Title and description of the data:
Nucleotide sequence alignment of human PNMT and rat Pnmt genes. Exons of the gene are boxed. mRNA start site is marked with +1. Translation start site is indicated by ATG (red/bold) and red arrow; translation end sites for human and rat are in purple/bold. Seven SNPs identified by resequencing PNMT in this study are marked bold with grey shading. The sequence of human-specific AluSp element in the first intron is marked in italics and its start/end sites are indicated by black arrows. Sequences of regulatory elements and transcription factor binding sites (TFBS) are underlined. Experimentally confirmed rat Pnmt expression regulating elements [6, 59-62] are typed in italics on green shading background. Predicted regulatory elements for human PNMT [12-13] are typed with regular font (no shading).
hPNMT 1192 GCAGGACCCATGGGGCAAGGCCGCCGAGCTAGAGC---GCCGAGACCTGAGCCCAAA
rPnmt  992 ........A---A.....---...T.AA.A.G.....GA.CGT...T......CG.AG.A.G

+1 rat exon 1

hPNMT 1249 GCAGGACCCAGCCCTGGCTGCGGCCGCCAGGCCGGCGGCTGCTGCCATACAGCG
rPnmt 1049 ..................A.GATG.A.T.........C.A.....T........A.A....C.C.T.....T....

hPNMT 1309 CTTTCGACGGCCGCTACCTCGACCAACACTACGCCGCCCCCTGCAGGGGACCTGCA
rPnmt 1109 ..............C............C.T..............T....A....A.GT......T....

hPNMT 1369 GCAGGACCCGCGTGGGCGTGAAGTGCGCTGCTGCAGAAGCTGCGATCCACGCCTTTG
rPnmt 1169 .........CCACCTTCTAGGAGGAGGGGGCCGAGCAGAGGGACCTGTCG

hPNMT 1429 GCAGGGGAAACTGAGGCACGAGGGACAAGAGGTCGTCGGGGAGTGAAAGCAGGG
rPnmt 1229 ..........ACT.........A..........A..GC...A...A.A...A.A.....-------.G...

hPNMT 1489 AAATAAAAAGAAGGAGGAGAAGCAGACGCAGCCCTAAAGATGAGGGAGCAAGAACA

hPNMT 1549 GAGATAGCTAGAGGGCTAGACTGAGGTGGAGATGAGGAAATGGAGGCAGATGTGGGACAG
rPnmt 1325 .G........G........G........G........G........G........G........G........G

hPNMT 1609 AGAGGAGAGAGGCTAGACTGAGGTGGAGATGAGGAAATGGAGGCAGATGTGGGACAG
rPnmt 1354 ---------------.....CGA.AG.-----GCTAG.G..AT.

hPNMT 1669 GAGATGAGACAGACTGAGGAGATGAGGAAATGGAGGCAGATGTGGGACAG
rPnmt 1387 G.G.............A............C.A.....A.GC.C.A-------

hPNMT 1729 GGGTGAAGAAGGCTAGACTGAGGTGGAGATGAGGAAATGGAGGCAGATGTGGGACAG
rPnmt 1419 ..T.A.A.ACACTACCCTTCTAGGAGGAGGGGC

Alu sequence

hPNMT 1789 CTTCCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT

hPNMT 2029 CATGTTGCTACAGCTGCTCTGCTCAGAATCCATCCACACCTTAGGATCCACCCACGCTCCTCCA
rPnmt 1524 ---------------.A.---------------------------------------------..A.

hPNMT 2089 AAGTGCTGAGATTACAGGTTGGAGAGCCACTGCGCCGCCAGCCAGTGGTAGATTGATCTCTTCTAGAT
rPnmt 1537 ..A.A-.A.GC.C.------------------------------------------.C.T....

Alu sequence

hPNMT 2149 GTGAAACCTGATCAGTGAAGCGGTGAAGGCTCCCTCCCAAGGCGCCAGCCATGAGTTATAGCTCTTCTAGAT
rPnmt 1560 ..C.G..---.GA-----------------..CA.TA...TT.TA-------.A....

hPNMT 2209 GGGTTCAGTCTAATCTCTGGGGCAAGATCCCCCTCCTGTAGGACACATTTTGAGAGGAG
rPnmt 1597 A.T....T.---.GTG....AA..CGA.T------....-....C.CTG.CA...C-----

hPNMT 2269 AAGGAAGAACTAGAGAGAGGACAGGGAGATGCAGGGGAGGGAAGGGTAAGGAGGCAGGGGC
rPnmt 1642 ......TG...G.G.-------------..C.C.AG..A.....GT.C--------AA.

exon 2

hPNMT 2329 TGCCCTGGCTGCTGGCCCACTGAGGACCCCTCTCCCTCTCTCTGCCCCTGCCCAGG
rPnmt 1688 CC....ATA.------------------------.C.C.AT....A..-.....G....T...