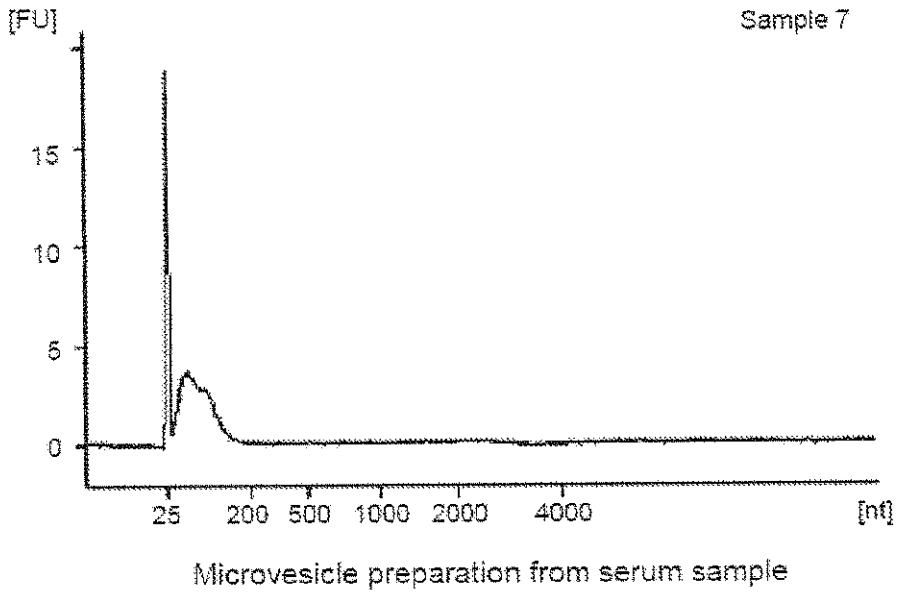
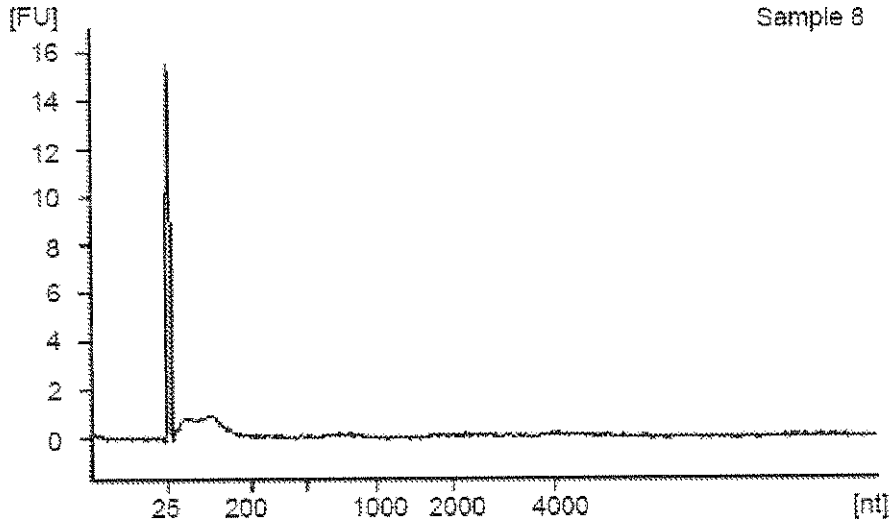
Fig. 1

A




Microvesicle preparation from serum sample

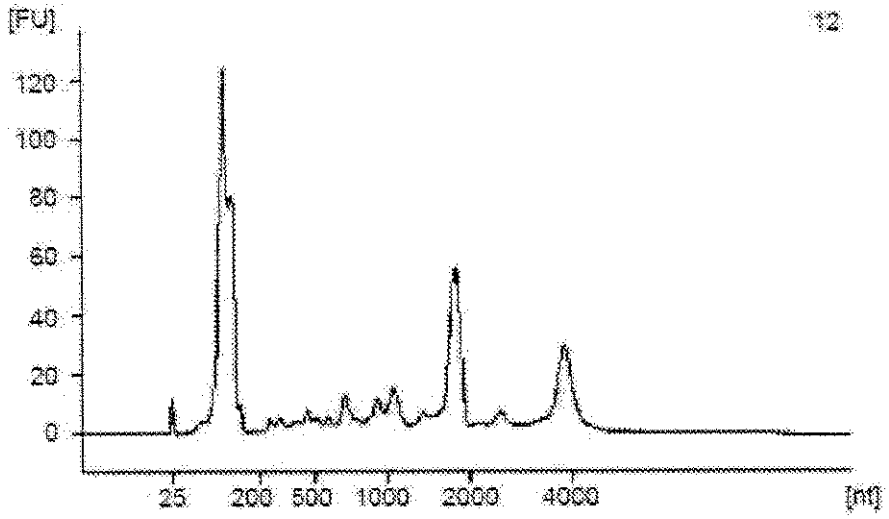
B




Microvesicle preparation from plasma sample

Fig. 1 (continued)

C




Thrombocyte preparation from plasma sample

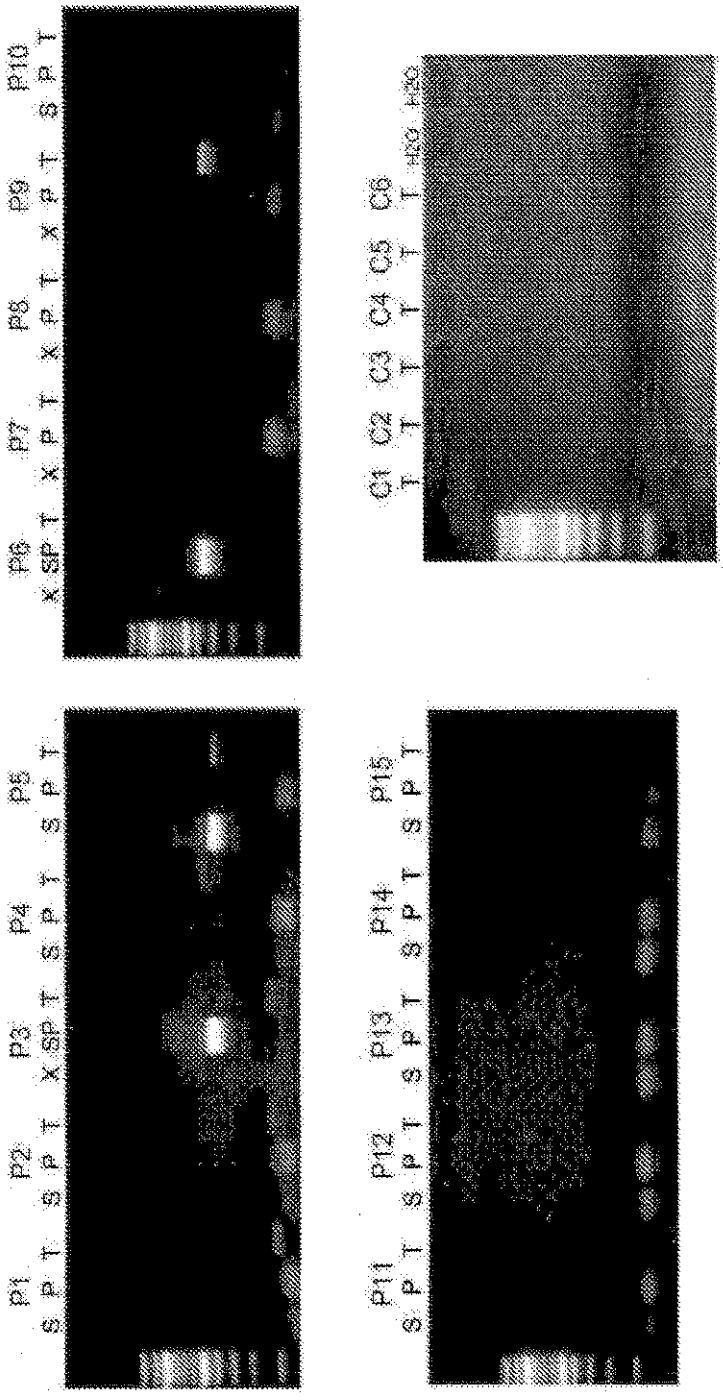

P1 P2 P3 P4 P5
S P T S P T X SP T S P T S P T
P6 P7 P8 P9 P10
X SP T X P T X P T X P T S P T
C1 C2 C3 C4 C5 C6
T T T T T T +20 +30

Fig. 2

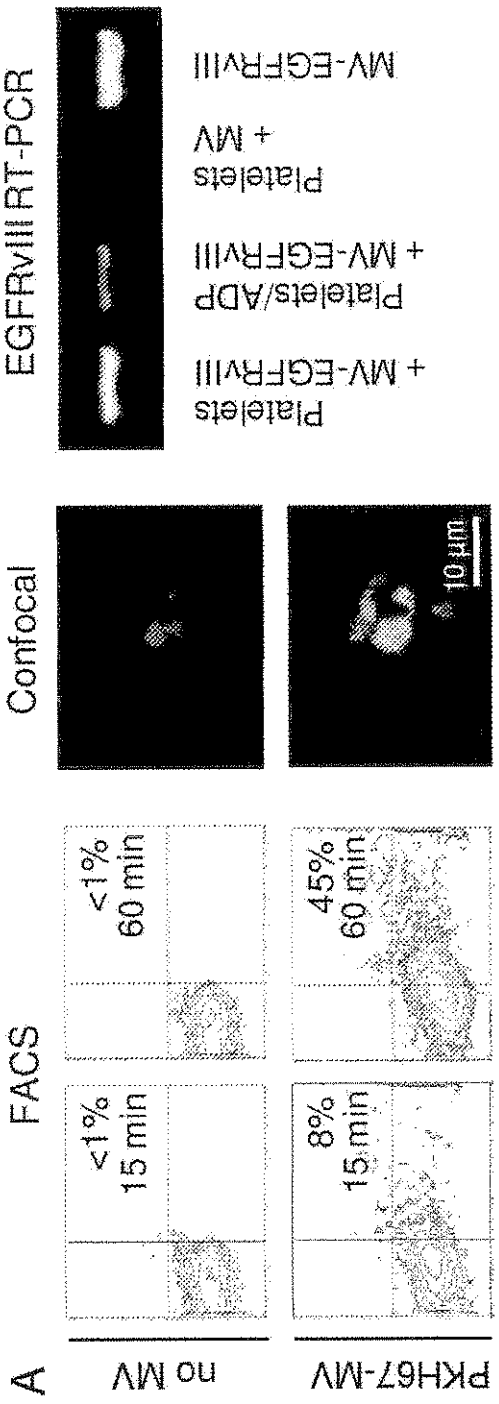

A
FACS
Confocal
EGFRvIII RT-PCR
no MV
PKH67-MV
<1%
15 min
<1%
60 min
8%
15 min
45%
60 min
10 µm
Platelets
+ MV-EGFRvIII
Platelets/ADP
+ MV-EGFRvIII
Platelets
+ MV
MV-EGFRvIII

Fig. 3A

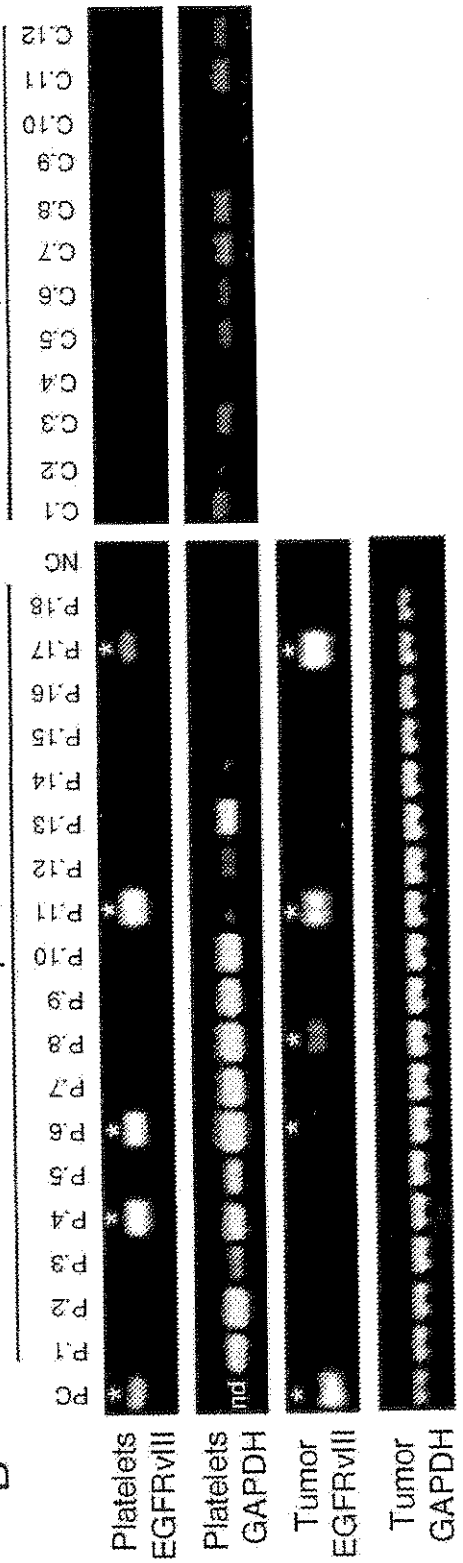
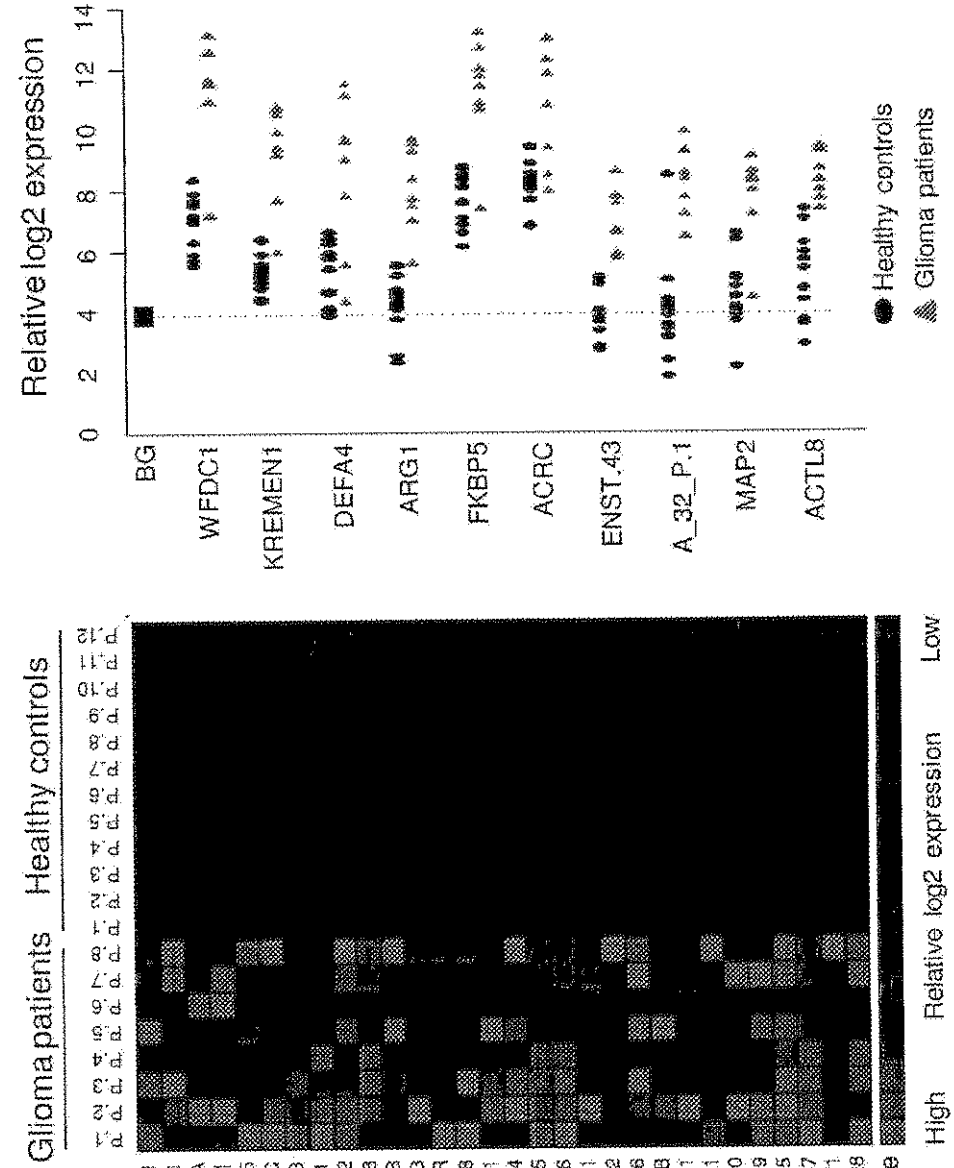

B
Glioma patients
Healthy controls
PC
P.1
P.2
P.3
P.4
P.5
P.6
P.7
P.8
P.9
P.10
P.11
P.12
P.13
P.14
P.15
P.16
P.17
P.18
NC
C.1
C.2
C.3
C.4
C.5
C.6
C.7
C.8
C.9
C.10
C.11
C.12
Platelets EGFRvIII
Platelets GAPDH
Tumor EGFRvIII
Tumor GAPDH
nd

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
TSPS0
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

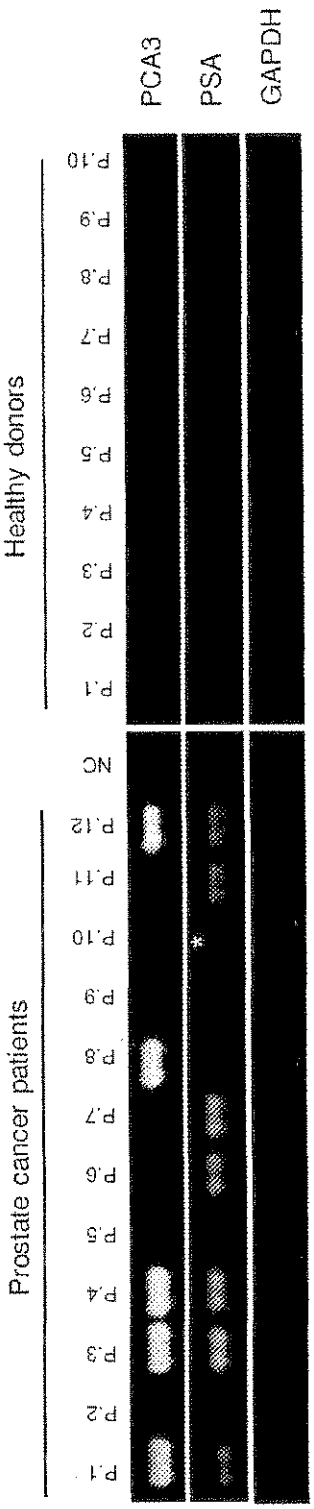

PCA3
PSA
GAPDH
Healthy donors
P.10
P.9
P.8
P.7
P.6
P.5
P.4
P.3
P.2
P.1
Prostate cancer patients
NC
P.12
P.11
P.10
P.9
P.8
P.7
P.6
P.5
P.4
P.3
P.2
P.1

Fig. 4

Fig. 5

| ProbeName | GeneName | |
|---|---|---|
| A_23_P106617 | WFDC1 | AAGCAGCTAGGTTGCAAGAACATTCCTCTACTTTCTGCTAAGCCTTGGAAACAGTTGGGA |
| A_23_P68851 | KREMEN1 | CATCGTGGGTCTCATGCCACGTCAAGACCTTCCCACATCCAAACTCAGCTTCCAGCAGGGA |
| A_23_P111206 | FKBP5 | CAATTCAGGGTCCCCTGGAGATCATCCTAACAATGTGGGGCTGTTAGGTTTTACCTTTTGAA |
| A_23_P259292 | C1QTNF5 | CTGGAATATTGTGAATGACTAGGGAGGTGGGGTAGAGCACTCTCCCGTCCTGCTGGCTGGCA |
| A_23_P5392 | TP53I3 | AGGAAGTCTGATCACCAGTTTGCTGAGGTCTAGGGACAATAAGTACAAGCAAATGCTGGT |
| A_24_P55092 | CD109 | TCAATCTAAGAAATGGTTTACGTTTTTCTCTTTAGCTCTATGGCATTTCACTCAAGTGGAC |
| A_23_P111321 | ARG1 | TGGAATCAGGAGACAAAGCTACCACATGTGGAAAGGTACTATGTGTCCATGTCATTCAAA |
| A_32_P175881 | THC2325987 | GGTTAAAAAGAGCTTGGCATCTGAAAACAGGGAGTGGTGTGGAGGGGAAGCAGCCTCCGT |
| A_23_P38154 | FDXR | CGATCTAACCCCTTACCCATCTCTCTACTGCTGGACTGTGGAGGGTCACCAGGTTGGGAA |
| A_32_P1671111 | A_32_P1671111 | GGCTGCCATTAGGAACTGCATGCAGTTAAGCCGTATAAACCTCTCTGATTTTTAGTTTCTC |
| A_23_P17811 | SEC14L2 | AGATCGCAATGAGAGTAGCAGGGTAGCTGGTTGCTAGAGTTACGGTGGGGATCAGAAAC |
| A_32_P132748 | BC018626 | GCTTGATCTGACGGCTCCTTTTCTAAATAACTTGGATGGATTATTCGTATTTTTTGGTAAC |
| A_32_P176018 | ACTL8 | TAGGAGTCCCAATTATTTTTTGACTAGGGGATGGGGGACAGTTGACATTTCTGGTCCTACA |
| A_23_P201587 | SORT1 | TTTTGAGTCCGGAAAAACAGAATTCCAAGTCAAATTCTGTTCCAATTATCCTGGGCCATCG |
| A_23_P85008 | MAOB | TATCTCTTTCTTCCTTTTTGTATCCTCCATTGTATCTTCATACAAAGGACAGTACACACTTG |
| A_23_P171237 | ACRC | AGAGGCAACACTTAAACACTAGGGCTACTGTGGCATCTATGTAGACAGGAAAGACAAAACG |
| A_23_P122863 | GRB10 | GAAAATAAACTGGAATGATCATCTATGGCTTGGGCCGCTTAGGAACAAGAACCGGGAGAGA |
| A_23_P326080 | DEFA4 | AGAGCTACAGGAAATGGTTGTTTCTCCTATACTTTGTCCTTAACATCTTTCTTGATCCTA |
| A_23_P330561 | MCEMP1 | CTGTCTCCCTGTTTTGTGTAAACATACTAGAGTATACTGCGGCGTGTTTTTCTGTCTACCCA |
| 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 | CCAAAAGTGTTTGTTGGCAATTATTCCCCTAGGCCTGAGCCTGCTCATGTACCTCTGATTA |
| A_23_P166848 | LTF | ATATTTGGGACCACAGTATGTCGCAGGCATTACTAATCTGAAAAAGTGCTCAACCTCCCC |
| A_24_P270033 | ENST00000278949 | GGGCCATATGCACAAATATTGTAACTCTTGGTATCTTTACTGCATCATAGTCAATAAACT |
| A_23_P126135 | MFN2 | TTGTTTTTTATGTTCATTTGCTGGAGCGCAAGACGGTGCTGACACAGTGAGTTTTCTCTGAT |