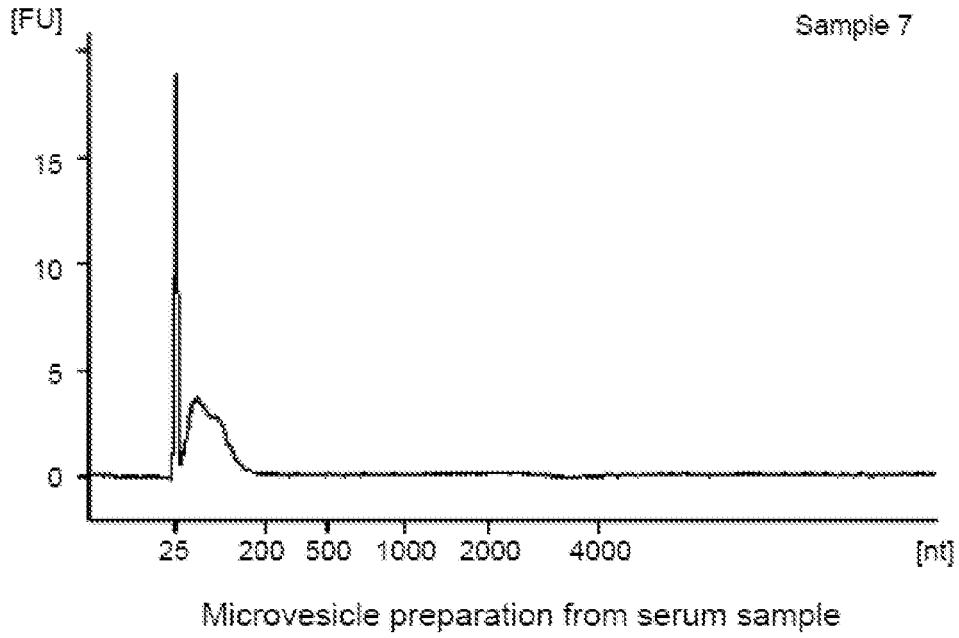
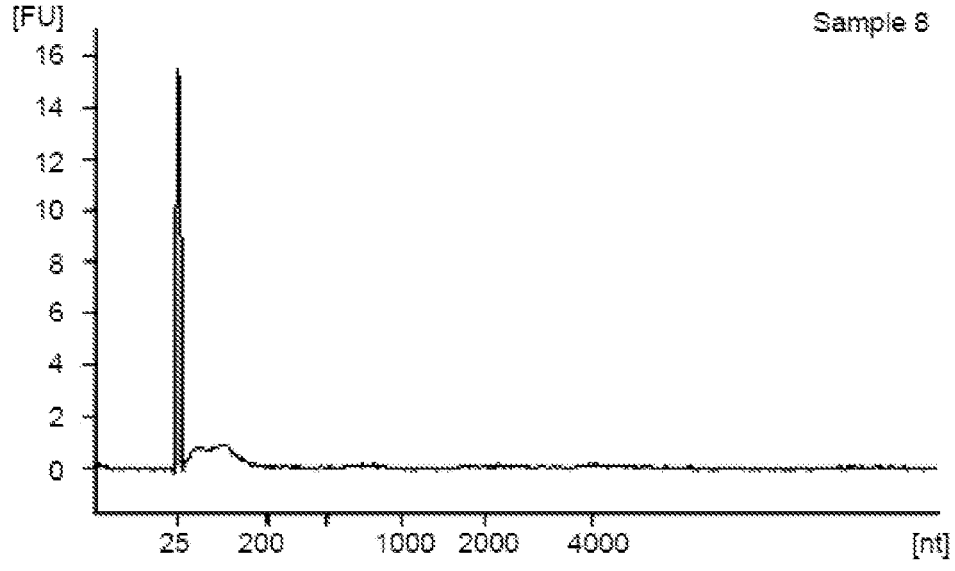
Fig. 1

A



Microvesicle preparation from serum sample

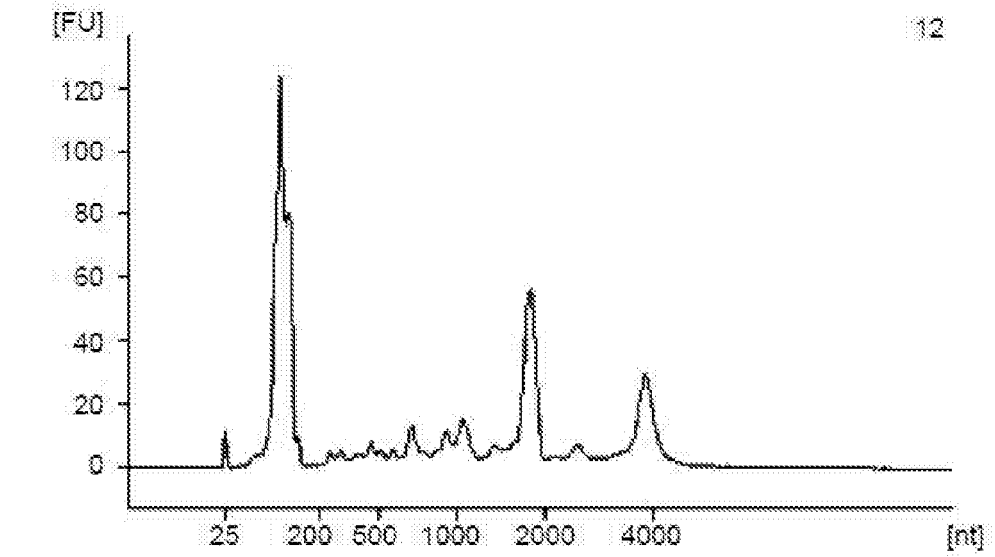
B



Microvesicle preparation from plasma sample

Fig. 1 (continued)

C



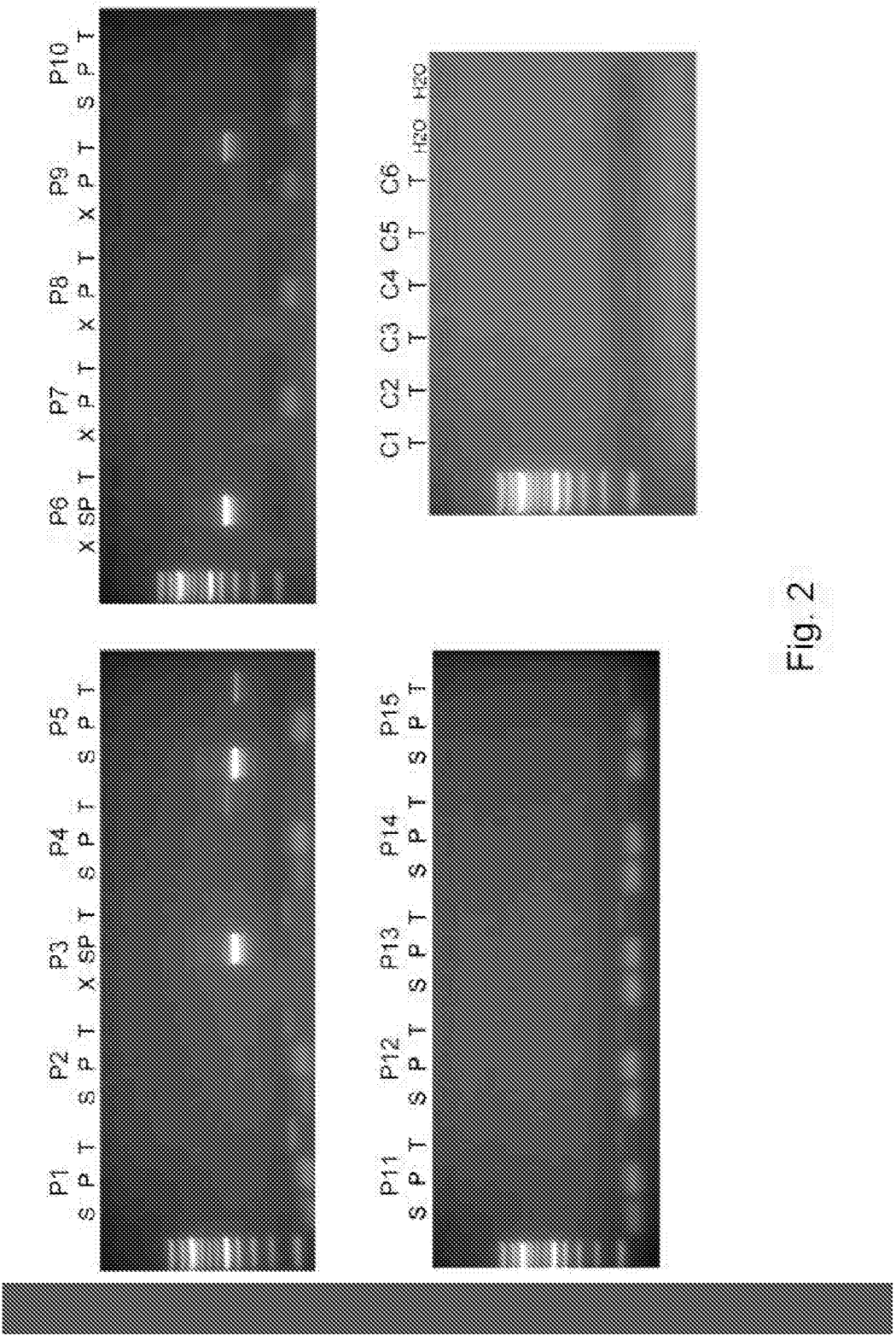

P1 P2 P3 P4 P5
S P T S P T X SP T S P T S P T
P6 P7 P8 P9 P10
X SP T X P T X P T X P T S P T
P11 P12 P13 P14 P15
S P T S P T S P T S P T S P T
C1 C2 C3 C4 C5 C6
T T T T T T H2O H2O

Fig. 2

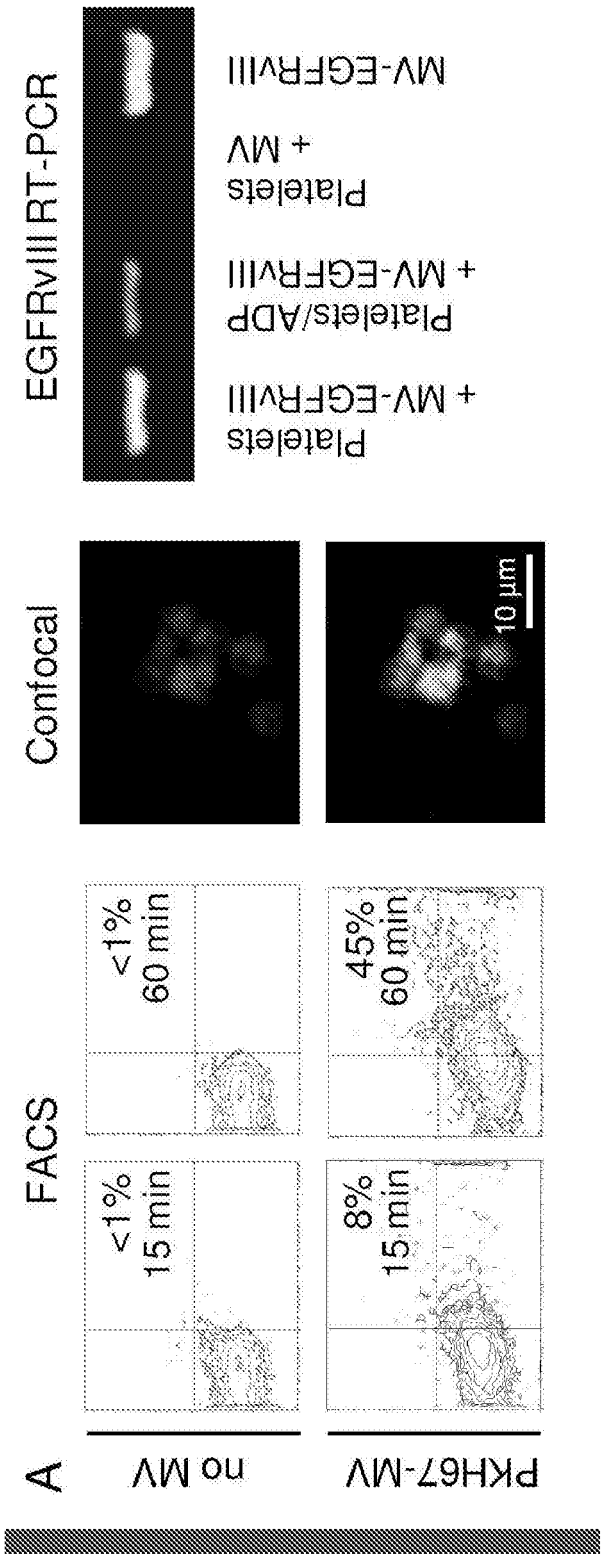

A
FACS
Confocal
EGFRvIII RT-PCR
no MV
PKH67-MV
<1%
15 min
<1%
60 min
8%
15 min
45%
60 min
10 µm
Platelets
+ MV-EGFRvIII
Platelets/ADP
+ MV-EGFRvIII
Platelets
+ MV
MV-EGFRvIII

Fig. 3A

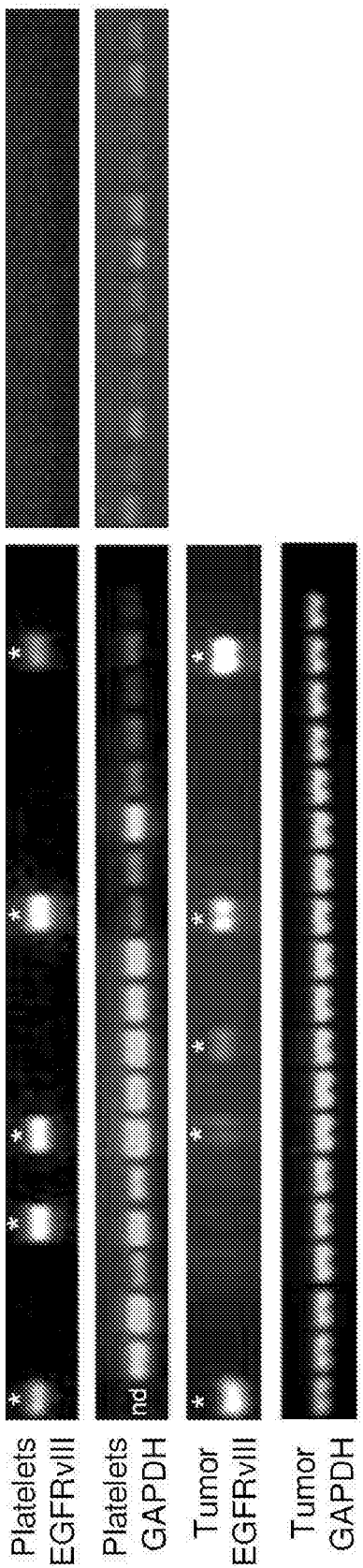

B
Glioma patients
Healthy controls
PC
P.1
P.2
P.3
P.4
P.5
P.6
P.7
P.8
P.9
P.10
P.11
P.12
P.13
P.14
P.15
P.16
P.17
P.18
NC
C.1
C.2
C.3
C.4
C.5
C.6
C.7
C.8
C.9
C.10
C.11
C.12
Platelets EGFRvIII
Platelets GAPDH
Tumor EGFRvIII
Tumor GAPDH
nd

Fig. 3B

Fig. 3C

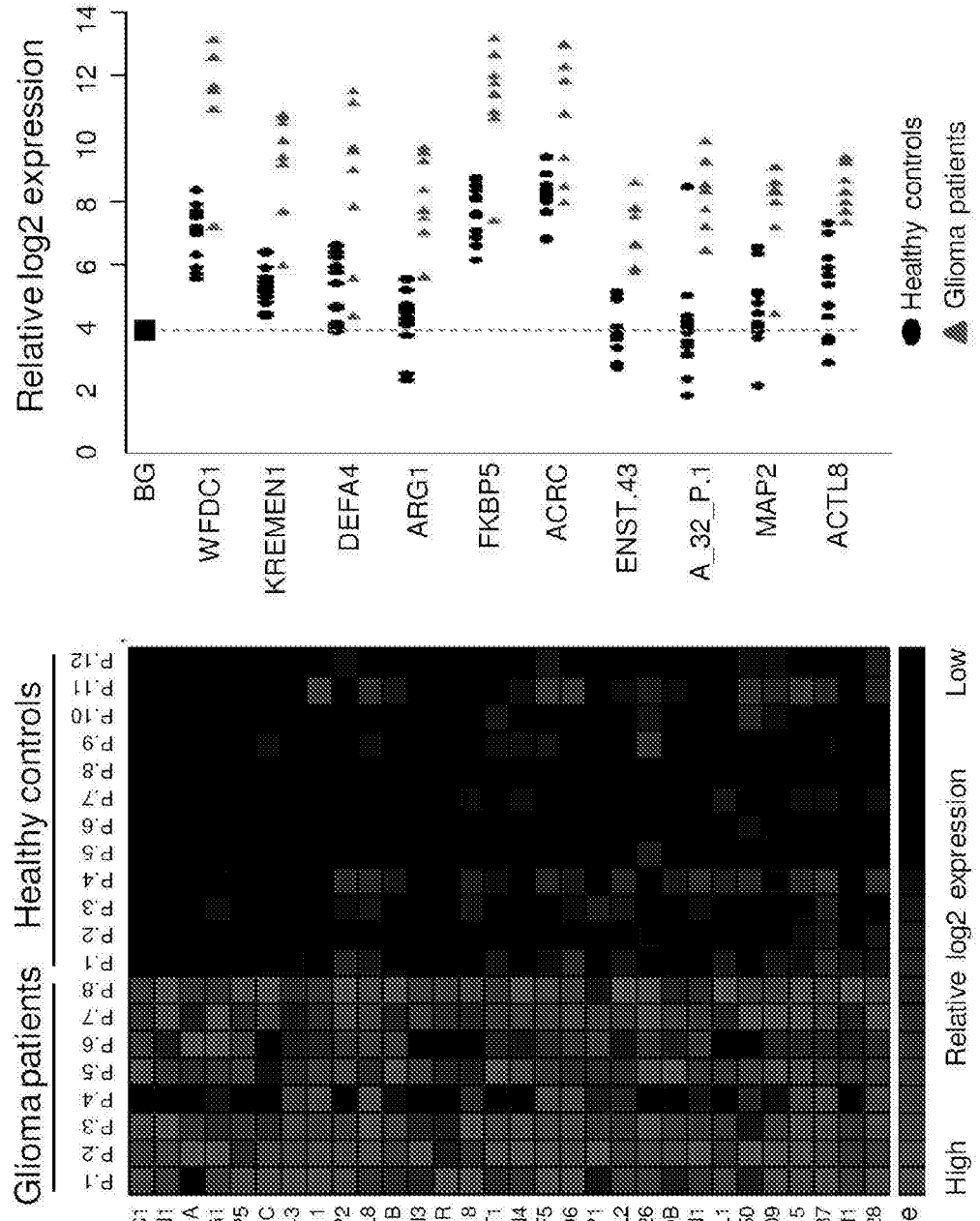

C
Glioma patients
Healthy controls
WFDC1
KREMEN1
DEF4A
ARG1
FKBP5
ACRC
ENST0328043
A_32_P167111
MAP2
ACTL8
UNC13B
TP53I3
FDXR
BX119718
SORT1
PFN4
C1QTNF5
A_24_P237896
PGLYRP1
SEC14L2
BC018626
MAOB
TCN1
AMOTL1
TSP50
CD109
A_24_P927015
THC2325987
C18orf1
LIN28
Scale
High
Relative log2 expression
Low
Relative log2 expression
0 2 4 6 8 10 12 14
BG
WFDC1
KREMEN1
DEFA4
ARG1
FKBP5
ACRC
ENST.43
A_32_P.1
MAP2
ACTL8
Healthy controls
Glioma patients

Fig. 4

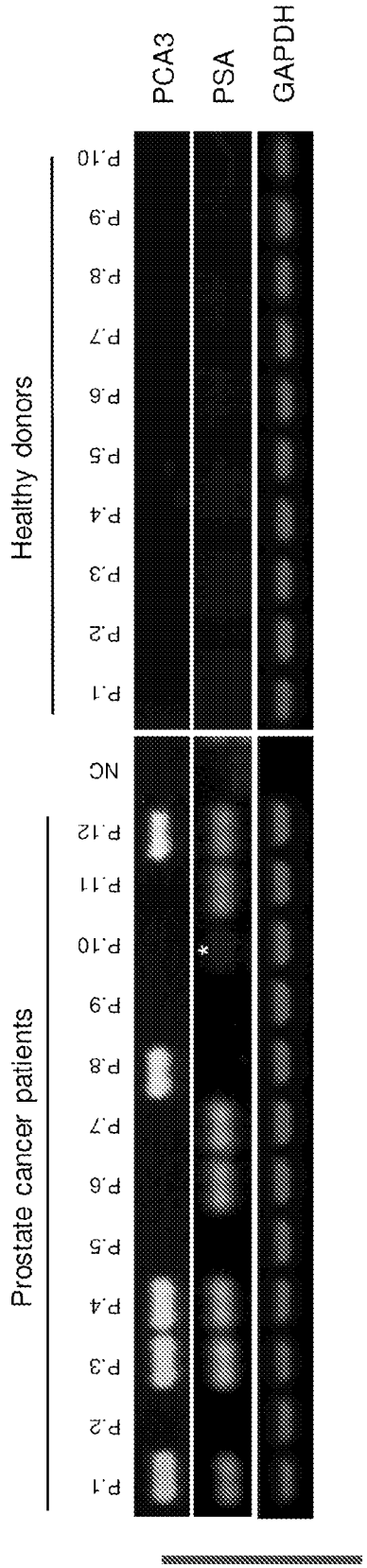

PCA3
PSA
GAPDH
Healthy donors
P.1
P.2
P.3
P.4
P.5
P.6
P.7
P.8
P.9
P.10
Prostate cancer patients
P.1
P.2
P.3
P.4
P.5
P.6
P.7
P.8
P.9
P.10
P.11
P.12
NC
*

Fig. 5

ProbeName	GeneName	
A_23_P106617	WFDC1	AAGCAGCTAGGTTGCAAGAACATTCCTCTACTTTCTGCTAAGCCTTGGAAACAGTTGGGA
A_23_P68851	KREMEN1	CATCGTGGGTCTCATGCACGTCAAGACCTTCCCACATCCAAACTCAGCTTCCAGCAGGGA
A_23_P111206	FKBP5	CAATTCAGGGTCCCTGGAGATCATCCTAACAATGTGGGGCTGTTAGGTTTTACCTTTGAA
A_23_P259292	C1QTNF5	CTGGAATATTGTGAATGACTAGGGAGGTGGGGTAGAGCACTCTCCGTCCTGCTGCTGGCA
A_23_P5392	TP53I3	AGGAAGTCTGATCACCAGTTTGCTGAGGTCTAGGGACAATAAGTACAAGCAAATGCTGGT
A_24_P55092	CD109	TCAATCTAAGAAATGGTTTAGTTTTTCTCTTTAGCTCTATGGCATTTCACTCAAGTGGAC
A_23_P111321	ARG1	TGGAATCAGGAGACAAAGCTACCACATGTGGAAAGGTACTATGTGTCCATGTCATTCAAA
A_32_P175881	THC2325987	GGTTAAAAAGAGCTTGGCATCTGAAAACAGGGAGTGGTGTGGAGGGGAAGCAGCCTCCGT
A_23_P38154	FDXR	CGATCTAACCCCTTACCCATCTCTCTACTGCTGGACTGTGGAGGGTCACCAGGTTGGGAA
A_32_P167111	A_32_P167111	GGCTGCCATTAGGAACTGCATGCAGTTAAGCCGTATAACCTCTCTGATTTTTAGTTTCTC
A_23_P17811	SEC14L2	AGATCGCAATGAGGAGTAGCAGGGTAGCTGGTTGCTAGAGTTACGGTGGGGATCAGAAAC
A_32_P132748	BC018626	GCTTGATCTGACGCTCCTTTTCTAAATAACTTGGATGGATTATTCGTATTTTTTGGTAAC
A_32_P176018	ACTL8	TAGGAGTCCCAATTATTTTTGACTAGGGGATGGGGGACAGTTGACATTTCTGGTCCTACA
A_23_P201587	SORT1	TTTTGAGTCCGGAAAAACAGAATTCCAAGTCAAATTCTGTTCCAATTATCCTGGCCATCG
A_23_P85008	MAOB	TATCTCTTCTTCCTTTTGTATCCTCCATTGTATCTTCATACAAAGGACAGTACACACTTG
A_23_P171237	ACRC	AGAGGCAACACTTAAACACTAGGGCTACTGTGGCATCTATGTAGACAGGAAAGACAAACG
A_23_P122863	GRB10	GAAAATAAACTGGAATGATCATCTATGGCTTGGGCCGCTTAGGAACAAGAACCGGAGAGA
A_23_P326080	DEFA4	AGAGCTACAGGAAATGGTTGTTTCTCCTATACTTTGTCCTTAACATCTTTCTTGATCCTA
A_23_P330561	MCEMP1	CTGTCTCCCTGTTTGTGTAAACATACTAGAGTATACTGCGGCGTGTTTTCTGTCTACCCA
A_23_P171336	NXF3	TCATCCTTCCAAAGGGGCCAGTTGTTCTGTGCACTTGTCCACCCCTGTTACCCCCAGGAT
A_23_P79398	IL1R2	CAAACACAGAACTGGAAAAGCAGATGGTCTGACTGTGCTATGGCCTCATCATCAAGACTT
A_23_P421843	ENST00000285206	TGGTGGCAGGGCCATGGGAGGTTGGAAGGCACCCACATCCTTAAAGCCATCAGTAGCTAT
A_23_P151415	KATNAL1	CTGTCTCTGCTGCAGACTTGGAGAAGTATGAAAAATGGATGGTTGAATTTGGATCTGCTT
A_23_P218086	TPCN1	TCCTAGAAAACCCATTGTGTCTCTGGATCTCTAGCACATTACTAAAAGAGCCTCTGCTTT
A_23_P253791	CAMP	GAATTGTCCAGAGAATCAAGGATTTTTTGCGGAATCTTGTACCCAGGACAGAGTCCTAGT
A_23_P31816	DEFA3	GAGAACGTCGCTATGGAACCTGCATCTACCAGGGAAGACTCTGGGCATTCTGCTGCTGAG
A_23_P58266	S100P	CCAAAAGTGTTTGTTGGCAATTATTCCCCTAGGCTGAGCCTGCTCATGTACCTCTGATTA
A_23_P166848	LTF	ATATTTGGGACCACAGTATGTCGCAGGCATTACTAATCTGAAAAAGTGCTCAACCTCCCC
A_24_P270033	ENST00000278949	GGGCCATATGCACAAATATTGTAACTCTTGGTATCTTTACTGCATCATAGTCAATAAACT
A_23_P126135	MFN2	TTGTTTTTATGTTCATTTGCTGGAGCGCAAGACGTGCTGACACAGTGAGTTTTCTCTGAT