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135

TARDBP

AGGTCTGGTTTTATTTAGCTTTCAGAGCTTCTCTGTAGGCTTGAATTTCCAGGAGGCAGCCGAGTCCCTGGGGAGAGGGTCATCGTGGCTCTCGTCGGTGCCTTCCACCTCTGGACAGGCAACCGGTGGGAG  
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270

TARDBP

AGGACGCCGGTGGGCGGGGGAGGAGCGGCCCTAGCGCCATTTTGTGGGAGCGAAGCGGTGGCTGGGCTGCGCTTGGGTCGCTCGCTTCCGTTGTCCTGTCGGGCTTCCAGCAGCGGCCCTAGCGGGTGA  
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405

TARDBP

TARDBP-201

TCGCGGAGCCTTCTCACTGAGGACGCCGTAGGTGCCTGGCTTCTGCATTGGGGCGGCCGAGGCAGACGACGCGGCTTCGGACCTGCCCGGGAAGTCAGCCGTGAGACCGGGCTAGTCTGCCGAGCGGG  
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540

TARDBP

TARDBP-201

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675

TARDBP

TARDBP-201

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810

TARDBP

TARDBP-201

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945

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TARDBP-201

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1080

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TARDBP-201

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1215

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TARDBP-201

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1350

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TARDBP-201

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1485

TARDBP

TARDBP-201

1 M S E V I R V T E D E N D E P I E I P S E D D G T V L L S T V T A Q  
ENSE0003910947  
TARDBP-201

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1620

TARDBP

TARDBP-201

35 F P G A C G L R Y R N P V S Q C M R G V R L V E G I L H A P D A G W G 70 N L V Y V V N Y P K  
ENSE0003910947  
TARDBP-201

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1755

TARDBP

TARDBP-201

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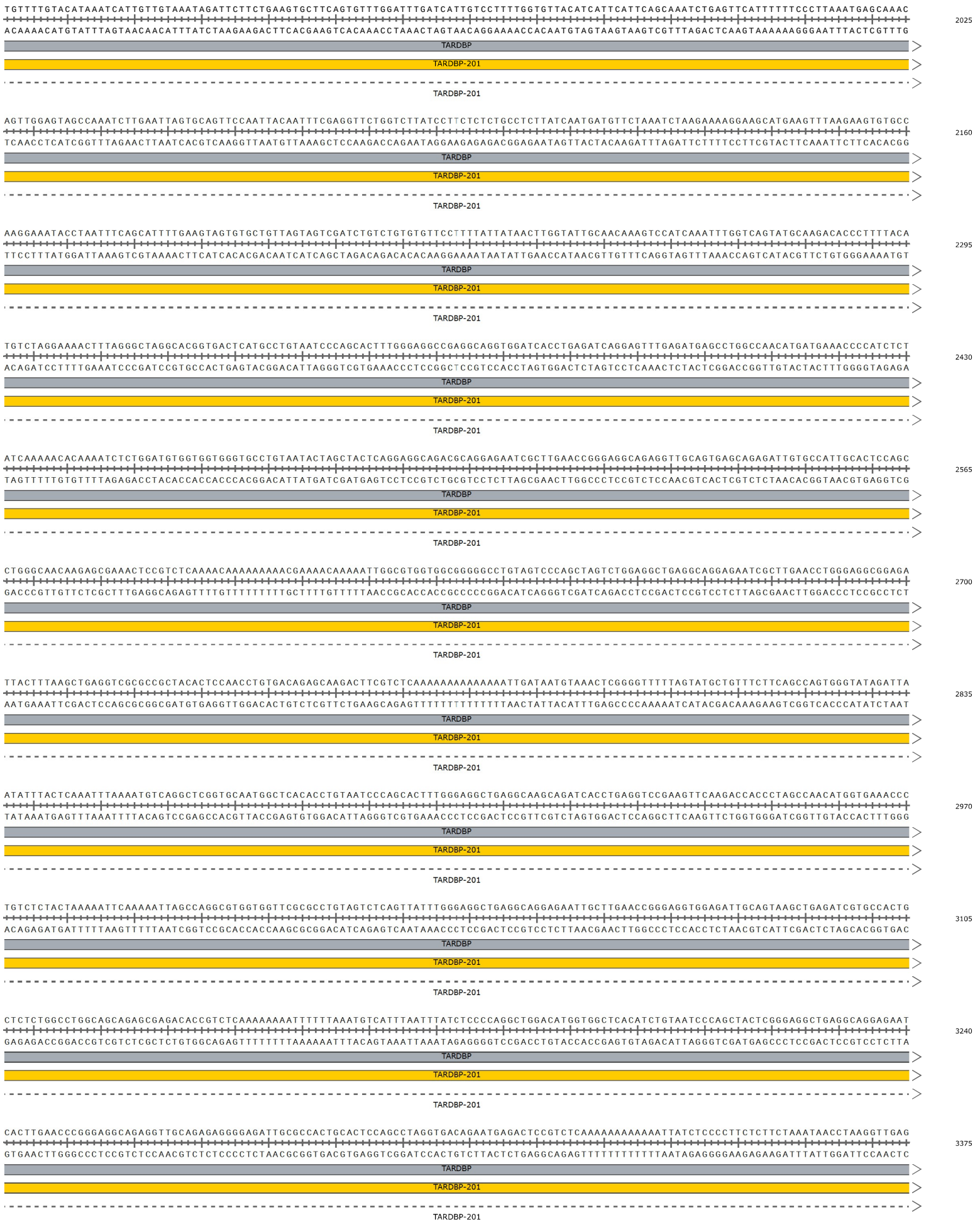
1890

TARDBP

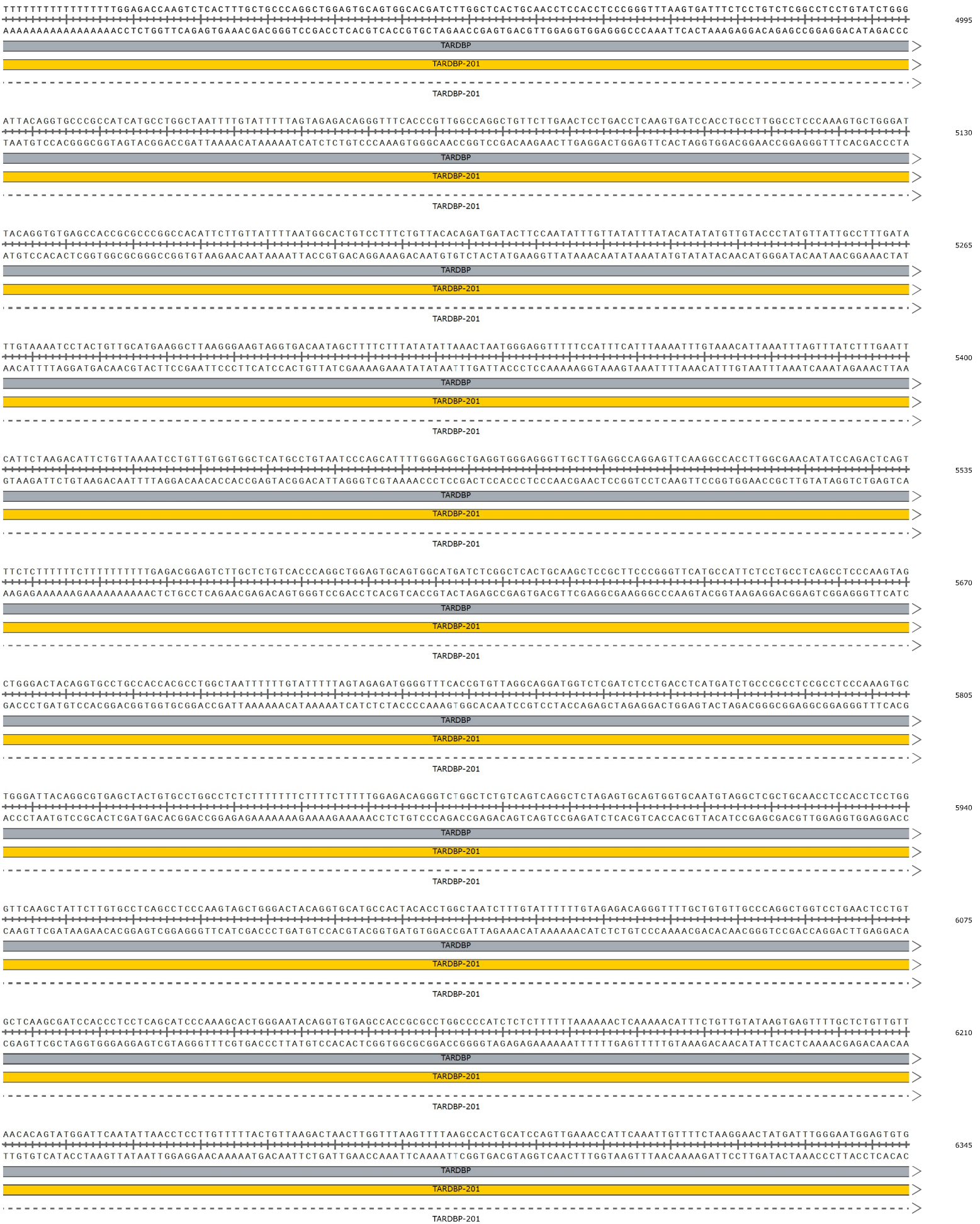
TARDBP-201

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TARDBP-201





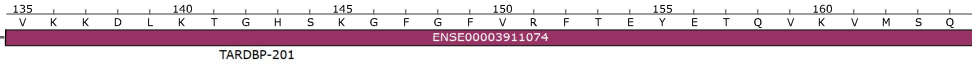


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6480

TARDBP

TARDBP-201

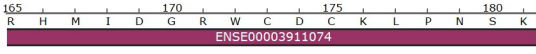


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6615

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TARDBP-201



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6750

TARDBP

TARDBP-201

TARDBP-201

CTTCCTTTTCGCTATGGATGAAAAGAGAAAAGGTTATTTGTCAAGTTAATAGTTTCTACATAGTTATATGTTAAAAACATAAAGAGAATCAGAATACATACATTAAATGTTATAAAGACCTAACCTTTTCCAAG  
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6885

TARDBP

TARDBP-201

TARDBP-201

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7020

TARDBP

TARDBP-201

TARDBP-201

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7155

TARDBP

TARDBP-201

TARDBP-201

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TATCCGATATGGTAGATCGGATCTACACCCATCCGATACGATAGACCCAAATATACTACAACCGTGTGCTGAAAAAATAAATCTCTCTCTCAGAGTGAGACAGTAGGCCCGACCTCACGTCACCACGTTAG

7290

TARDBP

TARDBP-201

TARDBP-201

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7425

TARDBP

TARDBP-201

TARDBP-201

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7560

TARDBP

TARDBP-201

TARDBP-201

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7695

TARDBP

TARDBP-201

TARDBP-201

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7830

TARDBP

TARDBP-201

TARDBP-201



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9450

TARDBP

TARDBP-201

TARDBP-201

AGGTGGGCTCCCTGTGTGCTAGGCTGCCAGGCTAGTCTTGAACATTGGCCTCACACAGTCTCCACCTTGGCCTCCAAAGCGCTAGGATTACAGGCATGAGCCACCATGCCAGCCTATGTCTTTTGA  
TCCACCAGAGGGGACACAAACAGATCCGACGGTCCGATCAGAAGTTGATAACCGGAGTGTGTACAGGAGGTTGAAACCGGAGGGTTTCGCGATCCTAATGTCCGTACTCGGTGGTACGGGTCCGATACAGAAAAC

9585

TARDBP

TARDBP-201

TARDBP-201

PCR Forward  
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AAATCGACTGAAATATCACTGCTGCTGTTAATAAACTAAAAGCTGATTGGGGGTTAAATGAAATGAGTGTTCATTGCTTATTTTTCTCTGGCTTTAGATAAATTAATGCTTGTAACTAAAGTTTTGTGCT  
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9720

TARDBP

TARDBP-201

TARDBP-201

ACTTTAAATATATGAATCAGTGGTTAATCTTCTTTGTTTACATCCCTTATTTCTTAGATTGGCGAGTCTCTTGTGGAGGAGACTTGATCATTAAAGGAATCAGCGTTCATATATCCAATGCCGAACCTAAG  
TGAAATTTATATACTTAGTCACCAAATTAGAAGAAACAAATGTAGGGAATAAAGAAATATCTAACCGCTCAGAGAAACACCTCTCTGAACTAGTAATTTCTTAGTCGCAAGTATATAGTTACGGCTTGGATTC

9855

TARDBP

TARDBP-201

I A Q S L C G E D L I I K G I S V H I S N A E P K  
ENSE00001145815

TARDBP-201

Sanger Sequencing Primer  
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CACAATAGCAATAGACAGTTAGAAAGAAGTGAAGATTTGGTGGTAATCCAGGTGGCTTTGGGAATCAGGTTGGATTTGGTAATAGCAGAGGGGGTGGAGCTGGTTGGGAAACAATCAAGGTAGTAATATGGGT  
GTGTTATCGTTATCTGTCAATCTTCTTCACTTCTAAACCACATTAGGTCACCGAAACCTTAGTCCACCTAAACCATTATCGTCTCCCCACCTCGACCAAACCTTTGTTAGTTCATCATTATACCCA

9990

TARDBP

TARDBP-201

H N S N R Q L E R S G R F G N P G G F G N Q G G F G N S R G G G A G L G N N Q G S N M G  
ENSE00001145815

TARDBP-201

gRNA Protospacer  
ACAGAGCAGTTGGGTATG

GGTGGGATGAACTTTGGTGGTTCAGCATTAAATCCAGCCATGATGGCTGCCGCCAGGCAGCACTACAGAGCAGTTGGGTATGATGGGCATGTTAGCCAGCAGCAGAAACAGTCAGGCCCATCGGGTAAATAAC  
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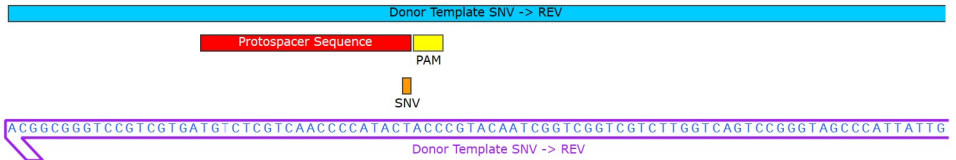
10,125

TARDBP

TARDBP-201

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ENSE00001145815

TARDBP-201



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10,260

TARDBP

TARDBP-201

Q N Q G N M Q R E P N Q A F G S G N N S Y S G S N S G A A I G W G S A S N A G S S G S G F N  
ENSE00001145815

TARDBP-201

Donor Template SNV -> REV

GTITGGTTCCG

Donor Template SNV -> REV

GGAGGCTTTGGCTCAAGCATGGATTCTAAGTCTTCTGGCTGGGAAATGTAGACAGTGGGGTTGGTGGTGGTGGTATAGAATGGTGGGAATTCAAATTTTTCTAAACTCATGGTAAGTATATTGTAAAATACATA  
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10,395

TARDBP

TARDBP-201

G G F G S S M D S K S S G W G M S  
ENSE00001145815

TARDBP-201



TGTAATAAGAAATTTTCAA... 10,530

TARDBP

TARDBP-201

GGTTGAAAGTGA... 10,665

TARDBP

TARDBP-201

CGGACTAACCATTTGGTGTGTGAT PCR Reverse

TTAGAACTACATTTTACCCCTTGT... 10,800

TARDBP

TARDBP-201

CCCCATACACAAAAGTACAATATGAAGCCTTCATTTAATCTCTGCAGTTCATCTCATTCAAATGTTTATGGAAGAAGCACTTCATTGAAAGTAGTGTGTAATATTTGCCATAGGAATACTGTCTACATG... 10,935

TARDBP

TARDBP-201

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TARDBP

TARDBP-201

AAGGCTGTCTGAAC... 11,205

TARDBP

TARDBP-201

AGATGTGTCTCTCAATCCTGTGGCTTTGGTGAGAGAGTGTGCAGAGCAATGATAGCAAATAATGTACGAATGTTTTTGCATTCAAAGGACATCCACATCTGTTGGAAGACTTTAAGTGAGTTTTGTCTT... 11,340

TARDBP

TARDBP-201

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TARDBP

TARDBP-201

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TARDBP

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TARDBP

TARDBP-201

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TARDBP

TARDBP-201

ACCTGATACCCAGACTTAATTGGTATTTGTTCTTGCATTGGCCAAAGTGA... 12,015

TARDBP

TARDBP-201

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TARDBP

TARDBP-201

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TARDBP

TARDBP-201

ATAGCTTTAAGAATTAGGGTGGGTTGTCTGTCTGGAAGTGTAAAGTGA... 12,420

TARDBP

TARDBP-201

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12,555

TARDBP

TARDBP-201

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12,690

TARDBP

TARDBP-201

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12,825

TARDBP

TARDBP-201

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12,960

TARDBP

TARDBP-201

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13,095

TARDBP

TARDBP-201

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13,230

TARDBP

TARDBP-201

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13,365

TARDBP

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13,500

TARDBP

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13,635

TARDBP

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13,770

TARDBP

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13,905

TARDBP

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14,040

TARDBP

GTAGTATTGGTTTTAACATGGAATTTTAGTCAATACCTGGGCTGAAGTATCAGTGTTCACACTACCCAAAAAAGGATTCAGGTTTATCCTCAATCAGTACTGCCATAATATAAAGCACTTACA  
CATCATAACCAAAATTTGACCTTTAAATCAGTTATGGAACCCGACTTCATAGTCACAAGGTTTGGATGGATGGGTTTTTCTCAAGTCCAATAAGGAGTTAGTCATGACGGTATTTATATTTCTGTAATGT

14,175

TARDBP

GAGATCAATAAGAACAAGTTTAAAAACAAGAGCATGGACAGGCAAGTTTACAGAAATGCCAACAGCCAGTATGAAAGAGACTGGCTTTTTAAGGTAATGAAATGTAATTTGAGCAGTGACATTACACTGGGTGG  
CTCTAGTATTCTGTTCAAATTTTTGTTTCTCGTACCTGTCGTCAAATGCTTTACGGTTGTCGGTCACTATTTCTCTGACCGAAAAATTCATTACTTTACATTAACCTCGTCACTGTAATGTGACCCACC

14,310

TARDBP

GCAAAGATGACTGTCACTCTCGTGGTTTATGTCCTTGAAGTCAATGGGTAAGGCTGGAATTAACCTGGCAAGTGGAGAAATGACAGCAGCCTCACCTGGAGTCTGTTTTTGGGTTGGAGCAACAACCTGCCATG  
CGTTTCACTGACAGTGAGAGCACCAAAATACAGGGGAACCTCAGTTACCAATTCGACCTTAAATTTGACGGTTCACCTCTTACTGTGCTGGAGTGGACCTCAGACAAAAAACCCACCTCGTTGTTGACGGTAC

14,445

TARDBP

TCCACAGTAATGATGAATGCTTCTCGAGCCACGTCGCTGCCAAGGCTTTCACAGGCATTTCTAAAAATGAAGAATCCTTGACTGCAGACACGCAAGTTAAAAATCACTAATTTATGTTCTCGATCCAGGGAAATATA  
AGGTGTCATTACTACTTACGAAGAGCTCGGTGACGCGACGGTTCCAGAAGTGTCCGTAAGATTTTTACTTCTTAGGAACTGACGTCGTGCGTCAATTTTTAGTGATTAATAAAGAGCTAGGTCCTTATAT

14,580

TARDBP

GTTAATAACTTTTTGTGACTCCATACTGACCTGCTTCCCAACAATTCATGGAACCCAGGACACTATTCTCCCAACAACACCTCTCTGTTTCACTATCTAGAAACACCAGTCCCCTCCGCTGTCACCTCT  
CAATTTTGAACACATCTGAGGTATGACTGGACGAAGGGGTGTTAAGTACCTTGGGGTCTGTGATAAGGAGGGTGTGGTGGAGAGACAAAGTATAGATCTTTGTTGGTCAAGGGGAGCCGACAGTGGAGA

14,715

TARDBP

GCAGCTGCTTGGCCCACTTTCTAAGCCAGCACAAGCATGTTAGCAGTTACACTTCCCTTGGATAGGGTGGCTTTTTCATATGCAGCAGTACATTTTTGATGGTCAACAATCGGTATGTGCACATACATTAG  
CGTCGACAGGAACGGGGTGAAGATTGGTCTGTTTCGTACAATCGTCAATGTGAAGGGGAACCTATCCACCGAAAAAGTATACGTCGTCATGTAAAACTACCAGTTGTTAGCCATACAGCTGTATGTAATC

14,850

TARDBP



CGCTCGAGTAGCTGGGATTACAGGCATGTACACACACACCCGGCTAATTTTGTATTTTTATTAGAGACGGGGTTCTCCATGCTGGTCAAGGCTGGCCTCAGGTGACCCACCTGCCTCGGCCCTCCAAAGTGTGG  
GCGAGCTCATCGACCCTAATGTCCGTACATGGTGGTGTGGGCCGATTAAAAACATAAAAAATAATCTCTGCCCAAAGAGGTACGACCACTCCGACCCGGAGTCCACTGGGTGGACGGAGCCGGAGGGTTTCAGGACC

17,550

TARDBP

GATTACAGGCGTGAGCCACACCTGGCCTAAAAATCATTTAATTTTTTATGCTTGCCTAGTTATAAGGTCAAAGAGAATCAAATGACTGATGCAGTCAGCACCTAACACCTCTGTATATGGGAAGGGGGTAATGA  
CTAATGTCCGCACTCGGTGTGGACCGGATTTTAGTAAATTA AAAAATACGAACGGATCAATATTCCAGTTTCTCTTAGTTTACTGACTACGTCAGTCGTGGATTGTTGGAGACATATACCTTCCCCATTACT

17,685

TARDBP

GAACATACTATTTGGAAATAATAACAGCCTAAGAGCCAAGTGTGAAGTTACATTTCTGCCTACCACAGCTAAAGCTCTCCTCACTGTCTCCTACCCAGTCTCTCTTCCATCAATTACCAGTCTCTTGTATAAA  
CTTGTATGATAAACCTTTATTATTGTTCGGATTCTCGGTTACAGCACTTCAATGTAAGACGGATGGTGTGCGATTTTCGAGAGGAGTGACAGAGGATGGGTCAGGAGAAAGGTAGTTAATGGTCAGAGAACATATT

17,820

TARDBP

TGTATCCATTACCAAGGCTCACAGACTGGGAGTGATTTTCTCCTTTGGAGCTCGTCCAGAATCCATCAGCCTCACACACATATTTACCTGCAAAATCATTGGAAAAGCAAAAATGTTAACTGCATGTATAAGATG  
ACATAGGTAATGGTCCGAGTGTCTGACCCTCACTAAAAAGAGGAAACCTCGAGCAGGTCTTAGGTAGTCGGAGTGTGTATAAATGGACGTTTAGTAACCTTTTTCGTTTTTACA AATTGACGTACATATTCTAC

17,955

TARDBP

GTTGTCAATTTGCTTGAATACCCCTTGAAAAATGTTGATTTCTGAGCATCAGTGGGACATAGAGGTGCTGAAGAACCATTTTACATGATTTTATAAATAGGAGGCTCTGCAATTACCATGTTTCTTGCAAAGT  
CAACAGTAAACGAACCTTATGGGGGAACTTTTTACAAC TAAGAACTCGTAGTCACCCTGTATCTCCACAGACTTCTTGGTAAAATGACTAAAGTATTTATCCTCCAGAGACGTAATGGTACAAACGAACGTTTCA

18,090

TARDBP

GGAAACCTTTTAGATGTGTAACCTTGAATATGTATCAAGATCTCAAGTGTCTAATGATAAGGTGTTGACTTGTAAATTAACCATTGGGAATACA  
CCTTTGGAAAATCTACACATTGAACCTTATACATAGTTCTAGAGTTCACGAATTACTATTCCACAACCTGAACAATTTAATTTGGTAAACCTTATGT

3'  
18,185  
5'

TARDBP

Feature	Location	Size	Type
<b>TARDBP</b>	1 .. 18,185	18,185 bp	gene
/note	= gene <a href="#">ENSG00000120948</a> Protein coding		
<b>TARDBP-205</b>	1 .. 8146	8146 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000473118</a>		
<b>TARDBP-236</b>	81 .. 11,266	11,186 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000639083</a>		
<b>TARDBP-237</b>	82 .. 11,840	11,759 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000639599</a> Nonsense mediated decay		
<b>TARDBP-235</b>	279 .. 10,905	10,627 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000629725</a>		
<b>TARDBP-203</b>	310 .. 10,515	10,206 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000439080</a> Nonsense mediated decay		
<b>TARDBP-201</b>	311 .. 13,149	12,839 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000240185</a>		
<b>TARDBP-204</b>	311 .. 9833	9523 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000472476</a> Nonsense mediated decay		
<b>TARDBP-207</b>	311 .. 8246	7936 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000476201</a>		
<b>TARDBP-219</b>	311 .. 6110	5800 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000613864</a>		
<b>TARDBP-221</b>	319 .. 18,185	17,867 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000614757</a> Nonsense mediated decay		
<b>TARDBP-231</b>	327 .. 9967	9641 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000621715</a>		
<b>TARDBP-206</b>	1373 .. 12,676	11,304 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000473869</a> Nonsense mediated decay		
<b>TARDBP-202</b>	1373 .. 11,840	10,468 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000315091</a>		
<b>TARDBP-222</b>	1385 .. 10,998	9614 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000616545</a>		
<b>TARDBP-232</b>	1385 .. 10,998	9614 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000621790</a>		
<b>TARDBP-222</b>	1385 .. 10,984	9600 bp	CDS
▶ 6 segments = 906 bp			
/note	= coding sequence <a href="#">ENSP00000484722</a>		
/translation	= MSEYIRVTEDENDPEIEIPSEDDGTVLLSTVTAQFPGACGLRYRNPVSQCMRGVRLVEGILHAPDAGWGNLVYVYVNYPK,,DNKRKMDETDASSAVKVKRAVQKTSDLIVLGLPWKTEQDLKEYFSTFGEVLMVQ,,VKKDLKTGH SKGFGFVRFTEYETQVKVMSQRHMIDGRWCCKLPNSK,,QSQDEPLRSRKFVVGRC TEDMTEDELREFFSQYGDVMDV/FIPKPFRAFAFVTFADDQ,,IAQSLCGEDLIKIGSVHISNAEPKHNSNRQLERSGRFGGNP,,GILSTCF bDQEMHDFRRL* 34.2 kDa		
<b>TARDBP-202</b>	1385 .. 10,905	9521 bp	CDS
▶ 6 segments = 888 bp			
/note	= coding sequence <a href="#">ENSP00000313129</a>		
/translation	= MSEYIRVTEDENDPEIEIPSEDDGTVLLSTVTAQFPGACGLRYRNPVSQCMRGVRLVEGILHAPDAGWGNLVYVYVNYPK,,DNKRKMDETDASSAVKVKRAVQKTSDLIVLGLPWKTEQDLKEYFSTFGEVLMVQ,,VKKDLKTGH SKGFGFVRFTEYETQVKVMSQRHMIDGRWCCKLPNSK,,QSQDEPLRSRKFVVGRC TEDMTEDELREFFSQYGDVMDV/FIPKPFRAFAFVTFADDQ,,IAQSLCGEDLIKIGSVHISNAEPKHNSNRQLERSGRFG,,VHLISNVYGR 595LHMLA acids = 33.5 kDa		
<b>TARDBP-232</b>	1385 .. 10,905	9521 bp	CDS
▶ 6 segments = 915 bp			
/note	= coding sequence <a href="#">ENSP00000482191</a>		
/translation	= MSEYIRVTEDENDPEIEIPSEDDGTVLLSTVTAQFPGACGLRYRNPVSQCMRGVRLVEGILHAPDAGWGNLVYVYVNYPK,,DNKRKMDETDASSAVKVKRAVQKTSDLIVLGLPWKTEQDLKEYFSTFGEVLMVQ,,VKKDLKTGH SKGFGFVRFTEYETQVKVMSQRHMIDGRWCCKLPNSK,,QSQDEPLRSRKFVVGRC TEDMTEDELREFFSQYGDVMDV/FIPKPFRAFAFVTFADDQ,,IAQSLCGEDLIKIGSVHISNAEPKHNSNRQLERSGRFGGNP,,VHLISNVYGR 594LHMLA acids = 33.4 kDa		
<b>TARDBP-235</b>	1385 .. 10,905	9521 bp	CDS
▶ 6 segments = 897 bp			
/note	= coding sequence <a href="#">ENSP00000486989</a>		
/translation	= MSEYIRVTEDENDPEIEIPSEDDGTVLLSTVTAQFPGACGLRYRNPVSQCMRGVRLVEGILHAPDAGWGNLVYVYVNYPK,,DNKRKMDETDASSAVKVKRAVQKTSDLIVLGLPWKTEQDLKEYFSTFGEVLMVQ,,VKKDLKTGH SKGFGFVRFTEYETQVKVMSQRHMIDGRWCCKLPNSK,,QSQDEPLRSRKFVVGRC TEDMTEDELREFFSQYGDVMDV/FIPKPFRAFAFVTFADDQ,,IAQSLCGEDLIKIGSVHISNAEPKHNSNRQLERSGRFGGNP,,VHLISNVYGR 598LHMLA acids = 33.7 kDa		
<b>TARDBP-238</b>	1385 .. 10,891	9507 bp	CDS
▶ 6 segments = 810 bp			
/note	= coding sequence <a href="#">ENSP00000497327</a>		
/translation	= MSEYIRVTEDENDPEIEIPSEDDGTVLLSTVTAQFPGACGLRYRNPVSQCMRGVRLVEGILHAPDAGWGNLVYVYVNYPK,,DNKRKMDETDASSAVKVKRAVQKTSDLIVLGLPWKTEQDLKEYFSTFGEVLMVQ,,VKKDLKTGH 269 amino acids = 30.7 kDa		
<b>TARDBP-238</b>	1385 .. 10,891	9507 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000649624</a>		
<b>TARDBP-201</b>	1385 .. 10,311	8927 bp	CDS
▶ 5 segments = 1245 bp			
/note	= coding sequence <a href="#">ENSP00000240185</a>		
/translation	= MSEYIRVTEDENDPEIEIPSEDDGTVLLSTVTAQFPGACGLRYRNPVSQCMRGVRLVEGILHAPDAGWGNLVYVYVNYPK,,DNKRKMDETDASSAVKVKRAVQKTSDLIVLGLPWKTEQDLKEYFSTFGEVLMVQ,,VKKDLKTGH SKGFGFVRFTEYETQVKVMSQRHMIDGRWCCKLPNSK,,QSQDEPLRSRKFVVGRC TEDMTEDELREFFSQYGDVMDV/FIPKPFRAFAFVTFADDQ,,IAQSLCGEDLIKIGSVHISNAEPKHNSNRQLERSGRFGGNP,,GILSTCF GFGNSRGGGAGLGNQGSNMGGGMNFGAFSINPAMMAAAQAALQSSWGMGMLASQNNQSGPSGNQGNMQREPQAFGSGNSNSYSGNSGAALGWGSA SNA GSGSGFNGGFGSSMDSKSSGWSGM* 414 amino acids = 44.7 kDa		

Feature	Location	Size	Start	End	Type
<b>TARDBP-236</b>	1385 .. 10,311	8927 bp	■	→	CDS
▶ 5 segments = 1245 bp					
/note	= coding sequence <a href="#">ENSP00000491203</a>				
/translation	= MSEYIRVTEDENDPEIEIPSEDDGTVLLSTVTAQFPGACGLRYRNPVVSQCMRGVRLVEGILHAPDAGWGNLVYVYNYPK,,DNKRKMDETDASSAVKVKRAVQKTSDLIVLGLPWKTTEQDLKEYFSTFGVEVLMVQ,,VKKDLKTGH SKGFGFVRFTEYETQVKVMSQRHMIDGRWCDC KLPNSK,,QSQDEPLRSRKVFVGRCTEDMTEDELREFFSQYGDVMDV/FIPKPFRAFAVTFADDQ,,IAQSLCGEDLIITKGISVHISNAEPKHNSNRQLERSGRFGGNPGGFGNQ GFGNSRGGGAGLGNNGSNGMGGGMNFGAFSINPAMMAAAQAALQSSWGMMLASQQNQSGPSGNQNGQNMQREPNQAFGSGNSYSYSGNSGAAIGWGSASNA GSGSGFNGGFGSSMDSKSSGWGM*				
414 amino acids = 44.7 kDa					
<b>TARDBP-231</b>	1385 .. 9967	8583 bp	■	→	CDS
▶ 4 segments = 730 bp					
/note	= coding sequence <a href="#">ENSP00000480690</a>				
/translation	= MSEYIRVTEDENDPEIEIPSEDDGTVLLSTVTAQFPGACGLRYRNPVVSQCMRGVRLVEGILHAPDAGWGNLVYVYNYPK,,DNKRKMDETDASSAVKVKRAVQKTSDLIVLGLPWKTTEQDLKEYFSTFGVEVLMVQ,,VKKDLKTGH SKGFGFVRFTEYETQVKVMSQRHMIDGRWCDC KLPNSK,,IAQSLCGEDLIITKGISVHISNAEPKHNSNRQLERSGRFGGNPGGFGNGGFGNSRGGGAGL				
243 amino acids = 26.7 kDa					
<b>TARDBP-207</b>	1385 .. 8246	6862 bp	■	→	CDS
▶ 5 segments = 827 bp					
/note	= coding sequence <a href="#">ENSP00000466842</a>				
/translation	= MSEYIRVTEDENDPEIEIPSEDDGTVLLSTVTAQFPGACGLRYRNPVVSQCMRGVRLVEGILHAPDAGWGNLVYVYNYPK,,GWTWWLTSVIPATREA EAGESLEPGRQLRGEIAPLHSSL,,DNKRKMDETDASSAVKVKRAVQK TSDLIVLGLPWKTTEQDLKEYFSTFGVEVLMVQ,,VKKDLKTGH SKGFGFVRFTEYETQVKVMSQRHMIDGRWCDC KLPNSK,,QSQDEPLRSRKVFVGRCTEDMTEDELREFFSQYGDVMDV/FIPKPFRAFAVTF				
275 amino acids = 31.4 kDa					
<b>TARDBP-205</b>	1385 .. 8146	6762 bp	■	→	CDS
▶ 4 segments = 604 bp					
/note	= coding sequence <a href="#">ENSP00000465240</a>				
/translation	= MSEYIRVTEDENDPEIEIPSEDDGTVLLSTVTAQFPGACGLRYRNPVVSQCMRGVRLVEGILHAPDAGWGNLVYVYNYPK,,DNKRKMDETDASSAVKVKRAVQKTSDLIVLGLPWKTTEQDLKEYFSTFGVEVLMVQ,,VKKDLKTGH SKGFGFVRFTEYETQVKVMSQRHMIDGRWCDC KLPNSK,,QSQDEPLRSRKVFVGRCTED				
201 amino acids = 22.8 kDa					
<b>TARDBP-233</b>	4516 .. 10,944	6429 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000622057</a>				
<b>TARDBP-233</b>	4516 .. 10,840	6325 bp	■	→	CDS
▶ 5 segments = 602 bp					
/note	= coding sequence <a href="#">ENSP00000481206</a>				
/translation	= WMRMLHQQ*K*KEQSRKHPI**CWV SHGKQPNRT*KSILVPLEKFLWCR,,SRKILRLVIQRGLALFVLRNMKHK*K*CHSDI**MDDGV TANFLILS,,KAKMSL*EA EKCLWGAVQRT*LRMSCGSSSLSTGM*WMSSPSHSGP LPLHLQ MIR,,LRSLFVERT*SLKESAFIYMPNLSIAIDS*KEVEDLV,,YMKPSF				
200 codons (14 internal stop codons)					
<b>TARDBP-223</b>	4522 .. 11,247	6726 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000617172</a>				
<b>TARDBP-223</b>	4522 .. 10,905	6384 bp	■	→	CDS
▶ 5 segments = 638 bp					
/note	= coding sequence <a href="#">ENSP00000479219</a>				
/translation	= RQMLHQQ*K*KEQSRKHPI**CWV SHGKQPNRT*KSILVPLEKFLWCR,,SRKILRLVIQRGLALFVLRNMKHK*K*CHSDI**MDDGV TANFLILS,,KAKMSL*EA EKCLWGAVQRT*LRMSCGSSSLSTGM*WMSSPSHSGPLPL LHLQ MIR,,LRSLFVERT*SLKESAFIYMPNLSIAIDS*KEVEDLV,,YMKPSF				
212 codons (16 internal stop codons)					
<b>TARDBP-225</b>	4535 .. 6843	2309 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000618606</a> Retained intron				
<b>TARDBP-215</b>	4623 .. 11,850	7228 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000611963</a> Nonsense mediated decay				
<b>TARDBP-226</b>	6437 .. 11,841	5405 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000619555</a> Nonsense mediated decay				
<b>TARDBP-229</b>	6437 .. 11,700	5264 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000620632</a> Nonsense mediated decay				
<b>TARDBP-212</b>	6510 .. 11,700	5191 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000610369</a>				
<b>TARDBP-212</b>	6510 .. 10,984	4475 bp	■	→	CDS
▶ 4 segments = 384 bp					
/note	= coding sequence <a href="#">ENSP00000482559</a>				
/translation	= CKLPNSK,,QSQDEPLRSRKVFVGRCTEDMTEDELREFFSQYGDVMDV/FIPKPFRAFAVTFADDQ,,IAQSLCGEDLIITKGISVHISNAEPKHNSNRQLERSGRFGGNP,,GILSTCFLIQEFVITHHRPL*				
127 amino acids = 14.5 kDa					
<b>TARDBP-220</b>	8090 .. 11,840	3751 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000614494</a> Nonsense mediated decay				
<b>TARDBP-214</b>	8163 .. 18,087	9925 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000611136</a> Nonsense mediated decay				
<b>TARDBP-208</b>	8244 .. 12,864	4621 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000477447</a> Nonsense mediated decay				
<b>TARDBP-217</b>	9801 .. 18,183	8383 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000612542</a>				
<b>TARDBP-217</b>	9801 .. 12,843	3043 bp	■	→	CDS
▶ 2 segments = 184 bp					
/note	= coding sequence <a href="#">ENSP00000478249</a>				
/translation	= RGLDH*RNQRSYICRT*AQ*Q*TVRKKWKIWW*SS,,TCTITQQQ*HGNT*NGTRGPPKTKL				
61 codons (7 internal stop codons)					
<b>TARDBP-228</b>	9965 .. 12,878	2914 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000620505</a> Nonsense mediated decay				
<b>Donor Template SNV -&gt; REV</b>	10,038 .. 10,137	100 bp	■	↔	misc_feature
<b>Protospacer Sequence</b>	10,056 .. 10,075	20 bp	■	↔	misc_feature

Feature	Location	Size			Type
<b>SNV</b>	10,075 .. 10,075	1 bp			variation
/note	= REV = A SNV = G				
<b>PAM</b>	10,076 .. 10,078	3 bp			misc_feature
<b>TARDBP-230</b>	10,205 .. 11,930	1726 bp			prim_transcript
/note	= primary transcript <a href="#">ENST00000621573</a> Nonsense mediated decay				
<b>TARDBP-213</b>	10,475 .. 13,149	2675 bp			prim_transcript
/note	= primary transcript <a href="#">ENST00000611008</a>				
<b>TARDBP-218</b>	10,702 .. 12,860	2159 bp			prim_transcript
/note	= primary transcript <a href="#">ENST00000613177</a>				
<b>TARDBP-234</b>	10,855 .. 18,154	7300 bp			prim_transcript
/note	= primary transcript <a href="#">ENST00000622108</a> Nonsense mediated decay				
<b>TARDBP-210</b>	10,855 .. 13,396	2542 bp			prim_transcript
/note	= primary transcript <a href="#">ENST00000496840</a> Nonsense mediated decay				
<b>TARDBP-224</b>	10,980 .. 11,809	830 bp			prim_transcript
/note	= primary transcript <a href="#">ENST00000617757</a>				
<b>TARDBP-209</b>	11,586 .. 13,149	1564 bp			prim_transcript
/note	= primary transcript <a href="#">ENST00000480464</a>				
<b>TARDBP-227</b>	12,450 .. 18,182	5733 bp			prim_transcript
/note	= primary transcript <a href="#">ENST00000620028</a>				
<b>MASP2</b>	14,180 .. 34,896	20,717 bp			gene
/note	= gene <a href="#">ENSG00000009724</a> Protein coding				
<b>MASP2-201</b>	14,180 .. 34,896	20,717 bp			prim_transcript
/note	= primary transcript <a href="#">ENST00000400897</a> Protein coding				
<b>TARDBP-211</b>	17,316 .. 18,185	870 bp			prim_transcript
/note	= primary transcript <a href="#">ENST00000607145</a>				
<b>TARDBP-216</b>	17,415 .. 18,185	771 bp			prim_transcript
/note	= primary transcript <a href="#">ENST00000612387</a>				

Primer	Length	Binding Sites	Tm	Date Added
✓ <b>PCR Forward</b> /sequence = ATCGACTGAAATATCACTGCTGCTG 44% GC / 7641.0 Da	25-mer	9588 .. 9612	→ 60°C	Apr 22, 2022
✓ <b>Sanger Sequencing Primer</b> /sequence = GGATTTGGTAATAGCAGAGG 45% GC / 6261.2 Da	20-mer	9928 .. 9947	→ 53°C	Apr 22, 2022
✓ <b>Donor Template SNV -&gt; REV</b> /sequence = GCCTTGTTTTGGTTATTACCCGATGGGCCTGACTGGTTCCTGCTGGCTGGCTAACATGCCCATCATACCCCAACTGCTCTGTAGTGTGCCTGGGCGGCA 57% GC / 30,748.9 Da	100-mer	10,038 .. 10,137	← 81°C	Apr 22, 2022
✓ <b>gRNA Protospacer</b> /sequence = ACAGAGCAGTTGGGGTATGG 55% GC / 6262.1 Da	20-mer	10,056 .. 10,074	↗ 56°C	Apr 22, 2022
✓ <b>PCR Reverse</b> /sequence = TAGTGTGTTGGTTACCAATCAGGC 44% GC / 7703.1 Da	25-mer	10,553 .. 10,577	← 59°C	Apr 22, 2022