Murine Dnmt1 Sequence (5’ UTR to Exon 2)
UCSC Genome Browser, mm10
Annotations from ENCODE datasets (if applicable): ENCSR000CED (CTCF), ENCSR000CCR (H3K4me1), ENCSR000CCQ (H3K27ac), ENCSR000CNH (DNAse I sensitivity). Datasets represent adult murine intestinal tissue.

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TAGCCAGGAGGTGTGGGTGCCTCCGTTGCGCGCATGCGCACTCCCTTCGG
GCATAGCATGGTCTTCCCCCACTCTCTTGCCCTGTGTGGTACATGCTGCT
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TCCCGGACCATGTCCGCAGGCGgtaggtgccacgcagggtggggtgtgagg
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cggccgctgacagccagggcgcgcatgcgcggggcagcgtttggcgcggg
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agatgttgtggccatggcctgtaacatcaggaggcaggagcaggagggtc
acaagttagaattcaactaaggtctcatttcagacattcacaccttgcaa
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Commented [A1]: Start of exon 1 (exons denoted by uppercase letters)

Commented [A2]: **Start of first intron** (introns denoted by lowercase letters)

Commented [A3]: Avoid **consensus splicing region**

Commented [A4]: CpG Island: avoid the region overlapping with intron 1 due to possible gene regulatory functions

Commented [A5]: Dnase-seq peak (in 1 of 2 replicates): avoid if possible due to potential gene regulatory functions

Commented [A6]: H3K27ac peak: avoid this region due to possible gene regulatory functions

Commented [A7]: Dnase-seq peak: avoid due to possible gene regulatory functions

Commented [A8]: Slight H3K4me1 peak: avoid if possible due to potential gene regulatory functions

Commented [A9]: Example of a repetitive region to avoid, as denoted by “n”. Avoid all instances of repetitive “n” stretches.

ggtgagggatttcttttcctgagcagggggtgtcctttccatagctgaga
ttccttggttggcatgggtttttcatttctttcagtttttttaaattaaa
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ctttacccagGCTCAAAGACTTGGAAAGAGATGGCTTAACAGAAAAG

Commented [A10]: Forward primer to evaluate landing pad insertion

Commented [A11]: PAM sequence (NGG on reverse strand)

Commented [A12]: 5' 60-bp homology arm for DNA template

Commented [A13]: sgRNA: CTAGTACCACTCCTGTACCG (reverse strand)

Commented [A14]: 3' 60-bp homology arm for DNA template

Commented [A15]: Reverse primer to evaluate landing pad insertion (primer sequence is the reverse complement of the highlighted sequence)

Commented [A16]: Avoid consensus splicing region