

Donor Template SNV -> REV

Protospacer Sequence

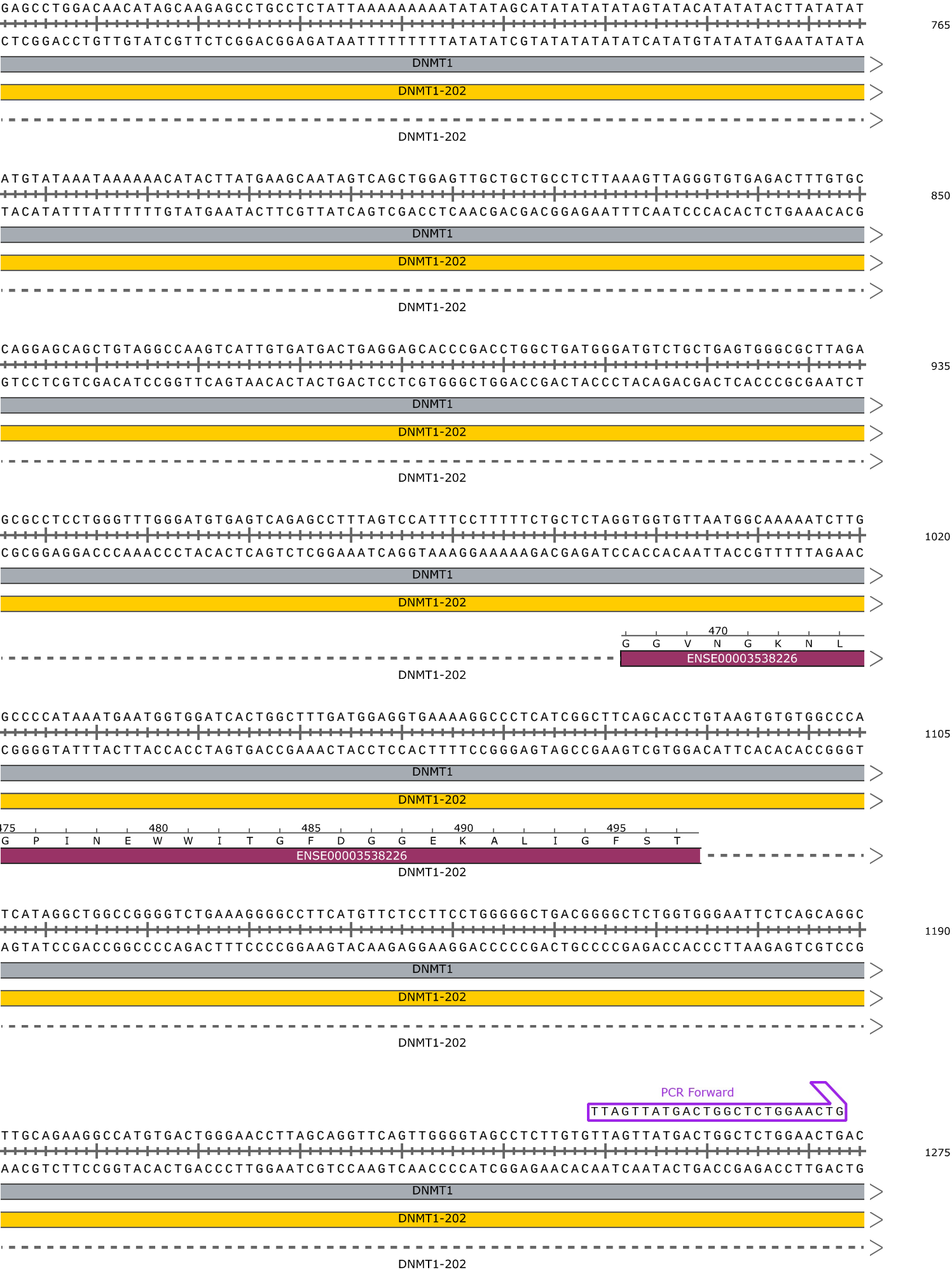
SNV

INK2J00048R_DNMT1_Y511C_A03_AA
5599 bp

Genomic alignment of DNMT1 and DNMT1-202 fragments. The figure shows DNA sequence reads aligned to a reference. Grey bars represent DNMT1 and yellow bars represent DNMT1-202. Purple bars highlight specific regions: ENSE00003606243 (430-445) and ENSE00003606243 (455-465).

Sequence alignment details (DNMT1-202):

- Region 1 (430-445): V Y C K H G H L C P I D T G L I E K N I E L F F S G
- Region 2 (455-465): S A K P I Y D D P S L E





Donor Template SNV -> REV

CTCTGTTACACCCAGCATTGCGGAATACATTCTGATGGATCCCAGTCCCAGATATGCGCCCATATTTGGGCTGATGCAGGAGAA
CTCTGTTACACCCAGCATTGCGGAATACATTCTGATGGATCCCAGTCCCAGATATGCGCCCATATTTGGGCTGATGCAGGAGAA
GAGACAAGTGGGGTCGTAAACGGCTTATGTAAGACTACCTAGGGTCAGGGCTCAACGCGGGTATAAAACCCGACTACGTCCTCTT

1955

DNMT1

DNMT1-202

S F A E Y I L M D P S P E Y A P I F G L M Q E K
ENSE00003601320

DNMT1-202

Donor Template SNV -> REV

PAM Protospacer Sequence

SNV

TCACACGCGGGTATAAACCC
gRNA Protospacer

Donor Template SNV -> REV

GATC

GATCTACATCAGCAAGATTGTGGTGGAGTTCTGTCAGAGCAATTCCGACTCGACCTATGAGGACCTGATCAACAAGATCGAGGTA
CTAGATGTAGTCGTTCTAACACCACCTCAAGGACGTCTCGTTAAGGCTGAGCTGGATACTCCTGGACTAGTTGTTCTAGCTCCAT

2040

DNMT1

DNMT1-202

I Y I S K I V V E F L Q S N S D S T Y E D L I N K I E
ENSE00003601320

DNMT1-202

Donor Template SNV -> REV

AGAGATCGAGGGTCTCTCAGCATCCGGGATTCCCACTGGAAACTTGCCTTCAGAACCAGCAGACACTGTTCTTCAGTTGGATTTAG
TCTCTAGCTCCCAGGAGTCGTAGGCCCTAAGGGTGACCTTTGAACGGAAGTCTTGGTCGTCTGTGACAAGAAGTCAACCTAAATC

2125

DNMT1

DNMT1-202

DNMT1-202

GCCAGTTTGGCTTAAGCATGAGAGAAACCTGTTCTCTTTCAAGACCACGGTTCTCTTCTGGCCTCAACTTGAACCGCTTCACA
CGGTCAAACCGAATTCGTACTCTCTTTGGACAAGAGAAAGTTCTGGTGCCAAGGAGGAAGACCGGAGTTGAACTTGGCGAAGTG

2210

DNMT1

DNMT1-202

T T V P P S G L N L N F T
ENSE00003615043

DNMT1-202

GAGGACTCCCTCCTGCGACACGCGCAGTTTGTGGTGGAGCAGGTGGAGAGTTATGACGAGGCCGGGGACAGTGATGAGCAGCCCA
CTCCTGAGGGAGGACGCTGTGCGCGTCAAACACCACCTCGTCCACCTCTCAATACTGCTCCGGCCCCCTGTCCTACTCGTCGGGT

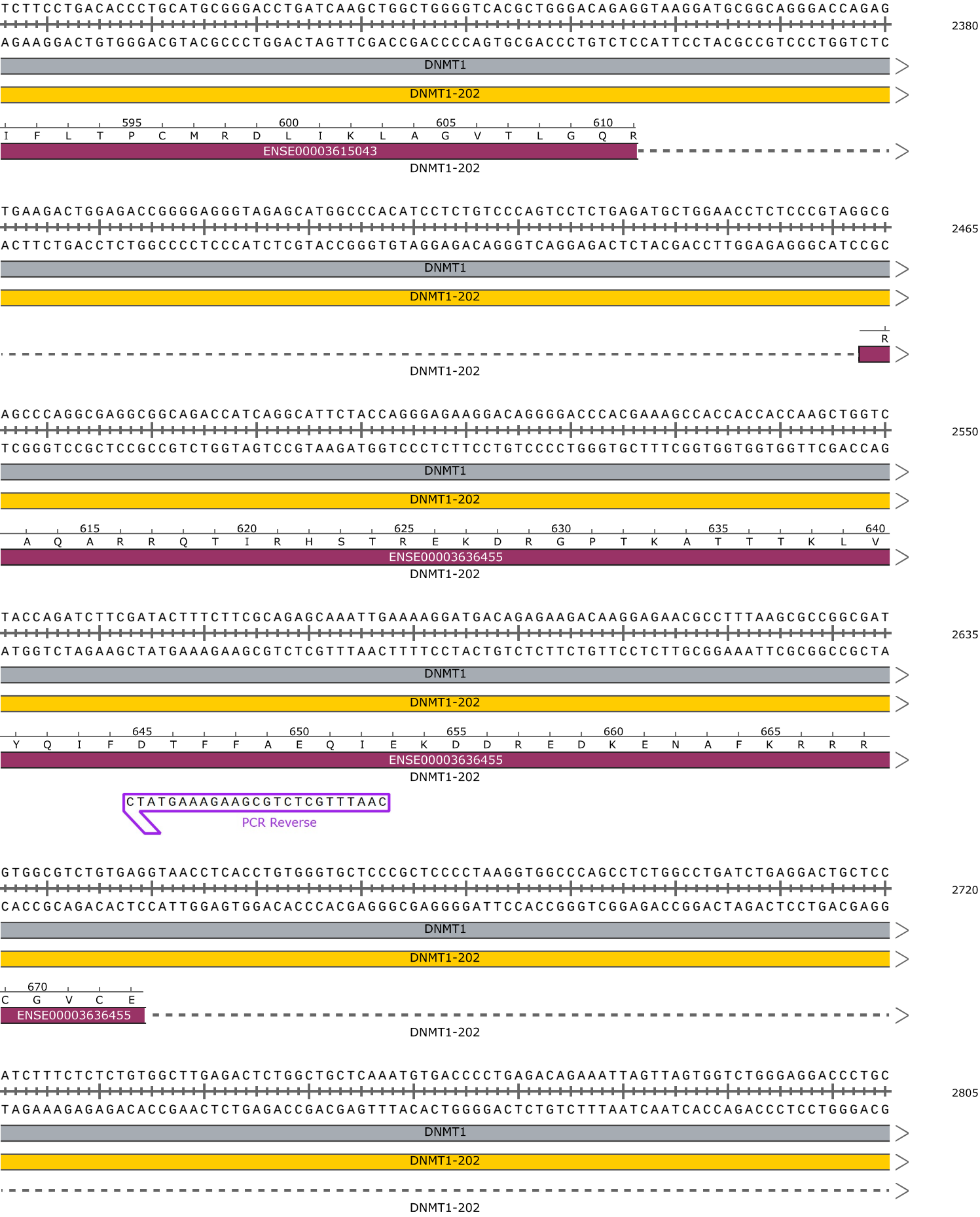
2295

DNMT1

DNMT1-202

E D S L L R H A Q F V V E Q V E S Y D E A G D S D E Q P
ENSE00003615043

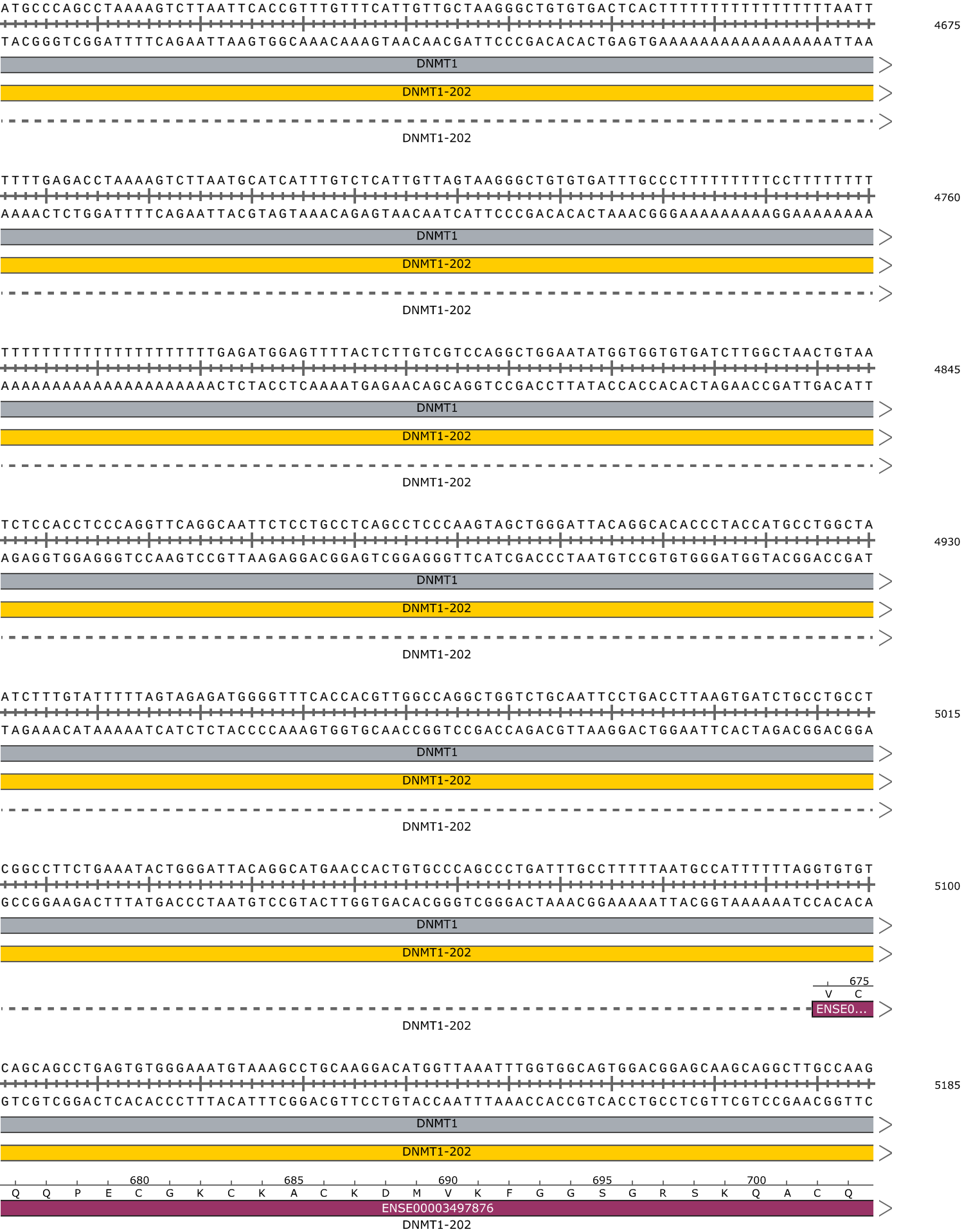
DNMT1-202

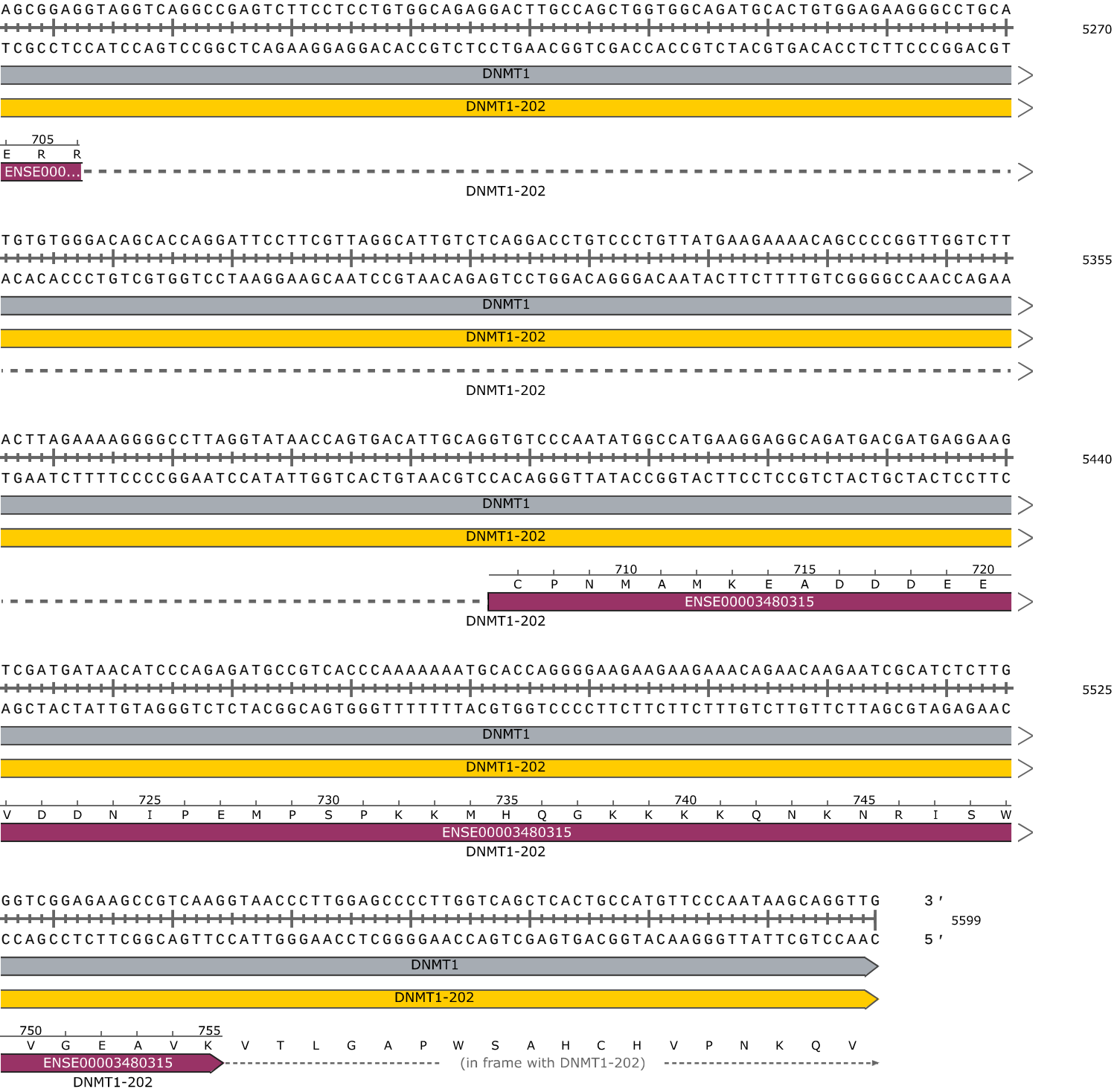



















































Feature		Location	Size			Type
✓	DNMT1	1 .. 5599	5599 bp			gene
	/note = gene ENSG00000130816 Protein coding					
	DNMT1-201	1 .. 5599	5599 bp			prim_transcript
	/note = primary transcript ENST00000340748					
✓	DNMT1-202	1 .. 5599	5599 bp			prim_transcript
	/note = primary transcript ENST00000359526					
	DNMT1-227	1 .. 5599	5599 bp			prim_transcript
	/note = primary transcript ENST00000592705 Nonsense mediated decay					
	DNMT1-229	1 .. 5599	5599 bp			prim_transcript
	/note = primary transcript ENST00000676604 protein_coding_CDS_not_defined					
	DNMT1-230	1 .. 5599	5599 bp			prim_transcript
	/note = primary transcript ENST00000676610					
	DNMT1-231	1 .. 5599	5599 bp			prim_transcript
	/note = primary transcript ENST00000676820 Retained intron					
	DNMT1-232	1 .. 5599	5599 bp			prim_transcript
	/note = primary transcript ENST00000676868 Retained intron					
	DNMT1-233	1 .. 5599	5599 bp			prim_transcript
	/note = primary transcript ENST00000677013 Nonsense mediated decay					
	DNMT1-236	1 .. 5599	5599 bp			prim_transcript
	/note = primary transcript ENST00000677250 Nonsense mediated decay					
	DNMT1-237	1 .. 5599	5599 bp			prim_transcript
	/note = primary transcript ENST00000677616 Nonsense mediated decay					
	DNMT1-238	1 .. 5599	5599 bp			prim_transcript
	/note = primary transcript ENST00000677634 Nonsense mediated decay					
	DNMT1-239	1 .. 5599	5599 bp			prim_transcript
	/note = primary transcript ENST00000677685 Nonsense mediated decay					
	DNMT1-240	1 .. 5599	5599 bp			prim_transcript
	/note = primary transcript ENST00000677783 Retained intron					
	DNMT1-241	1 .. 5599	5599 bp			prim_transcript
	/note = primary transcript ENST00000677946					
	DNMT1-242	1 .. 5599	5599 bp			prim_transcript
	/note = primary transcript ENST00000678024 Retained intron					
	DNMT1-246	1 .. 5599	5599 bp			prim_transcript
	/note = primary transcript ENST00000678694 Retained intron					
	DNMT1-247	1 .. 5599	5599 bp			prim_transcript
	/note = primary transcript ENST00000678804					
	DNMT1-251	1 .. 5599	5599 bp			prim_transcript
	/note = primary transcript ENST00000679103					
	DNMT1-252	1 .. 5599	5599 bp			prim_transcript
	/note = primary transcript ENST00000679313					
	DNMT1-203	1 .. 2278	2278 bp			prim_transcript
	/note = primary transcript ENST00000585843 Retained intron					

Feature	Location	Size			Type
DNMT1-201	433 .. 5544	5112 bp			CDS
▶ 7 segments = 985 bp					
/codon_start	= 1				
/note	= coding sequence ENSP00000345739				
/translation	VYCKHGHLCPIDTGLIEKNIELFFSGSAKPIYDDDP SLE,,GGVNGKNLGPINEWWITGFDGG EKALIGFST,,SFAEYILMDPSPEYAPIFGLMQE KIYISKIVVEFLQSNSDSTYEDLINKIE,,TTVPPSGLNLRFTEDSLLRHAQFVVEQVESYDEAGDSDEQPIFLT PCMRDLIKLAGVTLGQR,,R AQARRQTIRHSTREKDRGPTKATTTKL VYQIFDTFFAEQIEKDDREDKENAFKRRRCGVCE,,VCQQPEC GKCKACKDMVKFGGSGRSKQAC QERR,,CPNMAMKEADDDEEVDDNIPEMPSPKKMHQ GKKKKQKNKRISWVGEAVK 328 amino acids = 37.1 kDa				
DNMT1-202	433 .. 5544	5112 bp			CDS
▶ 7 segments = 985 bp					
/codon_start	= 1				
/note	= coding sequence ENSP00000352516				
/translation	VYCKHGHLCPIDTGLIEKNIELFFSGSAKPIYDDDP SLE,,GGVNGKNLGPINEWWITGFDGG EKALIGFST,,SFAEYILMDPSPEYAPIFGLMQE KIYISKIVVEFLQSNSDSTYEDLINKIE,,TTVPPSGLNLRFTEDSLLRHAQFVVEQVESYDEAGDSDEQPIFLT PCMRDLIKLAGVTLGQR,,R AQARRQTIRHSTREKDRGPTKATTTKL VYQIFDTFFAEQIEKDDREDKENAFKRRRCGVCE,,VCQQPEC GKCKACKDMVKFGGSGRSKQAC QERR,,CPNMAMKEADDDEEVDDNIPEMPSPKKMHQ GKKKKQKNKRISWVGEAVK 328 amino acids = 37.1 kDa				
DNMT1-230	433 .. 5544	5112 bp			CDS
▶ 7 segments = 985 bp					
/codon_start	= 1				
/note	= coding sequence ENSP00000504236				
/translation	VYCKHGHLCPIDTGLIEKNIELFFSGSAKPIYDDDP SLE,,GGVNGKNLGPINEWWITGFDGG EKALIGFST,,SFAEYILMDPSPEYAPIFGLMQE KIYISKIVVEFLQSNSDSTYEDLINKIE,,TTVPPSGLNLRFTEDSLLRHAQFVVEQVESYDEAGDSDEQPIFLT PCMRDLIKLAGVTLGQR,,R AQARRQTIRHSTREKDRGPTKATTTKL VYQIFDTFFAEQIEKDDREDKENAFKRRRCGVCE,,VCQQPEC GKCKACKDMVKFGGSGRSKQAC QERR,,CPNMAMKEADDDEEVDDNIPEMPSPKKMHQ GKKKKQKNKRISWVGEAVK 328 amino acids = 37.1 kDa				
DNMT1-241	433 .. 5544	5112 bp			CDS
▶ 7 segments = 985 bp					
/codon_start	= 1				
/note	= coding sequence ENSP00000504202				
/translation	VYCKHGHLCPIDTGLIEKNIELFFSGSAKPIYDDDP SLE,,GGVNGKNLGPINEWWITGFDGG EKALIGFST,,SFAEYILMDPSPEYAPIFGLMQE KIYISKIVVEFLQSNSDSTYEDLINKIE,,TTVPPSGLNLRFTEDSLLRHAQFVVEQVESYDEAGDSDEQPIFLT PCMRDLIKLAGVTLGQR,,R AQARRQTIRHSTREKDRGPTKATTTKL VYQIFDTFFAEQIEKDDREDKENAFKRRRCGVCE,,VCQQPEC GKCKACKDMVKFGGSGRSKQAC QERR,,CPNMAMKEADDDEEVDDNIPEMPSPKKMHQ GKKKKQKNKRISWVGEAVK 328 amino acids = 37.1 kDa				
DNMT1-247	433 .. 5544	5112 bp			CDS
▶ 7 segments = 985 bp					
/codon_start	= 1				
/note	= coding sequence ENSP00000503853				
/translation	VYCKHGHLCPIDTGLIEKNIELFFSGSAKPIYDDDP SLE,,GGVNGKNLGPINEWWITGFDGG EKALIGFST,,SFAEYILMDPSPEYAPIFGLMQE KIYISKIVVEFLQSNSDSTYEDLINKIE,,TTVPPSGLNLRFTEDSLLRHAQFVVEQVESYDEAGDSDEQPIFLT PCMRDLIKLAGVTLGQR,,R AQARRQTIRHSTREKDRGPTKATTTKL VYQIFDTFFAEQIEKDDREDKENAFKRRRCGVCE,,VCQQPEC GKCKACKDMVKFGGSGRSKQAC QERR,,CPNMAMKEADDDEEVDDNIPEMPSPKKMHQ GKKKKQKNKRISWVGEAVK 328 amino acids = 37.1 kDa				
DNMT1-251	433 .. 5544	5112 bp			CDS
▶ 7 segments = 985 bp					
/codon_start	= 1				
/note	= coding sequence ENSP00000503151				
/translation	VYCKHGHLCPIDTGLIEKNIELFFSGSAKPIYDDDP SLE,,GGVNGKNLGPINEWWITGFDGG EKALIGFST,,SFAEYILMDPSPEYAPIFGLMQE KIYISKIVVEFLQSNSDSTYEDLINKIE,,TTVPPSGLNLRFTEDSLLRHAQFVVEQVESYDEAGDSDEQPIFLT PCMRDLIKLAGVTLGQR,,R AQARRQTIRHSTREKDRGPTKATTTKL VYQIFDTFFAEQIEKDDREDKENAFKRRRCGVCE,,VCQQPEC GKCKACKDMVKFGGSGRSKQAC QERR,,CPNMAMKEADDDEEVDDNIPEMPSPKKMHQ GKKKKQKNKRISWVGEAVK 328 amino acids = 37.1 kDa				
DNMT1-252	433 .. 5544	5112 bp			CDS
▶ 7 segments = 985 bp					
/codon_start	= 1				
/note	= coding sequence ENSP00000504512				
/translation	VYCKHGHLCPIDTGLIEKNIELFFSGSAKPIYDDDP SLE,,GGVNGKNLGPINEWWITGFDGG EKALIGFST,,SFAEYILMDPSPEYAPIFGLMQE KIYISKIVVEFLQSNSDSTYEDLINKIE,,TTVPPSGLNLRFTEDSLLRHAQFVVEQVESYDEAGDSDEQPIFLT PCMRDLIKLAGVTLGQR,,R AQARRQTIRHSTREKDRGPTKATTTKL VYQIFDTFFAEQIEKDDREDKENAFKRRRCGVCE,,VCQQPEC GKCKACKDMVKFGGSGRSKQAC QERR,,CPNMAMKEADDDEEVDDNIPEMPSPKKMHQ GKKKKQKNKRISWVGEAVK 328 amino acids = 37.1 kDa				
Donor Template SNV -> REV	1860 .. 1959	100 bp			misc_feature
PAM	1919 .. 1921	3 bp			misc_feature

Feature	Location	Size			Type
✓ Protospacer Sequence	1922 .. 1941	20 bp			misc_feature
✓ SNV	1925 .. 1925	1 bp			misc_feature
<div> <div>/note</div> <div>= REV = A SNV = G</div> </div>					
DNMT1-208	1965 .. 5599	3635 bp			prim_transcript
<div> <div>/note</div> <div>= primary transcript ENST00000586799 Nonsense mediated decay</div> </div>					
DNMT1-250	4937 .. 5599	663 bp			prim_transcript
<div> <div>/note</div> <div>= primary transcript ENST00000679100 Retained intron</div> </div>					
DNMT1-245	5195 .. 5599	405 bp			prim_transcript
<div> <div>/note</div> <div>= primary transcript ENST00000678647 Retained intron</div> </div>					
DNMT1-207	5245 .. 5599	355 bp			prim_transcript
<div> <div>/note</div> <div>= primary transcript ENST00000586667 Retained intron</div> </div>					

Primer		Length		Binding Sites		Tm	Date Added
✓ PCR Forward		25-mer		1249 .. 1273		58°C	Nov 10, 2022
/sequence	=	TTAGTTATGACTGGCTCTGGAACTG 44% GC / 7703.1 Da					
✓ Sanger Sequencing		20-mer		1762 .. 1781		57°C	Nov 10, 2022
/sequence	=	ACATTTGGGTACGGGATGAC 50% GC / 6197.1 Da					
✓ Donor Template SNV -> REV		100-mer		1860 .. 1959		78°C	Nov 10, 2022
/sequence	=	TTCCACACCTCCTCTGTTCACCCCAGCATTTGCCGAATACATTCTGATGGATCCCAGTCCCGAGTATGCGCCCATATTTGGGCTGATG 52% GC / 13041.5 Da					
✓ gRNA Protospacer		20-mer		1926 .. 1941		55°C	Nov 9, 2022
/sequence	=	CCCAAATATGGGCGCACACT 55% GC / 6071.0 Da					
✓ PCR Reverse		25-mer		2563 .. 2587		57°C	Nov 10, 2022
/sequence	=	CAATTTGCTCTGCGAAGAAAGTATC 40% GC / 7665.1 Da					