

CATTCCGCTTCTCTCCAGGTGGCGGTGGGA
 GGTGTTTTGCTCGGGTTCTGTAAGAATAGGCCAGG
 CAGCTTCCCGCGGGATGCGCTCATCCCTCTCGG
 GGTTCCGCTCCACCGCGCGCGTTCCGCCTG
 CCGCCTGCGAGATGTTTTCCAGACGAATGATTC
 CACTCTCGGCGCCTCCCATGTTGATCCAGCTCCT
 CTGCGGGCGTCAGGACCCCTGGGCCCGCCCG
 CTCCACTCAGTCAATCTTTTGTCCCCTATAGGCG
 GATTATCGGGGTGGCTGGGGGCGGCTGATTCGGA
 CGAATGCCCTTGGGGGTACCCCGGGAGGGAATC
 CGGGCTCCGGGCTTTGGCCAGCCCGACCCCTGGT
 TGAGCCGGGCCAGAGGCCACCAGGGGGCGCTCG
 ATGTTCTGCAGCCCCCGCAGCAGCCCCACTCC
 CCGGCTCACCTACGATTGGCTGGCCCGCCCGAG
 CTCTGTGCTGTGATTGGTCACAGCCCGTGTCCGTC
 GCGGGCGCGGGGCGGATACGAGGTGACGCGCA
 GAGGCCAGCTCGGGGCGGTGTCCCGCGCGCGC
 GACTGCGGGCGGAGTTTCCCGAGGGCCGAAGCG
 GGGCAGTGTGACGGCAGCGGTCTGGGAGGCGC
 CCGCGCGCGCTCGGAGCAGCTCCCCTCCTCCGCA
 GCCGTCACCGCGCGCGTCCGCGCGCCCTGGCC
 TCCCGCACTCGCGCACTCCTGTCCGCGCCACCG
 GCCCACCTCCACCTCGATGCGGTGCCTGGCTGC
 TGCGTGATGGGGCTGCGGAGCGCGCCCTGCGG
 CTCCGCGCGCGCTGCTCGCGCTGAGGTGCGT
 CGGTGCCCGGCCCGCGCGCCCGCGCGCGCGC
 GGCTCCTGTTGACCCTGTCGCGCGTCCGTCTGC
 AGCGCGGCTGAGGTAAGGCGGCGGGGCTGGCG
 CGGTTGGCGCGCGGTCCGCGGGGTTGGGGAGGG
 GGCCTTCGCGGGGAGGAGCGCGCGGGCCGG
 GGTCGGGGCGGGTCTGAGGGGA

CTCTTAGTTTTGGGTGCATTTGTCTGGTCTTCAAA
 CTAGATTGAAAGCTCTGAAAAAAAAAACTATCTTGT
 GTTCTATCTGTTGAGCTCATAGTAGGTATCCAGGA
 AGTAGTAGGGTTGACTGCATTGATTTGGGACTACAC
 TGGGAGTTTTCTTCCCATCTCCCTTTAGTTTTCT
 TTTTTCTTTCTTTCTTTCTTTTTTTTTCTTTTTTT
 TTGAGATGTCTTGTCTAGTCCCCCAGGCTGGA
 GTGCAGTGGTGCGATCTTGGCTCACTGTAGCCTCC
 ACCTCCAGGTTCAAGCAATTCTACTGCCTTAGCCT
 CCAGTAGCTGGGATTACAAGCACCAGCCACCAT
 TCCTGGCTAATTTTTTTTTTTGTATTTTAGTTGAGA
 CAGGGTTTACCATGTTGGTGATGCTGGTCTCAGA
 CTCCTGGGGCCTAGATCCCCCTGCCTCAGCCT
 CCCAGAGTGTTAGGATTACAGGCATGAGCCACTGT
 ACCCGCCTCTCTCCAGTTTCCAGTTGGAATCCAA
 GGGAAGTAAGTTTAAAGATAAAGTTACGATTTTGAAT
 CTTTGGATTGAGAAGAATTTGTACCTTTAACACCT
 AGAGTTGAACGTTTCATACCTGGAGAGCCTTAACATT
 AAGCCCTAGCCAGCCTCCAGCAAGTGGACATTGGT
 CAGGTTTGGCAGGATTCTCCCTGAAGTGGACT
 GAGAGCCACACCCTGGCCTGTACCATACCCATCC
 CCTATCCTTAGTGAAGCAAACTCCTTTGTTCCCTT
 CTCCTTCTCCTAGTGACAGGAAATATTGTGATCCTA
 AAGAATGAAAATAGCTTGTACCTCGTGGCCTCAG
 GCCTCTTGACTTCAGGCGTTCTGTTTAAATCAAGT
 GACATCTTCCAGGCTCCCTGAATGTGGCAGATG
 AAAGAGACTAGTTCAACCCTGACCTGAGGGGAAAG
 CCTTGTGAAGGGTCAGGAG

Left: CpG sites at 1/10 nucleotides, constituting a CpG island. The sample is of a gene-promoter, the highlighted ATG constitutes the start codon.

Right: CpG sites present at every 1/100 nucleotides, constituting a more normal example of the genome, or a region of the genome that is commonly methylated.