

FIG. 1
Study design:

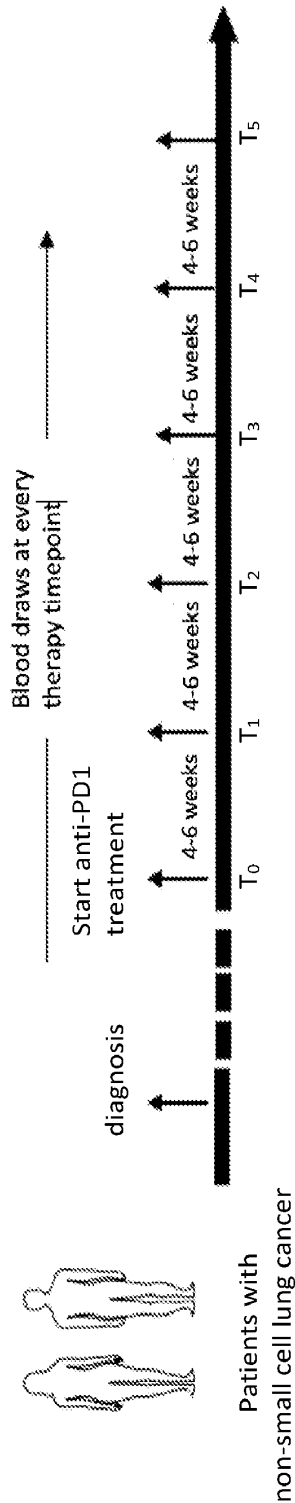


FIG. 2

	Responders (n=18)	Non-Responders (n=13)	Total (n=31)
Age ⁺			
Gender(%)	71.5	69.5	71
Female	55.6%	61.5%	58.1%
Stage(%)			
II	-	7.7%	3.2%
III	33.3%	15.4%	25.8%
IV	66.7%	76.9%	71%
Histology			
Adenocarcinoma	77.7%	76.9%	77.4%
Squamous cell carci.	22.2%	23.1%	22.6%
PDL1 status			
Positive	61.1%	61.5%	61.3%
Negative	5.6%	30.8%	16.1%
Unknown	33.3%	7.7%	22.6%
Treatment			
Nivolumab	33.3%	61.5%	45.2%
Pembrolizumab	66.7%	38.5%	54.8%

FIG. 3

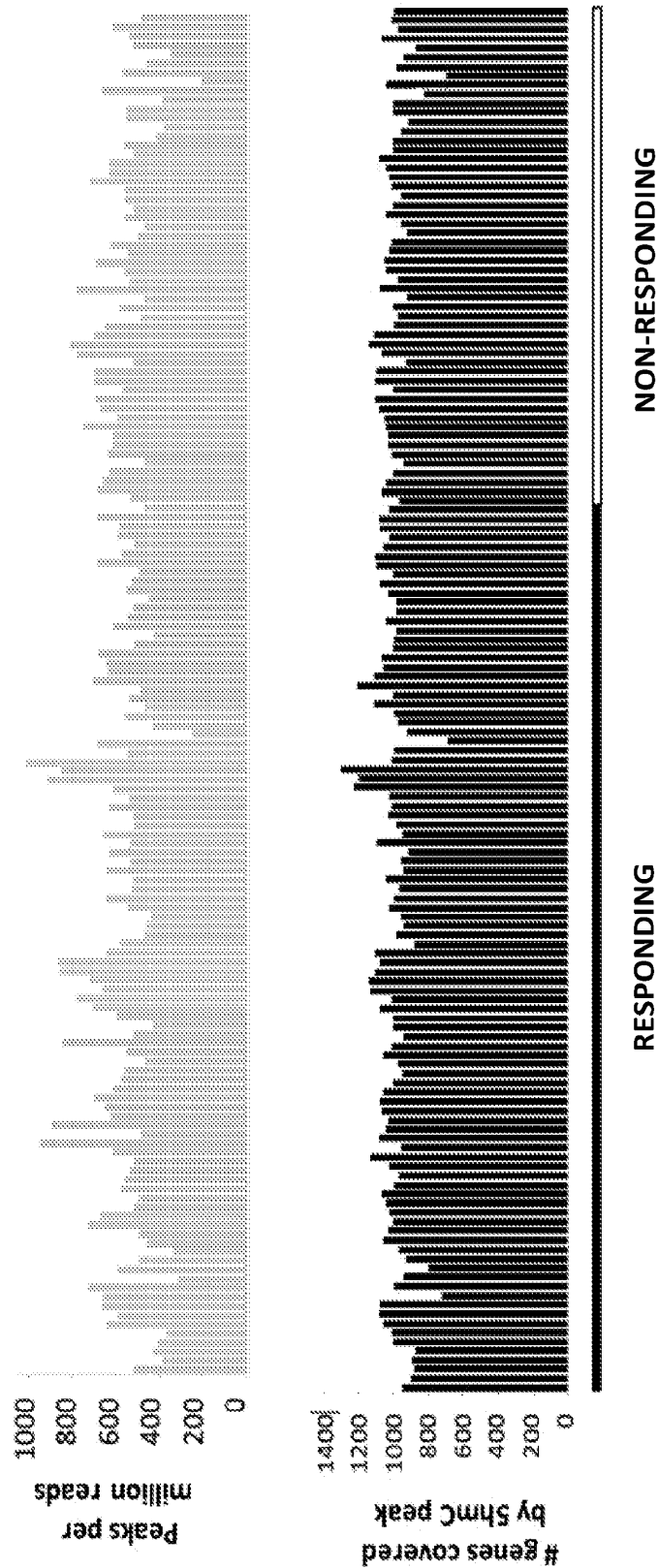


FIG. 5

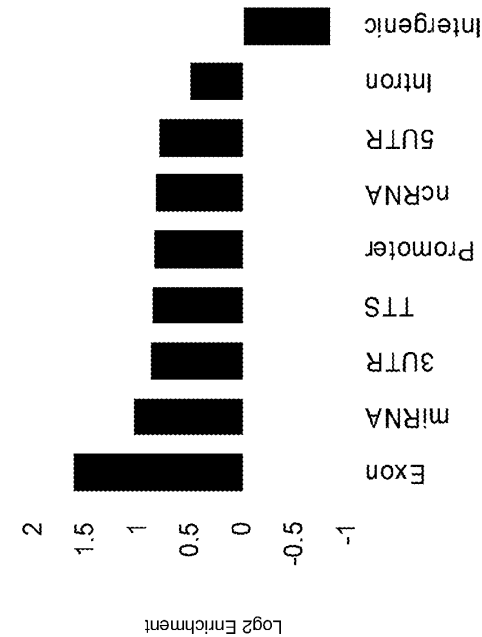


FIG. 4

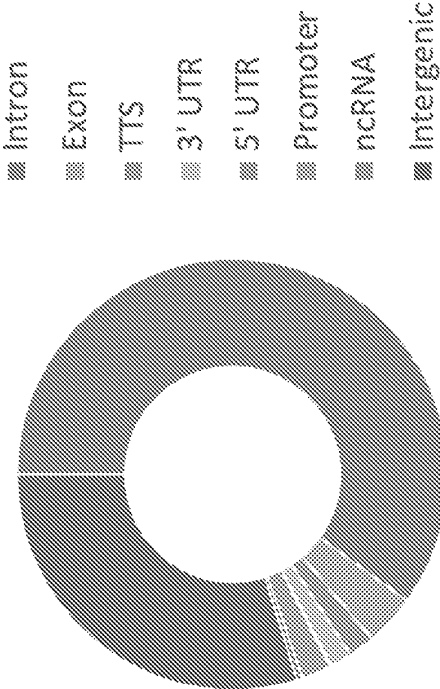


FIG. 6

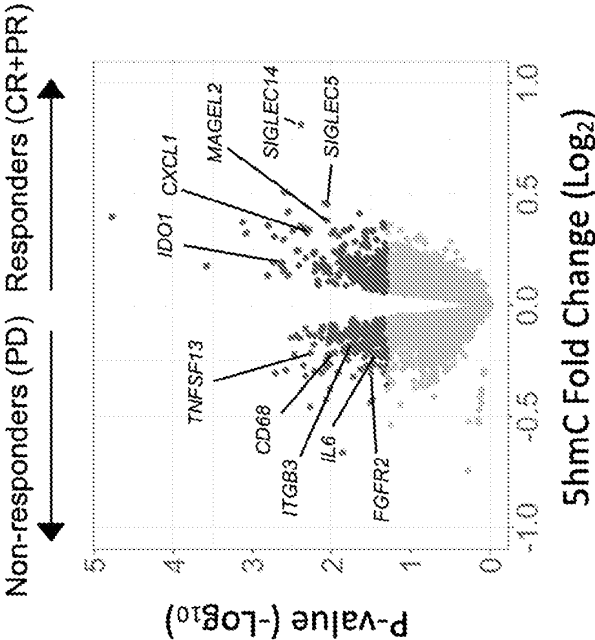


FIG. 7

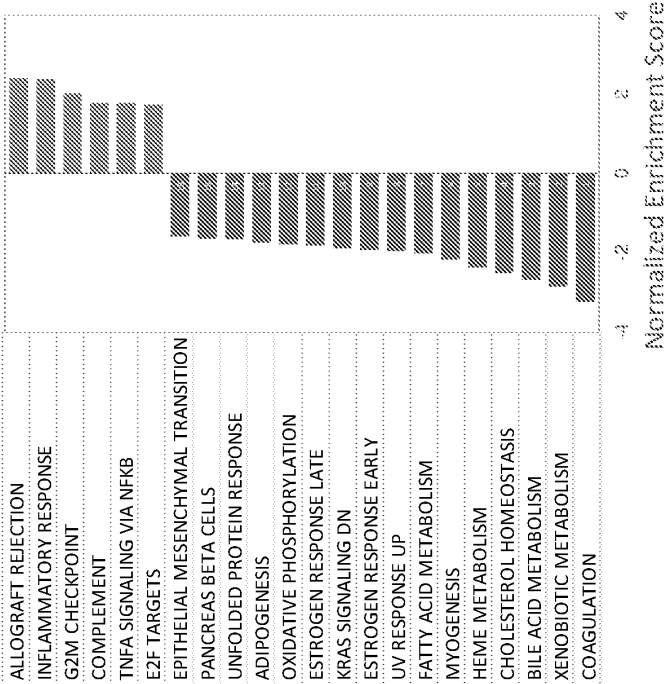


FIG. 8

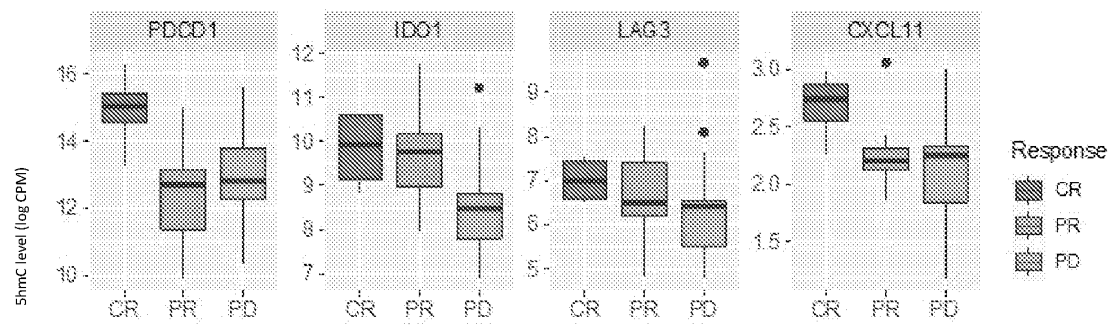


FIG. 9

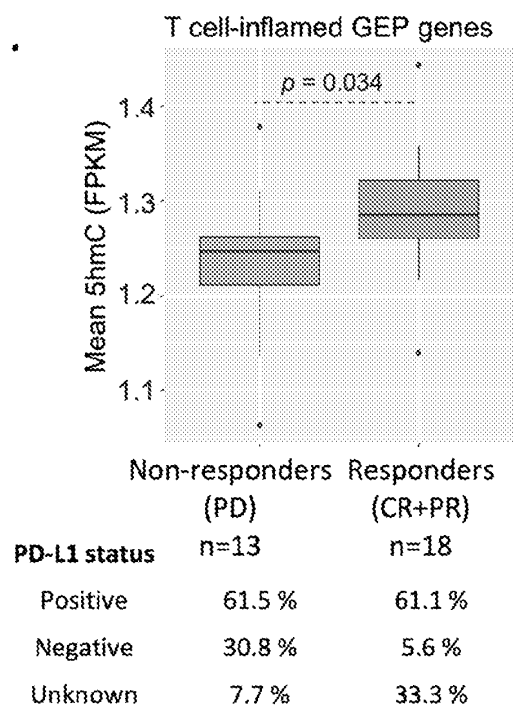


FIG. 10

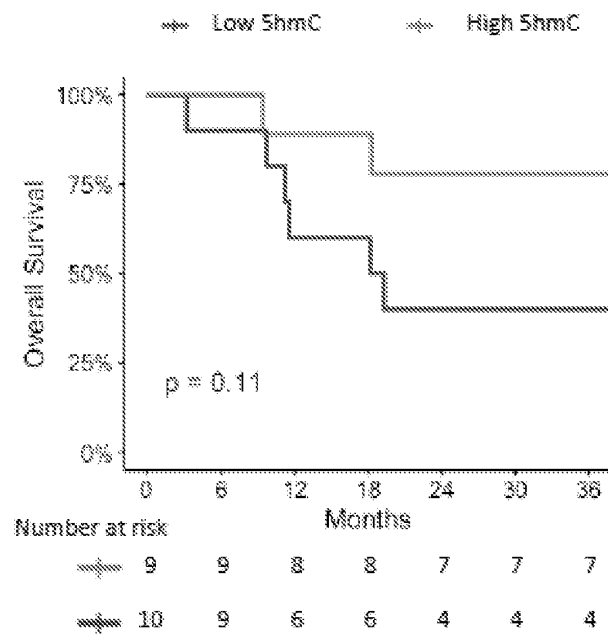


FIG. 11

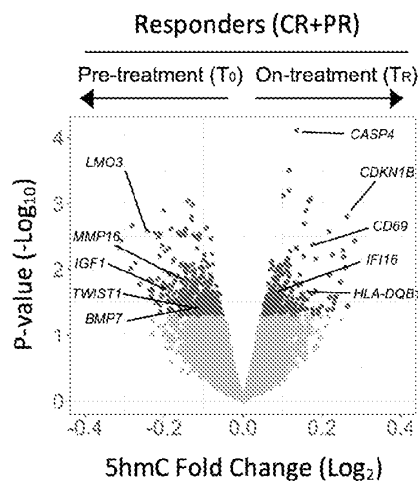


FIG. 12

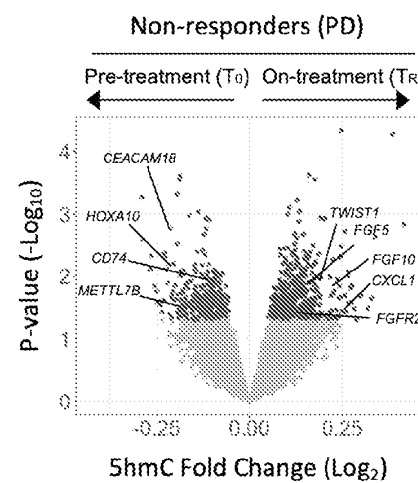


FIG. 13

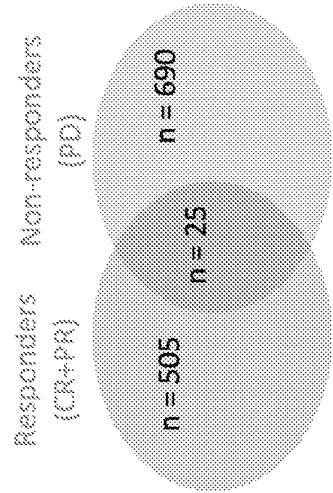


FIG. 14

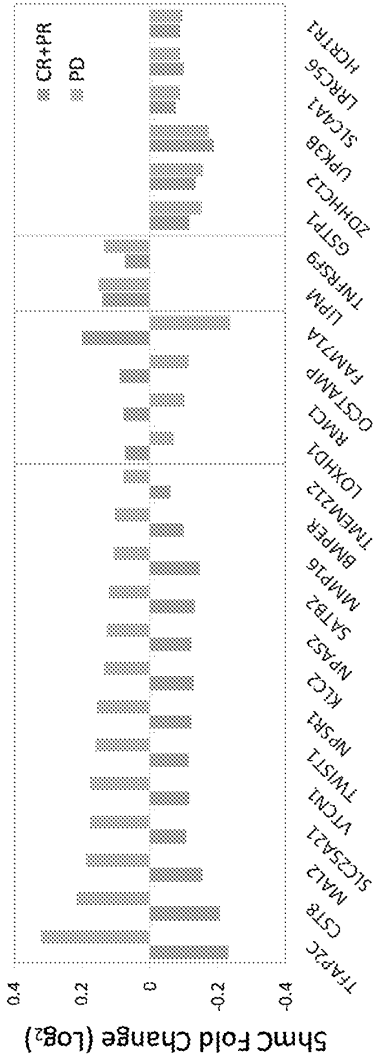


FIG. 15

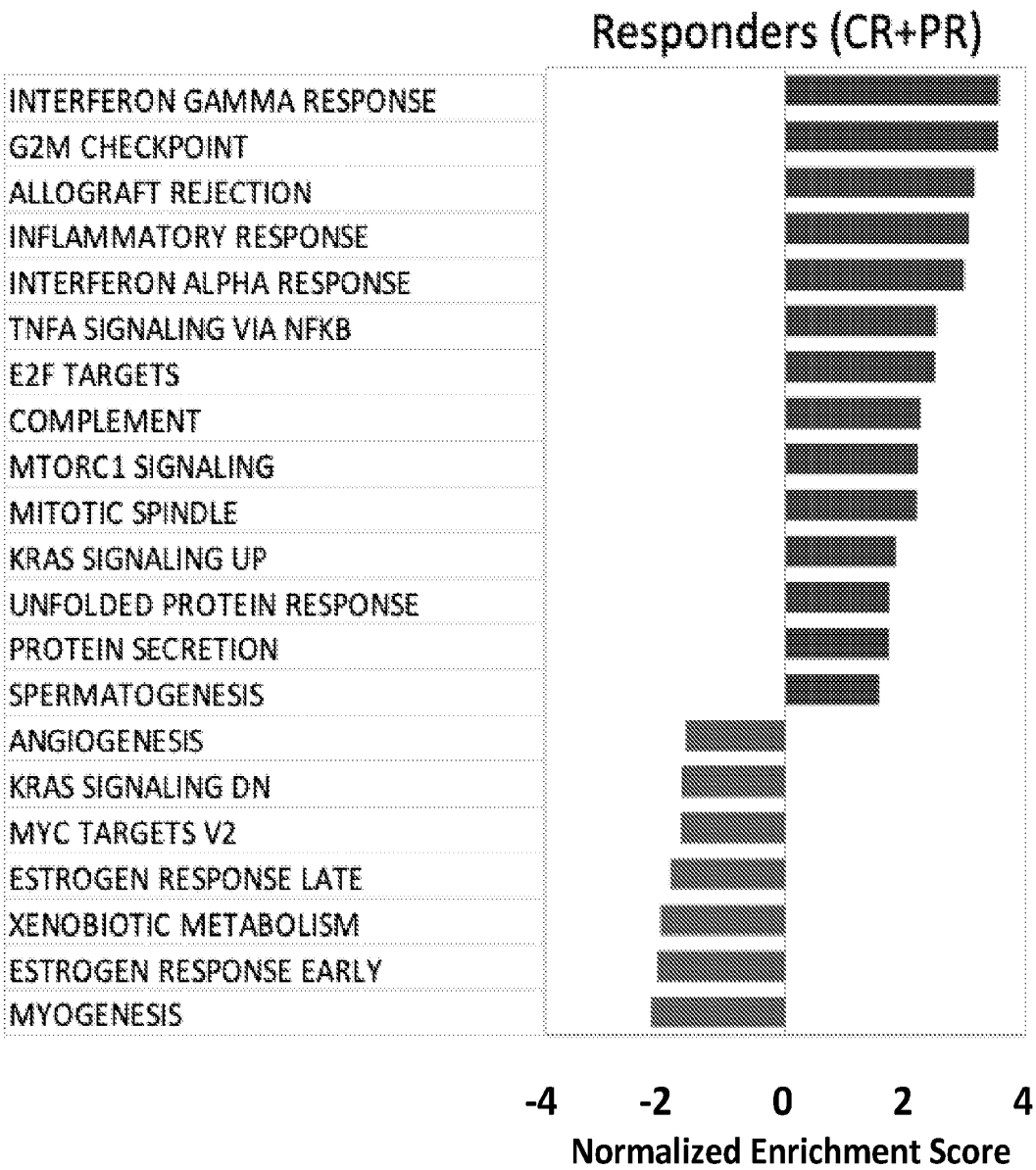


FIG. 16

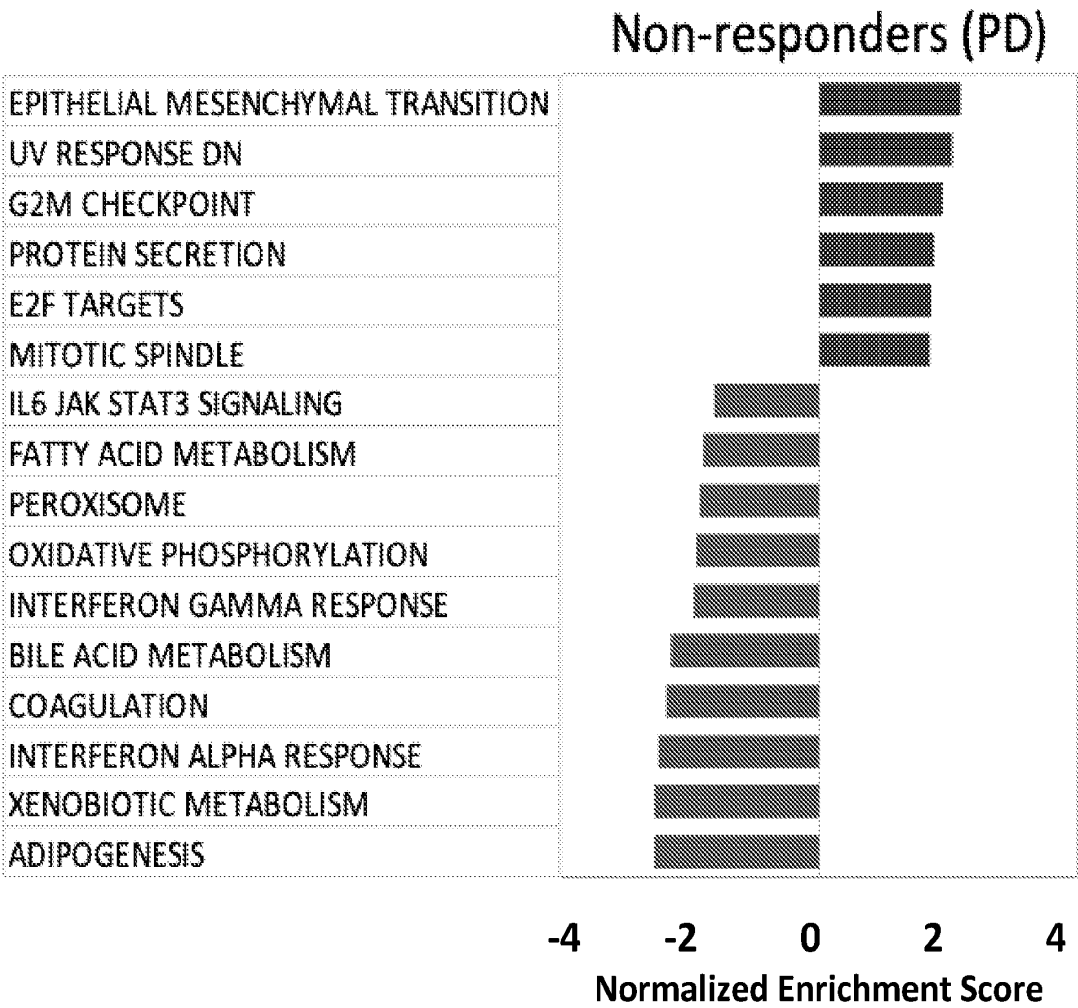


FIG. 17

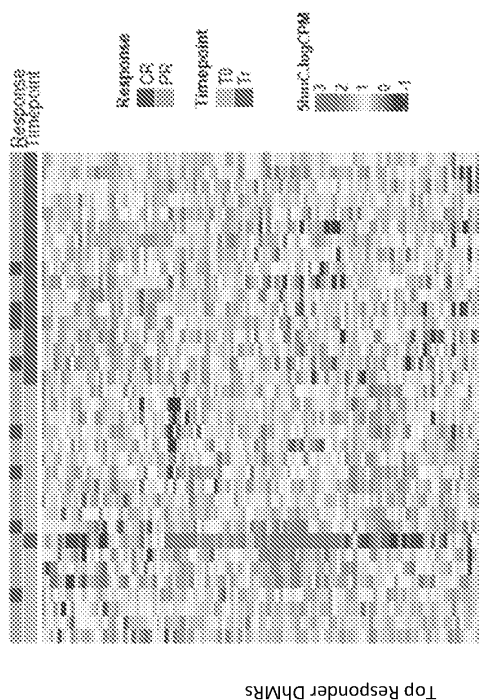


FIG. 18

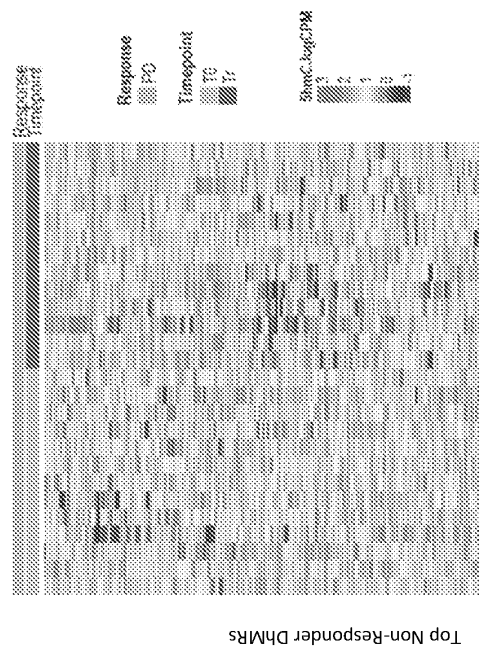


FIG. 19

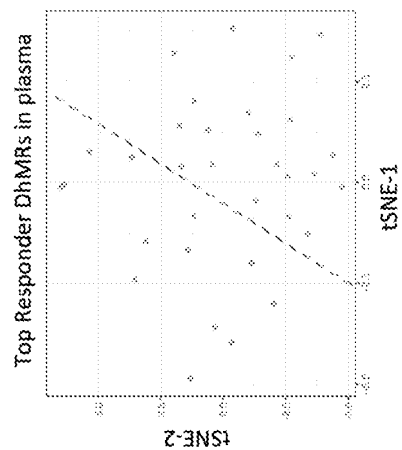


FIG. 20

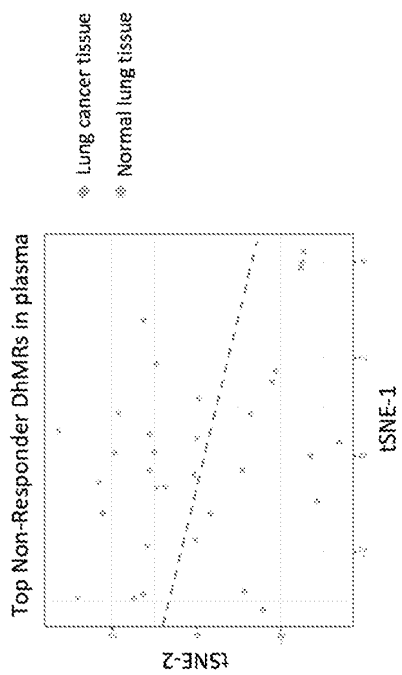


FIG. 21

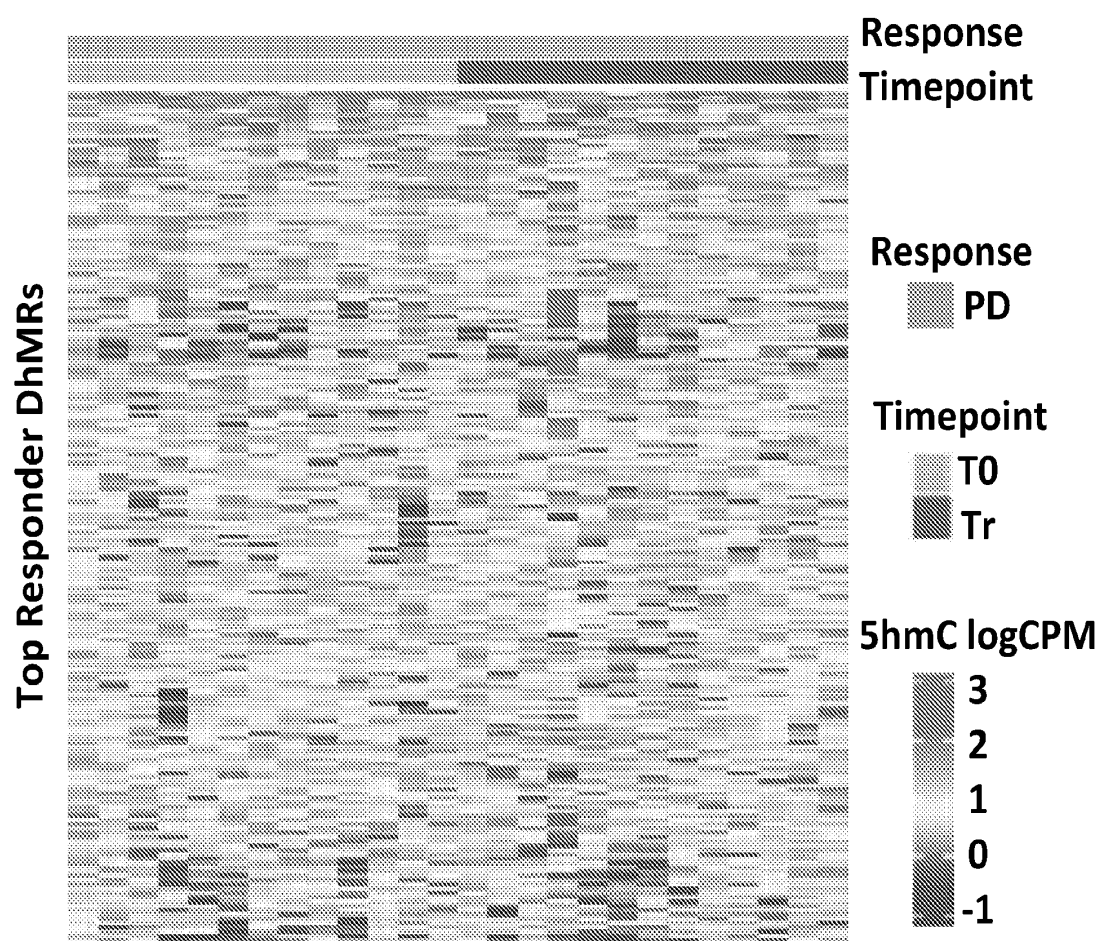


FIG. 22

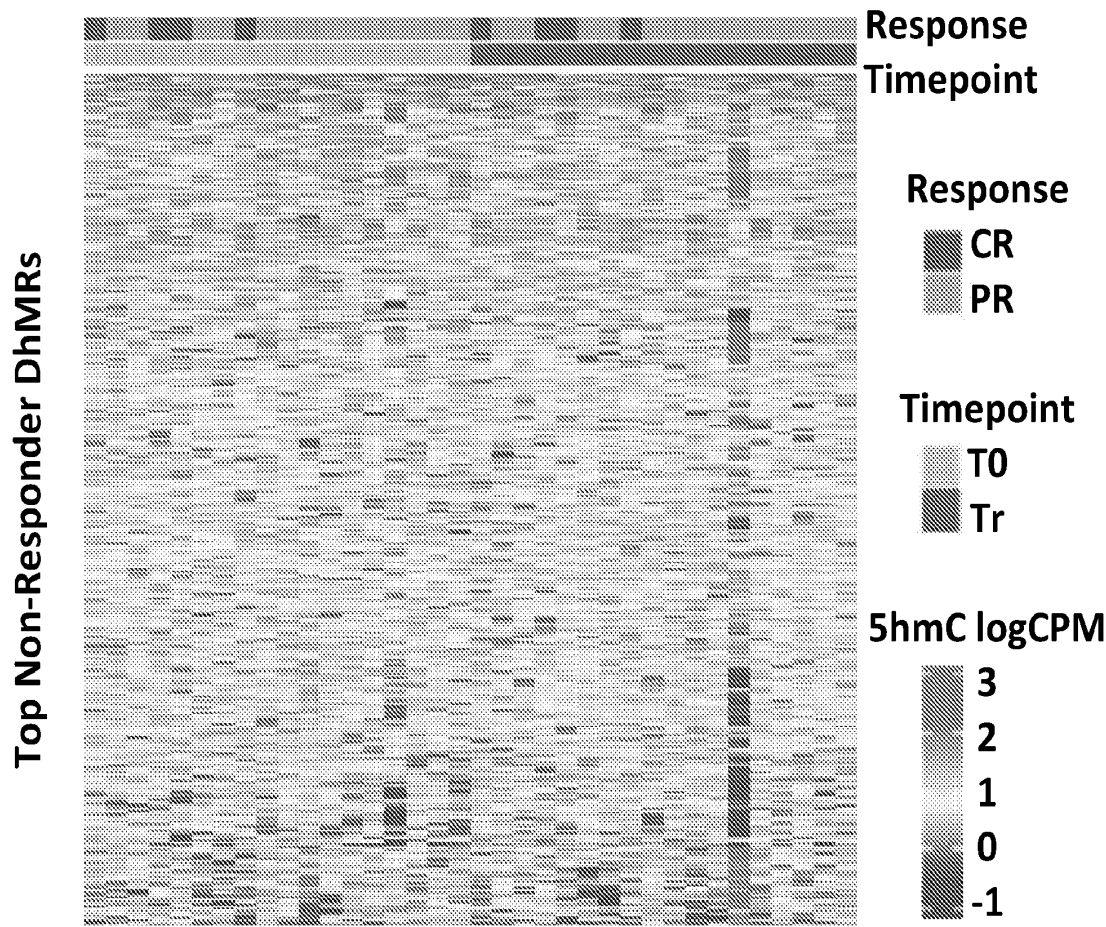


FIG. 23

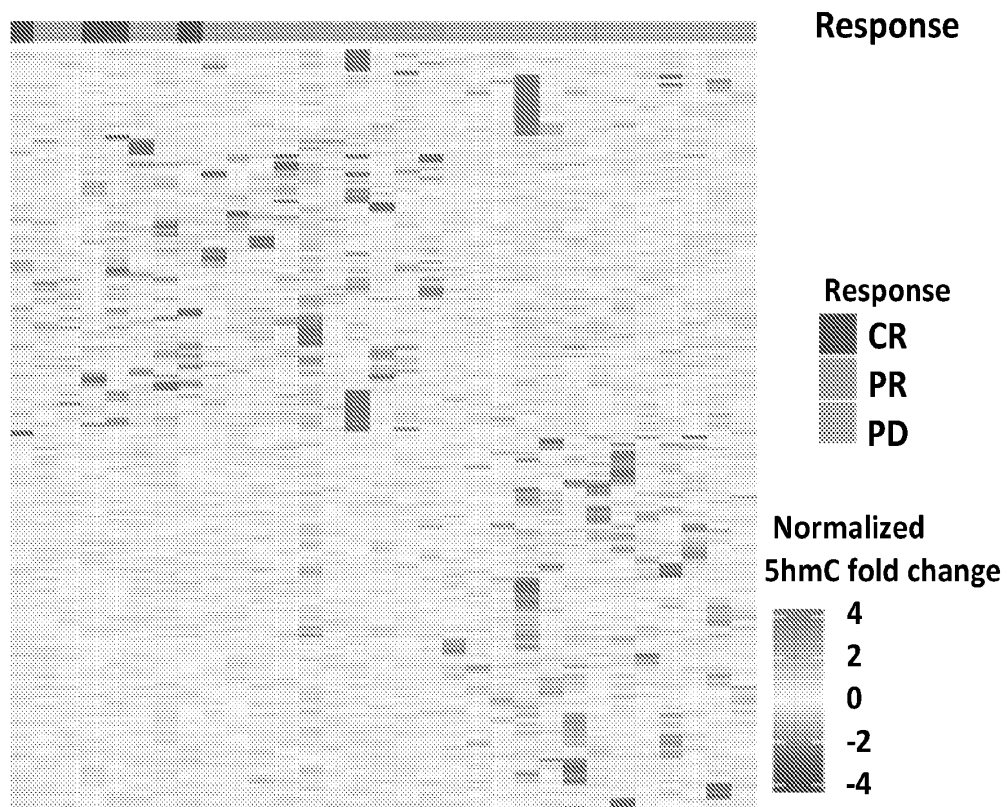


FIG. 24

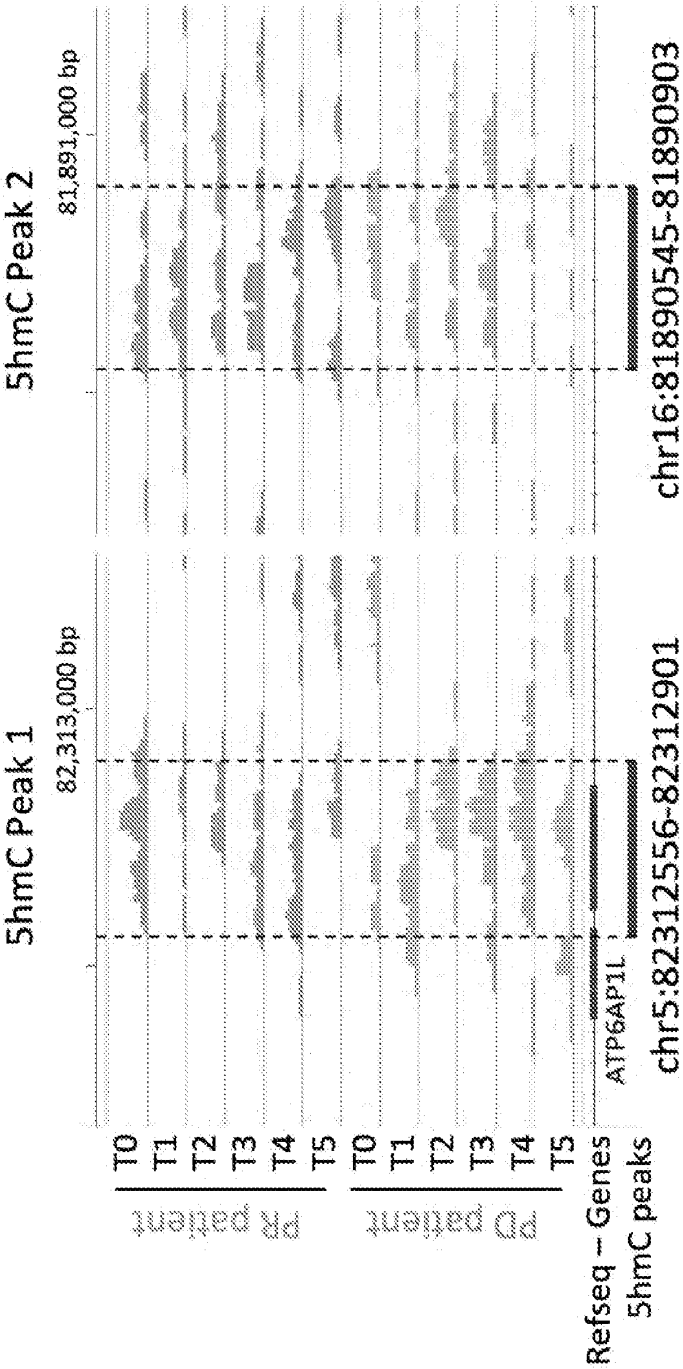


FIG. 25

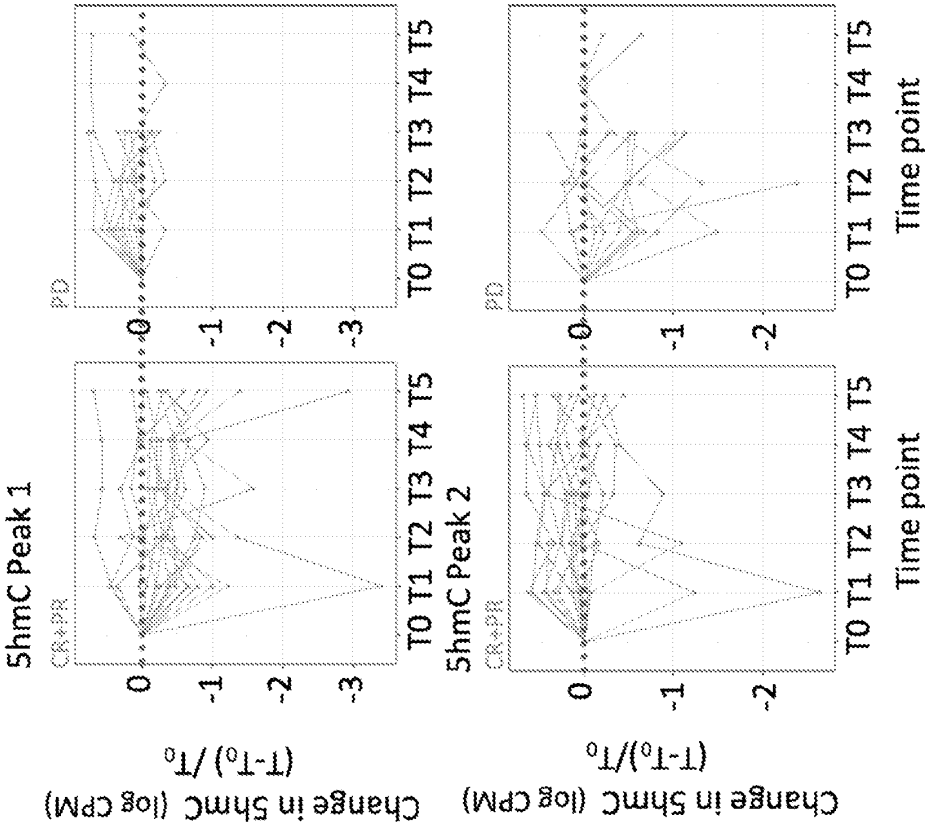


FIG. 26

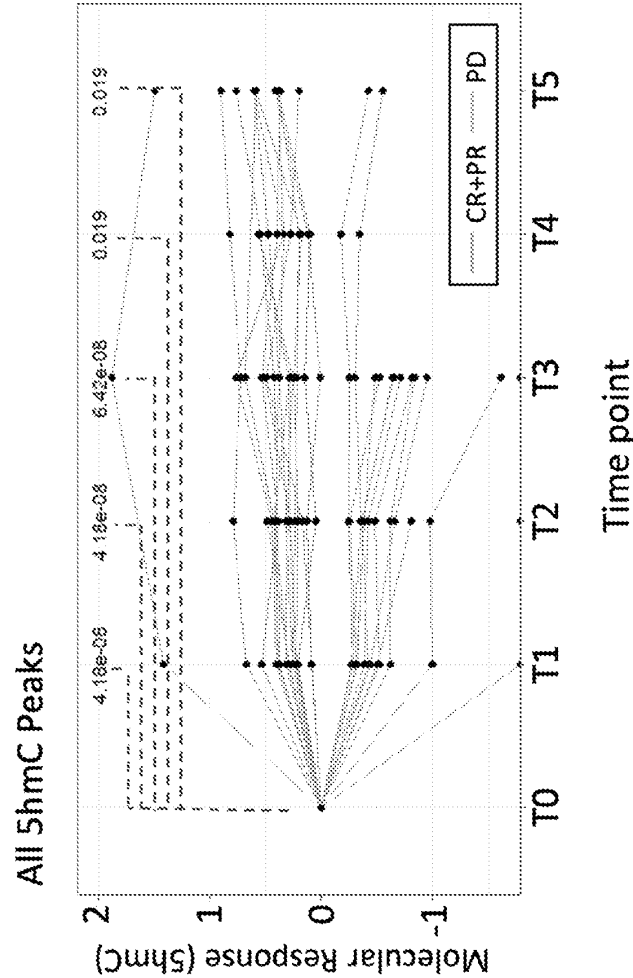


FIG. 27

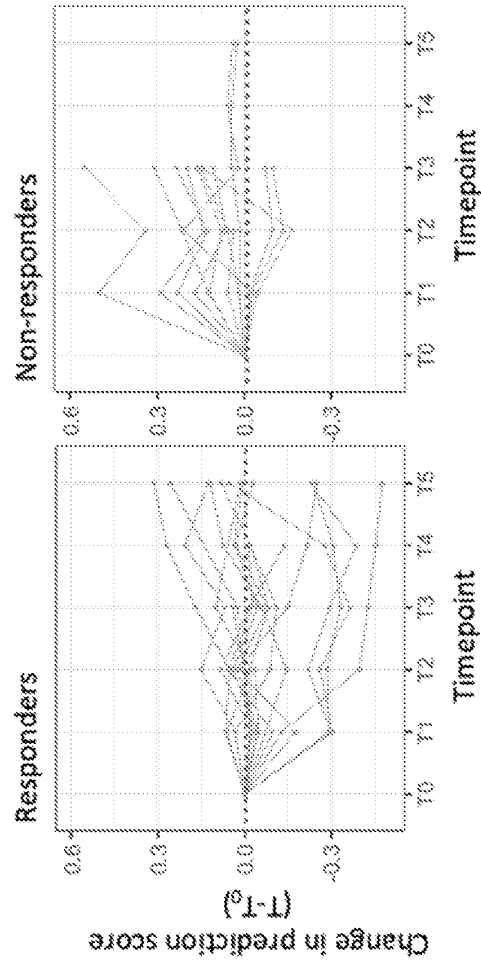


FIG. 28

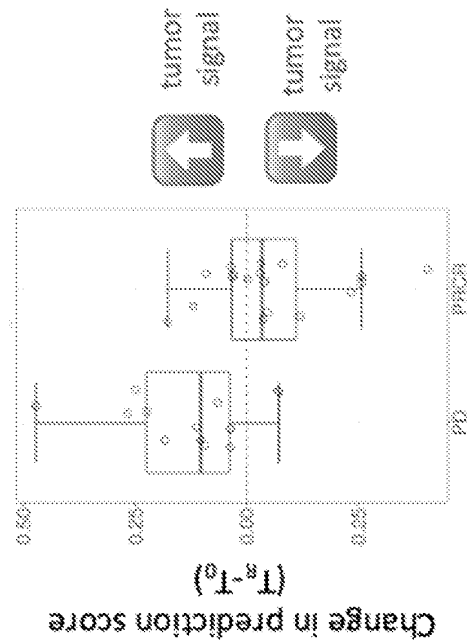


FIG. 29

Region	Chr	Start	End	Annotation	Detailed Annotation
1	chr8	58345645	58346139	Intergenic	L2b LINE L2
2	chr4	26121172	26121812	Intergenic	MIRb SINE MIR
3	chr7	142027489	142027861	exon (NM_001365693, exon 10 of 71)	exon (NM_001365693, exon 10 of 71)
4	chr20	45180753	45181715	Intergenic	MER30 DNA hAT-Charlie
5	chr1	56576333	56576793	intron (NM_003713, intron 1 of 5)	intron (NM_003713, intron 1 of 5)
6	chr15	94172674	94173041	Intergenic	L1MB2 LINE L1
7	chr4	41013360	41013627	intron (NM_004307, intron 6 of 17)	intron (NM_004307, intron 6 of 17)
8	chr7	48287990	48288654	intron (NM_152701, intron 20 of 61)	MER63B DNA hAT-Blackjack
9	chr8	135638625	135638982	intron (NM_006558, intron 7 of 8)	AluSc SINE Alu
10	chr2	224645766	224646062	Intergenic	Intergenic
11	chr9	120780896	120781573	intron (NM_012164, intron 3 of 7)	intron (NM_012164, intron 3 of 7)
12	chr4	121992567	121993325	Intergenic	Intergenic
13	chr6	166488650	166489049	exon (NM_001318937, exon 8 of 19)	exon (NM_001318937, exon 8 of 19)
14	chr4	10518457	10519026	intron (NM_052964, intron 15 of 18)	intron (NM_052964, intron 15 of 18)
15	chr18	56468741	56469013	Intergenic	Arthur1B DNA hAT-Tip100
16	chr3	53700512	53701121	intron (NM_000720, intron 8 of 48)	intron (NM_000720, intron 8 of 48)
17	chr12	131293631	131293934	Intergenic	MER68 LTR ERV1
18	chr16	22672084	22672471	Intergenic	L2b LINE L2
19	chr2	44082840	44083274	Intergenic	AluSx1 SINE Alu
20	chr6	7562514	7562876	exon (NM_001319034, exon 5 of 24)	exon (NM_001319034, exon 5 of 24)
21	chr4	80087984	80088343	Intergenic	MSTB2 LTR ERV1-MaLR
22	chr10	24245078	24245419	intron (NM_019590, intron 2 of 20)	intron (NM_019590, intron 2 of 20)
23	chr22	42528441	42528941	Intergenic	ORSL DNA hAT-Tip100
24	chr16	54176125	54176748	Intergenic	Intergenic
25	chr19	51635495	51636947	Intergenic	Intergenic

Region	Chr	Start	End	Annotation	Detailed Annotation
26	chr10	12099251	12099596	intron (NM_018706, intron 8 of 16)	AluSz SINE Alu
27	chr18	56805193	56805533	intron (NM_015285, intron 19 of 27)	Ricksha_b DNA MULE-MuDR
28	chr13	59357342	59358377	Intergenic	Intergenic
29	chr2	33903072	33903967	intron (NR_126403, intron 2 of 5)	LTR12C LTR ERV1
30	chr17	76368428	76368952	Intergenic	MER20 DNA hAT-Charlie
31	chr10	27851388	27851854	intron (NM_018076, intron 19 of 19)	L1ME1 LINE L1
32	chr11	4454390	4454985	Intergenic	HERVIP10B3-int LTR ERV1
33	chr2	175637274	175637830	Intergenic	Intergenic
34	chr3	3821811	3822314	intron (NM_001324188, intron 2 of 2)	MIR SINE MIR
35	chr2	89993190	89993551	Intergenic	Intergenic
36	chr15	55294246	55294673	Intergenic	AluJb SINE Alu
37	chr12	68736570	68736914	intron (NM_020401, intron 26 of 27)	AluSq2 SINE Alu
38	chr12	131651091	131651636	Intergenic	L1ME3G LINE L1
39	chr10	70690648	70691016	intron (NM_080722, intron 2 of 21)	intron (NM_080722, intron 2 of 21)
40	chr4	48173205	48173553	intron (NM_003215, intron 3 of 17)	intron (NM_003215, intron 3 of 17)
41	chr5	128071906	128072202	intron (NR_152810, intron 1 of 3)	THE1B LTR ERV1-MaLR
42	chr12	762706	763656	intron (NM_001184985, intron 1 of 27)	MER44B DNA TcMar-Tigger
43	chr9	138127339	138127705	Intergenic	Intergenic
44	chr1	247841561	247841874	exon (NM_001001959, exon 1 of 1)	exon (NM_001001959, exon 1 of 1)
45	chr17	72925451	72925788	intron (NM_139177, intron 5 of 9)	intron (NM_139177, intron 5 of 9)
46	chr2	66555601	66556292	intron (NM_002398, intron 9 of 12)	intron (NM_002398, intron 9 of 12)
47	chr8	133103686	133104014	intron (NM_003235, intron 43 of 47)	L2a LINE L2
48	chr17	46287634	46287934	intron (NM_001352769, intron 4 of 4)	intron (NM_001352769, intron 4 of 4)
49	chr9	89358401	89358786	intron (NM_001282688, intron 16 of 16)	intron (NM_001282688, intron 16 of 16)
50	chr5	52998262	52998613	intron (NR_073107, intron 1 of 28)	AluSx1 SINE Alu
51	chr2	218559055	218559513	intron (NM_020935, intron 3 of 25)	AluJo SINE Alu

FIG. 30

Region #	Chr	Start	End	Annotation	Detailed Annotation
1	chr1	1385191	1385724	TTS (NM_001350497)	TTS (NM_001350497)
2	chr1	1740291	1740752	intron (NM_182838, intron 1 of 5)	AluY SINE Alu
3	chr1	2474831	2475197	intron (NM_001303012, intron 1 of 21)	intron (NM_001303012, intron 1 of 21)
4	chr1	32312560	32312946	intron (NM_004964, intron 2 of 13)	AluSz6 SINE Alu
5	chr1	151285404	151285785	5' UTR (NM_001304763, exon 2 of 10)	5' UTR (NM_001304763, exon 2 of 10)
6	chr1	154204813	154205269	intron (NM_001010979, intron 2 of 3)	AluSx SINE Alu
7	chr1	155043282	155043577	exon (NM_001143687, exon 9 of 16)	exon (NM_001143687, exon 9 of 16)
8	chr1	204085723	204086209	intron (NM_005686, intron 1 of 13)	AluY SINE Alu
9	chr1	204473976	204474356	intron (NM_002646, intron 2 of 33)	AluSp SINE Alu
10	chr1	245704047	245704398	3' UTR (NM_018012, exon 15 of 15)	3' UTR (NM_018012, exon 15 of 15)
11	chr10	29266670	29266985	Intergenic	Intergenic
12	chr11	20494983	20495421	intron (NM_005788, intron 15 of 15)	AluSq SINE Alu
13	chr11	69009702	69009952	intron (NM_001098515, intron 2 of 2)	intron (NM_001098515, intron 2 of 2)
14	chr11	128491795	128492861	intron (NM_001143820, intron 3 of 9)	intron (NM_001143820, intron 3 of 9)
15	chr12	53481502	53482055	TTS (NM_001128911)	TTS (NM_001128911)
16	chr12	128771296	128771721	Intergenic	AluSz SINE Alu
17	chr13	45198203	45198555	intron (NM_198404, intron 1 of 1)	intron (NM_198404, intron 1 of 1)
18	chr13	49231307	49231985	Intergenic	Intergenic
19	chr13	109485718	109486199	Intergenic	L1ME3B LINE L1
20	chr14	73777379	73777789	intron (NM_001043318, intron 1 of 11)	L2b LINE L2
21	chr15	69996240	69996576	Intergenic	Intergenic
22	chr15	78398391	78398781	Intergenic	Intergenic
23	chr15	85071487	85071882	intron (NM_001243137, intron 3 of 21)	L1M6 LINE L1
24	chr16	12060778	12061105	intron (NM_032167, intron 8 of 20)	MIR3 SINE MIR

Region #	Chr	Start	End	Annotation	Detailed Annotation
25	chr16	29571755	29572488	intron (NR_135305, intron 1 of 13)	intron (NR_135305, intron 1 of 13)
26	chr16	69023135	69023513	intron (NM_024562, intron 16 of 17)	AluSz6 SINE Alu
27	chr16	70754327	70754739	promoter-TSS (NR_034083)	promoter-TSS (NR_034083)
28	chr16	84043724	84044078	Intergenic	Intergenic
29	chr17	2282638	2282987	exon (NM_017575, exon 8 of 19)	exon (NM_017575, exon 8 of 19)
30	chr17	19855100	19855473	intron (NM_014683, intron 3 of 26)	AluY SINE Alu
31	chr17	38569845	38570191	intron (NM_025248, intron 2 of 18)	intron (NM_025248, intron 2 of 18)
32	chr17	50745636	50746061	exon (NM_016424, exon 8 of 10)	exon (NM_016424, exon 8 of 10)
33	chr18	8771977	8772330	intron (NM_015210, intron 4 of 16)	intron (NM_015210, intron 4 of 16)
34	chr18	70294652	70295035	intron (NM_004232, intron 1 of 1)	intron (NM_004232, intron 1 of 1)
35	chr19	455516	455973	intron (NM_012435, intron 1 of 12)	MLT1D LTR ERV1-MaLR
36	chr19	40629454	40629772	3' UTR (NM_001042545, exon 30 of 30)	3' UTR (NM_001042545, exon 30 of 30)
37	chr19	47228621	47229043	intron (NM_001127240, intron 1 of 3)	intron (NM_001127240, intron 1 of 3)
38	chr19	51821231	51821800	intron (NR_163433, intron 9 of 11)	MER20 DNA hAT-Charlie
39	chr2	24145395	24145871	intron (NM_001145710, intron 5 of 10)	intron (NM_001145710, intron 5 of 10)
40	chr2	36817475	36817864	Intergenic	Intergenic
41	chr2	36907242	36907598	intron (NM_003162, intron 3 of 17)	AluSc8 SINE Alu
42	chr2	62020627	62021092	intron (NM_001321781, intron 2 of 2)	AluSp SINE Alu
43	chr2	71620909	71621345	intron (NM_001130987, intron 41 of 55)	intron (NM_001130987, intron 41 of 55)
44	chr2	111166061	111166554	3' UTR (NM_001204112, exon 5 of 5)	3' UTR (NM_001204112, exon 5 of 5)
45	chr2	175100486	175100813	intron (NR_045773, intron 9 of 13)	LTR10C LTR ERV1
46	chr20	2890796	2891530	intron (NM_080840, intron 1 of 22)	L2a LINE L2
47	chr20	23051152	23051862	Intergenic	CpG
48	chr20	49798502	49798971	Intergenic	MLT1K LTR ERV1-MaLR
49	chr22	17721520	17722002	intron (NM_001270733, intron 1 of 1)	AluSx SINE Alu
50	chr22	29733505	29734022	intron (NM_001318129, intron 5 of 5)	intron (NM_001318129, intron 5 of 5)
51	chr3	12877065	12877397	TTS (NR_136189)	TTS (NR_136189)

Region #	Chr	Start	End	Annotation	Detailed Annotation
52	chr3	16212352	16212656	intron (NM_001319051, intron 5 of 9)	intron (NM_001319051, intron 5 of 9)
53	chr3	72593102	72593561	Intergenic	AluY SINE Alu
54	chr3	128689701	128690107	Intergenic	AluSx SINE Alu
55	chr3	131006996	131007462	intron (NM_001001486, intron 27 of 27)	intron (NM_001001486, intron 27 of 27)
56	chr3	195983915	195984260	intron (NR_003264, intron 5 of 16)	intron (NR_003264, intron 5 of 16)
57	chr4	1360493	1360866	intron (NM_020894, intron 7 of 13)	intron (NM_020894, intron 7 of 13)
58	chr4	3557350	3559093	Intergenic	Intergenic
59	chr4	7937394	7937887	intron (NM_001371091, intron 1 of 17)	AluSx1 SINE Alu
60	chr4	9818638	9819197	Intergenic	AluY SINE Alu
61	chr4	86791103	86791448	intron (NM_080685, intron 40 of 47)	L1PA6 LINE L1
62	chr4	183912481	183912828	intron (NM_020225, intron 1 of 3)	intron (NM_020225, intron 1 of 3)
63	chr5	14557018	14557502	Intergenic	AluSc SINE Alu
64	chr5	95946131	95946485	intron (NM_012081, intron 1 of 11)	intron (NM_012081, intron 1 of 11)
65	chr5	134091608	134092049	Intergenic	MIR SINE MIR
66	chr5	149780761	149781292	intron (NM_001172699, intron 1 of 10)	AluSx1 SINE Alu
67	chr5	169717631	169717990	intron (NR_156756, intron 21 of 52)	AluSx1 SINE Alu
68	chr6	11225293	11225662	intron (NM_001142393, intron 2 of 7)	intron (NM_001142393, intron 2 of 7)
69	chr6	34865904	34866480	intron (NM_017754, intron 15 of 20)	AluSg SINE Alu
70	chr6	159986224	159986647	intron (NM_000876, intron 1 of 47)	AluSx SINE Alu
71	chr7	17069146	17069662	Intergenic	Intergenic
72	chr7	47454589	47454968	intron (NM_022748, intron 4 of 30)	(GCAG)n Simple_repeat Simple_repeat
73	chr7	55449273	55449722	Intergenic	CpG
74	chr7	65727455	65727915	intron (NR_038378, intron 2 of 7)	AluSz SINE Alu
75	chr7	138294885	138295191	Intergenic	THE1C LTR ERV1-MaLR
76	chr7	139130246	139130853	Intergenic	L1PA5 LINE L1
77	chr8	11463273	11463644	intron (NM_053279, intron 1 of 2)	intron (NM_053279, intron 1 of 2)
78	chr8	38469999	38470345	Intergenic	AluSc SINE Alu

Region #	Chr	Start	End	Annotation	Detailed Annotation
79	chr8	118348348	118348868	intron (NM_001363274, intron 4 of 4)	AluY SINE Alu
80	chr8	144515873	144516241	exon (NM_004260, exon 5 of 21)	exon (NM_004260, exon 5 of 21)
81	chr9	89876515	89877058	Intergenic	AluY SINE Alu
82	chr9	97909049	97909401	intron (NM_001330725, intron 5 of 5)	AluSx1 SINE Alu
83	chr9	132168379	132168915	intron (NM_032536, intron 2 of 7)	intron (NM_032536, intron 2 of 7)
84	chr9	137193698	137194031	intron (NM_001128228, intron 1 of 3)	intron (NM_001128228, intron 1 of 3)
85	chr1	10091565	10091845	intron (NM_006048, intron 2 of 26)	AluSx1 SINE Alu
86	chr1	30065208	30065679	Intergenic	Intergenic
87	chr1	60981811	60982321	Intergenic	AluSc5 SINE Alu
88	chr1	62618811	62619180	intron (NM_001367561, intron 13 of 49)	intron (NM_001367561, intron 13 of 49)
89	chr1	68228900	68229301	intron (NM_024911, intron 1 of 11)	MIR3 SINE MIR
90	chr1	77671865	77672248	intron (NM_001308237, intron 1 of 13)	MER44B DNA TcMar-Tigger
91	chr1	84319557	84320250	intron (NM_001134663, intron 2 of 3)	intron (NM_001134663, intron 2 of 3)
92	chr1	202302955	202303328	intron (NM_001017403, intron 9 of 17)	intron (NM_001017403, intron 9 of 17)
93	chr1	204480563	204480966	intron (NM_002646, intron 2 of 33)	intron (NM_002646, intron 2 of 33)
94	chr1	239858112	239858553	intron (NM_001347716, intron 7 of 7)	intron (NM_001347716, intron 7 of 7)
95	chr1	246816278	246816645	Intergenic	AluJb SINE Alu
96	chr10	1609541	1609935	intron (NM_018702, intron 1 of 9)	intron (NM_018702, intron 1 of 9)
97	chr11	8838027	8838514	intron (NM_005418, intron 3 of 22)	intron (NM_005418, intron 3 of 22)
98	chr11	77590434	77590848	intron (NM_001363477, intron 1 of 1)	intron (NM_001363477, intron 1 of 1)
99	chr11	129259999	129260502	intron (NR_145484, intron 1 of 1)	intron (NR_145484, intron 1 of 1)
100	chr12	2514602	2515176	intron (NM_199460, intron 9 of 49).2	intron (NM_199460, intron 9 of 49).2
101	chr12	20489011	20489407	intron (NM_000921, intron 1 of 15)	intron (NM_000921, intron 1 of 15)
102	chr12	20517765	20518199	intron (NM_000921, intron 1 of 15)	MER5A DNA hAT-Charlie
103	chr12	26979713	26980054	exon (NM_016551, exon 9 of 12)	exon (NM_016551, exon 9 of 12)
104	chr12	48698636	48698983	intron (NM_001240, intron 5 of 8)	AluSp SINE Alu
105	chr12	68031931	68032527	Intergenic	Intergenic

Region #	Chr	Start	End	Annotation	Detailed Annotation
106	chr12	107364517	107364824	intron (NM_001347944, intron 1 of 14)	MLT1 LTR ERV1-MaLR
107	chr13	27543194	27543592	Intergenic	AluSx1 SINE Alu
108	chr13	31826537	31826982	Intergenic	LTR26D LTR ERV1
109	chr13	100552318	100552670	intron (NM_001195087, intron 2 of 2)	intron (NM_001195087, intron 2 of 2)
110	chr13	110366962	110367277	intron (NM_001846, intron 4 of 47)	intron (NM_001846, intron 4 of 47)
111	chr14	72308931	72309583	intron (NM_001370288, intron 2 of 16)	intron (NM_001370288, intron 2 of 16)
112	chr15	39232677	39233100	Intergenic	Intergenic
113	chr15	51976614	51976973	Intergenic	AluSg SINE Alu
114	chr15	91966734	91967039	intron (NR_135775, intron 2 of 10)	intron (NR_135775, intron 2 of 10)
115	chr15	94322613	94323105	intron (NM_018349, intron 3 of 21)	intron (NM_018349, intron 3 of 21)
116	chr15	94613999	94614392	Intergenic	Intergenic
117	chr16	71711564	71711935	intron (NM_015020, intron 2 of 18)	intron (NM_015020, intron 2 of 18)
118	chr17	34359440	34359743	TTS (NM_002981)	TTS (NM_002981)
119	chr17	66383461	66383848	intron (NM_002737, intron 2 of 16)	intron (NM_002737, intron 2 of 16)
120	chr17	75136480	75136830	intron (NM_001002032, intron 3 of 3)	AluSg7 SINE Alu
121	chr18	12651435	12651865	intron (NM_020148, intron 1 of 15)	AluSc SINE Alu
122	chr18	79800569	79801141	Intergenic	Intergenic
123	chr19	41372948	41373634	intron (NM_001098825, intron 1 of 3)	intron (NM_001098825, intron 1 of 3)
124	chr19	54377433	54378131	Intergenic	Intergenic
125	chr2	2044249	2044836	intron (NM_015025, intron 4 of 24)	intron (NM_015025, intron 4 of 24)
126	chr2	46512424	46512765	exon (NM_001371281, exon 5 of 5)	exon (NM_001371281, exon 5 of 5)
127	chr2	127541789	127542176	intron (NM_001080527, intron 1 of 46)	intron (NM_001080527, intron 1 of 46)
128	chr2	128534488	128534924	Intergenic	AluSx SINE Alu
129	chr2	134138483	134138797	intron (NM_001371457, intron 1 of 16)	intron (NM_001371457, intron 1 of 16)
130	chr2	144875175	144875551	intron (NR_033870, intron 2 of 4)	intron (NR_033870, intron 2 of 4)
131	chr2	157894925	157895436	Intergenic	Intergenic
132	chr2	238015870	238016404	intron (NR_037904, intron 4 of 18)	L2b LINE L2

Region #	Chr	Start	End	Annotation	Detailed Annotation
133	chr20	41145187	41145629	intron (NM_182811, intron 1 of 31)	intron (NM_182811, intron 1 of 31)
134	chr20	47274287	47274618	intron (NM_001281774, intron 12 of 23)	intron (NM_001281774, intron 12 of 23)
135	chr22	20571133	20571474	intron (NM_001293234, intron 8 of 16)	intron (NM_001293234, intron 8 of 16)
136	chr22	44126016	44126553	intron (NM_001243386, intron 4 of 11)	intron (NM_001243386, intron 4 of 11)
137	chr3	73023128	73023546	intron (NM_001318025, intron 2 of 7)	AluSp SINE Alu
138	chr3	141689514	141690347	intron (NR_136190, intron 5 of 7)	intron (NR_136190, intron 5 of 7)
139	chr3	177644355	177644855	intron (NR_047568, intron 3 of 3)	LTR37B LTR ERV1
140	chr4	15996335	15997055	intron (NM_001371408, intron 14 of 24)	intron (NM_001371408, intron 14 of 24)
141	chr4	101018772	101019294	Intergenic	MLT1L LTR ERV1-MaLR
142	chr5	55062058	55062609	Intergenic	Intergenic
143	chr5	94868054	94868487	intron (NM_001002796, intron 17 of 22)	MER131 DNA? DNA?
144	chr5	168801442	168801968	intron (NM_003062, intron 9 of 35)	intron (NM_003062, intron 9 of 35)
145	chr6	26309642	26310015	Intergenic	Intergenic
146	chr6	35837289	35837824	intron (NM_003137, intron 15 of 15)	MIR SINE MIR
147	chr7	107091590	107091909	intron (NM_002736, intron 2 of 10)	MamRep137 DNA TcMar-Tigger
148	chr7	129997622	129997962	Intergenic	L2c LINE L2
149	chr7	157254959	157255681	intron (NM_014671, intron 21 of 22)	L1MB7 LINE L1
150	chr9	2235546	2235928	Intergenic	Intergenic
151	chr9	36072400	36072868	intron (NM_001316345, intron 8 of 22)	intron (NM_001316345, intron 8 of 22)
152	chr9	124763923	124764323	intron (NM_001278546, intron 1 of 9)	AluSx1 SINE Alu

FIG. 31

Region #	Chr	Start	End	Annotation	Detailed Annotation
1	chr1	9555113	9555497	intron (NM_032315, intron 2 of 6)	AluY SINE Alu
2	chr1	10975566	10975974	intron (NM_001170754, intron 2 of 12)	MIR SINE MIR
3	chr1	21806787	21807466	Intergenic	Arthur1B DNA hAT-Tip100
4	chr1	28958371	28958774	intron (NM_001166006, intron 1 of 14)	AluJb SINE Alu
5	chr1	41165147	41165549	intron (NM_001172218, intron 2 of 15)	L1MA6 LINE L1
6	chr1	96060467	96060915	Intergenic	Intergenic
7	chr1	107920999	107921339	intron (NM_006113, intron 1 of 26)	intron (NM_006113, intron 1 of 26)
8	chr1	145781958	145782280	intron (NM_014455, intron 3 of 8)	AluSq SINE Alu
9	chr1	147752592	147752925	Intergenic	Intergenic
10	chr1	169584810	169585301	intron (NM_000130, intron 1 of 24)	intron (NM_000130, intron 1 of 24)
11	chr1	183106579	183107009	intron (NM_002293, intron 2 of 27)	intron (NM_002293, intron 2 of 27)
12	chr1	184798098	184798535	intron (NM_052966, intron 12 of 13)	intron (NM_052966, intron 12 of 13)
13	chr1	185630762	185631179	Intergenic	Intergenic
14	chr1	223078216	223078514	Intergenic	Intergenic
15	chr1	247336293	247336875	Intergenic	Intergenic
16	chr1	247427029	247427669	intron (NM_001127462, intron 3 of 7)	intron (NM_001127462, intron 3 of 7)
17	chr10	927860	928464	intron (NM_001351277, intron 1 of 17)	AluSq2 SINE Alu
18	chr10	2010951	2011468	intron (NR_040253, intron 2 of 2)	intron (NR_040253, intron 2 of 2)
19	chr10	7272910	7273282	intron (NM_001029880, intron 7 of 20)	intron (NM_001029880, intron 7 of 20)
20	chr10	22812444	22812824	Intergenic	Intergenic
21	chr10	43758225	43758502	Intergenic	Intergenic
22	chr10	72794246	72794895	intron (NR_073062, intron 3 of 9)	MLT1G3-int LTR ERV1-MaLR
23	chr11	4214007	4214524	Intergenic	Intergenic
24	chr11	13348690	13348979	intron (NM_001351821, intron 3 of 19)	intron (NM_001351821, intron 3 of 19)
25	chr11	44948833	44949365	intron (NM_001258323, intron 1 of 7)	intron (NM_001258323, intron 1 of 7)

Region #	Chr	Start	End	Annotation	Detailed Annotation
26	chr11	76361868	76362164	intron (NM_004705, intron 2 of 4)	intron (NM_004705, intron 2 of 4)
27	chr12	30693113	30693522	intron (NM_006390, intron 1 of 24)	Tigger16b DNA TcMar-Tigger
28	chr12	45693117	45693459	Intergenic	THE1D LTR ERV1-MaLR
29	chr12	46269798	46270463	Intergenic	Intergenic
30	chr12	48918620	48919121	exon (NM_033124, exon 6 of 8)	exon (NM_033124, exon 6 of 8)
31	chr12	62266681	62267250	intron (NR_147080, intron 1 of 19)	intron (NR_147080, intron 1 of 19)
32	chr12	68473618	68474073	Intergenic	Intergenic
33	chr12	109897075	109897420	Intergenic	Intergenic
34	chr12	116100940	116101331	intron (NM_015335, intron 3 of 30)	intron (NM_015335, intron 3 of 30)
35	chr12	120937235	120937609	Intergenic	AluSx SINE Alu
36	chr12	121395108	121395529	Intergenic	AluY SINE Alu
37	chr12	123658934	123659532	intron (NM_001271867, intron 8 of 11)	AluSx SINE Alu
38	chr13	31931327	31931615	intron (NR_027062, intron 1 of 3)	L2c LINE L2
39	chr13	71643349	71643911	intron (NM_080759, intron 2 of 10)	intron (NM_080759, intron 2 of 10)
40	chr13	92173992	92174321	intron (NM_004466, intron 7 of 7)	intron (NM_004466, intron 7 of 7)
41	chr14	21805289	21805872	Intergenic	AluSp SINE Alu
42	chr14	34848877	34849425	intron (NM_013448, intron 3 of 26)	AluJr SINE Alu
43	chr14	68249886	68250272	intron (NM_133509, intron 7 of 10)	intron (NM_133509, intron 7 of 10)
44	chr14	71547639	71548044	intron (NM_001354289, intron 5 of 23)	intron (NM_001354289, intron 5 of 23)
45	chr14	77053056	77053380	intron (NR_110554, intron 1 of 3)	MIRb SINE MIR
46	chr15	20200923	20201411	Intergenic	L2a LINE L2
47	chr15	31091542	31091978	intron (NM_001252024, intron 1 of 27)	intron (NM_001252024, intron 1 of 27)
48	chr15	41430030	41430388	intron (NM_015138, intron 1 of 17)	AluSc8 SINE Alu
49	chr15	52121520	52121806	3' UTR (NM_016194, exon 13 of 13)	3' UTR (NM_016194, exon 13 of 13)
50	chr15	52311020	52311397	3' UTR (NM_000259, exon 41 of 41)	3' UTR (NM_000259, exon 41 of 41)
51	chr15	57194998	57195402	intron (NM_207038, intron 7 of 19)	AluSq2 SINE Alu
52	chr15	77688939	77689386	intron (NM_001301194, intron 2 of 3)	intron (NM_001301194, intron 2 of 3)

Region #	Chr	Start	End	Annotation	Detailed Annotation
53	chr16	2941624	2942036	intron (NM_032296, intron 9 of 9)	AluSg7 SINE Alu
54	chr16	23967719	23968066	intron (NM_002738, intron 2 of 16)	AluSx1 SINE Alu
55	chr16	57581626	57581967	Intergenic	MER50 LTR ERV1
56	chr16	68797830	68798489	intron (NM_001317185, intron 2 of 15)	intron (NM_001317185, intron 2 of 15)
57	chr16	69716975	69717438	intron (NM_000903, intron 3 of 5)	intron (NM_000903, intron 3 of 5)
58	chr16	72610065	72610533	intron (NR_159372, intron 1 of 7)	intron (NR_159372, intron 1 of 7)
59	chr17	19278480	19279242	intron (NM_001102664, intron 1 of 7)	AluSz6 SINE Alu
60	chr17	37727490	37727840	intron (NM_001304286, intron 4 of 6)	intron (NM_001304286, intron 4 of 6)
61	chr17	39992874	39993221	intron (NM_002809, intron 6 of 11)	MLT1B LTR ERV1-MaLR
62	chr18	6408659	6409042	intron (NM_001365765, intron 1 of 18)	AluSx SINE Alu
63	chr18	58867484	58867923	intron (NM_001353535, intron 2 of 6)	intron (NM_001353535, intron 2 of 6)
64	chr18	61581131	61581656	Intergenic	AluSx SINE Alu
65	chr19	15336631	15337039	Intergenic	AluY SINE Alu
66	chr19	41865635	41866355	intron (NM_001321485, intron 3 of 5)	AluSx3 SINE Alu
67	chr2	38120214	38120583	Intergenic	L3 LINE CR1
68	chr2	62462607	62462982	Intergenic	MIR3 SINE MIR
69	chr2	63817027	63817412	Intergenic	AluSx1 SINE Alu
70	chr2	143579371	143579774	intron (NM_018460, intron 11 of 13)	MamSINE1 SINE tRNA-RTE
71	chr2	172587248	172587648	intron (NM_002610, intron 9 of 10)	LTR12D LTR ERV1
72	chr2	175034819	175035274	Intergenic	Intergenic
73	chr2	201098748	201099115	Intergenic	AluY SINE Alu
74	chr2	201467344	201467631	intron (NM_018571, intron 3 of 11)	L3 LINE CR1
75	chr2	223970725	223971056	Intergenic	Intergenic
76	chr2	229957173	229957640	intron (NM_174899, intron 1 of 3)	AluSx1 SINE Alu
77	chr20	47456008	47456462	Intergenic	AluSz SINE Alu
78	chr22	21598867	21599375	intron (NM_001256355, intron 2 of 3)	intron (NM_001256355, intron 2 of 3)
79	chr22	31236994	31237552	intron (NM_005569, intron 2 of 15)	AluY SINE Alu

Region #	Chr	Start	End	Annotation	Detailed Annotation
80	chr22	43616317	43616652	intron (NM_198856, intron 18 of 29)	AluSz SINE Alu
81	chr3	4720354	4720841	intron (NM_001168272, intron 39 of 60)	intron (NM_001168272, intron 39 of 60)
82	chr3	20184823	20185344	intron (NM_001012409, intron 1 of 7)	intron (NM_001012409, intron 1 of 7)
83	chr3	31265686	31265994	Intergenic	Intergenic
84	chr3	49290433	49290905	intron (NM_199443, intron 14 of 20)	AluSx SINE Alu
85	chr3	57232611	57233047	intron (NM_012096, intron 1 of 21)	AluY SINE Alu
86	chr3	125083723	125084107	exon (NM_024628, exon 14 of 14)	exon (NM_024628, exon 14 of 14)
87	chr3	132492379	132492714	exon (NM_015268, exon 33 of 56)	exon (NM_015268, exon 33 of 56)
88	chr3	143008673	143009092	intron (NM_001080415, intron 1 of 27)	AluY SINE Alu
89	chr3	167721506	167721821	intron (NM_145860, intron 1 of 7)	L3 LINE CR1
90	chr3	169125020	169125597	intron (NM_001163999, intron 4 of 14)	intron (NM_001163999, intron 4 of 14)
91	chr3	179657512	179657883	intron (NM_003940, intron 1 of 20)	AluSc SINE Alu
92	chr3	180921640	180922062	intron (NM_001363882, intron 2 of 16)	intron (NM_001363882, intron 2 of 16)
93	chr3	197317357	197317803	Intergenic	Intergenic
94	chr4	39330668	39331056	intron (NM_001204747, intron 4 of 24)	intron (NM_001204747, intron 4 of 24)
95	chr4	73232151	73232522	intron (NM_032217, intron 1 of 33)	intron (NM_032217, intron 1 of 33)
96	chr4	143616665	143617027	intron (NM_001168235, intron 5 of 7)	intron (NM_001168235, intron 5 of 7)
97	chr5	32109209	32109581	3' UTR (NM_178140, exon 25 of 25)	3' UTR (NM_178140, exon 25 of 25)
98	chr5	36055881	36056530	intron (NM_001168316, intron 1 of 5)	MER70A LTR ERV
99	chr5	54022686	54023142	intron (NM_019087, intron 4 of 4)	L1MDa LINE L1
100	chr5	61508626	61508963	intron (NM_020928, intron 4 of 13)	MLT1H1 LTR ERV MaLR
101	chr5	91114087	91114597	intron (NR_003149, intron 87 of 89)	AluSx SINE Alu
102	chr5	171900518	171900943	intron (NM_012300, intron 3 of 12)	intron (NM_012300, intron 3 of 12)
103	chr6	6235458	6235819	intron (NM_000129, intron 6 of 14)	L1ME1 LINE L1
104	chr6	11354232	11354920	intron (NR_073131, intron 1 of 9)	intron (NR_073131, intron 1 of 9)
105	chr6	15376189	15376627	intron (NM_004973, intron 2 of 17)	intron (NM_004973, intron 2 of 17)
106	chr6	32119259	32119657	intron (NM_001136153, intron 9 of 17).3	intron (NM_001136153, intron 9 of 17).3

Region #	Chr	Start	End	Annotation	Detailed Annotation
107	chr6	34544898	34545163	intron (NM_012391, intron 1 of 5)	intron (NM_012391, intron 1 of 5)
108	chr6	36584706	36585043	Intergenic	AluSx1 SINE Alu
109	chr6	37876284	37876663	intron (NM_021943, intron 1 of 5)	intron (NM_021943, intron 1 of 5)
110	chr6	106663310	106663670	intron (NM_018292, intron 10 of 10)	MSTA LTR ERV1-MaLR
111	chr6	159116523	159117049	Intergenic	Helitron2Na_Mam RC? Helitron?
112	chr6	169905970	169906609	Intergenic	Intergenic
113	chr7	5011521	5011921	Intergenic	LTR79 LTR ERV1
114	chr7	43810665	43810993	Intergenic	HERV/P10F-int LTR ERV1
115	chr7	45232890	45233316	Intergenic	MER65A LTR ERV1
116	chr7	73395606	73396001	Intergenic	Intergenic
117	chr7	90720755	90721222	intron (NM_001287136, intron 1 of 13)	intron (NM_001287136, intron 1 of 13)
118	chr7	100417828	100418161	intron (NM_001258008, intron 5 of 15)	AluSz SINE Alu
119	chr8	11878533	11879039	Intergenic	Intergenic
120	chr8	19641420	19642051	intron (NR_148898, intron 1 of 9)	intron (NR_148898, intron 1 of 9)
121	chr8	53711641	53712024	Intergenic	Intergenic
122	chr8	67335677	67336097	intron (NM_006421, intron 1 of 38)	AluSx3 SINE Alu
123	chr8	109395972	109396469	intron (NM_177531, intron 11 of 77)	intron (NM_177531, intron 11 of 77)
124	chr8	127455130	127455668	intron (NR_024393, intron 4 of 4)	L2a LINE L2
125	chr8	144168758	144169236	intron (NM_001099281, intron 3 of 11)	intron (NM_001099281, intron 3 of 11)
126	chr9	75110111	75110387	intron (NM_012383, intron 1 of 9)	L1MC1 LINE L1
127	chr9	85671538	85672140	intron (NM_015239, intron 7 of 25)	intron (NM_015239, intron 7 of 25)
128	chr9	91220613	91220996	intron (NM_001698, intron 7 of 9)	intron (NM_001698, intron 7 of 9)
129	chr9	93002575	93002927	intron (NM_001369952, intron 3 of 16)	intron (NM_001369952, intron 3 of 16)
130	chr9	94590518	94590894	intron (NM_003837, intron 1 of 6)	LTR12E LTR ERV1
131	chr9	112399404	112399765	intron (NR_036651, intron 1 of 9)	MER11A LTR ERV1
132	chr9	114464970	114465437	intron (NM_001083885, intron 3 of 11)	intron (NM_001083885, intron 3 of 11)
133	chr9	127987121	127987518	Intergenic	Intergenic

Region #	Chr	Start	End	Annotation	Detailed Annotation
134	chr9	129702523	129702862	intron (NM_016307, intron 1 of 3)	intron (NM_016307, intron 1 of 3)
135	chr1	7099663	7100211	intron (NM_001349608, intron 3 of 21)	HAL1 LINE L1
136	chr1	9640757	9641255	Intergenic	L2a LINE L2
137	chr1	14802577	14802903	intron (NM_201628, intron 1 of 14)	intron (NM_201628, intron 1 of 14)
138	chr1	14933734	14934491	intron (NM_001370231, intron 2 of 8)	AluY SINE Alu
139	chr1	15435204	15435647	Intergenic	Intergenic
140	chr1	17688674	17689397	intron (NR_137287, intron 28 of 29)	MIRb SINE MIR
141	chr1	18144784	18145199	intron (NM_032880, intron 1 of 9)	intron (NM_032880, intron 1 of 9)
142	chr1	26804823	26805345	Intergenic	AluY SINE Alu
143	chr1	28325964	28326616	Intergenic	AluY SINE Alu
144	chr1	35911797	35912332	intron (NM_001317122, intron 12 of 18)	L2-1_AMi LINE L2
145	chr1	40687455	40688269	Intergenic	L2c LINE L2
146	chr1	41712619	41713094	intron (NM_024503, intron 1 of 8)	intron (NM_024503, intron 1 of 8)
147	chr1	50733781	50734142	intron (NM_007051, intron 6 of 18)	AluSz SINE Alu
148	chr1	50958326	50958763	intron (NM_007051, intron 1 of 18)	AluY SINE Alu
149	chr1	59979109	59979650	Intergenic	MIRb SINE MIR
150	chr1	92310643	92311183	intron (NM_024813, intron 6 of 12)	intron (NM_024813, intron 6 of 12)
151	chr1	92341638	92341986	intron (NM_024813, intron 10 of 12)	AluSg SINE Alu
152	chr1	15109841	151099448	intron (NM_001323912, intron 5 of 7)	intron (NM_001323912, intron 5 of 7)
153	chr10	4847516	4848066	non-coding (NR_073125, exon 10 of 10)	non-coding (NR_073125, exon 10 of 10)
154	chr10	6108544	6108962	intron (NM_032905, intron 6 of 11)	intron (NM_032905, intron 6 of 11)
155	chr10	6541022	6541337	intron (NM_001323265, intron 1 of 17)	L3 LINE CR1
156	chr10	13591875	13592246	intron (NM_003675, intron 1 of 9)	intron (NM_003675, intron 1 of 9)
157	chr10	28305191	28305495	Intergenic	Intergenic
158	chr10	35538380	35538677	intron (NM_181698, intron 9 of 11)	L1MB8 LINE L1
159	chr10	102763772	102764140	intron (NM_001083913, intron 1 of 3)	AluSx SINE Alu
160	chr10	124603560	124603907	intron (NM_022126, intron 6 of 6)	intron (NM_022126, intron 6 of 6)

Region #	Chr	Start	End	Annotation	Detailed Annotation
161	chr10	127075426	127075841	intron (NM_001290223, intron 23 of 51)	THE1D LTR ERV1-MaLR
162	chr10	129140465	129140879	Intergenic	Intergenic
163	chr11	3166109	3166701	Intergenic	Intergenic
164	chr11	5693255	5693699	intron (NM_001199573, intron 1 of 7)	AluY SINE Alu
165	chr11	47957159	47957771	Intergenic	AluJo SINE Alu
166	chr11	64435051	64435473	Intergenic	MERSA DNA hAT-Charlie
167	chr11	65978838	65979390	3' UTR (NM_005146, exon 20 of 20)	3' UTR (NM_005146, exon 20 of 20)
168	chr11	85973202	85973490	intron (NM_001008660, intron 19 of 19)	MER44A DNA TcMar-Tigger
169	chr11	123150692	123151002	intron (NM_024769, intron 1 of 6)	AluSz6 SINE Alu
170	chr12	1926298	1926779	Intergenic	MLT1L LTR ERV1-MaLR
171	chr12	64731026	64731550	intron (NM_002076, intron 9 of 13)	AluJb SINE Alu
172	chr12	80958198	80958566	Intergenic	AluJb SINE Alu
173	chr12	89163173	89163747	Intergenic	Intergenic
174	chr12	96191947	96192475	Intergenic	L1MC1 LINE L1
175	chr12	113158784	113159117	TTS (NR_106956)	TTS (NR_106956)
176	chr12	131821220	131821652	Intergenic	MER65A LTR ERV1
177	chr13	20231143	20231462	promoter-TSS (NM_006783)	promoter-TSS (NM_006783)
178	chr13	28001921	28002466	Intergenic	MERS2A LTR ERV1
179	chr13	33368589	33368931	intron (NM_001243476, intron 5 of 17)	intron (NM_001243476, intron 5 of 17)
180	chr13	39521593	39521906	intron (NM_005780, intron 2 of 3)	L3 LINE CR1
181	chr13	40527444	40527762	Intergenic	AluSq2 SINE Alu
182	chr13	113004055	113004540	intron (NM_001320815, intron 1 of 30)	intron (NM_001320815, intron 1 of 30)
183	chr14	45241093	45241512	intron (NM_018353, intron 4 of 16)	AluSx1 SINE Alu
184	chr14	54628162	54628468	intron (NM_015589, intron 1 of 11)	intron (NM_015589, intron 1 of 11)
185	chr14	55248200	55248674	Intergenic	Intergenic
186	chr14	69774714	69775093	TTS (NM_003049)	TTS (NM_003049)
187	chr14	81006424	81006749	intron (NM_001142626, intron 1 of 8)	AluSc5 SINE Alu

Region #	Chr	Start	End	Annotation	Detailed Annotation
188	chr14	81120200	81120699	intron (NM_000369, intron 8 of 9)	L1M3 LINE L1
189	chr14	89353706	89353950	intron (NM_001085471, intron 2 of 6)	AluSx SINE Alu
190	chr14	95094871	95095407	intron (NM_001291628, intron 23 of 26)	intron (NM_001291628, intron 23 of 26)
191	chr14	100545931	100546290	intron (NM_001159531, intron 2 of 5)	intron (NM_001159531, intron 2 of 5)
192	chr14	106141260	106141622	Intergenic	Intergenic
193	chr15	41792657	41792983	intron (NR_049762, intron 2 of 28)	intron (NR_049762, intron 2 of 28)
194	chr15	55299062	55299454	Intergenic	MER11C LTR ERV
195	chr15	64270397	64270839	intron (NM_001329607, intron 2 of 11)	AluY SINE Alu
196	chr15	69609092	69609783	intron (NR_126438, intron 1 of 3)	LTR88b LTR Gypsy?
197	chr15	75359460	75359787	exon (NM_006715, exon 16 of 26)	exon (NM_006715, exon 16 of 26)
198	chr16	1173962	1174298	intron (NM_001005407, intron 2 of 33)	intron (NM_001005407, intron 2 of 33)
199	chr16	49688159	49688677	intron (NM_001271620, intron 3 of 7)	intron (NM_001271620, intron 3 of 7)
200	chr16	56336709	56337076	intron (NM_020988, intron 6 of 8)	intron (NM_020988, intron 6 of 8)
201	chr16	89994810	89995609	non-coding (NR_003226, exon 11 of 11)	non-coding (NR_003226, exon 11 of 11)
202	chr17	859514	859866	intron (NM_022463, intron 1 of 7)	intron (NM_022463, intron 1 of 7)
203	chr17	3260598	3260998	Intergenic	MIRc SINE MIR
204	chr17	4043990	4044257	intron (NM_015113, intron 38 of 54)	intron (NM_015113, intron 38 of 54)
205	chr17	20908907	20909245	intron (NR_160710, intron 3 of 4)	intron (NR_160710, intron 3 of 4)
206	chr17	27541747	27542011	intron (NM_014238, intron 2 of 20)	Tigger12A DNA TcMar-Tigger
207	chr17	31000515	31000835	TTS (NM_032322)	TTS (NM_032322)
208	chr17	35951399	35951836	Intergenic	AluY SINE Alu
209	chr17	62012404	62013091	intron (NM_005121, intron 8 of 29)	intron (NM_005121, intron 8 of 29)
210	chr17	74914377	74914916	Intergenic	AluY SINE Alu
211	chr18	9112548	9112860	intron (NM_021074, intron 1 of 7)	AluSz SINE Alu
212	chr18	12052595	12053020	Intergenic	L2a LINE L2
213	chr18	48866474	48866859	Intergenic	MIRc SINE MIR
214	chr18	48940381	48940860	intron (NM_001190822, intron 3 of 3)	AluSx1 SINE Alu

Region #	Chr	Start	End	Annotation	Detailed Annotation
215	chr19	10296255	10296823	exon (NM_003259, exon 11 of 11)	exon (NM_003259, exon 11 of 11)
216	chr19	11099370	11099896	intron (NM_001195803, intron 1 of 15)	AluSq2 SINE Alu
217	chr19	24087899	24088382	intron (NM_001278678, intron 1 of 1)	AluSx1 SINE Alu
218	chr19	35704214	35704686	promoter-TSS (NM_001316903)	promoter-TSS (NM_001316903)
219	chr19	40876951	40877488	exon (NM_000764, exon 7 of 9)	exon (NM_000764, exon 7 of 9)
220	chr19	41618555	41619163	TTS (NM_001362493)	TTS (NM_001362493)
221	chr19	42246302	42246577	Intergenic	Intergenic
222	chr19	42350587	42350845	promoter-TSS (NR_107044)	promoter-TSS (NR_107044)
223	chr19	44613620	44614208	intron (NM_001205280, intron 1 of 4)	intron (NM_001205280, intron 1 of 4)
224	chr19	44735135	44735619	Intergenic	L1ME3B LINE L1
225	chr19	46314542	46314909	intron (NM_152796, intron 7 of 11)	AluSq2 SINE Alu
226	chr19	46723540	46723901	intron (NM_001039877, intron 12 of 17)	intron (NM_001039877, intron 12 of 17)
227	chr19	47646332	47646684	intron (NM_015711, intron 1 of 14)	intron (NM_015711, intron 1 of 14)
228	chr19	54220541	54220935	non-coding (NR_135495, exon 6 of 13).4	non-coding (NR_135495, exon 6 of 13).4
229	chr19	54629895	54630314	promoter-TSS (NM_001278398).3	promoter-TSS (NM_001278398).3
230	chr2	45980309	45980632	intron (NM_005400, intron 5 of 14)	intron (NM_005400, intron 5 of 14)
231	chr2	47228598	47228913	intron (NR_110207, intron 1 of 2)	intron (NR_110207, intron 1 of 2)
232	chr2	148678358	148678978	intron (NM_015630, intron 1 of 13)	LTR12C LTR ERV1
233	chr2	201151965	201152369	intron (NR_040030, intron 2 of 6)	AluSq2 SINE Alu
234	chr2	206798176	206798520	Intergenic	L1MB3 LINE L1
235	chr2	207561390	207561765	intron (NM_001371426, intron 4 of 8)	L3 LINE CR1
236	chr2	217790234	217790593	Intergenic	Intergenic
237	chr2	218822853	218823461	promoter-TSS (NR_128707)	promoter-TSS (NR_128707)
238	chr2	232569663	232569966	TTS (NM_004846)	TTS (NM_004846)
239	chr2	236870247	236871039	Intergenic	MIRc SINE MIR
240	chr2	238069308	238069695	intron (NM_016510, intron 4 of 11)	intron (NM_016510, intron 4 of 11)
241	chr2	241743527	241744103	exon (NM_001287249, exon 4 of 9)	exon (NM_001287249, exon 4 of 9)

Region #	Chr	Start	End	Annotation	Detailed Annotation
242	chr20	5725142	5725877	Intergenic	AluSx1 SINE Alu
243	chr20	12053131	12053373	Intergenic	MLT1G1 LTR ERV1-MaLR
244	chr20	13625420	13625841	intron (NM_017714, intron 2 of 13)	intron (NM_017714, intron 2 of 13)
245	chr20	35497363	35497658	intron (NM_007186, intron 25 of 34)	intron (NM_007186, intron 25 of 34)
246	chr20	37006018	37006581	intron (NM_002895, intron 20 of 21)	AluSq2 SINE Alu
247	chr20	53729260	53729681	Intergenic	AluSx1 SINE Alu
248	chr20	57713922	57714417	Intergenic	Intergenic
249	chr21	36889931	36890598	intron (NM_001352515, intron 6 of 10)	intron (NM_001352515, intron 6 of 10)
250	chr21	42028466	42028924	Intergenic	Intergenic
251	chr21	45331586	45331881	Intergenic	Intergenic
252	chr22	17974379	17974807	intron (NM_015241, intron 1 of 31)	AluSz SINE Alu
253	chr22	36116915	36117252	Intergenic	MIR3 SINE MIR
254	chr22	41044736	41045132	Intergenic	AluSz SINE Alu
255	chr22	41894993	41895427	intron (NR_103834, intron 14 of 21)	AluY SINE Alu
256	chr3	11599045	11599564	intron (NM_001128219, intron 2 of 4)	intron (NM_001128219, intron 2 of 4)
257	chr3	13107780	13108075	Intergenic	Intergenic
258	chr3	13186620	13187205	Intergenic	Intergenic
259	chr3	32258795	32259195	intron (NM_001320308, intron 1 of 2)	intron (NM_001320308, intron 1 of 2)
260	chr3	32832820	32833212	intron (NM_001039111, intron 1 of 3)	AluSq2 SINE Alu
261	chr3	100090917	100091871	intron (NM_001042459, intron 1 of 4)	intron (NM_001042459, intron 1 of 4)
262	chr3	130921043	130921376	intron (NM_001001485, intron 2 of 27)	AluSx1 SINE Alu
263	chr3	142866870	142867371	intron (NM_013363, intron 2 of 8)	LTR9C LTR ERV1
264	chr3	143326167	143326501	intron (NM_173653, intron 14 of 15)	L2a LINE L2
265	chr3	193512660	193513045	intron (NM_032279, intron 2 of 29)	MIRc SINE MIR
266	chr4	15412357	15413116	intron (NM_001135171, intron 1 of 2)	intron (NM_001135171, intron 1 of 2)
267	chr4	41119995	41120669	intron (NM_173075, intron 2 of 16)	intron (NM_173075, intron 2 of 16)
268	chr4	112209412	112209867	Intergenic	HERV9N-int LTR ERV1

Region #	Chr	Start	End	Annotation	Detailed Annotation
269	chr4	138955547	138956099	intron (NR_133945, intron 2 of 2)	L1MB3 LINE L1
270	chr5	775657	775833	intron (NR_147095, intron 1 of 16)	intron (NR_147095, intron 1 of 16)
271	chr5	55286980	55287463	intron (NR_144323, intron 8 of 26)	AluSx SINE Alu
272	chr5	79239360	79239717	intron (NM_152405, intron 1 of 10)	AluY SINE Alu
273	chr5	139481159	139481591	intron (NM_001367258, intron 2 of 6)	intron (NM_001367258, intron 2 of 6)
274	chr6	3254230	3254602	Intergenic	LTR12C LTR ERV1
275	chr6	7678810	7679462	Intergenic	AluSx SINE Alu
276	chr6	32643761	32644239	TTS (NM_002122)	TTS (NM_002122)
277	chr6	63806703	63807380	intron (NR_157848, intron 1 of 1)	intron (NR_157848, intron 1 of 1)
278	chr6	90177338	90177747	intron (NM_021813, intron 4 of 8)	MIRb SINE MIR
279	chr6	134241609	134242557	intron (NM_001143676, intron 2 of 13)	intron (NM_001143676, intron 2 of 13)
280	chr6	139834925	139835270	intron (NR_038399, intron 1 of 2)	AluSz6 SINE Alu
281	chr6	158098600	158099020	3' UTR (NM_001178088, exon 26 of 26)	3' UTR (NM_001178088, exon 26 of 26)
282	chr6	166513273	166513718	intron (NM_001006932, intron 4 of 21)	MIR3 SINE MIR
283	chr7	2504045	2504299	Intergenic	L2b LINE L2
284	chr7	5539959	5540360	Intergenic	Intergenic
285	chr7	15324544	15324923	intron (NM_001004320, intron 12 of 12)	MER1B DNA hAT-Charlie
286	chr7	27835514	27835804	intron (NM_175061, intron 4 of 4)	intron (NM_175061, intron 4 of 4)
287	chr7	66950125	66950587	intron (NM_017994, intron 4 of 6)	THE1C LTR ERV1-MaLR
288	chr7	81876647	81877120	Intergenic	Intergenic
289	chr7	105461571	105461970	intron (NM_001318164, intron 14 of 15)	Tigger3c DNA TcMar-Tigger
290	chr7	134855990	134856470	intron (NM_033157, intron 2 of 14)	intron (NM_033157, intron 2 of 14)
291	chr7	138252952	138253517	Intergenic	HERVL-int LTR ERV1
292	chr7	149691882	149692289	Intergenic	AluSx1 SINE Alu
293	chr8	66677617	66677982	non-coding (NR_161218, exon 3 of 4)	non-coding (NR_161218, exon 3 of 4)
294	chr8	124731374	124731757	Intergenic	Intergenic
295	chr8	125621955	125622382	Intergenic	AluY SINE Alu

Region #	Chr	Start	End	Annotation	Detailed Annotation
296	chr8	143531086	143531534	intron (NM_015117, intron 3 of 11)	intron (NM_015117, intron 3 of 11)
297	chr8	144193936	144194673	intron (NM_001099281, intron 9 of 11)	AluSq2 SINE Alu
298	chr8	144377844	144378352	intron (NM_174922, intron 1 of 14)	intron (NM_174922, intron 1 of 14)
299	chr9	77420759	77421261	3' UTR (NM_033305, exon 72 of 72)	3' UTR (NM_033305, exon 72 of 72)
300	chr9	129075822	129076124	Intergenic	THE1B LTR ERV1-MaLR
301	chr9	135728342	135728812	intron (NM_020822, intron 2 of 30)	intron (NM_020822, intron 2 of 30)

FIG. 32

Pathway Hallmark	p-value	Adjusted p-value	Normalized ES	Size	Leading Edge
HALLMARK_COAGULATION	0.00401606	0.02572016	-3.2405932	130	PLG THBS1 F11 F13B KLKB1 ITGB3 CFH C8B HNF4A GDA PLEK GP9 PDGFB APOC2 MMP11 JSCU P2RY1 CD9 CAPN5 F2RL2 PROS1 ITGA2 PROZ CLU HPN GNG12 GP1BA CFI CPB2 TIMP3 C8A C9 CSRPI SERPINC1 LGMN TF FN1 VWF COMP CTSO MMP7 SPARC PROC DUSP6 BMP1 F2 TMPRSS6 A2M SERPINE1 ACOX2 DPP4 FYN MMP15 MMPI4 THBD HRG RGJ ITIH1 DUSP14 MBL2
HALLMARK_XENOBIOTIC_METABOLISM	0.00404858	0.02572016	-2.869442	190	PLG CYP2C18 F11 FMO3 ADH1C SERPINA6 IGF1 CYP1A2 HES6 HNF4A TTPA CYP26A1 IGFBP1 TMEM176B CYP4F2 DDC MTNFD1 XDH FETUB PROS1 DDAH2 HSD11B1 ABCC3 HSD17B2 CES1 AKR1C2 SLC35D1 PDK4 JUP FAH TMEM97 SPINT2 SLC22A1 CYP2J2 GCKR FMO1 ADH7 IRF8 BCAR1 GSTA3 NDRG2 CROT CCL25 SLC46A3 ABHD6 SMOX PINK1 GSTO1 MAOA KYNUI PTGR1 PEMT CYP17A1 SERPIN E1 CASP6 CA2 ACOX2 TKFC ENPEP AOX1 GSTM4 ASL ENTPD5 HRG RETSAT PAPSS2 ATP2A2 ITIH1 DHRS1 MBL2 CYP2E1 CD36 MAN1A1 IGFBP4 ESR1 GSS TDO2 UGDH ECH1 MCCC2 AKR1C3 SAR1B F10 PTS PMIM1 EPHA2 AQP9 PC
HALLMARK_BILE_ACID_METABOLISM	0.00411523	0.02572016	-2.687128	107	GC BBOX1 SERPINA6 NR1H4 PEX11A AGXT TTR EPHX2 CYP39A1 PEX26 PAOX FADS2 PEX19 ABCA6 PEX12 GSTK1 AKR1D1 ABCA8 NR3C2 ISOC1 CYP7A1 ACSL5 CYP8B1 CROT ABCA9 OPTN SLC22A18 PECR IDI1 PHYH ABCA5 ABCG8 FDXR SLC35B2 SLC27A5 FADS1 HSD3B7 ALDH1A1 RETSAT ABCA1 ALDH8A1 PFKM SLC23A2 SLC01A2 BMP6 PIPOX LCK CYP46A1 HSD17B4 SLC27A2 IDH2 AQP9 PEX7 NPC1 SOAT2
HALLMARK_CHOLESTEROL_HOMEOSTASIS	0.003861	0.02572016	-2.5126571	72	ALDOC CD9 TNFRSF12A HSD17B7 HMGCR CLU FADS2 AVPR1A NSDHL TMEM97 LGMN ADH4 SQLE ACAT2 ACSS2 DHCER7 GLDC CYP51A1 STARD4 PMVK PDK3 GSTM2 FDPS

Pathway Hallmark	p-value	Adjusted p-value	Normalized ES	Size	Leading Edge
					IDI1 SEMA3B EBP HMGCS1 ACTG1 CXCL16 LSS GNAI1 ECH1 MVD ANXA13 PPARG ETHE1 JAG1
HALLMARK_HEME_METABOLISM	0.00390625	0.02572016	-2.3780285	184	MOCOS XK TAL1 HBD TRIM10 GATA1 ALDH1L1 PDZK1IP1 UROD ISCA1 FN3K DMTN ACKR1 DAAAM1 ALDH6A1 ALAD RCL1 ENDOD1 ALAS2 TNS1 RHAG NFE2 PRDX2 HBZ ARHGEF12 DCAF11 CLCN3 ARL2BP ADIPOR1 SLC30A10 OPTN TMCC2 SMOX UBAC1 SNCA EIF2AK1 NNT UROS CA2 ABCB6 MYL4 TRIM58 RBM5 FTCD LRP10 CPOX MINPP1 SLC2A1 ACSL6 ANK1 SPTB MPP1 HDGF GYPE GDE1 P4HA2 BMP2K ATP6VOA1 HTATIP2 ABCG2 HEBP1 PPP2R5B RANBP10 DCUN1D1 ICAM4 HAGH PC IGSF3 FBXO7 KHNYN RAP1GAP1 BTG2 GLRX5 NEK7 TMEM98 MFHAS1 BCAM SLC4A1 HTRA2 SELENBP1 XPO7 RIOK3 RBM38 GCLC SLC6A9 EPB42 UCP2 KLF3 MAP2K3 RHCE EPB41 TOP1 CIR1 LPIN2 NCOA4 C3 SLC22A4 OSBP2 CA1 FOXO3 CTNS BTRC MGST3 FOXJ2 HMB5 PSMD9 TENT5C CDC27 CTSE SLC11A2 MKRN1 CCND3
HALLMARK_MYOGENESIS	0.00793651	0.04409171	-2.1711383	187	OCEL1 IGF1 MYL7 TNNC1 IGFBP3 GNAO1 ACHE SORBS1 GJA5 CLU COL4A2 FGF2 COL6A2 BIN1 ITGB5 MYH7 MYLK KIFC3 LARGE1 MYOG EIF4A2 TPM2 HDACS AK1 MYL3 KCNH1 MYH8 PTP4A3 SPARC MEF2D TNNT3 MYH2 PSEN2 MAPRE3 FDP5 PTGIS HBEGF SGCA PICK1 GABARAPL2 CKB MYL4 AKT2 DES MYH3 PGAM2 TNNC2 WWTR1 GPX3 CACNA1H ITGA7 TEAD4 PFKM CD36 NAV2 LPIN1 ABLM1 FOXO4 MYOM1 MYO1C ITGB1 MYLPP KCNH2 TGFB1 SPEG PLXNB2 PC PRNP TNNI1 EFS FABP3 MYH9 CHRNA GSI TNNT2 NOTCH1 AGRN FYXD1 SMTN SIRT2 PDLIM7 PYGM TPD52L1 CKM MB SORBS3 CAMK2B SPTAN1 CSR P3 MAPK12 TAGLN COX7A1 CFD AEBP1 NQO1 CNN3 CDKN1A RIT1 ANKRD2 ACTN3 EPHB3 BHLHE40
HALLMARK_FATTY_ACID_METABOLISM	0.01619433	0.06228589	-2.0106956	151	CYP4A11 ADH1C1 HAO2 ME1 EC12 CRYZ UROD HSD17B7 APEX1 RDH11 AADAT GLUL ACADL ACOT8 PDHB ALAD H PGD NSDHL CYP4A22 PRDX6 ACAT2 ACSL5 FMO1 HMGCS

Pathway Hallmark	p-value	Adjusted p-value	Normalized ES	Size	Leading Edge
					L MGLL ADH7 LTC4S ACADS MCEE OSTC ALDOA PTPRG MAOA ECHS1 CPT2 HADH SUCLG2 UROS IDI1 CA2 HIBC H HMGCS1 SLC22A5 ACSS1 CPOX ALDH1A1 RETSAT PPA RA PCBD1 GCDH CD36 EHHADH TDO2 UGDH CEL ECH1 GSTZ1 HSD17B4 PTS CIDEA ODC1 HSDL2 HSPH1 SDHC S MS DHCR24 BPHL LGALS1 MDH2 BCKDHB CYP1A1 GPD1 GRHPR NTHL1 INMT IDH1 UBE2L6 CCDC58 ACO2 MDH1 VNN1 D2HGDH ALDH3A2 HCCS HMGCS2 ACADM IDH3B BLVRA ERP29 RDH16 YVHAH MLYCD SUCLA2 ACAA2 H SP90AA1 DLST FHI AUH ADIPOR2 ALDH3A1 FASN ACAA1 CPT1A SUCLG1 ENO3 ACSM3 CRAT CBR1 DECR1 S100A1 O GAPDHS SERINC1 ACSL1 NCAPH2 EPHX1 DLD HADHB SDHA ALDH9A1 RAP1GDS1 AOC3 CBR3 PSME1 ACSL4 ET FDH SDHD KMT5A AQP7 ADSL EC1 PDHA1 METAP1 IL6ST NFKBIA UROD NPTX2 MAPK8 IP2 C4BPB IL6 ONECU T1 YKT6 FOSB MSX1 CYB5R1 FMO1 APOM GAL BMP2 A LDOA RET BTG3 CLTB PPAT SELENOW MAOA CLCN2 RR AD TCHH IGFBP2 TYRO3 CA2 PPIF SULT1A1 E2F5 COL2A 1 ABC81 RXRB NR4A1 MMP14 CYB5B CASP3 GPX3 ATP6 V1F CDC5L IRF1 AP2S1 SLC25A4 TUBA4A MGAT1 BCL2L1 1 FGF18 TAP1 POLR2H KCNH2 CREG1 BTG2 GGH POLG2 RPN1 PARP2 HNRNP1 DNAJB1 BAK1 FURIN CDKN2B CY P1A1 WIZ ICAM1 OLF1 TACR3 FKBP4 PSMC3 PRKCD C CNE1 PTPRD LHX2 ATP6V1C1 SLC6A12 HSPA2 HYAL2 PD AP1 GCH1 STIP1 TGFB3 SQSTM1 AMID1 CNP CCND3 NXF1 FOS STK25 EPCAM EIF5 SOD2 NAT1 HMOX1 TST A RRB2 ASNS AGO2 ACAA1 PRKACA SHOX2 GRPEL1 DDX21 NPTXR MARK2 NUP58 CDC34 DGAT1 EIF2S3 CHKA ATF 3 RHOB EPHX1 KLHDC3 SLC6A8 BID STARD3 PPT1 PPP1R 2 PRPF3 TM6IM6 SIGMAR1 HSPA13
HALLMARK_UV_RESPONSE_UP	0.01619433	0.06228589	-1.9555131	148	
HALLMARK_ESTROGEN_RESPONSE_EARLY	0.02016129	0.0672043	-1.9282266	195	FRK FHL2 SLC7A2 PEX11A SEC14L2 SFN IL6ST CALB2 FAR P1 SLC37A1 ANXA9 DHRS2 NRIP1 HR MUC1 THSD4 WW C1 GFRA1 SLC1A1 ENDOD1 DLC1 AREG ELOVL2 KCNK5

Pathway Hallmark	p-value	Adjusted p-value	Normalized ES	Size	Leading Edge
					MLPH DHC87 FLNB PDZK1 SYBU NXT1 MAPT AKAP1 ELF3 RET CCND1 WFS1 MAST4 ASB13 TGM2 SYT12 TIPARP KRT8 SEMA3B SLC24A3 SIAH2 SLC16A1 PPIF MREG SLC22A5 ADCY1 CANT1 RHOD CLIC3 KAZN SLC2A1 RAPGEF1 PAPSS2 MINDY1 ZNF185 NAV2 SLC39A6 PGR TTC39A ABLIM1 IGFBP4 CELSR2 CBFA2T3 CISH CA12 GREB1 EGR3 SLC27A2 UNC119 ELF1 TUBB2B TSKU SYNGR1 TMPRSS3 DEPTOR SLC7A5 NBL1 LAD1 TIAM1 MSMB TPD52L1 AFF1 ISG20L2 TJP3 ABAT OLFM1 FKBP4 FAM102A DHR3 SCNN1A GLA B4GALT1 IL17RB TGIF2 PLAAT3 CHPT1 MYBBP1A SCARB1 BHLHE40 XBP1
HALLMARK_KRAS_SIGNALING_DN	0.0234375	0.07113821	-1.8893237	174	PTGFR THRB MAGIX PNMT TFAP2B CHST2 C5 CYP39A1 CLDN16 SSTR4 GP1BA PAX3 SLC29A3 CALML5 TGM1 MYH7 PDK2 THNSL2 SLC38A3 ZBTB16 ZC2HC1C HNF1A MYO15A UPK3B EDAR MSH5 KRT5 GPR3 KCNE2 NTF3 MTHFR SERPINA10 SPTBN2 CD40LG SNCB RGS11 IGFBP2 ARPP21 AKR1B10 GPRC5C SLC30A3 COL2A1 EDN2 TLX1 FGFR3 SCGB1A1 MFSD6 CALCB CAMK1D CDKAL1 SOX10 CELSR2 GTF3C5 COP2 HTRID VPS50 CDH16 P2RX6 COQ8A CNTFR EFHD1 RYR2 TF2 TGI KCNN1 ITGB1BP2 ABCB11 EGF BTG2 NPHS1 CHRNA1 SYNPO RSAD2 FGGY HSD11B2 DTNB NR6A1 CKM CAPN9 ITIH3 PAX4 SELENOP SLC12A3
HALLMARK_ESTROGEN_RESPONSE_LATE	0.0244898	0.07113821	-1.8159545	192	SERPINA3 SERPINA5 FRK MOC52 PRLR TNNC1 PRKAR2B SFN IL6ST CD9 FARP1 JASS1 CHST8 ANXA9 DHR32 NRIP1 HR CDC20 SLC2A8 LARGE1 HOMER2 AREG KCNIK5 DUSP2 PDCD4 DHC87 GAL FLNB CXCL14 PDZK1 NXT1 MAPT RET BTG3 CCND1 WFS1 EMP2 SEMA3B CA2 ACOX2 SLC24A3 SIAH2 SLC16A1 GJB3 PPIF PTPN6 CKB SLC22A5 LLGL2 FGR3 CLIC3 CDC6 MEST UNC13B RAPGEF1 PAPSS2 TRIM29 PGR IGFBP4 CELSR2 UGDH CISH CYP4F11 DLG5 IRNASEH2A PTGER3 CA12 EGR3 SLC27A2 IDH2 GINS2 TMPRSS3 CDH1 SLC7A5 NBL1 LSR TOP2A PLXNB1 TIAM1 TPD52L1 AFF1 MAPK13 GALE TJP3 HSPA4L OLFM1 STIL CAV

Pathway Hallmark	p-value	Adjusted p-value	Normalized ES	Size	Leading Edge
					1 FKBP4 FAM102A IMPA2 SCNN1A GLA IL17RB PLK4 PLAAT3 CHPT1 SCARB1 DNAJC12 ETFB XBP1 ALDH3A2 NAB2
HALLMARK_OXIDATIVE_PHOSPHORYLATION	0.02777778	0.07113821	-1.7854742	189	PHB2 SLC25A11 NDUFS8 ATP5F1E NDUFV1 NDUFA6 SCU ISCA1 NDUFA8 IMPC1 ATP5PO NDUFA5 MAOB PDHBI ALDH6A1 MRPS11 VDAC3 SUPV3L1 PDK4 MRPL35 VDAC2 FXN OXA1L ATP6V0C COX5B ATP5F1B VDAC1 NDUFAB1 ATP5MG ECHS1 NNT ATP1B1 PHYH COX6B1 TIMM9 NDUFS2 NDUFB6 COX11 ACADSB NDUFB4 RETSAT SLC25A20 ATP6V1F SLC25A4 CYCS NDUFC2 ECH1 MTX2 COX17 CYB5R3 MRPL15 ETFA NDUFA7 UQCRL1 HSPA9 IDH2 IDH3A NDUFB5 ATP5MC3 UQCRRF1 UQCRL1 PRDX3 BDH2 UQCRC2 GLUD1 NDUFS4 SDHC MRPS30 GOT2 MDH2 TCIRG1 FDX1 HADHA HTRA2 POLR2F COX10 DLAT NDUFA4 SLC25A3 AIFM1 IDH1 ACO2 MDH1 COX8A COX7B ETFB NDUFB8 ATP6V1C1 NDUFB3 HCCS MGST3 RHOT2 OPA1 NDUFB7 ATP6V1D ACADM IDH3B ATP5F1A MTRR LRPPRC PDHX UQCRC1 NDUFB1 ATP6AP1 MFN2 ATP6V1E1 SUCLA2 ACAA2 NDUFV2 RHOT1 LDHB DLST FH ABC87 NDUFC1 COX5A ATP5MC2 GPX4 ACAA1 GRPEL1 ATP5PB CPT1A SUCLG1 NDUFS1 PMPCA SLC25A12 ATP6V0E1 SDHB DECR1 ATP6V0B COX15 ATP5PF BAX TOMM70 AFG3L2 CYB5A NDUFS3 ATP5PD COX6C SURF1 ACAT1 IMMT ATP5MF LOGDH NDUFB2 COX4I1 DLD HADHB
HALLMARK_ADIPOGENESIS	0.02777778	0.07113821	-1.7385232	189	CAVIN2 PREB ADCY6 GPAM ME1 CHCHD10 SORBS1 ACADL EPHX2 ATP5PO NDUFA5 CMBL MIGA2 MYLK SLC5A6 ELOVL6 FAH MGLL PDCD4 DHC87 PLIN2 LTC4S DNAJC15 JAGN1 ACADS SLC25A1 CAVIN1 CMPK1 ANGPTL4 DNAJB9 ALDOA SAMM50 NDUFAB1 PEMT ECHS1 CPT2 HADH RMDN3 GPHN PHYH COQ3 ADIPOQ COQ9 HIBCH SULT1A1 ITSN1 CD151 QDPR RETSAT ESRRA ABCA1 SPARCL1 GPX3 ITGA7 CD36 GHITM DBT ECH1 NABP1 PIM3 PPARG MRPL15 UQCRL1 PTGER3 IDH3A ACLY CIDEA PRDX3 P

Pathway Hallmark	p-value	Adjusted p-value	Normalized ES	Size	Leading Edge
					TCD3 AGPAT3 MAP4K3 PHLDB1 SDHC MTCH2 RNFI1 M DH2 ANGPT1 ABCB8 APOE DLAT COQ5 COL4A1 G3BP2 R IOK3 STOM AIFM1 ATL2 IDH1 UCP2 STAT5A ACO2 COX8 A SCARB1 OMD COX7B ETFB C3 YWHAG MGST3 RREB1 MRAP NDUF7 SLC1A5 LAMA4 SLC27A1 LIPE ACADM AP LP2 PGM1 TALDO1 ORM1 NMT1 LPCAT3 UCK1 PFKL CH UK UQCRC1
HALLMARK_UNFOLDED_PROTEIN_RESPONSE	0.02845528	0.07113821	-1.6559626	104	PREB GFBP1 EXOSC2 NHP2 PDIA5 NOLC1 CKS1B IFT1 EI F4A2 FKBP14 EIF2AK3 SLC30A5 HYOU1 NFYB DNAJB9 W FS1 POP4 LSM4 EXOSC10 VEGFA LSM1 SERP1 EXOSC9 R RP9 PARN ALDH18A1 NOP14 CALR EIF4G1 TTC37 DDIT4 SHC1 NABP1 HSPA9 ZBTB17 ATF6 EXOSC5 EIF2S1 EXOSC 4 SLC7A5 RPS14 MTREX KDELR3 BAG3 XPOT PDIA6 NOP 56 SSR1 EIF4EBP1 YWHAZ XBP1 CNOT4 EIF4E EDC4 SRP RB ERN1 HSP90B1 IMP3 GEMIN4 YIF1A GOSR2 WIPI1 D NAJA4 HERPUD1 DCP2 PSAT1 DNAJC3 ASNS CHAC1 HSP A5 EXOC2 SEC31A KHSRP STC2 DCTN1 DDX10 EDEM1 A TF3 PAIP1 DKC1 SDAD1 ATP6VOD1 CEBPG MTHFD2 EEF2 ARFGAP1 SLC1A4 FUS
HALLMARK_PANCREAS_BETA_CELLS	0.0483871	0.10997067	-1.6401339	30	INS CHGA SCGN G6PC2 HNF1A ABCC8 GCK DPP4 FOXO1 VDR IAPP PKLR GCG PAX6 SLC2A2
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	0.04724409	0.10997067	-1.5765814	185	THBS1 ITGB3 CADM1 WNT5A COL5A3 ECM1 CDH2 TNFR SF12A IGFBP3 ITGA2 TPM1 SAT1 COL4A2 LRRC15 OXTR FGF2 COL6A2 NTSE1 ITGB5 TIMP3 IL6 CRLF1 MYLK PDLI M4 BDNF AREG TPM2 TPM4 MSX1 FN1 COMP PLOD2 S PARC SERPINE2 COL7A1 SDC4 BMP1 TGM2 VEGFC CALD 1 TGFB VEGFA SERPINE1 IGFBP2 CDH6 GPC1 EFEMP2 T HBS2 FSTL1 LOXL1 FBLN2 MMP14 SDC1 CXCL6 MYL9 M EST DAB2
HALLMARK_E2F_TARGETS	0.01960784	0.0672043	1.7440542	194	ORC6 POP7 MCM4 LBR PNN DSCC1 CCNB2 DCK DUT PP P1R8 POLE4 DEPDC1 DLGAP5 LMNB1 PLK1 CDKN2C DDX 39A KIF2C GINS3 AK2 KPN2 KIF4A HELLS ANP32E CDCA 8 SRSF1 NASP PTTG1 EED RAD51AP1 MMS22L MSH2 SN

Pathway Hallmark	p-value	Adjusted p-value	Normalized ES	Size	Leading Edge
					RPB1 STMN1 NBN PPM1D ILF3 DIAPH3 LYAR NAA38 ZW10 RACGAP1 BUB1B BRCA2 BARD1 MCM3 KIF22 NCAPD2 PRIM2 TRA2B RFC2 SMC3 CDK4 PRDX4 SYNCRIP HMMR RPA2 DCLRE1B ASF1A ATAD2 CIT MCM2 MCM6 MTHFD2 GINS1 RAD21 POLD3 POLD1 MRE11 CBX5 DEK MKI67 ORC2 RPA3 CHEK1 HMG3 NUP107 TUBB SMC1A RANBP1 JPT1 IPO7 XPO1 TCF19 PDS5B PAICS CCP110 UBE2T LUC7L3 RAD51C NME1 CTCF CDKN3 STAG1 PMS2 ASF1B TIPIN POLE RFC1 AURKA TMPO SMC4 CENPE SPAG5 HUS1 CDC25A MELK CHEK2 RPA1 PRKDC MYBL2 TK1 MC M5 CSE1L E2F8 MXD3 TBRG4 RRM2 XRCC6 POLA2 BRCA1 SSRP1 KIF18B UNG MYC MCM7 PSIP1 PA2G4 RBBP7 TRIP13 RAD1 BIRC5 TIMELESS CDKN2A PLK4 SPC25 CDKN1A CCNE1 DONSON WEE1 NUP205 CDC25B TACC3 LIG1 NOP56 ESPL1 UBR7 RFC3
HALLMARK_TNFA_SIGNALING_VIA_NFKB	0.016	0.06228589	1.77975562	180	CXCL1 PTX3 SERPINB2 KLF2 TNC GEM MARCKS SERPINB8 CCL20 CXCL11 TRIB1 INHBA DRAM1 MCL1 EGR1 KLF4 SLC16A6 IL1A GADD45B PDE4B SPHK1 BCL2A1 B4GALT5 ZFP36 IL23A LITAF DENND5A REL BTG1 ID2 TNFSF9 PTP RE IL12B PMEPA1 PTGS2 F3 TNFRSF9 OLR1 KLF10 ATP2B1 CD44 CD83
HALLMARK_COMPLEMENT	0.01176471	0.05882353	1.78789805	190	CXCL1 CTSV MMP8 SERPINB2 GNGT2 SERPINA1 MMP13 MSR81 LTF CASP1 FCN1 S100A12 PCLO GCA PIM1 GNG2 ITGAM CDH13 TIMP1 CTSS ANXA5 GZMB RASGRP1 PLA2G7 WAS APOC1 GZMK C1QA CTSL S100A9 CDA TIMP2 PDP1 CTSH RHOG GNB2 CTSC PSEN1 F3 OLR1
HALLMARK_G2M_CHECKPOINT	0.004	0.02572016	2.0242212	189	ORC6 HMG2 MARCKS EFNA5 LBR SLC12A2 CCNB2 EXO1 HIF1A PURA LMNB1 PLK1 DBF4 CDKN2C CDC7 DDX39A KIF2C MNAT1 KPNA2 KIF4A SRSF1 NASP PTTG1 TFDP1 KIF5B KIF11 STMN1 DR1 PBK CENPA ILF3 KATNA1 G3BP1 RACGAP1 BRCA2 BARD1 MCM3 CCNA2 KIF22 SLC38A1 HIRA PRIM2 TRA2B NUSAP1 ATF5 RBM14 CDK4 NUP50 SYNCRIP KIF15 HMMR RPA2 KMT5A MCM2 MCM6 FB

Pathway Hallmark	p-value	Adjusted p-value	Normalized ES	Size	Leading Edge
					XO5 MAPK14 SNRPD1 UPF1 SFPQ LIG3 FOXN3 PAFAH1B1 PRC1 RAD21 CBX1 MTF2 ATRX MKI67 TROAP CHEK1 HMG83 DKC1 PRMT5 POLQ NSD2 SMC1A JPT1 XPO1 SMC2 E2F2 ABL1 CHAF1A PDS5B PML RBL1 NOTCH2 INCEP CTCF CUL4A CDKN3 BUB3 STAG1 SAP30 PRPF4B POLE TPX2 TLE3 AURKA TMPO SMC4 CENPE HUS1 NCL ORC5 CDC25A KPNB1 CENPF ODF2 MYBL2 SRSF10 MCM5 MAP3K20 CUL1 NUMA1 SMARCC1 WRN UCK2 RPS6KA5 POLA2 CDC27 CCNF AMD1 MYC CUL3 KNL1 CHMP1A NUP98 SMAD3 TNPO2 TOP1 BIRC5 YTHDC1 MEIS2 PLK4 CUL5 FANCC CASP8AP2 STIL ARID4A RAD23B NDC80 CDC25B TACC3 ESPL1 KIF20B RAD54L
HALLMARK_INFLAMMATORY_RESPONSE	0.00389105	0.02572016	2.37552424	191	TPBG KCNJ2 CLEC5A MEFV MSR1 CCL20 C3AR1 MARCO CXCL11 CYBB CD70 GPC3 CCL24 INHBA FPR1 PCDH7 TIMP1 PTGER2 ITGB8 HRH1 RASGRP1 OSM TLR1 IL1A CXCL9 IL18RAP IL10 PDE4B SPHK1 CD48 HIF1A CSF3 TNFSF10 RHOG TNFSF9 TACR1 PTPRE IL12B PSEN1 EMP3 F3 TNFRSF9 OLR1 BDKRB1 ADRM1 SLC31A1 ATP2B1 PROK2 GABBR1 ACVR1B SLC28A2 KIF1B
HALLMARK_ALLOGRAFT_REJECTION	0.00404858	0.02572016	2.41465858	183	HLA-DQA1 CD1D GPR65 PSMB10 NCR1 HLA-DMB SPI1 INHBA TIMP1 IGSF6 RPS3A CTSS HLA-DRA GZMB CD8B TLR1 WAS CFP PTPRC IL4 CXCL9 IL18RAP IL10 KLRD1 CCR5 ETS1 HIF1A IL12A UBE2D1 CRTAM DEGS1 IL12B LY75 CAPG HCLS1 ITGB2 NPM1 IFNG ST8SIA4 KRT1 NCF4 CD86 TLR6 MMP9 TAP2 RPS9 GCNT1 NLRP3 TLR2 HDAC9 TRAF2 IL2RG TRAT1 CD8A STAT1 PRKCB FGR IRF4 IFNGR1 RPL9 EIF3D HLA-DOB MRPL3 CD47 LYN SOC5 GLMN JAK2 FAS CD80 RP L3L HLA-DOA IL7 IL13 BCAT1 TLR3 GALNT1 FCGR2B CD96 MAP4K1 INHBB CD3G CXCR3 CSK RIK2 IFNGR2 IKBKB LY86 EIF3A UBE2N ITGAL CCND2 EIF5A EREG AKT1 CD3E TPD52 SRGN

FIG. 33

Pathway Hallmark	p-value	Adjusted p-value	Normalized Enrichment Score (NES)	Size	Leading Edge
HALLMARK_MYOGENESIS	0.00352113	0.01764291	-2.247861	183	IGF1 TCAP LARGE1 CRYAB FST CRAT MYH2 CACNG1 NAV2 CNN3 CDKN1A CTF1 TSC2 MYBPH TNIN1 AGRN COX7A1 FXD1 TAGLN BCKRB2 COL6A2 ITGB4 MB SORBS3 PSEN2 CAMK2B GAA STC2 MAPRE3 FGF2 ANKRD2 WWTR1 CACNA1H ACTN3 TPD52L1 PC SH2B1 SH3BGR NOS1 SPDEF ADCY9 AEBP1 KCNH1 SORBS1 SOD3 MEF2D REEP1 KCNH2 DMPK HSPB8 BIN1 CKM ACHE FABP3 CKMT2 RYR1 PTP4A3 TNNC2 PLXNB2 TNNT3 SMTN KIFC3 ITGA7 MYBPC3 SPTAN1 AK1 MYOZ1 HDAC5 LDB3 ERBB3 CLU CA SQ1 SIRT2 LPIN1 PPFIA4 SPHK1 EPHB3 MYLPF SPEG CHRNA1 CFD MYL7 MYO1C MAPK12 GNAO1 COL15A1 ABLIM1
HALLMARK_ESTROGEN_RESPONSE_EARLY	0.00353357	0.01764291	-2.1367186	191	TFAP2C KRT15 NPY1R ELF3 AQP3 PDLIM3 CYP26B1 KRT19 SLC7A2 TSKU PGR OLFM1 TUBB2B ESRP2 THSD4 WFS1 FARP1 NAV2 SYBU INHBB TPBG WWC1 CELSR2 GFRA1 GREB1 MREG ADCY1 GJA1 KLK10 CELSR1 STC2 KLF10 KRT8 CCND1 CXCL12 MAPT TPD52L1 RAB17 MYC BLVRB SG20L2 TIAM1 SYT12 FOS ELOVL2 DEPTOR MYBBP1A FA M102A DHR3 ADCY9 LAD1 MED24 RETREG1 TTC39A ABAT PLAAT3 LRIG1 REEP1 PRSS23 BCL11B HSPB8 P2RY2 TJP3 HR RHOD FLNB ASB13 SULT2B1 AKAP1 ALDH3B1 PODXL CISH SEMA3B NBL1 EGR3 CHPT1 FRK CALB2 PDZK1 SCNN1A MLPH FASN SLC1A1 FDFT1 SLC39A6 ABLIM1 MYBL1 RBBP8 KRT13 PMAIP1 KDM4B SLC1A4 AMFR TGM2 CCN5
HALLMARK_XENOBIOTIC_METABOLISM	0.00359712	0.01764291	-2.0793422	185	F11 IGF1 ADH1C PLG ADH7 HGFAC HRG SLC22A1 FMO3 SERPINA6 CYP2J2 TPPA CYP27A1 SHMT2 DCXR TDO2 GNMT RAP1GAP ACOX2 CCL25 ITI4 VTN APOE SLC6A12 BCAR1 ASL DHR51 PTGR1 AKR1C3 CSAD TYR AKR1C2 ES

Pathway Hallmark	p-value	Adjusted p-value	Normalized Enrichment Score (NES)	Size	Leading Edge
					R1 PEMT SLC12A4 LCAT DDC ENTPD5 TIH1 NFS1 PCIF1 O PTGDS MPP2 HSD11B1 BLVRB ID2 ETFDH POR SERTAD1 GCKR EPA2 FBP1 UGDH BPP4 ATOH8 GCLC TMEM176B CROT JUP CYP17A1 COMT PSMB10 ABCC3 PPARD ACP2 SAR1B PYCR1 ENPEP ALDH3A1 AHCY PMIM1 CYP2C18 CNDP2 ABHD6 CES1 HSD17B2 CYP1A1 ACOX3 TMBIM6 DDAH2 GCNT2 TMEM97 TPST1 ALDH2 LONP1 SLC1A5 GAD1 NMT1 KYNUI XDH CYP2S1 TKFC ECH1 HNF4A PINK1 NPC1 CYP2E1 SERPINE1 CFB FMO1 ADH5 CYP1A2
HALLMARK_ESTROGEN_RESPONSE_LATE	0.00716846	0.02560164	-1.9235474	188	TFAP2C SERPINA5 NPY1R LARGE1 PDLIM3 CYP4F11 TH N MUJ CYP26B1 KRT19 PERP HMGCS2 PGR OLFM1 DUSP2 EMP2 WFS1 DCXR FARP1 PRLR ACOX2 PKP3 TPBG ASS1 CELSR2 RNASEH2A KLK10 LLGL2 ETFB FGFR3 CCND1 CXCL12 MAPT TPD52L1 CACNA2D2 BLVRB MDK LSR ID2 TIAM1 FOS FAM102A LAMC2 NAB2 UGDH METTL3 ST14 CAV1 PLXNB1 PLAAT3 XRCC3 PRSS23 HSPB8 CHST8 ALDH3A2 DLG5 TJP3 UNC13B HR FLNB DNAJC12 PCP4 SULT2B1 CPE ALDH3B1 SORB1 CISH SEMA3B SLC29A1 NBL1 EGR3 CHPT1 FRK CDH1 PDZK1 SCNN1A FDFT1 MEST RBBP8 KRT13 SLC1A4 AMFR SGK1 CCN5 TST ISG20 ITPK1 RABEP1 COX6C SLC2A8 TOP2A AREG SLC26A2 IL117RB GAL SERPINA1 GPER1 FKBP5 MYOF TSPAN13 SLC16A1 ATP2B4 TRIM29 CKB SCUBE2 FABP5 GINS2 CALCR DNAJC1 FKBP4 ABCA3 ARL3 SERPINA3 GALE OVOL2 SLC22A5 MICB KLK4 SCARB1 PDCD4 TNNC1 GJB3 IL6ST ZFP36 SLC27A2 CLIC3
HALLMARK_MYC_TARGETS_V2	0.02702703	0.07112376	-1.7436862	57	HSPE1 SLC29A2 TBRG4 SRM PPAN PUS1 DUSP2 RRP9 WDR74 GRWD1 DDX18 MRT04 PES1 MYC MPHOSPH10 FA RSA MYBBP1A TFB2M HSPD1 NOP56 MCM4 PHB SORD IPO4 BYSL TMEM97 CDK4 IMP4 UNG NIP7 TCOF1 NOC4L DCTPP1 NPM1 SUPV3L1 RRP12 PLK1 WDR43 MCM5
HALLMARK_KRAS_SIGNALING_DN	0.02517986	0.07112376	-1.7250584	167	SERPINA10 UGT2B17 TLX1 UPK3B CYP11B2 KRT15 GDNF PNMT KRT5 SLC6A3 TFAP2B ATP4A CACNG1 LYPD3 PR

Pathway Hallmark	p-value	Adjusted p-value	Normalized Enrichment Score (NES)	Size	Leading Edge
					OP1 WNT16 SPTBN2 KLK8 KRT4 CELSR2 IDUA SLC25A23 CYP39A1 DLK2 GP1BA SHOX2 CAPN9 EDN2 PKP1 ARPP21 PTGFR FGFR3 SKIL CNTFR PDK2 PRKN EFHD1 YBX2 PD E6B INTF3 TENM2 NOS1 SPHK2 CD207 KMT2D TGM1 GPR19 TCF7L1 CALML5 GP2 PDCD1 NRIP2 CKM FGGY LFNG HNF1A RYR1 KCNN1 KCNQ2
HALLMARK_ANGIOGENESIS	0.03832753	0.09581882	-1.6630214	33	KCNJ8 SERPINA5 APOH PGLYRP1 THBD VTN S100A4 NRP1 FGFR1 POSTN JAG2 PRG2 VAV2 PDGFA LPL FSTL1 PTK2 LRPAP1 SPP1
HALLMARK_SPERMATOGENESIS	0.04803493	0.11261261	1.5633125	117	PSMG1 TTK CRISP2 BUB1 TSSK2 HSPA2 PAPOLB TOPBP1 NAA11 SLC12A2 CCT6B PHF7 STAM2 ELOVL3 JAM3 DMC1 VDAC3 ODF1 CDK1 HBZ IDE NEFH AURKA SYCP1 GSG1 DNAJB8 TLE4 POMC SCG3 CCNB2 PARP2 HSPA1L TN N13 EZH2 ACRV1 NPHP1 ADAD1 HOXB1
HALLMARK_PROTEIN_SECRETION	0.02631579	0.07112376	1.72808125	87	BET1 M6PR ANP32E SEC22B DNM1L VPS4B AP3S1 CLN5 PAM SNX2 SCRN1 COPB1 PPT1 STX7 TSG101 NAPG STAM GALC ATP1A1 ICA1 COG2 ARFGEF1 MON2 SNAP23 DOP1A RAB22A SOD1 GOLGA4 TMED10 STX12 ZW10 ARFGEF2 AP3B1 VAMP4 VPS45 SEC31A CLCN3 STX16 CTSC GNAS MAPK1 ARCN1 ARFGAP3 RAB14 TMX1 SGMS1 SEC24D ARF1 TPD52 ADAM10 CAV2 LMAN1 AP2B1 ARFIP1 VAMP3 KRT18 COPB2 AP2S1 ATP6V1B1 CLTC KIF1B USO1 SSPN
HALLMARK_UNFOLDED_PROTEIN_RESPONSE	0.0173913	0.05797101	1.73716071	101	DDIT4 EXOSC9 NABP1 CEBPG XBP1 TTC37 HERPUD1 EXOSC5 NOLC1 ASNS DCP2 CALR DNAJC3 SSR1 EIF4E RPS14 DNAJB9 SLC30A5 IFIT1 EXOC2 TATDN2 CNOT6 SRPRA HSP90B1 ALDH18A1 LSM4 CKS1B MTREX MTHFD2 SERP1 FKBP14 PDIA5 EIF2AK3 EXOSC4 KIF5B SDAD1 NOP14 CN OT4 WIPI1 EIF4G1 NHP2 GEMIN4 XPOT DCP1A SEC31A YWHAZ ATF3 FUS DDX10 NFYB ATP6V0D1 ERN1 EIF4EBP1 LSM1 SEC11A SLC7A5 DCTN1 EDEMI1 PDIA6 SPCS1 HSPA5 NFYA VEGFA EIF4A2 KDELR3 PARN PREB NPM1 PAIP1 ZBTB17 EEF2 SRPRB ATF6

Pathway Hallmark	p-value	Adjusted p-value	Normalized Enrichment Score (NES)	Size	Leading Edge
HALLMARK_KRAS_SIGNALING_UP	0.02690583	0.07112376	1.8467282	180	NROB2 SLP C3AR1 IL7R EREG PEG3 IL10RA TMEM100 M YCN PRKG2 CLEC4A PTCD2 FCER1G PLAUR IRF8 IKZF1 H BEGF DOCK2 PDCD1LG2 CTSS KCNN4 SATB1 PECAM1 RE TN GUCY1A1 HDAC9 NIN ARG1 CMKLR1 PSMB8 IL1B GL RX ITGA2 GYPC CA2 EPB41L3 CXCR4 CCND2 LCP1 ANGP TL4 PLAU USP12 SCG3 MPZL2 PRDM1 SDCCAG8 PTGS2 ST6GAL1 LAPTM5 CDADC1 TNFAIP3 ALDH1A3 F13A1 PTB P2 LY96 FBXO4
HALLMARK_MITOTIC_SPINDLE	0.00446429	0.01764291	2.20638149	185	TTK BUB1 FBXO5 CENPE NDC80 SASS6 CNTRL CENPJ DL GAP5 CCDC88A BRCA2 KIF20B ARHGAP10 DOCK2 CDC42 VCL KIFAP3 NIN ABI1 RASA1 CDK1 CDC42EP1 ARHGDI A AURKA ECT2 ANLN SSH2 SOS1 GSN RAPGEF6 LMNB1 P RC1 NCK2 CCNB2 MARCKS ESPL1 SMC3 SMC4 RANBP9 CENPF CNTROB BIRC5 RASAL2 WASL WASF2 RFC1 NET1 ARHGEF3 CKAP5 TLK1 RALBP1 MYO9B ARHGEF2 PREX1 KIF2C FGD4 ARFGEF1 TUBGCP2 NUSAP1 YWHAE TUBA4A RASAZ LRPPRC TPX2 WASF1 CDC27 CLASP1 KIF11 PDLI M5 PLEKHG2 APC ITSN1 RHOT2 ARL8A CEP250 DLG1 RA CGAP1 CTTN KIF5B KNTC1 PKD2 MAPRE1 NEDD9 GEMIN 4 LATS1 KIF3C RABGAP1 ALMS1 ARHGEF7 TUBGCP3 ROC K1 PCGF5 NF1 SPTBN1 TSC1 MYH9 CEP192 LLGL1 ARAP 3 PPP4R2 PCM1 CDC42EP4 NUMA1 NOTCH2 CD2AP KIF1 5 STAU1 SYNPO CAPZB KIF22 RHOF SAC3D1 STK38L CDK 5RAP2 RAB3GAP1 AKAP13 NCK1 RAPGEF5 SUN2 PLK1 A RHGEF11 KATNA1 EPB41L2 PAFAH1B1 KIF1B EPB41 DYN C1H1 INCENP CSNK1D BCR CLIP1 ACTN4 TRIO RICTOR T OP2A TUBGCP5 ARHGEF12 PIF1 HOOK3 PALLD ALS2 EZR CYTH2 TUBGCP6 MARK4 ABL1 ARHGAP27 MAP3K11 PX N CLIP2 NEK2 TAOK2 ATG4B ARF6 KIF3B CEP57 PCNT B CL2L11
HALLMARK_MTORC1_SIGNALING	0.00454545	0.01764291	2.21779846	186	PSMG1 BUB1 FKBP2 STARD4 SLC2A3 DDIT4 BHLHE40 SL A CCNG1 XBP1 FGL2 RIT1 ACTR2 M6PR CYP51A1 DAPP1 TUBG1 LTA4H NUPR1 ACTR3 NFIL3 PNPIASNS PDK1 CA

Pathway Hallmark	p-value	Adjusted p-value	Normalized Enrichment Score (NES)	Size	Leading Edge
					LR EEF1E1 HK2 CORO1A SSR1 STC1 ELOVL5 UCHL5 CANX AURKA PGM1 RAB1A GLRX POLR3G CXCR4 STIP1 PSMA4 PSMD14 SKAP2 BCAT1 PSME3 SLC7A11 CACYPBP ALDOA IFRD1 IDI1 GSK3B EGIN3 GBE1 HSP90B1 IDH1 SQSTM1 DDIT3 TES UBE2D3 NUFIP1 HMBIS GAPDH DHCR7 UFM1 TM7SF2 NUP205 MTHFD2 TUBA4A ITGB2 PNO1 ARPC5L SERP1 TRIB3 ADD3 PSMC2 CDC25A GSR HMGCR SLC6A6 ATP2A2 ACSL3 TPI1 CD9
HALLMARK_COMPLEMENT	0.00446429	0.01764291	2.25604509	185	S100A9 CXCL1 CASP4 OLR1 RAB1F KLK1 PLA2G4A S100A12 CASP10 PLEK GMFB PIK3CG CCL5 RBSN RASGRP1 RCE1 APOBEC3G CR1 PFN1 GNG2 FCER1G PLAUR PIK3R5 LTAA4H ANG GPD2 DOCK10 ITGAM LCP2 IRF1 CTSS DGKG CASP1 CASP9 CASP3 LGALS3 SERPINB2 GNAI2 GP9 CR2 FCN1 AKAP10 PSMB9 CA2 GZMA PRKCD JAK2 LYN GCA IRF7 C9 GNB4 SCG3 ERAP2 ATOX1 IRF2 TIMP2 TNFAIP3 GRB2 C4BPB GZMK PRCP SERPINC1 PRDM4 CSR1
HALLMARK_E2F_TARGETS	0.00446429	0.01764291	2.50212464	187	CDKN1B CDCA3 CENPE CHEK1 WEE1 PSMC3 P CKS2 DEPDC1 ASF1B NBN UBE2S ANP32E MKI67 CBX5 DLGAP5 TUBG1 BUB1B SPC25 RAIN BRCA2 BRMS1L NOLC1 CENPM MMS22L TUBB DIAPH3 BARD1 RAD21 CDK1 MELK AURKA MCM6 MXD3 NUDT21 PCNA E2F8 HMMR LMNB1 CCNB2 SPAG5 ESPL1 SMC3 SMC4 DONSON POLE CDC25B BIRC5 EZH2 LIG1 NUP153 MRE11 PNN RFC1 ING3 EXOSC8 CKS1B GINS4 TK1 PSIP1 CTCF KIF2C POLE4 NUP205 MTHFD2 CHEK2 SMC6 GSPT1 HNRNPD CDC25A PDS5B IPO7 RPA2 TP53 UBE2T PRIM2 RAGGAP1 DCLRE1B LUC7L3 NAP1L1 NAA38 ZW10 RAD51AP1 RPA3 PLK4 STAG1 HEL DUT CDC20 PTTG1 RAD50 PAN2 STMN1 RRM2 CIT GINS3 AURKB LBR EED PA2G4 TMPO TIMELESS NCAPD2 HMGAI CCNE1 TACC3 JPT1 PPM1D DEK MCM2
HALLMARK_TNFA_SIGNALING_VIA_NFKB	0.00436681	0.01764291	2.52580691	179	CD69 CXCL1 MSC BTG1 OLR1 CXCL6 IL7R SLC2A3 DUSP1 RHOB TNFAIP6 IL18 PLEK MCL1 BHLHE40 NFKBIA CCL5 TNFRSF9 CCR2 PLAUR IRS2 NFI3 HBEGF TNFAIP8 IRF1

Pathway Hallmark	p-value	Adjusted p-value	Normalized Enrichment Score (NES)	Size	Leading Edge
					PLK2 ETS2 PTGER4 BIRC2 GPR183 MAP3K8 SERPINB2 TIPARP IL1B RCAN1 BCL6 ICAM1 RIPK2 PTPRE TAP1 SOD2 CCNL1 MXD1 PLAU BCL2A1 MARCKS PTGS2 KLF6 NINJ1 CD44 RNFI9B TNFAIP3 KDM6B CLCF1 NFE2L2 NFKBIE IER5 GADD45B LITAF BCL3 REL TSC22D1 IFIH1 SQSTM1 B4GALT1 F3 DRAM1 IL12B TRIB1 PLPP3 TGIF1 F2RL1 B4GALT5 CD83 PFKFB3 CD80
HALLMARK_INTERFERON_ALPHA_RESPONSE	0.0044843	0.01764291	2.99127826	91	IFITM1 SAMDN9 SAMDN9 IFITM2 SELL NMI TRIM21 CCR2 SP110 IRF1 GBP4 CD47 HLA-C LAMP3 CASP1 GMPR GBP2 EIF2AK2 RNFB31 EPSTI1 PSMB8 IFITM3 SLC25A28 IFI44 TRIM5 RSAD2 PSMB9 RIPK2 TAP1 IRF7 LPAR6 IFI44L IRF2 OASL HERC6 TMEM140 ELF1 IFIH1 PARP12 IFIT3 IRF9 ILJ5 C1S UBE2L6 NCOA7 TRIM25 IL4R
HALLMARK_INFLAMMATORY_RESPONSE	0.00446429	0.01764291	3.06402141	187	IFITM1 CD69 OLR1 C3AR1 CXCL6 IL7R CLEC5A EREG SELENOS TNFAIP6 IL18 IL10RA SELL NFKBIA NMI CCL5 ADGRE1 RASGRP1 PTGIR TNFRSF9 CCR2 GABBR1 LPAR1 PLAUR PIK3R5 NOD2 HBEGF ATP2C1 LCP2 IRF1 SLC7A1 LAMP3 PTGER4 IL10 SRI EIF2AK2 IL18RAP PTAFR GPR183 ABI1 CMKLR1 FFAR2 SLC31A2 NLRP3 TNFSF10 CD48 KCNJ2 PROK2 IL18R1 IL1B ICAM1 RIPK2 PTPRE LYN IRF7 CALCL SEMA4D MXD1 BEST1 KLF6 HIF1A CHST2 PTGER2 EBI3 TNFSF15 TACR3 MSR1 SLAMF1 MEP1A ACVR2A IRAK2 HRH1 CD82 F3 IL12B AQP9 ILJ5 PDPN HAS2 RNFI44B IL4R CD55 SLC31A1 NMIUR1 GNAI3 TAPBP TLR1 SLC28A2 RGS16 CSF3R ATP2A2 RHOG TACR1
HALLMARK_ALLOGRAFT_REJECTION	0.00438596	0.01764291	3.15951108	174	FASLG EREG IL18 FYB1 NCF4 PTPRC CCL5 FGR PRKCB CCR1 F2R DEGS1 LY75 HLA-DRA LY86 IRF8 SRGN EIF5A CCR2 LCP2 STAT4 CTSS ST8SIA4 EIF4G3 SPI1 CD47 MAP3K7 IL10 GBP2 IL18RAP HDA C9 ABI1 GCNT1 NLRP3 TAP2 IFNAR2 ITK BCL10 MRPL3 IL1B TGFB1 MBL2 ICAM1 RIPK2 GZMA TAP1 JAK2 NCR1 LYN IRF7 CCND2 CD86 ELANE GALNT1 BCAT1 IFNG HIF1

Pathway Hallmark	p-value	Adjusted p-value	Normalized Enrichment Score (NES)	Size	Leading Edge
					A CD96 IL16 FCGR2B BCL3 HLA-DOB ACVR2A HLA-DMA CD2 ETS1 ABCE1 IL12B STAT1 SIT1 IL15 DYRK3 CD88 PTPN6 CD4 ZAP70 IL4R CD80 TLR6 ITGB2 RPL9 PRF1 TAPBP TLR1 HCLS1 HLA-E GPR65 CRTAM RPS9 HLA-DMB
HALLMARK_G2M_CHECKPOINT	0.00458716	0.01764291	3.55201322	183	CDKN1B TTK BUB1 SAP30 HMG2 FBXO5 CENPE NDC80 CHEK1 POLQ ODC1 CCNA2 UBE2C CKS2 UBE2S MKI67 STIL HSPA8 SLC12A2 NUP50 BRCA2 KIF20B NOLC1 PML SLC7A1 BARD1 PBK RAD21 WRN CDK1 G3BP1 E2F3 AURK A MCM6 TGFβ1 RAD23B EGF SFPQ HMMR LMNB1 TRAP PRC1 CCNB2 MARCKS ESPL1 KMT5A SMC4 HIF1A CENPF CDC7 POLE CDC25B BIRC5 RASAL2 EZH2 BCL3 CDG6 RBL1 CKS1B E2F4 RPS6KA5 CTCF KIF2C LIG3 HNRNPUN USAP1 GSPT1 TPX2 EFNA5 HNRNPJ CDC27 CDC45 CDC25A PDS5B KIF11 AMD1 ATF5 RP2 MAPK14 PRIM2 RACGAP1 CCNT1 CUL3 KIF5B CASP8AP2 NCL UCK2 PLK4 TOP1 CUL4A CCNF STAG1 SNRPD1 DR1 CDC20 EWSR1 SRSF10 PRPF4B CHAF1A SQLE PTTG1 STMN1 DBF4 NUP98 MEIS1 AURKB LBR TMPO HMGAI TACC3 JPT1 MCM2 SLC7A5 CUL1 RBM14 KNL1 NUMA1 YTHDC1 NOTCH2 SLC38A1 CDKN3 KIF15 E2F2 FOXN3 NSD2 TFDP1 EXO1 SMARCC1 KIF22 SMC2 DTYMK MCM5 TNPO2 ARID4A KPNB1 PLK1 HUS1 KATNA1 GINS2 ODF2 PAFAH1B1 MYBL2 NASP CUL5 TROAP MNAT1 DDX39A INCENP
HALLMARK_INTERFERON_GAMMA_RESPONSE	0.00446429	0.01764291	3.56921198	185	CD69 CASP4 VCAM1 BTG1 SAMD9L IFITM2 PLA2G4A TNFAIP6 IL10RA NFKBIA SELP NMI BANK1 CCLE5 FGL2 ISOC1 TRIM21 P2RY14 VAMP8 IRF8 SP110 PNP EIF4E3 LCP2 IRF1 STAT4 GBP4 ST8SIA4 PML XAF1 CD274 CSF2R8 CASP1 CASP3 SRI EIF2AK2 RNFB3 CMKLR1 EPSTI1 PSMB8 TNFSF10 IFITM3 IFNAR2 SLC25A28 IFI44 RSAD2 IFIT1 MX2 IRCAM1 PSMB9 RIK2 GZMA RAPGEF6 TAP1 SOD2 JAK2 IRF7 PSMA2 XCL1 PELI1 CD86 HLA-B PTGS2 LAT52 HIF1A IFI44L IRF2 OASL TNFAIP3 HERC6

Pathway Hallmark	p-value	Adjusted p-value	Normalized Enrichment Score (NES)	Size	Leading Edge
					PTPN2 UPP1 IFIH1 HLA-DMA PARP12 IFIT3 NUP93 IRF9 STAT1 IL15 C1S UBE2L6 TRIM25 SLAMF7 PTPN6 IL4R RIPK1 MTHFD2 ZNF16 KLRK1 TAPBP NLRCS TRAFD1 CD38 ARID5B

FIG. 34

Pathway	p-value	Adjusted p-value	Normalized Enrichment Score (NES)	Size	Leading Edge
HALLMARK_ADIPOGENESIS	0.00396825	0.02561475	-2.5497022	185	DNAJB9 LTC4S COX8A PREB ACADS COQ9 GPX4 CHCHD10 NDUFA5 PHYH CYC1 DHCR7 ECH1 VEGFB TST UQCR11 ITGA7 CMBL UCP2 DRAM2 PEMT STOM CMPK1 ESYT1 QDPR PIM3 LPL APOE GRPEL1 SLC19A1 ESRRA CPT2 SLC25A1 IFNGR1 GPX3 ITSN1 PFKL ATP5PO SCP2 CAT BCKDHA ACADL ADCY6 ACO2 EPHX2 NDUFAB1 AGPAT3 ANGPTL4 ABCB8 ABCA1 C3 PDCD4 PPARG POR COQ5 ACADM DBT PGM1 MRPL15 MIGA2 ACOX1 SAMM50 STAT5A PP1R15B GBE1 PLIN2 NDUF7 ORM1 ACLY NABP1 SLC27A1 PEX14 MRAP GPAT4 SDHB DNAJC15 ALDH2 MGLL SORBS1 SCARB1 UQCRC1 MYLK ALDOA ACAA2 CAVIN1 IDH1 NDUFS3 UCK1 SLC1A5 NMT1 TALDO1 TKT SLC5A6 TIH5 CD151 DHRS7B CD302 MTCH2 REEP5 SDHC RNFI1 COL15A1 TANK REEP6 CS PFKEB3 CRAT FAH LPCAT3 DLD ECHS1 DGAT1 G3BP2 RMDN3 AK2 BCL2L13 DECR1 DLAT GPAM HADH APLP2 SOWAHC RIOK3 LIPE ETFB ADIPOR2
HALLMARK_XENOBIOTIC_METABOLISM	0.004	0.02561475	-2.5484896	187	HES6 CYP4F2 IMBL2 PINK1 CDA HSD11B1 CYP27A1 G6PC TMEM176B CYP26A1 CCL25 TTPA TAT CYP1A1 ECH1 FMO3 TKFC PDK4 DCXR ID2 PLG ACOX2 ATOH8 NPC1 ADH1C F10 SLC6A12 FBP1 IRF8 CYP2J2 HRG PEMT FAS VNN1 MTFHD1 SAR1B SLC22A1 MPP2 APOE ETS2 ETFDH ACOX3 ENTPD5 GSTM4 SLC46A3 HNF4A ITI4 CYP17A1 SLC12A4 JASL PC PYCR1 CAT LPIN2 BLVRB SLC35D1 PMM1 ACO2 EPHA2 DDC RAP1GAP ABHD6 PTGDS AQP9 MAN1A1 GCH1 CNDP2 POR ACSM1 ACOX1 CES1 TIH1 ARG1 DHRS1 ALDH9A1 CASP6 SLC35B1 GSR TMBIM6 F11 ALDH2 NINJ1 AOX1 IL1R1 CYP1A2 CYB5A AHCY ABCC2 IDH1 SERTAD1 SLC1A5 NMT1 NDRG2 SPINT2 JUP PAPSS2 PPARD BCAR1 MCCC2 GABARAPL1 HGFAC DDAH2 UPP1 UPB1 AKR1C2 ACP1 CYFIP2 ALDH3A1

Pathway	p-value	Adjusted p-value	Normalized Enrichment Score (NES)	Size	Leading Edge
HALLMARK_INTERFERON_ALPHA_RESPONSE	0.00390625	0.02561475	-2.4963202	92	CD74 DHX58 OGFR SAM2D9 GBP2 NMI TMEM140 TAP1 LY6E STAT2 CSF1 CNP IFITM2 BST2 UBA7 HELZ2 TRIM21 IRF2 IFITM1 MX1 LAP3 CMPK2 IFI27 ISG15 TRIM25 PROCR OASL PSMA3 MOV10 IRF7 ISG20 GBP4 PARP14 HERC6 CMTR1 HLA-C DDX60 SP110 IRF9 IFIT2 RSAD2 PSMB9 CCR2 GMMPR L4R IFITM3 PARP9 NUB1 IRF1 IFIT3 RTP4 TENT5A IMVB12A LGALS3BP BATF2 TRIM26 TRIM5 ELF1 UBE2L6 TRIM14 TDRD7 PARP12 IFI44L IFI30 EPST11 IFIH1 C1S CASP8 PSME1 EIF2AK2 NCOA7 IFI44 PSMB8 SAM2D9 IL7 LAPAR6 PNPT1
HALLMARK_COAGULATION	0.00396825	0.02561475	-2.3653134	125	APOC2 THBD MMP10 MBL2 GP1BA SERPING1 COMP CPB2 CFD CFH HPN MSRB2 HMGCS2 PLG F2 CLU ACOX2 F10 HRG SPARC PROC PROZ CTSO DUSP6 TMPSR56 CTSK ARF4 MAFF ISCU BMP1 C8B CAPN5 CRIP2 MMP11 A2M HNF4A OLR1 C9 DCT THBS1 MMMP8 SERPINC1 ITGB3 CSRP1 TIMP3 F12 LGMN C3 PECAM1 MMP9 MEP1A WDNR1 LRP1 ITIH1 SIRT2 PLEK CTSH TF CTSB MASP2 RAPGEF3 F11
HALLMARK_BILE_ACID_METABOLISM	0.00390625	0.02561475	-2.2964652	108	PAOX CYP27A1 SLC22A18 PHYH OPTN CYP8B1 HSD3B7 ABCA2 NPC1 PEX19 FADS1 TTR CYP7A1 AGXT SLC35B2 DI O1 CYP39A1 FDXR SOAT2 FADS2 NR1H2 RXRA PEX11G IDH2 ABCA6 ABCA9 SCP2 CAT BMP6 SLC27A2 PEX16 SLC23A1 EPHX2 NUDT12 AQ9 GSTK1 ACSL1 PECR ABCA1 GCLM PEX11A HAO1 CYP7B1 LCK ALDH8A1 ABCA4 ISOC1 ABCA8 DHCR24 ABCG8 ALDH9A1 PIPOX
HALLMARK_INTERFERON_GAMMA_RESPONSE	0.00393701	0.02561475	-1.9396123	186	METTL7B SERPING1 HLA-A CD74 DHX58 OGFR XAF1 NMI TAP1 LY6E CFH STAT2 IL18BP HLA-DQA1 CD69 IRF8 CCL5 FAS IFITM2 BST2 TNFAIP6 HELZ2 TOR1B TRIM21 IRF2 ZNF31 OAS3 XCL1 MX1 LAP3 CMPK2 IFI27 ITGB7 ISG15 TRIM25 LAT52 KLK11 IL2RB OAS1

Pathway	p-value	Adjusted p-value	Normalized Enrichment Score (NES)	Size	Leading Edge
					L15RA FGL2 NFKBIA PSMA3 BTG1 IRF7 IMX2 RIPK1 NLRC5 ISG20 GBP4 GCH1 RBCK1 PARP14 HERC6 HLA-DMA CSF2RB NOD1 CMTR1 DDX60 SP110 IRF9 IFIT2 RSAD2 PSMB9 DDX58 CIITA SOC1 CASP4 ICAM1 IL4R SPPL2A GZMA IFITM3 PTPN6 STAT4 IL6 EIF4E3 IRF1 IFNAR2 SECTM1 CASP3 ST3GAL5 FPR1 IFIT3 TNFAIP2 RTP4 PML PFKP LGALS3BP UPP1 BATF2 ZBP1 TRIM26 BPGM SAMHD1 TAPBP UBE2L6 TRIM14 NFKB1 NAMPT TDRD7 PTPN1 PARP12 VAMP8 LCP2 IFI44L NCOA3 RAPGEF6 STAT3 SOX2 IFI30 EPST11 PSMB2 IFIH1 C1S OAS2 SELP APOL6 CFB CD38 CASP8 IRF4 PSME1 EIF2AK2 GPR18 PDE4B PTGS2 STAT1 IFI44 SRI CD40 PTPN2 JAK2 PSMB8 SAMD9L IL7SLC25A11 NDUFS8 COX8A COX5B GPX4 TXA1L NDUFA8 NDUFA5 PDHB PHYH TIMM13 NDUF81 NDUFC2 CYC1 ECHH1 MPC1 UQCRI1 PDK4 ATP5F1A ATP6V0C TCIRG1 UQCRIH TIMM9 NDUFA2 NDUFB6 NDUFA7 PHB2 COX7A2 VDAC1 CYB5R3 COX11 GRPEL1 ISCU ETFDH MRPL11 MTRF1 CPT1A NQO2 ATP6V1F IDH2 ATP5PO MFN2 BCKDHA AC02 GOT2 COX5A NDUFB1 ATP5MC3 NDUFS1 ACAA1 SLC25A20 MRPL35 POLR2F ALDH6A1 POR MRPS11 NDUFB3 ATP5F1E ATP5PB ACADM COX6B1 ATP6V1C1 ATP6V1D UQCRIH FXN ATP6V0E1 MRPL15 SLC25A4 VDAC3 HSPA9 NDUFB7 NDUFV1 ATP5PD NDUFB8 COX10 SDHB UQCRIH TOMM22 CYB5A ACAA2 NDUFS2 IDH1 ACAT1 NDUFS3 SUCLA2 IDH3B BDH2 HADHB ACADVL COX15 SDHC SDHD OGDH CS ATP6V1E1 NDUUFV2 DLSD NDUFS6 ECHS1 CYCS VDAC2 FDX1 DECR1 DLAT NDUFA6 NDUFS4 ATP5F1C UQCRIH NDUFB2 ACADSB COX17 RHOT1 ALAS1
HALLMARK_OXIDATIVE_PHOSPHORYLATION	0.00409836	0.02561475	-1.9120272	180	
HALLMARK_PEROXISOME	0.02390438	0.09193993	-1.8563658	100	ACOT8 ECH1 HSD3B7 HMGCL FADS1 TTR CTBP1 ECI2 SLC35B2 DIO1 RDH11 HAO2 NR1I2 IDH2 TOP2A HSD11B2 SCP2 CDK7 CAT SLC27A2 EPHX2 UGT2B17 GSTK1 ACSL1 ACAA1 FDP5 PEX2 ABCB1 ABCB4 CTPS1 DHRS3 PEX11A

Pathway	p-value	Adjusted p-value	Normalized Enrichment Score (NES)	Size	Leading Edge
					SLC25A4 ACOX1 ISOC1 DHCR24 ALDH9A1 PRDX1 CLN6 P EX14 TSPO FABP6 SLC25A17 HSD17B11 CLN8 PEX6 IDH1 HSD17B4 LONP2 ABCD3 CRABP1 SCGB1A1 ALB IDI1 ER CC3 ABCB9 DLG4 PEX5
HALLMARK_FATTY_ACID_METABOLISM	0.02811245	0.09370817	-1.7985418	144	CYP4A11 LTC4S AADAT APEX1 ACADS GPD1 ACOT8 PDH B GLUL HSD17B7 CYP1A1 ECH1 UROS HMGCS2 HSPH1 P PARA HMGCL ADH1C ECI2 ACAT2 VNN1 AOC3 GCDH GS TZ1 CA4 RDH11 CD1D KMT5A ETFDH CPT1A CPT2 HAO2 CYP4A22 SUCLG2 ACADL RDH16 ACO2 INMT ACSL1 AC AA1 ENO3 ACSM3 ALAD ACADM ACOX1 LGALS1 DHCR24 OSTC ALDH9A1 MGLL UOD MCEE ALDOA HSD17B11 A CAA2 IDH1 IL4I1 HSD17B4 ADSJ SUCLA2 ACSS1 SLC22A5 GABARAPL1 IDH3B IDI1 NTHL1 HADHB ACADVL SDHC S DHD ALDH3A1 REEP6 HSDL2 CRAT METAP1 ERP29 UBE2 L6 D2HGDH DLI ACSL5 ECHS1 UGDH NCAPH2 FASN DEC R1 CA6 TDO2 HADH PTPRG CCDC58 MLYCD ADIPOR2 Y WHAH BLVRA PSME1 ECI1 SUCLG1 ALDH3A2 PTS HMG S1 AQP7 GAD2 PCBD1 HIBCH TP53INP2 HPGD SDHA RET SAT S100A10 DLST FMO1 MDH2 BPHL
HALLMARK_IL6_JAK_STAT3_SIGNALING	0.03383459	0.10573308	-1.6220649	72	INHBE EBI3 BAK1 TNF STAT2 TNFRSF1B CSF1 CSF3R FAS PLA2G2A TLR2 IL6ST CCR1 CXCL13 ACVR1B IFNGR1 A2 M IL15RA TGFB1 ITGB3 TNFRSF12A IL10RB LTB CSF2RB LEPR IFNGR2 PIK3R5 IRF9 IFNAR1 TYK2 IL4R IL12RB1 IL1 7RA
HALLMARK_MITOTIC_SPINDLE	0.028	0.09370817	1.71292711	185	ECT2 DLGAP5 CCNB2 RAPGEF5 ALMS1 PLK1 PRC1 KIFAP 3 NDC80 CDC42EP1 RASA2 FSCN1 ARHGAP5 LRPPRC AN LN TSC1 BIRC5 AURKA CCDC88A PALLD CDC42BPA RASA L2 KIF22 KIF11 WASF1 CLASP1 FBXO5 KIF2C DYNC1H1 A RHGAP10 CENPF DST NOTCH2 DYNLL2 EPB41L2 SMC4 F GD6 TLK1 PDLIM5 ARHGEF12 KNTC1 NIN BRCA2 ALS2 A RFGEF1 PPP4R2 RICTOR NEDD9 KIF15 DLG1 KATNA1 RH OT2 PKD2 ROCK1 ARHGEF2 TRIO TUBGCP5 NFI RABGAP

Pathway	p-value	Adjusted p-value	Normalized Enrichment Score (NES)	Size	Leading Edge
HALLMARK_E2F_TARGETS	0.02016129	0.08400538	1.74991347	186	1 NET1 TPX2 SHROOM1 KLC1 AKAP13 ABI1 SMC3 CDK1 BCL2L1 CLIP1 CSNK1D SAC3D1 RASA1 MAP1S SPTBN1 NCK2 STK38L BCR MAPRE1 TUBD1 ABL1 KIF20B GSN SORBS2 PIF1 EZR CDC42 RANBP9 CDC27 RAB3GAP1 MAP3K11 NCK1 RAPGEF6 CLIP2 BUB1 CEP192 KATNB1 DOCK2 TIAM1 ARHGEF3 RACGAP1 RALBP1 SSH2 CENPE SPTAN1 CDK5RAP2 PCGF5 CNTRL KIF1B CEP250 STAU1 ACTN4 SOS1 ATG4B LMNB1 CKAP5 ARF6 ARL8A TUBA4A ARHGA P27 PAFAH1B1 KIF3C KIF5B MARK4 WASF2 RFC1 TBCD BCAR1 APC MYO9B PCM1 EPB41 MYH10 KPTN VCL CD2AP ARHGEF11 YWHAE NUSAP1 CEP57 MYO1E WASL KIF3B FGD4 DOCK4 FLNB TUBGCP3 CENPJ TTK CDC42EP2 H OOK3 PREX1 SASS6 PXN CDC42EP4 CAPZB INCENP ESPL1 BIN1 ARHGAP29 TUBGCP2 SYNPO NUMA1 CTTN CYTH2 ARHGEF7 MARCKS TUBGCP6 PLEKHG2 FARP1 ARAP3 MYH9 PCNT CEP131 SUN2 TOP2A ITSN1 ORC6 MELK CKS2 DUT DLGAP5 SNRPB MCM4 CCNB2 RAD1 PA2G4 PNN DSCC1 PLK1 NOP56 KPNA2 UNG GINS3 RAD51AP1 CDKN2C SYNCRIP EZH2 LUC7L3 MSH2 CHEK1 RANBP1 ORC2 BUB1B BARD1 BIRC5 PPP1R8 MTHFD2 CDCA3 MKI67 AURKA NUP205 MCM2 MCM6 TRA2B HELLS SMC6 CHEK2 KIF22 BRMS1L SPC25 NBN ATAD2 ASF1A MMS22L POLD2 KIF2C CDC25A CDKN2A PRIM2 NASP CDKN3 STMN1 CCP110 NME1 GINS1 SMC4 EED CDKN1A RPA3 PTTG1 CIT BRCA2 DCK MCM3 ING3 TRIP13 NCAPD2 STAG1 ANP32E CBX5 DEK NOLC1 JMR1 SRSF1 CDCA8 CSE1L PRKDC POLD3 EXOSC8 ILF3 DONSON ASF1B PPM1D HMMR SMC3 JPT1 UBE2S DEPDC1 CDK1 E2F8 XPO1 PCNA CENPM MYBL2

Pathway	p-value	Adjusted p-value	Normalized Enrichment Score (NES)	Size	Leading Edge
HALLMARK_PROTEIN_SECRETION	0.02016129	0.08400538	1.78559053	87	VAMP4 AP2M1 TSPAN8 CLTA SSPN ATP6V1H CTSC STX7 SCAMP3 TPD52 NAPG BNIP3 SOD1 RAB22A CAV2 SEC2 4D GALC SCRN1 DST CLTC RAB2A DNM1L ARFIP1 ARF1 VPS4B ARFGEF1 RAB14 GNAS ANP32E ADAM10 COPB1 STX16 STAM PAM AP3B1 AP2B1 M6PR EGFR ATP1A1 VPS45 SH3GL2 RRR1 VAMP3 MAPK1 KRT18 ICA1 CLCN3 TSG101 STX12 TOM1L1 ZW10 ATP6V1B1 GOLGA4 YKT6 SNX2 GOSR2 BET1 AP3S1 MON2 COPE KIF1B ARCN1 PPT1 AP1G1 NAPA SNAP23 COG2 SGMS1 ARFGEF2
HALLMARK_G2M_CHECKPOINT	0.01185771	0.05928854	1.92063455	183	CCNA2 ORC6 MEIS2 CKS2 EXO1 EFNA5 PURA HIF1A TROAP CDC7 CCNB2 PLK1 PRC1 HNRNPJ DR1 KPN2 POLQ CDKN2C NDC80 ODC1 DBF4 SYNCRIP EZH2 HMG2N2 CHEK1 BARD1 BIRC5 SLC12A2 MKI67 AURKA G3BP1 MCM2 MCM6 TRA2B RASAL2 AMD1 KIF22 KIF11 SLC38A1 MNA T1 FBXO5 NCL KIF2C MAP3K20 CDC25A PRMT5 CENPF P RIM2 TNPO2 NOTCH2 NASP CDKN3 RPS6KA5 STMN1 SMC4 PTTG1 BRCA2 MCM3 STAG1 KIF15 NOLC1 KPNB1 CUL1 FANCC SRSF1 KATNA1 RBL1 UBE2C HIRA MEIS1 ILF3 TOP1 CENPA ORC5 TPX2 HMMR PRPF4B JPT1 UBE2S CDK1 ATF5 XPO1 MYBL2 RAD23B ODF2 SLC7A1 ABL1 KIF20B WRN BCL3 SNRPD1 TLE3 E2F3 CBX1 UCK2 TMPO KNL1 CDC27 GSPT1 SRSF10 RAD21 BUB1 MAPK14 DDX39A ARID4A CHAF1A RACGAP1 TENT4A MYC PBK CENPE HNRNPDSFPQ YTHDC1 HUS1 SMARCC1 CUL3 CUL5 EGF UPF1 SQLE CDK4 EWSR1 LMNB1 CTCF CDC45 PAFAH1B1 POLE KIF5B CCND1 STIL PML CDC6 CKS1B NSD2 PDS5B PLK4 MTF2 CDC25B NUP50 MCM5 NUP98 CUL4A NUSAP1
HALLMARK_UV_RESPONSE_DN	0.00816327	0.04535147	2.06096162	135	LPAR1 GJA1 EFEMP1 COL11A1 COL3A1 MMP16 RND3 F3 MET ANXA2 MAP1B PLCB4 HAS2 TJP1 MAGI2 SERPINE1 ATP2B1 COL5A2 TFPI RSA2 LAMC1 ADD3 ADGRL2 PIA S3 CDC42BPA INSIG1 AKT3 IGF1R ABCC1 INPP4B CDON KIT BDNF MAP2K5 ACVR2A PTEN ATP2C1 NOTCH2 SCHIP

Pathway	p-value	Adjusted p-value	Normalized Enrichment Score (NES)	Size	Leading Edge
					1 ADORA2B NIPBL ANXA4 COL1A2 SCAF8 NRP1 PDLIM5 TGFB3 GCNT1 IRS1 BCKDHB CACNA1A DDAH1 RUNX1 PLPP3 BMPR1A DLG1 ATXN1 SPOP MIOS NEK7 PHF3 AGGF1 SIPA1L1 NFIB SRI CDK13 SCN8A PRKCA VLDLR SLC7A1 NR1D2 ATP2B4 APBB2 ICA1 PIK3R3 CAP2 MAPK14 FYN IGFBP5 KALRN CELF2 CCN1 MRPS31 TENT4A TOGARAM1 MYC DBP PRKCE YTHDC1 CAV1 NFKB1 DYRK1A SFBT1 AMPH NR3C1 FHL2 ATRN PTPRM PRDM2 COL1A1 GRK5 SYNE1 LTBP1 WDR37 DAB2 MTA1 MGLL KCNMA1 PRKAR2B PEX14 PTGFR DMAC2L LDLR FBLN5
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	0.00396825	0.02561475	2.2092004	178	DKK1 CDH11 CXCL1 PRRX1 FBN2 GADD45B GJA1 PTHLH MATN3 COL11A1 DCN EDIL3 SGCG COL3A1 PFN2 THY1 SLIT2 PTX3 TPM2 ECM2 POSTN TNC SDC1 GEM CDH2 ITGA2 GREM1 LOX TNFRSF11B APLP1 MIFAP5 FBN1 IGFBP3 SGCB SERPINE1 MMMP2 ADAM12 WNT5A COPA CCN2 COL5A2 ITGAV CTHRC1 PMEPA1 IGFBP4 VCAM1 LAMC1 AREG BASP1 IL15 DPYSL3 PRSS2

FIG. 35

Chr	Start	End	CRPR.zeta	PD.zeta	p-value	Annotation	Detailed Annotation
chr1	5661693	5662036	-0.0786455	0.5657888	0.030711703	Intergenic	Intergenic
chr1	8721909	8722214	-0.1022858	0.7020954	0.00073492	intron (NM_001042681, intron 1 of 22)	LTR54 LTR ERV1
chr1	8908118	8908727	-0.1369095	0.59461119	0.00042631	Intergenic	HERVK9-int LTR ERVK
chr1	10027554	10027983	-0.1322477	0.55376848	0.00640113	Intergenic	AluSp SINE Alu
chr1	11676870	11677149	-0.2687887	0.33882553	0.00315027	intron (NM_001127325, intron 4 of 8)	intron (NM_001127325, intron 4 of 8)
chr1	15246903	15247192	0.42012512	-0.2067443	0.00421602	promoter-TSS (NM_052929)	promoter-TSS (NM_052929)
chr1	20606097	20606521	0.47065184	-0.2046283	0.04640106	intron (NM_001785, intron 2 of 3)	AluYa5 SINE Alu
chr1	24828402	24828720	0.56145099	-0.0289693	0.00950519	intron (NM_013943, intron 4 of 5)	intron (NM_013943, intron 4 of 5)
chr1	26083244	26083516	0.61192409	-0.2253846	0.00271209	Intergenic	Intergenic
chr1	32357410	32357901	-0.0100308	0.70174018	0.00051307	Intergenic	Intergenic
chr1	33260576	33260909	-0.0275859	0.60271174	0.01222808	intron (NM_152493, intron 1 of 8)	intron (NM_152493, intron 1 of 8)
chr1	43854083	43854359	0.53108964	-0.149633	0.02757414	intron (NM_001270466, intron 4 of 4)	L2 LINE L2
chr1	62456301	62456699	0.64999965	-0.0512812	0.00421602	intron (NM_001367561, intron 49 of 49)	LTR81AB LTR Gypsy
chr1	62618810	62619180	0.63925819	-0.0008878	0.00950519	intron (NM_001367561, intron 13 of 49)	intron (NM_001367561, intron 13 of 49)
chr1	65004382	65004707	-0.1079327	0.5079443	0.02208715	intron (NM_001321853, intron 2 of 26)	intron (NM_001321853, intron 2 of 26)
chr1	68228899	68229301	0.78517049	-0.1556456	0.00232819	intron (NM_024911, intron 1 of 11)	MIR3 SINE MIR
chr1	108146301	108146570	0.56641309	-0.1639144	0.01754732	intron (NM_013386, intron 7 of 9),2	L1PA7 LINE L1
chr1	116555965	116556249	0.64790082	-0.0281151	0.01079344	intron (NM_001779, intron 1 of 5)	AluS2 SINE Alu
chr1	150981046	150981491	-0.0768936	0.62287957	0.03415165	Intergenic	Intergenic
chr1	161620371	161620850	0.5703985	-0.0557967	0.04640106	Intergenic	L1PA5 LINE L1
chr1	168718208	168718486	0.73313907	-0.1042471	0.00558343	intron (NM_001937, intron 1 of 3)	intron (NM_001937, intron 1 of 3)

Chr	Start	End	CRPR.zeta	PD.zeta	p-value	Annotation	Detailed Annotation
chr1	170013619	170013996	0.5024212	-0.0967372	0.00170093	intron (NM_014970, intron 10 of 19)	MLT1 LTR ERV1-MaLR
chr1	184945676	184946040	-0.0335774	0.61681322	0.04197334	intron (NM_052966, intron 1 of 13)	L3 LINE CR1
chr1	186860893	186861406	0.57123879	-0.0266504	0.03789677	intron (NM_024420, intron 2 of 17)	intron (NM_024420, intron 2 of 17)
chr1	207852912	207853249	-0.0634314	Inf	0.02470338	Intergenic	Intergenic
chr1	211777936	211778358	-0.0352753	0.6559283	0.00170093	intron (NM_014873, intron 6 of 7)	AluY SINE Alu
chr1	223322657	223323219	-0.0629623	0.74850271	0.00061511	intron (NM_017982, intron 2 of 8)	LTR81AB LTR Gypsy
chr1	230641148	230641731	-0.1150161	0.49841011	0.00315027	Intergenic	Intergenic
chr1	231387120	231387670	0.47086723	-0.1367769	0.0073203	intron (NM_022051, intron 1 of 4)	AluY SINE Alu
chr1	232428826	232429176	-0.0950849	0.52218372	0.0073203	intron (NM_020808, intron 14 of 20)	intron (NM_020808, intron 14 of 20)
chr1	236059009	236059515	0.6071192	-0.0546224	0.03415165	intron (NM_002508, intron 1 of 19)	intron (NM_002508, intron 1 of 19)
chr1	247841561	247841874	0.6426535	-0.112288	0.03071703	exon (NM_001001959, exon 1 of 1)	exon (NM_001001959, exon 1 of 1)
chr10	6542527	6542831	0.8082461	-0.1496249	0.03071703	intron (NM_001323265, intron 1 of 17)	intron (NM_001323265, intron 1 of 17)
chr10	13633040	13633346	-0.1302577	0.51640274	0.00073492	Intergenic	Intergenic
chr10	17387816	17388193	Inf	-0.0980401	0.04197334	intron (NR_034129, intron 1 of 2)	MLT2B2 LTR ERV1
chr10	27740184	27740622	0.52117483	-0.087056	0.00364937	intron (NM_001242702, intron 3 of 6)	intron (NM_001242702, intron 3 of 6)
chr10	44016105	44016403	0.48290251	-0.164563	0.00035293	Intergenic	Intergenic
chr10	45204941	45205422	0.62088592	-0.1238141	0.01754732	Intergenic	Intergenic
chr10	76016465	76016962	0.53735246	-0.0491315	0.02757414	intron (NR_131178, intron 3 of 7)	intron (NR_131178, intron 3 of 7)
chr10	77451198	77451456	-0.0015654	0.60658529	0.00421602	intron (NM_001271519, intron 1 of 28)	intron (NM_001271519, intron 1 of 28)
chr10	78604232	78604614	-0.0018632	0.701207	0.03789677	Intergenic	Intergenic
chr10	92288942	92289322	-0.0412866	0.6794829	0.03415165	intron (NM_014912, intron 1 of 9)	AluX SINE Alu
chr10	97820113	97820836	0.50858539	-0.1526171	0.01754732	Intergenic	L1MB5 LINE L1
chr10	101430971	101431337	-0.1525899	0.76043474	0.02470338	intron (NM_001256856, intron 2 of 13)	AluX SINE Alu

Chr	Start	End	CRPR.zeta	PD.zeta	p-value	Annotation	Detailed Annotation
chr10	101934666	101935245	-0.0744415	0.92958857	0.04197334	intron (NM_024541, intron 23 of 25)	intron (NM_024541, intron 23 of 25)
chr10	102751227	102751550	Inf	-0.0465461	0.04197334	intron (NM_001083913, intron 1 of 3)	AluJb SINE Alu
chr10	119186451	119186822	0.85402501	-0.1409641	0.00640113	Intergenic	AluY SINE Alu
chr11	507799	508082	-0.1864095	0.48251982	0.02208715	promoter-TSS (NM_203387)	promoter-TSS (NM_203387)
chr11	9649475	9650136	0.3949485	-0.268761	0.00035293	Intergenic	AluSq2 SINE Alu
chr11	11218319	11218568	0.50629017	-0.1096345	0.01559077	Intergenic	Intergenic
chr11	13348689	13348979	-0.042642	0.57948615	0.00170093	intron (NM_001351821, intron 3 of 19)	intron (NM_001351821, intron 3 of 19)
chr11	32468837	32469216	0.53922946	-0.0954607	0.03789677	Intergenic	AluSx1 SINE Alu
chr11	57420197	57420500	-0.1287581	0.4606209	0.03789677	intron (NM_017611, intron 7 of 13)	MLT1L LTR ERV1-MaLR
chr11	59174712	59175058	-0.1319366	0.53686647	0.01382274	intron (NM_015177, intron 1 of 8)	intron (NM_015177, intron 1 of 8)
chr11	64159392	64159918	0.5278557	-0.1086638	0.00271209	intron (NM_014067, intron 1 of 10)	AluSp SINE Alu
chr11	65007163	65007523	-0.0568422	0.65573978	0.02208715	Intergenic	AluS2 SINE Alu
chr11	67648249	67648663	-0.2030695	0.41400359	0.00835151	intron (NM_080658, intron 1 of 7)	intron (NM_080658, intron 1 of 7)
chr11	69009701	69009940	-0.2773436	0.47348022	0.02757414	intron (NM_001098515, intron 2 of 2)	intron (NM_001098515, intron 2 of 2)
chr11	72331193	72331641	-0.094789	0.53461252	0.01222808	intron (NM_030813, intron 6 of 16)	AluY SINE Alu
chr11	75130984	75131312	0.54112389	-0.1556032	0.01382274	Intergenic	Intergenic
chr11	75506882	75507179	0.42295766	-0.168493	0.0073203	intron (NM_030792, intron 1 of 16)	intron (NM_030792, intron 1 of 16)
chr11	101514082	101514479	0.59605001	-0.0284319	0.01970718	intron (NM_004621, intron 1 of 12)	L2c LINE L2
chr11	119315356	119315356	-0.1714653	0.51520536	0.03071703	intron (NM_006500, intron 2 of 15)	intron (NM_006500, intron 2 of 15)
chr11	119885241	119885527	-0.0018538	0.6531138	0.02470338	Intergenic	L2a LINE L2
chr11	129274224	129274542	0.83899108	-0.0395948	0.01382274	intron (NR_145484, intron 1 of 1)	intron (NR_145484, intron 1 of 1)
chr12	2452758	2453241	-0.0393919	1.12254863	0.01222808	intron (NM_199460, intron 4 of 49).2	intron (NM_199460, intron 4 of 49).2
chr12	2607416	2607770	0.4857239	-0.1229221	0.00364937	intron (NM_199460, intron 27 of 49).2	intron (NM_199460, intron 27 of 49).2
chr12	6887471	6887858	-0.0572549	0.61056141	0.01222808	intron (NR_135083, intron 1 of 3)	Tigger7 DNA TcMar-Tigger

Chr	Start	End	CRPR.zeta	PD.zeta	p-value	Annotation	Detailed Annotation
chr12	13145038	13145337	-0.0765288	0.73118819	0.0073203	Intergenic	LTR33 LTR ERV
chr12	20555080	20555448	0.61554303	-0.0823018	0.02757414	intron (NM_000921, intron 1 of 15)	AluSx SINE Alu
chr12	25320978	25321303	0.52118952	-0.2332379	0.03071703	Intergenic	MIR SINE MIR
chr12	47814709	47815033	-0.152282	0.47897612	0.00144739	intron (NM_015401, intron 1 of 25)	L2a LINE L2
chr12	48698635	48699022	0.52384681	-0.158954	0.00170093	intron (NM_001240, intron 5 of 8)	AluSp SINE Alu
chr12	48918619	48919121	-0.0496849	0.66994987	0.00035293	exon (NM_033124, exon 6 of 8)	exon (NM_033124, exon 6 of 8)
chr12	68736570	68736914	-0.0309371	0.57888711	0.02208715	intron (NM_020401, intron 26 of 27)	AluSq2 SINE Alu
chr12	89163172	89163747	0.35282805	-0.2445177	0.00051307	Intergenic	Intergenic
chr12	94678104	94678399	0.37197434	-0.2352557	0.04640106	Intergenic	Intergenic
chr12	95358547	95358901	0.73783441	-0.1679454	0.04640106	Intergenic	Intergenic
chr12	113357684	113358150	0.5513021	-0.1076373	0.01970718	promoter-TSS (NM_001159727)	promoter-TSS (NM_001159727)
chr12	116100939	116101331	-0.1254916	0.57351473	0.00421602	intron (NM_015335, intron 3 of 30)	intron (NM_015335, intron 3 of 30)
chr12	121603724	121604241	0.60097709	-0.0935906	0.02470338	Intergenic	AluSp SINE Alu
chr13	40527443	40527755	0.35628323	-0.3417687	0.01754732	Intergenic	AluSq2 SINE Alu
chr13	40602932	40603201	-0.0088839	0.62626523	0.01382274	intron (NM_002015, intron 1 of 2)	intron (NM_002015, intron 1 of 2)
chr13	47463718	47464087	0.654967	-0.1899778	0.01222808	Intergenic	L1PA8A LINE L1
chr13	48358621	48358978	0.47663234	-0.1342397	0.00051307	intron (NM_000321, intron 6 of 26)	intron (NM_000321, intron 6 of 26)
chr13	100552317	100552657	0.61829767	-0.1066192	0.01382274	intron (NM_001195087, intron 2 of 2)	intron (NM_001195087, intron 2 of 2)
chr13	112619972	112620277	-0.0203854	0.58993043	0.01970718	Intergenic	MER51E LTR ERV1
chr14	22750388	22750675	0.50082329	-0.1739327	0.00364937	Intergenic	LTR50 LTR ERV
chr14	33991825	33992201	0.52689587	-0.1310604	0.00232819	Intergenic	Intergenic
chr14	59295419	59295854	0.5927325	-0.0113101	0.04197334	intron (NM_001270520, intron 3 of 24)	intron (NM_001270520, intron 3 of 24)
chr14	65185948	65186394	Inf	-0.0837092	0.03415165	Intergenic	Intergenic
chr14	68249885	68250268	-0.0797471	0.56649831	0.00271209	intron (NM_133509, intron 7 of 10)	intron (NM_133509, intron 7 of 10)
chr14	68387423	68387921	0.51827349	-0.0887034	0.03415165	intron (NM_133509, intron 8 of 10)	MLT10 LTR ERV-L-MaLR

Chr	Start	End	CRPR.zeta	PD.zeta	p-value	Annotation	Detailed Annotation
chr14	70737040	70737405	-0.1358678	0.46193359	0.0073203	intron (NM_033141, intron 8 of 12)	MIR SINE MIR
chr14	74622900	74623334	-0.1118434	0.5795953	0.04197334	Intergenic	L2c LINE L2
chr14	90512307	90512703	-0.0677018	0.60452204	0.02757414	Intergenic	Intergenic
chr14	101726820	101727547	-0.0287164	0.5774449	0.02208715	Intergenic	L2 LINE L2
chr15	39492530	39493315	0.704878	-0.0011364	0.03415165	Intergenic	Intergenic
chr15	42689427	42689688	-0.1051678	0.56111574	0.00144739	exon (NM_020759, exon 23 of 33)	exon (NM_020759, exon 23 of 33)
chr15	57194997	57195402	-0.1362331	0.47432273	0.00271209	intron (NM_207038, intron 7 of 19)	AluSq2 SINE Alu
chr15	62428321	62428617	-0.0428888	0.61391181	0.02208715	Intergenic	Intergenic
chr15	72108988	72109285	-0.1130937	0.65917665	0.00103815	intron (NM_006901, intron 1 of 41)	AluYm1 SINE Alu
chr15	72217317	72217751	-0.1596653	0.44115512	0.01970718	intron (NM_182470, intron 2 of 10)	intron (NM_182470, intron 2 of 10)
chr15	75493512	75493873	0.71958487	-0.0838249	0.04640106	intron (NM_002833, intron 7 of 12)	AluS2 SINE Alu
chr15	78546697	78547079	Inf	-0.1145855	0.04197334	intron (NM_001330676, intron 8 of 8)	AluSx SINE Alu
chr15	88985262	88985608	0.6182693	-0.1740327	0.01970718	Intergenic	PABL_A LTR ERV1
chr16	1405658	1406075	0.46598602	-0.1374668	0.00170093	intron (NR_160278, intron 2 of 15)	intron (NR_160278, intron 2 of 15)
chr16	12256929	12257344	-0.0332934	0.69443871	0.00835151	intron (NM_032167, intron 14 of 20)	MLT1E2 LTR ERV1-MaLR
chr16	15093044	15093398	-0.1496341	0.45736098	0.03415165	intron (NM_018427, intron 1 of 17).2	AluSx1 SINE Alu
chr16	17308961	17309293	0.47409993	-0.2007752	0.00640113	intron (NM_022166, intron 2 of 11)	intron (NM_022166, intron 2 of 11)
chr16	68900184	68900492	-0.1337421	0.51270811	0.00421602	intron (NM_024562, intron 7 of 17)	intron (NM_024562, intron 7 of 17)
chr16	69040254	69040612	-0.0998985	0.92310069	0.02757414	intron (NM_024562, intron 17 of 17)	intron (NM_024562, intron 17 of 17)
chr16	69199345	69199674	-0.017004	0.81331295	0.02470338	intron (NM_006750, intron 1 of 6)	AluJb SINE Alu
chr16	72530500	72530863	-0.1765391	0.45683447	0.01970718	intron (NR_159372, intron 3 of 7)	CR1-3_Croc LINE CR1
chr16	74843813	74844455	-0.1883326	0.52381046	0.00061511	Intergenic	AluJb SINE Alu
chr16	78543387	78543383	-0.0402112	0.60312121	0.04640106	intron (NM_001291997, intron 7 of 7)	intron (NM_001291997, intron 7 of 7)
chr16	81890544	81890903	0.43912441	-0.2790872	1.98E-05	intron (NM_002661, intron 10 of 32)	intron (NM_002661, intron 10 of 32)

Chr	Start	End	CRPR.zeta	PD.zeta	p-value	Annotation	Detailed Annotation
chr16	83952608	83953067	0.81625975	-0.2375839	0.00558343	promoter-TSS (NM_182981)	promoter-TSS (NM_182981)
chr16	85717650	85718024	-0.0044313	0.80231868	0.01382274	intron (NR_161452, intron 2 of 4)	MIRb SINE MIR
chr16	87460936	87461280	-0.112789	0.70567367	0.00051307	intron (NM_015144, intron 1 of 12)	intron (NM_015144, intron 1 of 12)
chr16	89994809	89995609	0.46108952	-0.2656475	0.01079344	non-coding (NR_003226, exon 11 of 11)	non-coding (NR_003226, exon 11 of 11)
chr17	6955689	6956027	-0.0925832	0.49238241	0.03415165	Intergenic	MSTB1 LTR ERV1-MaLR
chr17	7683722	7684091	0.4824334	-0.2281298	0.00835151	intron (NM_001126118, intron 1 of 9)	AluSz6 SINE Alu
chr17	31805084	31805559	-0.0704248	0.52096223	0.03071703	Intergenic	AluY SINE Alu
chr17	36537895	36538211	-0.1697905	0.63899225	0.02470338	exon (NM_001346754, exon 2 of 2)	exon (NM_001346754, exon 2 of 2)
chr17	46287634	46287934	0.41907153	-0.20248	0.01970718	intron (NM_001352769, intron 4 of 4)	intron (NM_001352769, intron 4 of 4)
chr17	48553222	48553523	0.49821144	-0.1141532	0.01754732	intron (NM_002146, intron 2 of 3)	intron (NM_002146, intron 2 of 3)
chr17	49267198	49267634	-0.0276359	0.58219067	0.00640113	Intergenic	AluSx SINE Alu
chr17	55481930	55482390	-0.0566751	0.57834394	0.02470338	Intergenic	Intergenic
chr17	78089622	78090078	-0.2038436	0.46708388	0.00144739	intron (NM_018996, intron 14 of 20)	L2b LINE L2
chr17	79981578	79982137	-0.0512986	0.61438055	0.01559077	intron (NM_019020, intron 3 of 11)	CpG
chr18	6408658	6409042	-0.0060537	0.60663537	0.03071703	intron (NM_001365765, intron 1 of 18)	AluSx SINE Alu
chr18	7438904	7439578	0.57185172	-0.0429692	0.03071703	Intergenic	Intergenic
chr18	12372611	12372984	-0.1368018	0.57520015	0.02208715	intron (NM_006796, intron 1 of 16)	L1MB7 LINE L1
chr18	23362923	23363489	-0.1395562	0.52643296	0.00364937	intron (NR_134876, intron 7 of 10)	AluSx1 SINE Alu
chr18	35321901	35322251	0.60355001	-0.2851055	0.00558343	Intergenic	AluSz6 SINE Alu
chr18	39506812	39507148	-0.131243	0.53449501	0.04197334	intron (NR_024391, intron 3 of 3)	intron (NR_024391, intron 3 of 3)
chr18	39555609	39556151	0.37704836	-0.2230603	0.04197334	intron (NR_024391, intron 2 of 3)	intron (NR_024391, intron 2 of 3)
chr19	7420335	7420955	-0.1010404	0.55420652	0.00950519	intron (NM_015318, intron 1 of 20)	Tigger13a DNA TcMar-Tigger
chr19	8393854	8394161	-0.186402	0.40353835	0.00640113	intron (NM_004218, intron 1 of 4)	intron (NM_004218, intron 1 of 4)
chr19	32648220	32648835	-0.0591183	0.63505756	0.04640106	intron (NM_032139, intron 3 of 28)	AluY SINE Alu

Chr	Start	End	CRPR.zeta	PD.zeta	p-value	Annotation	Detailed Annotation
chr19	47206187	47206623	0.6253809	-0.1192722	0.01079344	intron (NM_005500, intron 8 of 8)	intron (NM_005500, intron 8 of 8)
chr2	1934664	1935080	0.78563375	-0.1090195	0.04640106	intron (NM_015025, intron 9 of 24)	intron (NM_015025, intron 9 of 24)
chr2	11577517	11577957	-0.0765219	0.60435641	0.0073203	intron (NM_014668, intron 5 of 32)	intron (NM_014668, intron 5 of 32)
chr2	28606194	28606456	-0.1527771	0.81663189	0.00144739	intron (NR_138141, intron 20 of 35)	MIRb SINE MIR
chr2	29068341	29068724	-0.0171491	0.71742552	0.00640113	intron (NM_001029883, intron 1 of 1)	intron (NM_001029883, intron 1 of 1)
chr2	33903072	33903967	-0.090678	0.56229294	0.01222808	intron (NR_126403, intron 2 of 5)	LTR12C LTR ERV1
chr2	36365360	36366085	0.60187612	-0.055507	0.01559077	intron (NM_016441, intron 1 of 16)	intron (NM_016441, intron 1 of 16)
chr2	37391039	37391478	-0.0242624	0.66846329	0.04640106	Intergenic	Intergenic
chr2	45716712	45717022	-0.0107262	0.74437855	0.03415165	intron (NM_005400, intron 1 of 14)	THE1C LTR ERV1-MaLR
chr2	49775712	49776078	0.59035465	-0.13231	0.00485813	Intergenic	MSTA LTR ERV1-MaLR
chr2	70113810	70114157	0.57484193	-0.0750345	0.01754732	Intergenic	AluIb SINE Alu
chr2	74095606	74095943	-0.0193871	1.45718755	0.01559077	intron (NM_001287491, intron 10 of 11)	L1ME4a LINE L1
chr2	96474531	96475055	0.50984266	-0.0895486	0.01754732	Intergenic	AluSq2 SINE Alu
chr2	101796916	101797384	-0.1114984	0.54531745	0.00035293	intron (NM_145686, intron 3 of 30)	intron (NM_145686, intron 3 of 30)
chr2	109130092	109130856	-0.0095972	0.81741986	0.00640113	promoter-TSS (NR_029193)	promoter-TSS (NR_029193)
chr2	122220701	122221108	-0.0177862	0.62110095	0.03789677	Intergenic	Intergenic
chr2	126686306	126686721	-0.0121454	0.62080076	0.00485813	5' UTR (NM_001256584, exon 2 of 5)	5' UTR (NM_001256584, exon 2 of 5)
chr2	127541788	127542250	0.58438909	-0.018264	0.02757414	intron (NM_001080527, intron 1 of 46)	intron (NM_001080527, intron 1 of 46)
chr2	131001023	131001555	0.53432927	-0.1164326	0.02208715	intron (NM_001367493, intron 4 of 13)	AluSz SINE Alu
chr2	160369487	160369840	0.57158394	-0.0162737	0.04197334	intron (NM_002897, intron 1 of 13)	intron (NM_002897, intron 1 of 13)
chr2	175637274	175637830	-0.0118052	0.59823754	0.03071703	Intergenic	Intergenic
chr2	195863240	195863706	-0.0465959	0.56799284	0.02757414	intron (NM_018897, intron 41 of 64)	LTR33 LTR ERV1
chr2	201097049	201097756	-0.1798804	0.5850491	0.00364937	Intergenic	AluYa5 SINE Alu
chr2	201098747	201099115	-0.0315766	0.71046822	0.00950519	Intergenic	AluY SINE Alu

Chr	Start	End	CRPR.zeta	PD.zeta	p-value	Annotation	Detailed Annotation
chr2	222368286	222368725	0.40694093	-0.1904254	0.02757414	Intergenic	L1P2 LINE L1
chr2	224645766	224646062	-0.2368797	0.3683996	0.00835151	Intergenic	Intergenic
chr2	229912628	229913058	0.7445591	-0.0493033	0.01222808	intron (NM_001348325, intron 1 of 42)	intron (NM_001348325, intron 1 of 42)
chr2	231268388	231268745	-0.0680749	0.57661238	0.00558343	intron (NM_001352757, intron 11 of 19)	HAL1 LINE L1
chr20	2958738	2959210	0.47674793	-0.1096265	0.00421602	intron (NM_080841, intron 3 of 22)	intron (NM_080841, intron 3 of 22)
chr20	3886172	3886699	-0.063834	0.8235131	0.02470338	Intergenic	AluY SINE Alu
chr20	5827111	5827438	-0.1004342	0.52982425	0.02757414	intron (NM_001303478, intron 3 of 3)	LTR33 LTR ERV
chr20	32002999	32003293	-0.083166	0.58590994	0.01754732	3' UTR (NM_001011718, exon 3 of 3)	3' UTR (NM_001011718, exon 3 of 3)
chr20	34591861	34592253	-0.0043862	0.63828666	0.04197334	intron (NM_080476, intron 7 of 11)	AluY SINE Alu
chr20	39008667	39008930	0.53205606	-0.1614908	0.04197334	intron (NM_021931, intron 12 of 21)	intron (NM_021931, intron 12 of 21)
chr20	44077483	44078103	0.66112788	-0.0731284	0.02757414	Intergenic	HAL1 LINE L1
chr20	47456007	47456462	-0.0970868	0.56401367	0.00835151	Intergenic	AluS2 SINE Alu
chr20	50100264	50100574	-0.161593	0.46024376	0.03071703	intron (NM_001282579, intron 1 of 4)	AluSx4 SINE Alu
chr20	58556708	58557164	1.06213755	-0.2411674	0.01382274	intron (NR_034147, intron 6 of 6)	L2a LINE L2
chr20	58559975	58560245	0.58068635	-0.084823	0.04197334	intron (NR_034147, intron 6 of 6)	intron (NR_034147, intron 6 of 6)
chr20	59271330	59271736	0.49833926	-0.1427437	0.00950519	Intergenic	Intergenic
chr20	60645443	60645713	-0.1531004	0.58457269	0.0073203	Intergenic	Intergenic
chr21	38643091	38643432	-0.0173581	0.58018127	0.01970718	intron (NM_001243432, intron 1 of 11)	intron (NM_001243432, intron 1 of 11)
chr22	18021095	18021478	-0.0591665	0.52793436	0.04640106	intron (NM_015241, intron 1 of 31)	intron (NM_015241, intron 1 of 31)
chr22	19773839	19774107	0.50204154	-0.0985214	0.03789677	intron (NM_005992, intron 8 of 9)	intron (NM_005992, intron 8 of 9)
chr22	24623021	24623511	-0.0456146	0.5933905	0.01754732	intron (NM_013430, intron 10 of 15)	intron (NM_013430, intron 10 of 15)
chr22	29648465	29648832	-0.0675022	0.52250699	0.0073203	intron (NM_181833, intron 4 of 4)	AluJb SINE Alu

Chr	Start	End	CRPR.zeta	PD.zeta	p-value	Annotation	Detailed Annotation
chr22	43989077	43989513	-0.1610994	0.43017712	0.00364937	intron (NM_015380, intron 13 of 14)	intron (NM_015380, intron 13 of 14)
chr22	44141041	44141288	-0.0364816	0.64636211	0.03071703	intron (NM_001243386, intron 8 of 11)	intron (NM_001243386, intron 8 of 11)
chr22	44216015	44216320	-0.1243416	0.52630216	0.00364937	Intergenic	AluSx1 SINE Alu
chr3	3754199	3754741	-0.0111534	0.58581975	0.03789677	intron (NR_149025, intron 5 of 5)	L2c LINE L2
chr3	4501020	4501272	-0.1030155	0.54278041	0.01559077	intron (NM_001168272, intron 2 of 60)	AluJr SINE Alu
chr3	15610161	15610623	-0.0950343	0.5951014	0.01079344	intron (NM_001281725, intron 1 of 3)	MLT1H LTR ERV.L-MaLR
chr3	16212351	16212656	-0.150705	0.48353396	0.00364937	intron (NM_001319051, intron 5 of 9)	intron (NM_001319051, intron 5 of 9)
chr3	17686624	17686951	0.65539228	-0.2071592	0.01970718	intron (NM_001134381, intron 1 of 23)	MER20 DNA hAT-Charlie
chr3	23221524	23221880	0.55549623	-0.0487966	0.03789677	intron (NM_001370225, intron 3 of 5)	AluSq2 SINE Alu
chr3	75419569	75420191	0.55808577	-0.1068976	0.03071703	Intergenic	Intergenic
chr3	112530735	112531131	0.48717033	-0.1684668	0.01382274	Intergenic	L1MD3 LINE L1
chr3	113277716	113278100	-0.0537722	0.56374232	0.00950519	intron (NM_033254, intron 9 of 19)	intron (NM_033254, intron 9 of 19)
chr3	130921042	130921376	0.47849702	-0.241708	0.00199301	intron (NM_001001485, intron 2 of 27)	AluSx1 SINE Alu
chr3	133884237	133884740	1.3926348	-0.1723384	0.04197334	intron (NM_016577, intron 1 of 7)	intron (NM_016577, intron 1 of 7)
chr3	141646727	141647005	0.37741559	-0.2385579	0.00315027	Intergenic	Intergenic
chr3	154048144	154048590	0.81498076	-0.1400305	0.01970718	intron (NR_037901, intron 2 of 3)	MLT1H1 LTR ERV.L-MaLR
chr3	161395522	161395798	Inf	-0.0587995	0.03789677	Intergenic	MIRb SINE MIR
chr3	182709351	182709738	-0.0141351	0.80786782	0.01222808	Intergenic	Intergenic
chr3	183380394	183380789	-0.0858518	0.75920447	0.00315027	intron (NM_015078, intron 2 of 29)	AluSx SINE Alu
chr3	184357725	184358025	-0.0726572	0.58623278	0.03415165	intron (NM_001171088, intron 4 of 22)	intron (NM_001171088, intron 4 of 22)
chr3	185728003	185728330	-0.0073362	1.50874942	0.04640106	intron (NR_126326, intron 5 of 7)	intron (NR_126326, intron 5 of 7)
chr3	196302566	196302862	0.43686259	-0.1747634	0.02470338	intron (NM_152773, intron 3 of 4)	L1MC3 LINE L1

Chr	Start	End	CRPR.zeta	PD.zeta	p-value	Annotation	Detailed Annotation
chr4	2407649	2407947	-0.0531868	0.5479445	0.01222808	intron (NM_020972, intron 1 of 12)	AluSg SINE Alu
chr4	2457761	2458164	-0.0038266	0.63336324	0.00640113	intron (NM_001193282, intron 11 of 15)	MIRb SINE MIR
chr4	24978510	24978945	0.44666559	-0.1895182	0.0073203	intron (NM_173463, intron 1 of 12)	intron (NM_173463, intron 1 of 12)
chr4	51908664	51908944	0.63377038	-0.0549452	0.02470338	intron (NM_015115, intron 8 of 9)	MamRTE1 LINE RTE-BovB
chr4	73232150	73232522	-0.0557462	0.53515257	0.0073203	intron (NM_032217, intron 1 of 33)	intron (NM_032217, intron 1 of 33)
chr4	80087984	80088343	-0.0538969	0.78158371	0.02470338	Intergenic	MSTB2 LTR ERV-L-MaLR
chr4	82660745	82661065	Inf	-0.0554244	0.0073203	exon (NM_024906, exon 4 of 4)	exon (NM_024906, exon 4 of 4)
chr4	88015988	88016388	-0.0444014	0.69061783	0.03071703	intron (NR_156488, intron 1 of 13)	MER1B DNA hAT-Charlie
chr4	94336177	94336548	0.454692	-0.1395879	0.03071703	intron (NM_014485, intron 1 of 5)	intron (NM_014485, intron 1 of 5)
chr4	94516059	94516437	-0.0419515	0.57646018	0.01970718	intron (NM_001256428, intron 2 of 11)	intron (NM_001256428, intron 2 of 11)
chr4	109478615	109479042	-0.1216297	0.47571806	0.02757414	intron (NM_001042734, intron 3 of 22)	Charlie2a DNA hAT-Charlie
chr4	152435044	152435445	0.5402348	-0.1275943	0.01970718	intron (NM_001349798, intron 2 of 13)	L1MC4 LINE L1
chr4	184556963	184557311	0.38524649	-0.2383941	0.00315027	Intergenic	AluSc8 SINE Alu
chr5	1933952	1934396	-0.0431492	1.24624483	0.02470338	Intergenic	Intergenic
chr5	14849907	14850253	-0.1373433	0.46685785	0.01079344	intron (NM_054027, intron 1 of 11)	intron (NM_054027, intron 1 of 11)
chr5	42587404	42587953	0.50520354	-0.2136274	0.01754732	intron (NM_001242460, intron 1 of 7)	(T)n Simple_repeat Simple_repeat
chr5	56489333	56489621	0.60042327	-0.0672477	0.00315027	Intergenic	MIRb SINE MIR
chr5	59342744	59343029	0.68127053	-0.1221015	0.02757414	intron (NM_001165899, intron 3 of 16)	L1MA8 LINE L1
chr5	61508625	61508963	-0.0219657	0.59169783	0.00073492	intron (NM_020928, intron 4 of 13)	MLT1H1 LTR ERV-L-MaLR
chr5	72318839	72319196	0.57100053	-0.0546432	0.04640106	intron (NM_001286751, intron 1 of 10)	intron (NM_001286751, intron 1 of 10)
chr5	74869341	74869689	0.53673331	-0.1302177	0.01970718	Intergenic	MER9a3 LTR ERVK
chr5	82312556	82312901	-0.0824068	0.60858547	0.00199301	exon (NM_001349371, exon 9 of 10)	exon (NM_001349371, exon 9 of 10)
chr5	87395423	87395799	0.43749391	-0.1593429	0.01079344	intron (NR_157069, intron 6 of 8)	AluIb SINE Alu

Chr	Start	End	CRPR.zeta	PD.zeta	p-value	Annotation	Detailed Annotation
chr5	88926689	88927159	1.00540493	-0.0557672	0.00640113	intron (NR_109941, intron 3 of 3)	Tigger3b DNA TcMar-Tigger
chr5	100538709	100539056	-0.0807138	0.57524014	0.02757414	intron (NM_198507, intron 1 of 2)	intron (NM_198507, intron 1 of 2)
chr5	107542792	107543288	0.68357309	-0.2078878	0.00364937	intron (NM_001962, intron 1 of 4)	intron (NM_001962, intron 1 of 4)
chr5	128055582	128055848	0.57035398	-0.2504399	0.00170093	intron (NR_152812, intron 4 of 4)	LTR16E2 LTR ERV1
chr5	131494905	131495231	-0.0675495	0.75764343	0.00170093	intron (NM_016340, intron 13 of 27)	AluSx4 SINE Alu
chr5	154977866	154978227	0.34849523	-0.3004927	0.00558343	Intergenic	AluSc8 SINE Alu
chr5	173138701	173139112	-0.1537023	0.4931911	0.02208715	3' UTR (NM_153607, exon 9 of 9)	3' UTR (NM_153607, exon 9 of 9)
chr5	179823164	179823516	Inf	-0.092079	0.00087491	intron (NM_003900, intron 2 of 7).2	AluSx SINE Alu
chr6	14514714	14515184	0.63522501	-0.0552774	0.01754732	Intergenic	Intergenic
chr6	24546052	24546468	0.45344778	-0.1863922	0.00122772	3' UTR (NM_001350404, exon 20 of 20)	3' UTR (NM_001350404, exon 20 of 20)
chr6	31716969	31717182	0.43710893	-0.1596767	0.00421602	intron (NM_001353334, intron 5 of 5)	AluSp SINE Alu
chr6	31919770	31920179	-0.1534162	0.4380408	0.00042631	intron (NM_001178063, intron 1 of 13).3	intron (NM_001178063, intron 1 of 13).3
chr6	37122188	37122747	-0.1029763	0.48946667	0.03789677	Intergenic	Intergenic
chr6	38170846	38171233	-0.0429085	0.6567265	0.04640106	3' UTR (NM_152733, exon 10 of 10)	3' UTR (NM_152733, exon 10 of 10)
chr6	166488650	166489049	-0.1516604	0.497098	0.00199301	exon (NM_001318937, exon 8 of 19)	exon (NM_001318937, exon 8 of 19)
chr6	166513272	166513695	0.36024268	-0.3280833	0.00010397	intron (NM_001006932, intron 4 of 21)	MIR3 SINE MIR
chr6	166732761	166733130	-0.0647831	0.57754379	0.00950519	intron (NM_001006932, intron 2 of 21)	intron (NM_001006932, intron 2 of 21)
chr6	169905969	169906609	-0.0563313	0.66099178	0.00950519	Intergenic	Intergenic
chr6	170443274	170443594	-0.1772344	0.45091314	0.00558343	Intergenic	Intergenic
chr7	20012235	20012608	0.77995148	-0.1187881	0.00950519	intron (NR_110114, intron 3 of 5)	intron (NR_110114, intron 3 of 5)
chr7	41566688	41567046	0.4449041	-0.2454484	0.00315027	Intergenic	MLT1A0 LTR ERV1-MaLR
chr7	43810664	43810981	-0.0047566	0.61326281	0.01754732	Intergenic	HERVIP10F-int LTR ERV1
chr7	45163697	45163907	0.38983267	-0.3211225	0.00122772	intron (NM_005856, intron 1 of 2)	MIR3 SINE MIR

Chr	Start	End	CRPR.zeta	PD.zeta	p-value	Annotation	Detailed Annotation
chr7	48389071	48389445	0.61933536	-0.0156394	0.02208715	intron (NM_152701, intron 37 of 61)	intron (NM_152701, intron 37 of 61)
chr7	77404770	77405042	0.44735621	-0.1436446	0.00073492	intron (NR_146937, intron 2 of 31)	intron (NR_146937, intron 2 of 31)
chr7	80189650	80189935	-0.1991981	0.42273646	0.01559077	intron (NM_002069, intron 3 of 7)	MIR3 SINE MIR
chr7	128677167	128677753	-0.0625395	0.53819935	0.00558343	intron (NM_001290254, intron 3 of 5)	AluYe5 SINE Alu
chr7	139536676	139537066	0.63223392	-0.0105364	0.02757414	intron (NM_001080511, intron 2 of 4)	AluSx1 SINE Alu
chr7	143369298	143369705	-0.1908386	0.42013766	0.00144739	intron (NM_001371250, intron 1 of 6)	AluSx1 SINE Alu
chr8	1663367	1663934	0.51602478	-0.1035566	0.01970718	intron (NM_001346810, intron 8 of 14)	intron (NM_001346810, intron 8 of 14)
chr8	8513943	8514307	0.53125136	-0.1220151	0.04640106	Intergenic	THE1C LTR ERV1-MaLR
chr8	12821734	12822117	-0.0579053	0.53843363	0.01754732	Intergenic	LTR1A2 LTR ERV1
chr8	29657676	29658048	0.45072312	-0.2240091	0.00558343	Intergenic	Intergenic
chr8	47410865	47411403	-0.0330623	0.64440081	0.02208715	intron (NM_001080394, intron 7 of 19)	L1PA4 LINE L1
chr8	92955871	92956166	0.56400813	-0.0281325	0.01559077	intron (NM_001171797, intron 1 of 4)	L1MB7 LINE L1
chr8	95245907	95246379	0.72533146	-0.0990112	0.01559077	3' UTR (NM_177965, exon 6 of 6)	3' UTR (NM_177965, exon 6 of 6)
chr8	123407606	123407961	-0.0693759	0.55069818	0.00640113	Intergenic	AluSz SINE Alu
chr8	129894941	129895287	-0.011517	0.59340775	0.03071703	intron (NM_001353307, intron 4 of 13)	(GGGGTG)n Simple_repeat Simple_repeat
chr8	142700583	142701112	-0.1709331	0.64349167	0.01970718	intron (NM_017527, intron 1 of 2)	(CCTGCC)n Simple_repeat Simple_repeat
chr9	17203172	17203562	-0.1671054	0.48300475	0.00421602	intron (NM_001365029, intron 2 of 25)	L1PA7 LINE L1
chr9	68610035	68610331	0.91794169	-0.0603804	0.03071703	Intergenic	Intergenic
chr9	68806409	68806808	-0.1184845	0.5420444	0.00144739	intron (NM_003558, intron 2 of 15)	intron (NM_003558, intron 2 of 15)
chr9	70535923	70536376	-0.1790863	0.40885958	0.01079344	exon (NM_024971, exon 26 of 26)	exon (NM_024971, exon 26 of 26)
chr9	89346712	89346992	-0.1676885	0.46890048	4.18E-05	intron (NM_001282688, intron 10 of 16)	intron (NM_001282688, intron 10 of 16)
chr9	94191270	94191635	-0.1033335	0.53693739	0.00364937	intron (NR_160773, intron 2 of 2)	MSTA LTR ERV1-MaLR

Chr	Start	End	CRPR.zeta	PD.zeta	p-value	Annotation	Detailed Annotation
chr9	97927969	97928517	0.8035577	-0.1041842	0.02757414	intron (NM_018437, intron 4 of 4)	AluY SINE Alu
chr9	120624384	120625006	-0.0884207	0.53659713	0.00315027	intron (NM_001080497, intron 2 of 5)	AluSz SINE Alu
chr9	125660624	125660929	-0.001251	0.65443172	0.00950519	intron (NM_001006621, intron 1 of 9)	L2a LINE L2
chr9	127953793	127954254	-0.2035781	0.57700631	0.00950519	intron (NM_001035254, intron 1 of 10)	intron (NM_001035254, intron 1 of 10)
chr9	132253703	132254065	-0.0156944	0.57082767	0.01970718	Intergenic	L1MC4 LINE L1
chr9	134968534	134968898	-0.0204159	0.7086059	0.03789677	Intergenic	MIRb SINE MIR

FIG. 36

Chromosome	Start	End	Gene Symbol
chr22	42508343	42519796	RRP7A
chr2	197568223	197676045	RFTN2
chr8	88032010	88328025	MMP16
chr3	62318972	62336213	C3orf14
chr12	63844699	64162217	SRGAP1
chr8	56436673	56446671	PENK
chr8	39902274	39928790	IDO1
chr9	97029676	97039643	CTSV
chr19	57230801	57235548	AURKC
chr7	75092395	75149817	GTF2IRD2B
chr6	153004458	153131282	RGS17
chr1	117001749	117036476	CD101
chr17	40977715	40987135	KRT40
chr14	60981113	61083733	SLC38A6
chr8	81478418	81483263	FABP4
chr1	212624473	212626778	FAM71A
chr17	41393720	41397608	KRT31
chr4	118850687	119061247	SYNPO2
chr17	27756765	27800499	NOS2
chr4	163524297	164384050	MARCH1
chr9	137220246	137221581	RNF208
chr1	158179946	158184896	CD1D
chr14	64388030	64463457	MTHFD1
chr16	68245303	68261058	PLA2G15
chr4	119135783	119187789	MYOZ2
chr3	42581839	42595114	SS18L2
chr20	46557822	46684467	SLC13A3
chr12	8221259	8227618	FAM90A1
chr19	51642552	51646801	SIGLEC14
chr17	7558291	7561608	TNFSF13
chr11	102789918	102798160	MMP1
chr11	1888576	1891895	PRR33
chr10	71319258	71381423	SLC29A3
chr8	24384284	24406013	ADAMDEC1
chr20	23491100	23496018	CST8
chr19	44777868	44800652	CBLC
chr4	73869392	73871242	CXCL1

Chromosome	Start	End	Gene Symbol
chr3	100609600	100695479	ADGRG7
chr22	30409254	30428990	AC004832.3
chr15	65076815	65079939	KBTBD13
chr5	116032323	116060118	ARL14EPL
chr10	97614552	97633500	MORN4
chr19	55463001	55464707	C19orf85
chr1	86547077	86580754	CLCA4
chr16	4510668	4538828	CDIP1
chr6	96924619	97140754	KLHL32
chr7	93424486	93574730	CALCR
chr11	33376082	33674102	KIAA1549L
chr1	65792513	66374579	PDE4B
chr7	94907201	95296415	PPP1R9A
chr5	136132844	136188747	SMAD5
chr5	55935094	55995022	IL6ST
chr5	132866629	132868847	UQCRQ
chr19	21804948	21852125	ZNF43
chr7	143244092	143270854	GSTK1
chr5	147234962	147387855	STK32A
chr15	75598082	75626469	SNUPN
chr20	59863563	59933655	SYCP2
chr19	51612090	51646889	AC018755.2
chr1	114854862	114995370	SYCP1
chr11	66002227	66004149	BANF1
chr3	49171597	49176486	KLHDC8B
chr1	26280085	26281522	SH3BGRL3
chr2	62500217	62511894	TMEM17
chr19	51611926	51645545	SIGLEC5
chr19	10310044	10316015	FDX2
chr15	23643548	23647867	MAGEL2
chr16	3014711	3020071	CLDN6
chr20	45416083	45456934	PIGT
chr10	97713172	97718150	MARVELD1
chr12	55973912	55996683	AC034102.1
chr11	66975276	66977004	C11orf86
chr3	184031543	184039369	HTR3D
chr4	90127534	91601913	CCSER1
chr12	53708516	53727745	CALCOCO1
chr16	87881545	87936580	CA5A

Chromosome	Start	End	Gene Symbol
chr6	36854826	36874803	PPIL1
chr17	7579490	7582111	CD68
chr2	218270391	218346793	PNKD
chr17	40875940	40885227	KRT20
chr2	195575976	195737702	SLC39A10
chr3	190514050	190659750	IL1RAP
chr6	44126913	44155519	TMEM63B
chr9	129036620	129072082	MIGA2
chr14	95709946	95714196	TCL1A
chr1	154548576	154559028	UBE2Q1
chr17	39664186	39666555	TCAP
chr22	37807904	37817176	GCAT
chr4	61201257	62078335	ADGRL3
chr19	10221432	10231331	S1PR2
chr5	154887410	154938211	GEMIN5
chr4	76011183	76112802	ART3
chr11	60850932	60855950	PTGDR2
chr14	21032817	21034807	RNASE13
chr22	23966887	23972556	DDTL
chr5	107859034	108382098	FBXL17
chr16	46689642	46698394	ORC6
chr2	195737702	196068837	DNAH7
chr7	113876776	114075920	PPP1R3A
chr19	54724478	54736536	KIR3DL3
chr7	27163534	27180013	AC004080.3
chr3	149369021	149377692	TM4SF1
chr20	45841720	45857405	ACOT8
chr6	31528961	31530232	MCCD1
chr1	43269982	43274002	TMEM125
chr4	84583126	84651334	CDS1
chr7	19020990	19117636	TWIST1
chr2	181536671	181680665	CERKL
chr5	180988844	181006727	BTNL3
chr7	64307458	64356634	ZNF736
chr3	88338412	88467562	CSNKA2IP
chr20	35615891	35621049	SPAG4
chr17	47253845	47311816	ITGB3
chr5	80487968	80542563	FAM151B
chr17	47253896	47344292	AC068234.1

Chromosome	Start	End	Gene Symbol
chr20	1540143	1620009	AL049634.2
chr1	246566443	246668595	CNST
chr6	150061052	150069121	ULBP3
chr9	122144057	122159779	NDUFA8
chr1	244454376	244641177	CATSPERE
chr9	128920965	128942041	PHYHD1
chr1	151159747	151165948	LYSMD1
chr3	132317368	132368298	ACPP
chr5	79991310	80083287	THBS4
chr17	44011187	44023946	TMEM101
chr19	19710471	19733112	ZNF14
chr3	3799436	3847703	LRRN1
chr12	56360567	56362857	APOF
chr11	124739941	124747210	NRGN
chr1	32885993	32898441	HPCA
chr11	65122182	65127371	MRPL49
chr21	33903452	33915814	ATP5PO
chr16	19113931	19121629	ITPRIPL2
chr1	204190340	204196491	KISS1
chr8	80967809	81112068	PAG1
chr5	97091866	97142753	LIX1
chr1	107140006	107483458	NTNG1
chr17	30897335	30906238	TEFM
chr6	53794496	53924125	LRRC1
chr3	98732235	98821201	ST3GAL6
chr11	34150986	34358010	ABTB2
chr17	40861302	40867223	KRT12
chr4	55595228	55636698	NMU
chr1	22953042	22965338	LACTBL1
chr10	101570559	101609662	DPCD
chr11	90131514	90192894	NAALAD2
chr16	66878588	66895754	PDP2
chr2	88691672	88750929	RPIA
chr6	143494810	143511690	FUCA2
chr8	144082589	144086216	GPAA1
chr7	27170591	27180261	HOXA10
chr3	13316234	13420322	NUP210
chr7	12570576	12660182	SCIN
chr15	39581078	39599466	THBS1

Chromosome	Start	End	Gene Symbol
chr3	9749943	9788219	OGG1
chr4	112285508	112442621	ALPK1
chr5	64690441	64718190	SHISAL2B
chr22	26491224	26512505	TFIP11
chr1	54184040	54225464	MRPL37
chr4	76251720	76311129	FAM47E-STBD1
chr12	10412311	10436001	AC068775.1
chr1	206635535	206684419	DYRK3
chr10	79382324	79445627	ZCCHC24
chr1	156591761	156594299	NAXE
chr6	32164594	32168281	EGFL8
chr6	4115688	4135597	ECI2
chr1	162365406	162383531	AL512785.2
chr11	2301996	2318200	TSPAN32
chr6	149724314	149749665	NUP43
chr20	45534195	45547662	EPPIN-WFDC6
chr9	130693720	130704894	EXOSC2
chr5	160563119	160852214	ATP10B
chr19	12965158	12974762	DAND5
chr1	150487363	150507609	TARS2
chr4	80266598	80336680	FGF5
chr6	89146054	89165565	PM20D2
chr18	63752934	63805376	SERPINB7
chr9	127867849	127906022	AL157935.2
chr5	177511576	177516961	DDX41
chr12	77324640	78213010	NAV3
chr1	40979687	41012565	CTPS1
chr19	5678420	5680896	MICOS13
chr2	98997260	99154964	TSGA10
chr14	24305095	24311430	CIDEB
chr20	1563520	1620061	SIRPB1
chr10	59650760	59736002	SLC16A9
chr21	18269115	18485879	TMPRSS15
chr12	75391088	75432688	GLIPR1L2
chr3	146576554	146606216	PLSCR5
chr15	89677763	89690783	PEX11A
chr16	55509071	55586666	LPCAT2

Chromosome	Start	End	Gene Symbol
chr16	56191488	56357444	GNAO1
chr16	67229386	67247481	FHOD1
chr9	34521042	34522990	ENHO
chr10	90740822	90858039	HTR7
chr12	7765215	7774121	NANOGNB
chr21	41304211	41357431	FAM3B
chr16	14922801	14952060	NPIPA1
chr9	122370529	122395703	PTGS1
chr15	51447710	51622833	DMXL2
chr12	48766193	48789037	ADCY6
chr2	40097269	40611053	SLC8A1
chr2	105357711	105438513	FHL2
chr14	93333218	93707876	UNC79
chr14	24305733	24312053	LTB4R2
chr17	7583528	7592789	MPDU1
chr3	137998734	138033655	CLDN18
chr5	69217759	69230158	MRPS36
chr15	75195642	75212169	C15orf39
chr14	52775192	52791668	GNPNAT1
chr22	20859006	20891214	SNAP29
chr8	47960184	47978160	MCM4
chr8	144409741	144416895	SLC39A4
chr11	4593613	4596574	OR52I1
chr5	149141482	149260542	ABLIM3
chr17	1646144	1649866	RILP
chr2	219054423	219060921	IHH
chr4	26576436	26756223	TBC1D19
chr2	96497645	96508109	NEURL3
chr12	64780515	64881032	TBC1D30
chr15	67201032	67255195	AAGAB
chr1	183248236	183418380	NMNAT2
chrX	153179283	153183880	MAGEA1
chr9	34638132	34651035	GALT
chr15	80152489	80186946	FAH
chr13	97953657	98024297	IPO5
chr4	154781212	154828813	RBM46
chr3	157436849	157443633	PTX3
chr19	57363565	57398584	AC003002.1
chr17	7240007	7242449	GABARAP

Chromosome	Start	End	Gene Symbol
chr16	88453279	88537031	ZFPM1
chr15	41837774	41848147	PLA2G4B
chr15	59105125	59125045	CCNB2
chr7	123681942	123749003	WASL
chr7	135183838	135211534	WDR91
chr17	28573114	28576948	ALDOC
chr3	138123717	138132387	A4GNT
chr3	100709330	100748964	TFG
chr4	109848201	109872315	LRIT3
chr12	69825303	69959097	MYRFL
chr3	52048918	52056571	DUSP7
chr1	161623195	161631963	FCGR3B
chr9	96313443	96383711	SLC35D2
chr15	89664366	89679427	PLIN1
chr6	43243480	43288258	TTBK1
chr5	157625678	157671480	SOX30
chr20	5126878	5197887	CDS2
chr3	12153067	12158912	TIMP4
chr9	94374550	94461042	MFSD14B
chr15	79311111	79427432	TMED3
chr2	68974572	68980974	GKN1
chr14	88612430	88792752	AL121768.1
chr2	98793845	98936259	KIAA1211L
chr19	16324816	16327874	KLF2
chr9	127885320	127905408	ST6GALNAC6
chr13	113324163	113364148	GRTP1
chr11	67518911	67524517	CABP2
chr16	2968023	2980479	PKMYT1
chr7	31751178	32299329	PDE1C
chr5	138115174	138139443	NME5
chr20	45372556	45407889	TP53TG5
chr9	128945529	128947619	DOLK
chr10	79703226	79714681	NUTM2B
chr19	53467732	53496255	ZNF813
chr12	55716035	55724703	AC009779.3
chr5	53095678	53110063	MOCS2
chr5	160061800	160119450	PWWP2A
chr11	63552769	63563379	PLAAT2
chr10	121478333	121598458	FGFR2

Chromosome	Start	End	Gene Symbol
chr11	4598671	4608231	TRIM68
chr17	39626739	39636626	PPP1R1B
chrX	49071160	49074002	PRAF2
chr15	32765544	33194733	FMN1
chr16	72063147	72077246	HPR
chr10	61406642	61453450	TMEM26
chr2	189746659	189763227	OSGEPL1
chr10	49014235	49115522	VSTM4
chr8	97644183	97730260	MTDH
chr19	51371605	51372701	NKG7
chr6	89364635	89412270	RRAGD
chr20	44355699	44434596	HNF4A
chr3	194394820	194398354	GP5
chr2	55865966	55924139	EFEMP1
chr4	121667945	121696995	ANXA5
chr6	47878027	48068689	PTCHD4
chr11	1597176	1598294	KRTAP5-2
chr6	167146413	167196913	TCP10L2
chr17	76376583	76387860	SPHK1
chr17	49202790	49210574	GNGT2
chr18	20946905	21111813	ROCK1
chr4	55556518	55592245	PDCL2
chr7	22419443	22727613	STEAP1B
chr19	5623034	5668478	SAFB
chr17	75633433	75641404	SMIM5
chr22	30396940	30425303	SEC14L2
chr2	131476118	131482934	TUBA3D
chr8	86866441	87615219	CNBD1
chr1	74198211	74234086	FPGT
chr1	159918106	159925732	TAGLN2
chr5	77072071	77087285	ZBED3
chr17	41436445	41440921	KRT38
chr17	17476993	17493221	MED9
chr3	131381670	131388830	NUDT16
chr20	49293393	49484297	KCNB1
chr7	16599778	16645817	ANKMY2
chr18	32672670	32773062	KLHL14
chr12	64264761	64391192	C12orf56
chr9	97501179	97601743	TMOD1

Chromosome	Start	End	Gene Symbol
chr8	124450819	124462150	TRMT12
chr15	79432515	79472290	MINAR1
chr11	70398403	70436584	CTTN
chr17	58205436	58219605	MKS1
chr3	47495639	47513712	ELP6
chr4	100395340	100880126	EMCN
chr6	41053303	41064511	APOBEC2
chr6	13786556	13814568	MCUR1
chr20	34194568	34269344	ASIP
chr18	5392380	5630700	EPB41L3
chr15	84669537	84716460	SEC11A
chr2	218274196	218292586	TMBIM1
chr19	46918675	47005077	ARHGAP35
chr17	42038231	42050614	C17orf113
chr9	94318195	94328644	NUTM2F
chr7	93188585	93226524	HEPACAM2
chr19	41618970	41627074	CEACAM4
chr20	45648562	45670270	WFDC11
chr19	54850442	54867207	KIR3DL2
chr10	127135425	127196591	INSYN2A
chr17	18697997	18736118	TRIM16L
chr7	22725883	22732002	IL6
chr11	6019335	6034338	OR56A1
chr13	30422487	30428616	UBE2L5
chr14	92923149	92935285	CHGA
chr7	4905988	4959213	MMD2
chr1	25861209	25871253	PAQR7
chr9	33461352	33473930	NOL6
chr14	103084209	103090027	LBHD2
chr16	29812260	29820092	AC009133.6
chr3	187217284	187292022	MASP1
chr17	75827224	75844717	UNC13D
chr17	6996048	7010754	ALOX12
chr12	96489570	96875555	CFAP54
chr18	63871691	63903888	SERPINB2
chr17	42773448	42779599	VPS25
chr15	42210451	42273663	TMEM87A
chr13	66302833	67230445	PCDH9
chr1	22001655	22012539	CELA3A

Chromosome	Start	End	Gene Symbol
chr19	35106509	35124297	AC020907.6
chr2	55231902	55235853	RPS27A
chr19	32691960	32713796	NUDT19
chr6	36390550	36442854	PXT1
chr3	115802362	117139389	LSAMP
chr7	64666082	64711582	ZNF107
chr1	46340176	46365152	NSUN4
chr17	8204732	8210600	AURKB
chr9	89318505	89359662	SECISBP2
chr1	229431244	229434098	ACTA1
chr4	26163454	26435131	RBPJ
chr2	240560053	240564014	DUSP28
chr13	23180951	23325165	SGCG
chr8	66964098	67056604	PPP1R42
chr11	123069871	123195248	CLMP
chr12	89588048	89709300	ATP2B1
chr13	34942286	35673022	NBEA
chr3	9962536	10011116	EMC3
chr1	21217246	21345572	ECE1
chr16	75111859	75116771	LDHD
chr11	68030616	68036644	NDUFS8
chr11	60867561	60875693	ZP1
chr8	67952045	68237032	PREX2
chr8	30732246	30767006	UBXN8
chr12	3077354	3286564	TSPAN9
chr7	6590020	6608726	C7orf26
chr19	18249949	18255419	AC008397.1
chr9	115019574	115118257	TNC
chr4	36281621	36345756	DTHD1
chr16	25215730	25228932	AQP8
chr9	4662314	4665258	PLPP6
chr11	111782194	111871581	ALG9
chr15	22773062	22829789	NIPA1
chr6	44113450	44127452	MRPL14
chr2	68945231	68952893	GKN2
chr2	110732572	111118222	ACOXL
chr3	151733915	151761339	AADACL2
chr10	70052845	70112282	H2AFY2
chr3	158571162	158607252	MLF1

Chromosome	Start	End	Gene Symbol
chr9	133578414	133586197	FAM163B
chr5	39284139	39424868	C9
chr2	149038106	149215262	LYPD6B
chr19	49688663	49690575	ADM5
chr2	102714629	102736888	MFSD9
chr13	42781549	42791549	FAM216B
chr6	34877461	34888089	TAF11
chr1	115976512	116070054	SLC22A15
chr16	21233698	21253850	ANKS4B
chr5	157731419	157741449	THG1L
chr20	33273479	33309871	BPIFB1
chr15	51751596	51816363	TMOD2
chr8	103398657	103501895	AC012213.5
chr19	15878022	15898077	CYP4F2
chr19	47064186	47113776	AC008755.1
chr4	163323961	163344832	NPY1R
chr1	158461573	158470857	OR10K1
chr10	70098222	70132934	AIFM2
chr17	7613945	7633382	SHBG
chr12	55636859	55637854	OR10P1
chr4	168497051	168928457	PALLD
chr11	105137720	105531697	CARD18
chr4	122888696	122922968	NUDT6
chr7	16859411	16881987	AGR3
chr16	68636188	68722616	CDH3
chr10	17137335	17202054	TRDMT1
chr17	9576626	9643447	CFAP52
chr4	84669609	84966391	WDFY3
chr17	49132459	49176840	B4GALNT2
chr12	10226057	10329608	KLRD1
chr1	154321089	154325325	AQP10
chr12	75275978	75390928	CAPS2
chr9	89005770	89178818	SHC3
chr12	55444068	55453347	OR6C2
chr2	169509701	169526258	KLHL41
chr1	44805912	44806675	TCTEX1D4
chr16	28984825	28990783	LAT
chr3	101561867	101566446	TRMT10C
chr1	46929176	46941484	CYP4A11

Chromosome	Start	End	Gene Symbol
chr7	49773637	49921950	VWC2
chr3	3066325	3126613	IL5RA
chr13	77535673	77645263	SCEL
chr11	71814044	71821548	ZNF705E
chr1	156750609	156800815	PRCC
chr3	56620132	56683237	TASOR
chr7	50458435	50565405	DDC
chr5	65665927	65723035	SGTB
chr12	55716036	55720087	BLOC1S1
chr6	31686954	31703356	ABHD16A
chr2	172084739	172089677	DLX1
chr11	124747473	124752255	VSIG2
chr17	39603535	39609777	NEUROD2
chr3	51707067	51718613	GRM2
chr3	157259741	157533619	VEPH1
chr2	111898478	112029561	MERTK
chr4	76214039	76283783	FAM47E
chr17	3207538	3218896	OR1A1
chr1	41585305	41628816	AC119676.1
chr11	66257293	66267860	KLC2
chr11	85628572	85636539	TMEM126B
chr11	59142747	59155039	FAM111A
chr2	96123849	96138436	ASTL
chr2	70830210	70835816	CD207
chr3	28241583	28325142	CMC1
chr9	85546538	85742029	AGTPBP1
chr1	162378840	162386812	C1orf226
chr9	74722494	74888094	TRPM6
chr13	36168216	36214588	SOHLH2
chr19	8206735	8262421	CERS4
chr12	43353865	43551921	ADAMTS20
chr5	79111808	79132288	BHMT
chr1	114769478	114780685	SIKE1
chr4	67820875	67884032	TMPRSS11D
chr8	60678739	60868028	CHD7
chr2	130181736	130190729	MZT2B
chr2	65310850	65432637	SPRED2
chr16	2204247	2209453	MLST8
chr5	179614177	179634784	HNRNPH1

Chromosome	Start	End	Gene Symbol
chr1	162373202	162376870	SPATA46
chr20	6006089	6040053	CRLS1
chr3	194339767	194351328	CPN2
chr4	121035612	121073021	NDNF
chr14	102777475	102911500	TRAF3
chr15	90229974	90234047	CIB1
chr1	158560605	158570580	OR6P1
chr15	66702235	66782849	SMAD6
chr9	136992421	136993984	PAXX
chr3	9362970	9386791	THUMPD3
chr2	113067969	113075850	IL1F10
chr11	105092468	105101431	CARD17
chr11	116820699	116823304	APOA4
chr2	177623243	178072777	PDE11A
chr5	140670793	140673576	DND1
chr14	55366391	55411858	ATG14
chr14	23376772	23379772	CMTM5
chr7	2679521	2775500	AMZ1

FIG. 37

Chromosome	Start	End	Gene Symbol
chr11	104942865	104969366	CASP4
chr12	120687148	120701859	MLEC
chr3	194640790	194672463	LSG1
chr15	75598082	75626469	SNUPN
chr21	39174768	39183851	PSMG1
chr6	31879758	31897687	EHMT2
chr3	9837848	9844602	RPUSD3
chr14	102922655	102933596	AMN
chr1	192158461	192185815	RGS18
chr3	49857987	49869935	CAMKV
chr12	12715057	12722369	CDKN1B
chr19	4324042	4342786	STAP2
chr17	80219698	80253500	SLC26A11
chr1	192316991	192367285	RGS21
chr5	140966469	141012347	PCDHAC2
chr1	183023419	183145592	LAMC1
chr1	151847100	151853712	THEM5
chr22	19846137	19854896	RTL10
chr12	16548371	16610594	LMO3
chr17	1646144	1649866	RILP
chr5	33944622	33984693	SLC45A2
chr22	42553616	42574382	SERHL2
chr8	135457455	135656722	KHDRBS3
chr20	33161767	33181412	BPIFA2
chr11	61515312	61581148	SYT7
chr19	34481637	34512304	WTIP
chr19	42313308	42325064	TMEM145
chr19	50188185	50310542	MYH14
chr11	4680170	4697854	OR51E2
chr19	2977537	2995179	TLE6
chr22	19783222	19854939	GNB1L
chr1	31409564	31434680	SERINC2
chr11	114678385	114707069	NXPE2
chr4	154583127	154590745	FGA
chr12	9752485	9760901	CD69
chr8	144082589	144086216	GPAA1
chr14	64535904	64546173	HSPA2

Chromosome	Start	End	Gene Symbol
chr17	44004545	44009063	NAGS
chr22	30606837	30627278	TCN2
chr1	111290850	111320566	CHIA
chr1	161505429	161524013	FCGR2A
chr20	45534195	45547662	EPPIN-WFDC6
chr16	20359169	20404737	PDILT
chr1	13474972	13514003	LRRC38
chr15	30890558	30943108	FAN1
chr11	537526	554912	LRRC56
chr19	17226212	17229219	OCEL1
chr5	140926368	141012344	PCDHAC1
chr5	81301586	81313297	ZCCHC9
chr1	248046835	248063407	OR2L3
chr8	9136254	9151574	PPP1R3B
chr11	4482645	4493497	OR52K1
chr1	53226899	53238518	MAGOH
chr4	784956	826129	CPLX1
chr17	45160699	45170040	HEXIM2
chr5	98768649	98798643	RGMB
chr18	46476971	46657220	LOXHD1
chr14	94280459	94293268	SERPINA10
chr6	138161938	138344663	ARFGEF3
chr22	50263712	50270767	MAPK11
chr1	232397964	232561558	SIPA1L2
chr11	66362520	66372214	SLC29A2
chr2	110637527	110678063	BUB1
chr10	20779972	21174187	NEBL
chr11	111912735	111926871	HSPB2- C11orf52
chr19	1505021	1513604	ADAMTSL5
chr1	119794016	119811580	REG4
chr10	91798425	91865475	TNKS2
chr19	36687611	36727701	ZNF567
chr2	65227752	65271253	ACTR2
chr7	74453789	74602604	GTF2IRD1
chr7	75811664	75823356	CCL24
chr11	47177521	47186443	PACSIN3
chr10	274189	689668	DIP2C
chr11	71833199	71837710	DEFB108B

Chromosome	Start	End	Gene Symbol
chr7	45080436	45088969	NACAD
chr11	128686534	128813267	FLI1
chr10	114179269	114232304	TDRD1
chr2	68365281	68397453	PLEK
chr4	68053197	68129880	TMPRSS11F
chr4	68646596	68670652	UGT2B15
chr7	64307458	64356634	ZNF736
chr5	111662620	111997464	NREP
chr5	39105251	39274528	FYB1
chr19	35497219	35513658	DMKN
chr12	9985641	10013424	CLEC1B
chr2	197500139	197503449	HSPE1
chr12	49556543	49568145	MCRS1
chr10	100969517	100985871	SEMA4G
chr6	7326655	7389742	CAGE1
chr1	212035552	212107400	DTL
chr1	10456521	10472529	DFFA
chr7	142908100	142933808	TRPV5
chr5	37812676	37840041	GDNF
chr17	65538101	65641033	AC004805.1
chr14	105172937	105181323	NUDT14
chr19	55379244	55384598	TMEM238
chr4	103105805	103198409	CENPE
chr9	20999508	21031640	HACD4
chr7	73667830	73672112	VPS37D
chr1	1418419	1421769	ANKRD65
chr5	79236130	79327211	JMY
chr2	201182880	201229406	CASP10
chr15	89677763	89690783	PEX11A
chr16	30443630	30446181	SEPHS2
chr3	49162534	49166331	CCDC71
chr17	55392621	55421924	MMD
chr1	8317825	8344167	SLC45A1
chr5	140882123	141012347	PCDHA13
chr2	191678067	191696659	NABP1
chr10	100969457	100987515	MRPL43
chr20	37903110	37945350	VSTM2L
chr11	19117098	19176422	ZDHHC13
chr2	112721485	112742879	NT5DC4

Chromosome	Start	End	Gene Symbol
chr16	1911462	1918440	HS3ST6
chr12	109553714	109573580	MMAB
chr6	13786556	13814568	MCUR1
chr7	1688118	1747954	ELFN1
chr17	82057505	82065887	DUS1L
chr16	20333051	20356301	UMOD
chr1	31727116	31764893	ADGRB2
chr8	88032010	88328025	MMP16
chr6	24804281	25042170	RIPOR2
chr19	9178978	9188817	OR7D2
chr19	12317476	12333720	ZNF563
chr11	102110446	102233424	YAP1
chr1	16974501	16980835	MFAP2
chr3	108160811	108222435	IFT57
chr20	31944336	31952046	PDRG1
chr1	54998932	55017172	BSND
chr2	199269499	199471266	SATB2
chr16	58113591	58129381	CFAP20
chr4	499209	540200	PIGG
chr2	241149575	241183652	PPP1R7
chr12	53994894	54003337	HOXC9
chr17	43025230	43032041	RND2
chr11	76782250	76798153	TSKU
chr7	139523684	139544985	CLEC2L
chr1	248590486	248597700	OR2T10
chr1	149782688	149812373	HIST2H2BF
chr22	44752557	44862788	ARHGAP8
chr12	7304283	7328724	ACSM4
chr10	649947	669581	PRR26
chr5	115124761	115180546	TRIM36
chr2	98608578	98618515	UNC50
chr1	225919876	225924340	PYCR2
chr1	15756606	15786594	FBLIM1
chr4	3441886	3449495	HGFAC
chr6	154010495	154246867	OPRM1
chr8	144477968	144502121	PPP1R16A
chr2	112912970	112918882	IL37
chr17	42780609	42797066	WNK4
chr19	57487710	57496097	ZNF419

Chromosome	Start	End	Gene Symbol
chr20	25452696	25585531	NINL
chr12	90905621	90955176	CCER1
chr10	95036771	95069497	CYP2C8
chr3	50287731	50292918	IFRD2
chr16	87326986	87392142	FBXO31
chr12	49950740	49958881	AQP2
chr7	143244092	143270854	GSTK1
chr10	88802729	88820546	LIPM
chr13	19633658	19673441	MPHOSPH8
chr17	38530030	38605952	SRCIN1
chr11	6431048	6442617	HPX
chr7	152644775	152676141	XRCC2
chr3	167478683	167653983	WDR49
chr4	69589308	69639642	UGT2A2
chr17	41582278	41586895	KRT14
chr1	16018874	16034050	CLCNKA
chr5	36606354	36688334	SLC1A3
chr11	66257293	66267860	KLC2
chr15	43232594	43266857	TGM5
chr19	17933014	17943991	CCDC124
chr19	9324173	9382617	ZNF559- ZNF177
chr1	117143586	117210960	VTCN1
chr12	102395873	102481744	IGF1
chr12	51817839	51848766	FIGNL2
chr20	56629305	56639283	TFAP2C
chr9	32553000	32573184	NDUFB6
chr8	41645177	41650669	NKX6-3
chr1	169690664	169711702	SELL
chr1	7915893	7943165	TNFRSF9
chr22	35257451	35295807	HMGXB4
chr1	108875349	108934545	GPSM2
chr16	67184378	67190185	EXOC3L1
chr7	98291649	98401090	BAIAP2L1
chr1	111499428	111503760	ADORA3
chr3	165186719	165197109	SLITRK3
chr1	48727518	48776969	BEND5
chr6	144150525	144188370	STX11
chr10	117128520	117138301	VAX1

Chromosome	Start	End	Gene Symbol
chr1	228165803	228182257	IBA57
chr1	46757837	46819413	CYP4B1
chr1	6205474	6221299	RNF207
chr18	32091873	32131561	RNF138
chr10	122271305	122338162	BTBD16
chr1	52142093	52346686	ZFYVE9
chr17	31272012	31297539	OMG
chr12	57797375	57818704	AVIL
chr2	38813	46870	FAM110C
chr14	20425851	20436158	KLHL33
chr11	66563463	66568841	CTSF
chr11	59511367	59520703	OR4D9
chr4	1347265	1395992	UVSSA
chr17	42561466	42566277	COASY
chr5	140875301	141012347	PCDHA12
chr1	53087178	53142632	SLC1A7
chr1	161152775	161158856	UFC1
chr18	23503469	23531807	RMC1
chr20	3190349	3204685	DDRKG1
chr8	142212079	142403182	TSNARE1
chr12	52232519	52252186	KRT7
chr22	50486783	50490648	MIOX
chr22	41621118	41664048	XRCC6
chr2	235494042	236131800	AGAP1
chr8	43093505	43123434	POMK
chr2	206737762	206765328	MDH1B
chr1	33145398	33182059	TRIM62
chr3	121431426	121546641	POLQ
chr19	18683677	18782333	CRTC1
chr9	108934399	108950744	ABITRAM
chr19	58228593	58277495	ZNF544
chr11	62686405	62689530	LRRN4CL
chr14	96039323	96093889	C14orf132
chr2	191029575	191151596	STAT4
chr18	72536679	72638521	CBLN2
chr14	54474483	54489026	GMFB
chr4	42110852	42152878	BEND4
chr8	143368875	143384221	RHPN1
chr9	121074862	121177610	CNTRL

Chromosome	Start	End	Gene Symbol
chr21	42371836	42396091	TMPRSS3
chr18	57435373	57491298	ONECUT2
chr7	94656324	94669695	PEG10
chr14	94561441	94593118	SERPINA5
chr12	51047961	51060424	LETMD1
chr20	23491100	23496018	CST8
chr1	31617685	31632518	HCRT1
chr5	659861	693352	TPPP
chr11	2129111	2158391	AC132217.2
chr19	57977052	58003349	ZNF606
chr13	39009864	39038089	PROSER1
chr12	53479668	53500063	MAP3K12
chr13	41457549	41470871	RGCC
chr6	32659466	32668383	HLA-DQB1
chr10	35605409	35608935	GJD4
chr12	96907222	96953777	NEDD1
chr1	158999967	159055155	IFI16
chr5	73498407	73505635	BTF3
chr8	103371537	103382989	CTHRC1
chr2	72129237	72148038	CYP26B1
chr11	5880628	5887079	OR52E4
chr19	5784004	5785619	AC011499.1
chr9	128720869	128724127	ZDHC12
chr11	60914157	60923443	TMEM109
chr6	7268305	7347446	SSR1
chr6	6588107	6654983	LY86
chr15	67201032	67255195	AAGAB
chr6	89146054	89165565	PM20D2
chr16	67277509	67289499	PLEKHG4
chr16	1795619	1827157	HAGH
chr1	247670811	247679739	OR13G1
chr8	17576432	17644071	PDGFRL
chr1	24119770	24143140	IL22RA1
chr8	30995801	31033715	PURG
chr3	68975216	69013684	EOGT
chr11	111908618	111923722	CRYAB
chr22	26599277	26618027	CRYBB1
chr19	6426036	6433779	SLC25A41
chr2	96816244	96835382	CNNM3

Chromosome	Start	End	Gene Symbol
chr1	159062483	159147096	AIM2
chr13	36301637	36370180	SPART
chr1	220528182	220664461	MARK1
chr1	155897807	155911404	RIT1
chr14	24120955	24131829	AL136295.3
chr1	247711435	247716646	OR6F1
chr19	37312836	37369365	ZNF875
chr1	28329001	28335965	MED18
chr2	176136611	176173102	HOXD3
chr6	88139863	88166359	CNR1
chr5	140670793	140673576	DND1
chr3	58505135	58537283	ACOX2
chr8	89933335	90003228	NBN
chr1	161541758	161550737	FCGR3A
chr15	81000943	81005788	TLNRD1
chr7	76510427	76516521	UPK3B
chr2	74557882	74648338	M1AP
chr5	112976701	113022195	DCP2
chr14	35278632	35317493	PSMA6
chr11	64823051	64844653	CDC42BPG
chr6	136557045	136792477	MAP3K5
chr9	20658308	20995955	FOCAD
chr14	57268923	57298742	AP5M1
chr8	144529178	144605816	ARHGAP39
chr12	69239568	69274358	CPSF6
chr7	75027121	75074228	RCC1L
chr1	32862267	32872482	FNDC5
chr5	131806989	131945698	MEIKIN
chr6	162727131	163315492	PACRG
chr14	103715729	103733668	ZFYVE21
chr17	44248389	44268141	SLC4A1
chr5	140868182	141012344	PCDHA11
chr17	47951966	47957883	PRR15L
chr3	47282916	47346816	KLHL18
chr6	35497873	35512896	TULP1
chr2	143091361	143768352	ARHGAP15
chr11	106051097	106077459	KBTBD3
chr6	27247700	27256624	PRSS16
chr1	1534777	1540624	TMEM240

Chromosome	Start	End	Gene Symbol
chr2	19351484	19358623	OSR1
chr10	133355157	133358025	FUOM
chr5	132822140	132830898	SHROOM1
chr8	22245132	22254601	POLR3D
chr19	35718018	35738878	KMT2B
chr3	171843348	171938715	TMEM212
chr15	43323648	43330605	LCMT2
chr2	215942583	216034096	MREG
chr8	74234699	74321540	JPH1
chr5	73120568	73131809	TMEM171
chr11	34621092	34661057	EHF
chr17	42659283	42667006	TUBG2
chr14	23969873	24006408	DHRS4L2
chr1	32209093	32216196	DCDC2B
chr1	204131061	204152044	ETNK2
chr10	101061840	101068131	KAZALD1
chr8	56300009	56320776	SDR16C5
chr14	104085685	104115582	ASPG
chr19	45883607	45886141	IRF2BP1
chr5	140827957	141012347	PCDHA6
chr11	19182036	19210571	CSRP3
chr1	6424775	6461367	ESPN
chr19	416582	460996	SHC2
chr1	202878956	202889135	RABIF
chr20	56412111	56460387	CASS4
chr1	6185019	6209389	RPL22
chr4	185500659	185535612	PDLIM3
chr5	140855882	141012347	PCDHA10
chr5	140847462	141012344	PCDHA9
chr13	45333470	45341370	TPT1
chr6	17393504	17557790	CAP2
chr6	5102592	5260939	LYRM4
chr19	42387018	42390297	CNFN
chr5	151661095	151686975	SPARC
chr20	57168752	57266641	BMP7
chr1	202007944	202017183	ELF3
chr2	54972186	55112621	RTN4
chr2	46541805	46584688	RHOQ
chr20	46540945	46550574	OCSTAMP

Chromosome	Start	End	Gene Symbol
chr19	9412460	9435571	ZNF266
chr1	23956838	23963462	PNRC2
chr10	128096658	128126423	MKI67
chr16	85899161	85922606	IRF8
chr9	108854588	108856967	ACTL7B
chr19	2900897	2918473	ZNF57
chr11	125946055	125958647	VSIG10L2
chr14	99481168	99535044	CCNK
chr19	42297032	42303546	PAFAH1B3
chr8	142764333	142778224	LYNX1-SLURP2
chr22	41561009	41577741	CSDC2
chr16	2235815	2238711	DNASE1L2
chr16	58665108	58684770	SLC38A7
chr3	57268346	57292682	ASB14
chr5	180988844	181006727	BTNL3
chr2	218125288	218137251	CXCR2
chr19	45349836	45370918	ERCC2
chr8	142771196	142777810	LYNX1
chr8	144352218	144354914	TMEM249
chr12	131929199	131945896	PUS1
chr9	68705239	69009176	PIP5K1B
chr16	19167970	19268332	SYT17
chr14	23185315	23273477	RNF212B
chr1	212624473	212626778	FAM71A
chr4	76435228	76783253	SHROOM3
chr19	12142089	12156729	ZNF625
chr14	81471546	81533853	SEL1L
chr3	49422945	49429326	NICN1
chr6	5084580	5089487	PPP1R3G
chr5	170232446	170252575	C5orf58
chr3	150882996	150941743	AC020636.2
chr9	32551143	32568621	SMIM27
chr8	123013169	123042302	DERL1
chr14	93207240	93229215	UBR7
chr1	23359447	23369836	ZNF436
chr3	112921204	112975103	CD200R1
chr19	37551405	37614179	ZNF540
chr11	2163928	2171877	TH
chr7	34658238	34878332	NPSR1

Chromosome	Start	End	Gene Symbol
chr7	19020990	19117636	TWIST1
chr7	33904307	34156427	BMPER
chr3	37052625	37183689	LRRFIP2
chr11	111918031	111926871	C11orf52
chr1	52056198	52090716	BTF3L4
chr19	46143105	46161299	IGFL2
chr17	45784279	45835828	CRHR1
chr19	52555456	52587174	ZNF701
chr19	18637024	18671721	KLHL26
chr19	51331535	51342124	VSIG10L
chr8	133036727	133102912	SLA
chr5	173607513	173616660	BOD1
chr10	133420665	133424572	SPRN
chr9	136738166	136748453	AL355987.1
chr8	118995451	119108455	COLEC10
chr1	40258235	40294180	ZMPSTE24
chr4	102630769	102760994	MANBA
chr17	68267025	68291267	SLC16A6
chr10	63521400	63625128	REEP3
chr12	7711432	7717559	DPPA3
chr22	45920365	45977162	WNT7B
chr14	93202893	93207065	GON7
chr4	69588416	69653249	UGT2A1
chr14	69050880	69153150	DCAF5
chr18	31318159	31359246	DSG1
chr2	151270464	151290057	NMI
chr5	177511576	177516961	DDX41
chr12	95657806	95791152	NTN4
chr1	21596214	21669363	RAP1GAP
chr17	8173236	8176399	TMEM107
chr11	6474682	6481479	ARFIP2
chr1	43363397	43368074	ELOVL1
chr12	56638174	56645984	ATP5F1B
chr12	6965326	6970825	PHB2
chr21	41739368	41767089	RIPK4
chr17	36210923	36212878	CCL4L2
chr17	41307699	41309253	KRTAP16-1
chr7	141916398	141920625	OR9A4
chr10	28050992	28334486	MPP7

Chromosome	Start	End	Gene Symbol
chr6	42744480	42746096	TBCC
chr11	67583594	67586656	GSTP1
chr13	98142561	98455176	FARP1
chr7	15611211	15686683	MEOX2
chr19	15010725	15023276	CCDC105
chr3	125929274	125937039	ALG1L
chr7	30938668	30993254	GHRHR
chr16	77722491	77742260	AC092724.1
chr10	38094367	38360098	AL117339.5
chr8	143246820	143262705	ZFP41
chr17	28719984	28724359	RPL23A
chr6	159669068	159745186	SOD2
chr17	6057806	6124427	WSCD1
chr12	110434822	110450422	ARPC3
chr8	119165033	119245673	MAL2
chr2	6917411	7068286	RNF144A
chr12	16347141	16609259	MGST1
chr14	20640695	20641691	OR6S1
chr1	109249538	109275751	CELSR2
chr1	118883045	118989556	TBX15
chr3	133598174	133662380	TOPBP1
chr17	42667913	42676994	PLEKHH3
chr19	5782959	5784746	PRR22
chr16	57372476	57385044	CX3CL1
chr16	1943973	1957606	RPL3L
chr14	36678430	37172866	SLC25A21
chr3	23916544	23924374	RPL15
chr17	41712330	41715969	GAST
chr7	44748580	44769881	ZMIZ2
chr4	112539332	112636995	ZGRF1
chr19	43192701	43207299	PSG4
chr2	100820138	100996829	NPAS2
chr5	176620081	176630556	SNCB
chr10	119499816	119542719	RGS10
chr3	122421901	122514945	KPNA1
chr19	32581189	32587453	PDCD5
chr12	116738177	116853631	RNFT2
chr8	143857323	143878464	EPPK1
chr12	39293227	39443390	KIF21A

Chromosome	Start	End	Gene Symbol
chr8	144353227	144355609	AC233992.2
chr19	38941400	38975742	FBXO17
chr8	144876496	144902168	ZNF250
chr3	126103561	126197994	ALDH1L1
chr6	12716804	13290484	PHACTR1
chr8	132866957	133134903	TG
chr1	64203626	64267368	UBE2U
chr1	2425979	2505532	PLCH2
chr17	28607963	28614200	RSKR
chr13	52703263	52739820	CNMD
chr12	130396136	130716281	RIMBP2
chr20	35302565	35412031	UQCC1
chr2	108534354	108687246	LIMS1
chr11	19350723	20121601	NAV2
chr6	87408011	87511634	AL049697.1
chr5	1008828	1038943	NKD2
chr1	248013659	248024276	OR2L5
chr13	95578201	95644703	DZIP1
chr17	81712235	81721016	SLC25A10
chr1	186828948	186988981	PLA2G4A
chr2	157414618	157488961	CYTIP
chr15	90233807	90245811	GDPGP1
chr10	97153044	97292637	ARHGAP19- SLIT1
chr6	30908241	30926459	VAR52
chr8	18055991	18084998	ASAH1
chr10	62804856	62808483	ADO
chr2	218822382	218832086	PRKAG3
chr4	73836639	73849064	CXCL6
chr19	6772707	6857366	VAV1
chr9	124853416	124857890	WDR38
chr5	140834247	141012347	PCDHA7
chr1	1211339	1214153	TNFRSF4
chr5	140841186	141012347	PCDHA8
chr15	43777086	43802589	SERF2
chr12	54830517	54896008	MUCL1
chr12	118136123	118145584	PEBP1
chr15	43185117	43197177	CCNDBP1
chr11	122655721	122814473	UBASH3B

Chromosome	Start	End	Gene Symbol
chr7	36512948	36724549	AOAH
chr3	113532295	113629578	SIDT1
chr14	50975261	51096061	TRIM9
chr6	33162680	33192499	COL11A2
chr4	73052361	73069755	COX18
chr2	26692689	26733420	KCNK3
chr21	34787800	36004667	RUNX1
chr3	9779859	9793011	TADA3
chr22	38078133	38084093	SLC16A8
chr17	39200282	39204732	RPL19
chr8	144449581	144465677	CYHR1
chr10	10798396	11336675	CELF2
chr7	5970924	6009106	PMS2
chr6	49692357	49713590	CRISP2
chr11	448267	491399	PTDSS2
chr15	29699366	29968865	TJP1
chr1	84549610	84574480	CTBS
chr4	186587793	186726722	FAT1
chr14	60643413	60658259	SIX1
chr1	207043848	207052980	YOD1
chr20	7882984	7940458	HAO1
chr18	6941741	7117797	LAMA1
chr12	9951315	9995694	CLEC12A
chr6	127472793	127519191	SOGA3
chr16	19410495	19499113	TMC5
chr5	137745650	137754376	HNRNPA0
chr1	32361269	32364278	FAM229A
chr20	33407954	33443892	SNTA1
chr19	39984133	40021038	ZNF546

FIG. 38

Chromosome	Start	End	Gene Symbol
chr15	55538889	55588947	PYGO1
chr20	45648562	45670270	WFDC11
chr7	94907201	95296415	PPP1R9A
chr16	3088889	3099295	ZSCAN10
chr1	153774353	153780157	SLC27A3
chr1	117143586	117210960	VTCN1
chr11	68030616	68036644	NDUFS8
chr11	65122182	65127371	MRPL49
chr4	61201257	62078335	ADGRL3
chr5	107376888	107670937	EFNA5
chr2	164896185	164955525	SLC38A11
chr6	31686954	31703356	ABHD16A
chr1	241590101	241677376	OPN3
chr22	37570247	37582616	LGALS2
chr20	59300442	59325992	EDN3
chr6	31686961	31714072	AL662899.1
chr3	88338412	88467562	CSNKA2IP
chr11	842811	867116	TSPAN4
chr1	7915893	7943165	TNFRSF9
chr2	14632699	14650814	LRATD1
chr19	51478621	51490952	CEACAM18
chr16	28846599	28874212	SH2B1
chr12	45014671	45051099	DBX2
chr1	171700159	171742074	VAMP4
chr17	47694080	47712050	TBKBP1
chr8	62248590	62999652	NKAIN3
chr17	40875940	40885227	KRT20
chr2	49918502	51225575	NRXN1
chr9	136844414	136848801	AJM1
chr3	49171597	49176486	KLHDC8B
chr20	17570074	17609919	DSTN
chr11	99020948	100358885	CNTN5
chr14	36473287	36513829	SFTA3
chr1	244454376	244641177	CATSPERE
chr16	77788563	77980107	VAT1L
chr6	44809316	45377953	SUPT3H
chr12	69825303	69959097	MYRFL

Chromosome	Start	End	Gene Symbol
chr1	1635226	1659012	CDK11B
chr21	39556441	39673137	B3GALT5
chr18	6729717	6915716	ARHGAP28
chr17	4710595	4721499	ARRB2
chr7	126438597	127253294	GRM8
chr17	4937129	4940053	SLC25A11
chr8	119165033	119245673	MAL2
chr3	170996346	171026743	SLC2A2
chr10	81875193	82987179	NRG3
chr11	65866440	65873592	EFEMP2
chr12	63844699	64162217	SRGAP1
chr1	42162689	42164745	GUCA2A
chr4	20728605	21948772	KCNIP4
chr17	40977715	40987135	KRT40
chr5	138115174	138139443	NME5
chr2	219054423	219060921	IHH
chr3	93980138	94055668	ARL13B
chr1	114854862	114995370	SYCP1
chr3	96814580	97752460	EPHA6
chr9	99222063	99230615	SEC61B
chr1	215005774	215237093	KCNK2
chr6	167146413	167196913	TCP10L2
chr3	161104695	161253532	NMD3
chr6	22287243	22302826	PRL
chr9	112878919	112890876	SLC46A2
chr2	183117512	183161680	NUP35
chr6	24171754	24358059	DCDC2
chr16	24255552	24362801	CACNG3
chr7	27170591	27180261	HOXA10
chr9	96816471	96875623	ZNF782
chr11	2129111	2141238	IGF2
chr12	90963681	91005026	EPYC
chr16	1434382	1444556	CCDC154
chr11	67403914	67410089	TBC1D10C
chr19	40875438	40882752	CYP2A7
chr11	47407131	47416496	SLC39A13
chr15	36889203	37101299	MEIS2
chr12	77324640	78213010	NAV3
chr7	10931942	10940153	NDUFA4

Chromosome	Start	End	Gene Symbol
chr3	150408334	150466431	TSC22D2
chr3	101222545	101320575	IMPG2
chr14	100323336	100330372	SLC25A47
chr7	120273174	120750337	KCND2
chr1	172532348	172611833	SUCO
chr8	107899315	108083642	RSPO2
chr22	50525751	50530032	TYMP
chr17	75646242	75647975	SMIM6
chr17	81239304	81241310	NDUFAF8
chr4	90127534	91601913	CCSER1
chr11	64746388	64759974	PYGM
chr10	88802729	88820546	LIPM
chr8	52110838	52460959	ST18
chr16	29858356	29863414	CDIPT
chr17	14301080	14349404	HS3ST3B1
chr10	15075474	15088776	ACBD7
chr14	20190893	20201075	OR11G2
chr17	7583528	7592789	MPDU1
chr11	2899720	2925246	SLC22A18
chr2	134918234	134959342	CCNT2
chr5	127042557	127073492	C5orf63
chr19	3610644	3626815	CACTIN
chr6	47781981	47832780	OPN5
chr1	12063302	12144207	TNFRSF8
chr10	133379260	133391694	PAOX
chr15	80679683	80755621	ABHD17C
chr1	203083128	203086012	MYOG
chr4	157204181	157366075	GRIA2
chr12	106582906	106762803	RFX4
chr5	167284798	168264157	TENM2
chr2	240906329	240993311	CROCC2
chr1	150996085	151008375	MINDY1
chr3	108958238	109118142	MORC1
chr3	20160592	20186206	SGO1
chr7	121873088	122062036	PTPRZ1
chr17	82418317	82442645	HEXD
chr9	137251260	137253483	STPG3
chr15	45361123	45402327	GATM
chr3	42708268	42773253	CCDC13

Chromosome	Start	End	Gene Symbol
chr13	21153594	21176552	SKA3
chr4	80266598	80336680	FGF5
chr3	119498531	119525090	TIMMDC1
chr12	10412311	10436001	AC068775.1
chr5	19471295	20575873	CDH18
chr5	83940553	84384880	EDIL3
chr11	106674011	107018524	GUCY1A2
chr10	133160218	133226412	KNDC1
chr11	102047436	102084554	CFAP300
chr15	79898839	79923702	ST20
chr10	5638866	5666595	ASB13
chr16	67644987	67657569	CARMIL2
chr17	29614755	29622907	CORO6
chr2	108786756	108885477	CCDC138
chr5	31400496	31532196	DROSHA
chr11	537526	554912	LRRC56
chr11	119338941	119346705	MFRP
chr2	218356856	218368099	CATIP
chr6	55434368	55579214	HMGCLL1
chr5	21750672	22853622	CDH12
chr19	48600809	48614854	FAM83E
chr10	58269161	58289586	CISD1
chr20	2296000	2341079	TGM3
chr5	176647386	176659054	TSPAN17
chr5	150400040	150412929	CD74
chr11	105995622	106022403	MSANTD4
chr1	117929719	117966543	WDR3
chr19	50311936	50333515	KCNC3
chr4	44678419	44700928	GUF1
chr5	43526266	43557758	PAIP1
chr9	127815011	127854756	ENG
chr10	60026297	60733490	ANK3
chr7	19020990	19117636	TWIST1
chr22	17116298	17121367	TMEM121B
chr2	79185230	80648861	CTNNA2
chr15	36579625	36810248	C15orf41
chr3	75906694	77649964	ROBO2
chr16	89171766	89195492	CDH15
chr6	116529012	116558868	CALHM4

Chromosome	Start	End	Gene Symbol
chr15	59105125	59125045	CCNB2
chr4	105894774	106004027	NPNT
chr1	173799549	173824720	CENPL
chr4	158315310	158653372	RXFP1
chr12	12660889	12696207	GPR19
chr14	51489099	51730727	FRMD6
chr3	196762	409417	CHL1
chr9	27948077	28670286	LINGO2
chr1	9234774	9271337	H6PD
chr8	103398657	103501895	AC012213.5
chr19	13906200	13930879	CC2D1A
chr17	7613945	7633382	SHBG
chr17	7925930	7930622	AC104581.2
chr16	30524003	30526821	ZNF768
chr11	124739941	124747210	NRGN
chr2	241808824	241817413	NEU4
chr3	169772830	169789716	MYNN
chr17	31317559	31321884	EVI2A
chr21	45405164	45513720	COL18A1
chr20	57561079	57568121	PCK1
chr6	54846770	54945099	FAM83B
chr1	42767248	42779491	C1orf50
chr6	49605157	49636884	RHAG
chr17	78187316	78207701	AFMID
chr17	21238869	21253410	NATD1
chr16	72093612	72112912	DHX38
chr14	61811973	62112550	SYT16
chr8	58805411	59119147	TOX
chr8	108201215	108435333	EIF3E
chr6	53126960	53148841	GCM1
chr22	24719033	24774720	PIWIL3
chr16	67929613	67936017	AC040162.1
chr3	132317368	132368298	ACPP
chr15	23643548	23647867	MAGEL2
chr18	23503469	23531807	RMC1
chr11	62761564	62766710	POLR2G
chr3	113361900	113515151	AC112128.1
chr6	153004458	153131282	RGS17
chr4	64275256	64409468	TECRL

Chromosome	Start	End	Gene Symbol
chr1	30732468	30757774	LAPTM5
chr1	20633457	20651511	PINK1
chr3	158962927	159266307	IQCJ
chr3	42692662	42702827	HHATL
chr1	239386564	239915452	CHRM3
chr9	136428618	136439845	INPP5E
chr3	42653696	42667580	ZBTB47
chr7	69598295	70793495	AUTS2
chr7	44062726	44065567	PGAM2
chr13	37636635	37870425	TRPC4
chr7	34928875	35038271	DPY19L1
chr11	61873518	61892051	FADS3
chr12	103237590	103496010	C12orf42
chr6	114055585	114343045	HS3ST5
chr11	78100935	78139653	ALG8
chr5	43486708	43515148	C5orf34
chr6	99919909	99994247	MCHR2
chr22	38685542	38701556	JOSD1
chr11	67518911	67524517	CABP2
chr1	46929176	46941484	CYP4A11
chr2	240586733	240617705	CAPN10
chr3	115802362	117139389	LSAMP
chr5	26880596	27121150	CDH9
chr2	149329984	149474138	LYPD6
chr17	7661778	7687550	TP53
chr6	30699806	30717447	MDC1
chr2	29097704	29189643	CLIP4
chr7	116672195	116798386	MET
chr6	105096821	105137157	BVES
chr1	150574550	150579738	MCL1
chr11	57597386	57614853	SERPING1
chr2	136765544	137677718	THSD7B
chr10	120851304	120909524	WDR11
chr6	52977947	52995304	GSTA4
chr7	93424486	93574730	CALCR
chr19	15672756	15697174	CYP4F12
chr10	97640685	97676434	PI4K2A
chr19	1000418	1009732	GRIN3B
chr1	169394869	169460669	CCDC181

Chromosome	Start	End	Gene Symbol
chr11	65333851	65354262	DPF2
chr6	47878027	48068689	PTCHD4
chr12	70366289	70434292	KCNMB4
chr2	196189098	196593684	HECW2
chr17	28855009	28861061	ERAL1
chr15	59594874	59640239	GCNT3
chr17	39941473	39944734	LRRC3C
chr2	165469646	165689407	CSRNP3
chr2	212999690	213152427	IKZF2
chr16	11833849	11851580	RSL1D1
chr16	75472051	75495445	CHST6
chr1	74026014	74198187	LRRIQ3
chr2	221418026	221574202	EPHA4
chr2	73385757	73625166	ALMS1
chr7	4983717	5073221	RBAK- RBAKDN
chr17	17202648	17237185	AC055811.2
chr3	115623323	115721490	GAP43
chr4	151409175	151670503	FAM160A1
chr12	6310435	6328506	PLEKHG6
chr8	98102343	98117171	RIDA
chr6	50713827	50772988	TFAP2D
chr4	84583126	84651334	CDS1
chr3	184097063	184106995	HTR3E
chr19	42902078	42919563	PSG6
chr6	31572053	31574324	LTA
chr7	96481625	96709891	SEM1
chr5	44303543	44389706	FGF10
chr14	36657567	36679715	PAX9
chr17	10822469	10838087	PIRT
chr17	40122297	40136916	MSL1
chr18	46080247	46104334	ATP5F1A
chr3	158962234	159897366	IQCJ-SCHIP1
chr7	86643913	86864884	GRM3
chr1	150487363	150507609	TARS2
chr5	151276761	151303766	SLC36A3
chr2	233712991	233773299	UGT1A5
chr17	4163820	4263995	ANKFY1
chr8	124306188	124372692	TMEM65

Chromosome	Start	End	Gene Symbol
chr8	99960935	100131268	RGS22
chr5	100535373	100586741	FAM174A
chr20	42072751	43189970	PTPRT
chr4	106921801	107283806	DKK2
chr12	28133248	28581511	CCDC91
chr22	46576011	46679790	GRAMD4
chr15	47184100	47774223	SEMA6D
chr7	16087524	16421538	CRPPA
chr19	45485293	45497055	RTN2
chr1	54026680	54053504	TMEM59
chr17	75633433	75641404	SMIM5
chr2	218382028	218396894	SLC11A1
chr1	55039547	55064852	PCSK9
chr5	24487099	24644978	CDH10
chr12	43835966	44389762	TMEM117
chr11	72685068	72793599	ARAP1
chr1	170662727	170739421	PRRX1
chr17	18377777	18389647	EVPLL
chr20	45823213	45833745	TNNC2
chr8	78516339	78605267	PKIA
chr4	6909241	7033118	TBC1D14
chr11	44047980	44059977	ACCSL
chr19	53879189	53907652	PRKCG
chr3	132558141	132722459	NPHP3- ACAD11
chr2	231523186	231530445	NMUR1
chr3	180602162	180617828	TTC14
chr8	109240918	109334118	NUDCD1
chr18	63556159	63567011	SERPINB12
chr14	36678430	37172866	SLC25A21
chr4	82900683	82919969	THAP9
chr5	179614177	179634784	HNRNPH1
chr2	166403572	166611482	SCN7A
chr16	67229386	67247481	FHOD1
chr7	16599778	16645817	ANKMY2
chr11	33376082	33674102	KIAA1549L
chr1	203178930	203186704	CHI3L1
chr19	50943302	50953093	KLK5
chr8	88032010	88328025	MMP16

Chromosome	Start	End	Gene Symbol
chr12	52689625	52703463	KRT77
chr6	26124144	26139116	HIST1H2AC
chr3	139935184	140577397	CLSTN2
chr8	112222927	113436939	CSMD3
chr16	71430261	71442060	TLE7
chr2	100820138	100996829	NPAS2
chr14	51240161	51257655	TMX1
chr4	20251904	20620561	SLIT2
chr17	10628525	10657309	MYH3
chr8	53966551	54022456	TCEA1
chr6	96924619	97140754	KLHL32
chr9	106863165	107013634	ZNF462
chr17	744420	753999	GEMIN4
chr15	37921938	37967724	TMCO5A
chr9	122144057	122159779	NDUFA8
chr2	166888486	167259753	XIRP2
chr1	45340051	45343973	TOE1
chr7	22118235	22357154	RAPGEF5
chr1	11785722	11806920	MTHFR
chr5	140558267	140564781	APBB3
chr1	16562318	16613562	NBPF1
chr20	62804834	62814000	OGFR
chr13	98445184	98577940	STK24
chr15	71822290	72118577	MYO9A
chr8	65644733	65771261	MTFR1
chr1	117953860	118185223	SPAG17
chr3	105655460	105869552	CBLB
chr17	30316332	30334059	TMIGD1
chr5	127290795	127465737	MEGF10
chr19	49528002	49546962	RCN3
chr2	219597856	219616451	STK11IP
chr5	180784781	180815652	MGAT1
chr14	21568519	21580076	OR10G3
chr9	116425224	117415070	ASTN2
chr11	126269054	126278131	FOXRED1
chr2	69013177	69249327	ANTXR1
chr2	218259495	218263861	GPBAR1
chr11	6497259	6593758	DNHD1
chr19	12922478	12934037	FARSA

Chromosome	Start	End	Gene Symbol
chr14	88005134	88014811	GPR65
chr5	140332842	140346603	HBEGF
chr1	212624473	212626778	FAM71A
chr17	58205436	58219605	MKS1
chr16	560393	565529	PRR35
chr4	86594314	86815171	PTPN13
chr3	42856004	42876165	CYP8B1
chr17	75827224	75844717	UNC13D
chr12	120725773	120740008	ACADS
chr4	108047544	108168956	LEF1
chr7	76510427	76516521	UPK3B
chr17	82050690	82057470	GPS1
chr7	139230355	139308236	UBN2
chr10	49014235	49115522	VSTM4
chr2	241687084	241729478	ING5
chr19	35040505	35066571	HPN
chr17	41688884	41692668	EIF1
chr7	82754011	83162930	PCLO
chr6	32168211	32178096	AGPAT1
chr11	67398182	67421183	PPP1CA
chr19	50819145	50823787	KLK1
chr15	90966039	90995629	PRC1
chr11	66546394	66563334	ACTN3
chr6	30102896	30113090	TRIM31
chr3	50292830	50299405	HYAL3
chr3	52455117	52493068	NISCH
chr15	40323663	40326715	INAFM2
chr12	100573682	100628288	GAS2L3
chr12	56334173	56340410	IL23A
chr9	37582645	37592604	TOMM5
chr14	96392127	96489427	AK7
chr9	136949550	136955497	LCN12
chr7	112422967	112481017	IFRD1
chr1	47183581	47191044	PDZK1IP1
chr2	219002845	219041527	CFAP65
chr10	93566664	93604480	FFAR4
chr19	1578338	1605445	AC005943.1
chr1	86547077	86580754	CLCA4
chr1	50960744	50974634	CDKN2C

Chromosome	Start	End	Gene Symbol
chr3	44431704	44477670	ZNF445
chr3	179653039	179789401	USP13
chr12	30628987	30695869	IPO8
chr1	54641785	54742308	MROH7-TTC4
chr9	113410053	113429684	C9orf43
chr7	30752136	30892081	INMT-MINDY4
chr12	117208141	117452170	NOS1
chr1	120150897	120176515	SEC22B
chr12	75040076	75209868	KCNC2
chr12	43353865	43551921	ADAMTS20
chr2	37342826	37373322	QPCT
chr4	113900283	113979727	ARSJ
chr12	102073102	102120120	NUP37
chr2	158171080	158456753	CCDC148
chr11	4581742	4593340	OR52I2
chr10	125784979	125823258	UROS
chr14	61695512	61748259	HIF1A
chr3	113442717	113515187	SPICE1
chr8	55773141	55825448	TGS1
chr9	70529062	71446904	TRPM3
chr3	113286929	113441610	CFAP44
chr16	30989255	31010638	STX1B
chr1	54641753	54710266	MROH7
chr8	25419257	25424654	GNRH1
chr5	65517765	65563168	CENPK
chr3	33277024	33403662	FBXL2
chr14	23298789	23311759	BCL2L2
chr1	31617685	31632518	HCRT1
chr9	128720869	128724127	ZDHHC12
chr7	20330701	20415754	ITGB8
chr2	181536671	181680665	CERKL
chr7	93188585	93226524	HEPACAM2
chr12	85036313	85264457	LRRIQ1
chr6	73209745	73263196	AL365232.1
chr7	83363237	83649139	SEMA3E
chr7	26152197	26187137	NFE2L3
chr11	2132537	2161209	INS-IGF2
chr17	44248389	44268141	SLC4A1

Chromosome	Start	End	Gene Symbol
chr12	65278642	65491430	MSRB3
chr6	34877461	34888089	TAF11
chr12	78863992	79452008	SYT1
chr1	11806095	11848079	CLCN6
chr11	65375191	65383701	SLC25A45
chr8	27311481	27459391	PTK2B
chr17	3896591	3916476	P2RX1
chr2	197804592	198572581	PLCL1
chr4	44173902	44448809	KCTD8
chr22	41433493	41446801	TOB2
chr12	69801668	69855363	AC025263.2
chr6	32288525	32371912	TSBP1
chr11	8980575	9004049	NRIP3
chr2	240139025	240144562	OTOS
chr12	55681677	55684611	METTL7B
chr5	136028987	136063818	TGFBI
chr13	23180951	23325165	SGCG
chr2	233718777	233773299	UGT1A4
chr1	74235386	74544428	TNNI3K
chr11	2129111	2158391	AC132217.2
chr4	46993722	47426444	GABRB1
chr4	170060221	170091699	AADAT
chr18	23506183	23586506	NPC1
chr9	137220246	137221581	RNF208
chr11	62748318	62754160	ZBTB3
chr20	56629305	56639283	TFAP2C
chr22	37490361	37519542	CARD10
chr11	66257293	66267860	KLC2
chr11	105137720	105531697	CARD18
chr14	78170372	79868290	NRXN3
chr11	67428459	67435401	RPS6KB2
chr19	50958630	50969673	KLK6
chr5	43444251	43483893	TMEM267
chr20	2835313	2841190	PCED1A
chr1	230314489	230426332	PGBD5
chr3	179148113	179240093	PIK3CA
chr12	56994491	56998447	GPR182
chr8	79610813	79666175	STMN2
chr3	15450132	15521751	COLQ

Chromosome	Start	End	Gene Symbol
chr12	88492792	88580851	KITLG
chr2	158795316	158862781	DAPL1
chr17	12665889	12768949	MYOCD
chr11	46700817	46705912	ZNF408
chr3	125446649	125520202	SNX4
chr4	154535004	154550400	PLRG1
chr3	129087568	129122801	RAB43
chr6	127708071	127918631	THEMIS
chr17	42038231	42050614	C17orf113
chr7	74199651	74229834	LAT2
chr19	47870466	47886315	SULT2A1
chr11	124302830	124315099	OR8D1
chr1	165400921	165445355	RXRG
chr2	233729107	233773299	UGT1A3
chr3	124965709	125055997	HEG1
chr1	25959766	25998117	PAFAH2
chr7	94524203	94656572	SGCE
chr11	96352768	96389956	CCDC82
chr6	42929191	42939287	CNPY3
chr2	209771992	209999300	UNC80
chr22	41092591	41180077	EP300
chr7	39566384	39610320	YAE1
chr4	163524297	164384050	1-Mar
chr15	43533461	43590253	PPIP5K1
chr3	179396087	179451476	GNB4
chr16	30658430	30670814	FBR5
chr2	186827834	186849208	ZSWIM2
chr4	87975649	87983426	SPP1
chr19	8832397	8843340	MBD3L1
chr11	60867561	60875693	ZP1
chr2	101002228	101024032	RPL31
chr10	123706206	123940267	CPXM2
chr11	694437	727727	EPS8L2
chr5	147234962	147387855	STK32A
chr2	160272150	160493807	RBMS1
chr1	21217246	21345572	ECE1
chr16	50313486	50368934	BRD7
chr2	239892449	240025345	NDUFA10
chr2	8721080	8837630	KIDINS220

Chromosome	Start	End	Gene Symbol
chr4	73869392	73871242	CXCL1
chr16	28637653	28658682	NPIP8
chr22	39960396	39964718	Z82206.1
chr11	3638502	3642316	ART5
chr3	42809482	42942792	KRBOX1
chr3	51894875	51903353	IQCF1
chr4	46248426	46475230	GABRA2
chr19	48465836	48472431	AC008403.1
chr9	110873262	111038458	LPAR1
chr1	94529172	94541759	F3
chr7	117275450	117323289	WNT2
chr7	19695460	19709037	TWISTNB
chr2	182140035	182523192	PDE1A
chr17	5208919	5234860	SCIMP
chr20	14322984	14337614	FLRT3
chr1	173477329	173488815	PRDX6
chr1	196819756	196832189	CFHR1
chr12	91140483	91182824	DCN
chr17	76527355	76551175	CYGB
chr8	144409741	144416895	SLC39A4
chr12	7129697	7158945	CLSTN3
chr1	222872270	223005995	DISP1
chr11	71428192	71452868	DHCR7
chr4	2793070	2841098	SH3BP2
chr16	67148103	67150998	B3GNT9
chr3	180602857	180684942	CCDC39
chr17	36013055	36017972	CCL23
chr19	21932957	22010949	ZNF208
chr11	67583594	67586656	GSTP1
chr7	4775614	4794397	AP5Z1
chr13	114314481	114337626	CHAMP1
chr4	81030707	81057632	BMP3
chr3	171843348	171938715	TMEM212
chr14	23099061	23104989	LMLN2
chr12	123584532	123598582	TMED2
chr11	66593152	66606019	CCS
chr14	60981113	61083733	SLC38A6
chr5	151100705	151157785	ANXA6
chr1	170935470	171064765	MROH9

Chromosome	Start	End	Gene Symbol
chr7	81946443	82443777	CACNA2D1
chr9	122202576	122229626	LHX6
chr22	21009807	21028830	P2RX6
chr20	23491100	23496018	CST8
chr19	18782772	18791305	COMP
chr3	135965727	136147894	PPP2R3A
chr7	139133743	139191986	TTC26
chr1	221701423	221742089	DUSP10
chr7	108147622	108456717	NRCAM
chr4	36281621	36345756	DTHD1
chr11	61333209	61353295	TKFC
chr6	136231023	136250335	MTFR2
chr19	36916328	36998700	ZNF568
chr3	52495337	52524495	STAB1
chr1	200739557	200860704	CAMSAP2
chr1	225486834	225653142	ENAH
chr17	7435442	7437679	TMEM102
chr9	101387632	101398618	MRPL50
chr2	105038068	105099960	MRPS9
chr3	179562885	179588407	ACTL6A
chr18	21704956	21870957	MIB1
chr2	233691606	233773300	UGT1A6
chr3	151733915	151761339	AADACL2
chr1	241652277	241802133	WDR64
chr17	42900796	42913369	G6PC
chr20	46540945	46550574	OCSTAMP
chr2	19992051	20012668	MATN3
chr12	44508274	44921848	NELL2
chr13	27962136	27971139	CDX2
chr17	41717741	41734644	HAP1
chr4	177309873	177362936	NEIL3
chr20	6074844	6123544	FERMT1
chr1	74198234	74544393	FPGT-TNNI3K
chr5	173314712	173329503	STC2
chr3	51707067	51718613	GRM2
chr14	23295642	23302848	PPP1R3E
chr19	14789259	14835376	AC005255.1
chr1	160367070	160372846	NHLH1
chr13	113399609	113453524	ADPRHL1

Chromosome	Start	End	Gene Symbol
chr16	64943752	65126112	CDH11
chr1	145824087	145844402	POLR3C
chr13	20221961	20232365	GJB6
chr18	46476971	46657220	LOXHD1
chr2	130181736	130190729	MZT2B
chr14	75522424	75547015	BATF
chr2	175923881	176002839	LNPK
chr5	161847062	161899981	GABRA1
chr7	143954843	143997312	OR2F1
chr17	15699576	15720787	ZNF286A
chr3	14124939	14143679	TMEM43
chr15	48120971	48142672	SLC24A5
chr1	21509396	21578410	ALPL
chr4	176065833	176182818	WDR17
chr10	121478333	121598458	FGFR2
chr16	81035841	81047350	ATMIN
chr1	20589085	20618903	CDA
chr16	8881633	8885351	LITAFD
chr15	84669537	84716460	SEC11A
chr17	17505562	17591708	PEMT
chr2	26581204	26641366	CIB4
chr10	101131299	101137789	TLX1
chr19	38303557	38317273	YIF1B
chr8	100685815	100722809	PABPC1
chr8	100572888	100663415	SNX31
chr13	57631743	57729311	PCDH17
chr2	28849820	28870309	TRMT61B
chr11	65121779	65134533	SYVN1
chr2	156435289	156613735	GPD2
chr7	6577433	6589374	ZDHHC4
chr1	47216289	47232220	TAL1
chr11	72576140	72674591	PDE2A
chr7	110663050	111562517	IMMP2L
chr3	48625722	48635493	SLC26A6
chr6	36697825	36733184	RAB44
chr20	41340919	41360582	LPIN3
chr17	8753105	8758559	SPDYE4
chr2	55172546	55232563	CLHC1
chr1	16043735	16057308	CLCNKB

Chromosome	Start	End	Gene Symbol
chr1	175944830	176207286	COP1
chr2	199269499	199471266	SATB2
chr7	149776041	149833979	SSPO
chr1	22953042	22965338	LACTBL1
chr12	89588048	89709300	ATP2B1
chr5	10275874	10307902	CMBL
chr6	5997998	6007605	NRN1
chr3	42804751	42887974	ACKR2
chr1	45002539	45011324	HECTD3
chr12	56202174	56221933	RNF41
chr19	21291159	21329425	ZNF708
chr2	233681937	233773299	UGT1A7
chr15	82986209	82991057	RAMAC
chr11	66314493	66317044	CD248
chr12	101155492	101210407	SLC5A8
chr19	55229778	55259017	PPP6R1
chr3	167240286	167381346	ZBBX
chr17	35464248	35522379	SLFN12L
chr16	2204247	2209453	MLST8
chr22	46150520	46243756	PPARA
chr14	24114194	24125242	DCAF11
chr10	17315420	17454595	ST8SIA6
chr7	34658238	34878332	NPSR1
chr1	64470128	64693058	CACHD1
chr1	162373202	162376870	SPATA46
chr10	62374191	62670301	ZNF365
chr1	211571567	211579161	SLC30A1
chr17	49968969	49974959	DLX4
chr20	43540170	43569498	Z98752.3
chr11	103050685	103092194	DCUN1D5
chr6	96562547	96616636	FHL5
chr8	98189825	98294393	NIPAL2
chr12	122503453	122527000	RSRC2
chr8	115408495	115809673	TRPS1
chr3	139452883	139480747	RBP2
chr16	28499361	28512051	IL27
chr19	11721264	11739009	ZNF823
chr1	201380837	201399915	LAD1
chr4	99202637	99219537	ADH6

Chromosome	Start	End	Gene Symbol
chr19	34994783	35026471	GRAMD1A
chr10	103367975	103389065	TAF5
chr8	22578278	22598025	PDLIM2
chr20	45841720	45857405	ACOT8
chr7	100574010	100586129	LRCH4
chr8	123248450	123275541	ZHX1
chr15	70853238	71053657	LRRC49
chr12	122714755	122716892	HCAR3
chr12	53103485	53124535	SOAT2
chr20	63736282	63739103	LIME1
chr1	246566443	246668595	CNST
chr1	237877863	237890922	ZP4
chr3	63228314	63616924	SYNPR
chr19	19710471	19733112	ZNF14
chr7	93591572	93911265	GNGT1
chr18	55222330	55664787	TCF4
chr16	61647241	62037035	CDH8
chr16	55509071	55586666	LPCAT2
chr3	113002443	113019861	NEPRO
chr10	23694745	24547848	KIAA1217
chr6	63275950	63319977	LGSN
chr10	61406642	61453450	TMEM26
chr19	50996017	51009581	AC011473.4
chr9	99104037	99154192	TGFBR1
chr8	72537224	72938349	KCNB2
chr9	97029676	97039643	CTSV
chr11	47248299	47269033	NR1H3
chr14	20311367	20333312	CCNB1IP1
chr11	61897300	61920269	RAB3IL1
chr11	554849	560738	LMNTD2
chr2	188974319	189012746	COL3A1
chr17	75845698	75856507	WBP2
chr11	5232677	5243657	HBD
chr11	124766497	124800673	MSANTD2
chr7	73433782	73436120	FZD9
chr10	53802770	55627942	PCDH15
chr3	156540139	156555184	SSR3
chr17	19678287	19718979	SLC47A2
chr17	4538896	4555631	MYBBP1A

Chromosome	Start	End	Gene Symbol
chr2	219229756	219236669	ANKZF1
chr7	33904307	34156427	BMPER
chr5	156919291	156963226	TIMD4
chr2	72175983	72826041	EXOC6B
chr16	31083424	31089628	PRSS53
chr7	87152360	87196337	DMTF1
chr1	217426991	217631090	GPATCH2
chr20	5911509	5925353	CHGB
chr17	44011187	44023946	TMEM101
chr6	31652415	31658210	APOM
chr1	209686177	209734949	HSD11B1
chr7	93921698	93928610	GNG11
chr3	161344791	161372880	SPTSSB
chr14	62699463	63102037	KCNH5
chr19	7522623	7534009	MCOLN1
chr3	189631388	189897276	TP63
chr20	10401008	10434222	MKKS
chr4	92303965	93810157	GRID2
chr9	136994634	136996803	CLIC3