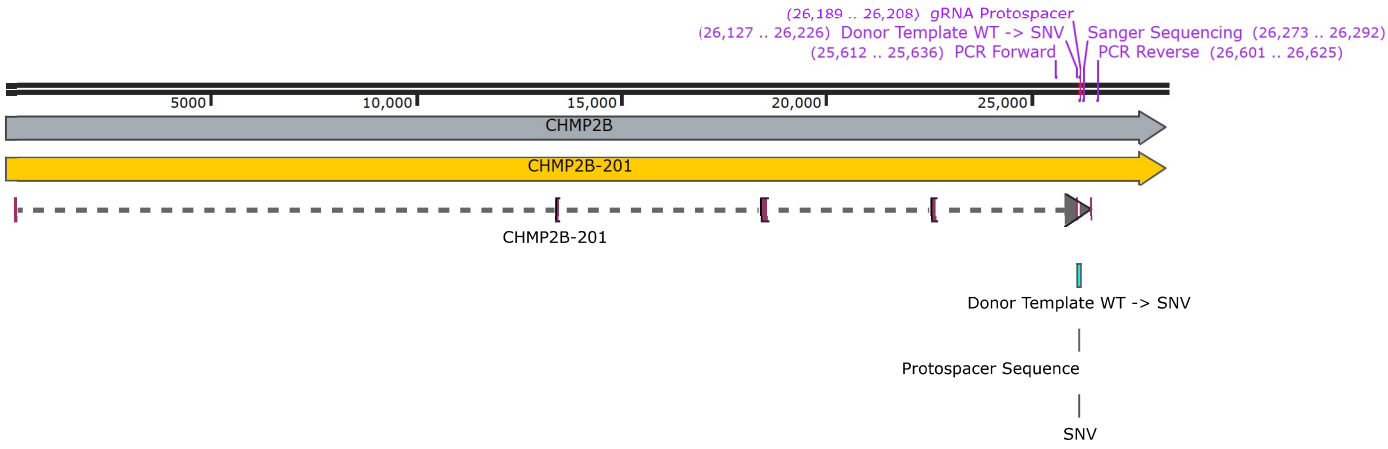

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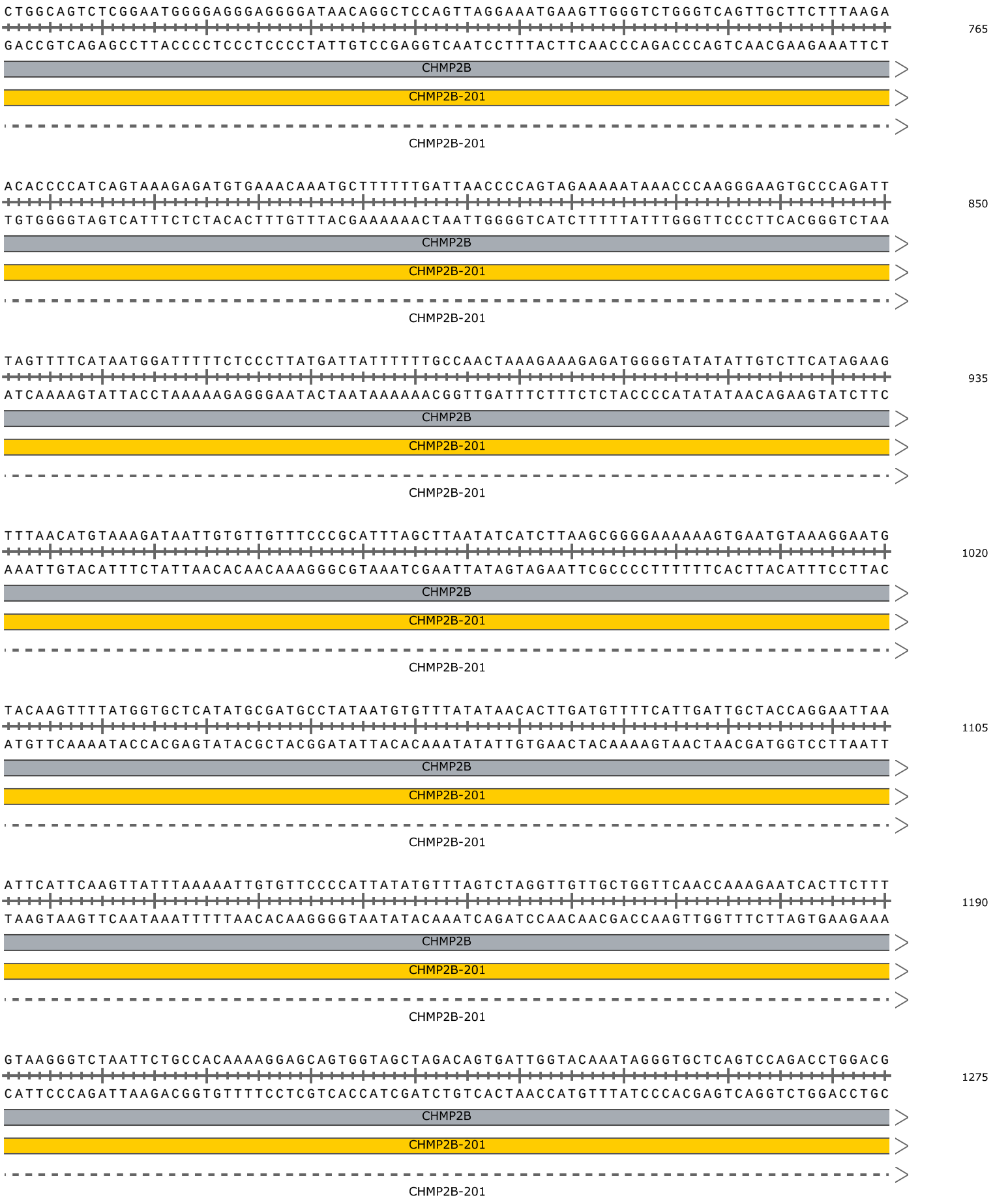
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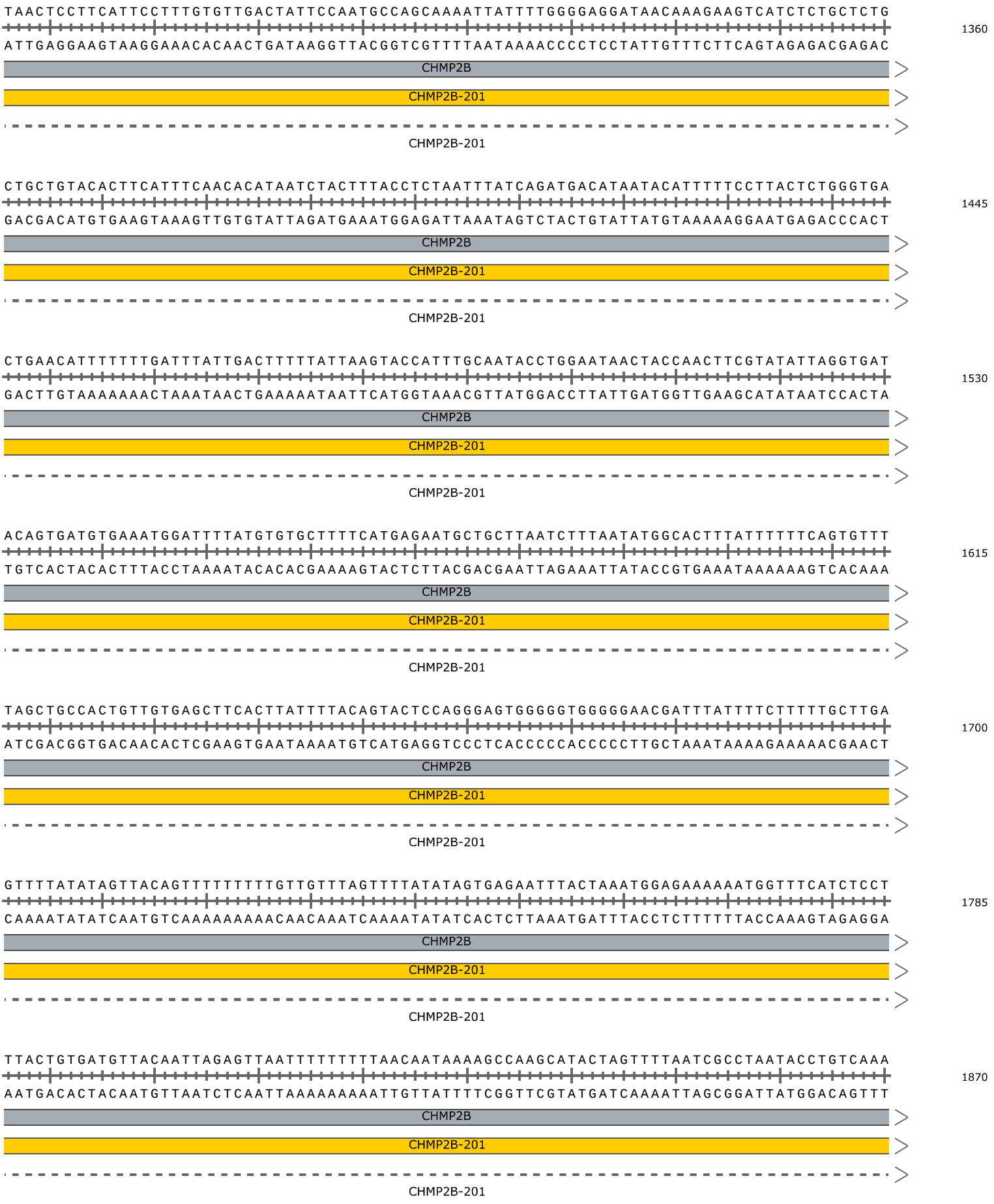
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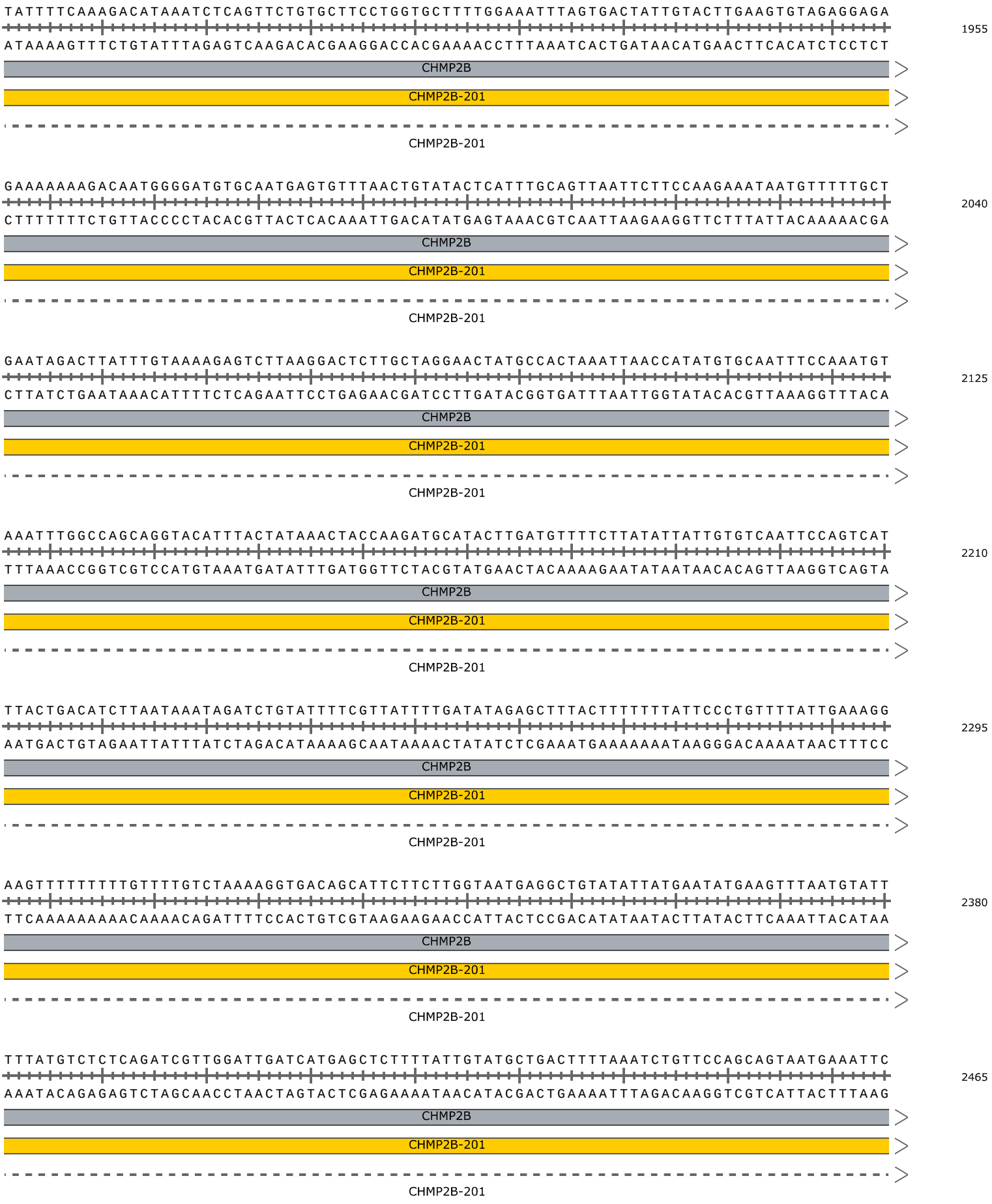
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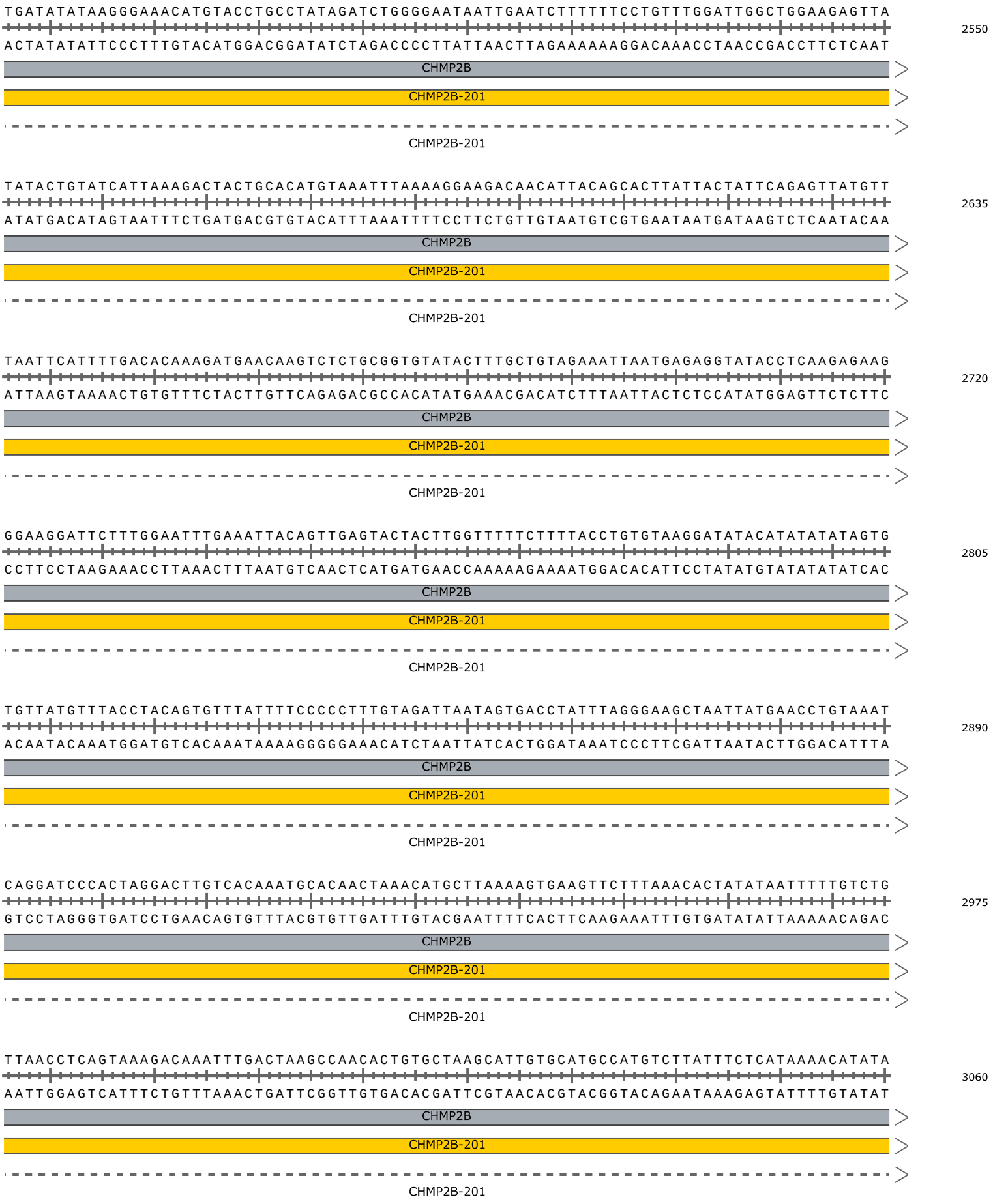
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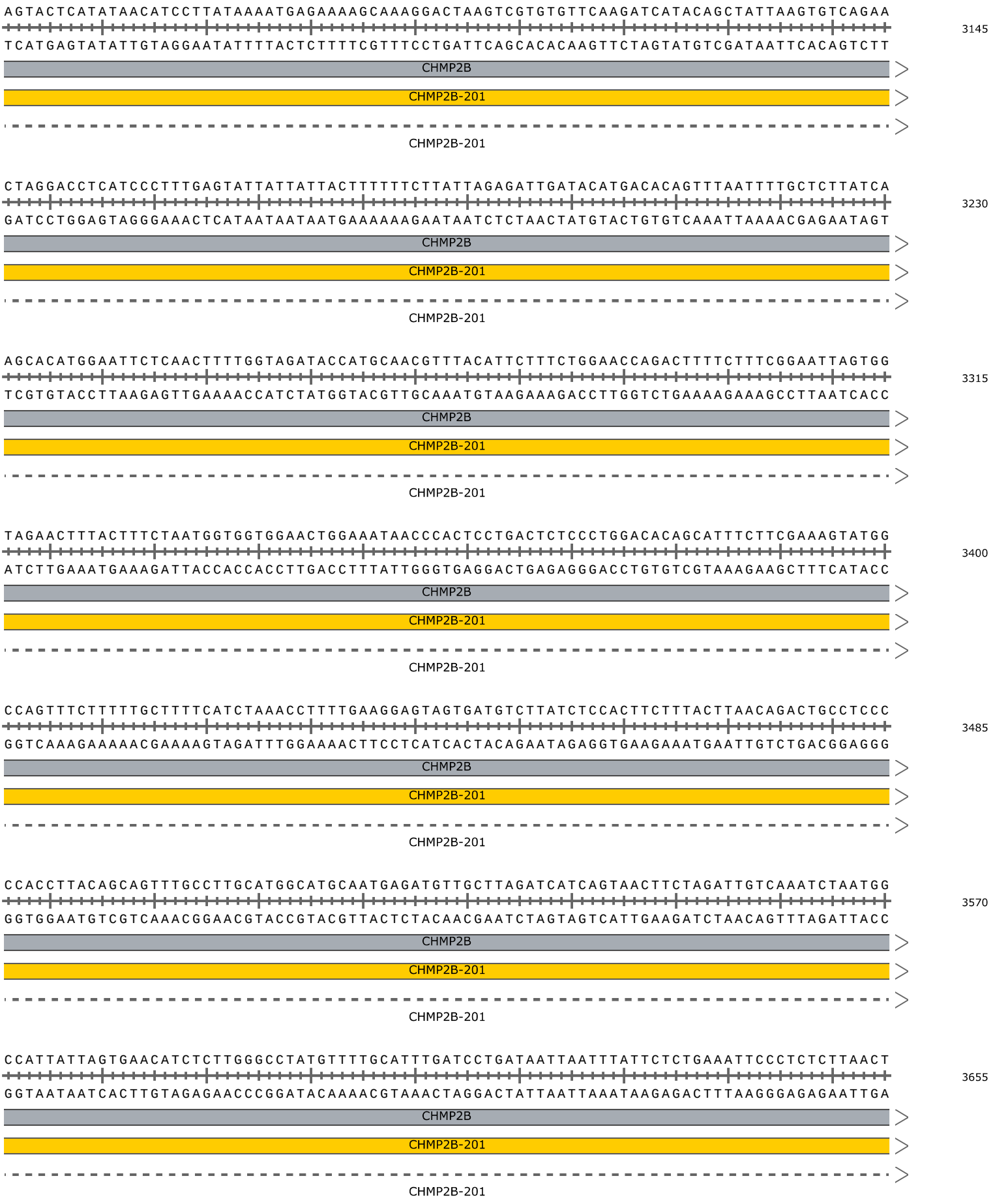
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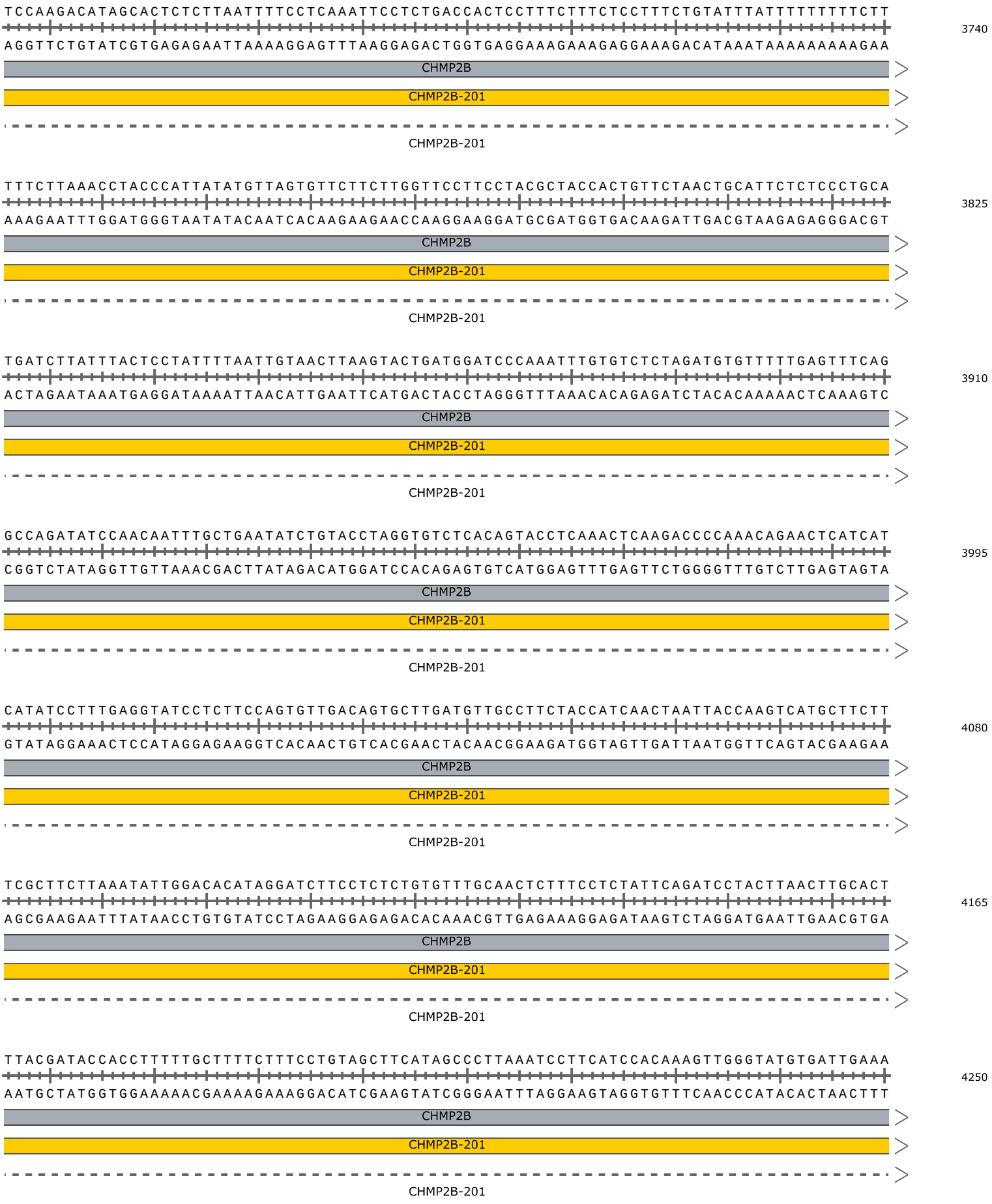
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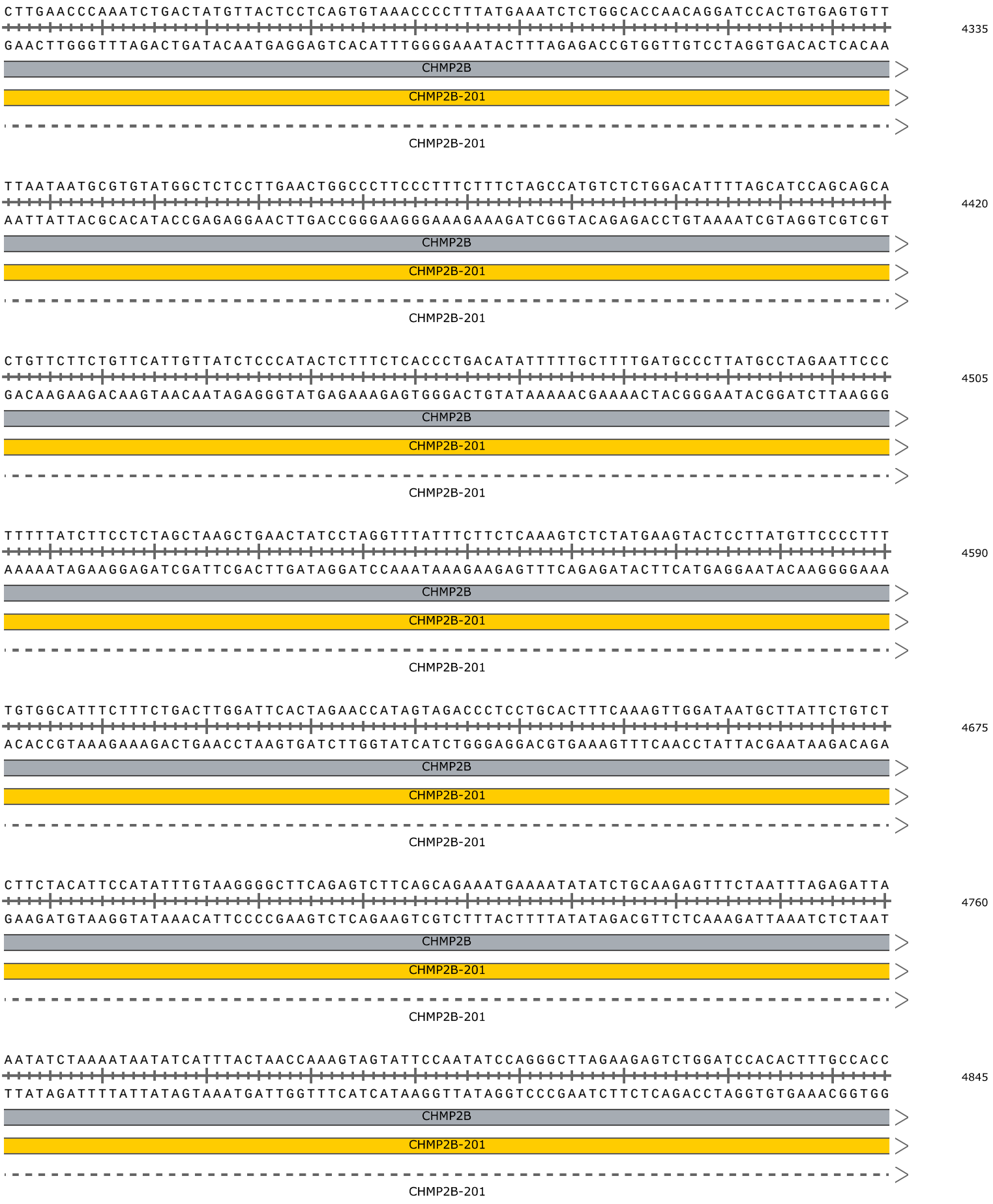
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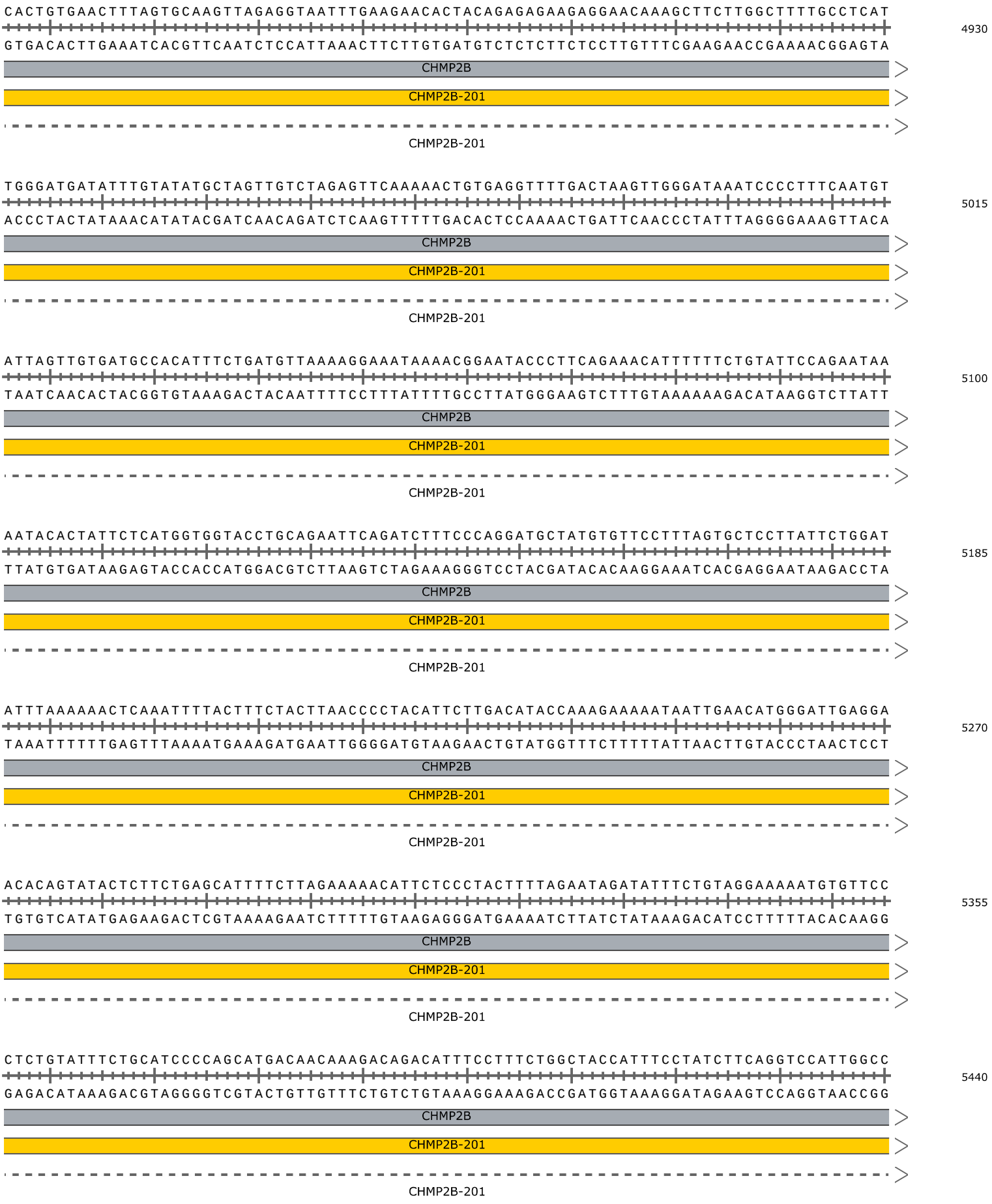
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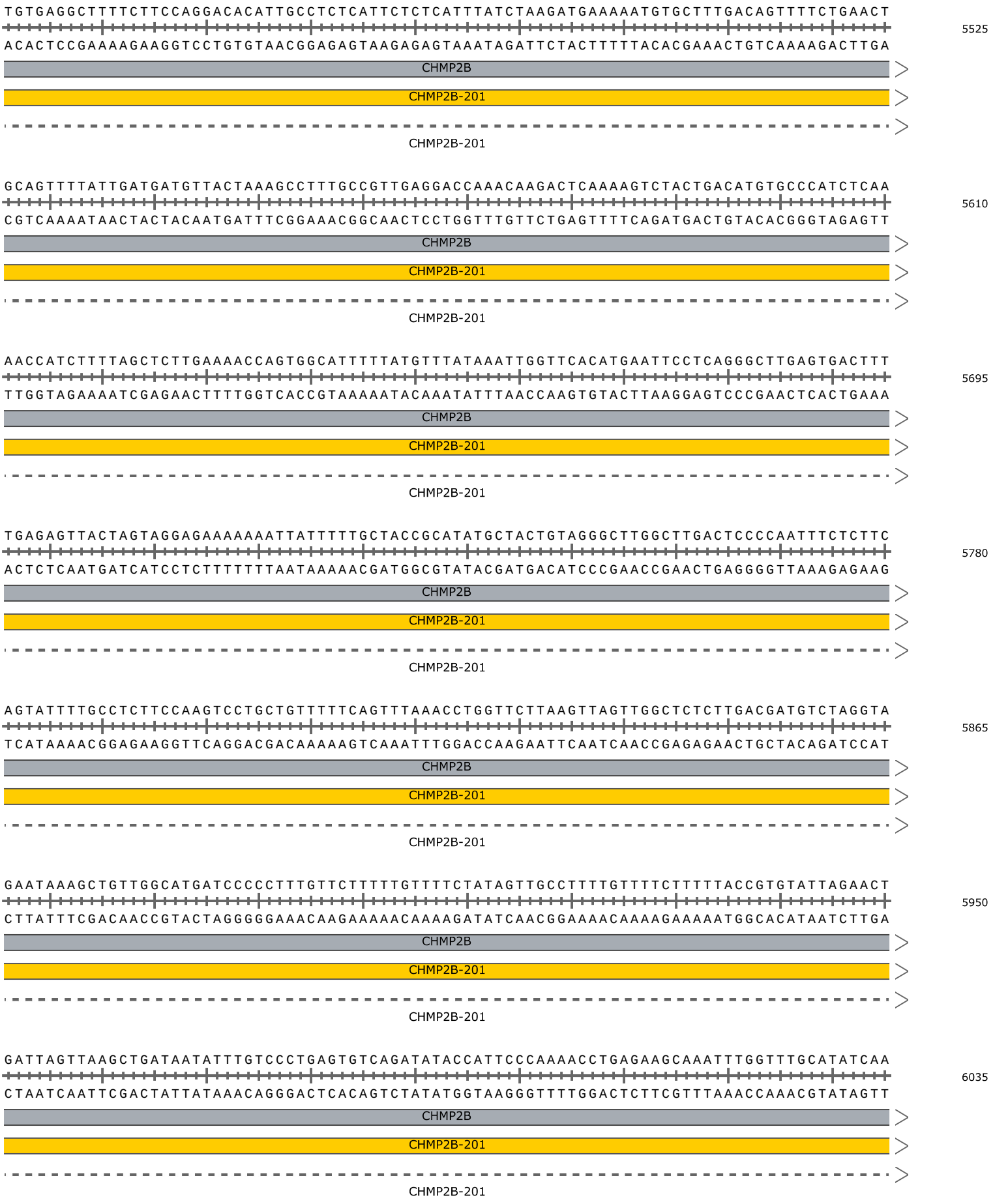
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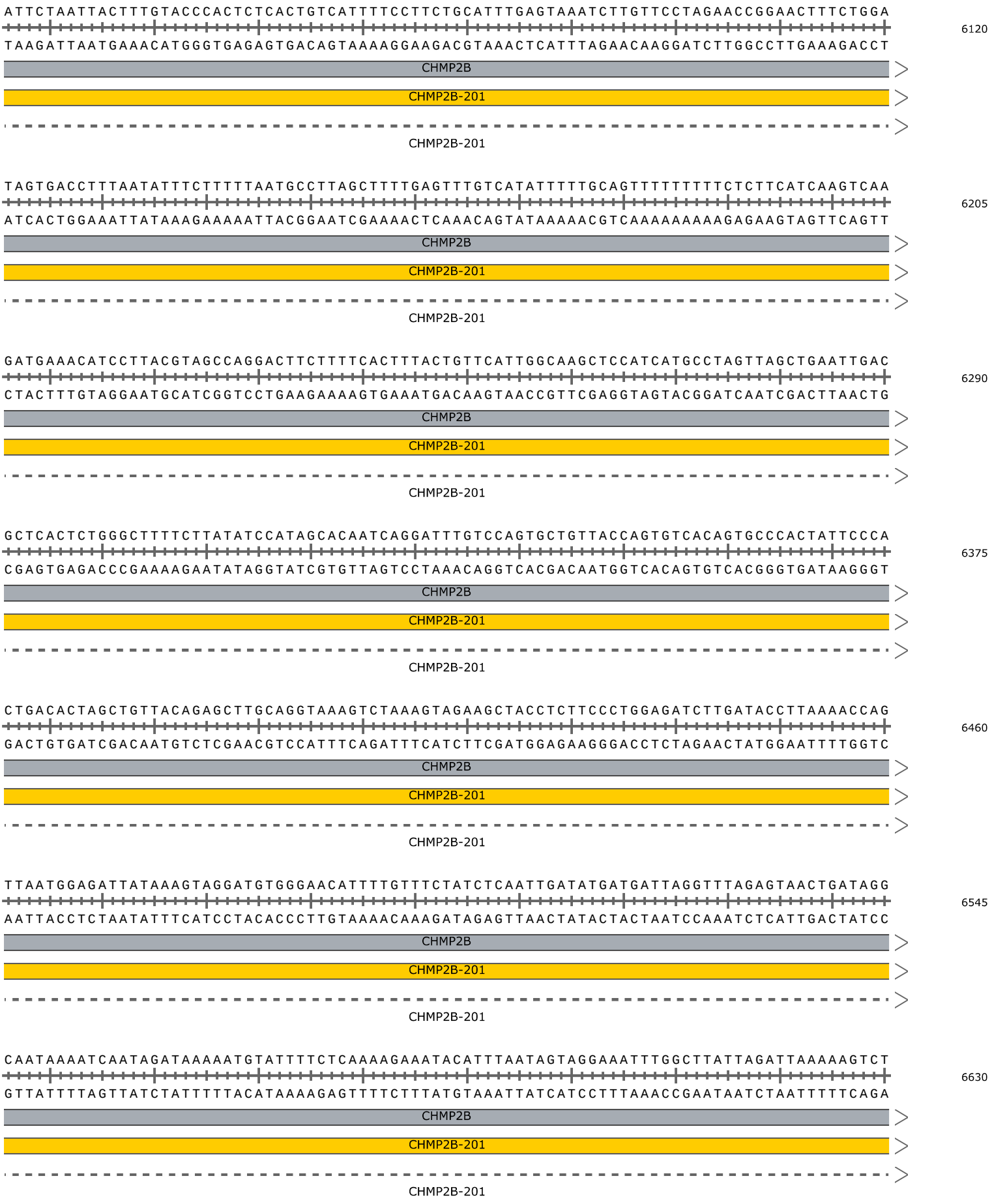
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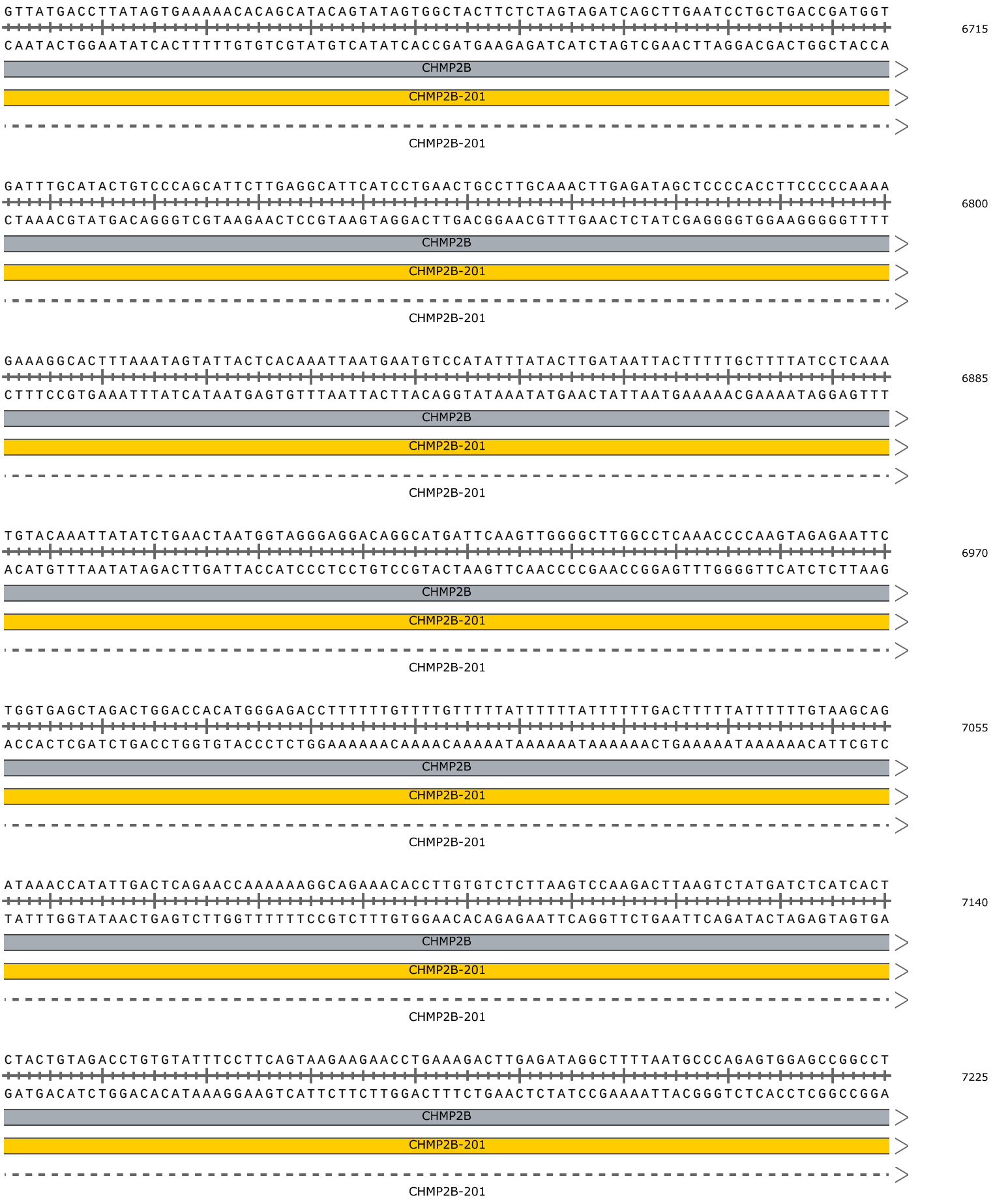
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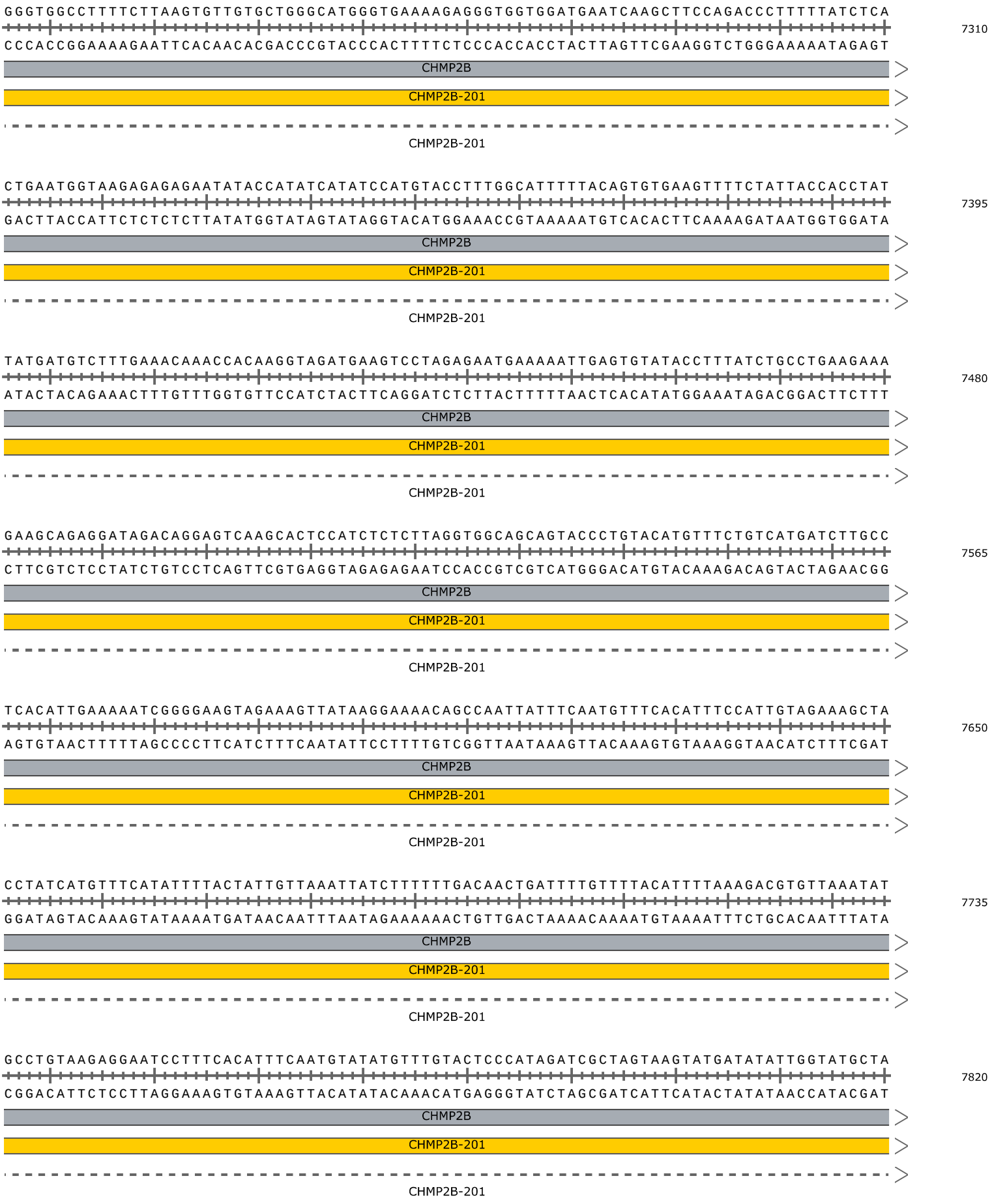
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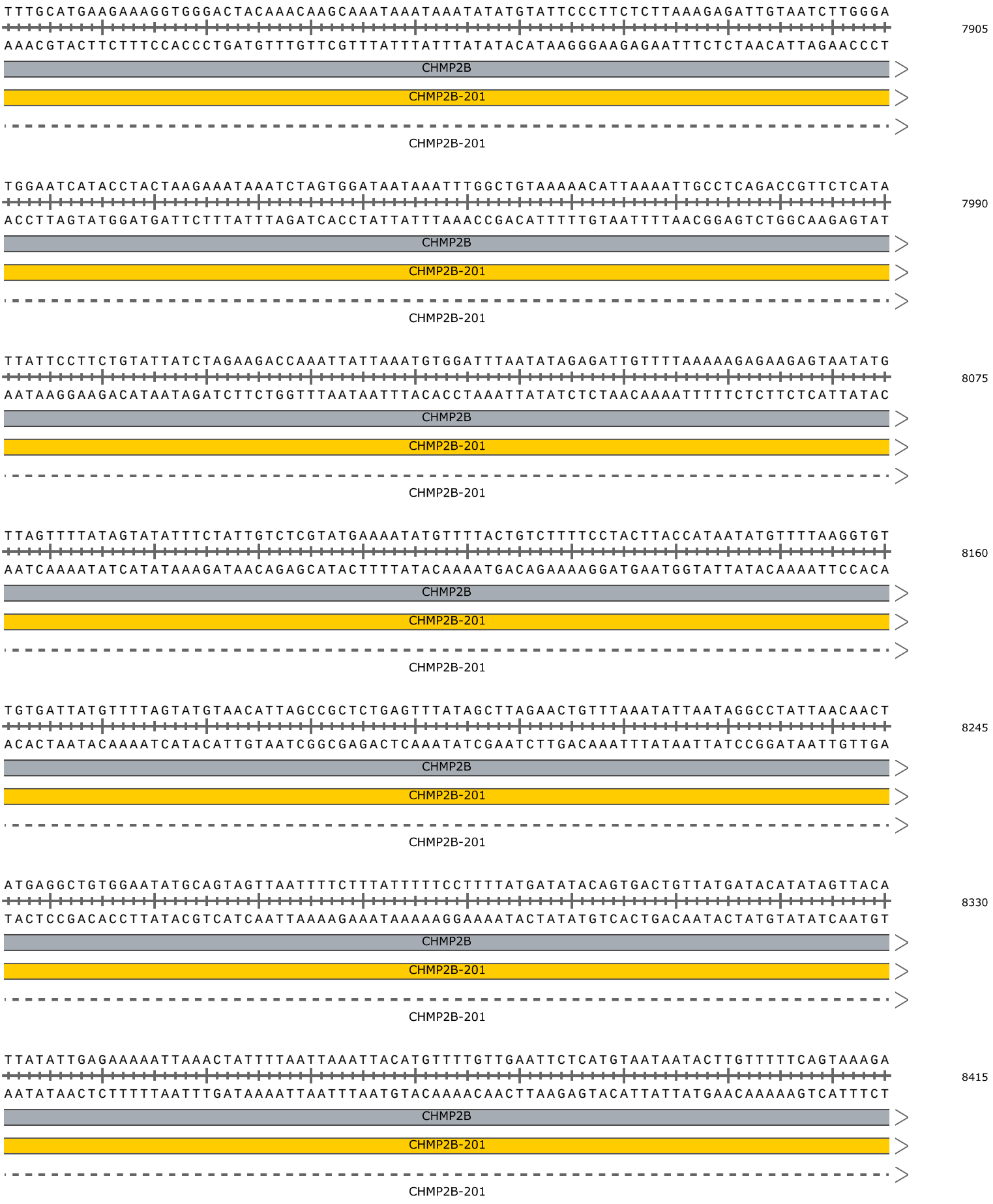
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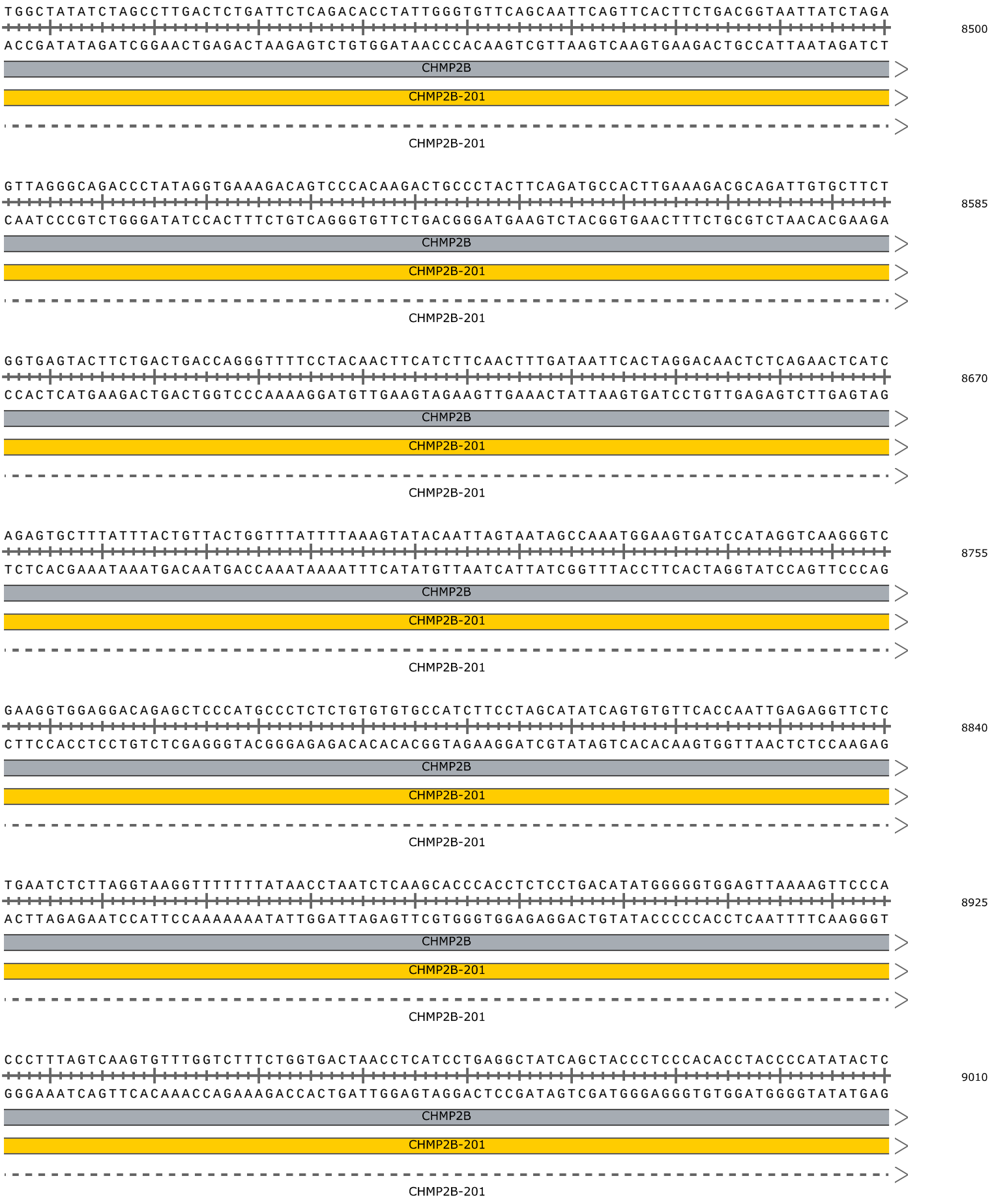
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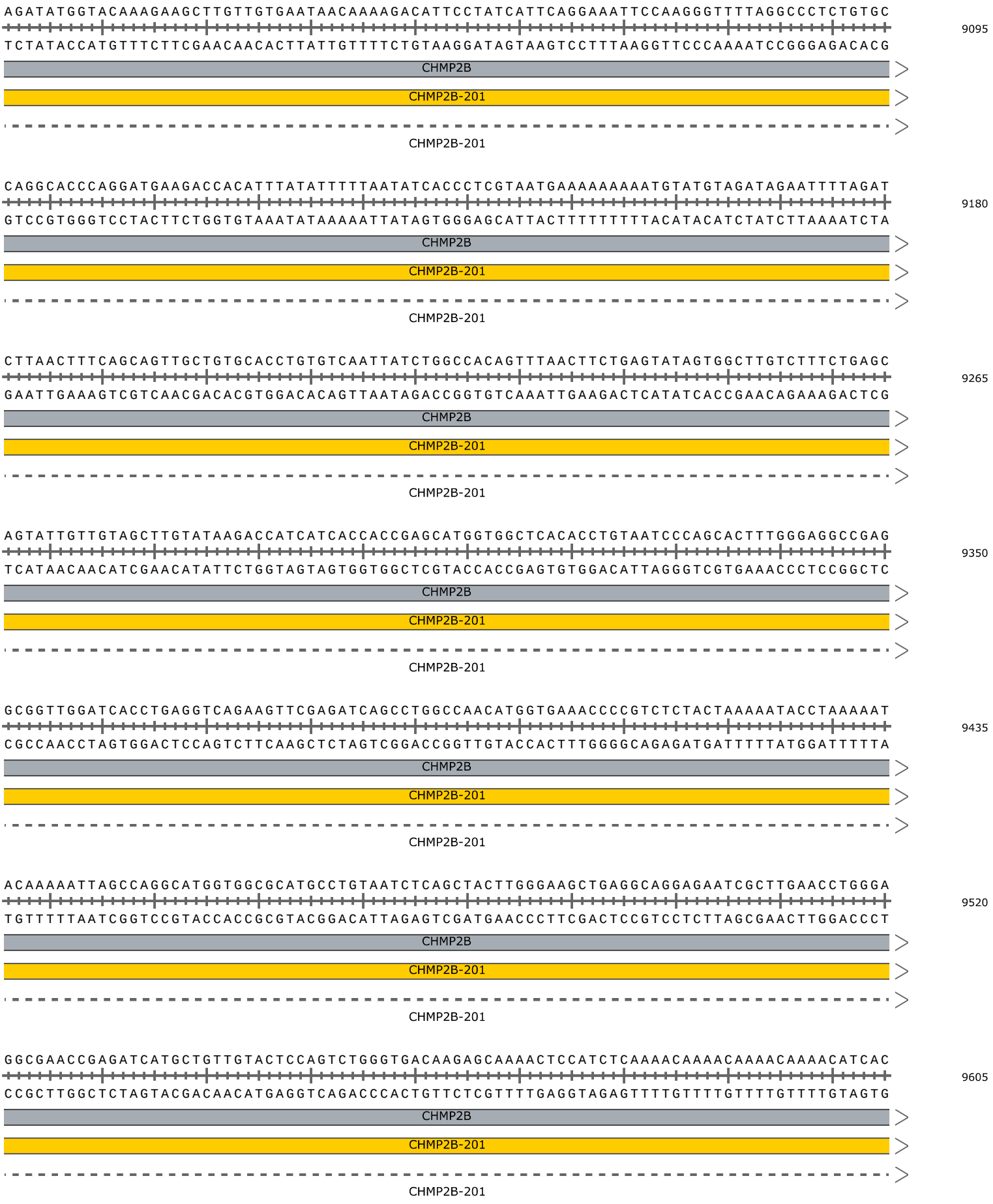
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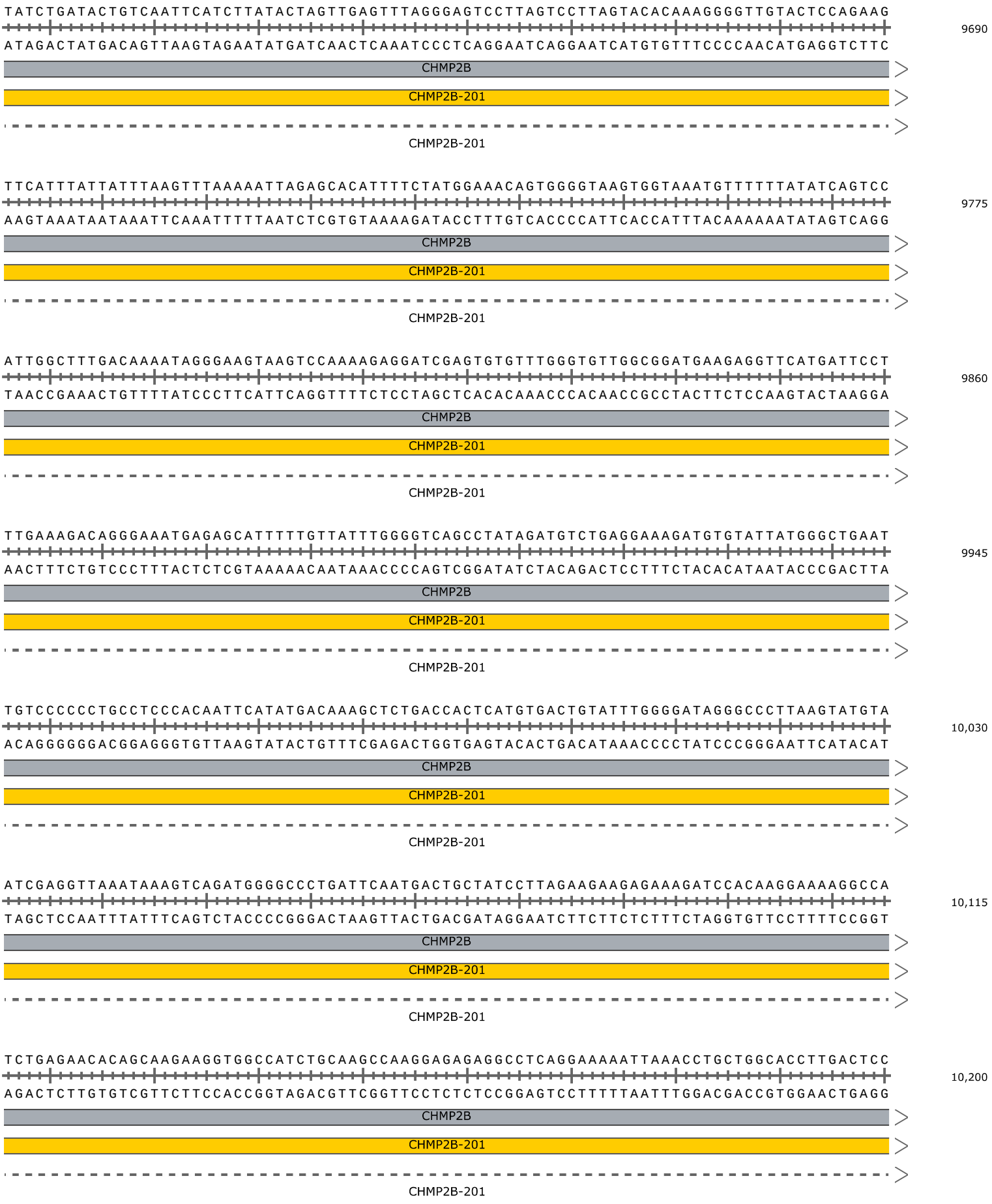
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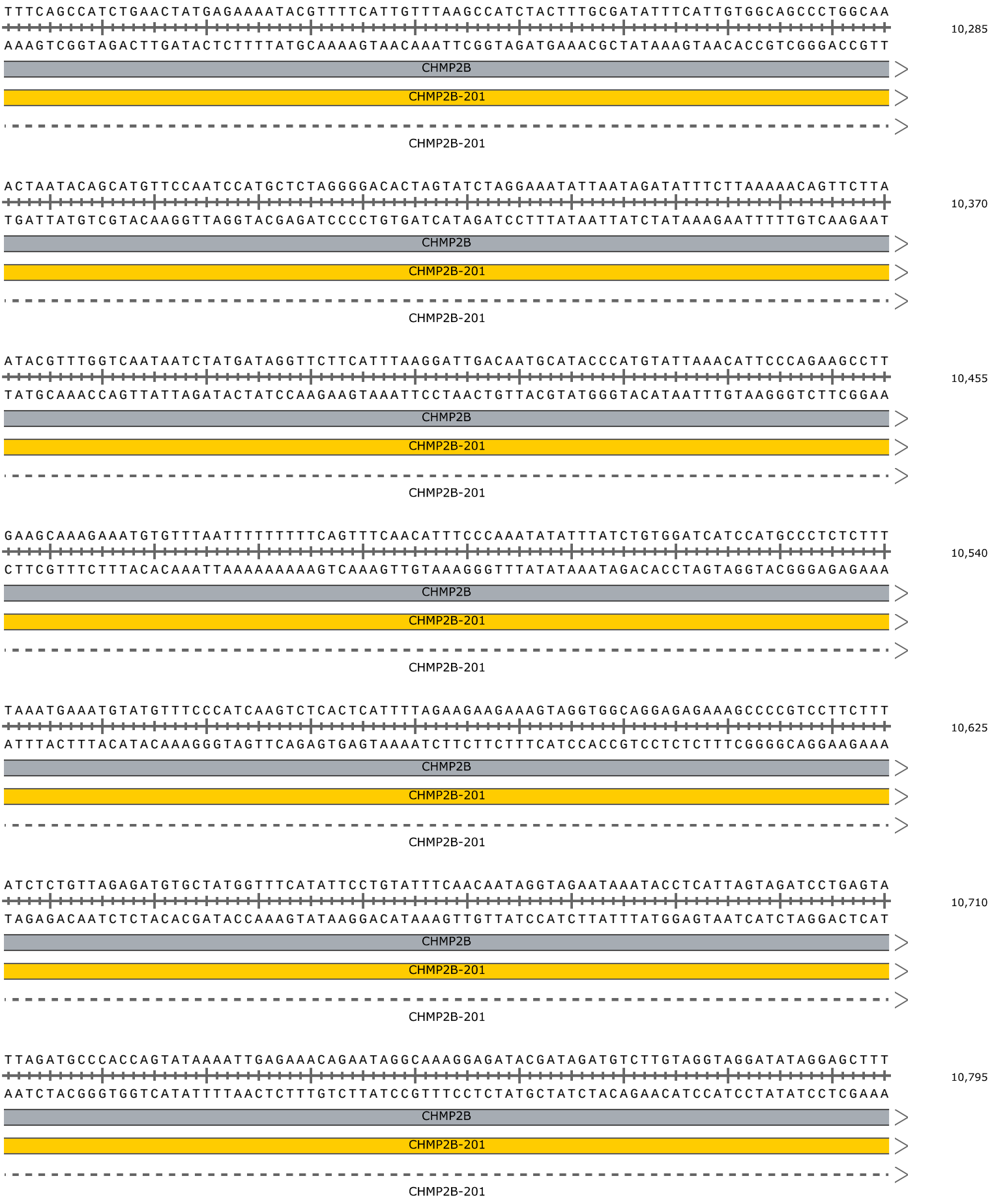
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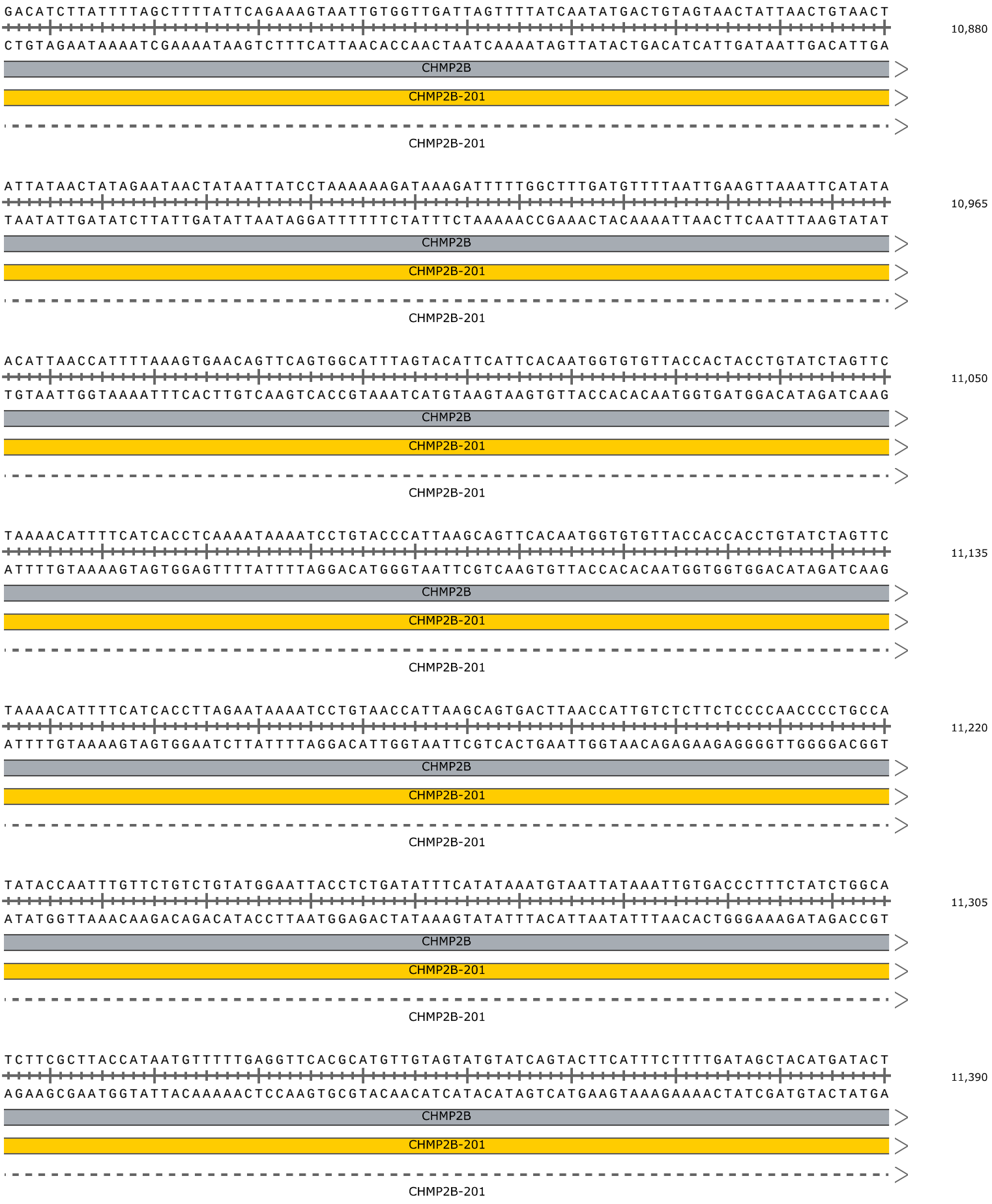
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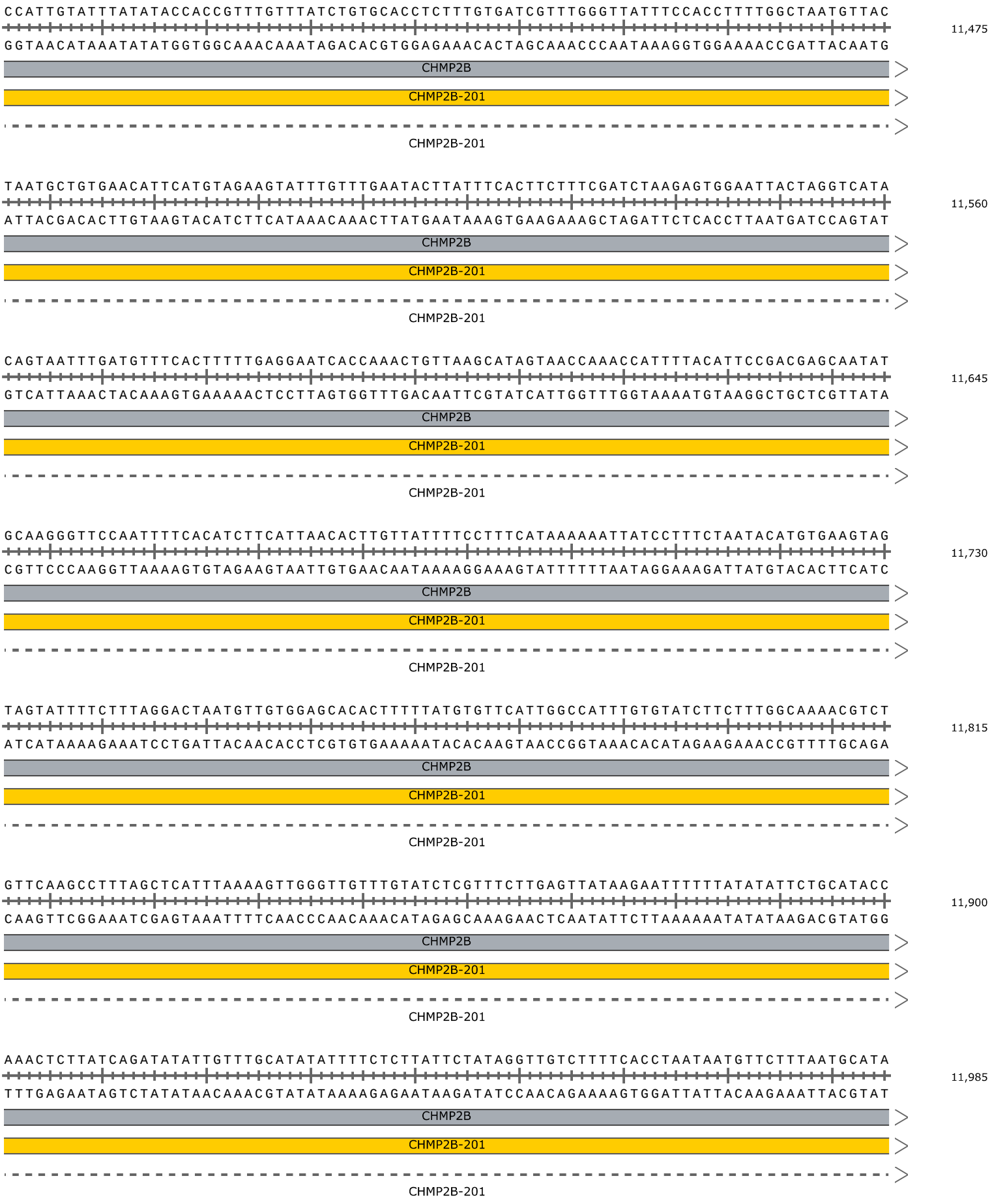
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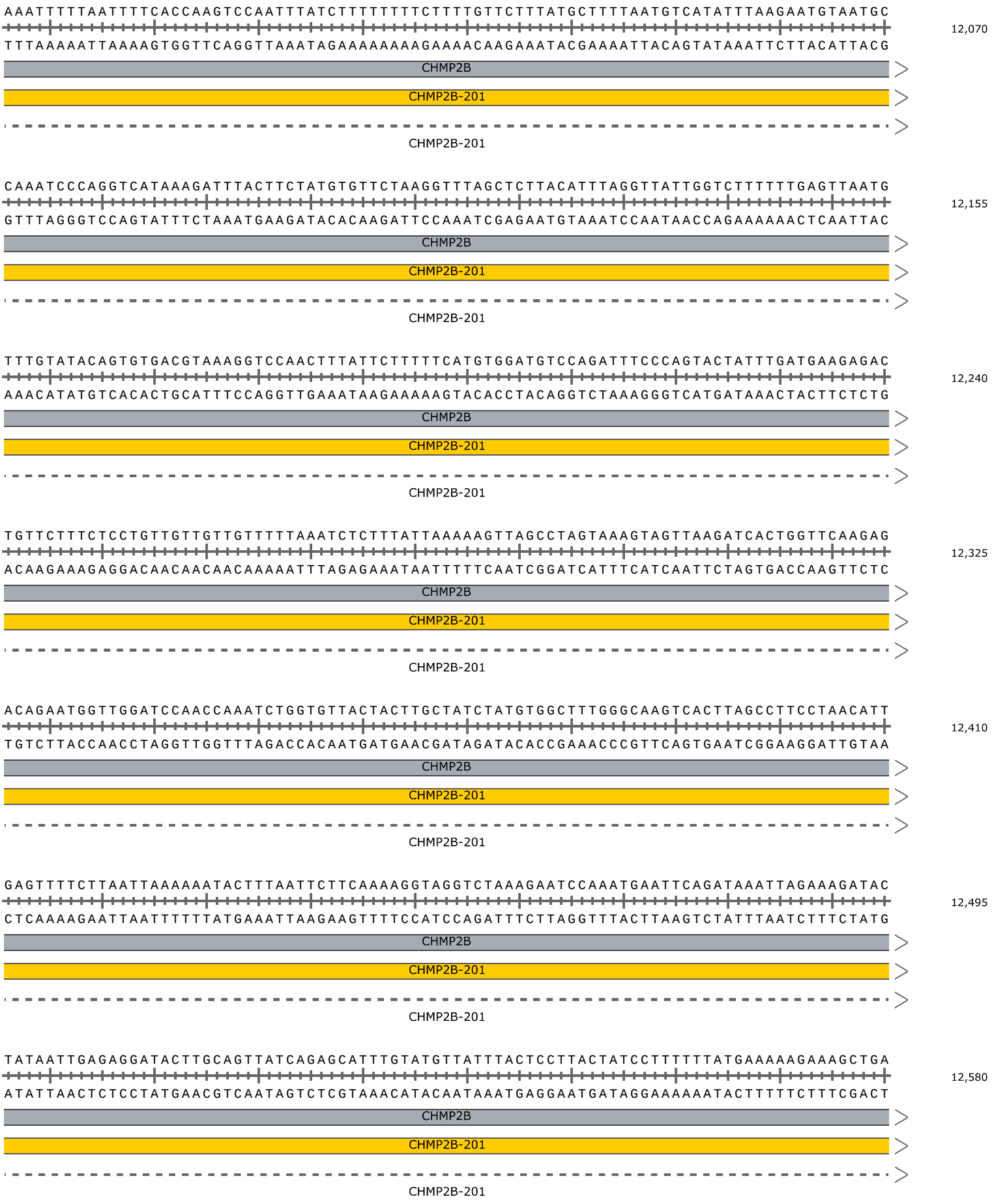
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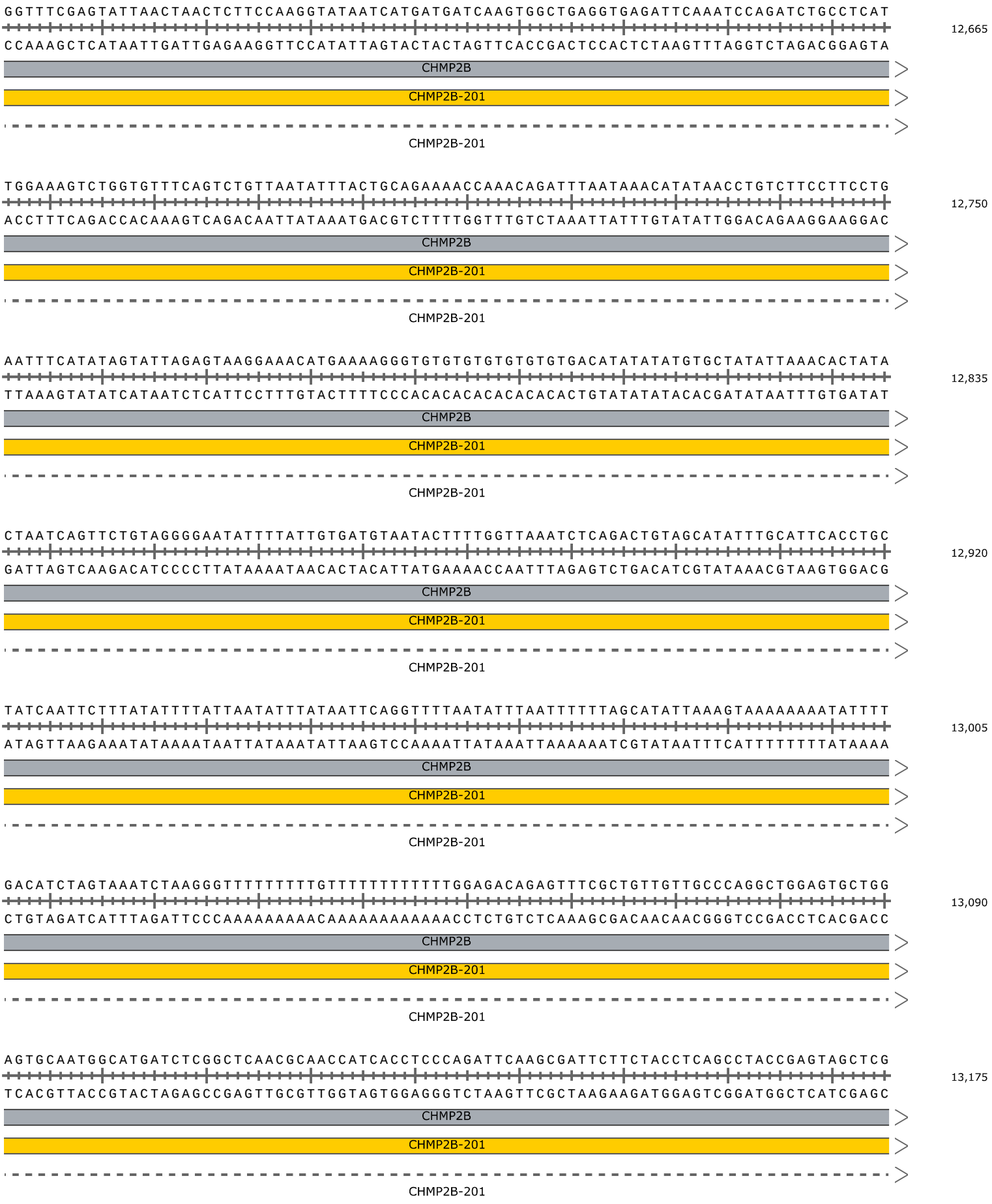
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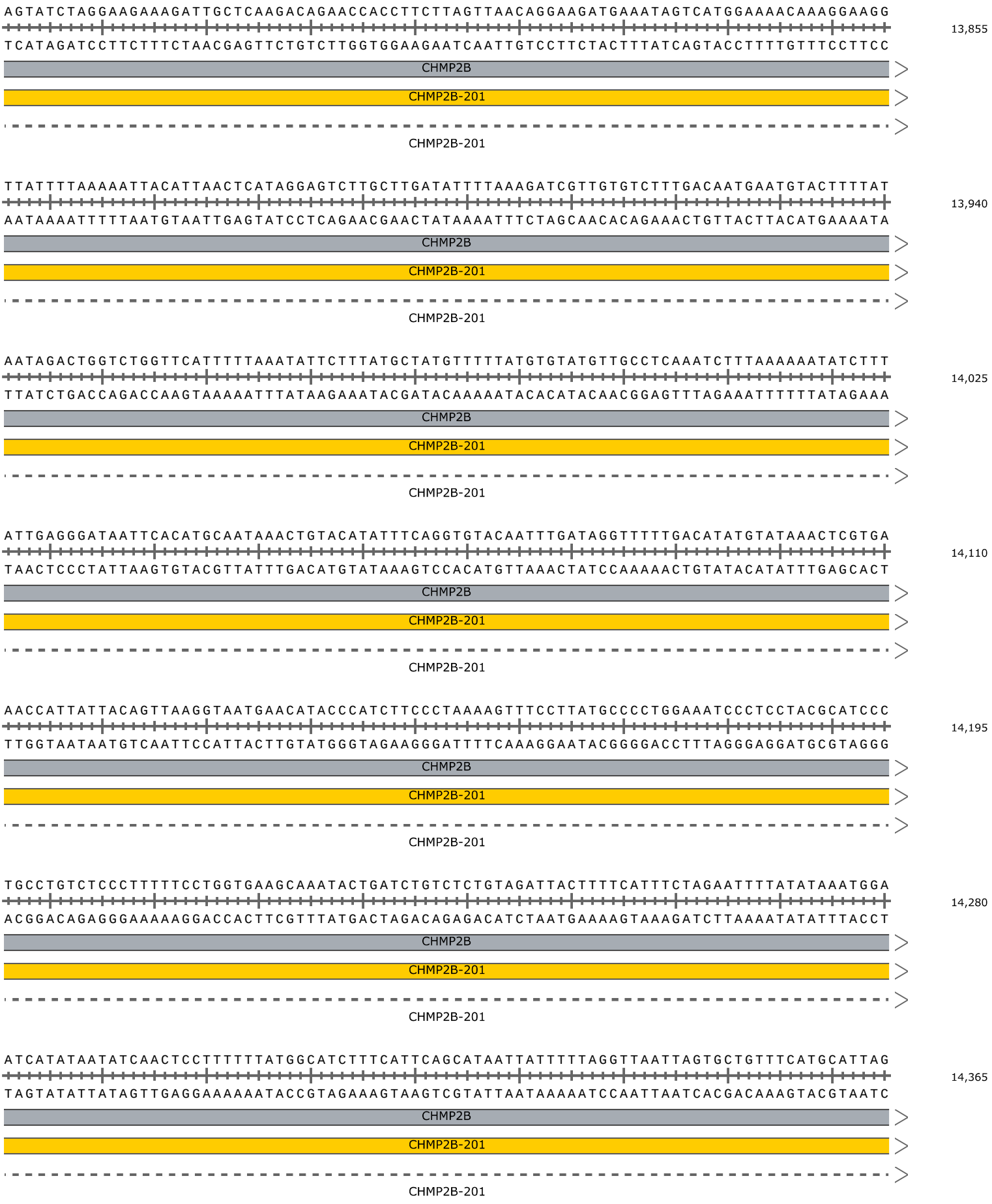
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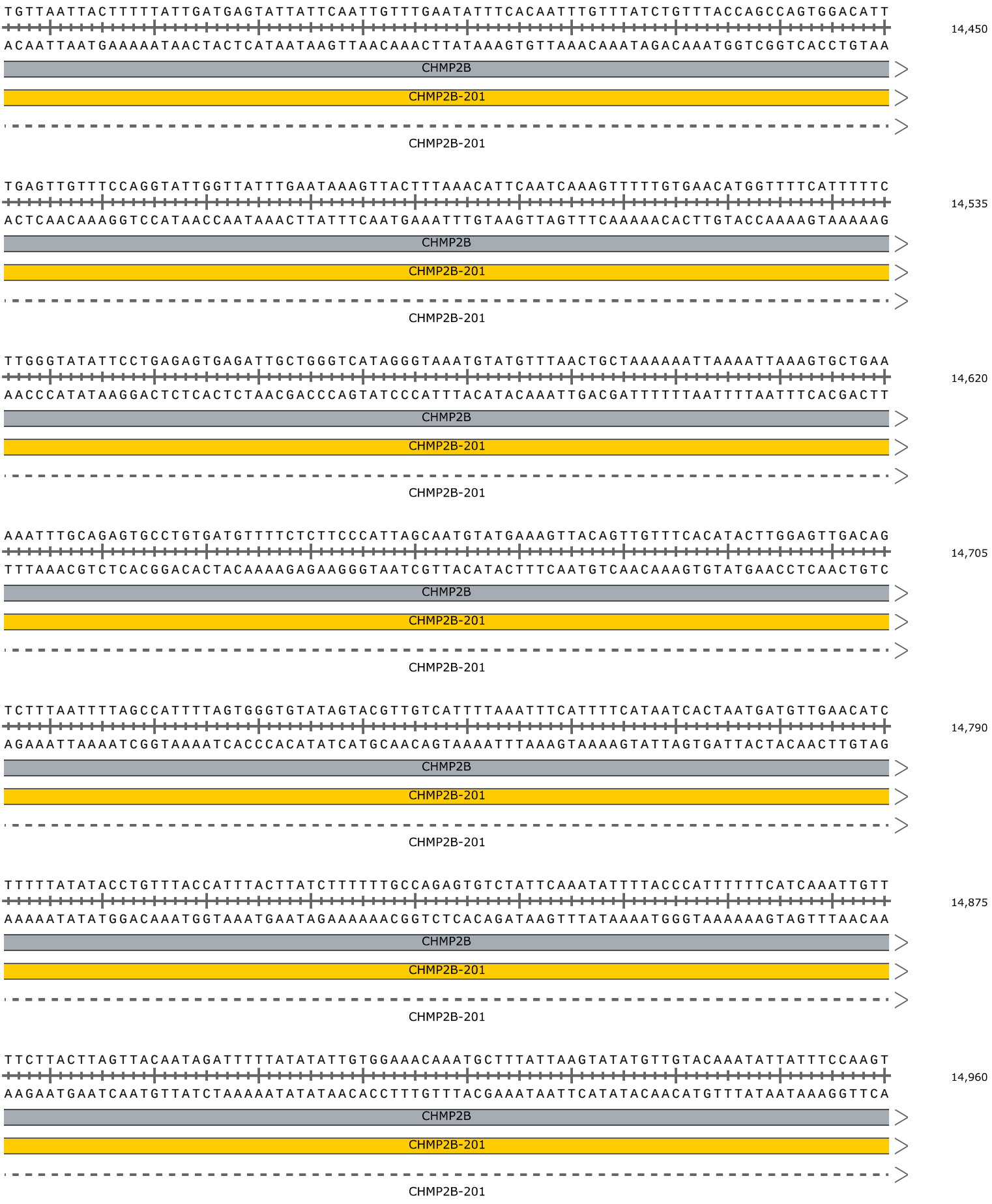
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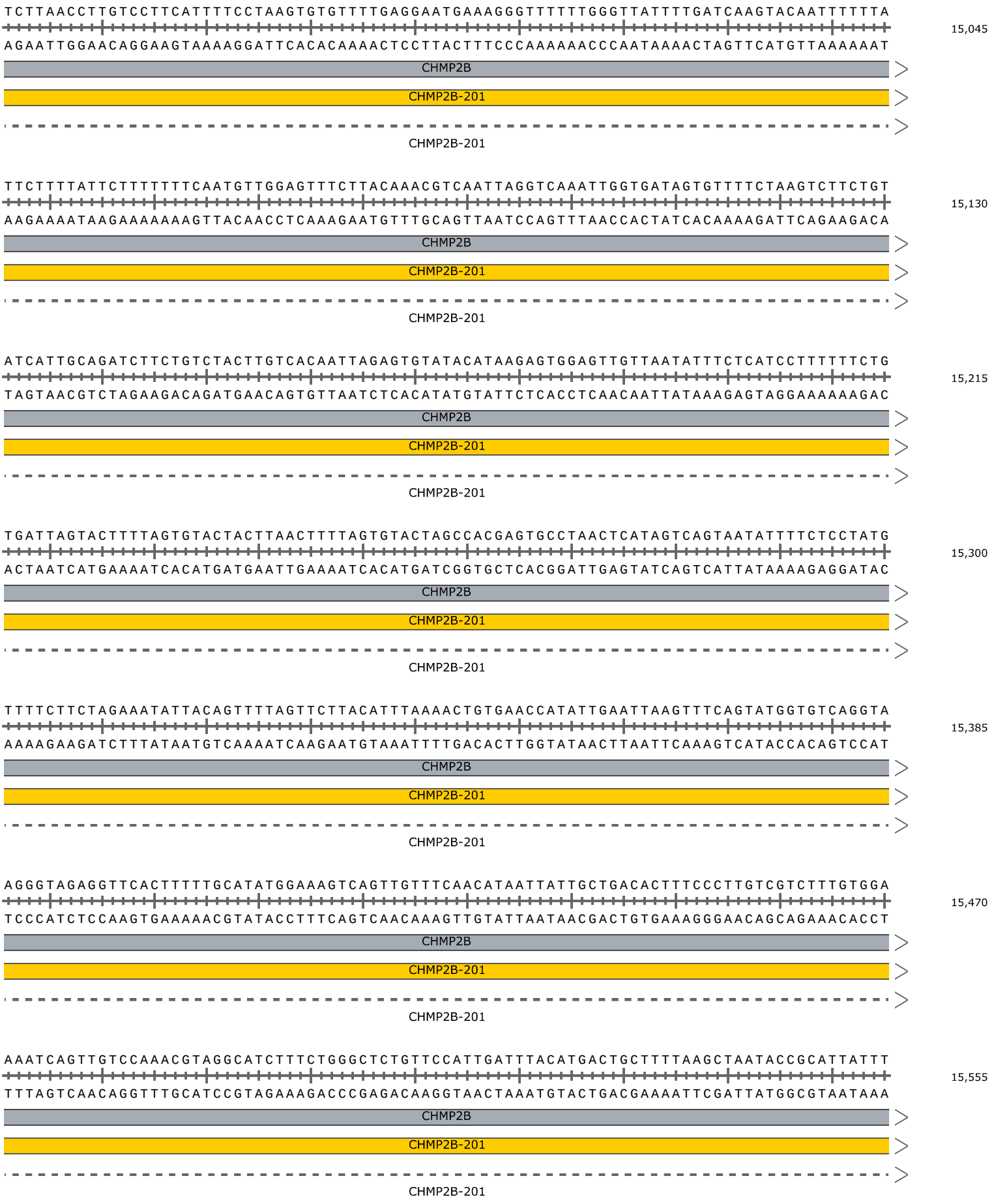
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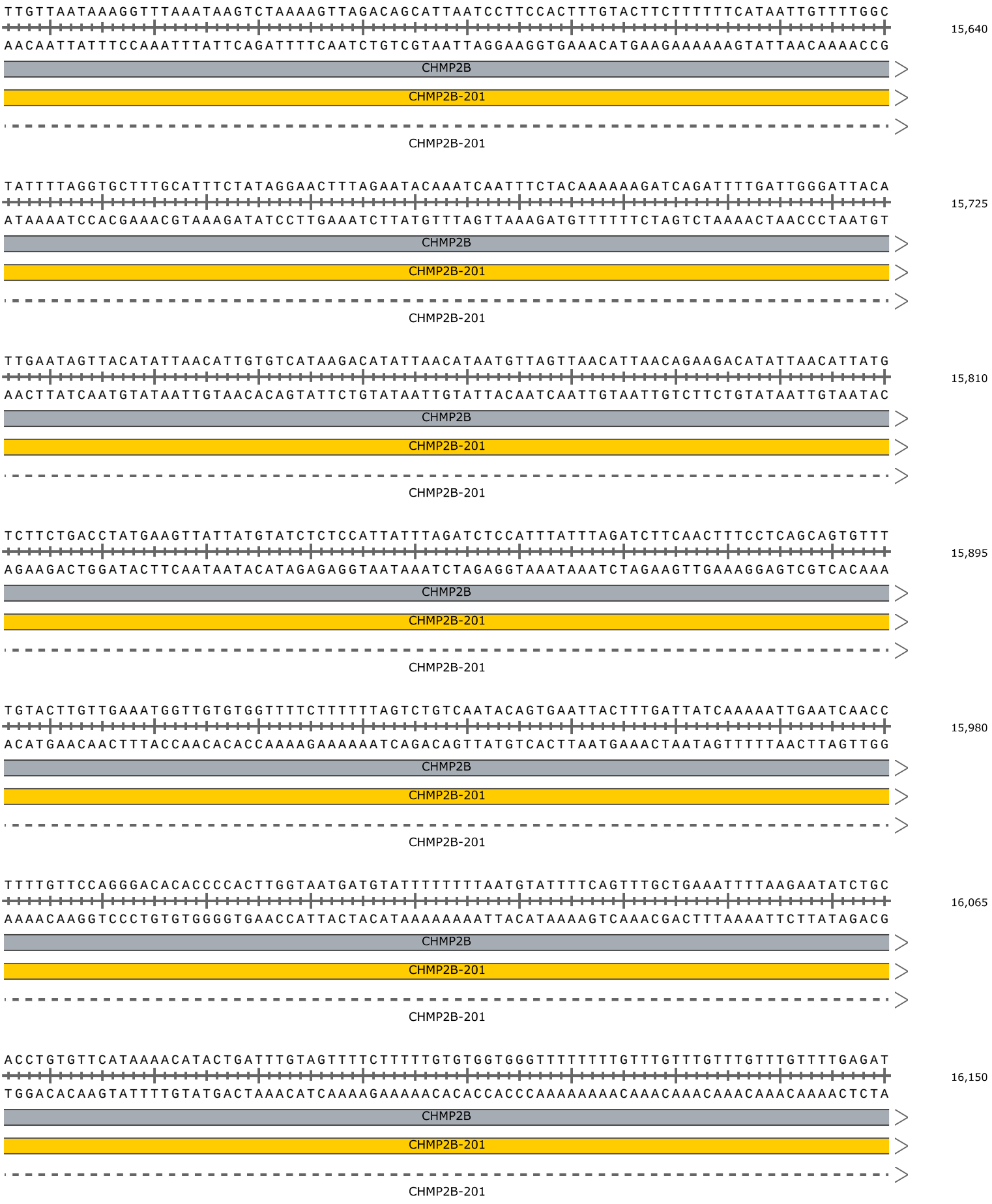
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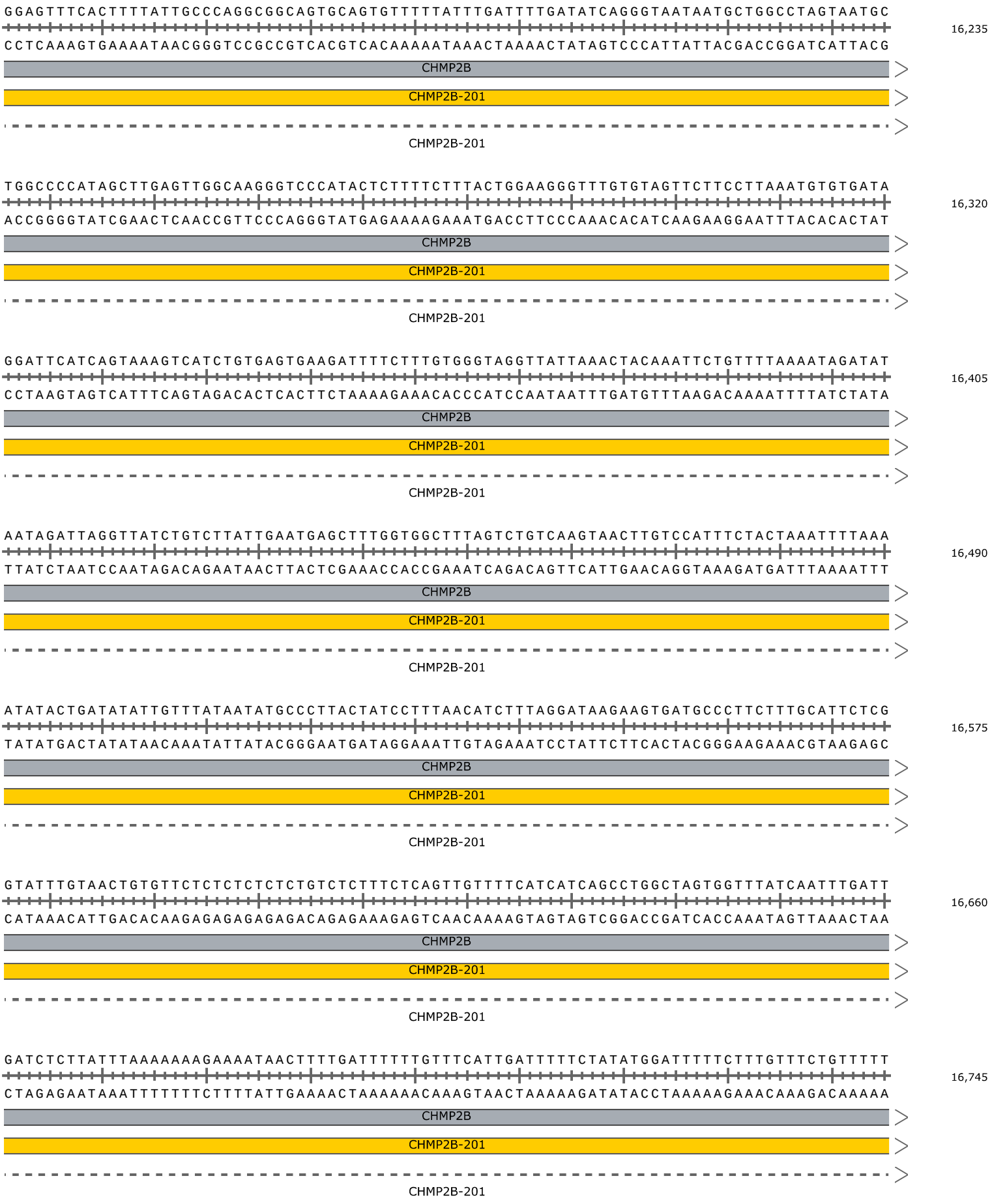
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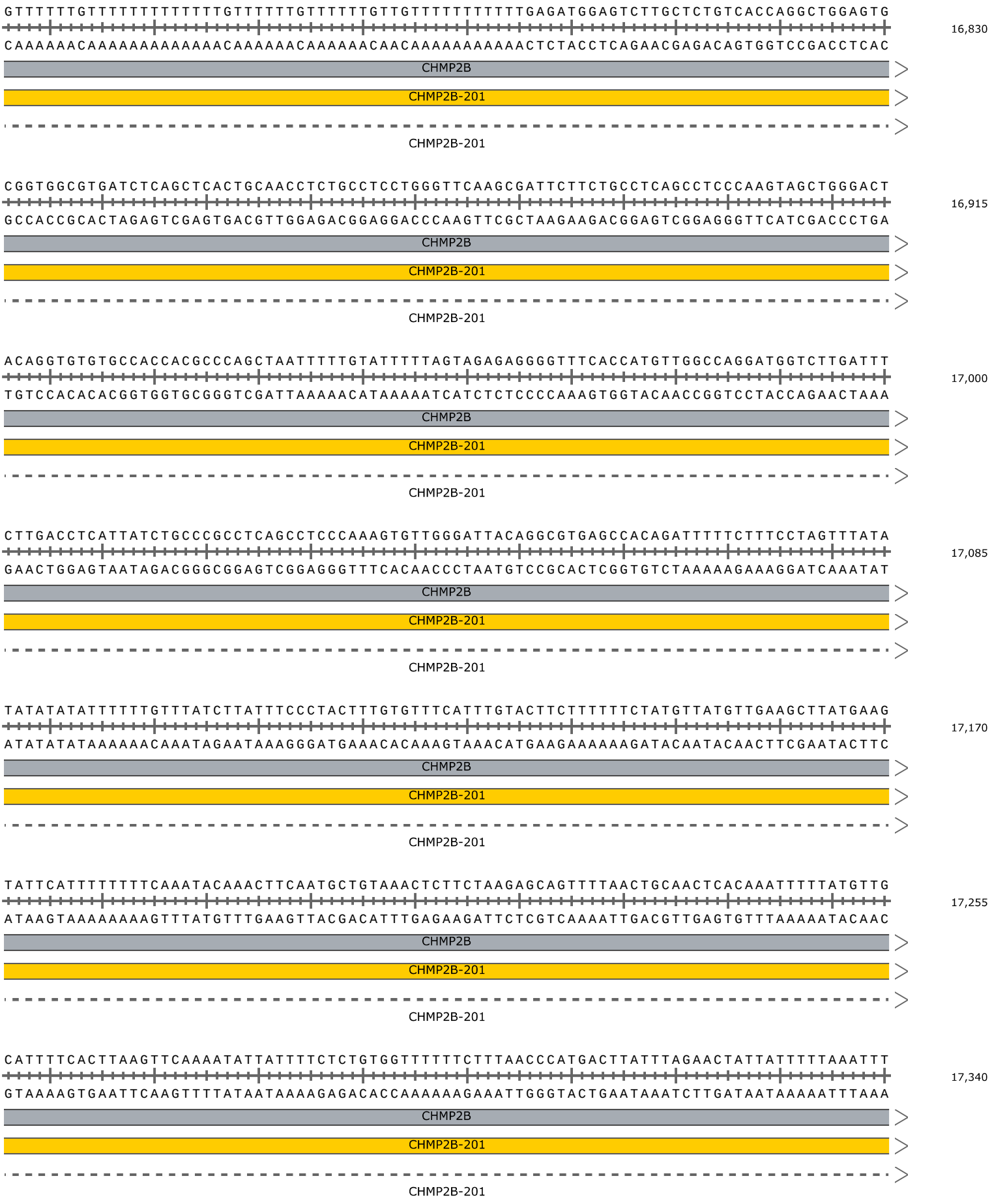
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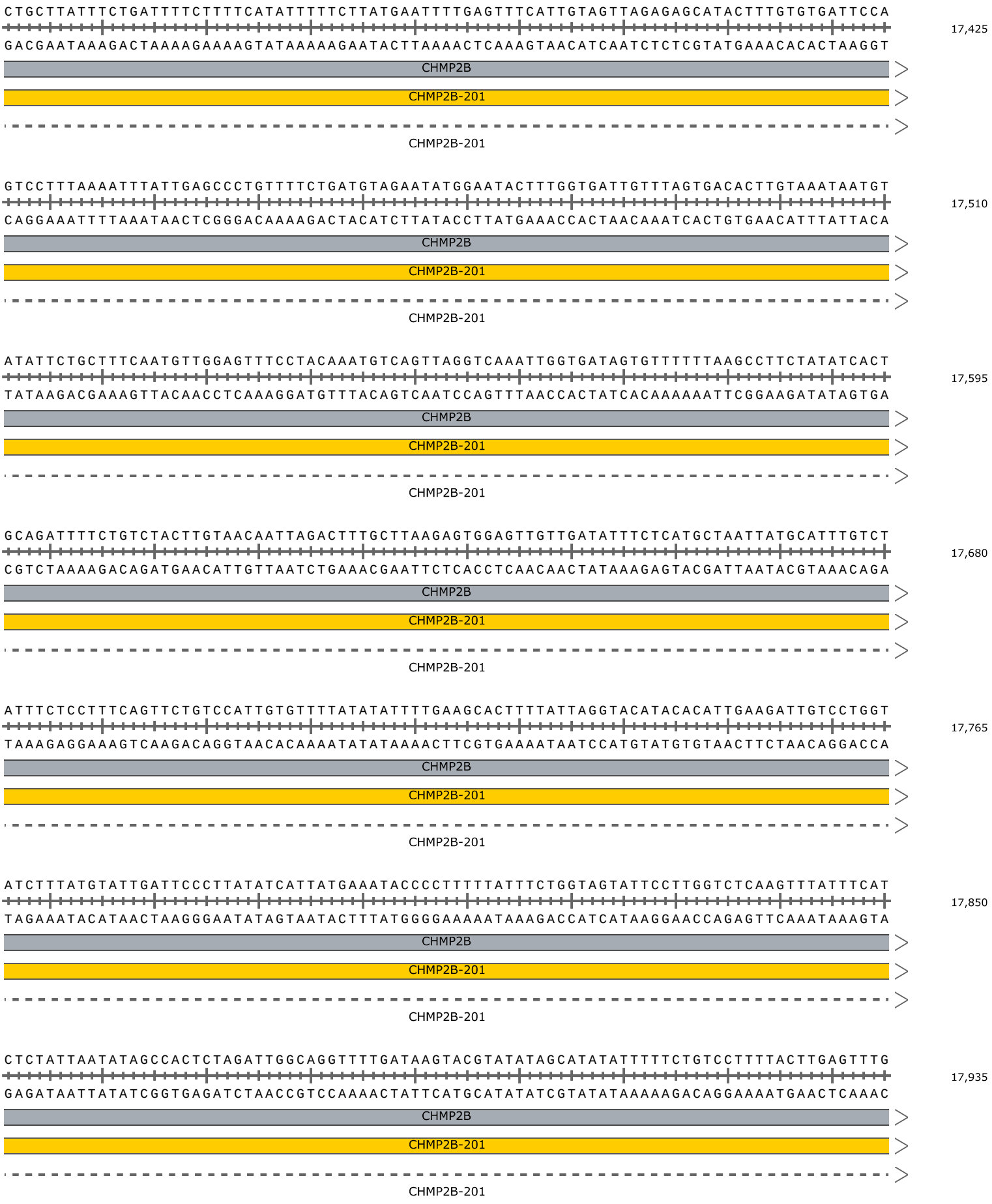
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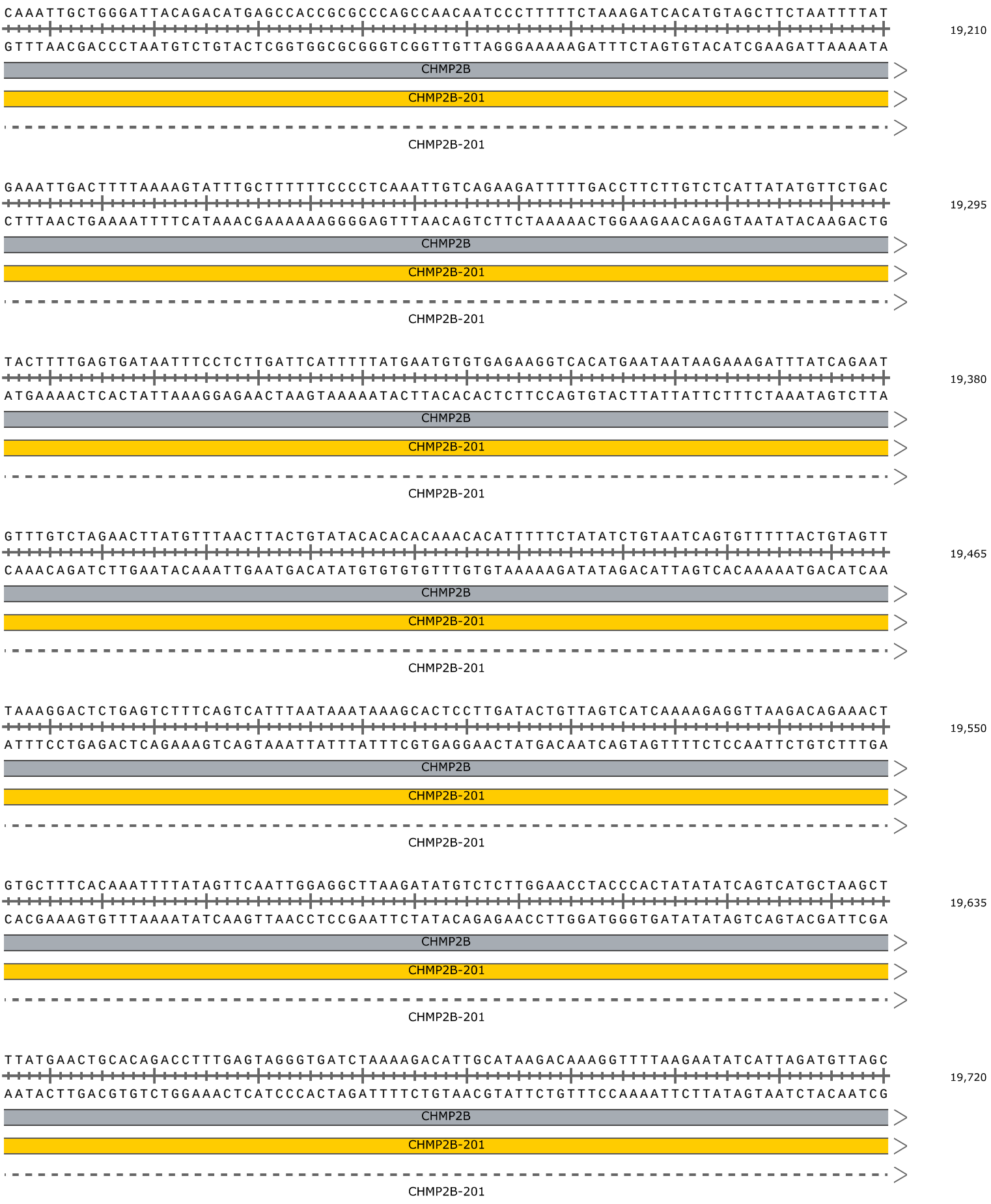
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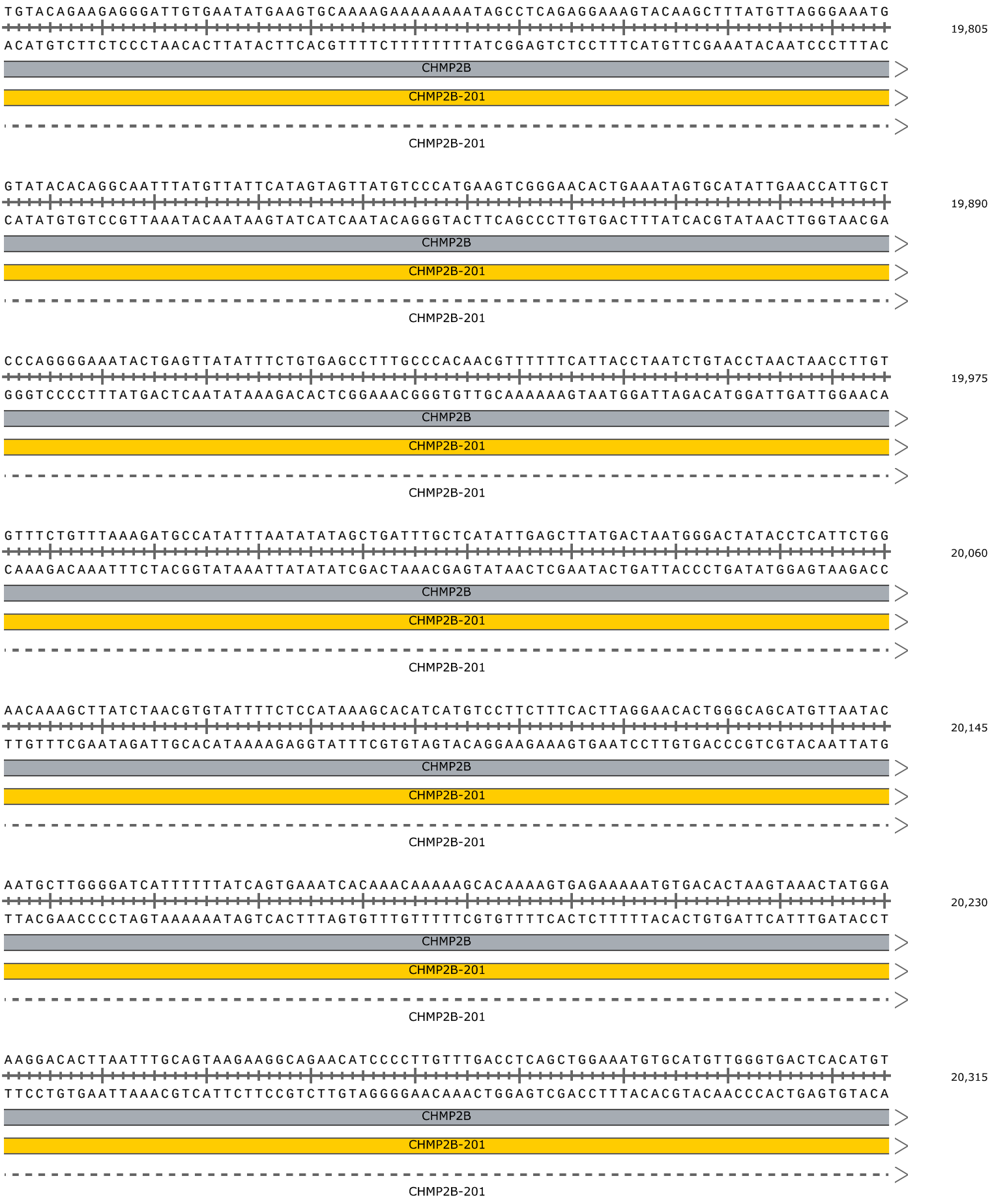
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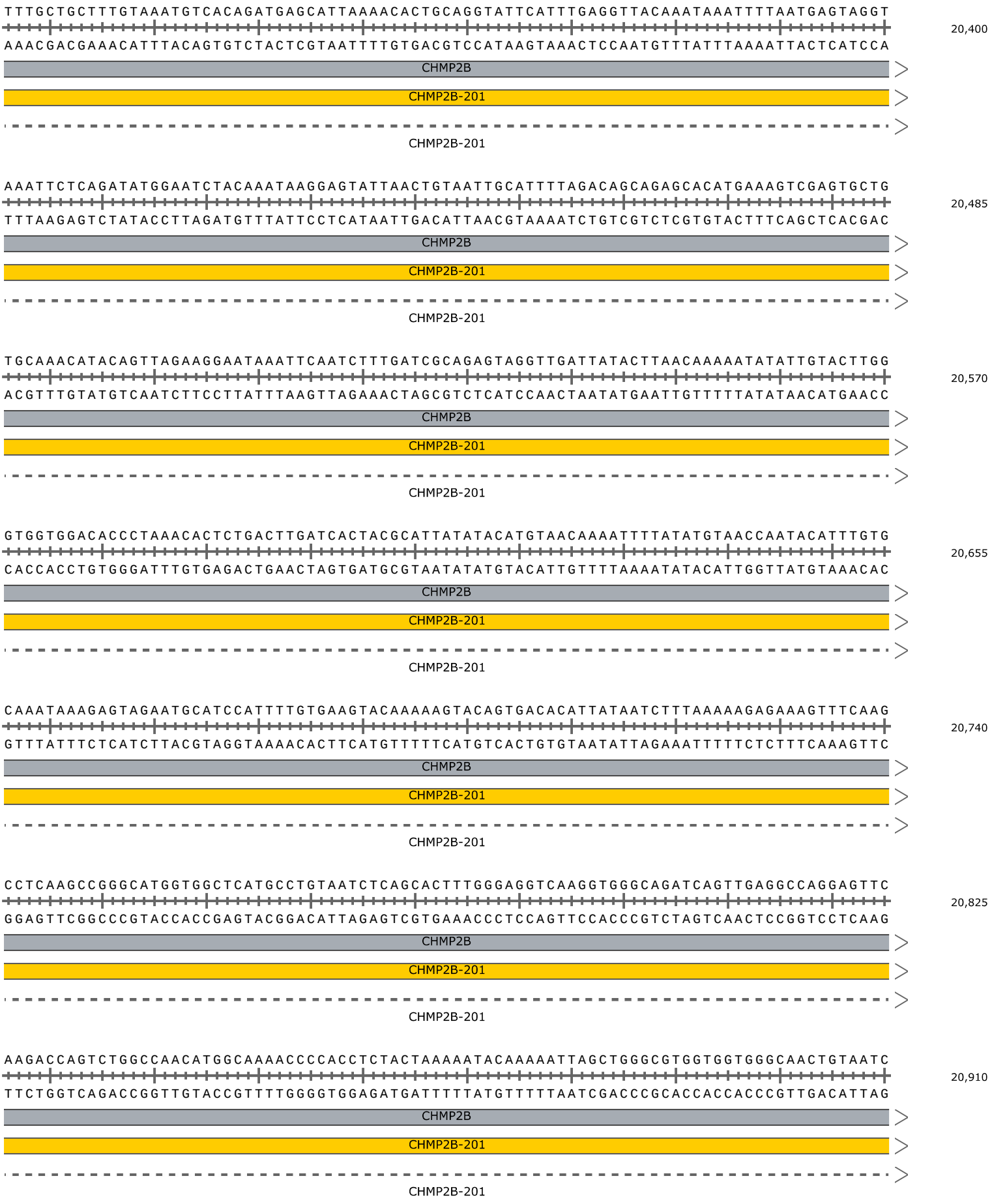
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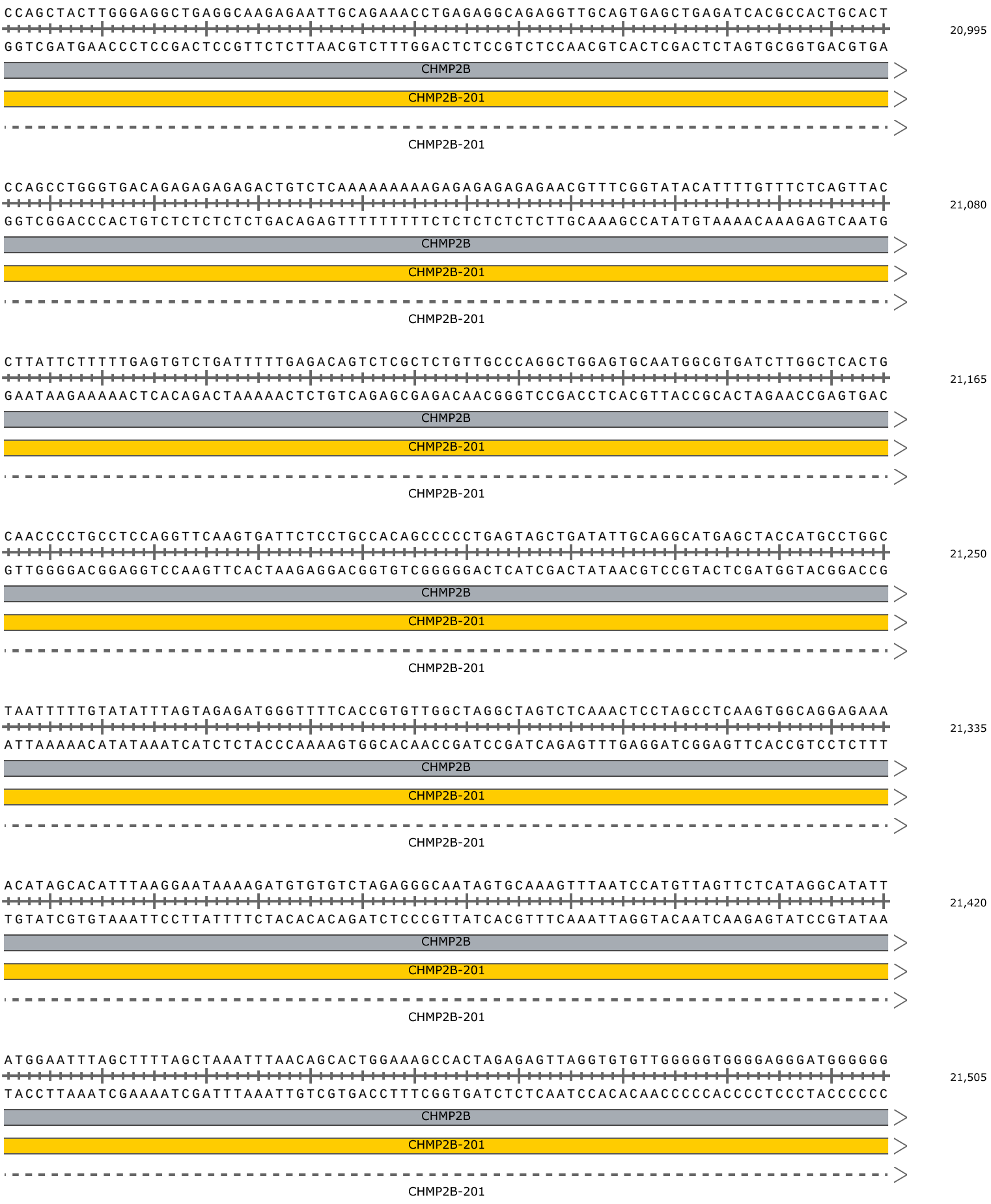
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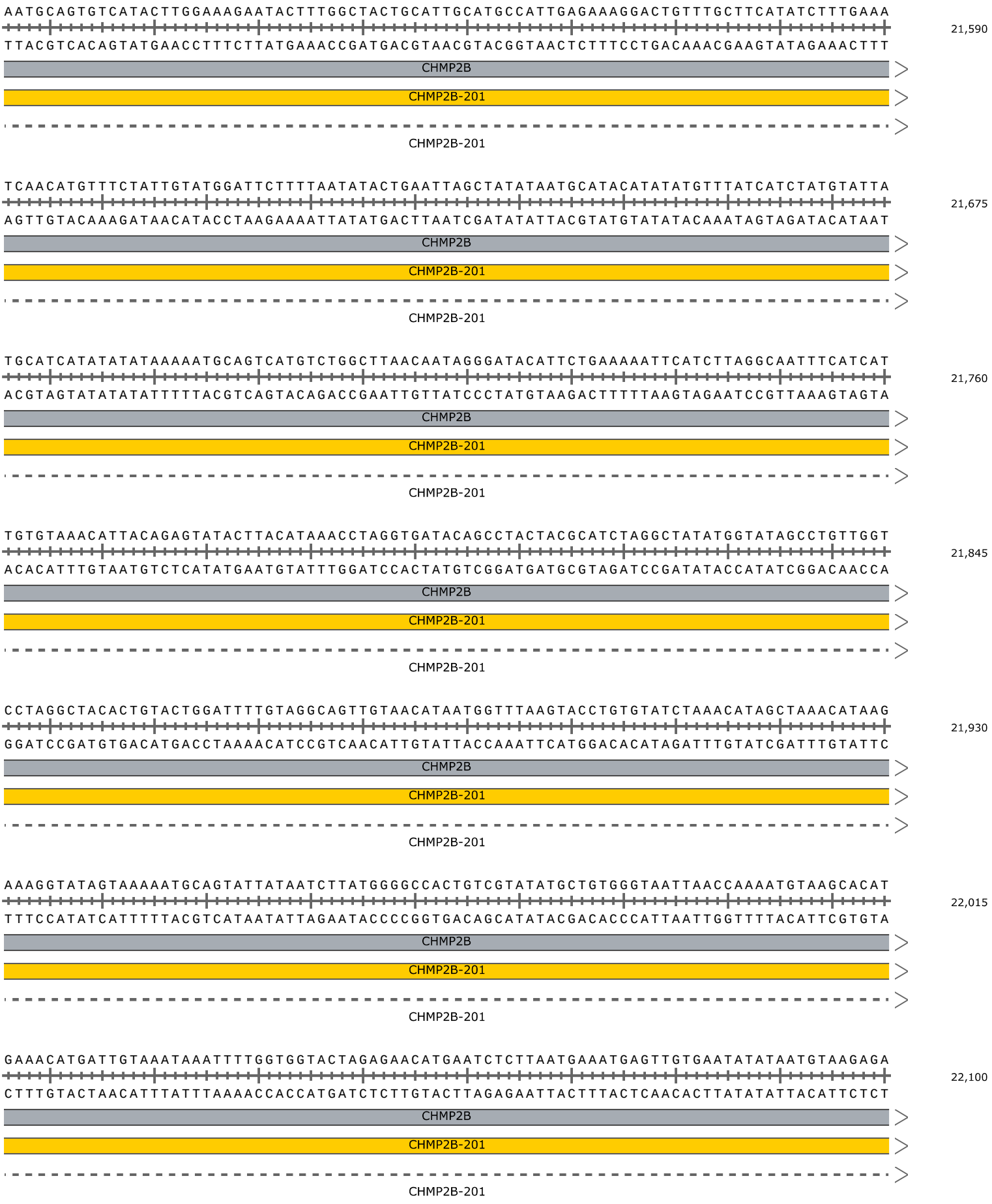
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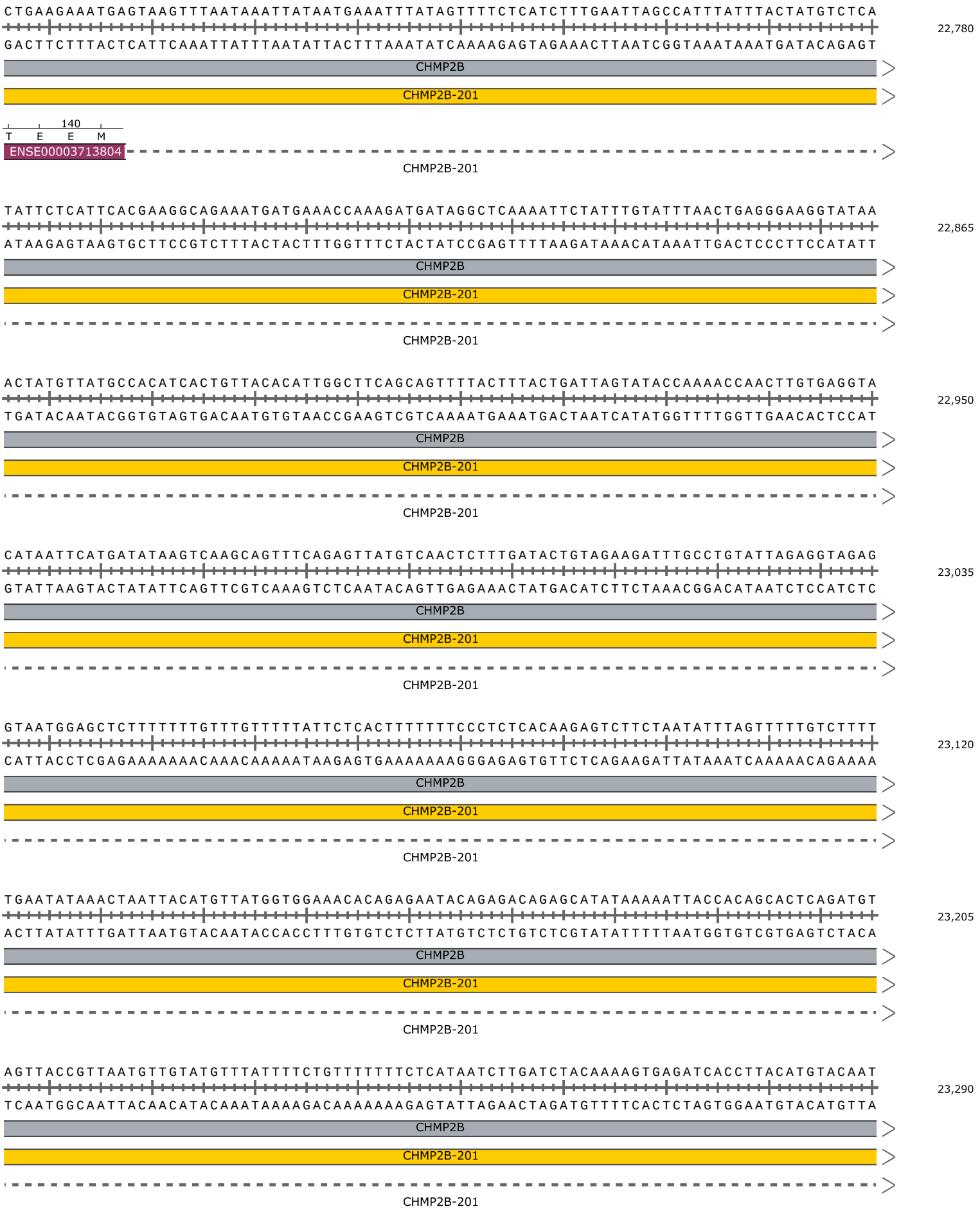
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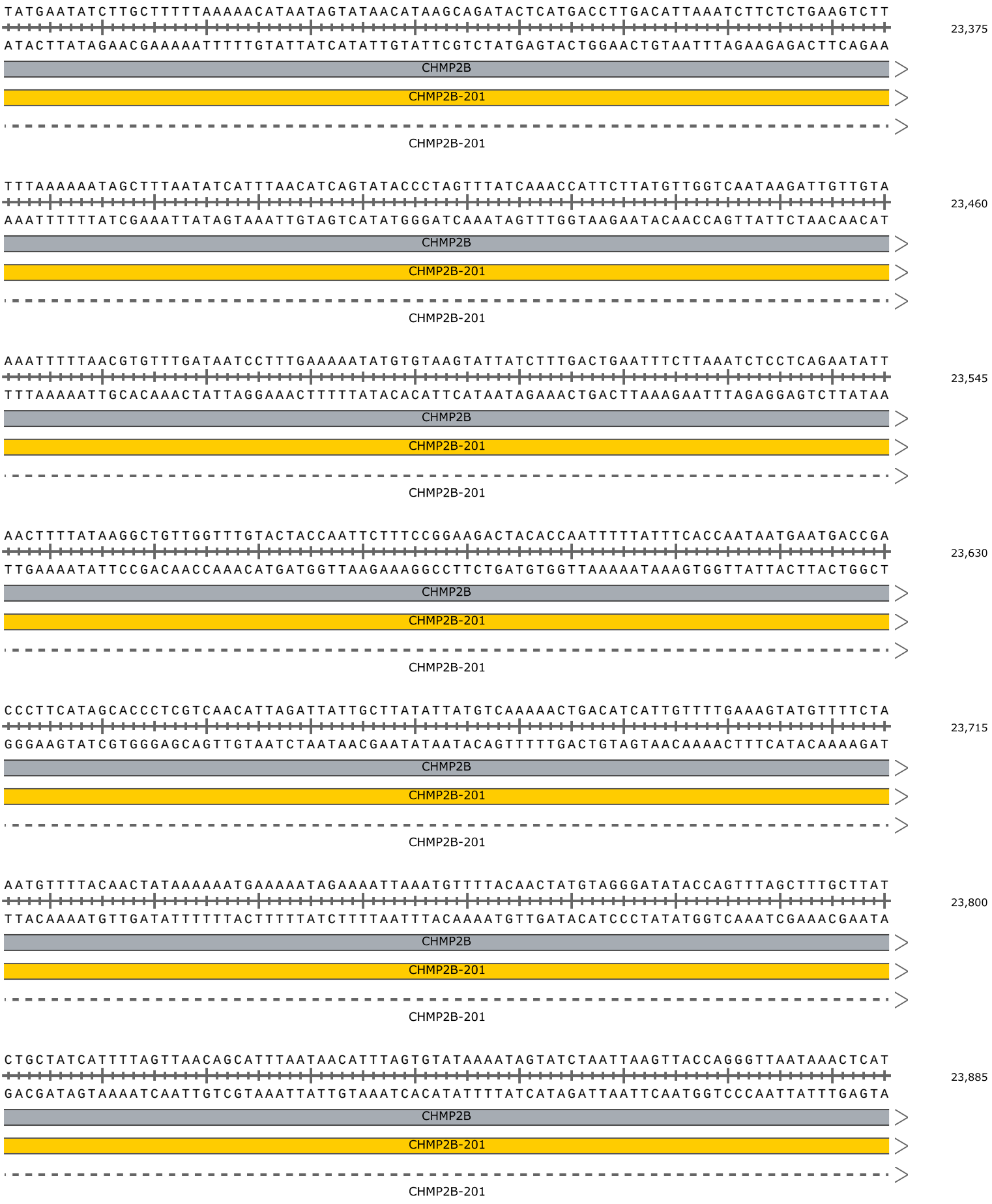
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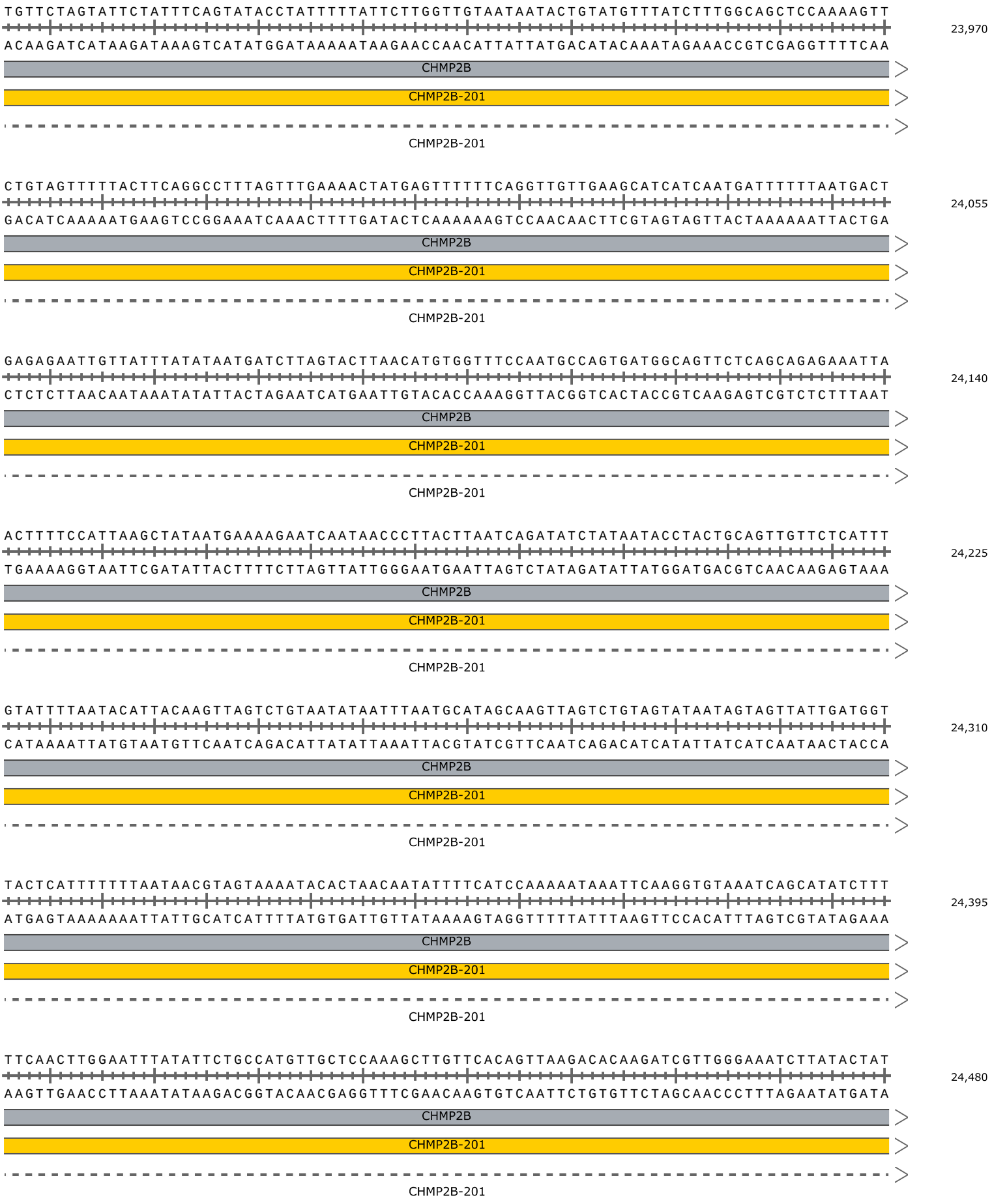
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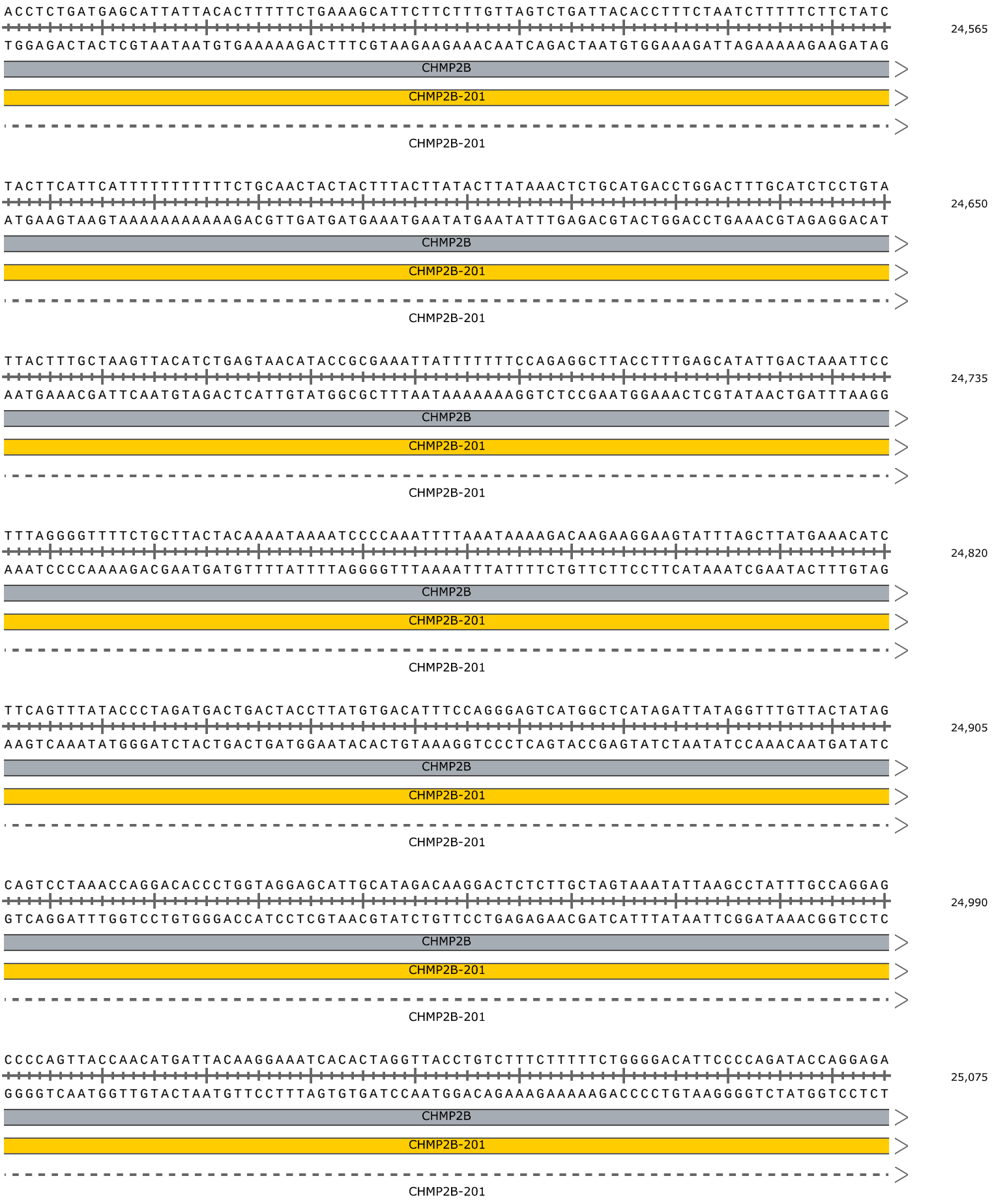
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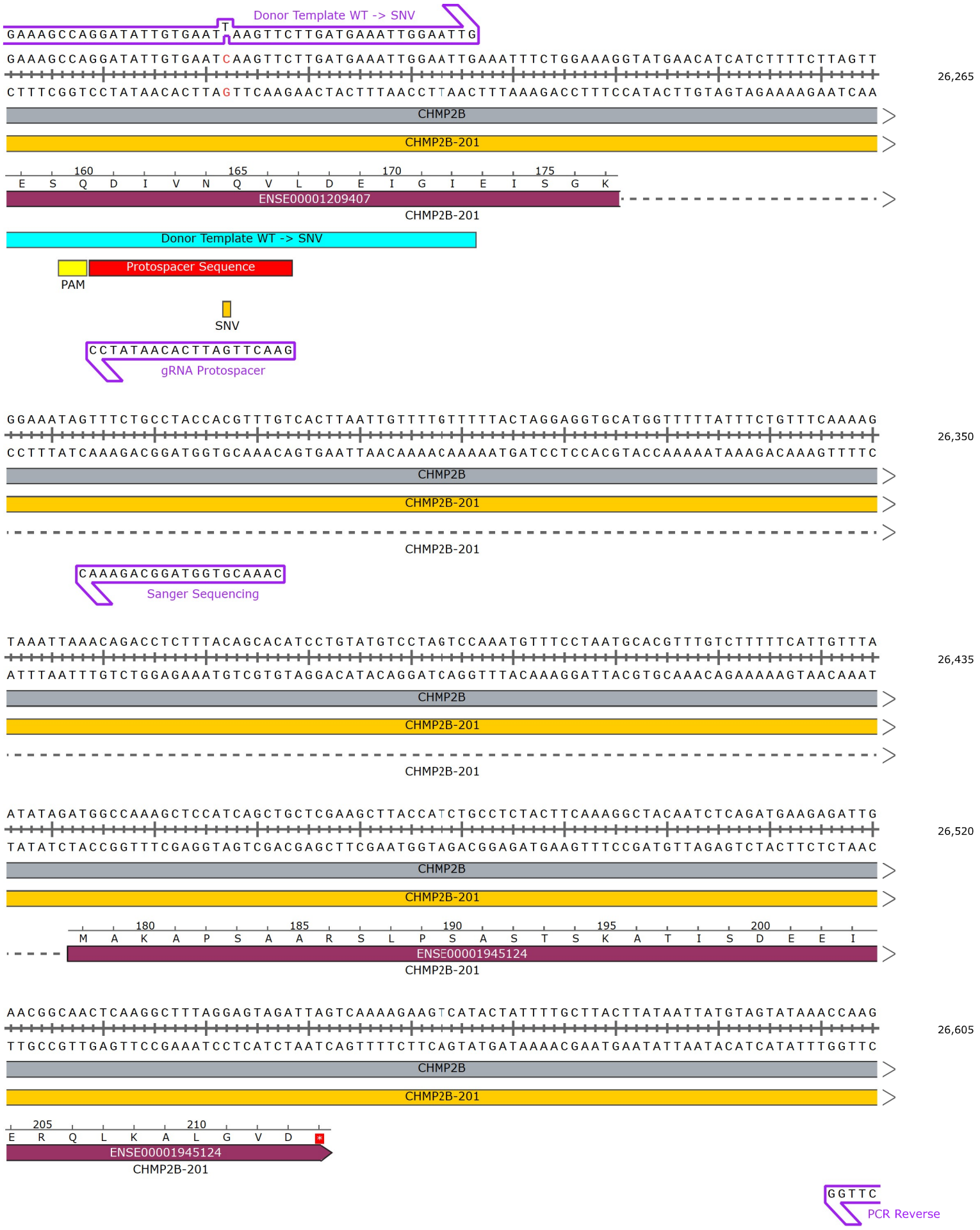
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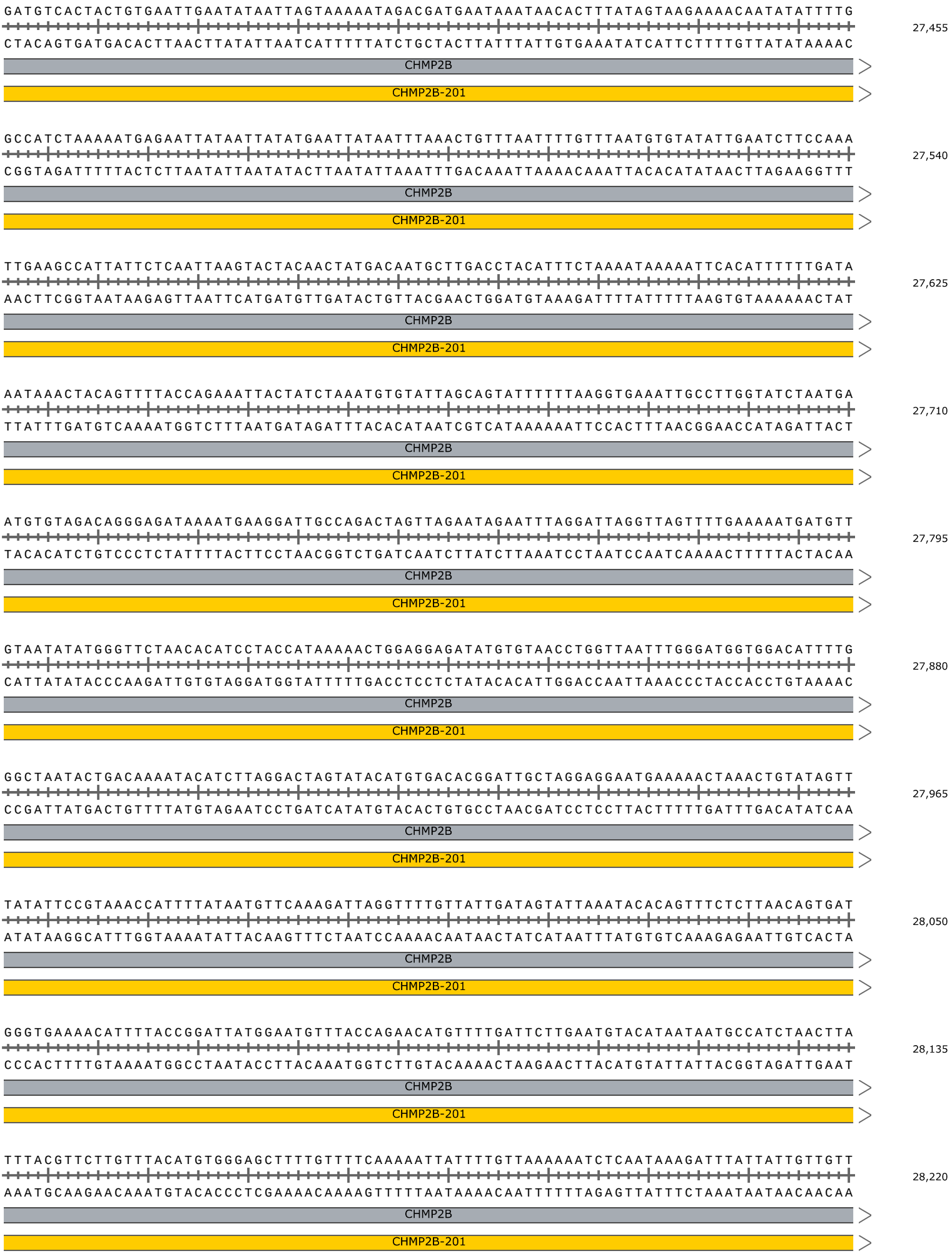
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CHMP2B
CHMP2B-201
TTGAAGCCATTATTCTCAATTAAGTACTACAACTATGACAATGCTTGACCTACATTTCTAAAATAAAAATTCACATTTTTTGATA
27,625
AACTTCGGTAATAAGAGTTAATTCATGATGTTGATACTGTTACGAACTGGATGTAAAGATTTTATTTTTAAGTGTAAAAAACTAT
CHMP2B
CHMP2B-201
AATAAACTACAGTTTTACCAGAAATTACTATCTAAATGTGTATTAGCAGTATTTTTTAAGGTGAAATTGCCTTGGTATCTAATGA
27,710
TTATTTGATGTCAAAATGGTCTTTAATGATAGATTTACACATAATCGTCATAAAAAATTCCACTTTAACGGAACCATAGATTACT
CHMP2B
CHMP2B-201
ATGTGTAGACAGGGAGATAAAATGAAGGATTGCCAGACTAGTTAGAATAGAATTTAGGATTAGGTTAGTTTTGAAAAATGATGTT
27,795
TACACATCTGTCCCTCTATTTTACTTCCTAACGGTCTGATCAATCTTATCTTAAATCCTAATCCAATCAAAACTTTTTACTACAA
CHMP2B
CHMP2B-201
GTAATATATGGGTTCTAACACATCCTACCATAAAAACTGGAGGAGATATGTGTAACCTGGTTAATTTGGGATGGTGGACATTTTG
27,880
CATTATATACCCAAGATTGTGTAGGATGGTATTTTTGACCTCCTCTATACACATTGGACCAATTAAACCCTACCACCTGTAAAAC
CHMP2B
CHMP2B-201
GGCTAATACTGACAAAATACATCTTAGGACTAGTATACATGTGACACGGATTGCTAGGAGGAATGAAAAACTAAACTGTATAGTT
27,965
CCGATTATGACTGTTTTATGTAGAATCCTGATCATATGTACACTGTGCCTAACGATCCTCCTTACTTTTTGATTTGACATATCAA
CHMP2B
CHMP2B-201
TATATTCCGTAAACCATTTTATAATGTTCAAAGATTAGGTTTTGTTATTGATAGTATTAAATACACAGTTTCTCTTAACAGTGAT
28,050
ATATAAGGCATTTGGTAAAATATTACAAGTTTCTAATCCAAAACAATAACTATCATAATTTATGTGTCAAAGAGAATTGTCACTA
CHMP2B
CHMP2B-201
GGGTGAAAACATTTTACCGGATTATGGAATGTTTACCAGAACATGTTTTGATTCTTGAATGTACATAATAATGCCATCTAACTTA
28,135
CCCACTTTTGTAAAATGGCCTAATACCTTACAAATGGTCTTGTACAAAACTAAGAACTTACATGTATTATTACGGTAGATTGAAT
CHMP2B
CHMP2B-201
TTTACGTTCTTGTTTACATGTGGGAGCTTTTGTTTTCAAAAATTATTTTGTTAAAAAATCTCAATAAAGATTTATTATTGTTGTT
28,220
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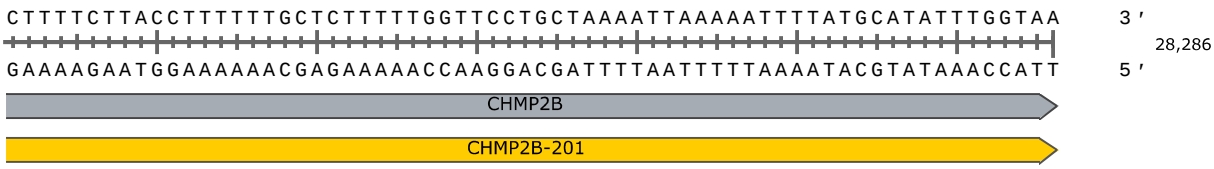
CHMP2B
CHMP2B-201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3′
28,286
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5′
CHMP2B
CHMP2B-201

	Feature	Location	Size			Type
✓	**CHMP2B**	1 .. 28,286	28,286 bp		→	gene
	/note = gene ENSG00000083937 Protein coding					
	CHMP2B-203	1 .. 28,278	28,278 bp		→	prim_transcript
	/note = primary transcript ENST00000471660					
	CHMP2B-208	15 .. 28,145	28,131 bp		→	prim_transcript
	/note = primary transcript ENST00000677929 Retained intron					
	CHMP2B-205	32 .. 26,954	26,923 bp		→	prim_transcript
	/note = primary transcript ENST00000494980					
✓	**CHMP2B-201**	39 .. 28,286	28,248 bp		→	prim_transcript
	/note = primary transcript ENST00000263780					
	CHMP2B-204	39 .. 28,216	28,178 bp		→	prim_transcript
	/note = primary transcript ENST00000472024					
	CHMP2B-206	42 .. 28,216	28,175 bp		→	prim_transcript
	/note = primary transcript ENST00000676705					
	CHMP2B-210	57 .. 28,145	28,089 bp		→	prim_transcript
	/note = primary transcript ENST00000678859 Retained intron					
	CHMP2B-207	100 .. 19,461	19,362 bp		→	prim_transcript
	/note = primary transcript ENST00000676947 Retained intron					
✓	**CHMP2B-201**	253 .. 26,552	26,300 bp		→	CDS
	▸ 6 segments = 642 bp					
	/note = coding sequence ENSP00000263780					
	/translation = MASLFKKKTVD,,DVIKEQNRELRGTQRAIIRDRAALEKQEKQL,,ELEIKKMAKIGNKEACKVLAKQLVHLRKQKTRTFAVSSKVTSMSTQTKVMNSQMKMAGAMSTTAK,,TMQAVNKKMDPQKTLQTMQNFQKENMKMEMTEEM,,INDTLDDIFDGSDDEEESQDIVNQVLDEIGIEISGK,,MAKAPSAARSLPSASTSKATISDEEIERQLKALGVD* 213 amino acids = 23.9 kDa					
	CHMP2B-205	253 .. 26,552	26,300 bp		→	CDS
	▸ 6 segments = 552 bp					
	/note = coding sequence ENSP00000418920					
	/translation = MASLFKKKTVD,,DVIKEQNRELRGTQRAIIRDRAALEKQEKQL,,ELEIKKMAKIGNKEACKVLAKQLVHLRKQKTRTFA,,TMQAVNKKMDPQKTLQTMQNFQKENMKMEMTEEM,,INDTLDDIFDGSDDEEESQDIVNQVLDEIGIEISGK,,MAKAPSAARSLPSASTSKATISDEEIERQLKALGVD* 183 amino acids = 20.8 kDa					
	CHMP2B-203	284 .. 26,552	26,269 bp		→	CDS
	▸ 5 segments = 519 bp					
	/note = coding sequence ENSP00000419998					
	/translation = M,,ELEIKKMAKIGNKEACKVLAKQLVHLRKQKTRTFAVSSKVTSMSTQTKVMNSQMKMAGAMSTTAK,,TMQAVNKKMDPQKTLQTMQNFQKENMKMEMTEEM,,INDTLDDIFDGSDDEEESQDIVNQVLDEIGIEISGK,,MAKAPSAARSLPSASTSKATISDEEIERQLKALGVD* 172 amino acids = 19.1 kDa					
	CHMP2B-209	12,122 .. 19,765	7644 bp		→	prim_transcript
	/note = primary transcript ENST00000678818 protein_coding_CDS_not_defined					
	CHMP2B-204	13,102 .. 26,552	13,451 bp		→	CDS
	▸ 6 segments = 690 bp					
	/note = coding sequence ENSP00000480032					
	/translation = MISAQRNHHLPDSSDSSTSAYRVARIT,,DVIKEQNRELRGTQRAIIRDRAALEKQEKQL,,ELEIKKMAKIGNKEACKVLAKQLVHLRKQKTRTFAVSSKVTSMSTQTKVMNSQMKMAGAMSTTAK,,TMQAVNKKMDPQKTLQTMQNFQKENMKMEMTEEM,,INDTLDDIFDGSDDEEESQDIVNQVLDEIGIEISGK,,MAKAPSAARSLPSASTSKATISDEEIERQLKALGVD* 229 amino acids = 25.6 kDa					
	CHMP2B-206	13,102 .. 26,552	13,451 bp		→	CDS
	▸ 6 segments = 690 bp					
	/note = coding sequence ENSP00000504098					
	/translation = MISAQRNHHLPDSSDSSTSAYRVARIT,,DVIKEQNRELRGTQRAIIRDRAALEKQEKQL,,ELEIKKMAKIGNKEACKVLAKQLVHLRKQKTRTFAVSSKVTSMSTQTKVMNSQMKMAGAMSTTAK,,TMQAVNKKMDPQKTLQTMQNFQKENMKMEMTEEM,,INDTLDDIFDGSDDEEESQDIVNQVLDEIGIEISGK,,MAKAPSAARSLPSASTSKATISDEEIERQLKALGVD* 229 amino acids = 25.6 kDa					

	Feature	Location	Size			Type
	CHMP2B-202	25,779 .. 26,643	865 bp		→	prim_transcript
	/note = primary transcript ENST00000466696 Retained intron					
✓	**Donor Template WT -> SNV**	26,127 .. 26,226	100 bp		⊢	misc_feature
✓	**PAM**	26,186 .. 26,188	3 bp		⊢	misc_feature
✓	**Protospacer Sequence**	26,189 .. 26,208	20 bp		⊢	misc_feature
✓	**SNV**	26,202 .. 26,202	1 bp		⊢	misc_feature
	/note = WT = C SNV = T					

	Primer	Length	Binding Sites		Tm	Date Added
✓	**PCR Forward**	25-mer	25,612 .. 25,636	→	58°C	Jan 18, 2023
	/sequence = TTAAATCGGACATCATTCTTTGGGC 40% GC / 7647.0 Da					
✓	**Donor Template WT -> SNV**	100-mer	26,127 .. 26,226	→	71°C	Jan 18, 2023
	/sequence = CCCCTAGTCAATGATACACTTGATGACATCTTTGACGGTTCTGATGACGAAGAAGAAAGCCAGGATATTGTGAATTAAGTTCTTGATGAAA 38% GC / 30,996.3 Da					
✓	**gRNA Protospacer**	20-mer	26,189 .. 26,208	←	48°C	Jan 18, 2023
	/sequence = GAACTTGATTCACAATATCC 35% GC / 6060.0 Da					
✓	**Sanger Sequencing**	20-mer	26,273 .. 26,292	←	56°C	Jan 18, 2023
	/sequence = CAAACGTGGTAGGCAGAAAC 50% GC / 6184.1 Da					
✓	**PCR Reverse**	25-mer	26,601 .. 26,625	←	59°C	Jan 18, 2023
	/sequence = TAAAAGAAATCTGCACTGTGCTTGG 40% GC / 7705.1 Da					