCCAGTCA
7072	TIA1	NM_022173	CGGAAGATAATGGGTAAGGAA	CACAACAAATTGGCCAGTATA	CTGGGCTAACAGAACAACTAA	AACGATTTGGGAGGTAGTGAA
7074	TIAM1	NM_003253	CGCCTGAAATTTCTAATAGAA	AACGGAAATGGTAGAGTTTCA	CTGGTTCTGTCTGCCCAATAA	ACGGCGAGCTTTAAGAAGAAA
7075	TIE1	NM_005424	CCAGTGAGAACGTGACGTTAA	TACTTGTATATCGCTATTGAA	GCGCTTCAAGGTCAATGTGAA	CCCAGTGAGAACGTGACGTTA
7077	TIMP2	NM_003255	CAGGCACATTATGTAAACATA	CTCAAATACCTTCACAATAAA	CTCGCTGGACGTTGGAGGAAA	CTCGACATCGAGGACCCATAA
7078	TIMP3	NM_000362	CAGGTGAAAGACTGAGATGAA	CCCTGCGGAGTCGATAAATTA	CGGCGGCATTATTCCCTATAA	CACGCTGGTCTACACCATCAA
7080	TITF1	NM_003317	CCCACTTGTCACTGACACAAA	TGGCTTAAATATAGTTCCTAA	TACCTTGTCATCAGCATGTAA	CTCCGTTACGTGTACATCCAA
7084	TK2	NM_004614	AAGGTGTTCAATTAATCTGCA	CTCCCGATAAAGAACAGGAAA	CGGGATCGAATATTAACTCCA	ATGCCAGAAGTGGACTATGTA
7087	ICAM5	NM_003259	CCGGGAGAACGTGACCATCTA	CAGGAGGAAACTTCACGTTGA		
7088	TLE1	NM_005077	AAGGTTAAACATTTGTATAAA	TCGAATTTATAGAAATAGAAA		
7089	TLE2	NM_003260	CTGCATTGATATTTCCGATTA	CAGCGAGAAGACGGAAATGCA		
7090	TLE3	NM_005078	CAGGATCAAAGACGAATTCCA	CACAGTTTATGAGGTCATCTA		
7092	TLL1	NM_012464	GAGGCGTTATTCCTTATGTTA	CAGATCGAGATAACCACGTAA	TAGAATCAATCTCGACCTATA	CAGCATTACAAGGATATTTGA
7096	TLR1	NM_003263	CACCATTTATATGTGGTATTA	CTGGTTTGGCATACAACTGTA	CCGCAAAGTTATATCTATGAA	CAGGGTCTTCATGAACACTAA
7097	TLR2	NM_003264	CTGGGCAGTCTTGAACATTTA	AACATTTAGACTTATCCTATA	CAGGTAAAGTGGAAACGTTAA	CCGCAACTCAAAGAACTTTAT
7101	NR2E1	NM_003269	CCGGTTGATGCTAACACTCTA	TACGTTATGTTGGAGCATTTA	TCCCGTTAACATAGTGCTGAA	CTCTATACTTATGGAAATGTA
7102	TM4SF2	NM_004615	CACGGACGCTATGCAGACTTA	AAGGGTTGTTATGATCTGGTA	CCGGTTCATCACGGCCAATCA	CAGGCTGCCTAAGACATGTAA
7104	TM4SF4	NM_004617	AAGGAAGAAAGCACATTTAAA	CAGGTCAGGGAGAATGTATAA		
7108	TM7SF2	NM_003273	CCGCATCATGCCCTACATCTA	CACCATGGATATCACACATGA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
7112	TMPO	NM_003276	ACCCATCAAATTACAGTATAA	GAGGAGAAGTATGCAAAGTAA		
7124	TNF	NM_000594	AACCCAAGCTTAGAACTTTAA	CAAGCTTAGAACTTTAAGCAA	TAGGGTCGGAACCCAAGCTTA	CCGACTCAGCGCTGAGATCAA
7126	TNFAIP1	NM_021137	CTCACATACGGTAAAGCCAAA	TGCCCTCTTGAGGTCCTTTAA	CAGGAGGTGAGTTCCTCTTTA	ACCCATGTCTTTCTACCCTAA
7127	TNFAIP2	NM_006291	CTGGCTGTGTAACCTAACATA	TAGGAGTTAGCGTGTTTGATA	CCGGATGTCCATGGAGCAGAA	CAGGGTGATGCTGAAGATGAT
7128	TNFAIP3	NM_006290	CTCGGCTATGACAGCCATCAT	CAGATGTATGGCTAACCGGAA	CCGAGCTGTTCCACTTGTTAA	CAGCCTTTACTCATACTATTA
7130	TNFAIP6	NM_007115	CTGGCACATTAGACTCAAGTA	CCCACTGCATAGAAATAACAA	TGGCGTCTTTACAGATCCAAA	AAGGCGGTGTGTGAATTTGAA
7139	TNNT2	NM_000364	CAGGCAGCTCCTGTTTGGAAA	CCACTCCACACCAGTAATAAA	CCGAAACAGGATCAACGATAA	CAGGATCAACGATAACCAGAA
7140	TNNT3	NM_006757	AAGCGTCAGAACAAAGACCTA	GAGGAGCAGTACGAAGAAGAA		
7142	TNP2	NM_005425	CAGAAAGAACTTGGAAGGCAA	CAGGATGGAAATCCAACTAAT		
7151	TOP1P1	M55632	CTCACAATTCACACCAATAAA	TTGGGACATCATGAAAGTTTA	TGCCTTCATATTAATATATAA	GTGGAAGTTTACTGACAGGAA
7153	TOP2A	NM_001067	CCCATTGTAAAGGTATCTAAA	CAGACTATAGGGAATACCATA	CACGTAGGCTGTTTAAAGAAA	ACGAATAACCATAGAAATGAA
7155	TOP2B	NM_001068	GTGGATTATGTGGTAGATCAA	CTGATTGAAGTAGTTAAGAAA	CAGCCGAAAGACCTAAATACA	TCGGGCTAGGAAAGAAGTAAA
7158	TP53BP1	NM_005657	AAGCAGTAACACCTCTTACAA	CTCCAGAACTACCGTAATTAT	TTGTTTGACCAGAGCAATAAA	CAGGACAGTCTTTCCACGAAT
7161	TP73	NM_005427	CCCGCTCTTGAAGAAACTCTA	CCGGGCCATGCCTGTTTACAA	CCCGGGATGCTCAACAACCAT	ATCGAGTATTTCACCTCCCAA
7164	TPD52L1	NM_001003395	CAGCTAGAAGACGAAATTACA	CAGCAATAGGATGATTTACTA		
7166	TPH1	NM_004179	AAAGACAATGTCTACCGTAAA	CGGGAGGATAATATCCCACAA	TCCATTTGGAGTGAAGTATAA	CGGAGTATTCAGATCCTGAAA
7167	TPI1	NM_000365	CCGAGGATGGCTGAAGTCCAA	ATGGAAGGCGTGGTGGGATTT		
7168	TPM1	NM_000366	CACACTGTGCTTTCTATTGTA	CTCAAGGGCACCGAAGATGAA	TGCGGAGAGGTCAGTAACTAA	AACGATATGACTTCCATGTAA
7171	TPM4	NM_003290	AGCGTTTGCTTTCGCCTGTAA	ATAGTAATTAATAGATGGTAA		
7172	TPMT	NM_000367	ACCGAAATTCCTGGAACCAAA	AGGGTTCAAGGTGGTCCCAAA	CACCGGTTGAATGGACAACTA	ACCGGTTGAATGGACAACTAA
7175	TPR	NM_003292	CTGAAGGAAGATCTAAATAAA	CAGGAGGTTTCTAGAGAACAA		
7177	TPSAB1	NM_003293	CTGAGTGCTGGACCTCATTAA	CTGCCTGGGACCGGACGTCAA	CTGGACCTCATTAAAGTGCAT	CAGGATCATCGTGCACCCACA
7187	TRAF3	NM_003300	CTGGAAGATTCGCGACTACAA	ACACTTCACTCTGAAGAATTA	TCCGATGATCGCGCTGCAGAA	AGAGAGCATCGTTAAAGATAA
7188	TRAF5	NM_004619	AAGGTAGGCTGTTCCAGTTAA	AAGCATTTCTTTAGCCCACAA	CTGGAGGGTACTTGCTATAAT	AGGGTACTTGCTATAATGGAA
7189	TRAF6	NM_004620	CAGGAAACTATTCACCAGTTA	CAGCGCTGTGCAAACTATATA	CAGGGATGAGTTTAAACCCTA	AGGGATGAGTTTAAACCCTAA
7224	TRPC5	NM_012471	CAGAGCTATCGATGAGCCTAA	GAGGCCTGTTCTCAAAGTGAA	CACACTAAGTCCATCTTACAA	ACCAGCTATCAGATAAGGCAA
7252	TSHB	NM_000549	GAGAGTGTGCTTATTGCCTAA	CCCAGGATGTTTGCACATATA	CTGCATACATGAAGCCATCAA	AAGACAAACTACTGTACCAAA
7253	TSHR	NM_000369	TCCAGAATCTACGTATCTATA	CAGAATCTACGTATCTATAGA	TACGCAGACTCTGAAGCTTAT	AGCACTGATATTCAGGTTCAA
7262	PHLDA2	NM_003311	CACTGTGCCCATTGCAAATAA	CGGCTTTGAATGAATAAATGA	CTGGTTCTTTGTAGTCACATA	CGCGCTCGGCACGACATGAAA
7266	DNAJC7	NM_003315	AAGCTTATAATTATTATACAA	AAGGAAGGAAATTACAAACTA		
7270	TTF1	NM_007344	AAGGAGATACTGAGAAGTTAA	CAGTTTGATTATATTTATATA		
7272	TTK	NM_003318	ATCCGACTTTATGATTATGAA	TTGGACTGTTATACTCTTGAA	TCCGACTTTATGATTATGAAA	CAGCAATACCTTGGATGATTA
7273	TTN	NM_003319	TGCGGCGAGTATACATGCAAA	TCGGGACGGTCAAACCTATAA	CGCATTCTAGCTCGAGTCAAA	ATCGACTATTACATCGTAGAA
7280	TUBB2	NM_001069	CAGATCAATCGTGCATCCTTA	CATGGTCTTTCTACTTGTAAA	CTGTGAAGGTATCTATACTAA	GAAGGTATCTATACTAATAAA
7297	TYK2	NM_003331	ACGAAATTCCTTGAGCTCATA	CTGATGCTATATTTCCGCATA	CGGGTCTGTGCTGAATGTGTA	CACCATCTGGTAATAAACTCA
7299	TYR	NM_000372	ACCCATGTTTAACGACATCAA	AAGGATTTGCTAGTCCACTTA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
7314	UBB	NM_018955	GAGGCTCATCTTTGCAGGCAA	CCAACTTAAGTTTAGAAATTA	ATGGCATTACTCTGCACTATA	CAGGATCCTGGTATCCGCTAA
7316	UBC	NM_021009	TTGCACTTTCCTTTCAATAAA	AACGTCAAAGCAAAGATCCAA	GAGGTTGATCTTTGCTGGGAA	GAGGTTGATCTTTGCCGGAAA
7317	UBE1	NM_003334	CCCGCTCACCTTTGATGTCAA	CTGGGATGTCACGAAGTTAAA		
7318	UBE1L	NM_003335	TTGGAGTTTGACACCAACCAA	CGGCCGGATGGTCACCTGAAA	CAGCAGAAGGAACTGAACAAA	ATGCTTGTTAAAGGAAGGCAA
7320	UBE2B	NM_003337	CTCATTAGAAAGGCTAACAAA	TTGGATTACAGTATGGCAATA	CCCAGTATTAGCAATGAATTA	ACCTCTCATTAGAAAGGCTAA
7325	UBE2E2	NM_152653	TCCGATGGAGATCAACGTGAA	CCGCTGCTAAATTGTCAACTA		
7334	UBE2N	NM_003348	ACCTTGTCTCTTGCAGTTTAA	AAGATGAAGAATTAACTATTA	TAGCCAGTCATAAATACATAA	CAGATTTGTGTTAAGATAGTA
7335	UBE2V1	NM_021988	ATCCATGCGAGTAAACATTTA	TTGGATGTAACGGCTTGGTAA	CACGGGAATTATTATTGTCAA	AAGGAAGACTTGAACCTAGAA
7343	UBTF	NM_014233	CCGGAGAAGAAGAAGATGAAA	CAGGACTTCCAGAGAGAGAAA		
7350	UCP1	NM_021833	TCCAGTGTTATTAGGTATAAA	CAGAATAATAGCAACAACCGA	TGCAATGAAAGTGTTCACTAA	AACGAGAACTGTCAAAGTCAA
7358	UGDH	NM_003359	TACAATCATGTTTGAAATTAA	ACGGTTGTTGATGTCAATGAA		
7363	UGT2B4	NM_021139	CTGGGAAACCCAATAAATGAA	CCCAATAAATGAACTCCTTTA	ATGAGGTTATATTGAAATGTA	AGGAAGCTAATAAATAATTAA
7367	UGT2B17	NM_001077	CACATTGTATTTGAACACAAA	TTGGGAATATTCTGACTATAA		
7376	NR1H2	NM_007121	CAGGGCAACAGGAGTAGTTCA	CCGGAAGAAGAAGATTCGGAA	ATCGTGGACTTCGCTAAGCAA	CTGGGCGAGCCTGTAGACCTA
7378	UPP1	NM_003364	CAGGAAACTAATTTCCTGATA	CACACTTTACACAAGAATCTA		
7380	UPK3A	NM_006953	CACGGAGTACAGGTTCAAGTA	CAGTGTGACTTTCGCCACCAA		
7384	UQCRC1	NM_003365	CCGGGAGCACACAGCTTACTA	CGCCACCGTGATGATGCTCTA	CCGGACAATGTGGCCTTGCAA	CCACAGGTGACCACCAATAAA
7385	UQCRC2	NM_003366	TACATCCAGTCTGACGACAAA	CCAGAATTTCGTCGTTGGGAA	ATCAAGGCTGCCTATAATCAA	AAGGCTGCCTATAATCAAGTA
7392	USF2	NM_003367	CCGGGAGTTGCGCCAGACCAA	CAGCAAGACGGGAGCGAGTAA	AAGACTGTAACGCAGACAACA	AAGAGCCCAGCACAACGAAGT
7399	USH2A	NM_007123	CAGGTACAATTTGACCATTGA	CAGAGGGAAACTTGACTTTAA		
7407	VARS2	NM_006295	CCGGATTTACCACCAGTTGAA	CTGTTTCACCATGGACCCTAA	CACGAGGAAGGCATCATCTAT	CCGGTTTGGATTATGTGCCTA
7414	VCL	NM_003373	CGGATTAGAACCAACCTCTTA	AAGAGAGTAATGGGTTTCATA	TAGGTGTTTGTTCATCTGTAA	CTGATATAAATGCAATATTAA
7415	VCP	NM_007126	CACAAGCAGTTTCTAAACCAA	CCCATTGATGACACAGTGGAA		
7422	VEGF	AF022375	GAGGGTTTCAATATACATCTA	CTGGAATTTGATATTCATTGA	ATAGAGAATTCTACATACTAA	AAGAAAGATAGAGCAAGACAA
7423	VEGFB	NM_003377	CAGGACAGAGTTGGAAGAGGA	CCGGATGCAGATCCTCATGAT	CAGTGTGAATGCAGACCTAAA	AAGACCCAAACCTCTGCATAA
7425	VGF	NM_003378	CCGGAGGAAGAAGCAGCTGAA	CGGCAGCCTCTTGGTCATGAA		
7434	VIPR2	NM_003382	CACCGGTTGCTGGGATACAAA	CTCCAGCATTTAGATAATCTT	CCCGCTGTTCGGCGTCCACTA	AACGGAGACCTCGGTCATCTA
7436	VLDLR	NM_003383	CCCTGAAAGAGTGTCATATAA	ATCCAACTAGTTGAACAGCTA	CAAGGTTGGTAGACATGTTAA	CAAGATCGTAGGATAGTACTA
7441	VPREB1	NM_007128	AGGCTATGTATTACTGTGCTA	CTGCTGAGATATTTCTCACAA	TCCCAGGTTCCTGCTGAGATA	AGACTGCATTAGGGAATTAAA
7442	TRPV1	NM_018727	CAAGTGGGACAGATTCGTCAA	CAGAACCACATCCCAAAGGTA	CTCAATTGCTGTGCAGGTTAA	CCCGAGGAAGTTTATCTGCGA
7447	VSNL1	NM_003385	TAAGCGTTTACCCGAATTAAA	CGGCTTAAGCGTTTACCCGAA	CAGAGACGGCTTAAGCGTTTA	AGCGTTTACCCGAATTAAATA
7450	VWF	NM_000552	AAGGGACGAGATCGTTAGCTA	AACATGGAAGTCAACGTTTAT	CCCACCATCTCTGGTCTACAA	ACGGCTTGCACCATTCAGCTA
7453	WARS	NM_004184	CAGAAGGGAAACTGAAAGAAA	AAAGAGCTAATAAACCGAATA	CAGGTTCTTGATGCCTATGAA	AGGGTTCCAAGTATACTCTTA
7455	ZAN	NM_173059	TGCGATCTTAATAAACCCTCA	CCGTGTGCTAATCAACAGCAA	CCCGGCTATGTGCTGAGTGAA	CAGCTTAAGAATGGCCAGTAT
7461	CYLN2	NM_003388	CACCTTCTGAACCTTCTTCAA	CAGGACAAAGCTCAGAAACAA		
7462	WBSCR5	NM_014146	AAGCTTGTACAGTTAACTTAT	AAGGACCATTTCCCAGAGCTA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
7472	WNT2	NM_003391	AAGGCATTTATTGCCATATTA	CTGGAGAAGAATGGCTTTCAA		
7474	WNT5A	NM_003392	CAGAGTAAATACTCTGAATAA	CCGGATAACCTTGTAACATAT	CCGGGTCTGCAGAGAATGAAA	CACACAAACTTTACACTTTAA
7480	WNT10B	NM_003394	AAACCTGAAGCGGAAATGCAA	CAGGCACTGTTTGGAGCCATA	CAGGATCGGCTGAGGGCCAAA	ACGAATGCGAATCCACAACAA
7483	WNT9A	NM_003395	CCGGCTGAAGCTGGAGCGGAA	CCGTGTGGACTTCCACAACAA		
7484	WNT9B	NM_003396	CAGCACCAAGTTTCTGAGCAA	AAGCAAAGCCTCCTCCCTTAA		
7498	XDH	NM_000379	GACAGTCTTTGCGAAGGATAA	CTGCACCATTGCTGTTCCAAA	CGGGATTGTGGTTCGAGTGAA	ACAGGTAATAACGTGAAGGAA
7499	XG	NM_175569	CAGCCAGTTATTTCAAACTAA	ACGGTGGAGATCACCATTCAA		
7511	XPNPEP1	NM_020383	AAGGAGAACCTCGTTGACAAA	ATGAGATTGCGTGGCTATTTA	CCCGACTGGAACCAAAGGTCA	CCCGACTTCTTTGGCCAGTGA
7514	XPO1	NM_003400	TACATGTTACTCCCTAATCAA	CTGTGTCAGTTTGTAATGGAA	CCCATTGTAAAGCGACTTCAA	CAGCAAAGAATGGCTCAAGAA
7516	XRCC2	NM_005431	CACGATGTATACTTCCCAAAT	AGGGTACTACGCAAGCCTTAA	TTGCAACGACACAAACTATAA	CAGGGTACTACGCAAGCCTTA
7517	XRCC3	NM_005432	AAGCCAAACTGAAATCGGTAA	CCGCTGTGAATTTGACAGCCA	GAGACACTTAAGGGAAATTAA	CAGAATTATTGCTGCAATTAA
7520	XRCC5	NM_021141	GACGATTTATTGGACATGATA	ACCCTCATAAGTCGTCACTAA	AAGCGAGTAACCAGCTCATAA	AAGCATAACTATGAGTGTTTA
7525	YES1	NM_005433	GAGGCTCCTGCTTATTTATAA	CCAGCCTACATTCACTTCTAA	AAGTATAATGCAGTACATTAA	AACAGTCAGTATGCAATCTTA
7529	YWHAB	NM_003404	AAGGTTTAATCTGATATCAAA	CTGCCGTTGTTCGGGACTTAA	CTGGATAATACCTTTAAGAAT	CAGCAATATGTTCACTATGTT
7533	YWHAH	NM_003405	ATCAAGATGGGTGATTATGAA	ATGGGTGATTATGAAATGCCA	TTCCATCAGCTTTATAATAAA	CAGGCTACAGTTGATATTTAA
7555	ZNF9	NM_003418	CAGCAAGACAAGTGAAGTCAA	AAGAGTTGAGTCAGACCAGTA	CTGACCTCAGTAGCTATTAAA	CACATAGATGGTGATGGCAAA
7559	ZNF12	NM_006956	CAGCAATGGATTATAGTTTAA	CTCGCAGAAGTCAGCACTTAA		
7567	ZNF19	NM_006961	CAGGCTATTGTAGCTATTATA	CACCAGTGAATCCATTCTCAA		
7579	ZNF31	NM_145238	CAGGGAAGTTATCTTGGTATA	ACCAGGTAATTTGGAAGTGAA		
7592	ZNF41	NM_007130	CAGCATATCCTGGGACATAAA	CACAGTGTATATGCAATTCTA		
7593	ZNF42	NM_003422	CCGCAGGTCCAGGTAGTGTAA	CTGGCGATTACATAAGTATAA		
7596	ZNF45	NM_003425	AACGAGATGATTTGCACTATA	CACCAAGATCAATGTATACAA		
7617	ZNF66	NM_001009883	CAGGATCAAATTCTCACATAA	CAGCATATAAACAGAACCAAA		
7620	ZNF69	NM_021915	AAGAAAGTCAATGAAATTAAA	CAGGCTGAACTTCCAGGAGAA		
7629	ZNF76	NM_003427	CCGCTCCTTCACCACATCTAA	CATGGATGAATGAGTATTTAA		
7634	ZNF80	NM_007136	CAGGGTTATATGCAATGTTCA	CTGGAGGAAGATGAGCCCTAA		
7675	ZNF121	NM_001008727	CACATTTGAATTCACACTGAA	TAGGAATTTCTCATACCATAA		
7681	MKRN3	NM_005664	CCAGTGGGACTTGCTTCATTA	TCCTGTTTAGCTTGACATGAA	AAGCCAGTAATTAGCATCTAA	GAGGACTTACAAAGCACTATA
7695	ZNF136	NM_003437	ATGCTTAATCTCACAAAGAAA	ATGGAAGGACCAGAACATTAA		
7705	ZNF146	NM_007145	CACGAATGAGGTTAACTTTAA	CTGGATTCATTTCCAATTAAA		
7707	ZNF148	NM_021964	CAGGAATGAATTCTCCACTAA	TCGGATGGCATAAGTGATTAA		
7712	ZNF157	NM_003446	CCGAATGAAGATGACTCTCAA	CAGGGTGAACATGCCAGCTAA		
7730	ZNF177	NM_003451	CCTGAGTACATTTATATTTAA	CTGGGTATAAGTAAGCAAGAA		
7739	ZNF185	NM_007150	CGCAATTATAATAAATGCTAA	CTCCCTGAACTTCACACATAA		
7743	ZNF189	NM_003452	AACACTAACATTATCCGTAAA	CTGCCAAGTATTGGAAATGAA		
7748	ZNF195	NM_007152	AAGACCTTTCATGAAATATAA	CACAAGAGTATTTCTTCTGAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
7750	ZNF198	NM_003453	ACGGGCGAGATATGAACTTAA	CGCCATGAAGTCAGCTTTAAA	CACGCTGGGTATTACCATGTA	ACGCTGGGTATTACCATGTAA
7756	ZNF207	NM_003457	CAGGTACATAAAGAAACAATA	CAGGAACTATTGGACATTTAT		
7780	SLC30A2	NM_001004434	AAGGGCTGTATTTGGGCCTAA	GAGAGGCTTCTTACTAGGTAA		
7799	PRDM2	NM_015866	CTGGCACTAATTTATAACTAT	CTACACGTAAGTATAAATGAA	CCCGGGTGATTGAGATCCAAA	CAGATGTATGTCTACACGTAA
7804	LRP8	NM_017522	TTGCGGAAAGGTAACCACAAA	CTGGACTGACTCGGGCAATAA	CCGGATGGTGTATGACTGGAT	CAGTACCTTACTCATCATTTA
7809	BSND	NM_057176	CTCGGTGTTTAGGCTGAACTA	CCAGATGAAAGTCATGAGCTA	CTGGACATGGACTCCAGTGAA	TGGGATGATATGGAGGTTCAA
7818	DAP3	NM_033657	CCCGAGGAATTAGCACTTGTT	CGGCACTGTGCCTACCTCTAA	TTGGCTCTGGACCTGCATTAA	TCGCTTTGTGATGCAGGTGAA
7837	D2S448	XM_056455	TACCTGCACTTTAATCAGATA	ACGGAACAAGTTACCACTACA	AACAACCGGATTACACATTTA	CAGGAGTGGAATGTACATATT
7857	SCG2	NM_003469	ATGACTGTGTTTAATAGTATA	CTGGATGAGAATAATACTCGA		
7862	BRPF1	NM_004634	CCGAAAGGTCTACAAGAGTTA	TCCCAAGTCAGGCAAACATAA	AAGGGAGACGATCAAGGTTCA	CAGCAACTGCCTCAAGTATAA
7866	IFRD2	NM_006764	CCGGATCTACGCTGCCTTCAA	ACGCTTTGAGAAGCACCTGTA		
7874	USP7	NM_003470	ATGGAGTTGCGTGGGATTCAA	CCCAAATTATTCCGCGGCAAA	CGGGCCGACACCAGTACATAA	CGAGTATGAAGTAAATTTGAA
7879	RAB7	NM_004637	AACGTTGATTTGCATAATACA	TCCCGTTAGATCAGCATTCTA	TAGATCAGCATTCTACTACAA	CACGTAGGCCTTCAACACAAT
7884	SLBP	NM_006527	TACGATCGTTATATTAAAGAA	ATCAGTTAATTTACCATGTAA		
7903	SIAT8D	NM_005668	ACGAGATGTGTCAGTGGTCAA	CACAATGTAGAAGGTTGGAAA		
7915	ALDH5A1	NM_001080	AAGAAAGACTCCGTAATCTTA	ACCCTCTTTCAAAGACAATAA	TTCGGAAGTGGTACAATTTAA	AAGGAGACTTATCTACATATA
7917	BAT3	NM_004639	CAGCGGTTGATCAACTTGGTA	ATGATGCACATGAACATTCAA	CCGGTTGCTGGAGTTGTGTAA	CAGCTCCGGTCTGATATACAA
7919	BAT1	NM_004640	CCAGGTGGTGATCTTTGTGAA	CTCAACCTCAAACACATTAAA		
7940	LST1	NM_007161	ATGGCTCACCCTTCCACCCAA	TTCAAATTGATCATCATCAAA		
7942	TFEB	NM_007162	CAGCAGCCACCTGAATGTGTA	GAGACGAAGGTTCAACATCAA	CCGCCTGGAGATGACCAACAA	AAGCAGGAGCTGCCTAGCGAA
7979	SHFM1	NM_006304	CCGGTAGACTTAGGTCTGTTA	AAGAAGTGTTGAAGTAACCTA		
7988	ZNF212	NM_012256	CAGAAACGTGATGGAGAGTAA	TAAGTAGAAGAAATAATTTAA		
7991	TUSC3	NM_006765	ACGGATGTTCATATTCGGGTT	CACGGCTATCCTTATAGTGAT	CAGGATTGAAATAAATGACAA	ATGGTAGCATTTAGTAATCTA
7993	D8S2298E	NM_005671	CGGGTGAAGCCTGGAAATTAA	AAGGATTGCTTTCTATATATA		
7994	MYST3	NM_006766	CGGCGCTATACTAATCCAATA	AAGTTGTTTCTTGACCACAAA	CTGGACTTCCGTAGTGACCAA	CAGCTGAATTTGCGACCTGTA
8000	PSCA	NM_005672	CCCAGCATTCTCCACCCTTAA	CCCAGTAAAGGCTGAGATGAA		
8021	NUP214	NM_005085	CCCGGAGATGATCCCAACAAA	CAGAGATATTTGTGAACTTTA		
8022	LHX3	NM_014564	CCCACAGATGTCTGTTGCCAA	CTGGCCTGTGTGTAAGTCAAA	CAGCTCTTTCCAAGACTTCAA	CTGCTATTTCTAGACATGAAA
8029	CUBN	NM_001081	CGGAACCATCTCTCACATTAA	CACCTATGTCATAGAGGCTAA	CAGCTGCAATTTGAAGATCGA	CCGGTTAGAATCCATGGACAA
8031	NCOA4	NM_005437	AAGAGAAGTGGTTATATCGAA	CCCACGTTAGTTCTACATTAT	CTGGTCAATAGTGATTACCAA	ACCGACTAAGCAAATAGGCAA
8048	CSRP3	NM_003476	ATGGGAGAGGCAATAAATAAA	AACGAGTTGCAGAGCATATAA		
8061	FOSL1	NM_005438	CTGGACAGTATCCCACATCCA	CACAATTTGCACTAAATCAGA	CCGAGTAAGGCGCGAGCGGAA	CCCACCTAGAACACTAACTCA
8065	CUL5	NM_003478	CTGGAGGACTTGATACCGGAA	CCAGCTGATTCAGTTAATATA	CAGGTTTGAATCAGTCACCTA	CAGCTGGTTATTGGAGTAAGA
8073	PTP4A2	NM_003479	AGGGACTGTGTTGCTTGTGAA	ATGCAACAATAGATTCCATTA	CAGAGAATGCTGGTAGCTTAA	AACAGCATACCTGCTAAGCTA
8085	MLL2	NM_003482	CTCGGAGTGGTTTGAGAACTA	CCCGTTGAGTCCCATAGGGAA	CGGCCGGAGTTTGTAATCAAA	CACCAGCATGTCTAAGGCATA
8111	GPR68	NM_003485	TAGAGCTTGAACCACCTTCTA	CAGGATGGCGGTGGAGAGACA	CCGCGTGTGCTTTGAGCACTA	CAGCGTGGTCATCTGGGCCAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
8131	C16orf35	NM_012075	CCCGGCGTCCCAGACAAGTAA	CAGACATGGGTTGATCACCTA		
8139	GAN	NM_022041	AACGTTGGCAATGAAAGATAT	CACCATAACATAGCTCCGAAA	ATCATGATGAATTGAAATGAA	CCGCACAGTCATGTAATTCAA
8153	ARHN	NM_005440	CAGGTTCCTCTTACTATGATA	CAGCTATTCTCACACATCTAA		
8175	SF3A2	NM_007165	CCCGGGCTACAAAGTGACCAA	CTGCCTGACACTTCACAACAA		
8178	ELL	NM_006532	CCGAAGTGCCATTGTCATCAA	AAGGAATTATGAAGCTAAGAA		
8190	MIA	NM_006533	CTCCTTGGGTTTATGCAAATA	CAGGGAGATTACTATGGAGAT		
8192	CLPP	NM_006012	CCGGGTGGCGTCATGCAGGTA	GCCCATCCACATGTACATCAA	CACGATGCAGTACATCCTCAA	GCCCAGGAGTTTGGCATCTTA
8200	GDF5	NM_000557	CACTATGGGACTGGATACAAA	CAGCTCCTTCCTGCTGAAGAA	CTGTTAGACTGTTAGATTTAA	TAGATTTAAATGTATATTGAT
8204	NRIP1	NM_003489	GCGGAGAAGAATGAGTATGAA	ATGGTTGACAGTGTCCGTAAA	AAGCGTGCTAACGATAAAGAA	AACCAACCCAATACTATATTA
8209	C21orf33	NM_004649	ACCACATTTATGGACCATGAA	CAGGAAGAAAGGGAAATTGCA		
8214	DGCR6	NM_005675	CAGAGAAATAAAGATGCCTCA	TGGCTTCTACGTGACCACCAA	CTGGGCAGAGTTCATCTTCTT	ACCCTAGGATAGTCTCATAAA
8237	USP11	NM_004651	CCCATTGAACGCAAGGTCATA	AAGGTCGAAGTGTACCCAGTA	ACCGATTCTATTGGCCTAGTA	CTGCGTCGGGTACGTGATGAA
8241	RBM10	NM_005676	CAGGACTATCGGACCGAGCAA	CCAGAAGGTGTCGATGCACTA	CTCCAACGTGCGCGTCATAAA	ACCACTCACTATCGACGGCAA
8243	SMC1L1	NM_006306	TCGGAAGTGAATGACAAGAAT	ATGGAGGAGATTCGTAAGAAA	CGGCGTATTGATGAAATCAAT	CACCATCACACTTTAATTCCA
8260	ARD1	NM_003491	CCGGGCCGCCCTGCACCTCTA	ACGAGCTTTCACAATAAATTT	CACAGAGAGCACAGATGTCAA	CCGCCCTGCACCTCTATTCCA
8266	UBL4	NM_014235	TCCCTTCTGTTCAGTAAACAA	CTGTTCAGTAAACAAACTGAA	CAGGGACACACTCGTGAGCAT	TAGGCTGTTTCTGATATCCAA
8270	DXS9879E	NM_006014	CTGGTTCTTAAATGTTTGTTA	CCGAATTTCCGTCATCAACTT		
8273	SLC10A3	NM_019848	CAGGGACAGCCCTGCCATCAA	ATCAAGAACGTGAGTGCTATA	GCGGAGAGACTTCTGCATCAA	CATGGTGTTAATGCAGGACAA
8284	SMCY	NM_004653	CTGACGATTGCTTAGCATTAA	CGCGTCCAAAGGCTAAATGAA	CCCAGAGACGTTGGATCTCAA	CAGGGTAGAAACGTTGAGAAT
8291	DYSF	NM_003494	CACCGTCAAGGTCATCGATAA	CCGGGATGAGCCCAACATGAA		
8292	COLQ	NM_005677	TCCAATGACTTTGGGAATTTA	AACAGCGTTCTTCCAATCTCA	AAGAAGCGTGGTGGCCACAAA	AAGGACAAATTCCTGCTACTA
8309	ACOX2	NM_003500	ATGGCATATATGCAACATTAA	CTGCCTATGAGGAATATATAA		
8312	AXIN1	NM_003502	CGGGAAAGGTGTTGGCATTAA	CTGGATACCTGCCGACCTTAA	CAGCATCGTTGTGGCGTACTA	CAGCTACAGATACTACTTCAA
8318	CDC45L	NM_003504	ACGGATCTCCTTTGAGTATGA	ATTGAAGAGTCTGCAAATAAA	TAGGCCAGTCAATGTCGTCAA	TACGAGCAGTATGAATATCAT
8322	FZD4	NM_012193	ATGGTGCTTAATGAATCTCCA	CTGGAGAGAGTTGCTATTCCA	TAGGTGATCGATACTTGTCAA	CAGAATGATAGTGCCTTTAAA
8339	HIST1H2BG	NM_003518	CTCCAAGTAAATGTGTGCTTA	GCCACTCAAGTCTCACATAAA		
8340	HIST1H2BL	NM_003519	TTGCCACTATTGTTTCATTAT	CAAGCTCTTGTCCAACCCAAA		
8341	HIST1H2BN	NM_003520	CAAGGCCATGGGCATCATGAA	TTCGGTCAGTCTCGGCCCACA		
8347	HIST1H2BC	NM_003526	TAACGACATATTTGAGCGCAT	CCAAGTAAACATTCCAAGTAA		
8356	HIST1H3J	NM_003535	CTGCTCTATCTTGGGTTTCTT	ATCCGTGGCGAGCGAGCATAA		
8370	HIST2H4	NM_003548	CCGCAAGGTCTTGAGAGACAA	GCGGATCTCTGGCCTCATTTA		
8379	MAD1L1	NM_003550	CAGCTGGACCTGCAACACAAA	CAGGACCAAAGTGCTGCACAT	CAGGCGACTGCTCATCTTCAA	CAGCGATTGTGAAGAACATGA
8382	NME5	NM_003551	GAGGAGATACAAGATATTATT	CTCGAAAGAACAAATCATGAA	CATGATATTAGCTAGACATAA	ATGATATTAGCTAGACATAAA
8392	OR3A3	NM_012373	CAGGTGTCTTCAGCTACATGA	TGGAATCTTCAGACAAGGATA	CTGGGTTCAGTGGAATCTTCA	CAGGGCGCTCTGTGTCAGCTA
8396	PIP5K2B	NM_003559	CACGCGTTTCCTCACCACCTA	CCCATTTGACACCCAGGTTAA	CCGCTTTAAGTTTAAGGAGTA	CACGCCATACGATACAAAGAA
8417	STX7	NM_003569	CAGCAGATTATCAGCGCAAAT	TTGCTGTAGATTGCCTAGTAA	CAGCAGTATACTAACCAGCTT	TCTGATGAAATTAGCGAATAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
8419	BFSP2	NM_003571	CAGGGTGTGAGCTGGAACAAA	CAGGCTGAGACAGAATCCTTA		
8425	LTBP4	NM_003573	AACCGGCTTTGAAAGAGTTAA	ACACGTGATCTCAGAGGCCAA	GCGGCTGGAGTGCATCGATAA	TACGAGTACGGCCCAGACTTA
8435	SOAT2	NM_003578	CAGGTTAGGTTCCTGATGAAA	CAGGTGGAATTATGTGGCCAA		
8438	RAD54L	NM_003579	CGCGCGCTTTGGGAACAGGAA	CTCGCTAAAGAAGCTTTGTAA	ATGGAGGATCTAAGGATGAAA	AAGCATTTATTCGAAGCATTT
8440	NCK2	NM_001004720	ATCTCACAATTATGTATTTAA	GACACTAATACAGATGATTAA	TAGCCGTTTGTTGACACTAAT	TCGGCTTGTTTGAATCTCACA
8446	DUSP11	NM_003584	ATGATGCAATTGAATTATTCA	CACAATAAGCCTGTTAAACAA	CCCTTATGTATTCAAGCTTAA	CAGAAACTGTTCCTTACTTAA
8448	DOC2A	NM_003586	CACGAGTGTGTTGCACGTTTA	GCGGAGTTCTATATTCACATA		
8456	FOXN1	NM_003593	TCCCGTCAGCGAGATCTACAA	CAGCGTTTGCCTGGTCTGGAA	CGGGCTCACCTTAAAGGTCAA	CACACAAATTATTCAGATGTA
8459	TPST2	NM_001008566	CAGATTTGCCATCCTCCTTAA	AAGCATATTGCTTGCTATTAA		
8460	TPST1	NM_003596	AAGATATGCCTTTAATATTTA	GAGGCTGGTGTTACTGATGAA		
8468	FKBP6	NM_003602	CAGGCTTTGATCATTGACCAA	CAGGTTTCTGTTCAAACCGAA		
8476	CDC42BPA	NM_003607	ACGGCTTTCATTACCAAATAA	TCGGAAAGATATACCCTGTAT	CAGATAATAGTCGGAAACAAA	CAGACTTTCCGTAGCAGCTTA
8481	OFD1	NM_003611	CCGCCCGGGCTGGGCACTAAA	CTCAGACAAGTTCGACATTTA	CCCAGTCTTTGGCAATAACAA	TACCATCGGAGAGTCATTAAA
8493	PPM1D	NM_003620	TACATGGAGGACGTTACTCAA	ATGGCCAAGGGTGAATTCTAA	CTCGGCGTCGTCGAAGATAAA	ACGGGTCTTCCTAGCACATCA
8498	RANBP3	NM_003624	AACGAACTATTTCCTCCAGTA	CAGAGTTAAGCTGATAAATGA		
8499	PPFIA2	NM_003625	ACCGATGAAACTAGTCAAATA	TCCAATGAACGCCTACAACTA	TACCAGCTGGATTTAGGTTAA	AACGTTTGGGTGACTCATGAA
8504	PEX3	NM_003630	GCGGGTCCAGTTAAACATAAT	CGAGACATTACCACTATTAAA	TGGGTAAATCACCTATACTTA	ATGGTGAATTCCAACAACTAT
8507	ENC1	NM_003633	AAAGGCATTGTCCAAAGTTTA	CACCTTAGTACTTTAGACTAA	CAGCGGCTCCATTAACATCTA	ACGGCATGTATCACAGATGTA
8511	MMP23A	NM_004659	CGGCCAGAAGATCCTCCACAA	CCAGAAGATCCTCCACAAGAA	CCGGGCGCTCATGCACCTGAA	CAGAAGATCCTCCACAAGAAA
8513	LIPF	NM_004190	CAGCTTTGATGAAATGGCTAA	CACAATCGACTTCATTGTAAA	CAGCAATGCCTTATTTATAAT	CAGGCTGTTAAGTCTGGGAAA
8517	IKBKG	NM_003639	GAGGAGCTTCTGCATTTCCAA	ACCATAAATAATGGCATAGTA	TTCGGAAATGCCTCACATATA	CTCCTCTAGTTCAGAGACATA
8518	IKBKAP	NM_003640	ACTGGATATTATAGAAACCAA	AGCATGGTAACTTATATTGAA	GCGGTTTACTATAGACAAATA	CAGCGGTTTACTATAGACAAA
8520	HAT1	NM_003642	CACGCTAGAAGGGTTTATGAA	AAGACTAATTAGCCCATATAA	CCCTTCTTAAACAGTATAATA	TACCGGCGTGTTATTGAACGA
8526	DGKE	NM_003647	ATCCATTAATCAGATGCGTAA	CTAGATCGATGGAAAGTTCAA	CTGGAAGTCGTTGGAGTATAT	ATCGATGGAAAGTTCAAGTAA
8532	CPZ	NM_003652	CGCGCAGAACCTGGATCTGAA	CCCGGAGACAAAGGCAATCAT	CCGGATCTCAGTCAAAGGCAT	TACGCCAAAGTCATCAAGAAA
8535	CBX4	NM_003655	CAGCCCGAGGTCATCCTGCTA	CTGCCTCACCGTTACTTTCAA	GAGGCTGGTCGCCCAAATATA	AAGCCCTTCTTTGGGAATATA
8536	CAMK1	NM_003656	CAGCCTGGATGAAGACTCCAA	CAGGAGATACAGCTCTAGATA	CTGCATGACCTGGGCATTGTA	CAGGTGCTGGATGCTGTGAAA
8539	API5	NM_006595	CTCGAGTGGCAGATATACTAA	CCGACCTAGAACAGACCTTCA	CAAGTTTGCTATTCAAATCAA	AAGAGTAATGGTCAATCTTAA
8541	PPFIA3	NM_003660	CTGGTGGACGCTCGAATGTTA	TCGAATGTTAGATCACCTTAA	CACGGGTAAAGAGAACTGTTT	ACGGCTCAACTATGACCGGAA
8542	APOL1	NM_003661	CTGGACAACCTTGCAAGACAA	CAGGTGGAGAGGGTTAATGAA		
8543	LMO4	NM_006769	ATGGTGTATTTAAATAATAAA	ATGACTGAATATGAACATTAA		
8555	CDC14B	NM_003671	CCAAATAATGTCGGCTTACAA	CAGAATTGATGTGCTGCTAAA	CCGTACAGTGATGATGACGAA	CAAGATCAGCAAGAACCCGAA
8559	PRPF18	NM_003675	AACGGATATTATTAAATTCAT	CAGAATGATCTGAAAGTTCAT		
8564	KMO	NM_003679	TAGTGTTCTGCTTATAATTAA	CAGAGTTACCCTCTAAAGATA	AAGGCTATTAATATCATACTA	TGGGTACAACATCGAATAATA
8566	PDXK	NM_003681	CCCTGTATTAAGCAAGAATTA	CCCGGGCATGTTCGTCTCTCA	TCGAGTGACTTTCTAACCCAA	CCGGAGCTTCATCTAGTGATT
8567	MADD	NM_003682	CCAGGAAATGATCGACAGGTA	CTCAACAAGTTCTATACTAAA	CAGGAGGGCGTTAGTGGATCA	CAGACCCACTACTATAGTAAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
8568	D21S2056E	NM_003683	CAGGGAATTCAGCTCCAGTAA	TCCGAGCAGTGTGGTGGTTTA		
8600	TNFSF11	NM_003701	ATCCATGCTCTTGACCTTGTA	CAGCGTCGCCCTGTTCTTCTA	CAGATGGATCCTAATAGAATA	ACGGGTTGACCTTATGAGAAA
8601	RGS20	NM_003702	TAGCATGTTGTCAGTGGCCAA	TCGGTTTGAATACGTCACTTA	CACATATTCGATGATGCTCAA	CTGCTATATATTCACCATGTA
8612	PPAP2C	NM_177543	CATGGTGTTCTTGGCGCTGTA	ACCCGCGTGTCTGATTACAAA	TCGCTCGGACTTCAACAACTA	CCGGGTCAACTGCTCGGTCTA
8620	NPFF	NM_003717	TTGGGAAGAAGTGACATGTCA	TCCGCGGAGGAAGACAGCGAA	CCCAGAGGTTTGGCAGAAATA	CAGGGATCCTGGAGGAATGAA
8635	RNASET2	NM_003730	CCGGATTACTGGACAATACAT	CAGGATGAGGAAGTACAGACA		
8638	OASL	NM_003733	GCGGGTGCTGAAGGTAGTCAA	CAAGTACTACACACTCCACAA	CAGGTGCTCCTTAGCCAAATA	CAGCTGGAATTCCAAGGCCAA
8642	DCHS1	NM_003737	CACGGTATTGCTACCACCAAA	CTGGTGTTGCTTGAACCTCTA		
8644	AKR1C3	NM_003739	TAGAATGTCATCCGTATTTCA	CCGGAGTAAATTGCTAGATTT	CTGGGATCTCAACGAGACAAA	CACCCTAATTATCCATATTCA
8649	MAP2K1IP1	NM_021970	AAGAGCTAGCATATAGATGTA	TTGCATTGAGTGAGGAACATA	TAGCATATAGATGTAATTTAT	ATGCCCAGGCTTGCAGAATAA
8651	SOCS1	NM_003745	CTGTAGGATGGTAGCACACAA	TAGGATGGTAGCACACAACCA	CCCGCCGTGCACGCAGCATTA	CTGGTTGTTGTAGCAGCTTAA
8654	PDE5A	NM_001083	TCGGTTCAATGCAGAAGTTGA	AACAACAATCATTAGAAGTAA	TCGGATGTTTACTGACCTCAA	CAGAGATGGTGTGTTCTGCAA
8659	ALDH4A1	NM_003748	CCGGAAAGAGTGGGACCTGAA	CAGGGTAAGACCGTGATCCAA	CAACTTCTACATCAACGACAA	CAGGGTAAAGTGTAACTCAGA
8661	EIF3S10	NM_003750	GAGGATCTAGATAATATTCAA	CAGGAACATGAACAAATCAAA		
8663	EIF3S8	NM_003752	ACCGTGATTTCGAGTCCCATA	GGGCGTCATTGTCAAGATCAA	AACGAATGGATGAAGAATTTA	CCGCCGACGCATGATCAGCAA
8664	EIF3S7	NM_003753	TCGGAACATGTTGCAGTTCAA	CCGCCAAGTTTCAGTGATGAA		
8665	EIF3S5	NM_003754	CGGAGTTGACCTGATCATGAA	CACAATGAGTCAGAAGATGAA	CCGCATGAGCATCAAAGCCTA	TACGCGTACTACGACACTGAA
8666	EIF3S4	NM_003755	CACGCAGAACAAGACAGGGAA	GAGGTCATCAACGGAAACATA		
8668	EIF3S2	NM_003757	CAGATTAAGTATAACCGCGAA	AAGAAATAAATTGGTTTGGTA		
8673	VAMP8	NM_003761	CTGGTGCCTTCTCTTAAGTAA	AAGACCTTTCAGTATCCCTAA		
8675	STX16	NM_001001433	CTGGGATCAGTTATAATATAT	TCCAACGTAATTGGTCAGATA	ACCATCATTGATGTTAATTAA	CCGGATTAAGCAGAAGATGAA
8685	MARCO	NM_006770	CAGGACTTTGGCCATCTATAA	CCCAGGGATGTTCAGAATCAA	CAGGATTGTCGGCAGTAGTAA	CTGAAGTTTACTACAGTGGTA
8688	KRTHA7	NM_003770	CTGCATTAAATGGTCAATAAA	CCAGTGTTTCAGAATCTCCAA		
8692	HYAL2	NM_003773	TCCCTTGCCCTAGATAGTTTA	AAGGGCTCTCTTAGGCATGTA	CTGCCAGTACCTCAAAGATTA	AAAGATGTGTATCGCCGGTTA
8697	CDC23	NM_004661	CTGCAATAGCAAGAAAGCCTA	TAGGGACAGCTTGTATAATTA	TACGAGAAACTCAATCAACTA	ACCCATCTTAATTAAGCCTTA
8698	EDG6	NM_003775	TTGAAGTTCGATCATGGTAAA	CCGGCTCATTGTTCTGCACTA	CCGGAGCTTCCACCACCGACA	CAGCCGGCTCATTGTTCTGCA
8701	DNAH11	NM_003777	CACCGTCAAATGAAAGGATAA	CAGGTGGCTGTTAACATCTTA	GAGCTTGTTAACCATAATTAA	TACGTTGTACACGCTTTGCAA
8702	B4GALT4	NM_003778	CACAGTGAACTTGGGAATGAA	TACATATTAACTAATAATAAA		
8704	B4GALT2	NM_001005417	CCCATGGATGACCGCAACCTA	CAGAGGTTTACCAAGATTCAA		
8707	B3GALT2	NM_003783	ATGGAAGTATTTACAATGAAA	AACCGTGGATTTCATATTATA		
8708	B3GALT1	NM_020981	CAGAGTTAAGAGGAAGATTTA	CACACTGGATGTGATTATTAA		
8711	TNK1	NM_003985	AAAGAGCTACTATACATCATA	CCCTATTACATACATCTTTCA	ATCGGTCATGATGAACTTGGA	AAGGATCTAGTCTGCCCACTA
8717	TRADD	NM_003789	CAGGGTCAGCCTGTAGTGAAT	CCGAATGTTAAGCAATGATAA	CCCGAATGTTAAGCAATGATA	AGCAATGATAATAAAGTATAA
8718	TNFRSF25	NM_003790	GAGAACCACCATAATTCTGAA	CACAAGAAGATTGGTCTGTTT	CACCGTCCAGTTGGTGGGTAA	CGCGGTATTAAATCTGTGAAA
8720	MBTPS1	NM_003791	CACAGGAAGAATTGTAGATAA	CAGAACGGAGACAACATTGAA	CAGAACAGACTTCAACAGTAA	CAGGGATAATTTAAGGATGAA
8721	EDF1	NM_003792	CGGACGGGCCATACCCAATAA	CTAGGGCGAAATGAACACAAA	CAGAAGGACCTGGCCACGAAA	CACGGTGACGGTGCTGCGCAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
8722	CTSF	NM_003793	CCTGTCCGTCTTTGTCAATAA	CGGACATATGAGTCAAAGGAA	CACCTTTGTTGAATTGTGGTA	CCCAATCTCCGTGGCCATCAA
8723	SNX4	NM_003794	AACATTATGCAGATCAGTTAA	TACCTAGTATACATAAACATA	CCCATCCTTTGTAGAGACAAA	CTCGTTATTTCTAATGATGTA
8724	SNX3	NM_003795	ACCCTTCACATGGAAGATTAA	CAAGATGAAATAATAGATAAA		
8725	C19orf2	NM_003796	AAAGAGGGTTTCAAAGTTTAA	CTGGAAAGAATACCACTTTAA		
8726	EED	NM_003797	AAGGAATCTTATGATTATAAT	AAGCAACAGAGTTACCTTGTA	AGGCATAATTAGGATAATAAA	CTGAACGCCCTGATACACCTA
8727	CTNNAL1	NM_003798	CTGCAGAGGGTTTAAAGCTTA	CGGATGGGTCTCAGTTACAAA	ACGCTTATTAATCATAAAGAT	AAGCTTGGGAATCCCAAATTA
8729	GBF1	NM_004193	AAGAATATTTACATCATTCAA	ACGGGAACTAATTGAAATTAA		
8731	RNMT	NM_003799	CTGGTCTTAATTAACAGGTAA	CAGGGTGACTCTCCAAAGAAA		
8736	MYOM1	NM_003803	CACCAACTAATGACACTTTAA	CAGGTCTTTCACTCATATAAA		
8739	HRK	NM_003806	AGCGAGCAACAGGTTGGTGAA	ATACAGCTCTATATATATAAA	CGAGAAGGAAGTGGAGAGTAA	AGCGATCGTAGAAACACAGAA
8747	ADAM21	NM_003813	TACCACAAACATTGTCATTAA	CAGGAATATGTCGTCCACCTA		
8767	RIPK2	NM_003821	CAGGGACTTGATCATGAAAGA	CCAGGCTTAATTGCCCTACAA	CACAAGGACATCGACCTGTTA	ACGTATGATCTCTCTAATAGA
8772	FADD	NM_003824	TCCTAAGGTAATCCTATTAAA	CAGGACGAATTGAGATAATAT	CAGCGGGATCTCGTATCTTTA	AGCGGGATCTCGTATCTTTAA
8773	SNAP23	NM_003825	AAGAGGTTGTTACCTCAGTAA	TACCACATGAATTCAGATTTA	CAGGCCTATTAACATCATACA	CTGGCAAGGCTTATAAGACAA
8775	NAPA	NM_003827	CCGGGAATGCAAGTTGATGAA	CACCGAGTCGGTGAAGGAATA		
8778	SIGLEC5	NM_003830	TTGTGGCAATGTTAACATTAA	CTCGGAGATCAAGACAAGCAA	AAAGGTTGTTGTGAACATTAA	CAGGAACGGCATAGCCCTAGA
8784	TNFRSF18	NM_004195	CAGCAGAAGTGGGTGCAGGAA	CCCTGGGAACAAGACCCACAA	TCGGGATTCTCAGGTCATGAA	CAGGAGGGAGAGAGAGACACA
8787	RGS9	NM_003835	AAGCTATTGACCCTCAGGAAA	AACGATGGGCCTTCAACTTCA	CAAATAGGTGTTTGAACTGTA	CTGACACCAGTTTCAAATTTA
8792	TNFRSF11A	NM_003839	CCCAGTGTGTGTTCATTGTAA	TAAGTTTGTGTCGTTCCTTAA	CCCGCTAGGTGGTTAATTTAT	ACCCGCTAGGTGGTTAATTTA
8797	TNFRSF10A	NM_003844	CAGGAACTTTCCGGAATGACA	CAGGCAATGGACATAATATAT	CCGGGTCCACAAGACCTTCAA	ATCAAACTTCATGATCAATCA
8798	DYRK4	NM_003845	ACACGGCTCCTGAGAAATTTA	CAGATGCTTTCGGTAGAGAAA	CTGCATCACGGCGGAGTTGTA	CTCCATATGAACAAAGTGAAA
8802	SUCLG1	NM_003849	CAACATCTCTATGTTGATAAA	ATGGATCACGTAGACATGTAA		
8807	IL18RAP	NM_003853	AGCGGTAACCTGGTACAAGAA	ATCGTAGTGGATGAAGTTTAT	CCCAGTATCTTTGAACTACAA	CCCAGCCTAAGGAATGGTGAA
8808	IL1RL2	NM_003854	CAGGAGTCTACCAATGTGTTA	TAGGTGGTTTACCAAATTTAT	TGGGTCCAATAAAGTGGTATA	AAGGACTGTAACGAGATTAAA
8809	IL18R1	NM_003855	CGAGAAGAGATGAAACATTAA	CCGAGTCTTAATCTTCAGAAA	AAGAGTGAGATTGTCAGTGTA	TTGCTATTGCATAGTCTCTAA
8811	GALR2	NM_003857	CTGCACCTTCGTCTTCAGCTA	GACGGTTGATGTGGCCTGAAA	TACCAACCTGTTCATCCTTAA	CCCGCTCACGCGCGCCACTTA
8812	CCNK	NM_003858	CAGCCATATTGGCTCAATAAA	CTCAATAAATAGCTTCGGTAA	ATCCTGGATCTTTACTCACAA	AAGCAACTCAAAGGTGATAAA
8816	WDR22	NM_003861	CTGGTTAACTTGAGAAGCCAA	TAGAATTACTTTGGATTTGTA		
8818	DPM2	NM_003863	TAGCCTGATCATCTTCACCTA	CAGCATGTCATCCACAAGTAT		
8821	INPP4B	NM_003866	CTCCATAGATTTGAAACAGAA	ATCGATGTCAGTGACACTTGA	CCCGGAAAGTGTGAGCGGAAA	AACGATTTGCCGCAAACTGAA
8822	FGF17	NM_003867	CTGGAGGTGGCTGTCCTCAAA	CTGCTGATTCTCTGCTGTCAA		
8828	NRP2	NM_003872	CGCAAGTACTGTGGACAAGAA	CTGGTCTGTCATAAGACAGAA	CTCGTGATATTTGTAGGATAA	CAGGCTCTGAAGATTGCTCAA
8831	SYNGAP1	NM_006772	CAGAGCAGTGGTACCCTGTAA	ACGAACGAAGTCACAACCCAA	CCCGGCTGATGCAAAGCTTTA	ACGCTTGCCACTAAAGCCATA
8832	CD84	NM_003874	CTGGGACTTCAAGCTATGAAA	ACCCACAGAAATTATTATGAA	CTCAGAAATCTTCACAGTGAA	CAGAATGTGGGCTGCATATAA
8836	GGH	NM_003878	ATGCCGTAATAAAGTCATGAA	AAGCATTGATTTATCAGTTCA	TCAGTCCAATTTATACTGGAA	CTGGCTCTGATTCTTCATTAT
8848	TGFB1I4	NM_006022	AACTTTCAATAAAGCATATAA	CTCACTTTGTGTAATCTGAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
8851	CDK5R1	NM_003885	CACATGCACTACTGAAATTTA	CTGGTCATCAGTATTGTGTAA	TGAGCTGGTTTGACTCATTAA	CCGGAAGGCCACGCTGTTTGA
8852	AKAP4	NM_003886	CTGCCTTATCATGGCTAAGTA	CAAGACTCTCTTGGACATGAA	TACAGTGTCTATGCCGATCAA	GTCGGTGAACACATTCTCAAA
8875	VNN2	NM_004665	TGGGCGTTTGGTAAACAAGAA	ATGGCTACTTTCAATACAATA	AGGAGCTTTGCTGTCATTTAA	CAGCAATAACTTACCTGCTAA
8881	CDC16	NM_003903	AAAGAACTTCTTGAATCACTA	TAGAATATGGTTTGACCAATA	CCCATGCACTTCGGTCACGAA	ATAGTGGAATAAAGAAGGTAA
8882	ZNF259	NM_003904	GAGGAAGATCTCAGAAATGAA	CTGGAGGACATGAACAGAGAA		
8883	APPBP1	NM_003905	CAGGTATTGGTTCGTTTACAA	ATGGATTGTGATCATAGCTAA		
8888	MCM3AP	NM_003906	CAGGAGCATTTACGGATTTAA	CTGAGTGAAGATGGTCAGATA		
8893	EIF2B5	NM_003907	CTTGTATATGTTAATATTAAA	CAAAGTGAAGATGAAAGGTTA		
8896	G10	NM_003910	ATGAGAGAAGCTGAAACAGAA	CAGCAGAGAACTCTATGAATA		
8900	CCNA1	NM_003914	CAAGCAAGGGTTTGACATCTA	AAGCAATTAGGGAGAAGTACA	TTCGAAATATGAAGAGATATA	CACCGATGATACATACACAAA
8905	AP1S2	NM_003916	ATGGCATTAGATGGCTCTATA	ATGGCACATCATATACATGTA	AAGGGAACTTTAGTTAATTAA	CAGGCAGTATACATTTATTAA
8906	AP1G2	NM_003917	CCGCCAGGTGGTGTCCATCTA	CCCACAAATAAAGCCCAATAA		
8910	SGCE	NM_003919	CAGGTAAATGGTATCCCTGAA	TAACATTTAATACAAATTTAA		
8914	TIMELESS	NM_003920	CCGGCTCATGGGATCAGTAAA	CAGCCGCATCATCAAGAACAA		
8926	SNURF	NM_005678	GAGGTGGAAGTCCAAGTCAAA	CAAGAGGTGGTTAAAGCCATA		
8932	MBD2	NM_003927	ACCCTTCAGGTGTTACTAGAA	CTCGCGAGTGTAACTTTCATA	TGGAAAGATGATGCCTAGTAA	AAGATGATGCCTAGTAAATTA
8936	WASF1	NM_003931	TACACTCAGAAAGTACATTTA	TTGCTTGCCTATAGGAGTTAA	GCCCTATAACCGATTAATTAA	CAAGAACGTGTGGACCGTTTA
8938	BAIAP3	NM_003933	CTCGCCTGACTCCATCCAGAA	CAGCCAGAGGACCCAGGTGAA	GTCGACCTTGCTGGACATTAA	TGGGATCATGACGACGATGTA
8940	TOP3B	NM_003935	CACGGAGAAGAAAGAAGCTAA	CACGGACACAGACATCTGTAA		
8942	KYNU	NM_003937	CCACATGTAACTAACAATAAA	CAGATTTAAGATGGATAACAA		
8945	BTRC	NM_003939	CTGGTTTCAGGTGGAACTTAA	CTGGAGGCAGATGACATCTAA	CTGGGCTAGAATAAATGTAAA	CAGGATGAGCAACAACAGTAA
8972	MGAM	NM_004668	TCGGCATGATATGAATTGGAA	CTGGCCCATATTTAACAGAGA	CCCAATGGAAACGGAACTAAT	TGGGAGGAATAATATACCTAA
8976	WASL	NM_003941	ATGCTACATATGAATGTTGAA	CACATTGAGTAATATGCATAA	CAGATACGACAGGGTATCCAA	AACCTTAATGTAATTTACTTA
8986	RPS6KA4	NM_003942	CGGCCAGGAGTTCGCAGTCAA	AAGGAGATAGGTGGCTCCTAA	CGCCACCTTCATGGCATTCAA	CAGGCTGTGCCTTTGACTTTA
8989	TRPA1	NM_007332	CAGTAGACAGTTGCACATTAA	CCACGAATTCATATCTAATAA	CACGAATTCATATCTAATAAA	CTGGTTCTAACTTTCAATTTA
8992	ATP6V0E	NM_003945	AACGTTAACAGCACATTTGAA	AACCCTCTCTTTGGACCGCAA		
8993	PGLYRP1	NM_005091	CTGGTGCGACGTGGGCTACAA	CAGCTTCATGGGCAACTACAT	TGGCATCAGCTTCATGGGCAA	GAGGTCCAACTATGTGCTCAA
8996	NOL3	NM_003946	CCCAGTACCGCTGGAAGTGAA	ACCCTGGAGATCCCAAACCTA		
8999	CDKL2	NM_003948	TGCGAGAAATCAAGTTACTAA	TCAGGCATTTATAACATTAAT	TTCTACGGACTTTAAATTAAA	ATGATGTGTTTAGGTAATCTA
9002	F2RL3	NM_003950	CAGGCTGGTGCCCGCCCTCTA	ACGCGTGAAACACAGAAGAAA	CACATTCACGATACTGTGCAA	AAGGCTGTACTGGGTCGAACA
9015	TAF1A	NM_005681	AAGCAAGATCACCAAATCTTA	CCGGATGCACTAAGAATATAA		
9019	MPZL1	NM_024569	CTGGTTGCAGATAACGAACTA	CCAGTCATATATGCACAGTTA	CACCTTCTTTATAAAGCGTCA	AAGGCATTACTTAGAGATTGA
9025	RNF8	NM_003958	CAGCCTGTGATAGGCATTCAA	ATGGACAATTATGGACAACAA		
9026	HIP1R	NM_003959	CTCCGACATGCTGTACTTCAA	AAGTGTTCTGTTGGCAATAAA		
9028	RHBDL1	NM_003961	CCGCTGGTACTTCTACCGTCA	TGGGATGAGATGTCCCTACAA		
9038	PNR	NM_003967	CAGGCTCAGCAGATTACCACA	CCCACTGGTCTTTGACATCTT	CTGCCTCATTATGATCAGCTT	CACCATAGACACGATGGTCGA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
9045	RPL14	NM_003973	CAGATTGATAGTAGGATTATA	CACCAGAAGTATGTCCGACAA		
9046	DOK2	NM_201349	TGGGTGAGTCACCATCCCAAA	GACAATGTTGTACTAAAGAAA	CAGCAGACGTTTGGAAAGAAA	CAGATTTCTTGGTGGCATTAA
9048	ARTN	NM_057090	CTGGTGTTGATAGAGATGGAA	CCGGTGGGTGATGGATATCAT	CCCGAACAGGTGAAGGGACAA	CAGCATTTGAAGGACACATAT
9050	PSTPIP2	NM_024430	ACGAATAAACTTCTTCCGGAA	CTCAGTGGTGCAAGATTTAAA	CCGGCTAGTGCTTCTGTGATA	CCACGTTATGTCAGCAATGAA
9053	MAP7	NM_003980	AAGCTGTTGTACGGCGCACAA	AAGGGCTGTATCTCCATCTAA	GTGCTCCTTCTTAGCAATCAA	CAGGCATATGGTCTTTAGTAA
9056	SLC7A7	NM_003982	CCCTTCTTGCTTAAATCCATA	ATCAGATATTTGGAATATTTA	TAGAGAGACATGAAACTATCA	CAGGTGCTGGATGACAATAAA
9064	MAP3K6	NM_004672	CAGGAACTGAATGTGGATTCA	TACCAGACAAAGCGTATTAAA	TCAGAGGAGCTGAGTAATGAA	CACCATCCAAATGCTGTTGAA
9068	ANGPTL1	NM_004673	GAGGCGGGTCATACTCCTTAA	CAGAAAGTTTGGACAGCTTTA	CTCGTGTTACTCAACTCTATA	CGGGAGATAGATGTTCTGCAA
9075	CLDN2	NM_020384	AAGGCTAAGGGCTATAGACAA	CCAGACTAATTTGTGCATGAA		
9081	PRY	NM_004676	AAGGACTCAGAGAGACATGAA	AAGAAGGATCTTAAAGACTCA		
9086	EIF1AY	NM_004681	TTGGCTTTCATGAACAAGTAA	ACCATAATATTTGCTGTTAAA		
9088	PKMYT1	NM_004203	CTCCTACGGAGAGGTCTTCAA	CTGCCTGGCCGTGTCTAATAA	CTGGGAGGAACTTACCGTCTA	CCGGCCAGAGTCCTTCTTCCA
9091	PIGQ	NM_004204	ACGCTGCTGTGTGCTCCTGAA	CAGGTGTTGCTGTCACAGCTA		
9092	SART1	NM_005146	CTCAACCTTCATATTAAATAA	CCCGTGTACAGTGACCCAGAA		
9096	TBX18	XM_496819	TCGCCTGAAGATAGATAGGAA	CAGCAATGCCTTCGCCACTAA		
9101	USP8	NM_005154	CACGGAAAGAAGCACTTGTAA	AAGGCTCGTATTCATGCAGAA	CAGGTTCAGGCAAGCCATTTA	CAGGGTCAATTCAAATCTACA
9110	MTMR4	NM_004687	CCGGCTGCATATCAAATTCAA	AAGAGTGGCTCTCACGGCTAA	TTGCCATAGATGTAACCTAAA	TCGGCACTGGAGAGTACCAAA
9114	ATP6V0D1	NM_004691	CACTTTCATGTTCCTCCCTAA	CCGCGCCTTCATCATCACCAT		
9118	INA	NM_032727	CAGCTAAATAATCTTACTCTA	CAGCCTATTCCTGAACTATAA		
9126	CSPG6	NM_005445	AACCGGTTACCAATCGATAAA	TACCCAGGAACTGTAAATTTA	GAGGACTAAGTTGGAGCTTAA	ATGGAGGATATCGAACGCCAA
9132	KCNQ4	NM_004700	GACGATTACATTGACAACCAT	CTGGTACTACTATGACAGTAT	CGGGCATCTCTGAGACTCAAA	CCGCTCCATCAGGATTCTCAA
9136	RNU3IP2	NM_004704	CTGGAGGAAACTGCACAGGAA	CACTCTTATCCTCCTTATTTA		
9138	ARHGEF1	NM_004706	CAGCAGCTCTGAGAACGGCAA	TCGGAAAGTGCTGTCCCTGAA		
9140	APG12L	NM_004707	ATGGTATGTAGTAGAATTCAA	CAGCTTCGATTTGAATGACTA		
9141	PDCD5	NM_004708	CAGAACAAGGTTTAATAGAAA	CAAGTCTAGGACAGAAGTTAA		
9146	HGS	NM_004712	TACGAGCAGCTGAACAGGAAA	CACGTCCGGAGTAACACTACA	GCACGTCTTTCCAGAATTCAA	CCGGAACGAGCCCAAGTACAA
9149	DYRK1B	NM_004714	ACGGAGATGAAGTACTATATA	CTCGCTGAACCTGACCCGGAA	CCGGACCTACCGCTACAGCAA	CACGGAGATGAAGTACTATAT
9150	CTDP1	NM_004715	CCGAATATTATCAAGGGATGA	CCCGACAAACTTCCCGATAGA	CTCCATGGTTTGCATTATTGA	CCGGCTGTACGCACACACCAT
9156	EXO1	NM_003686	GAACGAGTGATTAGTACTAAA	AGGGTTAAATCTCCCAAGGAA	CAGATGTAGCACGTAATTCAA	ATGGATGTACTTTACCTTCTA
9159	PCSK7	NM_004716	CAAGCGCAGCGTCCACTTCAA	TAGCTATGACCTCAACTCTAA	ATGCCTTTCTATGCAGAAGAA	TCGGAGCATTGTGACCACTGA
9169	SFRS2IP	NM_004719	CACGAGGAAATGATCGGTACA	ATGGTTCTCAGCTACCTATAA	CTGGACAGGATTCTAGCCTAA	AAGGAGGTGATCCATTGGAAA
9170	EDG4	NM_004720	CTACCTGAGTCTGATTCTTTA	AAACCTTTCTTTACACTCTAA	GACCATCGGCTTCTTCTATAA	CCCGCGAGTCTGTCCACTATA
9181	ARHGEF2	NM_004723	CTGCAATGTGACTATCCACAA	CCGGCGGGACCGAGTGCTTTA	CAGCGATTGGTCAATCTCTAT	CAGCACCCTACTGCCCTTTAA
9183	ZW10	NM_004724	CTCGCCTATCAGACTTTACTA	GCCAGTGAATATATATTGCAA	TACCACGAAGTGATGAATTTA	ACCGGTGAATTTACAGACTTA
9187	SLC24A1	NM_004727	CACTGACTTACTACACCTCAA	CAGTGACATTACAGCAACCTA	CACAATGGGCATGGATCAGAA	ACTGCAGATTATGATGGTAAA
9196	KCNAB3	NM_004732	AACCCTAGGGAACATCCTCAA	AGGGAACATCCTCAAGAGCAA	CCGAGCGAGGTTTAAGCCGAA	TCGAGTAGTGATACGCATGAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
9200	PTPLA	NM_014241	AAGTGAGTTCAAGAATCTTTA	CTGGTGAACTTCTTACAATAT	CACTGTTTAATTGGAATTGTA	ACCACTTGCCATACTTCATTA
9201	DCAMKL1	NM_004734	CACCTTTAGGTTACCTATATA	CAGTGGAATGTGACCAGTCAA	CCGGAAGTGATAACACGCAAA	CAGGTTTATAACTTCGACACA
9211	LGI1	NM_005097	GCCGTGTGTACTTGTACCAAA	TCCCAGCGTCCTGTAATTTAT	AAGCAACACAATTATTCACTA	AAGATTCATTGGTGATTCCAA
9214	TOSO	NM_005449	TACCGTGGTATCCACCACCAA	CAGGTAAGCTGTAGGCATGTA	CCGAGTTACTCTGAAGCAATA	CAGGGTTGGGTCTTACACAAA
9215	LARGE	NM_004737	CACGGCCAAGAACCTACATTA	ACGGCCAAGAACCTACATTAA	AAGGGTTATCATCTTACTGCA	ACCAGCGAAAGCTGCATTTAA
9219	MTA2	NM_004739	TAGACGGATTGAGGAGCTCAA	ACGGCCTTATGCTCCTATCAA	CAGCCAAGCGTCAGAAACTAA	ACGCCAGTTCTCAGAAATAAA
9220	TIAF1	NM_004740	CAGATTCTTATGCACGCTTGA	CACGCTTGAGTCCGAGACTCA	TACCCGATGTATGGAAATAAA	AGGAGTGTCATTTGTCCCTAA
9228	DLGAP2	NM_004745	CAGGATGGAATTTCACAGGAA	CTCATTATTACTCAAAGTAAA		
9229	DLGAP1	NM_001003809	CACGAGGTAAAGATGATGAAA	CAGGAAGAAGGACCACTTTAA		
9244	CRLF1	NM_004750	CTGCTGGTCCAAGAACATGAA	CTCAAGGATTTCCTCTTTCAA	AACGCTGGATATCCTGGATGT	AACACCAACTACTCCCTCAAG
9247	GCM2	NM_004752	ATGGATTACCATTGTACTAAA	ACCCTGGTTATACAAATTCAA		
9256	BZRAP1	NM_004758	CCGCCGTCTGGTGGTCCTCAA	CAGGTCTTCCTAGCACGTTAT	CAGAGCTAAATGGCTCCTTAA	CACAGTGAGTATGTAACTTGA
9263	STK17A	NM_004760	TGCCTAAATACTAGTAACATA	TACTAGTAACATATCAGTGAA	TCCATTGTAACCGAAGAGTTA	AACCAGGATATTTAACAGGTA
9267	PSCD1	NM_004762	AAGGATGAGATAGCAGAAGTA	CAAGTTCTTGTTGGGCTTTAA		
9276	COPB2	NM_004766	CAGTACGTATTTGGCATTCAA	CCCAGTCAGGTTTCAAGGGTA	CAGGTTTCAAGGGTAGTGAAA	ACGATTCTTCAGAGTATGCAA
9278	ZNF297	NM_005453	CCCGCCCATTCTACTACTCAA	CAAGGTATTTCCAGAACTAAA		
9282	CRSP2	NM_004229	CGGGTTGGGACTTAACTTTAA	CGGGTGAAGTTTCGTGTTGAA	CACGTTTACCTGACATATGAA	CACGACAAGGTGAATGCACAA
9287	GPR58	NM_014626	CTGCCCAGTGATGTTCAACAA	CACCTTGTTTATGGCAGGTTT	CAGGATCCATATTCATCACAA	CACATGTAATCCGTTAATATA
9289	GPR56	NM_005682	AACCGACATGCTGGGAGATTA	CACCATCAAGGTGCACATGAA	TCGGCCGCCCATCATGGTTAA	GAGGGTCTGGCACATCCTTAA
9290	GPR55	NM_005683	CCGAGAGTTTGGACCCACATA	TTGATTAATCTGATTCGCCAA	CTGAGAGGACCTGATCATGTA	CCGGTTCTTGGCCATCCGTTA
9293	GPR52	NM_005684	CAGGAAGCACAAGAACCCAAA	AACGGGCTAATTCTTGCTCCA	CAGGTGTCCACGAGTCATTAA	AACCTGGCTTGCAGTAAGTAA
9294	EDG5	NM_004230	TCCAGGAACACTATAATTATA	AGGCGTGGCCTTCGTAGCCAA	CACCCTGAATTCCCTGCTCAA	ACCCACGTTTCTGGAGGGCAA
9296	ATP6V1F	NM_004231	CAGTGTCATTGTTGATGTTAA	CCGGCAATTTCTAAACCGGGA		
9311	ACCN3	NM_004769	CACCCGGATGGGAAAGTGCTA	TGGGAAAGTGCTACACATTTA	CTGGGCAGCCATCGAACCCAA	CCCAAATAAAGTCCTAATGCA
9312	KCNB2	NM_004770	CTGCGGCTTTGTCCAGTTCAA	CCCAATTATTGTGAACAATTT	CCCAGTTGACATAACTGTGAA	GCGGTTAATAATGCCTGTGAA
9319	TRIP13	NM_004237	ACCCAAATTGATCAGATTAAA	CAAGACTATTTAATGGATGTA	TTGACACAGAATTAAAGGTTA	GAGGATTCACATTAATATAAT
9322	TRIP10	NM_004240	TTGGAAGAACGCAGTCGTGAA	CACCATTGATGTACATACTCA	ACGGCTGAAATTGGAAGTGCA	ACGGCTAGACCAGGATATCAA
9329	GTF3C4	NM_012204	CAGGTCAAGCATAACAACGAA	CAGGTAGATTTAATAGACCTA		
9332	CD163	NM_004244	CCCGCCCAGAAGGAACTTGTA	CACATGGGAGATTGTCCTGTA	TCGCATTATTCTTCTTGACTA	CGCATTATTCTTCTTGACTAA
9333	TGM5	NM_004245	CAGGAGTATGTCATGAATGAT	CTGCCTGAAGCTGCTAGACAA	CTCCCAGTTCAAGGACCTCAA	CAGATCCAAGCTAATATGAGA
9337	CNOT8	NM_004779	ATGGCTTTCTTTAGGATGAAA	ATGCTTGTAAATACTATTTAT		
9343	U5-116KD	NM_004247	CTGATTGAAGGTGTTGATCAA	AACGCCTAATAAGAAGAACAA		
9349	RPL23	NM_000978	TGCGAAATTCCGGATTTCCTT	TTGCATGATTCTCCAGTATAT		
9356	SLC22A6	NM_004790	CACCAGAACCACATCATTAAA	CCGGAAGGTACTCATCTTGAA		
9360	PPIG	NM_004792	CAGGAAAGGAGTAGAAGTAAA	CTGGATAATTTGTACTGCTAA		
9361	PRSS15	NM_004793	CCCGCGCTTTATCAAGATTAT	CAGCCTTATGTCGGCGTCTTT	CCGGGACATCATTGCCTTGAA	TAGAAGCTATTTAATGATTAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
9364	RAB28	NM_004249	TTGGGAAACAGTACAAACAAA	ACCCTTCAAATTTGGGATATA	CAGGGCAGAAATAGTGAAGTA	CAGCGTATTGTCAGGGCAGAA
9368	SLC9A3R1	NM_004252	CAGGGCATCTGTTATCCTGAA	CAGAAGGAGAACAGTCGTGAA	CACCAGAAACGCAGCAGCAAA	AGCGAGGAGCTGAATTCCCAA
9369	NRXN3	NM_138970	CTGGAGGGTCATATATACAAT	CATGGCTTACTTGTTCCATAA	CAGGATTATAAAGAGATATCA	ACCAGTGTGCGTGTAACTTTA
9371	KIF3B	NM_004798	CAGAAATGCATGGGTAAGGTA	TTAGGGAAATAGCTTCTTTAA	CAGAGAATTCACCGAATCCTA	AACGCTAAGGTGGGTAGCCTA
9373	PLAA	NM_004253	TAGGTGTTGATTCTCAAATAA	AAGAGTGTGAACACAAATTTA		
9392	TGFBRAP1	NM_004257	CCGCCGATCGTCAAGAGGATA	CAGGTACATAGTAATCCAAGA	CACCCACTTAGCTGTGCTGTA	CACAGAGGTAGCAAATGGCTA
9394	HS6ST1	NM_004807	CCCGTACAACCTGGCCAACAA	CCGCGCGGCAGGACCATGGTT		
9404	LPXN	NM_004811	ATGGAAGAGTTAGATGCCTTA	CAGCTCGTGTATACTACCAAT	CTGCTTAATAGTCTTATAGAA	ATGACTAGGCTGATAATCTTA
9409	PEX16	NM_004813	CCGGACCATCCTGCTGCTCTA	CCGCGGAAGTTAAGCAACCAA		
9424	KCNK6	NM_004823	TCCGTCTGTGTCTCTCAATTA	CCGTCTGTGTCTCTCAATTAA	CTGGTTGAGCTCAAATCCCAA	ATCATCATAATACAACTTCAA
9427	ECEL1	NM_004826	CAGCATCCAGCTCTCAGTTAA	CCGGCTCAAGTACACACATGA	CAGGTGCTGACTGACAAGCAT	CTGCAAAGTCTGGTCAATAAA
9429	ABCG2	NM_004827	ACGGATTAACAGGGTCATTGA	ACCGAGCTCTATTAAGCTGAA	CTGGCGAAGAATATTTGGTAA	CTGGTCTAATTTATTAATCTA
9435	CHST2	NM_004267	ATCGTAGTGTGTTTAAATAAA	CCCTGTGGTGATACCTATAAA		
9436	NCR2	NM_004828	CAGGCTCTCAGGCACAATCCA	CAGGACATTACTGGTGTAGAA	CACGGGCAGTCTCTACGAGAA	ACACACTTTGTGAATAATAAA
9437	NCR1	NM_004829	TCGGTTCATCCTGGACCCGAA	CTGGATCTGGTGGTAACAGAA	ATGGTTGTATATTCCTAATAA	AAGCATGTTCTTACTGCTCAA
9440	CRSP6	NM_004268	TCAGTTCGTAATGGACCTGAA	GTCCAAATTCCTAGTGATTTA	CAGGTACATGCAGTTCAGCAA	CAGCCTACTCTAAATTATTGA
9443	CRSP9	NM_004270	TTGGAAAGTCAGGGCATCGAA	TAGCATCATATATTAGTTCAT	ATCAAGGAATATACGGATGAA	AGGCAGTAATTTCGCTGTATA
9446	GSTO1	NM_004832	GCCCTGCTTACTAGTGAGAAA	CAGGCATGAAGTCATCAATAT	CAGGAGTCAGCAATAAAGCTA	CAGCAATAAAGCTATGTCTGA
9448	MAP4K4	NM_004834	TCGGAGCTGCACCGAGGGCAA	CAGGACTTTAGTTAGAATTAA	AGGCAAGATCCTACCCGGAAA	AACCATTAATGTTTAATTTAA
9453	GGPS1	NM_004837	AGGGATGATTATGCTAATCTA	TACACTCGTAATACCCTTAAA		
9455	HOMER2	NM_004839	CGGAGCCAAGGTGATCATAAA	CAGCACAATCACACCGAATAT	CAGAACTAGGTCTACCTTCAA	ACCGAATATGACCTTCACCAA
9468	PCYT1B	NM_004845	AAGAGCCATGATCTAATTCAA	CACCATAATACTCCTCTGAAA		
9469	CHST3	NM_004273	CAGGTTGACTTAATTTATTTA	CAGCTGTATATTCTAGTCCAA		
9472	AKAP6	NM_004274	CTGCGGATGATTGCAAGTCAA	CCGGGAGACTTGCAATCTGAA	CACGTTTGTCACTGCCGTTTA	AAGCATGTGGATGTACATCTA
9479	MAPK8IP1	NM_005456	ATGCAGTTTATTGTAATATAT	CCGGCTCACCGTGCACTTTAA	TGGCATCAGCTTACAGTGCAA	CTGGAGGAGTTTGAGGATGAA
9493	KIF23	NM_004856	CAGAATAAACTCTGGGTTAAA	CACCTTTGCCGTCATGCGAAA	CAGAAGTTGAAGTGAAATCTA	AAGGCTGAAGATTATGAAGAA
9498	SLC4A8	NM_004858	TGGGACCAGTACAATTCTCAA	AAGCATCATCATCAGAATGAA	AGCCGTCATTATTAACAGGAA	GACGGCTATCTTAAAGTTTAT
9508	ADAMTS3	NM_014243	CAGGAAGCTTGGGTACCTTAA	CCGCTCTAGCCTGACATATAA	AACAATGTGATACGTAAATTA	TAGGCAAATTCCAGATAGTAA
9509	ADAMTS2	NM_014244	GACAGGCAAGTTCATCTTAAA	CCGGGTCTCACTGACGTACAA	CCGCCGGAGGCTGGACCACAA	CAGGCGAATGGGAGCCATGTA
9510	ADAMTS1	NM_006988	CGGCAGTGGTCTAAAGCATTA	TAGGATAGTTAGTGAGGATTA	CTGAGCAGTGATATAGCATAA	CAGCAACGTGAAATAACGCAA
9516	LITAF	NM_004862	CAAGGTCGTAAATGCATGCTA	CTGGGCCTGAACATAATTTCA	TGCCAATGTAGTCTCACTTAA	GCCAATGTAGTCTCACTTAAA
9520	NPEPPS	NM_006310	CAGACCAATGGGTGAAGTTAA	CATGGTGATGGCACTACTTTA	GAGGGATTTGCAGTTGATAAA	CTGGGAATGGTTAAACACAAA
9522	SCAMP1	NM_004866	AACACTGTTGTTAACATCTAA	CACCACATTTCTTATATTAAA		
9524	GPSN2	NM_004868	GTGGATGGCCTATTACATCAA	CTGGATCGGTTTCGCCATCAT		
9542	NRG2	NM_013982	TTGTCTTATAATACTAGCTAA	AGGGAAACTATTTATATGTAA	CCGAGACATTCGCATCAAATA	ACCCGTGGTGGTGGAGGGCAA
9554	SEC22L1	NM_004892	TAGGACATTCTCAAATTTCAA	CCACAATTTGCTAACATTTAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
9555	H2AFY	NM_004893	CTGGCTGTGGCCAATGATGAA	AAGGCTTTGGTTTCCAGTTTA		
9559	VPS26	NM_004896	CTGCATAATGTTGATTATAAA	CACCAAGGAATTAGAATTGAA		
9562	MINPP1	NM_004897	ATGAAATTCTTCCTACTTATA	AAGTCGGAAAGTACAATGAAA	CCGAGTGCAGATGTTATTAAA	CACGGTCAAACAGATCCGCAA
9570	GOSR2	NM_004287	TTGGGAGTGATTGTGGTCTAA	CAGGACAAGTACTTTATGATA	CAGCATTCCCACAGCCTGCAA	AACGAAATCCAAGCAAGCATA
9575	CLOCK	NM_004898	AAGGAGCCATCTACCTATGAA	GACACGCATGATAGAAGCAAA	ATCGGCAACAAGAAGAACTAA	ATCCAGCAACTTGCACCTATA
9580	SOX13	NM_005686	AAGGAACTCTATGGAAGCCAA	CACCATCAAGTCAGAGGAGAA		
9586	CREB5	NM_004904	TAGCTTTAAATACATCATTAA	CAGCAATAAACTTACAAGTAA		
9589	WTAP	NM_004906	AAGGTTCGATTGAGTGAAACA	GGGCAAGTACACAGATCTTAA	CAGACTAAAGACAAACTGGAA	ATGCAAGAGTGTACTACTCAA
9598	CSAG2	NM_004909	CAGCTGTGTGGTCAAACAGTA	CTACCACAAGACTAACATAAA		
9605	C16orf7	NM_004913	CTGGGTGTATCTCAGAGATAA	CGCCGTGTATACTCCGATGAA		
9609	RAB36	NM_004914	AAGACAGTACAAAGCATATAA	GTGGCCATTCTTGTAGTTATA	CAGCTCAGCGATTGCCAAATA	AGGCACTGTGGTGATCCCATA
9611	NCOR1	NM_006311	CCCGGTGGTTTCCTAGAAACA	CCCGCTCACCAGGGAGTATAA	AGGCAATTCAGTGGACTATAA	ACCGCAGTATTGTCCAAATTA
9620	CELSR1	NM_014246	CACCATGATGGAGCTGGACTA	TGGCGTTTCCTAAGTACGAAA	CGGGATCCTGGATGTGATCAA	CGCCAACAGTGTGATTACCTA
9625	AATK	AB014541	CCGGTTCCGCTGAGATCAGAA	CTGACTCAGCTAGACCCGTAA	TCCGCTGAGATCAGAAGGCAA	CTCCAACGTGTCAGCCAACAA
9629	CLCA3	NM_004921	CAGAGTACTTTCGGTTCTGAA	CCCAGCGAAGAAATGGATAAA	GAGAGCTACATTATAAGAATA	TAGGCCCGAAATGACTAGCAA
9636	G1P2	NM_005101	CAGGATCAAGGGCCGGAAATA	CCGGAAATAAAGGCTGTTGTA	AAGCACCGTGTTCATGAATCT	AATGCGACGAACCTCTGAGCA
9638	FEZ1	NM_005103	CACAGATAAACTCATCCTGAA	ATGGAGGACCTCGTAAATGAA		
9640	ZNF592	NM_014630	TCAGACTATATTTCAAATAAA	CCCACTAAAGAGAGTTCTAAA		
9648	GCC2	NM_014635	ACGGGAAGACTTAGAGTTTAA	ATGGATAATTTCCATAAGAAA		
9673	KIAA0446	NM_014655	AGGGTGATGTGTGTATAATTA	CCCGTGGTGGGCACAGTTCTA	CAGCATGGAGGACAAACGCAA	CCGGAAGTTTGTAGCTGACTA
9674	KIAA0040	NM_014656	ACCCTGTGAATCATAATTTAA	CCGAGTGATCTTCTCTTCTAA		
9679	FAM53B	NM_014661	ATGGCGAGACCTGGACAGGAA	GACAAGAAGGTCGGTGTTAAA	CGGGAGATGCTTCCTTCTGTA	TACTTGTACTGTGTAAATAAA
9688	NUP93	NM_014669	TCGAAGTTTCCTGAACATTAA	AGGGATGAGAAAGATAGTCAA		
9706	ULK2	NM_014683	CAGCCTGAGATACGTGCCTTA	TAGGATAATCGGTACAGTTAT	ATCGGTACAGTTATTCTTAAA	ACCGGGAAGTTATCAGATCAA
9716	AQR	NM_014691	ACGATTGGAATTAGAATTAAA	CAGGATGGATTTAGCCGACTA		
9717	KIAA0420	XM_032693	ACGGTCCACCCTGAGAATGAA	CAGGCGGAAGTTCCTCATCTA		
9719	ADAMTSL2	NM_014694	CCAGGAGTTCTTCTCGGCTAA	CACCCTCAATGAGACTGTGAA		
9720	KIAA0565	XM_113947	TAGTCTTGTAGTATGTTTGAA	TAGCGTTACAATAGAATAGTA		
9722	CAPON	NM_014697	ACGGTATGAGTTTAAAGCCAA	CAGCAATATCTTCAGGTGTAA		
9726	ZNF646	NM_014699	AACAATTTATTTAAGTTTAAA	CGGGAGCTAGAAGACAATGAA		
9727	RAB11FIP3	NM_014700	CACATGAAATATATATATATA	CCCGTCCATCCTGGAGGTCAA		
9728	KIAA0256	NM_014701	AAGGATGAGAATATTCAACAA	CCACATAAGTTTATAATTTAA		
9730	VprBP	NM_014703	CAGAGTGAACTCAACAACCAA	CAGGGTGTTACTCCTCACCAA		
9733	SART3	NM_014706	CAGCAGCTGGAGAAATATAAA	ATGGAGTTGATCATCAAGTAA		
9735	KNTC1	NM_014708	CAGCACATTAAAGCTCACGAA	CAGGCAGTATATCCAGTTAGA	TGCTCTTAATTTCGAAATTAA	TCCCGTGGATCTAGAATATCA
9737	GPRASP1	NM_014710	TGGGTCTATAGATGTAATTAA	GGGTCTATAGATGTAATTAAA	CTAGCAGTAAATCCAGACCAA	ACGCCCTAAGAGTAAGGCCAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
9744	CENTB1	NM_014716	CACCGTGAGCCTGAACCACAA	ACGGGCCAGCAACGCATTTAA		
9746	CLSTN3	NM_014718	CCCAGTCAAGTTCCTCTGGAA	CAGGTGAAGCCCACCTGTAAA		
9748	SLK	NM_014720	GACCATTAACTGAGTCCCAAA	TCGAATGGCCATGTTTAAGAA	TAGCATCTTGTGATCACCCAA	CCAGATCAGGACCGTGATAAA
9751	SNPH	NM_014723	CACGATGTTCATCCAGGCCAA	ATGAGGGTTCCTAAACCTTAA		
9761	KIAA0152	NM_014730	AAAGATATAATTAACGATCAA	CAGGATTGTGCTGGCAGCCAA		
9767	PHF16	NM_014735	TCGGTGGGCCTTAGTCTGCAA	CACGCTAGCTGTGGACTTTAT	CACCAATAGGTGGGTGAAGAA	ACCATGATTATCAGACACTAA
9775	DDX48	NM_014740	CCGGAAGGGTGTGGCCATTAA	CCCATAAACTCTATACTTCTA	CCGCATCTTGGTGAAACGTGA	AAAGAGCAGATTTACGATGTA
9780	FAM38A	NM_014745	CTGCGTCATCATCGTGTGTAA	CAGCCTTGTATGCACCGTCAA		
9781	RNF144	NM_014746	TGCGATGACCACAACAAGGTA	AAGGATTAGAAACCGCAATTA	GTGGAGAAAGTGTATTCTTTA	CAGGAATAACTGTCCAAATTA
9783	RIMS3	NM_014747	CTCCAGTATCCTGACATGTAA	CAGGGAAGAATCATCTCCAAA		
9784	SNX17	NM_014748	ACGGAAGTTGCAAGAGTTTGA	CTCCGCCTACGTGGCCTATAA	CAGCGAGACTTTCAACAGTTT	CTGGCCCTCGATGCCAAATTA
9797	TATDN2	XM_376203	ACAGTTCTAAAGGGCTTTATA	CAGCCATGTGTGGATCTTGAA		
9806	SPOCK2	NM_014767	CACATGCATAAAGGAAATCAA	CACGTTTGTGTGTCCTTGTAA		
9810	RNF40	NM_014771	CAGCTTAACTCTGGCTACTAT	CACGCTGGCCCAGGTACGCAA	GCGCATCGAGTTTGAGCAGAA	AAGCGGAAGCTTCGAGAAGTA
9811	KIAA0427	NM_014772	CCCGGATTAGTGGGAGATCAA	CAGAACGAGACTGGCAAATTA		
9815	GIT2	NM_014776	CCCGTTGATTATGCAAGGCAA	CAGCGTTGAGAGTCAAGACAA	CTGCCTATGGCTGAAACTATA	AAGCATCGTGCAATAAGTGAA
9818	NUPL1	NM_001008564	AAGGTACAAGAAGATATTAAA	AAGCAAATAATTCACATATAA		
9819	KIAA0669	NM_014779	CAGGATTGCATTTAATAGATA	CTGGCATATTTCTAACACTAA		
9825	SPATA2	NM_006038	CACAATGTTAAGGGATTTATA	CCCAGTTCAATGGATACTAAA		
9826	ARHGEF11	NM_014784	CACTTGTATCTCCTTAGTTAA	AAGCGATTCAATCCTGATCAA	CTGGAGGATCAGCAAGGATAA	CACAACGACTCTCGACCGGAA
9830	TRIM14	NM_014788	CACCGAGAAGCTCAAGGCTAA	GCGCCTCACCTTAGCATTCAA	CAGGTGCCTATCACTGAGTAA	AAGCAGAGCTGCGTAAAGTTA
9832	KIAA0555	NM_014790	CTGCATTTAATGAAACATGTA	CACCTGCTTGAAAGAAATTAA		
9833	MELK	NM_014791	CACCTCGATGATGATTGCGTA	AAGACTAAAGCTTCACTATAA	CTGGATCATGCAAGATTACAA	CGGGTTGTCTTCCGTCAGATA
9834	KIAA0125	NM_014792	CAGCATGGTGACTATAGTTAA	CAGGAACAGTTCTGAAGTCAA		
9836	LCMT2	NM_014793	TAGATTTATAAGTGTCAATAA	ATGGCCATTAATGTTACACAA	ACCCACTAAAGTAGACAATAA	CAGAGGCATTTCCTCGCGTAA
9837	KIAA0186	XM_375911	ACAATTGATGTTGAACTTGTA	TTGGGAGAATTGACATCTTAA		
9842	PLEKHM1	NM_014798	CCCATTCATATTTCAACAGAA	CAGGCAGCCTCTGGAACTCAA		
9846	GAB2	NM_012296	CAGACCAGACGTTTCATTCTA	CACTAAGGACACAAGAATCAA	CACCAATTCTGAAGACAACTA	AACCTCAAACCTGATCGGAAA
9848	MFAP3L	NM_001009554	CCGAAACTGCAGAACCTTCTA	CACCATCGTCATGGTCCTCAA		
9851	KIAA0753	NM_014804	CAGAGAAAGGAAGAAACTTAA	CTGGCTCAGTTTGGTGATGAA		
9853	RUSC2	NM_014806	ATGTATTTATTTATTTATTTA	CCCGATCAAGACCTAGGACAA		
9854	TMEM24	NM_014807	TAAAGTCAAATTGGAGTTTAA	CACAATTGAGGAACTGATCAA		
9855	FARP2	NM_014808	CAGGAACATGCGCCAGTTAAA	CAGGTTTGGACACAACTACAA		
9860	LRIG2	NM_014813	AGGGATGTCATTGTAAATATA	CTGGAATATACTAGTATCTTA		
9863	AIP1	NM_012301	AACCCATTCATCGTAAACAAA	CAGACCTAAACTGATCCTAAA	TTGGATGTCATCCAAACTTTA	ACGCAGTGACTACGCAACCTA
9871	SEC24D	NM_014822	CAGCTGCTTAATTAATTGAAA	AAGGTACAATTGTACCATAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
9877	KIAA0663	NM_014827	AAGATTGATAGTGAAATTAAA	CAGCTAATGATTACAGTTTAA		
9880	KIAA0352	NM_014830	AAGCTTAACATCAGAATGAAA	CTGGGTGGTCTGTGTACTTAA		
9890	LPPR4	NM_014839	AAGGAGTTGTTTACAGATGAA	CACATTGTTAAGGACATATAA		
9894	KIAA0683	NM_016111	CCAGTTTGTGATGACCCAGAA	CCGGGAGACGCTGCTGGGCAA		
9896	KIAA0274	NM_014845	GAGGGTGATGTTGCAAATGAA	AAGAAATTCCACAAATATGAA		
9899	SV2B	NM_014848	CTGGTTGATTTGAGAGATAAA	AAGATGGATCTTGTAAATTTA		
9901	SRGAP3	NM_014850	AACCAGCAAGTTGTTCATTTA	AACCTAGTTAGTAGTCTTCAA		
9908	G3BP2	NM_012297	ACCAGCGTGTGTACACATAAA	CAGCCAAGAGTCGAAGCTAAA	TTCAGTGAATGTCATACTAAA	CCGAGTGGCTCCTGAATTTAA
9914	KIAA0703	NM_014861	ACGGACCTCTTGGTGGATGAA	CAGGCTGAAGAGACACCTAAA	ATGGACTTAAGTGATATTAAA	CCGAGAGTTGGCGTGAAGGAA
9915	ARNT2	NM_014862	CAGAATAACCACCATGAGGAA	TAGCTTTAGCCGAGAAAGAAA	CCGGAACAGCTCTAGGAATAA	GTGGACAGTTTAAGTACTTAA
9921	RNF10	NM_014868	TCCAAGCGTTATAATCGCAAA	CCGGGTAGTTCTGGAGGAGAA	TTCGATGAAGAAACCACGGAA	CAGGATTGAGATAGAGGAGAA
9936	DCL-1	NM_014880	CAGAATTATGTGCATACCAAT	ATGGCGTATTATGTGAACTAA	GAGGCTATTTAAGTAAATTTA	TAGCTAGTAATAACAATATAA
9940	DLEC1	NM_005106	ACAGCCTGACATGGAATTTAA	CAGGTTCTGCATTATGCCCAA		
9941	ENDOGL1	NM_005107	CTCGGGCAAGATGGCTATCAA	CAGAGGCAAGGTGTTACACTA	AAGAAGCTAGAAGAACTCAAA	AACAGTGGAATCCTAAATTTA
9949	AMMECR1	NM_015365	CCCACTGTTTGTAACATGGAA	CACACTTACCAGTGCCCTTAA	CTGACCAGGTATCGTAGTGAA	CGCCAGCATCATCATTTCCAA
9950	GOLGA5	NM_005113	CTGGACCTAAATCTACGTATA	AAGCAGGAGTTCCACTATATA	AAGAAGATCTTTATCGAACAA	CACGACCAACCATATGGCAAA
9951	HS3ST4	NM_006040	CCGTGTTGTTATAAAGCTTAA	CAGAGGATAAATAGTTGTCAA		
9958	USP15	NM_006313	ATGAATAATGTTGTAACTCGA	GACACAATAGATACAATTGAA	AAGATGATACCAGGCATATAA	TATGTCGGAATTCTTAATTAA
9965	FGF19	NM_005117	TTGTCTGATCATAACATTGTA	AAGAAACATCTAGAAGTTGTA	CAACATGATATTTATGAGTAA	CCGTAAGGCGCTACTATATAA
9970	NR1I3	NM_005122	AAGCCACAGGCTACCACTTTA	TTGAACAGTTTGTGCAGTTTA	CACACACTTCGCAGACATCAA	AACACTTTCATGGTACTGCAA
9976	CLECSF2	NM_005127	AAGCAGTAATGTCCTAAAGAA	CCCAGTTGAGAAAGTAAGAAA	CAGCTAGATGTTACACCGAAA	ACGTGTCAGGCTACACATAAA
9978	RBX1	NM_014248	CACATTATGGATCTTTGCATA	TTGCATAGAATGTCAAGCTAA	CTGCTGTTACCTAATTACAAA	AAGAAGCGCTTTGAAGTGAAA
9985	REC8L1	NM_005132	CCGGAGAAATTCCAGGAACAA	CAGAGGGACAATGTTCTACTA		
9988	DMTF1	NM_021145	ATGGATAAGCATAGTAACAAA	CAGATTATTGTTCATGCTTTA		
9989	PPP4R1	NM_005134	CAGCTAGTAATGAGAATGATA	AACCTGGTAACTACAAATCTA	TGGGAGTGCTGCAGTCTTTAA	CAGGCGTTGTTAGATCAGTAT
9993	DGCR2	NM_005137	TCGCTGGGAGGTGGCATTCAA	CTCCCTCAATACTGTGGTGTA	AAGCCCAGTTGTGAATATCAA	GAGGTGGGATTTGATACTGTA
9994	CASP8AP2	NM_012115	CAGCTGATGTGCGGAAGTCAA	CAGTATTCAAATAGTCAGAAA	CAGTCTGATCTCAATAAGGAA	AACGAAGTTTCGAGATTCTTA
10001	MED6	NM_005466	TCCCACTAGCTGATTACTATA	CACCCAAATTTGTGCAGCTAA	AAGGGTATTGGTGGCACTTCA	ACCCAAATTTGTGCAGCTAAA
10002	NR2E3	NM_014249	CAGGCAAGACTAATTGACAAT	AGGGAATACTCCAATGGAGAA	CACGGAGTTTGCCTGCATGAA	CACAAATGTATTCATACGTAA
10003	NAALAD2	NM_005467	CAGCAAGTATCTATAATCTAT	TCGATTGTGGATGAACATGAA	AAGAAACATGATCAACAATTA	ACGGTGGAAACTGGTATCCGA
10004	NAALADL1	NM_005468	CACAGAAGAGTTCTTCAACAA	ACGCATATCAACACTGCAGAA	TCCCTTTACTCCGGTGCTTTA	CTCCGGTGCTTTATATTTACA
10019	LNK	NM_005475	CAGCTTTACAGTGATAGTTAA	CAGCACATTGTGATAACATAA		
10020	GNE	NM_005476	CTGCTTACTAATGTATTAATA	ATGAAGGTTTCTACAACATAT	CCCGATCATGTTTGGCATTAA	ATGGAAATACATATCGAATGA
10025	THRAP5	NM_005481	CACCCGGATCCTGGCCATGAA	CAAGGTCATGATCAACCTCAA	TGGGAAGGACAGGTCCAATAA	CACGTGCAGCCCAGTATGGTA
10039	PARP3	NM_005485	CCAGACCAACATCGAGAACAA	CCCAGTGAGGACTGTGACTAA	CACGCAGAAGCTCATCACTAA	CAGCAAGGAGATGTTCAAGAA
10044	SH2D3C	NM_005489	CCAGAGAAACTCCACAAGGAA	CAACCAGGCCTTGCACTTCAA	CAGGCGAGAGCTACACACACA	CCACACCAATGCTGAAGTCAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
10046	CXorf6	NM_005491	AAGAATAAATTTGCAGGTCAA	CCGTCTAACATTACTCATGTA		
10048	RANBP9	NM_005493	CAGTGCAATATTAGAAACCCA	ACGGTGTGGTTATGACCTTTA	CAGGTTGGGATAAGCATTCAT	AAGCAATGAGTGAACAGCTAA
10050	SLC17A4	NM_005495	ACGCTAGTTATTTAACTGCAA	GAGCAAGATAGTACACTTTAA		
10053	AP1M2	NM_005498	CTCCGAGGGTATCAAGTATAA	CTGGATTGAGTCTGTCATTGA		
10054	UBA2	NM_005499	AAGAGTAGATTTGATATCAAA	CTGGGTATCTTGGACAAGTAA		
10055	SAE1	NM_005500	TACCAAGTCTTTGGATGTTAA	TCCAGGGATGTCATAGTTAAA		
10060	ABCC9	NM_005691	AACAGAGGACATTGCAATAAA	CAGCCAGATATTGACTTATTA	CTGCATCTATAGCATCCATTA	CCCAAATTTGTTCGCCCACAA
10062	NR1H3	NM_005693	CCCACAGAGATCCGTCCACAA	CAGGAGTGTCGGCTTCGCAAA	GAGATAGTTGACTTTGCTAAA	CATGAATGAGCTGCAACTCAA
10063	COX17	NM_005694	CTGAAGAATGAAGAAGATTAA	AAGGAATGCATGAGAGCCCTA		
10068	IL18BP	NM_005699	CTGCTTCGGATCCACACTGTA	TCCCATGTCTCTGCTCATTTA	CAGGATGTGGACGGACTGGTA	ACCGATCAAGTCAACTCAGTA
10077	PHEMX	NM_005705	CAGCAATGGTGCATTGAGCAA	TCAAATATACATCACATCAAA		
10086	HHLA1	NM_005712	CCCAAGTGGGCTACATTTGAA	CTGGAGGGTCTCTCTGGGAAA	AAGCATGTTAATGTTACCATT	CTCCAGCTAGATCATCAGTTA
10092	ARPC5	NM_005717	CAGCCTCTGAATGAAATGCTA	CAGGGTAGTTGGGATCTCAAA		
10094	ARPC3	NM_005719	GCGCTTAATAAGAATAAGTAA	CTCATGGATCCTGATACCAAA		
10095	ARPC1B	NM_005720	AAGCACTATGCTGGTCATGAA	TCGTGTGATCTCCATCTGTTA		
10102	TSFM	NM_005726	CAGGAAGGAAACACAACTGTA	CAGCAAGGAGCTCCTCATGAA		
10105	PPIF	NM_005729	CTGTGTGTTAAAGAAATTCAA	ATGGATTTGTGTTCACCTTAA		
10107	TRIM10	NM_006778	ACGGACATCAGAAGCACTCTA	TTAGTTTGTGTTAACTATGAA	TCCAATAATGTTAGAGTTCAT	CAGTTGTATGACTTTAAACAA
10111	RAD50	NM_005732	TAAGATTGAATTGAATCGTAA	CACGAGTAAGATTAAGAGCAA	CAGGAACAGATTCAACATCTA	CAGAAAGTGTATAATAAGAAA
10131	TRAP1	NM_016292	CCCGGTCCCTGTACTCAGAAA	AAGGATGTCGGTGAGTGGCAA	CCGCTACACCCTGCACTATAA	CGCGCTCATCAAGAAGCTGAA
10134	BCAP31	NM_005745	CTGCACGTTGACTGTGGGAAA	CACCTTCTTTGTGGTTCTCAT	CAAGAAGTACATGGAGGAGAA	AAAGGTGAACCTCCAGAACAA
10136	ELA3A	NM_005747	CACATCCTGAATAAAGAATAA	TGGCTGCAACTTCATCTGGAA	CTGGCTTTGGCTGCAACTTCA	AAGAATAAAGATCTCTCGGAA
10139	ARFRP1	NM_003224	CCGATTTAACAAGAACTACAA	CACCACCACCGTGGGCCTAAA		
10140	TOB1	NM_005749	CAGCCTGTTATGGCTAACTAA	AGCCTGTTATGGCTAACTAAA	CCAGCCTGTTATGGCTAACTA	CAGATATGGCCTCTTACAGTA
10142	AKAP9	NM_005751	CAGGTTCGTGAATATATGGAA	ACAGATTATATCACTCGGCTA	CAGCTTCAAAGGGATATACAA	CAGCCTATCAGTGAACATCAA
10154	PLXNC1	NM_005761	TTGGTGAGAATTTGACTTCAA	CCCAACCAGAGCAACCTACAA	TCGAGGGAAGCACAAGTTCAA	GACGTCGTACATATTTGGAAA
10158	MAP17	NM_005764	CCCTAATTTCTGTGAAATAAA	CCGGCCCTACCCGCCCTTGAA		
10165	SLC25A13	NM_014251	CAGACCAAAGATGGATTAATA	CTCAGAAATTTGGTCAGGTTA	TAGCAGATTTATATGAGCCAA	CAGTATCTACCTCAAAGGCTA
10166	SLC25A15	NM_014252	AGCCTTATGCACCTAATTCAA	CACCAGCAGGGTATCTCCCAA	ATAGGCCTGGATCGAAGTAAA	AGGCCGTCCATTAGAGATTTA
10168	ZNF197	NM_006991	TCAGGCCTAATTATACATCTA	CACCAATGAGTCCAAGATTGA	TCCCAACTTTCAAGTCTACAA	CACCTACACTTTAGACAATTA
10178	ODZ1	NM_014253	CCCAGTCATATCAACCATAAT	CCGACCTGCCTTTACCTTTAA	AAGGCTATAATCCGGCCTTAA	CTCTATGATTTCCTTACTAAA
10180	RBM6	NM_005777	CAAGCAAGAATTAATAACCTA	CAGACTGGTCTTCAGATACAA		
10188	TNK2	NM_005781	TGGCCTTACCATGGACTTGAA	CAGGATCTTGTGCCTGGAAAT	CGGCAGTCAGATCCTGCATAA	ACGCAAGTCGTGGATGAGTAA
10189	THOC4	NM_005782	CAGGAACTCTTTGCTGAATTT	CCAGTTAAACAGACCAGCAAA		
10194	SDCCAG33	NM_005786	CACGGGCAAGGTCAACATCAA	ACCGCGGAACATTGCACTAAA		
10202	DHRS2	NM_005794	CAGCACCGGGATAGACAGGAA	CTGGAAGAACTTCAAGGAACA	TAGATTTGGCTGATCCAATTA	CTCTCTGTAATTTGTGCTTTA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
10206	RFP2	NM_001007278	CAGAATTTGTGTGCAAATATA	AAGGAGATCATAAGAAATTAA		
10208	C13orf22	NM_005800	CAGCCTCAGTTTCACAGTTAA	CTGAATGAAGTTAGAGATGAA		
10213	PSMD14	NM_005805	TAGGACATGAACCAAGACAAA	CAGGCATTAATTCATGGACTA	AGAGACATTATTACTCCATTA	TTGGATACTGTCGTATTTAAA
10218	ANGPTL7	NM_021146	TCGGGCTTGGAAGGAAAGCTA	CCGCATCTCTGGAGTGTATAA	ACCGCCTGGGTGAGCACAATA	CTGAAGGTAGATGGTGTTATA
10220	GDF11	NM_005811	AAGGTGATGTTCACAAAGGTA	TTGGCAGAGCATCGACTTCAA	CAGAGCATCGACTTCAAGCAA	CTGAAATGGAGTAATAAATGA
10228	STX6	NM_005819	CAGGCTGAAGCTAAATAGAGA	TCCCAGGTTTCTTAAGAATAA	CTGAAGCTAAATAGAGAACAA	AACCTAGTCATTAATGAGTAA
10231	DSCR1L1	NM_005822	ATGGATTACTTTAGATGCAAA	CTCAAAGAGCTTAGACTTCAA		
10234	LRRC17	NM_005824	AGCGTAATAATTACTATAGTA	ATGCAGGGTAATCCAGCTAAA	AAGGAACAATTGGACCCGAAA	CCCGTGTGACGTGTACACATA
10244	RAB9P40	NM_005833	TAGGTGAAGAAACTAATGCAA	AAAGAGGATTCAGCTGACAAA	ATTGATATAAGTGACATGAAA	AAGCAACATGGTACACCTTGA
10245	TIMM17B	NM_005834	CAGCACTTCCTCCAGCTCCAA	GGCACCCTGATGAGTATTTAA		
10250	SRRM1	NM_005839	CAGAATAAATTTCTAAATTTA	TAGGTTGAAGTTCAACATGTA		
10257	ABCC4	NM_005845	TTGGCTATACTGCATCACTTA	TACAACCAATAGGAACAACAA	CTCCTAGTACTTAGAAATACA	GAGGTTAAAGACAGTCATATA
10261	IGSF6	NM_005849	CAGAATGTAAGGAAACTATAA	CAGGAAATTGCTCAAGAACTA		
10262	SF3B4	NM_005850	CTGGATGAGAAGGTTAGTGAA	CACAGGCAACTCCAAAGGTTA		
10267	RAMP1	NM_005855	CACCTGGCACATGGCGGAGAA	CCCGCCCGGCAGCATCCTCTA	CAGGTTCTTCCTGGCAGTGCA	CAGGGACGTGACCTTGACTTA
10276	NET1	NM_005863	ACGGAAAGAGACTTTGGTGTA	GAGCATCATAGGGTTACTTTA	TCGGTGTGGATTGATTGGAAA	CTGGAGGATGCTATATTGATA
10279	PRSS16	NM_005865	TCCGAGTATAATGACGTGGTA	ACGTGGTATCCCGAAGCCTAA	CAGAGAGTTATGGAAATATAA	CTGTTCTTTCCTAAAGATCAA
10280	OPRS1	NM_005866	CAGCGTCTTCCATTCCAGAAA	TGGGAACAAATGAGACACATA	CCGGCTTGAGCTCACCACCTA	AGGGATATCCATGCTTATGTA
10282	BET1	NM_005868	TCAGATTAAATAGCATTATAA	ATCATTTATTGGATTATTAAA	CAGAATAAATTATTAGCTGAA	CACTGATGTCGTGGCGCTTTA
10284	SAP18	NM_005870	AAGCCACGGGATTGTATGAAA	TCCCTTTAGTTTGTTACAGTA	AACGGCCTATAGGATTGTTAA	AGCCACGGGATTGTATGAAAT
10290	APEG1	NM_005876	CCCGAGGACACCACCACCGAA	CAAGTGTATCATCACTGCCAA	CAGCTGGAATAACAAGCCCAA	AACACCTATTTCTTAACTCAA
10291	SF3A1	NM_005877	CAGGTGTGTTACCGAGTGGAA	CGCAAGGATTATGATCCCAAA	CAGGATAAGACGGAATGGAAA	CAGCATGTAGGTAGCGTCCTA
10293	TRIP	NM_005879	CCGGCTCAGGAGCAAGATGAA	AAGGAAATCATGAGCCTGAAA	CGGGACCAGCCTGAGGTGTAA	CCGTGATGATATTGATCTCAA
10300	KATNB1	NM_005886	CTGCTGTAATTTATAAGGCAA	CAGGGAGGAGAGGCTGCATAA		
10322	SMYD5	NM_006062	CTCGAGGAGCTGGGCTAGATA	TTGGATGCTATGGGAATTACA	CTGGCCTTATGGAGTATGGAA	AACATTGAAGTCTTCCAGAAA
10328	NOC4	NM_006067	CTGGACAAACCCAGAGATCAA	TGCAAGATTGTTCCTATTAAA		
10329	TMEM5	NM_014254	CAGCCTCAGGAAACAAATGAA	TCCCTTTATCTTTATCAAGAA		
10344	CCL26	NM_006072	AACAATTGTGACTCAGCTGAA	TCCCAGAGTTACTTTAATAAA	AAGCTATGAATTCACCAGTAA	CAGGGCCGTCTCAGTCTCATA
10352	WARS2	NM_015836	CCGGCATTCAACCTACAGGAA	CTACCTCGATTACAACATTTA	GCCAATGGATGCGAACTTAAA	AAGGTAGATCTATCAAGCCAA
10360	NPM3	NM_006993	TTGGATAAAGGTTGAAATAAA	CACCCGCTCCTTCACCTTTAA		
10361	NPM2	NM_182795	CAGGAACGTTATGAAGCATCA	CAGGCGAGCGTGGCTAAGAAA		
10363	HMG20A	NM_018200	AAGGAAGATAACGGACTGTAA	CAGGAATGCATGAGATTTCAA		
10369	CACNG2	NM_006078	CCGTGTGATCTTTATAATTTA	ATACATATATCCATTATATTA	ATCCATTATATTAGTAGTGGA	TCGGTTGGGTGTTTATATAAT
10370	CITED2	NM_006079	TGGAAACAAAGTAAACTATAA	CTCCCTTATGTAGTTGAAATA	CAGATTTACGAGTGAAAGGAA	TGGAATGTCGTCAGTGGCAAA
10381	TUBB3	NM_006086	CACGGTGGTGGAGCCCTACAA	CCAGCAGATGTTCGATGCCAA	GCGGATCAGCGTCTACTACAA	TTGCTGTCAGATACCCTTAAA
10385	BTN2A2	NM_006995	AACTCCAAACATCGCGATTAA	CTCATTGAAATCAAGGCCCAA	TACGTCAGCATTCAGGTTCAA	AACGATTAATGTTTCATTATT

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
10395	DLC1	NM_006094	CAGCTTGATCAGGACATAGAA	AAGGTATTTCAGAGAAGGAAA		
10396	ATP8A1	NM_006095	GAGGATAAATTACAAGATCAA	ATGCAATGTAATGCAGTTTAA		
10398	MYL9	NM_006097	GAGGCACCCATTGATAAGAAA	ACCCATTGATAAGAAAGGCAA		
10403	KNTC2	NM_006101	CACAATTAGCAGAGTATCACA	TCCAAAGGTTATGACTTTGAA	TCCCTGGGTCGTGTCAGGAAA	CCGAGACCACTTAATGACAAA
10407	SPAG11	NM_016512	ATGGCAGATCTGGGATCTAAA	TTGAATGAATTTAGCACCAAA		
10412	TINP1	NM_014886	AAGAGATTTATTAAATTGTAA	AAGGCTAAGCTTTACCATAAA		
10423	CDIPT	NM_006319	CACCATGTGCCTGTTGGTCAA	CCGGATTGTCTTCGCCATCAT		
10424	PGRMC2	NM_006320	CCCTAAATCAAATCAATATTA	CACATCAATTTGAGTTGTTCA	CCGGCGGGTCCATATGGAATA	CAAGATAAATTAATCTCACTA
10426	TUBGCP3	NM_006322	TCGCATGGACTTTAACTGCAA	CCACTACCTAAGAGTATTTAA	TACGACTTTGTATCAGCATAA	TACCGCGAATGCATCAGCTAA
10431	TIMM23	NM_006327	CAGGCATGTTGTATAAATGTA	CCCGCTGTTATTGAGGAGTAA		
10436	C2F	NM_006331	CAGAAGAATGTTCTGATTGAA	AAGGTAATTAAGAATCCAGTA		
10450	PPIE	NM_006112	CAGATTCCTCTGGATTATGAA	AAGACGCTTGAAGAGAATAAA		
10454	MAP3K7IP1	NM_006116	ACGCCTTGGCTGAGAAGGCAA	CACGAGGACATGACCCTGCTA	CTGCAGGTGAGAGGATTTAAA	CACCTTGGACAAGCCACACAA
10457	GPNMB	NM_002510	CCGTGAGAATTCAGCATGGAA	ATCGAAATTCATCCGACGAAA	CTACTATTGATTAGAGCCTAA	TCCATGTAACTGTATGCATAA
10458	BAIAP2	NM_006340	AAGAAATACCAGACTGAGCAA	CACGGGCAACCTCCTGGACAA	CAGCAAGAATCCTCAGAAGTA	CTGCTTCTCCTGCCTAATAAA
10460	TACC3	NM_006342	CAGGAAGTTCTGAGAACCAAA	AAGGAACTTTCCAAAGCTGAA		
10465	PPIH	NM_006347	CAGGGTCATAAAGGATTTCAT	CCGCATGAAGATCGAGCTCTT		
10469	TIMM44	NM_006351	AAGAAATGAAAGAAAGTATAA	CTAGATAATGTCAAACAAGAA		
10474	TADA3L	NM_006354	ACCGACTGGCAGGATAAGAAA	CTGACCGAACTGGACACTAAA		
10478	SLC25A17	NM_006358	CTCCTGGAGATCATTAAAGAA	CTCATTGCTGTTGGTCTTCAA	CTGGACCTGTTGTCACCTTAA	ACCCAAATGATTCTCTTATAA
10480	GA17	NM_006360	ATGGATAAGAATACTCCTGTA	TTCGTGCTTATCTGAAATCTA		
10482	NXF1	NM_006362	CAGAACAAGTAGAACAGCTAA	AACGCGTTAATTTCCCTCAAA		
10489	MUF1	NM_006369	CCCAGGCTTTAGAGAAGTATA	CCGGCGTAAGAGTGAAGCCAA		
10490	VTI1B	NM_006370	AAGCAACAGGAAGCAAATGAA	ATGATATACCAAGGTAATAAA	AAGGTAATAAATGCTGTTTAT	CAGTATGATATACCAAGGTAA
10491	CRTAP	NM_006371	CAGCATGTCAGTGGCATTTAA	CAGGGAGATCAAGGACTTCAA		
10494	STK25	NM_006374	CCGGCCGAGTCCACACAGCAA	AAGACCTGACTTGGAGACAAA	CACCAAGCTATGGATCATCAT	AAGGGCATCGATAACCACACA
10499	NCOA2	NM_006540	CAGTCTAGTGCCAAAGATTAA	CCAGGAATGATGGGTAATCAA	AAGGATTGGCATTCAGTCAAA	AGGGCTGTTAACATTAGCAAA
10500	SEMA6C	NM_030913	CGCCCTGGAACCCAAATTCAA	CCGCGTAGCCCGAGTATGTAA		
10516	FBLN5	NM_006329	CAGATCTGCATCAATACTGAA	CAGATGGATGAAAGCAACCAA		
10517	FBXW10	NM_031456	CCGGTGTATATCCGAAATGAA	AAGGAAGGTCTTGAATTTCAA		
10521	DDX17	NM_006386	CACGTAAATGAAACCACTCAA	CTGGGACATTGTAATCATAAA		
10522	DEAF1	NM_021008	CAAGTCATTAACACACTTTAA	CAGCGGCACTCTGTACAAGAA		
10525	HYOU1	NM_006389	ACGCAAAGTCATCACCTTTAA	CAGCAAAGCCTTTAAAGTGAA		
10536	LEPREL2	NM_014262	GAGGCTGATGCTTTAAATGAA	CAGGAGTGGATAGAAGCCAAA		
10537	UBD	NM_006398	AAAGCATTCTTTGTCTATTAA	CTGGACAAACACAGCAATCCA	ATGGGATTTAATGACCTTTGA	AACCCATATGACAGCGTGAAA
10539	TXNL2	NM_006541	AACGAAGTTATGGCAGAGTTA	AGCGCTAATGAACATCTTAAA	TTCGATATATTGGAGGATGAA	TACCCTCAGCTGTATGTGAAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
10561	IFI44	NM_006417	CTGGGATATCTGAGAAGTATA	TCAGATGATAGTAAAGATCAA		
10562	OLFM4	NM_006418	CTCATTGTCCACCTTACTAAA	CGGGAATATTGCCAGAGTTAA	TAGGGATTCTTTGTACAGGAA	CAGAGTTAACCTGACCACCAA
10563	CXCL13	NM_006419	CTGAATGGATACAAAGAATGA	CGCTTCATTGATCGAATTCAA	AAGGGTGATGTACACATGTAT	ACGGAGGAGAATTAAGTCCTA
10569	SLU7	NM_006425	CTGGCTTTAATAAATATTTCA	CAGGCAGATCCTACAAAGCTA		
10571	SMA3	NM_006780	AAACTCATTCAAGGAGGTGAA	CAGCCGGGATGCACTAGGCAA		
10573	MRPL28	NM_006428	CAAGTTTGGGATGGACCTGAA	CAGTGAGATCCTGGACAAGAA		
10575	CCT4	NM_006430	CTCGATAATCTGGATAACTGA	TTGCCTGAAGTTGTATTGAAA	TTGCTCATATTGACCAATTTA	TAGAGTTGGCCCTACGATTAA
10577	NPC2	NM_006432	CCCGAGCTTGGAACTTCGTTA	GTGGATGGAGTTATAAAGGAA	AAGGACAGTCTTACAGCGTCA	CAGATCGTTTCTCATCTCTAA
10578	GNLY	NM_006433	CAGAAATTTCATGAGGAGGTA	CAGGGTGACCTGTTGACCAAA		
10580	SORBS1	NM_006434	TCCGGAACACTGAGAGATCAA	CTGAACAGAGATGATGATTCA	CAGGATTCCAGTCCTCTACTA	ACCCGGCAACACGAAAGCAAA
10581	IFITM2	NM_006435	ACCATGAACCACATTGTGCAA	CCAGGACCTCCACACCATTAA		
10594	PRPF8	NM_006445	ACGGGCATGTATCGATACAAA	CAACGTCGTCATCAACTATAA	CCGAAAGTCATATAAGATGAA	ATGGCTTGTCATCCTGAATAA
10595	ERN2	NM_033266	CAGCCACTCGACGACCCTGAA	CAGGGATTAATGAAACTGCCA	CACCTGCATTCTTTACACATA	AAGGATGAAACTGGCTTCTAT
10606	PAICS	NM_006452	CACGTGGAAATCTCCGTTATT	GCCCAAGGACTTCTAACAATA	CTCGACTAACAGGGACTATAA	CCCAAGGACTTCTAACAATAA
10613	SPFH1	NM_006459	CACTGGAATGTTAAACACTAA	CCCGGAATATCTGGAGCTCAA		
10615	SPAG5	NM_006461	TCGACATGACTTGGAAGATAA	CCCGAGTAGCATCAATGGTTT	TCCCGACAACTCACAGAGAAA	CCAAATTAGCTCTACTCCTAA
10623	POLR3C	NM_006468	CAGCTTGATAGGGAAAGGTAA	CCCACACTTGTCATTAATGAA		
10628	TXNIP	NM_006472	TAGAGGGCAGGTGTTCATAAA	TAGAGCTGATTTGATGGACAA	AAGAATACCTTAATTCCTTAA	AAGAGCCAATTTAACAAACTA
10630	T1A-2	NM_001006624	CGGGAAGGTACTCGCCCTAAA	CTCAAGTGTGTTTGAAACCAA	CAGGAAGTCGATAGTCTCAAA	ATCGAGGATCTGCCAACTTCA
10631	POSTN	NM_006475	ACGGATCTTGTGGCCCAATTA	CACGAGAAGAACGAATCATTA	ACCAGATTCATTACAATTCAA	CTGCTTATTGTTAACCCTATA
10634	GAS2L1	NM_006478	CTGGGACACGCTGGAGCATTA	CAGCAGAGCCTCTGACAGTAA		
10651	MTX2	NM_001006635	CTGCAGAACCTTGGCCTGAAA	AACCTCAAATTATATAATGTA		
10653	SPINT2	NM_021102	CAGCGATATGTTCAACTATGA	AAGGAGGAGTGCCTCAAGAAA		
10658	CUGBP1	NM_006560	TTCTAGAACTTCATAAGATAA	CGGCTTAAAGTGCAGCTCAAA	CGGGAACTCTTCGAACAGTAT	CAGGGTCCTCACCTAGCTCTA
10659	CUGBP2	NM_006561	CTGAAATTTATTATTAGACAA	CAGGAGAAAGGTTACTGTAAA		
10663	CXCR6	NM_006564	CTGCTATTCAGTCATAATCAA	CACCAGCATGTTCCAGTTATA	TCGTTTCATTGTAGTGGTTAA	CAGGTCATGTGCAAGAGCCTA
10668	CGRRF1	NM_006568	CTGATAGGACTTATAAACTAT	TCCATCTGTGTTGATACATAA	CGGGAAATTTATGATATTATT	CCGGGAAATTTATGATATTAT
10670	RRAGA	NM_006570	CCGGTTTGAGAAGATCAGCAA	TTGGTATGGTGTAACACTAAA		
10673	TNFSF13B	NM_006573	CACGCAGGACATCAACAAACA	CAGACAGTGAAACACCAACTA	CGGAGGGTAAATGCCAGCAAA	CACGCCTTACTTCTTGCCTTA
10683	DLL3	NM_016941	CCCGGTGAATGCCGATGCCTA	CCGGATGCACTCAACAACCTA	CCTGAAGATGTAGACCCTCAA	AAGGCTATTATTGTGATCAAA
10692	RRH	NM_006583	CTGGAAGAATCTGAAATAAGA	CACTGTACTGATGACCTTTAA	CAGACATGGATCATTGTCCTA	CACAAATGCAATTATTATTAA
10693	CCT6B	NM_006584	CAGGAGATGGTACTACTTCAA	TAGAACATCATTACAAACTAA		
10694	CCT8	NM_006585	AACCTTCGAGATATTGATGAA	CTGGACTTGAACAGTATGCTA	GAGGCTGTGTATAGAAACATA	AAGGCTGTATTTGTAGTAGTA
10713	USP39	NM_006590	GTGGCTGATGATGGTAAATAA	AAGAGGCGAGATAATGATGAA		
10716	TBR1	NM_006593	TCCCATTATCTCGACCACTGA	CTGGTTTGTGACGCCGGCCAA	ATGGCCGTCTGCAGCGAATAA	AAGTCTCGGCCTCCACATTAA
10717	AP4B1	NM_006594	TGGAACAATTGAAGAAATAAA	GAGGAAATTCTGAAACAGGAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
10724	MGEA5	NM_012215	CTGGTACAAATCAAACATGAA	CAGGGAGAGAGTCTTCAATAA		
10726	NUDC	NM_006600	TGGCCTACTGTTACACATTAA	CACCAAGAAGATTAACCCTGA		
10730	YME1L1	NM_014263	TTCCAGATTGACCATGAATAA	GAGGCATTAGATAATGCCTTA	TCGGCATTTATGGACTTCTAA	TCCGTTGATCCAGAAATTATA
10735	STAG2	NM_006603	CAGAAATATATTGAAAGTTTA	TTGCTTGTCCTTTAAGATAAA		
10748	KLRA1	NM_006611	CTGGAATTAATTCTACAATAA	TCGGATTATCATATGATGAAA		
10749	KIF1C	NM_006612	ACCTCCATCATCAATCCTAAA	CCGGCTGATTAGAGAGCTGCA	CACGGTCCAGACCATTGTCAA	CTGGAGAATCAGTACCGGAAA
10753	CAPN9	NM_006615	CCCGAGAACTTCTATGAGATT	AAGGAGTTCATTCATCTCAAT	GAGGAGTGTAGTTTCCTTGTA	GAGAACTTCTATGAGATTCTA
10761	PLAC1	NM_021796	CCGGTTCAGGACAAAGTCCAA	AAGGATTTGTATAAAGAGTGA		
10765	JARID1B	NM_006618	TAGGGTTGTGTGATTAATCAT	CAGGAATGTAGTAAGCCACAA	ACGCACCAAGCCGAAAGTAAA	TCGTCCTAACATAACACTAAA
10768	AHCYL1	NM_006621	CAGGGTGGTAAAGCTAAATGA	AAACAGTTGTATCGTATGCAA	CTGATAGAACTCTATAATGCA	CCCACTTGGATTTATAGTATA
10771	ZMYND11	NM_006624	CCGGATGAAGTCGGACCACAA	ACCAGTGGGTATATGATTGAA	CACCTCATGTATCGTAAGTTA	TAGGAATGGATCGATAGTTGA
10773	ZNF482	NM_006626	AACGTTTGTATTATTCTATTA	TACAGGGTTAATAATCCTTAA		
10776	ARPP-19	NM_006628	CACATGAAAGATTAATCTGAA	CACTCTGTCATTGTTAATCTA	CGGCATGTTTGTAGCATACAA	CCCGGCCGGCTTATGATTTAA
10780	ZNF234	NM_006630	AAGGGTTTCATTTACAGTTCA	CAGGACTATATACAACTCACA		
10781	ZNF266	NM_006631	CTCGCCTTAGTGAACATACAA	TTGCTATTTCTTCAAATCTTA		
10783	NEK6	NM_014397	AAGGGATAAAGTGGAAATCAT	ATGCAAGTTAGCTAATACAAA	ACCGGAGAGGATCCATGAGAA	ACCACGGAAGTCGAGAATTAA
10785	WDR4	NM_018669	CAACGTGACCTCCTACCTGAA	CAGCTTCAGCAGTCTCTACAA		
10791	VAMP5	NM_006634	CTGCAGCAGCGTTCAGACCAA	GACGGAAATTATGCGTAACAA		
10797	MTHFD2	NM_006636	AGCGAGAAGTGCTGAAGTCTA	AGCCATTAACCTAGTGATTAA	TAGGATTATTCCTTGCTATTA	CTCGCGGCAGTTCGAAATGAA
10803	CCR9	NM_006641	TTGGAAGAAATGAGAAATACA	CCCACTTTATTCTGAGGAATA	CAGTCTTGTTATCCTTGTCTA	AAGGGATGAATCTGAACTATA
10811	NOXA1	NM_006647	CAGGTGGAGCAAGTTGGCAAA	CAGCAGGGAGATCAGCCCTAA		
10815	CPLX1	NM_006651	AGCCATAACGTTAGACTGCAA	CCGTGTTCACTTCTAAACTAA	AACGTTAGACTGCAATACTAA	CACGGCCGTGTTCACTTCTAA
10844	TUBGCP2	NM_006659	CCCGGTGGCTAAAGAGATCAT	AAAGAGATCATCTACACGTTA	CCAGGAGGATTACAACGACAA	CAGCGTCTGGATCAGCAACAA
10846	PDE10A	NM_006661	ATGCAGGGAGTTGTATATGAA	AACCCTTTGCATAAAGAACAA	TAGACTCTCATTCACAATGAA	CAGTATTACTATACAATGTAA
10849	ASE-1	NM_012099	CCGGGAAACTGAGGAACTAAA	AAGGAGCTGTTTCCTGGGTAA		
10858	CYP46A1	NM_006668	CACGAGTCCTGAGTCGGTTAA	CCTGATGTCAACCAAGTACAA	AGGCTTGGTGTCCGAATGCAA	GCGGATGGACACATACTTTGA
10859	LILRB1	NM_006669	CAGAAAGTGCATTAAACTGAA	ATGAATGAATTAGGAAAGAAA		
10863	ADAM28	NM_014265	TCGGATAATTTGCCCTGGAAA	CACCTAAGGACTCAAATCCAA	AAGAAATATCTCCGAAGTTAA	CACACTAATCTTGGAGGAATA
10869	USP19	XM_496642	CGGCCTTAGCTAGAAGTCGAA	GACCCGCATTATAAACATTAT	CCGGGCTGTGGAGAAGGATAA	ACCCGCATTATAAACATTATA
10874	NMU	NM_006681	CCAATATTACCTCAAGGATTA	CAAAGTCCCTTTGCAAGTCAA	CAGAGTGGACGAAGAATTCCA	GAGCAATGCTATGGAATACAA
10881	ACTL7A	NM_006687	CTGCTCGGAGATGTTCTTCAA	CACAAGAACCTACTGAATCAA		
10886	GPR74	NM_004885	CAGCTTGTCCAGGAATCTACA	CTACTACGCATTATATATTTA	CTGGCCATAAGTGATTTACTA	CCGGGAAGACTGGCCAAATCA
10890	RAB10	NM_016131	AAGGGACAAACTAGTAGGTTT	AAGCACTGATGTAACTTGCTA	CTGATGTAACTTGCTAGGTAA	CAAATTCGGTTTCATATTCTA
10897	YIF1	NM_020470	CACGAAGGCCTTCATTACTTA	CTGGCCTACAGTGGCTACAAA		
10901	DHRS4	NM_021004	CAGGATGCTCTGGATGGACAA	AACCCTTTCTTTGGAAGCATA	AAGGAGCAGAGTTGCAAATTA	TTGCGCGGCTTTGAATCCAAA
10906	FLN29	NM_006700	TACTGTTATAATAATTATTAA	CAGGAAAGGAATAGAGGCCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
10907	TXNL4A	NM_006701	TGGCAACAACAACAAGATTAA	CAGCATCGCCGAGAAGGTTAA	TGGCCTAATCTTAACTAATTA	AAGGTTTACTCTGGTTATAAA
10908	NTE	NM_006702	CCGGCGGTCTACAGACCTTAA	ACGCATGAGGAAGAAACTGAA		
10933	MORF4L1	NM_006791	CAGAAACAGCGAGAACTTCAA	TCCGGAGAGCAGAGTACTCAA		
10934	MORF4	NM_006792	GGGCACCCAGCTACTCAACAA	GCCGAAATTCTTGCAGATTGT		
10936	GPR75	NM_006794	CTCGGATTGAACCTTACTACA	ATGCATTATCACACCACTAAT	CCAGCTCGTATCAGCCATCAA	ATGGACTTTATTCTAACTTGA
10939	AFG3L2	NM_006796	CCGGCACCAATCGACCAGATA	GAGCGAGTGATTGGTGGCTTA	CATGGTATTGGAGAAACCTTA	ATGATGAAGTACGAATACTTA
10945	KDELR1	NM_006801	CCGCACGCTCTATCTCTTCAA	TAGCAAGTTCAAAGCTACTTA	CCACTGGTTGCCAAACACTAA	CACGTGTATGAAGGTGGTCTA
10946	SF3A3	NM_006802	AAGGAAGAATGCAGAGTATAA	CAGAGACTATTCAGTACCAAA		
10947	AP3M2	NM_006803	CCCAGTGTATGTCAAACATAA	CACAATTAACCTGCAGTTTAA		
10956	OS-9	NM_006812	ACCCACCATGTTCTTGAACAA	AACAATCAGGTTTCTAAATAA		
10957	PNRC1	NM_006813	TTGTATATATACAATGGATAA	TTGCCTTGTTGCAACATACAA	TACACTTGTATGAGCAACCAA	CAGATTTCAGTATGTGTGTAA
10966	RAB40B	NM_006822	AACGGTGATATTGGAGTGATT	ACGGTGATATTGGAGTGATTA	TCGGCGAATGCTGCTTGCGAA	CCGTCGGACTTCGAATTTCTA
10982	MAPRE2	NM_014268	AACGCAGGTCATACAGCTTAA	TCCCAATATCTTCTAGAATAA	GACCTTATTAATAGGAGCATA	CAGCAGGTGCAGCTAAATCAA
10983	CCNI	NM_006835	AAGGCTGTAGAAGGAAATATA	CAGCGTTATTTAAGCACATAA		
10985	GCN1L1	NM_006836	CTGGAAGATTGTTGTCTCCAA	CAGGTTCAGCTGGAATGTGAA		
11001	SLC27A2	NM_003645	CAGCCACTTGATATAATCCAA	CTGAGAGATGTCTTTAAGAAA		
11012	KLK11	NM_006853	CCAGGAGACGATGAAGAACAA	ACAGGAGATGCTGTCACTTAA	ATGCTGTCACTTAATAATCAA	CAGCTCCTGGCCATATATCAA
11016	ATF7	NM_006856	CGGGCTGTGGACAGAGATTTA	CAGCTACTGTTAGCTCATAAA		
11017	RY1	NM_006857	ATGACTTGCCATTATAATTAA	ATGGTTCTCTCCGCAAGTATA		
11027	LILRA2	NM_006866	CAGGCTGAGGAGTACCATCTA	GAGGCTCTGGAGGACAATCTA		
11031	RAB31	NM_006868	CGGGCACATTAGGCAGTTGAA	CACACACTGATTCATACTAAT	CAGGATTCACATAAACATTGT	AAGGAATACGCTGAATCCATA
11033	CENTA1	NM_006869	CACCCGTAACATCTTCATCTA	CGCAGTGGAGGCGCACTTCAA	CCGGAAGTTTGTGCTGACAGA	GAGGCGCACTTCAAGCATAAA
11035	RIPK3	NM_006871	ATGGCAAGTCTGGATAACGAA	CACAGGGTTGGTATAATCATA	CAGCCTGATGTCGTGCGTCAA	ACCGCTCGTTAACATATACAA
11041	B3GNT6	NM_006876	ACCGATGACAATGTGTAAATA	AAGTCTGAATACTTAATGAAA		
11045	UPK1A	NM_007000	AAGCATATACTAGATAGTCAA	CAAGCAGATGCTGACCTTCTA		
11054	OGFR	NM_007346	CACGGTGGGCCGAGCACAGAA	CAGGAGTGAACTGGCATGCCA	CACGCCAAACCTGAGTTTCTA	CAGAATGACAGGGTCCAGAAA
11068	CYB561D2	NM_007022	CACAAAGAGCAGCTTGGCAAA	CAGCTCATACTTGTACTGTAT	CAGGTGAGCAATGCCTACCTA	CACCAGCTTGGTCATTATGAA
11072	DUSP14	NM_007026	TAGCTGTTAAGTAACTATAAT	CCCAGGATTATATTAGCATTA	ACCCTTATTATTTAGCTGTTA	AAGGGAATGCATACATTGCTA
11073	TOPBP1	NM_007027	CAGCAATATTTCCAACATAAA	AACGAAGTTTGGAAACAGAAA		
11079	RER1	NM_007033	CACGATGAAGAGGCAAATCAA	CGGAATTATAAATATATATTA		
11092	C9orf9	NM_018956	CAGCATCGAGCAGAAGTACAA	CAGGTGCAGAGCTACATGGAA		
11098	PRSS23	NM_007173	ATGGTAGTCTTTGAACAGTAA	CACATATTAAACTATACCTTA	AACAGTTGTGGCCACACTAAA	CTGCATTGTAGCAATTTGTAA
11099	PTPN21	NM_007039	CCCACCGCAGTTGCACTATAA	AAGCACCTCCTTACCGGGCAA	GTGCATAGATTTCTATCTTAA	GAGGAGACCATTCAATTTCAA
11113	CIT	NM_007174	CCGGAAGCTCCAAGAAATCAA	AGGAATTTAGTCGGCGTCTTA	CAGGATATACCGTAACACGAA	ATGGAAGGCACTATTTCTCAA
11119	BTN3A1	NM_194441	TCAGCCTATAATGAATGGAAA	CTGGAGGAACTCAGATGGAGA	CAGATGGAGAAGTATCCAGTA	AAGACTCAGTTCAGAAAGAAA
11126	CD160	NM_007053	CTCAGTTGATGTTCACCATAA	ATGACCTCTTGTCATAGTTAA	AAGGAACGCGACTAAACTTAA	AAGAGATGCTAAATATACCAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
11127	KIF3A	NM_007054	GCCGATCAATAAATCAGAGAA	CCCAATTCATTTGCTCACATA	CTGGTTCAGAAAGACAGGCAA	GTGCCTTATCGTAACTCTAAA
11128	POLR3A	NM_007055	ACCAAGAAAGTCAGCATGTAA	ACGGCTGTAAAGACAGCTGAA		
11131	CAPN11	NM_007058	CAGGATGGCCATCAAATTCAA	CCCAAGAATACTGGCCATATT	CACATTCTTTCTAACCATGGA	ATGCGCCTGGTTATTGAGAAA
11132	CAPN10	NM_023083	CAGCAGGAACTTTGCCTCATA	CAGGATTGACAGGCCATCCAT	CTCCGTCATGGCAGTGATGAA	CAGATCTTCTTTATAACTATT
11135	CDC42EP1	NM_007061	GCCCAGCACAGTGCAAGCAAA	CTGGGAGAGACGAGCCATGAA		
11141	IL1RAPL1	NM_014271	GCGGGATACTTGTGAAATATA	ATCGGGCACTTTGAGAACTAA	ACGCATTGTGATGACCAGCAA	ATGCAACAAGTTGAACTCCAA
11146	GLMN	NM_007070	TAGCTATGCTTCAGCTGTATA	TAGCATCGAAACTAGGAGAAA	GAGGAACTTCAGTCTATAATA	AAGGCATATTCAATTGGATTA
11154	AP4S1	NM_007077	ATGCTCTTTCATTGAATATAA	CTGGTCCTTATCAGGAACCAA		
11157	LSM6	NM_007080	CTGGATGGCTACATGAATATA	CTGACATGTGAGTAAGATAAA		
11163	NUDT4	NM_019094	CAAATTCATGTTAGTGAAGTA	ATGAAACTGGTACCAATTTAA	CAGGTACTATTTGTCACATAA	AACATTTGTTCTACAAATTAA
11166	SOX21	NM_007084	CCGGTTTGTATGTACATAGAA	TTGAGCGAATATCAAAGTTAA		
11176	BAZ2A	NM_013449	CACTGAGAAGGCTAAGACTAA	CACCACTACAGAGATATCATA	CCCGCAGTGACGGCCAGTAAA	CTCGGTAGCTTTGAATCTTAA
11177	BAZ1A	NM_013448	CAGCTAGACCAGCTTATTGAA	AACGAGGAAGACCACAAGTTA	CACAAGTTAGATTGCCAGTTA	AACCCTCGTAACACAAGTGAA
11181	TREH	NM_007180	CAGGCCTGAGTCCTACAGCAA	CTCGCAGAAGTCAGCCATGTA		
11194	ABCB8	NM_007188	CACGATGCTGGTGCATTTATT	CACCTTCTTTGACGCCAATAA	AGGAATTTAAGTCATCCTTCA	AAGCTGGAAGCTTCCGATGAA
11197	WIF1	NM_007191	CACAAGGCATCAGTTGTTCAA	CCCTGTCGAAATGGAGGTAAA	TTGCATTGGCTTGAAGCAATA	AAGCAATATAATATATTGTAA
11211	FZD10	NM_007197	CAGGTGTGCAGCCGTAGGTTA	ACCTCACATTTGTGAACTCAA	CCCGATTATGGAGCAGTTCAA	CAGCCGTAGGTTAAAGAAGAA
11212	PROSC	NM_007198	AAGGTTCTCCTGAAAGGTTAA	ATGGCTCAGGTTAATTCTCAA		
11218	DDX20	NM_007204	CAGGGCATGGCAAGAATATTA	CCAGATGAAGACAAGACTTAA	CTGGACTATCAGTCAAATCAA	GGGCTCGATTTAATTGTTCAA
11221	DUSP10	NM_007207	CCGAAGATACTACACACTTTA	CAGGGCAGCTTAAGTGGTCTA	CAGGTTCATAGACCGAAGATA	ATGAGAATACAGGCTCTCTAA
11222	MRPL3	NM_007208	GCCGCCGAAACAGACAGTTAA	AGGGCATAAATATATCATTCA	CCGCCGAAACAGACAGTTAAA	CACATTAAATATATGAGTTAA
11224	RPL35	NM_007209	CGAGGAGAACCTGAAGACCAA	CAGGAAATTCTACAAGGGCAA	TGCAGCAATGGCCAAGATCAA	CCGTGTTCTCACAGTTATTAA
11226	GALNT6	NM_007210	CAGCGTGATCATTGTGTTCCA	CACCTTCTATGGTGCCATCAA		
11232	POLG2	NM_007215	CAGATACGAAATGGTGTTAAA	AAGGAACAAACTTTACTACAA		
11240	PADI2	NM_007365	CAGCAAGCGAATCACCATCAA	CAGCCTTGACTCATTTGGAAA		
11243	PMF1	NM_007221	AAGGATCTGCACAGTGTTATA	GAGGAAATCTCTGACATCAAA		
11248	NXPH3	NM_007225	CAGCGTCCACTTCCAACACAA	CGACTTCTACTCCAACATCAA		
11259	DOC1	NM_014890	AAGACTGAAACTGAAGCTAAA	GAGGATTTAACTAAACTGAAA		
11279	KLF8	NM_007250	CTCAGTCAGTCTGCCAAATAA	CTGAGATAGAATACAGAAGTA		
11283	CYP4F8	NM_007253	CAAGGACATAGTCTTCTACAA	TGCCCTTGTAGTGAAACGGAA	AGGGAATGTCTGTAACATCAA	CAGAGTCTAAGTAAAGACTTT
11284	PNKP	NM_007254	CAAGCTGGTGATCTTCACCAA	CGGGAAGTCCACCTTTCTCAA	CACGTGTGAGACAGCCCTGAA	CACGTGAACAGGGACACGCTA
11316	COPE	NM_007263	CAGAGCTGTCAGGACCATGAA	CCGGAAGGAGCTGAAGAGAAT		
11317	RBPSUHL	NM_014276	TCCCTTGTCCTTACACATACA	CTCAAAGGTCTCCCTCTTCAA	CCCATGATCATCCGTAAAGTA	CAGGTCCTTCCTGGAATATTA
11326	VSIG4	NM_007268	CAGACTCCTGATGGCAACCAA	CTGGTGCTCAATAAATATCTA		
11328	FKBP9	NM_007270	CAGCGGCGACTTCGTGCGCTA	AAGCTTGCCTACGGAAATGAA	TCGAGTCACAATCGCATGAAA	CTGGTGTTTGATGTTGCATTA
11329	STK38	NM_007271	AAGGCGTTGACTGGGAACATA	CCATAGTACTAAGGAAATAAA	TACGTCGGCCATAAACAGCTA	AACCTTATCGCTCAACATGAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
11331	PHB2	NM_007273	TCGCCACATCACAGAATCGTA	CAGAATCGTATCTATCTCACA	CACAGCTGCTGTAGAAGCCAA	AACCCAGGAATTCTCAATAAA
11334	TUSC2	NM_007275	AAGGCTGGTGCCAGTAGTTAT	CCAGTAGTTATGAGTAGCCTA	CCGCGGCTCTATGTTCTATGA	CAAGCTGAGGCGAGTGCATAA
11336	SEC6L1	NM_007277	CTGGAGCAACATCTGAATGAA	CACGCTCACTTCAAACATCAT		
11340	EXOSC8	NM_181503	CAGGAGATTTCTGAAAGAGAA	CAGAATTTGCAGCACCATCAA		
11343	MGLL	NM_007283	CCCGATTTGCCTGGTTCTGAT	AAGACAGAGGTCGACATTTAT	CTGGACCTACCTTAATGGTTA	TCAGAGCTTGATGCTACTGTA
11344	PTK9L	NM_007284	AAGGAATTCTTTGCCAAGGCA	CCAGATGAAGCTGGACCTAGA	TTGGGATGGTTGAATGCTGTA	AAGACAGAGATCAGTGTGGAA
22795	NID2	NM_007361	CCCACAGAAAGTAAAGTATCA	CTGGAATAGAGAAGCTCCTAA	AAAGCACATGTGATCAATATA	CACGTATAATGCTGCCAACAA
22803	XRN2	NM_012255	ATGGATTACATTAGAAGGCAA	AAGGAGGTTCAGGGCATCAAA		
22818	COPZ1	NM_016057	AGCGATTTAAATTGTATTGAA	TTGGCTGTGGATGAAATTGTA		
22820	COPG	NM_016128	CAGGAAAGGGACATTGTAAAT	AGGCCCGTGTATTTAATGAAA	CACCGACTCCACTATGTTGAA	CCGAGCCACCTTCTACCTAAA
22827	SIAHBP1	NM_014281	CTGGGACTCCGTCACCATGAA	CTCCGTCACCATGAAGCACAA		
22828	RBM16	NM_014892	CACGGTCGTATTCAAGTGAAA	CAGAATGATCCTGAACTTTAT		
22838	RNF44	NM_014901	CAGAGGGATATTCACTAATAA	CAGGTGACGTTTCTATATTTA		
22841	RAB11FIP2	NM_014904	TTGGAAGTATTTAATATGCAA	CTCGTTATAAACACTACTAAA		
22843	PPM1E	NM_014906	CCGCCTAATCATGTGTTTATA	TTGGTTCTATAAACTAGATAA	GAGGCGGTTTATAGTCAGAAA	CCCATTTAGGTCTGTACTAAA
22848	AAK1	NM_014911	CTCCTCGGACCTCTCAACAAA	CCCGAGAAGCTTGGAGGCTCA	CCAGGTGGTAAACCTGATGAA	AACGTGAGTAGCGGTGATGTA
22850	KIAA0863	NM_014913	AAGCAATTTCTTAAAGATTAT	CAGGAGAGAAATACTTTCATA		
22853	LMTK2	NM_014916	AGCGACTATTATATCCAGTTA	ACGGCTCTTAGCTGCGTTCAA	CAGATCAGACTAAGTATAGTA	CACCTCCGACTTAAATGTGAA
22871	NLGN1	NM_014932	CCGCCTCAACACAATGCCTTA	CGGAGGTATATTCTACCATTA	GAGGAATATTATGTGAATATA	AAGAAACATGACTGTCTCAAA
22882	ZHX2	NM_014943	ACGGCAGATCTTCCAAATCAA	CAGTACTATTGTGACATTAAA		
22888	UBOX5	NM_014948	CAGACAGTAACTTTGGTGTAA	TCCCTACAACTTGGTACTCTA	CCGGCACATTCCTTTCCTTTA	TCCGGTGTGCTTGTGTTCTTA
22901	KIAA1001	NM_014960	TCGCAATGGAGTCACACGCAA	CACAGGGTGATGGACCATCAA	AAGGACAAAGTTGACCACACA	CTGGAAGACGATACCGCAGAA
22902	RIPX	NM_014961	TTGGTATAAGTTCCTAATTAA	AACATTGTAAATAATCCTATA		
22913	RALY	NM_007367	CGGGCAGACCCTGGACATCAA	CTCAGCCAAGATCAAGTTAAA		
22915	MMRN1	NM_007351	CACAACTTACTTAGAAATGAA	TCCCTGTATATAAATATATAA		
22920	KIFAP3	NM_014970	TCGAGTTAGCTACAAACATAA	CCACATCTTGATGCTAAGTAA	CACAAGAGACGTCATAATCAA	CAGCATGATGGACCAACTAAA
22925	PLA2R1	NM_001007267	ATGCGTGGAAATATTATGCTA	ACGGTGTAAATACATCTGATA	AAGGTTTGGCTCATAGAGAAA	AAGGAGGTACGCTGTTAAGTA
22927	HABP4	NM_014282	AAGCGAGAATTTGAAAGATAT	CAGACCAAAGCCTGAGTTTAA		
22936	ELL2	NM_012081	CTGGGATTTATACAAGATAAA	CAGAAAGATGGTGTCAATCAA		
22937	SCAP	NM_012235	CCCGGTAGACCTGGAGGTGAA	CACCTGCTTAATTGACACCAA	CCTGACTGTAATAATATTAAA	CTGGCCGACGCTCTTCAGCTA
22938	SKIIP	NM_012245	CACAGGTCTCTCCAAAGTGAA	TCGGATGGTAGAAATGCAGAA	CTGGATATGGGACGAAAGAAA	CCCGATGAAGAAGCTATTAAA
22943	DKK1	NM_012242	CAGTAAATTACTGTATTGTAA	CCCTGTGATTGCAGTAAATTA	CACACTTGTCAGAGACACTAA	ATGTACTATCTTAATGCTTAA
22947	DUX4	NM_033178	GAGCTCTGCGGCACCCGGAAA	AGAGAGGAACGGGAGAGACTA		
22949	LTB4DH	NM_012212	CGCGCCGGAGGGAATAGGAAA	CACTGTTATCGGCCAGATGAA	CCGCATTTATGGGAATGCTGA	GGCCATTTAGATGATTAGTTA
22954	TRIM32	NM_012210	CTGGGTAGTTCTAGAACTTTA	CAGCAGGAATTTGACCCTCTA		
22977	AKR7A3	NM_012067	CTGGGCAGAGATGTACAGGAA	AAGGCTCTTCTGTAACATCTT	AACTGGAAGGAGCACCACTTT	AAGCGACTGCAGAGTGAAAAT

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
22979	KIAA0953	XM_039733	CTCAAGGATATCAGAAGCCAA	CAGCATTTGCGGAATTAACAA		
22980	KIAA1049	NM_014972	CCGGTCACTGTTGCCAAACTA	CCGCTTCGAGCTGATAAACAT		
22986	SORCS3	NM_014978	CAGGCTATTCTGAGCTCAGAA	ATGGAGGAGGGTGATCTACAA	AAGGCAGTCAGTGGATCTTAA	CACAACTTCCTTAAAGTCAAA
22987	SV2C	XM_043493	CCAGATTTAGCTGGAGATTAA	CTGCTCCTAATTTAACATTAA		
22992	FBXL11	NM_012308	AAGCCAGACTGAATCAACAAA	AGCGCTATGTGTACTGCATAA	CTCACTGGAGTTCCTATAGTA	ACCCATTTCGTTGCTACCCAA
23001	WDFY3	NM_014991	CGGCATTAATACTTTAATTTA	AACATGAAACTTCAAACTAAA		
23015	GOLGIN-67	NM_015003	CTGAAAGACAAGAGCATTTAA	ACCGGTCATCGTACAAAGAAA		
23030	JMJD2B	NM_015015	CCCGGCCACATTACCCTCCAA	CAAATTGAAGATGGAGATCAA	AAGCAATGTTTATATTATAAA	CACCTGACAAATCCTAGCGAA
23032	USP33	NM_015017	AAGAATTCCTTCGATGTTTAA	AAGAAGATCCGCAAACCATAA	CTGCAAGTAGTGGACACTATA	CCGGTTGTTCATGTTGATCCA
23033	KIAA1117	NM_015018	AAGGAGGGATATGTCTCTGAA	AACGAGAGATCTCCATATAAA	CCGGATTTCTGTTATGGGCAA	CCGGAGTTCTATGTACATAGA
23040	MYT1L	NM_015025	ACGGAAATGTATACAAATCAA	CAGGACTGAGTCAGAAATGAA		
23043	TNIK	XM_039796	CCGGAATATTGCTACATACTA	ATGGCGTTATTTCTAATTTAA	CTGGAATATAAGCGCAAACAA	AAGGACCATATTGATAGAACA
23045	KIAA0826	XM_093839	ATGCAAATTAATAGACATCAA	ACGCATTGGTACCAAATTTAA		
23049	SMG1	NM_014006	TTCGTTTGCATCACAGTTTAA	ATGGGTCAGGTTCGAAGTCAA	CACCATGGTATTACAGGTTCA	ATCGATGTTGCCAGACTACTA
23052	KIAA0830	XM_290546	AAGATCTATATGTTAAGCTAA	CAGCCAAACTATTATTTGATA	CCGCCCAGGATCAATCAGAAA	AACGAATGGTACAATCTCAAA
23053	KIAA0913	NM_015037	CTGGTATTTATTTGGCATTTA	CACGGGCAAGAGACTCCAATA		
23063	KIAA0261	NM_015045	CTGGATCATATTGTAGATAAA	AAGGAGATAAATCAAAGGAAA		
23081	JMJD2C	NM_015061	CAGATATTAATGGGAGCATAT	TCCCAGAAGTTCGATTCACTA	CCCAGAAGTTCGATTCACTAA	AGCGGGTAGGGCGATAATTTA
23082	PPRC1	NM_015062	AAGGAGCGTGCAATAGAAGAA	CAGGCTTTCATCAGTGAGATT	CAGACTAATAAACATCAACTA	AAGGGTGGTCTTCATTGGAAA
23085	RAB6IP2	NM_015064	CTGAAGTTATATAGCCTTGAA	AACGGGCTTTAACATGTTTAA	TAGAAGTAAATTAAAGTTGTA	CAGGAACTTAACCCAAATCTA
23086	SLAC2-B	NM_015065	AAGGAAGATTATGGAAACCAA	CAGGAGAATAAGAGATATGAA		
23090	ZNF423	NM_015069	CAGCAAGAAGTATAACTGTAA	CAGAGAGAAATGCTTAGTCAA		
23091	KIAA0853	NM_015070	CTGGCATATAGTAATACCCAA	AAGAAGCGCTATAGAAATGAA		
23098	SARM1	NM_015077	CTGGTGGTTAAGGGTAGCAAA	CAGGATCGGGATTACAGGCAA	CTGCTATTAAATCCACATTAA	AGCGGTGTTGGCGACTAACAA
23108	GARNL4	NM_015085	CACATTGTATTTGTTAATGTA	CAGGGAGTTTCTGCTCACCAA		
23116	KIAA0423	NM_015091	AAGGCGTATTTGGAAGTTTAA	CTGGAGCTATTTCACAGTATA		
23118	MAP3K7IP2	NM_015093	ATCCTAGGTAATTAAACCATA	CTGGGTAAACTATCTTTGTAA	TGGCTGGGTATCTCAGTTTAA	CAGTCAATAGCCAGACCTTAA
23126	POGZ	NM_015100	CAGGGATTTCCTGTAAGGAAT	CCGGGTGTAAGGTCCCTTTAA		
23129	PLXND1	NM_015103	CAGCCGCACTGCACAAGTGTA	CATGACAGTCATGGTCTATAA	CACGAGTACCGGGTCAAGATA	CACGCTCTGCAAGGTTCTCAA
23144	ZC3HDC3	NM_015117	AACGTGGTCATCAAAGTTAAA	CAGCGACTTCCTCAAAGGCTA		
23148	KIAA0363	XM_166571	CCGGGTGAGGCTGGAGTGCAA	ACGATCAGATCTGTCCTGCGA		
23149	FCHO1	NM_015122	CAGGAAGTTTGCAGAGAGTAA	CAAGTTCTATGTGCACATCAA		
23158	KIAA0882	NM_015130	CTGCAAGATAATGTAACTGAA	CTGAATGGATGTGGAAATGAA		
23163	GGA3	NM_014001	CTGGAGTCCTGGCTCAATAAA	AAGGAATAAATCCAAGAGCTT	CACGTTAGAGGAAGTTAACAA	CAGGGTGTCTGAGAAAGTGAA
23165	NUP205	NM_015135	CTGCGTCAGTTTAAATTTCAA	CTGACAGGAATTATAAGTAAA		
23166	STAB1	NM_015136	CACCTCGTGCGCGGCCATCAA	CACGAAATACTCCTACAAGTA	CACGCCAACTGTAGCCAGGTA	TAGGAACAATGGTCACTTGTA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
23170	KIAA0153	NM_015140	CGGCCACATCTTCAAGGTCTA	ACCCAGAACCTTCACCAGCAA		
23177	KIAA0582	NM_015147	CGGCAATTTAAGAAAGATATA	CACCCTCAAATCACCTACTAA		
23180	RAFTLIN	NM_015150	CAGGCAGATGAGGAAATCAAA	CTGAAATTCGTTGGTGTTATA		
23191	CYFIP1	NM_014608	TCGAAAGGTTATAGAAATAAA	CCAGCCAAATTTCAACACTAA		
23203	PMPCA	NM_015160	CAGAATAAGTTTGGACAGTTT	CAGGATCGAGATATGAAGCGA	CTCACCGAGATGATTCATGAA	TCGAGAAATGGTAGAAATCAT
23213	SULF1	NM_015170	AGCATGGATTTGATTATGCAA	AAGAGGCAAATTTCTACGTAA	TCCGTCGAATTTGAAGGTGAA	CTGGTGTTTGCGTACAGTTAA
23218	KIAA0540	XM_291064	CTCGGGAGAGACGGAATACAA	CACACAGAATGTATACTTCTA		
23231	KIAA0746	NM_015187	TAGAAGATTCTTAGTACTTAA	CCGGGAGGATTTCCATTATAA		
23235	SNF1LK2	NM_015191	CGGGTATGTCCTGGTGAATTA	ATCTACCGAGAAGTACAAATA	CCGAAGGATGTTGGTCCTAGA	AAGGGCAAGATTATTTGCTTA
23236	PLCB1	NM_015192	AAGCGAGTTGAAACTGCTTTA	CACACTACCAAGTATAATGAA	CAGAGATGATCCGGTCATATA	TCGAGATTACATGGATGTTAA
23258	RAB6IP1	NM_015213	CCGATTTGTCACTGCAATCAA	ACCATTGAGAAGAACATTCAA		
23259	DDHD2	NM_015214	CAGGATGAGTATGGACCTTAA	AAGAAAGAAGATATTAAACTA		
23268	DNMBP	NM_015221	TCCGAGGTTCCTCAAAGTTAA	CCAGCTCTTCACAAACTTTAA		
23277	KIAA0664	NM_015229	CAGCCCGACCTTCAAGAAGAA	CCGAGAAAGGGCCATATTCAA	AAGGGCCATATTCAAGGTGCA	CTCGGCCAAGCACATCTTCAA
23283	CSTF2T	NM_015235	CAGGATAAGGTTACACTTGTA	CAGCCATTTAGTCCTAATATA		
23284	LPHN3	NM_015236	CAAGCGTACAATGACAGGTTA	AAGTATGGGAGTAAAGCTAAA	CAGGAACTATAGGTGTATCAA	AAGCTAAACATTGCATATCAA
23303	KIF13B	NM_015254	AAGGTTATTCTTAATCCTGTA	ACGGGAAGCATTAGCAAGAAT	CCCACTAATGTCTTAACCTAA	ATGTCTTAACCTAAACCATAA
23304	UBR2	NM_015255	ATGGATCCAATTACACGTCAA	CCAGATTTATTACTACCATAA	CAGAACAATACTCTAATAGAA	CAGGTAAATGCTACAGATGAA
23309	SIN3B	NM_015260	CACATTAAAGTTAATAATTGA	CAGCTATGTGAATAAGATTAA		
23313	C22orf9	NM_001009880	CTCGCCCTTTGTAATAACCTA	AAGAATGTACCTGCACTCAAA		
23315	SLC9A8	NM_015266	CACCCTGGTTGTCACGACGAA	CTGGATGCCTATTTAGAAATA	CAGAGTCGCCTTAGTCCAGAA	TTGGCTCACCTTGGTAACAAA
23316	CUTL2	NM_015267	AACATTCTCATAAACATTTAA	AGGGAGGAACTCAACCATCAA		
23324	MAN2B2	NM_015274	GTCCAATATCAGAACTATTAA	CCGGACGTTCTTTATTCACTT	CACGGGTTTCTCTATGAAACA	CGGGCTTTCTTTGGAAGATGA
23326	USP22	XM_042698	AAGGTGAATTTCATAAATGTA	CTGAGTTTATACAGAAATTTA		
23332	CLASP1	NM_015282	CAGGATTAGAAACACACTTAA	AAGCGTAATGTTACACTTTAA		
23347	KIAA0650	XM_113962	AAGGATCTTAACAGTCAATTA	CAGGGATAAAGTAATTCCTAA	AGGACCAATTATCTCAGTCTA	CCCGTTCGTCTCAATGTTAAA
23352	RBAF600	NM_020765	CTGCGTGAAGGTGAAAGTCAA	CAGCAGGGTTATGCCCTTAAA		
23367	LARP	NM_015315	CAGGCTGAAGTGATTCATTCA	CACCTAATCCACAGAAAGTAA		
23378	KIAA0409	NM_015324	AAGGGTAGTACTACAAATGAT	AAGGGAAGAAGAAATGTCAAA		
23379	KIAA0947	XM_029101	CTGGCAGTTTATTGCTCTTAA	CCGCATCATTCAGAACATAAA		
23385	NCSTN	NM_015331	CCCGAATGGCTGAGCCCTGAA	CAGTGCCAGGATCCAAGTAAA	AAGGTTTAATGTCAGGGTCAA	TCAGATTGGGATTAACATAAA
23386	KIAA1068	NM_015332	AGGCAGGAACTTGAAGAGAAA	CCCTGCTTTAATAAACAGCAA		
23396	PIP5K1C	NM_012398	CGGCGAAACCACCTACAAGAA	GACGGCGAGAGCGACACATAA	CGGCAAGACCTATTTATAATA	CCGCGTCGTGGTCATGAACAA
23398	KIAA0073	NM_015342	AAGGTTGATGCTGTAAGATTA	ATGGGAGACATTCACACCAAA		
23403	FBXO46	XM_371179	CAAGATCACATGTGACTTATA	CCCGCCTTCTGCGGCCCTCAA	CAGCGATAGCTCCAAGGCCAA	CTAGATGGTTTGCCTATTAAA
23404	EXOSC2	NM_014285	CTGGTAAAGTTGGAAGAATAA	CTCCATTCCTATATCCTTTAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
23411	SIRT1	NM_012238	CAAGCGATGTTTGATATTGAA	TTGGGTCTTCCCTCAAAGTAA	CAGGATTATTGTATTTACGTT	ATAGCTGTTCTTTATGCATAA
23413	FREQ	NM_014286	CTGCGTGGCTAGGATGATTAA	CCCGGGCTGGTTGGTCTTGAA	GCGGAATAAACCCAATGGTTA	CGGAATAAACCCAATGGTTAA
23416	KCNH3	NM_012284	CCGGCGGGAGCAGGTGGTAAA	AGGGTAGTAGATGGCATTGAA	CCGTACCACATTCGTGTCCAA	CAAGGACATCAGCGAAACCAA
23417	MLYCD	NM_012213	CCCGGGTTCCTGAACCTAGAA	CAAGGTGTGTGTAGTAAGTTA	AAGTTGGATAATAGGCTTTAA	TAGGCTTTAAATGATCAGGGA
23428	SLC7A8	NM_012244	CTCCCAATATATTTACACGAA	TGGTGAGAAATTGTAAACAAA	CAGGCGGTTGAGGAACATATT	CCCGAATTCTGTCTGCTTAAA
23451	SF3B1	NM_001005526	AAGACTCACGAAGATATTGAA	CAGGTTATTATGACCAGGAAA		
23456	ABCB10	NM_012089	ACCCTGCTTCTGGAACTATTA	CCCAGTGTGGCTGAGATCCAA	CTAGGTATTATTAAGAATGAA	TAGACCCTAAGAAGTAATTAA
23457	ABCB9	NM_019624	CTCCCTAGCCTCCTAAGCAAA	TTGAGAGAACCCGGTCAATAA	CTGCGTGACCACGGCCATCTA	CCCGGTCAATAAAGTGTACTA
23463	ICMT	NM_012405	CAGAAATATGACTTATTTCTA	CAGAGTGTAAGTAAAGGATAA		
23468	CBX5	NM_012117	CAGGGAGAAGTCAGAAAGTAA	GCCGATGACATCAAATCTAAA		
23471	TRAM1	NM_014294	CCGGAACAATTGTGTGCTTTA	CTGGCATTATACTGAACTATA	ATGGTGTGAATGGAACATTAA	CAGGGTAACATGGAAATACTA
23474	ETHE1	NM_014297	TCCCTGGAGCTCCCTAAATAA	CAGCTGTGAGGAGTTTGTCAA		
23480	SEC61G	NM_014302	CAGCAATAGGATTTGCTATAA	CTAAATTAAAGTAATTTCAAA		
23484	LEPROTL1	NM_015344	TCCCAATGTTATGCAGACATA	CACAGTCATCTTTGCAACTAT	CAGAGACTTGCTGAAGGATTA	CAGACGGTTGGCATACGTTAT
23495	TNFRSF13B	NM_012452	CTGTAGGTCGTCATCACCTAA	CAGCGGAGTGGAGAAGTTGAA	AAAGGAGCAAGGCAAGTTCTA	AACCCTAAGCAATGTGCATAC
23506	KIAA0240	NM_015349	TTGGATATAGTCAACATATAA	CCCAATTAATATACAGCCAAA		
23507	TA-LRRP	NM_015350	AAGCATATTGGATTTATTTAA	CAGATCAACCTCAATAATGAA		
23511	NUP188	XM_497078	AACAATGTTATTCGGCTGAAA	AACAACCTCATTGCTGTTCTA		
23513	SCRIB	NM_015356	CTGGGAGGCAACGATCTGGAA	CAGGATGAAGTCATTGGAACA		
23524	SRRM2	NM_016333	CCCACTTGGTACAGAAATGAA	CTGGGTCATCTCCAGAAACAA		
23531	MMD	NM_012329	CGCCATTTGGAAATACCTTTA	ACGGACTTTATGCGGCATTTA	AACCATTTATGTATTTCTCTA	AACCACTAATATGTATGTAAA
23532	PRAME	NM_006115	AAGGAAGGTGCCTGTGATGAA	CAGGATGTGCATGCATCTTGA		
23533	PIK3R5	NM_014308	CAGGATCTATAAACTCTTCAA	TAGGATCCTTTCTAGAAGGAA	ATCGCAGATCAAAGTGGACAA	ACCGGTGCTGCTGCAACTCTA
23543	RBM9	NM_014309	TAAGAAGATGGTCACACCATA	TCCGTTTGGTTTATGGAGAAA	ACGGCTGCTTTGAAAGGTTTA	AACGGTATAAAGAGAGATCAA
23548	OSRF	NM_012382	CAGGAAGATACTATTGGTGTA	CCGCTTTATGTTAAAGATCTT		
23549	DNPEP	NM_012100	CACGAGGGTGATGAAGGCCTA	CAAGTACTTCATGACCAGGAA	GAGCTGAAGCTGGATTATTAA	AAGTGGATTGTCACTCAGAAA
23550	PSD4	NM_012455	CTGCCAGGAATTCATAACCAA	CACGGCCAAGGTGAAGCGCAA		
23551	RASD2	NM_014310	CTGGGAGGGATCCGACAGAAA	CTCCGTGTACACTATCAATAA	TCCGTGTACACTATCAATAAA	ATGGATCTCCGTGTACACTAT
23562	CLDN14	NM_012130	AACAAGTTTAATATAAAGTGA	ACGGCCGTGTCCTACCTGAAA	CGGGTACAGGCTGAACGACTA	CACGGCCGTGTCCTACCTGAA
23563	CHST5	NM_012126	CAGGGAGTAAGTTACTGCTAA	AGGGAGTAAGTTACTGCTAAA		
23564	DDAH2	NM_013974	CTGGATCTGGCCAAAGCTCAA	TAGGATAGTATAGGAAGTAGA		
23567	ZNF346	NM_012279	ATGGGCCAGACTACAACTTAA	GGGCCTCATGAAGGTCTTTAA	CGCAAAGAACTTAAAGCTGAA	ACGCAAAGAACTTAAAGCTGA
23584	VSIG2	NM_014312	CTGCCTGGTCAGGTTCCAGAA	CAGCACCGTGACGACCACCAA	CCCACCAGATTTCTACACCAA	ATCCAACTGGTTCTAAGTCAA
23586	DDX58	NM_014314	AAGGATAATACTGAACTGTAA	CAGGAATGTGAAGAAATTCTA		
23589	CARHSP1	NM_014316	CACCATCTGAAGAGCATTAAA	CTGCACATCTCTGATGTGGAA		
23590	TPRT	NM_014317	CTGGCACGAATTGGAAATACA	CAGAGTGATGGTGTGCAACAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
23604	DAPK2	NM_014326	ACGCCGGTGGACAACCAGCAA	AACCCTTGGTACCACAGAATA	CTGGTTAAAGAGACCCGGAAA	CGGAATTTGTTGCTCCAGAAA
23613	PRKCBP1	NM_183048	TTGACGCAAATAGCGAAAGTA	ATCGACACGTTCCGATCACAA	CACCATTGAACAGTTATCCTA	AGCGAACTTGTCATAGATTTA
23616	SH3BP1	NM_018957	CCCTGGAGACATCAACTTCAA	CAGCCCAGTCTCTTTGAGTAA		
23620	NTSR2	NM_012344	CAGCTTCGTGTGGTTCCACTA	CAGAGCCATCGTGGTCATGTA	TCGTATGGAAGAAGACCTTTA	CCGGACCTGAATGTAATGCAA
23624	CBLC	NM_012116	CAGACCATCCCTGCCAACAAA	CAAGATCTGTGCTGAGAGCAA	CTGGGAGGCCGTGAGTATCTA	CAGCCGAAAGTGAGACTCCTA
23626	SPO11	NM_012444	TACCTTCTACGATACAACTAA	ACAACTAATGTTAACGCATAA	TACATATATTATCTACATCAA	CAGAGTGTACTTACCTAACAA
23632	CA14	NM_012113	GTGGGTGAGACTAAGAATATA	TTGCATGAAGTCAGGCATAAA	AAGCAGGATCCTCGTATACCA	CGGGATCTCTCCTTAGGATAA
23633	KPNA6	NM_012316	CAGGTACTTATTATTGGCCAT	ACGCTTGGATTGAGTTATTTA	CTGGGTGGATTACATATGATA	AACCATTCTCTTACAGTTTAA
23636	NUP62	NM_016553	CTGGAGAGCCTGATCAACAAA	CCGCGAGGTGGAGAAGGTGAA	CGGCTTTGCCTTGAATTTAAA	ACCGGCTTTGCCTTGAATTTA
23645	PPP1R15A	NM_014330	CAGGATCAGCCGAGGATGAAA	GTGGGTTTATATAAGGAATAA	TGGGTTTATATAAGGAATAAA	CCAGTTGTTGATCTTATGCAA
23650	TRIM29	NM_012101	CTCCATGTACCTGACACCCAA	CCGGCCATTCTACGTCAACAA		
23673	STX12	NM_177424	AAGAATTTGATGAGCCAGCTA	CTATATTTAATTGGAAGGTAA	TCCTTCTGTTATTATACTTAA	CTGGGTTTAAAGTTTACTTCA
23678	SGKL	NM_013257	CCGAGATGTTGCTGAAATGTA	CATGGTATGATCGAAATGTAA	CCACAGCGAGACCCTAGTTAA	ACCAACTAACTTACATGCTTA
23682	RAB38	NM_022337	ACGAGGGTCTATTACCGAGAA	CAGCAAAGGCCTCAAGTCTTA	CTCCAAGTTAAGTCTCCCTAA	ATGATTTGGACTCCAAGTTAA
23683	PRKD3	NM_005813	CAGGCGGGAAACTGAATAATA	CTGAGCCTATTTCTAGTATAA	CGGGAGAGTGTTACCATTGAA	CACGATATGTCAGTACTGCAA
23704	KCNE4	NM_080671	CTCGGAGAACATCCATCAGAA	TCGGAGAACATCCATCAGAAT	CCCAGCCCATTTGCACACTAA	CCAGCCCATTTGCACACTAAA
23760	PITPNB	NM_012399	AACAAAGTAAATGAAATTTAA	CAGGATAAAGACTGATGTTTA		
23761	PISD	NM_014338	TTCCTTCTGCCTACAAATAAA	CAGCTTCGTGACGCACACCAA		
23765	IL17R	NM_014339	CAGGTTTGAGTTTCTGTCCAA	CAGGAAGGTCTGGATCATCTA	CGGCACCTACGTAGTCTGCTA	CAGCGGTCTGGTTATCGTCTA
23770	FKBP8	NM_012181	CTCCTACGACCTCGCCATCAA	CTGCCAGGAACTGACCACCTA	AAGACAACATCAAGGCTCTCT	AATCCCATGGAAGTGGCTGTT
23786	BCL2L13	NM_015367	CAGGCATTTCGGGAATGTACA	CTGGATGGTCCCTGTCTATAA	TTGGGCTTATAGAGCCAGTTA	CCGTGTCTTTCCAGCCCTAAA
24139	EML2	NM_012155	CAGCAGCTGCTTTGTCACCAA	CTGCGGGAAATCTCACATCTA		
24142	NAT6	NM_012191	CTGCTGGAGACACAATATCAA	CCGCCTGTCACGGGTGCTGAA		
25764	HYPK	NM_016400	CAGCAGAGTTACTGTACTCAA	CTGGATTAATTTATGGCAATA		
25776	PGEA1	NM_001002880	CGGCTGAAAGTGGACATCTTA	CTGGAAGAGAGTATCATATAA		
25777	UNC84B	NM_015374	CTGGGAGTGTGTATATATGTA	AAGGAGGATTTCCGCAGGGAA		
25778	RIPK5	NM_015375	CTGGTCCATTAGATTCCGAAA	CACCGCTTTATCGCCAGCTAA	TTGCTTCATCGTAAACCTAAA	TAGAGCTTGTTTGATGTTAAA
25788	RAD54B	NM_012415	CACGAACTTCGACCTACTGAA	CAAAGGCAGATCAGTAAGCAA	CTGGATCAAATTAAGAATATA	ACCCAAGAAATTATAAATAAA
25793	FBXO7	NM_012179	CCGATTTACAATTACATTGAA	CAGGATGAACAACCAAGTGAT	GACAATACTGTCAGAGTTCAA	CACAGATTGGAAAGAACTGTA
25796	PGLS	NM_012088	AAGCCAGGTGATCACCATTAA	CAGCGTGTGACCCTCACACTA		
25804	LSM4	NM_012321	ACGGATCTGCTCAGAAAGGAA	CGACAACTGGATGAACATTAA		
25822	DNAJB5	NM_012266	AACGAGGATGAGATCAAGAAA	CCGGAAGATGGCCTTGAAGTA		
25824	PRDX5	NM_012094	ATGGTGGTACAGGATGGCATA	CAGCCAGGAGGCGGAGTGGAA	CTGAGTGTTAATGATGCCTTT	CACCTGCAGCCTGGCACCCAA
25828	TXN2	NM_012473	CCCGGACAATATACACCACGA	CAGGATGGACCTGACTTTCAA	CGGGAAGGTGGTGATGGCCAA	CCCAAACTAGTGAGAGTAATA
25830	SULT4A1	NM_014351	AAGCAGATGCTTAATAGTAAA	CCGGAGGTTTATGAATGATAA		
25832	DJ328E19.C1.1	NM_015383	AACGATGACGATGAAGATGTT	AACGAGAGCTGACCCAGTTAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
25839	COG4	NM_015386	CAGGGATGTTCTGTGTAATAA	CAGGAGCTAATTGGCTTATAT		
25847	ANAPC13	NM_015391	CTGGAATTATTTGCCTGTTAA	ACGGTTTGTTTCAGTCTCCAA		
25853	WDR40A	NM_015397	CAGCATCAATGTGATTAGTAA	AACACTGATAATAGGAAGTAA		
25859	PART1	NM_016590	ATGAGATATTCTACACATTAA	AAGAAAGTCACTCATGAGTAA		
25865	PRKD2	NM_016457	CCGGCAGGGCCTGCAATGCAA	CAGCGGCACCTTCCCTTTCAA	TTGGGTGGTTCATTACAGCAA	CACGACCAACAGATACTATAA
25873	RPL36	NM_015414	CGGGAGGAGCTGAGCAACGTA	AAAGAACAGCTTGACAGGAAA	GCCCTCAAATTTATCAAGAAA	CTGCCCTCTCCCTGAAATAAA
25874	DKFZP564B167	NM_015415	AAGCTAAAGCACACAAATAAA	CAGGGTTTATTTGGTCAAGAT		
25886	DKFZP434C245	NM_015426	CCGGGCTCACACACAAATGAT	TAGAAATTGATTGCACATTGA	CTCCAGTGACTCAACCCTGAA	CCGGGAATGTGTCCACTCGTA
25903	OLFML2B	NM_015441	CAGGCTGCTGTTCGAGAATGA	TCGAGAATGAGTATTCCTATA	TTGTATAATATTGCAAATGTA	GCGGATTTACGTAACCAACTA
25911	DPCD	NM_015448	ATGGTCATATTTCCTGAGTAA	AAGGAAATGGCTGAAGAATAT		
25913	POT1	NM_015450	CAGGCTGAAGATTCAAGTATA	CAGGGTCTTGCCAGAAAGTAA		
25917	THUMPD3	NM_015453	AAGAGGATGTATCAACATTAA	CAGGAGAGAAACATTGCTTTA		
25926	DKFZP586L0724	NM_015462	CAGGACAGTCATCCTCTATAA	TTCGGGAGCTACAGAAATTAA		
25927	C2orf32	NM_015463	AAGGATGGTAACAAACTAGAA	CAAGGTTGAGGTGAAGATTAA		
25932	CLIC4	NM_013943	CACGAACATGCAGTTATTGAA	CTGGATATGTACTAACGAATA	TAGCAGTACAATGATTAGTAA	CAGGGAAGTTAGTCAAATGAA
25937	WWTR1	NM_015472	AGACATGAGATCCATCACTAA	CTGGCTGTAATCACTACCATT	CTGCGTTCTTGTGACAGATTA	ACAGTAGTACCAAATGCTTTA
25938	C14orf125	XM_113763	TCGATTTATGAGAAAGATGTA	TAGGTTCATATCTACATTGTA	CAGCCTTACAGTGCAACATAA	CTAGGCATAATATTAGCTAAA
25942	SIN3A	NM_015477	CAGAGGATATATGCTGATAAA	CAGATCCGCAGACATCCTACA	GAGCGTGTAAGCAAGCGTCTA	CTGGTCACTCGAGCACATCTA
25943	C20orf194	XM_045421	ACCGGGAAATTGAGAAGTATA	AAGGTAATTATCAGCATTGTA		
25959	ANKRD25	NM_015493	CAGGTTCATTAAAGAAGGCAA	AAGCTGATTGGAAACAATTAA		
25963	DKFZP564G202	NM_015497	AAGATTGTCATCAACACCATA	CAGAAGTTGTAGCTTATACAA	AGCGCTGATTGTTACAATGAA	CTGGCTTAATTTAAACAGTTA
25972	UNC50	NM_014044	CCGGCTGAAACTGCTTTCTTA	AAGAAAGAGCATTTAGTATAA		
25977	NECAP1	NM_015509	CGGGAACATTACAAACAAGAA	TAGCTTCTCCATCACATTCAA		
25979	DKFZp566O084	NM_015510	GAGGATGAAGTTGATTGACTA	CCGAGATGGAACAGTATGAAA	TTGCATTTGTTGAGACTTTAA	CAGATGTTATGTCACCTGAAA
25980	C20orf4	NM_015511	CAAGAGCATAATGTACATTAA	TAGGAGCTTAGGAAACAAGAA		
25981	XLHSRF-1	NM_015512	CAGGATGTACATCACCACCAA	CAGCCGTACATCGATAATGAA		
25988	MIZF	NM_015517	CCCAAGGACTTTCATGATTAT	CAGGGCATTATTCTAGAAACA		
25992	SNED1	XM_059482	AAACCTGTTCTTAGACTCCAA	CTCAGTGAAGCGAAACAGTAA	CAGGTAGTAAACACGATCTTA	CACCTAGGCTTCAGCCTTAAA
25998	IBTK	AB037838	AAGCATGGTGTTAGTCTGTAT	GAGGATTTAAATTATCCTAAA	TAGAAGAGTCATTACACCATA	CAGATTGAGGAGCATGCCATA
26009	ZZZ3	NM_015534	CAGCCTGATGGGAACACTAAA	TAGGAATTTACCTGAATATAA		
26015	RPAP1	NM_015540	AAGGAGGATAGCTGAAGCCAA	CAGCAACATCTGGTAAGAGAA		
26020	LRP10	NM_014045	TACAGAGAATCCTAATGATAA	CAGGGTGCCATCCCACCTGTA	ACCCTATGTAGCTGCTATAAA	CACCGGAATGCCAATTAACTA
26030	PLEKHG3	NM_015549	AGGAATGAAGCCAATAATTTA	CCGGTCTTCCTGCAAGAAGAA		
26031	OSBPL3	NM_015550	CTGCATTGTACTAATCTGTTA	AAGAACCAAGGTAGAATTTAA		
26033	ATRNL1	NM_207303	CAGGTTATTATGGAGATCCAA	CAGGGTGACAAGATATGTATA	CAGCTTTCCGCCTAACTAGAA	TTGGTCGTAGGTAAAGGTCAA
26038	CHD5	NM_015557	CCCACGGTACATGATCCTCAA	CAGCTACAAGATTGATTACAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
26040	SETBP1	NM_015559	ATGGAATGCCTTACACATCAA	CAGAGGGAAGTCTGAAGCTAA		
26043	KIAA0794	XM_087353	CAGCTTGAAAGGAGTGTTTAA	CAGCACGTGCATATTCATTTA		
26050	SLITRK5	NM_015567	TTGCATCTAAACAATAATAAA	CAGGCTAAACCTGAGGAGTAA		
26063	DECR2	NM_020664	CAGAATCGACATTCTCATTAA	CTGCACCACCTGTTTGCATAA	AAGATAATCTATTTACTGTAA	AAGAAAGAGGATTAAAGAGAA
26088	GGA1	NM_001001560	CAGAGGCCTACCAGATGCTAA	TCGGACATCGGAGAAGGTGAA	TCGGTGTGTCTCCTTCATTCA	CCGAAGAATGTGATCTTTGAA
26091	HERC4	NM_015601	TACGTTAGCGCTAAATGACAA	CAGAGTACCCAGAAATATTAA	TAGAAATACTACATAGGGTAA	GAGGGAATTATTGGATCCTAA
26127	FGFR1OP2	NM_015633	CCCGCCGGTGATGGCGTTGAA	TACGCTAAATTTCATCCTTAT	TAGACATATTTAGTAGGTTAA	ACGGAGGATTTGTACGCTAAA
26145	IRF2BP1	NM_015649	CTCCGATTTCGAGAAAGAGAA	CCCGTTCAATGTGCGCTTCAA	TTCAAGTACCTCGAATATGAA	ACCGCTGCCGCGGATAAATTA
26148	C10orf12	NM_015652	CAGAGGATTTATAATTATAAA	CAGGATTTAGAGGCAAATGAA		
26154	ABCA12	NM_015657	CACTCAGTTAATACCGATCAT	TTGCGACTCTTAATCAACGAA	AAGCCTAATGATCCGACTTTA	CAGGTGACTCCGATAATATAA
26155	DKFZP564C186	NM_015658	AAGGATGAGGACAGGAAGCAA	CACGGACAGTGCTGCATTCAA		
26165	C9orf36	NM_015667	GGGAAGAGAAAGAGTCCAGTA	CTCAGAAGCTCTCAGATCCTA		
26166	DKFZP434I092	NM_015668	CCCAGACTATATAAACTTCAA	TCGGACCAAATTGCTTATAAA		
26175	C14orf109	XM_058628	CAACATAGTGATGATTCAGAA	CTGGCCTTGGAACACATTCAA		
26190	FBXW2	NM_012164	CAGAGTGTATGCACTTTACTA	ACGGAATGGGTCACCAAGGTA	CCAGTGGGACTTTGCCAGTTA	CACGCAGTGCACAATCATTTA
26212	OR2B6	NM_012367	CCACAAATGCTAGTAAATTTA	CAGCATCATACAGGAGTTTAT		
26226	SHFM3P1	NM_012165	CCGGGAAGAGTACAAGGACAA	ACCGCTGGCTGTGGCACTTCA	CTGGCTGTGGCACTTCACCAA	CCCAGTGAAGGTGTCTCAGAA
26227	PHGDH	NM_006623	CTCGAGAATACTGCCCAGTTA	TGGGATGAAGACTATAGGGTA	CACGACAGGCTTGCTGAATGA	CAGCAATAACCGTCTAATAAA
26228	BRDG1	NM_012108	GAGGCTTCATTCTTACAGTAA	CACCTGAACACCAGAATTAGA	AAGGAACCAACTGAAGATTAT	CACCAGAATTAGAATTAAACA
26232	FBXO2	NM_012168	CACAAAGTGGGCTCTCAATAA	TCGAGGGTAGATAGGCCTTAA	AAGCTCACCGTTAAGCTACTG	AACGATGAGAGCGTCAAGAAG
26233	FBXL6	NM_012162	CCGGCTGACTCTAGCCAAGGA	CCCGGGCCTGCTCTACCTCAA		
26235	FBXL4	NM_012160	CACCGGTCTTTCCCATGTTAA	TTGGCTGGTGTACCAAATGTA	TCCGAATTAGTACGCCTTGAA	AACGACTTGTTCTCTATCGAA
26254	OPTC	NM_014359	CACCTGCAGAATAACCTGATA	CAGGGACAGCTTCTCTCCCAA		
26256	CABYR	NM_012189	ACCAGTGTAATGTATCAATAA	CCAGTGTAATGTATCAATAAA		
26261	FBXO24	NM_012172	CCACCACTCAATGACCTTCAA	CCGAATCTTCATGCAAGGAAA	CCCAAGGTGTGACACAGTTTA	CAGGCGAGTGACTGTCAAGAA
26273	FBXO3	NM_012175	CTGACGATTATCGATGTTCAT	CTGCCAGAACTTAGCTCTGTA	GTCGGGTATATGAATACACAA	TCGCTAAGACCTTGACTTTAA
26275	HIBCH	NM_014362	CAACTTAGGTATACAATATAA	CACGGGAGTCATAACACTAAA		
26276	VPS33B	NM_018668	CCGGAGAGGCATGGACATTAA	CAGCGTTGGATCAACACTGTA		
26292	MYCBP	NM_012333	AAGCAGGAGAATCCAAAGTAA	CAGGACAGAGGCAATATACAA		
26298	EHF	NM_012153	CAGCAATAATATGCAAATGAA	CTGGAAGTAAGAAGAATTAAA		
26330	GAPDS	NM_014364	CAGGCCAATGATAACCTTATA	CCCGGAATACATGGTGTACAT	CTCCATGAACATTGTGAGCAA	CCGAGACAAGTGAAACGGGAA
26338	OR5L2	XM_372387	CCGCTTTGTGGCCATCTGTAA	TTCACTCGTCCTTAGCTCTTA	CACCACTATCCTGAAGATACA	AACAGTGGAGATGTTGACAAA
26469	PTPN18	NM_014369	CCGGGTGTAAGTCTAACGCCA	GTGGGCCTGGATCAAAGTTAA	CCCAATGACTGTAGCATTCAA	CAGGCAGACATCAGTCCACAT
26507	CNNM1	NM_020348	CAGGTCTTAAGTGCAAATCAA	CAGGTGCAATTCCAAGCATAA		
26515	FXC1	NM_012192	CACCGAGAAGCTGAAACGGAA	CAAGTATTTGTTGGTTCATAA		
26523	EIF2C1	NM_012199	CCAGACCTCGACCATGATAAA	CAGCTACAACTTAGATCCCTA	CTCCAAGAATTGTGCAAGTAA	TAGGCTTAACATAAAGCCGAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
26533	OR10G3	NM_001005465	CTGCGTTTATCCTGACAGGAA	CTCATGATGAACTTCACTTTA		
26538	OR10H2	NM_013939	AGAACTGAAGGTTGCCATGAA	TGCCTCTGTCATCTACCTCAA	TTGGCCTGTGGAAATAATGTA	CACCCTGATGGCCACCACCTA
26539	OR10H1	NM_013940	CACCTTGATGGGCATCACCTA	TTCAGTAAACTCTACCCAGAA	GACCTTCTTCAGTAAACTCTA	AAGAAGACCTTCTTCAGTAAA
26578	OSTF1	NM_012383	CAGATGCAGTTCGAACATTAA	GAGGACTATCTCGATGATGAA		
26583	DUX2	NM_012147	AGCCAAAGCAAGGCCCTACAA	CTGAGGCAGCACTGGCATTAA		
26610	ELP4	NM_019040	AAGGAATTTGATGAAGATGTA	TTGGACCAGTATCATCTTCAA		
26658	OR7C2	NM_012377	CTGTGGAATCCTATTCTCTTA	CGCAGAGGACTCTGACATGCA	CTGGTGAATATCCAAACACAA	CTGCAGTTACACCACCTTCTA
26659	OR7A5	NM_017506	AAGATAATTTATTGGCTATAA	AACTGGTCTTGTAGAATTTAA	ACAGTCAGAGATGACCTTAAA	AAGCTTAGTGCCCATATATAA
26716	OR2H1	NM_030883	CTGCTAGACAACGTTTGATCA	TACGTAGGTCATGTAAGCAAA	TAGCTCCATAAGGCACACAAA	CCACATTAAAGTTGCAAATAA
26762	HAVCR1	NM_012206	AACGCTGATCCCATAATGCAT	TCGGAAGGACACACGCTATAA	GGCCTTTGGAATAACAATCAA	CACCATTGTACTCTTACACAA
26873	OPLAH	NM_017570	CTGCCTCATCATCGACAGTAA	CTGCTGCACATTGGCACCCAA		
26985	AP3M1	NM_012095	ACGGTCTTCCTGCATATTTAA	CTGGATTATGTAGAAGATTTA		
26993	AKAP8L	NM_014371	TAGCTCTGACACAAATGCAAA	CCGGCCAATGGCCTCAGGCTA	CAGGATAACACCACCAACTAT	AAGGAACACTTTAAGTACGTA
26995	TRUB2	NM_015679	AAGCTGTAACAGAAAGGTCAA	CTGCGGAAGTTGGTTCATGAA		
26998	FETUB	NM_014375	ACCGCTCAAGTCTGCCTTAAA	CAGCAGTATATATGTGCTGAA		
27012	KCNV1	NM_014379	CCGATATGTCCTGCACTACTA	AAGCTATGTACAATTAACTAA	CTGACACATTTGAGTGTCCAA	CTGTATCCCATTATTACTATA
27013	C2orf24	NM_015680	CTCCATGATGGTGGCCAGTAA	CTGGCTCTGGTGTACATTGAA		
27018	NGFRAP1	NM_014380	CTGCCATTTATCATGAGATTA	TGCCATTTATCATGAGATTAA	CTGGGAAAGAATCCCGGGAAA	ATGGCAAATATTCACCAGGAA
27020	SDFR1	NM_012428	TACATAAAGATGAGTAATATA	ACAGGTATATACAGCATATAA	CTGGTACATAAAGATGAGTAA	CAGGTATATACAGCATATAAA
27032	ATP2C1	NM_014382	AAGGTGCTTACGAACAAGTAA	AAGGGCAGACCTTGACACTTA	TAGGGTAACAGTGTCCATAAT	TACGTATTAAATGCACGTTAA
27034	ACAD8	NM_014384	CTGAATGTAAATCATGATAAA	AAGCTCTTTGCTACAGATGAA		
27036	SIGLEC7	NM_014385	CCGAATATAGTGAGATTGTAA	CAGGGAATGATATAAGCTGGA	TAGTGAGATTGTAACGTGAAA	CTGGAGGAGTCTGACCCTGTA
27040	LAT	NM_014387	CTACTCTGTGTAATAGAATAA	CCTCAGATAGTTTGTATCCAA	CCTCTTGTGGTTCTCAATAAA	CCCGTAACTTATTATCACTTT
27071	DAPP1	NM_014395	TCGGTCGTTCATCTTTAAATA	CTGGAAATTGGTCAAGGACAA	TAGGTAGTATAATAAAGGTAA	CTGGGCCTTATTAAAGAGCAA
27086	FOXP1	NM_032682	CAGGCGGTACTCAGACAAATA	CAAGACCTCCTTAATAATGAA		
27089	QP-C	NM_014402	CTGAAAGACCTTTCTCTGGAA	CCGCACGTCTTCACTAAAGGA		
27092	CACNG4	NM_014405	GACGACGAACAATGAACTAAA	CTAGGTGGTTACAAATCATAA	CAGGAGAGCAACTTACCTTCA	CCCTGTGTGTTTCGCCAGTTA
27098	CLUL1	NM_014410	CAGGTTGGTCAATGTATCCAA	CAGGAAAGTATGTTAGCTATA		
27099	NAG8	NM_014411	CAGGTTGTTATCTGTCTATTA	AGCCAGTATATTTAAAGGTAA		
27104	EIF2AK4	BX640919	CACCCATTATATTTCATTGAA	CAGGTATAATTACTAATTATA	TCCGATAATCTTGCAGTGCAA	CTGCAGGAATTTAGTAACATT
27120	DKKL1	NM_014419	CCGGGCTGTGGTCTAGCATAA	CAAGCACCATATGGAAATAAA		
27124	PIB5PA	NM_014422	ATGGGAATACCTACCAGGTAA	CTGGAGGTCATCCATTAGGAA	CTGGGACTGGATCGGCTTATA	CAGGTAACATTCAGTGAGGAA
27129	HSPB7	NM_014424	CAGGTGGACCATCCTCCCAAA	CAGAGGGAAGGTCACAGGCAA		
27148	STK36	NM_015690	CTCACCAGTTCTAGCGAGTAA	CTGGTCATGTCACCATAATAA	CCAGTTGGTGTCAGCCCTGTA	ATGGATGCTGACCTCCTTATA
27154	BRPF3	XM_166450	CCAGATTACCTGGAATTCATA	CCAGGATATCACCGAATGCAA	TACCAACTGCATGAAGTATAA	CCGGCTTGAGAAAGAGTCATA
27156	RTDR1	NM_014433	CTGCAGAGCTTCATTTGGAAA	CAGCATATCTCGAGAGGGCAA	CACAGTGATCACTGAAGGGAA	CAACAGTATGGTGCGCATAAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
27163	ASAHL	NM_014435	CCGGAGAACATCTGCCATCAA	CAGTGGATGTGCAATTCTTAA		
27177	IL1F8	NM_014438	CTGAGTGGAAATTCTTTAATA	CAAGCCTACTTTGCAGCTTAA	TTGGAATTCACACATGCATAA	AACGCTCTGTTTAGTATGTAT
27179	IL1F6	NM_014440	CCAGCCCACACTGCAGCTGAA	TCCAGTCACTATTGCCTTAAT	CTGGGCCTGAATGGACTCAAT	AAAGGATATAATGGATTTGTA
27190	IL17B	NM_014443	CGGAATGGACTGGCCTCACAA	TTGCACCTTTGTGCCAAGAAA	CTGCTGTTTCTTCTTACCATT	CCAGAGAAAGTGTGAGGTCAA
27199	OXGR1	NM_080818	TACATCGTTTCTAGACCATTA	CTCAATGGAACTCCTGGTAAA	CCGCTACTGTGTGATCATTCA	CACCAGTTCGGATGAACTCAA
27202	GPR77	NM_018485	TCGGGCCTGCCTGGTGGTCTA	TAGAGATATAGCAGTGACCAA	CAGCAAGAAATCCACCAGCCA	CACGTGCTGGACAAATCTTAA
27229	76P	NM_014444	CTGGATGTTACCACCAAGTAA	CAGGATCACCATCCATCTCAA		
27232	GNMT	NM_018960	AGGGAAGAACATCTACTATAA	AACATCAGTGCTGATAGTGAA	CAGACGGAAGGGTAAACAATA	GACGGAAGGGTAAACAATATA
27235	CL640	NM_015697	CTGGAGTTATGTGGACACTAA	TTGGAATAAATTTATCTCCAA		
27237	ARHGEF16	NM_014448	TACATTAAAGTTATTTCTTAA	CACCATTGTGGTCAAGAGCTA		
27239	GRCA	NM_014449	CCCGCCCAGTATGAAAGCTGA	TTGGACTTCCTTTGGGACTAA	CCGACTATGACTGGAACGAGA	ATCAATTGCAGGGATGCTTAA
27240	SIT	NM_014450	CAGACTGGAGTGGACCTGGAA	CCGGAGCTCTATGCCTCAGTA		
27247	HIRIP5	NM_001002755	CAGGTTATGGATGATGAATCA	AAGAAGCAAACTCACCTTAAA		
27254	PIPPIN	NM_014460	CAGGAGGTAGGTGGAGGGCAA	CACGTCAAACTCTCTTCCCAA		
27255	CNTN6	NM_014461	GTGGGTGTGTATAATAATGAA	CTGCAAAGGATTCATCTGTAA		
27257	LSM1	NM_014462	CAGCAAGTATCCATTGAAGAA	CCGCTGTGCATTGCAGCATTA		
27286	SRPX2	NM_014467	CCACTCGTTCTAGGAATGTTA	CTGGCTACTATCCGGATGAAA	CCCGATGGTGTTATACATTAA	GAAGATTAACGTCAACGTCAA
27291	C10orf28	NM_014472	AAGGAGCATAATTGTAGAGAA	CCCACATGTCATTGAAATTTA		
27292	HSA9761	NM_014473	CAGGTGTGCTATACTTATGTT	TTGGCACGTGTGGACCATCTA	TGGGATGGTCTAGTAAGGATA	CTGGTCCAATCTATTCATAAT
27295	PDLIM3	NM_014476	CGGGAACTACTTTGAACACAA	CAGGATTACACCAGGAAGCAA		
27302	BMP10	NM_014482	AAGGATGAGTTTCTTAAGACA	AGAGTACATGTTGGAACTCTA	TACGATGGAGTAGACCGGAAA	CCCGCTCTACATCGACTTCAA
27303	RBMS3	NM_001003792	CCGACAGCTGTTTCTATTGAA	ACCGTACAGTATTGCAACCAA		
27314	RAB30	NM_014488	CTGCGGGAGATAGAACAATAT	TAGGGCTTCGGTGGTAATCAT	TCGGTCCATTACCCAGAGTTA	AAGAGAGATTTCGGTCCATTA
27329	ANGPTL3	NM_014495	CAGTTGGGACATGGTCTTAAA	CTCAGAAGGACTAGTATTCAA	CAGGTAGTCCATGGACATTAA	ACCGTGGAAGACCAATATAAA
27330	RPS6KA6	NM_014496	TTGGATCATCTGCACCAATTA	CGGGAGGCTAGTGATATACTA	GGCGAGGTAAATGGTCTTAAA	CAGCGGTATACTGCTGAACAA
27334	P2RY10	NM_014499	CTGACGTGCATCAGTCTTCAA	TCAGAGTTTCGTGACCAACTA	CTCCCTATCATATTAACTTTA	AAGTTGAATAGTTTACCTTAA
27335	EIF3S12	NM_013234	AGCCAAGAAGAGAGCATTAAA	AAAGATGTGTTGACTCAGAAA		
27338	UBE2S	NM_014501	CCGCCTGCTCTTGGAGAACTA	CCGGCCGGCCGCAGCCATGAA	TCCCTCCAACTCTGTCTCTAA	CCCGATGGCATCAAGGTCTTT
27342	RABGEF1	NM_014504	ACGGAATTCTTTATCAATAAA	CAGGAAGAAGATGAGCCTTAA		
27345	KCNMB4	NM_014505	CCCGCGCTGCAGGATCTGCAA	AAGGAGGCTTGTAGAAAGCAA	CTGGAAGACTTGGAACCTCAA	ACCCTCAGTTTCCACTATTAA
27350	APOBEC3C	NM_014508	CAGCATAACCAAATCTTACTA	ACGCTGTAAGCAGGAAGAGAA		
27434	POLM	NM_013284	CTGAATGTCTCCAAGCAAATA	TAGGAGCTGGGAGGAAGATAA	CGGGAAGGACTGCGAACCTTA	CCCAGAATGCCCAGAAGAGAA
27436	EML4	NM_019063	CAGATGCAAATACCATAATTA	CGGCAATTCACTAACAAGAAA	CAGGAATCGATCGGATTGTAA	TCGGATTGTAAGGACATTGAT
28231	SLCO4A1	NM_016354	CTGCAGGGAAATGCACTTCAA	TGGATTGTAGTTAGAATACTA		
28232	SLCO3A1	NM_013272	TAGGACAAAGTTTATCTATAA	TCGGATGGCCATGCTCGTCAA		
28234	SLCO1B3	NM_019844	ATGGATAAGTCTATGCATCTA	CTAGAATATAAGGGAGGTAAA	TAGCTATGCCTTTATGGTTAA	TTCATCTATGTTGCAATTCAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
28951	TRIB2	NM_021643	TCGAAGAGTTGTCGTCTATAA	TACCCTTTCCATGACATTGAA	CAGGTTGTCCCACATGTATAA	CACGTGGACTCTAGTATGTAA
28952	CXorf37	NM_014008	CAGGAAGGAGGAGGTCTATAA	CAGAAGGAAATCAACTCCCTA		
28955	DEXI	NM_014015	ATGAGTGTTGTGCCTACTTAA	AAGCAATACTTAGGAGGCTTA		
28956	MAPBPIP	NM_014017	TAGAAGAACCTTCTTAGACAA	CACCGCTGCCATAGCCAGTAA		
28959	LR8	NM_014020	CCGGGCAAACTTGCTGGCTAT	CACAATGCTGATTAAACATAA	CTGATTAAACATAATAAACAA	GAGGAAGTTGTTCACAGCAAT
28964	GIT1	NM_014030	ATGGCTGACAGCCTTGACTTA	CACCTTGATCATCGACATTCT	GCCGCTGAGGATGTCCCGAAA	CAGCCTTGACTTATCCGAATT
28965	SLC27A6	NM_014031	TAGACAGATTTGGAAATATAA	AGGGAACTTTATGATCAAATA		
28977	MRPL42	NM_014050	CAGTAATATATAGTAAAGTAA	TAGCTTATGTATGATCCTTAA		
28988	DBNL	NM_014063	TGGGCTCTCTTTACCTATGAA	ATCCGTGTCTCTGAAGAACAA		
28989	AD-003	NM_014064	AAGGCCCGAACAAGACAGGAA	GAGGTGGATATGGTCGACATA	ACGGAGGACTTCCTGGTTCAA	CTCCAGCAGCATCGACATCAA
28990	HT001	NM_014065	AAGCAACTTTATGAATATCTA	GTGGAAGATCATAGTAATGAA		
28996	HIPK2	NM_022740	CCGAGTCAGTATCCAGCCCAA	ACGGGTCGGGACACCAGTGAA	TCCCGAAGTCTCCATACTAAA	AACCAGTACCCTTACATATAA
28998	MRPL13	NM_014078	CAGGTGGATTTAGACAAGTAA	CAGGAAGGTATAGTCCTTCAA		
29028	ATAD2	NM_014109	CTGGTACTTAGGCACCATAAA	AAGAATAATTAGCAGCGTTAA	CCGGATAAAGAAGAACGGACA	AAGGCATTTATAAAGATCGAA
29068	HSPC063	NM_014155	CAGGAAATGCTTGGAAAGCTA	CCGCAGGACATTTCTGATTTA		
29085	PHPT1	NM_014172	TAGCCTGGCCACAGAATTAAA	CCGATTCCACGTTTCCTTTAA	TCGGGCGACATGCAGAAGCAA	CACGCCATTTCAACTGAGAAA
29087	THY28	NM_014174	TCAGTTGATCCTAATTAGCAA	AGCAAATTACTTCATCATCTA		
29095	ORMDL2	NM_014182	TCCGGCTATATGGGCAACAAA	TCAGCTATAGCTGCAGTTTAA		
29097	HSPC163	NM_014184	CTGGTTCATCTTCCTTCTCAA	CTGCTTCTTCATGTATCTTTA		
29109	FHOD1	NM_013241	CACGGTCACCCTCATCAACAA	CAGCGAGAGGAGCATCTACAA		
29110	TBK1	NM_013254	CAGGATATCGACAGCAGATTA	CCCAATTTATCCAAGTTCTAA	CTGACTTGACACGTTTGTAAA	CAGAACGTAGATTAGCTTATA
29113	C6orf15	NM_014070	ATCGGTGTTGTGGAGGAGAAA	CTAGAGCACGATAGAGGGAAA		
29114	TAGLN3	NM_001008272	CTCTGTTTGATTATTTATTTA	ACCCAAGATCTCAGAGTCAAA		
29115	HCNGP	NM_013260	CTGGTCTGGATTCCACTTAAA	CAGCTCATTGTTTACAGGCAA		
29116	MYLIP	NM_013262	CCCAATTAATAGGATAGCTTA	TGCACTATTATAAACTATTAA	AAGTAAGTGCTTAAGTATTAA	ATCGGGTGCAATACTAGCTAA
29121	OCIL	NM_001004419	TCAGATATCTTGAGACAAGAA	CTCATAGAAACTGGAGGCAAA	TAGAAGCATATTGGAACTGAT	CAGGAGAGTGTGCCTATTTGA
29122	TSP50	NM_013270	CAAGCTCAAGCAGGAACTCAA	CACTCTGGTTCAGATCATCAA	CAGGGAGAAGTTCTGCTATGA	GAGGTGCTCAATTAAACATTA
29124	LGALS13	NM_013268	TACGTACATTACAATGAGTAT	TGGCAATCATGTGGTCATGAA		
29127	RACGAP1	NM_013277	CAGGTGGATGTAGAGATCAAA	CACCACAGACACCAGATATTA	CTGGTAGATAGAAGAGCTAAA	CTGAATGTATCTCCTAGCTAT
29775	CARD10	NM_014550	CACAGGGAGTGTGACACTTAA	CTGCACATTATGGAGCATTAA		
29798	C2orf27	NM_013310	ATGCTTCAGATTCAAGTGCTT	ATGATAGCAGAGTACCTTCAA		
29799	YPEL1	NM_013313	CAGGGTCTCTTTAGATAGCAA	CTGTCAGATATTAGAATTGAA		
29802	VPREB3	NM_013378	CTGCTGGTCTTCCCAGGCCAA	AATATTCAACATGTCAACAAA	TGGGTTAATAATATTCAACAT	AAATGGGTTAATAATATTCAA
29841	TFCP2L2	NM_014552	AGGGATGAAGAACGAAAGCAA	CTGCACTGTTTAACAAATGAA		
29851	ICOS	NM_012092	TGGGATTATGTTGTAGTTTAA	CCGGAATTGAAAGCAAATTTA		
29881	NPC1L1	NM_013389	AAGCACCTTGGTCATGGATTA	CAGCTTTGAAGGTTCTATCAA	AAGCCTCATGACACTCTCCAA	CCGAGTGATGGTGGACTCCAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
29882	ANAPC2	NM_013366	CAGCGGTGCAGTCCCGCCAAA	GAGAGTCTATATGCAGAGTAA	CTCACTGGATCGTATCTACAA	AAGGTTCTTCTACCGCATCTA
29894	CPSF1	NM_013291	CCGCGGCTTCCTGTACTTCAA	CAAGATGGTCATCTCCCTCAA		
29922	NME7	NM_013330	CGGCAAACACTGCTAAATTTA	CAGGTTGGGACATTTAGACAA	TTCATGTAGATCACCAGTCAA	CCCGGCATTTACGCCCTGGAA
29924	EPN1	NM_013333	AACTTTGGGAATAAATGGCAA	TCCCGCGACGCTCACCCTGAA		
29927	SEC61A1	NM_013336	CCGAGTGGACCTGCCAATCAA	AAGGTGAATAAGTGACAAATA		
29930	PCDHB1	NM_013340	CGCGCTGAGAACCATGGATTA	ACGTTTCAGATTGACCCTCAA	ACCAAGCATTCTAGAAAGGTA	CTCGGCCTTGTCCATATGAAA
29933	GPR132	NM_013345	CAGGATTGCCGGGTACTACTA	TACCAATTTCTCGTTCCTGAA	CTGGGTCACCATCGAGATCAA	ACGGACCATTCCCGCCAAGAA
29945	ANAPC4	NM_013367	TGGCTCGGAGTCTTTATTATA	CTGAGCTAGACTCCTAATCTA	CAAGGCTAGATGAACAGTGTA	CAAGCTGGTGCTGCCGCTTTA
29946	SERTAD3	NM_013368	CAGCCTGATCCAGTCTTCTTA	CAGGCATGTCCTCATCCATAA		
29947	DNMT3L	NM_013369	CCACTGCAAACCGGCACTGAA	AACTCACTTCCTCTTTATAAA	AAGCATGTGGTTGATGTCACA	AAGGCTAACCAGCGAAATATA
29948	OKL38	NM_013370	CCCGGTCATCATTGTGGGTAA	CAGAAGCAGGTCCCAAATAAA		
29953	TRHDE	NM_013381	CTGGAGATTATTAATTGATCA	CAGGAACAGAATACCACTAAA	CCGAATCTATAGAATAAAGTA	CACCACTGAATTCATGTAATA
29954	POMT2	NM_013382	ACCAACCATCATTAATGTTAA	AACCTGTGGATTATCAAGAAA		
29956	LASS2	NM_013384	AACGAAGAGAGTCTTTCTTAA	TTGGAGTAGAATGGCAACTAA		
29959	NRBP	NM_013392	AGGCGAGAAGAGGTGAATCAA	AACATGGATACTAGTGCCGTA	TCGGTGGAGGAGGGAGTCAAA	CCGGTTGACTTCTCTGCTAGA
29965	C16orf5	NM_013399	CACGTAGGACAGGGTCACAAA	CTGCCTCATCAATGACTTCAA		
29982	NRBF2	NM_030759	TTCGGTTTCTCCTGATACAAA	TTATGTGTAATTAATCTATAA	CACACTTTGCACTACTCATAA	CAAAGGGATAGCCATATGAAA
29984	RHOD	NM_014578	CCGGTGGTACCCAGAAGTGAA	AACCTGCAAGTGAAAGGCAAA		
29997	GLTSCR2	NM_015710	TCGAGAGAGAGCCAAGTTCAA	CAAGTTCAAACGCAAGTACAA	CTGACAAAGAAGAGAACCAAA	CCGGAGCTTCCTACAATCCAT
29998	GLTSCR1	NM_015711	CCCGCAGAACCTGACGTTCAT	CAGGCCATGCTCAATAAATAT	CGGGCTCAAGCTCAAGATCAA	CCGCATCGGGCTCAAGCTCAA
30000	TNPO2	NM_013433	CCCGAGCATCTCTCTCTGTAA	ATCGTGCAGGATAAACTCAAA		
30008	EFEMP2	NM_016938	CCTGGAGATGGTCACCATGAA	CCGCTCCTGTGTTGATGTGAA	CCGCTCCGCTGCCGTCATCAA	CACGGAATGCACAGATGGCTA
30009	TBX21	NM_013351	CCGCGTGAGGACTACGCGCTA	ACCTGTTGTGGTCCAAGTTTA	CCGCCTGGACCCAACTGTCAA	AACAAATACACGTATGTTATA
30010	NXPH1	NM_152745	AAGCAGCAAATCCACACTAAA	TAGGAGTATCTGCTTGTTAAA		
30062	RAX	NM_013435	CCGCACGACTTTCACCACGTA	CCGCGAGGAGCTGGCCGGCAA	CAGGCTGAAGCTCCTAAACTT	CCAGATAACCATAACAGGGAA
30811	HUNK	NM_014586	AACTAAGTACGTTGCAAATAA	TACGTTGCAAATAATAGTACA	TCGGACCAAGATCAAACCAAA	CACGGGCAAAGTGCCCTGTAA
30814	PLA2G2E	NM_014589	AAGCTGGGCTGTGAGCCCAAA	CTGGGCACCTACAACCGCAAA	CAAGTCCGCCCTGCAGTACAA	AACCGCAAATATGCCCATTAT
30817	EMR2	NM_013447	TAGGTCAGTGTAAGAATTAAA	TTGCTTGATATAGACTGCTAA	ACGGGTTTGATTATTTAGTCA	AAGCATGGTGATGATATAGGA
30818	CSEN	NM_013434	CCCGGCTGACCAACATTCAAA	TCCAGGAACATTCCCACATAA	CAGGAACATTCCCACATAATA	CCCACATAATACATTCCATCA
30836	ERBP	NM_014597	ACCACTGTGTTCCACCATATA	CCACTGGGAAGCAAAGTTTAA	CACGAACAGGCCAATGTTGAA	AAGAAGAAATTTCGCAATTAA
30837	SOCS7	NM_014598	CAGCTTTGAAGAACCAAATTA	CCCAAGTTGACAAGAACTCAA	CCGAAAGTTCTACTACTATGA	ACCAAATTAAGCTACCATGAA
30845	EHD3	NM_014600	CACTTTATATACATTATTCTA	CTGGTGGTGGATCCCAAGAAA		
30850	HUMPPA	NM_014603	CAGCGTCACCTTTGAAGTATA	CAGGCTGGTGCTGGAGAGTAA		
43849	KLK12	NM_019598	TCCCGGGAGAATCACGAGCAA	TCCCTGGAGTCTACACCTATA	TGGGAACTTCTTGGAACTTTA	TGCAATAGTCTGGAATAAATA
49861	CLDN20	NM_001001346	TACAAAGAAAGTAGAATGTAA	CTGCAGGAATCTCTAGTTTAA		
50484	RRM2B	NM_015713	AAGGGCTTATGGACTGAGAAA	AAGGAGCAGGCCATAACTTTA	GAGCAGTTCAGTGGTACATAA	AACCAGGAGGTTATCATGGTA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
50485	SMARCAL1	NM_014140	CCCGCAGAGCTGAGAAGTTAT	CAGAACAGCATCAGAGGACTA	TTGAGTTATGAGTTAGGTCAA	CAGCTTTGACCTTCTTAGCAA
50488	MINK1	NM_015716	CACATGTCTCATCAAGACTTA	CCGGAACAAGATTCTGCACAA	CGCAGACTTTGTGTTGCTGAA	CACGTACGGGCGCATCATTAA
50489	CD207	NM_015717	CTCGGTGACCTCAGAGAGTGA	CCAGGATGACTTTGCACGTTA	ACCCTGGATTCTGAAATTAAA	CAGGATGACTTTGCACGTTAA
50515	CHST11	NM_018413	CAGCATAGTGAGAATTATTTA	CCGCAACAAGTTCACCCAGAA		
50613	UBQLN3	NM_017481	CGAGGAGTCAGTAGCAATCAA	CTCCATATGCTGCAAGATTTA	CAAGATTTAGTTAGTACAAAT	TTGAGATGCAATTACACCCAA
50614	GALNT9	NM_021808	CCCGGAGATGAGGGTCTACAA	CACCAGGAAGCCCTACAACAA		
50615	IL21R	NM_021798	CCCGGTCATCTTTCAGACCCA	CTGCAAGAAGTCCATATTGTT	CCAGAGCAGACCCTCAATAAA	ACCTGTTGAAATGTGAATTAA
50616	IL22	NM_020525	CTGATAGGTTCCAGCCTTATA	CCTGCGTTAGTTACAAAGGAA	AAGGTAGACTTTCTAAGCATA	AACATGTTTATTTGACCTCAA
50628	GEMIN4	NM_015721	CCGCCATATGGAAGTGTGCTA	CAGCCAGAACGCGACGCTCTA	CACCGCAAGTTAGAACAGCTA	CAGCCTGGACTTTACAGTTAT
50649	ARHGEF4	NM_015320	AAGGTTGGCCTTGGCTCATAA	CAAGCCAGAAACCACATTTAA	CCGCGACGTGTTGTACTACAA	CACATTTAATTTCATAAATAA
50700	RDH8	NM_015725	CAGGGTGTCATCTTCAACGAT	AAGGATGAACAGACTCTTCAT	CAGCTGTCTCTGGGAAAGCAA	CACACCAGCAATGTATGTATA
50717	WDR42A	NM_015726	GAGGAATAAGTCATTAATCTA	CAGCTGAATTCTTGCCCTTAA		
50835	TAS2R9	NM_023917	CTCCCTAGTTAGACACACCAA	CCAGGTACTTTCAAACAGTTA	TGGATTCATTGTACTAGTTAA	CTGGCTGAAGCTAAAGATCAA
50846	DHH	NM_021044	ATGGCTCTCCTGACCAATCTA	TCGGTCAAAGCTGATAACTCA	ACCGAGTGGCCTCCACGCAAA	CCCAGGCATAGAAACCTCGAA
50852	TCRIM	NM_016388	AAGGTTGAGATGACAATGTTT	ATCAGTATTTCAAATAACTTA	AAGCATGAATGCGTTCTGGAA	AAGGATGGAGATGAGCAACTA
50861	STMN3	NM_015894	CACGTAGTAAAGTGAACTTAA	TTCAATCAAATGAACAATTAA		
50862	RNF141	NM_016422	ATCACGGATCATGAATTTATA	TTGGTGAGTAACACACATATA	CACTGATAAATTGTGCAATAA	CTCGATTTCCTTATATCTAAT
50939	IMPG2	NM_016247	GAGGATGGAGTCACAAGTATA	AAGGTTGGTAGTTATGTGGAA	TCAGGCATTCATCTAAATAAA	AAGGAAATTCGTGTACTTGAA
51015	CGI-111	NM_016048	TACCAACATCTTGAATATATA	AGGGATTCTAATATTTATTTA		
51020	C6orf74	NM_016063	AAGGCTAGGTTCATTGAATAA	CCAGATGAAATTGCTGCCTTA		
51031	C17orf25	NM_016080	CTGATGTAATTTAGAAATGAA	AACGATTTCTTCAGCCTGAAA		
51043	ZFP67	NM_015872	CAGAGGGTTCTGGAAGATGAA	CCCGGAAAGCTTTCCTGCAAA		
51056	LAP3	NM_015907	CCCAGTCTTCTTGGAAATTCA	ATGGGAGGAGCTGCAACTATA	AAAGCTTAATTTGCCCATTAA	AAGCTTAATTTGCCCATTAAT
51060	TLP19	NM_015913	CTACGTGATCTGCACCTTTAA	AAGGGAATATTGAGGAATCAT	AACAATTAAGCCGACCAGGAA	AAGTGTAAATCAGTTATTCTA
51062	SPG3A	NM_015915	ACGCCTCAAGGTCTCAGGGAA	TCCCGAGAGCCTAGATATTAA	CCCGAGAGCCTAGATATTAAA	ACAGCAGAAGCTAACAATTTA
51068	CGI-07	NM_015938	CAGCATGAAGATAATGGCTAA	CAGAATACACTTCGTATCAAA		
51070	NOSIP	NM_015953	CAGGATGACGCGGCATGGCAA	CCCGTGCACTTCACACCGCTA		
51076	CUTC	NM_015960	CAGGATGAAGGTAGAACTATA	CAGAATATTCCCTAAAGGTAA		
51077	C14orf111	NM_015962	AACCATAGATACAACATTGAA	AAGGAAGTATGCGACCATGAA		
51084	CRYL1	NM_015974	CAGCTTGATTGCATTTGACTA	CAGCCAGTGATTGTAGTTTCA		
51095	TRNT1	NM_016000	ACGCAGAGATCTCACTATAAA	AAGGATTTGGGTGGAACTGAA		
51097	CGI-49	NM_016002	CAGCTTATAAGTTGCTATCAA	AAGAAATGTATCAAATCTGAA		
51099	ABHD5	NM_016006	AAGGCCTGATTTCAAACGAAA	TACGTCTATATCACACCTTAA		
51101	CGI-62	NM_016010	CCAGGTGTGCTTACAAACAAA	CAGGTAAAGTGTCTTCAAGTA		
51105	PHF20L1	NM_016018	ATGGCTAAGTGGATAATTTAA	TCCGTTGATCTTAGTGGTGAA	CAGCTGAAGATTGGAATACTA	ACGGAAATTTAGGGTATTTAA
51112	TTC15	NM_016030	CAGGCTGGCACTACTAGTGAA	ATCCAGGGAGATGCAGTTAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
51116	MRPS2	NM_016034	CACGACATCATCGACCTGGAA	CACGCTCAACAACATCTTTGA		
51121	RPL26L1	NM_016093	AAAGAAGAACTTATTGAGAAA	GAGGGTCACCATGAAGTTCAA		
51130	ASB3	NM_016115	AACGCTTGGATTCTACAGCAA	ACCCATCTTTGTCGTTTGGAA	TACGGTCTGACAGTTATATTA	CTGAGGATGTATGAAGTTCCA
51131	PHF11	NM_016119	CACCGTGGGATGTGATTTAAA	ATGGAGTTCGAGGAATTTATA	GAGATCTTATGTCAAGTTCTA	ACAGCCCATGATAGCCTCTTA
51135	IRAK4	NM_016123	GTCCATTATTAGATTATGTTA	CAGCTTAGAAGAGTACTCCAA	TTGCAGGACAGTGGTTATTAA	ATCCTATTAGTCATATATTTA
51138	COPS4	NM_016129	CAGGAAGTACAAGCATTTAAA	CAGAATGAATCAACCAATGAA		
51162	EGFL7	NM_016215	AGGAGTGGACAGTGCAATGAA	CAGCACCTACCGAACCATCTA		
51167	NCB5OR	NM_016230	CAAGCTATGATTGGTTCCAAA	TTAAGGATTGTTTATATCTTA	AGGCTTCACACCAATGGTTAA	TCGATCATGTTTCCATGCAAA
51168	MYO15A	NM_016239	CAAGATTAGATTTGAACGGAA	CAGGATCGTGTTTCAGGCCAA		
51179	HAO2	NM_001005783	CCGGTCGGTCGCTGAGATCAA	CAGGAGGATCACAAACTCACA		
51182	HSPA14	NM_016299	CGCGAGCCATGATGAAATTAA	ATCCCTATTGGTGCAGCTATA	AATGGATTACGTGATATATTA	CTCTATTGAGATAGCATCTTA
51184	MGC14560	NM_016301	TTGGACCTAGATAACAAGTAA	CAGCCTCATGCCTGAATCAAA		
51187	C15orf15	NM_016304	CAGCATTTGTATAGTAACTAA	CCCTTTGTTAATGTTATAGAA		
51191	HERC5	NM_016323	CCGGACGCCGAAATGCATTAA	ACCATTTGAGTATGACAACTA	GAGGAGAATGGTAATGTTCAA	TGGAAGTAGCATAACTGTCAA
51194	IPO11	NM_016338	CAGCTACAACTTTGAAGTTAA	GAGGAGATTCTTGGAAATATA		
51195	RAPGEFL1	NM_016339	ACGGAGAAACTTCAATATTCA	CCCATTGCTCCTTCAAGCCAA	ACGGTGGAACTAAAGATTCCA	ACCCAAAGCTCTGGAATTGTA
51199	NIN	NM_016350	CTGGAAGAATATCGTGCACAA	CTGGAAGACCTAAGAAATGTA		
51205	ACP6	NM_016361	GAGGCCAAACTTGAAATACAA	GTGCCTTTATACAATGCCAAA	CCCGCTGGACATGTTCTTGAA	CCATGTCAGTTTATACCTTAA
51207	DUSP13	NM_016364	CAGGTGGACACAGGTGCCAAA	ACCCAATTCAGAGATTCTTTA	TCAGTCCATCTCTATAATAAA	ACCCTGAGATGTAAACAGCAA
51208	CLDN18	NM_001002026	AAGGATGAGCAGACAAGTCAA	CCCAACTTGGCTAGTAATAAA		
51214	IGF2AS	NM_016412	CAGGCGGTGGACGCTGCTGAA	CTCAATCTGCCCAAAGCCAAA		
51222	ZNF219	NM_016423	CCCAATAAACAGGTGTCTTAA	CAAGGGAGTCACAGTGCCTTA		
51234	LOC51234	NM_016454	CACAAAGAAACTATACCATAA	ATGGTTGAGAACAATGCATAA		
51237	PACAP	NM_016459	CAGGACTACGGAGTTCGAGAA	AAGGCAGAGACCAAACTTCAT		
51239	MGC41816	NM_016466	TGGACAGATGATCATATTCTA	CTGGGCCGAGTGAAGCATTTA		
51256	TBC1D7	NM_016495	CCGGGTGTGTTTGCACTACTA	ACGCTTTGTGAACCAATTAAA		
51258	MRPL51	NM_016497	AAGGGCCATGTTCGGAGTGTA	GACCTGCACAACCTTAATAAA		
51260	CXorf26	NM_016500	AAGGACATCTTTCTAGTCTAA	AACCGGGAAGGCTATAACAAA		
51265	CDKL3	NM_016508	CTAAAGCAATTTCATCACGAA	AGCTCCCGAATTAGTATTAAA	TGGGCAGATAGTGGCCATTAA	CAACATTATTGTCATGGACTA
51266	CLEC2	NM_016509	AAGGTGGACCAACTACCTTAA	ATACATCACCTTAAATATTAA	CTGACAGATACTGAAATTGTA	AGGGCTTTATTGTACAATAAA
51275	FLJ39616	NM_016534	CAGGATTGTATAGAATATATA	AGGATTGTATAGAATATATAA	GAGCATAAGTTAAGTAAGTAA	CTCCACCGATAACCTATCAAA
51276	ZNF571	NM_016536	CAGGGATTTCTGAATAATGTA	CTGAATTATATCCTTTATTAA		
51295	SITPEC	NM_016581	TACGAGTTTGACATCAATGAA	CCGCAACAAGTGTGTGTATTA		
51296	SLC15A3	NM_016582	CAGGAAGGGTAGGGCAAGAAA	CAAGGACTTTGGGAACATCAA		
51298	THEG	NM_016585	CCGGATCATCTCCCTGGCCAA	AAGGATGAGGAGGACAATAAT		
51301	C2GNT3	NM_016591	AAGGATGAAGTCAGGTATGAA	CAGCTTAGTTCCAGAGAGAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
51307	FAM53C	NM_016605	CAGGATGTTGGGTTTGCTCAA	CAGGTGCTGAGTGAAAGCGAA		
51312	MSCP	NM_016612	CACCAAGGAAACAGCCACCTA	CCGGACGGTGTACCAGCTCAA		
51317	BHC80	NM_016621	TACGGAAGAACCTGATAGTAA	ACGGAAGAACCTGATAGTAAA	ACCGGACAAGTTCCAAATACA	ACCATGCCAAGTGAAATAATA
51321	LOC51321	NM_016627	GACAACTATTATATTCCAGAA	ACCCATGAGATCGGACACATA	CAGCATTGTAGAAAGATACAA	CCCGTGGAAGCCTTTAAGGAA
51330	TNFRSF12A	NM_016639	CGCCCACTCATCATTCATTCA	CTCAGATGTCCTGAAATTCCA	CAGCTGACACTGACTAAGGAA	GAGGGAGAATTTATTAATAAA
51332	SPTBN5	NM_016642	CCGGCGTATGTTAGAAGAGCA	ACGGGCCACATTCGCAAGCTA		
51334	LOC51334	NM_016644	CCGGGAAAGATTCCTCACCAA	CTCAGCTATATATGTAATAAA		
51335	NEUGRIN	NM_016645	CTGGGCAAGTATTAATGTATA	CCCGGTTGCCCTTGCGATCAA		
51339	DACT1	NM_016651	CACAGAGACATTCACTATTAA	CCGCAGGAGAACAAAGTTGTA		
51343	FZR1	NM_016263	TCGCCAGATCGTCATCCAGAA	CAGGATTAACGAGAATGAGAA	TGCAGTGACGCTGTCATTAAA	CGGGTCGATCTTCCACATTCA
51347	TAOK3	NM_016281	CAGAGACTGTACTACGACAAA	ACGCAGCGAGAGAATAAAGAA	CAGCTCCTCCGTCGTGCATAA	CAAACAGTATAAAGCACTCAA
51352	WIT-1	NM_015855	CCCGGCCTCGAAGGTGCATAA	GCCTCTATTATTATACCGTAA	TAGGCCCATGAAATTGATGAA	CAGTCTGAGGTTACAATTAGA
51364	ZMYND10	NM_015896	CTGCAGGGAGTGCCAAGTCAA	CTGCAGGGTGGAGGACTTCAA		
51368	TEX264	NM_015926	CAGGACCCAGAATAAAGCCAA	CCGGGCCAGAGGAGAGGCATA		
51373	MRPS17	NM_015969	TGACATGTTTATGTTATGGAA	CTCTGTGGTGTTTATGAAATA	TCCCTATTTATTAAAGTATTT	CAGGCTTGTTCTGGATCCCTA
51374	C2orf28	NM_016085	ACCTCTTATATAGACAACCAA	AACCAAATCTGTCAAGGGCAA	CTGGAATACTATCACCTCTTA	AAGCCAAGACTTCATGAACTA
51382	ATP6V1D	NM_015994	AAAGAAGATAATAGAGACTAA	ATGGATGAAAGAGATCTGTAA		
51389	RWDD1	NM_001007464	AAGGGCCACGATGACAGATTA	CAGGAGAATATTCTTCTGATA		
51390	AIG1	NM_016108	CAGAGAGATGATATACCCGAA	CAGATGTTTCTCATTGCATAA		
51393	TRPV2	NM_016113	TCAGATAAGAGTCAACCTCAA	CTGGCTGAACCTGCTTTACTA	CAGAGGATCTTTCCAACCACA	CCAGTGAATTCTGGTGGCAAA
51400	PME-1	NM_016147	ACGGCAGCGATTATTAGTAGA	AGGAAGGAAGTGAGTCTATAA	AGGCGATACATCTGAGTTCAA	AACATCGAGCTCTGTTGTAAA
51409	HEMK1	NM_016173	CAGGGTGGCAACCAACTATAT	CAGTAAAGTATTGAGAGACTA	CAGGGATTGATTAGTCCTCCA	ATCCACGTTCATTTAACTGAA
51411	BIN2	NM_016293	CAGGGAAATGAGCAAGCTGAA	AACGATTTGAACAAAGCGCTA		
51412	ACTL6B	NM_016188	CACCTACAGCAAACACGTCAA	CACGGCCATTCCAGTACATGA	CTGGCATAACTACATGTGTAA	CAACAGCACCATGGAGCGCAA
51421	AMOTL2	NM_016201	AAGCATATTGCTCCAATTCAA	AAGGGTGTTAGTCTTGGAGAA		
51422	PRKAG2	NM_016203	AAGCGCGGTTATGGACACCAA	CGCGGTTATGGACACCAAGAA	CCGGAAAGCATTCCTCTCGAA	AAGCACGAGCCTGAACGGTTA
51426	POLK	NM_016218	AAGGATAAACCCATTGCTGTA	CAAGGATTTACCCATTAGAAA	TAGGATGGGACTTAATGATAA	CCGGGTGACGACGGGTAGAAA
51429	SNX9	NM_016224	ACAGATCTCAATGATGCAATA	CAGCCGCTTTCCAGTGATGTA	CCCATCATTGTTGGAGATTAT	TACCCAGTGTCAGATAATTAA
51435	SCARA3	NM_016240	CCCTGAGAAGTTCAACATTTA	ATAGTATTACTGACTCAGTAA	CCAGAGGAAGAGACCATGAAA	CACCATCTTCACCAACATCAA
51442	VGLL1	NM_016267	CTGCATATTGTTCCAGATAAA	CAGGTGATGGTCCAGAATTAA		
51449	PCYOX1	NM_016297	AAGCATCCAAATGGTAATTAA	CAGGATGGCTTATATGAGAAA		
51466	EVL	NM_016337	CACACAGTAATAAACGGTTTA	CGGCTTAAACTTTGCAAGTAA	CAGGTTGTGATCAATTATTCA	CCGGATCAACATCTACCACAA
51475	CABP2	NM_016366	CAGAAGCTGGAGGCAGCATAA	CAGCATGTTCCTTGAAGCCCA		
51490	C9orf114	NM_016390	AACGCTGCTAGGAGAATCGAA	TCGCAGGACCCTCGCACCAAA	TCGGGTGACTGTGCGACTGAA	CCGGCACACCTGAAAGTTCTA
51491	HSPC111	NM_016391	ACGAATAAATTGAGCCTTGTA	CAGGGTGGGTGATGTAAATAT	TCGGAGTAAGATCAACGTCTA	CGGGACCTCATTGACTATGTA
51496	HSPC129	NM_016396	CTCAGTTACAATCAATTTAAA	AAGTACAGTATTGGAAATTAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
51497	TH1L	NM_016397	CAGGAGGATGATTCTGGAGAA	AAGCGAGTGAGCATCAATAAA		
51513	ETV7	NM_016135	CAGATGTGAAGCTCAAATTAA	TGCGCCACTATTATAAGCTTA	GCGCCACTATTATAAGCTTAA	CCCGATATGAGCCCTACATCA
51524	HSPC196	NM_016464	CTAGCTGTGTTCAGCATTCAA	TAGAGAATAAATTGAATTCTT		
51526	C20orf111	NM_016470	CACAATGAAATCCGAAGCCAA	AAGGCTTGTCAAAGAGATTTA		
51531	C9orf156	NM_016481	CAGACTTTAATTTACAGAATA	AAGGTAGAAGGTGGAGCTATA		
51535	PPHLN1	NM_016488	CAGAATGAAGGAAATCCTGAA	AGGGACGATATGAATATGAAA		
51548	SIRT6	NM_016539	GTCGAGGATGTCGGTGAATTA	CACGGGAACATGTTTGTGGAA	CCGGCTCTGCACCGTGGCTAA	CTCCCTGGTCTCCAGCTTAAA
51550	CINP	NM_032630	ACGGATATCTGTGGACCTTAT	CAAGGGAATTTGTGAACTAGA	GCGGCTGATTGGCACAATTTA	CGGCTGATTGGCACAATTTAA
51552	RAB14	NM_016322	AGGAATCGAACTAACAATACA	AACGGTTCACGTCTAGCCAAA	TCCATTGATCCCGTATCTTAA	CACGTTAATAGAGGTAGTACA
51554	CCRL1	NM_016557	AACCCACTATGCTATAAGTTA	AAGAACGATTTCCCTGCATAA	TTCCATGGTAGTGGCAATTTA	CGCCGTGGTTGCAACTTATAA
51560	RAB6B	NM_016577	ATGGCCAGAGTGGGTCGTCAA	ATCCATGTTCTTAGAGCCTCA	CGGCTGTTACTTAAACAACTA	CAGGGATCACATCACTCTTAA
51561	IL23A	NM_016584	CGCGCTGAACAGAGAGAATCA	AACAGAGAGAATCAGGCTCAA	CCAGATTTGAGAAGAAGGCAA	CAGATTTGAGAAGAAGGCAAA
51574	HDCMA18P	NM_016648	TCAGGTGATTTAGTAAATAAA	CAGGAGAAAGTTAATGCAACA		
51582	OAZIN	NM_015878	CCGGATTTGCTTGTTCCAGTA	CGGATTTGCTTGTTCCAGTAA	CAGGTTAAGCTTGTCTGGTCA	ATCATAGTATTTGTTGACCTA
51592	TRIM33	NM_015906	CGCCAAGAATGCAGACAGATA	AAGGGTGCAATTGAGAATCTA	CTGGGCAAAGAATGTAGTCAA	TCCCGTAGTATCGGTACACAA
51596	C6orf82	NM_015921	TGAGGTGCTGATGATGATTAA	ACGTGTGGCCTTTGAGATCAA		
51599	LISCH7	NM_015925	CACGTCGTTTACGCTCATTAA	ACGTCGTTTACGCTCATTAAA	GAGGATTACCATCACCGGAAA	CGGGACGACCTCTATGACCAA
51606	ATP6V1H	NM_015941	CAAGAGATGCTTCAAACTGAA	CAGCAGAAGTACGATGATGAA		
51616	TAF9L	NM_015975	TAGGCTGAAGTCCTTAATTAA	ATCACTGATAGTAGCATTTAA		
51637	C14orf166	NM_016039	CTGGCATGTTTGGAAATCAAA	AAGATTCAAGATCGACAAGAA		
51639	SF3B14	NM_016047	TCGGATATTGTATATAAGAAA	AACATTCGACTTCCACCTGAA		
51645	PPIL1	NM_016059	CAGCTTCTAGATGACATAGAA	AAGGAAGTTAATACCTATGTA		
51659	Pfs2	NM_016095	CTGGGACATTCTTCAATTCCA	AAGCCTTAGGTAAATAAGTCA	CTGGCGATTAACCTGAAACAA	CTCCTGTTAAATCATGCTTCA
51660	BRP44L	NM_016098	CTGTAACTTAATGGCAATAAA	CAGTAATATGTATATCATCTA		
51661	FKBP7	NM_016105	CTGGCTAAAGACGGCTCGAAA	ACGGAGCATTGAGACATTTAA	CGGAGCATTGAGACATTTAAA	CACGATGAACTATAGCATATT
51667	NYREN18	NM_016118	AAGCAGTACTCTGACAGACTA	ACCGTACTTAGACATAGCTAA	TAGAGGCTTATGAGTATCTTA	ATCCTCAGATGTGGTGGTTAA
51676	ASB2	NM_016150	CCGAGAGACACCGCTCTACAA	CAAGTACGGTGCTGACATCAA	CGGCGCGAACATCGACGCCTA	CCCAGGCAGGCTGATTAGATA
51678	MPP6	NM_016447	TTGGTTGGTATACTCAAAGAA	ACGGATTCAGAGAGCATACAA	CTGATGATTCAGTAAGGTTAA	TGGAAGGTGTACTAATATATA
51684	SUFU	NM_016169	ATGGACGGCACTTTACATATA	TGGGACTGTTACAATACTTCA	GAGCGTACATCTGAAATTCAA	CCAGGTTACCGCTATCGTCAA
51700	CYB5R2	NM_016229	CCCTTGATTGAGAAAGAGAAA	CAGAGGCTTTGTGGACCTAAT	TCAGTATTTGGAGAACATGAA	CCAGGGAATCTTGGAATCAGA
51702	PADI3	NM_016233	TCGCTAATAAATCAACAGAAA	CACAGAAATGTTTGAGGTCTA		
51704	GPRC5B	NM_016235	CGCAAACTAAAGCAAAGCTAA	CTGCAGATACTCTAATCACTA	TCCGTTTAGAAGCAACGTGTA	CTCGCCCTGTTCCTACACTTA
51710	ZNF44	NM_016264	CACGCTGAATAGAAACTATAA	CAGGGATAGTCTACAAATGTA		
51715	RAB23	NM_016277	ATGATAAACTCTAGACATATA	TTCATTATTTGTACTAAACAA	CAGAATTTATATTGTTTATTA	AAGGTTAAAGTTAAGATTCTA
51716	CES4	NM_016280	CCACAGCAGAATCTAAAGAAA	CAAGCTTCTTGCTATAATGTA	ATGGAGGATTTCGGTAGATTT	ATCGATAGGAATCCAGACCTA
51720	RAP80	NM_016290	CAGATTGCTTAGTGGACTTTA	ACGACATGCCATGTACTGCAA	CACGTCGTGACTTAAATGAAT	CAGTATTGACTCGGAGACAAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
51727	UMP-CMPK	NM_016308	TCCGAGGTTCTTAATATGAGA	TACAGAGGTGGTTTAATCAAA	CGCGTATATATCCCTCTAGTA	AAGTATTGCTAAGTACTATAA
51738	GHRL	NM_016362	CACGACTGTTGTACAAGCTCA	CCGACAAGTGATCGCCCACAA	CAGGAGGCGAATAAATGTTCA	CGCCCGGAAGATGGAGGTCAA
51755	CRK7	NM_016507	CCGCTTGGTATCGAAGCACAA	AACGGCGACGTCAGCGACAAA	ATCGGGATATTAAGTGTTCTA	ACCGGATATCGGGAAGTTCAA
51759	C9orf78	NM_016482	ACGGTGTGATAATACTCTTTA	CAGGATGAGATCAGAAGGATA		
51760	LOC51760	NM_016524	CAGCTGGTGCATGGACTCAAA	CCGGAACGCAGGGAAAGGCAA		
51761	ATP8A2	NM_016529	CAGGAAGAAATAAGACATGAA	ATGCAATATCATGAACTTTAA		
51763	SKIP	NM_016532	ACGGTCGGAGTCCGGAAGAAA	CACGTTCGACTTGGAGCTGAA	CTGGAATTAGCCGCTTAAATA	CAGCCAAGTGTCGTCCACATA
51773	HBXAP	NM_016578	CCGGACGTCGGCAACGGAGAA	CAGCCAATTGGTCGAGACAAA	CACCGAGTCGTGTACCATGAA	ACGCACAAAGATTGAGTCCAA
51780	JMJD1B	NM_016604	AAGGAACTTTGTCACATCTAA	ACCCTGCATCAAAGAAATTAA		
51802	ACCN5	NM_017419	CAGTCTGATCACGATCATAGA	CACGATCATAGAAATTATTGA	ATCATAGAAATTATTGAATAT	AGGAGTGTTAATGGTCACTTA
51805	COQ3	NM_017421	CTCGGCGGTTTATGTGAAGAA	TCAGTGGGACTCTACAGATAA	AACCATATGGTTCAAATCCTA	CTGGAATCAAATGGTCTGTCA
53340	SPA17	NM_017425	ACCCTTGGATTTAGAATTATA	ATCCATCAACCTTCTTATTAA		
53342	IL17D	NM_138284	CTGGGCCTACAGAATCTCCTA	CAGCATCAACTCCAGCATCGA	TGGCTGGAAGCTGATGGGAAA	TGGGTGCTTGCCAAAGAGATA
53343	NUDT9	NM_024047	TTCGATTTAAGCATGGCTTAA	AAGATTAGTGCCACACTGAAA	ATGGATAATCTTATGCTAGAA	CACGCTGCAGATCCCATTATA
53347	UBASH3A	NM_001001895	CCCGCAGACGTCATCCGGGAA	CTGGGTGATTGGGATCTCACA	ACGGCCAAACTCATCCTGGAA	AACAGGTGTAATAGTCAATAA
53353	LRP1B	NM_018557	AACGTTTATACTGGACAGATA	CTGGATGGTGGTAATTTAGAA	CCCTACTATACTCGTTAGCAA	TAGATGATTCATGTAAGTTAA
53373	TPCN1	NM_017901	CGCACACAACTGGGAGATGAA	CCGAATGAACTACAGCCGCAA	TAACACAATAGTATTACTCTA	CGAGCTGTATTTCATCATGAA
53635	PTOV1	NM_017432	CCCAGTCCAGATCGTCAACAA	CAGATCGTCAACAACAAGTTT	CCGGCGTGTCATTGCCAACCA	CTGGAGCAGGAGCAACAGCAA
53826	FXYD6	NM_022003	CCCAGAAAGCAGAGAACTGAA	CAGGTGCAAGTGCAGTTTCAA		
53827	FXYD5	NM_014164	CACCAGAGGACAGACGTTGAA	CCCGGTTATGCCGGAATCGTT	GAGGACAGACGTTGAAAGATA	CTCAACTATCATGGACATTCA
53829	P2RY13	NM_023914	CAGGATGTTAATATGCTATAA	AAGGAGTAGTTAAGCTCTGTA	CAACTGTTTATTGCTAAAGAA	AAGACTGACTGTAGACTGCAA
53905	DUOX1	NM_017434	CCAACTAATCTTAGAAGGTAA	CCCGGGCAGATCCGTGTGGTA	TCGGCGGAGGTTTGGCAAGAA	CCAGTCTAACACCACAACTAA
53916	RAB4B	NM_016154	CTACATAAGAGTTATCTGTTA	AAGAGTTATCTGTTACTGTTA	CCGCACTATCCTCAACAAGAT	CAGGAGCTATAGTGGAGTGAA
53918	PELO	NM_015946	CATATTTGATTTAGAGGGTAA	AAGCAGTGGGATAGTGTGGTA	CTGAAGAGGATTAATGATTGA	ACGTACTACCATCTTGATTAA
53947	A4GALT	NM_017436	CAGGATCGCACTCATGTGGAA	CACGGACTTCATTGTTCTCAA	CACGTGCTGGTCCTGATGAAA	AGGAGAATAATCAATAGAATA
53981	CPSF2	NM_017437	CACATTTGGTTCAGAAATTAA	CTGCTTGACCTTTCTAAGAAA		
54039	PCBP3	NM_020528	CCGGCATGCAGTGGTAATTAT	ATGGATCTGCTCTAAACCTTA		
54058	C21orf58	NM_058180	CAAAGTCTAATTTAATAACTA	TAGGTGGAACTTGGGAAACTA		
54067	C21orf49	NM_001006116	TAGGTAATGTGTAGTTCTCAA	CACAGAAATGCTAGTTGGAAA		
54102	CLIC6	NM_053277	CCGAATCTAATTCCGCAGGAA	CACGCATATTCAGATGTTGCA	ACACACAATTTCATTCATATA	TGGTATGTGTTTGATGCTATA
54107	POLE3	NM_017443	AAGCTTTAGGAAACTACTAAA	AGGGATGAGGACAATGATGAA		
54112	GPR88	NM_022049	GGCGTTGAGTGTTATAGTGAA	CTCCTAGATGCTAGAACTTAT	TACCACGACATTTAACATCAA	ACCAGTATGAGTTGCCATTAA
54207	KCNK10	NM_021161	CGGGAGTCAGTCCAATAGGAA	TTGGCTGGAATTGGAGACCAA	CAGCGTGGAGATCCACGATAA	CTGGAATTTGTTGGAAGCAGA
54209	TREM2	NM_018965	CAGGGCTGAGAGACACGTGAA	AACACTTACAAATAAATCCAA	AAGGAAGATGATGGGAGGAAA	ATCCAAGACTGTCATATTTAA
54212	SNTG1	NM_018967	CTCACAAAGCACAATATTAAA	GAGGATTTGGATTAAGCATAA		
54329	GPR85	NM_018970	CTGTATGTCACTACATATGAA	TTGGAGCATAGTACCATAGAA	CAAGGGAACCTTACTGTGTTA	AAGCACAAACTAGGAAGACTA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
54332	GDAP1	NM_018972	ACGCATTCCTTCAGCTCTCAA	ACCCAGGTTAATGCCTGATAA	TCCCGGCTTATGCAACTACAA	CGAGCGTGTCTTGAAGAGAAA
54344	DPM3	NM_018973	CCCATTAAAGAGCCAGTTTAT	TCCCATTAAAGAGCCAGTTTA		
54361	WNT4	NM_030761	CAGGGAAGGCCGATAATTTAA	TTGGGTCCTCATGTTATTTAT	CTCATGTTATTTATTGCCGAA	CAGACCTAAGGTGGAGTAACA
54429	TAS2R5	NM_018980	TCAGCTCAATTCAGGAAGTTA	CCAAATTGGCTTAACATTCTA	TCGGTTTAATTGGAAATGGAA	GCCGTTGGCTTCGCTATCTTA
54431	DNAJC10	NM_018981	CTGGAGAACTGTGGTTTGTAA	CAGGGCCTATCCAACTGTTAA	CAGCTTAAGTTTGGTACACTA	CTCGACGGACTTATAATGTTT
54433	NOLA1	NM_018983	CTGCATGATCTGTTTCTACTA	ACCAGTTGACTTCTGCATTAA		
54439	RBM27	XM_291128	CAGGGAAAGATCGAAGTTTAA	AAGCAAGGAAATAACAATCAA		
54443	ANLN	NM_018685	CTCAATCTAAAGACAAATCTA	AAGGTTTCACTGAATGCGAAA	CTGATGCTTGCTACAAACCTA	CACCGTTTCCATCGTCTCGTA
54457	TAF7L	NM_024885	CTCCATAAGATTCAGAATAAA	CTGGTTGTTATTCACCAACTA		
54458	DKFZp564J157	NM_001005354	GAGCGGCCACATAATTACCAA	CGGCCACATAATTACCAATTA		
54461	FBXW5	NM_018998	CACCCAGTTCTCCCAGTTCAA	CTGGACCACGTCATAGACATA	CACGAGGATGTGGTCAACTCA	CCCGTTCAGGGCCCTGAATAA
54462	KIAA1128	NM_018999	GAGCATAATTATCTCAGGTAA	ACGAGTTGGCCTTATCCTTAA	ACCGTATATTTATGAAGCATA	CCGTATATTTATGAAGCATAA
54475	FLJ10458	NM_018096	ATGACCAAATAAGTAACTTAA	CAGCAGTGACAGCACACTGAA	AAGGACAAATGCCTCCGGATA	CCCAGGTTCTATGACCAAATA
54495	TXNDC10	NM_019022	TTCGAGGTTATCCAACAATTA	CAGATTGAAGTCAATTATTCA	ATGCTGTTAATTTAACAAGTA	TAGGATATTAAGACTATCAAT
54498	SMOX	NM_019025	CCAGTCAATGCTGAAAGTCAA	CACGTCATCCAGCTAGGGAAA	ACCGACAAGATCTTTCTGGAA	CCGGCACGATAAACCAGTCAA
54499	LOC54499	NM_019026	TTGGGTATGATTAGAGTGAAA	AAGAATAACAACAGAGATCTA		
54503	ZDHHC13	NM_001001483	TGGATACATATTGGACTTCAA	CAGCTCATTATTCATATGCTA		
54508	FLJ11235	XM_496773	CCGTAGCACAGTAGAAATGAA	CAGGATCAGCATAACCGCCAA		
54510	PCDH18	NM_019035	CTGAGTATAGTTTGACTGTAA	CCCGAAGCAACTGGTAAGCAA	CTGCGCCATAGTAGCAGGTAA	CCGGAGAATATTTCTCTCACA
54512	EXOSC4	NM_019037	CCCTAGTGAACTGTCAATATA	CAGGCAGATGGTGGGACCTAT		
54514	DDX4	NM_019039	CTGAATAACAACATTGCTAAA	AAGGTTTAAATGAAGAAGTAA		
54518	APBB1IP	NM_019043	AAGATTTAAATGAGTCCTTAA	CAGCATCTCTACAAGCATCAA		
54538	ROBO4	NM_019055	CCGGGCCTGTGAGTTAGGAAA	CCGGGAGGATTTCCAGATCCA	CACCTCAGGAAGTGACTCTAA	CTCCTGTAGATTACTCCTGAA
54540	FLJ10404	NM_019057	CCGAGAGGTGGAGTACTTTAA	CAGAAACTCAGAGCAACTAAA		
54554	WDR5B	NM_019069	AAGACTGTCCAGAAACTTTAA	AACCGTAACCTCACACATTAA	TAGCACAATAATTTAACTGAA	ATCAGAGTTACTAGTAGGGTA
54556	ING3	NM_019071	GAGGCGATCTTTGGAATTAGA	CGGCACTTATGACAACATTAA	AACCAAGATTGCCCTATAGAA	CTAGAGTACCTGGGTACATAA
54558	SPATA6	NM_019073	CAGGCTCATCAAAGACATTTA	CAGGATAAATTTATTTACCAT		
54575	UGT1A10	NM_019075	AAGCACAGGCACAAAGTATAT	CTGGAAGATCAGAACCGGGAA		
54579	UGT1A5	NM_019078	CACACTCAATCGTTCTTTGAA	CACCCTGGAGGTGAATATGTA		
54581	SCAND2	NM_022050	CTCCAAATAGTTAAACTGGAA	TAGAGTTAACTTTGTAATGTA		
54584	GNB1L	NM_053004	CCCGTCATGGACCTTGACTTT	CACGATCCGGCCAGATCGCAA	CAGCCTTGGCCTGAAACCTCA	CAGGTGCGTGGGACTCATGAA
54585	LZTFL1	NM_020347	AAGACGTATATTCAACATAAA	AAGCATTAAGATAAACAAATA		
54620	FBXL19	NM_019085	CCGCTGGATCGAGGATGTTAA	CACTCTTTCATCGTCATGGAA	CCGGGTCTGTACAATACGGTT	TACAATACGGTTTGCTATAAA
54658	UGT1A1	NM_000463	AAGGGAAGCTTTGTACCTTTA	CTGATGTTTCCTACAACTAAA	ATGGTTGCAATTGATCCTTAA	TTCCCACTTACTGCACAACAA
54662	TBC1D13	NM_018201	CCGGTGGAACACGTACTTCAA	CACAGAAATCTTGGAAACCAA		
54663	FLJ10439	NM_018093	AAGGTTTATCTCAAGTCTCAA	CACCGAGACTGGGATCTTGAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
54716	SLC6A20	NM_020208	CGAGATGTTCCCGCAAATCAA	TGAGATGTTGTTAGCCTATAA	CCCGTGGATTCAATCTTCTTA	TCCAATTATATGGAAGAGTTA
54734	RAB39	NM_017516	TCAGTTCAGGATAAATACCAA	AAGGTTACAAACCCACACCAA	TAGCTTCACAACGTCAAGTTA	CAGGAGCGGTTCAGATCAATA
54737	HSMPP8	NM_017520	AAGGGTGAAATAAGAGATTTA	CTGGTGAACTTCTGTGCTTAA		
54741	LEPROT	NM_017526	ATGGCGTTTACTGGCCCTTAT	CTGGCCCTTATTCGTCCTGAT	CGGCCTTGTGTTGGCAGGCAA	AAGCATCATCATAGAGAAGTA
54752	DKFZp434H2215	NM_017559	ACGGGTGTCATCCCGAACAAA	GAGGATGATACCATCAACCTA		
54754	DKFZp434I1117	XM_030729	CCGGCCGGACGACTCCTGTAA	CCGCAGGAAGAGGACGGGATA		
54763	ROPN1	NM_017578	CTGGGATGGTGTGGTGAGCAA	CACACTAAGGATAGCAATTTA	AGGATAGCAATTTATCTCAAA	TACACACTAATAAACAATTAA
54790	FLJ20032	NM_017628	AAGGCCTTTCATATAAATTTA	CAGCTGTAGACTAACAATATA		
54795	TRPM4	NM_017636	CTGCACGACGTTCATAGTTGA	CAAGATCGTCATCGTGAGCAA	CGGGTTTACCTTTCTAAGGAA	AACGTGGGAATCGGTGCATAA
54801	FAM29A	NM_017645	CCGGAAGAAGTTGGTCATCTA	AAGGAACACTGTCAAACTATA		
54820	NDE1	NM_017668	ACGCAGCTGCAACAAATTGAA	CGCGCAGACCAAAGCCATTAA		
54828	BCAS3	NM_017679	CAGATTTAAATGATACATCAA	CTGGAAGAGATTGAACAAGAA		
54831	VMD2L1	NM_017682	CCGCGACAACAGCGCCCTTAA	TCGAGTTGTCATGAGGATGAA		
54836	BSPRY	NM_017688	CAGCTGATTCAGAAGGAGCAA	GTCGGAAATGTTAAACTTTAA	CTGGATGGTGAATGTCCAGAA	CCAGAACAGTTGTGCCTATAA
54841	BIVM	NM_017693	CTGCTGGAAATAATTCATCAA	GAGGTGGTTTAGACAAATTAA		
54843	SYTL2	NM_032379	AAGGGATTTAAATATAACAAA	CCGGTGGAATCTGATCTTGAA		
54847	SIDT1	NM_017699	CCGGACCAAGATGTTCCTTTA	CACATTCCTCTTAACAAGTAA		
54850	FBXL12	NM_017703	CTGGTGGATGTAACTACTCCA	CACCTTGAAGAGGGCAGATAA	TCGCGATTCAATGATCGATAT	AATGATCGATATGCTCATAAA
54855	FAM46C	NM_017709	TTGGAACATATTCCAATTCAA	CTGGTCATTCATGACCTTAAA		
54866	PPP1R14D	NM_017726	GAGCCTGAGATTGACCTGGAA	CAGGCCTGCCCTGAAACTCCA	CCGCCTGACAGTGAAGTATGA	CAGGAGCTCTTCCAGGATCAA
54873	PALMD	NM_017734	CTGGGTATTGGTGTAAATGAA	TAGGTTAAGGAAGGAGATAAA		
54901	CDKAL1	NM_017774	TAGCACATCCTTCAAATTAAA	CAGCGTACTCATGGAAATGAA		
54913	RPP25	NM_017793	TGGAGTCTTGTTTCCAATAAA	GACAGGTAGCATGGACCTTAA		
54918	CKLFSF6	NM_017801	AAGAATTATAAGAGAAATGAA	ATGGGAATTTAACATATTTAA		
54919	FLJ20397	NM_017802	CTGCAGCTGATTTGAAATTAA	GCCAAAGTGATTAGAAAGAAA		
54935	DUSP23	NM_017823	CAGGAGATGCCATTGCTGAAA	TTGGCTGAAGACACTGAAGTA	GAAGTGGACTAAAGTATTAAA	CAGTTCTACCAGCGAACGAAA
54937	FLJ20449	NM_017826	CAGAAACTATTTGCAAACATA	CTGAATTGTTCTTATATGTAA		
54938	SARS2	NM_017827	CACCTGGAAATTGGCGAGAAA	CTGGATATGCCCACCCAAGAA		
54939	COMMD4	NM_017828	ACCCTGGATGTTACATATAAA	AAGGAACCTATCGAAGAATAA		
54941	RNF125	NM_017831	CAGAAGTACATAGATAAGTAT	CTGGATCATTGTATTACTCAT	CTCGGTTTGCAAATTAGATAA	ATGGTTAGGCACGATAACTAA
54946	SLC41A3	NM_001008485	ACCCATCGTGAAGATCCTGAA	AAACCTCTATTTAGATTTCAA		
54955	FLJ20508	NM_017850	CAGGATATTGAGAGACATTAT	CCAGATAACTATTATTAATAA		
54957	TXNL4B	NM_017853	AAGGAAGTAGACCAGGCGATA	CCACCACTCTATTCAGGTAAA	CTCGTGGTGGTTATTGAAACA	TCGATATGCTAAGAAGAACAA
54958	FLJ20512	NM_017854	ATGGGTCGGGAAGCAGCATAT	CCCGAGGACTGGGACATTAAA		
54962	FLJ20516	NM_017858	ATGCTATTGCCAATACTTTAA	CAACAGCAACTTGATGCTACA	CTGAGTTAAGTAGAAGCCTAA	AAGCTTGGCGTTACTATGTAT
54973	FLJ20542	NM_017871	CCGCAAGATCGCCGTAGACAA	GAGGAACATGTTTGAGTTCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
54988	FLJ20581	NM_017888	TAAGATGATCACACAGCATTA	AAGAATATCATTGGCCCTGAT		
54989	FLJ20582	NM_014106	CAGGTAATAATGTTAACTATA	CAGGAGAATCACATGCTTTAA		
54998	AKIP	NM_017900	AAGCAGATCAAGTTCGAGAAA	CTCAGAGGACTCAGCCTTTAA	CTGCTGTGATCCGTAGTAATA	ATCCGTAGTAATAAATTCTCA
55002	C13orf11	NM_017905	CACGTGCAGATCACCACTTTA	CGGGCTCTTCATGGCCGTCAT	GAGGAGCAGCCAGTACATCAA	TAGTCAAATATTTGTTATTAA
55006	FLJ20628	NM_017910	CGGCGCCTTCGCGAAACACTA	CTGGCTAAGAAGAATTACAAA	GGCGTGATTCATGGAAATTAA	CAGGAGCAACCGAAGACATAA
55010	FLJ20641	NM_017915	TCCCAATTTGCTTGTACTTAT	ACAGAATAGATTGTACGGCAA	CCCAATTTGCTTGTACTTATA	CAGAATAGATTGTACGGCAAA
55011	FLJ20643	NM_017916	CAGGGAGGGCCTTGAGGACAA	TCCGGAATGGCGCATGATGAA	CCCGCTGCAGATCAACTCTCA	ACCGGAAGAGAAAGCAATTAA
55014	STX17	NM_017919	TTGAGGTTTGTTAGTGAGGAA	TTGCAATTTGGTCCAACTATA	CTCCTATAACCTCTAGGTAAA	ACCCTGAATTGGAGACCTTAA
55016	MARCH-I	NM_017923	TACCTTAACCAAGATGCCAAA	ACCAAGATGCCAAATTATCTA	AAGAACTTCTCATGTAATGTA	TAGGCAGTAATCAAAGATTAA
55049	FLJ20850	NM_017967	CCGCTCTTGTAGGGTAATTAA	CAGCTTCGCGGCAGCAGCTAA		
55066	PDPR	NM_017990	TTGGAGCAAGTATGTACTTAA	TAGCTACAAGATTCAGCTTTA	ATCTCTTATCTCCTTGATATA	ACCACATAGCCCAGTGATTAA
55072	RNF31	NM_017999	CTGGCGTGGTGTCAAGTTTAA	CCGAGATGTGCTGCGATTATA	ACGCATGAACGACCCAGAATA	CAGGACAATAACGTCATGTTT
55082	FLJ10154	NM_018011	CAGATTGTAGATGACAATATA	AAGGATGAAATTGAACGAGAA		
55083	FLJ10157	XM_371354	CAGCAAACACATTCCATACAA	CAAGCTCATAAACGAACGCAA	ATCAGTATTGCTTATGAATAA	AAGCACTTTGAGGAACCTTAA
55089	SLC38A4	NM_018018	CAGGACTGGATAAATAATTAA	ACCCAAATACTTTGTATTCAA		
55102	C14orf103	NM_018036	CTCCAACATGTTGACAGTGAA	CTGGGTGGCATGAGAAACCAA		
55104	FLJ10246	NM_018038	CAGGTTCATCTTTGACTTCAA	CAGGTTGTATCTCCAGATAAT		
55111	PLEKHJ1	NM_018049	CAGGGTGCTTGTTCTGTTCAA	CCCGTGCTGAATGAATGTACA		
55117	SLC6A15	NM_182767	TGGAATTACATAAGCCCTAAA	CACGCCTATTGTGGACACTTT	CCAGCAGATATTACTACTATA	CCCAATGGACGGTATGGAATA
55118	CRTAC1	NM_018058	CACCAGTCACTTAACTTGTTA	CCGGGACATCGCCTCACCCAA		
55122	C6orf166	NM_018064	CTGCAGCATCCTCACCATTAA	TTCACTGGTTGTGTAAATAAA		
55124	PIWIL2	NM_018068	AAGGATGTACATAAGATTGAA	AAGAAGCAAGTTTCTGAGTAA		
55128	TRIM68	NM_018073	TTCATGTATGTAGGAGTTAAA	ACGCATTCTGTCCACCATGAA	TAGGCCAAACTGGAGAAATAA	AAGAGAGATCCTGAAGACTTA
55129	FLJ10375	NM_018075	CAGACCCTTTATCAACATAAA	TAGACCATTGTTAAATAAATA		
55139	FLJ10415	NM_018089	CCGAAGGTTCATGGAGAAGAA	CAGGAGGAGCGTGAACGAGAA		
55148	C14orf130	NM_018108	AAGCCTCAACGCAGAATCAAA	CAAGGTTGCACTATTAGTATA	CACAATAGTACCGATCAGTTA	ATCAGTTAACTCAGCGCTGAA
55154	FLJ10504	NM_018116	AAGGAGCTAGTTTGCAATAAA	CTGATCCTTAGTAACATGTTA		
55166	C6orf139	NM_018132	TTGGATATTCTTCATAATTCA	ATGGAAGATTTAACTAATGTA		
55167	FLJ10546	NM_018133	CTGGCACGGGATATAATAGAA	CAAGGCGTTTACTGAGATTAA	CAGTGTCTTATGAAACATGTA	AGGGCCTTGATTGTTATGTAA
55170	HRMT1L6	NM_018137	CCGCCTGGGTATCCTTCGGAA	CCGCAGCGCTTTGCTCAGCTA	CACACCTTATCTAAGTCTGAA	ATAGCCTAACATTTATTGTAA
55174	FLJ10569	NM_018142	CTGGTTCTTCTTGAAGATGTA	CCAGTGTGAAATGTTACTAAA		
55180	WINS1	NM_018148	AACCCGGATATTGTCTGTCAA	AAGAAACTTCTTAGAGATTCA		
55182	FLJ10597	NM_018150	CAGGCAGCTCGCGAACACAAA	ACGGCAAGTCTTAGGAGGGAA	CCCAATCAGTATGCTGAATCA	CTCGGTGTTCAGTGGTGTATA
55183	RIF1	NM_018151	CTCATGGAAATTACAATTAAA	AAGGAAATGCATGTAAAGTAA		
55192	FLJ10634	NM_018163	ACCCAGAAACTTGATGAGAAA	AAGGAAGAAAGTGAAGCTTGA		
55193	PB1	NM_018165	CAAGGATGCAAATTCAATTAA	TCCCAGGTTTATAATGATGCA	CCGGAGTCTTTGATCTACAAA	CAGGCTTACATCGCACATACA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
55194	FLJ10647	NM_018166	CTCCGTTTACTTGATCTGCGA	GAGGTGAAGTGACCAAATGAA		
55200	FLJ10665	NM_018173	AAGGCAGAGGAGTATGTTCAA	CCCACAGAAAGTTGTGCATAA		
55206	SBNO1	NM_018183	CAGGTTCAACTTTGATAATAA	CTGGATGAACTTATCGATGAA		
55218	C14orf114	NM_018199	CAGAATCTCAGCAGAAGCCAA	GTGGGTAAATTTGGAAGGCAA		
55219	FLJ10747	NM_018202	ATCCTCTTTGTTTATATTGAA	CAGGCTGGAACAAGACATTAA		
55228	FLJ10781	NM_018215	CAGGTGTATGGTAGTAAGTAA	CACCATGACTAGTAAATGTAA		
55234	SMU1	NM_018225	CAGAATGTTCAAATACCTTTA	CAGGTTGTTCTGGAATTGATA		
55239	FLJ10826	NM_018233	CCGGATTGCCTTCATCCTGTA	TTGCCTGACAGTGTTCTTAAA		
55243	KIRREL	NM_018240	CTGGGAGGAAAGAGAGATAAA	CCGGGTCATGAAGGCCATCTA		
55247	FLJ10858	NM_018248	TCGGATATACAGCATATTCCA	AAGGATTATGCGACACAATAA	CCTGGATATTCTAACAGTGAA	ACGGATTCATTTCGGAATGAA
55256	MTCBP-1	NM_018269	AAGCCTTAAATGTTTAAGTAA	AACAGGAGTATTAGTACATAA		
55257	C20orf20	NM_018270	CTCGGATTAGCAAGCAATAAA	TCGTGTGACTGCGAACATTAA		
55265	KIF24	AK001795	AAGGTTATCAAATTCACTTAA	AAGGGCATGTAGTTTAATTAA	AACAAGTAATCCCTAGTACTA	TAGCGTAACATGATACATCTA
55274	PHF10	NM_018288	ACGAATTACAGACCATTATAA	CGGACAGTTCCAGGAATATTA	TCCAGGGAAGACAGAAATCAA	ATGGCAGTGTATGGAATGTAA
55275	FLJ10979	NM_018289	AAGGAGATTTAGATCAACCAA	ACCCGTGATATTAAGCAATTA		
55283	MCOLN3	NM_018298	TCAGTTAATCTTCGCAGTAAA	CAGACAGTTCGTCATCAAGAA	ATGACTTTACTCTGACTATAA	CTGATACATACGAAACAATTA
55284	FLJ11011	NM_001001481	AAGGTTAACAGCATGAATTAA	CTGGTTATAGTGGGAATATAA		
55295	FLJ11078	NM_018316	AAGAATTAACCTCCTATCTTA	CACGGGCATCGTACAGGTGTA		
55304	C20orf38	NM_018327	AAGCATCATATTTGAAGGAAA	CAGAGCTTCTTTAAAGCATAA		
55308	DDX19L	NM_018332	ATCAAGGAAGAGAAAGTCAAA	GGGAATTATGCTGTTCATTTA		
55314	FLJ11155	NM_018342	TAGGTTATCAGTAACAATTTA	ATCCTTTGTTTCATAAAGTAA		
55317	C20orf29	NM_018347	CACCGGAGTAAGAAACTACAA	CCCACAGTCATCGAAACACAA		
55324	ABCF3	NM_018358	CAGGGAAATAGCCAGGTGCTA	CCCAAGTGGCTGCTATGTAAA	TCGGTTGGAATCATCTGGCAA	CGAGGCTCGACTTAAGGCAAA
55342	STRBP	NM_018387	AAGGATGTATAGAGTCTCAAA	CTGGAAATTCTACAACTGAAA		
55359	STYK1	NM_018423	GCCCAAGAGTGTTATTCTCAA	CCGATTAGACTAAGGAGACTA	TTCACCTTAGGTATAGATAAA	CTGGGCTGCAAGATATCAATA
55361	PI4KII	NM_018425	TCCAAAGATATCGGACCCTAA	TCCGCACACAATCATAGAGAA	CCGCATCGGGCTACCACCAAA	ACGCAAATGTATGAATAACAA
55364	IMPACT	NM_018439	CAGGATGGATTCTGAAATATA	AAGAAGAGGAATGAACATTAA		
55366	LGR4	NM_018490	CACACTTGGGCCAATAACTAA	TCCAGCTAGATTGCAGTTTAA	TAGGTGTAGTAGAGCAATATA	TAGGATTTCATAGTAATTCTA
55437	ALS2CR2	NM_018571	CAGGATTTACATGGGTATAAT	ATGCTGTTACAGAAACTGAAA	CCAGTGGAACTCACACAGTAA	CAGGAACACTGGTAACTATAA
55503	TRPV6	NM_018646	CAGCAGAAGCTACTTCAGGAA	CAGGCCTGCATTACTCCTTCA	GAGGAGTAGCATGAACGCCAA	CTGCATGTCAGAGCACTTTAA
55511	SAGE1	NM_018666	AAGGGAGCTGTTTAAATTTAA	CTGGTATTTCATGCAGAAGTA		
55520	ELAC1	NM_018696	ATGAGTGGAATTACTAGGTAA	ATGAATTGGCTCAGTATTTAA		
55530	DKFZp761H039	NM_018711	CCCATGAAAGCCAGAGCTAAA	CCCGGCCAAACCCTCAGTGAA		
55534	MAML3	NM_018717	CTGACTTATGGCAACACTAAA	CAGCAGCTTTGGAGACACAAA		
55561	CDC42BPG	XM_290516	CACAGTCATTATATTGTTATT	CCGGCCCGTGTACACACTCAA	CTCGCCGCCTACCAACTTCAA	CGCCGGTGGCTTTGCACTCTA
55572	H17	NM_017547	CCCGCTAGTTGTCAACATGTA	CAGCTTTCTACGGAACATCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
55578	FAM48A	NM_017569	CTGAAGTTAAGCAGAAATTAA	AAAGATGATTATGTATTTGAA		
55600	ITLN1	NM_017625	CTCAGACAAGATTACAATGAA	CCCGGTGATCCCTGTGGTCTA	CTGCGGGATTTGTTCAGTTCA	ACCCAGTAGCTAGAATGTTAA
55601	FLJ20035	NM_017631	CCCAGTGTCAGTATTTATAAA	AAGGGTATTTGCTACCTTTAA		
55611	OTUB1	NM_017670	CAGCAGGACCGAATTCAGCAA	CAGGGCTTCACTGAATTCACA		
55621	FLJ20244	NM_017722	AAGGATCGTCTCTGTGGCTAA	CCAGGAGAGAAGGACACGCAA	ACGCCGGAATGTCCAGCTCAA	CAGCATCAGCGCTGACTTCTA
55622	FLJ20272	NM_017735	AAGCCATATTCTTAAATTCAA	CCGCAGGTGTATTTACGGTAA		
55626	FLJ20294	NM_017749	TGCGTAGAATTTAGAGTTATA	CTCCTAATGAATGCTAAATAA		
55627	FLJ20297	NM_017751	TAGGCTGTCGTCTGCCATCAA	CAGTGGTACTTAAGTATTCAA		
55629	PNRC2	NM_017761	CTGAAGGTTTAGTATATTAGA	AAGATGTAAACTCTTGCATAA	ACAAGTTTATGTAGTACTTAA	CCCAATGGCCCTGTTTATTAA
55632	KIAA1333	NM_017769	AACGACATTAAGTGATAAATA	CTCATTACATTGGACATTAAA	AAGGAATATTATAGCCACTTA	TAGATTAATCTGTATGGTCAA
55636	CHD7	NM_017780	CAGGGATTAGTTAACAATACA	TACCATTGGTATTATAATAAA		
55640	C14orf58	NM_017791	ATCAGATATTCTAAACTTAAA	AAAGGTATTAACAAATGTTTA		
55643	BTBD2	NM_017797	CCGCATCAGGTTCTCAGTCAA	CACGCTATACACCGCCAAGAA		
55644	OSGEP	NM_017807	CTGGACCACGGGAAAGAGATA	CTGGAGGGACTAATAAGATCA	TAGCAAAGCTATAGACTCCAA	CCAGGATGACTCAGCAATAAA
55652	FLJ20489	NM_017842	CTGGAGCTTCATTTCCTTCAA	GTGAGGAATCTTTGTACTTAA		
55662	HIF1AN	NM_017902	CACTGTGAACTTCTGGTATAA	CACCCACAAGTTCTTGTACTA	CAAGCTCAAGCCATACATAAA	AACACATAGGCTTGCGTCTTA
55663	FLJ20626	NM_017908	CCCAATGTCGATGGACAGGAA	AAATTCCACTTTCATAATAAA		
55667	C9orf55	NM_017925	CAGCACAATAATGTTCTTAAA	CAGCTTGAGATGGAAATTCAA		
55669	MFN1	NM_017927	ACCCAGCAAGAAATTATTGAA	AAGGCTTGTTATAGTCACTTA		
55680	RUFY2	NM_017987	AAGAATTATGTTGAAGAATTA	CAGGATGTAGAGAATGAGCTA		
55683	FLJ10081	NM_017991	CCGGATGCTTGTGTCATCCAA	CCGACCTGCCTTTATGATAAA		
55687	TRMT1	NM_001008568	CTGACAGAGATGGATCTGCTA	AACGAAAGAGTTTGTAAAGAA		
55690	PACS1	NM_018026	CCCGGAGGAAACTAACCTCAA	CCCGGTGCAGATGAACCTGTA		
55699	FLJ10326	NM_018060	CAGTCGTTCAATATATGTAAA	ACCGAATTATACAAACAATAT	ACCACTGAGCATATTGTTAAA	AAGAGTCTTCCTATAAAGTAA
55702	FLJ10374	NM_018074	CTGGAGCAGCTTCCAACACTA	TGCGAGGTGATCAGAAGGCAA		
55711	MLSTD1	NM_018099	CAGGTTGGGTTGATAATATAA	CAGGATGACAAAGCTCATGAA		
55718	POLR3E	NM_018119	CAGGAGGTGGATAAAGTACTA	CCGCGGAGAGATCGAGCTGAA		
55732	FLJ10706	NM_018186	CAGGATTTCTAAAGCACACCA	CAGGTAGCAGATCAACCTTAT	CAGCCTGGCTTTCAATGGAAA	CTGGGTTTGATGCTTTGTCAA
55734	ZFP64	NM_018197	AAGGACATGGAGCGGCATTTA	CAGCAGTTTAACAACCTGGAT		
55743	CHFR	NM_018223	AACAGTGATTAACAAGCTGAA	TCACCACGCCATGAAATTCAA	TCCCGTGGAGCGGATCTGTAA	AACCAGAGGTTTGACATGGAA
55754	TMEM30A	NM_018247	ATCGATGGCGATGAACTATAA	ACCGGATAACACGGCCTTCAA	CTCGAGATGATAGTCAACTAA	AACGATTTAAAGGTACAACAA
55760	DHX32	NM_018180	ATGGATCAGGTAACTACTTAA	ACGCCTTATCTTTGAAATTCA		
55769	ZNF83	NM_018300	ACGCAATTTAAATGTGATATA	AAGGAGAGTAATACAGGAGAA		
55779	FLJ11142	NM_018338	CTGAGATTAATAGAAATTGAA	AACTATCACTTTCAACATTAA		
55781	RIOK2	NM_018343	CTCATAAATGGTTATCCACTA	GAGCTATGAATCAGTATAGAA	CGCGGTTGAAATGGGCATGAA	AACGCGATTATCATAAACATA
55793	FLJ11280	NM_018379	TCCAGTTGTTTCAGAGCTTAA	TAGCACCATGACTAAGCATAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
55794	DDX28	NM_018380	CAGGGCAATGAGGAACAACTA	CACGTACTTGATCACTTTGTA		
55795	FLJ11305	NM_018386	AAGGATGATTCTGATCTATTT	AAAGCGTATTCTGAATTTATA		
55801	IL26	NM_018402	AACTTAATTTAAAGTATGTAA	AAGCAGCATGGCTCAAAGCAA	CAAGTACATTGTGTCAACTTA	CAGTGTGAACTTAGTACTTAA
55802	DCP1A	NM_018403	CAGGATACATTAATACATCTA	CTGGAGCAGAATAAGTCTAAA		
55805	DKFZp761O0113	NM_018409	CTCAAAGATCTTAATGAGTAA	CCGCTAAACACTATTATTCTA		
55813	HCA66	NM_018428	CACGCATTGGATATTCATTTA	CTGGCCATTTATGAAGATGAA		
55814	BDP1	NM_018429	CAGAGCAAGGATAGAAATTAA	AAGGTTCTTAATGAATGTCTA		
55815	TSNAXIP1	NM_018430	CCGCACGCAGATGGAACTCAA	CAGGAGGGACTTTGAAATGCA		
55819	RNF130	NM_018434	CAGAATGATGTCGTCCGAATT	CTGTCCTATGTGCAAACTTAA	CAAGCTGTTAACCGAAGATCA	TCCGAGAACAGGAGAAATCAA
55829	SELS	NM_018445	AAGGAGATTTATGGACTTCAA	CTGGCGGATGAGGCTAAGAAT	AACCCTTAACCCTCGATTCAA	AGGCCTCTAGATGATTAGCAA
55830	GLT8D1	NM_018446	TACCGAGATCTCAAACATAAA	CAGACAGACTATAGACTATAA		
55836	C6orf35	NM_018452	TAGGCTCTAATTAGTCAGCAA	CTGCCTTTCATTTGTAACTAA		
55837	C14orf11	NM_018453	CCGGAGAAAGTGAATCATCTA	ATGAATTGTTCTATTAACAAA		
55844	PPP2R2D	BC047379	CCGCTCCATTAAGAACAGTGA	TTCATCCATATCCGATGTAAA	TAGGTGGTTACCACAACAGAA	CAGAGACTACCTGTCGGTGAA
55848	C9orf46	NM_018465	CTGCTTGGCTTCCACCTTTAA	AAAGGAGTTCATGCTTATGAA		
55850	MDS032	NM_018467	TCGAATCATGCCTAAACTCAA	ACCGGCCTCTGAGGTGATCAA		
55851	PEN2	NM_172341	CTCCCAGGACAGGCTCCTTAA	ACAGAACAGAGCCAAATCAAA	CTCGCCCAAAGAAGACTACAA	CACAGAACAGAGCCAAATCAA
55870	ASH1L	NM_018489	CAGGCTGTCGTATCAATGCAA	CCGAGATGATGGGAATATCAA	TCGACTGTTATCTCACATTAA	ACGGTAGTTCTTGCAATTATT
55872	PBK	NM_018492	AACGCTGTAAACTGTAACATT	TCAGTAGTTATTAGACTCTAA	CTCATTCTCCTTGGGCTGTAA	AAGTGTGGCTTGCGTAAATAA
55884	WSB2	NM_018639	CACGTTAATTCGGAAGCTAGA	CGGAAGCTAGAGGGCCATCAA	CACGGCTTCTTACGATACCAA	AAAGATGTCTTAATTGTGTAA
55889	GOLGA6	NM_018652	CAGGAGAGACTGTGTGAACAA	CGGACGGGACGGAGCAGTGGA		
55894	DEFB103A	NM_018661	TACCATTGGGTTCCTAATTAA	CAGGTCATGGAGGAATCATAA		
55897	MESP1	NM_018670	ACCCATAGGGCTAGACACTTT	CACGAGCTGCGCCGCTTTCTA	CTGCCTAATGTGAATTTATTT	GTGAATTTATTTATTTGTGAA
55908	LOC55908	NM_018687	CCGAGAATTTGAGGTCTTAAA	ACGGCTGACAAAGGCCAGGAA		
55914	ERBB2IP	NM_001006600	CTGCAGTAACTCGAAGTACAA	CAAGTTTGATTCAAATCATAA	CAAGATGTTATCAATTGGTTA	CCCGAAGAGCCAAATATAATA
55915	LANCL2	NM_018697	AAGGAAAGAATTTGAAGTCCA	CAGATGGGTTATTGCAGATTA	CTGGCAGTTCCAGAACATTTA	ACCCAGGTATATGTTACTAAA
55922	NKRF	NM_017544	TCGCTTATTTCTGGAATGTAA	CAAGATGTCAATTGAATACAA		
55929	DMAP1	NM_019100	GCGGATGTACGGGACATTCTA	CAGCTTTATCTCCACGATGAT		
55959	SULF2	NM_018837	CTCCATGGAGACGATTTACAA	TCGGTGCTACATCCTAGAGAA	TCGAAAGTGGCCAGAAATGAA	ATGACAGATTCTGGAGGATAA
55968	NSFL1C	NM_016143	CAGTAAATGCTTGACAAGTAA	CACCAGCATGTTGTACGGAAA		
55969	C20orf24	NM_018840	TGGATTCAGATGAAACATTAA	CTGGATTCAGATGAAACATTA		
55997	CFC1	NM_032545	CTGGAGTAAAGACACCTTCAA	TTCCTGGAAACTGATCTTCAA		
55998	NXF5	NM_032946	CAGGAAGCTAGTGAAATGACA	AAAGTATACTCTACCATTAAA		
56000	NXF3	NM_022052	CTGAATTTGATTCAGAATGAA	CCAGTTGAGTTTCACTATGAA		
56107	PCDHGA9	NM_018921	CAACGGATTTACCGAGTTAAA	ACGGAATAGAAATAGAAGTAA		
56108	PCDHGA7	NM_018920	AACATCCTGATGGAAGATAAA	AAGGATTAGATTATGAAGAAA		

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Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
56110	PCDHGA5	NM_018918	TCAGATTATAATATCACTTTA	CAGATTATAATATCACTTTAA		
56124	PCDHB12	NM_018932	AAGCTACACAATAAATCCGAA	CTCCAGGTCAAATAAGTTCAA		
56132	PCDHB3	NM_018937	CCGGAACTAGTACTGGATAAA	ATGGACACAAATATAGACTAA		
56143	PCDHA5	NM_018908	CACAATTGAGATACAGGTTAA	AAAGTCCAAATTTATAATTAA		
56156	TEX13B	NM_031273	CAGGAGAGACTCCGAACTCCA	CGGAGCTATTGTAGCAGGCAA		
56171	DNAH7	NM_018897	CAGGATAAATCGGCCAGCAAA	TTGGAGAGTTATGCTAAGCAA	TCGGAAGGCAATATATTAGAA	CGGGCTAATATCATTCGATCA
56172	ANKH	NM_054027	CACGCTCTGTTTCGTGATGTT	CACGGAGTTCGAAACCATCTA	ATCAATGAACATTGTACCTTA	TTGAATGTAAGGCTCAGTAAA
56204	FLJ10980	NM_019600	CAGCACCATAACCCAAATGAA	CACATTGTTGTGGAAGAATAA		
56241	SUSD2	NM_019601	CGGCACCAACTTCACATTCAA	CAGCCTGACCTGGCATGTCAA		
56255	DJ971N18.2	NM_021156	CTCCAATAACAGCCAGGTTTA	CAAGGTAGTCTTGTGAAGAAA	CTGGGTCTTGAACTACTTTAA	CTCCAGTACCTGAAAGTGAAA
56256	SERTAD4	NM_019605	AGGGAGTTATTTGGTAAGCAA	ATCCAAGATCACATACTTTAA		
56259	CTNNBL1	NM_030877	CAGGCATATCATCAAGGAGTA	TCGATTTGCTTCAGGAATTAA		
56265	CPXM	NM_019609	CCGGATTCGAGTCATCAAGAA	CTGGAGGACGGCGATCTATAT	CAACCAGAGCATCGATCTTAA	GAGCATCGATCTTAACCATAA
56270	WDR45L	NM_019613	AAGACTGTTATTGAAATAGAA	GCCGGTTTCTTTAGTTCTTTA		
56271	BEXL1	XM_043653	CTAATGGAAATTAGAATTCTA	AGGGCAGATGATGGAAATCAA		
56301	SLC7A10	NM_019849	TGGCTGGAACTTCCTCAACTA	CCCACTGGTGACCTTCGTGTA	CACGTTCACCAACATTGCCTA	CAGCTTCATCTCAGAGCCTAT
56311	ANKRD7	NM_019644	CCGGTTAAGTGAACTATGATA	AAGGATGGGTATACTCCACTA		
56341	HRMT1L4	NM_019854	CAGGCTCTTATGGGCATGAAA	CAACATCATCACCATATTTAA	CGCGTGTGCCTAGAATATATA	CAGATGTTAAGCAGCTATGAA
56479	KCNQ5	NM_019842	CGGGTTGCTGTTGTCGATATA	CAGAGTATTAAGAGCCGACAA	AAGGGCAAATCACATCAGATA	TCCAAGGTGCATCGACATTAA
56606	SLC2A9	NM_001001290	CACGTTGGACAATTATGTCAA	ACCCATTATTGGGAAGCTTAA		
56649	TMPRSS4	NM_019894	CAGGATCCTGACAGTGATCAA	CAAGGTGATTCTGGATAAATA	CAGGATCTGGATGTTGTTGAA	CTGGATGTTGTTGAAATCACA
56650	C3orf4	NM_019895	ACCGGAAAGAGTACACCTTAA	ACGGTGTATCACCATACCCAA		
56652	PEO1	NM_021830	CAGGCACCTAAGGCATTTCAA	CAGGATCGCAGCTCAAGACTA	TAGGATAGGCTGGAGCATAAA	CTGGCAGGCTAGTGTAGATAA
56659	KCNK13	NM_022054	ATCCTTATTCTTTAAGTCTAA	CCAGGCTTCCTTCAAAGCATA	TAACTAAAGAACATAGCTTAA	TGCAAAGATGATGACTATTTA
56660	KCNK12	NM_022055	TGGGACCATCCTGTTCTTCAA	CTGCATTTACTCGCTCTTCAA	CGCGCTGGGCATCATGAACAA	CTGGCGCTTTCTTAATCTTTA
56729	RETN	NM_020415	CAGCATTGGCCTGGAGTGCCA	CAGGAGGTCGCCGGCTCCCTA	CTCCATGGAAGAAGCCATCAA	CCCTAATATTTAGGGCAATAA
56848	SPHK2	NM_020126	CACGCTTTGCCCTCACCCTTA	CAGGTGGAGTATGGGCCGCTA	CCGAGGGTAGTGCCTGATCAA	CAGGATTGCGCTCGCTTTCAT
56851	C15orf24	NM_020154	TACATTATGTATATTAATTAA	CAGGTCCACCTTCTTACTTTA		
56888	KCMF1	NM_020122	CTCCTAATACTCCACATTCAA	CAAGAACATGTTACTTCTGAA		
56889	SMBP	NM_020123	CACGTCTTTCTGGGCATATAA	CAGATGTACATAGATGATTTA		
56893	UBQLN4	NM_020131	CACATGCTCAATAACCCTGAA	AGAGATGCTAATGGAATTTAA	CACACTGGCCTTTGTAAATAA	CCAGAGGAAATTCGTGTGAAA
56897	WRNIP1	NM_020135	ATGAATTAATGTTATAAGGAA	CGCCATGTTCATAGAGGATAA		
56900	AD-020	NM_020141	CTGGAAATTCTATTTACTTTA	AAGGTAATTTACAGCCAGAAA		
56904	SH3GLB2	NM_020145	CACCAAGAACTGGACAGAGAA	CAGACAGAGTTTGACCGGCAA		
56911	C21orf7	NM_020152	CTGAGAATTGTTGTAAAGTAA	AAGGTGTGGAATAACCCTTAA		
56915	EXOSC5	NM_020158	CCCAGCAAGGATAACATTCAA	ATGGAATGGATGAATCAATAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
56919	DHX33	NM_020162	ACGGTTCCTCTTAGCTATTTA	CTGGGTGAAGGTTGATTTGTA		
56922	MCCC1	NM_020166	CAACATTGACTTCTTACTCAA	TAGCATGCAGATTGAAGATAA	CATGGTTATGATCGCCATGAA	ATGCATTTGGGTCACTAATTA
56928	SPPL2B	NM_020172	CACGGTGAGGGCGGCGCTGTA	CAGGTTTGACATCCAGGTACA		
56930	LOC56930	XM_373790	CACCAACCCAGTTCTCAGTTA	TTGCCACGTGTTTCCTGTTAA		
56935	FN5	NM_020179	AAAGGAGATAATAGCCTTAAA	CTGGTCTTTGACTTGATTAAA		
56943	e(y)2	NM_020189	CGCGGTGATGGTGGTTAGCAA	AAGGAGCTCCTACAAAGAATA		
56949	XAB2	NM_020196	CCGGACCTTGTCTTCGAGGAA	CAGCTACGTTTGTACATCAAA	CCGCGTGTACAAGTCACTGAA	CACGTACAACACGCAGGTCAA
56950	SMYD2	NM_020197	AAGATAGAAATGACCGGTTAA	ACCGGTTAAGAGATTCTTATT	CCGGAGGGCCAAGCACTATAA	GAGGTTAGTCTGAATCTTGAA
56951	C5orf15	NM_020199	AAGGATATTTGTGTACAATTA	TAGGATAATGATATTGCTCAA		
56952	PRTFDC1	NM_020200	CAGGGTATGACTTGAATTTAT	TACCGGGAATGCAGCTATTAA	CCGGGAATGCAGCTATTAATA	CTCGAAACTAAGCAAGTATAA
56956	LHX9	NM_020204	CCGGCACTGCGACCACTTTAA	CAAAGTGTATTTGGATTTAAA	AACCAGATAATTAATTAGTTA	CCGGGCGTGTGTATATGGAAA
56961	SHD	NM_020209	CCAGGGCTTCCTGCATCTGAA	TCCGGAGACCTCCGCCCAGAA		
56967	C14orf132	NM_020215	CGCCATAAATTCTGAAATAAA	CAGCATGAAAGTGATGAGCTA		
56970	ATXN7L3	XM_375456	CAGCATCTATGATGACATCAA	CCACAAGAGTTTACAAATGAA		
56974	DKFZp547K054	XM_498167	CGGGTCGATGTGCAAATCCAA	CCGCATTAATGTCCTCTGGAA		
56981	PRDM11	NM_020229	CTGGCTGATTGTGGACAAGAA	CTGGATGAGGTACGTGGTCAT	CAGGTTCTGGATAACCCAGAA	ACGCCTACAGTCAGTGTGCAA
56988	C8orf17	NM_020237	AAGAGCAATAATACAATTCAA	ATCAAATTTCTTTATCTATAA		
56990	CDC42SE2	NM_020240	ACGGCGGATTGACAGAAGTAT	CCCACAAACTTTGTGCATACA	CAGGAGACCTGTTCAGTGGAA	AAGGGAGGTTATGGAGGTGGA
56992	KNSL7	NM_020242	CTCTATACACTCAGAATTCTA	CAGGATTCCTATGACAACTTA	TTGAGATTGACCAACTTTCAA	ACGCAATAACAAATTATCATT
56995	TULP4	NM_020245	CCGTTTCTTGATCACCACTTA	CTCGGTGCAGTAATCTATAAA	CACACTGTGTTGGACCAACAA	ATGCATTACTGTAAACATGAT
56996	SLC12A9	NM_020246	CAGCAGTACCCTGAAGGACAA	CACGATCGTCGCCGTCGCCTA	CCCACTGGTGTTGATCGGAAT	CTGGTGTTGATCGGAATCTAT
56998	CTNNBIP1	NM_020248	TCCCTTCAGACTGGCCCTTAA	CAGTATCGTTTGTTTATGAAA	TGCGTTTATAATTGGCTTAAA	CACCTGTTTGCCTGAAGTTAA
57007	CMKOR1	NM_020311	CACGCTCTCCTTCATTTACAT	CTGGGTGAATATCCAGGCCAA	CCGGAAGATCATCTTCTCCTA	CACTATTGGTGTACCTTATAA
57018	CCNL1	NM_020307	TTGGATATAAGGGATCTTGTA	CAGTGTGATGTATGGACTCAA	CTCCAAGAAGACACTATAATA	CCCTAGCAGTATCTAATTAAA
57019	CIAPIN1	NM_020313	CAGGTTGAACATGATGATCAA	CAAAGTGAAGACAGCATCTAA		
57026	PDXP	NM_020315	CAGGTTTCAGTCAGTAAATAA	CCAGTTTAGGTTCCTAAGTAA		
57048	PLSCR3	NM_020360	TAGCATCTGCTTGGCCAATTA	TACATTCATATAAACTTTGTA		
57060	PCBP4	NM_020418	AAGGGCGAGACTGTAAAGCGA	ACAGGAGTTCTTGGTTCCCAA		
57085	AGTRAP	NM_020350	TTGGGTCTTCTCAGGACCGTA	AACCTGAAGGTGATTCTCCTA	CTGCTTCGTCTACCACATGTA	CAGGGATTGCCTGAACCAAGA
57093	TRIM49	NM_020358	CAGGATCTCACATTTGCTTAA	TACGTATTGGTTCTTTATTAA	CAGGCCTTGTTTCTACCTCAA	ATGATATCTTTGTGTATGAAA
57105	CYSLTR2	NM_020377	CAGATTATGCCAGGCACTTTA	AAGGGTGGAGGTGATATGGCA	TGGGATCATATGGATCCTTAT	CAGGCTTTCTAAATTCTTCAA
57113	TRPC7	NM_020389	AACGGTGATGTGAACTTCCAA	CCGGATCAAACTCGCCATTAA	CGGATCAAACTCGCCATTAAA	CAGGCTTACGTCAACAGTCTA
57115	PGLYRP4	NM_020393	CCAGTGAATGTCCTTGTTATA	CAGGATGACTCTCCCAGCGAA	CAGCGAAGTATGGCATCATTA	TCAGCAGTGTCTGAAATTTAA
57117	LOC57117	NM_020395	CCAAGTTGTACTGAACGCCAA	AACCTGCTACTTCGTCAGCTA	TACGCCCACTGTACCTTTAAA	CAGGACCTAGTGGAAGTACTA
57118	CAMK1D	NM_020397	CTGAGAAAGATTAAGCATGAA	ATGGAGAAGGACCCGAATAAA	CCAGGCGCTTTCTATACTTAA	CAGGCGCTTTCTATACTTAAT
57122	NUP107	NM_020401	CAGCTTTAAGTGGGAATCTTA	CAGGTGAATATACTGAGTAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
57124	CD164L1	NM_020404	CAAGCGCATCACTGACTGCTA	CCAGCAGATGTGTGTCAACTA	CCCTATGATCTCAACCAAATA	CACGCTGGCTGTCGACGGCTA
57130	ATP13A1	NM_020410	CAGGAGCTGCACTTCATTGAA	CACCTTCGCCATCAATTACAA		
57140	RNPEPL1	NM_018226	CACCTACTCTGCCGTCGTCAA	CCTGATGAACCTGTTCACCTA	CCGAGCCTATGTGGAGAAGTA	CCGGGCAGGGCTGGAATTCGA
57144	PAK7	NM_177990	ACGCCTCTAGTAGCAAACCAT	AAGGTGGATTACGATCGAGCA	ATGGTGTGCACGTTTCATTAA	ATGATCTGGATCCGTATTATA
57146	LOC57146	NM_020422	AAGGTGTAGTTTCCACTGTAA	CAGATGGATGAAGACCACTAA		
57147	PACE-1	NM_020423	TGAGGAGTATTCAGTCAATAA	CAGGAGGTGGAATCACTGCTA	CAGGACAATTCCGGAAGTAAA	AAGCTCTATTATGAAATACAA
57148	KIAA1219	NM_020336	CCGGTACTTTGTCTTGGATAA	CCGGGCTGTTACTGTGAATAA		
57151	LYZL6	NM_020426	AAGCAAGTTCAACATATCAAA	CAGCAGCTTTCTTGCCCTAAA		
57152	SLURP1	NM_020427	CTGCTTCCGAGACCTCTGCAA	CAGCTCCTGTGTGGCCACCGA	CAGGGCGGAAGGTGCTCCTCA	CAGGACCATTACCCGCTGCAA
57153	CTL2	NM_020428	CCGGGACTTTGAGTACTATAA	CACAGTGAACACCCACGTTTA		
57161	PELI2	NM_021255	CAGAACTGTTTGGTTGATTAA	CAGGGTTAGGGTTTAAAGAAA	CACGTGATATAACTGGTTATA	CTCGGGTACAATGGTGCTTTA
57162	PELI1	NM_020651	CAGGACTACATTATAAATTTA	CAGGCTATATATTGTAGCTTA		
57167	SALL4	NM_020436	CCGAACCAACACATCCATTAA	CGCGGTGGATGTCAAACCCAA		
57172	CAMK1G	NM_020439	CTGGAAGAAACAGACCACCAA	TAGAAAGAAGTTCATGAGTAA	CAGGTCTTGTCGGCAGTGAAA	AACAGGCCGCCTGAAACTCAA
57176	VARS2L	XM_373419	CCGGAGGAACCGTGAAGCCAA	TAGTATTGTATGAAATCCCTA	CATGCAGGAATTGCTACACAA	CGCTTTATCCTCAATGCTTTA
57238	KIAA0492	XM_378914	CTGTGTTATAATGATACTTAA	TAGCAATTGAATAAACATAAA		
57325	CSRP2BP	NM_020536	CTGGAAGGAAGTGGACGTCAA	CAGGCGTGATTATGAAACAAA		
57404	CYP20A1	NM_020674	TAGAGAGACCCTCGTCCTTTA	ATCCTAGAAGACAGTATGATA	CAGAGTTGAGGTTTGCATATA	CCAGGGATTACTCCAACTGAA
57405	Spc25	NM_020675	CGGGACTAAGAGATACCTACA	ACGGTTTATAATTAACATACA	CTCGTCATTTCATTAGGTATA	CCACGGTTTATAATTAACATA
57407	HSCARG	NM_020677	CACCTTCATCGTGACCAATTA	AGGCACCAACATCTGAATAAA		
57413	AD026	NM_020683	CAGAGGAGCTATGATAGACCA	TGGGAAAGACCTATCAGGCAA	CTCGCGTGTCCTGACTCCAAA	CACGGCTTCTGCCATCTGCAA
57452	GALNTL1	XM_031104	AAGGATCCACATACCCATAGA	AGCAGCTAGGCGCGAGCGAAA		
57462	KIAA1161	NM_020702	CGCGGCCGCCATCAAAGTCAA	AGGACTCTCGTAGGAAATAAA	CAGGCCAGACTTCGTGCCTTA	CACCTCTATACCACCCATTAA
57472	KIAA1194	NM_015455	CCAGGATATATTGAACCTTTA	CAGAGGCAACTTATTCATGAA		
57484	RNF150	XM_371709	TCCAGAGGTTTCGATATGCAA	AACCCGGAACTTGCAGAAATA	CCGGAACGCGTTCCTGCAGAA	CAGAAGGACTGTTGCCTTGTA
57504	MTA3	NM_020744	AAGAAGGATAGAAGAACTCAA	ACGGCCGTTTGTTGCTATTAA		
57508	KIAA1287	NM_020748	CAGGTAAACCCTAATCATTAA	ATGAGTGTTAGTGGAATTTAA		
57510	XPO5	NM_020750	ATGGTACAGGCTACTGCTAAA	CACGGTTTGCTGTGTTTCAAA	CCAGATGTTTCGAACACTAAA	CTGTCTCGAATTGTAGTGGAA
57514	CDGAP	NM_020754	CAGGATGTCACCATAGATAAA	CTGGATCAGACTCCAAATCAA		
57520	HECW2	XM_038999	CTCCATCACTTGAGAAGTATA	ACGGTCTACTATCATCAGTAA	AAGGCTCTTCTCAGAATTCTA	CAGGATTGGTGCGCCTTTCAA
57529	RGAG1	NM_020769	CACCATCTCACTACATTCTTA	AAGCAATATCCTCACTGATAA	CAGGGCATATATGACTCCCTA	AAGGCCCATACCAACAAGTAA
57533	TBC1D14	NM_020773	CAGCAGGACTGTGTTCATGAA	AACACTGGAGTTGGCCTTAAA		
57538	ALPK3	NM_020778	CAGGTGGATGCTGGGACACAA	CAGGCAGATGGGAAGATACAA		
57558	USP35	XM_290527	GTGGATCATTGCACTGCTGAA	ATCGAGGTTTCGCTCACCAAA	CCCTTCTAACTTCTAACCGAA	ACCCATGTTCATAAATAAATA
57560	KIAA1374	NM_020800	AAGGAATGAAATTCTGATAAA	CCCAAAGTTATTACCACATAA		
57565	KLHL14	NM_020805	CCAAATTTAATCCATAATAAA	AAGCATTTATGAGAATTATAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
57572	DOCK6	NM_020812	CACGGTGAAGATGAAGGAACA	AAGACCAAGGATGAAATGGAA		
57579	KIAA1411	NM_020819	CAGCAATTACATTAAATTCAA	AAGGTGCTGAATAGCATTAAA		
57582	KCNT1	XM_029962	CTGGCTCTTTCCAAACTAGAA	AGCGCTGGAAACTTCTATTAA	CAGGTCATCGTGGCCATAATA	ACGAGGACGTAGCAAATTTAA
57585	CRAMP1L	NM_020825	CTGCATAATGATCCCATTTCA	CAGATCGTCAGTGGGATTGAA	CCCGACAACCTTGCCACCCAA	AAGGGCCACCACTGTACGTTA
57592	KIAA1441	NM_020832	CCGCCTGGTCTTCTTCAACAA	CAGGCTCTCAGGAATCCTTTA		
57593	KIAA1442	XM_044921	CAGGGAGAAGTGACCTGGAAA	CAAGTTCTTCCTCAAATGCAA		
57599	WDR48	NM_020839	CAAGTTTGTCATATAAAGTAA	AAGGGAGATCATAGTGAGTTA		
57605	PITPNM2	NM_020845	CTCCAAGATGATTATAAAGGA	CTCGTGCAAGCAGGAGAGAAA	CTCGAGTTTCTCAACTGTTCA	ACGGGAAGGCTTGGACTCCAA
57608	KIAA1462	XM_166132	CTGGAAGTAACTTTACTTATA	AAGGTAAATAATAGCCTATAA		
57609	KIAA1463	NM_173602	CCGGCATACATTGAGTATAAA	ATGGAATTAATTTACACGTAA		
57613	KIAA1467	XM_370682	GTGAATCTCTTAAGTATTTAA	CGGCGCAGTGATGGATGTTAA	CATGGTGTATTTGCAAACTAA	TTGGTTTAGTATAGAATTTGA
57617	VPS18	NM_020857	CCCGATTATCTCGCTGCATAA	ATGGAGGTGGAGAGCATTAAA		
57621	ZBTB2	NM_020861	AACGTTTAATTAAATGAGTAA	CAGGAGTACCTTTCACATCTA		
57633	LRRN1	NM_020873	AAGATTGATAACCCTCACATA	AACCTCTTCAATCCCACTAAA	CTGGTTTGATTCTACACCCAA	AAGACTTTGCTTGAATGTTTA
57636	ARHGAP23	XM_290799	CTCCTTCATCTCGGCCGTCAA	CTGGCTGAAAGCAGCACTGAA		
57642	KIAA1510	NM_020882	CCCGACCTTCACGCTCTTCAA	CTGGGAAGAGAGCAAGTTCAA		
57646	USP28	NM_020886	CTGGAACAGTTTGCAGATAAA	AAGGATTAGGTGGGCACATAA		
57647	DHX37	NM_032656	CCCAGTGACTGTGCATTTCAA	CCAGATCAACTTGGATCATTA		
57650	KIAA1524	NM_020890	ACCACTCTTATAGAACAACAA	CAGCTAGTAGACAGAGAACAT	CGGCACAATCTTTCTGTTCAA	CAGAAAGAGCGCAGAGTGATA
57654	KIAA1530	NM_020894	CACGGTGATCTCGAACTCCTA	ATCCAAGATCACAGAGATTTA		
57657	HCN3	NM_020897	CTGAGTGGGAACATACTTCTA	AGGGACAAGAGTAGTCCTTTA	CAGCTTTCTGCCAACATGTAA	CCCGCCTTGGATCGTCTTCAA
57661	KIAA1542	XM_290536	CACACGAACCATCTCCATCAA	CGAGCTCAATTTGGTGGTAAA	CGCGTCCTTGATAAATCTCTA	CCGGATCAATATTCCTGGAAA
57665	RDH14	NM_020905	TATAGTAAGTATAATGAATAA	ACAAGTCTTACTTGGAATAAA	CTGCCTGGTGTGTGCACACAA	CAAGCATGGATGACATATTAA
57666	KIAA1545	XM_495939	CCGAAGTTACAGATTATATTA	TAGTCTGTTGATATAAATATA		
57693	ZNF317	NM_020933	CCGCTGGAAGTCCAACTTTAA	CAGCTTGGCATTTAATGTCAA		
57703	KIAA1604	NM_020943	CAGGAACAGATTACAGATAAA	CAGCAAACAAATGATAGGAAA		
57707	KIAA1609	NM_020947	CAGGCAGTGCACTTAGAGAAA	CGCGTTGCAAACTATTATAAA		
57711	ZNF529	NM_020951	ATGGATTTAATAGGTAATCAA	AACCTTGTATACAGACATTAA		
57716	PRX	NM_020956	CAGGCTACTTCGAACCAGGAA	CCCGCTGCTCCTGAAGTTGTA	AGGGATGGAATTTGGCTTCAA	CCCGCCGTGGAAATTGAGGAA
57717	PCDHB16	NM_020957	ACAGCATTAAACAGTCAATAA	AACCTGATTTATAGTCCTGTA	AAGCAAGAGCTGAATATAATA	AACGGGTACGGTGATAATTAA
57722	NOPE	NM_020962	CCGGCTCAAGAAGAAAGTGAA	CCAGCCTATGATAACACTAAA		
57729	KIAA1639	XM_290923	TCGGAAGCACTGCTCAGTGAA	CACACAGAGGACCTACACATA	CACAAAGACCTTCGCATTCCA	CCGCACGGCATGTGTCAGCAA
57733	GBA3	NM_020973	AACCATGATTTGCAACTGTAA	CAGATAGACCTGGAAACATAA		
57758	SCUBE2	NM_020974	CAGGACAAGTGTAACCTTTAA	CAGGAACTCATTGAAGACATA		
57763	ANKRA2	NM_023039	CACAGTGTGATTGTTTACAAA	CTCGATTTGTGAAGTCCTTAA		
57787	MARK4	NM_031417	TAGGAGTTAGTTAGGCATTGA	CAGTAGGGCCTTGAAGGTTAT	CTGCAGCCTGTTGCCCAATAA	CCGCATCATGAAGGGCCTAAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
57801	HES4	NM_021170	CCGCCACTCGAAGCTGGAGAA	TGCCGAGACTGTAGCAGAGAA	CTCCAAGCCGGTCATGGAGAA	AAACGTATTTATTATTCCAAA
57804	POLD4	NM_021173	TTCACTAATGCTTATCAATAA	GAGGCTCAACTCCTCCATCTA		
57805	KIAA1967	NM_021174	CCACTTAACAACTAAATACAA	CCGGTTCCACTTAACAACTAA		
57820	CCNB1IP1	NM_021178	AAGATAATTTAGCTAACTTTA	TAGCAGGGCCTTCAAAGTAAA		
57823	SLAMF7	NM_021181	ATGTATTAATTGGCTCTATAA	CACCATGGGTCTGCAGAGCAA	AACAGATATTGTGAGATTCAA	CACTAATAGAACAATCCTAAA
57864	TSCOT	NM_033051	AAGGAAGAGGAGGTACATTAA	CACCTTGTACAACAAGATCTA		
58189	WFDC1	NM_021197	CCGGATGTGCTGAGGCCTAAA	CTCAAATGTTCCCAAGATAAA		
58190	CTDSP1	NM_021198	CAGCTCCTTCAAGCCAGTGAA	CTCCTTCAAGCCAGTGAACAA		
58475	MS4A7	NM_021201	TCGGAGTACTATTATCCAATA	CAGGAAGGATTTGACTATCAT	CACACTCATATTGCTTAAATA	CACGGTCTTGGATATAAGTAA
58480	RHOU	NM_021205	CACCTCTAATCTGGATGTTAA	TACCCAGTTACTTATGATTTA	CCCAGGTATTACACAAGCCAA	ACCCAGTTACTTATGATTTAA
58484	CARD12	NM_021209	AAGGTTCAAGCCAAAGTATAA	CCGGGATTTCAGCAAGTTGAA		
58490	C20orf77	NM_021215	AAGCTTAAATTTGTATATTAA	ATGGTTGGAAATAACCTTCTA		
58493	C9orf80	NM_021218	AAGTGACTTTGTAATATCAAA	TGCGTTTATAGTCAACATGTA		
58496	LY6G5B	NM_021221	CCGCATGTACTTGTTCCTCAA	CACCATCTATTATGATGTCAA		
58497	PRUNE	NM_021222	CTGGTATACTGTTCTCATAAA	ATGGCTGAATTTCTATTCTTA		
58499	ZNF462	NM_021224	CCCGGGATCCTTAAATTATAA	AAGAAGGGCAAGAATAATTAA		
58508	MLL3	NM_021230	ATCAGAGTTCACGACCATTAA	ACCAGTGATCACTTTACTAAA	CTAGAACAGATTCGTAAACAA	CCCAGTGAGCTTCCTCAACAA
58510	PRODH2	NM_021232	CAGGAGCTGCTCAGCCAAGAA	CAGGATGCTCCGGACCTGTTA		
58513	EPS15L1	NM_021235	AGCCTTGTTATTTAGCAACAA	CCGGATCCTTTCCAGACAGAA	AACCATCATCAAGTCCCTGAA	CAGAACCTTCTAGCACACATA
58533	SNX6	NM_021249	CCGAAACTTCCCAACAATTAT	GCCACTCTTATTTACCTTTAA	TCGCCAGTAGTTATATTACAA	CCGCGGACTTAAAGCAATAAA
58538	MPP4	NM_033066	CAGGCCACTAGTATCCTACTA	CAGGTGTTATCCTATGAGGTA	TCGAGGCACAATCATGTTCAA	TACGGTCAGAAGTTCTTTATA
59082	ICEBERG	NM_021571	CAGTGGGTGCAGGCACAATAA	AGCCAGGAAGACATGAACAAA	CCAAGTCTTGCTGCAAATTTA	AAGATATTCTCGTGAAAGAAA
59283	CACNG8	NM_031895	CACGCGCGCCCTCATCTGCAA	AGGCGTCTGCGTGAAGATCAA	CTGCGTGAAGATCAATCATTT	CACCAACACGCTCAACAGGAA
59286	UBL5	NM_024292	AACCTGGAGCTTTATTATCAA	TTGGAACAAGATTGTCCTGAA		
59341	TRPV4	NM_147204	CACCAAGTTTGTTACCAAGAT	CCCGGGCAAGAATGAGACCTA	CTGGAGTGAATTCTCTCTTCA	CTGGGATTTGCCGGTGCTCAA
59343	SENP2	NM_021627	ATGGTCGGAATCAGATTTGAA	CAGATTATATTTCTAGGGACA	CCACACAAGAACAAACGCTAA	AAGAACAAACGCTAACTAATA
59345	GNB4	NM_021629	TACCTTATATTTGCAGGTGAA	AAAGTAGGTAATAGCATATAA	TACGATGACTTTAATTGTAAT	CTGCTCTATATATAACTTAAA
59350	LGR7	NM_021634	CTGCAGTTACCTGCTTTGGAA	CAGGAGATGCCACCTGAGTTA	ACAGACTAGAATGGCTGATAA	AAAGGATGTTTAGACCTCTTA
60385	TSKS	NM_021733	GTGGAAGATGCTGAAATCAAA	AAGCTGTTCACCGGCATCGAA	CACCAACGTGTCACTGCTCAA	AACCAACGTCTTGAAGCAGAA
60386	SLC25A19	NM_021734	CTCCCTGTGATCAGTTACCAA	CTCGTATGAATTCTTCTGTAA	AACCTATTTAATAGACATTAA	ACCTATTTAATAGACATTAAA
60437	CDH26	NM_021810	CACAAGTTACACTTTCTTAAA	CACACTATTAGTTTGAATTAA		
60468	BACH2	NM_021813	CCGGGAAGATAACTCTAGCAA	CTGATGCAAGTGCACCTCTAA	CAGGTGATAATTATGTAGGAA	CACGAGGCATTGTGTGTTGAA
60490	MDS018	NM_021823	CCCGTATAACATGGTGGTTAA	ATGAAATAAACTATAACTAAA		
60526	FLJ21820	NM_021925	TTCGATATGTTCTCTATGTTA	AGGAGCATTTATGTAAGCTTA	CTGCACTAGACAGAGAATAAA	GAGATACTCACTGATACTAAA
60529	ALX4	NM_021926	CAGGTTCCCTGCTACGCTAAA	CAGCAGCTACCTGAGTGTCAA	CCGGACCACCTTCACCAGCTA	CAGCCTCAGCCCAGGCCTCAA
60592	SCOC	NM_032547	TAGGATTAGTAAGATATACAA	CTGGATGAGAACAGTTACAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
60673	FLJ11773	NM_021934	CACAGGCAAGTTCCACTACAA	CGGGAGAAGGTGGGTGAGAAA		
60675	PROK2	NM_021935	CAAGGCTCTTACCTTACTTTA	TCGCTCTGGAGTAGAAACCAA	TAGCCACATCTTACCTGTAAA	CGGTATTAAGTTGTAATTTAA
63027	C6orf85	NM_021945	ACGGAGTGAAATGTACATGAA	AAGGATATGCTAAGTGATGAA		
63891	RNF123	NM_022064	CACATGCGTGTACAAAGGGAA	CCGCAAGTTTCTGCTTAGCAA	CTGCGCTACTATTGGGATGAA	CAGGGCCACAGTGAGCATTAA
63892	THADA	NM_022065	CAGACTTCTATTGATGCTAAA	CACCTTGAGTTCACAGATTAA		
63925	ZNF335	NM_022095	CTGGAGGAGGATAGCGACTAT	CGGGCAGCGTTTCAACCGTAA	CAGGCGCTTCCTAGGCAAGAA	TGGCCTGTCAGTCTCAATAAA
63939	C20orf177	NM_022106	AAGCAAGATATTCTATACATA	AAGGGAAGTGTCTTTCAATAA		
63940	GPSM3	NM_022107	TTGGTTGTGTGAATAAATATA	CGGGCTGTGAATGGACCTTCA		
63971	KIF13A	NM_022113	CCGGCAGGCCGTCACAGTCAA	AACCTATGAAATAGTATCCAA	CCGCAACAACTTGGTAGGAAA	CTGGCGGGTAGCGAAAGAGTA
64061	TSPYL2	NM_022117	CAGACATATCTCCATGGGCTA	CAGCGAGAATCCTGACCACAA	CCAGAGGTTAGTTGACCCGAA	CACAAACATGGTGATTGTCAA
64072	CDH23	NM_022124	CCGGCTGCCCTTCTTCACCAA	CAGCGGAGTGCTGACCTTGAA		
64083	GOLPH3	NM_022130	CACCATTGGTTTCATAATGTA	CACAGTAAATACTTAATATAA		
64087	MCCC2	NM_022132	CCCGAGCACTTCACATATCAA	AACAATTACGGGCCCAAGAAA	ACCCTTACTATTCCAGCGCAA	CCCATAAAGCGGAGACAGTAA
64090	GAL3ST2	NM_022134	CACCAACATCATGTTCCTGAA	CACAGTCACCGAAGAAATGAA		
64100	ELSPBP1	NM_022142	AAGCTTAAATAACCACCTTTA	CAGCTGGTCCTTTGTGAAGAA		
64101	LRRC4	NM_022143	ACCACTATCTCTGAACCTTAT	AAGCCACAAGTTAACTTGCTA	CAGAAGGGATTTCTGGTATAA	AAGCTGTGAGATCCACAGTTA
64102	TNMD	NM_022144	CAGATTAAAGTGATTCCTGAA	TTGGAAGTACACGACTTTAAA		
64106	GPR147	NM_022146	CTACGGCTACTTCAACGAGAA	CACCAACATGTTCATCCTCAA	CTGTTTCATCGTGCTCAAGAA	CTGGTGGCCATTGCTGTGGAA
64109	CRLF2	NM_022148	AACCGTGCAGGTGACATGGAA	ACACACCACTGTCAAAGTCAA	CACATGAGTCTCTGTGTTCAA	CAGGATCCACGTTGACATTTA
64127	CARD15	NM_022162	CTGCCACATGCAAGAAGTATA	CAACATGGCCGTGAACTTTAT	TAGGCCGTTCCTTCAAAGCAA	CAGTTATGGATTGAAAGTTTA
64129	LCN7	NM_022164	AACGTACTGGGACAACTGTAA	CCCATCTTCCTCGGTCATGAA	CCGGCCTGGGATCCAGGCTAA	CAGCCCTGTATTCTTATTCTT
64131	XYLT1	NM_022166	CAGGGTGCTGACGAAATCCAA	CAGCAGGATCTCAACGGGAAA		
64132	XYLT2	NM_022167	CCGGGACAAGAATTTCCTCAA	CACACCCATTTCAGCCATCAA		
64145	ZFYVE20	NM_022340	CAGGATGGCAGCATCATTAAA	ATGGAGAAAGTTGACCAGAAA		
64146	PDF	NM_022341	CCGGTGGAGCGGGCGCAGCTA	CTGGTGCTGGGTCCTCCCGAA		
64147	KIF9	NM_182902	CCCGGACCTTATCAGAGGAAA	CACGCTCTGAAGGACTCGTTA	AACAGACAGACTGGTCGTTTA	CAGGACTTGGTTTATGAGACA
64149	NJMU-R1	NM_022344	AACTGTGGTAGTGGAGATATA	CACTGAGTCCTAGATAGATAA	TTGGCAGATACTAATCTACCA	TTGAGTTACACTCCTGTTGAA
64170	CARD9	NM_052813.1	CAGCGACAACACCGACACTGA	ATGCACTGTATTAGTGTTAGA	CCGCGTCTTCTCCATGATCAT	ACGTAAGGACTCCAAGATGTA
64174	DPEP2	NM_022355	CTCCATCTTACGTACCTTCTA	CTGGGCATGATGGTAGACTTA	CAAGGCTGTCATTGGATCCAA	CAGGCACAAATATTTCTTGAA
64211	LHX5	NM_022363	CAGGTACAAGCTAATACTCAA	GCCAATTTAGATATGCTATAA	TTAGATATGCTATAAATTTAA	AAGCAGCCTCCTGAAACCAAA
64223	GBL	NM_022372	CCAGGTGAACGCACCCATTAA	CAGCTACATGGCAGCTGTCAA		
64232	MS4A5	NM_023945	TAGACTGAAGTACCAACTAAA	CAGCATTATTGAATTATTCAT	AAGAACATGGTCTAGACTGAA	GAGGATTGTGATTGTGAACAA
64236	PDLIM2	NM_021630	AGACATAATCGTGGCCATCAA	CTGAGAGTCAGTCCTCCTTAA		
64328	XPO4	NM_022459	CAGAACTTTATGCTTAATTTA	AAGGAATGCCTTGGTAAGTAA		
64332	NFKBIZ	NM_001005474	ACCATTAAGTGCCTAATTCAA	TAGCTGCTGCTTATCATGTAA	CACTAAGTCTTTGTAGATAAA	TCCGACGTATCCTGAAGGGAA
64344	HIF3A	NM_022462	CAGACTCTTCACCTCCGGGAA	CTGTCGGAGAATGTCAGCAAA	CGGGCGCACCCTCAACCTCAA	ACCAATCTCTATACACCATAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
64359	NXN	NM_022463	AAGCTCAAACTTTGGAACAAA	CCGGGTCCTGGTGGAATCCTA	AACCGGCTGTACGGAATCCAA	AAGGTAATGGTTCATATCATA
64374	SIL1	NM_022464	CCGAAATAATTTGAAAGGCAA	AAGGCTGGATATCAACACCAA		
64375	ZNFN1A4	NM_022465	CAGACCATCACTGCACTTTAA	TTCCTTGAGATTCAAACCAAA		
64377	CHST8	NM_022467	TTGGATTAAGGTTCCAAATAA	CAGGAATAAAGTTCAACATCA		
64393	WIG1	NM_022470	CAGGCTCATTATCAGGGTAAA	CAGCATTTAGAGAGCAAGCAA		
64400	FTS	NM_022476	CTGCACTGTCTTACTGATTTA	AAGGTGAAGAGAAGACATTAA		
64409	WBSCR17	NM_022479	CTGGTTAGGGTGCACATATAA	CAGAAATGAGAAGATACAATA		
64419	FLJ22405	NM_022485	CAGCGTGATTCCAAACACGAA	CACGTTTGAGAGTACCGTACA	CTGCCCAGTAATCCTGTTCAA	AAGGTGAAGTTTGGCATGAAT
64421	DCLRE1C	NM_022487	AAGAAACGAATTATATCTATT	CCCAGTGGGAAGTATTCTTTA	CAGGTTCATGTGAATAAGCTA	AAGTACGGAGCCAAAGTATAA
64423	C14orf173	NM_022489	CAAGATCAGCACATTGCTGAA	CAGCGATGTCCTAACCACTGA	CCTGATTCTGATGATAATAAA	CCCGGCCTTGATGCTACAACA
64429	ZDHHC6	NM_022494	TAGAAGGTGTTTCAAGAATAA	TACGTTCTGTTCGGTTATCAA		
64446	DNAI2	NM_023036	CAGGGTAATGCTTAGCATATA	CCGGAAGAAAGTGGAGAAAGA		
64478	CSMD1	NM_033225	ACGGGCGAGCGCAATAGGATA	CCGGTTCAGTATGAAGATAAT	CAGGAAGTCGAATTCACCTAA	CAGGACTGATTCATAGCCATA
64582	GPR135	NM_022571	AAGACAATGTCCCTTCTTCAA	ACCAAGCATTGTGAACTGCTA	CAACAGGATGTCCTCTTCCAA	ACCAAACAGCCTAAATCCGAA
64601	VPS16	NM_022575	CTGCATGAAACAACATAACAA	CCGCACGGAGCTGGCCATCAA	CAGCATGGACTGGGACCTGAA	GAGGCCAGTGCTCGATATATA
64648	SPANXD	NM_032417	AAGCCTGCCGCTGACATTGAA	AACCTTGGGCAATGACAATAA		
64710	NUCKS	NM_022731	TACCACGGTTGTAAAGCAATA	CCCGACCTTATTTGAGGGTAT	ACCCTAGAATTTAATCAACAA	AAGGTGTACCACGGTTGTAAA
64711	HS3ST6	NM_001009606	CCGGCGCCTGCAGGAGTTCTA	TCGCCTGGTACCGGAGTCTGA		
64714	PDIP	NM_006849	CACTGTGGTTCTCTTCAAGAA	GCGCCTGGTCACGGAGTTCAA	CTGCGCTTGGTCAACCTTGAA	GAGCTGTGCATTGTGAATAAA
64747	FLJ14153	NM_022736	CAGGTGAAGTTATTAAATTAA	AACCTGGTGTTTGGACTTCAA		
64748	LPPR2	NM_022737	CCGCGTGGCCGAGTACCGAAA	CTGCGTTGTGCATAACTTTCA	CCGGGACAACTTCAGCCCTTA	CCCGTGTCTAAGCATGTGCAA
64759	TENS1	NM_022748	AAGGCGGATATTTCAAGAGAA	ACGGTCTCTACCCATGTTTAA	CGGTGTGATTGTGGACTACAA	CAGGACCTCGATATTATCGAT
64768	C9orf12	NM_022755	CACGCATGAGATGAAGCATAA	CAGCTTTGTTTAAAGATACAA		
64772	FLJ21865	NM_022759	CAGGCAATTAATTAGGAGTAA	CGGCTTCTTCACTAACTATAA		
64779	FLJ12998	NM_022764	CAGCCTTACATTTGCTCATTA	CAGGTCGTGGACATCCCTGAA		
64782	FLJ12484	NM_022767	AGGGTTGTAATGAGCACTAAA	AACCATTTGTTCTAGAATAAA		
64783	RBM15	NM_022768	AAGGTGATAGTTGGGCATATA	TTCGGTGATGTAAGTGTGAAA		
64785	FLJ13912	NM_022770	TAGGAGCTGGTTGACCTTGTA	AAGAATCACTGCCATATAATA		
64805	P2RY12	NM_022788	TCGGTCTAGTCTGGCATGAAA	TAGTCTGGCATGAAATAGTAA	CCGGAGTAAATCAAACTTTAT	CAGGGTCAGATTACAAGAGCA
64838	FNDC4	NM_022823	CTGGGACGTCCCAGAAGGCAA	CCAGGTGACATCACAGTGGAA		
64839	FBXL17	NM_022824	CTGTCTGAACTGGATCATAAA	AGGCATGATCGTCATAGCTAA	ACGAAAGTTAATTATACATTA	ACGAGAGGGTAGTCACATTAA
64840	PORCN	NM_022825	ACAGATGATTGTGGCCATGAA	CTGGATATCCTTCCACAGCTA		
64850	AGXT2L1	NM_031279	CACGACAACATTGTTGAGTAT	ACCAACTTGATAGGATTCTAA	CAGAATAAACCAAGTGATAAT	ATGTGTCAAATTAGAGAGCAA
64853	FLJ12806	NM_022831	CAGGTCATTAGCTTACTATAA	AAAGAATATTCTTACATATAA		
64854	USP46	NM_022832	CCGGGAGAATGTGTTGGCATA	CAGCACGGCATTGTTCCTTAT	TAGGGAAATGTTTGTACTATA	CAGTTATTTAATCGAAGTAAT
64856	WARP	NM_022834	CGGGACCGCACTGACAGGAAA	CACTAACATCCCAGACTTTAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
64924	SLC30A5	NM_022902	CTCACTCTTTGTGGACCACTA	TCGAATCATATGATCTCCTAA		
64926	FLJ21438	XM_029084	CACAACCTAACAAGCAATGAA	CAGTATGAAGTTGCCCAGTAA		
64943	FLJ12442	NM_022908	CCGCGTGGACTTCACCTTCTA	TAGGTCTTCAATCAAGGTTTA		
64951	MRPS24	NM_032014	CTCAAAGGTTGTGTATAAGTA	CAGTGAAACTTTGCTGTCCTA		
64965	MRPS9	NM_182640	AACAGTCATACTATTCATTAA	CCGCAGAAAGTTTACGTGGAA		
65009	NDRG4	NM_020465	AAGGGTCAGGTAGAAGAGAAA	CCGCAGAGACCTGGACATTAA		
65055	C2orf23	NM_022912	CTGAGCCGAAATATAAGAATA	CACCAATACCTAAATCTGTTA	AAGCCTGTAAGTGTACATGTA	CCCAGAATTATCAGAAACGAA
65083	NOL6	NM_022917	CACTACAGACCTGACAGTCAA	CACGCACACGGATGTCCTTAA	CCGGCCGCCCTTGGACATTTA	CAGGAGATCCATCCACCTATT
65084	FLJ22104	NM_022918	AAGATGTTGCTTAATAATTAA	AAGGTGTATTTCTACAATTTA		
65109	UPF3B	NM_023010	AAGGTGGTAATTCGAAGATTA	CAGAGCATACATCAACTTTAA		
65121	LOC65121	NM_023013	GACGGTTAGTTGCCAAATTCA	CCCACAGCACTCATTCCTGAA		
65123	FLJ21919	NM_023015	CTGCCTGATGATGGACATGAA	AAGGATAGCATTATGAACATA		
65217	PCDH15	NM_033056	ACCATAGTTGCTATTGATGAA	ACACGAGTCAATCTTAATGAA	ATCGCTATGTTCAGGAACAAA	ATGGATTTAGTAGTATGCTTA
65220	FLJ13052	NM_023018	CCAGACCATCATGCACATTCA	CACGCACCTCATGGAGGAGAA	CCAGGAGAACATGATCGTGTA	AAAGAGCGTCCTTGTCATCAA
65250	FLJ13231	NM_023073	AAGGCTCATCTTAAATTTGTA	ACCAGAGAATTCCATAATTAA		
65266	WNK4	NM_032387	CAAGGTCACTTCGGGCAGAAA	CACTAGTGTCTCAGACCAGAA	CAGGAGGAGCCAGCACCATTA	CAGCTTGTTGGGCGTTTCCAA
65268	WNK2	NM_006648	GACGCTGAAGACATACCTGAA	CACGTATATGGTGGAGCATGA	ACCTATAAGTCTAGTAGCAAA	AACGTTCATCGAGCAGATGAA
65975	STK33	NM_030906	TCCATAAGTGACTGTGCTAAA	CAGTGGTTAACAGGCAATAAA	CAGGATGGTAATAGGTTAAGA	ATGTGTCTAGTGCATCCTTAA
65977	PLEKHA3	NM_019091	CAGGGTGTATTGTAGCTTATA	CAGGAATTTGTTCACCATGAT		
65981	C1QDC1	NM_001002259	AAGCTTCGAACTATACTTCAA	CAGTACAGTATTGACAATAAA		
65983	NS3TP2	NM_023927	CTCGGTAACCCTAATAAAGAA	CAGGTTTGCTTCAAACAAGTA		
65987	KCTD14	NM_023930	CTGCCTGGAGATGGACATTAA	CAAGGTATTCTCCAAGTTCTA		
65989	EGFL9	NM_023932	AAGTTCTGTGACAAAGATGAA	CAGCCTCACACCAGAAATATT	AACCTGCCTTGACGGCATAAA	AAGACCTGTGAGCTTGTCTTA
65990	MGC2494	NM_023933	CTGAGTATTAGACACGATAAA	CAGGATCGTGCTGGCGGCCCA		
65999	MGC3036	NM_023942	CTGCAACTTAGTGGAAGGAAT	AAGGGCTGTGAGCAGGTGTAA		
66000	MGC3040	NM_023943	CAGGGAGATCCAGTCCCTTGA	CAGGACCAGATGATACCATGA	CACTGGGATGGTCCTTGTTAA	CCCTCTATTGCCAACTGTTAA
66002	CYP4F12	NM_023944	GTCCTATATAACGATCTTCAA	ACCTGCCTCATCGATATTATA	CCGCAGGAAGCTGGAATTGAT	TTGCAGATTGTCATGAATAAA
66036	MTMR9	NM_015458	TACGTTGGAATAGATCCTCTA	ATGCCTGAACCTGTTATCTAA	CAGGTCTAAGGATTAACTATA	CAGACCTAGTATTCTAAGTTA
78989	COLEC11	NM_024027	CCCAGAATTGCTCTTCCATAA	CCCAATGTCATTATGTAATTA		
78990	OTUB2	NM_023112	CAGGGAGATCTTCAAGTTCAA	CAGCCGATAAACATTGATTAA		
78994	MGC3121	NM_024031	ACCAATCAGGTTGAACAAGAA	CAGCCTCTGACTCGAGCATTA		
79000	MGC2603	NM_024037	CAAGACTAAATTGGAAAGAAA	CAGGAGGATGGGCCAACTCAA		
79012	MGC8407	NM_024046	TCGGAGGTGACTGACAGATAT	CTCGTGCTGCAAAGAGTGATA	AAGGTAGGGCAGTATGTTTAA	CTGCATGGCAATAACTCATAA
79016	PCIA1	NM_024050	CAGGAGCAAGTGGAGCTGGAA	CTGCGCTACCTGCATCAGCAA		
79018	C17orf39	NM_024052	GAGGGCAATACTAAACTTAAA	CTCCTCAATCCTGAAATTCAA		
79027	ZNF655	NM_024061	GTGCAGGACACCGACATGGAA	AGGAAGCAGCAGGGTCACCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
79048	SECISBP2	NM_024077	CTAGATTTGTTTGATAATCAA	CTGGAAATTGATCAGCATTAA		
79054	TRPM8	NM_024080	TCGAATGTTCTCACCTATTAA	CCGGGACGAGATGGACATAGA	CAGAATGTTATCATACTACAT	AAGGTTAGATTCCAATAAATA
79066	MGC3329	NM_024086	AAGGAGGAGCTTCGCATACAA	ATGGATGCTCTTAAAGAAGAA		
79068	FTO	XM_051200	AAGGAGATGTTAATAATTAAA	CAGGGTCATTACAGAGATTAA		
79073	MGC5508	NM_024092	CAGGTTTGATGTGGAATCACA	CACCGCCAGTGTCATACCAAA		
79075	DCC1	NM_024094	TTGGTTTAGATCAAAGTTCAA	AACGAGTTTATAATCCTATAA		
79080	MGC2574	NM_024098	CAGCCAGAGTACAGTCCTGAA	AGCGTCCAAGAAGTTGAATAA	CTCGGAGTTGGCCCAGAATAA	CCGAAAGGCCGCCGAAGACAA
79092	CARD14	NM_024110	ACGGACGGTTATAAGAGGCTA	ACCAGTGTGTTTACTTGTAAA	CCGCATCGTCAGTATGGACAA	CACCTGGATTATGAGCTCCTA
79094	MGC4504	NM_024111	TCCCATACTGTTACCCATAAA	CTGCTTGACACTGACTTACTA		
79095	C9orf16	NM_024112	CTGGCTTAGACACCTTCTCAA	GGCCTTGAGTGTCCACATTAA		
79097	TRIM48	NM_024114	CAGGCCCTGTTTCTACCTCAA	CTGGGAGAAGCTGTTAAAGAA	TTGCATTCTAATGTTATTAAA	AAGAATCAGAATGGCAATATA
79143	LENG4	NM_024298	AAGCATAAGCTTCCCATTTCA	TCCCAATAAAGTGTTGCACAA		
79153	MGC4171	NM_024307	CAGAGTGGTGGTGGTGTCACA	GACGCTATGACCGTAATGAAA	CCGGACCTCCTAAGTCCAGAA	ACCCATGAGCGTAGAGATCAA
79155	TNIP2	NM_024309	CCGGAAGTTAAAGCACACTTA	CGGGCTCAAAGTAGGATTCAA		
79169	C1orf35	NM_024319	TTGACTCTTTGTATTTCAATA	CTGGGAGGACGTGAAGACTGA		
79171	MGC10433	NM_024321	CCGCCCAATTATCGCGACCAA	CCGCTTCCCATCCTTCCTTAA		
79176	FBXL15	XM_370575	CAGCCTCTCTCTGGCCGTCAA	CTGAGGAAGAAGAGATAGCAA	CTGAGCTGTAGGGAAACTGAA	CACCCTGGAGCTTCAAATAAA
79178	THTPA	NM_024328	CAGGCTTTGCATCCTTGGGAA	ACGGAGTATAAGGAACTCACA		
79184	CXorf53	NM_024332	CAGCATTTGCAGGAATTACAA	CAGATTGAGATGAATTTGCAA	TACGATGTTGATTATAACATT	ATGGACCTACATACACACAAA
79187	FSD1	NM_024333	CAGAGGTACTCCATCTCCCAA	TCCGGCTATCATTGAAAGCGA	CACGGCCAAGCACGCCAACAA	AGGTCTCAAGTTTGACATGAA
79258	MELL1	NM_033467	CTCCCGAGAGTACTACTTCAA	CTGGACCGCATTGGTAGCCTA	CACGCACGGCTTTGACGACAA	TGGCCGGAACTTCGACAAGAA
79369	B3GNT4	NM_030765	CACCCTGTTAGCTCTGATTAA	CAGGAACACTAAGGTCAAATA		
79442	LRRC2	NM_024512	CAGGAGAGACTTGTAGGTACA	CCGCAAGATATAGACAGGCTA	AAGACCAAATACTGAAGTTAA	CTGGAGCTATATATAAATCTT
79573	TTC13	NM_024525	CAGGGTGATTTCTATAAATCA	TCCGATTATGAAGCAGTTTAA		
79574	EPS8L3	NM_024526	CAGCTTAGACACCTCCAAGAA	CAGGAAGAAGAAATTTGGGAA	AGCCATTTACTTGCACCGGAA	CCGGAAGGAGTACTCCCAGAA
79585	CORO7	NM_024535	CAGCCACATCACCAACCTCAA	CTGCAGCTTGATCGCCTTCAA		
79603	LASS4	NM_024552	CAGGTTCTGGTTACCACCCAA	AAGGACATTCGTAGTGATGTA		
79607	FLJ21103	NM_024556	CAGACAGTGTTTAACAAGTAA	CAGGAGGAAAGCAGTGACAAA		
79629	FLJ22709	NM_024578	TCCCAGTGAAATAAACATGTA	ATCCAGAAATTCGATGACCAA		
79631	EFTUD1	NM_024580	CACCAAATGAAAGAAGATCAA	CCCAACATACTAGTCAATAAA		
79635	FLJ13646	NM_024584	CTGGAATACCTGACTAACAAA	TCCCATTTAGTATAACTATAA		
79640	FLJ23584	NM_024588	CAGGGTCAGTTAGGAAATGAA	CAGAAACAATTAAGTCATGAA		
79642	FLJ23548	NM_024590	CTGATCTAACTTCTAGCTAAA	AGGCATATTGTTCATGTTTAA	CAGATTGATGAGGACATTCAA	CCGATCCATTATCAACATAAA
79654	FLJ21156	NM_024602	ACGGATCTACATCTACCCAGA	ACCACTGTACTGAGTGACCAA	TCGGGACATGTATGTACCCAA	CCCGAGGTATTTCACCTCTTA
79660	PPP1R3B	NM_024607	CTAGGATGACATGATGTTATA	CAGACAGTACTTTAAATGTTA	CCCGCTAGATATGCCATTCAA	CACCCAAGTTCTTATACGTTA
79671	NOD9	NM_024618	ACCTGACTTGCTGCTATTAAA	CTGCGGTTTCTCTGATACCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
79673	FLJ12586	NM_024620	CGGGAAATCCTTCAACAGAAA	TACCTGTGAATGAACAATGAA		
79679	B7-H4	NM_024626	ATCGTTCAAGAGAATGATTAA	CTCCAATATGAACAAGATAAA		
79684	FLJ23342	NM_024631	TACAGTTGTGTTGCCATTTAA	CTGGAAAGATGTTTACTACAA		
79686	C14orf139	NM_024633	AAGGAGGAATTTGTTTCTAAA	CAGGATGTTCAGGGCCTTAAA		
79692	ZNF322A	NM_024639	AGGGTTGGAAATACCAAGTAA	TACATATAATATGTATGAGAA		
79696	C14orf140	NM_024643	CAGGAGCAGAGTTAAAGGTAA	CTGGTAGCAAGCAATAATAAA		
79697	C14orf169	NM_024644	GAGGTCCAGGAAGATACGAAA	CAGATTCTAAGGATCCGCGAA	ACCCAAGTGCTTGGAAATATA	CTGCTTGAGACAGATATTAGA
79703	FLJ22531	NM_024650	CAGCTAGTGATTTCCATAGAA	CAGCATTATGTGAGACCAAAT		
79706	PRKRIP1	NM_024653	AACGATGATGATGAACACAGA	CAGCTGTGATTTCATCCCGAA		
79707	FLJ23323	NM_024654	CAGATTAAACCTGAATATTTA	ATGGAGTTTCATGGCCATGAA		
79714	FLJ12436	NM_024661	AAGGTTCATTTACATTAATTA	CAGCTTAGTCATTCCAGGCAA		
79718	TBL1XR1	NM_024665	TAGATACTAGATTGTATTGAA	AAGGAGCTATCTGTTTATGTA	ATCACAAATGATCATACTTAA	AAGCAAGATAACGGCATATAA
79724	FLJ23436	NM_024671	AGCCCAGAATTTGAAGCTCAA	AGGGAGCTAGAGGAACCTTTA		
79728	FLJ21816	NM_024675	CAGGAGGATTACCTATACAAA	CTCCTTGTAAATAAAGCTATA		
79733	FLJ23311	NM_024680	CGAGCAGATTATGATGATCAA	AAGACAAGTCTTTAAGGGTAA	CAGAGGATGTCCATTAATCAA	CACGTGGGAAACCAAACTTTA
79741	C10orf68	NM_024688	AAGCAATTTATAGAACATATA	ACCAAGAAACTTCAAGCTAAA		
79742	CXorf36	NM_024689	CTGGTTTGAAATGAAACCTTA	AACACCTAGATTAGCATTCAA		
79770	C5orf14	NM_024715	TACTATAAGGGTTATAGTAAA	AACTAGTATTGCAATAAGCAA	CTGCATGAACGTAATCCAGTA	CCGGCAGAATAGTGAGTAGAA
79784	MYH14	NM_024729	TCCCAGAATCGGGAAAGTGAA	CGCGGGCAAGGTCGACTACAA		
79794	FLJ21415	NM_024738	CCCGTGGAAAGTGCAGTTTAA	AACGTTGAGGCAATTCCTAAA		
79797	ZNF408	NM_024741	CAGCCTGGTGCTAATCCATAA	CCGAGACATCCTCGCTTTAAA		
79807	FLJ13273	NM_024751	CCAACTATACCTGTAGAAATA	TTGGTAATTATCAGCAGGAAA	AAGACTCAGAATCTTAAGGAA	GAGGTTTATAGGTTTAAGTAA
79811	FLJ13213	NM_024755	CAGCTTCGTTATGAACAAGAA	CAGAAGGTACTGTTACATTAA		
79815	FLJ13955	NM_024759	CACCTTTCAAGTACTAAGTTA	CTGCACAAGGCTGACACATAA		
79816	TLE6	NM_024760	CTGAATTATCAGGGCATTCTA	CACGATCTAGTCTGTGGTGTA		
79823	FLJ23451	NM_024766	CAGCCTTGTTGATGCAATAAA	CACGCCGAGGGAATACTTTAA		
79829	FLJ13848	NM_024771	CTGGATGTTGCTGCATTCTAA	AACGAATATGCAAACCATGTA		
79830	ZMYM1	NM_024772	CACCACTAATTTGAAGATAAA	CAGGAGTTGGTAAATAAACTA		
79836	RNF127	NM_024778	ATGGAGGAGCTCATAGCTAAA	CAGCGGGATGGCTACAACACA	TTCGCTCAAATTATCCCTAAA	CAGAGAGAAATTGAGTAGAAA
79837	PIP5K2C	NM_024779	TAGGATTCATTCTCCATGTAA	CTGTCCTGTCTTATACTGCAA	TTGATGTGTGATAATCTCATA	CCGGAGCAGTATGCTAAGCGA
79838	TMC5	NM_024780	CCGGGCTTATCGGAGATCCAA	TAGGGACACAGTGATGTACTA	CAGGAATGATTGGTTCTTAGA	CGCGATTATTGCTAATTGGAA
79841	FLJ23598	NM_024783	CAGCCTACCATCCAGAAGTAA	CAGCTTTGGAAACGCACCTAA	CCAATAGATATTCTCTCTAAA	CATGTATTACCCAGAATTTAA
79846	FLJ21062	NM_024788	CTGAAGTTAATTGTACTATAA	TTGGAGAAATATGGAATGAAA		
79852	ABHD9	NM_024794	ATGTATGTTAATTGAAATGAA	CTGGCATTTCTCCATCTACTA		
79864	FLJ23554	NM_024806	CAGGGCGCCAATAACAGGCAA	AAGACTTACATCGGATTTCAA		
79872	CBLL1	NM_024814	CGCGAACTCAAAGAACTATAA	CTCGATCGGTCAGTCAGGAAA	CCGCCTCAACATGGTGGTCCA	ACCATTATAATCCTAACTCAT

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
79875	FLJ13710	NM_024817	CAGAAGAGAGAGAATCTTGTA	ATGAATATTGTGCTTTATTTA		
79884	FLJ21159	NM_024826	ATGGAATATCTTAAAGAGAAA	AAGGATGGACTAGAAGATAAA		
79896	THNSL1	NM_024838	CAGGATGTTGGTAATGAGCAA	CAGGCTTTAAAGATTAAAGAA		
79897	RPP21	NM_024839	CAAGCAGATTCCAAACCACTA	CTCAATGATCCCGGGCATTTA		
79908	BTNL8	NM_024850	GTGGACGGAGGACACAATAAA	CACGGGATATGTTGATAGAGA	CACAGTATCAAGGCAGGACAA	CAGGATTAGTTCCCAGTCTTA
79912	FLJ22028	NM_024854	CAGCGAGTTCAGGAGACTCTA	CTAGATCCAAATATTGATATA	TAGCAATATCTCGTTTGCTAA	AAGAATAATGATCATAGGGAA
79923	NANOG	NM_024865	ACCGAGTGTTTCGATGAGTAA	TTGGTTTAAGTTCAAATGAAT		
79924	ADM2	NM_024866	AAGGGCTCCTTCTGCTATTTA	CACTGAGCATTTAATTTACAA	CTGGTACGTCAAGGAGCCTAA	TAGCGAACACTGAGCATTTAA
79943	FLJ14129	NM_030895	CAGGCCTTTGTAAGTTGTCAA	CAGGTGCTAAAGAGAGCAGTA		
79953	C20orf39	NM_024893	CACCGCATTAGCAATATACAA	CCGGCCCAACATCATCCTCTA		
79958	FAM31C	NM_024898	CAGCTCAAACACACCAATAAA	TACCTTGGAGACGACCTTTAA		
79960	PHF17	NM_024900	ACTGACCAATGAAGAATTTAA	AAGCGGGAGCAGGATGTCTTA	CGCCCAGAGCAAGAAATGATA	ACCGATTAAATTCATTAGTGT
79962	FLJ13236	NM_024902	CAGGTGATAGTTGGCATCTAT	CAGCTTGAGGGTCTAAGGATA		
79963	FLJ14297	NM_024903	CACGAAGTAGAGGAACTCATA	CCCTAGGTGTCTGGAAATGAA		
79968	FLJ12973	NM_024908	AAGGGATTATCTAGCATTAAA	CAGGATGGAGACAGTGATGAA		
80006	FLJ13611	NM_024941	AAGCTTAGGCTGTTAAATAAA	CAAGAGCATATTTGCAACCAA		
80013	C10orf97	NM_024948	TCGCTCTCCTTCACTAAATTA	ATCACAGTTACTATTGATAAA	TTGAATGATTCCGGCTTGTAA	ACGTTATTTATTATGATCCTA
80028	FBXL18	NM_024963	CAGCACAGATCTGATTCTGAA	CCTGCAGCACATGAAATTCAA	CCGCGCGGCTTTGGCAAGAAA	CAGCCAGTTTCTGTTGTTTGA
80036	TRPM3	NM_020952	CAGACTAGAGGAATTGTACAA	ACGGCCTGAAACTCTTCATAA	ATCATCGTGTATAGACATCTA	CAAGGTAACAGTCATAGTTCA
80045	GPR157	NM_024980	CTAGATGATCTTGACTTTCCA	AAGACCTTACTTTGCGATTCA	CACCTGGGTGTCACACGGCAA	AAGGGCTTCTTTGATAAAGAA
80069	C6orf208	NM_025002	TTGGAGGTTGGCAGAATTCTA	CAGCAGGTGGATGAGACACAA		
80086	TUBA4	NM_025019	CCCAACCTACACCAACCTCAA	AAGGAGTTCATCGACCTGCTA	AGGCTTTAAGGTTGATATCAA	CTGTGTGTCTGTCCTACATAA
80094	FLJ14107	NM_025026	CACAAATTCCATTATTGTCAA	CCGCCACACCTTCCTCCATAA		
80099	FLJ21075	NM_025031	AAAGATAAATACGGTCCTGAA	TTCCACTTAATTTCACTATTA		
80110	ZNF614	NM_025040	CTGAGCTTAATTGTACATTAA	CACCACAAAGTCAGTACTCAA		
80115	FLJ22582	NM_025045	CAGGTCCACCATGGCCATCTA	TTGTAAATGATGAGAAATAAA		
80118	FLJ22684	NM_025048	AAAGAAATATTTAGTAAATTA	CTGGCCTAGGACCTTAAATAT	ATGGGCTAATTAGAATTATCA	AAAGCATATGAAAGAATTCAA
80122	FLJ23074	NM_025052	GTGGTACATCGCGATATCAAA	CGCGATATCAAAGGAAATAAT	CTGACCAGGTAAGAAACTGAA	ATGTCTAATTGGAGATTTCAA
80127	C14orf45	NM_025057	CACAAGCTGCTTTCAATTTAA	CAGGAGTGATGCATCCAGAAA		
80129	C6orf97	NM_025059	CCGATCCAAGATGCTTTCTAA	CACCAATGAACTGAAGATTAA	AAGCTCTAGCATGAAATTAAA	CAACCGTTCGTGAGTCATCAA
80139	FLJ14299	NM_025069	ACCGGACTGTGTATTTATTTA	CTGGGAATATAAGTGCATTAA		
80145	NIF3L1BP1	NM_025075	CAGACAGGCATGAGACATTAA	AAGCATGGAATCAGATCCTAA		
80146	UXS1	NM_025076	TAGAATTTGCTCAGTTAATTA	CTGGAGGAAGGTTTAAACAAA		
80161	CXYorf2	NM_025091	CACACTGGAAATCGTGCAGAA	TGCACTGATGATAACTTCAAA		
80167	FLJ21106	NM_025097	CAAGTGAATATTGAACCTTAA	ATGGATGAATGTACTCATGTA		
80184	Cep290	NM_025114	CCGGAAGAAATGAAGAATTAA	AACGATCATTATCAACTTCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
80194	FLJ21749	NM_025124	CTGCTCTGTGCCTTAACTTAT	CAGCATTGATGATGCCTTCGA		
80195	C10orf57	NM_025125	TAGAGGAGGTGCAGTAATTTA	CCAGTTGTTACTTAAGAAAGA	ACCCTGAAAGATTATGAACTA	AACCATAGAGTTAGGCATCAT
80207	OPA3	NM_025136	CCTGATCAGTGTTAACCTTTA	CTGAATCAATGTGTTATTGTT		
80209	C13orf23	NM_025138	CACCTGGGAAAGCGCCTTCAA	ACGGTGCAAGAGAATACTTGA	AAGGAAGACCTAGCCGCATAA	TACAAGTAAGACTTAGGATAA
80210	FLJ12584	NM_025139	CCAGATAGAATTCATCATCAA	TCGGATCTTCTTGGCCATGAA		
80213	BLP2	NM_025141	CTCAGCTTCAGTCATGTGTAA	TCGGGCGGTGAAAGTACTGAA	CTGAACTATGCTAATCTGGAA	CAGAATGTTTATGTCTAGTTA
80216	ALPK1	NM_025144	CACCCAATTCATCGTAATCAT	CCGCAGGTGGTTATTCGCCAA	CAGGCCCTACATTTAAAGCTA	CAGCCCTTGGTCCTATCTGAA
80217	C10orf79	NM_025145	AAGGACCAAATTGAAAGGCAA	CAGACTGAAGTTGAAAGATTA		
80222	TARSL1	NM_025150	CAGGCCGAACAGGTCCTTAAA	TCGCCAGTTGTTCAAGGATAA		
80223	RAB11FIP1	NM_001002233	ACAGAAGGAAACGATAAGCAA	AGGGCTTAATGTAGTTAATAA	CAGGTTAATGATTACAATTAA	CACAGAGTTCGGAATTCACAA
80233	FLJ22175	NM_025161	TAGGAGCAGAACGCTCATGAA	AAGCCTCAACGAGGCCATGAA		
80274	SCUBE1	NM_173050	CAAGCTCTGGATCCAGTTCAA	CAGGTGCTACAGGACAGCAAA	CACGTGTGGTTGCCACCAGAA	CCCGGCTTTGACCTTGCCCAA
80309	SKIP	XM_051221	CACCAACATGTTAATTCATGA	AAGAAGATGAGTCATATTGTA	GGCAAGTATGCTACAAATTTA	CTGAAATTCTGGACACCTTAA
80313	LRRC27	NM_030626	CTCCGGTACAATAGAATTAAA	CTGCTTTCTGATAGTGATCAA		
80318	GKAP1	NM_025211	CTGCAAGTTGATGAATCACAA	TAGCTCCCTAATGGTCTATAA	CATGCTGTTTGTAACGCTCAA	AACGCTCAACATGATCTTCCA
80329	ULBP1	NM_025218	AACCTGTATATGTACCTTGTA	ACCCTACAATTAAACACTGTA	TATGATGATAATTGTATAATA	TCGGGATATACCCACAGGAAA
80341	BPIL1	NM_025227	CTGCACATTGGGAGCCTTATA	CTGGTGCAGAAGCACATTAAA	CAGGCGAATTTCTCATTTCAA	ACCATACTTAGTCATCACCAA
80342	T3JAM	NM_025228	ACCCAGGACCTACAAGATCAA	CAGGACCTACAAGATCAACTA	TAGCAGGGACTTACAGATGAA	CAGACTTGGCACCAACATTAA
80343	C20orf50	XM_046437	AACGAAATCAAACAATATTTA	CAGGATTACTACAAAGCATTA		
80346	C8orf20	NM_025232	TCGGTTCCGTGCAACTTTCAA	CGCGTACATCGTGCAGGCCAA	CCCTTTCTACTATGAGATCAA	CAGGGATGCACCCACAATGTA
80347	COASY	NM_025233	CCGGGTGTTTGGGAATAAGAA	TCCGATTATGGGATAGGAGAA		
80381	B7H3	NM_025240	AAGAAGATGATGGACAAGAAA	CTGGCAGCTGACAGATACCAA	CTGAAACACTCTGACAGCAAA	CAGCATGACCCTGGAGCCCAA
80723	TMEM22	NM_025246	CAGGACTACCAGGAAATACTA	CTGATTATTATTGTCTCATTA		
80725	SNIP	NM_025248	CCGCAGTATTATCAAGATCTA	CTGGCCCAGATCCGAAGGCAA		
80736	C6orf29	NM_025257	CCCGGACAACAAGAAGAGGAA	CCGGGTCATCTTGGAGTATAT		
80740	LY6G6C	NM_025261	CAGGACAGCAATGCCTGACAA	TAAGCTGGGTCTGACATATAA		
80742	PRR3	NM_025263	ACCCATGACATGTCTTATAAA	AAGCTGGTCTCTTATCAAGAA		
80755	MGC2744	NM_025267	ACGGCAGTTGCTGACCATCTA	CTGGCTCATGTGGAACATTAT		
80759	C6orf148	NM_030568	CTCCTTCATTCCTACCGTCAA	TTGGCAAAGCAATCCAATAAA		
80761	UPK3B	NM_030570	CTCCTTCATGGGCAAGCGCTA	CTGGTTTCTCTCCCTCTCCAA		
80762	NDFIP1	NM_030571	TAGGATACAAATGAAGCTTAA	AAGTCTTTAATTGGTAAATAA		
80776	MGC4093	NM_030578	TCGCGGAAGTATCGCGGCTTA	CCAGCGGTTTCTCGGAAAGTA		
80789	KIAA1698	NM_030628	ACCCAGTTATATGCAGGGCTA	TCAGCAGGAAGTGATCTATAA	CTGGGTAATATGCATGAAGTA	CACGCGTACATTAATGGACAT
80824	DUSP16	NM_030640	AACCCAGTTGTTACTCTCTTA	CAGGACAAAGTGTTAATTACA	CCGGCCATTTGTGGAATACAA	AAGGTTGTAGTTTACGATCAA
80831	APOL5	NM_030642	GAGGAATAAATTGGTCTGAAA	TGGGAGAAGGTTGTAAAGAAA		
80832	APOL4	NM_030643	TTGCTCATATATAGTAGACAA	CAGCAATTGTTCAGGGAATAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
80834	TAS1R2	NM_152232	CACAATTTGCATCTCCTGTAT	GGCATTTATCACGGTACTCAA	CAGCGTGTACTCTGCGGTCTA	CACACTGAAGATGAATATGAA
80835	TAS1R1	NM_138697	CACTGTGGCGTTTAATGACAA	CTCCGGGCTGCCAATAAAGAA	CTCCATGAGTTCTGCCTACAA	CAAGGACACTGTGGCGTTTAA
80864	EGFL8	NM_030652	CAGCACTTACAGGACCATGTA	TCCCTCAGAGAGAGTCAGGGA		
81061	OR11H1	NM_001005239	CAACATATGCACTGACTATAA	ATCCTATACTCTTGTCCTGAA		
81127	OR4K15	NM_001005486	CAGCAGTTACTCAGTTGACAA	CCAGTTGGCATTCACTGTTAA		
81282	OR51G2	NM_001005238	CCCAGTTCTCTCACATTCTTA	CCGGGCAACTGCACAATTCTT		
81285	OR51E2	NM_030774	ATGGTTAGCTGTCACATACAA	ATGAGAGATAACCTTGCCCTA	TGGCTGGAATAGTAAACTAAA	ACGGGTGCTGGCTATGTTCAA
81300	OR4P4	NM_001004124	CACAACATTCTCAGAAGATAA	CCACTTGTAGTTCTCATGTAA		
81488	GRINL1A	NM_015532	CAGGGAGATACCGAGAAGTAA	CAGCAATTTGATTATGTATTA	CCGGGACTTAATTAAATACAA	ATATTTGAATATTGTGTTTAA
81494	CFHL5	NM_030787	AAGAATTTAATCATAATTCTA	AAGGGAAATTTGAATATCCTA		
81502	HM13	NM_030789	CAACCTCCTGCTGTCCATGTA	ATGCTTCAGACATGCCTGAAA		
81544	PP1665	NM_030792	CCGGGACGTCAGCATCATGAA	CAGGCCTGCCTCCATGCTTAA		
81553	FAM49A	NM_030797	CACCTAGACATTGAGAATGAA	AACAACATCTATAACGATAAA		
81554	WBSCR16	NM_030798	CTGGTGTTAAGGGTCACGCAA	CACAGGAGCCGGAAAGATAAA		
81557	MAGED4	NM_030801	AAGGATGTCATCAGAGAATAT	CCAGATGTTAGTCACCAGTAA		
81563	C1orf21	NM_030806	CACGTTCTTTATGAAAGGCAA	CCACGTGTATCTGAACATTAA		
81565	NDEL1	NM_030808	CAGGCTGAACAAAGAAATAGA	AAGACTTTGAACAAAGGCTAA		
81566	C12orf22	NM_030809	CTCCATCTTGATGATATATAA	CTGCGTAGTGCTGAACATTAA		
81577	MGC11335	NM_030819	CTGAGAAATGTTAATAAATAA	CACAGTGACACTCAACTTCAA		
81607	PVRL4	NM_030916	CTGCTTTGAATCCTTTACGAA	CTGCTTGACCTTTACCTCCAA	CCCTGATAGTCTCAAGGACAA	CAGAGCAGTATTAATGATGCA
81608	FIP1L1	NM_030917	ACCTGTAAATCTTAACATCAA	CAGGGAAGAACTGGAAACTCA		
81617	CAB39L	NM_030925	CTGAGAGATCCCAGAAGGTAA	GCCAATGTCTTTGGACTGTAA		
81620	CDT1	NM_030928	CCGGGCCAGAAGATAAAGAAA	CACCTGGTGGATTCACATTAA		
81622	UNC93B1	NM_030930	CTGCCCGACATCGACAGCAAA	CACCAGGATGGCGCAGAAGTA		
81693	AMN	NM_030943	CGCATTTGACCTGGAGCGGTA	CCAGGTGGTGCTGGTGGAGAA	CAGCCACAGTTACTTCGTCAA	CAGGGTGGCCTTACTCAGTAA
81706	PPP1R14C	NM_030949	CCGCAGAAGAAGAGTGTATGA	AACCCTTAATTTGAAGAACTA	TAAAGTTGTATGAACCCTTAA	AAGAGCTGCTTTCTCGGATAA
81787	DKFZP547L112	XM_375153	CAGGGCTGTACCCTGGACTGA	CTGCCAGGCCCTAGACCAAGA		
81792	ADAMTS12	NM_030955	CCCGGAGTGATCTATGATGTT	CCAGTGGAACGGGAACTATAA	CCGGAGAGTTCTGAAACCAAA	CAGGAAAGACGGCAAACCGTA
81794	ADAMTS10	NM_030957	CGGGCACACATTCGGCATGAA	CAGGACTTTGTGTACCCGACA	ACCGATTAATGCATCTCTCAT	CCGGAAGTTATTTATTGGGAA
81797	OR12D3	NM_030959	CCGGATAATGGCCATCATGTA	TACATTACTGTCCCTGCATTA	CCCAAATAACCAAACGCGTAA	CACAATCAAGCTAAACCTACA
81833	SPACA1	NM_030960	CTGGATAATAATGAAATAGTA	ATGAATGATGTTTGAATGATA		
81844	TRIM56	NM_030961	TTGGCTAAGATTAAGTATTAA	CAGCGACTTCCTGGCCTGTAA		
81858	Sharpin	NM_030974	CAGGAGGGCCTGGAACCCTCA	CCCGGAAGCCTCCACACTCAA	CAGGCTGCAGGTCACACTTGA	AGGCTGCAGGTCACACTTGAA
81875	FLJ12671	NM_030980	CAGGGCATACTGGGAAATGTA	CAGACTTAATACCCATTGAAA		
81930	KIF18A	NM_031217	CACATGAAGAGAAGTATTCAA	ATCCGTCTACAGTAACCTTAA	CAGGTGGAACTAATCTGGTTA	CAGGAGGACTTGGACTCTACA
81932	HDHD3	NM_031219	ATCGCTGAACAGCTTTATAAA	CAGTGTTATTACCTCCAGTAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
83259	PCDH11Y	NM_032971	CAGGAGATTATTTCACCTCAA	CAGGCAGATGATAATGATGAA		
83394	PITPNM3	NM_031220	CAGCAGTGGTCGCATCACATA	CTCGCGCATGATCCTGCGCAA	CACGAAGGACATCTCTGTCTA	CCGGGAGAAGTGGCTTCGTAA
83401	ELOVL3	NM_152310	CTGGGTCTTTCTTCTCAGCAA	ATCGATAATTCCACAGTCAAA		
83445	GSG1	NM_031289	AAGAGCAGTGTTAGGAGTTAA	CAGGATGGTGCTGGAGTTCAA		
83446	DKFZP434K1172	NM_031290	CCAGAAGAAACTAATGCACAA	CCGGCTGATAAGGAAGATGTT		
83449	PMFBP1	NM_031293	CAGGATGATCTCATTCAAGAA	AAGGGTGATCATTCAAAGGTA		
83468	GLT8D2	NM_031302	CCCGATGGTCCTCAAAGGGAA	CTGAGAGAAATAAACTTTAAA		
83479	DKFZP564B1023	NM_031306	AAGGTCAAACTAGGCCTTAAA	CAGGCCCATTATTGACTTTGA		
83482	SCRT1	NM_031309	TCGAATAATAATGACACATAT	CCCGGCTTTCTCCCAGCAATA		
83539	CHST9	NM_031422	CAGAATCTATGTAGAAGATAA	AAGGCATTATGTGATTTACAA		
83549	UCK1	NM_031432	TCCCTCTAGGTCACTGAGAAA	AAGGCTGGTTGTGGCCTACAA	TGCGGTTTAAAGATCCCTCTA	AACGGTGGAGGTGCCGACCTA
83552	MFRP	NM_031433	CAGGGAGTTTGTGGTCAGCGA	CGGACACAGCATAGAACTACA	CAGCATAGAACTACAGTTCCA	CTGCTCCTTCCTGTCCCTTTA
83650	AMAC1L2	NM_054028	CCGCACTCCAATGAGGTCACA	CAGGAGAGTTCCAGGGAAGAA		
83660	TLN2	NM_015059	CTCCTTGAATAACTGCGTAAA	CCAAGTGATAGGGAACCTCAA	CAGATGTTGTATGCAGCCAAA	CTGCATGATCGTGATGTCACA
83690	LOC83690	NM_031461	CTGGTGGATTTACATATTAAA	CTGCTGGTGGATAAACATTAA		
83698	CALN1	NM_031468	CCGGATGACCTTTGTAAGTTA	CAGACTCAGGTCATAAATCAA		
83706	URP2	NM_031471	CCAGCGAAAGTTCAAGGCCAA	CGGCCAGAAGTTCTGCATTAA		
83707	MGC11134	NM_031472	AAGGAGGAGGATCCAACAATA	CTGGCCATCCATCCTACTCAA		
83729	INHBE	NM_031479	AAGGGTTAGGGTGATGGTCCA	TGGCTTATACTTTCTTAATAA	AGGGCTGTTGAGGTACCTTAA	TAGGGTGATGGTCCAGAGCAA
83733	SLC25A18	NM_031481	CCCACTGTTTGCCAACCTTAA	CAGCACCTAGTTTGAGACCAA		
83743	GRWD1	NM_031485	TCCCAGGAGTTTCCAGGGTAA	GCGGATCTCATTAGGCGGAAA		
83844	USP26	NM_031907	TACCTATAATATAGAAATCAA	AAAGATTTGTATGAAGATAAA		
83849	SYT15	NM_031912	GCGGCGCTTCCTCCAATCCAA	CAGCCGCATGCTAGGACCCAA		
83855	KLF16	NM_031918	CTGCCTGGCCTCATCCTTGTA	TTGTATTTAATTAATTAAACA	TGGCCTCATCCTTGTATTTAA	TCCTTGTATTTAATTAATTAA
83861	RSHL2	NM_031924	CAGCGTGAGTATGAAGAACTA	AAGGCTATATTGTAATTCTAA		
83862	TMPIT	NM_031925	CTGGTGGGTGTTCCATCACTA	CTCGCCCTGAAGAAATGCAAA		
83872	FIBL-6	NM_031935	CTGCAGATTCTGAATACTCAA	CCGCCTGACATTACATGGCAT	TAGACTCTAAGCAATTGCCAA	CCGAGTATATGTTCCGCCAAA
83873	GPR61	NM_031936	TGGATTTATGAGGAAACTGAA	TACCCAGAACTGGGACTACAA	GTGGGATAGTCTCCCATTTAA	CCCATTTAAGCAGCTAATAAA
83876	MRO	NM_031939	CGGGATAACAATAGTAGGTAA	ATGGATGGTTAGAAATGTTAA		
83877	BLP1	NM_031940	TTGGTGGTTTGTTGACCTTAT	ATGGCCGTGGATTGTAATACA	CACTACTTCATAACCACTTTA	TGGATTGTAATACACACTGAA
83879	CDCA7	NM_031942	CAGAGTAAAGAAGAACTTAAA	CACAATAATAGTATTAACTAA		
83884	SLC25A2	NM_031947	TACAATTTGGTCTGTCGTGAA	GTCGTGAAGGGTATCCTTAAA	TACCCTAAATCTTAACTTTAT	CCCTATGTACCTAATCTGAAA
83886	MPN	NM_031948	ACCAGTGCCCTTCACCAATTA	CCCACCAGACTCATTTGTAAA	AACCCAAAACCATCAAGAATG	AAGTGCCCTTCACCAATTACA
83893	NYD-SP12	NM_031955	CAGGTAGAAATCACACTTGAA	CAGAATTGCTGCAGTCACTAA		
83899	KRTAP9-2	NM_031961	CCCTGGTAGCAGAAATCCTTA	ATCGATGATCTTTGCAATCTT		
83903	GSG2	NM_031965	TTCGGGCAGATGGGAAGAATA	CAGGCTCATGAAGAAGGAGAA	ACAGTCTGTTTAAGTAAGCTA	CAGTCTGTTTAAGTAAGCTAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
83933	HDAC10	NM_032019	CGGGTTCTGTGTGTTCAACAA	CCGTTAGTAAACATCGCTCAA	CGCCCTTGCGCCGTTAGTAAA	CAGGTGAACAGTGGTATAGCA
83938	C10orf11	NM_032024	CAGAAAGTAACCAGACAAGAA	TTGCCTTGAAATGAATGGAAA		
83941	BBP	NM_032027	ACGCTACGCAAGAACCAGTTA	AGCACCCAACATAACTTGTAA	AAGTAGTTACATTATAGATTA	ACGCAATTATATCCATAAATA.
83954	FKSG83	NM_032030	TGGGCATGGCTCAAACTCAAA	AACGTGTGTCTTTCCACTTAT	AAGACTGTTTATATACTACCA	ACGTGTGTCTTTCCACTTATA
83956	FKSG42	NM_032032	AAGGAAACGAACTCCAATTTA	CAGATTTGGGAGCAAAGGCAA	CAGGTGGATGCAGACATCCAA	AAGGAAGGAAACGAACTCCAA
83959	SLC4A11	NM_032034	CCGAAAGTACCTGAAGTTAAA	CCGGGAAATCGAGATGAGCAA		
83983	SSTK	NM_032037	CGCAGTCACTTCACAAGGCAA	CAAGGGTACCGTGGCCATCAA	CCGGTTGGAACCTGCAATAAA	ATCGAGGTGTGCAACGGGAAA
83990	BRIP1	NM_032043	TAGCATGGCAACAATCTCTTA	CAGGCCCTTGGTAGATGTATT	AAGATAAACAGTCCACTTCAA	CCTGAACTTTACGATCCTGAA
84000.	MSP	NM_032046	CTCAGTTGTTTCAGAAACATA	CAGCAACTGGAATGACTCCTA	CTGGAAATTACCTGGAGACAA	ACGGGAATGCATCTCCAGCAA
84034	EMILIN2	NM_032048	ACGGGTCATGATGGAATTAAA	CACCTGAAGGACAAAGTTCAA		
84058	FLJ12953	NM_032118	CCCTGTGGTATTCATAAAGTA	CAGGGCCAGAATTCACATTAT		
84062	DTNBP1	NM_032122	CTGCTGGATTAGAATTACTTA	CAACTGGAGAATTACAAGAAA	CACCCAGCAAATGAAGCTGAA	TTGGCTGTATGCGGAATTCCA
84066	DKFZP564J047	NM_032126	CTGAGGGAAGGTGAAGCTTAA	CCAGCTTGAAATGAGAGTAAA		
84083	ZRANB3	NM_032143	TTGCCAGTGTATGACACCTTA	TGCCAGTGTATGACACCTTAA	CCGGATTCACATCTATACTAA	TGGATAGTTCTATAGAATTAA
84106	PRAM-1	NM_032152	CCGGAAGAAGTTCAAGTTTGA	CCGAAGCCTGAGTTTGGTAAA	CCGCAAGTTCTCACAGCCTGA	CCGGAGCATCAAAGCAAAGTT
84108	PCGF6	NM_032154	TAGGAGAATTTGAGAAGTTTA	AAAGATTTCCATGAAATGTAA		
84109	GPR103	NM_198179	ATGCTTATTCTGTACAGTAAA	TTGTTATTGCATAGTAAATAA	ATGGAAATTCAGGAATTACAA	AGGAATTACAATGATGCGGAA
84132	USP42	XM_374396	CAGCCCGTGATGAATGGCAAA	CAGGACGAGGCGAAAGCCCAA	TTGGAGGATACCTAAGATCTA	CACGACAGAACTGCACTTGTA
84152	PPP1R1B	NM_181505	CTGAGTCTCACCTGCAGTCTA	CAGGGATTTGCCCTTCACAAT	CAGCTTGTTTGAAGCCCTTGA	ATAAATCTTTGTAAATAACAA
84162	KIAA1109	XM_371706	AAGGATGCAGCTTGACTTTAA	CAGGTGTGGAGTATAGATGAA	CTCGAAGAGATTCACTTTCAA	CACCTCTTAAGCGAATGGAAA
84168	ANTXR1	NM_018153	CAGCAGTGTTTGATACCGTAT	CTCCCATTATAGGGCAAACAA	CTGACAGAAGACAGAGAACAA	CCGAGGAACAACCTTAATGAA
84171	LOXL4	NM_032211	CCGGGTGGAAGTGCTCATGAA	CAGAGTCAGATTTCTCCAACA	CAGGATTGGTCTAAACTTCAA	CTCATTATGGACTGCTACAAA
84174	SLA2	NM_032214	CTCGTTGAGACCACCACCATA	TCGGACAGTCTAGGTCCTCAA	CATCAACAGGTTCTCAATTAA	CAGGTTCTCAATTAAAGATTT
84186	ZCCHC7	NM_032226	CAGGGAATTGAGCTTCAGCAA	ACAGATTTCCTAAACAAGTAA		
84196	USP48	NM_032236	CACAGTCTGGTGAATGGTATA	ATGGCTGAGATGCGTAAGCAA	CCGAAGTATGCGACATAGAAA	ACCAGATGCGTTGGTCCATAA
84197	FLJ23356	NM_032237	AACACTATGCTTACTGAATAT	ACGGGTCATGTGCGACTCCAA	CAGGATGATCTCATGCCCTCA	AAGGTCTTGGATACACTTAGA
84203	TXNDC2	NM_032243	TAGCTTCTCATGTGTAAACTA	CACCTTGAAGCTCTCAAATAT	AGCAGTCATTGCAGAATTAAA	CAGAATTAAAGTAAACATGTA
84217	ZMYND12	NM_032257	CAGCATATTAAGGGAATATAA	CAGCTTGATGTCCATGAGCAA		
84220	RANBP2L1	NM_005054	CAGCATGAAATAAACACTCTA	CAGGCGTTCAGTGGAATTAAA	CAGCATGGTAATAATGTTCAA	CAGAATTATGATAATAAGCAA
84229	DKFZp434I099	NM_032269	CAGGACAATGACAGAGTACTA	CACACTGACCATCTCCATCTA		
84231	TRAF7	NM_032271	AAGGAGTGCGAGCACATCAAA	TCGGAGAAGATCGACCAGCTA	GCGGGACGCATCCATGTTAAA	CACGCTGGTCTCCTCACACAA
84233	DKFZp586C1924	NM_032273	CAGGTGATTTGGATTGTGAAA	ATCGGTTTATGTTGGATTAAA		
84259	MGC2714	NM_032299	AACATTTATTTCAGAACAATA	TCCCACGTGTATACAAGCTAA		
84263	HSDL2	NM_032303	AGGCACCTACCTTGCATCTAA	AAAGAGGTGACTTAAGTTCAA	ACCCAGTTCATGAATCGCTAA	CAGTTCATGAATCGCTAATAA
84265	MGC3200	NM_032305	AAGGGAGAAAGGAGAATTGAA	ATAGAGGATGATGACAGTTTA		
84266	SPATA11	NM_032306	CGGGACTCTGAGGGAAGTCAA	CAGGCGGGAGGTGGCGCCCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
84270	C9orf89	NM_032310	CAGGATCATCCTCCAGCTGAA	CAAGGTGCTGACCATATTAAA		
84279	C2orf7	NM_032319	CATGATTATTTGTACTTTCAA	CTGGCTAGAACCCGAAACAAA		
84284	MGC13186	NM_032324	AAAGATTTCTTGTTTATTTAA	AAAGATCAAATTAGCCTTAAT		
84288	MGC12458	NM_032328	AAAGATGATCGTAACACTTTA	AACGAGTAGCAGTGTAATGAA		
84289	ING5	NM_032329	CTGCGTGGACCTTACCACGAA	CCGGATCCGAGGAGCAAGTTA	AACCGTGAGGGATGTTAATTA	ACCGTGAGGGATGTTAATTAT
84291	MGC2408	NM_032331	CAGACACTATGCCCAAGCCTA	CAGCTCCAACTAGATCCAGAA	CTGGAGGCCGGTTTATCTCAA	TCCGGAGTTACCGGAGCGGAA
84292	MGC4238	NM_032332	CCGGCTCTATTGATTCCAGTA	ACGATTTAATGTGGATGGCAA		
84296	SLD5	NM_032336	CAGCACTTGATCCGATACAAA	TCGCCTCATGAAGATAGAGAA		
84298	MGC14817	NM_032338	CAAGCTCTACTGATACTTTAA	ATGAAAGATGTTCAAGAGATA		
84299	C17orf37	NM_032339	TGCCTTTGAGATAGAGATAAA	CCCAGGGTAAGTGCCCACGAA		
84302	C9orf125	NM_032342	CAGGGTTTAGCTGGCCTGTAA	CTGCAGGTATTTCACTGTTTA		
84310	MGC11257	NM_032350	CAGAGCGTGGATGCTCTGGAA	TGGCCTCACTTTCCATCATAA		
84311	MRPL45	NM_032351	AAGAAATAATTTATCCCTTAA	CACGCATATCATCTCTTTCAA		
84312	BRMS1L	NM_032352	CACAGCATTGATATTACCTCA	TAGGTAGTACTCTAAATAGAT	CCGCTGGCAACTTTACAGGAA	ATGCAAATTCGTACAAAGGTA
84318	MGC13183	NM_032358	AGGCTTTAAGACAGATATTAA	CACCAGAGAAATCAGAACAAA		
84321	THOC3	NM_032361	CAGCGTCTTCTTGCTGGAGAA	ACCAGCTTTGTTGGCATCCAA		
84324	CIP29	NM_033082	CAGGCATATCTTGAAGAACAT	CTCCTTCTTCTTGGTCACATA		
84327	ZBED3	NM_032367	CCTGGTGACTTTGAAAGGATA	CCCAGAATCCTTGGGAAATTA		
84329	MGC15619	NM_032369	CCCGGCCTTCTCCTTTAAGTA	TGGGAGCTCACTAAGAACAAA	CAGGTTCCAGGCCATCAGTAA	CAGCCCGACAAGAATAACTAT
84330	MGC15716	NM_032370	CACAGCAAACTGCACTACAAA	CACACAGTCCCTGGAAGGCAA		
84334	C14orf153	NM_032374	AAGGATTTGGAACAAGCTTAA	TCACAAATAAATTGTAATTAA		
84337	MGC4549	NM_032377	CCCGTGGATGTGTACAGTGAT	CTGGACAAGGGAAGCCCACTA		
84366	PRAC	NM_032391	CTGTCTCTATTTATACAATAA	TAGGCCGATGCTTGCTTGCAA		
84376	HOOK3	NM_032410	CTGCCAATAATTGATATACAA	CAGCATGAGAATAAGATGTTA		
84433	CARD11	NM_032415	CTGGATGATGACAGTCACGAA	CCCGTTGGACACATGCACCAA	CACAGTACTCGCAGTGCTTAA	CAACTCGAGATCGATCAGCTA
84435	GPR123	NM_032422	CCGACTTTCCTAGGCAACAAA	AAGCCGTGTTCTGATTATCAA	CTGCCCAAGGGTAAATTGCTA	CACTGTAAAGCTCTTCACCTA
84436	ZNF528	NM_032423	TAGGATTTACACAAGAAGTAA	AACGCAGATAATCCTTACAAA		
84439	KIAA1822	NM_032425	CAACAAGAACCTCAACTCAAA	GAGGATAATCCTGGAGGTCAA	CAGGAACACTTGATGAATAAA	GCGCATCGACGTGGACCGTAA
84441	MAML2	NM_032427	CCAGTCGAAAGTAATGGCTAA	CTCCAAATAAACAATGGACAA	CAGAGTTCAATTTCAGCTCAA	CAGGATACAGTATCCAATTTA
84450	ZNF512	NM_032434	CAGCACAGTTCCAGAAAGTAA	CAGCCAGGAAGTACTACATAA		
84465	MEGF11	NM_032445	AAGCAGCTATGTAGAAATGAA	CAGCAAGTTTACACTGCTTAA		
84498	KIAA1838	NM_032448	AACCCTGAAATTAAACAAGAA	CTGAAGTAAAGCAACAAGTAA		
84504	NKX6-2	NM_177400	CTCGGACGCCGAGAAGCTGAA	CGGCTGCTCAAGAAGCACAAA		
84520	C14orf142	NM_032490	CTGATTTATCATGTACCTTAA	AACAATCTGCATTGATTACAA		
84536	C21orf67	NM_058188	CAGAGGAAGATCAAAGATCAA	CAGAAGGACCACAGTAGAGAA		
84614	ZBTB37	NM_032522	CAGGGTTACACCAAATCTCAA	ATGCAGCATATTATAGACAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
84630	TTBK1	XM_166453	TGGCAGGAACGAGAAGTTTAA	AACGAGAAGTTTAACTATGTA	TGGCAGGAACGAGAAGTTTAA	CAGGAACGAGAAGTTTAACTA
84639	IL1F10	NM_032556	CCGGATAGCCTCAGTCAGGGA	CCATGGCAAGATACTACATAA	GCAAGATACTACATAATTAAA	AAGGCTCTATACACAAGAGAT
84641	FLJ14753	NM_032558	CACCAGTAAATGGACCATTAA	ACGAGTGAAGTTTATATCCAA		
84643	LOC84643	NM_032559	CACGGTAGAGTGGGTGGAGAA	AAGAGTCTTCTAGCCCTCAAA	CAGAGGGATGAATTTATTAAA	CTGGTGGAGTACACCATGATA
84645	C22orf23	NM_032561	AAGGGTCTTGCCACCACTTAA	CCGCCTTAGGCAAGTATTCAA		
84651	ECG2	NM_032566	CTCCATGGACATAGAGAGAAA	ATGGAGAAAGTTTCTGTGCTA		
84658	EMR3	NM_032571	CTCCGGGATGTGGAATCGAAA	AAGGAACGTGTCTCTCTCCAA	GTGGTTTAGAGAGATCGTAAA	AACGATAGTGTAGCTATTGAA
84659	RNASE7	NM_032572	CCACTTCATATTTGTATAGAA	CAGCACGAAGACCAAGCGCAA		
84675	TRIM55	NM_033058	TACAAACATATCACACATTAA	CAGAACATAAGTGTAACTTTA		
84676	TRIM63	NM_032588	AAGGAAGAAGGACACCAGTAA	AAGGAGCACGAAGATGAGAAA		
84678	FBXL10	NM_032590	CCGGCAAGACCGGGAAACAAA	CAGATCTAACAAAGTAGGCTA	TAGGAGTGGACTAGAAGTTTA	AGGAGTGGACTAGAAGTTTAA
84680	PHACS	NM_032592	CTGGGTTGACTTGAGAAAGTA	CAGCAGGTGCTTGCAGGCAAA		
84687	PPP1R9B	NM_032595	CCGGGAGGTGCGCAAGATTAA	CACTGAGGAATTCCAATTCTA	CCCGGGAGGTGCGCAAGATTA	CAACTCGAAGCTGGTCAGCAA
84691	NYD-SP18	NM_032599	CAGGTATGTGACCACTATCAA	CTGAGAAGATTTATTACCTAA		
84692	NYD-SP17	NM_032600	ACGGCTTTATTTGTTCCTTAA	CTGAAGAAACGTAACCATCAA		
84699	CREB3L3	NM_032607	CCCGAGAAGAGTCTCCAGGAA	ACGATGCAATCTCACCGTGAA		
84701	COX4I2	NM_032609	CTGGAGCTTGGTGCTGAGGAA	CCGCTGGGACTATGAGAAGAA		
84708	LNX	NM_032622	ATCATCCTCGATAGTACTCAA	CACGGTGCTTGTATAACTGTA	CTCGCTCAGAGAATTAATTAT	CACAGCTAACACAGCTCTTTA
84720	PIGO	NM_032634	CAGGTACTGGATGATCTGCAA	TAGGACTTCATTATTCTATAA		
84733	MGC10561	NM_032647	CACCTGCGGGTGCACCTTAAA	GCCGGCTGGATGTGACTCAAA		
84749	USP30	NM_032663	CAGAAATAACTCCCAAACAAA	CACACCAGTATTTATCCTTAA		
84750	FUT10	NM_032664	CAGCGCGAGAGTAGAAGTGAA	TAGGATCATTGCACAGTATAA		
84775	ZNF607	NM_032689	TAGGTTCATTTCTGTACTTAA	TAGGCTCAATTCATCCCTTAA		
84787	SUV420H2	NM_032701	AACCTTGTTATAAGCAGCAAA	CCGGCGCTATGGGCTGCCTTA	AAGAAGAATGAGCACTGTGAA	AATGACTTCAGCATCATGTAC
84816	RTN4IP1	NM_032730	TTCGAGCATTTCATATGCGAA	ATCATACACTATCCAAATGAA	CACGAGGAAAGACTGTAATTA	ACGAGGAAAGACTGTAATTAA
84833	USMG5	NM_032747	CAGCTGTGAAAGCAACATAAA	TACCAGTTCACTGGTATTAAA		
84836	MGC15429	NM_032750	CAGGTTACACACTAAAGTAAA	CTCAGGAATCAAGGAACATAA		
84844	PHF5A	NM_032758	ATGGCTAAACATCATCCTGAT	CTGGCACACCATATCGGAGAA		
84864	MINA	NM_032778	TTGGCTCGAATGTGTACATAA	CTGTTGCTACAAGACGATTAA	TACCTGCGTATCTACTAACAA	AACCAGTATTTAAGTCTATAA
84868	HAVCR2	NM_032782	AACCATCAGAATAGGCATCTA	CAGGCATAATGAATGATGAAA	CTGATATAAATCTAACACAAA	TTGACAGAGAGTGGTCCCTAA
84870	THSD2	NM_032784	ATGGAACTCGATATCCAGATA	ATGGAATACATCGGCAGCCAA	AAGGGAAGCATTACTGGGTTA	CTCGATATCCAGATATAAATA
84872	FLJ14451	NM_032786	CACCAAGAGTGGCAAGATAAA	CTGCCATGACTTCCAGAACAA		
84873	GPR128	NM_032787	CTCGATCAAAGTGCTGTGGAA	AAGAAGATTGTTAGCACATTA	CACAGCTCTATTACCTTCTAA	ACGCGAGTGGTTGGACAGATA
84875	PARP10	NM_032789	CAGGCAGATCATGAACTACAT	TTGAATAAACGTGAACGTGAA		
84888	SPPL2A	NM_032802	CAGCAATAATATTATGTGGAA	TGGGCTGTGTTTCGAAATGAA		
84893	FBXO18	NM_032807	CCCGCTGTTCATTCCTTGGAA	CTGCATAGCCGTGCTTCTCTA	TAGGGCGGAAGTACCAGTCAA	CACCGTCCTTACCATGAAGAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
84894	LRRN6A	NM_032808	CAGCGAGAACAAGATCGTTAT	CCGCTGGCGGCTCAACTTCAA	AAGGACTTCCCTGATGTGCTA	CAAGGGCAACACAAAGCACAA
84896	ATAD1	NM_032810	CTGGATTAATTTATCTGATAA	CAGGTGAACAATGGATAACAA		
84898	PLXDC2	NM_032812	TCCAGTGGATTTGATCGTCAT	CCAAGATAGCACTACATCTAA	CACAGTACATAGCACCTTTAA	ACAGACCACAATTACTATATA
84904	C9orf100	NM_032818	CTGGATTGTGGGAGAACTAAA	CCCAACTAAACCTCAAATGAA		
84918	LRP11	NM_032832	TACGTATTTCTAGACCATAAA	CAGAAACTTAGTTGAAGGCAA		
84925	DIRC2	NM_032839	ACAGATTATCACATTAATTTA	CACAGACTTGAAGGAGTTTAA		
84926	FLJ14800	NM_032840	CAGACCAGAGATGTTTATACA	CCCTACGATGTATGAAATGTA	CCAGTTTGGGTCAAAGTGCAA	CCGGTTTGTTCTCATGAACAA
84934	FLJ14827	NM_032848	ACCAAGGAAGAAGAACAAATA	CAGCTTTATAGGTGTGACCTA		
84938	APG4C	NM_032852	CACGTAATTGCAGGAAATGTA	ACAGATGAAGTTGACAAGCTA		
84948	TIGD5	NM_032862	CACAATCATCTCAGTGGCGAA	CCGCAAGGCCTACTCCATCAA		
84950	FLJ14936	NM_032284	AACCTGGATGTGAGGCATTAA	TCCGACGGAAATAGAATTGAA		
84959	STS-1	NM_032873	AAGAGAGTTGTTCTTAGGTTA	AACCAAATCATCAGTTATCAA	CCGGCTTATTTGAGTGGACAA	CCGCTTAAGGATGCTAACATT
84961	FBXL20	NM_032875	ATGGCAGTAACTGGCAGCGAA	CAGGACCCATTTACCCAATAT	GACCCATTTACCCAATATTAA	CTTGGCGAACTGAGTATTTAA
84972	MGC15912	NM_032886	ATGGATGAGGTCATCATGAAA	CTCGCTGGGTTTATATTTGAA		
84991	RBM17	NM_032905	TCCGCTGACTGAAATACTTAA	ATGGAGTATGTGGGTATAGAA		
85013	MGC13159	NM_032927	CAGCTTTAGTAATTACTATAA	TTGCATATGCATAAATTATTA		
85014	MGC14141	NM_032928	ATGGCTTATCCTTCTCTCCAA	CTGCATCTCCAACAAGTCCAA		
85015	USP45	XM_371838	AAGCATATATAATGTTATCAA	CAGAGAAAGCATGTTAAATTA	CGGGTGAAAGATCCAACTAAA	CAGGAAATTATCGGAACATAA
85236	HIST1H2BK	NM_080593	AAGAGAATCATTTACAAGTTA	AAGGAGGGACTTTCTCTGGAA		
85285	KRTAP4-10	NM_033060	AAGGGCATCCATCTACATTTA	TACATATTAACTGTTCTTCAA		
85300	ATCAY	NM_033064	CAGCGTCAAGTTCATCAACAA	CTCGCCTTTGTTTGCCAGTAA		
85315	C6orf33	NM_133367	TAGGAATTTAAGTCCATAGAA	AAAGCTAGAATTGCTTATCAA	AGGAAGCTTATTCTCATATAA	CTAGAATTGCTTATCAATCAA
85317	BAGE4	NM_181704	CCGAGGCAAGTCAAAGCTGAA	GAAGATCAAATTGAAGATAAA	CTGCAGATATTTCATCAAATA	ATGGCTGGAAATGCAAATGAA
85320	ABCC11	NM_032583	CCGGTGTATTTGAATAAACCA	CCGCTCATGATCCAAAGCTTA	CTCCTCCAGTTGGATCATCAA	AGGCTACTTGATGGCTCTCAA
85358	SHANK3	XM_037493	CAGGGATGTCCGCAACTACAA	CCGCAAGTTCATCGCCGTGAA		
85359	DGCR6L	NM_033257	AACCCTAGGATAGTCTCATAA	CCGCGCTCGGGATGTCGTGAA		
85360	7h3	NM_033025	CTCCATCTTTGTGGATAATAA	GCGCCTCTCCATAAAGATGAA		
85409	NKD2	NM_033120	CTCGTCTGTGTAACCCATAAA	CACGCTCTATGACTTTGACAA	CAGCCTCATGCACACCATCTA	CACGGAGCGCAGAAACCACTA
85411	C6orf114	NM_033069	TGGAATCAGAATTCAACTTAA	AACCTCCAATGTGGACATTTA		
85414	PCANAP6	NM_033102	CACAGGCATTTAAATATTTAA	CAGGCTCAGGGTTAACAGCTA		
85417	CCNB3	NM_033031	GTGCAGGATGTCAATATGGAA	TAAGGAGTCGTTAGCCTTTAA	AGGGCTAAGCATGCATGTTAA	AAGGCTGTGTATTACAAGTAT
85439	STN2	NM_033104	CAGATGTACCTTATAATTCAA	AAGCTGGATATTTCCTCTTTA		
85443	DCAMKL3	XM_047355	GAGGAAACTGTTTAACCTCAA	CTCGAGAATCACAGAGCGGAA	TCGAAGGAGCTCAGAGTTCAA	CCAGCTAATGAAGATAAACTA
85452	KIAA1751	XM_372193	CACCTTCAAGCCGATGATAAA	CAGGACTTTGATATTGGCAAA		
85455	DISP2	NM_033510	CCGGAACAGTCCGGACTACAA	CAAGAACTTCAGTGAGACTAA		
85459	KIAA1731	XM_374922	CAGCAGATACAGAAACATGAA	CAGCATGAACTTAGTGCTATA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
85464	SSH2	NM_033389	GAGGGTTTGCCTGGAAGTTAA	CAGGAGTCTTTGAGTATCATA	TTGAGGATGAATTAAACTTAA	CAGATTTAGTCTAGCATGAAA
85465	SELI	NM_033505	CAGGCATAGTTTCCACTTTAA	CACCACTGTGTTGATATGTAA		
85480	TSLP	NM_033035	GAGAAATTTCTTTGTCTATTA	TTGGTGGACTAGTATAGTATA	AGCACCTAAACTTACATTTAA	CTGGAACAAGTGTCACAATTA
85865	LOC85865	NM_033107	CAGCTTGGTGACTGTAATTAA	AAGCCTGAACTTGGAAAGATA		
89765	TSGA2	NM_080860	AACATGGTGAATATCGTTTAA	CCGAGAGGAGATCGTATCATA		
89777	SERPINB12	NM_080474	TAGGCAAAGATGATCGTCATA	TACGATCTTGGGTGGAGTTTA	ACGATCTTGGGTGGAGTTTAA	TTGGGTGGAGTTTAATGCCAA
89780	WNT3A	NM_033131	CAGGAACTACGTGGAGATCAT	GCCGCGCTACACCTACTTCAA	CCCGACTGTGCTGCTCGCGAA	ACCGCCATCCTCTGCCTCAAA
89792	GAL3ST3	NM_033036	CAGCCGCAAGGTGGACATTAT	CTCGAACTACCTGTTGCGCAA		
89796	NAV1	NM_020443	CGGGATCATCTAAGAAATGTA	TAGGTTGTCATTCAGACTTTA		
89797	NAV2	NM_145117	CACCTTTAACGTGGACCATAA	CAGCAAGAATGTGGACCTCAA		
89822	KCNK17	NM_031460	CCGGGATGTCGTCCAAGCATA	ATGGCTGGCCTTGATCATCAA	CAGCTCTAAGGAAGACTTCAA	CTGGGTGCAGCTATATGATTA
89832	CHRFAM7A	NM_139320	AACATTAAGATTACAAGTGGA	TCCATACAAATGCACAACATA	CACCGCAACATTAAGATTACA	ATCGGTTAAATTTGATGCAAA
89845	ABCC10	NM_033450	AGGAAGGGAGTTGATTCCTTA	ACGGCTGTGGAGGGCCTTGTA	CTGCTGGTACCCGTCAACAAA	AGCCCAGATTGTGGTAGATTA
89853	C9orf28	NM_001011703	AAGCCTTGCCAGAAACGTCAA	CTGGAAAGACGGCTTATTTAA		
89858	SIGLEC12	NM_033329	CAACAGGACATCAGAACTTAT	CAGGAAATGGAACTACATATA	CCGAGACTGATTCCTTTAGAA	ATGGAACTACATATATGACAA
89869	PLCZ1	NM_033123	CAGAAATACGAGCCTATCGAA	ATGGATTCACGTGAATGTCTA	CAGCAGACTCGTGTAATTAAA	TTAGCTATGCATCGCAATAAA
89870	TRIM15	NM_033229	CAGGAGTAAAGAACTGGCTTA	GAGGGATGAATATATCACAAA	CCGGCTTGGAGCCCAGGTCAA	ATCCGTGATTTCCACAGGAAA
89882	NYD-SP25	BC033792	AACAGGTATAGCCAAATTCAA	TAGACGAAATGTGCCATTATA	CACGTTAAATCAAGGAAGGAA	TTGAATGGACCTAACTATACA
89884	LHX4	NM_033343	CCGGACCACCATCACAGCCAA	CAGAACTTGGCCACACCAATA	CACCAATAGGATTTATGGCAA	TCGAAAGTACGCCAATGTGAA
89886	SLAMF9	NM_033438	CTGGCAATAAAGTCAAATTAA	CAGGCATGGATATGACCTACA	TCAGGGCTTTACCAAGCTCAA	CTGGCTGGCAATAAAGTCAAA
89890	KBTBD6	NM_152903	CAGTATTTATTTGATTATTTA	TAGGTTTGTATTGTTGATCTA		
89894	LOC89894	NM_138341	CTCGTGTTACCTTGATGGATA	CAGGGTCTACTCAACTGTGGA	ATGGCTACTCTGAGTGTTATA	CACCGTCAATTACATCTGGTA
89953	KNSL8	NM_201521	GACCAGAATAAGTATAAGGAA	CAGCTTCGCCGTTCTATGGAA	CAGCGGCTACAGCGCAGTGAA	AAGGTTGCGGACGTTGCACAA
90007	MIDN	XM_028067	CTGTCTTGGATACCTATTTAA	CCCTTTATGTGTTGAAAGTTA	ACCGGCTTCGGCAGACAGAAA	ACCGTTGTTCTCGTAGGTGAA
90024	LOC90024	XM_028217	TACGGTCGGAAGGAAAGTAGA	CCGACCAACTGCAGCACCCAA		
90025	C6orf157	NM_198920	ATGAATGATTATCAAATTAAA	CTGCGGTGAAGTCATAATAAA		
90102	PHLDB2	NM_145753	AAGCATGAAACTAAATTGAAA	CAGAATAACTTTATCACCCAA		
90133	LOC90133	XM_029323	TACCAGCGAATTCCCACCCTA	TACAAAGACTCAGATCTCCAA		
90231	MGC33867	NM_138346	CAGCCCAGGAGTGGAAATGAA	CCAGATGGAGTCGACGCTCAA		
90249	UNC5A	NM_133369	CACACCCATTGCCCACACTTA	CCGCATAGCCTATTTGCGCAA	CCGCATTAATGTCTCAAGGCA	CACCATGGAGGTCCGCATTAA
90316	TGIF2LX	NM_138960	AGGGCCCAGTGGTCCAGACAA	AAGGTCAAGGTTTCTGTCACA		
90378	SAMD1	NM_138352	CAGCTTTCCAAGAGCAGGAAA	CTCCATGGCAGCCATGAACAA		
90379	LOC90379	XM_373433	CTGCGTGGACATGGTCATGAA	CCGGGTGTGCGTGTCCCTCAA		
90390	THRAP6	NM_080651	ATGAAAGATTATTGTAATAAA	CTACAGGATAATCTTCGCCAA	CTGAGATTGGTATATGACAAA	CAGGAAGCTGAGATTGGTATA
90427	BMF	AK024472	GAGGTCTTCAGTACTATTGAA	CCAGAGGAACTCAGTTAAGAA	GACGCTAGAAACTAAATTATA	CAGACGCTAGAAACTAAATTA
90441	ZNF622	NM_033414	CAGGCACATATGAATGACAAA	CTCCTTGATGAGATACTACAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
90485	BC37295_3	NM_001005850	CTCGCTTATAGAGCACCAGAA	AACGCGATGAATTCAGCCGAA		
90507	SCRN2	NM_138355	CACAGGGTTACTGGAGCACTA	CAGGCTTATGCGTAAGCTTCA		
90529	LOC90529	NM_178122	AAGCTTTATGAAAGCTCTCAA	ACCCAGGTGATTCCAATGATA		
90594	ZNF439	NM_152262	TTGCTTTATGGAAGAAAGTAA	CTAGGATTCTTTGAATACAAA		
90637	LOC90637	NM_182491	GAGGGAGATGGTACTATAATA	CAAGATTTCTGTAAAGATCAT		
90736	CXorf44	NM_138362	TCCTGGATGAATAATATTGAA	CTGGGCTTCCTGGGTCAAGTA		
90737	PAGE-5	NM_130467	ATGCTGGAAATTTGACTGCTA	AACCAAGAATATTGTTCTTAT		
90780	PYGO2	NM_138300	AACATGAACTTTCCCAGCCAA	TCGGAGTGAGGTGAACGATGA	ACGTATCTTCTTCATACCAAA	CAGCCCATCTGTTGCACATTA
90835	LOC90835	XM_373675	CCCAGTCTCTCTCACATTCAT	CTGGAACATTCTGGAAACTTT		
90874	MGC45731	XM_371286	CACCAGGACTCAGAAGACAAA	CTGGCCTTGGTTTCTATGTAA		
90952	ESAM	NM_138961	CTGAAATTAGCTACTCACCAA	CAGAGGATAGGGAATCTCTTA	TCAGGTGTTGTCCTACATCAA	ATACATAATGTTTGTATGAAA
90987	ZNF251	XM_291262	CAGACTCGTGTTGGAGAGAAA	AAGCATAATTTATAAACAATA		
91050	DKFZp761B107	NM_173463	CAGGCTAATCTTGCACAACTA	AAGAAACTAATTATACTACAA		
91074	ANKRD30A	NM_052997	CTGCAGATATATGTGGAGTAA	AAGGCTAACTGCGGAATGAAA	CAGGAGATGCTTGTTTGCAAA	AACCGTATATATCAATATGAA
91151	TIGD7	NM_033208	CAGACGGAACTCATAAATTAA	AAGGTTCTAAGTAGAATTGAA		
91181	NUP210L	NM_207308	AAGGAGTACTTTGAAGAGCAA	CAGGATGAAGTACAGATTGAA		
91227	GGTL4	NM_080839	GAGGACAAGGCTGACAAGCAA	CACCAGCACCATCAACCTCTA		
91304	C19orf6	NM_033420	GCCCGATGACATGAACAACAA	CGAGTTCTTCGTGCTGCTCAA		
91316	LOC91316	XM_498877	CTGCTGTGGTCTCTGCTTCTA	ATCGTGGTATCCCAAGGGTTA		
91319	DERL3	NM_001002862	CACGGCCGACTTCGTCTTCAT	CTGGGAAGAGTCCCATGCTAA		
91351	FLJ31033	XM_037817	CTGGGTATTCCAGCATATTAA	TAAGAATAAGATAGTCATTAA		
91355	DKFZp434O0213	NM_182492	TTGGCTCTGTGCATCCTTGAA	AGCACTATAATATTTATTGTA	CACGTGCAGCCTATATGGGAA	CTGGAACAAATCAGTGAACAA
91368	MGC13017	NM_080656	CCCAGGAGTTATCACTGTAAA	TCCTGGTATTACCAACATAAA		
91369	MGC15396	NM_052855	CTGGGTGTTAATCCAGATCAA	AAGGATGTTGCTCGACTCCAA		
91404	SESTD1	NM_178123	CGCCAACAAATTGACTCGTTA	TCGGTTGATCCTGAAACAGTT	CAGCGTCGATTTAATGGCTCA	ATCCCGCATGTTGTCAACATA
91409	DKFZp434E2321	NM_207310	AAGCTCATAATGAATCAGACA	CTCCAAGAAATGCCTGCTTCT		
91445	FLJ38628	NM_152267	ACAGCCAAGGATGGCAAGCAA	CCTGAGTTTAATATTACAGAA	ACCACCATCCTCAGAAGCCAA	CTGAATCTTATTGAGGGACTA
91452	ACBD5	NM_145698	CAAAGTGATAATGATAAGAAA	ACCGTTAATGGTAAAGCTGAA		
91464	LOC91464	NM_001008494	ACGGGATACAGAGATAAACAA	CTGGATGAAAGGAGAAGGCTA		
91522	COL23A1	NM_173465	CAGGATCTTGGATGCCCTCAA	CAGGAAGGAGATGAAGGTAGA		
91561	LOC91561	XM_039218	CAGGGCCGCAGAGCTCGCGGA	CGGCTTCTCTCAAGGATGAGA		
91574	FLJ38663	NM_152269	CAGCATTATTATAGTGCTTCA	TTGGATGAGAATGAACTCGAA		
91584	DKFZp434G0625	NM_181775	CCGCATCGTCCAGACCTGCAA	CTGGCCTTTGTGGGCACCAAA	TACCTGGGAATTCTTCCTAAA	CAGCCGGAAACTGACCAAGAA
91607	FLJ34922	NM_152270	CCCGATAACCTTCACACTCAA	CAGATACAACTCAGCATTAAA		
91608	RASL10B	NM_033315	ACCAATTTAGAAATAACAATA	CAGGGCAAGCAGAGGCAGCAA		
91647	ATPAF2	NM_145691	CTCCGAGAGCACCACAGTCAA	GAGACATTAGTGGAACTTCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
91662	NALP12	NM_033297	CTCATGCAGATTGAGATCAAA	CCAGACCTTGACCGACCTTTA		
91664	LOC91664	XM_039908	AAGTATGATGATTGCAGCAAA	CGCTGCGAGTGTGGTGTTTAA	AACCTGGTGTCAAGATACAAA	ACCGCCGCTATTCTCCAGATA
91754	NEK9	NM_033116	CAGGTGTCATGTGGTGATGAT	TCGGGAATTATCAACCATGAA	TACACTTGGGTGAACATGCAA	CACGAACCAGTGAAGTCTATA
91833	WDR20	NM_144574	TGGGAACATGTACTTATATAA	CACGAGGAACCCTCTCCTTAA		
91860	CALML4	NM_033429	CACGGTGCTCTTAGCATTCAA	ATGGAATTTATGGTAACTTTA		
91862	MARVELD3	NM_052858	ACGAGAGGAGGTGGAATATTA	CTGGAATGCCACAAATGCAAA	CTGGGAGAGCCTGCTGCCAAA	CAGGCGCTGTACCAAAGCAAA
91942	LOC91942	NM_174889	CCAGTTCAAACTCAAATTAAA	CCCGCAGTACAAGAACTGGAG		
91966	CXorf40	NM_178124	ATACATTAGGTTAAATCTGAA	AGGGCCAGGTAAAGAAGCTAA		
91977	MYOZ3	NM_133371	CACTAAGGATATAACAGTTAA	CTCCAGGTGATTCCAGCATAA		
91978	C19orf20	NM_033513	GAGGGCCGCCTTCAACAACAA	CGGAGGTTACACCCTCAGCAA		
92002	MGC29729	NM_152274	CAGATTTGTAGGGAGAATGAA	TACAGGCATGACATCAATGAA		
92017	LOC92017	NM_001009607	CAGCGTCATGAACAAAGTCAT	ACGGAGAAAGCAGCTCCAGAA		
92106	MGC15763	NM_138381	ATCGTCTGCTTTAACGCCTTA	AACCAGCATAATGAAATCCAA	TACCAGCGAACTCCTGTTTAA	ATGCAGTTTGCATGTTACAAA
92181	DC-UbP	NM_152277	CTGCTCTAAATTCCCTATGAA	CAGGCTTTGAGACTCATGTAA	AAGGCAGTTAAGAAATAGATA	AGGCAGTTAAGAAATAGATAA
92211	PCDH21	NM_033100	AGGGCTGAGAATTGACGAGAA	AACCTGCTATCAGGAAATCTA	CAGGTTGGTAGCAAAGATCTT	CAGGTACAACTTCTATGTGAA
92235	LOC92235	XM_043739	ACCGTCTGTTGCAAGCATGAA	AAAGCTGGCCTCAGACAACAA	TCCGATATTCTTCCCGCAGTA	CAGAACTGGATTGCCAATGTA
92249	LOC92249	XM_499179	CTGCACTAAATTCCTTCATTA	AAGTTCCTATCTAATATTATA		
92255	DKFZp434H222(	NM_001007527	AAGGACTTTAAGAAAGATCAA	AAGATTAAGATTATACTTCAA		
92312	LOC92312	XM_044166	CCGCTCCAGGGCTTCTCTAAA	CAGGCCCAAATCGCCACCTCA	CAGGCAAGGCTGCAAGATTAA	ATCCTCGAGTACAACAATGAA
92369	SSB4	NM_080862	CTCGCTCAACGTCTTCGTCAA	CATGGCTGTCACAAAGCTTTA	AAGCTTTATTTGAGCAAATTA	ATGAAGAGCGTTTCTAATAAA
92454	MGC20460	NM_053043	CCCGGTGTAACCATTTATGAA	ATCGAGATCAATGAACCTTTA		
92579	G6PC3	NM_138387	CTGGGAAATGGCCAGAAGATA	CACATGTTCAGTGCCCAGGAA	GTGGCTCAACCTCATCTTCAA	CAGGTGCTGGCTGGCCTAATA
92609	TIMM50	NM_001001563	CCGGACATACAAATATTTCAA	CACCCTGGTCTCGGAATCTAA		
92610	TIFA	NM_052864	TAGGATTATTTACTTACCAAA	CAGAATAATGATTTCTCCTAA		
92714	ARRDC1	NM_152285	CACCAAGAAGTTCTCCTACAA	CCGGTCTTCATTGGCAATATT		
92715	C9orf112	NM_138778	CAGCCTTTCATACTTGTTTAA	CAAGGGTGGAATGGAAGTTAA		
92736	OTOP2	NM_178160	CAGGCAGGCCCTGGTCATCTA	AACGCTCTGGATCCTCTTCTA		
92799	SHKBP1	NM_138392	CAGGGCCTCCTTGGAATAAAT	CCAGCTAGTGTTCATCCAGAA		
92806	MGC16385	NM_145039	AAGCGAGTTCACAAATAGCTA	CGCCTTTAGACTTATCTTAAA	AAGGTGTAATCTCGACCTTGA	CTCGGTTGACTCGCCATCGAA
92815	HIST3H2A	NM_033445	CGGAAATGTCCGGTCGTGGTA	CCGCGGTGCTCGAGTACTTGA		
92822	ZFP276	NM_152287	CGGCATGAAGAAGCACATCAA	CAGGTTAGAAGACATACAGAA		
92999	ZNF651	NM_145166	CCCGAGTGATCTGAGGATTTA	GAGGCTAGCACTAATAGGAAA		
93010	B3GNT7	NM_145236	CAGGAAAGACAACAAATACTA	CTGGGACGTGACCACCACTAA		
93034	NT5C1B	NM_001002006	TTGGATGTTTGTAGATAACAA	TAGGATAAGTTTAGAACTTGA		
93082	LOC93082	NM_138397	CACGTGTATAATGGAAATGAT	CAGAGAGACCATGCATCTGAA		
93107	KCNG4	NM_172347	CCCGCTGAGCCGCCTGAGCAA	CAGCCAGGAGTTCTTCTTCGA	ATGAACGATGTCAATGACCTA	TTGCCTATCATGCACATGTAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
93134	ZNF561	NM_152289	CAGGCTGTGGACCGCAAATAA	CACGCCTAAGTAGACATGAAA		
93145	OLFM2	NM_058164	CGGAATAAACAGGACCTTTGA	CAACGGCTCCCTGTTCTATAA	CACGGACGTGCCCTTCCACAA	CAGGACCTTTGACATTTGAAA
93185	IGSF8	NM_052868	TGGGCCCAGATTGCAGAGAAA	CCGGCATTTATGAGTGCCACA		
94033	FTMT	NM_177478	CAGGTGAAGTCTATCAAAGAA	CCGGGATGACGTGGCCTTGAA		
94086	HSPB9	NM_033194	CAGAGACGGTTTCCAAATGAA	CCCGGAGGAACTGGTGGTGCA		
94097	SFXN5	NM_144579	CCCGCTCGCTGCGGTTGATTA	TAGGCCAGAGGTGAACATTCA	CAGCCGGACAGTGGTGTACAA	CAGGCTGGTAAATTTAGGATA
94104	C21orf66	NM_013329	CATGTTAAGGATACAAATCAA	CAGCATGAGAAACATCTGCAA		
94122	SYTL5	NM_138780	CAGAATTCAATGAAACACTAA	ATGGATTTGGCTGCTATTGAA		
94134	ARHGAP12	NM_018287	CACCATTGTATTGGACACTAA	CAGGGCGTTGCTATTACTATA		
94137	RP1L1	NM_178857	CCGGAGGATACTGCTGATTAA	TTGGATAAAGTTTGTTCTCAA		
94234	FOXQ1	NM_033260	CTCCATCAAACGTGCCTTAAA	CCGATGCTTCACTGTGCCAAA		
94235	GNG8	NM_033258	CTGGCTTTCTGCGAGACGCAT	CAAGATTGCCGAGGCCCGCAA	CAAGACGGTGGAACAGCTGAA	ACAGCTGAAGCTGGAGGTGAA
94241	TP53INP1	NM_033285	CAGAACGATGTTGACCTGTTA	AAGGGACATTTGGTTAGGTTA	CTGGGAGACACTAGTAGTATA	CCGCGTCAGTACAATTACTAA
96764	NCOA6IP	NM_024831	AAGGATCATAGTGAAATACTT	CCGGCCAAAGTGAACCACGTA	TCGCAATAATGCAGAAGTTTA	ATGGAAACTTACAGGACTTAA
112398	EGLN2	NM_017555	CCCTGTAGACAGAGAAACCAA	CCGCATGGCAGACAGCTTAAA	CAGGGAATTGTGTCTGCAGAA	CTGGCTAGGGTTACCCAGCAA
112479	MGC16943	NM_080663	TAGGTGCTTTCTAGAATCAAA	CCCAATATGAGTAAACAGGAA		
112597	MGC4677	NM_052871	CACCAGCCTCTCCTTGAATAA	AAGTTTCAAATTGACATTCCA		
112609	C6orf117	NM_138409	AAGCTGCACACTGGTATTAAA	ACCTATTGTTCTGGAAACTAA		
112616	CKLFSF7	NM_138410	CAGGCTGGTGGGCACCAGGAA	AAGCATATGGCTGTCCTATAA		
112724	RDH13	NM_138412	CCGCTTAAGGAAGGAAGGAAA	CTGGCAGACGAGGAAGTATAA	ACGAGGAAGTATAACACCAAA	AAGTACTTCGATGGACTCAAA
112770	MGC31963	NM_144580	CTGCAGAACCTGCTTCATATA	CAGCACTCCATCGACGATGAA		
112858	TP53RK	NM_033550	TTGGCTCGAATGCACGATGAA	CTAAGTAAAGGTGTTAAGATA	TAAGTTTATACCGCTAAACAA	AAGTATTGGCGTATAACATTA
112939	BTBD14B	NM_052876	CCGGCAGATCTGCAACATGTA	CCAAGTGAGATTGCACATTTA		
113026	PLCD3	NM_133373	GCGGATGAACTCAGCCAACTA	CCGGTTTGTGGTGGAAGATTA	AAGCAAGGGTACCGCCACATA	TAGGTTTGTAACTGTTTCATA
113177	C19orf36	NM_052878	CCCGAGGAGGTGGAACCTCAA	CCGCCACCATGTGAACTTCAA		
113178	SCAMP4	NM_079834	ACCCGTCAAATCTGTGCCTTA	CCGAGCCGACAGCTCCTTTAA		
113230	LOC113230	XM_053966	CCGCAGAAAGGTCTCGGAGAA	CAGGAGGAGCGCAAACCTTGA		
113246	GRCC10	NM_138425	CAGGAGGTTATCAAAGCCTAT	TCCGCTGAACCTAGAGCTTCA		
113451	ODC-p	NM_052998	TAAGCAAATTGCACAGATCAA	AAAGTTTGGAGTGTCACTGAA	CACCTCCAAGACCATCGTGTA	TAGTTCAAGTATGCAACATAA
113510	HEL308	NM_133636	TCGGTATGAGTGCAACATTAA	CAGCATTACTACCATAGGCAA		
113540	CKLFSF1	NM_052999	CCAGCCTAAATGTGACCATAA	CAGCCTAAATGTGACCATAAA		
113612	CYP2U1	NM_183075	CAGCGCTTTGATTACACTAAT	CAAGGGTATACCATTCCTAAA	CCGGAGGATTTCTACCCTAAT	CGGGTGTGTATGGGAGAACAA
113675	SDSL	NM_138432	TCCGACAACTCCGGCCAATAA	CTGCCAGGAGATGGCCAAGAA		
114026	ZIM3	NM_052882	CAGGAACTCTTAAACACTGAA	ATCAATCAACTTGCTAATTTA		
114041	C21orf88	NM_153754	CAGCCTTAATTCTACCTGCAA	TCCCGTCTCTTCCATTCTCTA		
114049	WBSCR22	NM_017528	CTGAGTGGAAGTTATCTGTCA	CCGAGCTGTCCTGCAGCTGTA	CCCTAACAGTGCCAAAGCAAA	CAGGGAGTCTGTGTTCACCAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
114131	UCN3	NM_053049	CCACAAGTTCTACAAAGCCAA	CAGAGGCACCCGGTACAGATA		
114294	LACTB	NM_032857	AAGCCAAATGCCGGAATTCAA	CTGGATCTTGATATTCCAGTA		
114548	CIAS1	NM_004895	AAGGCAGACCATGTGGATCTA	AAGCCAAGAATCCACAGTGTA	TTGATAATTTATATCTCTCAA	ACAGAACTAGTTGACTATATA
114625	ERMAP	NM_018538	AACTAGGTACAGCGACTTTAA	CACAAGACCATTGTACTGCAA	TTGGGAAAGGCTGATGAGTAA	TTGGAGAGTATTGATTTCAAA
114659	LOC114659	NM_052888	CTGAAGAAAGATCTAGCTGAA	TGGGTTCAAACTACAGATCTA		
114769	COPI	NM_052889	CAAACTGGAACTCATAAATTA	AAGGATCTCTATATCCTAGAA		
114771	PGLYRP3	NM_052891	CAGCCACTTCTTCTGAAAGAA	CTGCCAGACTGTCGTCCGAAA	CAGGATGGTGGCGTGTATGAA	CAGACTGTCGTCCGAAACATA
114783	LMTK3	XM_055866	GCCGCCTTTCTCGGAACTGAA	CCGGATGGGTAGACAACACGA	CCGGGAGACAGGACCCAGGAA	GCGGGAGGATGTGACAAGGAA
114788	CSMD3	NM_052900	CTGGTACACCCTTATATGGAA	CTGGCATTCCTCAATATGGTA	CAGGTGTATGATGGACCAAAT	CACGGTTTGCACAATGGTATA
114789	SLC25A25	NM_052901	CACGGTTGCACTTCCATTCCA	CAGGCCTGACTTCCCAACCTA	CAGAGTTATGTCCTAACTATT	GACGTTAGAAGTTGTCATTTA
114793	FMNL2	NM_001004417	CCGGTTTGTGAAAGCATATAA	ATGCAGTTTATTAATATTGTA		
114799	ESCO1	NM_052911	AAGCTACATGATAGAAATATA	TAGGCTGTTAACAAATCTCAA		
114804	RNF157	XM_290732	CAGGACGATCTCGCCTCTTGA	AAGCCTGGTCAATATCCGAAA	AAGCGTGAAAGCACTGGACAA	TCGGGTAGCCATCACCATCTA
114818	KBTBD9	XM_496546	CAGGACAGAATGGGAATTCAA	CCGGTTTGAGTTGTTATATAA		
114823	LENG8	NM_052925	TTGGAGAAGGGTGACCATGAA	CAACGTCTTCATGAAGGACAA		
114836	SLAMF6	NM_052931	CTCCAGTCCTTCGGACTTAAA	CTCCATTGTTTGAGCCAAGAA	CAGGGAATGTAGTTTCACAAA	CACAATTTACTCCACAATTAA
114881	OSBPL7	NM_017731	CGCATTGACCTTGACACTGAA	CTGGCAAGATATGAAGTGGAA		
114882	OSBPL8	NM_001003712	CAGAACTATAATGTGATTCAA	ATGGTTTAAATTAGTTAATTA		
114904	C1QTNF6	NM_031910	CAGCAACAAGTTAGTATTGCA	CAGGAAGACCTGTGCTATAAA		
114971	PLIP	XM_374879	CAGGAGTGGAAGAGACTAGGA	AACCTCCAGAAGGGAGTCCAA	CACCTTGGACAACCTCCAGAA	CAGCTGCGGCTCAGCACAGTA
115330	GPR146	NM_138445	CAGCATTCAGTTTGTCAATGA	CTGGTGTTAAATGGAGCTATT	CAGGGTTCTGAGAACATTTCA	AGCATTCAGTTTGTCAATGAA
115426	UHRF2	NM_152306	CACATACATAGTGTTACTAGA	AAGCGGTACTCTAGAAATGAA	CAGATATGATGGCATTTATAA	CACTATATTCCCTAAAGTATA
115548	FCHO2	XM_291142	AAACATATTAATAAAGTATAA	CGGGCGGGCGCGGACGCGGAA		
115557	GEFT	NM_133483	CAGGACCATATGAGAACTGGA	CTGGATATGTATACAAGAACA		
115650	TNFRSF13C	NM_052945	CCCATGGAGTTTGGTGTGCTT	ACGGCCGGCCCTGAGCAACAA	CTCCTGTTCCTGTGCCTTCAA	CCGGGAATCTCTGATGCCACA
115708	C14orf172	NM_152307	CACCATGAGCTTCGTGGCATA	CACGGTGGAGTTCCACCAGCA	CCGCAGCGGCACGCCCATGAA	CCAAGTGTGAGTGATGAGCAA
115827	RAB3C	NM_138453	AAGGACATTTGCCAACAATGA	GTGGCAAATATGTGATCTTAA	TACAAGATTGGTCAACTCAAA	ATGCAGTACAAGATTGGTCAA
115861	TXNL6	NM_138454	CCGCATCCTGATCCGCAACAA	CCGGCTGGTGCTGCTGTTCTT	AGCCCAGAGGTTCGAGATCAA	CTCAAGGACATGCCAAAGAAA
116068	LOC116068	XM_371760	TAGCAATTAGCTCATAATCAA	AAGGAGATACATTAAATGCAA		
116093	DIRC1	NM_052952	TTCGTTTGTACTCATACTCAA	CAGAGTTTCTCTTGCCCTTAA		
116115	ZNF526	NM_133444	CACGGAAGACTGAAGCAGAAA	CAGAGATGATGGAGATGTCAA		
116143	LOC116143	NM_138458	CACCGGCGTCATTCAGCTGTA	AAGGAGCACCTGAAATTGTGA	AAGGTGTGGGACCCAAGGCAA	ACGGTGGGAGACAAACATCAA
116166	LOC116166	XM_007651	ACCCATGATGCCATACCTACA	AAGCCGAAGCTCAGAGAGGAA		
116173	CKLFSF5	NM_138460	CTAAGTCATTCCCAAATTAAA	CAGGATGTGGCTTCTCATGAA		
116225	ZMYND19	NM_138462	ATGGGAAGGGTAGAAATTACA	ATCATTTGCTGTAATCCTTAA	CACGGGAGTTGTGTCCACAAA	CAGGACGGTTCTCATTATTTA
116285	BUCS1	NM_052956	CCGGAGGAATTTAACTTTGCA	AACATTGGCATCAGAATCAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
116362	RBP7	NM_052960	CAGGCTCACCTGTATCCAGAA	CAGCGACAACTTCGAGGGCTA		
116441	LOC116441	NM_138786	CTGGAGAATAATAACAACTAT	CAGCAATAAACTCACCAACTA		
116443	GRIN3A	NM_133445	CTGAAGAACGATCCAGAGAAA	CAGAGATTACACAGAGCAATA	ACCGACGGAAATACATCTTTA	CACCCAGGGAATAACAACTTA
116447	TOP1MT	NM_052963	AAGCCGGTGTACAAGAACTTA	AGCAGCTAAGATCTTATCCTA	CCAGACGAAGATCCAGGCAAA	GTGGAGAAGATCTACAGCAAA
116511	MAS1L	NM_052967	CCAACGGGCGTTAGCAGATAA	CAGGGTCGATGTGGAAACATA	CACGAATCCCTACATGGTATA	AGGGTCGATGTGGAAACATAA
116541	MRPL54	NM_172251	CAGGCCCTGGAGGCCAATAAA	CCGGATGCTGAGTACCCTGAA		
116841	IMAGE3451454	NM_053052	CTCCAGCATAGTTGAGATCAA	CAGCGGTTTATTGGAAAGCCA		
116844	LRG1	NM_052972	ACGGCTACATCTAGAAGGCAA	ACACCCTGGTATTGAAAGAAA		
117065	PRRXL1	XM_060970	CAGAGAAGAGCTCGCCATGAA	CCGGACGACGTTCACTCTTCA		
117194	MRGX2	NM_054030	CTGGTTAATGTTTAAGTTAAA	TACCAGATTTGAGTCACTAAA	CCGAAGAACTCGGAGCATTTA	ATCAATGTCAACACATATTTA
117248	GALNTL2	NM_054110	CTGGGAAATGATTATTACATA	CTCCAGGATACATAAATTCAA		
117283	IHPK3	NM_054111	CTGAGATACGTTACCCAATTA	AAGACTGGTGGACAAGTGTAA		
117285	DEFB118	NM_054112	CACCAATATGTAATTCTATTA	CAGCTGTGTAAAGAAGTCTAA		
117286	CIB3	NM_054113	TGGCAGCATGCCCGAGCTGAA	ACTCTGGTTTCTGAGAATAAA	CTGGAGCAGACGGTGACCAAA	CACGAGCAGCTGGAAGCGTAT
117289	TAGAP	NM_054114	CAGGAGAGCAGCCAACGAGAA	CTCACTATTCTATGCCTTAAA		
117579	RLN3	NM_080864	CAGGTACATGCTGCTGCTGCT	CCGGTGGAGACGATCAGACAT	CCCGGTGGAGACGATCAGACA	CCGGATGCAGATGCTGATGAA
117584	RFFL	NM_057178	TCGCAACTTTGTCAACTACAA	CCGGCTATACAAGGATCAGAA	ATCGGTTTCTTCAGTGCCTTA	TTGGTGAGAAATGAAATACAA
117854	TRIM6	NM_001003818	TTGAGATGTGCTCAATGTATA	CAGCTGTTGAGTGAGCTGCTA	CTACACTTTCTCTAAATATTA	TAGGAAGTTCTGATCTGTTAA
118425	GDEP	NM_058168	AAGAACTTAATGTGTAATTAA	AGCGATGTGCTGTGAAATCTA		
118426	LOH12CR1	NM_058169	CCCGATGTCATCAAGTTGCAA	ATGGATGATATTGTGGTTGTA		
118430	LOC118430	NM_058173	CTGCAATTGGTCACAACTATT	TCCTGTGATTTCATCCAACTA		
118442	GPR62	NM_080865	TAGGCTCCATTCTGCCATCTA	ATGGGCAGGTGTCACAAAGAA	CTGGACCAGTTTGGTATTAGA	CCCTAAGGGCTCACAACCAAA
118472	ZNF511	NM_145806	CCGGTTTGATAAGCCAAAGAA	CACGGAAATGTTTGCTCCTTT		
118670	FAM24A	XM_058332	CAAAGTAGCTAAGGCACTAAA	ATGAGCAATATTTCTTTCTTA		
118738	ZNF488	NM_153034	TGGCATATTGTTGGTGCATAA	CACATTGTGAGTATATGAATA		
118788	PIK3AP1	NM_152309	AAGTACGACTGTAGTTATCTA	TCCCATGGGATTATTCTCTAT	CAGCAGGGTATTTAAGTGCTA	ATGCTCAAGAGTCACATTAAA
118812	C10orf83	NM_178832	CAGCTGATAAGTATTGGGTAA	CAGGCTGTCTTCTTTCATCAA	CAGATTGTGGTGGAAGTTATA	AAAGGTGTTTATAAAGAATAA
118856	MMP21	NM_147191	ATGGTGAGATTTAGCACATAT	AAGGATCAGGCCCTCACAGAA	CCGCTTATTACTCCTATGCAT	CACACTGAACATGTAATAAGA
118945	LOC118945	XM_497242	ATCCATATGAAGGAAAGGTTA	ATGGACCAAGTGGAAGGCAAA	CAGGAATACAGCCAAGGGAAA	CAGCTTCACAATGGCCATGAA
119016	CTGLF1	NM_133446	CAGCATAGCCTCGGCCTAGGA	CAGCGGGAGTGCGTGGCCAAA		
119391	GSTO2	NM_183239	ACGGCTTGTCTTGGGAACCAA	CAGGAATTCAGCAACCTGGAA		
119764	OR4X2	NM_001004727	CAGGTGTGTACTGTCCTTGTA	CTGGCTGAAAGGAAAGTCATA		
119775	OR52P2P	XM_061677	ACCACCTTACTTGGCCATGAA	CTGCATGCTATCCACCATTGA	CGGCACATCCACATCCTTCTA	AAGCAGCTGTCTTATGGCATA
120105	LOC120105	XM_061864	GAAGATCTGTTTATAAACTAA	CACCCACAACATACTCTGTTA	TACGATGTGAGCATAAGTGAA	CCGATAGATGTGGAATACAAA
120114	FAT3	XM_061871	CACCATGCTCGGAACCTGTAA	TGCAAACTAAAGGAAACTTTA		
120318	LOC120318	XM_497316	GAGGCTAAAGAGAAGCATCAA	AACAGTGGGAACGACAAACAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
120793	OR56A4	NM_001005179	CACACTCTACTACGTCTAGAA	ATCCATTGAGATACCCGTCTA		
120796	OR56A1	NM_001001917	CTGTGATAATTTCACCCTTAA	AAGAGCTGTGCTTAGATTCAA		
120824	LOC120824	XM_062300	AGGGATTCAGAGTTTATCTTA	AAACCTGAATATGGCAACCAA		
120863	DEPDC4	NM_152317	CAGGATATGAAATGATTTCAA	CAGCATCTCTCTGAAACGAAA		
120872	LOC120872	XM_497349	GAGGAGTTAGCTGCATTTAAA	CAGGCTTATTAGAATGAACTA		
120939	FLJ31166	NM_153022	CAGCACAGCCATCGACATTAA	CCGCAGCACAGTGCTAATCTA		
121275	OR10AD1	NM_001004134	CTGGTTCTTTGGGCTGATCAA	CTCAGTTTAGTCTGTGGGCAA	CTGGTTCTTTGGGCTGATCAA	AGCTATGTTCTCTTACATGAA
121278	TPH2	NM_173353	AACGTGAAGCTGCTACCGAAA	ATGAAGTTGGTGGATTGGTAA	CTCAGTATACTTCAATCCCTA	CTGAAATAACGTATTATGTTT
121504	HIST4H4	NM_175054	CAGAATGTCTGGGCGAGGTAA	CAGCTTCTCTACAGACTCCAA		
121506	FLJ32115	NM_152321	AACAACCTGCATAATAAATAA	CTGGTGGACAGTGGTATGAAA		
121512	FGD4	NM_139241	CCGGTATGAGATGCTCCTTAA	CAGAGTCATTCTACCGATAAA		
121793	MGC35169	NM_152324	CAGCAGCAAGTTAGGGCTGAA	ATGATGTAACAGGGACAATAA		
122585	LOC122585	XM_063202	CACATATGTGTTCAGGGTGGA	CTGCGACTCGAGGCCACCCAA		
122664	C14orf8	NM_173846	CTGCGTTTGGAGAATCATCAA	ACGGGAAGAGATGACTGACAA		
122773	KLHDC1	NM_172193	CAGGCTTTATTTAAAGGATAA	CAAGTTATCTCTGAAATTTAA		
123624	FLJ32310	NM_152336	CCAGGTGATGTTATAAATAAA	AAGGAGGATCTTCTTGGCAAA		
123688	LOC123688	XM_058719	AAGACACTGCAGAGATTCCAT	CAGTAAAGATCTGTTGAATAA		
123803	NTAN1	NM_173474	TGGCATTGCTGTCAACATTAA	CAAGAAGATGACATTCACTTA		
123876	LOC123876	NM_001010845	TCCAGCATGACTAGAATATAA	CACCCTTAATCTGGGTAGGAA		
123879	MGC48972	NM_173475	CAGGAGTTATTTATTATCTTT	TAGGTTGAATTAACATTACAA		
124044	MGC26885	NM_152339	CAGGAAATGACCTGACCTCAA	AACACTCAGAGGGACGGTCAA		
124274	GPR139	XM_064062.4	CTCCATCTTCTTCATCTTGAA	CCGCATCATCATGATTCTTTA	ACCGTTAACCATTGACAGGTA	AAGAATTGTCGTGCACCTCAA
124402	LOC124402	NM_145253	AAGAACGAATTCCAAACCAAA	CACCATGTTCTCCCGTCTCAA		
124446	LOC124446	XM_378175	AGCCCTAGAATGGGTGAGGAA	TTTCTCAGGTGTGAATCAACT	TGAAGGCCTTGTGCTGACCAA	GGACAACTGGTCCTTATCACA
124460	SLIC1	NM_153337	CAGTACTGGCAGAACCAGAAA	CTGGCTGCATGGGACCCATAA		
124512	LOC124512	XM_497558	TCGGCAAAGCTGCCAAATGAA	CAGGAAGACATACAGTTGAAA		
124535	FLJ40311	XM_064190	TAGAAATATTACAGAGATCTA	TAGGAATATGAAACTAATTAA		
124538	OR4D2	NM_001004707	CCGGCTGGTTTGAGAGTGACA	CTCACCAATTTGCTTAAATTA	CTGGATGGCGTTATGATTTCA	ACCAATTTGCTTAAATTAGTA
124602	FLJ37300	NM_153209	CGGCCGGGCCAAGAACATTAA	CACCGAAGTCTCCACCATCAA	CCGGGAGAAGTCCTACCTGTT	CCGGGTCAAGAACATCTTGCA
124637	FLJ32499	NM_144607	CCGGAGCATCCGCATCATTAA	CAGGAAGATGGGATTTACAAA		
124641	OVCA2	NM_080822	CAAGGCCTTAATGGACATTGA	ACGATGGTGACTGCCACATAA		
124783	FLJ25414	NM_152343	CCGGAGTTTCACGGAGGAGAA	AACGAGGAGTCTGACTTTGAA		
124808	FLJ31795	NM_144609	AAGGAGCAGAAACATAATCAA	ACCACATTAAATTGTAAATAA		
124817	FLJ40137	NM_173478	CAGCAACATTACAGTCTTGAA	CAGCAAGTGCTTTCATCCAAA		
124930	FLJ25555	NM_152345	CCCAAGTAGACTGGACACAAA	CACCAAGACACAGAAGTTCAA		
124935	SLC43A2	NM_152346	TCGGTGCTAATTCCTTTGTAA	CCCGCTCTACCTGATCTGCTA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
125058	TBC1D16	NM_019020	CAGGGACATCTTTGCAAGCCA	GACGATAGAAACCTAAGGAAA		
125111	GJC1	NM_152219	CACAGCATCCTTGACAGCTAA	CCCGGTGCTGTTCGTCGTCTA		
125206	SLC5A10	NM_152351	ATGGGTGTTCGTGCCCATCTA	CAGCGGGCAACTCTTCATCTA		
125476	C18orf37	NM_194281	AAGGTGTTTGACAAGAAGATA	CTGGAAGAACCTGAAACAAAT		
125875	MGC33839	NM_152353	CACCGTGAAGAATGCGTGGAA	AAGTCTCAAGGTCTCCAGTAA		
125950	RAVER1	NM_133452	ACGGACCTTTGCTGAATTAAA	CCAGCACTCCATGAAGATAAA		
125958	OR7D4	NM_001005191	CTGTGTGGTCTCCTTGTTCTA	CTCAGATTGTCTCCTCCTTAA	CTGCTCTAACACCCTCCTCAA	ACAGATCGTGTAGAAGAGAAA
125963	OR1M1	NM_001004456	CAGGAAGCTGGTCAACAGAAA	CAGCGTCATAATCGCCATGAT		
125972	CALR3	NM_145046	CACGAACATTACTTCAATCAA	CTGGAACTTAACATCACTCAA		
126014	OSCAR	NM_130771	AAGGAGTAGCTGAAAGGAAGA	CCCGCTGTGCCCTGTGCTGTA	CCCAGCTTCATACCACCCTAA	AAGGTAGTAGTGAGACGTGAA
126037	LOC126037	XM_058967	AAGGCCAAGAAGCCTGCATTA	CTAGAAGGCCCTTTCATCAAT		
126074	FLJ35119	NM_175871	CCCAATCAATATGTTGTTTAT	CAGGGACATATGCAGATCCAA		
126119	SBBI54	NM_138334	CTACTACAACCTGGACTCCAA	ACCGGCAACTATGATGTCAAT	CTGGGAAAGGCCAGCACTTCA	CTGCCGCTGCTGCCTCAATAA
126133	MGC10204	NM_153329	AAGCCTGAACACAGAAATTCA	CAGGAGTCTGTGTGGGATGAA	CCGGCTGTCCTGCCTCTCCAA	CCCAATAAACTCTCTGACCAA
126205	NALP8	NM_176811	CAGGAAATGGGTGTTAGGTAA	CTGAGATACTTGGAAATACAA		
126353	C19orf21	NM_173481	CCCAAACTGCCCTGAAATAAA	TTCCGTTTCTATCTTCCTTTA		
126374	WTIP	XM_059037	CACCGTGGACGTGGAGAACAA	AAGGACAAGATTTGACTTAAA		
126402	FLJ40365	NM_173482	CACCTTGGTAGAAATGGCAAA	TTGGAGCTGAAGGAAAGATTA		
126410	FLJ39501	NM_173483	CGGGAGCTGGCCCTAAAGCAA	AAGGACCTGAGTGCAAGTAAT	CTGGACAACATGCACCATGTA	CAAGAGAAGATGAGTGATTAT
126526	FLJ36888	NM_178830	CTGGATCTCAATAAGGAGATA	CGAGGTCAAGGTCACCATTAA		
126537	LOC126537	XM_497611	CTGGTTCATGACTTCACAGAA	AAGGAGTTGTCTGATGAGGAA	CTCAGCCACCATTGCACCAAA	AAGCCGGAGGTCATAATGTAT
126626	MGC29891	NM_144618	AAGGAAATATACAGAAGACAA	CACCAATATATATGCCTTTAA		
126661	LOC126661	XM_059061	TTGGCAGTTGGAAGCTCTTAA	CCGCTAGGAGAGCAAGCACAA		
126792	B3GALT6	NM_080605	CCCGTCTCTCACGTACTTTAA	CCCGCTGCTGCCCGTGTTTAA		
126823	KARCA1	NM_001007255	ATGGAAGCATCTACACATTAA	CAAATGCTTATTAAATTTCAA		
126859	DKFZp686H1423	NM_144696	CCGGAGGACTATTTCAAATTA	CTCAAGATTATTAAACATTTA		
126868	FLJ38716	NM_152367	AACCAAGACATTAGATTTCAA	AAGGCATTGGATCAACACAAA		
127059	OR2M5	NM_001004690	CTCTATGGATGCAATCATTGA	ACTCAGGAAAGTGTTAGGAAA		
127247	ASB17	NM_080868	AACAATGAGTAAATCTACTAA	AACCTCGACTTCACTGAAATA	CTACTGCAATATGGAATCTTA	ACCATCAGGAATCAACTATTA
127281	MGC26818	NM_152371	CACCATTGCAGTGGCCATTTA	CCGGCAGCAACGAGCCATTAA		
127385	OR10J5	NM_001004469	AGGCCTGATATTTATCTCCTA	ATCAATGAGATAATAAATTAT		
127602	LOC127602	XM_059166	CAGGCTCATTTGGGAATTTAT	CCCAATTTAAACATAGAACAA		
127623	OR2B11	NM_001004492	CAGGTGGTCCTGACGGTGCAA	CCCAAGAGCAGGGCAAATTTA	ACCGCTGTGAATGACACCATA	AAGCCTTATCCTCGGAAGTAA
127670	HE9	NM_172000	ATGGATCATGGTTATGTTTAA	TTGGCTTCATTTCAAACTTTA		
127733	UBXD3	NM_152376	CACCAGGACTTGAGCACATAA	CTGGTAAATAACCACAGTGTA		
128077	MGC46719	NM_153713	CCGATTCATGCTGGAATCCAA	AGCCATTTCAGTAGCACTAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
128136	LOC128136	XM_497739	TTGAGCCAAATGCAACTTTAA	TGGGATAATGCTGCAATCCAA		
128239	IQGAP3	NM_178229	CACACGGACCTGAGCAAGCTA	ATGGTAGGACATGGACCTTGA	GAGCACTAAGACCACCTTCTA	CTCCGTGGTTCCGTTGAAGAA
128312	HIST3H2BB	NM_175055	GCGCCCAAGAAGGGTTCTAAA	TTGGAGAGACTCAGCCATCAT		
128322	LOC128322	XM_060943	AAGAACATCAACGATGGCTTT	CAGGTTTGCCCTGCACAATTT		
128414	C20orf58	NM_152864	CAGCGTCAAGAGAGTTTGTAA	AAGTTGGTAAATAAACAGGAA		
128486	C20orf142	XM_371399	CTGGTAAGACTTGACCTTTAT	AAGCAAGATAGTTACAAGAAA		
128497	C20orf165	NM_080608	ACGGAAGGAATACAGCCGAAA	CTGCTTGTAGATGGATGAAAT		
128853	DUSP15	NM_177991	CCGAAATAAGATCACACACAT	CTGGAGGGTATTAAAGAGACA	CACCACGATTGTGACAGCGTA	ACGGGCCTGGAGGGTATTAAA
128859	BPIL3	NM_174897	CCCGGACTTTCTGGCCATGAA	CTGTAGCTTATCCCAAGTCAA	CCTGGTCAATGTGAAGACTAA	CTGGCTGAGCTGGACATAGTA
128939	LOC128939	XM_066243	CAGCAGGTGTTTGTTGGGCCA	CAACGAGTGCATGGATGGAAA		
128989	DKFZp761P1121	NM_152906	CTGGATGTGCTCAACAATAAA	CAGGAGTAGGCTTGTATTTAA		
129049	RUTBC2	XM_059318	ACGGACTTTGCTTAAATCCTA	CAGGTGAGAATTCTTGAGCAA		
129285	LOC129285	NM_152994	AAGGAAGTTCATGTCAATAAA	AAGGCTAAACTAGAAGTGAAA		
129530	LOC129530	NM_174898	CTCAAATGTTACACAGATAAA	CAGGTTTCCCAGACAACTGAA		
130063	LOC130063	XM_059396	CATGACTTTATTGTCTTTCAA	CAGCAGAACTGTGGACAGCAA		
130162	FLJ31438	NM_152385	CAGAATGGCTTTGACAAATTA	ACGGTTAGATTTAGTTACCAA		
130399	ACVR1C	NM_145259	AAGTGTGAAACTTGTGCCATA	CAGCAAATAGATATTCCTCTA	CACAGAGTAATGAATATTTAA	TACTTTGGTAAACGAGATTTA
130576	LOC130576	NM_177964	CACATTGGACCTCAAGGCGAA	CAGGTCAAACCCTCTTGTTTA	AAGACAAATGGTGTCCACAAA	AACGGTGAACTTTGGAGTGAA
130940	LOC130940	NM_138803	CTGAATGAAGTCAGATGTAAA	CACGAGAAATATTGTGACCAA		
131034	CPNE4	NM_130808	CCGAACTGAGGTTGTGATGAA	CAGCGTCAGAGGAAACTAACA	CACCAAGGAGGCATCGCAATA	AATGTTGATAGACGAAATATA
131096	KCNH8	NM_144633	TCGCACGTTATTTGCCATGTA	TTGGAGCAAATCTATCAATTA	CAGACTTTGGTAACAATCCAA	CAAGACTATCAAACAAATCTA
131118	TIM14	NM_145261	ATCAATGAAGCTAAAGATTTA	TAGAATTTATACACTAATAAA		
131601	GPR175	NM_016372	TACCCTGATGCCCATCTCTCA	CACCATGGTGGATGGACTGAA	TCGGAGGAGCTTCTACGTGTA	CAAGATCCTCTTCTCCTACAA
131616	TMEM42	NM_144638	AAAGCCAGTCATGTAACTCTA	ACGGACCAGCTGGAAAGATCA		
131973	LOC131973	XM_497912	CAGGAAGGTATCCTCCATGAA	CTCGGCCTGCTGCATGCACAA	CCCATCAGAGGCAGCACTCAA	CCGGAGTCCGCGGTTACTCAA
132001	MGC16471	NM_138807	CTGGAGTTTACTACAATTCAT	ATGGTGGTTGGAGAAGATAAA		
132320	FLJ30655	NM_144643	CAGCTGGAAATGGCAAATGAA	AAGGTTGCACAGTGAATTAAA		
132332	FLJ30834	NM_152399	AAGAATGGTATTTGGAATTAA	CAAGATTGTCTGAGAAATGTA		
132671	LOC132671	NM_145263	CAGCTTTGAGATAAATGTTAA	AAGGCTAAGTGTAGAAGATAA		
132789	GNPDA2	NM_138335	AAGCGTGTAATAAATAAGTTA	CTGGCTATTTATTATAAAGTA		
132946	ARL9	NM_206919	CTGGAGATTGGTGGCAGTAAA	CTGGGTAATAGTCAACTAATA		
133308	LOC133308	NM_178833	ACGTACAAAGACTGAGACAAA	GGGCTGTAGTTTGGTCAATTA	CAACGATAATGTGCAGATCAA	CTGCAGAAAGTTGAACATCAA
133396	IL31RA	NM_139017	CTGGACGATCCAGCAAGATAA	TTGGGTGTCTATGATTTCTTA	AAGAATAACGATCCCAGATAA	CGGGACCAGCATAAATTTCAA
133688	FLJ34658	NM_152404	CACACTGACACTTACAATGAA	CTCAATGTAGTTATTTGCTAA		
133746	JMY	NM_152405	TTGGATAACATTAGATCCAAA	ATGGCTGTACTGTCTATTCAA		
134145	LOC134145	NM_199133	CCAACTGTTTGTAGTATCCTA	CACATCTTTAACTAAACTTAT	CTGGGATAATGGTACACATAA	CACCTAGTCTTTGGTCCATAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
134391	GPR151	NM_194251	TGGAAATGGATGATAACCAAA	AGGGAAGGCTTGAAAGGTGTA	CTCCTTCACAATGCTTGGAAA	CCGAGCTACGGCGTACTCCAA
134466	LOC134466	XM_376436	CAGGGTCAGTTCAAGCCTTAA	CAGGCAAGTTGTAGTCATCAA		
134505	LOC134505	XM_068889	CCCAGCAGATCTTCATCTGTA	CCAGGGTATCAACAGGAACAA		
134860	TRAR3	NM_175057	CTGGCAGCGTTTGGAAACTTA	AAGCATCAGGCTAGGAAGATA	TAAGGACTGATTCGTCAACAA	CATGGTGTTTATATACAGTAA
135112	NCOA7	NM_181782	ATGGATATTGACTATATGTAA	CTCCATAGCACTGAAATTTAA	AACAATTATTATACTCCTTAA	CCGGAAATCGGCATCACTAGA
135295	SRrp35	NM_080743	CACAGTCAAGTTCACCTCAAA	AACTCTCATTATGTTAAATAA		
136242	LOC136242	XM_059830	CAGGAATTCCTTATGTGTGAA	ACGGTACTGAACAGACAATTA	ACCAATGTTTACAAATATGTA	CACCATGAAATATGTCTTCTA
136306	LOC136306	NM_174959	CCGCTGGAAGGTTAATCATAA	CGGGCCCTCCAGCAAATTAAA		
136371	ASB10	NM_080871	AGGGCTTGAGTGAAAGGAGAA	ATGGAGGGATTTCCGCTTCAA	CAGCGCCAACACCATGGACTA	CCGGGTGATGTCTGATGAAGA
137075	CLDN23	NM_194284	TAGCTACATATCATTGCATAA	CAGCAGCTTAATGGATTTCAT		
137362	MGC33309	NM_152413	CAGCTTGTTAAAGACCTACAA	CAGCTGTATCAATGCCAACAA		
138050	FLJ32731	XM_372038	ATGGATGTCTTTGGAACTTCA	CTGGACCAACTTGACCGTCTA		
138162	C9orf116	NM_144654	CTGCCATTTCACATCTAATAA	CTCCGTGTACAGGACCAGTAA		
138199	C9orf41	NM_152420	CCGGAAATGCATTGATCATAA	CACAATGTAATTGATTATATT		
138240	C9orf57	XM_059954	TACTGCATTAATTTAATTTAA	CACATTCAAGGTGGCATTCAA		
138428	C9orf115	NM_001002913	ACGGCGGCTTATGAACGCCAA	CCAGGCTGCCTGCGGATTAAA		
138429	PIP5KL1	NM_173492	ATGCTGGAACCAGGACTCAAA	ATCAAGATCATTCAGCAATAA	AAGATGGAACTGGATACCACC	AACGTCTCCACGAGGATGAGA
138639	PTPDC1	NM_152422	AACAGAGGGTTTCAAAGCATA	AGGCTATACATAAGTATTGTA	TACGTAGATACCAGAGGCCAA	CGGAATGTTGAGTGCCTTCAA
138724	MGC41945	NM_203299	CAGGAGAACCCTCAAACTCTA	CAGAAGCTACATGGAAGGATA		
138805	OR13F1	NM_001004485	CCGCTGTAGATTCACAGGAAA	TCAGTGGAAGGTCGAAGTAAA		
138864	LOC138864	XM_498304	TACCTGAGAATAAACCATCTA	TTGGGAGAGCATATCCCGAAA		
138883	OR1N1	NM_012363	CAGGAGTATTGTTTCCTCTTA	CTGCGTTGTTTGTGTGTTCTA		
139105	CXorf20	NM_153346	CAGCGAATTATCCAACTTTAA	AAGGTAGAGAAAGAAATTCAA		
139135	PASD1	NM_173493	ATGTTTGTAATTGTTTGTTAA	CAGCCTGTTTCTTGGAAGTTA		
139231	CXorf39	NM_207318	CAGGTGGAATATATTGAGTAT	TTGGTTATTAATAGAGCTCTA		
139411	PTCHD1	NM_173495	TCCGTGGAGTTTGGAGTGATA	CCCGTGTGGTTGACCAAATTA	AAGGATTTCACAAGAACTAAA	TCCCGGTTTGAGAGCTATTTA
139562	HSHIN6	NM_207320	CAAGACGACAGTAGCATTGAA	TGCGTATAACTTCACCACAAA		
139604	LOC139604	XM_498354	TGGGATCATGATGAAGGACAA	ACCCTTTGACACTGAAATAAA		
139760	GPR119	NM_178471	CAGTCTCTGCTTCACCTTGAA	CGGGCTGTGGTTAGTGTCTTA	CAGGAGTGTCACCTCTACCTA	CTCCCTCATCATTGCTACTAA
140432	ZNF183L1	NM_178861	ATCCCATGCCTGAGTATGTAA	CACTGCAGTATTATTTGCAAA	AACGGGAAGGAAATCCTCTTA	AAGGATCACATGCTACAACTA
140469	MYO3B	NM_138995	ATGGCCGTACACAGACTTCAA	CACCCATTTATTAAAGGAGTA	ACCCTGGTTGATAAATTTGAA	AACCAGTTAAATGGAACTCTA
140545	RNF32	NM_030936	CAGTATCAAACCCGAGTGATA	TGGGTTAAGTACTACAATGTA	CCGCTAATAGTCTGTCCTAAA	TTCAGTGGTATTCAACATCAA
140576	S100A16	NM_080388	CAGGGAGATGTCAGACTGCTA	CACCTGTTCAGTCTCATCTAA		
140609	NEK7	NM_133494	CGGACAATTTAGTGAAGTTTA	CCCATTTATGTCTGGTGTTAA	CCGGATATGGGCTATAATACA	ACGACCGGATATGGGCTATAA
140612	ZFP28	NM_020828	AAGGAAATTATTAAACTATAT	CCGGGCTTGGTGACTATCAAA		
140628	GATA5	NM_080473	CTGGGTTGGATGATACCTTAA	AAGGGCCTTGTTCTAGCTGAA		

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Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
140706	C20orf160	NM_080625	CACCATGGAATATGAAGTCAA	ACCATACTAAACAGTGTAGAA	CTGAGGGTTAAGACCTTAGAA	CACCCGATAAGAGCTCAATAA
140730	RIMS4	NM_182970	GTAGCTCATGTTGAAATTAAA	CAGAGTGGACAGAAAGCATTA		
140766	ADAMTS14	NM_080722	CAGCACCGACTTCTTCATTGA	CACCGGCAGCTTCATCCTCAA	CAGGAGTGTGTGTACACTGGA	CCGCTTGATCATGGTTGGCTA
140803	TRPM6	NM_017662	CACGAGCCTATTGCTCACTTA	AACCTGAAGTCAAACAATCAA	GAGCAGAATCCTGCACATTAA	TTGCCCAATTGCCAAACTAAA
140809	C20orf139	NM_080725	CACCTTCTATCAGAAAGTAAA	ATGGGTATTTATTTGGATAAA		
140823	C20orf52	NM_080748	AACCATGGTTGCCAACTACAT	CTGATGGGCGGCATTGGGAAA		
140862	C20orf82	XM_097736	CCGAGTCACTTCGGTTTCTAA	AAGCGAGTTCTTAAAGAAGTA		
140870	WFDC6	NM_080827	CAGCCTTACTTTATACCATAA	CAGGATTTGGCTCATAATCCA		
140873	C20orf173	NM_080828	CAGGAGGAAATTGTAAGATCA	TTGGATCAGAATAGCAAGGAA		
140876	C20orf175	NM_080829	CACGGAGTTGGGTACCATCAA	CAGGAAGGGCTCCTTGTACAA		
140880	CST11	NM_080830	TAGGCAATAAATGTTTGTCAA	CAGGATCTTCCGAGTCCTTAA		
140883	SUHW2	NM_080764	TCAAATGTTTAAGAAGCCTAA	CAGTGGATGTAGCATCCATAA	TAGCCGTTAGTGGAGAATGAA	CCCAACTTGAATCGAGATCAA
140885	PTPNS1	NM_080792	CCCGAGAAGAATGCCAGAGAA	ACGCCTGTAAATTACTGAGAA	CTCGCTGTGGACGCCTGTAAA	CGCCTGTAAATTACTGAGAAA
140901	STK35	NM_080836	CTACGTGTGAACAACTTTATA	GACTGAGGCTTTGTAAATTAA	TTGGGTTGGTATGATACATTA	CTCGGCTGTTAGGGATCTGAA
142679	DUSP19	NM_080876	AAGGTCATATATACTATACAA	TACGGTCCTCTTTCTCACATA	CAGAGTTAACCTAATGAGTCA	ATGGTCAGTATCACTGGATAA
142686	ASB14	NM_130387	CCGGTTAACTGCCTCCAGATA	AAGGCTGGACATCTACAGTTA	ACGACCTTTATGGACAAGGAA	CTCACTATATATTATAGTAAA
143187	VTI1A	NM_145206	TCCCATAAGAAGATAATTAAA	CAGAGCTTTATGATTCTGTAA		
143379	C10orf82	NM_144661	TTGCATGTCATTAATGATAAA	TCCCAAGGAGGTGAACTTTAA		
143458	LOC143458	NM_174902	CAGCACCTCTAGTTAGAGTTA	CTGCTGGGTAGTTACCTTATA	AAGGGACTATTTATATGTGTA	AACCTGTTTGACGCTAATTAA
143503	OR51E1	NM_152430	CTGGTTCAATTCCACTACCAT	GCCCTAGGTGTCAGTGATCAA	CTCATATCTGCTTATTCTTAA	CAGTTTGATGCTTGTCTGCTA
143872	FLJ32810	XM_370651	GTGGATCTATTCAAAGCTTAA	ACCGGAAATGTTTAAATTAAA		
144106	FAM10A5	NM_153291	CTCTAATTTGAGTGAAATAAA	ATAAAGCCCTGCTGAAGGAAA		
144195	SLC2A14	NM_153449	AGGGAGTCAATTCCTAGGATA	CAGAGAGATGGACAACAGACA		
144203	OVOS2	XM_495917	ATCCAGTGAGATCCAGTTTAA	TAGGCCTGATATTAATAGCAA		
144348	ZFOC1	NM_152437	AAGGAATGTTTAGAAGACCAA	CAGCGCATAAAGGAGATTTAA		
144360	FLJ32894	NM_144667	ACAGGATTTCATACTTATTAA	CTGCAGTAGCTAAGACTATAA		
144631	LOC144631	XM_096642	TTGGAGGCTAAAGGAAGTAAA	CAGCAGTTATTTGGGTGTGAA		
144742	LOC144742	XM_378388	TACGTTGTTGTGGGAGATTTA	CAGGGAATTCACAGCAAACTA		
144809	FLJ40919	NM_182508	CAGCATTATGAGGATTTACAA	CACAATGTCAATATACATTAT		
144962	LOC144962	XM_084990	TTGCAATATTATTAGATTAAA	CAGCAAGGGTATATTTATAAA		
145173	B3GTL	NM_194318	AACCATATTATTGATGATGAA	AAGGAATAATACTGTACATAA		
145389	SLC38A6	NM_153811	CCCATATACTGTGAACTTCAA	AAGGTTATAGTAAATACTTAT		
145414	LOC145414	XM_085138	CTTGGGATTTACAGCAATTAA	CTGCATGATGTCTCACAGAAA		
145501	THSD3	NM_182509	CAGCACCGACTTCTCACCTAA	CAAGAGCGACTTCCTAATCAA		
145645	MGC33951	NM_152448	TGGATGGTTTCTAATAATAAA	CAGAGCCTTGATTACATAGAA		
145660	LOC145660	XM_085200	CCAGCTCATTTGGTCACATAA	CCGGCTGAGGTGTTCAATAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
145773	MGC26690	NM_152450	CAGGAATACTTTAACAATTAA	TCCCAGTAGATTAGACTTCAA		
145790	UNC13C	XM_496070	ATGCAGTAGGAGAACAATGTA	CACTGCAAGCTAAATACATAA	ATGGGAATGTTTAGTTCACTA	CAAGCTGATCTAATACGTTAA
145846	LOC145846	XM_096883	AAGAAATTCATCAGCCTTCTA	CAGATCAGTGGCAATCATTTA		
145853	LOC145853	XM_096885	CCGCTTCTTCACGGCGCTCAA	AACCTCGGTATTCCAACTTTA		
145946	SPATA8	NM_173499	CCCACTGATTCAGAAGATAAA	ATGGTGTATTCTGGATGTCTA		
145978	FLJ31461	NM_152454	CCAGTAATGAATAATCATTAA	CACATGTGTCTTCACATTCAA		
146057	TTBK2	NM_173500	AGGCATCACCTCAAGATGAAA	AAGAGTAAGCCAGCCAGTAAA	CACATTGGTCATGACATGTTA	ACGGCCCAGGTTAAATGGAAA
146059	CDAN1	NM_138477	CAGCATGAGCCCAATGATGAA	CCGGAGGATGGTGACTGCCAA		
146110	LOC146110	XM_018432	CAGGGACTCAGTATGAACCTA	CAGCATTCTATGTGCAAGATA	CAGTATGAACCTACTGTCAAA	CTGCAGTCGTTCCGACACAAA
146167	LOC146167	XM_085347	CGGGCTGGTCATCCTGGGCTA	CGCTGTCTTCATCCTCATGAA		
146310	RNF151	XM_370927	CCGCCTGGAAGTCAAGTGCAA	CAGGGCCAACATACCTTGTAA	AAGGTTGTCCACATGAATAAA	TCCGGTGGCTAGCCAGACAAA
146378	FLJ25404	XM_375333	CCAGTTCTGCACCCACATAAA	GCCCAGTTTATTGGAGAGAAA		
146723	FLJ31882	NM_152460	CAGCACAATTTGCGATTGAAA	TCCAATCATAGTTGAGAACAA		
146849	FLJ32734	NM_144681	CCGCGCCATGAAGAAAGCCAA	CTGGGCGTTAAGGAAGCCCAA		
146880	MGC40489	XM_373742	CCGGAGCTGGCAGGTCTACAA	CTCACTGGTTATAGTGCTATA		
147011	PROCA1	NM_152465	CAGGACGACGCTCACAATTGA	CACAATTGAAAGATGGACTAA	CAGACGTGAGCCGATCATTAA	CAGGGTGGTCAGGGTGCAGAA
147179	WIRE	NM_133264	AAGCTTGGCAGGTATATTATA	CAGAGGATATATCCCAGCAAA	CAGGTATATTATATTTCATCA	CCCGCCTACAACAGAGAGAAA
147199	SCGB1C1	NM_145651	CACATGGAAATGTATCCTCAA	ATGGACTTCCTGCAAACACTA		
147339	C18orf25	NM_001008239	AAGAATCAGAATGTACCATAA	CAGTTTATTCTTGGCAATCAA		
147381	CBLN2	NM_182511	AAGGTCTTAAGGAGAAATGAA	CTGAATCATATAAGTTGGTAA		
147687	MGC34079	NM_152475	AACGTCATTCATCCACATTAA	CAAGAACTTTATGTTATCCAA		
147808	LOC147808	NM_203374	CCCATTGTGGTCCGTCCTTAA	TTCAGTTCTGTTCCTATTAAA		
147945	NALP4	NM_134444	AACAACAAGCTTGGAACATAA	AAGAAGCTAACTTTCATATTA		
147968	CAPN12	NM_144691	CACGCCCTGGGAAGAAAGCTA	GACAGACACAGGAGAAATAAA	CAAACCATCAATTAATATTAA	CAGGGCAGGGTTGCTGAGCAA
148003	LOC148003	XM_086001	TACGTGTGTCTCAATGAGTAT	AAGGTAAATGGTGAATACATT		
148022	TRIF	NM_014261	TACCACCTCTCCAAATACCAA	ATCGGAACAGAAATTCTATAA	CTCCCAGATCTTCGCCAGGAA	ATCATCGGAACAGAAATTCTA
148066	ZNRF4	NM_181710	CACGCGGTCATTCCAACTCAA	ACGGGCCGTGCTGGAAGACAA	CAGCTTTGACTCCACCACCTA	AAGAATAAAGTGGGTTTGAAA
148103	ZNF599	NM_001007247	AAGATTCATACCAGAGTTTAA	AAGAATTATATTAAAGATTCA		
148223	C19orf25	NM_152482	CAGGGTGTCCTGAGTCTCATA	CAGCACATAGACAGCGATGAA		
148252	DIRAS1	NM_145173	CTCGGCCAAGATGAACTACAA	CAGGGTTGTGTCCAACATACA		
148430	LOC148430	XM_042500	CCCTGGAGATCGCGGAGGCAA	CTCCGTGCTGGTGCACCTTAT		
148479	PHF13	NM_153812	CCCTGCCATTTAGGTGCCTAA	CAGCCTGTTAATGAACAGCCA	CAGCTGGTGGTTCTTAGGTTT	ATGGCCCGTGTTCATAACTCA
148523	LOC148523	NM_144697	CAGCTAGGACATCTAGCTTTA	CAGAAGTGTAAAGAACTCCAA		
148545	FLJ32833	NM_152488	ACCGCTGAGAGTGGACAAGCA	CAAGTGTGAAGAGTACAGGAA		
148870	FLJ32825	NM_152492	CAGAATGGAAACCGCACCAAA	CAGGAAGACGAGTGAACCCAA		
148898	LOC148898	NM_001008896	CCCTCCTTGTATATCCTTAAA	ACCCTCCTTGTATATCCTTAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
149041	KIAA2025	XM_086409	CAGCACCTTATCAGCAGGGTA	CTCCATATTCACCTCATCAAA	CTGCAAGCAATTCAGATTAAA	CAGCAAACTTGAACCGACTAA
149095	FLJ32785	NM_152494	AACAGACTCATGGACATTAAA	CACCGTGGAGCTGCAGATCAA	CAGAGACAGTGATGGAATCAA	TACAATGACCTATTGAAGAAA
149466	MGC52423	NM_182517	CCCGGCCAGCTTCTTAATGAA	CAGGCTCTGCACAGTACCCAA		
149478	LOC149478	XM_378860	CACCACAGGCTCGGCGAGAAA	CCCATTGACCTCCAGGACAAA		
149483	FLJ33084	NM_152500	CAGGAGATTCGAGAACTACAA	CCGGCGAGAGGCAGAACTTTA		
149620	LOC149620	XM_086604	AACATTCATAAGTAGGAAATA	CTGCAGAGTACAAGTTGCAAA		
149685	SMAF1	NM_174906	TAGCCACACATGCGCCATGAA	AGGGTGTGGGTCCATATTAAA		
149708	WFDC5	NM_145652	CCAGAGGCTAATTCTGATTTA	CAGAATGAATATTCTTGCAGA		
149709	LOC149709	XM_086637	CAAGAAGTGTTGCTACTACAA	CTGAGCTCTTCTAACACTAAA		
150051	LOC150051	XM_097792	CTGGGATGTATGTTCCTTACA	ACGCTGTGGAAGATAAACCTA		
150142	C21orf121	NM_198078	CCAGATCTCCGTGAAATTAAA	CCCACTGATGGTGGTTCACAA		
150147	C21orf128	NM_152507	CAGGCAAATGTTGGGAAGCAA	CACAAGTGAGTTAACATTTCA		
150159	LOC150159	NM_139173	CCTAATAATACTGCACATGAA	CATGCATACCACAGAATCAAA	TAAGAGGAGTATTGAATGTAA	CTCATTGATCCTAATAATACT
150209	FLJ30473	NM_144704	AACTAAGAAGGTCGTGTTCAA	CCGGGTGAAGTTCTACATGCA	CAGAAGATGCTCAACCCTCAA	AACATGTTAGACATTACCGTA
150244	FLJ31568	NM_152509	TCGCAGCCTGTCCTACAATAA	CTGGCATTTCTTTGATAACAT		
150248	C22orf15	NM_182520	CTGGCTGAGGATGGCAACCTA	CACCAACTCCACGCACATATA		
150291	FLJ35801	NM_153044	CACAGTGATACAAAGAATGAA	CAGGTTAGTGGTACAAAGTCA		
150353	DNAJB7	NM_145174	CCAAACATGTATCTCAATATA	CTGCGGACAATTAGTATTCAA	CAGGTTCAGACTACACAATTA	ACGACAGTCCGGGTAACATAA
150383	LOC150383	NM_001008917	CCGGGAGAACATCAATGCTTT	ATGCAGTTTATTCTACTCCAA		
150696	PROM2	NM_144707	CAGCATCATCTTTGCCGTCAA	CTGCATCTTATAAACCAGCAA		
150709	FLJ25415	XM_371586	ACGGGTATTGTGTATAGGAAA	CTCAATTACATGAACAATTTA		
151011	NA	NM_144710	CTCCAGGAAAGTAATGTTCAA	AAGGTGGATGTGAAACATGAA		
151121	LOC151121	XM_379133	TTGAATGAGTACAGTAATGAA	AAGCAACACATCTAACTTATA		
151242	PPP1R1C	XM_087137	AATGAGTTTAATTGACTTCAA	TAGGATTTATGTTATAGATAA	TTGGAACTGGTTAGTACCTAA	CTCGATCTGGAATTACAGCTA
151306	GPBAR1	NM_170699	CTACCTGTACCTCGAAGTCTA	TCGACCTGGACTTGAACTAAA	CAGGACCAAGATGACGCCCAA	AAGCCTCATCATCACCGCGAA
151313	DKFZp434N062	NM_199336	CCCGACATAGGATGAGGGCAT	CTAACAAGACGCAATGGGAAA		
151443	LOC151443	XM_087200	AAGCAAGGATTCTACATCAAA	ACGGCTTCTAATAGAGCTATA		
151449	GDF7	NM_182828	CCGGCCCTGGTCTCCACTCTA	CCACTTCATGATGTCGCTTTA	GCCGTTGCACGTGGACTTCAA	AACAACGTTGTCTACAAGCAA
151516	FLJ25084	NM_152792	TAGGAGCTCAGTACATGTAAA	AAGGTGGCCAATGGTGCTGAA	CAGGAGCTATCCCACTGAGAA	CAAGCTGCTGTTGATGACAAA
151531	UPP2	NM_173355	CAGAATAGGATTCGAGATTTA	CTCACACTAAATTAAATTCAA		
151636	DTX3L	NM_138287	CAGAGGGATATTTGCCTCCTA	AAGAGACAAGTCCTTACTATA	TGGAATGATATTCACCACAAA	TGGGCAAGCATTGGTAATAAA
151742	PPM1L	NM_139245	CTGTAGAGTCACATATATGAA	AAGCGTGAACCCATATTGATA	CTGGTGGTCTTAGGTCTATAA	CAGGACTACGAGAAAGACAAA
151760	LOC151760	XM_098117	CACCTTCAACACCACCACAAA	CCCACAGTAAACGCAAAGTAA		
151887	URB	NM_199511	TCCAGTAATATTGGCCACAAA	AAGGACCTTATTTGGCATATA		
151963	LOC151963	NM_178496	CTGCAAAGCCATCATCATTAA	AAGGGTAAGAAGGACAATGAA		
152028	MGC34923	NM_144717	CAGAATAATCCTTGAGAGAAA	CACCCAGCACTTGCAAGGCTA	CACGGACAAGGGATGAGAGAA	CTGGAGAAACAGTGTACTATT

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
152118	LOC152118	XM_098163	CAGAGAGAAGTGTAAATGACA	TAGTTGTTTGGTCACAAATAA		
152138	LOC152138	XM_093644	TTCTGCAGAGCTGGACTTCAA	CAGAACAATCTCCCTGGGAAA		
152404	IGSF11	NM_152538	CAAGAGCAGAATAGTACTTAA	AACCATTTCAGTATTGATAAA		
152485	LOC152485	NM_178835	AAGGAGAACACTGGTATGGAA	AACACAGATGGTGAAGATTAA		
152519	LOC152519	NM_207330	CAGAATTTCTACAAACTTTGA	CAGAAAGGTATAATCATGTAA		
152579	SCFD2	NM_152540	TACAAGTTCATTAGTTCTAAA	CAGGCTGTCTTTCACAATCCA		
153297	LOC153297	XM_098350	TCGGTCCTATTAAATAACATA	CTCATTTATAATAGTGCCAAA		
153571	CEI	NM_178569	CCCTGAGATTTGTGTTGTCAA	AACGGCATCGAGGCATTTCAA		
153745	MGC26988	NM_130899	ACGGAGATGATCGTCTTTGAA	AACGAAGAGAACCATGAGCAA		
154092	LOC154092	XM_379434	CCGGGTGTGCCCAGAAGTCAA	AAGCACTTAATCATACTTAAA		
154141	OACT1	XM_371801	TCGACTTGCTATCAAAGTGAA	CCGAATATACATCTTCCACTA		
154197	PNLDC1	NM_173516	AAGCAGAATATCCACAGCCTA	AAGGAGAGGCAAACAAGTATA		
154386	C6orf195	NM_152554	CACGGCCGACTTAGTAATTCA	CAGAGGGAGATTAGCAATGAA		
154810	AMOTL1	NM_130847	TAGGTTTGCAAACAAAGTTAA	CAGGAATGATTTGAACTGATA		
157724	SLC7A13	NM_138817	TACCATTGGTAAAGTCTCCAA	CCCAATCTATCTATACCTTAT	CGGGTTCATTATGGTCTATAT	AAGGTTAAACATATGATAGAA
157813	LOC157813	XM_098828	ACCCGCCATAGCAGTGACCAA	CCGAGAAGCCCTGGAGATAAA		
157869	RPESP	NM_153225	CACGGTGTGTGTGGATTGTCA	CAGAGGATGCTGGATACTGTA		
157983	C9orf66	NM_152569	CTGAGACACTAAATAAATATA	CGGCCTCAAACTCAAGATAAA		
158038	FLJ31810	NM_152570	CAGTAGGAGGATAATTAACAA	TGCGGGAATTATCATGATCAA	AAGGCGTTTCATCACCACCAA	ACCCAGGAGGTTCAACATGAA
158056	AEGP	NM_206920	ACGGCGCTGGCTGCAGAAGAA	CACGACCACACCACAGGCCAA	CAGGCTGCAGGTCTCAGGATA	CTCCACCTGGCTTATTATTTA
158228	C9orf122	XM_379636	CAGACCGAGTGAGCCCAGCTA	CACGCTCAGCCGAGCTCATCA		
158248	TTC16	NM_144965	CTGGTGGACTTCTATGCCTTA	CAGGACCTCACCTACTATGAA		
158399	ZNF483	NM_001007169	TAGAGTTGATTTCCCAGCTAA	CAGGATTTGGGTAAAGTCACA		
158511	CSAG1	NM_153478	CCGAACCAGGAACTCAATCAA	CAGCCAGTAATTCCCAGGCAA		
158835	DGAT2L4	NM_001002254	CAGCGATTATTTCCCTCTCAA	TTGGATGTGATTGAACTTTAT		
158880	USP51	NM_201286	AGGCCTGAGAGGGCTAATCAA	CCAGAGACTAGGAAACGTAAA	GAGGACTTACTCTACAGTGAA	CCCAGAGACTAGGAAACGTAA
159163	RBMY1F	NM_152585	TAGATGTAATATCTACCTTAA	CAGGCTCTTTGTCCTACTAAA		
159371	TMEM20	NM_153226	CTCCATTATTCTCTAAATGAA	ACGCTTTATGTTATACATTAA		
159491	C10orf64	NM_173524	CTGGGACATGCTGGAAAGGAA	AAGGCTGAAGACAGAAATGAA		
160065	PATE	NM_138294	CTGGATCACTTTCAATGAGAA	CTCCATCTTCTGCACACGAAA	AAGGAGGAAAGGGTAGTTTAA	AAGCCTGGAAAGAGTGATGAA
160287	LDHAL6A	NM_144972	AAGAATGTGTTTACTGTGTTA	CAGAAGGAGCTCAAGCTTTAA		
160760	TA-PP2C	NM_139283	CTCAATTCTCAGGGACTTTAA	CCCTCAAAGCCTAGAAATTTA	CACAAATTGTACGTAATGATA	AAAGGGATGGTACAAGTCTAA
160851	DGKH	NM_152910	TGGGAGTTCGATTATCAACAA	CTCCTAGTGCTTAGTGGTCAA	CCGGATCTAGATTCCGTAGAT	CAGGTGGAGTATAATGACATA
160897	ITR	NM_180989	CTCCCATTTAACTGAGTATAA	TCAGTTGACAATGACCATGAA	CCCAATCATAATTAAGCCGTA	ATGCCTCATCTTAATAGCTAA
161003	STOML3	NM_145286	CTCCAGATAATTTATAAGTAA	AAGGCATAGAATATAAATGAA		
161725	C15orf16	NM_130901	CTGGTTCTGGCCTATGATCAA	CAGGACGACATTGCCCAAGAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
161823	LOC161823	XM_091156	CAGCTTACTAGTAGCCCTGAA	TCGAAGTTTCTCATCAGGAAA	TAGGTATTTGATAGCAGTTGA	TAAGATAGTTCTGAAAGGTAA
162073	LOC162073	XM_091331	TTCCTTGAAGGTGAACCGTAA	ACCCAAGAATTGGTTCAAATA		
162333	FLJ35757	NM_152598	AAGAGAGAGGTTGTCAAGAAA	AAGCAGAAGATACTACTTTAA		
162394	MGC19764	NM_144975	CAGAGTTAATTCACTATTAAA	TCCATTTAATTTAATAATCAA		
162466	PHOSPHO1	NM_178500	CCGTCCCTATCTATTCAGTTA	TACAACTATAAAGGAGGTGAA	TCGGGTCCGGACAGCCAGTAA	CGCCAACATGTGCAAGCACAA
162494	RHBDL4	NM_138328	CAAGTGGTACTATGACAGCTA	AGGCATGAAGTGCCAGTTCAA		
162605	KRT25D	NM_181535	CTGGGAATTCATCTAAAGATT	AAGACAGTGGTTGAAGAGCTA		
162835	LOC162835	XM_091830	CTGGAACACCTCATCATGCCT	CGCAAGGTGGTTGGCGCTGTA		
162993	LOC162993	XM_091914	CAGCACTTGCTAAACATCTAA	CAGGTATTCCACATACCTTAA		
162998	OR7D2	NM_175883	CCCATGCGTATACATTGTTTA	AACAATTAATCTCCAAGTAAT	ACCAATTACCTGAATAGTGAA	CAGCACGTTGATATACTTTAT
163259	FLJ37099	NM_198459	GTGGGTCTAGATATAAATGAA	AAGGAATAGACTCATCACATA		
163479	FLJ35838	NM_173532	CAGCACTTATCCCAAGACAAA	CAGGGCAACCTGAGATAACAA		
164091	MPRA	NM_178422	CCAGGGAGAGGGAAAGAGTTA	TGGCCTGGATGCAATAAAGTA	TCCTTGGAAGTCCAAACTCTA	CTGAATGGTCTTTGCTAAGAA
164118	LOC164118	XM_089384	CCCTAGCATCTTGGTACCCAA	CAGGCTGGCCAGAACCATGAA		
164153	LOC164153	NM_203412	CAGACCAAGAATAGCAGGAAA	CCCGATGTTCCTCACAGTCAA	GAGGCAGCAGCTGATCAGTAA	CTGCTTGTGCTTCCAGCTTAA
164395	LOC164395	NM_001008409	CTGCATGTTGTGGACATGGAA	CACAGGTTTATTTCAAGGCAA		
164656	TMPRSS6	NM_153609	CCGCCTGATGTTGTTACTCTT	CCGCCTGGGAACTTACTACAA	CACGCTGGGTTGTTACCGCTA	CACGGCCGGGATCACCATCAA
165140	OXER1	NM_148962	CAGGGCGAGGTCTCTCTGGAA	GTCCCTTCCAATATTAATAAA	CCGGGTGGAGGAGACAGGCAA	CCAGCTGATAGTGCCAATCAT
165257	C1QL2	NM_182528	AAGGCCACTCTCGATTCATAA	CCGCATGATCTGGGAACCTTA		
166614	DCAMKL2	NM_152619	CCGCACTATCTACACCATCGA	TACGTGTGTGCATCCAATGAA	CTGAGCTTGACCGTTGCATAA	ACAGATGCTCTGAATCATCAA
166647	GPR125	XM_291111.1	CAGCCTTACTTTGCTCTTATA	CAGGCTTGTATTTAATATAAT	CAGCTTGATAATAGTCTGACA	ATGGATTTGACGGGATCTGAA
166752	FREM3	XM_094074	AAGGAAGGGCTTTATGAGAAA	CTGGCTGATCGTTATGATGAA		
166979	FLJ37927	NM_152623	ACCGCTGAAAGTCATAACCCA	CACTGCTAGGTTGAACATCTA	CAAGGACAACCTATTACCAAA	AAGGAGATTGCAACTGGTCAA
167227	DCP2	NM_152624	TTGGAAATTGTCAAACATTTA	CTGGGTTATCAGAGTAATGAA		
167681	PRSS35	NM_153362	CCGAACCTTAACCAGGGTGAA	AAGGGAGTATCTGTTAGGAGA	TACGGCTAACAGAGACCTGAA	CCGTAGTGAGATCACTTCATA
167838	C6orf198	XM_371849	AAAGACTTCCACTGCAATATA	TGGGTTTCTCTCTCCCTTGTA		
168433	RNF133	NM_139175	CAGTGGAGTGATCATCTATAA	GTGGTTATGATTGGTAACTTA	ACCGGAGATGGCAGCGATTAA	AACGCTATAAGCCTAATGACA
168451	THAP5	NM_182529	TTGGAAGATGAGAAAGAAGTA	CACCATTTAAGATACGTGAAA		
168507	PKD1L1	NM_138295	CACCCTTATGGCATCATGGAA	CACGAATACAGGATGCATTAA	AACGAGTTTCATGGAACCGAA	CAGGTTGACCTCAAAGGTGTA
168544	ZNF467	NM_207336	GTGGATGATTCGGAAGGTGAA	CACCAGCTCATTCACGGCGAA	CCCGCTCTTCTTCTGAGCCTA	CAGGAAAGAGTGGTTATTTAT
169270	ZNF596	NM_173539	CCGCTCGGATTTGTCTTCTTA	CAGCTGTAGCGTTAACACTAA	TACCACTTTGCTCAACCTAAA	CAGCACTTCTATAATAGATCA
169436	C9orf96	NM_153710	CTCGGATCGAATAACGATAAA	CTGCCTGGTGATGGAGTTCAA		
169522	KCNV2	NM_133497	CACGTGATCCATCCTCCTAGA	ACGGAGAATGAGGGCAGCCAA	TACGAGGAGCAGACAGACGAA	CTGGACAGAGGGCAACTATAA
170082	MGC17403	XM_372198	CGGGAGCAAAGAGATGATTAA	CTGACCCATAATGGACATTAA		
170302	ARX	NM_139058	ACCACTCAAGACCAAATGGAA	GACGCCTGATATTGAAGTAAA		
170463	SSBP4	NM_032627	AAACATGTACACTATCATGAA	CCGCGAGAAGTTGGCGCTGTA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
170626	GAGED4	NM_130776	ACAGGCAACCACAGGTTTAAA	CCAGAAGGAGGTGACAGGCAA		
170692	ADAMTS18	NM_139054	AACCAGCATAAAGCAAATGAA	CAGGTTTAATAAGGACACGAA		
171568	POLR3H	NM_138338	CTGGTTCTGTTTGTTTCTCAA	CTGCACATTCATGATCAGAAA		
192669	EIF2C3	NM_024852	AAGGCTGTACAGATTCACCAA	CGGGATGAAATGGCTCATGTA	CTCCTATAGGAAGTATCGCAA	CTGACTGATTCTCATCGGGTA
196051	PPAPDC1	XM_113641	ATCCTTGAATTTGCAAGTGAA	AACAGACAAGACTGAAATTAA		
196264	LOC196264	NM_198275	CACAGTATCAATATTTCATTA	AACCACTTATTTATTGAATAA		
196335	OR56B4	NM_001005181	TACCATTTGCTGGGCATATTA	AGGGTTCATCATGCTCAGGAA	CTCATCATAATCACCATTCAA	ATGGCAGTAGACAGATACATA
196337	LOC196337	XM_113696	CCCATCTTTGATACCTTCATA	CACCTTCATCCTCTCAGATTA	AAGACACAATACGGACACTAA	CAGCTTATTTAAGATCCAGAA
196403	DTX3	NM_178502	TCAGATACAGTTCTCCCTTAA	CACCGTGTGTCTATCCTCATA	CGGCACCATTGTCATCCAGTA	ACCGAATGTCATCACCTGGAA
196463	LOC196463	NM_173542	CAGGCTGATGAGGTACAATGA	CTGGATGAACACGGTGGTGAA		
196743	PAOX	NM_207126	CTGGACACATAAAGCAAGTTA	CACGGAGATGCTGGACACATA	CCGGACTTGAGTCTGAGTTCA	CGGAGATGCTGGACACATAAA
196792	FAM24B	NM_152644	CTGGAGCAGAGGAGCCATTAT	TTGAATAAATGTACACTATTA		
196883	ADCY4	NM_139247	CCCGCCTTCAAATACTATGAA	CCGGCGCAACGAGGATCTCTA	CCCGTAGTAGCTGGAGTTATT	CTCGCCTTCTAAGAACCTCAA
197131	UBR1	NM_174916	CACGTCATATACAGCCTACAA	ATGCAGTAATATGTGACCTAA	AACCCACAATATGGACAGAAA	CAGGAATATTGGGATACTGTA
197187	MGC23284	XM_378628	AAGGCTTTGTGACTAACTCAA	CCCGCCCAGATATAAATATAA		
197258	FUK	NM_145059	CAGAATCATGGCGTCTACCTA	TCCCTATGGCTTAGAGTTGTA	TGGCTTAGAGTTGTAGACTTA	CCGAAGGGAGTTGATTGGACA
197322	LOC197322	NM_174917	CTGGCCTCCCTTAAACCTGAA	CCGGACCTCAGTGGACATCAT		
197358	NOD3	NM_178844	CTGGCTGGGAAGGGCAGTCAA	CAGCTTAGATTTACAGGAGAA	CTCCGGAGACTCAATCTTCAA	CAGGATGATCTCAGAGGCCAT
199692	ZNF627	NM_145295	ACGGTCTAATTTGTGTAGTAA	AACCATGTGCATACAACTTAA		
199897	LOC199897	XM_117152	CAGGACTACTTCATGAGCCAA	CCCACTGGGTTGTGAAATGAA		
199953	RP13-15M17.2	NM_001010866	CAGCAGTGGGTGAGCAGCCAA	CAGCCTCAGTTTGCCATCTAT		
199990	FLJ31031	NM_182533	ATGGATGTGCAAGACCTTGAA	ATCCTTCACTTTAATTTATAA		
200081	DKFZp451J0118	NM_175852	CGCGAGGAGCATATCGACAAA	CACATACTGTGTGGACAATAA	CTGGTGTATCCTTCACATCTA	CCGGACCTATGTGGCAAGGAA
200172	FLJ23878	NM_144990	ACCCATCTGTGTAGCCAAGAA	CTGGAACTTGTGACTGTCAAA		
200186	TORC2	NM_181715	CAGGACTTCATTCACCTCTCA	CCGGCCAATGAGTGACTTCAA		
200213	LOC200213	XM_114156	CCGCTTTAAGCAGGCCACCAA	CAGGGTTATTCTATGGAGTAT		
200312	LOC200312	XM_117224	ACCCACGAAAGTACAAGATCA	CCGCATCTGAAGTTACCCAAA		
200315	APOBEC3A	NM_145699	AAGCAGTATGCTCCCGATCAA	CAATGTATTAATGAAATGAAA		
200350	FOXD4L1	NM_012184	TAGCGTTCCTGCTTCTTGCAA	CCGGACGTTGTTGCAAAGGAG		
200407	CREG2	NM_153836	CAGCAAATCTCTAGAAATTTA	AAGGAGTAGCTTTGACATTAA		
200424	MGC22014	XM_371501	CCGGATCGAGAAGGTCATCTA	CCGGCTCTATGAAACCTTCAA		
200491	LOC200491	XM_117239	AAGACATGCAGTCTCATTGAA	TCCCTGGAGCTCAGAAGCCAA		
200539	ANKRD23	NM_144994	AAGAAGAAACTTGAAAGATTT	CCGGGAGAAGCTGAAATTGGA		
200624	LOC200624	XM_117257	AGCCACCATGCTGACAAGTAA	CAGGTAGTCTGTGGAGCATTA		
200728	TMEM17	NM_198276	ACCATGTTTCTTGACATGGAA	AAACAGTATATTAACCCTAAA		
201163	FLCN	NM_144606	CTCCTTTGCCTGGCTCCTGAA	CGGTCTTTGCTCCTTTACAAA	CAGGCCTGTTGCAGTCTCCAA	CCGGGATATATCAGCCATGAT

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
201175	LOC201175	XM_371057	AAGGGAGTTCCTTACTTACTA	AAGGGAGTTCCTTACTTACTA		
201516	ZSCAN4	NM_152677	AACCAATAAATTTCTGTTGAA	AAGGGATTTCTGAGTTCTCAA		
202018	FLJ90013	NM_153365	AGGGTACTTCCTTGAACATAA	TACCACCAGAATAACCCTTAA	CAGTGTTAACTTTAAGGTATA	TCCGCTTGAATTATTCTGTTA
202020	FLJ39653	NM_152684	CCGCATATAAATGGGCCTTGA	CGGAACCTTATTATTTATGAA		
203054	ADCK5	NM_174922	CTGGGTCCTCCAGGACCTGAA	CTGGGAGATGCTCAAGTTTGA	CCGCTACTTCCTTATGGCTAA	AAGGCCTTTGCTGAGCAGATA
203074	UNQ9391	NM_198464	CAGACCAATGCTGCTGACAAA	TAGCCCATCCATGGAAATAAA	CACCTCGTTGGTGAACTACAA	AGGGAAGAACTCGGTATTCCA
203076	LOC203076	XM_114621	CAGGTGGTCAAGTTCACAGAA	AAGGAAAGAAAGCGAAGGCAA		
203100	HTRA4	NM_153692	TACCTGAAACAATCAATTAAA	ACGATGTAATTGTCAACATAA	CCCGCTCAGGAGGAATTACAA	TAGGCAGTTCTTGGCAGAATA
203859	TMEM16E	NM_213599	TACGTTGATGACGTAAAGAAA	CAGGATCATGCTTGAACTTTA		
204219	LASS3	NM_178842	AACAGTAATGACTACAATAAA	CTGGAGATACCTGGAAATGAA		
204801	NALP11	NM_145007	CAACATAAGATTCGAGTTAAA	CAGCGATATCTGTCAATATAT	GCCAGGTTCAATAATACCTAA	CAGCCATGAGAACGTCAAATA
204851	HIPK1	NM_152696	CGGGCAGTGCTGCTACATCAA	CAGGAGTTCTCACGCAGGGAA	CTGAGCTATGTTTGTAATGCA	AGGGAAGCTGTACACCACTAA
205147	FLJ38377	NM_152698	TCCCAAGTGTTGAGAATCCAA	CAGGAGAGCCTAGGACTCAAA		
205564	SENP5	NM_152699	CACGATTGTGGTCACCTTGAA	CAAGGTTTGCAAGCTAAGAAA	GTGCCTGATTGCCACACTAAA	CAGAACATCGTTCTAATACCA
205655	LOC205655	XM_497917	CTGGTGCTCAGTTGTATGCAA	AATGATGAAGTTGGAAATGAA		
205860	FLJ25801	NM_173553	CACATGGTGTGTGGGATACAA	CAGGTGGCAAGTGGGCATATA	CAGCATGTTCAGAGTACTCCA	CGGGCAGATATCATTCTACAA
206426	MGC26597	NM_152700	AAAGTTGAGGTTATCCTGTAA	CTCTTAGTTTGTAATTTAATA	AGGGTACCACTTATTCTTCAA	ACGGACCCATATACTTTATAA
219402	MTIF3	NM_152912	GAGGAGATATTTCATCAAATA	AAGGCATATAAAGAAACTCAA		
219414	LOC219414	XM_169434	CTGAGTGGATTTGGAAACTGA	AAGGAGCTCGTTGAAATATCA		
219429	OR4C11	NM_001004700	CCGCTTGCACGTCTCACATAA	CTGGATAGGGTCTTTAATACA	CCCTATTTGATTGATCATTAT	TAGGGTCTTTAATACACTCTA
219445	OR7E5P	NM_153024	TTCAAAGTTGTTTACTTATAA	CAGTGACATCAATAACATATA	TAGCGTAAACATCACGACTGA	AACGTTGATGAGGAATAAATT
219464	OR5T2	NM_001004746	CAAGTTTGTTCTAGATTTCAA	CAGGTTATCAATAAAGTATAT		
219469	OR8H1	NM_001005199	CAGATGGCCCTCTTTATACTA	TACGACATTGAAATCATGATA		
219487	OR5M11	NM_001005245	CACCATCGTCTTGGTGTCCTA	AAGACTGTTGAGGAATCTAAA		
219537	CHASM	XM_166203	AAGGAGAAGGCTACTGATGAA	CAGGAGATGACTGGCAGGAAA		
219770	CX40.1	NM_153368	CAGGGTGTCAGGGCACACGAA	CAGGAGGATCGTTTGAGAATA		
219927	MRPL21	NM_181512	AAGGATCTTGTTCGAGTAGAA	CTGATCTTAATTGGAAATGAA		
219928	MRGPRF	NM_145015	GGCGGTGTTCTCCATCCTGAA	AAGGCATTATCAGTGAGCAAA	TAAGGCATTATCAGTGAGCAA	CAGGAGAAGAAAGATCTGTTT
219972	MPEG1	XM_166227	ATGGACGAAGTTGGAGTTCAA	CACCGTGAACTTCAAATTTGA		
219995	MGC35295	NM_152717	CAAGGCTACCACAGAAGGTTA	CCGGAATCCTCCAGAATGGAA	AAGGACAAGGCTACCACAGAA	CGCCTTCAGCGCAGACTTCAA
220001	FLJ32009	NM_152718	AAGCTGCTTGTTCCCACCCAA	CACAGGCAGAATCTTCTATAA		
220032	LOC220032	NM_182833	ATGGCTGAATACTCCAAATAA	AAGGAGTGACTGTGCATATAA		
220081	FLJ32682	XM_495949	CAGATGGAAACTGGTAATTAT	AGGCAAGTTATTCATCACAAA		
220158	GTSCR1	XM_496277	CAGGATAGAAAGACATCACTA	CTGGTTTATTGCTCCTATTTA		
220164	DOK6	NM_152721	ATCGTATGAACAGTTATTTAA	TACGCCAAACCTGGATATTTA	AACCATAATTTGGTGCATTAA	CTGAGCAACATGAAAGATTAA
220416	LOC220416	XM_166971	CCAGTAGAAGTTCAGAAGTTA	CTGACTGTTGATGGGAATGAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
220441	RNF152	NM_173557	TAGGTTAGATATAGACACTAA	TAGGATTTATTTGGTATTAAT		
220717	LOC220717	XM_165448	AAACAAGGAAATAAAGGCTTA	CGGGAAGGTCGTGGTGCTGAT		
220972	MIR	NM_145021	CTGCTAGAGTCTACAGAAGTA	TCCAGCGGGATTGACACTCAA	TGGGAATTAGTGGATGCTAAA	TGGATGCTAAATGGCAATTAA
221044	C10orf49	NM_145314	TTGCTTATGGCTTACAAATAA	TACGAGGAACAAAGGAATGAA		
221060	C10orf111	NM_153244	AAGTACCTATGTAGAACCTAA	CAGGGAATCTTGAGCCCGAAA		
221078	NSUN6	NM_182543	CACCACGGATTCAGTTACTAA	CAAGACACTCGTCACTATTAA	CTCGTCACTATTAATTCGGAA	CAGAAGCAGTTTAATGGATTA
221120	DEPC-1	NM_139178	AAGAATCACTATGGAACCAAA	CACGCACATTTGAGATGAGAA	CAGAGAGGATATAACTTATCA	ATCGCTATCATCTTTAGGCAA
221178	SPATA13	NM_153023	CAGGGACATGCTGTACTACAA	CACGGTGATTACAGCAACATA		
221188	GPR114	NM_153837	CGGGCGTGTCTACAACATCTA	AAGCGGCTTTGTTTCAGCCTA	AGGCATGGGTCTCGAATCTTA	AGCGGCTTTGTTTCAGCCTAA
221223	FLJ31547	NM_145024	CTCAAGGTGCATTACCCGAAA	TTCCATTATCGGAGTCAATAA	CCCGCAATCATTAGCTTCTTT	CAACAAGATTTCTTCAATAAA
221241	C18orf20	NM_152728	CTCCTATTAAACATTTGTTTA	CTGGTTTATCAGCCACACTTA		
221261	C6orf184	XM_168053	ATGGAGGACCATTCCCAGTTA	CCCAGATACCCTAGAATATAA		
221357	GSTA5	NM_153699	CACAGAAGGTATAGTAGATTT	CACGACAGTGACAGAGTTTAA		
221391	OPN5	NM_181744	CAGCCTTTCACCATACTGGAA	CAGCCTTTCACCATACTGGAA	CACCGTAACCACAGTCAGGAA	CGCTGAAATAATGACTATCAA
221393	GPR115	NM_153838	CAGGTAAATGGTCTGGTGCTA	AGGCTCTCACTTTAACATTAA	TAGGCTCTCACTTTAACATTA	TAGGAGAATGTTCCCACTATA
221458	C6orf102	NM_145027	CAGCGTTACCATCGATGACAA	AGCGAGAAAGCTACAAATTTA	AAGATTGTCAAGAACCATTAA	ACGGTCCCAACTCCTCTCTAA
221527	ZBTB12	NM_181842	CGGCAAGTGCTTCACACAGAA	CAGCCAGTTCATTGAGCCCAA		
221656	AOF1	XM_173173	AACCTATTTCATCACTCTAAA	TTGGGTGATAGGACACTTTAA	AGGGACTAAATATGACTTTAA	ATCGATGCGGTATGAAACCAA
221662	RBM24	NM_153020	TAGTAGCTAATAAGAGAGTTA	TAGGAGCGTGGCAGTGGGTAA	AAGGTTAATGATAATGTGGTT	AACGATATATTGCTAGTTTCA
221785	ZNF498	NM_145115	AAGGTAAATGGTAATGACTAA	AAGGGTTTCATTTCTGTTTAA		
221830	TWISTNB	NM_001002926	CACATTCATCTTAACATTGAA	CTGGTTGAAGCTGGTAATCAA		
221895	JAZF1	NM_175061	ACGACCTATTAGAGTAATCTA	CAACAGCTAAACAGTCATAAA	ACGCAACTAGTTGGTGCATAA	ATGAGCCTTATTGACAATTAA
222171	LOC222171	NM_175887	CTGGTGGAAATCGCTCACCAA	CCCGAATCACTTGGCAAATAA		
222183	FLJ37078	NM_153043	TACATTTGACCCTGAGGTTAA	CAACATGGAATTTGCAAGTAA		
222229	DKFZp434K1815	NM_152892	AAGGACCAGGGACACAGCTAA	ATGGCAAGGATGCGTCCTCAA	CACAGCTAACTAACTTATTCA	GACGGTCAATGACAACCTGAA
222255	ATXN7L4	NM_152749	CAGGGAGGTTATGAGGCTTAA	CACGCAGAAGTCAGAATCAAA		
222389	C10orf30	NM_152751	CAGGTTGTACTCCATGAGAAT	AGGAAATTAATGCAAATTCAA		
222546	RFXDC1	NM_173560	CACGCAGATTGTGAAGGATAA	ACCCAGTTTAATAATGACAAA		
222584	C6orf143	XM_294139	CAGAATTATGGGTATGATGTA	TAAGATTAACTTGAAGTTCTA		
222642	BZRPL1	NM_001010873	AAGCACTTGGAGGAAGGCCTA	CAGCACTGATCTGGCATCCCA	CCCATTCTACAAAGTCTTATT	CAGAGGAGTGCTGTGGAGAAA
222658	C6orf69	NM_173562	CGGATGCTCATTAGAGGTTAA	AACATTCGCATTGGAATTGAA	TAGCATCACTGTGGAAATTAA	CCGGTCTGAAGTCATCTATAA
222698	C6orf194	NM_001007531	AAGCAGCAGTTCAGATTCCAA	AAAGAGAAAGATGACAAGTAA		
222699	LOC222699	XM_498063	CAGATGCTCTTTCTCCTCGGA	GGAGCTGGACATGAAGATCAA		
222967	LOC222967	NM_173565	CAGAACGAAGATGCCAGCCAA	CCGGACGGCAGCATGTATGAA	ACCGAGAACATTCGTCCAAAT	CTGGATGCTGAAAGACTTTAA
245934	DEFB121	NM_001011878	AAGAAAGTGAAGTATACTATA	CAGGTGCAGAACAACATGTAA		
246176	GAS2L2	NM_139285	CACAGTGTACCTCGTCAGGAA	CCCGTCCATCTACAAGCTGAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
246181	AFAR3	NM_201252	AAGACGTGTTAAGTTAAAGAA	CAGACTATTATTCGGCCATTA	CACGTTGTATGATTTCGTTTA	CCCGCTTTGTCTAATTTAGAA
246721	POLR2J2	NM_032958	CACCATTAACAAGGACACCAA	TCCGGAAGAGGCCTCTTATTA		
246777	SPESP1	NM_145658	CAGGTGAAACTGCGATAGAAA	CAGAGGAACCTTATATTGAAA		
252839	TMEM9	NM_016456	CAAGGTCATCATTGTCATCTA	CCGGATGCATATACTGAGCAA		
252884	ZNF396	NM_145756	AGGGAAGAGACTCATAGTAAA	ATGGATGATCATCTTAATATA		
252983	STXBP4	NM_178509	AAGAACTGAACTATTATTAAA	CAGCAATTTATTGAACACTAA		
253143	MGC50372	NM_173566	CAGGCATGGAAGCTACATATA	AAGAAGGAGTTTAGTTTAGAA		
253150	MGC14276	NM_153248	AAGGAAATCGAGCTTAATGAA	CACCCAATTCAACTTAATAAA		
253558	LYCAT	NM_001002257	CAGATTAGATATAGCCCTAAA	CAGAATATTATTAAACAATCA		
253582	C6orf191	NM_001010876	CAGAAATAATGTTAAATAGAA	ATGGCTCAACATAAACTATAA		
253650	FLJ35740	NM_147195	ACGGAGAAACAGCGGATGAAA	TAGGTGCTCAAGGGAAGTTTA		
253738	DKFZp667B021(	NM_001005463	CACGTTTAGTATATTAAGACA	CCGGGTGATCCCGAAAGGTTA		
253769	MGC43690	NM_182552	ACAGAATTTGGTAAAGTTAAA	CTGGATGAATGTAGAGAGAAA		
253832	FLJ25952	NM_153251	CAGCATTGACTTAGAGCTACA	CAGAATGATGCCTTAATCTTA		
253962	LOC253962	XM_172968	CTGGCACAGCCGATTCCCAAA	CTGCGAGAAGAGGAAGCCTTA		
254102	EHBP1L1	XM_170658	CAGGGTTAGAAGCTGATACAA	ACCCGTAAGACAGAAATTATA		
254263	CNIH2	NM_182553	CGCGGGCACGCGAGCGTTTAA	CTGGTGCAAACTTGCCTTCTA		
254439	LOC254439	XM_170659	ACGGAGCTTGATGAAGCCAGA	CACGGTGTCCTGATGAAGGAA		
254786	OR6C3	NM_054104	CACATCCATCATGAACAGGAA	CAGGAATAAGACTATTTCCTA		
254950	KRTAP15-1	NM_181623	TTGGATCTCTTGGTTGTGGAA	CCCGCCAGACTAACTACATAA		
255061	TAC4	NM_170685	AAGCCAGTTCTTTGGGCTGAT	CTGGGTAATTGTGGCCTTGGA		
255187	LOC255187	XM_173160	TAGGATTGAGATACACAGTTT	CAGGCACCTTATATCCTCAAA		
255239	ANKK1	NM_178510	CAACATGATGATGATTATTAT	CTGAGTGTCATCAACCTCCTA	GCGGACGGAGTACGCCATCAA	AGGAGCCGAGATGGAAATTTA
255275	LOC255275	XM_171855	CACTGGAACATCATAAGGGAA	CAGCAGGATCCTGAAGCCCAT		
255324	LOC255324	XM_171078	CACCTAGATGGGCCTCTCTAA	CACAATGAAATGAGAAGATAA		
255620	LOC255620	XM_173132	GCCTTAGTTTACCACTTCTTA	CTGGGCTGTTCTGGACTTCAA		
255714	MGC87693	NM_207341	CAGGATCACACTGGCCAACAT	CCCAATAAACAATCATTTCAA		
255738	PCSK9	NM_174936	TCCCTGATTAATGGAGGCTTA	CAGGTCTGGAATGCAAAGTCA		
255743	LOC255743	NM_198278	CAGGCAAATAGTGTCATCGAT	ACGGCAGAATATATGGCTGTA	CTCATGTATATTGGAGGCAAA	CTGGCTTAGACTAGAGTATAA
255967	PAN3	NM_175854	ATGGCTAAAGACCTTAACCAA	AAGGCAAGTTTACATCACAAA	CCGGATACAGAAATCAAGTAA	TACCTATACTTTGATACTGAA
256006	ANKRD31	XM_293911	TCGGCATGTCATAGAGATTTA	CCCAGTAATCGGCAAATTAAA		
256051	ZNF549	NM_153263	AAGCCTTATGTGTGCAATATA	CAGAAGGTACATATAACAGAA		
256076	FLJ35880	NM_153264	AACAGTATACACCAAATGAAA	CAGCTTGGGAGAATACATAAA		
256112	ZNF37B	XM_497219	ATGGGAAATCTTATGCATGTA	CACCTGTGAAGCCAACTATAA		
256130	MGC42090	NM_152774	CAGAAACATTCTAGTACAATA	CTGCTTTGATGTATAGTTAAA		
256144	OR4C3	NM_001004702	CTCCTTGTCTTTATAGGCAAT	TGCAATTAGTTCTATTACTTA	CTGCTACATTGTCATCCTGTA	CTCAGTGACCTTGGAATCTAT

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
256236	NAPSB	XR_000169	CCCGCTGGATGTACTGGTGGA	TGGGACCAAGTTTGCCATTCA	CGGGTGCTCAGAAATCCCAAA	CAGGATTACGTCATCCAGTTT
256309	MGC33607	NM_152775	AAGCAAGTATTTATAAGAATA	AACGAGAATATTTAAGTTTAA		
256356	MGC40579	NM_152776	TCCCTGGATATGACCAGAATA	AACAGTGTTAGGGCAACTTAA	TACCATCTTGTACGAGCAATA	CAGCCAATGGGTGTAATTTCA
256453	LOC256453	XM_172917	ACCTCTTGCCTTTCATTTCAA	CAGGCAAATTCCACAAACATT		
256472	MGC33486	NM_153266	CAGGAGAAGAAGCTTCCAGAA	TTGGAGGAAGTGGAAGCCTAA		
256892	OR51F1	NM_001004752	CAGCGTGATCCTGTTTGTCAT	CACGTGAAATCAGTCTATATA		
257039	LOC257039	XM_172230	TCGACCTACAGTTGAGATAAA	AGGAATCAACAGAGAATGAAA		
257169	C9orf43	NM_152786	AAGAAAGAACTCGGCAGTGAA	CACGGAGAGACCAAAGATGAA		
257177	LOC257177	XM_170909	CCGGATCACTTCCATCGCTGA	CACCTTGTGTCAAGAAGGCAA		
257202	GPX6	NM_182701	AGGGCTAGCGACTGACAGAAA	AACGGCGAGGAGTACATCCAA	CAGACTATCCTGTGTCCCTAA	CCCGAGAAGTTGTGACATCTA
259249	MRGX1	NM_147199	CAGGAACGCCTTCTCCATCTA	CTGATTCTGCTTGGTGTCAAA	CGCCTTATATATTCCCTGTTA	CACGTGGACAGGGAAGTCTTA
259285	TAS2R39	NM_176881	AACATACTTGTCTGAGATCAA	ATGGCTATACATGCAGCTGAA		
260293	CYP4X1	NM_178033	AAGCCGAGTGTTGAATCAGTA	TGGGATGTATTTGCACCTGAA	CACCAATAGACTTTCATATAT	ATAGATGTGATCATTCCTATA
267012	DAOA	NM_172370	CAAGGAAATAACTTCTACCAA	TTGCAACTCTCTGGTCAGTAA	AGGCATTTACAGAGATCATTA	AAGAGAGACGGTAACAAGGAA
280636	C11orf31	NM_170746	AAGTATTTGAGTAATAGAGTA	CTGGTGATGTTGGAACATTAA		
282617	IL28B	NM_172139	CCGGGCCTGTATCCAGCCTCA	AGGGCCAAAGATGCCTTAGAA	CTGCCACATAGCCCAGTTCAA	CAGGCCTTTAAGAGGGCCAAA
282969	C10orf125	NM_198472	ACGGAGTACGAGTCCATCCTA	CTGCAGGGAGACGGCCCTCTA		
282973	C10orf39	NM_194303	CAGCAGAGAATTAAAGAGTTA	CAGCAGAATTCAAGTATTTAA		
283008	FAM22A	NM_001009610	CCCTATGAATGGAATATACAA	CAGATTTACATTGGTTTCTAA		
283092	OR4C13	NM_001001955	AAACAAGACTATCTTATTCAA	CAGCATGTTTGTAGCCTGCTA		
283117	LOC283117	XM_210184	CACCCTGCGAGTCTTCCAGAA	ATAGTTATTGATTCTGACAAA		
283130	LOC283130	NM_182556	TCCCGCCAGGGTTAAACATTA	CACGCCCTTAGACGTGATCAA	CCCGGCTGCCTTCACCTCTTA	GCGCTTCTTCAGAGTCATTAA
283135	FLJ90834	NM_173578	CCCGATTGTATGCTCCATCTA	CAGATGATCAATAAATACTAA		
283140	LOC283140	XM_498528	CGGCACCATCTAACACATTAA	CAGGCAGTCAGCACAAATTTA		
283149	BCL9L	NM_182557	CACCTACTTCTTATCAAAGAA	CAACATGAACATGAACATGAA		
283150	FOXR1	NM_181721	CCCTTCCTCTTTGATCTTTAA	CTGGATGTGGGTAAATCCCAA		
283155	LOC283155	XM_208545	CTCCTTTACAACCATACTTTA	CTGCATTTGATAGCAATGTAA	AAGAAATGTTATAAAGTAGAA	TTGGAACGGATGAAGCATTTA
283162	OR8B4	NM_001005196	CTGAATGACTTTGTTTCAGAA	CAGGGACATTCACCTACTTAA		
283177	LOC283177	XM_378327	CAGGAGCAAGGGTGTCATTTA	AAGGCGCTGTTTCTTAACCAA		
283189	OR9G4	NM_001005284	ACCCATTGCTTTATTCAGGTA	CACAGACTATACAACCACAAA		
283197	MGC39681	NM_174939	CACATTGTGTTGAAAGAAGAA	ATGGATGAATTTAAACAGTTT		
283202	LOC283202	XM_208563	CAGATCACTTGTCCTCCTCAA	AGGCTGTAAGGTCATCGTATA		
283209	PGM2L1	NM_173582	AAGGATTAATGCCAAACTAAA	CAGGTATTAATTTACAAATTA		
283212	FLJ33790	NM_173583	ATGGCTGATGCTAATAATAAT	CAGGGATAGTTTCCAGCTCAA		
283237	MGC29649	NM_173810	ATCCATCTGTTTATTTCTATA	CTGGGCATGTTTGGTTAACAA		
283238	MGC34821	NM_173586	CACCGTTGACTTATCAGGAAA	CACAATAAATTTATCTACATA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
283259	LOC283259	XM_208061	TTGAATTGCATTCTAATGTTA	CAGGCCCTGTTTCTACCTCAA	TTGCATTCTAATGTTATTAAA	ACGAATCAGAATGGCAATATA
283297	OR10A4	XM_208604.1	CACCTCTGTGTTTGAACTGGA	CACCATGGCATATGACCGCTA	CTCAAGGAATAAAGAAGTGAA	ACCATTTACTTGGTTACTTTA
283377	LOC283377	NM_207344	CAGGCCTTTCTCAGACTGTAT	CAGCTTTGTTTGAATTTATTA	AAAGCTAGGCATACAGCCAAA	TACCAGATGGCTGAAGAGTAA
283383	GPR133	NM_198827	TCCGGATGAGATCGCCATGTA	CAAGGAGGGCCTGAAAGTCTA	CAGCATGCACTACTACCTGAA	CAAGCACAGATTGACACGTAA
283389	LOC283389	XM_211009	TGGCAAAGGTTTGGTGAAATA	ATCAGGTTGCTCAGCAATGAA		
283440	LOC283440	XM_211040	TACAATGTTCAAGATAGAGAA	CCGGTACTCATAAACCTTCTA		
283455	KSR2	NM_173598	CAGGCTTACCGTGGACGCCTA	AAGGAAATCCATTACTTCAAA	TCCGTTGTGAGGGATGCCAAA	ATCCGGTGACCTCGAATCCAA
283483	LOC283483	XM_378431	CACACAAAGCTTTCTCTTAAA	AAGGTGGATTTGGAAGAACAA		
283551	LOC283551	XM_378455	CACCTTTGTCTTACAGTTTAT	CCAAATAAATACATAATACAA		
283553	LOC283553	XM_211086	CTCACTGGAGTTGACCATCAA	AAGCAGGAACTTAATTTAGAA		
283579	FLJ25976	NM_174943	CCGCAAGATGCTCACGCGAAA	CCGGAGGGTATGGGAAGAGAA		
283600	C14orf68	NM_207117	ACGCTGCACCTGCCACTTAAA	CAGGATCCAGACGGAGCCAAA	TTGGGAACTGTTGTCAATAAA	CACGGTGAAGGTCAGGATCCA
283601	C14orf70	NM_001007560	AAGGATGTGACTCTCCTAGAA	CCCAGGCAGATGAAAGCTTAA		
283659	FLJ25756	XM_370866	TAGGAAATGAAGAATCTTTAA	CAACAGTAAATTGGTAATTAA		
283677	LOC283677	XM_208778	CCCAGGGCAACTGAAAGTCAA	CTGGCGGGTTTGAGAAATTAA		
283685	FLJ36144	NM_182561	CACTGTGTGAATATAGTCTGA	TCCCTCCAAAGTTCTTTGTAA		
283694	OR4N4	NM_001005241	ATGTGCACCACTCGTGTCATT	CACCACTCGTGTCATTATTAT	TAAGCTGGCTTAAGAGATCAA	AAAGATGCTAACGGTAGCATA
283761	LOC283761	XM_378542	CCCACAGGGTTTGAACTGTAA	CCCAGTCAAGTTGACCTGTAA		
283777	FLJ39743	NM_182562	AAGGGTCCAATTGACTAGAAA	TAGGATGAATATGGACTTTGA		
283848	FLJ37464	NM_173815	CCCACTGAAAGTGGCCAAGAA	CCGTATGATGGACATAGTTCA	AAGAGTGGGCATGAAGCTCAA	CAGGTTGTGACATGGAGCAAA
283902	LOC283902	XM_211251	CCCATGCTAGTTGCAGAGAAA	CAGGACATTATCTCACCATAA		
283933	MGC46336	XM_290712	ACCGCATCTCTGTGAAATAAA	CTCCTTTCCCTTATACATTAA		
284029	FLJ34790	NM_173621	CCGCCCGTTATTGCTGCTCAA	CAGCGACACCATGATGATTTA		
284040	FLJ36674	NM_173622	TAAGAAATCAGTAAATATTAA	CAGGAAGGGAATACAAAGGTA		
284058	LOC284058	NM_015443	CAGAAGAATTGGAGAGATTTA	CAGGTTGAGAGGCATATACAA		
284067	LOC284067	XM_208990	ATCCAATATATCAATGATGAA	ATGCATGTGAATATACAATTA		
284069	MGC34829	XM_208993	CCGCCCTGGCTTCCTCACCAA	CCCGCAGGAGATCCTGATCAA		
284076	FLJ35808	NM_173623	CCAGTTGGTCTTCATCTCCAA	CTGGGAGAGTCCGAACACAAA		
284086	NEK8	NM_178170	CCAGTCGGGTGTGACCATCAA	CAGGAAGCTCAGCGAGTTGTA	CCAGAAGCTGGTGATCATCAA	ACGGACAGTTGGGCACCAATA
284111	SLC13A5	NM_177550	CAGGAGTCATAATGAACATAA	CAGACTGAGGAAGAAAGGAAA		
284114	FLJ36878	NM_178518	CACCCTTACTGCTTCCCATAA	CTGGACGGCACTGAACTGCAA		
284119	PTRF	NM_012232	CAACTTTAAAGTCATGATCTA	GAGGAAAGATTGAATCCTAAA		
284121	LOC284121	NM_001007533	CACGATGGACTGAGCCAGCTT	CGGGACCGGATACATTATTAA		
284131	FLJ35220	NM_173627	TTGGCCAAGGTTAGCGATTAT	TGGGTCTAGGATTCTCAGTAA	ATGGGTGAGAGTTGAAATGAA	AAGAGAGAGATTGGTGTTAAT
284134	LOC284134	XM_211345	TCCATCTGGACTAGCAATAAA	AAAGGTATTGAATGAATTGAA		
284185	FLJ39421	NM_178519	AGGGAGGGAGATGGACTCGAA	AAGGGCTATGGATCTAAATAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
284186	FLJ38792	NM_178520	CACACAAGAGTTCCCTTTCAA	CCCTGCGGGAATTCTATTAAA		
284207	METRNL	NM_001004431	AGGCCTGACCCTGGTACCGAA	AACAGGTGCTCTCATCGTTAA		
284222	C18orf58	XM_290817	GTGTCTTGCAGCAGACTTAAA	AAGTCTGCCAGTGCCTATTAA		
284230	LOC284230	XM_208185	AAGAGAATGCTGGCTATTAAA	CCCACCAGACTTTCTGTAAGA		
284266	CD33L3	NM_213602	CCCAGGAGTCCAATTATGAAA	ACGCATTAGCTTGAGCGTGAA		
284269	LOC284269	XM_209097	CAGGTTTGTGGTGGGAGAGAT	CAGCAGCTCTTCACAGTCTCA		
284273	ZADH2	NM_175907	ACCCGTAGGTACCGTCCTTAA	AACGCTTACATTCAATTCTTT	ACGCTTACATTCAATTCTTTA	TACGATGGTCTCAACACCTTT
284293	LOC284293	XM_209104	AAATGGCACATTTGCATTAAA	GTGGCAAATTCTACCAAGCAA	CAGCTAGACTTTGTGAATGAT	AACAACTATGCAAACATTAAA
284296	LOC284296	NM_175908	CAGGATTTCATTCAAACATGT	CAGAGACATCCTCTACTGAAA		
284312	ZSCAN1	NM_182572	CACACCAAAGGTGGTACCCAA	CCCTTGGAACCTAACAGATAA		
284352	LOC284352	XM_113978	CGCCACGGCCCTGAAGATGAA	CTCGACTGTCTGGACCTGAAA		
284353	NKPD1	NM_198478	AGCCGTGGACATAGCTTCCAA	CAGGGTATACATGCAATAAAT		
284361	LOC284361	NM_175063	CCGGGATGTGGCAGCCCTGAA	CTCCCTGTAAGTCTATTTAAA		
284393	LOC284393	XM_209178	CCGAATTTGTGCCAATAAGTA	ACCAAGTTCAATGCTGATGAA	CCGCACCAAGCTGCAGAACAA	CCCGTTGTTACCGGTATTGTA
284397	LOC284397	XM_209180	CAGGAGGATTAATAGGTGGAA	TCCCATGAGTATGTAGCCATA		
284427	MGC34725	NM_173637	AAGAATTACTTCTGTGGAATA	CTGGGTCAGAAGATTCCTGAA	ATGCATGACAACAACCTTGAA	AATGGTGAACATGTCACACAA
284475	LOC284475	XM_378886	TGGGATTTGGTGAGAATCTTA	AAGGGCAAACTTGAAACATAA		
284485	FLJ36032	XM_371311	AAGAAGTAGAGTGGCTCATAA	CAGACTCGGATTGCTAACGAA		
284498	DKFZp434E141C	XM_209234	CTGGCTTTACAGCAGAAACAA	CTCAGCTTTCTTATCTTTATA		
284593	FAM41C	XM_496333	GAGGACCTTGTGCATGAATAA	TGGAATGAAATGAATTCTCTA		
284610	KFZp434D177-like	XM_371388	CAGCTGAAATGGCACATTCTA	CAGGGCTGTCATCAGCATCAA		
284672	LOC284672	XM_208234	GCGGCAGTTGTGATAAATAAA	AAGCATTTAAATGAAATTGAT	CTGGAGAGAAGTGGACTCCAT	CAGCTTAGGGAAAGAGAGCTA
284988	LOC284988	XM_209429	CAGGGTCCCATTCGGCCTCTT	TTCCGGTTAATTGTTCTGGTA		
284992	FLJ39660	NM_173646	TACACTGAACTTTCACATAAA	AGGATTGTTGTTAATAATATA		
285033	LOC285033	XM_379111	ATGCCACATGATGAATACATA	CAGGTTTCAGATCCCAAGCTA		
285095	LOC285095	XM_211764	CCGGAGGGTCATGGAGAAGGA	CACAGGATCTTCATCATGGAA		
285188	LOC285188	XM_209505	CTGCCTGAACCTCGACTCCAA	AAGGAGCAACTGGACCAGGAA		
285189	PRGA	XM_376111	TGGAGGTTTCTTGAAGACCTA	AAGACCTAGAACATAGAAGAA	CAGAGAAGAATGTGCAGCAAA	ATGAAGATACGTGAAATTCAA
285195	SLC9A9	NM_173653	TACGATATGCTACAGCACCAA	TCGGCTCTTCAGAATGTGGTA	AAGGGAATGCCCAGCTATTTA	CCACTGTTTGTTAGGCCTTAA
285220	EPHA6	XM_114973	CACTGTTTATGTACTCATGTA	CACGTGAATTACACCTTTGAA	AAGGGTTATTTCCGAGCTGAA	CAGGTATGTAATGTAATGGAA
285248	LOC285248	XM_211816	CTCGCAGAAGTTATGGAGAAA	CAGGAAGTATTTATTGTGAAA		
285267	ZNF619	NM_173656	AAGGGAGGAGATAGCCAGGAA	CAGCTAAACATTTCTAAAGAA		
285268	ZNF621	NM_198484	CAGGCTGAACTGTCACTTTAA	CAGCATAAACTCTATGGTTAA		
285296	LOC285296	XM_208312	TGTGGGCAGCTCCCTGAACAA	CTGGGCTGTTCCGGACTTCAA		
285307	LOC285307	XM_211837	TGCCATCTAATCTAACTTCAA	CACGGAATCAAAGAGAACTAA		
285313	IGSF10	NM_178822	CACCAACAAACTATTATTAGA	AAGCAGAATCACAGTCCATAA	ACGCATCAATTTAGGATACAA	CAGGCGTATATCACTGTATAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
285326	LOC285326	XM_211843	CACAAGGACCAAACATATGAA	CAGATGGGATCTCAAAGCCAA		
285335	SLC9A10	NM_183061	AAGCCTCATCAGTTTAATTAA	AAGTTTGTTCCTAAACATAAA		
285362	SUMF1	NM_182760	TTGAGTGATACTAATCATGTA	CAAGTGAAGACCAATATTCAA		
285386	FLJ41238	NM_198485	AACAATGGGATAAGCATTTAA	AAGGATGACTTCCAAATTTAT		
285412	LOC285412	XM_208319	CAGCTGCTACTGTTGCTTCTA	AAGCAGAAATACCAGTGGTAA		
285453	LOC285453	XM_209616	CAGCTGCTTCAGACTACCAAA	ATGGATGAGGATGAATTGGAA	TGGCAGCTACTGCAAGGTTAA	GACATTCTTAATTACAGGTAA
285521	FLJ38991	NM_173827	AAGTATTAGAATAGAACCAAA	CTGGCAATTCCTAGTTAATAA		
285643	LOC285643	XM_209695	CTGCCTGGATCTATAAATGCA	CTGAGTGAGCACCGCCACAAA	AAGGAAGGTATTGCAGCTCGA	GCGGTAGAAGAAGAAGCTCAA
285671	LOC285671	NM_178532	CTGGATCATATGGTAAGTATA	AAGCAAGGAATTGATAACTAA		
285676	ZNF454	NM_182594	CAGGGATTTCAACCTAGCAAA	AAGAGTTCAACTCTTAATAAA		
285692	LOC285692	XM_498992	CAGGAACTCCTTCATAGATGA	CCCAGCCAAGTCAGCATATAA		
285703	LOC285703	XM_209728	ATGAGAGTGAATTCTGAAGAA	CTGGTTGAGCACTCTATACAT		
285733	LOC285733	XM_379432	CTGCACTTGATTACAATGAAA	CTGCAGCATCTTACTACATAA		
285741	LOC285741	XM_209741	CTGCGCTTGCTGCAAGCTTCA	CATGTTATGTATGTTGTCGAA		
285759	FLJ34503	NM_173673	ATTGATTGAATTAATGTTTAA	CAGACTATATTTCATCAGCAA		
285761	DCBLD1	NM_173674	CACAATGACATCTAAGAATTA	ACCGATTAATCTAGAGATAAA		
285770	LOC285770	XM_209753	AAGGTATTGGTGCCTATGAAA	CTCCTGCTATCTTTAAATCAA		
285830	FLJ35429	NM_001003807	ATCTATCATATTAGAAATCAA	AAGGAGAAGAATGACTATTTA		
285940	LOC285940	XM_376585	CTGCATCATCTTTGAGTACTA	CCCGGATGATCCGAAAGACAA	TACAGTCTTTGTGAAATGAAA	GTGAATATGTGAAACAGTAAA
285966	FLJ40722	NM_173678	CTCCTAATAAGTGTTCCATAA	CCCTGGTAACATCATCCTCAA		
285973	NOS3AS	NM_173681	CAGCTCTGGCACAGTCAAGAA	CAGCCTCACCTTTGCTCTCAA		
286094	LOC286094	XM_212170	AAGAATGGACTCTTCTATTAA	CAAGCTGTTTATAAACTATAA		
286122	FLJ37131	NM_173687	AACCATACTGTTAGTCTATTA	CTGGCTTTCCATGACTACCAA		
286183	FLJ39630	NM_173688	CACCGATCTAATGACATTCAA	CAAGTAGTTATTGAACTTCTA		
286187	LOC286187	XM_209936	AAGCATTCTGTTTCTGGAGAA	AAGCAATTCACTCATAAGTAA		
286204	CRB2	NM_173689	ACCGGAGGAGAGACTCATCTA	CAGGGTCAGTTTACTAAGTTA		
286207	C9orf117	XM_209941	CGGGACCAGCTTCCTTAGCAA	CAAGGAGATGAAGGAGTTCTA		
286238	LOC286238	XM_379684	CTCAATGAATATAGAAGGGAA	CAGCCAGGATTCAAACTATAA		
286262	C9orf75	NM_173691	CACAGTGGTGCCCAAGAGGAA	CTCCTCAAGAAAGAAGATGAA		
286327	LOC286327	XM_497054	ATCATTCTCATGAGTCGCAAA	CTGTATATCTGGAATGTTTAA		
286336	C9orf59	NM_033387	CAGCAGAATCCTTATTTATAA	AACCGCATAATTATTCATTAA		
286423	LOC286423	XM_210042	TAGGCAGATCTCCGTGAAGTT	TTGTACCAACGCAATGAACAA		
286453	dJ341D10.1	NM_001007535	TACAAAGACCAGTGAATTATA	TTGAATTCTATTAGTATGTAA		
286561	LOC286561	XM_210515	CTGGGCCAATGTTGTATCCTT	GAGGGAGGAGGCAACCTTGAA		
286749	SALF	NM_172311	TTGCTACAACATCCAGCCTAA	CAGTCTAGGTTCTACATCTTA		
286753	TUSC5	NM_172367	CAGCATTACCCTCATCATCAT	CAGGGAGAGGACAGAAATGAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
286826	LIN9	NM_173083	TTCCTTTAGATGTCTCATAAA	TAGGCTTCCAACACCAAATAA	ACGAGTGGTTCTATTCAAATA	CCAGTAGAATTTCTTATCCAA
286828	CSN1S2A	XM_379270	CCCATTTAGAAGAACATGTAA	CAAGAAGAAACTGCAAATAAA		
317702	VN1R3	NM_174980	TAGCACAAAGACAAATGATTA	CCGATTTATGTGGATTGTCTT	CTGGCAAGTGGAACAGCATAA	CTCAGTGATATTGGATGCAAA
317781	DDX51	NM_175066	CAGGAGAGCCTCGTCCAGAAA	CTGGAGGAGTCTGTCAAGGAA		
326340	ZAR1	NM_175619	CAGCACTTTCAGCTTCAAATA	CACGATTTATACATTGCATAA		
337867	PHGDHL1	NM_177967	TCCGTTGTCCATCACAAACAA	CACGCTGGACATCCAGAGACA	TGCCATTACATTAGCATGTAT	GAGGGTAATGTTACTTCACAA
337976	KRTAP20-2	NM_181616	TACTATGGTGGTCTGCGTTAT	GTGCTACTACAGCAACTACTA		
338328	LOC338328	NM_178172	CTGCAGCTTCCTGCAGAGGAA	CCAGATGACTACGACGAGGAA	AAGTACAGAGTGAGACTTAAA	CACCAGTTCAACACTCCATTA
338382	RAB7B	NM_177403	CAAGGCTGGTGTAGAGAGAAA	AACGAGCAGACTAAGGAGTAA	TCGAGGTACCAGAGCATCTTA	CAGCATCCTCTCCAAGATTAT
338398	TAS2R60	NM_177437	AACTATTTAAGGAACCATCTA	TGGCGATAGCATACGGAGCTA	TCCGATGGCCTTCCCATACAA	CAGGCTGAGAGCTGTGCTGAA
338440	TP53I5	XM_374860	CACGGTGGTGTTCGCCATCTT	CTGCCTCAAGGGCTACGTCAA	GACCATCATCATCATGACCAA	CGGGAGCAGCCAGTTGATGAA
338611	LOC338611	XM_291745	CACAGCCATGTGCAGCCTATT	TCCAAGCAGTATATGAAGCTA		
338645	LOC338645	NM_001009909	CAGACCAATTATGATCCTTAA	AAGGAAATCTTTAATCAATAA		
338657	DLNB14	NM_198489	ATCATTGTCTTTCTTAGGAAA	CAGGACCATCTCTGACATTCA		
338661	LOC338661	XM_290501	AACATTTGTTGTTAATATAAT	AAGTATCCAGGATGACCTGAA		
338692	LOC338692	NM_207354	CACCGTGTTTGAAGTGCCCAA	CCGGAGGAGCTTCATCTTCAA		
338751	OR52L1	NM_001005173	CTGGTAGGGATTCCAGGTTTA	CACCGCTTTGGTCATCATGTA		
338879	RNASE10	XM_292225	AACGCTGGTGCTTAGCAACAA	CTGAATCTGGAGAGTGATCAA		
338949	LOC338949	XM_294751	AACAATGTTTAGAGTCATGAA	CAGAAATGGAATAAATATCAA		
339005	LOC339005	XM_370838	CAAAGTCACATCTTTGTGGCA	GCGAAGTTAGAGCCTAGTGTA		
339022	LOC339022	XM_294775	ATGGATTTATAGAGAACATCA	AGAGAATACATTTAAATTAAA		
339059	FLJ40448	NM_182605	AGGAGAATCACTTTCACTTAA	CACCATCTGGTTGCCTGGCAA		
339065	LOC339065	XM_294794	AAGCTACGATAGAGTCAGATA	CAGGGTAGTGATGACCTCACA		
339145	FLJ44299	NM_198491	CAGCTGAGTAGGGCAAATGAA	CAGAGTGGCTTAGAACAGTAA		
339201	DKFZp762C2414	NM_178542	CCCGGCTGATTGGATTCGTTA	CTCCATGAGGCTGGTCCTGAA		
339210	LOC339210	XM_378687	CTAATAAACATTGGTATTAAA	CTGCAAAGAAATACTTGATAA		
339324	LOC339324	XM_290838	AAACATCACAATATTCATACA	AAACATAATATGGAACAATTA		
339390	LSECtin	NM_198492	CTCCTGGAGCTGATTGCCAAA	AATAAATATTTGAGAAATGAA	CAGCCTGAGGAAGCATCAATA	CTGAGGAAGCATCAATAAATA
339398	LRRN6D	NM_001004432	CACCTTGAGGCTGTCTGGCAA	ATCATTAAACCTGCTGTCAAA	CACGGCTATAAGATTATTTCA	AGCGCTAGTCAGCTAGTCTAA
339403	RLN3R2	NM_181885	CCCGGGAGAGCCGCCCTTCTA	TTCAGACACCTTCGTCTTCAA	CAGGCGGTGGGTCGCAAGCAA	CCGATGCCTGTCAAATTCCTA
339451	KLHL17	NM_198317	CACGCTTGATGGGAACCTGTA	CAGCCTCAACTCCATCGAGAA		
339457	LOC339457	NM_001003808	CAGGCGAAGTTTGACACATTT	CAGGGTGTGGTCAGCCGCAAA		
339483	LOC339483	NM_178546	GCCGCTGACTGTAACATGTAA	TAGGGAGGTCTCAATAATAAA		
339488	TFAP2E	NM_178548	TATGTTGTAATTAAATTTGAA	CTCAAGGAACAAAGAAGATAA		
339512	MGC48998	NM_178550	CAGGGTGAAATGAGCCTTGAA	AAGGGATAATTTATACTTCAA		
339559	ZNF642	NM_198494	CCAGGAATTGTTGACTTTCAA	CAAGTGTAAATTGGTGATTTA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
339669	MGC35206	NM_178552	CTCCGTCTTCTCAGACTACTA	TAGAGGTGTCTTCTACTCAAA		
339766	LOC339766	XM_291007	CAGGATCTTCTTCGACAACGA	CCGGAGGAGATGAACCTGCAA		
339778	LOC339778	XM_496547	AAGGACTTTCTGTCCATCTAA	CACCATCATCCTTACTGATAA		
339788	LOC339788	XM_379074	TTGGTAGAATTTACCTTATAA	CTGAATGTTTGTACCCTCTAA		
339799	LOC339799	XM_290345	CGGAGTTGAGCTGATCATGAA	CACAATGAGTCAGAAGATGAA	TACGCATACTATGACACTGAA	CCGCATGAGCATCAAAGCCTA
339843	LOC339843	XM_290351	CTGGGTTGTGAGCTCCTTGAA	TACCATGGAATGGGTCAGAAA		
339862	LOC339862	XM_376212	CAGCTAAATAATTGCTAAATA	TAGGTTCAACTTCAGCATATA		
339879	LOC339879	XM_291054	CTGGGCGGCACGCACTCTCCA	TAGGCTGGTGACACGTCTCCA		
339983	FLJ37478	NM_178557	CAGCCTGAAACCAACACATTT	CACATTCAGCTTAGAAGTGGA		
339997	LOC339997	XM_295126	TACAGTACATTAGACATTCAA	CAGAGCCTATGTCAATGGCAA		
340024	SLC6A19	NM_001003841	CCAGAAGATCTCCTACCCGAA	CACGAACATCCTGACCCTCAT	CTCGGTGATTGTGTCCATCAT	CAGGTTCAATAAGGACATCGA
340074	LOC340074	XM_379355	CCGGCATACAGTCACCACCAA	ATGCATCTTAATCATTTACAA		
340094	LOC340094	XM_295155	AGGCAATAAACTTAAACAATA	AAAGGCCATTACAATATTTAA		
340096	LOC340096	XM_293943	CTCCGTGGAGAGGGTGCCGGA	CCTGGGAAACCTTGCACTCTA		
340113	LOC340113	XM_379324	CAGATGTTTGTTTCTGCTCTA	AAGGAGCAGAACATCTGTTAA		
340146	SLC35D3	NM_001008783	CAGGTATATGAAGAAGGATTA	CTGGAATATAATTCAGAATTA		
340156	LOC340156	XM_373109	ATCGGGATGCTAAGCAAATAA	AAGCTTCTGGGTAAACACATA	AAGAATAAACATGGACCTTAT	TTGGTGTTGATAAGAAATTAA
340168	LOC340168	XM_291161	AGAGCTAGAGTGATTCCTTAA	ACCAGTTTCCAGCCAATGCAA		
340265	GRID2IP	XM_294249	CAGGACTGTCCGAGTCTACAA	GCGCAGGACTGTCCGAGTCTA		
340267	LOC340267	XM_295195	CTGGTAGGTTGTGCTCAACTT	TACAGGATATCTTATTTGAAA		
340348	MGC50844	NM_178562	GCGGACATACTTAGATCCTAA	CAGCATTGTGCCAGAGTGATA		
340359	LOC340359	XM_294387	AAGGTATGACAGCATCTGCAA	CCGGGAGAAGAGTGAAGCCAA		
340393	LOC340393	XM_291270	CTGCCTGACTCAGATGCCTAA	CCGGAAACTCAACATCAACTA		
340485	ASAH3L	NM_001010887	TTGGGTCAGATGCTTGATGAA	CAACAAGAAATCATCAGTCAA		
340515	LOC340515	XM_379650	ACCAATGTATATGCACTTGTA	TAGGAAGAAGTGGTAAGCTAA		
340526	RGAG4	XM_291322	AAGGATGAAGAAGATGAAGAT	TGGGCAGTCGCTGTCGCATTT		
340542	LOC340542	XM_291335	AACATTGATATGATAGATGGA	AAAGTTAATAAAGCAATTTAA		
340595	FLJ46608	NM_001004308	CTGATTTATAACCTGCATTAA	CTGCAGTAGTTTCTAACTCTA		
340654	LIPL3	XM_291663	CAGCTTTACCACTCTGATGAA	CAGGCAGTGAATTCTGGTGAA	CAGGATACTCCCTCAAATCAA	CAGGACTAAATTGGCTGTTAA
340665	CYP26C1	NM_183374	GCGCTATGGGACAGTGTTCAA	CCGGGTGATGCCCTCGACCTA	CACCTTCGAGCTCGACGGCTA	CTGGAGCGTGATGTATAGCAT
340900	LOC340900	XM_291767	AACCTGGTATTGGAGATGTTA	CTGATTTATTAATTAGCTATA		
340913	LOC340913	XM_291770	AACAGCCATGTGGAAGTAATA	CTGAGTCATGTTTCTACCTAA		
341032	MGC50104	NM_198498	AAGGAGTGAGAGTGAAGCATA	CCGGGCAGACAAGTAACTCAA		
341356	LOC341356	XM_292023	AGGGTGGTGAGAAGAATTACA	ATGGAGTTGGTTTCAAGAAGA		
341418	OR6C4	NM_001005494	ATCCCTTCATATATACTTTAA	CAGCATGACAACAGGAAATAA		
341457	LOC341457	XM_292085	CAGGGAGAAATTTGATGACAA	CACCGTGTTCTTTGACACGGA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
341511	LOC341511	XM_292109	TAAGGACGTTAAAGCCAACAA	CAACATGCTTGTGTTCATTAA		
341784	LOC341784	XM_497370	ACCAACGTTCATGCTGAGGTA	CGGGATCATGAGGGAGTTTCA		
341883	FLJ46156	NM_198499	CTGAACCACAATACAATTAAA	CCGGTTGTTTGTAATATTTCA		
342346	LOC342346	XM_296817	CAGGAGTGCCCTGGCAGGCAA	AAGGACGTGAACACCAAGTTA		
342372	PKD1L3	NM_181536	CCGGTAGAAGACATCCTGGAA	CACCAGTTCTCGGAAATCAAA	ACGGAGATGCCCATTATGAAA	CAGCTGGATGATTTCAATTAT
342538	MGC71999	NM_199290	GAAGCTGTCGGAAACATTCAA	ACAGCATCTGATAGTGGTGAA		
342600	LOC342600	XM_292624	CCCGCTAGGCTTCCTGGGAAA	CTGGATTCTCTGAACACCCAA		
342618	LOC342618	XM_496207	AAGGACTTGTTTCACTGCAAA	CAGGAAGAGGTACAATTTAAA		
342669	LOC342669	XM_292674	CCAAGTGAACCTATCCGCAAA	CAGGGCATCTGCACTGGAGAA		
342853	LOC342853	XM_497574	CAGCATGTGGCACAAGAGACA	CATCAAGATCGCGGAGATCAA		
342931	LOC342931	XM_292796	GGCGCTGGTTTCCATCATCAA	AACGTTGTACTCTCTTCAGAA	GAGGGAAATACCAGTGCTTTA	AACGATCTCATCGTTTCTGAA
342933	LOC342933	XM_292723	AGCCGGGAAGGAGAAACTCAA	ACGTGTGCAATAAATCATTTA		
342934	LOC342934	XM_292724	CTGAATCTGAGAGGTCTCAAA	AAGGAATATCTTATGCAGGAA		
342945	HKR2	NM_181846	CCCGAGCAACCTCTCCAGTTA	CTCAGTATCTACAACACACAA	TAACCTAAAGCTTATCTGTAA	CAGGGTATAAGTATGCTGAGA
342969	LOC342969	XM_292824	CACTCATTCCTCACACCTAAA	ATCGGTTAAGATCGATGGCAA		
342970	LOC342970	XM_292810	AACATTGAAGATCAGTACAAA	CAGGAGGAGAAACCCTATGAA		
342977	NANOS3	XM_292819	ACGCCTGTGCTCTTTCTGCAA	CACCCGAAACTCGGCAGGCAA		
342979	LOC342979	XM_292820	ACCACTGGGCATAGAGAGAAA	ACGGAGGGAGATCTGAATCTA		
343035	C1orf36	NM_183059	TTGAGGGAAGGAAATAATTTA	AAGAGTTGATTGGCTTATTAA		
343169	OR6F1	NM_001005286	CACCTTTGTCTCCTATGTGTA	CTGGGCTTTCCTGGTTCTCAA		
343295	LOC343295	XM_497684	ATGATTGTAAGGGAACAGCAA	CCCATGGAATATGAGCATGAA	TGCCACATTGGTGATCCTCTA	ATGTATAACGATGACCTAGAA
343406	OR10R2	XM_372798	CCCAAGATGCTTATCAACTTA	ATGGAAGGTAGGGATAATGTA	TACAGGTAATTAGATGATTTA	CACAACTGTTATTCTGCCCAA
343413	LOC343413	NM_001004310	CAGGGATGGAAGAATACACCA	CACCAGAAAGGGAAAGATGAA	CAGACATTCACACAAACTTCA	CAGAGAGAGGAGTGAGCCCAA
343472	BARHL2	NM_020063	CACACAGAGTGCAACCAGTAA	CGCCTTATTTCTATCACCCAA		
343505	LOC343505	XM_291607	ACCAAGGAGCTTGATAAAGTA	TTGGCACTAGTTGAACAGAAA		
343563	OR2T29	NM_001004694	AACTGTGAGATTCGTCCTTTA	AACCCTTTAATCTATAGTCTT		
343629	LOC343629	XM_293121	CAGACCTGCATTCATATACAT	CAGAGGTTGAACATACCCTAA		
343990	MGC42367	NM_207362	ATGGAACTTGCCAGAAAGAAA	CACAAGGGTGATGGACATTAA		
344018	FIGLA	NM_001004311	CAGCAAAGTTGATATCCTTAA	TACCTTCTAGAGACAAATAAA		
344065	LOC344065	XM_292895	AAGCTCTTAGTGAGCATTTAA	AAGGATATTTCTGAAGAAGAA		
344165	LOC344165	XM_292957	AAGCCAGAGGATTGCAACCAA	CACGAAGACTGGAATCTGTAA		
344172	LOC344172	XM_497885	ACGGAACCAGTCGGTCAGGAA	CTGAATTCGAATCACTGTTTA		
344328	LOC344328	XM_497894	AAGAGTTAAGAAGGCATGAGA	CAGGATCCGAGCAAAGCTAAA		
344561	GPR148	NM_207364	GAGGATCTATGCAGAGGCCAA	CGCCATTGTGCTGCACACCTA	CCACTTATGACTAACTTCTTA	CAGCACAATATAATAGTGGAA
344709	LOC344709	XM_298233	CAGGACCAACTTCGCAGATCA	AAAGATTCACATGATGAATAA		
344805	TMPRSS7	XM_293599	TAACTATTCAATAACCAAGAA	CCCAGCGTTGTGATGGAGTAA	CCCGAGCTACTATCCTCCAAA	TCGGATTACTCGTCAACCATA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
344807	CD200R2	NM_001008784	AAGGATAGAAGCCACTCAGTA	CCAAGTCTGTTGATTGATTTA	CTGATCATTCTTTATGTGAAA	AGCGTTGTCCTTACTGATCAT
344838	PAQR9	NM_198504	AAGGCGTGTGTCATGATACAA	ATGCATGGAATGTGAACACAA	CAGGGCTTAACCTGCTAGAAA	CACACTCTTCGTGCACTTCTA
344892	RTP2	NM_001004312	CAGCGCTGCCTCTGAAGCCTA	CACATGATGTGGAGAATGCTA	CGGAATGAGAGGATTGCATTA	TAGGGTGTCGTACTTACCATA
345051	LOC345051	XM_293680	CAGAGGCTGGGCGATGTTGAA	CAGGATGATCCCAGCTTTGAT	CCAGCTTTGATTCACTGGAAA	CAGCTTCTTACCTCAGTCAAA
345079	LOC345079	XM_293687	AAGGCCAAGAGCAAGGAAATA	AAGCTGCTGAGAGTTGGTAAA		
345275	SCDR9	NM_178135	AAGAAAGAAGTGGGTGATGTA	TACCAAGACATTTGAGGTCAA	TCCATCGATGATGGAGAGAAA	CTCCCACTACATCAAGACTAA
345378	LOC345378	XM_293802	CTGCTGTTCTGTCTGAATTAA	ACCCTAGTAAATCATCTGCTA		
345537	LOC345537	XM_293868	TAGAATTTAGGTCCCTTGTTA	CTGGATGAGAGATCTTCCTAA		
346007	EGFL11	NM_198283	AACGATCCTGAAGATAATAAT	ATGTGGTAAATTGGACACTAA	GAGGAATAATGCTACATGTAA	AAGCTTGGAGCAAGACATATA
346305	LOC346305	XM_498257	CAGGGAGGCTTCTCAGACCTA	CACGGTGGAGACCATATTGTT		
346517	OR6V1	NM_001001667	CAGGATGCTCTCAGACCTGTT	CAGTAGTACCATCTTTCTGTA		
346702	LOC346702	XM_498271	CAGAAGGTCATTATTCACAAA	AGGCACCAATGGTATCTTCAA	AAGAGCCCTGCTCAAAGTTTA	CTCGTCATGGTTACCATTTCA
347051	SLC10A5	XM_376781	TAGAAATATCCTAATGCTTAT	CAGTGGGATTAGTGTTCTTAA	ATGCCTGTCAATTCTTATATA	ATCAATTGGAATAGTCATCAA
347088	GPR144	NM_182611	CAGCGAGTGGGCCAAGGCCAA	CTGCTGCAAATCTATGAAGTA	CCGAGTCAATGCCTTGGCCAA	CTGGCTCAATGTGCACACAAA
347292	LOC347292	XM_294581	TATGGCCATGGGCCTCTTCAA	AAGCGGCGTGCCATGGAGCTA		
347376	LOC347376	XM_293312	CTGAGTGTTGTGGGTGGGCTA	AACGTGTTTCAGAATACACCA		
347527	LOC347527	XM_293401	CACCGCTGGCTCAGGATCAAA	AAGCTCATTATGTGACTCCTA	GACGTTGGAATTGCATCCTTA	CAGCCATAAGAGAGCATCGTA
347549	LOC347549	XM_293416	CAAGAGGTGGCTGGGAAAGTT	CGCCATGGGCAGAGTGAGGAA		
347689	SOX2OT	XR_000282	CAGGACTTATCAGCTGGGATA	AGGAAGGTTGATTGGAAATAA	CAGGTGTAGATCACCTATTAT	TCCGGGTTCCCAAGAACTAAA
347731	LRRTM3	NM_178011	AAGGCTTGATTTATCAGGCAA	CAGAAATAATACATTAACCAA		
347732	CATSPER3	NM_178019	CCCAATGGTCTTGGATGATTT	CAGACAATGGTGACCATGATA	GCCCAACATTCAAGAAATTTA	CCGTTTCTTTAAGATAATTAT
347734	SLC35B2	NM_178148	CTCGCAGTTCCTGGTGCTAAT	CCCTGTCATGCTGATGGGAAA	CCCGATGTGGCAGGCCCTGAA	CAGCTTTATGGTACCTGGCTA
347918	FLJ33915	NM_182613	CTGGAGATGTGAATTCCATAA	AAGCATCTAAGAGGCAATGAA		
348035	MGC40069	NM_182615	CAACAGATGTTCATATTTCTA	TACCTTTGATAAGATGGCTAA	AACGGGATTATTCAGTAGGAA	CCCAGTCACCTGACAAATCTA
348094	LOC348094	NM_182703	CACACTGATGCCAGATGTTAA	ATGGACTTTAGTTAATAGTAA		
348174	LOC348174	NM_182619	GACACGGCCATCGGTCACTAA	CACTAATCTGCAGCACCGGAA		
348303	SELV	NM_182704	CAGCAATTTCCGAATCACCTA	ATCGATGAGGAAATCAAGAAA		
348327	ZNF530	NM_020880	CAGGTATCTGTCCTCATTCAA	CTGGATGAGTTCAAACCTTCA		
348487	FLJ36766	NM_182623	CTGTGTCATTGGCAAGGACAA	CCGGGCCCGCGGAGACATGAA		
349136	LOC349136	NM_198285	CAGCACAGATGGCACAGCCAA	CAGGATCCTGGTTGCCAACAA		
349236	LOC349236	NM_182635	ATGCATGACTGGGACAAGAAA	AAGGTGAGACTCCACATGGAA		
349565	NMNAT3	NM_178177	AAGGTCTAAATCACAAGGATA	AAGGGATAAATAATAAATTGA		
350383	GPR142	NM_181790	ATGGTGTCCCATGCACAGAAA	CAGGAGGCCCTCCTACTACTA	AACACTGGACGAGGTCCTCAA	CCGGGTCTTCGTCATGCTCTA
353145	LCE3E	NM_178435	CTGACGCATGCCTTCCCATAT	AGCGATCTTTGGAGGAAACAA		
353299	RGSL1	NM_181572	CAGGTCATTAGCCAGAATAAA	CCCGCTCTTACTTACAGTATA		
353376	TICAM2	NM_021649	CAGGAAGTATTTCTCATTTAG	CTCCGTTAACAGGCAGCATAA	TCGGGTACTATCACCCAGAAA	TTGCCTGAGATGAAACATATA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
353514	LIR9	NM_021250	ACGGCTGAGATTCGACAGGTT	CAGGAATACCGTCTGGTTAAA		
359948	IRF2BP2	NM_182972	CCTGATCTTAGTAGCAGACAA	CTCCGTCCTCTATGAACCAAA	CCCAATGATTACCCTTAATTA	CTGCTTGAATTGTATATATAT
360023	FRBZ1	NM_194314	AAGGCAGATAGTATATATATA	AAGCCTAATGTCTGTAATTAA		
360132	FKBP9L	NM_182827	GAGGACCGTGTATGAGAGAAA	CTGGAATATTCTGTCATAAGA		
373856	USP41	XM_036729	ATGCAAGCTACTGTGAATTAA	CAGCAGGATGACTATCCTTGA		
373863	DND1	NM_194249	GAGGGTGAATCCAGAGAACAA	CAGCCCTGTGTTCCTCACCAA		
374355	C10orf96	XM_495849	AAAGAGTGAATTGATACAAGA	AAACAGTACAGTGAAATTACA		
374383	)KFZp686O2416	NM_001009913	CTGGATCAAGTGGGCATGAAA	TAGGTTGTTAATACTCGTGAA		
374387	)KFZp779M065:	XM_374877	CCAGGAAAGATGAACATCCAA	ACCCTGGAAGGTAGCACATAA		
374618	TEX9	NM_198524	GAGGATGAAATTCAGAATTTA	ACGAAGATGATTACAGTTTAA		
374654	KIF7	NM_198525	TCCGTTACCCTTGACCTGGAA	AAAGAACTGGACCCTCATTTA	TACCCTCACTGGGATCAACAA	TTGGCCAAGAATCATCACGAA
374860	ANKRD30B	XM_371111	CACTTTGAGCCTGCCACTGAA	CAAGAGCTTGGCGATACAGAA		
374890	LOC374890	XM_373798	ATCCAGTTCTATGTCCTATAA	CCAGGCAGGACTGACAATAAA		
374920	LOC374920	NM_199341	CCCGCTGGAGTTCGCCTACTA	ACGGGTAGAGACGAAATGCAA		
374955	LOC374955	NM_198546	CTGGATATTCCTGAAATGCAT	TAGGAGAATACTGTTTACAAA		
375035	LOC375035	NM_199344	CTGAATTCCCATGAATACAAA	AAGCAACAATACATTCTCGAA		
375108	LOC375108	NM_198996	ATGCACTTGCTTGTGAATTAA	TCCAATGGTTTAGGCATTCAA	AAGGATTCCTTCAGAGATTTA	ACCATATAGCAGATTAGATTA
375189	PFN4	NM_199346	AAGAATGAATTAAGGGAGCAA	AAGGACTGTATTTCAAGGGAA		
375295	LOC375295	XM_374020	CCCGCTCAGTTCAATATTTCA	CAGGTTAGACCTGGCAGTAAA		
375298	CERKL	NM_201548	ACACTTGATCTTATTAATTTA	CAGCAGAGAAGTGGTACTTTA		
375318	AQP12	NM_198998	CTCCCAGTGGGCGCCTATGAA	CAGGCCGATGGCAGGTCTTAA		
375341	FLJ43654	NM_198562	AAGGATCTGCTTGATATGATT	ACCAAGTGAAGTATAGTATAA		
375347	FLJ44290	NM_198564	CTGGGTGGTATGGGAAGTGTA	AAGGATTCAACTATATTTATA		
375444	FLJ32363	NM_198566	CTGGTAATTTGTCAAACTGAA	CAACATATTATTAAAGTTTAA		
375484	FLJ44216	NM_198567	CACCAATATTATGTCATTCAA	CCGAAAGGACTTAATAATCAA		
375757	C9orf119	XM_372143	CTGCACCTTGACATTCAGAAA	CAGAAGGGTGTGGACATGATA		
376267	RAB15	NM_198686	CTGCACCAACCTCAACATTAA	AAGGACTATATTTGTACTGTA		
377630	DUB3	NM_201402	TCCGATGTCACAGGCAACAAA	CTGCTGGAGATCTCAAATCAA		
377677	CA13	NM_198584	AAGGGCAATGGGATAAAGCTA	ATGCACTATAAGTTAATATAA	CTCAGTGATGTTAGATGGAAA	CAGAGGGACACTAAGCATTAA
377841	UNQ2492	NM_198585	CACAGTTGAAGGGACAGGCAA	CAGCGTCTACACTCACAGCTA		
378832	C21orf123	NM_199175	CCGTGAAAGGATGGAAACAAA	CTGCAGGAGTGAGCAATTTAA		
379025	FLJ31306	XM_495990	CAGAGCTGTCAGAAAGAATAA	ATGAAACATACTCAAGATTTA		
386678	KRTAP10-11	NM_198692	GTCCAGCTGCTGAGTGCTCAA	AAGCAGGATTCTCCAGTCTCA		
387032	ZNF307	NM_019110	TTGGAAGAAGTCATTTGATAA	CGGAATAGAAGTCTTATTGAA		
387054	FOXD4L3	NM_199358	AAGCACCTGCTCCTCCATGAA	AAGATTAAGCCTAGTTATATA		
387082	SUMO4	NM_001002255	TCCGGTGTTCACCATGGCCAA	TCCGATTTGGTGGGCAACCAA		

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Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
387332	TBPL2	NM_199047	CAGAATATAGTTTCCACTGTA	TACAAGTACGTTACTTATTAA		
387357	C6orf190	NM_001010923	TACGCAGATAATGATCATTAA	AAGCCTGTTTATGAAATTCAA		
387509	GPR153	NM_207370	ACGGGCCTCGTGACCACCATA	CAGGACGTCGGGAGCAGGGAA	GACCACCATAGTCTTCATCTA	CAGCGTTGGCGCCAAGCAGAA
387601	LOC387601	NM_199352	AACGTCATAGTATACCATCAA	CTGCTAGTATTGGACATATAA		
387643	LOC387643	XM_370537	TTGAGTTGTCATGTAGATTAA	CAGGCAGTTTGTGAATATTAA		
387710	LOC387710	XM_373474	CCGGCTCTACTGAACTTCAGA	CTGCTCAGATGTGAGAAGTAA		
387715	LOC387715	XM_373477	CCGGGTGATAGGCATTAACTA	CAGCATCAATGTGAAGCCAAA		
387717	LOC387717	XM_373478	GAGGCAGGCCTCGCCATTTAA	CCCGGCTGGAATCCAGCTCAA		
387720	LOC387720	XM_370584	AACACAATGATTTGACAGGAA	AACAACTAATTTATGGAACAA		
387723	LOC387723	XM_370586	AAAGATAGACTTCTTCTTAAA	CTGAAGAATGAGGAACATAAA		
387748	OR56B1	NM_001005180	CACCAGTTCCTTAATCTTAAA	CACAGCGTGATTATTGCTCCA	ACCCTCTTCGCTATCCATCAA	AAGTCTTATTATACTGTCATA
387750	LOC387750	XM_370607	CAGCAGGCACTGAATATACAA	CAGGCCCATTTCTTTCATCTA		
387753	LOC387753	XM_370611	AAGAAAGACGCCAAAGAGAAA	AACCTATTTCCTATGAATTCA		
387758	LOC387758	NM_203371	AAGAAGATTAATGATCACTTA	CAGGTCTACATTATTTAATTA		
387763	LOC387763	XM_373497	ATGGCTGAAGGCATTTATTTA	AGGGAGAGACTTATACTTTAA		
387781	LOC387781	XM_370634	CACCTACTAAATACAAATAGA	CAGCCAGATATTTGTGGACAA		
387804	LOC387804	XM_370648	CAGCCTCATGTGGGTTTGTAA	CAGGGCCGTGCTGACACATAA		
387820	LOC387820	XM_370665	AACAGAAATGTTAAACTATAA	AAACAGGACATCTATGACAAA		
387823	LOC387823	XM_373519	CCGTGTGATCCTAAACATGTT	ACACCTCTTCCCATCATTTAA		
387825	LOC387825	XM_370668	CAAGGTTGTTAGAGACTTCAA	CAGAAACATGTTGCATGTTAA		
387836	UNQ5792	NM_207375	CAGAAATTGGACAGCCAGTAA	AAGGAGATTCTTGGAAATGGA		
387849	REP15	XM_370686	AAGGAGTACCTTGGATTTGAA	AAGAGAGATAATAAAGTCACA		
387851	AK3L2	NM_001002921	AAGCAGTTGCTGCCAGGCTAA	AAAGCCAGTCATTGAATTATA		
387856	LOC387856	XM_370691	AACCCGTGAATTGTGTAAATA	AACAATTTACCTGGAAATTAA		
387871	LOC387871	XM_373539	TAGGTATTTAATGTATTAATA	AAGGTACTTGAGAAACATTAA		
387873	LOC387873	XM_373541	CTGGGATTACAGAAAGAAGAA	CCCGGCCAAATGAGCTATTTA		
387880	LOC387880	XM_370704	GAGGGAATCATGGCAAGCCAA	CTCAATGGTGAACACCCGAAA		
387882	LOC387882	NM_207376	CACGACAATCTCATCATATTA	ACCAATGTATTTCAACAATTA		
387887	LOC387887	XM_373549	CACAGAGTCTTTCCAACTCAA	AACGCTGTTTCTAGTGCTTAA		
387895	LOC387895	XM_373553	ATGGACAATGAGAAACATGTA	CTCAGTAACAATAACAAGAAA		
387898	LOC387898	XM_373556	CGCGCAGATAATCTGGCATAA	CTCTTGGGACTCAGAAATCAA		
387911	LOC387911	NM_001007537	AAAGGCATCAAAGGTGATCAA	AAAGGAGATCGAGGAGAGAAA		
387917	LOC387917	XM_373562	ACAGGTGAAGAAACCCTTTAA	AAGGATGCTCTTGACGCCAAA		
387923	C13orf21	XM_370724	AAGGAACTGGCTGGCCCTGAA	ACCGGCAACTGAGATGTTTAA		
387930	LOC387930	XM_370727	CAACATTTCTGGCAATTTCTA	AGGCATCAACATTTCTGGCAA		
387937	LOC387937	XM_373569	CTGGACATCATTTAGCATATA	CAGGAAAGAGATTACTTGGAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
387950	LOC387950	XM_373578	CCGGGCATTGGTGTTTGCAAA	AAGGAGGAAACGGATCACCAA		
387974	LOC387974	XM_373583	ATCGGATTCATCTGACATTTA	CTGGTTTAAATGCCACCTTTA		
387991	LOC387991	XM_370763	CCCAGAAACAAGGCAAATGAA	CAGATACATCAAATAAAGTTA		
387992	LOC387992	XM_373594	TAACAGATCTTTGAACACTAA	CACTTAAAGAAGAGAATTTAA		
388007	SERPINA13	NM_207378	CAACATAGACTTTGCCTTCAA	CCAAATGCTTTCTATCTCTTA	TCCGTGCATGATTGCTTTGAA	AAGGATAGTAATGGTGATCAA
388019	LOC388019	XM_373611	CAGCAATACAGTCACATTCCA	CAGGGTGTGTTTGCTGGATTA		
388021	FLJ42486	NM_207379	CTCAAATGAGAATCAGCTTAA	CACGCTCTTCTTCCTATGCAA		
388022	LOC388022	XM_370779	CTCCACAGAACTGCCAGTAAA	ACACGCTAAGTTTATGTTTAA		
388069	LOC388069	XM_370829	TTACAATGCAGTAAACTTTAA	AAGGAACCATGGAAATAACAA		
388076	LOC388076	XM_370833	AAGAAATATCATGAAAGGAAA	AACGATCATCGATGTTGTCTA		
388116	LOC388116	XM_370856	CAAAGCAGAAACGGAATTACA	CACCTGGTGAATGAAATCAAT		
388129	LOC388129	XM_373631	ACGGAGACCCAGGAAAGATAA	CAGCCGAGGGCGAGAAATGAA		
388142	LOC388142	XM_373638	CAGCCCTCACTAGACTACAAA	ACCATAAACCATGCAATACAA		
388143	LOC388143	XM_370879	TCCCTGCGCCATCTTCCAGTA	AACAGGTGTTAATAAATAAAT		
388159	FAM42B	XM_370893	ACAGTTGATCGCAAACTAGTA	CAGATTGACTATCCAGTTTAT		
388166	LOC388166	XM_370898	AAGAGGTTTCAGGCTGCCTTA	CTCCCTTAACATAGACATTGA		
388174	LOC388174	XM_370905	CAGCAATCTCTGCATGCCTTT	CCCAAGAGCTTGTGTATCTTT		
388177	LOC388177	XM_370909	AAGCCCTCTCAAAGACACTAA	ATGGGTGATAGTGGCTTTAAA		
388180	LOC388180	XM_373650	TGCAATCAGACTAGAAGGAAA	CCGGGCATGATTCTCAACTTT		
388205	LOC388205	XM_370930	CAGAACCGATTTGGATTTGGA	AGCCAGGATTCCAGTACAGAA		
388214	LOC388214	XM_373666	GCGGCTGGATCTGTAATGAAA	TAGGCTGATGTTAATAAATAA		
388227	LOC388227	XM_373670	TCCGATGACTTCTGTCCCTAA	CCCGCTGTTGGGAGTCCTTTA		
388231	LOC388231	XM_373671	CAGGAAGAACCTCATACCCAA	CAGCATGTTTCTGATCATATA		
388248	LOC388248	XM_370968	CAGGGATGGAAGTGAAGTGAT	CCAGGTCTTTAGGAGAAGAAA		
388255	LOC388255	XM_370973	CAGCATCTGAATTACACTTAT	CAGAGTTGTGTTCACGAAGAA		
388276	LOC388276	XM_373685	CAGAATGCCAAGCTCCAGTAA	CAGAAGGAGCTTGGGAATACA		
388295	LOC388295	XM_373693	CAGGCAGAATTAGTGACCGAT	CCCAATAAGGCTGCTGACTCA		
388298	LOC388298	XM_370992	CAGCAGGCTAGTGATGGTTAA	CTGGGTGTTTGAAAGAATCAA		
388300	LOC388300	XM_373695	TTGGGATTCATGCTAGATCAA	TTGGCTGTTTCTAGAAAGATA		
388325	UNQ5783	NM_207103	CTCACTGGTAAATAAAGTTAA	ATGGTTCTGAGTGATATTAAA		
388344	LOC388344	XM_371023	ACCGGTCATGCCCATCCGGAA	AAGGGAGACAGTTCTGCTGAA		
388364	UNQ9372	NM_206832	CAAGAGTAGATCTGAGTTTAA	CACCTGATTGTTAAAGATAAA		
388387	FLJ31222	NM_207388	CAGCCTCCAAATTTCTTTAAA	CCGGCTGAAATTGTATACTTT		
388394	LOC388394	NM_203400	CCGGCGCCGCGCGGCGATGAA	TGGAAAGAAATCTTGTAATAA		
388419	LOC388419	XM_371078	CAAGTTCATCAGGTACCTGTA	CGCCAAGTTCTTCGACGTCAA		
388420	LOC388420	XM_373749	TAGCCTTGTTTGGGATACAAA	CAGCTATTTGGCACATTTCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
388428	FLJ44861	NM_207389	CGGGTCCTTCAACTACCTCAA	CAGGTACATCCTGTCCATCAT		
388429	LOC388429	XM_373756	CTGGTGGAAGCTGCAGGAACA	ATGGGCGTCTCCTAACCGTAA		
388489	LOC388489	XM_373786	CACGGTCAGCGTGGCGAAGTA	TCAGATCATCTTCATGTTGAA	CAGGCTGTGCAGGTCCTGGAA	TAGCGTGTTCACCGAGTGGAA
388491	LOC388491	XM_371125	ATGCAGGCACTTGACATTTAT	CACCTTGAACATAACAGGAAA		
388494	LOC388494	XM_373788	CAGGAAGTATTTATCCAATGA	CAGAATCACAAGTGAAATAAA		
388514	LOC388514	XM_371145	ACCCTATATAAAGATCTTCAA	ATCTGCATCATCAACATTATA	CGGGACCCAGTTTATGGGAAA	CGCCTTCAGTACTTTCCACAA
388524	LOC388524	NM_001005472	ATGGAACAGTACATCTATAAA	AAGGAGGAATTTCAGGGTGAA	CACGGAGGCATCTTATGTTAA	CCCGTCGTAACTTAAAGGGAA
388531	FLJ45744	NM_207391	CAGGAGCTTTATTCCCTATTA	CAGCTTTAACTTGGGATTTAA		
388532	LOC388532	XM_371160	CTCACAAGTGTCACCATGGTA	CTGGGATAGCTTCCTGAAATA		
388533	UNQ467	NM_207392	CTGGGTGGTCCTGAGGAAGAA	CTGATTCTCAACCTACCATAA		
388536	MGC62100	NM_206894	CTGGTGGACTTGGAATGTTAA	CAGCGATCACATCTTATTAAA		
388538	LOC388538	XM_371165	AACCTTGGAGTGTACACTGAA	AAGGGCAGACATGGAGAAGAA		
388551	LOC388551	XM_371177	CCGCACAGGCTGCACCATCAA	CAGGCCCTAAAGAACGGCCAA		
388554	LOC388554	XM_371182	CTGGAGTGGGTCCAATATGAA	CACGGCCTTTGTGAAAGCCAA		
388564	LOC388564	XM_371196	CTCCCTCCTCACTTGGATAAA	CAGCGAGTGAGGCCCAGACAA		
388565	LOC388565	XM_371197	CAGCGCTTCGAGCCCATGGAA	CAGGGAGAGTCTGAAGCGCCA		
388566	FLJ26175	NM_001001668	AAGGCTTTCACTGATCACATA	AAGCATAGAGAGGATAAGTAA		
388579	LOC388579	XM_371207	AACAAATGTTCAACATTCAAA	ATGAGGGAGGTGGATGAACAA	CTGGTGTCTGAATATCAGCAA	CCAGCAGATGTTTGATGCTAA
388587	LOC388587	XM_373822	CCGGTTAGAAATGGCCGCGGA	CTGAGTGGATGTAGATGAGAA		
388605	HS6ST1P	XM_371230	CAGAGGTAGCTGCGTCCTGAA	ACCCATCTGTAGCTCCCTCAA		
388616	LOC388616	XM_373837	TACCATGGGATGGTTACTGTA	CCGTGTTATTTGGGAAACTCA		
388621	LOC388621	XM_371243	AAGCCGAGATAGCTTCCTGAA	AAAGAAAGAAGCCAAAGAGAA		
388624	LOC388624	XM_371244	CTGGCACTACTTCTCTCTCAA	AAGGATGTTACCAGTGCCTTA		
388630	LOC388630	XM_371250	AAGGGAGTGGATGTTAGGGAA	CAGGACATCCATGGCCAAATA		
388633	LOC388633	XM_371253	AAGCTTGTATAACACTGACAA	CACATCATTTCTGAATAGGAA		
388648	LOC388648	XM_373852	CCGCCAGCAGCCGGATTACAA	CAGGGATGTGCGGGTTCTCAA		
388652	LOC388652	XM_373854	CTGGCATTGTTTACTGGAGAA	AAGGGAAGTCGACGAAATAAA		
388662	SLC6A17	XM_371280	CACCCTCTCCGTGTCCTACAA	CAGCTACAATAAGCAGGACAA	GTGGTCGAGAATGCTGAGAAA	CTGGATTTATGGAACCAAGAA
388714	LOC388714	XM_371326	CAGGAATATATAAAGACATAT	CCGGATGATTACCCAAACTAT		
388720	LOC388720	XM_371330	CTGACTTACTGTTTCAACAAA	CGGATACAATAGATAATGTAA	AAGGTGGATGAGAATGGCAAA	TCGGATACAATAGATAATGTA
388730	LOC388730	NM_203376	TTGGTGGTGACTACACCTAAA	CTCCCACTTTGTGAAGTTTAA		
388818	LOC388818	NM_203405	CAGCTTCTTTGTTCCAGTGAA	CACCTTCTAGGGATAAATAAA		
388830	LOC388830	XM_371418	CAGGAGGGAAAGTCTAATGAA	AAGAATTGTGTTGGTCATGAA		
388882	LOC388882	NM_001006606	CACCTTGGTGAGAATCAGGAA	CCACAGATACAGATTATTAAA		
388885	LOC388885	XM_373949	ACCGTCAGCCACCTCAGTAGA	AGGCTACTACGTGAAGGAACA		
388900	LOC388900	XM_371466	CAGAGAAGAATTAATGTTGTA	CAGGAAGATGGAGGTCATCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
388903	LOC388903	XM_373962	CGGGAAGCACTTAACCAATGA	CAGCCAATCCTAGCTCGTTAA		
388907	LOC388907	XM_371470	CAGACAATAAACTTAGGGCCA	TTCGTGTAACTGACAGAGATA		
388917	LOC388917	XM_373970	CCATATGAAATTTGCAGTTAA	AGGGAGAATCTCAGACTACAA		
388922	LOC388922	XM_371476	AAGGATAGCAAGACAAATGAA	AAGGAAGTTGAAGGAAATCAA		
388927	LOC388927	XM_371478	CAGCTCCTTTCTCAAGCTTTA	CAGGGCTTTCAAGGTAATGAA		
388929	LOC388929	XM_371480	CCAGATTTATTACAACATAAA	CGCCATAATGTGATAAATAAA		
388931	LOC388931	XM_371481	CACGTTCTTCCAGGTGCCCTA	ACCCAATGTTCACACAAGTAA		
388939	LOC388939	XM_371488	AACCTCTTCATCCCAGCTGAA	AAAGAACAGCTGATTAAACTA		
388942	LOC388942	XM_373981	CAGGTTGACATCACATATGTA	CAGGACGAAGTCACACACTAA		
388954	LOC388954	XM_371495	ATGGAACAGTACATCTATAAA	AGGAGGAATTTCAGGACGGGA		
389002	ANKRD20B	XM_371535	AGAAGTAGTCACCGCCATGAA	GTTATTATTCATATTAATTTA		
389033	LOC389033	XM_374010	GCCAGGCAGCACCCTCTGATA	TCGGACTGAGAGCATTTCCTT		
389055	LOC389055	XM_374016	TAGCAGTGTGTGACACCATAA	CGGGAGTGCTCTGCAACTGAA		
389058	SP5	NM_001003845	CAGGGCGGTTCCAAACTCTAA	CAGCATGATATGTCTCTGTAA		
389067	LOC389067	XM_374021	CAACATTATTGTGACTATCAA	AAGAGTTATAATTACATTTCA		
389070	LOC389070	XM_374022	CAAGTTTCAGTGCTCAATATA	AAGAGATCAGTCATTACAATA		
389075	RESP18	NM_001007089	TAAGGAAGAAATTATCTATAA	CAGATTTGAATCATTAAAGTA		
389077	LOC389077	XM_374025	CACCTTACAGGCTGACCTTAA	TCCCACAAAGTTAGAAGCAAA		
389089	LOC389089	XM_374029	TACAGCATTCTCGACCTGTGA	TGGGAGGCTTGTGTTGAGTTA		
389090	OR6B2	NM_001005853	CCTGAGGAACAAGGAATTTAA	CACCGTGGTCACCGTCTTCTA	CACGCCAATAATTAACCCTTT	TTGGGTCAAACTTCACACTAA
389108	LOC389108	XM_374038	CAGGTTTCTGCCCGCCAAGAA	CACGTAGTTGCGAGAGCCCAA		
389118	LOC389118	NM_001007540	CAGCCTGCCCTGCTTTATAAA	CAGGCACAGCCTGAAGAGGAA		
389123	IQCF2	NM_203424	AAGCATTGAATGGAAGACATT	CAGGGCTAATGAACCATCTAA		
389127	LOC389127	XM_371645	CCCTGGAGACTCATTCCTACA	TCCCGAGGCTACAACACAGAA		
389145	LOC389145	XM_374048	GTGCATATTCCTGATCCTAGT	AGGCATGCCTGCCATCTTCAT		
389147	LOC389147	XM_371663	AAGGCCAGTAAGACCAGGGAA	CAGCACTGGCAAGGCCAGTAA	CACACAGTATTTGTTTCTTCA	AAGGAACAACTGTATCTTATA
389151	LOC389151	XM_371665	AAGGTATATTCTAGACCTCAT	AAATGTTAGTTTATTACTGTA		
389153	LOC389153	XM_374053	CCGGTCCTCTCTTGCCCACTA	TCGGGCTTGGATTTGGAGAAA		
389189	LOC389189	XM_374071	CCGGCTCTGGCTCCAAACAAA	CCGAGTGTGGTTTGCTATCAA		
389197	FLJ46481	NM_207405	CCGGGCTTCCCTTGATGTTAA	ACCGCTGGAGTTAGAAATGTA		
389233	LOC389233	XM_374091	CAGAAAGTCTGAGAAAGGATA	CAGGTTGTCATTGGAAGTCCA		
389239	LOC389239	XM_371714	AAGGATATCTGTCACAGATAT	CACAACTAAATGAAAGCCTAA		
389246	LOC389246	XM_371718	AGACATGAAATATGACATATA	CAGATTGGCTCAGAAACCATA	AAGCAACAGGAAGCAAATGAA	CACCAAGAGTAGACTGATAAA
389247	LOC389247	XM_374099	CAGGATAGAAATTGGAGGCTA	AGGGAATGATTTAGCAATAAA		
389253	LOC389253	XM_374104	CCGGGCAGCTGTCTCCCTCTA	CAGGCGGAATCCATCCAAGTA		
389288	LOC389288	XM_374120	TGGCACCTGAAGAAAGCATTA	AACGCCATTCATTTCTCTAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
389290	LOC389290	XM_374121	AAGGAACTAAGAGTTGCAGAA	CAGCTGAGAATACATACCAAA		
389293	LOC389293	XM_371741	TCCCAGAATAGCCCACATTAA	CACGGGAGAACTCATAATGAA		
389305	LOC389305	XM_371757	AAGAATGAACTAAGGTGTCTA	AACCTTTGTGAAGCTCAACAA		
389308	LOC389308	XM_371758	CAGAATGTCCGGCCTTATATA	CAGCGCCTATATTTGAATAAA		
389321	LOC389321	XM_371769	CAGAATCGAGGCATCTGTTGA	CAGCATCGAGAACAAGCTAAT		
389332	LOC389332	XM_374141	CGCGCTCAGAGCCGCCAGAAA	CGGGCTGTTGTAAAGCCGAAA		
389333	LOC389333	XM_374142	CCGGGACGCCTCACAGCCCAA	CAGGAAGCTCAGAATGGGTTA		
389338	LOC389338	XM_374145	CTCTCCGAATTGAAACACTAA	TAAGAAGATTGGCGAAATTTA		
389342	LOC389342	XM_371781	ACCAAGTTCAATGCTGATGAA	CCAATAAATTCTACTAACTCT		
389345	LOC389345	XM_374150	CACAGAGGCTACAACTAGAAA	CAGGCATTATCGGGACTATAA		
389352	LOC389352	XM_371791	CTGGGAGACAAGAGTCCGGAA	CCGGATGTCCAGAATGATGAA		
389383	UNQ3045	NM_207409	CAGCTTAGTATCTGCACATAA	CAGGGATTGCATCATATTCAT		
389389	LOC389389	XM_371820	TCCAACAAACTGTGTCTTTAA	TAGGATGGGAAACAAGGTTAA		
389390	LOC389390	XM_374167	TTGTTCCAGTTCAATGATTAA	ATGGAATCTGTCTCTCCTTAA		
389398	LOC389398	XM_374170	CAGCTATGATACTCAGAGAAA	CAGGAATATTTCACCCAAGTA		
389413	LOC389413	XM_374175	CTGCATCAACTGCCTCCCTTA	CTCACCTTACTTTCACCTTAA		
389415	LOC389415	XM_374177	CCAGCCCTTTGGAAGAGAGTA	CCAGGCCTTAGCCCTGAGCTA		
389425	LOC389425	XM_371843	AAGACTGATCTTTGCTGGAAA	CTGGCTGTCCTGAAATATTAT	CTGATCTTTGCTGGAAAGCAA	AAGGTGGATGAGAATGGCAAA
389427	LOC389427	XM_371845	GAGGATCAAATTATAGTTTCA	GCGGTTGAATCCAGTCATAAA		
389435	LOC389435	XM_371853	AAGAGCTGAGGAGAAGATTAA	CAAGCAGGCTGTCACCGTGCA		
389458	LOC389458	NM_203393	CCGGATGCTAACACCCAGGAA	CCCAGATGCATTTATTAGAAA		
389469	LOC389469	XM_374203	CAGGATAGTCAAGGACCTCTA	AAGAGAGAATGTAATACACAA		
389533	LOC389533	XM_374226	CCACCTTATATTATAGTCAAA	CAGGCACTCCTTGATGAAATA		
389541	LOC389541	NM_001008395	CGGCTGCACCGCGGCATGAAT	CTGTCTGTGGTCTTTGGAGAA		
389599	LOC389599	XM_372002	CGGGAACGCTGGTAACTACAA	CAGGATTTACATGGCTGGGTA		
389618	LOC389618	XM_372019	CTGGAATGCCTTTGTACATAT	CTTGCCTGAACTTCCCAAGAA		
389634	LOC389634	XM_374252	CAGGGATGGCAGTCCCAGGAT	CCCGCCGCTACCGGGCAGGAA		
389641	LOC389641	XM_374260	TTCAATCTATCTGAAGCTTTA	AAGAGTCTTGAAAGTCCTTAA		
389643	HMFN0672	XM_372035	AAGAGTCATCTTCAATACCTA	TAGAAAGAAATGAAATGATAA		
389674	LOC389674	XM_372050	AAGAATTGGATGCAGCTATGA	AAGCTTGTGTATCATCCATTA		
389676	LOC389676	XM_374276	GAGGATTTAGAGGGCAAGCAA	CAGGACTTTGACAGCATTCAT		
389727	LOC389727	XM_372092	CTGGCGGTGAATGACTTTGAA	CCGGGAGAAGTTCTATGCCAA	CCACGCAGAGATGACAGCCAA	CACGTACACACGGGAGCGCAA
389734	LOC389734	XM_372097	TAGCATTTACATGATGTTTAT	AAGGATTGGAATTAACTTTAT		
389753	LOC389753	XM_372112	CCCAATCTCCTTTGGATATAA	CTGATTTGTGGTCTTCATTTA		
389756	LOC389756	XM_497059	CCCGAGGTGGATGAGGGTGCT	CTGCCTCTTGCCTGCAGCGAT		
389757	LOC389757	XM_372114	CAAGTCCATCTTTGAACAATA	CGGGACCGAGGTGCAGCAGTT		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
389773	LOC389773	XM_374297	AAGAAATTGTAGCGCCAGTAA	AACCTAAATTTAATTAATAAA		
389777	LOC389777	XM_374300	AAGATGCTATGAATCCAGAAA	TCGCATCTGGATAATCCTTCA		
389792	IER5L	NM_203434	TCGAGCCATTGTCGCCTTCTA	CAGAAACAGCAGAAGCGTTAA		
389813	LOC389813	XM_372159	CAACGCCTGCCTCTACTTCAA	GACCGTGTACCAGGACATCAA		
389832	LOC389832	XM_372190	CAGGAGAACGCCAGCCCTTAT	CTACCATAACACTGAAATAAA		
389840	FLJ16518	XM_372199	ATCCCTCTATTCGGGAATTAA	CTGGATGTTCGCGATGGACAA	CTGATTGTTGCTGGACAACAA	GCCGATCAGCATAACATTAAA
389844	LOC389844	XM_372202	GTCCTTGATTCCAATCATGAA	CAGCTGCGAGGTCGCCATCAA		
389846	LOC389846	XM_374325	CAGGATTGGGTGGATAAATAT	CTGGATGCCAATCGAGATTTA		
389848	LOC389848	XM_372204	AAGGAGGAATTTCAGGGTGAA	TCCGGGAATACTGGCCAGGGA		
389878	CXorf35	XM_374333	ATGGGTGGCGATGTTGAAGAA	CAGCACCATACTGGAACTTCA		
389907	LOC389907	XM_372274	CCGCCTGCCAACCGCCTTCAA	CACGCTGGTCACCGTGGGTGA		
389932	tAKR	XM_372302	CAACGGCACTGTGAAGAGAAA	CTCAGCTTATACACACCTGAA	AAGATATATTCTATACCACAA	AAGGTTGCTATGAGTAATGTA
389950	LOC389950	XM_372307	TTGGTGTGTGATGTGGCTTAA	CTGGGTAGTCTGGACAATGCA		
389953	LOC389953	XM_372310	CAGCTAAGGAACACTGTGTAA	CAGGAATGGATTCTCCACATA		
389988	LOC389988	XM_372323	TACATCCAAAGTTGCCCATAA	CTCACTGAGACTGGAGTCGAA	CAGCCAGAGACAAGAAGAGTA	AAGGTTGTTATCTTTATTGAT
390003	LOC390003	XM_497249	CACAACTTATGATGTTTATAA	ATCCGTTACGTTGGTGACCAA	CTCAATGACGTGTACAGTTTA	CAGCATGAGATACACCAACAA
390020	LOC390020	XM_372337	TTCCAACATCATCACCATCAA	ACCCACCTTCTTTGAAATATA		
390036	OR52K1	NM_001005171	CCCAGTGATTGCCCATTGCTA	CCCATGGTCAATCCTATCATA		
390054	OR52A5	NM_001005160	CACAGGTTTGGTTCACACATA	TTAGTTATAATCAAATATGAA		
390058	OR51B6	NM_001004750	TCGGAGTGACATTGACCACAA	ACCCATTTATCTATAGCATTA		
390059	OR51M1	NM_001004756	CACAGATACCACCTTCAATAA	CCCAATCATATACAGCATTAA		
390063	OR51I1	NM_001005288	ATCCATGTTAACAACATTTAT	CAGGCATTCCTGGGATACAAA		
390067	OR52H1	NM_001005289	TCCCAAGATGCCTGCCAGAAA	TCCCAGGATGCCTTACACAAA	CAGATCAGAGATAAGGTTATA	TACCACCATCTTGACTCCCAA
390072	OR52N4	NM_001005175	ACCAGCTTCATTTATTCTGAA	TCCCTTTACTTTCCTCACCAA		
390083	OR56A3	NM_001003443	CCCAAGAAATTAAGCAGGGAA	CTGCGATGATGTCACCATCAA		
390144	OR5D16	NM_001005496	CTCCCTGATATCACTCTCTTA	TAGGCATTGGTATCCATTTAA		
390158	LOC390158	XM_372396	GCCCAAGACAGAAGTTATGAA	CTGGATGATAGTTCATGTAAT		
390167	OR5M10	NM_001004741	CAAGAACATTTGCATCTCTCT	TTACATGTATGGCTTCCTTAA		
390183	LOC390183	XM_495875	TTCCCAGCTTAACAGACTTAA	CAGGAGGGAATTTCTGTCTGA		
390190	OR5B2	NM_001005566	TGGGACAGTAATCTTCATCTA	AAGAAAGTGTTGAGAAGGCAA		
390205	LOC390205	XM_372416	CGGCCTCTGGCTCTACGGCAA	CTGCCTCTGGATCGAGGGCAA		
390212	GPR152	NM_206997	CCAGCCACAGGCAGACACTAA	CAGCTAGATTCTGAGGGTCCA	CAAATGGACACTACCATGGAA	CAGGACCATTCTGTCAGCCTA
390221	LOC390221	XM_497309	CCCACTGCTCTGTGCAGTGAA	CTGGACCTCAGGGTCTAACAA	CTCCTACACCTGCAAGAGCAA	CTGCCTGCAAACGGCACTTTA
390226	LOC390226	XM_495887	TACCAGGAGGCTGGCATTCCA	ACCAGGTTACCATATACTTCA		
390231	LOC390231	XM_372423	CTGGACAAAGAGGAATGACAT	AAGACTCTTGTAATTGGGTTA		
390233	LOC390233	XM_372424	AAGGAAGAGGATAATCACTAT	CTGAGCGAAGCAGACATGGAA	ACCCAGACTATGTGTCATTAA	CACTCTGATTACTCAATCTTA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
390234	LOC390234	XM_372425	AAGCTGAACCTCAACCAAATA	CAAGAGATTTGTTCAATGAAA		
390260	OR6X1	NM_001005188	CACAGTAATCACAGAATTCAT	AAGACTGGTCATGCAAAGTAA		
390264	OR10G4	NM_001004462	ATGGATGCCATGGATGGAGTT	GCACATCCTCAGAGGAAATAA		
390281	LOC390281	XM_497327	AAGCACCTATATGCCCTTCTA	CTGGAAGGACAGGTTGTTAAA		
390282	LOC390282	XM_372447	AAGCTGTTGAGAGAAAGGAAA	AAGGAAAGTTAAGGCCACCAA	CGAGATCATGCTCAACGGTAA	AACGTCAGAGTGAAATATGTA
390284	LOC390284	XM_372448	CCAGACAAACTCAGAGCTTCA	CTGGTGGTGGTCATCGAAGAA		
390335	LOC390335	XM_372466	AAGAAAGAAGCTGCCCAGAAA	CAGCTCTCATCTTGCAGTACA		
390349	LOC390349	XM_372472	CAGGTGTGCAGAGATACTTGA	CAGCACCAATGAAGACAGGAA		
390377	LOC390377	XM_372486	CACCCACCGTTTCATCACCAA	CAGAAGAGCTGGCGTCATGAA		
390387	LOC390387	XM_372490	CAGGGTCTCCATGGCCTGTCA	ATGACTCTGATTCCACATTAA		
390407	LOC390407	XM_497376	AGGTAGATGGTTTGACCTTAA	TCGAGACATCAGGACCTTCTA		
390421	LOC390421	XM_497382	CTGCCTGCATTTGTTCCTAAA	CAGGAGTGAGATCCCACCCAA		
390429	OR4N2	NM_001004723	AACAGTGATAAGAGAATTCAT	AAGGTGTTTAATAAGCACATA		
390442	OR11H4	NM_001004479	TTGGATTCCTTGGATACCCAA	TGGGACAGTCATGGTAATGTA		
390443	RNASE9	NM_001001673	AACGTATTCCTCATACTATAA	AAGGAGTGTATTGTAATTTAA		
390445	OR5AU1	NM_001004731	CAAGAGGAAAGTGATCTCTTA	CTCCTACTTCTTAATTCTCAA		
390529	LOC390529	XM_372542	GACCCTGGAGGAAGAAGCAAA	CAGGCGTTTGCTGCCTCCTTA		
390550	LOC390550	XM_374354	CCCACTCTCATGGATGCCTTA	ACACTCAGTATTGGTAGATAA		
390551	LOC390551	XM_372556	CTGAGGTGGGTCTGACTCAGA	AAGCAGGTAGGTGCGAATGAA		
390560	DNM1DN4-1	XM_497444	AGCAGTGTTTCTTCTCTATCA	CAGCTTCATCATCCTGGTTCA		
390564	LOC390564	XM_372562	ACCGATGGGTACAGAGGCCCA	CTCCCTACTCTTTGCGAGGAA	CAGGGTCAGCCGAATGCCAGA	ATGGACGACCTTCTGAACAAA
390570	LOC390570	XM_372566	CTGTCTCACCGAAGATGTTAA	CACGAATGTACCAGTGAACAA		
390577	LOC390577	XM_372569	CCGAGCTGGGTCGGAGCATGA	TGGCCCGGAGTTAGAGGCCAA		
390641	LOC390641	XM_497469	CAGGTGGACATGTAAAGAAGA	CAGCAGCTGAAGGACAGATAA		
390667	LOC390667	XM_372607	TTGCTCGTGGAGGAAGACCTT	CTGGAGGAACAGTTCCGGAGA		
390736	LOC390736	XM_372641	CGGCTCGATGTCTGCAGGCAA	GTGGAGGAAGATGGACAACTA		
390801	LOC390801	XM_372676	CACACTGAACTTCCAGAACTT	CACCACTGTGGACAACAACTA		
390842	LOC390842	XM_497583	CTGAGGAACCTGCAAGACTCA	ACCAATGACAGTATCCAGTAT		
390919	LOC390919	XM_497622	AAGGGCTTTCCTGCAGCGCAA	CAGAGAAAGTCTATACATCTA		
390975	LOC390975	XM_372749	CTGGTCCACGCAGATGTCAAA	CTGGTCACCCATCGTCAGAAA	CCCGGCAAACAGTCTGAGGAA	ATGAACTAGATCCAAATCCAA
390988	LOC390988	XM_372755	CCGCCTGGAGGAGACCCACAA	GACGGCCATGTTCGACTTCAA		
391039	LOC391039	XM_497673	CACCCTCTATGACACAACCTA	CAAGGACATGAAGATGCATAA		
391053	LOC391053	XM_497689	ATGATGGATAGTGACACCATA	ATGAACAACTCTACAACATAA		
391059	LOC391059	XM_372784	CACCTTTACATGACCCAAGAA	TCCTATAATTTCACAACCAAA	CAGATTGAAGTTACTTTGTCA	CTGAAGGTTCATGGTGCCTTA
391105	LOC391105	XM_497715	CAGCTCTGCTAAGGACTTGAA	TTCATCTGAGTTTGAGATTAA	CAGTTTCATTTGACTCCTCAA	CTGGATTTAACGGAAGTAATT
391109	OR10K1	NM_001004473	CACCCTAATATCTGTGTCATA	CCAAGACTAATTACACTTCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
391123	LOC391123	XM_372802	AAGGTCATTGTCACTGTCCAA	ATGAGGCTAGGTGGGAAGGAA		
391126	LOC391126	XM_497721	GTGACTTCCAACCAAATCAAA	CCACATTCACAGGAAGATTAT		
391137	LOC391137	XM_372805	TTCCTGCTTCACCACCCTCAA	AGGATTCTGCTCAGCCAGTAA		
391142	LOC391142	XM_496426	CCAGCAGAGACACTACAATCA	CAAGAGGGCACGGGAGGCCAA		
391192	OR2L3	NM_001004687	CTCCATATTCCTTATTGCCAA	CACCCTCACTCCAATGCTCAA	ATGGCTCTAATTGGAAACCTA	TAGGATTCTTCCCACCATCAA
391205	LOC391205	XM_372838	CTGGAGGAGCAGCGTCACGCA	CGACATCGTCTCTGCTCTGAA		
391209	LOC391209	XM_372840	CTGGTCGATCGCACTTGTACA	CACGGGCTGTGCTGAATGACA		
391253	C20orf137	XM_372869	CCGAAATAAAGACACAAGAAA	CCGGCTGTAATGGCAACCTTA		
391265	LOC391265	XM_497576	CCCAAGAAGGGCAGAGGAACA	CGGGACCAAGTCTGTCACTAA		
391340	LOC391340	XM_372908	ATCCCTATATTGAGGAGCAAA	CTGCCCATCATCTGTATCCTA		
391347	LOC391347	XM_372913	CAGGCCCTGCTGAGCTAGCAA	CAGATATGTGTTGTCCTGTTA		
391370	LOC391370	XM_372926	CAAAGGCTTTGGTGTGTTCAA	AAGATTGGGCTTCACCCATAA		
391429	LOC391429	XM_372954	CAGATGGCATAGAGCATCCAA	AAGATGGGATAGAGCATCCAA		
391599	LOC391599	XM_497949	CAGGGACTTCATCAGCTGCTA	CAGGACCTGTTTGGAGAACGA	CAGGAGATATTTAGGTACCAA	TCGGACAAGGATGGAAACTTT
391634	LOC391634	XM_496686	CCACATCTACTGCATGATCAA	AAGATTGGATGTTATATATTA		
391711	LOC391711	XM_373037	AAGAGAAGGATGATAAAGAAA	AAGAATTATAAGCACATTTCA		
391717	LOC391717	XM_496725	ATCAGGTGAGAGCGTGTGAAA	CTGGTGAATTTGAGAAGTGTA		
391722	LOC391722	XM_373042	CACCAGAACAGTGGTCATCTT	ACAGAGAAATGTGAATAAGAA		
391730	LOC391730	XM_497990	CTGGATGGAATTCCTTCCCAA	AAGAACTTGCTCCATCATTAA		
391733	LOC391733	XM_373053	GTCAGAGACGGAGAAAGATAA	CACCATCACGGCACACTCCAT		
391769	LOC391769	XM_373079	CACGCAGCTGCTCCTGCGCAA	CTCCGCAGAGAGGGTCCTTAA		
391773	LOC391773	XM_497999	CTCATCAACAATTACGGCCCA	CAGCGTCATGATAACGTGAAC		
391804	LOC391804	XM_498008	CACACTTTCTAGCCCGTACAA	CCGAAGGGCGTAGTCACAGAA		
391819	LOC391819	XM_498013	CTCAGTTTGGAGGAATTGGAA	CCAGGACATGGCGGTCAACAA		
391827	LOC391827	XM_498018	TGGGTTGATGGTGGAGGTAGA	CCCTGGAATCTCTACACTAAA		
391833	LOC391833	XM_498020	CCGGACTTCGCTGCTCCCGAA	CAGGCCAGCAGCATCCTTATA		
392169	LOC392169	XM_499232	ACGGGCGCGGTCAGTGCCTGA	ACGGTGAAGACCTGAGATTTA		
392222	LOC392222	XM_373253	ACGCACCAGTTTCTTGCTTTA	CTGAGTGATGAGGAAATGAAA		
392238	LOC392238	XM_374372	AAGGGAAGAATTACACAGGAA	CAGGTACACGTAAGAAAGAAA		
392262	LOC392262	XM_373263	CACCTATGACACAAATGTCAA	CTGCTGAAGAATCAAGTATAA		
392267	LOC392267	XM_496992	CACCTCAGCCCTTACCTGGAA	TGCCATGGTGTATTACGTCAA		
392281	LOC392281	XM_497005	TGGACCCAAATTGCTTACGAT	CAGGTACATTACTCCTCAGCA		
392309	OR13J1	NM_001004487	CAAGATCCTGGCAGTGCTGAA	CCCTCTGTGCTCAGCCATGTA		
392376	OR13C2	NM_001004481	AAGGGACTTTCTGGTCACCCA	AAGGATGTGAAAGAGGCAGTA		
392392	OR1K1	NM_080859	CCGTGTGGCCACTGTCATGTA	TGGGACAGTCATTGCAGTCTA		
392395	LOC392395	XM_373319	CAGCCAGGCCATCGCCAACTA	TGGGACAAAGAAAGAGACCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
392459	LOC392459	XM_373344	ATGGAGCACCATTTCCATGAA	CAGGCTAGCAACAAAGGTGAA		
392517	NCBP2L	XM_373362	CAGGCCTGTGATTAAGAGCAA	CCCAAGTGTTGTAGCCTTAAA		
392546	LOC392546	XM_373372	GCGGTCCGCATTACTCACATA	CACCCTCTTAACGATGATGGA		
392556	LOC392556	XM_498396	CACTCTATGGAGCCAATCTAA	CACGATTATAATGGAGGGCAA		
392583	LOC392583	XM_374379	CCGCCTTGTGAGCCAGAGCCA	CCAGCGGAGGTCCTCAGGAAA		
392702	LOC392702	XM_374730	CTCCTGGGCAGCGGAAACAAA	CTCCCGGAATCTGGTGGACAA		
392758	LOC392758	XM_374498	TCCAGTGGTCTTTGGAGAACA	CGGCTGCACCGCGGGCATGAA		
392895	LOC392895	XM_499284	AAGGTGCACCAGGTAAGATGA	CAGTGGGAAGAGGAATTTGAA		
399665	EEIG1	NM_203305	CAGGAAGGTTGGAGCAAGCAA	TGGAATCTTCTTGAAAGTTTA		
399668	MGC39606	NM_203306	CAGCGTGAAGGGCCTGAACAA	CAGGTCCTGAATGAAGCTGTA		
399671	MGC48595	NM_203309	CACTATGTTTATAAAGAGAAA	CTGCTTGGATATGAAACATAA		
399706	RP11-529L18.1	XM_378200	AAGAGCTTCGTGTTAGAGAAA	AAGACAAATGAGACAGAGCTA		
399708	LOC399708	XM_378203	CAGGGTATCAAGAGTCAGTAA	AAGGATAGAATTATCCATCTA		
399715	LOC399715	XM_374766	ACCCAATAGCATAAGTATTAA	CAGCCTCAGTACTGTAAGAAA		
399763	LOC399763	XM_374803	CGGTATATAAATAGAATTAAA	CAGGTGTTTCTGAAAGATTAA		
399833	FLJ44653	NM_001001678	AACCCTAAGCCTAAACCTTAA	ACCCTTAACCATAACCCTTAA		
399851	LOC399851	NM_207427	TGGCTTGAACCCAGAGGTGAA	CAGAGTCACACTGGATTTACA		
399919	LOC399919	XM_378299	CTCGCTCAGGTGAGCATTCAA	TAGAGAGGTAATTAAGTTAAA		
399921	LOC399921	XM_374904	CCCATCCAGGAAGGTTATATA	CAGGGTCAAAGTTCTGAGCAT		
399937	LOC399937	XM_374917	AAGAGACAGAATGACAAGATA	CTGAAGCAAATGTACCATAAA	CAGCAACTCAATGAAAGCCAA	CAGAGTGTGAGTGATACTTTA
399940	LOC399940	XM_374920	AAGAGACAGAATGACAAGATA	CTGAAGCAAATGTACCATAAA	CCGGCCCTGTTTCTACCTCAA	CAGCAACTCAATGAAAGCCAA
399961	LOC399961	XM_378317	CTGAGAAATGAAAGTGTGAAA	ATGGTGCTTCCTATAATCCAA		
400047	LOC400047	XM_378363	TTGGACTTGACCCTACTGTAA	AAGGAGTCTTCAGGAATCAAA		
400083	FLJ43808	NM_207438	TACATTTAATATCCCAATTAA	AAGGATGAAATTTGACGAATA		
400099	LOC400099	XM_378399	AAGGTCTGACAGAAACTTTAA	CAGGTTCATGTCCCAATGAAA		
400156	LOC400156	XM_375035	CAAGCTGTATGTGAAGCTACA	AAGGACAACGCCATTAAGAAA		
400201	LOC400201	XM_378449	ATGGAGCTATGAAATGGCAAA	AAGGATATTACCAACAATGGA		
400224	LOC400224	XM_375090	AGGGTGGGTGATGACCTTCTA	AAGAGCTTTGAAACCAATAAA		
400238	LOC400238	XM_378473	CAGGTCAACTGTGGAATTTGA	CACCATTTAGAGGACAATGAA		
400263	LOC400263	XM_378491	AAGAGCCATCATGGTGATCAA	ACGGAGCAACGTCCAGTTTAA		
400353	LOC400353	XM_375183	CAGGCATAACTGAAGGTGAAA	CAGGCAGGAGAATCACCTAAA		
400400	LOC400400	XM_378529	CAGGGTCTCACCTTACAGCAA	CACATCTAGCATGGCATATAA		
400446	LOC400446	XM_496093	AAGGCTTTCTTAGGTGTGAAA	CTGGTTAAGTTGTGTACTAAA		
400475	LOC400475	XM_378553	TTGCAGAGTCTCAATACCCAA	TAGCTATAAATTATCATATAT		
400481	LOC400481	XM_375284	CAGCAGCAACAACAACAACTA	CCCGACCTACCTCCTGTTCAA	AGGCACCTTTCTAGAGATTAA	CAGGGTGAAGAGAATCTTCTA
400496	LOC400496	XM_378562	ACCAATTTAGGTGTAATTTAA	AACGCTTTGCTTTATCATTAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
400523	LOC400523	XM_378582	AACGCAGGATATTGCATCATA	CTCGTGGGTCTTCATACCTAA		
400552	LOC400552	XM_378623	CCAGAGTGTATTGCTTATAAA	ACCGTGTTTGGCAGACATTAA		
400569	MGC88387	NM_001001683	CGCGCTCTGGAAGACATTGAA	CAGAGTGATAATGGCTACCTA		
400586	LOC400586	XM_375424	CCCGCAGAATGGAGGAGATAA	CTGGAGAAACATCATCCTTAT		
400591	FLJ44815	NM_207454	CAGGATTTCATATATAGCAAA	CAGGAGAATGTCAGCAGTGAA		
400619	LOC400619	XM_378703	CTGGAGTAACTATTCCACTAA	CTGAGTCTTCTCTTTCTTCAA		
400623	LOC400623	XM_378708	CTGCGACATTTAGTCCTTTAA	ACCAGTGTGTTTGAGCATTAA		
400624	FLJ45079	NM_001001685	CAGGGTCTGAACTAAGAGCAA	CTGGGTCTGCGTGAAGATAAA		
400642	LOC400642	XM_378735	CACATCTTCCATATACTTTAA	CCAGAGTTTCTTATCAAGTAA		
400651	LOC400651	XM_378747	CAGGCTGAATTTGACGTTAAT	AAGGACATACATGCAAATGAA		
400658	FLJ44313	NM_207460	TCCGCGAGTCCTCAAATGTAA	CAGGGCATTGTCTGTCTACAA		
400664	LOC400664	XM_375549	CTGGTGATTTCCAGTAGGTGA	CGCCCACTAATTCTACATTAT		
400668	PRSSL1	NM_214710	CACACCCATTCCACATGCAAA	CGCCCTGATGCTGCCCGTGAA		
400673	VMAC	XM_375560	TTCGAAAGTGCTGCAGTTATA	CTGTCTGTGCTCAAGAATAAA		
400679	FLJ46230	NM_207463	CCCGGAAGGAAAGGAAAGGAA	CTGGACTTTGGTCAAGTACTA		
400681	LOC400681	XM_375589	GACCCTATATTTGGAATTTAA	TAGATTAAATTGGCTAATTAA		
400684	LOC400684	XM_378793	CCACTGTTTATTTCAGCATAA	CACGAAATCCTCCCATCTCAA		
400685	LOC400685	XM_378795	TAGAGTAATACTGGCCTTATA	CTGCTTGTGGTGGAAACATAA		
400709	SIGLECP16	XM_375634	CTCCGTGTGGCCTCCCTGGAA	AAGGGCAGCATTGGGCATGGA		
400721	LOC400721	XM_375664	CACACTGGTCACACCACCTTA	GTGGGAAATCATTTAGTTCAA		
400729	LOC400729	XM_378824	CGGCTCCTGTCTGACCAGGAA	ATGATGTACTAGATCCCTTAA		
400764	LOC400764	XM_378880	CAGGGAGCAGAAGACATTAAT	AAGGGCTATGAAGAAACATAT		
400790	LOC400790	XM_375814	CAGGAGCTCCTGCTACATAAA	AAGGAACATATTTCCACATAA		
400800	LOC400800	XM_378925	AAGGTACAAATTACAGATATA	AAGGAAATGATTTAACTTCAA		
400842	LOC400842	XM_375914	CCCATGAAGAATGAAGCACAA	CCGAGCGATCGCAGAGACCTA	TTCATACAGAATGGCACTAAA	CTGGGATTATTGATTACAACA
400846	LOC400846	XM_378981	CACGTACTTTCTGAATCTAAA	CACAAAGATGTGAGCAATAAA		
400850	FLJ44790	NM_001001691	CCCGGCGTTCCTGGAAGCCAA	CCCGCAGCAAGTTAAATCTAA		
400865	LOC400865	XM_379006	AAGGCAAACCATAGCCATTAA	AAGAATTTGCATCATAATTAA		
400876	LOC400876	XM_379023	CAGCTCGGACAGCATCCATAA	CTGTCTGAAATTGAATGTTTA		
400888	LOC400888	XM_375955	CAGGCATCACCTTGCCTGGAA	CCGGTGATTGATGATACTACA		
400890	LOC400890	XM_379036	AACCAGAATAATCAGCCCTAA	ACGCAGAGATGCACACATTAA		
400916	C22orf16	NM_213720	CCCAGATAGCTGGGATTGGAA	CACAGATAACCCAAGACACAA		
400921	LOC400921	XM_376001	CTGGCTGACGTGCTCCATCCA	CATTGTGGACTTGGACATTTA	CTGACACTAAGCTCGGCTTCA	GCCCTCTACTCAGCATGGATA
400931	FLJ27365	NM_207477	CTGGGTAAGTCTAGCCCAGAA	CAGGTGATGCCTGAAGCTCAA		
400932	FLJ46257	NM_001001693	ATGCATTCGTTTATCAATCAA	CCGGGAAGTGTTCACAAATAT		
400934	FLJ44385	NM_207478	AAGAAGGAAACTGGACACATA	CAGGACAATTATTAAGTTCCA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
400937	LOC400937	XM_379068	CAGGATCTACGTTATAATTAT	CACAATTATGAAATAATGTAA		
400944	LOC400944	XM_379077	CACCAACTCCTTGTATTGCAA	CTGGGATGGAATCCTAATGAA		
400945	LOC400945	XM_379078	CAGGTTTATAATATGCATTCA	CAGCAATTTAATAATAATGCA		
400964	LOC400964	XM_379106	CTGGGATTACACAGTCGGTAA	CAGGTTAATGGAAATAATTAA		
400997	FLJ44006	NM_001001696	ATGGAGATATACAATTGTTAA	AAGGTCTTAATGAGAATGAAA		
401025	LOC401025	XM_379149	CCCATCCTGAGTGACTACTAA	CCAGCATGTCTTTCCACTATA		
401034	LOC401034	XM_376179	CCACCGGAGACTCAAGATGAA	CACACTCACAGTTACCAGCTA		
401037	LOC401037	XM_379161	CCAGTGCAGCTAGAAATGTAA	TCCCTCAGAATTTACATCTAA		
401050	LOC401050	XM_379173	TTAGATAATAATGGAACTGAA	CCCAGTTTAGTTTATATATAA		
401054	LOC401054	XM_376207	TTGGCTGGACACAATCCTGAA	CAGGTTGACCTTGGTGAACTA		
401056	LOC401056	XM_379180	TAGGACTCTGGAGAAGATCAA	TGGAAGCTCTTTGGAAACCAA		
401058	LOC401058	XM_379182	AAGAATACATAAGAAGTCAAA	TACAATATATTCTTAATTTGA		
401059	LOC401059	XM_379184	TACATTCTGAGTTGAAGGAAA	TCCAAGTATGATTGGAAATTA	TAGATATTTATTATCCAGGTA	ACGAAATTCATTGGCAGATTA
401078	LOC401078	XM_379200	CTGCGTGGTGGCAGTTGTTGA	CGGGTTTGTAGTTACCTATAA		
401081	LOC401081	XM_379206	AAGCAGGTATTTGTATTAGAA	CTGATAGAAGAAGACATTAAA		
401087	LOC401087	XM_376267	AACAAGTACGAATTTGCCAAA	CTCCTTGTGTTTCATTGGCTA	ACGAATTTGCCAAATGGACAA	ACGGTCTATGGTGGCACAAGA
401089	LOC401089	XM_376269	CACGTTCCAGATACACTTTAA	TTGGATTTCTATCACCATAAA		
401097	LOC401097	XM_376281	CGCCAACTGCCTCAGACCTTA	GCGGGCTGCCTCTGACATTTA		
401101	LOC401101	XM_379234	AACGATCTGCGATGAAGATAA	CAGCTGTGACTTGATAAACAA		
401103	LOC401103	XM_379235	CAGGACCTCTGAATCCTATAA	ATGTAGTAATATACTCAATAA		
401114	FLJ35816	NM_207489	CTGACTTTACTCTGAGATCAA	AAAGGTAATGACCAAGATAAA		
401123	FLJ45721	NM_207490	TAGGAAGTAATTACTAATAAT	AACCATGTAGCTCATAAGTAA		
401149	LOC401149	XM_379273	CCGGGACAACAGGCTCTCCAA	CTGGCTGTAGATCCCAATGAA		
401165	LOC401165	XM_379299	TAGGGTTAATGCTACATGGAA	AAGGCAAATTCTATCTTCAAA		
401172	FLJ33360	NM_001001702	CAGGCTTTGCTTCTCTCCCAA	AGGAACCTTACTGATAATTTA		
401176	LOC401176	XM_379318	AACCAAGAGTTATAAACTATA	AACGTAAATATTATTACGTTA		
401180	LOC401180	XM_379325	CACGTCCTCCTTACTCCCGAA	CAGAAACTAAACCGACACCAA		
401206	LOC401206	XM_376420	AACCAGCTGTACATTTGGAAA	GACGAGAAGAAGGACGCTGGA		
401207	LOC401207	XM_376423	AAGGGAGAGACAGACAATAAA	AAGATACAACTTAACTTTAAA		
401210	LOC401210	XM_379359	CCGGTCCACTGTGGAAGGCAA	CAGCCAGAATCTCGCATGTAA		
401215	LOC401215	XM_379368	AAGCTCAGGCTGTGAAATTAA	AACGATAATTTGTGAAAGTAA		
401217	FLJ40453	NM_001007542	AAGAGATTGCTTTGTCCTGAA	CACGATGTCTATTAAACAGAT		
401220	LOC401220	XM_379378	AAGAAATTAGGTGAAGAATTA	AACAATCACTATAGTAAGATA		
401224	AACSL	XM_376454	CTGGTTGACCTTGCAAATTGA	AAGCAGATGCTTGTAAGCTAA		
401236	LOC401236	XM_376469	ATCAATCTATATTATCTTAAA	AAGGTTAGTTGAGTAAATTAA		
401254	LOC401254	XM_379406	CCAAATGGGACTGAACTTTAA	CAGGAGAACCATCACAAGCTA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
401262	CRIP3	NM_206922	ATGCCTGAAGTATGGCATGTA	AAGTGATGTCATTAAGCAGAA		
401278	FLJ44955	NM_207500	CCCATTTCATCTAGAAAGTAA	TAGAGGTTTGTTAATCTAATA		
401281	FLJ27255	NM_207501	CAGCTAGGTAAGATCATGTAA	GACCATGATACTAACAATAAA		
401308	LOC401308	XM_376576	TGCCCAGTTTGAAGAATTGAA	ATCCTCTATTGTTCTGACAAA		
401328	LOC401328	XM_379485	AACGTTTAACACAGACATTAA	AACCTAATAGTCTTAGCCAAA		
401400	LOC401400	XM_379518	CTGGAATTCTACAGCCATGAT	CTGCTGGGAGAAAGAATGGAA		
401431	LOC401431	NM_001008745	ATGACTTTGATTTCTGCATAA	CAGGGAATTATTCACATGGCA		
401470	LOC401470	XM_376787	AAGGGCAAGGCCATTAAGAAA	CCGCCACCACGCGCAGCCTAT		
401472	FLJ45248	NM_207505	AGGGTATTTCCTAGCAAGAAA	TAGGAAGAATTTCCTGACAAA		
401476	LOC401476	XM_379603	AAGCAATTTGCTCAAGATAAT	ACCCATCAAGAGATTAAGTAA		
401477	LOC401477	XM_379605	CAGGATGCTGTCACAATTACA	TCAGGAGTAATTGTTAACTAA		
401480	LOC401480	XM_379608	CAGCTTTGAGGTCCTAGGAAA	CAGAGTTTCCTTCCCAGCTAA		
401495	LOC401495	XM_379625	TACCAGGAAACTTGAGACCAA	CACACCCTTACCAGACTTCAA		
401497	LOC401497	XM_376822	CACAACAACAGTATAACATAA	TTCAATAAAGTTATCAATAAA		
401499	LOC401499	XM_379628	AACGGGAAAGCTCTTGGAACA	TTGAGCCAGTTTACAAAGAAA		
401508	FLJ45202	NM_207507	CTCAAAGGCTGTCCACAAGAA	AACCCTGTCTGTCTCTACTAA		
401537	LOC401537	XM_376888	CCAGATGAAACAGTACATCTA	CACCTACATCACAAATCTGAA	CACGGAGGCATCTTATGTTAA	CAGACTGGTTTGAAGGAAGAA
401539	LOC401539	XM_379648	AAGACGTAATAGAGATTTCAA	CTCGTAGTCAGTGACAAGTAA		
401550	C9orf148	XM_379667	AAGAAGAATCCTAACCTCAAA	AAGGGTCGTGGTGAGAATCAA		
401584	LOC401584	XM_376986	ACCAAGTACTCCAGATTAATA	CAGCTTGAACTGTTGCCTTAA		
401607	LOC401607	XM_379717	ATTGATCAGCCAGCAGTCAAA	CACTCGCCAATTAGAGATTGA		
401679	LOC401679	XM_377185	CTGCAAGGCGTGCCACCTGAA	CCGGTGCTCCTGCCTTGTGAA		
401704	LOC401704	XM_377231	CTACTGGATGATGACAATGAA	AAGCAGTAGATATGAATAATA		
401713	LOC401713	XM_377259	TGCCAATATGGTCAACAGGAA	TCACAAGACCTTCAATTTAAA		
401855	LOC401855	XM_497509	CTGGCCTACAAGAACACATAA	AAAGTGGGTCACCAAATGCTA	CCAGGCCGCTTTGGAAGCGAA	CCCTCGAGAGTTGGAAGTCAA
401876	LOC401876	XM_497534	CATGGTATCAAGGGAAATATA	CCCACTTGAATTGCTCAACAA		
401891	LOC401891	XM_377488	CTGCTCGTAATGGATCAACAA	CAGATTTAACTGCAATAGATA		
401895	LOC401895	XM_377500	AACAGACCTTCCGCAACTTCA	CAGCAAGACGGCAGAGGTACA		
401896	LOC401896	XM_377511	ACCAAGTTCAATGCTGATGAA	ACGCTCGGAAGGGTTGACATT		
401921	LOC401921	XM_497630	CAGGTCTTCGGTGGCAAGAAA	CCCGGTCACTACACTATGAAA		
401943	LOC401943	XM_497659	TGGGAGGACGAGAAGAGCCAA	AAGCCCTTGGAGAATGAACTA		
401945	LOC401945	XM_377579	ACCGGATATGCAGCTCTGAAA	CCGGAGAAATCTGCAGGTAAA		
401980	LOC401980	XM_497729	CTGAGTGACGTTAATCACTCA	CGGGAAGCTGCTGGTGATCAA		
402011	LOC402011	XM_497758	CACAATATTGGTGGTATCAAT	TACCATCAACTTGTCCAACTA		
402036	LOC402036	XM_377696	CACGGTGCTCTGGACCGTCTT	CCTCATCAACATTGACTTTCA	CTGGAGAATGACAGCCACACA	CACGGAGGTGAGAGAGAGCAA
402037	LOC402037	XM_497793	CTGGGCCTGCCTGGACCATAA	AAGGATGAGAGGGAAGCAGAA	CAGACGCTGAGGATTCTTGTA	CCCGAAAGATGTGGGCATTAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
402055	LOC402055	XM_377713	CCAGGATTGAAGGAAGGGAAA	CAGGAGTTTGCTAGTGGGACA		
402057	LOC402057	XM_377716	AAGAAGCTCCGCAACAAGATA	CACGCATCTGATGAAATGGAT		
402072	LOC402072	XM_377741	CTGGTACTTCTTATGACACTA	AACATGGTCTATAATGTGTAA		
402094	LOC402094	XM_377755	CCGGGCATCTGCATTCCGGAA	CAGAAGGAAGAGAAAGTGCTA		
402095	LOC402095	XM_377756	TGCCATGGAAATGGTCCAATA	CAGGTTTAACCACCAGTTTAA		
402112	LOC402112	XM_496610	CTGTCTCAGGAGATTCTCAAA	CACCCAAGAGATTATCCTGAA		
402146	LOC402146	XM_497943	AAGCCTGAGCCCATGGAGAAA	ACGGTTATGTATGTAGCAAGA		
402184	LOC402184	XM_497977	GACAAGAAACTAGAGCAATAA	CCAGCATGTGGAATTCTTGAA		
402196	LOC402196	XM_497991	CTCCTTGTGGCCCACAGCCCA	AAGCCATTCCTCATGCCAGAA		
402199	LOC402199	XM_377875	CCGCTGCAGCCCAAGCATTTA	CTGCAGAAGAATCATGTTCTA		
402200	LOC402200	XM_377877	TGCCATGGCTGGAATAGCCAA	CCGCTGCAGCCCAAGCATTTA		
402253	LOC402253	XM_377935	TCGCCTCAGATCTGACCAGAA	TCAGAGTGTTTCAAATGTGTA		
402330	LOC402330	XM_378015	GAACTACGATAAGTTCTCATA	GAGAACTACGATAAGTTCTCA		
402353	LOC402353	XM_378043	ACGGGACGGCTGCCCAATGAA	CGCGGATAATCGAGACTGCAA		
402367	LOC402367	XM_378064	CAGGCACATGCTCCTGCTTCA	CCCAAGCATTCCCGACAGGAA		
402388	LOC402388	XM_378103	CAGATGTGCATTGGAGACTCT	GACGTGGGCATTGGAGACTGA		
402397	LOC402397	XM_497102	TCTGGAAGTATGTATCTACCA	CAGGATTTGATGGTGCTAGTA		
402485	LOC402485	XM_380104	CTCATTGACAAGATTAACATA	AACGTTTAACACAGACATTAA		
402504	LOC402504	XM_380107	CAGAGCTGGATCTACCATGAA	AAAGATGACTGAAGAATGGCA		
402522	LOC402522	XM_379849	CGCCGAGGATTTCAGAAGATA	CAGGAGGGTTGGACACGGCAA		
402523	LOC402523	XM_380114	AAGGGCATACATGGTAATTAT	AACGTGCTAAGTATCAGTAAA		
402532	LOC402532	XM_380117	CGGAGAAAGACTGGTCTTGAA	CAGACTTGGTGTTATGGTAAA		
402563	LOC402563	XM_380128	GCCGGGAGGTTGAGTAGAGAA	CAGAAGGAGTGGAGACATTGA		
402604	LOC402604	XM_379939	CAGGAATTCCTTATGTGTGAA	ACGGTACTGAACAGACAATTA	ACCAATGTTTACAAATATGTA	CACCATGAAATATGTCTTCTA
402634	LOC402634	XM_379987	CAGAAGGTGGAGAGGTCATCA	CCGGCGATGCTGCGTTGCCAA		
402641	LOC402641	XM_379995	AAGACATGAGGGAATCATTAA	ACAGCTGGATATAAACCTGAA	CAGAAGAAGTCTTGTCATCAA	TTCCAGGTTATTGATAAGAAA
402669	LOC402669	XM_380011	AGGCACCACTCTGAAGACAAA	CAGGTGGTGTCTATGATGCAA		
402716	LOC402716	XM_380072	AACACTGGTTATGGGAACAAA	CAGGGTTTGGAGAACATTCAA		
403282	OR6C65	NM_001005518	CCCGTGATTATGGGCCTCCAA	CTCCTACACACTCATCCTTAA		
404033	FLJ34077	XM_495846	AAGGGAAACAAGAGCATAAAT	CAGCCTGATGATGCAGTAGAA		
404550	MGC17624	NM_206967	CCCAGATGATGGAGAAATCGA	CCGCAGTGAGCCCACCAAGAA		
404552	SCGB1D4	NM_206998	AAGAAACGACTCTCATTGAAA	CTCCAAGTTGCCAAACTTAAT		
404785	POTE14	NM_001005356	CAGAAGCAACTTTCTGAAGAA	CAGGAAGAAATTGTCATGCTA		
407835	LOC407835	NR_002144	CAGGGAGATCAGCATCTGCAT	CAGCCCGTGGTCGACAGGGAA	CTGCTGGACTATATTGTGAAA	TTCCAGGAGTTTGTCAATAAA
408263	MGC27121	NM_001001343	AAACAAGATAATATTAAATAA	CAGCCTTATATTACTCCATAA		
414153	SNRPEL1	XM_034623	AACCTCATCTTCAGATACTTA	TTGCAAGTGTGCTCTTTGTGA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
414918	MGC33692	NM_001001794	CCGCGACAAGGCGCTGCTCAA	CACCATTGTCTCAGCAGTAAA		
415116	PIM3	NM_001001852	CACCGCGACATTAAGGACGAA	GAGCGTTTAATTTATTCAGTA	CTGTCAGAAGATGAACATGTA	ATGAACATGTATAGTGGCTAA
439919	LOC439919	XM_498448	TGGGTATTAATTCTCACTGTA	CTGTATAAGTGAAGACATTAA		
439928	LOC439928	XM_498427	AACCAGCAGAACAAATACAAA	TTCTTACTTTGATGGGAACAA		
439952	LOC439952	XM_495799	ATGCTGAAACATCGAAGTCCA	CCGAGAAATCAACGACCTATA		
439957	LOC439957	XM_495805	TACCCTTACCATCAATGCCAA	CCGGGAGACAGCCAGACTCAA		
439959	LOC439959	XM_495806	CACCAAGACTATCAATTTGAT	AGGGAAATTCATCTATTTATA	AAGATGCAGGATCATGGCCAA	TAGGTATTCAATAGCATTAGA
439982	LOC439982	XM_495828	CAGAATCAGATGTTCCAGCTT	ACGGGCTTATTGAGACCCTCA		
439985	LOC439985	XM_495832	AAAGCGATACATTGTCTATTA	AAAGATAAGAAGAAGAAGTAA		
439994	LOC439994	XM_498491	CAATGTCTTTCTTGTATTAAA	TACAGATAGGATTACACTAAA		
440000	LOC440000	XM_498494	CCGGCTGCTCGTCACCGCGAA	GACAATTTACTTGACTGGAAA		
440004	LOC440004	XM_498497	ATGGTATTTCTGGTTATTAAA	CCGGAGTGGTTCTGACTTTAA		
440021	KRTAP5-2	NM_001004325	CTCTCATGTCTGTAAATCAAA	AATGAATTTCCTTGCAATAAA		
440042	LOC440042	XM_498516	ATAGTAGATTCTATCAATCAA	CAGGTGAACAGAAGTTCTCAA		
440050	LOC440050	XM_498520	AGGGTCCATTCCTCACTATAA	AGGAGAGTCCACCCTAATTAA		
440055	LOC440055	XM_495885	CAAGATTCAGGTTCACCCGTA	CAGGTTCACCCGTAACCCACT		
440058	LOC440058	XM_498524	TTGGAAGAATTGTGTTATATA	AAGGGTAGACTGAGTCTTGAA		
440066	LOC440066	XM_495897	TAGGGTCAAATCAGTCACTCA	CACCTGCATTGTGCAAGGAAA		
440071	LOC440071	XM_498531	CCGGAGAGGCCGAGTGATCTA	CACAATTCTCTCTCTCCTTAA		
440077	FLJ16353	NM_001004328	CAGCACATAGTTAGTGCTCCA	TTGACAAATCAATATATTAAA		
440079	LOC440079	XM_498535	TGCAAGGTACTTGACACGCAA	AAGAGAGAATAGATAACTTCA		
440083	LOC440083	XM_498536	AAGAAGATGAGAGTGATTCAA	AAGGAGACAACAAGTCCCGAA		
440093	LOC440093	XM_495919	ATGCATGTTTCTGTATGTTAA	ACCAAGCAGACTGCTCGTAAA		
440098	LOC440098	XM_498543	ATCGGGTAAAGGAGTCGATAA	CTGGAGACAAGTGGACCCTAA		
440101	LOC440101	XM_498545	CAGAAGTTTATTTCTCACTTA	CACATAGATTACACTAAATAA		
440102	LOC440102	XM_498546	GAGAATGTTGCTGCCACTCAA	AAAGAAAGGAATATCATTATA		
440106	LOC440106	XM_495929	AAGAGGGTCCATCGCCATCAT	AGGGCTGGAAGTAGGCCTGAA		
440112	LOC440112	XM_498548	AAGATGTTGTTTCAACCTGTA	AAGCTTTAAGTTGCAAATGAA		
440134	LOC440134	XM_498562	CCACTCCATAGTGAATGGTTA	TTGATTGTCTTTCATCGGAAA		
440138	LOC440138	NM_001004127	AACGGTCAACAGATACTAGAA	CTCATTGTATGTGGAACTTTA		
440142	LOC440142	XM_495960	ATCCAGTTCATCTCACTTCAA	AAGCCTTTGAGAAGCATGAAA		
440151	LOC440151	XM_498568	CACCAGCATTCCAGAGTCCAA	CTGGAAATAAATAATTCATAA		
440153	LOC440153	XM_495967	CAACATATGCACTGACTATAA	CTCACTCTTTACTACAACATA	CAGCAACTTCACAACCCAGTA	CAGGCCTCAGATAGACGCCAA
440155	LOC440155	XM_498569	TACAAATGGAGACACAGGAAA	CCGGCTGCTGCTTACACCTTT		
440157	LOC440157	XM_495969	AAGGGAAGCCAGGCTGAGATA	CAGAGTCTGCCTCCATGAGAA		
440186	LOC440186	XM_498579	AGCCTCGGAAATTTCCTTTAA	CCCGGAAAGCAGGGCATTCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
440190	LOC440190	XM_498580	AAGGAACTTTGGGAAGATGAT	CCGGGCCTCCTTGAAGGTTGA		
440191	LOC440191	XM_498582	TAGCATAAGATGCTTCCTTAA	TACTTAATAAATAAACATTTA		
440228	LOC440228	XM_496031	CTCCTGGGTAGATGCATATAA	CAGCCCAAGGACAGCCAATTA		
440232	LOC440232	XM_496036	CTGTGCCTGGCCTGTATTGTA	AAGCAGGTGGATGCAAATGAA		
440233	LOC440233	XM_496037	CAAGAAGGCAAAGACAATAAA	CACCTGGAAGCTGCCATCTAA		
440242	LOC440242	XM_496040	TGCAGAGATCCAGGATACAAA	ATACAACAGCTTCTTAGGTAA		
440243	LOC440243	XM_496041	CACCTGGAAGCTGCCATCTAA	GTGCATCCTCACGTAAGTGCA		
440245	LOC440245	XM_496042	CCCAAACGAGGTGATCGACTT	CTCCTTTCGGTGCATGAACAA		
440252	LOC440252	XM_496049	AACAAGAAACAGAAAGCCAAA	AGAGATGAGTATTCTGAACAT		
440254	LOC440254	XM_498602	CAGCTGCTGCGGCGCCATGAT	TTGCAAATAATGAGAAGCCGA		
440266	LOC440266	XM_496062	CTGCAGCAAAGCACATACAGA	GATGAGTGTGCTGAACATATA		
440274	LOC440274	XM_498608	CTTGAGAATTATGTAGAATAA	CAGAGGTCATCTTTAAGTAAA		
440277	LOC440277	XM_498610	AACATTGGCCAGGGAAGTTAA	CAGGATGGTGACTTGTCTTTA		
440284	LOC440284	XM_498614	ACGGAAAGCCTTTATAATGTA	CAGAATGTTATTAATCTTTAA		
440298	LOC440298	XM_496086	CCGGGACCCTGCAGAAATGAA	ACCCGGGATCCTCAAATAGAA		
440301	LOC440301	XM_498620	ATAAATTCTCACACACACATA	CTGCCCTGTTCTATAGCTATA		
440303	DNM1DN11-13	XM_498621	TTGACCGTTGCTGAAACTTGT	CTGAGCATTCATCTGAACTAT		
440307	LOC440307	XM_496092	ACGCAGATCACTGGCCATCAA	ATCGAGGACATCATCATCAAA		
440317	LOC440317	XM_496097	AACCCTAGTGTTGGTACAGCA	CAGAGCGTTTCAGGCAATGAA		
440329	LOC440329	XM_498628	TCCCAAGTCAAAGACACTCCA	CGGCTTGAAGGAACAGGGCTA		
440334	LOC440334	XM_498631	TTGTAACTACTTGAAGTTAAA	ACGGTCTTTCTTTGCCAACTA		
440344	LOC440344	XM_496123	CACGGGAGGTGACATGAGCAA	GAAGGAGAAATTCCAAAGAAA	CAAAGAAATGTAGTTTATTTA	CTGGCTGTGAAGGACCCTTTA
440361	LOC440361	XM_496145	AGGGAGCAGTGAGGACACCAA	CACAACGATGTGCTTAGTAAA		
440370	LOC440370	XM_496158	CTCCTTGTATCTTCAAATGAA	ATGGTATACTTTATTAAGAAA		
440372	LOC440372	XM_496161	GCCGATGGAGATGCCTATGAA	CACGGAGAATGACCAGCTCAA	ATGGACAAGAAGAAAGAGTAA	CGCGGGCGTCTAGGCAAGAAA
440374	LOC440374	XM_370980	ACCTATTTATGAATATACAAA	AAACCATTAAACAGATTTCTA		
440380	LOC440380	XM_498645	AACCCAAGAGAAAGTCAGAAA	ATGGAGGAATGAGGAGTTCAA		
440387	LOC440387	XM_496169	TACCACCACGCCCGCTGTGTA	CTGCCTTAAGATTTCCCATTA		
440391	LOC440391	XM_498650	ATGGTATTGGTGTAACATGTA	AAGGATCGCATGGCAGAACTA		
440414	LOC440414	XM_496194	CGCGGATAGTGTGCAGGCATA	CCTGGTGTTGTCAATCATGAA		
440426	LOC440426	XM_498662	TCCCAAGTGGCTAAGACTTAA	CAGGATTAGCTTGTGGTTTAT		
440432	LOC440432	XM_498666	CCGGGCATACTTAGTATCTTT	CTGGTTGGTAAAGAACATTAA		
440434	LOC440434	XM_496214	GCCGCAGGCGTTATTCCTAAA	CAGCCGAAAGAGCAACTCATA		
440435	GPR158L1	NM_001004334	AACCAAGGAAATGGCCGCAAA	CAGGTGTGTATAAATCTGACA	ACAGAAGAATTCACTACTGAA	CACCATCATACTCAAGCTTTA
440447	LOC440447	XM_496231	TCCCAGGGTCTCTACAGATTT	AAGGAGTTGCAGGAAGCATTT		
440449	LOC440449	XM_498675	CTAGATGAAGAGTTATCTTAA	CTGGAGTTCCTTGACTAGGAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
440455	LOC440455	XM_498678	CCCGAGGCTCCACGTACTCAA	CGCGCTTGTCAGGGAACAGAA		
440461	LOC440461	XM_498680	CTTGTGATGTGTGGAGATCAA	CTCCCTGGTTATACTGTTATA		
440462	LOC440462	XM_498681	CCGGGCCTTGTGAACCTGCAA	CACCCTGGTCTTCTCCTGTAA		
440472	LOC440472	XM_496255	ATGGCTATAACAACAAACTAA	CAGACTCTTCTTAGAAGTCTA		
440484	LOC440484	XM_496268	CAGGATCATCCATACCCTAAA	CACTGTAACATAATCCATTAA		
440493	LOC440493	XM_498698	GCGGCTCAGTTTCACTAACAA	CCCGACTTTCCGTGCAATAAA		
440495	LOC440495	XM_498700	GGCGACATATACTAACAACAA	CTGGTGTTACATTATCAACAT		
440498	LOC440498	XM_498704	ATGGTGCAAGCTGGCATTGAA	CTGGTAGATTATCATGGAGTA		
440501	LOC440501	XM_498706	CGGAGCAGAGTTCTCCTCAGA	CAGATTTCAGTGGTACTGCGA		
440508	LOC440508	XM_496285	CAGGGCTACTCCCACTGGTTA	CTCCATAAGCCTCAGAATGAA		
440526	LOC440526	XM_498718	CAGCAACCACGCCACCATGAA	CTGAACAGGGTTCTAACCAAA		
440536	LOC440536	XM_498721	CAGGCATCACATCCAGACTCA	AGCCTTTGTAGGAACGAGAAA		
440546	LOC440546	XM_496328	AAGCAGAGAAATGCAAACTAA	TTGCTTCAAATAGGGCCAGTA		
440551	LOC440551	XM_496331	GAGGGAGATGCGCTCCCTGGA	CCCGCCTCTCGTGGTGCTCTA		
440552	LOC440552	XM_496332	CTCCAAATATCTCATCAACAA	AACCAACACACTAACCATATA		
440554	LOC440554	XM_498731	AAGCACAGTTTCCTATGACAA	CACGTCACTCAGAAAGTTGAA		
440563	LOC440563	XM_496344	TCGAAACACCAGCGCATATCA	ACCAGCTTCATTTGATCAAGA		
440567	LOC440567	XM_496348	GAGCTCTATGATGAGCATGTA	CTGCTCGTGTTAAATCTAGAA		
440568	LOC440568	XM_496349	AAGGTCTTAAGTGCAGCAGGA	AAGCTCTTTGTTGGAGAAGGA		
440572	LOC440572	XM_498736	CCGTTTAATATCAGAGAGAAA	AACCATATTTATGAAAGTAAA		
440583	LOC440583	XM_498743	CCGGGATGACCTAAGGAACAA	CAGAGAGTGATGACTGCTTAA		
440586	LOC440586	XM_496361	TCAGGTTATGTTGGAGCTAAA	AAGCGAATTTATGATCTGAAA		
440587	LOC440587	XM_496362	CAGGCAGTCATGTGGCCCGAA	CCCAAACATCTTATTGATACT		
440596	LOC440596	XM_498746	TTGGGTTTCCTTCAGTCTCAA	GTGGGTGAAGTGGAAGAACAA		
440606	LOC440606	XM_496385	CTGGAACATGTAGGCCTTGTA	TAGCTACAGCATATTATTTAA		
440607	LOC440607	NM_001004340	ACTGTGAAAGGCCTCCAGTTA	CAGCAGGAATATCACAATACA		
440609	LOC440609	XM_498754	AAGCCTTGTTAACTTGCTGAA	CACATCGTGTTTGGGATCAAA		
440665	LOC440665	XM_498809	CACCAAGAAGTTTCTGACAAT	GAGAATGTTCCTCTTCAGTAA		
440667	LOC440667	XM_498810	CAGCAGCTGTTGCCAAATGAA	CACGCGGGTTCTGCCCTCAAA		
440678	LOC440678	XM_496401	AAGGATGTCATCAAAGTAGTT	TAGGAGATCTTTCACTTGTAA		
440683	LOC440683	XM_496404	GAACATAAGTTTCTATTTCAA	CAGAGGCGCTTCAGGAAGCAA	AGGAATGAACATAAGTTTCTA	GTGCAATTCGTCAGAACTTAA
440684	LOC440684	XM_496405	CTCCTTGTCAGGAGCACCTAA	AGGGATTATTACTCACTGCAA	CTGCAACTTAGCCTAGCATTA	TAGCATTAAGTTGCTTGACTA
440692	LOC440692	XM_498820	AAGCAGATCAGTGCTCAAGTA	TAGGAGTTGTAGAGCAGAGAA		
440696	LOC440696	XM_496420	AAGCCAATTGATGACATATAT	AAGCGTAAAGCTTGAAATATA		
440705	LOC440705	XM_496427	CACCTTCATGCTCAGCATTCA	TCCGAATTTCTTGATCAAGAA		
440707	LOC440707	XM_498827	CCGAGACTCAGACTTACCCAA	CTGCATCTTCTCATCCCATAT		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
440722	LOC440722	XM_498831	AGGCATCACGTCCACATGCAA	CAGTGTGGCATGGGCATGTAA		
440724	LOC440724	XM_498833	AAGGGAAAGGGTGACCACATA	CACTGTGAAGAATATATTAAA		
440725	LOC440725	XM_498834	TTGCATCAAATGGGACCTTAA	ACGAGACTTACAAATAATAAA		
440730	TRIM67	NM_001004342	CTGGCTTTAATAGTGATTCAT	TACCTAAGTTCTGGTATCTAA	CCGGGAAGTGTACGTCGGTAA	CACAACTATCTCAGGCCTTAA
440747	LOC440747	XM_380170	ATCCAATTCTCTACACCATAA	ATGCAGAATCAACAACAACAA		
440752	LOC440752	XM_498844	CTGCTTGAAGCTGGCATTTGA	ATGGCTGGTTACTGTGCTAAA		
440757	MGC44328	NM_001004344	ACAAGTGTTAATCCCAATAAA	CAGGGAAGACACAGTCACTAA		
440764	LOC440764	XM_496476	CACGGTGCTCCTGGAGGCCTA	CACGCTCACGGTCAAGTATGA		
440765	LOC440765	XM_498851	CAGCAGTAACTTATTAAATCT	CACAGCCGAGTTGCTAGCTAA		
440766	LOC440766	XM_498852	ACCCATGAACATGTACAATTA	ATGGCTAATAATCACATGATA		
440771	LOC440771	XM_498856	CCGGTAGCCAGTCAGAATTTA	CACGGTCAAGACGGAAGCAAA		
440772	LOC440772	XM_498857	AAGCAAATGGCTCATTTCCAA	AACCTCTAAGATTTGAATGAA		
440773	LOC440773	XM_496481	CAGGTAGATGATAAGGAGATT	AAAGAAGAATCTGAAGTGAAA		
440786	LOC440786	XM_496488	CTGGCGTTAAAGAGGTCCATA	TAGAATATGGAGGCCCTGAAA		
440787	LOC440787	XM_496489	TAGACTCAGAGAGATGGCAAA	CAGAACAAACATAGTACGGCA		
440788	LOC440788	XM_496490	ACGGAGCATTACATTCCCAGA	CCCGGAATCAATGGGAATGAA		
440790	LOC440790	XM_498869	AACATTCTTCATTATGCATAA	CAGCAGGTGTTGCTTAGTGAA		
440793	LOC440793	XM_496494	AAGGTCTTCTCAAATATTGTA	CTGCAGCGGAGCCATGGCCCA		
440804	LOC440804	XM_036936	AACAGAGATCCTGGATACCAA	CTGGAGGAAGACAGCTTATTA		
440815	LOC440815	XM_498875	GCAGATGGCGAGCATGGCAAA	AAGGGAGACCAAAGTTGGAAA		
440824	LOC440824	XM_496523	CAGATCCATGCTGATCCCGCA	CAGGGCGCTGAGTACCATGTA		
440839	LOC440839	XM_496539	TTGAGGGATTTCAGACTTCAA	AAGTCTTATTTAAGAAATATA		
440843	LOC440843	XM_498885	TTGAATTTGTGTTCAAAGTAA	CTGGGAAGAAAGCAACACAAA		
440854	CAPN14	XM_496548	CTGGAGTGACAGTTCAAGTAA	CAGGATGAATTCTTCACCAAA		
440855	LOC440855	XM_498894	CTGGACATATTTCTTCTGGAA	CCGGAACAGAGATTTACTCAA		
440856	LOC440856	XM_498895	ACGAACGTAATTTGTTTCTGA	AAGGGAGAGAAGAGAGTTGAA		
440857	LOC440857	XM_498896	TCCAGTCTGTTTACTATACAT	GGGACTCAAAGTATTAGCTAA		
440859	LOC440859	XM_498898	CCGGGAAGCCTGGCTCCGAAA	CACATTACAGTTAATCTGTAA		
440866	LOC440866	XM_496551	CAGAAAGTTTGTGAAGATCTT	ATGGTCTGACTTTCACAGAAA	CCGGTTCATCTAATACAGACA	CAGATTTGTCAAGGTTTGAAA
440867	FLJ16124	NM_001004345	AAGGAAGGAATTTATCTACCA	CACGAGAAATATTACGTTGTA		
440872	LOC440872	XM_496559	AAAGAGATACGTATGTACTTA	CAGTGGCTGTGAAGAATATAA		
440900	LOC440900	XM_498909	ATCCGTCACACTAGATGCATA	CCGGAGCCGTTTACAGTTTGA		
440923	LOC440923	XM_498916	AACAGTGAATAAGCACCATAA	TAGGAGGAAGGCCACAACTAA		
440925	LOC440925	XM_496609	CAGAGGTTAGCCTAACTACAA	ATAGGTTTAAGAGTTAATATA		
440927	LOC440927	XM_496612	AAGATCAATGCCCTCATTAAA	AAGAAAGTGGAAGCAAAGAAA		
440930	LOC440930	XM_498918	CCGCTAGGTGTAGGACCGCTA	TTGGCAGAATACTCAGGTCAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
440937	LOC440937	XM_498922	ACCTGAGAATTCAATGATGTA	CCCAACCTACAGGAAGCATAA		
440940	LOC440940	XM_498923	CAGGGCGACAGTGTAGGGCCA	AGCCTGCGTCTCAGCAGCAAA		
440954	LOC440954	XM_498932	CTCATTTACCTTCCACATAAA	AAGGAACAGATGTACAGTAAA		
440959	LOC440959	XM_498934	CTGCACCAATTCGCTCATTTA	CAGCCAGTTCATAGACACCAA		
440960	LOC440960	XM_498935	CGGGAGAATATGCAGCAATAA	CCGGCTCAGGTATTTATTGAA		
440965	LOC440965	XM_498938	CGGCAGACACACCACGTTCCA	TAGGTCTATCAGTGCTTTGGA		
440970	LOC440970	XM_496650	AAGGAAGAGAGTGATTATATA	CAACATCTTATTGCTATTTAA		
440971	LOC440971	XM_496651	ATGGAGTAAACTACAGCTTAA	TAGGATATATTTGTCCCTTAA		
440978	LOC440978	XM_496659	CAGGGTAATCACGGAATCCCA	AAGGGAGAGATTGGTGATGTA		
440990	LOC440990	XM_498952	GAGGATGTATGTGATGAGTAA	CTGCTGTAAACCAATGTTAAA		
440992	LOC440992	XM_496668	TTCGCTCTCGCCGCCGAGGAA	AAGGAGGAGTTCGAATGCCTT		
440995	LOC440995	XM_498955	CCAGAACTGGCAGCCCTTAAA	TAGCGTGCCGTGGCCATTGAA		
440997	LOC440997	XM_498957	AAGGTTCATAGTTGTGTTGTA	TAGGCTATTTCAAGAAATTAA		
440998	LOC440998	XM_498958	TGCAGAATTCATTATAATAAA	CAGGTGAGACTTCACCGTGAA		
441022	LOC441022	XM_496700	CACCCTATGGATGAACAGGAT	CACAAGCATCTGATGAAGCAA		
441023	LOC441023	XM_498970	TCCCTCCATCCTTGCCCTAAA	ACCATGAGTTGTCACATCTAA		
441027	LOC441027	XM_496707	CGGAATGACCTTACTTGGTAA	TACCATTAAATTCAGCTGAAA		
441030	LOC441030	XM_498973	AAGAATCTTTACAAAGCTGAA	AAGGATGAGAGTGGATGTCAA		
441035	LOC441035	XM_496713	CAACTTGGTAAGAACACATAA	GTGAGAAATAATACTCATAAA		
441042	LOC441042	XM_498981	AAGGTTTGCTCTAACCTAGAA	TAGCAGGAATTCTTATATCAA		
441050	LOC441050	XM_496721	CTGGAGTAAGAAATATTTCAT	CTGGCTTAGTATGGACTTCAA		
441053	LOC441053	XM_496723	ACCATTTGCAATGAAGAGGAA	AGGAAAGGAATTTGACATTAA		
441059	LOC441059	XM_498991	AACTCCCAATTTGGAAAGTAA	CTGCTAAAGAATAAATGTAAA		
441068	LOC441068	XM_496743	CTACAAGAAATCGAAGAGAAA	CACCAAGGAAATGAAAGTTCA		
441069	LOC441069	XM_498996	CGGGACCTGAACCGAGAGCAA	CAGGGTTCCATCAGGAAGGAA		
441071	LOC441071	XM_498997	CAGCTTGAACAACTCAGCTAA	CCCATGGATATTGAAAGGATA		
441073	LOC441073	XM_496746	AAGAGCTGAGACAGAAGTACA	AAACTGGACAAAGACTGTGAA		
441077	LOC441077	XM_496748	AGGGTTCAACCTCCAACCTTA	CCTGAGATCGATAAAGCTTAA		
441093	LOC441093	XM_499007	AAGATGGAGTTTGGAAGGATA	CTGGAAGATTCTGTTCATGTA		
441099	LOC441099	XM_496770	AAGCCTCAGAGTATTTCGAAA	AACATTTCACTTTACATCTAA		
441113	LOC441113	XM_496782	AACCACAGATCTCGTAGGAAA	CACGATGTATTTATTTGATTT		
441117	LOC441117	XM_496786	GTGGAAGAATTCATATATGAA	AAGGATCTTAGCTTTGAGAAA		
441118	LOC441118	XM_496787	CTGGAAGAGTAGAAACAGAGA	CAGGTGGTGTTTGGGTGCATA		
441128	LOC441128	XM_496793	AAGCCCAAATAGAGAACAGTA	AAGAGGCACCTAATTCCTTAA		
441129	LOC441129	XM_499026	CCCACTCACCGCACACCATCA	CAGGGCGCCTCTAGTCCCTCA		
441140	FLJ45422	NM_001004349	TTGGGAGGTGATGTCATATAA	CAGACGGTACATACACTCTAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
441141	LOC441141	XM_499031	CAGAATGACTACCCATGCAAA	AAGACAGGTACTGGAAGATAA		
441157	LOC441157	XM_499037	CCGGGATTCAGAATTGATCCA	CTGCACGTCACGGCTACTCAA		
441162	LOC441162	XM_499039	ATGGGACATGCATATAAACTA	TACCTAATACACTGCAATATA		
441165	LOC441165	XM_496820	CACCCTTAAACTACAAAGAGA	AAAGAAGACATCACCCTTAAA	CACCTGCTACTCAGAAAGCTA	TTGGAAGAGATTCTTATTAAA
441167	LOC441167	XM_499042	CAGGCAAGCTTTCAACTATAA	CTGAAGGTAATCAGAGATTAA		
441171	LOC441171	XM_499044	CCCAGAAACACTGTACTTTAT	ATGATGAATCACCAACACTAA		
441173	FLJ39824	XM_496827	CAGGACCATTTGACTATTTCA	TAAGTTATTTATACTCATTTA		
441189	LOC441189	XM_496843	CCGGGCCTCAGTTTCCCGGAA	CCCGGAGGAGATCGCGCGCAA		
441199	LOC441199	XM_496855	AAGGATACTTGTTAACCTTAA	TCCAGCTTTGTTGGTATTCAA		
441209	LOC441209	XM_496859	CTGGCTGTCAATTTATCAGTA	AGGAAGATTGTTGGTGATGAA		
441215	LOC441215	XM_496862	TTGCAAAGAGAAGAAGATCAA	CAGGGTGTATGAGGAGAGAAA		
441220	LOC441220	XM_496867	CAGCATGTCTTCAGCCAGGAA	CTGGTGGTTGTACTCAGATAA		
441221	LOC441221	XM_496868	CTGAGAAATGGAATAATCGTA	CAGGATGAACGGCGCCAGGTA		
441235	LOC441235	XM_496880	CAGGTCATATCCTGAGATCAA	CACTGTCCTGATTATAAATAA		
441243	LOC441243	XM_376622	AGGCCAAAGCTTTGTATTTCA	ACAGAGTGGTGTGGAGAATAA		
441268	LOC441268	XM_496908	TTGCTCCATACAGACCTCCCA	CTGCTGATTTCTTCACTTGCT		
441307	LOC441307	XM_499093	AAGGATGTTTGGAGGCTTCAA	CCGGCCTTCGTTTCCATTCAA		
441309	LOC441309	XM_496942	CTGAATGATATTTAAGCTGAA	GGCGACCTTGCTGCAGGACAA		
441313	LOC441313	XM_496945	GACGTTGTAGTTGGCGTGGTT	CTGGAATGCCTTTGTACATAT		
441328	LOC441328	XM_496957	ACCAAAGAGCGTGGAAGGAAA	TCCGGATCAGAAGGAGCAGGA		
441333	LOC441333	XM_496962	TAGGGAAGGGTGGTTCTGCAA	CACCTTGGATCTAGGAGACAA		
441336	LOC441336	XM_499101	CACCAGGACCTGAAATGTTAT	CCAGCTGGATATCACGGGAAA		
441377	LOC441377	XM_496991	AAGGAACAACGGTCACACCAA	CCCACCTTGATTTAGACCTGT		
441386	GD:PTPRD	XM_497007	CCCAAGCTGTATGTGAAGCTA	AAGGACAAGGCCATTAAGAAA		
441395	LOC441395	XM_497014	ACAGATCCTGGTCAGAGTAAA	CAGGTGCTGGTTATGCTTTAT		
441401	LOC441401	XM_499136	CAGCCGGTCAAAGCAGCAGAA	ATGACAGATTATGAGAATGAA		
441421	LOC441421	XM_497042	AAGGCGTGCTGTCGCCTGCAA	AAGAGGTTTCTGGGTCATCTA		
441424	LOC441424	XM_497044	AACACCCATAAGAATTCCTAT	CAGAAGGAACAAGCACAATAT		
441432	LOC441432	XM_376852	CAGGAAATATGATGCGAGGAA	CAGGGTGTACCATGGCATGAA		
441447	LOC441447	XM_497061	AAGGAGGAATTTCAGGGTGAA	TAGCACGATTTCCTATGACCA		
441450	LOC441450	XM_499151	CTGGGTTCTGCTGACATGTGA	TAGGACGAATTTCTTGCTCCA		
441454	LOC441454	XM_499153	CAGCTCTGAAATCATTGCCAA	TTGGTTTATATGATCTAGTTA		
441455	LOC441455	XM_497068	AACTGCTGTGGAAACCAAGAA	GTGCCTCTCCATGGAGATTCA		
441458	LOC441458	XM_499155	CTAAGTGGAGTGGACCATAAA	ATGATAATAGCTTACCACAAA		
441460	LOC441460	XM_499156	TGGGAACAATAAAGCACTTCA	CTGCACCTATTGTCACAGCAA		
441464	LOC441464	XM_499160	CTGGGATTAAGACACAAACAA	CAGGGACAACTTGGATCTTCA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
441467	LOC441467	XM_499164	CTGCTTGGCGGTAGACCTTAA	CAGGATCCTAACGAAGACCAA		
441468	LOC441468	XM_499165	AAGCAAGGTCTCGCTGTGTTA	TAGGACTTTCTTTGCATTCAT		
441471	LOC441471	XM_351854	AAGCGTCTTCGTCTTGCTCAT	CTGCACCTCACTGGAGCGGAA		
441474	LOC441474	XM_499168	CGCCGCCTGCTTCACTTCTTA	CCCAGGAGATAGAACCTTCTA		
441483	LOC441483	XM_497093	GGCCCTGATAAGGCCACCCAA	CCACGCTGGGTTTAAGTGACA		
441490	LOC441490	XM_497100	ATGGAATCAGCGACCACACTA	TTTGACCATTGTTAACAATAA		
441491	LOC441491	XM_499175	CCCAGTGGAGCACGTCCTCAA	CTCCAGAAACATGAGCACAAA		
441494	LOC441494	XM_499177	CAGAGGCATGAAGCTAGAATA	CAGGTTCATCTCATTAGTGGA		
441515	LOC441515	XM_497146	CTCACTAAAGCTCTAGTGCAA	CAGCACATTCAGTTAATGTTA		
441525	SPANX-N4	NM_001009613	CTGGAGAATAACCAGCCTACA	CAGAGTTTGAAAGAGACAGAA		
441528	LOC441528	XM_497181	CTGGCCCAGCATTTAAACTTA	CTGAATATTGTGCGCATGAAA		
441529	LOC441529	XM_497182	CTGGAGGAATCACCCAGTGAA	CAGGCCACTCAGGATATCCAA		
441531	LOC441531	XM_497185	AAGCCATTCCTCATACCAATA	AAAGTATAGTATATATTAATA		
441540	LOC441540	XM_351948	CTGGCACCCTTCAGATCCTTT	CCTTACGGATTTCGCGGTTTA		
441542	LOC441542	XM_497201	CAGCATTCTGACGCTGAAGTA	CAGGACATATGAGACTTATTA		
441551	LOC441551	XM_497216	TCGACCAATTTGCCAACGTTA	CTGGGAATATGGCTCCTGAAA		
441560	LOC441560	XM_497230	GCGGATGAGCACCAACCCTGA	CAGACGGCTTGTATCTCGCAA		
441561	LOC441561	XM_497231	ATGGACCAAGTGGAAGGCAAA	CAAGAGATTATATGACATGAA		
441569	LOC441569	XM_499192	ATCAGAAGACATAGCCAGAAA	CTGCAAGAAAGGCCTCAACAA		
441599	LOC441599	XM_497281	ATGGGTGACTCTTAAAGGTTA	CTGAATCTAGAGCTCATTAAA		
441631	LOC441631	XM_497334	ATGGTCCATTATAAGACTGAA	CAGCATGATGCCATTGCTGAA		
441634	LOC441634	XM_497338	CTGGAGCTCACTCGCATTCAT	CGGGAGTTGAAGGACTTGGAA		
441636	LOC441636	XM_497341	CAGGAACAACTGAACCATCAA	ATCCATATTGATGACAATAAA		
441663	LOC441663	XM_497381	TAGCAACAAGATGAAGACCCA	TAGCCGCAAACTAGACCCAAA		
441665	LOC441665	XM_497385	CCGGGACCTGTGACCCACTCA	CACCTGAGACCTGTCCTGTGA		
441682	LOC441682	XM_497406	CACCATCCAAGGTATCGTGTA	CAGGCCTAGCATAGTCCTTTA		
441696	LOC441696	XM_499197	CTCAGACATGCCTCCGCGTAA	CACAAAGAGTTTGTTACTGTT		
441706	LOC441706	XM_497431	TGGGATGACAGATGCATTCAA	CCAGGATATCTAATTCGCTAA		
441709	LOC441709	XM_497434	TCTGGTATTTATTACTAGAAA	CACCCTAAGTCTGCACTTCAA		
441740	LOC441740	XM_497477	ACAGCTGTACATATTATACTA	CAGGAAACTGCCAGAAAGTAA		
441754	LOC441754	XM_497493	TTGGAACATCGGCAACACAAA	CAGGATGAAGCTCATGCCTCA		
441755	LOC441755	XM_497494	CAGGCAATGGAAGATGCATAT	TAGATGAAACTTACAATATAA		
441759	LOC441759	XM_497498	CTGGCCGAGTTGCACCCTTGA	ACGGACGATGGAGGTCTGTGA		
441790	LOC441790	XM_497536	TCCAAACAGATTCCTTGGGAA	CAGCTTGTGATTGAGGACCTA		
441798	LOC441798	XM_497553	TCCGCGGTCTTTACCCTGGAA	CAGGAGCATGCAGGCCTACAA		
441816	LOC441816	XM_497584	CAGCAGGTGTGGGAAATCCTA	ATGGACTTGGTCAACATCAAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
441821	LOC441821	XM_497592	AAAGATTGCTCCAAAGATTAA	CAGCAATATCCCATCCACAAA		
441826	LOC441826	XM_499202	CTGGGAATTCTGGATGTTCCA	CTGGGTATTCTGGGCATTCCA		
441827	LOC441827	XM_499203	AAGCCTATCTAGATCTACTAA	CAGCCTATCTAGACCTACTAA		
441833	LOC441833	XM_497603	CTCTCGGACATTAGTCACCAA	TCCCGAGAATGTGACATCTAA		
441842	LOC441842	XM_497614	AAGCTTCTAACGGGTTCTCAA	CTGAATGTGAGATAATTTATA		
441847	LOC441847	XM_497623	ACCCACCTTGTTAGGCATAAA	TCCAACCTCATTAAATATAAA		
441848	LOC441848	XM_497624	CAGTTGAAGATCAATAAGAAA	ATGCATCGAGTTCACACTAAA		
441866	LOC441866	XM_497645	ACCCTGATTTGTCCTGATAAA	TCCTGATAAAGAGAAGGCATA		
441874	LOC441874	XM_497654	CACGTCAATTACCGCGAGGAA	CAGTTCTGTATCAGTCTTGAA		
441898	LOC441898	XM_497698	AAGCTCCTTCTCCTATTATTA	TAGGCAGAATCCCGTCAAGAA		
441915	LOC441915	XM_497724	CCAGTTACATCTGGTGATCAA	AACGCTTATGGTATGAAGAAA		
441916	LOC441916	XM_497726	ATCCAGAGTATGGAGAAGTAA	CAAATCCAATATATTAAGAAA		
441922	LOC441922	XM_497733	CAGGAGAGACAGGACCCATTA	CAGGAGAGACAGGACCTATTA		
441925	LOC441925	XM_497740	CAAGTTCATGCTTATAAATTT	CAGGGACTACAGTGCCTTGAA		
441928	LOC441928	XM_497743	TGGGAAATATGAGGTCATGAA	CTGGAGGTACCTGCAGCGGAA		
441955	LOC441955	XM_497773	AGGGATGAGGTAGCAGAGAAA	AAGGCTATGAGAATACACCAA		
441959	LOC441959	XM_497777	CAGACCATGACAACAACATCA	TGAGCAGATCGCGGAGATCAA		
441994	LOC441994	XM_497814	TCGACAGACCCTGGAGGTGTA	CAGCACCATATCCGACATCAT		
442008	LOC442008	XM_497828	GACGACAAGAACTTTAGCAAA	CAGAATCAAATGATCCTGCAA		
442011	LOC442011	XM_497831	AAGCTTATTGATGGCATTCAT	ACGGCTTCATTTAACAGTGAA		
442016	LOC442016	XM_497838	CAGATAGATCTGTTTCAAGAA	AAGGGAAATGCTTGATGGTTA		
442020	LOC442020	XM_497844	CAGCATCATGAGCCAGTTTCA	CAGGCTGACTCGGTACGCAAA		
442022	LOC442022	XM_497846	CGAGCAACTCTCTGGGAACTA	TGAGGTGGTGTCCTTCCGTAA		
442044	LOC442044	XM_497872	CCAGGTGTCAAGGACAGCAAA	CAGCTCCATTGTCTCCCATAA		
442081	LOC442081	XM_497923	CCGCCAGACATTCCAATTGGA	CACGGGCTACATGACCTGTGA		
442093	LOC442093	XM_497939	ATCGTCATTGTTAATGAGCTA	AAGGCTGATTACGAGAGCAAA		
442099	LOC442099	XM_497951	TCGGACAGACCTCCACTTCAA	AACCCTCAGCTTCCATTTAAA		
442108	LOC442108	XM_497964	AAGGGACATGTGGAAGTAATA	CAGATTAGTCAAGAAGATGAA		
442119	LOC442119	XM_497984	CAGGATTTGAAGGAAGCCACA	AACGACATCTTTGGCACCAAA		
442121	LOC442121	XM_497986	CAGAATAGCTTTGCACATACA	CAGCTGGACTTTAAGAATGTA		
442124	LOC442124	XM_497989	CCCGCCTTCGTTATCATTTGT	CACCTTCTACCTCTTATTCCA		
442140	LOC442140	XM_498021	CTCATGGCTCTTGGAAGGAAA	CACCCTGGAAGAAACCATCAA		
442141	LOC442141	XM_498022	CTCAAGGAGCCTCATATGGAA	CCGGAGCATGGCAGAACTCCA		
442145	LOC442145	XM_498027	CCGGGTCCTAAACTCTGGATA	TAGGCTCTGGGTATAAGCTTT		
442158	LOC442158	XM_498040	TGCCAGCAAAGTCCATGTAAA	AGGAACAATAATTGTGCCAAA		
442174	LOC442174	XM_498056	CTGGCTCTGTGAATTCGAATA	CTGGTGGGAGTGAGAATTGAA		

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
442208	LOC442208	XM_498091	GCGGATCAGGTTCAAAGTGAT	CAGGACCAACATCCTCTCCAT		
442209	LOC442209	XM_498092	AACAATAAAGGCGAGATGAAA	CAGATCAAGGGATCAAGGGAT		
442228	LOC442228	XM_498111	ACGGAAGTACTTGGCATATAA	CACCATGTAGTTGTAATTCAA		
442243	LOC442243	XM_498127	CTGACACCTCAGGGTCAGAAA	CAGAGGCACCTATACCACCAA		
442272	LOC442272	XM_498157	AAGCAGAAGGACACAGATGTA	CCGAACCAGATGAAACCCAAA		
442339	LOC442339	XM_498230	GTGACTTTGAAGATAGCTTCA	CCGGTGAGTGGCAAACAACGA		
442350	LOC442350	XM_498243	CAGAAACAGGGAAATCCTGAA	CGGAATGGAAATACTTTCTAA		
442375	LOC442375	XM_498266	ATGGCTTTGCAAAGGAGCCAA	TGGCATCATCTCAGGAAGAAA		
442397	LOC442397	XM_498297	CCCGTAACAGATTTCCATGAA	CAGGTAGTAGTGACACATATT		
442398	LOC442398	XM_499238	GTGCGAGATGAGAAATCTCAA	CCGGGACAACTGCACCAGTGA		
442400	LOC442400	XM_498299	AACGACAACATGAAGTTCGAA	CAGGGACGCTTTAGCACTCGA		
442401	LOC442401	XM_378044	CCGCCTCTTTGGGCACCTTAA	CAGCGAGATGACCAAGACGAA		
442410	LOC442410	XM_498312	CGGTGTGAGCATGGCAGAGAA	CAGGGCCATTTCCATTGTCAT		
442429	LOC442429	XM_498335	CTGGCCAAGAAGCCATTCACA	CAGAGCCTGCGCAGTGTGGTA		
442451	LOC442451	XM_498366	CATGATGAACACAGTGTGAAA	CAGCTGAAAGTCAGGATAGTA		
442454	LOC442454	XM_498369	TGCATTGGACCTGACCATGAA	TACCTTGAACTGTATGTGCAA		
442481	LOC442481	XM_498410	CAGGATGGAGGCTACGAAGGT	CCGACCCACAGGCTCCAGTAA		
442524	LOC442524	XM_499272	CAGACTTGAGGGCCCAGACAA	CTCGAAGATGCCAGTATTTCA		
442535	LOC442535	XM_499279	TACTATGACGTCTCCAACTCA	ACTGTTTGTCATAGTGCCGTA		
442562	LOC442562	XM_499306	CAGTCACAATGAGTAATTTAA	CCCGTCGAACACAGCCACCTA		
442573	LOC442573	XM_499315	ATCGGGTATTGAGTCCATGGA	AAGGGTGGAGCACAACGTCAA		
442578	LOC442578	XM_499318	TGGAATTGGCAGCGTGGCAAA	TCCACCTTACATGCAGTTGTA		
442606	LOC442606	XM_499352	GAACAACATCATGGAGTATTA	CCGTGCCTTCTTCCACTACAA		
442608	LOC442608	XM_499354	CTTCCACTTCCTGGCCAGGAA	TGCAGTCCAGGAGGATTTGAA		
442616	LOC442616	XM_499536	TTGGACATGCATATTCCCAAA	CCCGGCGGTTATTCCGTTTAA		
442622	LOC442622	XM_499365	CAAGGAGAAACTGGACTAATA	CTGGAGGGCCTTTGACTTCAA		
442625	LOC442625	XM_499368	AAGCAGGAGATTAGTAATGGA	AAGGAGAAATTGAGCGATGTA		
442696	LOC442696	XM_499441	CAGTTACATGTTCTCATTTCA	CTCAAGCGGTACTACACATAA		
442699	LOC442699	XM_499444	AAGCTCCACAATTGCCAGGAA	AGCTGTGACCTTAATAATTTA		
442708	LOC442708	XM_499454	AAGAATTTGACAAGAAGGATA	CTGCCTTGTCAAGGCCATTAA		
442709	LOC442709	XM_499455	ACAGATCACATTGCATGCAAA	TAGGAACAATGTGGCCTTCAA		
442711	LOC442711	XM_499457	CAGGAACATCAGCTTAACCAT	CTGGTGCATTTAGGCCACCTA		
442721	LOC442721	XM_499467	CACCACAGAAGTCAATTTGAA	AAAGTCAAATAGAGAACATAA		
445328	FLJ43692	NM_001003702	ATGTGTTTCATCAGCACTCAA	CTGGATGATTACTATCTCTTT		
445449	HBM	NM_001003938	TTGGTCTGTGCCTGTCAATAA	CAGGACGAGTTCACCGTGCAA		
474338	LOC474338	NR_002190	CAGAGAATTGCTGATAATCAT	CTCATTATTCATTATTGTTTA	AAGGAAGGTGAATATATTAAA	CAGGCTTGTGGTGATAAATAA

Table 4 (continued)

GeneID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
474343	SPIN-2	NM_001006681	CAGCAGGGAGGCGGAGGGCTA	CAAACTTGTGTGTACATGAAA		
474344	GIMAP6	NM_001007224	AGCGATCAATTTCCCATTGAA	CCCATTGAACTGAACATGCAA		
494143	LOC494143	NM_001008708	CAGAACCTCAATTGCATATAA	CTGGAAGACATTGCTGAACAA		
497049	FLJ25758	NM_001011541	CAGGCTGTTCCTAGTCATGGA	CACCCTCGAATTCTTCTTGAA		
503497	MS4A13	NM_001012417	CTGCAGTAACTCTAACAATAA	CTGGAATTATAAGTACTTTAA		

Table 5

Gene_ID	GeneSymbol	GenbankID	Target Sequence 1	Target Sequence 2	Target Sequence 3	Target Sequence 4
19	ABCA1	NM_005502	CCGGAACATGCTACAATACCA	CACCGACAATAAGCTGAATAA	CTGGATGTACAACGAACAGTA	CTCAGTGGCTGTGATCATCAA
1537	CYC1	NM_001916	CCCATCATGGGAATAAATTAA	TACCATGTCCCAGATAGCCAA	CAGCATGGACTTCGTGGCCTA	GCGGGAAGGTCTCTACTTCAA
5270	SERPINE2	NM_006216	CAGGATGGCTGGAACACTGTA	CACCAGACTGGTCCTCGTCAA	CTGGGAGGTATTGGAGGGAAA	AACGCCGTGTTTGTTAAGAAT
6183	MRPS12	NM_021107	CAGGACCACTATTAAGCCATA	CTGCTGGGACAAGACACTGTA	TTCCATCAGGACCACTATTAA	CACGTTTACCCGCAAGCCGAA
9493	KIF23	NM_004856	AAGGCTGAAGATTATGAAGAA	CACCTTTGCCGTCATGCGAAA	CAGAAGTTGAAGTGAAATCTA	CAGAATAAACTCTGGGTTAAA
9994	CASP8AP2	NM_012115	AACGAAGTTTCGAGATTCTTA	CAGTATTCAAATAGTCAGAAA	CAGTCTGATCTCAATAAGGAA	CAGCTGATGTGCGGAAGTCAA
84056	KATNAL1	NM_032116	AAGGAAATTAATATTAGTAAA	AAGGAAATTAATATTAGTAAA	TAGGTTATATTTGGTAATAAA	TAGGTTATATTTGGTAATAAA
3384	ICAM2	NM_000873	CCCGAAGATGTTGGAGATCTA	CAGGTCATCCTGACACTGCAA		
10036	CHAF1A	NM_005483	CACAATAAACTAAATTCTGAA	AAGGAAGAAGAGAAACGGTTA		
10336	PCGF3	NM_006315	CACGTTGTACGTGAATGTTTA	ACGGTTTGAGTTACTCAGTTA		
23151	KIAA0767	XM_027105	AAAGAGGAACAAAGTCATCAA	AAACTTTGTTTGTTTAAAGAA		
26064	RAI14	NM_015577	TAGGATGATAGATGAACTCAA	ATGGATGAAGATGTCCAGAAA		
26073	POLDIP2	NM_015584	CACGTGAGGTTTGATCAGTAA	TAGGTATGGATTGATGACTAA		
50804	MYEF2	NM_016132	AACATTTATTTAATAATTATA	AACCTGCTATTAAATAGTAAA		
51186	WBP5	NM_001006612	CAGGAGTTTAAAGAAGATATA	CACATTATTATTGCTAGAATA		
55004	FLJ20625	NM_017907	AAGGAAGTATATTCATCCAAA	CTGCTACTAATCACAGAGAAA		
55707	FLJ10420	NM_018090	CCGGGCATGTTTGGCAGTAAA	CTGGTTTATAAGAAATCTGAA		
57194	ATP10A	NM_024490	CAGGAAATGATAACAACCCAA	CACCTGGGCATTGAAACCAAA		
57479	KIAA1205	XM_046305	CTGAATGAGCACAAGAAGAAA	ACGCCAGGACACGGTCATCAA		
57591	MKL1	NM_020831	CCGCATTTCATGAGCAGAGAA	TTGGTGTAGTGTAACCATTTA		
58506	SR-A1	NM_021228	AACGGTTTCTCCACAGTCGAA	CTGGGCTCCATTGGCGTCAAA		
60677	BRUNOL6	NM_052840	ATGCAGGTAATTAGAACGTTA	CAGGAGTTTGGTGATGCGGAA		
121053	MGC40397	NM_152318	ATGGGACAGGTTGCTCATCAA	CCTGGTCGTTTCAATATTGAA		
127703	FLJ38984	NM_152374	TAGGAGAATGGGAATTCTAAA	ACGCCGGAAGGTGGTGACTAA		
146850	C17orf38	NM_001010855	CAGGAGGTGGAAGCAATCAAA	ACCCATCTATTTCCAGATCTA		
221491	C6orf1	NM_001008703	CAGATGTATAGTATTCAGTAT	CCAGATGTATAGTATTCAGTA		