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135

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270

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405

TARDBP

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540

TARDBP

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945

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1080

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1620

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1755

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2025

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2160

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TARDBP-201

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2700

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2835

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3105

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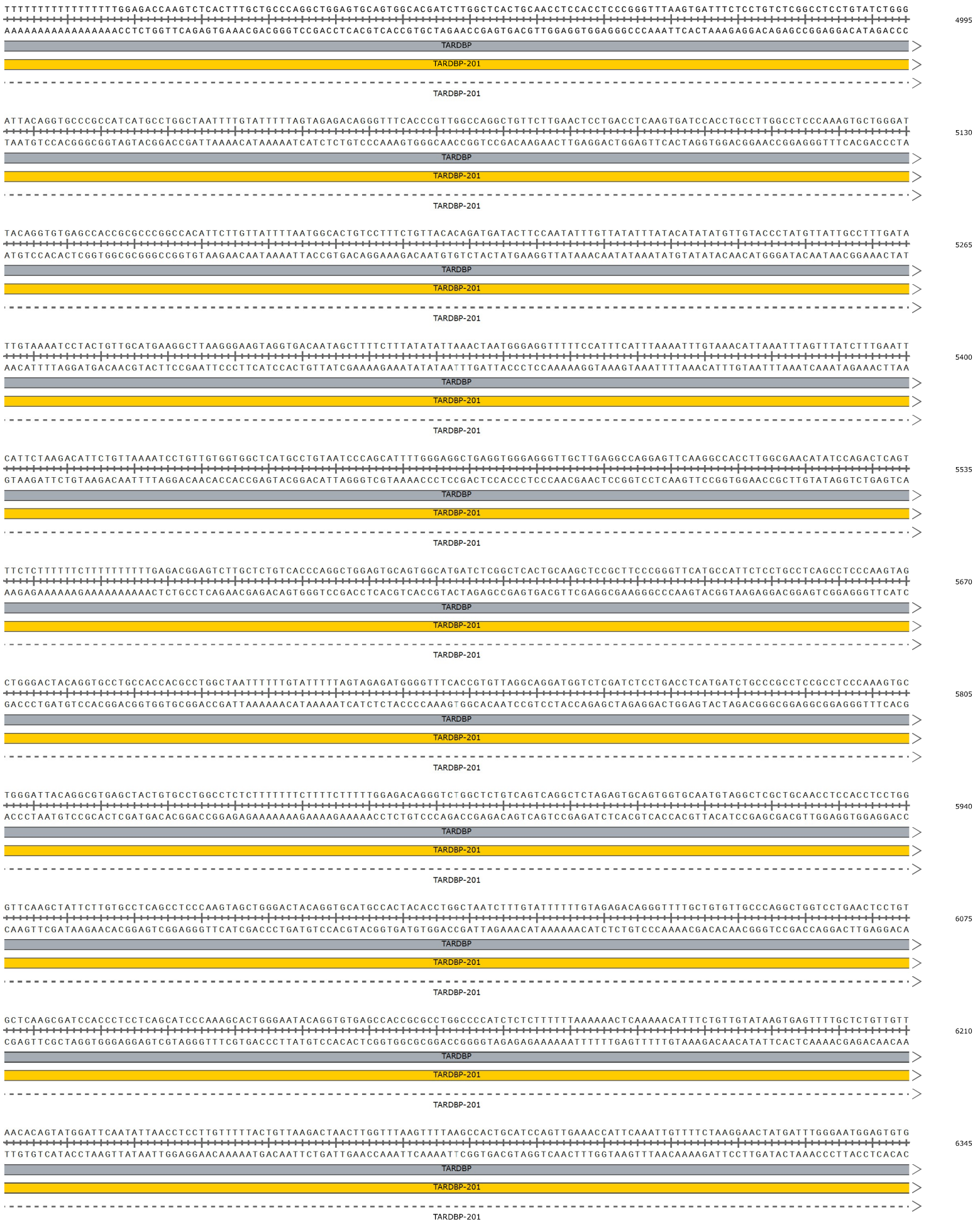
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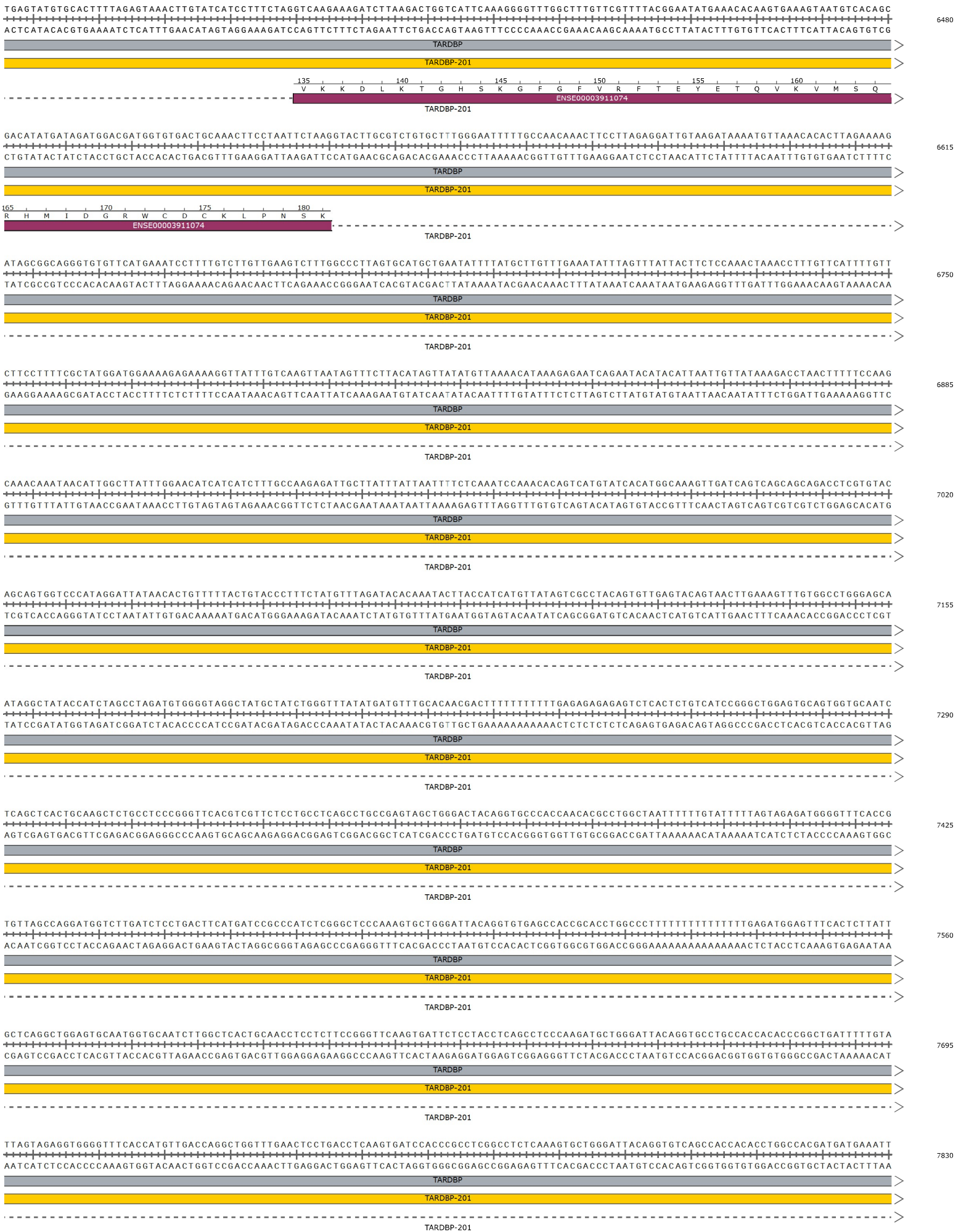
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7965

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TARDBP-201

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8100

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8505

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8640

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8775

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8910

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9045

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9180

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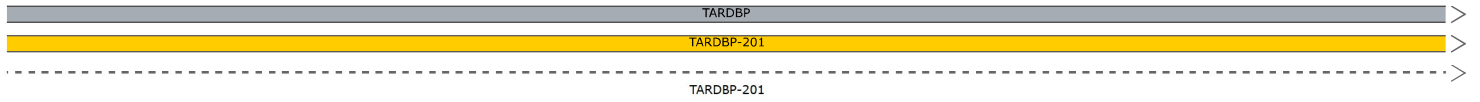
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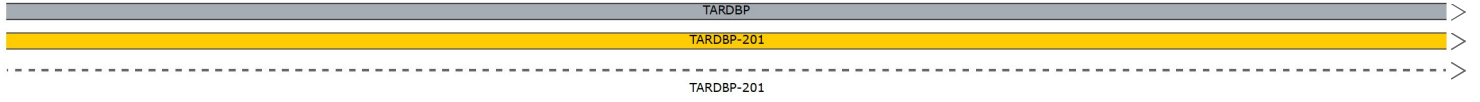
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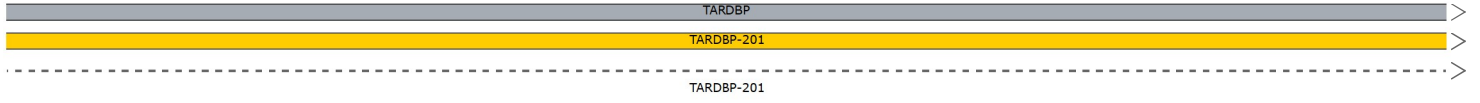
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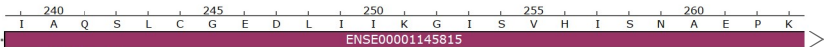
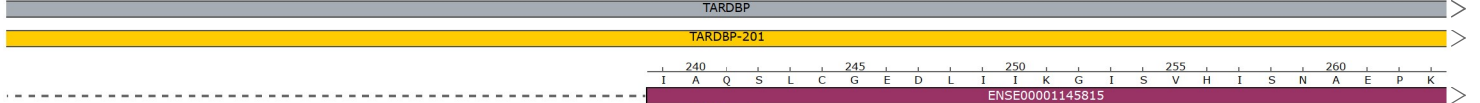
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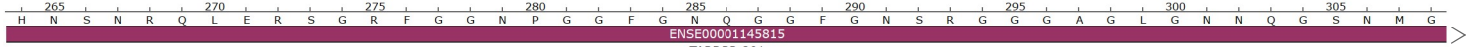
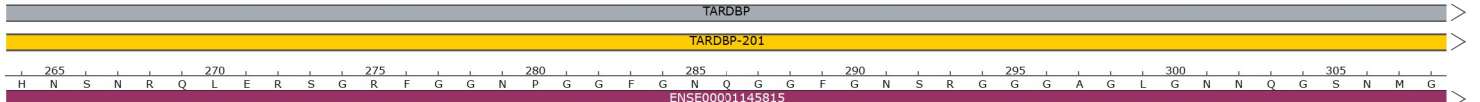
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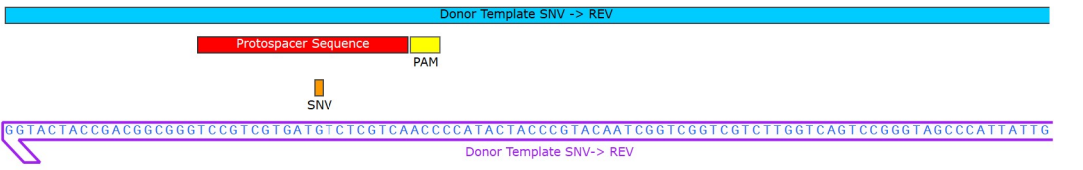
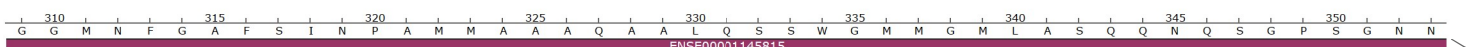
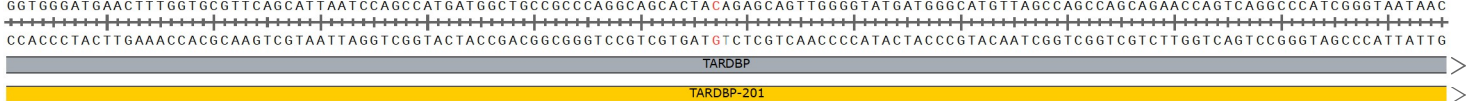
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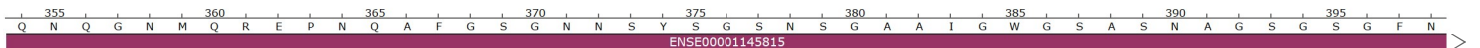
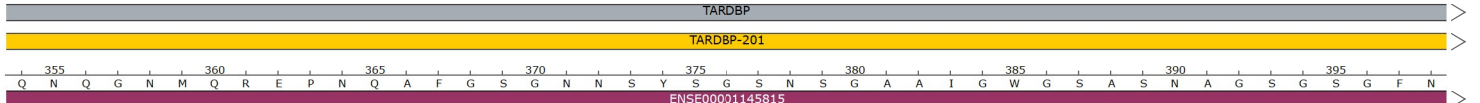
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10,125



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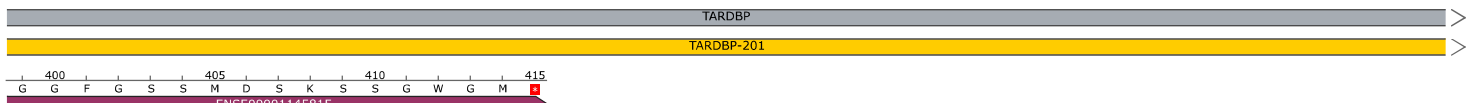


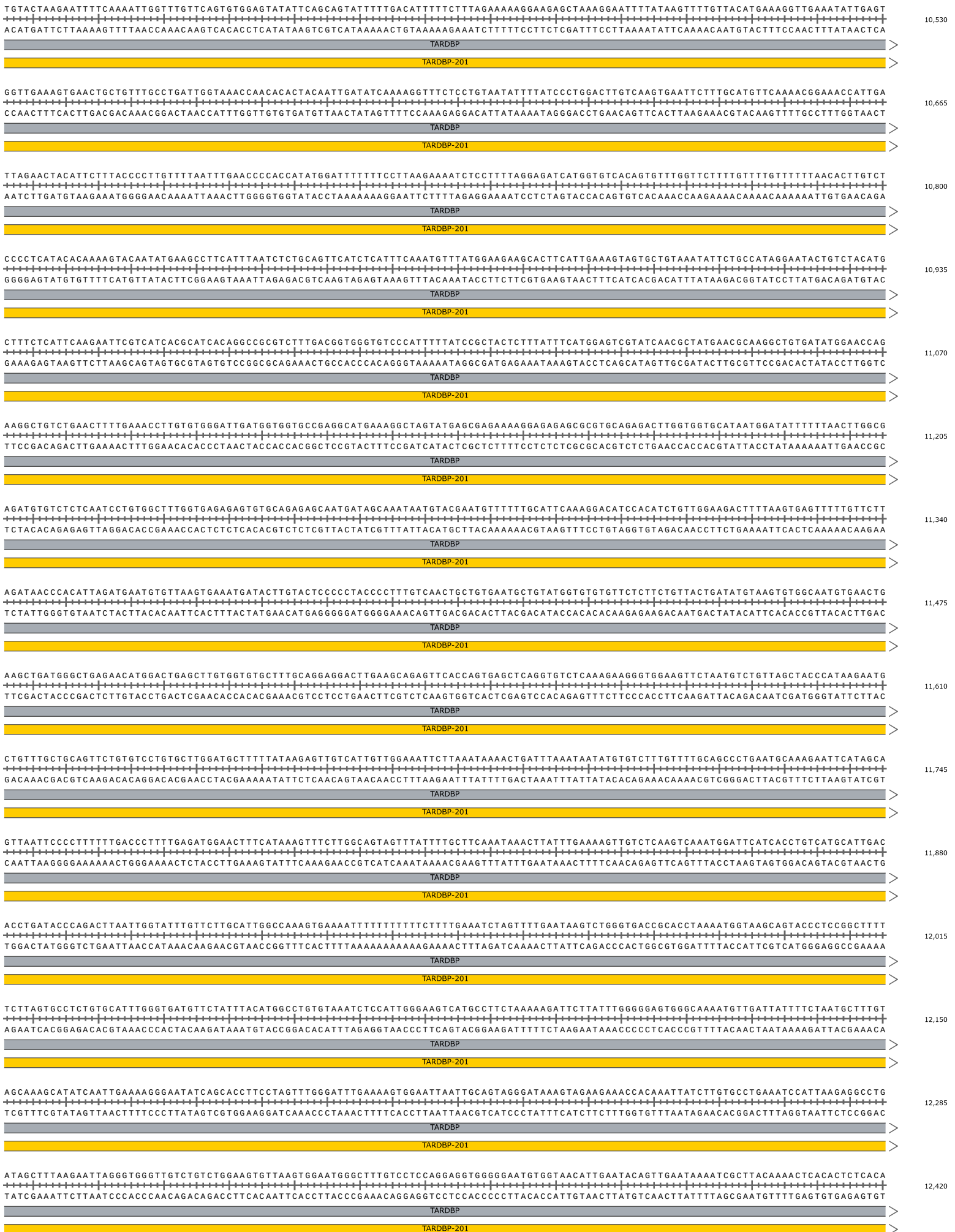
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10,395





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17,820

TARDBP

TGTATCCATTACCAAGGCTCACAGACTGGGAGTGATTTTCTCCTTTGGAGCTCGTCCAGAATCCATCAGCCTCACACACATATTTACCTGCAAAATCATTGGAAAAGCAAAAATGTTAACTGCATGTATAAAGTG
ACATAGGTAATGGTCCGAGTGTCTGACCCTCACTAAAAAGAGGAAACCTCGAGCAGGCTTAGGTAGTCGGAGTGTGTATAAATGGACGTTTAGTAACCTTTTTCGTTTTTACA AATTGACGTACATATTCTAC

17,955

TARDBP

GTTGTCAATTTGCTTGAATACCCCTTGAAAAATGTTGATTTCTGAGCATCAGTGGGACATAGAGGTGCTGAAGAACCATTTTACATGATTTTATAAATAGGAGGCTCTGCAATTACCATGTTTCTTGC AAAAGT
CAACAGTAAACGAACCTTATGGGGGAACTTTTTACAAC TAAGAACTCGTAGTCACCCTGTATCTCCACAGACTTCTTGGTAAAATGACTAAAGTATTTATCCTCCAGAGACGTAATGGTACAAACGAACGTTTCA

18,090

TARDBP

GGAAACCTTTTAGATGTGTAACCTTGAATATGTATCAAGATCTCAAGTGTAAATGATAAGGTGTTGACTTGTAAATTAACCATTGG AATACA
CCTTTGGAAAATCTACACATTGAACCTTATACATAGTTCTAGAGTTCACGAATTACTATTCCACAACCTGAACAATTTAATTTGGTAAACCTTATGT



3'
18,185
5'

TARDBP

Feature	Location	Size	Type
TARDBP	1 .. 18,185	18,185 bp	gene
/note	= gene ENSG00000120948 Protein coding		
TARDBP-205	1 .. 8146	8146 bp	prim_transcript
/note	= primary transcript ENST00000473118		
TARDBP-236	81 .. 11,266	11,186 bp	prim_transcript
/note	= primary transcript ENST00000639083		
TARDBP-237	82 .. 11,840	11,759 bp	prim_transcript
/note	= primary transcript ENST00000639599 Nonsense mediated decay		
TARDBP-235	279 .. 10,905	10,627 bp	prim_transcript
/note	= primary transcript ENST00000629725		
TARDBP-203	310 .. 10,515	10,206 bp	prim_transcript
/note	= primary transcript ENST00000439080 Nonsense mediated decay		
TARDBP-201	311 .. 13,149	12,839 bp	prim_transcript
/note	= primary transcript ENST00000240185		
TARDBP-204	311 .. 9833	9523 bp	prim_transcript
/note	= primary transcript ENST00000472476 Nonsense mediated decay		
TARDBP-207	311 .. 8246	7936 bp	prim_transcript
/note	= primary transcript ENST00000476201		
TARDBP-219	311 .. 6110	5800 bp	prim_transcript
/note	= primary transcript ENST00000613864		
TARDBP-221	319 .. 18,185	17,867 bp	prim_transcript
/note	= primary transcript ENST00000614757 Nonsense mediated decay		
TARDBP-231	327 .. 9967	9641 bp	prim_transcript
/note	= primary transcript ENST00000621715		
TARDBP-206	1373 .. 12,676	11,304 bp	prim_transcript
/note	= primary transcript ENST00000473869 Nonsense mediated decay		
TARDBP-202	1373 .. 11,840	10,468 bp	prim_transcript
/note	= primary transcript ENST00000315091		
TARDBP-222	1385 .. 10,998	9614 bp	prim_transcript
/note	= primary transcript ENST00000616545		
TARDBP-232	1385 .. 10,998	9614 bp	prim_transcript
/note	= primary transcript ENST00000621790		
TARDBP-222	1385 .. 10,984	9600 bp	CDS
▶ 6 segments = 906 bp			
/note	= coding sequence ENSP00000484722		
/translation	= MSEYIRVTEDENDPEIEIPSEDDGTVLLSTVTAQFPGACGLRYRNPVSQCMRGVRLVEGILHAPDAGWGNLVYVYNYPK,,DNKRKMDETDASSAVKVKRAVQKTSDLIVLGLPWKTEQDLKEYFSTFGEVLMVQ,,VKKDLKLGHSKGFVFRFTEYETQVKVMSQRHMIDGRWCDCCLPNSK,,QSQDEPLRSRKFVVGRC TEDMTEDELREFFSQYGDVMDV/FIPKPFRAFAFVTFADDQ,,IAQSLCGEDLIKIGSVHISNAEPKHNSNRQLERSGRFGGNP,,GILSTCF		
TARDBP-202	1385 .. 10,905	9521 bp	CDS
▶ 6 segments = 888 bp			
/note	= coding sequence ENSP00000313129		
/translation	= MSEYIRVTEDENDPEIEIPSEDDGTVLLSTVTAQFPGACGLRYRNPVSQCMRGVRLVEGILHAPDAGWGNLVYVYNYPK,,DNKRKMDETDASSAVKVKRAVQKTSDLIVLGLPWKTEQDLKEYFSTFGEVLMVQ,,VKKDLKLGHSKGFVFRFTEYETQVKVMSQRHMIDGRWCDCCLPNSK,,QSQDEPLRSRKFVVGRC TEDMTEDELREFFSQYGDVMDV/FIPKPFRAFAFVTFADDQ,,IAQSLCGEDLIKIGSVHISNAEPKHNSNRQLERSGRFG,,VHLISNVYGR		
TARDBP-232	1385 .. 10,905	9521 bp	CDS
▶ 6 segments = 915 bp			
/note	= coding sequence ENSP00000482191		
/translation	= MSEYIRVTEDENDPEIEIPSEDDGTVLLSTVTAQFPGACGLRYRNPVSQCMRGVRLVEGILHAPDAGWGNLVYVYNYPK,,DNKRKMDETDASSAVKVKRAVQKTSDLIVLGLPWKTEQDLKEYFSTFGEVLMVQ,,VKKDLKLGHSKGFVFRFTEYETQVKVMSQRHMIDGRWCDCCLPNSK,,QSQDEPLRSRKFVVGRC TEDMTEDELREFFSQYGDVMDV/FIPKPFRAFAFVTFADDQ,,IAQSLCGEDLIKIGSVHISNAEPKHNSNRQLERSGRFGGNP,,GILSTCF		
TARDBP-235	1385 .. 10,905	9521 bp	CDS
▶ 6 segments = 897 bp			
/note	= coding sequence ENSP00000486989		
/translation	= MSEYIRVTEDENDPEIEIPSEDDGTVLLSTVTAQFPGACGLRYRNPVSQCMRGVRLVEGILHAPDAGWGNLVYVYNYPK,,DNKRKMDETDASSAVKVKRAVQKTSDLIVLGLPWKTEQDLKEYFSTFGEVLMVQ,,VKKDLKLGHSKGFVFRFTEYETQVKVMSQRHMIDGRWCDCCLPNSK,,QSQDEPLRSRKFVVGRC TEDMTEDELREFFSQYGDVMDV/FIPKPFRAFAFVTFADDQ,,IAQSLCGEDLIKIGSVHISNAEPKHNSNRQLERSGRFGGNP,,VHLISNV		
TARDBP-238	1385 .. 10,891	9507 bp	CDS
▶ 6 segments = 810 bp			
/note	= coding sequence ENSP00000497327		
/translation	= MSEYIRVTEDENDPEIEIPSEDDGTVLLSTVTAQFPGACGLRYRNPVSQCMRGVRLVEGILHAPDAGWGNLVYVYNYPK,,DNKRKMDETDASSAVKVKRAVQKTSDLIVLGLPWKTEQDLKEYFSTFGEVLMVQ,,VKKDLKLGHSKGFVFRFTEYETQVKVMSQRHMIDGRWCDCCLPNSK,,QSQDEPLRSRKFVVGRC TEDMTEDELREFFSQYGDVMDV/FIPKPFRAFAFVTFADDQ,,IAQSLCGEDLIKIGSVH,,FISFQMFMEALH*		
TARDBP-238	1385 .. 10,891	9507 bp	prim_transcript
/note	= primary transcript ENST00000649624		
TARDBP-201	1385 .. 10,311	8927 bp	CDS
▶ 5 segments = 1245 bp			
/note	= coding sequence ENSP00000240185		
/translation	= MSEYIRVTEDENDPEIEIPSEDDGTVLLSTVTAQFPGACGLRYRNPVSQCMRGVRLVEGILHAPDAGWGNLVYVYNYPK,,DNKRKMDETDASSAVKVKRAVQKTSDLIVLGLPWKTEQDLKEYFSTFGEVLMVQ,,VKKDLKLGHSKGFVFRFTEYETQVKVMSQRHMIDGRWCDCCLPNSK,,QSQDEPLRSRKFVVGRC TEDMTEDELREFFSQYGDVMDV/FIPKPFRAFAFVTFADDQ,,IAQSLCGEDLIKIGSVHISNAEPKHNSNRQLERSGRFGGNP,,GILSTCF		

Feature	Location	Size	Start	End	Type
TARDBP-236	1385 .. 10,311	8927 bp	■	→	CDS
▶ 5 segments = 1245 bp					
/note	= coding sequence ENSP00000491203				
/translation	= MSEYIRVTEDENDPEIEIPSEDDGTVLLSTVTAQFPGACGLRYRNPVVSQCMRGVRLVEGILHAPDAGWGNLVYVYNYPK,,DNKRKMDETDASSAVKVKRAVQKTSDLIVLGLPWKTEQDLKEYFSTFGEVLMVQ,,VKKDLKTGH SKGFGFVRFTEYETQVKVMSQRHMIDGRWCDC KLPNSK,,QSQDEPLRSRKVFVGRCTEDMTEDELREFFSQYGDVMDV/FIPKPFRAFAFVTFADDQ,,IAQSLCGEDLIITKIGSVHISNAEPKHNSNRQLERSGRFGGNPGGFGNQ GFGNSRGGGAGLGNNGSNGMGGGMNFGAFSINPAMMAAAQAALQSSWGMGLASQQNQSGPSGNQNGQNMQREPNQAFGSGNSYSYSGNSGAAIGWGSASNA GSGSGFNGGGSSMDSKSSGWGM*				
414 amino acids = 44.7 kDa					
TARDBP-231	1385 .. 9967	8583 bp	■	→	CDS
▶ 4 segments = 730 bp					
/note	= coding sequence ENSP00000480690				
/translation	= MSEYIRVTEDENDPEIEIPSEDDGTVLLSTVTAQFPGACGLRYRNPVVSQCMRGVRLVEGILHAPDAGWGNLVYVYNYPK,,DNKRKMDETDASSAVKVKRAVQKTSDLIVLGLPWKTEQDLKEYFSTFGEVLMVQ,,VKKDLKTGH SKGFGFVRFTEYETQVKVMSQRHMIDGRWCDC KLPNSK,,IAQSLCGEDLIITKIGSVHISNAEPKHNSNRQLERSGRFGGNPGGFGNGGFGNSRGGGAGL				
243 amino acids = 26.7 kDa					
TARDBP-207	1385 .. 8246	6862 bp	■	→	CDS
▶ 5 segments = 827 bp					
/note	= coding sequence ENSP00000466842				
/translation	= MSEYIRVTEDENDPEIEIPSEDDGTVLLSTVTAQFPGACGLRYRNPVVSQCMRGVRLVEGILHAPDAGWGNLVYVYNYPK,,GWTWWLTSVIPATREAEAGESLEPGRQLRGEIAPLHSSL,,DNKRKMDETDASSAVKVKRAVQK TSDLIVLGLPWKTEQDLKEYFSTFGEVLMVQ,,VKKDLKTGH SKGFGFVRFTEYETQVKVMSQRHMIDGRWCDC KLPNSK,,QSQDEPLRSRKVFVGRCTEDMTEDELREFFSQYGDVMDV/FIPKPFRAFAFVTF				
275 amino acids = 31.4 kDa					
TARDBP-205	1385 .. 8146	6762 bp	■	→	CDS
▶ 4 segments = 604 bp					
/note	= coding sequence ENSP00000465240				
/translation	= MSEYIRVTEDENDPEIEIPSEDDGTVLLSTVTAQFPGACGLRYRNPVVSQCMRGVRLVEGILHAPDAGWGNLVYVYNYPK,,DNKRKMDETDASSAVKVKRAVQKTSDLIVLGLPWKTEQDLKEYFSTFGEVLMVQ,,VKKDLKTGH SKGFGFVRFTEYETQVKVMSQRHMIDGRWCDC KLPNSK,,QSQDEPLRSRKVFVGRCTED				
201 amino acids = 22.8 kDa					
TARDBP-233	4516 .. 10,944	6429 bp	■	→	prim_transcript
/note	= primary transcript ENST00000622057				
TARDBP-233	4516 .. 10,840	6325 bp	■	→	CDS
▶ 5 segments = 602 bp					
/note	= coding sequence ENSP00000481206				
/translation	= WMRMLHQQ*K*KEQSRKHPI**CWVSHGKQPNRT*KSILVPLEKFLWCR,,SRKILRLVIQRGLALFVLRNMKHK*K*CHSDI**MDDGV TANFLILS,,KAKMSL*EA EKCLWGAVQRT*LRMSCGSSSLSTGM*WMSSPSHSGP LPLHLQ MIR,,LRSLFVERT*SLKESAFIYMPNLSIAIDS*KEVEDLV,,YMKPSF				
200 codons (14 internal stop codons)					
TARDBP-223	4522 .. 11,247	6726 bp	■	→	prim_transcript
/note	= primary transcript ENST00000617172				
TARDBP-223	4522 .. 10,905	6384 bp	■	→	CDS
▶ 5 segments = 638 bp					
/note	= coding sequence ENSP00000479219				
/translation	= RQMLHQQ*K*KEQSRKHPI**CWVSHGKQPNRT*KSILVPLEKFLWCR,,SRKILRLVIQRGLALFVLRNMKHK*K*CHSDI**MDDGV TANFLILS,,KAKMSL*EA EKCLWGAVQRT*LRMSCGSSSLSTGM*WMSSPSHSGPLPL LHLQ MIR,,LRSLFVERT*SLKESAFIYMPNLSIAIDS*KEVEDLV,,YMKPSF				
212 codons (16 internal stop codons)					
TARDBP-225	4535 .. 6843	2309 bp	■	→	prim_transcript
/note	= primary transcript ENST00000618606 Retained intron				
TARDBP-215	4623 .. 11,850	7228 bp	■	→	prim_transcript
/note	= primary transcript ENST00000611963 Nonsense mediated decay				
TARDBP-226	6437 .. 11,841	5405 bp	■	→	prim_transcript
/note	= primary transcript ENST00000619555 Nonsense mediated decay				
TARDBP-229	6437 .. 11,700	5264 bp	■	→	prim_transcript
/note	= primary transcript ENST00000620632 Nonsense mediated decay				
TARDBP-212	6510 .. 11,700	5191 bp	■	→	prim_transcript
/note	= primary transcript ENST00000610369				
TARDBP-212	6510 .. 10,984	4475 bp	■	→	CDS
▶ 4 segments = 384 bp					
/note	= coding sequence ENSP00000482559				
/translation	= CKLPNSK,,QSQDEPLRSRKVFVGRCTEDMTEDELREFFSQYGDVMDV/FIPKPFRAFAFVTFADDQ,,IAQSLCGEDLIITKIGSVHISNAEPKHNSNRQLERSGRFGGNP,,GILSTCFLIQEFVITHHRPL*				
127 amino acids = 14.5 kDa					
TARDBP-220	8090 .. 11,840	3751 bp	■	→	prim_transcript
/note	= primary transcript ENST00000614494 Nonsense mediated decay				
TARDBP-214	8163 .. 18,087	9925 bp	■	→	prim_transcript
/note	= primary transcript ENST00000611136 Nonsense mediated decay				
TARDBP-208	8244 .. 12,864	4621 bp	■	→	prim_transcript
/note	= primary transcript ENST00000477447 Nonsense mediated decay				
TARDBP-217	9801 .. 18,183	8383 bp	■	→	prim_transcript
/note	= primary transcript ENST00000612542				
TARDBP-217	9801 .. 12,843	3043 bp	■	→	CDS
▶ 2 segments = 184 bp					
/note	= coding sequence ENSP00000478249				
/translation	= RGLDH*RNQRSYICRT*AQ*Q*TVRKKWKIWW*SS,,TCTITQQQ*HGNT*NGTRGPPKTKL				
61 codons (7 internal stop codons)					
TARDBP-228	9965 .. 12,878	2914 bp	■	→	prim_transcript
/note	= primary transcript ENST00000620505 Nonsense mediated decay				
Donor Template SNV -> REV	10,028 .. 10,127	100 bp	■	↔	misc_feature
Protospacer Sequence	10,046 .. 10,065	20 bp	■	↔	misc_feature

Feature	Location	Size			Type
SNV	10,057 .. 10,057	1 bp			variation
/note	= REV = C SNV = A				
PAM	10,066 .. 10,068	3 bp			misc_feature
TARDBP-230	10,205 .. 11,930	1726 bp			prim_transcript
/note	= primary transcript ENST00000621573 Nonsense mediated decay				
TARDBP-213	10,475 .. 13,149	2675 bp			prim_transcript
/note	= primary transcript ENST00000611008				
TARDBP-218	10,702 .. 12,860	2159 bp			prim_transcript
/note	= primary transcript ENST00000613177				
TARDBP-234	10,855 .. 18,154	7300 bp			prim_transcript
/note	= primary transcript ENST00000622108 Nonsense mediated decay				
TARDBP-210	10,855 .. 13,396	2542 bp			prim_transcript
/note	= primary transcript ENST00000496840 Nonsense mediated decay				
TARDBP-224	10,980 .. 11,809	830 bp			prim_transcript
/note	= primary transcript ENST00000617757				
TARDBP-209	11,586 .. 13,149	1564 bp			prim_transcript
/note	= primary transcript ENST00000480464				
TARDBP-227	12,450 .. 18,182	5733 bp			prim_transcript
/note	= primary transcript ENST00000620028				
MASP2	14,180 .. 34,896	20,717 bp			gene
/note	= gene ENSG00000009724 Protein coding				
MASP2-201	14,180 .. 34,896	20,717 bp			prim_transcript
/note	= primary transcript ENST00000400897 Protein coding				
TARDBP-211	17,316 .. 18,185	870 bp			prim_transcript
/note	= primary transcript ENST00000607145				
TARDBP-216	17,415 .. 18,185	771 bp			prim_transcript
/note	= primary transcript ENST00000612387				

Primer		Length		Binding Sites		Tm	Date Added
✓ PCR Forward		22-mer		9621 .. 9642	→	57°C	Apr 22, 2022
/sequence	=	ACTAAAAGCTGTATTGGGGTT 41% GC / 6829.5 Da					
✓ Donor Template SNV-> REV		100-mer		10,028 .. 10,127	←	82°C	Apr 22, 2022
/sequence	=	TGTTATTACCCGATGGGCCTGACTGGTTCTGCTGGCTAAGCTAACATGCCCATACACCCCAACTGCTCTGTAGTGTGCCTGGGCGGCAGCCATCATGG 58% GC / 30,751.9 Da					
✓ gRNA Protospacer		20-mer		10,046 .. 10,065	→	54°C	Apr 22, 2022
/sequence	=	AGGCAGCACTAAAGAGCAGT 50% GC / 6184.1 Da					
✓ PCR Reverse		20-mer		10,192 .. 10,211	←	59°C	Apr 22, 2022
/sequence	=	GCTGCACCAAGAATTAGGCC 55% GC / 6111.0 Da					
✓ Sanger Sequencing Primer		20-mer		10,192 .. 10,211	←	59°C	Apr 22, 2022
/sequence	=	GCTGCACCAAGAATTAGGCC 55% GC / 6111.0 Da					