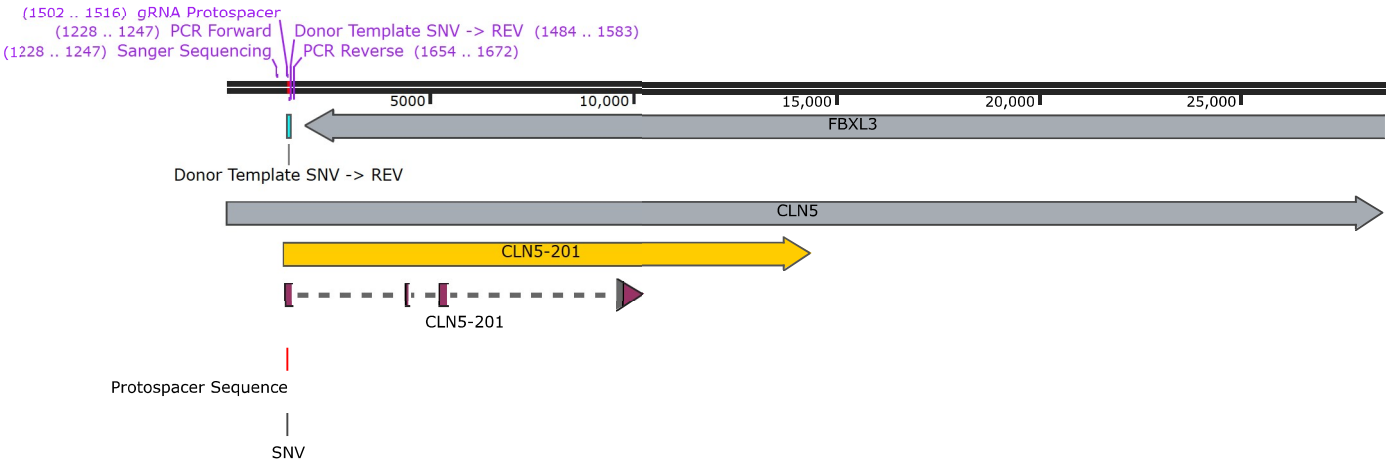

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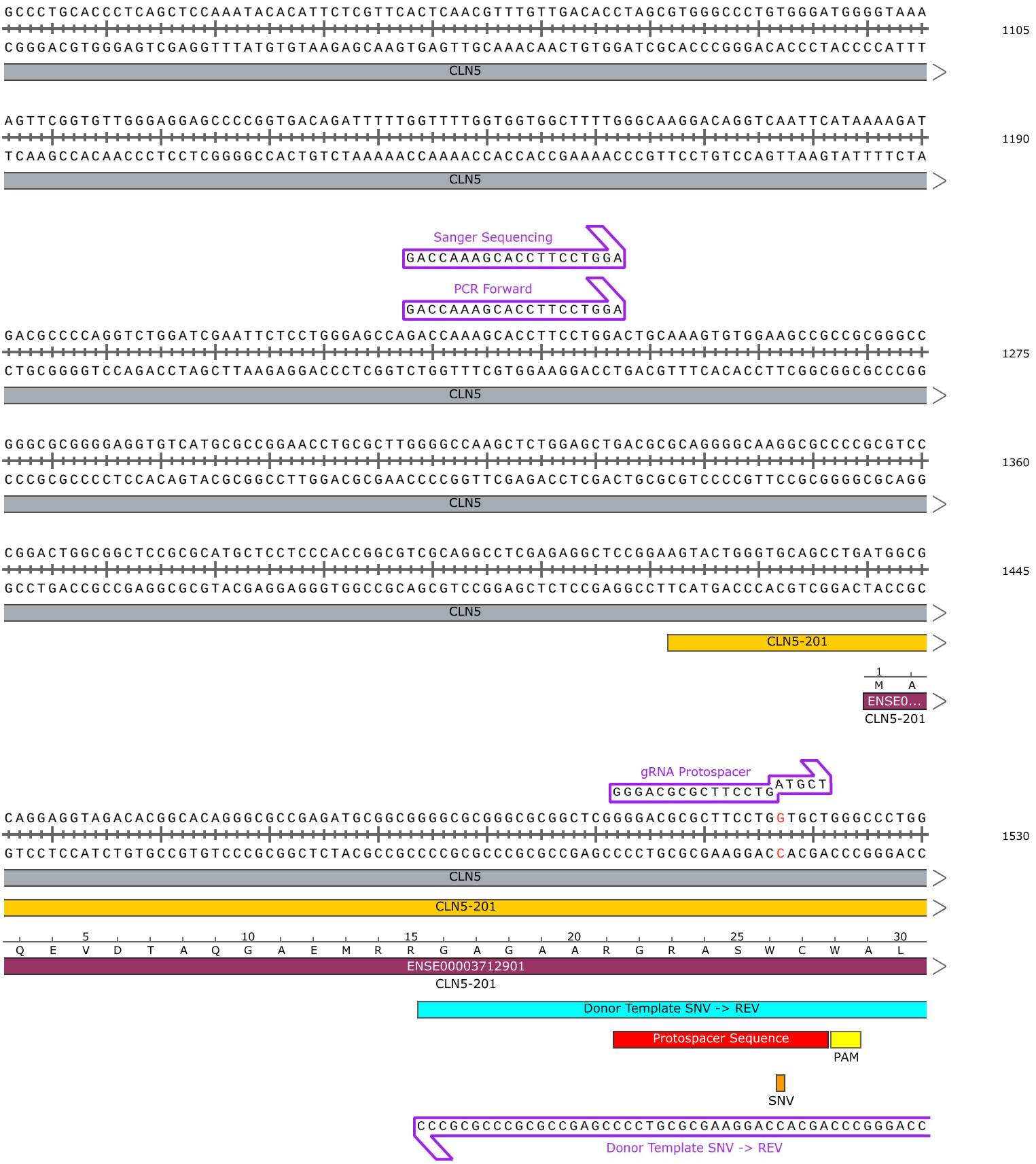
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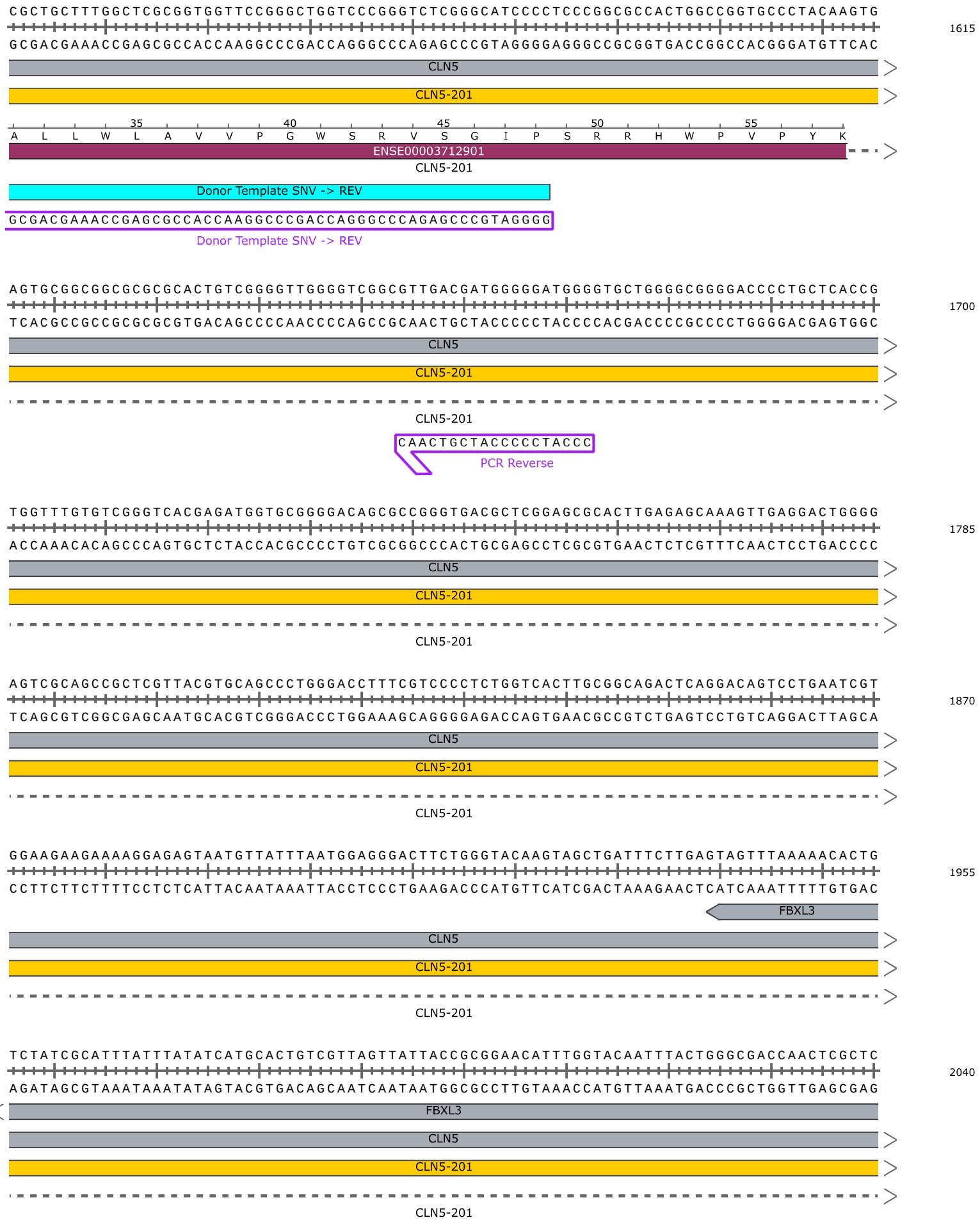
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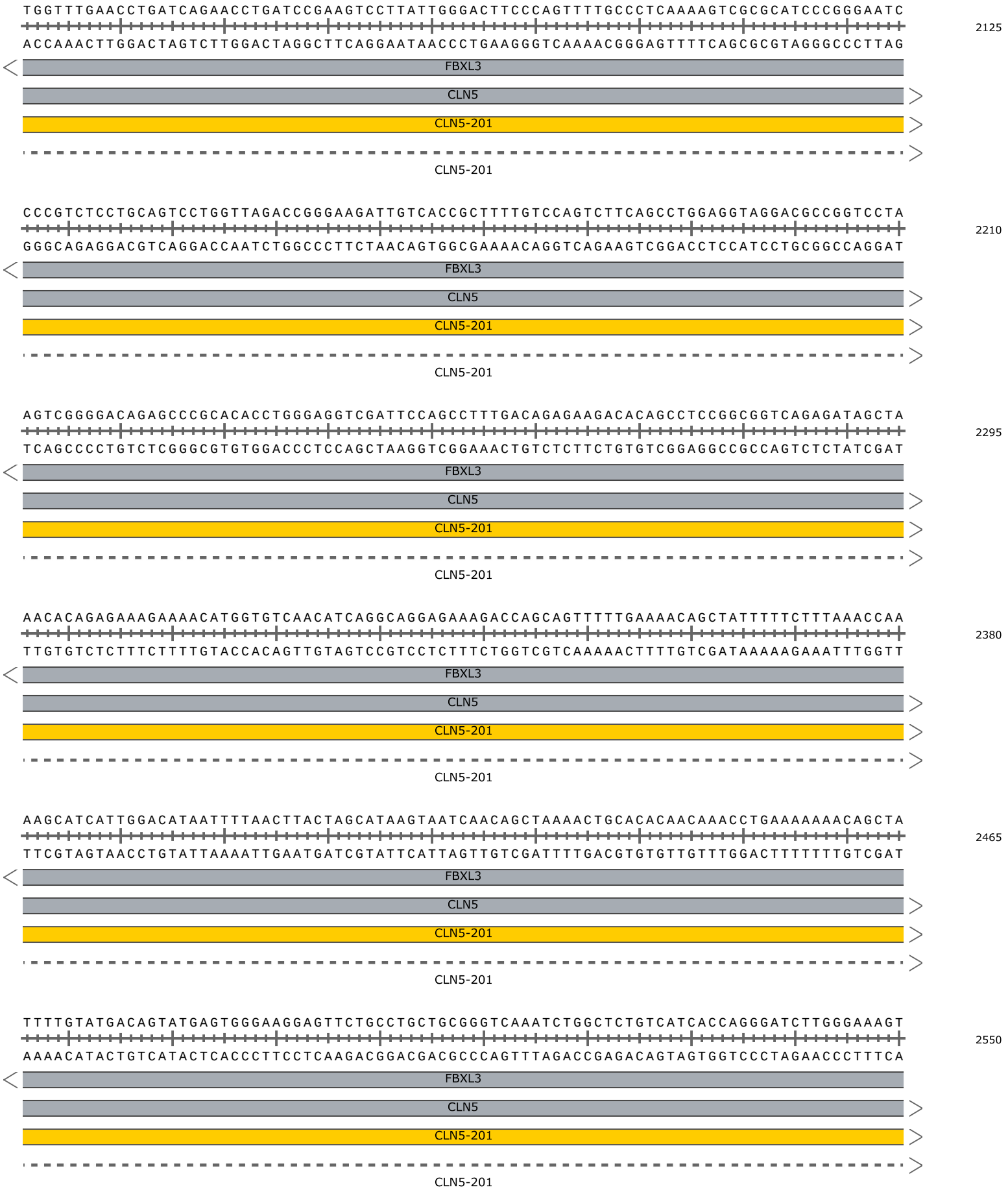
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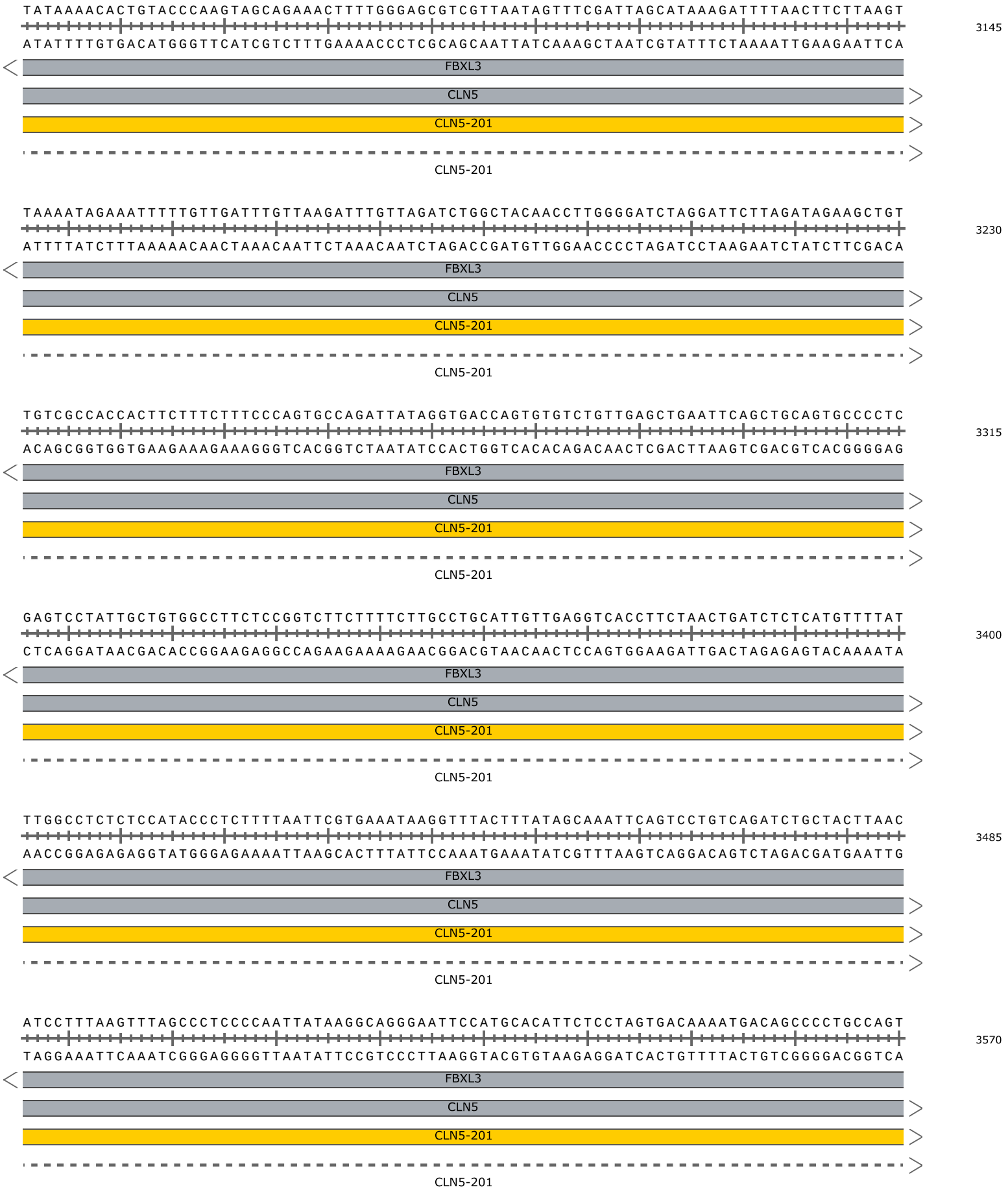
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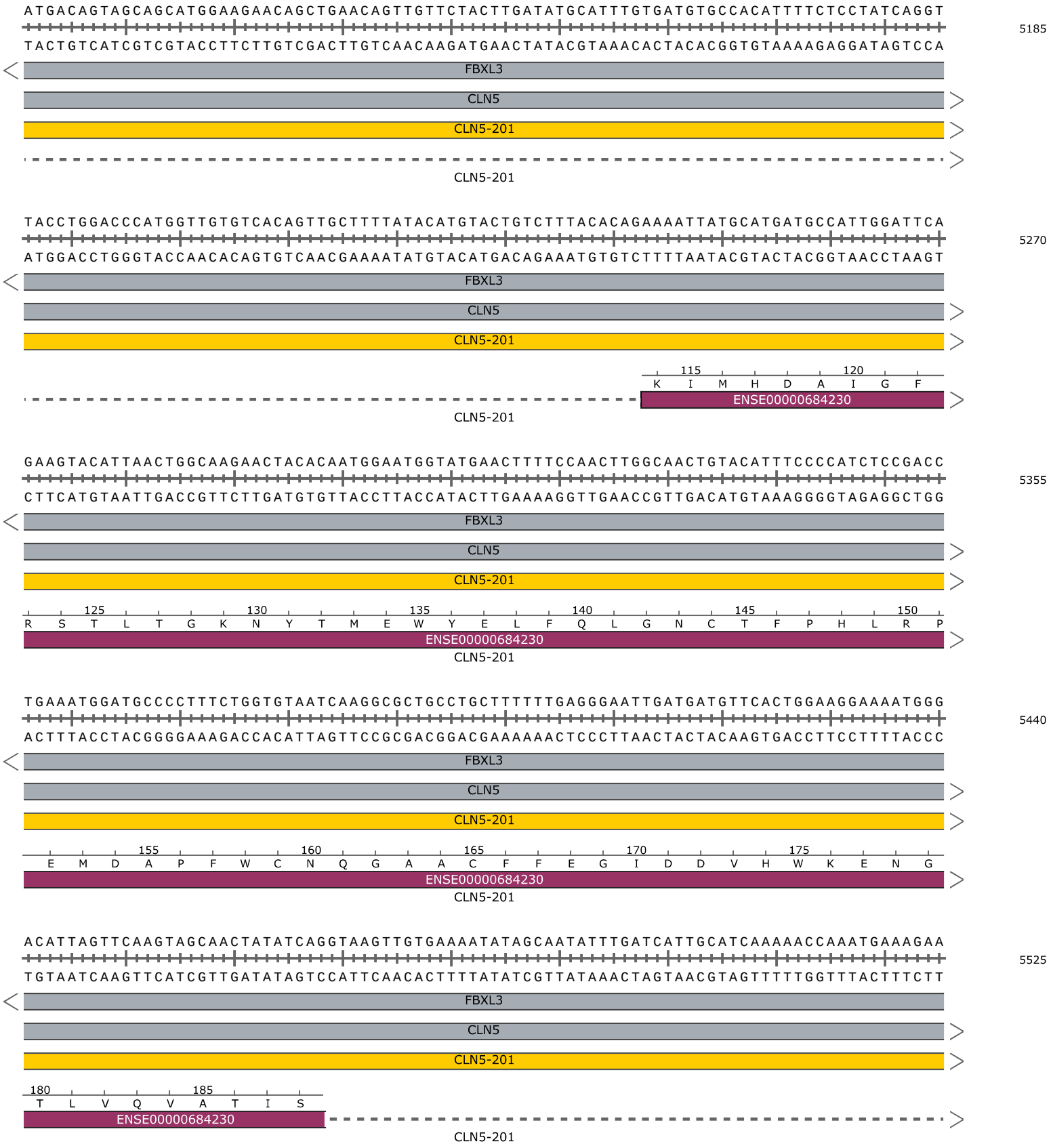
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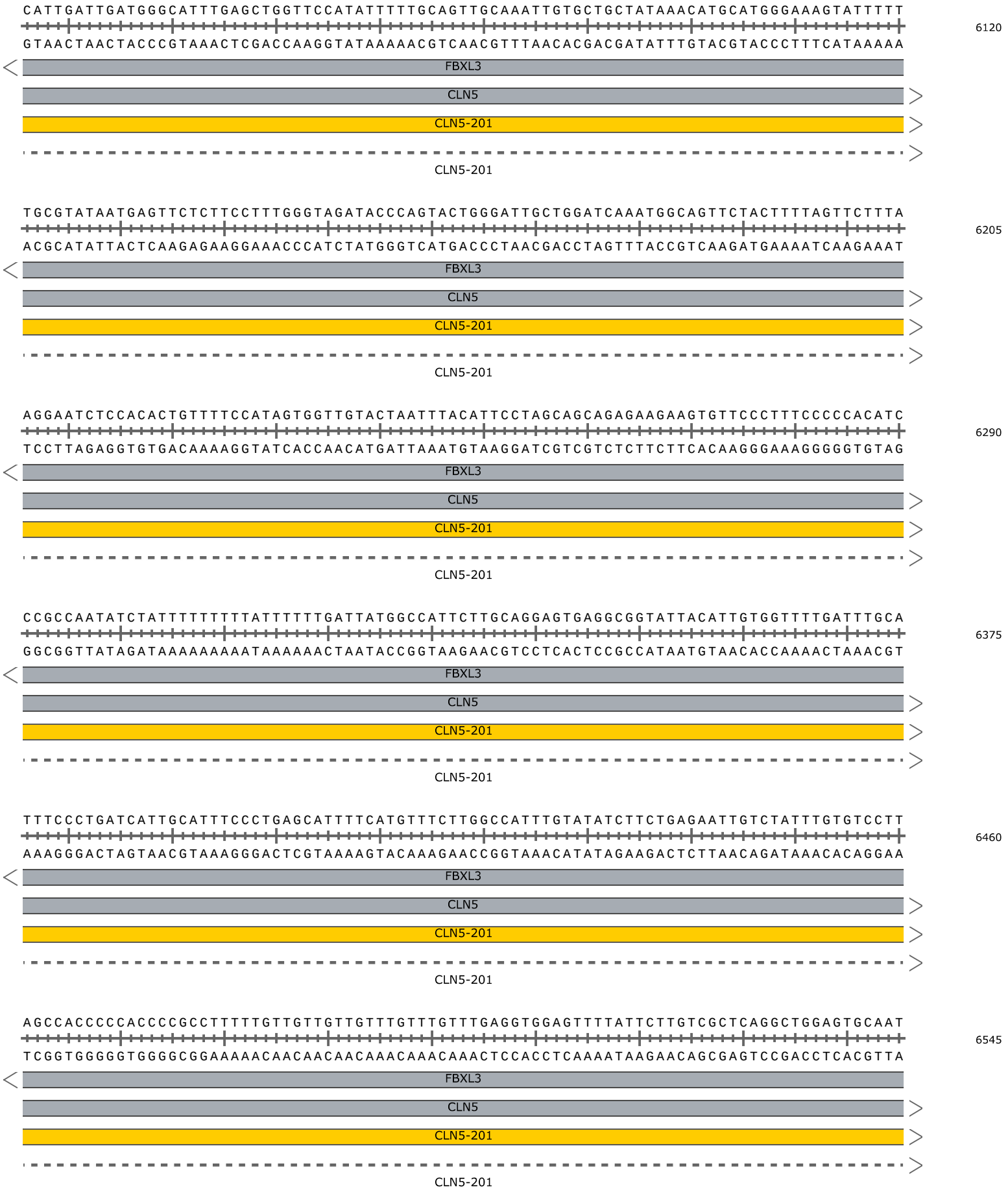
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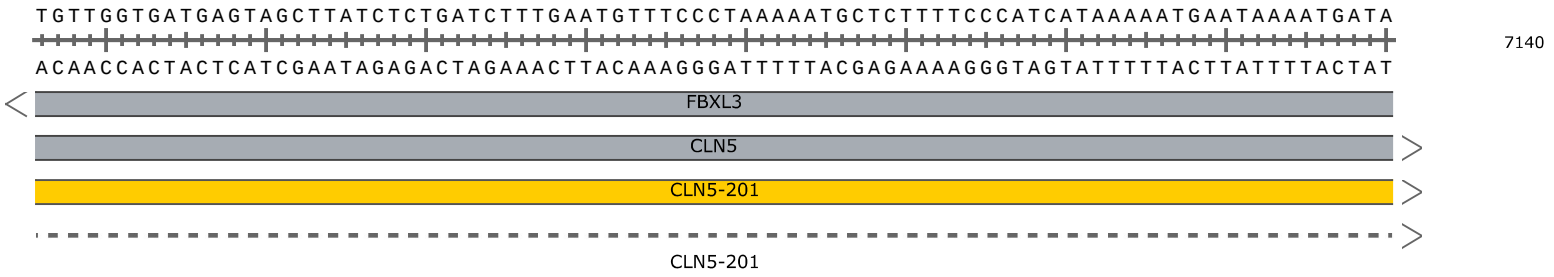
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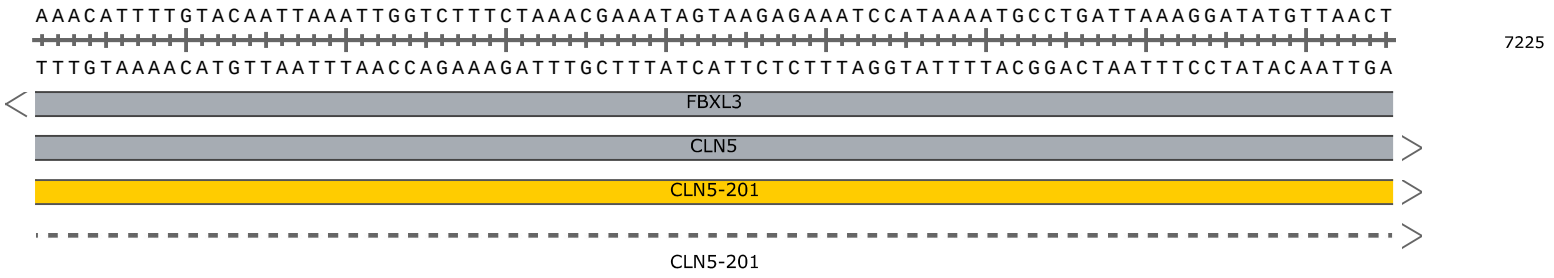
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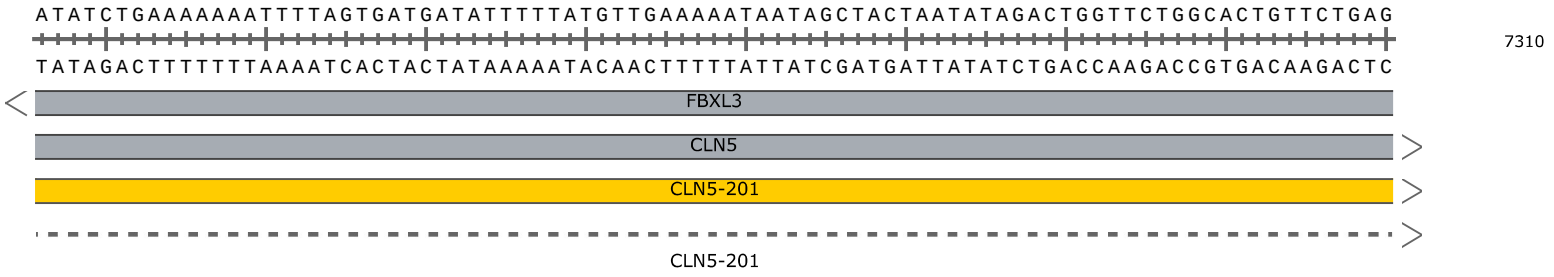
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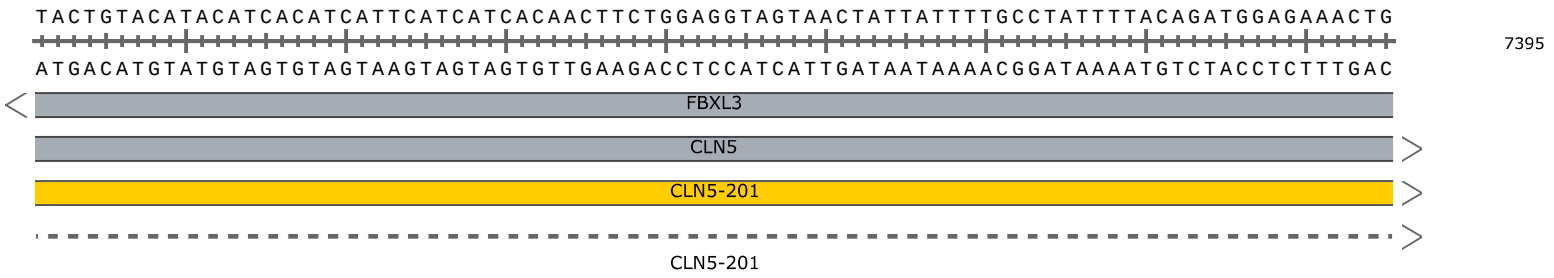
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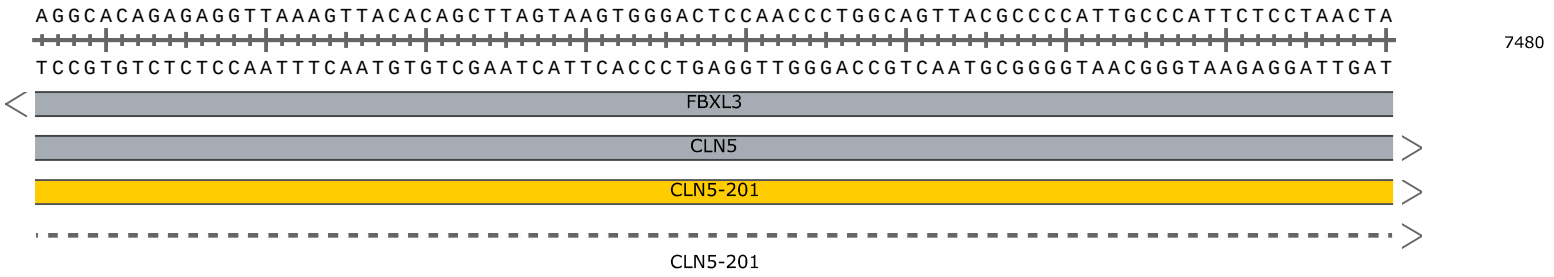
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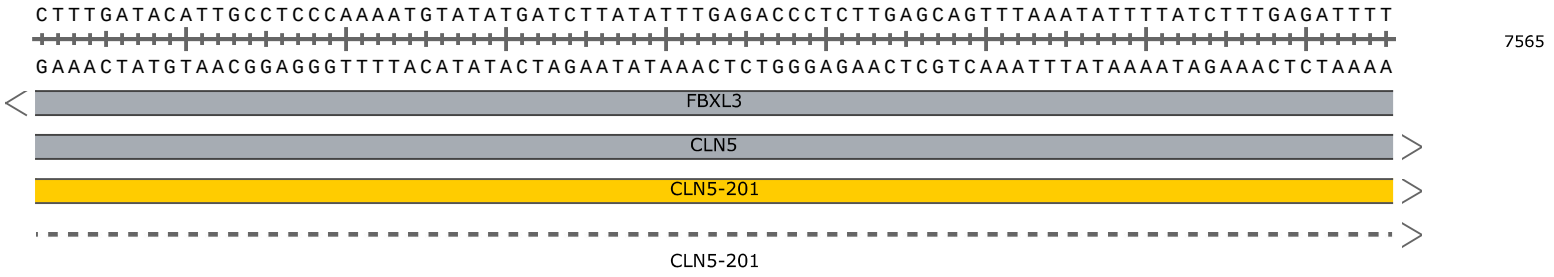
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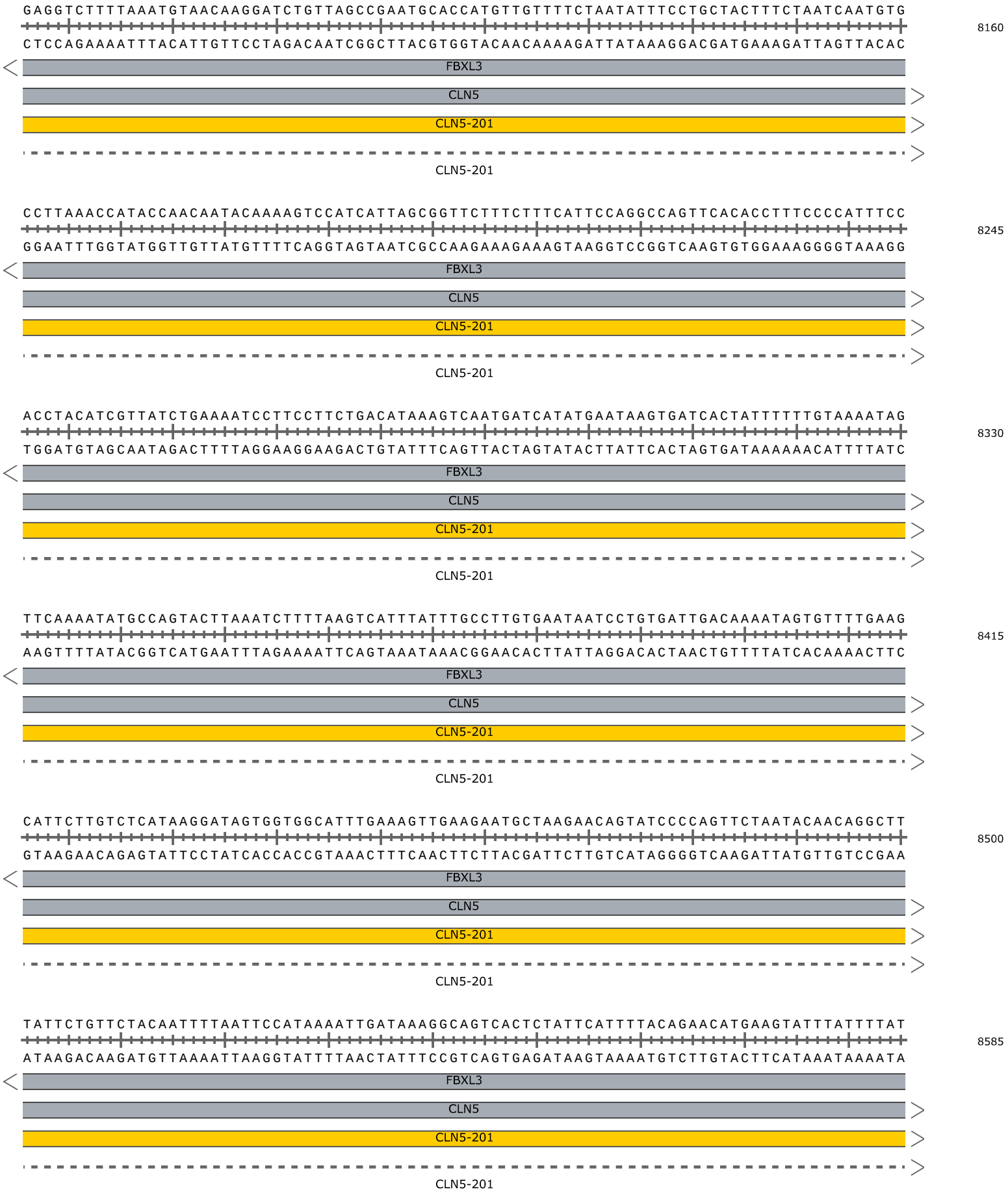
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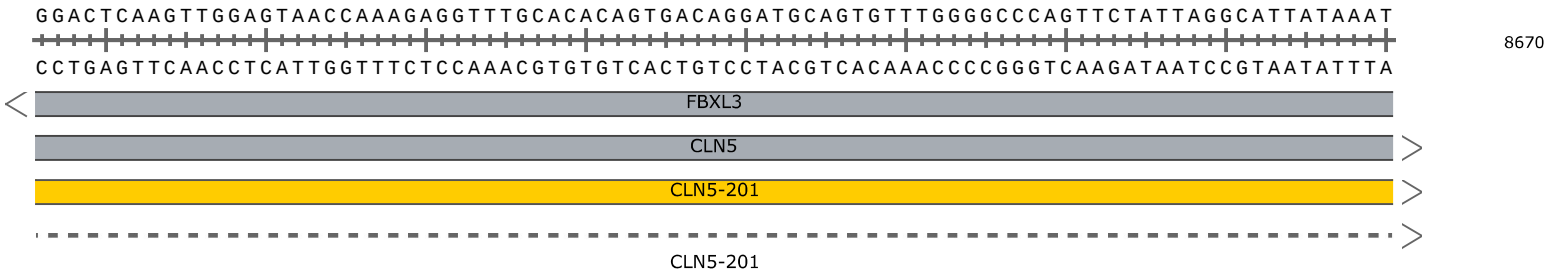
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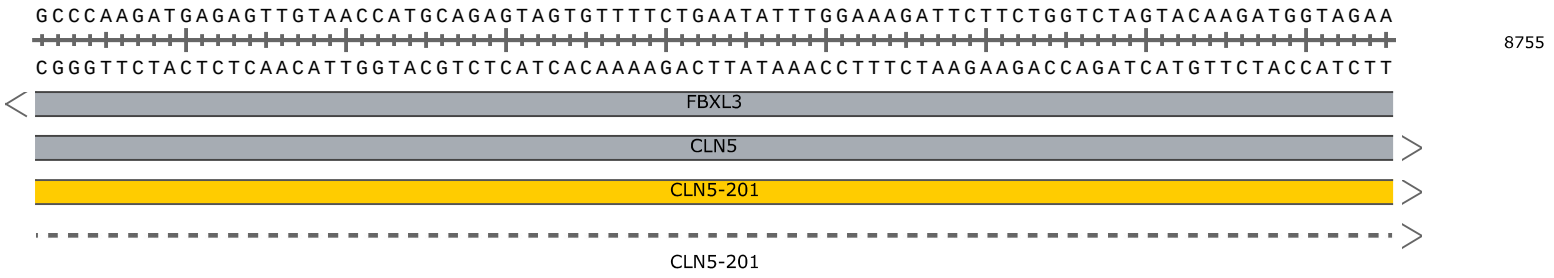
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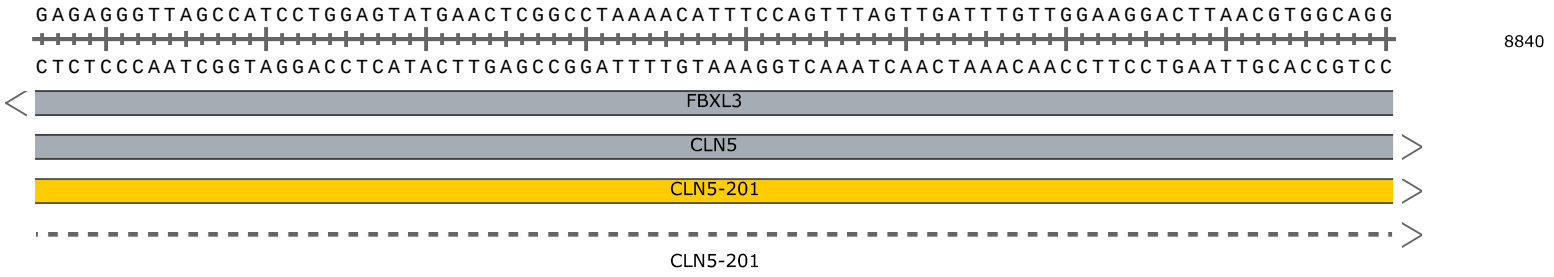
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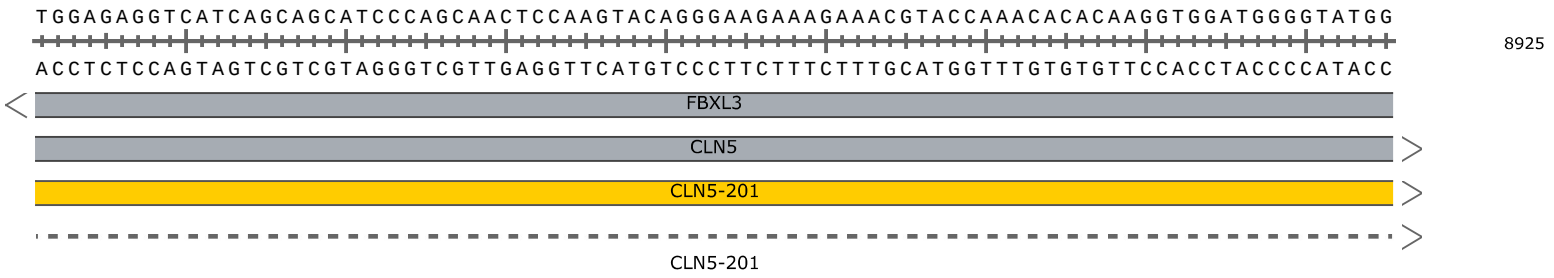
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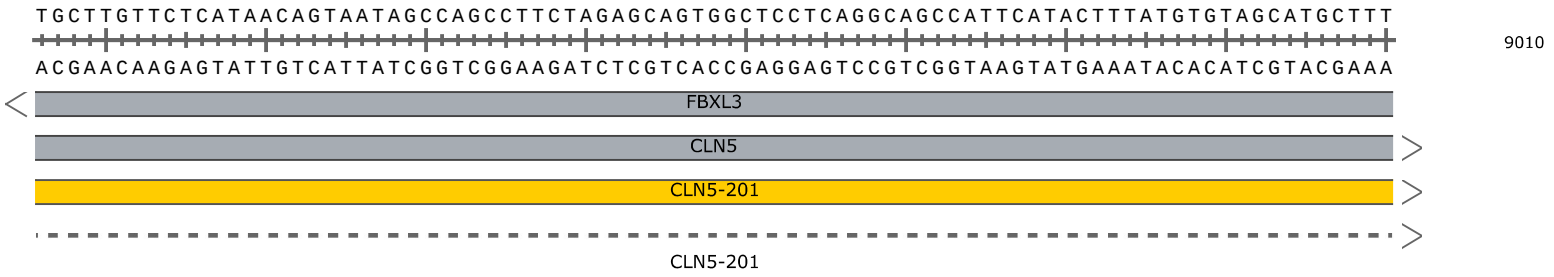
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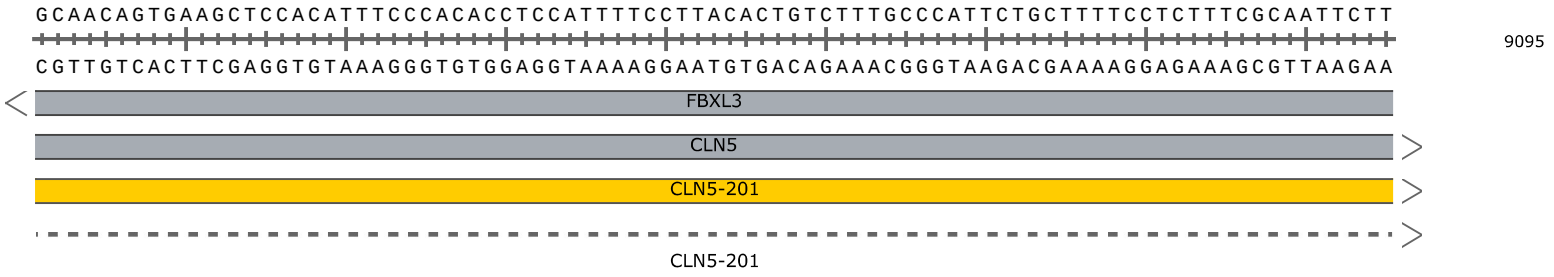
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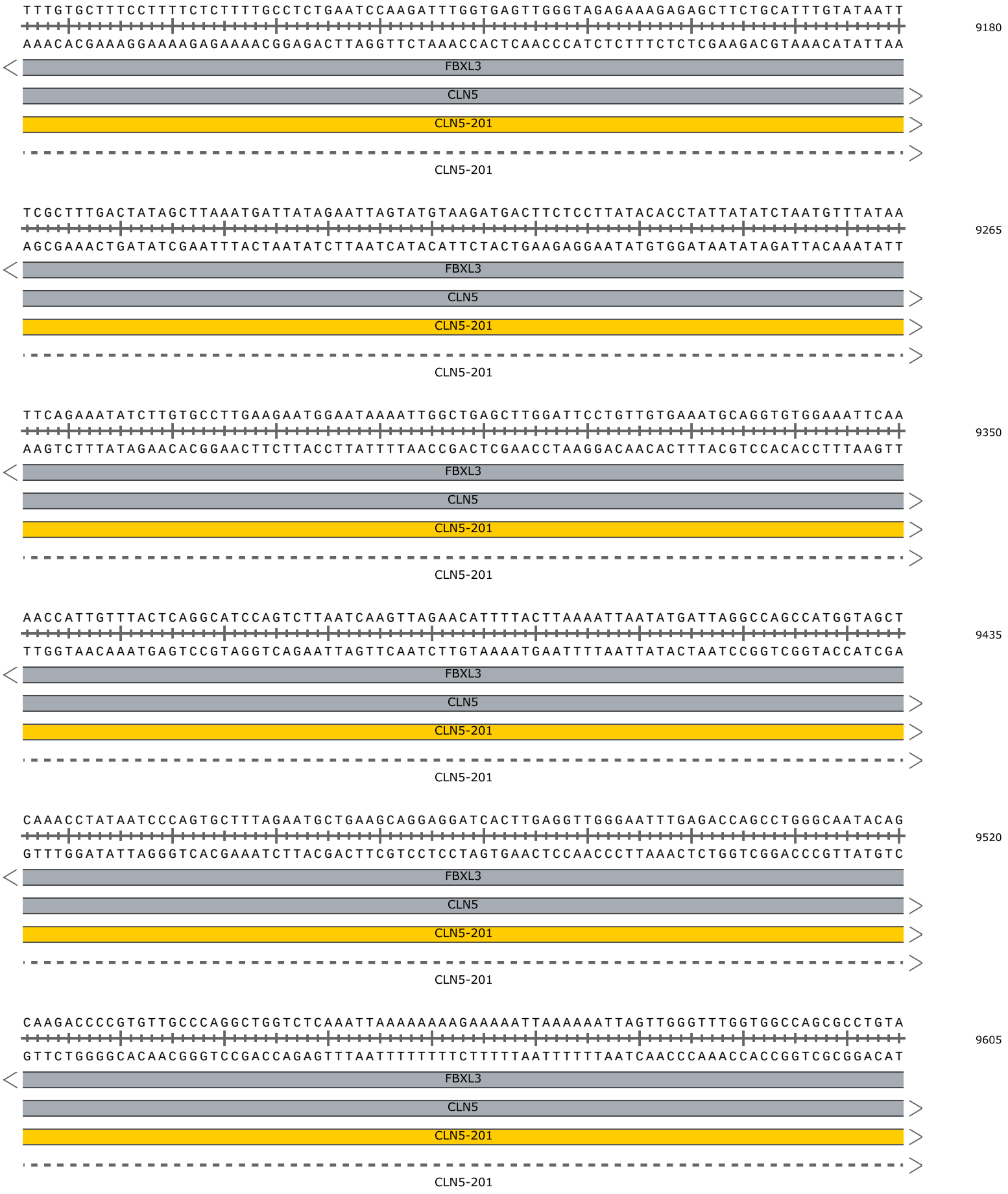
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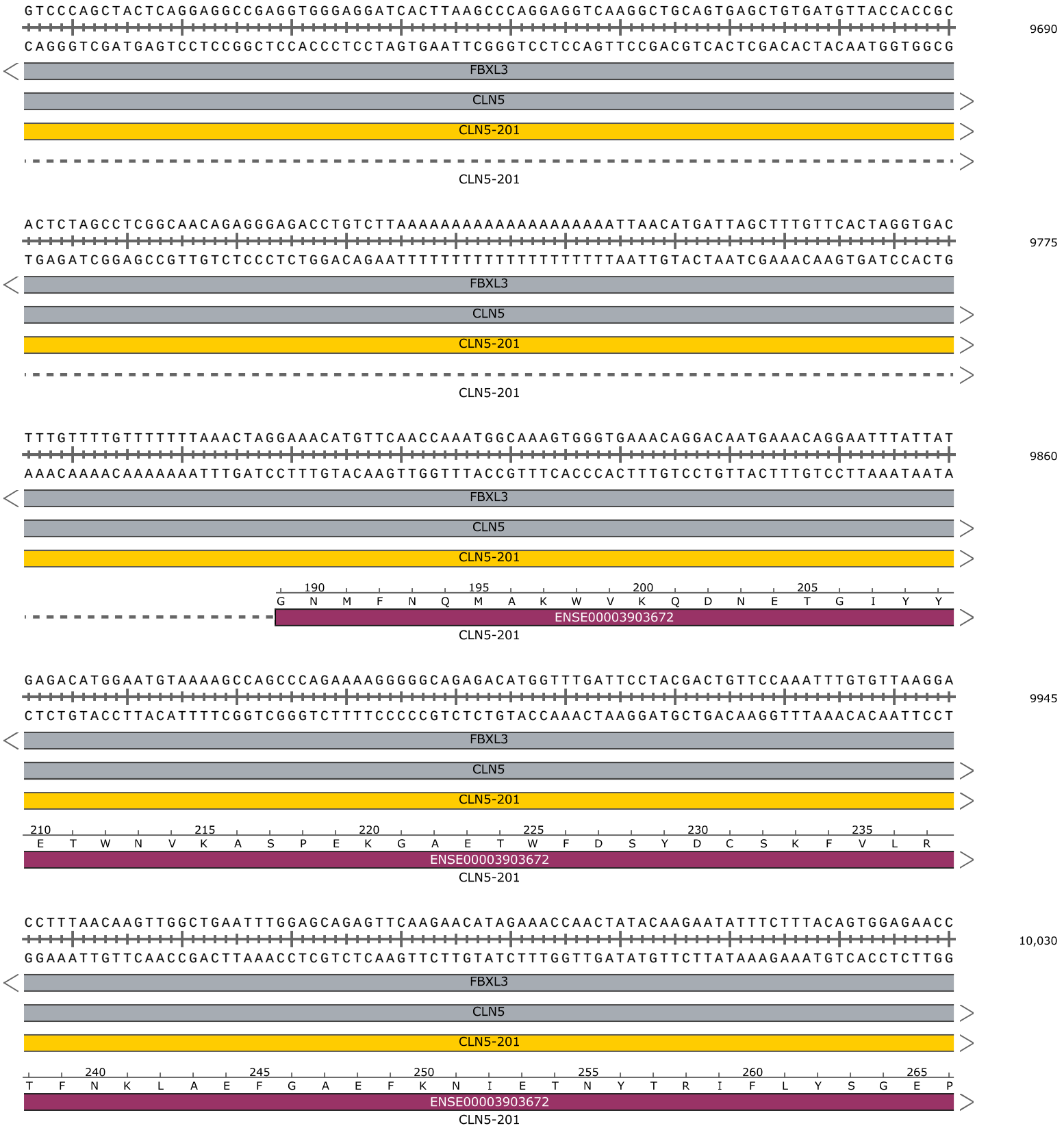
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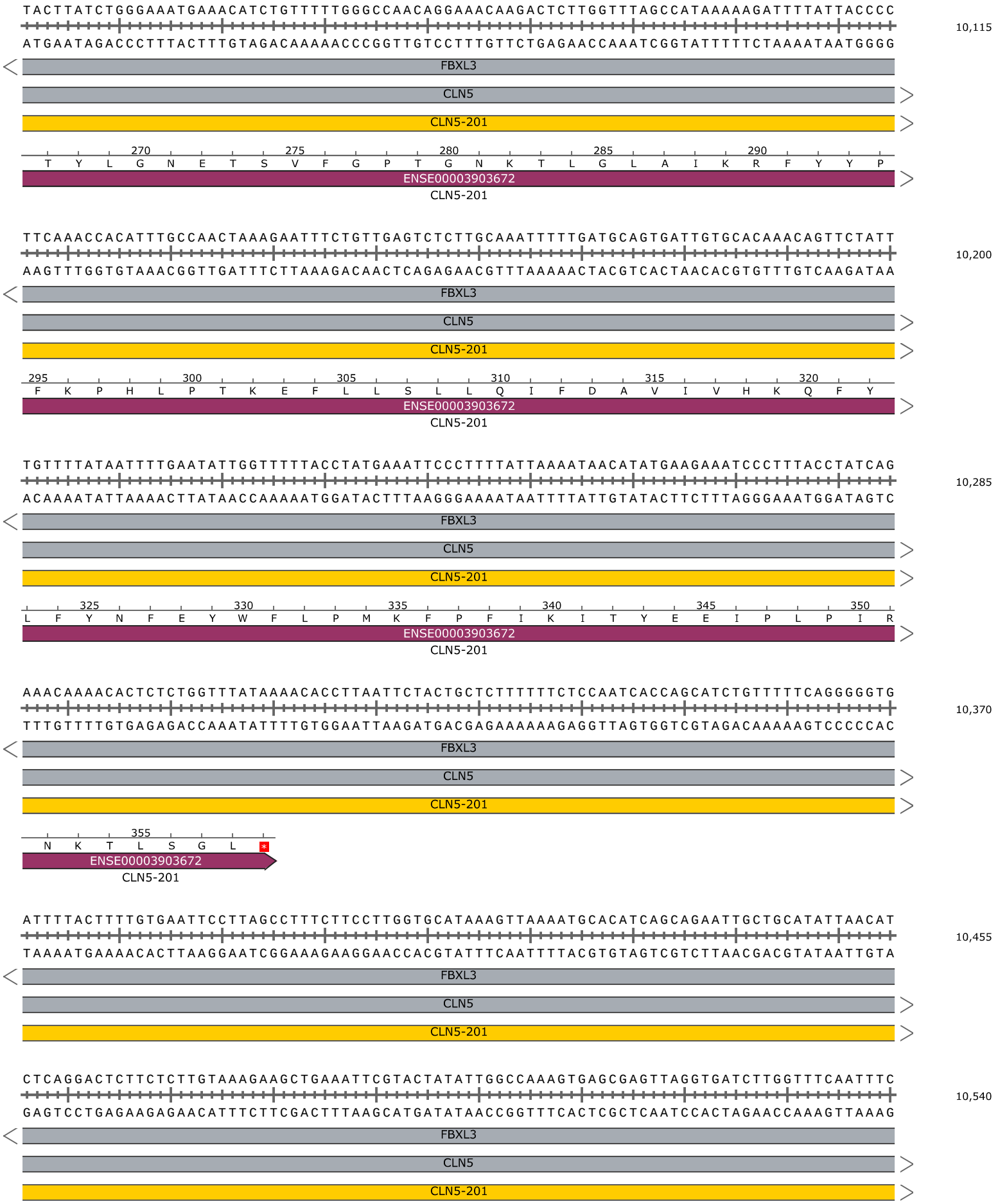
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CLN5
CLN5-201
295 300 305 310 315 320
F K P H L P T K E F L L S L L Q I F D A V I V H K Q F Y
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CLN5-201
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CLN5
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L F Y N F E Y W F L P M K F P F I K I T Y E E I P L P I R
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CLN5
CLN5-201


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CLN5-201


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CLN5-201


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CLN5-201


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CLN5


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CLN5


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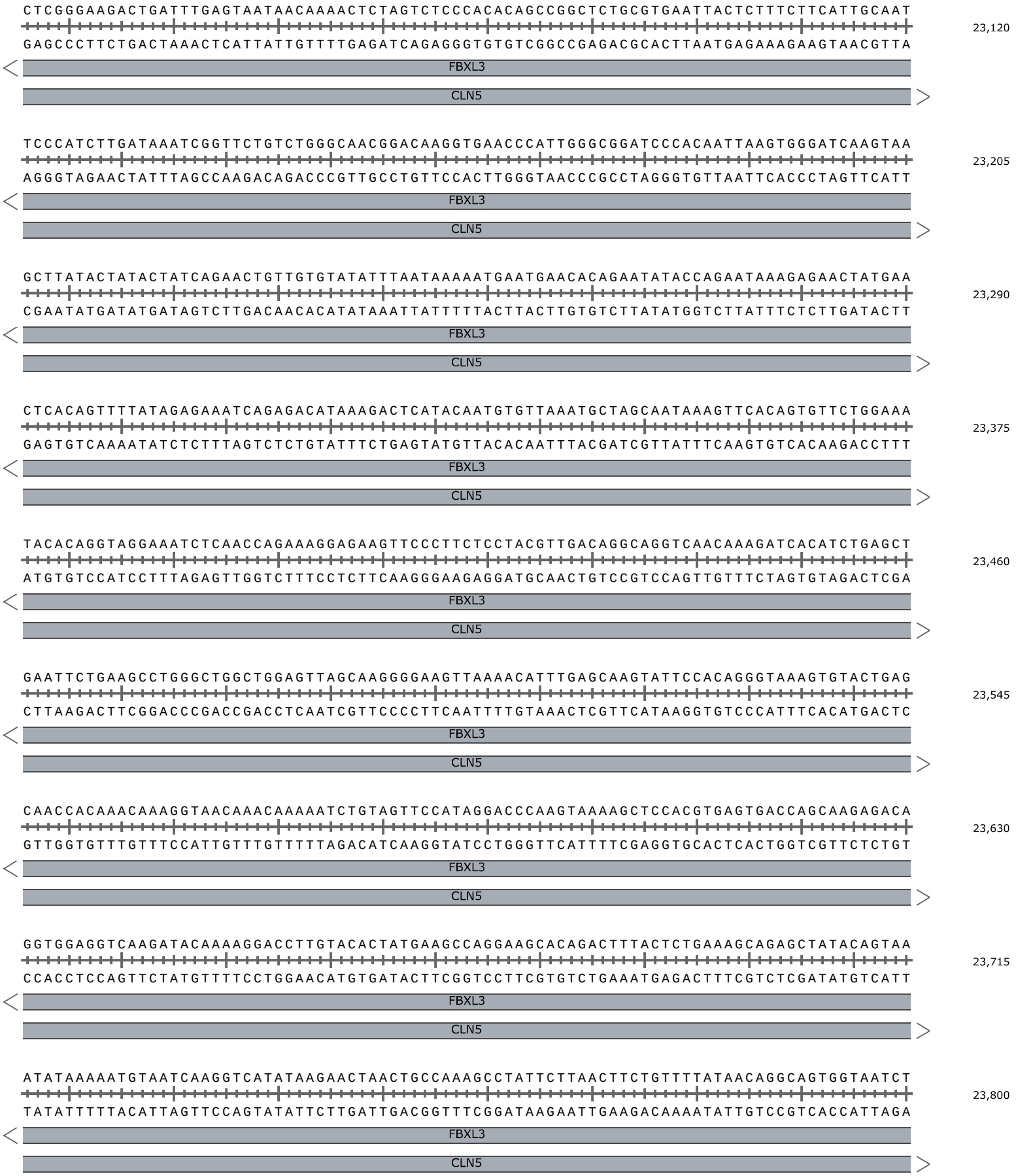
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CLN5


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CLN5


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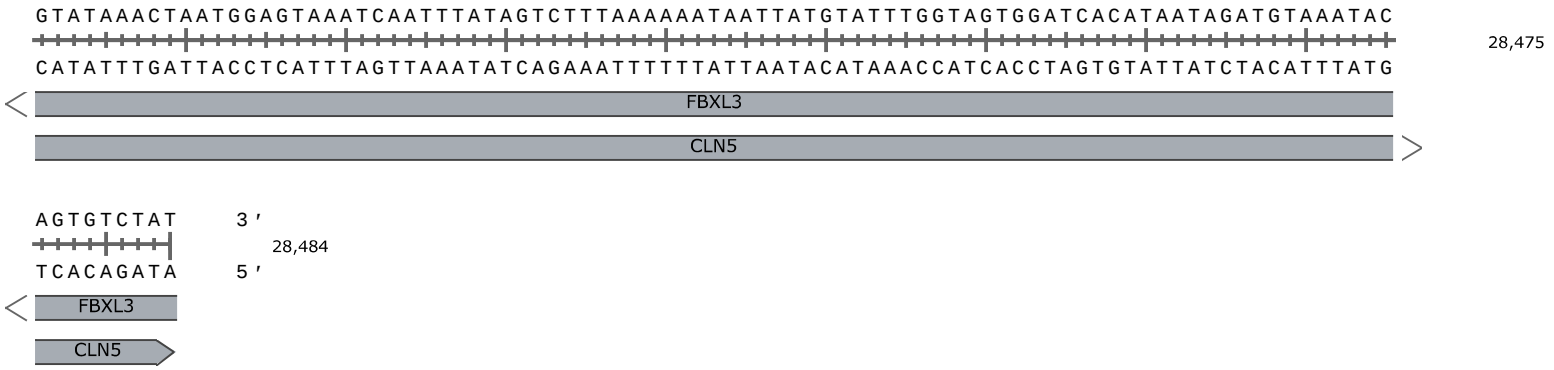
CLN5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CLN5
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CLN5

	Feature		Location	Size			Type
✓	**CLN5**		1 .. 28,484	28,484 bp		→	gene
	/note	=	gene ENSG00000102805 Protein coding				
	CLN5-208		1 .. 14,458	14,458 bp		→	prim_transcript
	/note	=	primary transcript ENST00000636183				
	CLN5-216		1385 .. 11,818	10,434 bp		→	prim_transcript
	/note	=	primary transcript ENST00000636780				
	CLN5-202		1400 .. 7204	5805 bp		→	prim_transcript
	/note	=	primary transcript ENST00000485938				
			1419 ..138,930	137,512 bp		→	gene
	/note	=	gene ENSG00000283208 Protein coding				
			1419 .. 87,366	85,948 bp		→	prim_transcript
	/note	=	primary transcript ENST00000638147 Protein coding				
	CLN5-219		1419 .. 9317	7899 bp		→	prim_transcript
	/note	=	primary transcript ENST00000637537				
✓	**CLN5-201**		1422 .. 14,458	13,037 bp		→	prim_transcript
	/note	=	primary transcript ENST00000377453				
	CLN5-218		1428 .. 26,472	25,045 bp		→	prim_transcript
	/note	=	primary transcript ENST00000637397				
	CLN5-207		1430 .. 5440	4011 bp		→	prim_transcript
	/note	=	primary transcript ENST00000635989				
	CLN5-203		1432 .. 11,686	10,255 bp		→	prim_transcript
	/note	=	primary transcript ENST00000616833				
	CLN5-211		1437 .. 28,484	27,048 bp		→	prim_transcript
	/note	=	primary transcript ENST00000636525				
	CLN5-215		1439 .. 27,707	26,269 bp		→	prim_transcript
	/note	=	primary transcript ENST00000636767				
	CLN5-205		1439 .. 20,309	18,871 bp		→	prim_transcript
	/note	=	primary transcript ENST00000635905 Retained intron				
	CLN5-211		1440 .. 26,486	25,047 bp		→	CDS
	▸ 5 segments = 813 bp						
	/note	=	coding sequence ENSP00000490078				
	/translation	=	MAQEVDTAQGAEMRRGAGAARGRASWCWALALLWLAVVPGWSRVSGIPSRRHWPVPYK,,RFDFRPKPDPYCQAKYTFCPTGSPIPVMEGDD DIEVFRLQAPVWEFKYGDLLGHL,,KIMHDAIGFRSTLTGKNYTMEWYELFQLGNCTFPHLRPEMDAPFWCNQGAACFFEGIDDVHWKENGTLV QVATIS,,GFHHVGQDSIELRTSSDPPILASQSAGITDVSHCTRPTIRILPQRGTLYYL,,LWTKTFLLCSLQFSWDFQNIATPYFNLLPKP* 270 amino acids = 30.7 kDa				
	CLN5-215		1440 .. 26,087	24,648 bp		→	CDS
	▸ 5 segments = 747 bp						
	/note	=	coding sequence ENSP00000489855				
	/translation	=	MAQEVDTAQGAEMRRGAGAARGRASWCWALALLWLAVVPGWSRVSGIPSRRHWPVPYK,,RFDFRPKPDPYCQAKYTFCPTGSPIPVMEGDD DIEVFRLQAPVWEFKYGDLLGHL,,KIMHDAIGFRSTLTGKNYTMEWYELFQLGNCTFPHLRPEMDAPFWCNQGAACFFEGIDDVHWKENGTLV QVATIS,,GFHHVGQDSIELRTSSDPPILASQSAGITDVSHCTRPTIRILPQRGTLYYL,,RWVLLCCPG* 248 amino acids = 28.0 kDa				
	CLN5-218		1440 .. 22,246	20,807 bp		→	CDS
	▸ 5 segments = 822 bp						
	/note	=	coding sequence ENSP00000490422				
	/translation	=	MAQEVDTAQGAEMRRGAGAARGRASWCWALALLWLAVVPGWSRVSGIPSRRHWPVPYK,,RFDFRPKPDPYCQAKYTFCPTGSPIPVMEGDD DIEVFRLQAPVWEFKYGDLLGHL,,KIMHDAIGFRSTLTGKNYTMEWYELFQLGNCTFPHLRPEMDAPFWCNQGAACFFEGIDDVHWKENGTLV QVATIS,,GFHHVGQDSIELRTSSDPPILASQSAGITDVSHCTRPTIRILPQRGTLYYL,,SLALLPGWSTVVRPRLTATSASRIQTIFLPQPPK* 273 amino acids = 30.7 kDa				

	Feature	Location	Size		Type
✓	**CLN5-201**	1440 .. 10,310	8871 bp		CDS
	▸ 4 segments = 1077 bp				
	/note = coding sequence ENSP00000366673				
	/translation = MAQEVDTAQGAEMRRGAGAARGRASWCWALALLWLAVVPGWSRVSGIPSRRHWPVPYK,,RFDFRPKPDPYCQAKYTFCPTGSPIPVMEGDD DIEVFRLQAPVWEFKYGDLLGHL,,KIMHDAIGFRSTLTGKNYTMEWYELFQLGNCTFPHLRPEMDAPFWCNQGAACFFEGIDDVHWKENGTLV QVATIS,,GNMFNQMAKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNIETNYTRIFLYSGEPTYLGNETSV FGPTGNKTLGLAIKRFYYPFKPHLPTKEFLLSLLQIFDAVIVHKQFYLFYNFEYWFLPMKFPFIKITYEEIPLPIRNKTLSGL*				
	358 amino acids = 41.5 kDa				
	CLN5-208	1440 .. 10,310	8871 bp		CDS
	▸ 4 segments = 1077 bp				
	/note = coding sequence ENSP00000490181				
	/translation = MAQEVDTAQGAEMRRGAGAARGRASWCWALALLWLAVVPGWSRVSGIPSRRHWPVPYK,,RFDFRPKPDPYCQAKYTFCPTGSPIPVMEGDD DIEVFRLQAPVWEFKYGDLLGHL,,KIMHDAIGFRSTLTGKNYTMEWYELFQLGNCTFPHLRPEMDAPFWCNQGAACFFEGIDDVHWKENGTLV QVATIS,,GNMFNQMAKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNIETNYTRIFLYSGEPTYLGNETSV FGPTGNKTLGLAIKRFYYPFKPHLPTKEFLLSLLQIFDAVIVHKQFYLFYNFEYWFLPMKFPFIKITYEEIPLPIRNKTLSGL*				
	358 amino acids = 41.5 kDa				
	CLN5-203	1440 .. 9329	7890 bp		CDS
	▸ 4 segments = 624 bp				
	/note = coding sequence ENSP00000479547				
	/translation = MAQEVDTAQGAEMRRGAGAARGRASWCWALALLWLAVVPGWSRVSGIPSRRHWPVPYK,,RFDFRPKPDPYCQAKYTFCPTGSPIPVMEGDD DIEVFRLQAPVWEFKYGDLLGHL,,KIMHDAIGFRSTLTGKNYTMEWYELFQLGNCTFPHLRPEMDAPFWCNQGAACFFEGIDDVHWKENGTLV QVATIS,FISCALKNGIKLAFLGFLL*				
	207 amino acids = 23.4 kDa				
	CLN5-216	1440 .. 7412	5973 bp		CDS
	▸ 4 segments = 594 bp				
	/note = coding sequence ENSP00000489809				
	/translation = MAQEVDTAQGAEMRRGAGAARGRASWCWALALLWLAVVPGWSRVSGIPSRRHWPVPYK,,RFDFRPKPDPYCQAKYTFCPTGSPIPVMEGDD DIEVFRLQAPVWEFKYGDLLGHL,,KIMHDAIGFRSTLTGKNYTMEWYELFQLGNCTFPHLRPEMDAPFWCNQGAACFFEGIDDVHWKENGTLV QVATIS,DGETEAQRC*				
	197 amino acids = 22.4 kDa				
	CLN5-219	1440 .. 7412	5973 bp		CDS
	▸ 4 segments = 594 bp				
	/note = coding sequence ENSP00000489711				
	/translation = MAQEVDTAQGAEMRRGAGAARGRASWCWALALLWLAVVPGWSRVSGIPSRRHWPVPYK,,RFDFRPKPDPYCQAKYTFCPTGSPIPVMEGDD DIEVFRLQAPVWEFKYGDLLGHL,,KIMHDAIGFRSTLTGKNYTMEWYELFQLGNCTFPHLRPEMDAPFWCNQGAACFFEGIDDVHWKENGTLV QVATIS,DGETEAQRC*				
	197 amino acids = 22.4 kDa				
	CLN5-202	1440 .. 5479	4040 bp		CDS
	▸ 3 segments = 576 bp				
	/note = coding sequence ENSP00000482959				
	/translation = MAQEVDTAQGAEMRRGAGAARGRASWCWALALLWLAVVPGWSRVSGIPSRRHWPVPYK,,RFDFRPKPDPYCQAKYTFCPTGSPIPVMEGDD DIEVFRLQAPVWEFKYGDLLGHL,,KIMHDAIGFRSTLTGKNYTMEWYELFQLGNCTFPHLRPEMDAPFWCNQGAACFFEGIDDVHWKENGTLV QVATISGKL*				
	191 amino acids = 21.7 kDa				
✓	**Donor Template SNV -> REV**	1484 .. 1583	100 bp		misc_feature
	CLN5-206	1501 .. 11,752	10,252 bp		prim_transcript
	/note = primary transcript ENST00000635915 Nonsense mediated decay				
✓	**Protospacer Sequence**	1502 .. 1521	20 bp		misc_feature
✓	**SNV**	1517 .. 1517	1 bp		misc_feature
	/note = SNV = A REV = G				
✓	**PAM**	1522 .. 1524	3 bp		misc_feature
	CLN5-209	1698 .. 4208	2511 bp		prim_transcript
	/note = primary transcript ENST00000636405				
	CLN5-213	1726 .. 10,672	8947 bp		prim_transcript
	/note = primary transcript ENST00000636681 Nonsense mediated decay				
	CLN5-214	1914 .. 11,805	9892 bp		prim_transcript
	/note = primary transcript ENST00000636705				

	Feature		Location		Size		Type
	CLN5-214		1914 .. 10,310		8397 bp	→	CDS
	▸ 4 segments = 913 bp						
	/note	=	coding sequence ENSP00000490937				
	/translation	=	WVQ,,AL*LPSKT*SLLSS*VYFLSNWLTYPSYGG***H*SFSITSPSMGI*IWRPPGTL,,ENYA*CHWIQKYINWQELHNGMV*TFPTWQLYISP SPT*NGCPFLV*SRRCLLF*GN**CSLEGKWDISSSSNYIR,,KHVQPNGKVGETGQ*NRNLL*DMECKSQPRKGGRDMV*FLRLFQICVKDL*Q VG*IWSRVQEHRNQLYKNISLQWRTYLSGK*NICFWANRKQDSWFSHKKILLPLQTTFAN*RISVESLANF*CSDCAQTVLFVL*F*ILVFTYEIP FY*NNI*RNPFTYQKQNTLWFI 504 codons (27 internal stop codons)				
✓	**FBXL3**		1939 .. 36,536		34,598 bp	←	gene
	/note	=	gene ENSG00000005812 Protein coding				
	FBXL3-206		1939 .. 24,922		22,984 bp	←	prim_transcript
	/note	=	primary transcript ENST00000485797				
	CLN5-210		3392 .. 9280		5889 bp	→	prim_transcript
	/note	=	primary transcript ENST00000636520 Retained intron				
	CLN5-212		4570 .. 5618		1049 bp	→	prim_transcript
	/note	=	primary transcript ENST00000636602 Retained intron				
	CLN5-217		4578 .. 11,770		7193 bp	→	prim_transcript
	/note	=	primary transcript ENST00000637278 Retained intron				
			5256 ..138,930		133,675 bp	→	prim_transcript
	/note	=	primary transcript ENST00000637192 Nonsense mediated decay				
			5295 .. 85,539		80,245 bp	→	prim_transcript
	/note	=	primary transcript ENST00000635838 Protein coding				
			5300 ..109,741		104,442 bp	→	prim_transcript
	/note	=	primary transcript ENST00000638101 Protein coding				
	FBXL3-205		8478 .. 28,027		19,550 bp	←	prim_transcript
	/note	=	primary transcript ENST00000477982				
	CLN5-204		9123 .. 9724		602 bp	→	prim_transcript
	/note	=	primary transcript ENST00000635761				
	FBXL3-201		14,601 .. 36,500		21,900 bp	←	prim_transcript
	/note	=	primary transcript ENST00000355619 Protein coding				
	FBXL3-202		16,906 .. 36,536		19,631 bp	←	prim_transcript
	/note	=	primary transcript ENST00000417323 Protein coding				
			17,943 .. 86,519		68,577 bp	→	prim_transcript
	/note	=	primary transcript ENST00000461131 Retained intron				
	FBXL3-203		24,506 .. 28,085		3580 bp	←	prim_transcript
	/note	=	primary transcript ENST00000470210				
	FBXL3-204		24,852 .. 36,426		11,575 bp	←	prim_transcript
	/note	=	primary transcript ENST00000472949				

	Primer	Length	Binding Sites		Tm	Date Added
✓	**PCR Forward**	20-mer	1228 ..	1247	56°C	Oct 16, 2022
	/sequence = GACCAAAGCACCTTCCTGGA 55% GC / 6071.0 Da					
✓	**Sanger Sequencing**	20-mer	1228 ..	1247	56°C	Oct 16, 2022
	/sequence = GACCAAAGCACCTTCCTGGA 55% GC / 6071.0 Da					
✓	**Donor Template SNV -> REV**	100-mer	1484 ..	1583	90°C	Oct 13, 2022
	/sequence = GGGGATGCCCGAGACCCGGGACCAGCCCGGAACCACCGCGAGCCAAAGCAGCGCCAGGGCCCAGCACCAGGAAGCGCGTCCCCGA 68% GC / 30,720.7 Da					
✓	**gRNA Protospacer**	20-mer	1502 ..	1516	59°C	Oct 16, 2022
	/sequence = GGGACGCGCTTCCTGATGCT 65% GC / 6125.0 Da					
✓	**PCR Reverse**	19-mer	1654 ..	1672	58°C	Oct 16, 2022
	/sequence = CCCATCCCCCATCGTCAAC 63% GC / 5613.7 Da					