

**Caveolin 1: Mus musculus strain C57BL/6J chromosome 6, GRCm38.p1
C57BL/6J, from 4776 bp to 6715 bp.
NCBI: NC_000072.6**

ttgaacctct aagtaaaatt ttctgcagtt gaaaatactc aaagtgctta tggttactgt -661
 ataacctgct ggtagggatt tcatttttctt tattgcagag gcccacac agattgctt -601
 gttgtgttta tatttaaaaa aaaaaaaaaat gttccctcag gttcccagcc atctgcttc -541
 tatacttttc tctgtgaaac aaggagacag atcagttcta cgtgggcaa ttgggagggg -481
 aggcagctta ggacagggca gaattctttc tgcagagcc gatgccata ctgggcatct -421
 ctgcagactc ttgggctccc tccaccctg ctgagatgat gcactgggaa aacacgctc -361
 ctcccctgga tgcctctctg taggtttata gctgggaaa cgttgctc agtctaaaat -301
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 gtccctagcca actgagagca gaacaaacct ctggcaaca gccagaggc tcctcccag -121
 ccaccgccc ccgccagc ctttcccc tctatacaat acaagatctt ccttctcag -61
 TSS →
 ttctcttaa tcaagccca gggaaacctc ctcaagcct gcagccagcc accgcccagc -1
 CDS →
 ATG tctgggg gcaataact agactcag gtaggcttgg gtgagggctc caaagtgcct +60
 gcttttgcta tcttccactc caaatgctc gactgctttc ctgccccag ccgctctcc +120
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42-43
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46
47
 gtaccaccgc cattgtcaac tccttcttgg cactcagggt gactaaact ggagaccgc +660

48
 gttcccaaat agggctaega ttcagcttgg agtagacagc ctgagagtga tctaagtaag +720

ggtgggtcag gcagttcttc agatggcatg tcctctgggg catgggggtg ggggtgacag +780

gtcttggcac atgcctcagc ctaaagaagt atgttagatt gtgagccact tattcacccc +840

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 cacggcctaa gaaaaaccag ggagtaaagg tgggttttaa aaggggtag gggctgtggc +900

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51
 aggtgcaagg aagaagcaeg gagggacagt gaagatggga ccattacgc tgtcagtttg +960

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58
59-60-61-62
63
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66
67
 ctctgcctgg taccagggg tgtggtgtcc tccctcct cctcttaaaa agcttgagc +1260

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69
 gctggagttt tctgtgtgca agcctttcct tcgaggttga agctagcaaa agttgtagc +1320

70
 ccaggctacc ccgcacagc caggctgact ctgactctt gttttcttt ctgaactttt +1380

Figure S1: Genomic localization and nucleotide sequence of the Caveolin 1 gene analyzed in this work by MassArray Epityper technique. CpG dinucleotides located in the proximal promoter, exon 1 and intron 1 of the Cav-1 gene (from -619 to 1272 pb from ATG codon (+1)) are shadowed. ATG codon indicates the Translation Start Site (CDS) and TSS indicates the Transcription Start Site. Due to the limitation of the technique, DNA methylation of some CpGs sites could not be measured (crossed out), or were measured together with others (indicated as boxed CpGs sites).