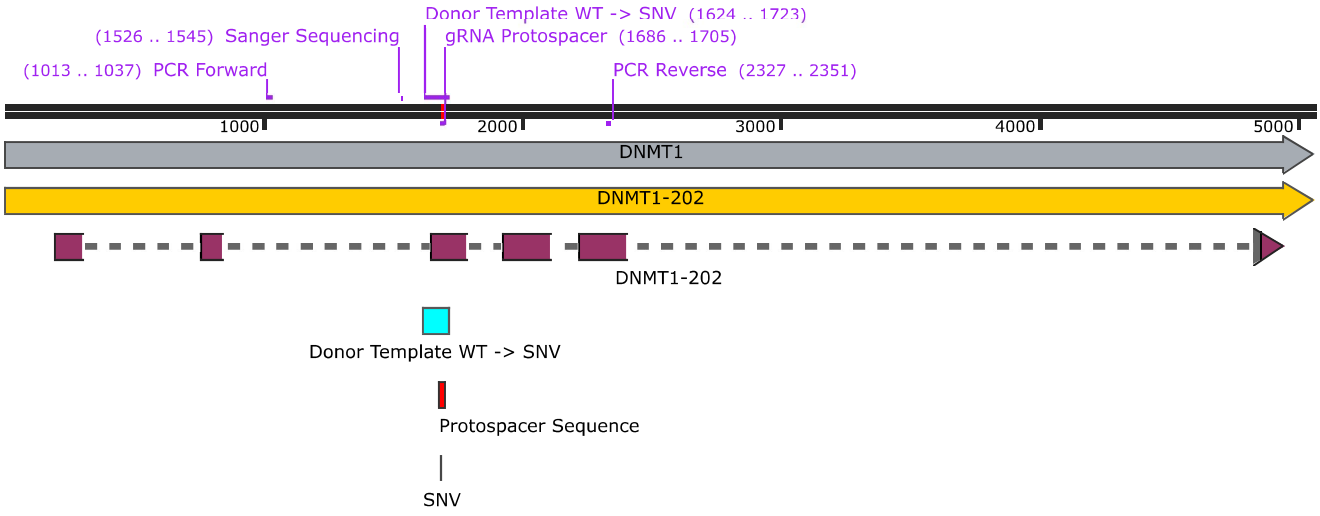

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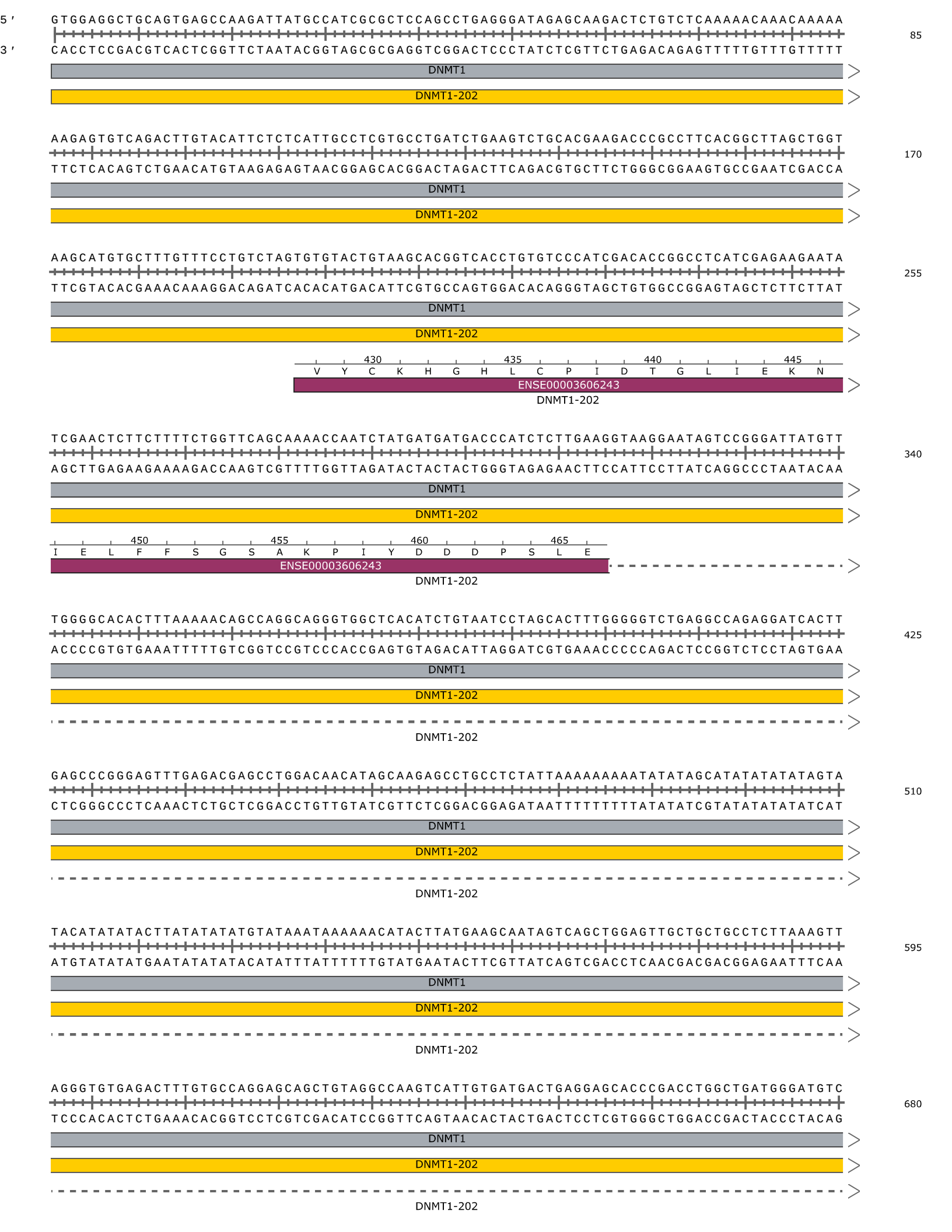
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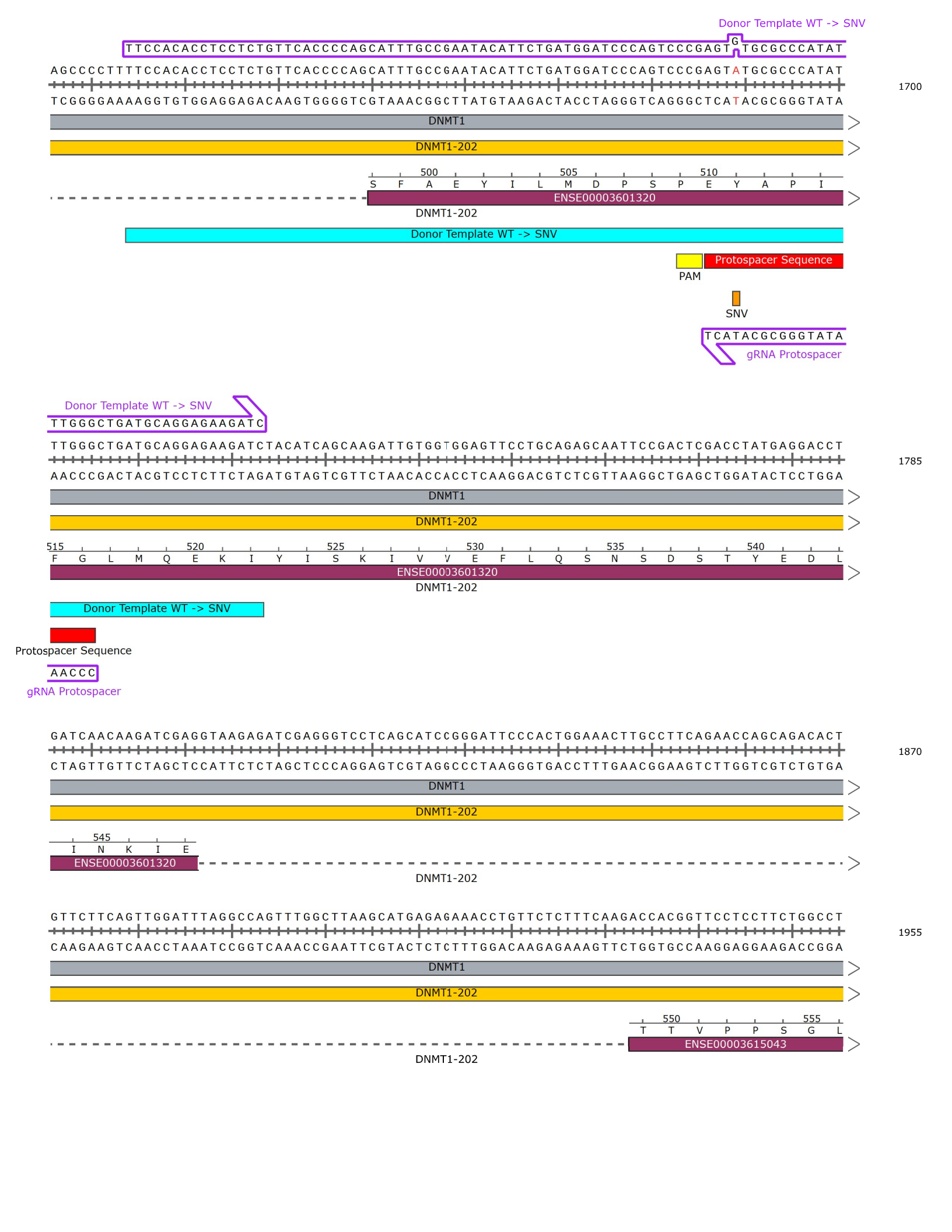
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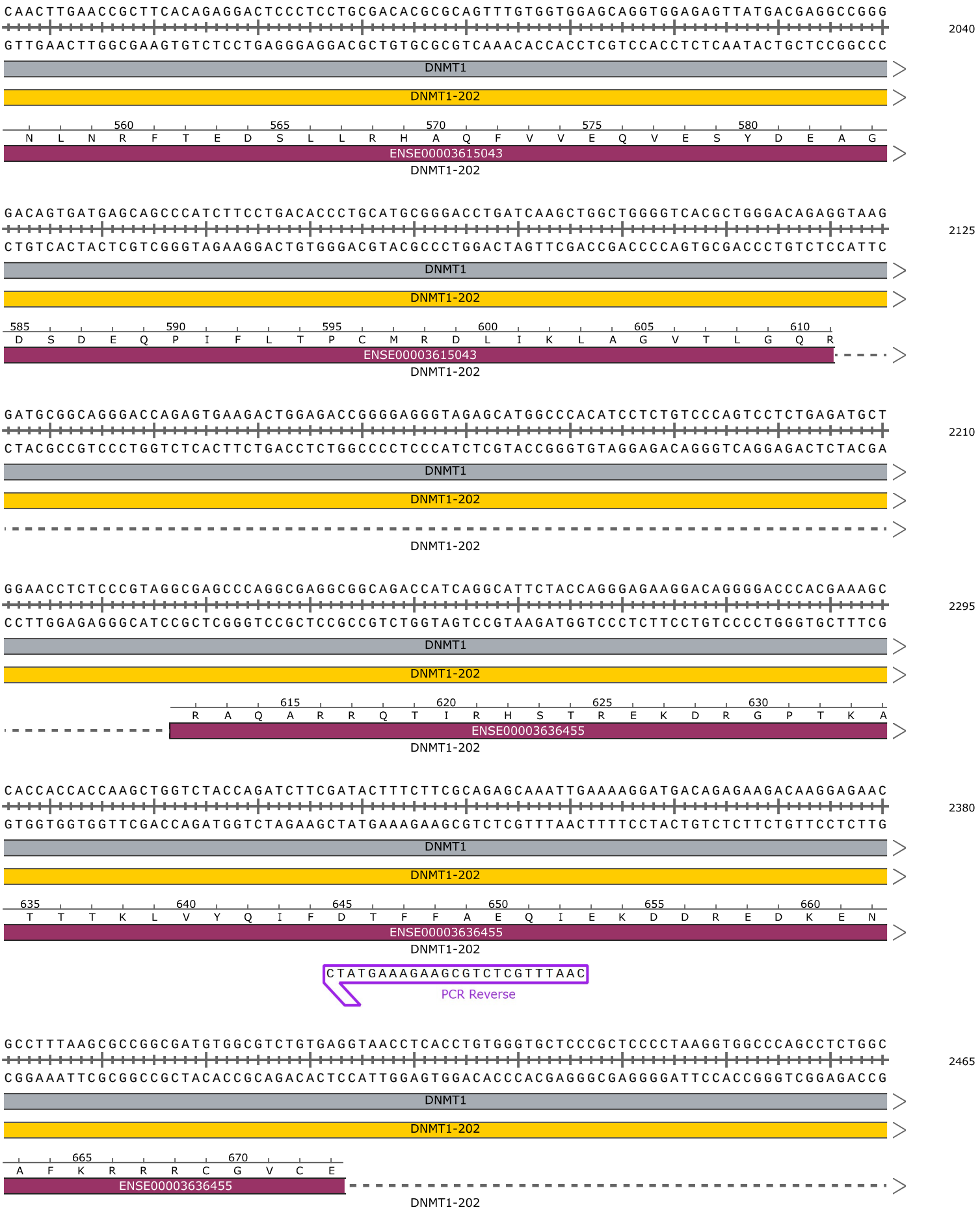
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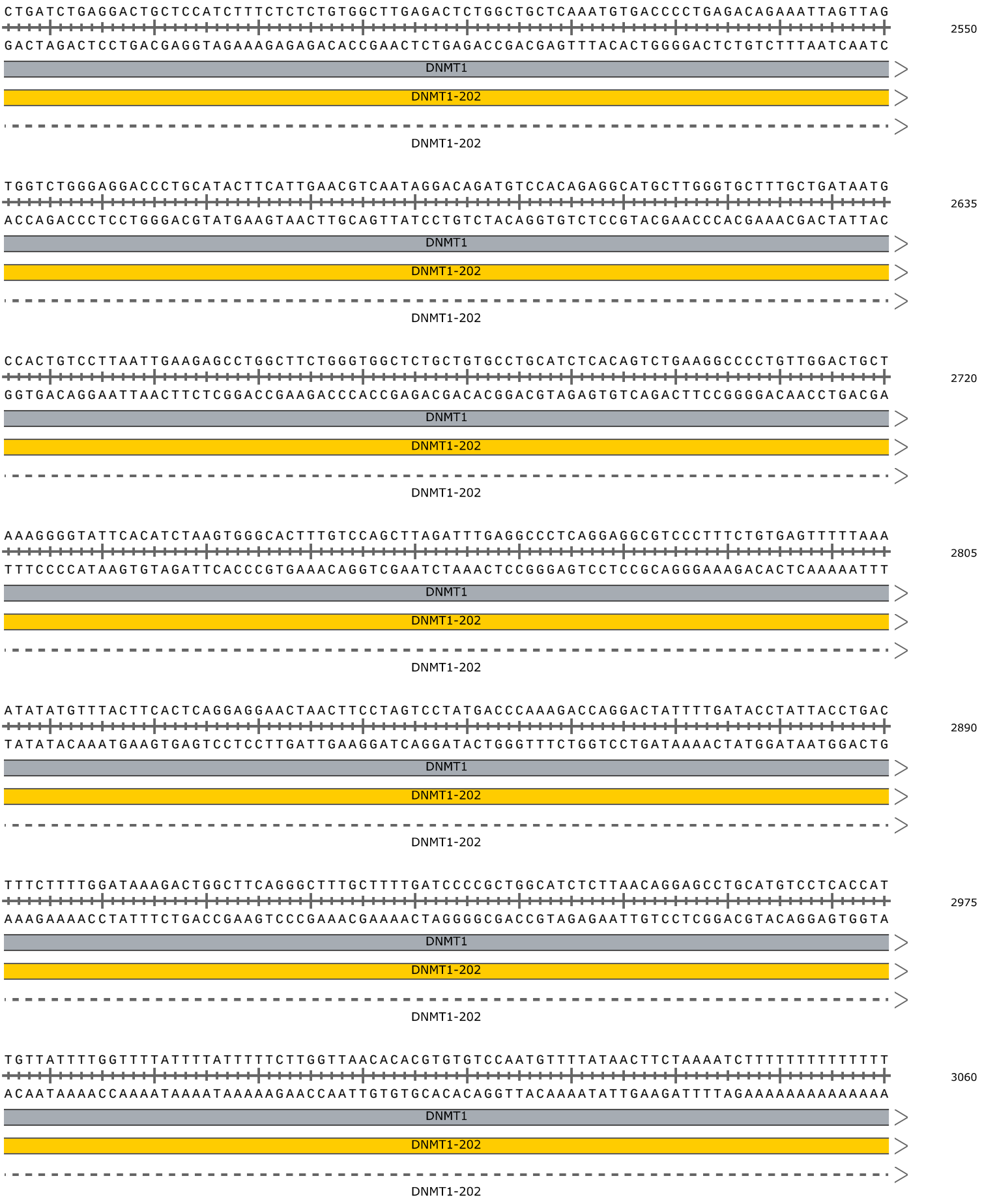
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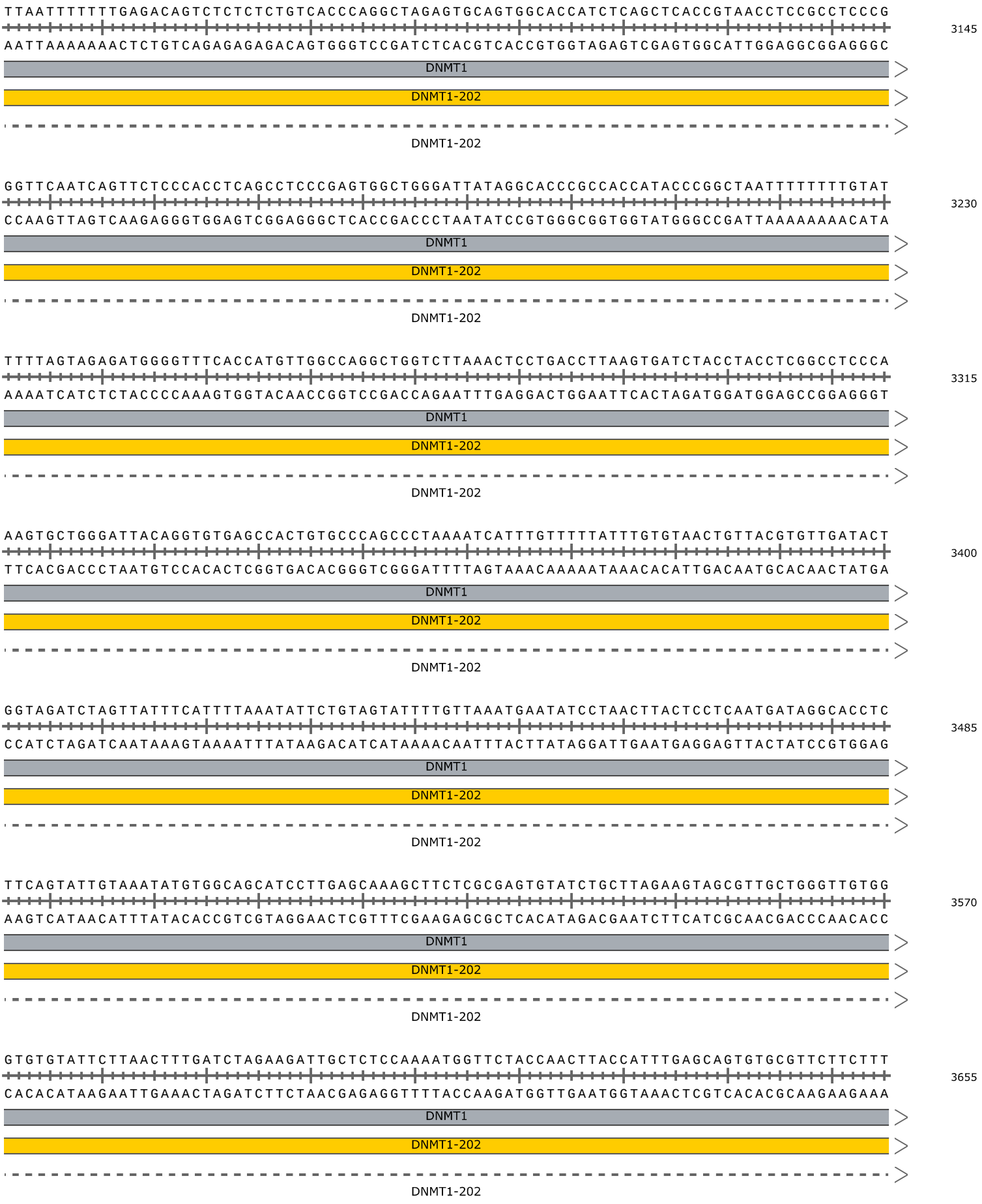
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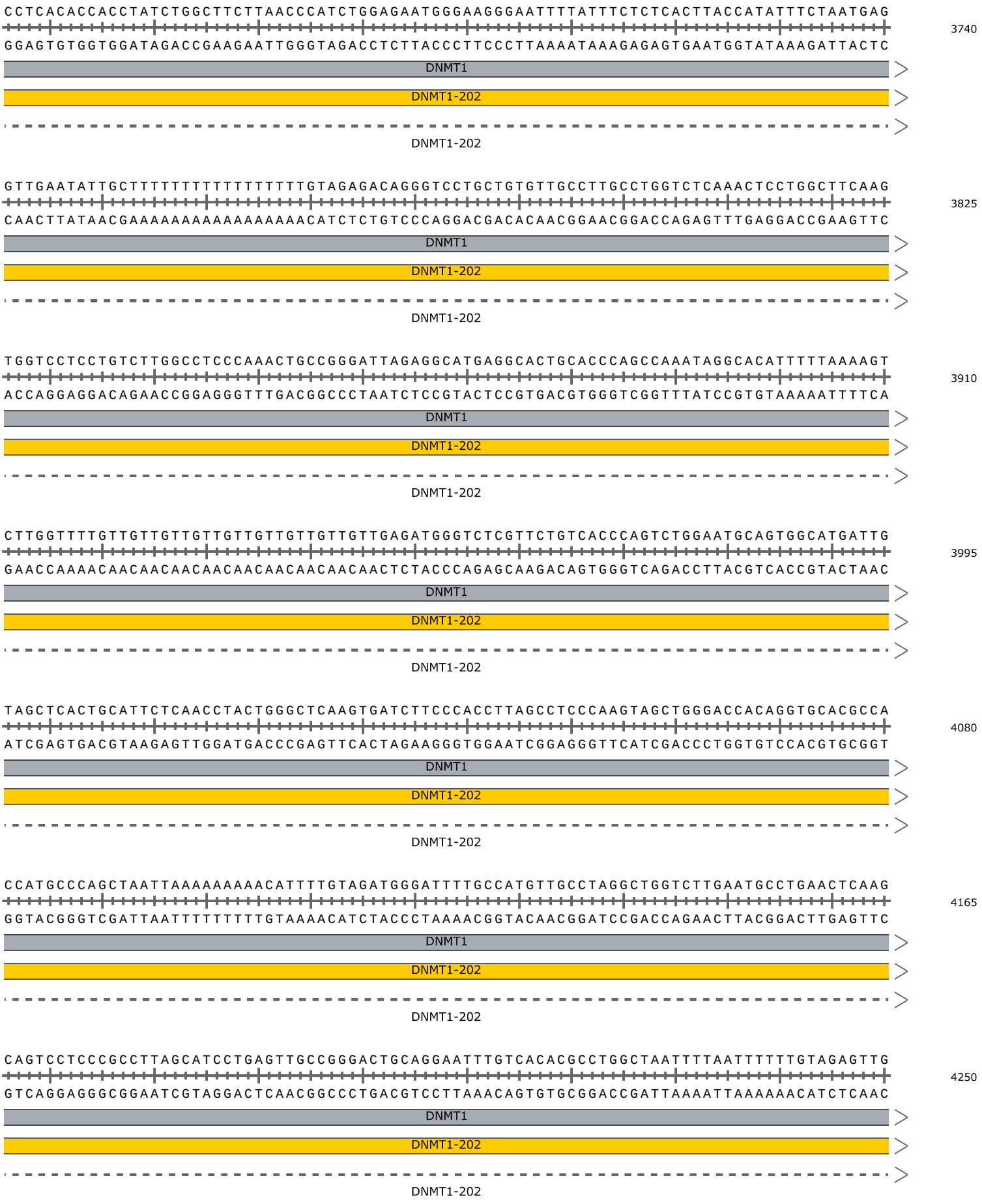
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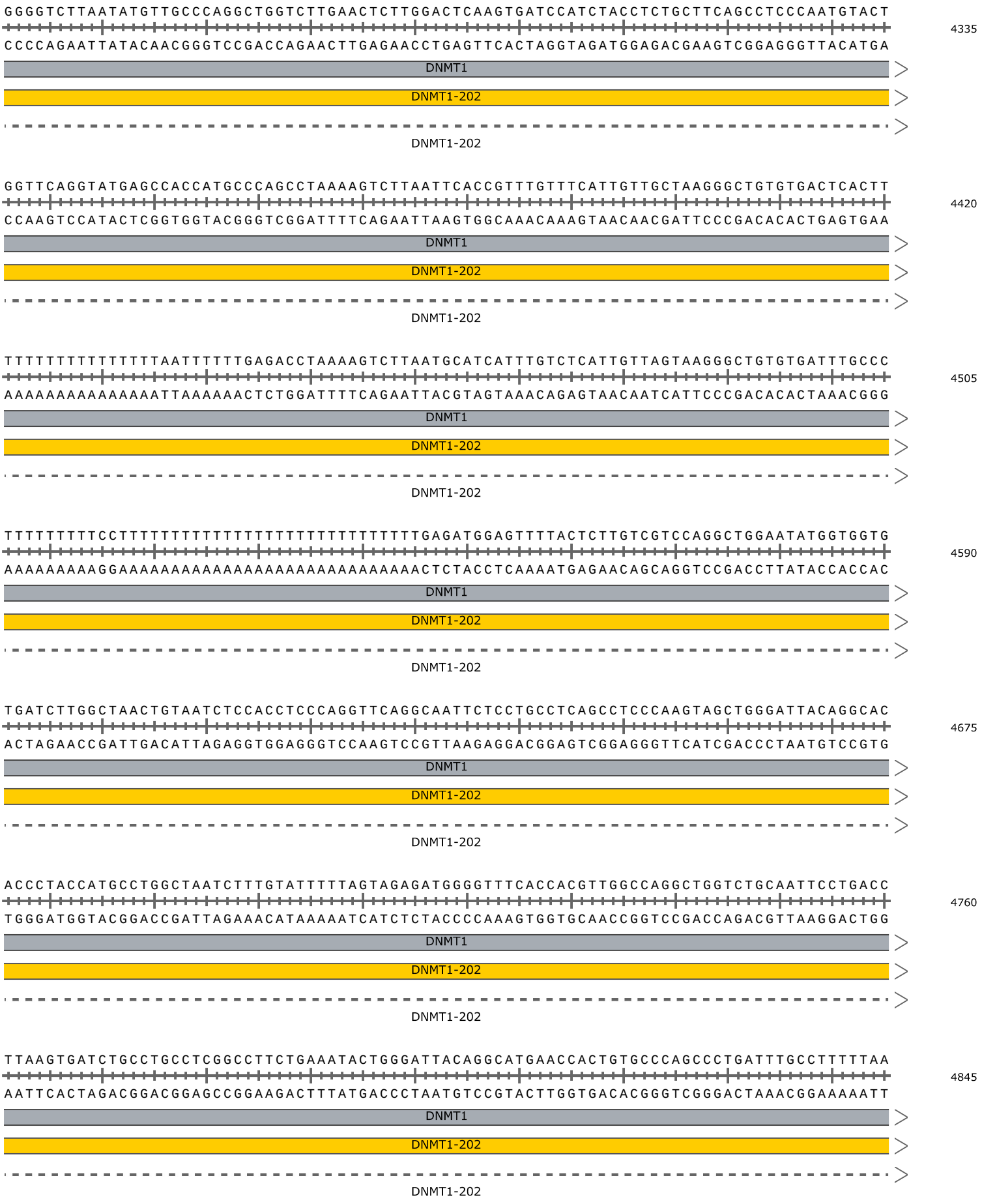
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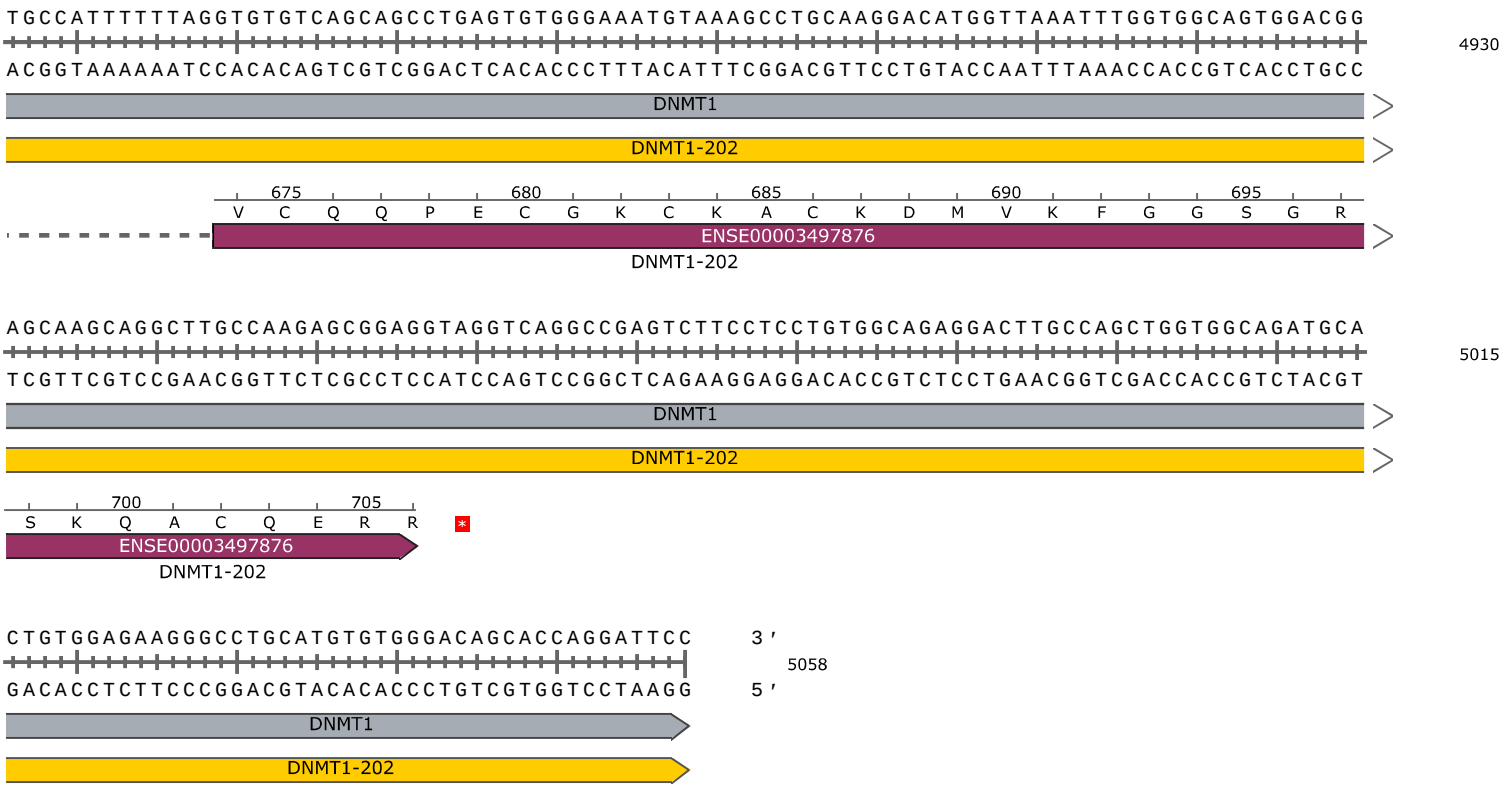
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	/note	=	primary transcript ENST00000340748						
✓	**DNMT1-202**			1	.. 5058	5058 bp		→	prim_transcript
	/note	=	primary transcript ENST00000359526						
	DNMT1-227			1	.. 5058	5058 bp		→	prim_transcript
	/note	=	primary transcript ENST00000592705 Nonsense mediated decay						
	DNMT1-229			1	.. 5058	5058 bp		→	prim_transcript
	/note	=	primary transcript ENST00000676604 protein_coding_CDS_not_defined						
	DNMT1-230			1	.. 5058	5058 bp		→	prim_transcript
	/note	=	primary transcript ENST00000676610						
	DNMT1-231			1	.. 5058	5058 bp		→	prim_transcript
	/note	=	primary transcript ENST00000676820 Retained intron						
	DNMT1-232			1	.. 5058	5058 bp		→	prim_transcript
	/note	=	primary transcript ENST00000676868 Retained intron						
	DNMT1-233			1	.. 5058	5058 bp		→	prim_transcript
	/note	=	primary transcript ENST00000677013 Nonsense mediated decay						
	DNMT1-236			1	.. 5058	5058 bp		→	prim_transcript
	/note	=	primary transcript ENST00000677250 Nonsense mediated decay						
	DNMT1-237			1	.. 5058	5058 bp		→	prim_transcript
	/note	=	primary transcript ENST00000677616 Nonsense mediated decay						
	DNMT1-238			1	.. 5058	5058 bp		→	prim_transcript
	/note	=	primary transcript ENST00000677634 Nonsense mediated decay						
	DNMT1-239			1	.. 5058	5058 bp		→	prim_transcript
	/note	=	primary transcript ENST00000677685 Nonsense mediated decay						
	DNMT1-240			1	.. 5058	5058 bp		→	prim_transcript
	/note	=	primary transcript ENST00000677783 Retained intron						
	DNMT1-241			1	.. 5058	5058 bp		→	prim_transcript
	/note	=	primary transcript ENST00000677946						
	DNMT1-242			1	.. 5058	5058 bp		→	prim_transcript
	/note	=	primary transcript ENST00000678024 Retained intron						
	DNMT1-246			1	.. 5058	5058 bp		→	prim_transcript
	/note	=	primary transcript ENST00000678694 Retained intron						
	DNMT1-247			1	.. 5058	5058 bp		→	prim_transcript
	/note	=	primary transcript ENST00000678804						
	DNMT1-251			1	.. 5058	5058 bp		→	prim_transcript
	/note	=	primary transcript ENST00000679103						
	DNMT1-252			1	.. 5058	5058 bp		→	prim_transcript
	/note	=	primary transcript ENST00000679313						
	DNMT1-203			1	.. 2042	2042 bp		→	prim_transcript
	/note	=	primary transcript ENST00000585843 Retained intron						

Feature	Location	Size	Type
DNMT1-201	197 .. 4956	4760 bp	CDS

6 segments = 837 bp

/codon_start = 1
/note = coding sequence ENSP00000345739
/translation = VYCKHGHLCPIDTGLIEKNIELFFSGSAKPIYDDDPSLE,,GGVNGKNLGPINEWWITGFDGGEKALIGFST,,SFAEYILMDPSPEYAPIFGLMQE
KIYISKIVVEFLQSNSDSTYEDLINKIE,,TTVPPSGLNLNRFTEDSLLRHAQFVVEQVESYDEAGDSDEQPIFLTPCMRDLIKLAGVTLGQR,,R
AQARRQTIRHSTREKDRGPTKATTTKLVYQIFDTFFAEQIEKDDREDKENAFKRRRCGVCE,,VCQQPECGKCKACKDMVKFGGSGRSKQAC
QFR
279 amino acids = 31.4 kDa

✓	Feature	Location	Size	Type
✓	**DNMT1-202**	197 .. 4956	4760 bp	CDS

6 segments = 837 bp

/codon_start = 1
/note = coding sequence ENSP00000352516
/translation = VYCKHGHLCPIDTGLIEKNIELFFSGSAKPIYDDDPSLE,,GGVNGKNLGPINEWWITGFDGGEKALIGFST,,SFAEYILMDPSPEYAPIFGLMQE
KIYISKIVVEFLQSNSDSTYEDLINKIE,,TTVPPSGLNLNRFTEDSLLRHAQFVVEQVESYDEAGDSDEQPIFLTPCMRDLIKLAGVTLGQR,,R
AQARRQTIRHSTREKDRGPTKATTTKLVYQIFDTFFAEQIEKDDREDKENAFKRRRCGVCE,,VCQQPECGKCKACKDMVKFGGSGRSKQAC
QFR
279 amino acids = 31.4 kDa

Feature	Location	Size	Type
DNMT1-230	197 .. 4956	4760 bp	CDS

6 segments = 837 bp

/codon_start = 1
/note = coding sequence ENSP00000504236
/translation = VYCKHGHLCPIDTGLIEKNIELFFSGSAKPIYDDDPSLE,,GGVNGKNLGPINEWWITGFDGGEKALIGFST,,SFAEYILMDPSPEYAPIFGLMQE
KIYISKIVVEFLQSNSDSTYEDLINKIE,,TTVPPSGLNLNRFTEDSLLRHAQFVVEQVESYDEAGDSDEQPIFLTPCMRDLIKLAGVTLGQR,,R
AQARRQTIRHSTREKDRGPTKATTTKLVYQIFDTFFAEQIEKDDREDKENAFKRRRCGVCE,,VCQQPECGKCKACKDMVKFGGSGRSKQAC
QFR
279 amino acids = 31.4 kDa

Feature	Location	Size	Type
DNMT1-241	197 .. 4956	4760 bp	CDS

6 segments = 837 bp

/codon_start = 1
/note = coding sequence ENSP00000504202
/translation = VYCKHGHLCPIDTGLIEKNIELFFSGSAKPIYDDDPSLE,,GGVNGKNLGPINEWWITGFDGGEKALIGFST,,SFAEYILMDPSPEYAPIFGLMQE
KIYISKIVVEFLQSNSDSTYEDLINKIE,,TTVPPSGLNLNRFTEDSLLRHAQFVVEQVESYDEAGDSDEQPIFLTPCMRDLIKLAGVTLGQR,,R
AQARRQTIRHSTREKDRGPTKATTTKLVYQIFDTFFAEQIEKDDREDKENAFKRRRCGVCE,,VCQQPECGKCKACKDMVKFGGSGRSKQAC
QFR
279 amino acids = 31.4 kDa

Feature	Location	Size	Type
DNMT1-247	197 .. 4956	4760 bp	CDS

6 segments = 837 bp

/codon_start = 1
/note = coding sequence ENSP00000503853
/translation = VYCKHGHLCPIDTGLIEKNIELFFSGSAKPIYDDDPSLE,,GGVNGKNLGPINEWWITGFDGGEKALIGFST,,SFAEYILMDPSPEYAPIFGLMQE
KIYISKIVVEFLQSNSDSTYEDLINKIE,,TTVPPSGLNLNRFTEDSLLRHAQFVVEQVESYDEAGDSDEQPIFLTPCMRDLIKLAGVTLGQR,,R
AQARRQTIRHSTREKDRGPTKATTTKLVYQIFDTFFAEQIEKDDREDKENAFKRRRCGVCE,,VCQQPECGKCKACKDMVKFGGSGRSKQAC
QFR
279 amino acids = 31.4 kDa

Feature	Location	Size	Type
DNMT1-251	197 .. 4956	4760 bp	CDS

6 segments = 837 bp

/codon_start = 1
/note = coding sequence ENSP00000503151
/translation = VYCKHGHLCPIDTGLIEKNIELFFSGSAKPIYDDDPSLE,,GGVNGKNLGPINEWWITGFDGGEKALIGFST,,SFAEYILMDPSPEYAPIFGLMQE
KIYISKIVVEFLQSNSDSTYEDLINKIE,,TTVPPSGLNLNRFTEDSLLRHAQFVVEQVESYDEAGDSDEQPIFLTPCMRDLIKLAGVTLGQR,,R
AQARRQTIRHSTREKDRGPTKATTTKLVYQIFDTFFAEQIEKDDREDKENAFKRRRCGVCE,,VCQQPECGKCKACKDMVKFGGSGRSKQAC
QFR
279 amino acids = 31.4 kDa

Feature	Location	Size	Type
DNMT1-252	197 .. 4956	4760 bp	CDS

6 segments = 837 bp

/codon_start = 1
/note = coding sequence ENSP00000504512
/translation = VYCKHGHLCPIDTGLIEKNIELFFSGSAKPIYDDDPSLE,,GGVNGKNLGPINEWWITGFDGGEKALIGFST,,SFAEYILMDPSPEYAPIFGLMQE
KIYISKIVVEFLQSNSDSTYEDLINKIE,,TTVPPSGLNLNRFTEDSLLRHAQFVVEQVESYDEAGDSDEQPIFLTPCMRDLIKLAGVTLGQR,,R
AQARRQTIRHSTREKDRGPTKATTTKLVYQIFDTFFAEQIEKDDREDKENAFKRRRCGVCE,,VCQQPECGKCKACKDMVKFGGSGRSKQAC
QFR
279 amino acids = 31.4 kDa

✓	Feature	Location	Size	Type
✓	**Donor Template WT -> SNV**	1624 .. 1723	100 bp	misc_feature
✓	**PAM**	1683 .. 1685	3 bp	misc_feature
✓	**Protospacer Sequence**	1686 .. 1705	20 bp	misc_feature
✓	**SNV**	1689 .. 1689	1 bp	misc_feature

/note = WT = A
SNV = G

Feature			Location			Size			Type
DNMT1-208			1729	..	5058	3330 bp			prim_transcript
/note	=	primary transcript ENST00000586799 Nonsense mediated decay							
DNMT1-250			4701	..	5058	358 bp			prim_transcript
/note	=	primary transcript ENST00000679100 Retained intron							
DNMT1-245			4959	..	5058	100 bp			prim_transcript
/note	=	primary transcript ENST00000678647 Retained intron							
DNMT1-207			5009	..	5058	50 bp			prim_transcript
/note	=	primary transcript ENST00000586667 Retained intron							

	Primer	Length	Binding Sites		Tm	Date Added
✓	**PCR Forward**	25-mer	1013 .. 1037	→	58°C	Nov 10, 2022
	/sequence = TTAGTTATGACTGGCTCTGGAACTG 44% GC / 7703.1 Da					
✓	**Sanger Sequencing**	20-mer	1526 .. 1545	→	57°C	Nov 10, 2022
	/sequence = ACATTTGGGTACGGGATGAC 50% GC / 6197.1 Da					
✓	**Donor Template WT -> SNV**	100-mer	1624 .. 1723	→	78°C	Nov 10, 2022
	/sequence = TTCCACACCTCCTCTGTTCACCCCAGCATTTGCCGAATACATTCTGATGGATCCCAGTCCCGAGTGTGCGCCCATATTTGGGCTGATG 64% GC / 30431.8 Da					
✓	**gRNA Protospacer**	20-mer	1686 .. 1705	←	57°C	Nov 9, 2022
	/sequence = CCCAAATATGGGCGCATACT 50% GC / 6086.0 Da					
✓	**PCR Reverse**	25-mer	2327 .. 2351	←	57°C	Nov 10, 2022
	/sequence = CAATTTGCTCTGCGAAGAAAGTATC 40% GC / 7665.1 Da					