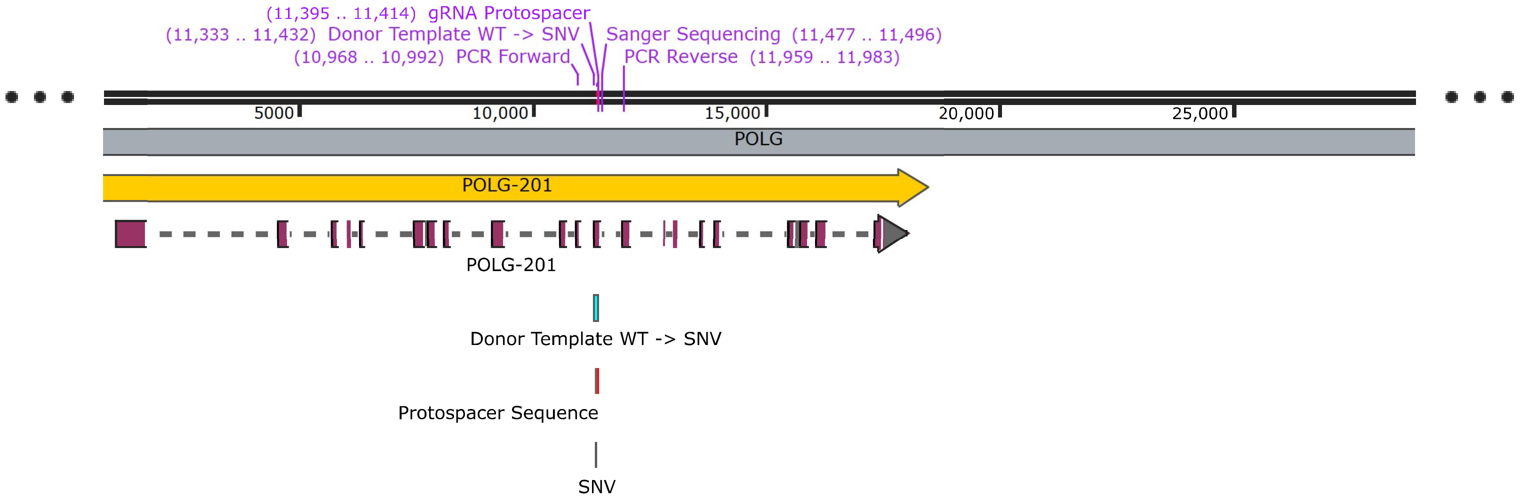

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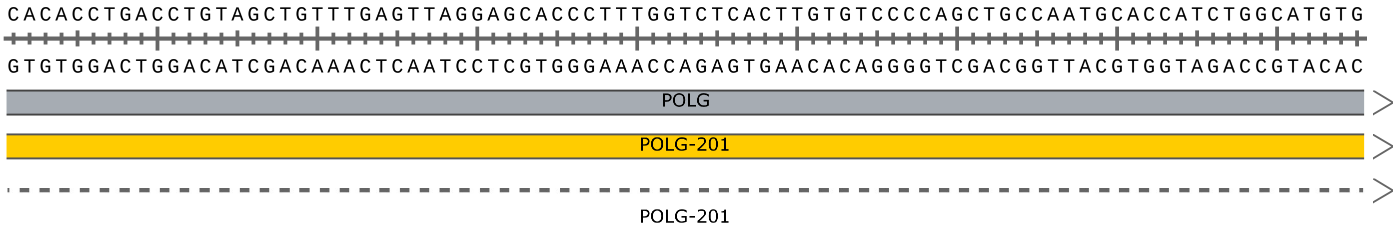

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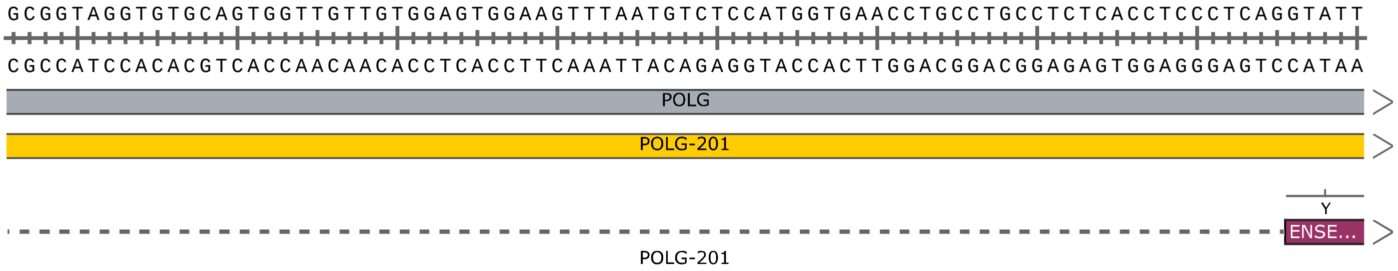

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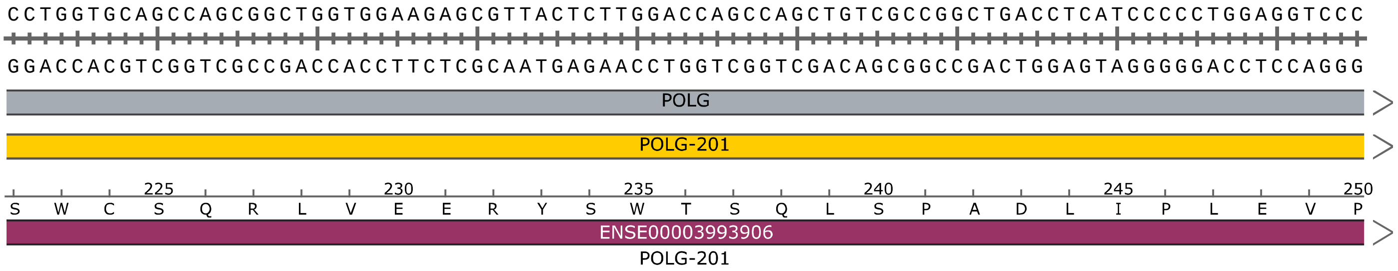

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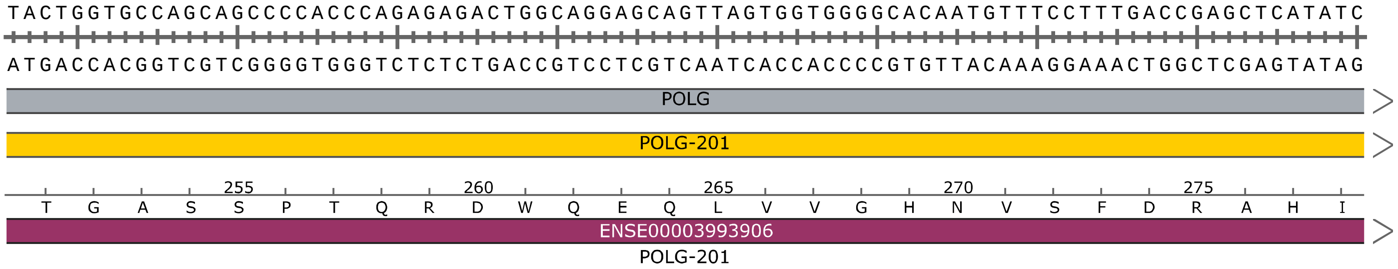

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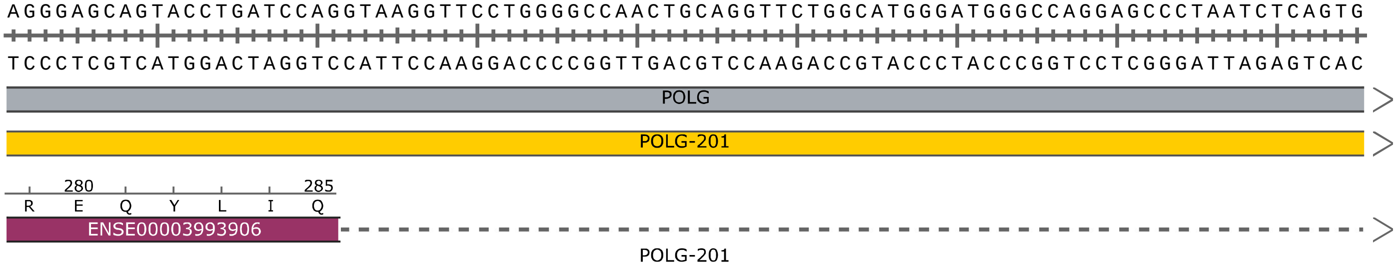

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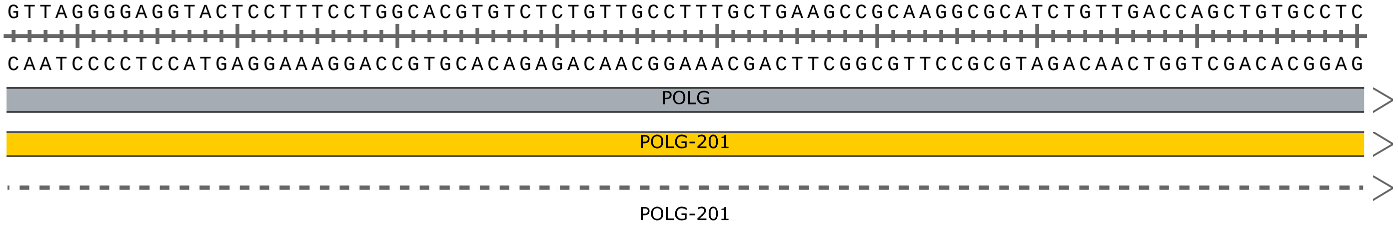

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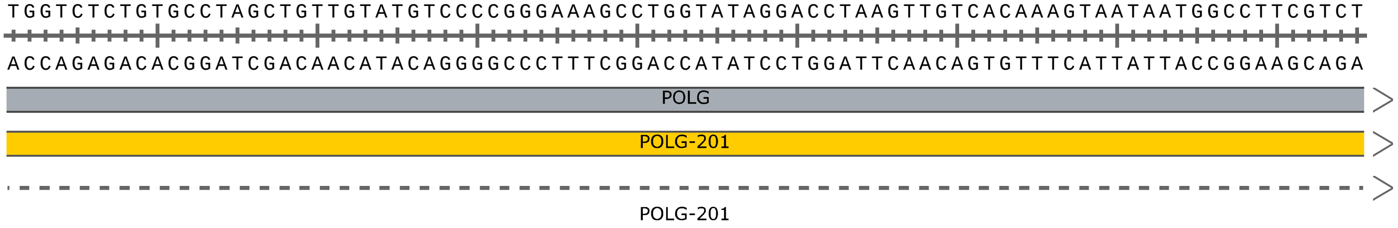

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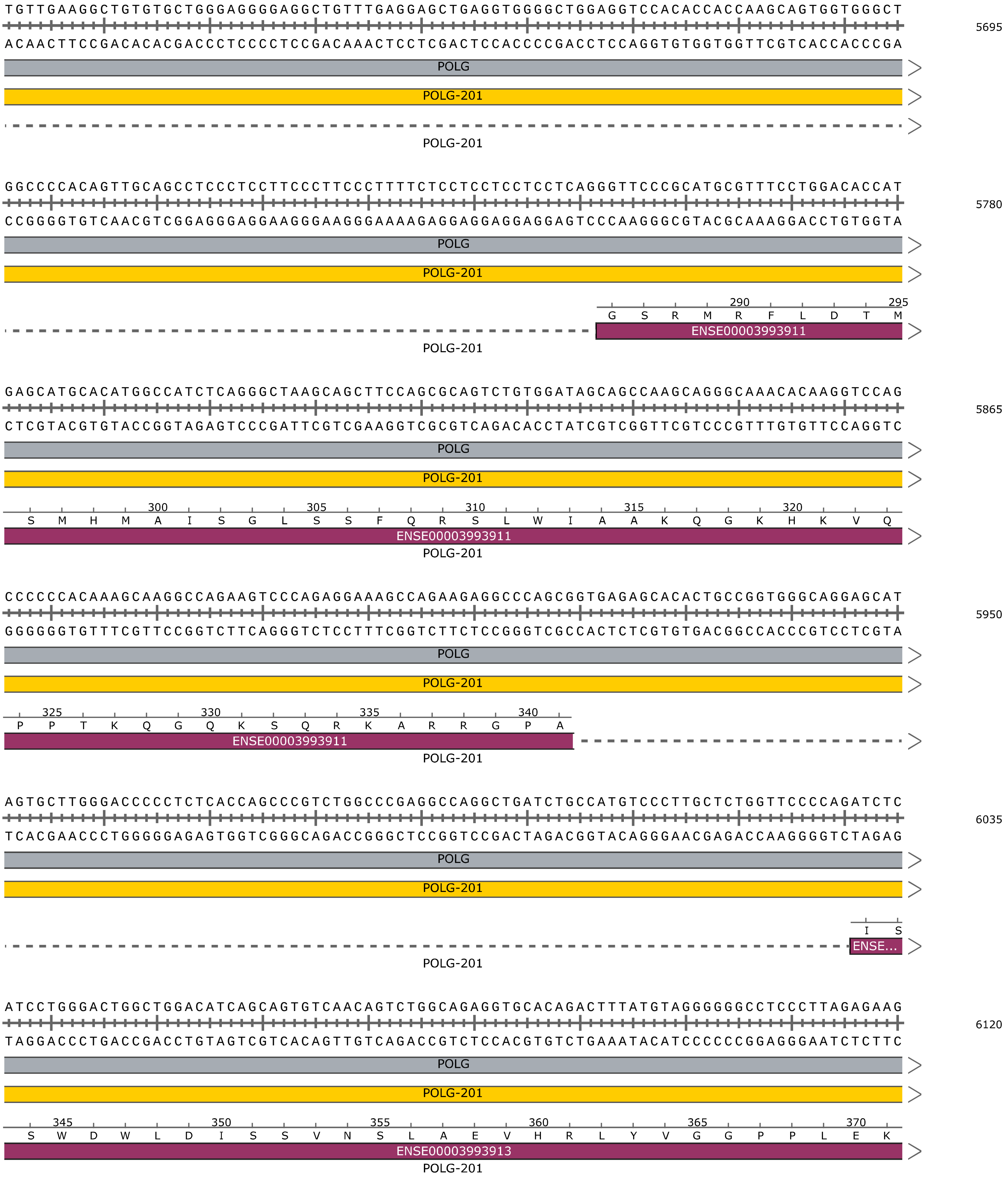
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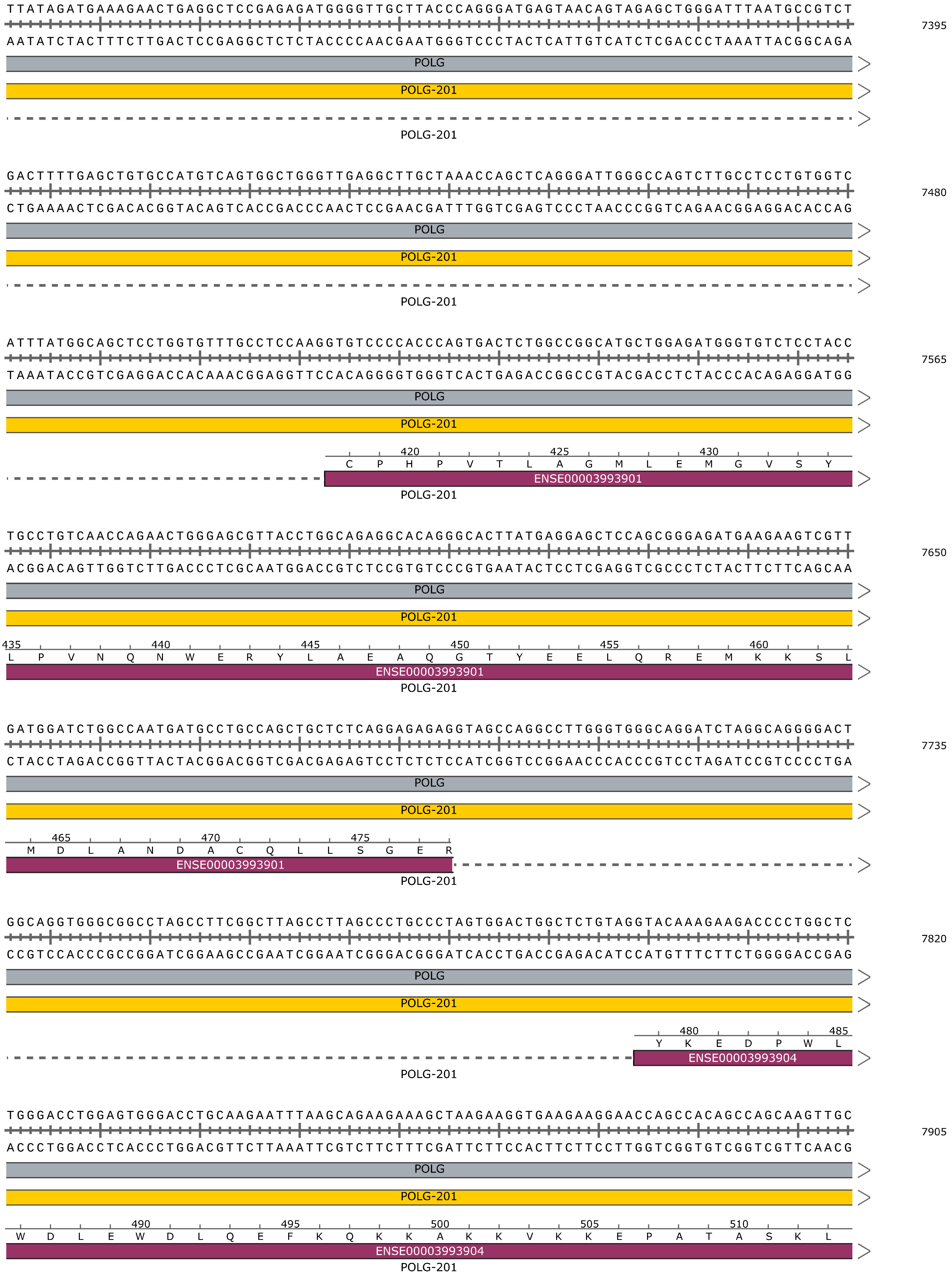
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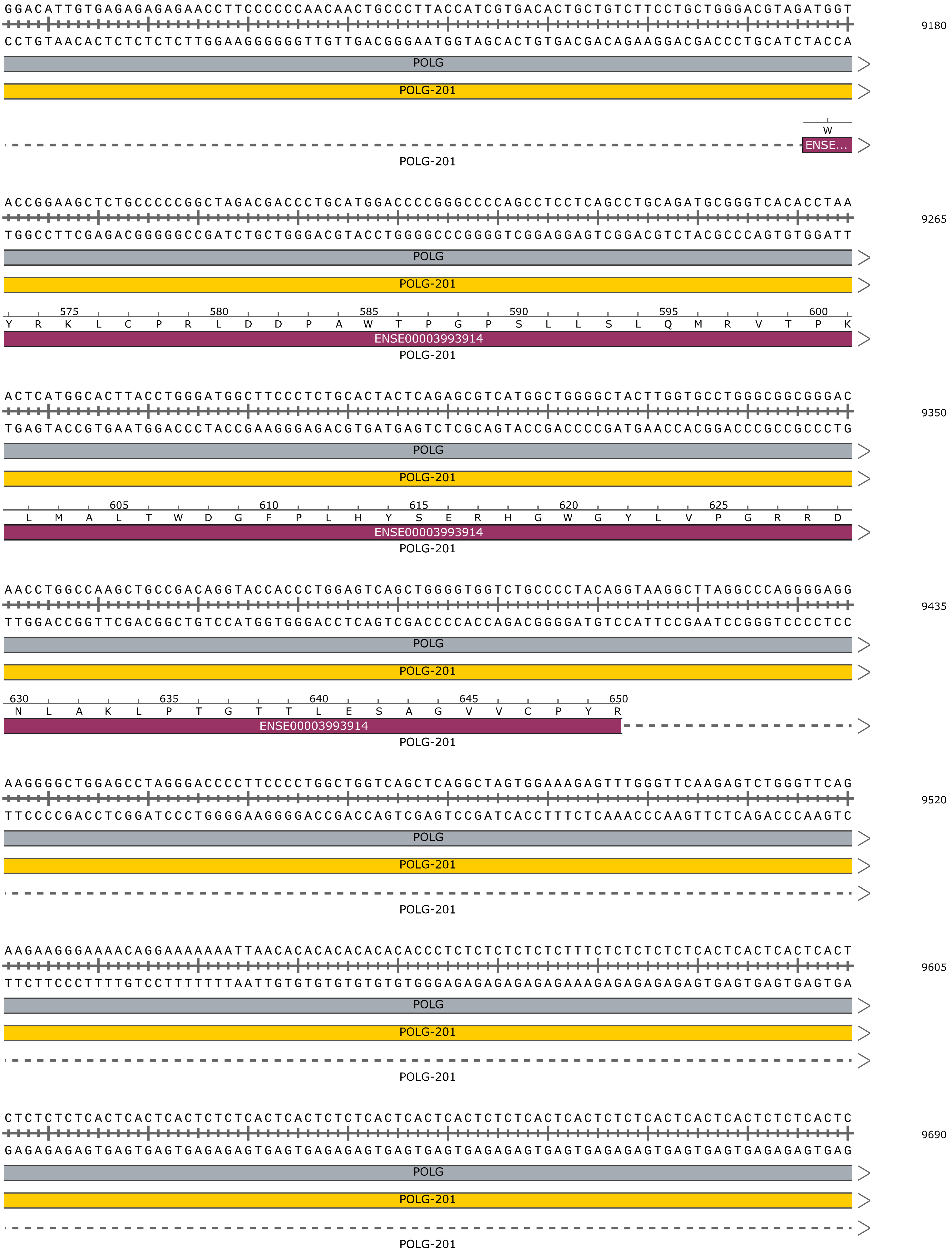
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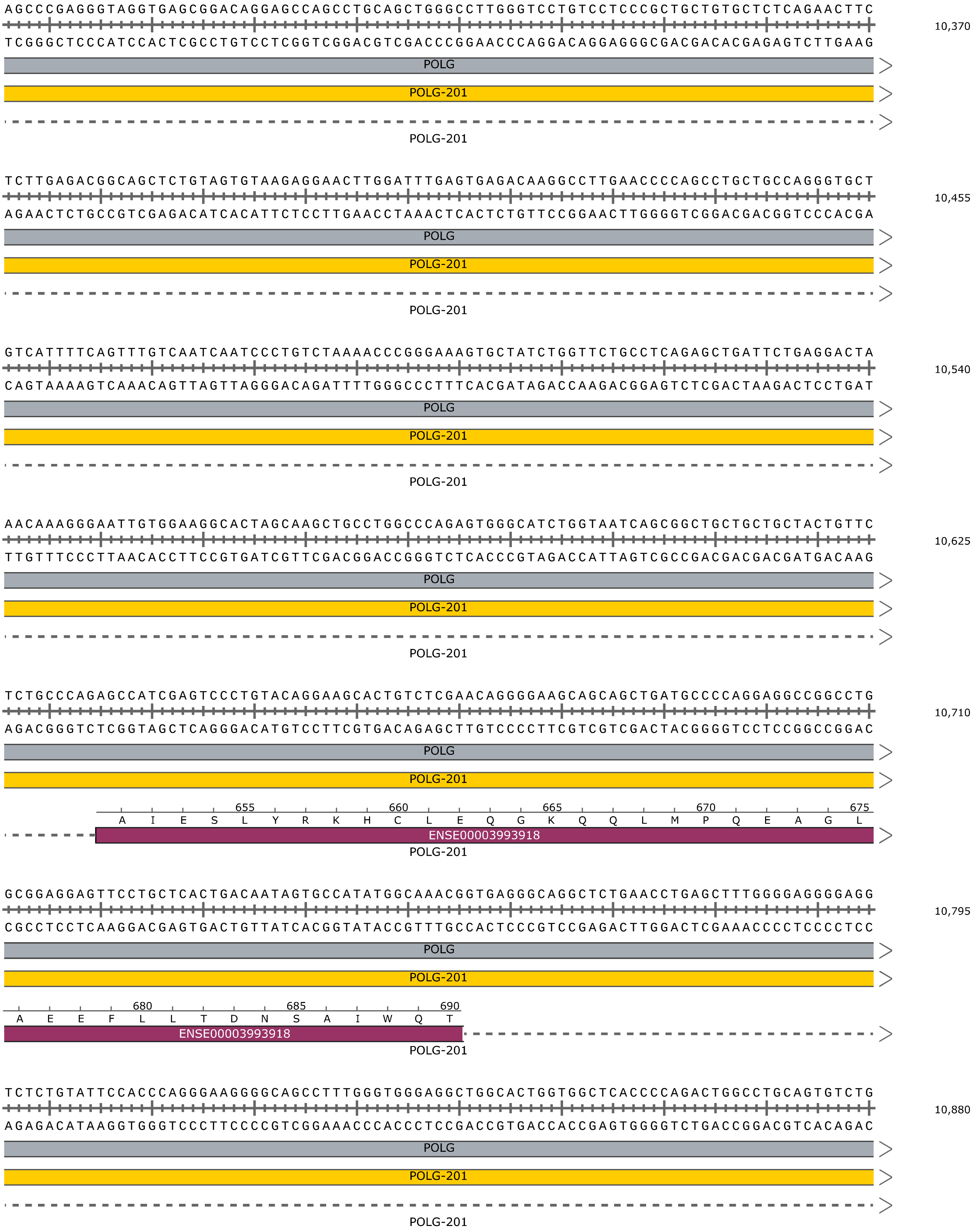
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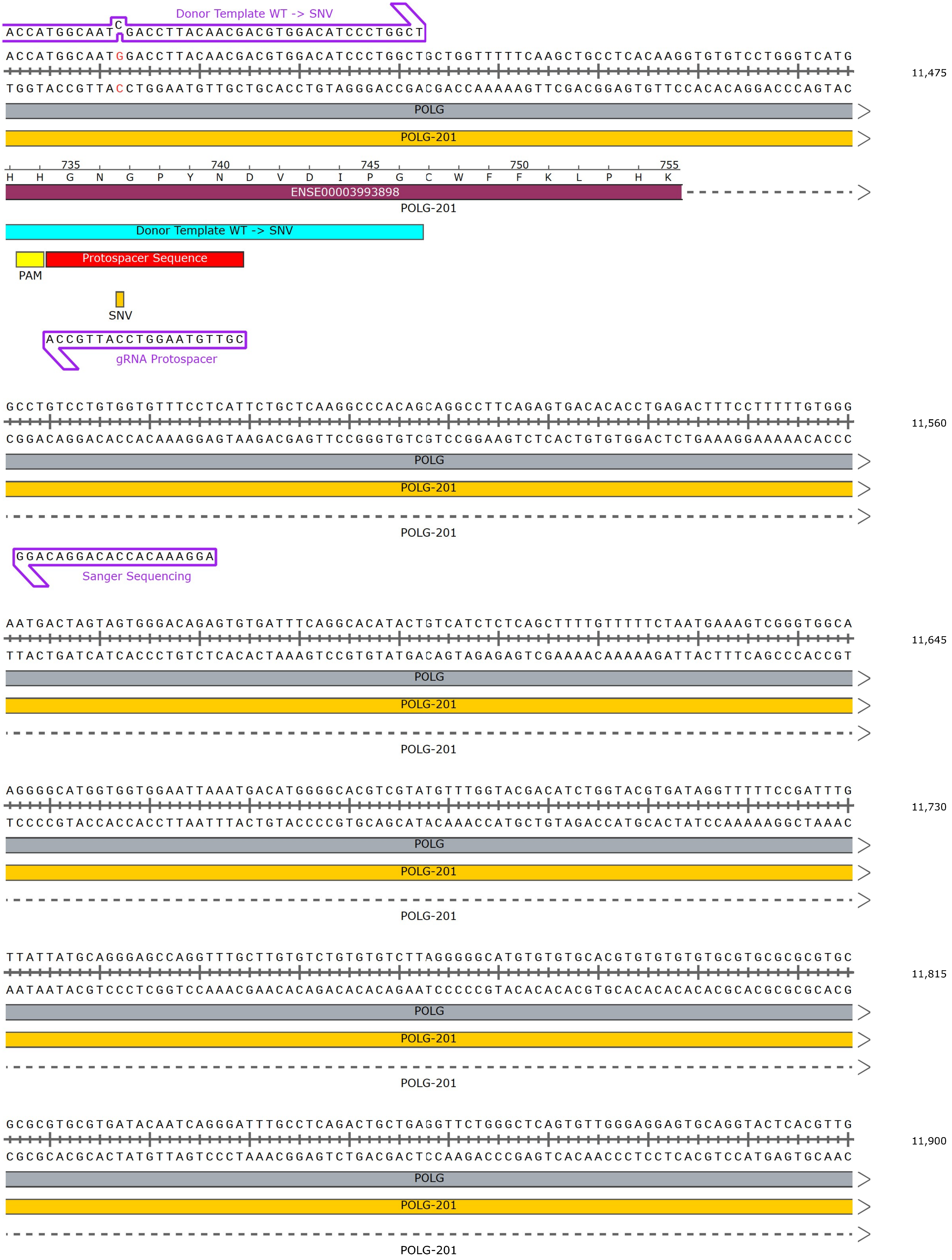
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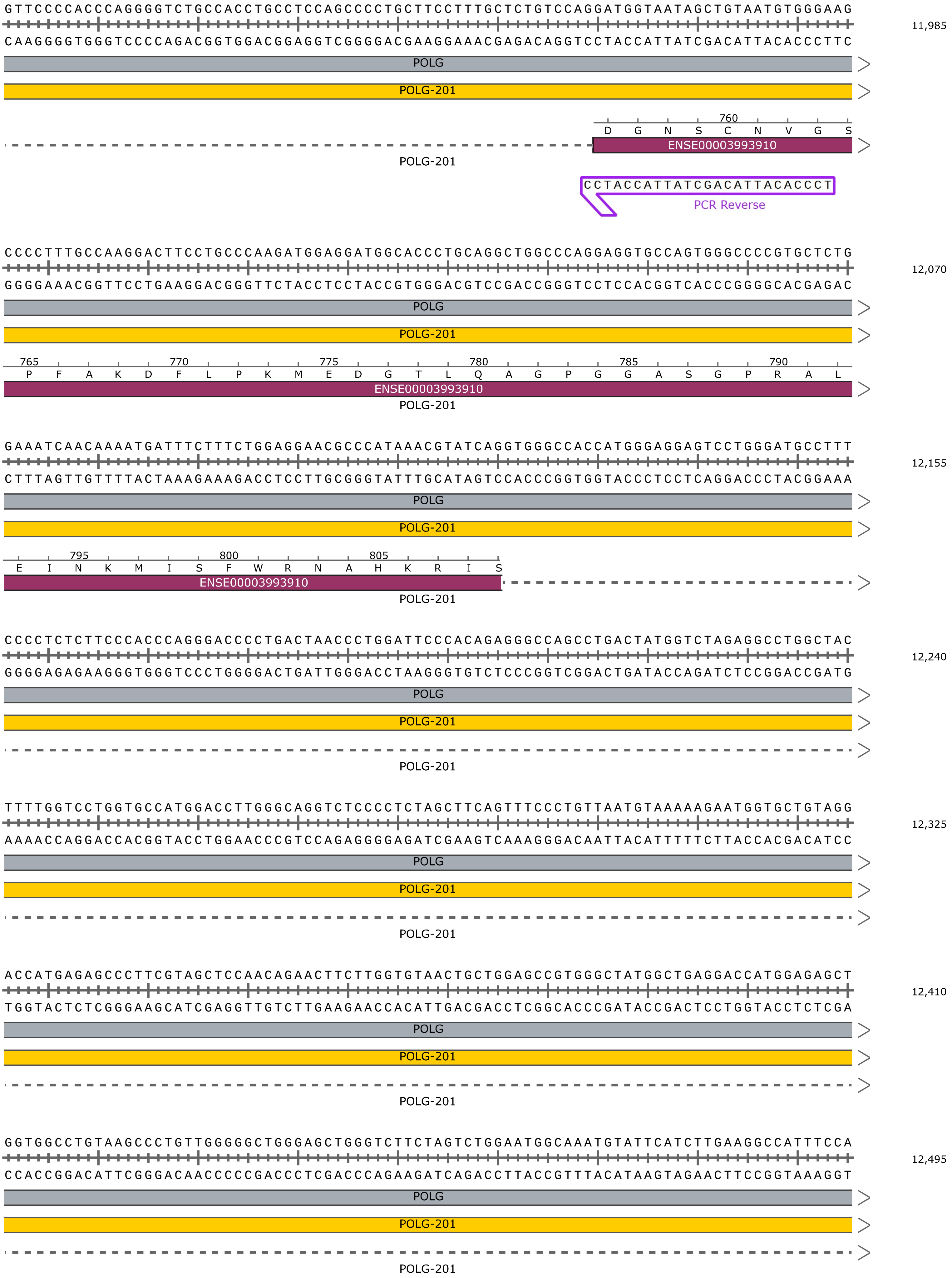

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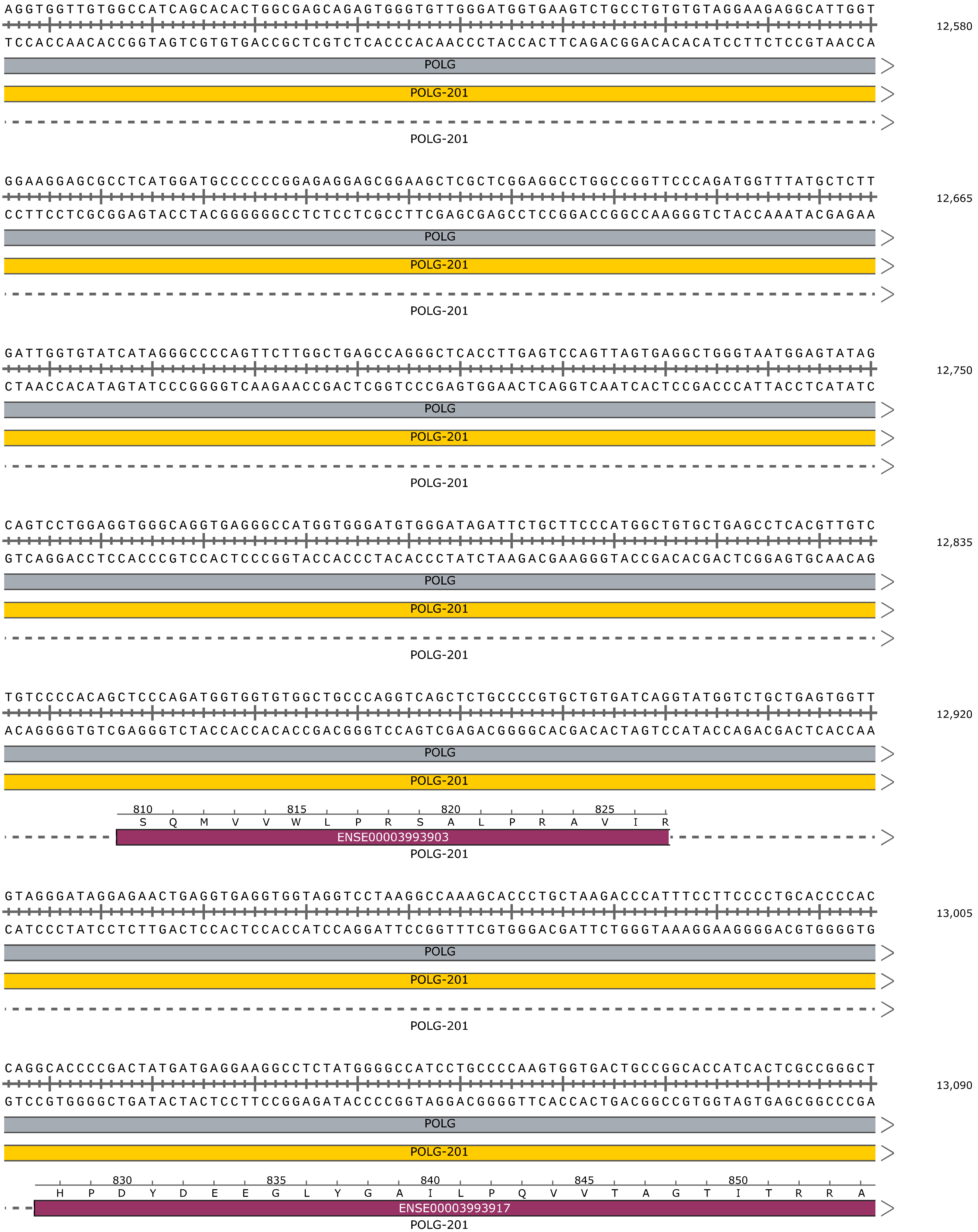
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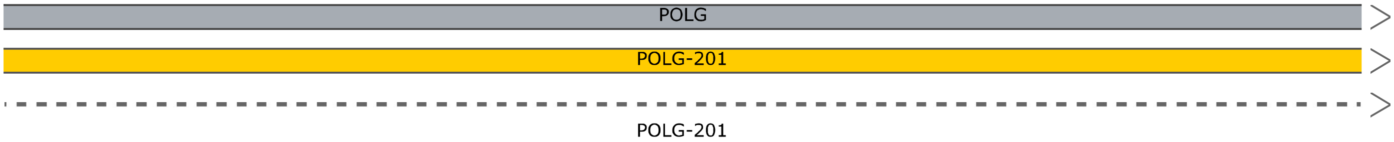

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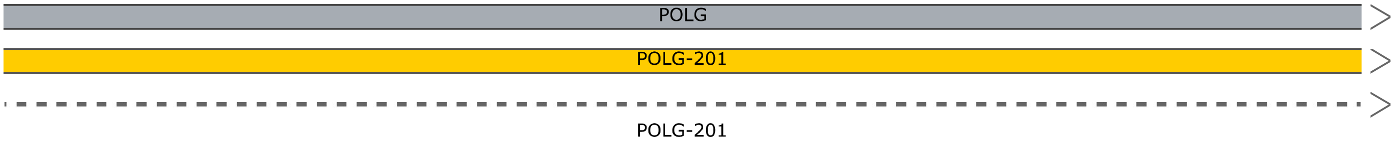

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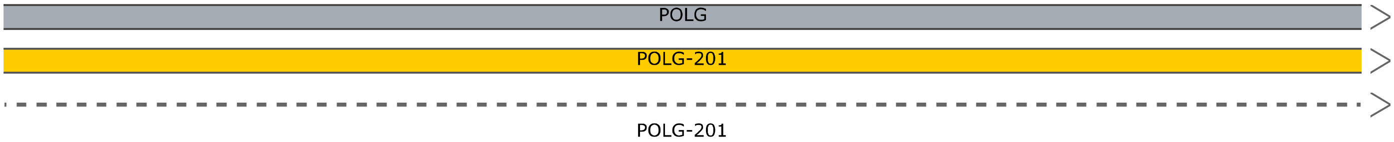

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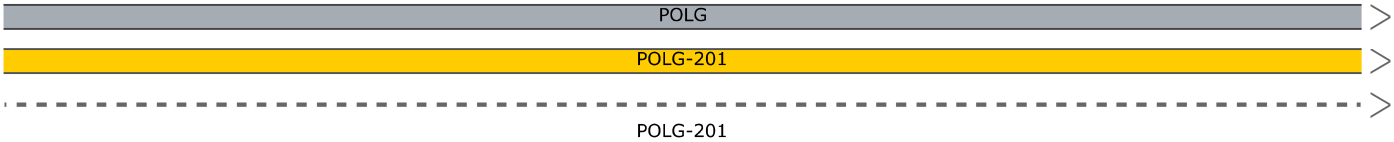

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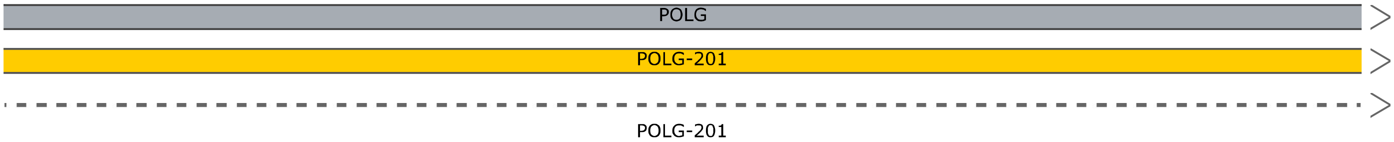

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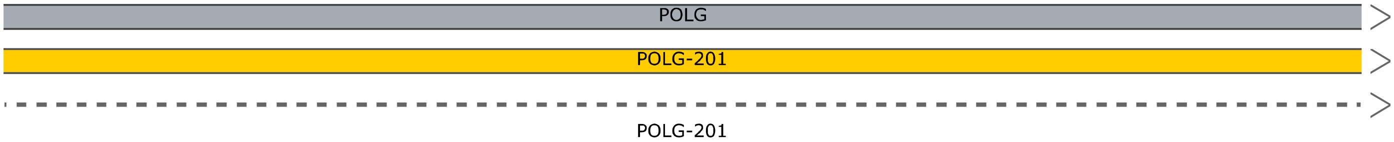

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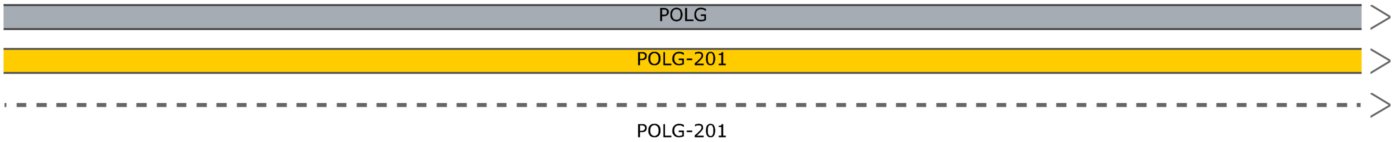

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14,960

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POLG-201

POLG-201

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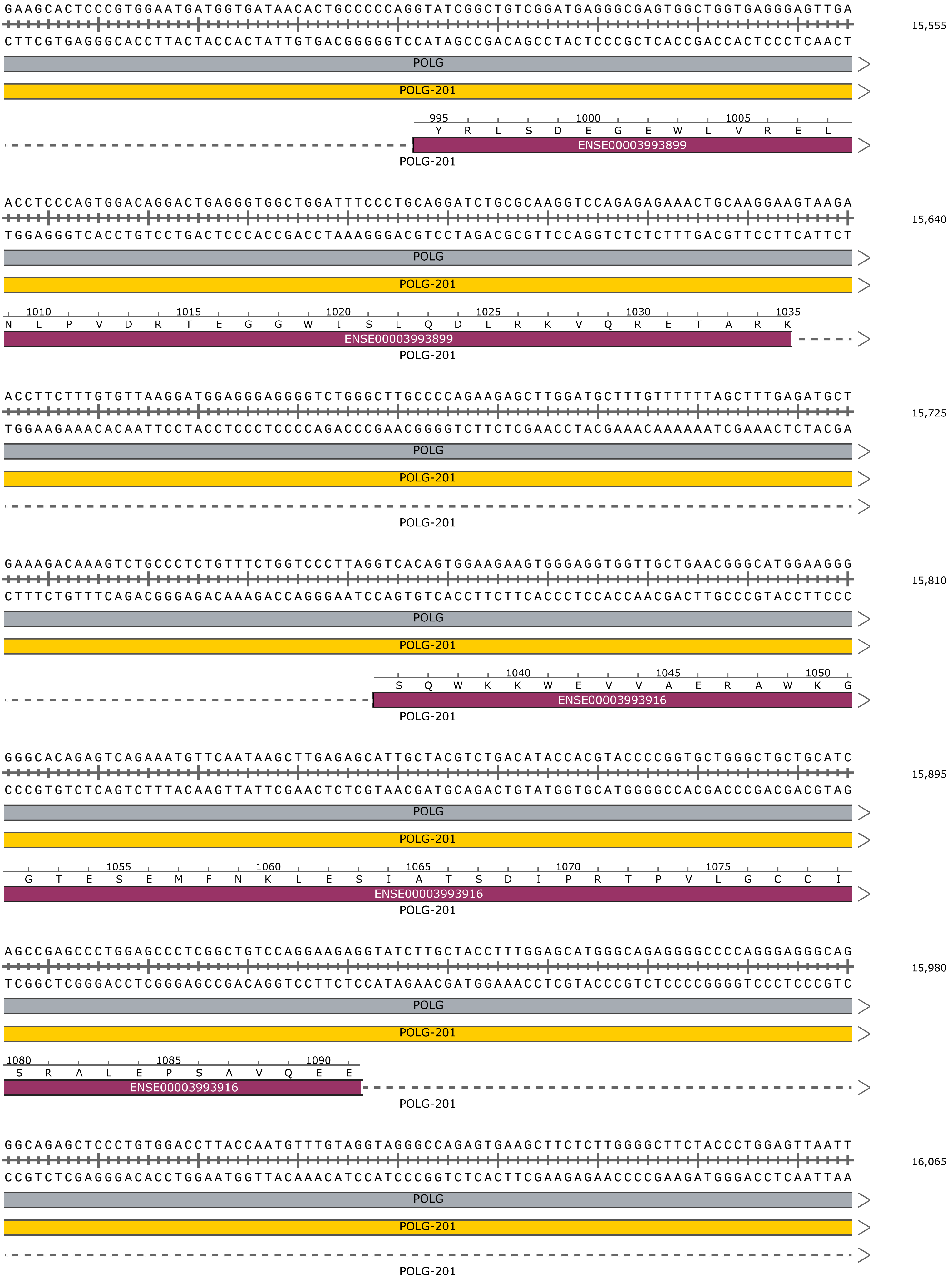
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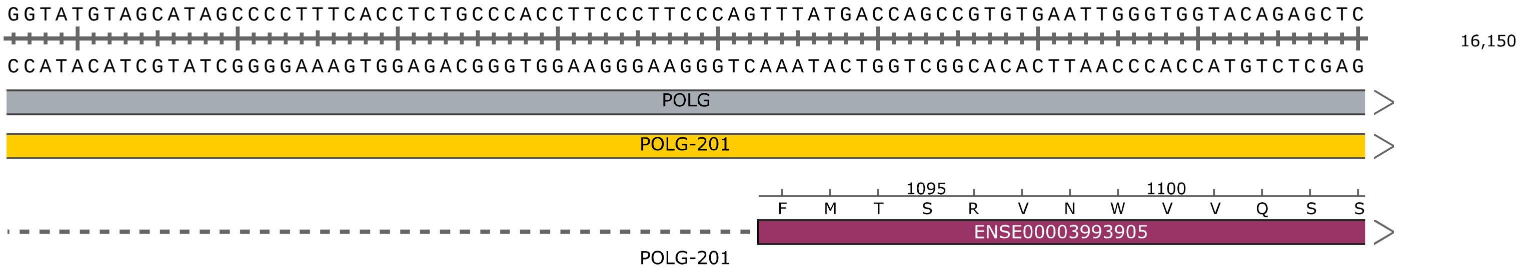
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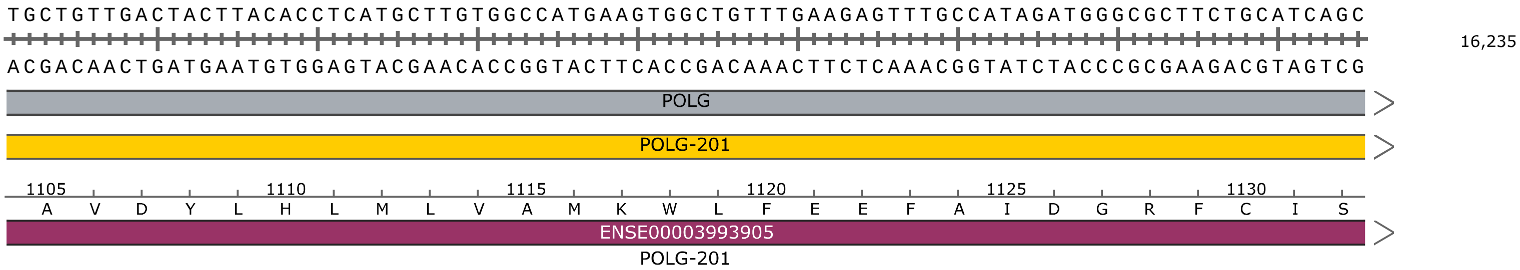
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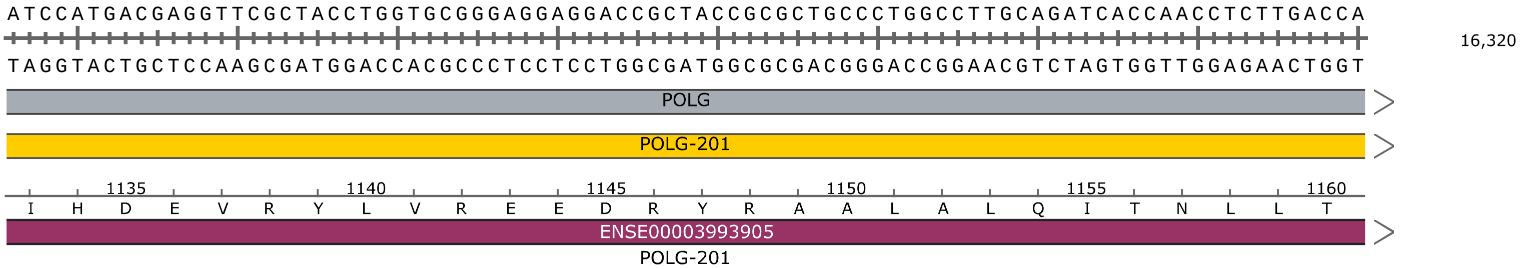
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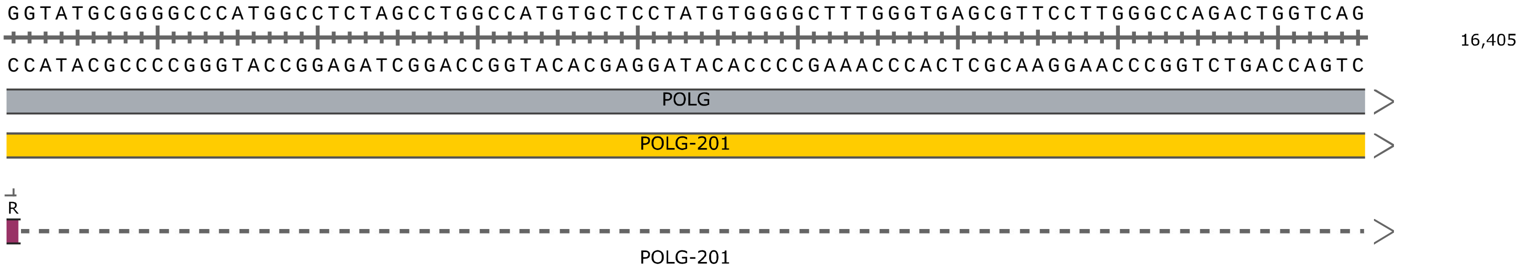
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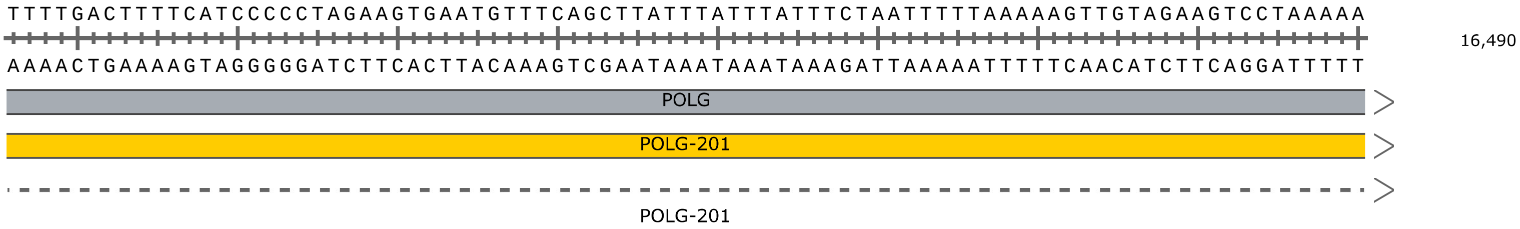
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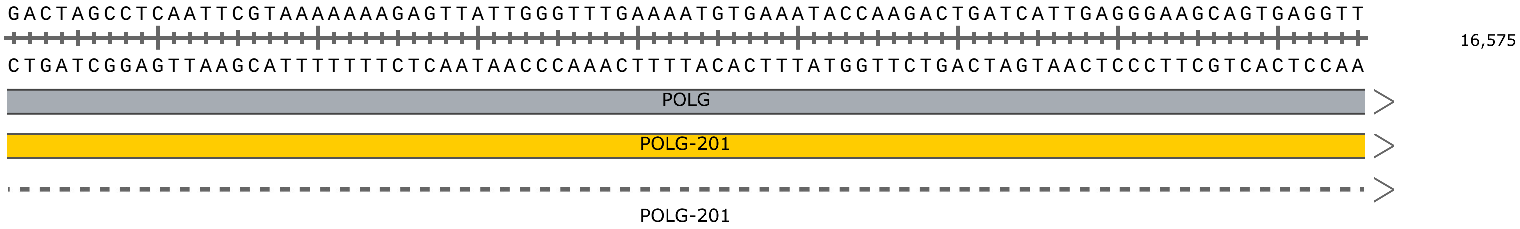
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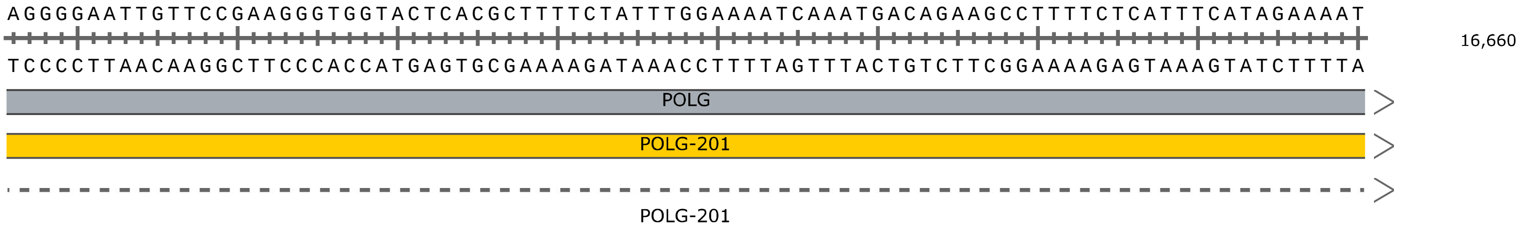
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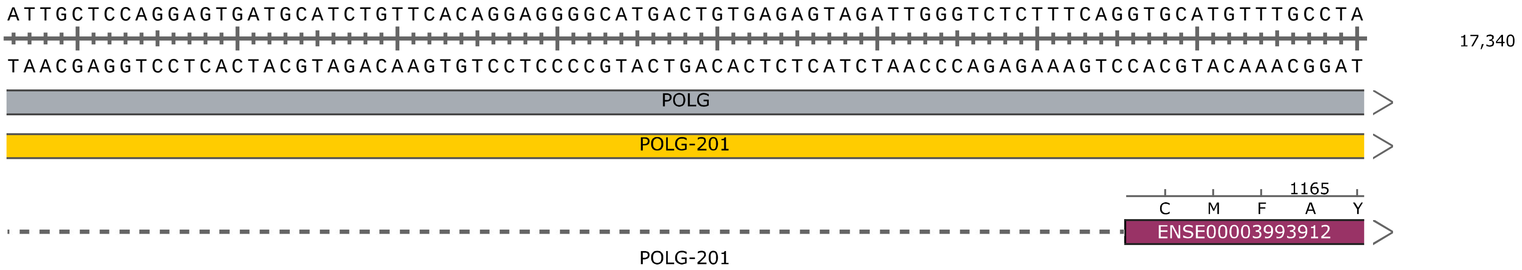
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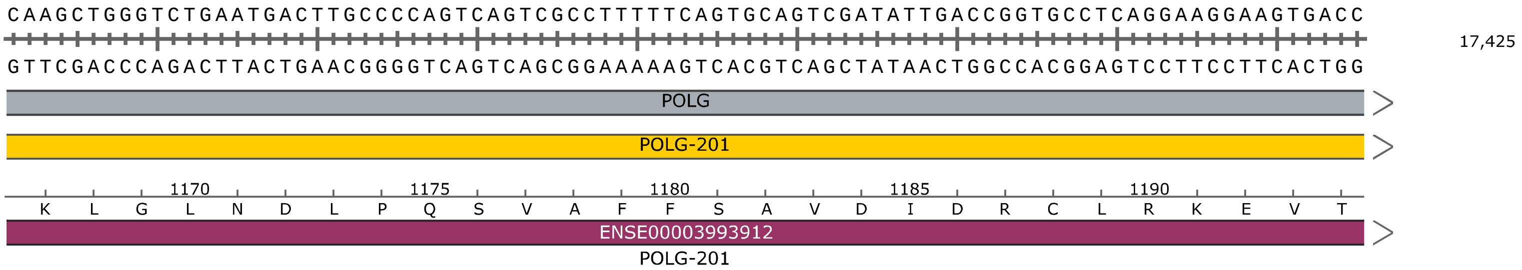
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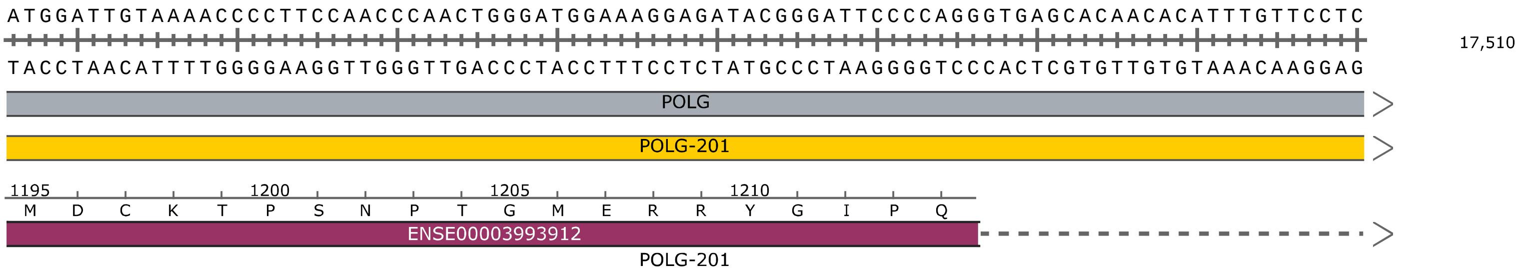
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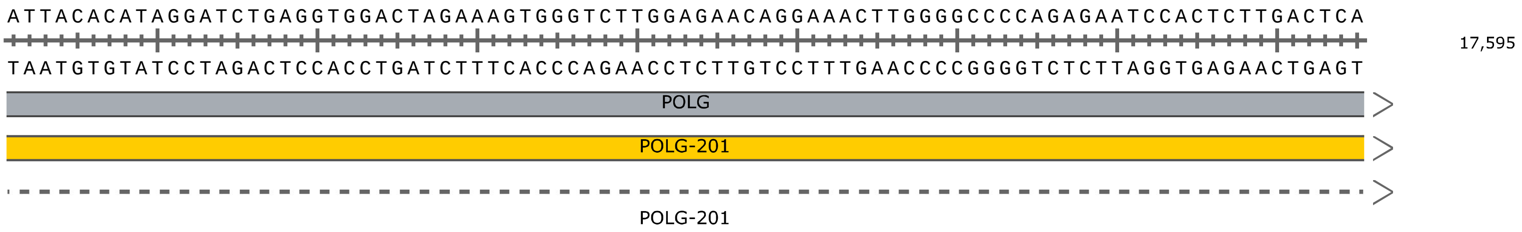
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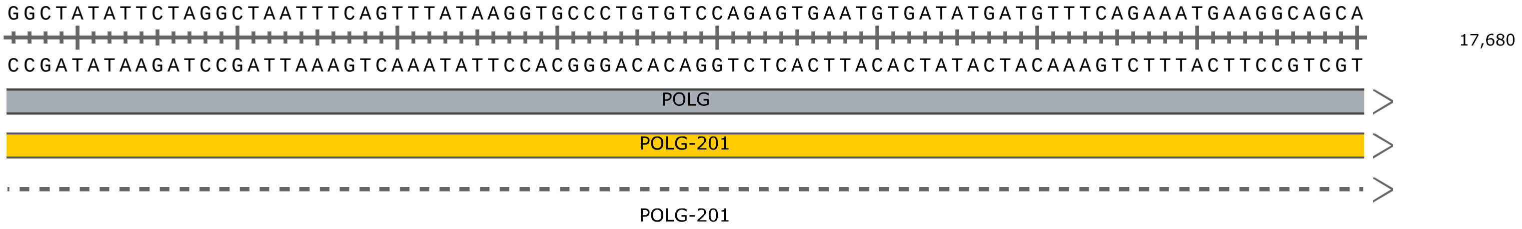
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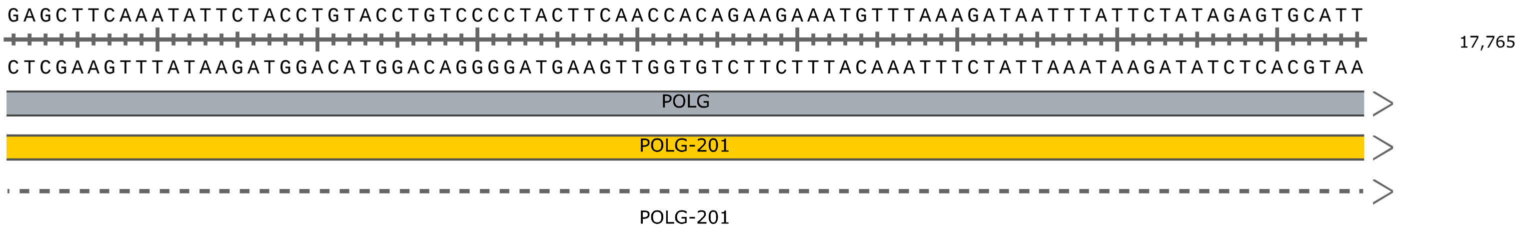
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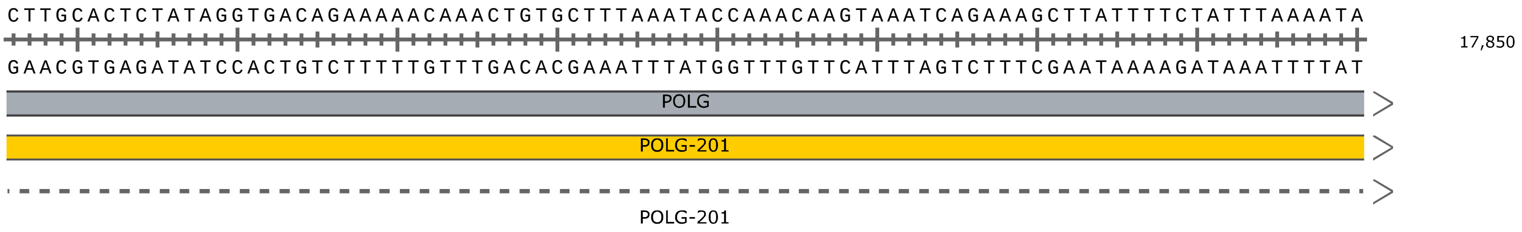
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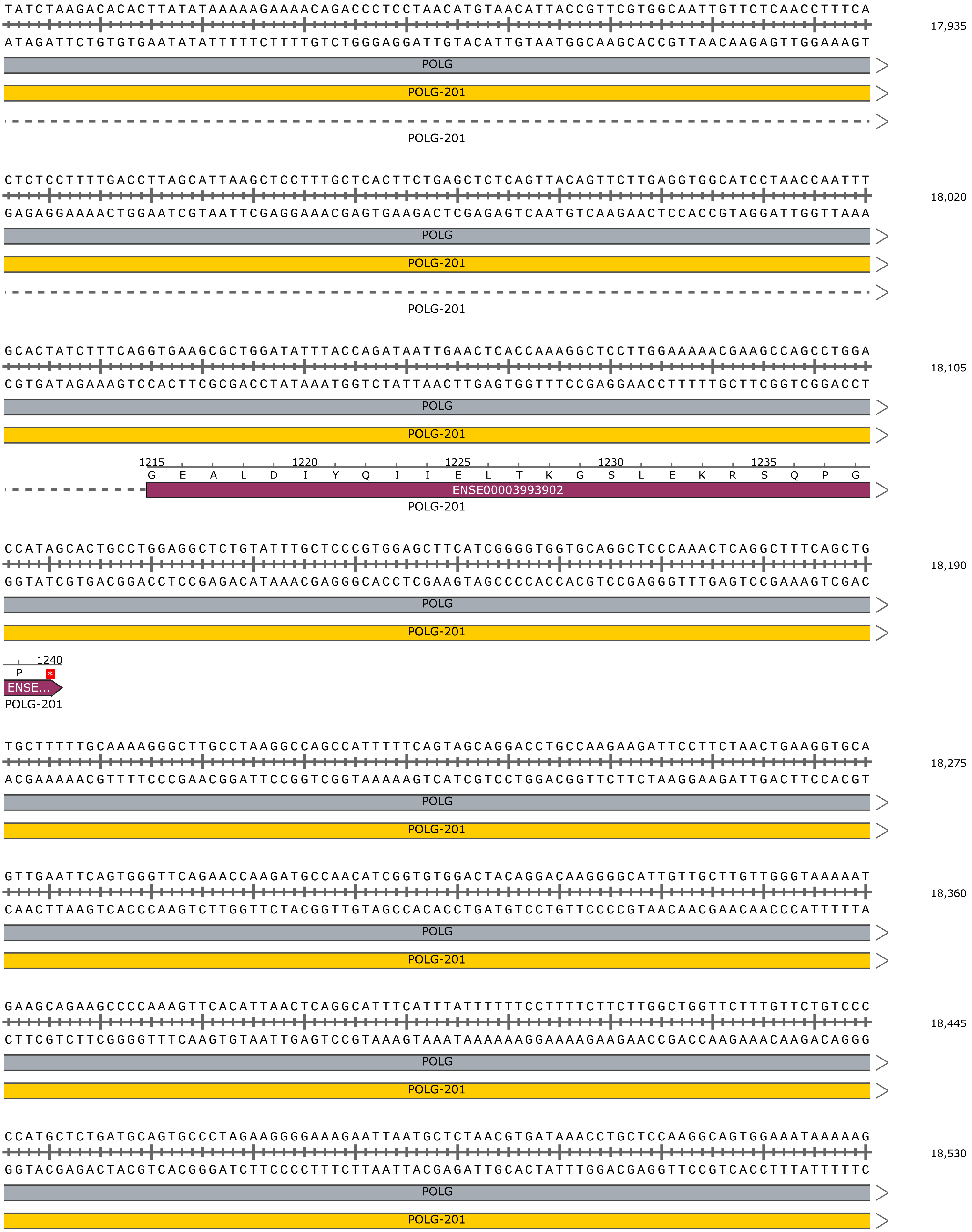
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AGTAAGGCTTTAAGTCAAATATGGATGGAGGAGGAGGAAAATGCCTAGGGAGGAAATGAAACTGATTACTGTGTAATGAGGGGAA
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TCATTCCGAAATTCAGTTTATACCTACCTCCTCCTCCTTTTACGGATCCCTCCTTTACTTTGACTAATGACACATTACTCCCCTT
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                                                                                        24,820
TAGCTCAGATTGATCGACCCAAGTTCAGAGTCTAGACGGAAAATGAGTACCAGACAAGAACCCGTAAGACTAATTGGAAAGAGTA
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CATGCATATGGGGATAACTACTAATCATAACCTATAGCTAGGATGAATGAGATGATGTATGAAAAGAGCTTAACACATCAGACAC
                                                                                        24,905
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                                                                                        24,990
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                                        POLG

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                                        POLG

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                                        POLG

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                                        POLG

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AAAACTGGTTTAAGCAAACAGTAAAGGAGATTCAAGTACTGCAGGAATCTGATGGTATTTAGGACCAAATGACACTTACAAAGCC    26,775
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                                        POLG

ACGTCCTTCCACTTCCCTGAAAGTGCCCTCACTGCACTGCCGTCTCATCACAACCCTTCTTCATGTGCTTGCTGCTACTCTGCTC    26,860
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                                        POLG

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                                        POLG

CCTTGCTCCAAATGCAAACATATATGCTTCCTTTCTCCAAATTAAGTGAAACAGTTTTCTTTACATAAAGATGTCCTTGCTGCAA    27,030
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                                        POLG

AGCCCTCAAGCCTTGGCTTGGTCTCTGATGGGTGCCTCCAGCTTGTGGTAAGCAGGGAAAAAGTTTATATATGCTCAGTTCAGG    27,115
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                                        POLG

AAATGAAAGAATAACACAGGGGGGTCAGATGAGAACCAGACAGCTTCACCTGCACAACAAGGGAGAAGGAAACCAATGTAACCAG    27,285
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CAGTAAAAGTGCTTCCCCCATTCCTAGGAAAGGCATTCTCAACTCACCAGCTTTTCCATATTTTTTGGAATTCCTCCGGAGCTCT
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                                                                                        28,305
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                                   POLG

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GATCCGCCCGTCTCAGCCTACCAAAGTGCTGGGATTACAGGCATGAACCACCGTGACAGGCCCAAAAGCAGATTAGAATTATAAA
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                                                                                        28,560
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POLG

ACAGCTGCCTGATGGCAGAGCTGTCTGCACCAGCTCGTGGAAAAATGTAAGCAGAGTTCCCAGTTGCATGATGATAGCTTTCTCA
                                                                                        28,815
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POLG

ACAGGCTGA   3′
          •••   28,824
TGTCCGACT   5′
POLG
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Feature			Location	Size		⇄	Type
✓ **POLG**			1 .. 29,664	29,664 bp	■	→	gene
/note	=	gene ENSG00000140521 Protein coding					
POLG-202			1 .. 18,542	18,542 bp	■	→	prim_transcript
/note	=	primary transcript ENST00000442287					
✓ **POLG-201**			38 .. 18,542	18,505 bp	🟨	→	prim_transcript
/note	=	primary transcript ENST00000268124					
POLG-217			38 .. 18,178	18,141 bp	■	→	prim_transcript
/note	=	primary transcript ENST00000636774 Nonsense mediated decay					
POLG-219			43 .. 18,542	18,500 bp	■	→	prim_transcript
/note	=	primary transcript ENST00000636937					
POLG-213			45 .. 18,557	18,513 bp	■	→	prim_transcript
/note	=	primary transcript ENST00000631044 Nonsense mediated decay					
POLG-215			151 .. 18,523	18,373 bp	■	→	prim_transcript
/note	=	primary transcript ENST00000635986 Nonsense mediated decay					
POLG-228			151 .. 18,507	18,357 bp	■	→	prim_transcript
/note	=	primary transcript ENST00000672071 Retained intron					
POLG-224			418 .. 1012	595 bp	■	→	prim_transcript
/note	=	primary transcript ENST00000637711 protein_coding_CDS_not_defined					
POLG-225			1053 .. 4654	3602 bp	🟥	→	CDS
▸ 2 segments	=	783 bp					
/note	=	coding sequence ENSP00000497242					
/translation	=	LEPKARCSDSQRGGPCTNHEPPALEEGGRRHRRARAGSSSGALGLQLRPRVRPQRRAAAAAAAAAAAAAAATAASAAASAILGGRAAA AQPIGHPDALERAARANLRARRGDAWRGRGAPQRRAPAEARALGAASRALARRGAAPAAPLRGQPGPALPPPGPEAEPALPGGGQLAV AGPAAPEAPGLGLGGGLDPVRPRGGGRTRGHPRGAGPGVRRGGLLGRGNLPHIGGGHIPLGL,,VFLVQPAAGGRALLLDQPAVAG* 260 amino acids = 25.5 kDa					
POLG-225			1053 .. 4654	3602 bp	■	→	prim_transcript
/note	=	primary transcript ENST00000650303					
✓ **POLG-201**			1108 .. 18,111	17,004 bp	🟥	→	CDS
▸ 22 segments	=	3720 bp					
/note	=	coding sequence ENSP00000268124					
/translation	=	MSRLLWRKVAGATVGPGPVPAPGRWVSSSVPASDPSDGQRRRQQQQQQQQQQQPQQPQVLSSEGGQLRHNPLDIQMLSRGLHE QIFGQGGEMPGEAAVRRSVEHLQKHGLWGQPAVPLPDVELRLPPLYGDNLDQHFRLLAQKQSLPYLEAANLLLQAQLPPKPPAWAWAEG WTRYGPEGEAVPVAIPEERALVFDVEVCLAEGTCPTLAVAISPSAW,,YSWCSQRLVEERYSWTSQLSPADLIPLEVPTGASSPTQRDWQE QLVVGHNVSFDRAHIREQYLIQ,,GSRMRFLDTMSMHMAISGLSSFQRSLWIAAKQGKHKVQPPTKQGQKSQRKARRGPA,,ISSWDWLDI SSVNSLAEVHRLYVGGPPLEKEPRELFVKGTMKDIRENFQ,,DLMQYCAQDVWATHEVFQQQLPLFLER,,CPHPVTLAGMLEMGVSYLPV NQNWERYLAEAQGTYEELQREMKKSLMDLANDACQLLSGER,,YKEDPWLWDLEWDLQEFKQKKAKKVKKEPATASKLPIEGAGAPGDPM DQE,,DLGPCSEEEEFQQDVMARACLQKLKGTTELLPKRPQHLPGHPG,,WYRKLCPRLDDPAWTPGPSLLSLQMRVTPKLMALTWDGFPLH YSERHGWGYLVPGRRDNLAKLPTGTTLESAGVVCPYR,,AIESLYRKHCLEQGKQQLMPQEAGLAEEFLLTDNSAIWQT,,VEELDYLEVEAE AKMENLRAAVPGQPLAL,,TARGGPKDTQPSYHHGNGPYNDVDIPGCWFFKLPHK,,DGNSCNVGSPFAKDFLPKMEDGTLQAGPGGASG PRALEINKMISFWRNAHKRIS,,SQMVVWLPRSALPRAVIR,,HPDYDEEGLYGAILPQVVTAGTITRRAVEPTWLTASNAR,,PDRVGSELKA MVQAPPGYTLVGADVDSQELWIAAVLGDAHFAGMH,,GCTAFGWMTLQGRKSRGTDLHSKTATTVGISREHAKIFNYGRIYGAGQPFAER LLMQFNHRLTQQEAAEKAQQMYAATKGLRW,,YRLSDEGEWLVRELNLPVDRTEGGWISLQDLRKVQRETARK,,SQWKKWEVVAERAWK GGTESEMFNKLESIATSDIPRTPVLGCCISRALEPSAVQEE,,FMTSRVNWVVQSSAVDYLHLMLVAMKWLFEEFAIDGRFCISIHDEVRYL 1239 amino acids = 139.6 kDa VREEDRYRAALALQITNLLTR,,CMFAYKLGLNDLPQSVAFFSAVDIDRCLRKEVTMDCKTPSNPTGMERRYGIPQ,,GEALDIYQIIELTKGS LEKRSQPGP*					

Feature Location Size ▨ ⇄ Type

POLG-202 1108 .. 18,111 17,004 bp ■ → CDS

22 segments = 3720 bp

/note = coding sequence ENSP00000399851

/translation = MSRLLWRKVAGATVGPGPVPAPGRWVSSSVPASDPSDGQRRRQQQQQQQQQQQQQPQQPQVLSSEGGQLRHNPLDIQMLSRGLHE
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WTRYGPEGEAVPVAIPEERALVFDVEVCLAEGTCPTLAVAISPSAW,,YSWCSQRLVEERYSWTSQLSPADLIPLEVPTGASSPTQRDWQE
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SSVNSLAEVHRLYVGGPPLEKEPRELFVKGTMKDIRENFQ,,DLMQYCAQDVWATHEVFQQQLPLFLER,,CPHPVTLAGMLEMGVSYLPV
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DQE,,DLGPCSEEEEFQQDVMARACLQKLKGTTELLPKRPQHLPGHPG,,WYRKLCPRLDDPAWTPGPSLLSLQMRVTPKLMALTWDGFPLH
YSERHGWGYLVPGRRDNLAKLPTGTTLESAGVVCPYR,,AIESLYRKHCLEQGKQQLMPQEAGLAEEFLLTDNSAIWQT,,VEELDYLEVEAE
AKMENLRAAVPGQPLAL,,TARGGPKDTQPSYHHGNGPYNDVDIPGCWFFKLPHK,,DGNSCNVGSPFAKDFLPKMEDGTLQAGPGGASG
PRALEINKMISFWRNAHKRIS,,SQMVVWLPRSALPRAVIR,,HPDYDEEGLYGAILPQVVTAGTITRRAVEPTWLTASNAR,,PDRVGSELKA
MVQAPPGYTLVGADVDSQELWIAAVLGDAHFAGMH,,GCTAFGWMTLQGRKSRGTDLHSKTATTVGISREHAKIFNYGRIYGAGQPFAER
LLMQFNHRLTQQEAAEKAQQMYAATKGLRW,,YRLSDEGEWLVRELNLPVDRTEGGWISLQDLRKVQRETARK,,SQWKKWEVVAERAWK
GGTESEMFNKLESIATSDIPRTPVLGCCISRALEPSAVQEE,,FMTSRVNWVVQSSAVDYLHLMLVAMKWLFEEFAIDGRFCISIHDEVRYL
VREEDRYRAALALQITNLLTR,,CMFAYKLGLNDLPQSVAFFSAVDIDRCLRKEVTMDCKTPSNPTGMERRYGIPQ,,GEALDIYQIIELTKGS
LEKRSQPGP*
1239 amino acids = 139.6 kDa

POLG-219 1108 .. 18,111 17,004 bp ■ → CDS

22 segments = 3720 bp

/note = coding sequence ENSP00000516154

/translation = MSRLLWRKVAGATVGPGPVPAPGRWVSSSVPASDPSDGQRRRQQQQQQQQQQQQQPQQPQVLSSEGGQLRHNPLDIQMLSRGLHE
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WTRYGPEGEAVPVAIPEERALVFDVEVCLAEGTCPTLAVAISPSAW,,YSWCSQRLVEERYSWTSQLSPADLIPLEVPTGASSPTQRDWQE
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SSVNSLAEVHRLYVGGPPLEKEPRELFVKGTMKDIRENFQ,,DLMQYCAQDVWATHEVFQQQLPLFLER,,CPHPVTLAGMLEMGVSYLPV
NQNWERYLAEAQGTYEELQREMKKSLMDLANDACQLLSGER,,YKEDPWLWDLEWDLQEFKQKKAKKVKKEPATASKLPIEGAGAPGDPM
DQE,,DLGPCSEEEEFQQDVMARACLQKLKGTTELLPKRPQHLPGHPG,,WYRKLCPRLDDPAWTPGPSLLSLQMRVTPKLMALTWDGFPLH
YSERHGWGYLVPGRRDNLAKLPTGTTLESAGVVCPYR,,AIESLYRKHCLEQGKQQLMPQEAGLAEEFLLTDNSAIWQT,,VEELDYLEVEAE
AKMENLRAAVPGQPLAL,,TARGGPKDTQPSYHHGNGPYNDVDIPGCWFFKLPHK,,DGNSCNVGSPFAKDFLPKMEDGTLQAGPGGASG
PRALEINKMISFWRNAHKRIS,,SQMVVWLPRSALPRAVIR,,HPDYDEEGLYGAILPQVVTAGTITRRAVEPTWLTASNAR,,PDRVGSELKA
MVQAPPGYTLVGADVDSQELWIAAVLGDAHFAGMH,,GCTAFGWMTLQGRKSRGTDLHSKTATTVGISREHAKIFNYGRIYGAGQPFAER
LLMQFNHRLTQQEAAEKAQQMYAATKGLRW,,YRLSDEGEWLVRELNLPVDRTEGGWISLQDLRKVQRETARK,,SQWKKWEVVAERAWK
GGTESEMFNKLESIATSDIPRTPVLGCCISRALEPSAVQEE,,FMTSRVNWVVQSSAVDYLHLMLVAMKWLFEEFAIDGRFCISIHDEVRYL
VREEDRYRAALALQITNLLTR,,CMFAYKLGLNDLPQSVAFFSAVDIDRCLRKEVTMDCKTPSNPTGMERRYGIPQ,,GEALDIYQIIELTKGS
LEKRSQPGP*
1239 amino acids = 139.6 kDa

POLG-226 1451 .. 18,512 17,062 bp ■ → prim_transcript

/note = primary transcript ENST00000666746
Nonsense mediated decay

POLG-208 1507 .. 18,534 17,028 bp ■ → prim_transcript

/note = primary transcript ENST00000530292
Nonsense mediated decay

POLG-223 1718 .. 4651 2934 bp ■ → CDS

2 segments = 100 bp

/note = coding sequence ENSP00000490427

/translation = QRELAPHWRWPYPPRP,,ASGWWKSVTLGPASCRR
33 amino acids = 3.9 kDa

POLG-223 1718 .. 4651 2934 bp ■ → prim_transcript

/note = primary transcript ENST00000637307

POLG-222 5825 .. 18,532 12,708 bp ■ → prim_transcript

/note = primary transcript ENST00000637264

POLG-222 5825 .. 18,111 12,287 bp ■ → CDS

20 segments = 2732 bp

/note = coding sequence ENSP00000489844

/translation = VCG*QPSRANTRSSPPQSKARSPRGKPEEAQR,,SHPGTGWTSAVSTVWQRCTDFM*GGLP*RRSLENCL*RAP*RTFVRTSR,,T*CSTV
PRTCGPPMRFSSSSYRSSWR,,GVPTQ*LWPACWRWVSPTCLSTRTGSVTWQRHRALMRSSSGR*RSR*WIWPMMPASCSQER,,GTKKTP
GSGTWSGTCKNLSRRKLRR*RRNQPQPASCPSRGLGPLVIPWIRK,,TSAPAVRRRSFNKMSWPAPACRS*RGPQSSCPSGPSTFLDTL,,D
GTGSSAPG*TTLHGPRAPASSACRCGSHLNSWHLPGMASLCTTQSVMAGATWCLGGGTTWPSCRQVPPWSQLGWSAPT,,EPSSPCTGS
TVSNRGSSS*CPRRPAWRRSSCSLTIVPYGKR,,*KNWIT*KWRLRPRWRTCELQCQVNP*L*,,LPVVAPRTPSPAITMAMDLTTTWTSLAA
GFSSCLTR,,MVIAVMWEAPLPRTSCPRWRMAPCRLAQEVPVGPVLWKSTK*FLSGGTPINVS,,APRWWCGCPGQLCPVL*S,,GTPTMMR
KASMGPSCPKW*LPAPSLAGLWSPHGSPPAMPG,,LTE*AVS*KPWCRPHLATPLWVLMWTPKSCGLQLCLETPTLPACM,,AAQPLGG*H
CRAGRAGALIYTVRQPLLWASAVSMPKSSTTAASMVLGSPLLSAY*CSLTTGSHSRRQLRRPSRCTLPPRASA,,GIGCRMRASGW*GS*T
SQWTGLRVAGFPCRICARSREKLQG,,SHSGRSGRWLLNGHGRGAQSQKCSISLRALLRLTYHVPRCWAAASAEPWSPRLSRKS,,L*PAV*
IGWYRALLLTTYTSCLWP*SGGLKSLP*MGASASASMTRFATWCGRRTATALPWPCRSPTS*P,,VQSILTGASGRK*PWIVKPLPTQLGWK
GDTGFPR,,VKRWIFTR*LNSPKAPWKNEASLDH
910 codons (33 internal stop codons)

POLG-230 5900 .. 18,521 12,622 bp ■ → prim_transcript

/note = primary transcript ENST00000672923
Retained intron

POLG-210 6150 .. 7849 1700 bp ■ → prim_transcript

/note = primary transcript ENST00000532363
Retained intron

	Feature	Location	Size			Type
	POLG-221	7526 .. 18,505	10,980 bp	■	→	prim_transcript
	/note	= primary transcript ENST00000637238 Nonsense mediated decay				
	MIR6766	8052 .. 8123	72 bp	■	→	gene
	/note	= gene ENSG00000275101 miRNA				
	MIR6766-201	8052 .. 8123	72 bp	■	→	prim_transcript
	/note	= primary transcript ENST00000622641 miRNA				
	POLG-203	8157 .. 12,120	3964 bp	🟪	→	CDS
	▸ 5 segments = 700 bp					
	/note	= coding sequence ENSP00000432389				
	/translation	= NKMSWPAPACRS*RGPQSSCPSGPSTFLDTL,,DGTGSSAPG*TTLHGPRAPASSACRCGSHLNSWHLPGMASLCTTQSVMAGATWCLGGGTTWPSCRQVPPWSQLGWSAPT,,EPSSPCTGSTVSNRGSSS*CPRRPAWRRSSCSLTIVPYGKR,,*KNWIT*KWRLRPRWRTCELQCQVNP*LW,,MVIAVMWEAPLPRTSCPRWRMAPCRLAQEVPVGPVLWKSTK*FLSGGTPINVS 233 codons (7 internal stop codons)				
	POLG-203	8157 .. 12,120	3964 bp	■	→	prim_transcript
	/note	= primary transcript ENST00000526314				
	POLG-227	8219 .. 15,570	7352 bp	🟪	→	CDS
	▸ 8 segments = 859 bp					
	/note	= coding sequence ENSP00000499709				
	/translation	= KRPQHLPGHPG,,WYRKLCPRLDDPAWTPGPSLLSLQMRVTPKLMALTWDGFPLHYSERHGWGYLVPGRRDNLAKLPTGTTLESAGVVCPYR,,AIESLYRKHCLEQGKQQLMPQEAGLAEEFLLTDNSAIWQT,,VEELDYLEVEAEAKMENLRAAVPGQPLAL,,TARGGPKDTQPSYHHGNGPYNDVDIPGCWFFKLPHK,,DGNSCNVGSPFAKDFLPKMEDGTLQAGPGGASGPRALEINKMISFWRNAHKRIS,,SQMVVWLPRSALPRAVIR,,YRLSDEGEWLVRELNLPVD 286 amino acids = 32.1 kDa				
	POLG-227	8219 .. 15,570	7352 bp	■	→	prim_transcript
	/note	= primary transcript ENST00000670281				
	POLG-211	9262 .. 13,087	3826 bp	■	→	prim_transcript
	/note	= primary transcript ENST00000532584 Retained intron				
	POLG-204	9275 .. 12,057	2783 bp	■	→	prim_transcript
	/note	= primary transcript ENST00000526398 Nonsense mediated decay				
	POLG-205	9378 .. 11,348	1971 bp	■	→	prim_transcript
	/note	= primary transcript ENST00000526573 Retained intron				
	POLG-212	10,571 .. 11,342	772 bp	■	→	prim_transcript
	/note	= primary transcript ENST00000533857 Retained intron				
✓	**Donor Template WT -> SNV**	11,333 .. 11,432	100 bp	🟦	⊢⊣	misc_feature
✓	**PAM**	11,392 .. 11,394	3 bp	🟨	⊢⊣	misc_feature
✓	**Protospacer Sequence**	11,395 .. 11,414	20 bp	🟥	⊢⊣	misc_feature
✓	**SNV**	11,402 .. 11,402	1 bp	🟧	⊢⊣	misc_feature
	/note	= WT = G SNV = C				
	POLG-207	11,425 .. 14,042	2618 bp	■	→	prim_transcript
	/note	= primary transcript ENST00000528881 Nonsense mediated decay				
	POLG-209	11,435 .. 15,594	4160 bp	■	→	prim_transcript
	/note	= primary transcript ENST00000530715 Nonsense mediated decay				
	POLG-229	13,939 .. 18,542	4604 bp	■	→	prim_transcript
	/note	= primary transcript ENST00000672695 protein_coding_CDS_not_defined				
	POLG-218	14,061 .. 15,524	1464 bp	🟪	→	CDS
	▸ 2 segments = 100 bp					
	/note	= coding sequence ENSP00000490403				
	/translation	= PADVRCHQGPPL,,RGTGSTPVE*W**HCPQVSAV 33 codons (3 internal stop codons)				

Feature		Location	Size	▨	⇄	Type
POLG-218		14,061 .. 15,524	1464 bp	■	→	prim_transcript
/note	=	primary transcript ENST00000636812				
POLG-216		15,483 .. 15,798	316 bp	■	→	prim_transcript
/note	=	primary transcript ENST00000636530 protein_coding_CDS_not_defined				
POLG-220		16,853 .. 17,419	567 bp	■	→	prim_transcript
/note	=	primary transcript ENST00000637042 protein_coding_CDS_not_defined				
POLG-206		17,034 .. 18,345	1312 bp	■	→	prim_transcript
/note	=	primary transcript ENST00000526671 Retained intron				
FANCI		17,601 .. 90,917	73,317 bp	■	←	gene
/note	=	gene ENSG00000140525 Protein coding				
FANCI-201		17,601 .. 90,913	73,313 bp	■	←	prim_transcript
/note	=	primary transcript ENST00000300027 Protein coding				
FANCI-202		17,731 .. 90,883	73,153 bp	■	←	prim_transcript
/note	=	primary transcript ENST00000310775 Protein coding				
FANCI-212		17,734 .. 56,175	38,442 bp	■	←	prim_transcript
/note	=	primary transcript ENST00000566895 Retained intron				
FANCI-222		17,751 .. 90,882	73,132 bp	■	←	prim_transcript
/note	=	primary transcript ENST00000696717 Protein coding				
FANCI-219		17,759 .. 25,939	8181 bp	■	←	prim_transcript
/note	=	primary transcript ENST00000675352 Retained intron				
FANCI-223		17,760 .. 90,866	73,107 bp	■	←	prim_transcript
/note	=	primary transcript ENST00000696718 Protein coding				
FANCI-224		17,782 .. 90,845	73,064 bp	■	←	prim_transcript
/note	=	primary transcript ENST00000696719 Protein coding				
FANCI-221		17,888 .. 25,190	7303 bp	■	←	prim_transcript
/note	=	primary transcript ENST00000676110 Retained intron				
FANCI-220		18,028 .. 90,879	72,852 bp	■	←	prim_transcript
/note	=	primary transcript ENST00000676003 Protein coding				
POLG-214		18,084 .. 29,664	11,581 bp	■	→	prim_transcript
/note	=	primary transcript ENST00000635831				
POLG-214		18,084 .. 18,111	28 bp	🟪	→	CDS
/note	=	coding sequence ENSP00000490231				
/translation	=	GKTKPAWTI 9 amino acids = 1.0 kDa				
FANCI-203		18,381 .. 90,858	72,478 bp	■	←	prim_transcript
/note	=	primary transcript ENST00000447611 Nonsense mediated decay				
FANCI-218		18,391 .. 90,917	72,527 bp	■	←	prim_transcript
/note	=	primary transcript ENST00000674831 Protein coding				
FANCI-226		18,393 .. 35,663	17,271 bp	■	←	prim_transcript
/note	=	primary transcript ENST00000696721 Retained intron				

Feature	Location	Size	■	⇄	Type
FANCI-204	18,418 .. 71,425	53,008 bp	■	←	prim_transcript
/note	= primary transcript ENST00000561894 Protein coding				
FANCI-211	18,436 .. 27,003	8568 bp	■	←	prim_transcript
/note	= primary transcript ENST00000566615 protein_coding_CDS_not_defined				
FANCI-210	20,216 .. 90,612	70,397 bp	■	←	prim_transcript
/note	= primary transcript ENST00000565522 protein_coding_CDS_not_defined				
FANCI-227	26,133 .. 28,003	1871 bp	■	←	prim_transcript
/note	= primary transcript ENST00000696722 Retained intron				

	Primer	Length	●	Binding Sites	⇄	Tm	Date Added
✓	**PCR Forward**	25-mer		10,968 .. 10,992	→	58°C	Jan 11, 2023
	/sequence =	AACTGGATTACTTAGAAGTGGAGGC 44% GC / 7770.1 Da					
✓	**Donor Template WT -> SNV**	100-mer		11,333 .. 11,432	→	82°C	Jan 11, 2023
	/sequence =	GGTGTGTGGCCCTCACAGACTGCCCGTGGTGGCCCCAAGGACACCCAGCCCAGCTATCACCATGGCAATCGACCTTACAACGAC [illegible] 62% GC / 30,656.8 Da					
✓	**gRNA Protospacer**	20-mer		11,395 .. 11,414	←	58°C	Jan 11, 2023
	/sequence =	CGTTGTAAGGTCCATTGCCA 50% GC / 6108.0 Da					
✓	**Sanger Sequencing**	20-mer		11,477 .. 11,496	←	59°C	Jan 11, 2023
	/sequence =	AGGAAACACCACAGGACAGG 55% GC / 6178.1 Da					
✓	**PCR Reverse**	25-mer		11,959 .. 11,983	←	58°C	Jan 11, 2023
	/sequence =	TCCCACATTACAGCTATTACCATCC 44% GC / 7480.9 Da					