

Figure S2. Genomic sequences of rDNA, LINE-1 and Alu amplicons. List of genomic sequences amplified by rDNA, LINE-1 and Alu amplicons assayed through target-bisulfite sequencing. CpGs are highlighted and identified via their relative position within each amplicon.

>18S1

4 24 30 45 52
 TAGCCGTTTCTCAGGCTCCCTCTCCGGAATCGAACCCTGATTCCCCGTCACCCGTGGTCACCATGGTAGGCA
 72 75 85 104 108 117 120 123 128 135 139
 CGGCGACTACCATCGAAAGTTGATAGGGCAGACGTTCGAATGGGTGTCGCGCCACCGGGGGGCGTGCGA
 143 148 173 176 179 183 190 194 200
 TCGGCCCGAGGTTATCTAGAGTCACCAAAGCCGCCGCGCCCGCCCCCGGCCCGGGGCGCGAGAGGGGCT
 215 242
 GACCGGGTTGGTTTGTATCTGATAAATGCACG

>28S

29 56 62
 GTATTTAGCCTTAGATGGAGTTTACCACCCGCTTTGGGCTGCATTCCCAAGCAACCCGACTCCGGAAGACC
 72 78 81 83 86 93 99 110 116 128
 CGGGCCCGGCGCGCGGGGGCCGCTACCGGCCTCACACCGTCCACGGCTGGGCCTCGATCAGAAGGACT
 153 157 160 163 170 179 183 195 197 202 205 207
 TGGGCCCCCAGAGCGGCGCGGGGAGCGGGTCTTCGTACCGCCACATGTCCCGCGCCCCCGCGCGGGG
 212 220 223 246 249
 CGGGGATTCGGCGCTGGGCTCTTCCTGTTCACTCGCGTTACTGAGGGAATCCTGGTTAGTT

>Alu

26 30 38 40 42 62
 TCTCTACTAAAAATACAAAAATTAGCCGGGCGTGGTGGCGCGCGCCTGTAATCCCAGCTACTCGGGAGGCT
 84 94 101 118 124 126
 GAGGCAGGAGAATCGCTTGAACCGGGAGGCGGAGGTTGCAGTGAGCCGAGATCGCGCCACTGCACTCC
 AGCCTGG

>LINE-L1

27. 34. 37 49 61 70
 CTCTGAGCCAGGTGTGGGATATAGTCTCGTGGTGCGCCGTTTCTTAAGCCGCTGTAAGGCGCAATATTC
 85 99 103 123
 GGGTGGGAGTGACCCGATTTTCCAGGTGCGTCGTCACCCCTTTCTTTGACTCGGAAAGGGAACCTCCTGA
 149 173 183 188 190 194 199
 CCCCTTGCGCTTCCCAGGTGAGGCAATGCCTCGCCCTGCTCGGCTCGCGCACCGGTGCGCACACACTGG
 217
 CCTGCGCCCACTGTCTGGCACTCCCTAGTGAG

>RiboProm1

5 27 36 38 42 50 59 65
 GTCCCCTGTGTAGCTAGGCAGAGCTCCGGAAGCCCGCGGTGTCAGCCCGGCTGGCCCGGTGGCGCCA
 79 81 84 106 135
 GAGCTGTGGCGCGTCTTGTGAGTCACAGCTCTGGCGTGCAGGTTTATGTGGGGGAGAGGCTGTCTGCTG
 140 152 154 157 161 173 178 182 189 191 194 203
 CGCTTCTGGGCCCGCGGCGGGCGTGGGGCTGCCCGGGCCGCGTCCGACCAGCGCGCGTAGCTCCCGAGGCC
 210 215 217 222 224 232 232 235 237 244 246 260
 CGAGCCCGCGACCCCGCGGGGACCCGCGCGCGTGGCGCGGGAGGCTGGGGACGCCCTTCC

>RiboProm2

GTGTCCTTGGGTTGACCAGAGGGCCC²⁶CG³⁰GG³⁵CGCTC⁴⁷CGTGTGTGGCTG⁵⁶CGATGGTGG⁵⁶CGTTTTTGGGGACA
GGTGT⁷⁶CG⁸¹TGT⁸³CG⁸⁵CG⁸⁸CGCCTGGGC⁹⁷CG¹⁰⁰CG¹⁰³GCGTGGT¹⁰⁹CGGTGA¹¹⁵CG¹¹⁷CGACCTCC¹²⁵CG¹³¹GGGGGAG
GTATATCTTT¹⁴⁹CG¹⁵⁴CTC¹⁵⁹CGAGT¹⁷²CG¹⁷⁵GCATTTTGGGCC¹⁷²CG¹⁷⁵GGTTATTGCTGACA¹⁹¹CGCTGTCCTCTGG²⁰⁴CGACCTG
²¹²
T²¹²CGCTGGAGAGGTTGGGCCTTGGGATG