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-1320 aaccctgcag ttgcttccat gtttaggcgc tgcccaccaa ggttccaag ttggaaagga
-1260 aggaggagag aggcagagag agagagagag agagagagag agagagaagc gcgagagcgg
-1200 ccctgtaatt gagcagaaag gaaagggaga aaaatgaatc ccaaactttg ggcttacctc
-1140 tttctgctgg ctggctcgcc aaaatatggt aadggtagag gatgtccagg ttcttggcat
                                     ARE I
-1080 cttgaacaaa caattggaca aaatgcacaa acaaagcaag aaaggaatga aggattttat
-1020 tgaaaatgaa agtacctcc acagtgtggg agcgagcatg agcatagggg ctcaaaggcc
-960 ctgttacatt ttgtgagttt aaataccctc tacttggggg acaccctatg taaatgaaga
-900 ggatgaagta aagttacagt taciaagtta ttaatggcgg gcatacgccc tatggagagg
-840 atatttcccg ttataactga agtgtgaatt ggccttatgt tccctgtctc tagacctat
-780 tctcctgctt cctgtgaaag cagagggttt tgtttgttt ttgctttttg ttttttgaga
-720 cggagtcttg ctctgttgcc caggctggag tgcagtggg cactcggctc actgcaactt
                                     ARE II
-660 ccgccttccc gggttcaagc gattctcctg gctcagcctc cggagtagct aggactacag
-600 gcgcgtgtca ccatgtccca gctaactctt ctttattttt agtagagacg tgttagccag
-540 gtttcaccgt gttaccgtgt taccgtattc cagccgggct ccgcccctgg attcggtgga
-480 cagaccagct ttacctccag agactcccc tgtcttcct gcaccggctg actataccta
-420 cacacttcgg tggcacaatc tttgtttaga tatgctgatg ccttccttcg ctgggaacgg
-360 tccagtcctg cccgcctggc gctcagctct gcgatctca ggggatggag tggcaatctc
-300 attgctcccg cctctcctga cccctctgc cttctcctc agaccgggt taagtgggca
-240 gagggctccg agggctctct cccgcctggg gattgcacag agggctgggt ccgcaggctg
-180 gctaaaagga cctagcccag gattgcgagg cagcgcctc cctgcagctg gacagactcg
-120 ggcgcccggc ccaaagccg gcaggggctg gtccgcgcg tcacctgcta ttggccaggt
-60 ggggctgtcg gctgccagca gtgcttatgc ttaagtgcg gagcgggtg ctgaggagcc
1 AGGCGCGCGC CAGGATGGTG GACAGCGTGT ACCGGACCCG CTCCTGGGG GTGGCGGCCG
+1
                                     ARE III
61 AAGGGCTCCC GGACCACTAC GCGGACGGGG AGGCGGCGCG CGTGTGGCAG CTGTATATCG
121 GAGACACCCG CAGCCGACC GCCGAGTACA AGGCATGGCT GCTTGGGCTG CTGCGCCAGC
181 ACGGCTGCCA GCGGGTGCTC GACGTAGCCT GTGGCACTGG gtgagcccag gccggggccg

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Supplementary Fig.2. Human *GNMT* gene sequence from promoter region – 1320 bp to + 240 bp (intron 1) is shown. The sequence was retrieved from the UCSC hg19 human genome assembly (<http://genome.ucsc.edu>). Boxes indicate the three predicted AREs. Exon 1 is shown in uppercase letters, with sequences 5' to the transcription start and intron 1 sequences shown in lowercase letters. The 5' untranslated region (UTR) is indicated in blue and the coding region in red. +1 indicates the transcription start site.