



Supplemental Figure 1. Summary of differential HERV expression in M059J (A), H4 (B), and A172 (C) cell lines.

| HERV | Locus | FC HERV | Differentially Methylated Gene | FC Gene | Methylation | Gene Function | Potential Anti- sense RNA |
|-------------------------|--------------|--------------------|---|--------------------|--------------------|--|--------------------------------------|
| PRIMA4 | 10p12.1 | -14893 | PDSS1 | -1.35 | 0.63 | Key respiratory chain element | Yes |
| PABLA | 16p13.3 | -22070 | MLST8 | 1.34 | 0.74 | mTOR-associated protein | Yes |
| HML6 | 19q13.43b | 13162 | ZNF208 | 1.10 (NS) | 0.45 | Zinc finger | Yes |
| PABLA_Xp22.2 | Xp22.2 | -2537.73 | CTPS2 | 1.22 | 0.46 | Rate limiting enzyme in production of cytosine nucleotides | No |
| ERV316A3_11q24.2 | 11q24.2 | 181.43 | DDX25 | 2.74 | 0.57 | RNA helicase involved in several functions: translation initiation, nuclear and mitochondrial splicing, and ribosome and spliceosome assembly. May also involve cellular growth and division | Yes |
| HARLEQUIN_7q22.1 | 7q22.1 | -871.225 | DGAT2L7P | 1.32 | 0.56 | Pseudogene associated with metabolism | No |

Supplemental Table 1. Summary of DEG-DEHERV pairs at differentially methylated sites along with identification of potential antisense RNA sequences in A172 and M059

Sequenced PCR Product at 19q13.43b

tggtaccTCCAGTACGAGCCATGAGCCAGCGGAATCTGAATGCAAAGACAGAACAAGGG
CCGACCGGAGTCAACAATGACATCCAACCCCAACATGGGGACAGATCAAGAAAAC
GACACAAGAAGCTGAGAACTACTGGAGCGCCAGGGTCAGGC AAAAACCCCTGACT
CCAgttct

Alignment of YourSeq and chr19:58312254-58312433

Click on links in the frame to the left to navigate through the alignment. Matching bases in cDNA and genomic sequences are colored blue and capitalized. Light blue bases mark the boundaries of gaps in either sequence (often splice sites).

cDNA YourSeq

```
cacgactgaa taacctcac taaagggact agtcctgcag gtttaaacga 50
attcgccctT GTTACCTCCA GTACGAGCCA TGAGCCAGCG GAATCTGAAT 100
GCAAAGACAG AACAAAGGCC GACCGGAGTC ACAATGACAT CCAACCCCAT 150
AACATGGGGA CAGATCAAGA AAACGACACA AGAAGTTGAG AAACACTG 200
AGCCCGCAGG TCAGGCAAAA ACCCTTGACT CCATGTTCTa agggcgaatt 250
cgcgcccgct aaattcaatt cgccctatag tgagtcgtat tacaattcac 300
tgcccgctcgt tttacaacgt cgtgactggg aaaacctcgg cgttacccaa 350
cttaatcgcc ttgcagcaca tccccctttc gccagctggc gtaatagcga 400
agaggccgc accgatcgcc cttccaaca gttgcgcagc ctatacgtac 450
ggcagtttaa ggtttacacc tataaaaag agagccgcta tegtctgttt 500
gtggatgtac agagtgatat tattgacacg ccggggcgac ggatggtgat 550
ccccctggcc agtgacagtc tgctgtcaga taaagtctcc cgtgaacttt 600
acccggtggt gcatacggg gatgaaagct ggcgcatgat gaccaccgat 650
atggccagtg tgcgggtctc cgttatcggg gaagaagtgg ctgatctcag 700
ccaccgcgaa aatgacatca aaaacgccat taacctgatg ttctggggaa 750
tataaatgtc aggcagaga ttatcaaaaa ggatcttcac ctagatcctt 800
ttcacgtaga aagccagtc gcagaaacgg tgctgacccc ggatgaatgt 850
cagctactgg gctatctgga caagggaaaa cgcaagcgca aagagaaagc 900
agtagcttg cagtgggctt acatggcgat agctagactg ggcggtttta 950
tggacagcaa gcgaaccgga attgccagct ggggcgcctc ctggttaagt 1000
tgggaagccc tgcaaagtaa actggatggc tttcttgccc ccaagatct 1050
ganggccag gggatcaatn tttgat
```

Genomic chr19 :

```
gtgtttttac aggagatgga caaacctgtt gggcgccctc caggtgtgtg 58312203
tgacctatgga acgggagacc ggagggatcc atggtattca accgtgggcc 58312253
TGTACCTCC AGTAGAGCC ATGAGCCAGC GGAATCTGAA TGCAAAGACA 58312303
GAACAAGGCC CGACCGGAGT CACAATGACA TCCAACCCCA TAACATGGGG 58312353
ACAGATCAAG AAAACGACAC AAGAAGCTGA GAAACTACTG GAGCCCCAGG 58312403
GTCAGGCAAA AACCCCTGAC TCCATGTTCT tggccatgct agctgtagtg 58312453
tcctgtgagg tatgtttccc ctgtgtagag gcaaaaaacat attgggcata 58312503
tgttcttaac ccactggtag tacgactggt
```

Sequence of C2 Probe

NR_144445.1 ERVK3-1

C2 probe

2 gcagtgtg aagacgtca eggcgcgcg gactatcggg cgctaggct ctctgaggag

61 gctgccacag tgaagcaacc gtgacaagtg gtgcccgacc agggacctga acgaggaagg

121 tctgccagag cagagaaagt gaaactgatc agacgaaacta cgaacctctg gacgggagag

181 tctgccggcg gagaatataa ggagatggac aaacctgtgt ggtgccctcc agtgtgtgt

241 gaccatggaa cgggagaccg gagggatcca tggatttcaa ccgtgggctt gttacctcca

301 gtacgagcca tgagccagcg gaatctgaat gcaaagacag aacaagggcc gaccggagtc

361 acaatgacat ccaaccccat aacatgggga cagatcaaga aaacgacaca agaagctgag
421 aaactactgg agcgccaggg tcaggcaaaa acccctgact ccatgttctt ggccatgcta
481 gctgtagtgt cctgtgcgtc tataggatcg ggtgaaccac caaccggcaa ttgaaagctg
541 cacagcctga aattaccttt attcaattaa tgcaaaaaca aaaggggaga tgttgagggc
601 cgaaggaatg agggctctga ccaactcagt ataccactgg aggctctgtg agcaaacagc
661 aaactgttct catgaaagca ggatgttggc gaactgacaa actctgtctg ccgccagaag
721 gaatgctggg ggcagtcatg tcccaggtec cgtgtctctt gaggttatcc acaggaacat
781 ccagaacctg ttgaacaaag aaaggaatca tgtgggctg tgttaaatca aatagctgac
841 cgacagttat ccttctctcc ctattcactc tacctaataa atatgaaggc ctgtaaaage
901 tcaggtcctt gttccctaat atcaaggagc ccctgaccc cttctttcaa acagatcctt
961 ttgtctgtct catttctgca ttcgtcgtcc ttcgttcggt ccagaagcaa ccgcgacagt
1021 cctgcatgtg ttgatccac ctgtatgtc aggtgtgacc tcagggtgtg gagtatcctt
1081 cataccctt atcatcactg cctatteget ctctctccag cctctggcaa ccaactaatc
1141 acgttatatg tctagat