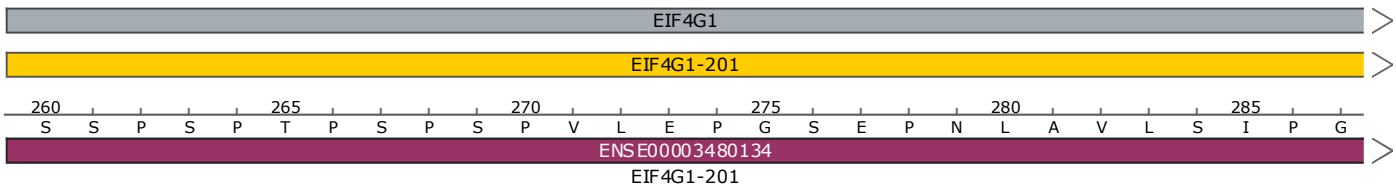


5'
3'

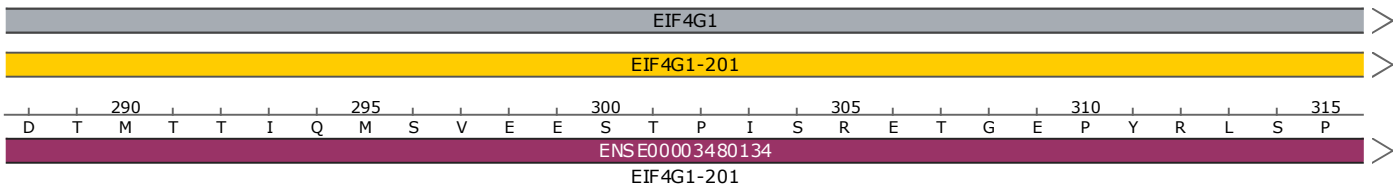
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85



GACACTATGACAACTATACAAATGTCTGTAGAAGAATCAACCCCATCTCCCGTGAACCTGGGGAGCCATATCGCCTCTCTCCAG
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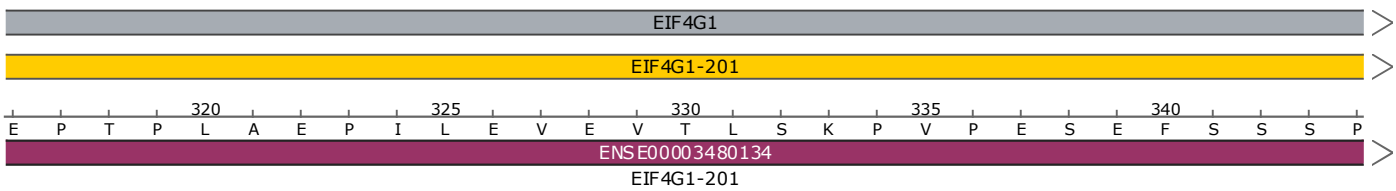
170



PCR Forward
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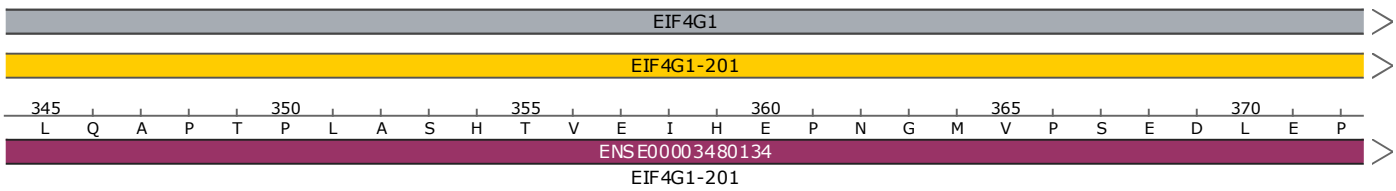
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255



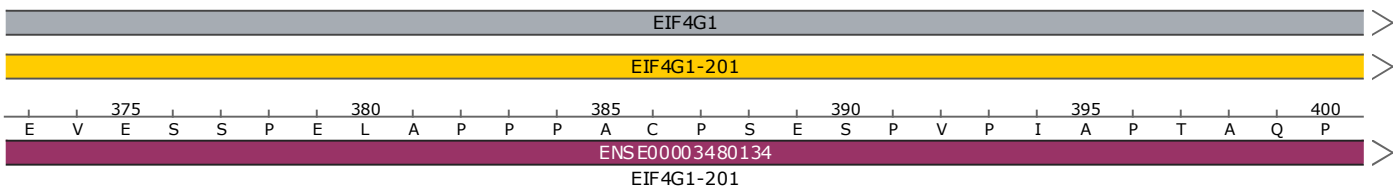
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340



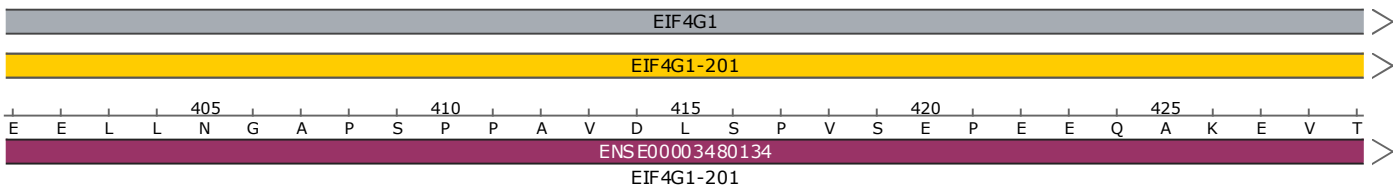
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425

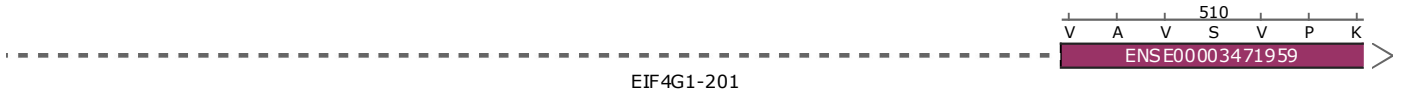
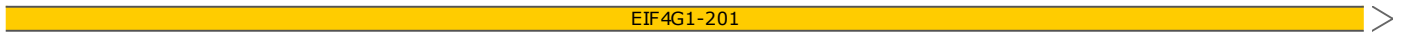


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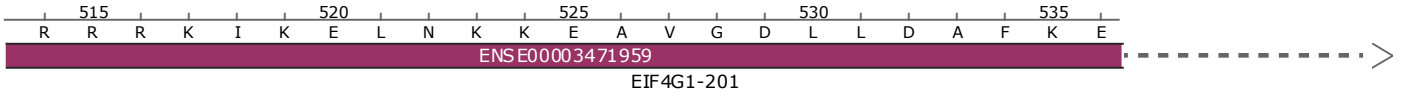
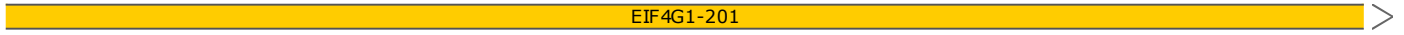
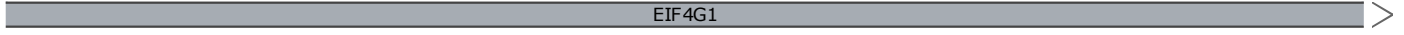
510



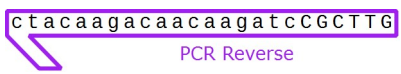
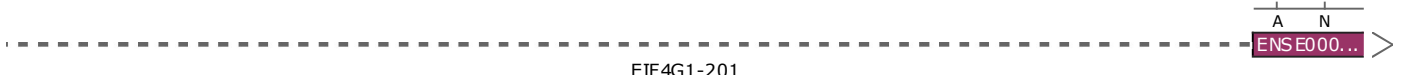
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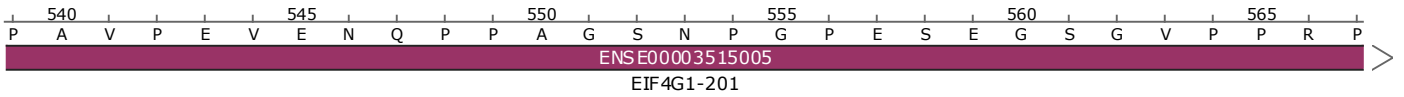
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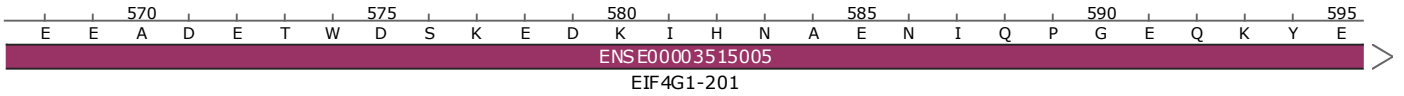
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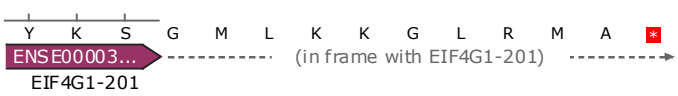
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GCCGTCATGGTCTCCACCTTTTAGTCGGAGGACGTCCTCGTCTAGGTCCGGGTCAGACTCCCGTCACCACACGGGGGTGCAGG



TGAGGAAGCAGATGAGACCTGGGACTCAAAGGAAGACAAAATTCACAATGCTGAGAACATCCAGCCCGGGAACAGAAGTATGAA
ACTCCTTCGTCTACTCTGGACCCTGAGTTTCTTCTGTTTTAAGTGTACGACTCTTGTAGGTCCGGCCCTTGTCTTCACTT



TATAAGTCAGGTATGCTGAAGAAAGGGTTGAGAATGGCTTGAGTTTTCTTATTAGGGCCAGAGGAGGCAGTATGATTGCTTCATT
ATATTCAGTCCATACGACTTCTTCCCAACTCTTACCGAACTCAAAGAATAATCCCGGTCTCCTCCGTCATACTAACGAAGTAA



CTGCCTGGGCAGGGGGAAGGGGGGGCACGGTGCCTGTAATTATTAACATGAATTCAATTAAGCTCA

GACGGACCCGTCCCCCTTCCCCCGTGCCACGGACATTAATAATTTGTAAGTTAATTCGAGT

3'

1512

5'

EIF4G1

EIF4G1-201

Feature	Location	Size	Start	End	Type
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/note =	gene ENSG00000114867 Protein coding				
✓ EIF4G1-201	1 .. 1512	1512 bp	■	➔	prim_transcript
/note =	primary transcript ENST00000342981				
EIF4G1-204	1 .. 1511	1511 bp	■	➔	prim_transcript
/note =	primary transcript ENST00000352767				
EIF4G1-202	1 .. 1507	1507 bp	■	➔	prim_transcript
/note =	primary transcript ENST00000346169				
EIF4G1-203	1 .. 1507	1507 bp	■	➔	prim_transcript
/note =	primary transcript ENST00000350481				
EIF4G1-209	1 .. 1507	1507 bp	■	➔	prim_transcript
/note =	primary transcript ENST00000414031				
EIF4G1-222	1 .. 1507	1507 bp	■	➔	prim_transcript
/note =	primary transcript ENST00000442406 Nonsense mediated decay				
EIF4G1-206	1 .. 1505	1505 bp	■	➔	prim_transcript
/note =	primary transcript ENST00000392537				
EIF4G1-212	1 .. 1505	1505 bp	■	➔	prim_transcript
/note =	primary transcript ENST00000424196				
EIF4G1-218	1 .. 1505	1505 bp	■	➔	prim_transcript
/note =	primary transcript ENST00000434061				
EIF4G1-240	1 .. 1505	1505 bp	■	➔	prim_transcript
/note =	primary transcript ENST00000676453 Nonsense mediated decay				
EIF4G1-205	1 .. 1448	1448 bp	■	➔	prim_transcript
/note =	primary transcript ENST00000382330				
EIF4G1-207	1 .. 1448	1448 bp	■	➔	prim_transcript
/note =	primary transcript ENST00000411531				
EIF4G1-208	1 .. 1448	1448 bp	■	➔	prim_transcript
/note =	primary transcript ENST00000413967 Nonsense mediated decay				
EIF4G1-210	1 .. 1448	1448 bp	■	➔	prim_transcript
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EIF4G1-213	1 .. 1448	1448 bp	■	➔	prim_transcript
/note =	primary transcript ENST00000426123				
EIF4G1-216	1 .. 1448	1448 bp	■	➔	prim_transcript
/note =	primary transcript ENST00000427845				
EIF4G1-219	1 .. 1448	1448 bp	■	➔	prim_transcript
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EIF4G1-221	1 .. 1448	1448 bp	■	➔	prim_transcript
/note =	primary transcript ENST00000441154				
EIF4G1-224	1 .. 1448	1448 bp	■	➔	prim_transcript
/note =	primary transcript ENST00000444861				
EIF4G1-226	1 .. 1448	1448 bp	■	➔	prim_transcript
/note =	primary transcript ENST00000450424				
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▶ 3 segments =	1019 bp				
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/note =	coding sequence ENSP00000343450				
/translation =	SSPSPTPSPSPVLEPGSEPNLAVLSIPGDMTTTIQMSVEESTPISRETGEPYRLSPEPTPLAEPILVEVTLTKVPPESEFSSSPLQAPTPLASHTVEIHEPNGMVPSDELPEVESSPELAPPACPSESPVPIAPTAQPEELNGAPSPPAVDLSPVSEPEEQAKEVTASMAPPTIPSATPATAPSATSPAQEEEEEEEEEEEEEEGAGEAGEAESEKGGEE LLPPESTPIPANLSQNLEAAATQ, , VAVSVPKRRRIKELNKKEAVGDLLDAFKE, , ANPAVPEVENQPPAGSNPGESEGGVPPRPEEADETWDSKEDIHNAENIQPGEQKY EYKS				
	339 amino acids = 35.7 kDa				

Feature	Location	Size	Start	End	Type
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▶ 3 segments = 1019 bp					
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▶ 3 segments = 1019 bp					
/codon_start = 1					
/note = coding sequence ENSP00000317600					
/translation = SSPSPTPSPSPVLEPGSEPNLAVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEPILVEVTLTKPVPSEFSSSPLQAPTPLASHTVEIHEPNGMVPSEDLEP EVESSELAPPACPSESPVPIAPTAQPEELNGAPSPPAVDLSPVSEPEEQAKEVTASMAPPTIPSATPATAPSATSPAQEEEMEEEEEEEEEGEAGEAGEAESEKGGEELLP PESTPIPANLSQNLEAAATQ, , VAVSVPKRRRIKELNKKEAVGDLLDAFKE, , ANPAVPEVENQPPAGSNPGESESGVPPRPEEADETWDSKEDIHNAENIQPGEQKY EYKS 339 amino acids = 35.7 kDa					
EIF4G1-204	1 .. 1370	1370 bp	■	→	CDS
▶ 3 segments = 1019 bp					
/codon_start = 1					
/note = coding sequence ENSP00000338020					
/translation = SSPSPTPSPSPVLEPGSEPNLAVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEPILVEVTLTKPVPSEFSSSPLQAPTPLASHTVEIHEPNGMVPSEDLEP EVESSELAPPACPSESPVPIAPTAQPEELNGAPSPPAVDLSPVSEPEEQAKEVTASMAPPTIPSATPATAPSATSPAQEEEMEEEEEEEEEGEAGEAGEAESEKGGEELLP PESTPIPANLSQNLEAAATQ, , VAVSVPKRRRIKELNKKEAVGDLLDAFKE, , ANPAVPEVENQPPAGSNPGESESGVPPRPEEADETWDSKEDIHNAENIQPGEQKY EYKS 339 amino acids = 35.7 kDa					
EIF4G1-205	1 .. 1370	1370 bp	■	→	CDS
▶ 3 segments = 1019 bp					
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▶ 3 segments = 1019 bp					
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/note = coding sequence ENSP00000376320					
/translation = SSPSPTPSPSPVLEPGSEPNLAVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEPILVEVTLTKPVPSEFSSSPLQAPTPLASHTVEIHEPNGMVPSEDLEP EVESSELAPPACPSESPVPIAPTAQPEELNGAPSPPAVDLSPVSEPEEQAKEVTASMAPPTIPSATPATAPSATSPAQEEEMEEEEEEEEEGEAGEAGEAESEKGGEELLP PESTPIPANLSQNLEAAATQ, , VAVSVPKRRRIKELNKKEAVGDLLDAFKE, , ANPAVPEVENQPPAGSNPGESESGVPPRPEEADETWDSKEDIHNAENIQPGEQKY EYKS 339 amino acids = 35.7 kDa					
EIF4G1-207	1 .. 1370	1370 bp	■	→	CDS
▶ 3 segments = 1019 bp					
/codon_start = 1					
/note = coding sequence ENSP00000395974					
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EIF4G1-209	1 .. 1370	1370 bp	■	→	CDS
▶ 3 segments = 1019 bp					
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/note = coding sequence ENSP00000391935					
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Feature	Location	Size	Start	End	Type
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EIF4G1-212	1 .. 1370	1370 bp	■	→	CDS
▶ 3 segments = 1019 bp					
/codon_start = 1					
/note = coding sequence ENSP00000416255					
/translation = SSPSPTPSPSPVLEPGSEPNLAVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEPILVEVTLTKVPPESEFSSSPLQAPTPLASHTVEIHEPNGMVPSEDLEP EVESSELAPPACPSESPVPIAPTAQPEELNGAPSPPAVDLSPVSEPEEQAKEVTASMAPPTIPSATPATAPSATSPAQEEEMEEEEEEEEEGEAGEAGEAESEKGGEELLP PESTPIPANLSQNLEAAAATQ, , VAVSVPKRRRIKELNKKEAVGDLLDAFKE, , ANPAVPEVENQPPAGSNPGESESGVPPRPEEADETWDSKEDIHNAENIQPGEQKY EYKS 339 amino acids = 35.7 kDa					
EIF4G1-213	1 .. 1370	1370 bp	■	→	CDS
▶ 3 segments = 1019 bp					
/codon_start = 1					
/note = coding sequence ENSP00000403269					
/translation = SSPSPTPSPSPVLEPGSEPNLAVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEPILVEVTLTKVPPESEFSSSPLQAPTPLASHTVEIHEPNGMVPSEDLEP EVESSELAPPACPSESPVPIAPTAQPEELNGAPSPPAVDLSPVSEPEEQAKEVTASMAPPTIPSATPATAPSATSPAQEEEMEEEEEEEEEGEAGEAGEAESEKGGEELLP PESTPIPANLSQNLEAAAATQ, , VAVSVPKRRRIKELNKKEAVGDLLDAFKE, , ANPAVPEVENQPPAGSNPGESESGVPPRPEEADETWDSKEDIHNAENIQPGEQKY EYKS 339 amino acids = 35.7 kDa					
EIF4G1-216	1 .. 1370	1370 bp	■	→	CDS
▶ 3 segments = 1019 bp					
/codon_start = 1					
/note = coding sequence ENSP00000407682					
/translation = SSPSPTPSPSPVLEPGSEPNLAVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEPILVEVTLTKVPPESEFSSSPLQAPTPLASHTVEIHEPNGMVPSEDLEP EVESSELAPPACPSESPVPIAPTAQPEELNGAPSPPAVDLSPVSEPEEQAKEVTASMAPPTIPSATPATAPSATSPAQEEEMEEEEEEEEEGEAGEAGEAESEKGGEELLP PESTPIPANLSQNLEAAAATQ, , VAVSVPKRRRIKELNKKEAVGDLLDAFKE, , ANPAVPEVENQPPAGSNPGESESGVPPRPEEADETWDSKEDIHNAENIQPGEQKY EYKS 339 amino acids = 35.7 kDa					
EIF4G1-218	1 .. 1370	1370 bp	■	→	CDS
▶ 3 segments = 1019 bp					
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/note = coding sequence ENSP00000411826					
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EIF4G1-219	1 .. 1370	1370 bp	■	→	CDS
▶ 3 segments = 1019 bp					
/codon_start = 1					
/note = coding sequence ENSP00000404754					
/translation = SSPSPTPSPSPVLEPGSEPNLAVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEPILVEVTLTKVPPESEFSSSPLQAPTPLASHTVEIHEPNGMVPSEDLEP EVESSELAPPACPSESPVPIAPTAQPEELNGAPSPPAVDLSPVSEPEEQAKEVTASMAPPTIPSATPATAPSATSPAQEEEMEEEEEEEEEGEAGEAGEAESEKGGEELLP PESTPIPANLSQNLEAAAATQ, , VAVSVPKRRRIKELNKKEAVGDLLDAFKE, , ANPAVPEVENQPPAGSNPGESESGVPPRPEEADETWDSKEDIHNAENIQPGEQKY EYKS 339 amino acids = 35.7 kDa					
EIF4G1-221	1 .. 1370	1370 bp	■	→	CDS
▶ 3 segments = 1019 bp					
/codon_start = 1					
/note = coding sequence ENSP00000399858					
/translation = SSPSPTPSPSPVLEPGSEPNLAVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEPILVEVTLTKVPPESEFSSSPLQAPTPLASHTVEIHEPNGMVPSEDLEP EVESSELAPPACPSESPVPIAPTAQPEELNGAPSPPAVDLSPVSEPEEQAKEVTASMAPPTIPSATPATAPSATSPAQEEEMEEEEEEEEEGEAGEAGEAESEKGGEELLP PESTPIPANLSQNLEAAAATQ, , VAVSVPKRRRIKELNKKEAVGDLLDAFKE, , ANPAVPEVENQPPAGSNPGESESGVPPRPEEADETWDSKEDIHNAENIQPGEQKY EYKS 339 amino acids = 35.7 kDa					

Feature	Location	Size	Start	End	Type
EIF4G1-224	1 .. 1370	1370 bp	■	→	CDS
▶ 3 segments = 1019 bp					
/codon_start = 1					
/note = coding sequence ENSP0000398145					
/translation = SSPSPTPSPSPVLEPGSEPNLAVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEPILEVEVTLSKVPPESEFSSSPLQAPTPLASHTVEIHEPNGMVPSEDLEP EVESSELAPPACPSESPVPIAPTAQPEELNGAPSPPAVDLSPVSEPEEQAKEVTASMAPPTIPSATPATAPSATSPAQEEEMEEEEEEEEEGEAGEAGEAESEKGGELLP PESTPIPANLSQNLEAAATQ, , VAVSVPKRRRKIKELNKKEAVGDLDDAFKE, , ANPAVPEVENQPPAGSNPGESEGSVPPRPEEADETWDSKEDIHNAENIQPGEQKY EYKS 339 amino acids = 35.7 kDa					
EIF4G1-226	1 .. 1370	1370 bp	■	→	CDS
▶ 3 segments = 1019 bp					
/codon_start = 1					
/note = coding sequence ENSP0000391412					
/translation = SSPSPTPSPSPVLEPGSEPNLAVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEPILEVEVTLSKVPPESEFSSSPLQAPTPLASHTVEIHEPNGMVPSEDLEP EVESSELAPPACPSESPVPIAPTAQPEELNGAPSPPAVDLSPVSEPEEQAKEVTASMAPPTIPSATPATAPSATSPAQEEEMEEEEEEEEEGEAGEAGEAESEKGGELLP PESTPIPANLSQNLEAAATQ, , VAVSVPKRRRKIKELNKKEAVGDLDDAFKE, , ANPAVPEVENQPPAGSNPGESEGSVPPRPEEADETWDSKEDIHNAENIQPGEQKY EYKS 339 amino acids = 35.7 kDa					
EIF4G1-229	1 .. 667	667 bp	■	→	CDS
/codon_start = 1					
/note = coding sequence ENSP0000399969					
/translation = SSPSPTPSPSPVLEPGSEPNLAVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEPILEVEVTLSKVPPESEFSSSPLQAPTPLASHTVEIHEPNGMVPSEDLEP EVESSELAPPACPSESPVPIAPTAQPEELNGAPSPPAVDLSPVSEPEEQAKEVTASMAPPTIPSATPATAPSATSPAQEEEMEEEEEEEEEGEAGEAGEAESEKGGEL 222 amino acids = 23.0 kDa					
EIF4G1-229	1 .. 667	667 bp	■	→	prim_transcript
/note = primary transcript ENST00000457456					
EIF4G1-215	1 .. 301	301 bp	■	→	CDS
/codon_start = 1					
/note = coding sequence ENSP0000409545					
/translation = SSPSPTPSPSPVLEPGSEPNLAVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEPILEVEVTLSKVPPESEFSSSPLQAPTPLASHTVEIH 100 amino acids = 10.5 kDa					
EIF4G1-215	1 .. 301	301 bp	■	→	prim_transcript
/note = primary transcript ENST00000427607					
EIF4G1-217	1 .. 243	243 bp	■	→	CDS
/codon_start = 1					
/note = coding sequence ENSP0000411707					
/translation = SSPSPTPSPSPVLEPGSEPNLAVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEPILEVEVTLSKVPPESE 81 amino acids = 8.4 kDa					
EIF4G1-217	1 .. 243	243 bp	■	→	prim_transcript
/note = primary transcript ENST00000428387					
EIF4G1-223	1 .. 194	194 bp	■	→	CDS
/codon_start = 1					
/note = coding sequence ENSP0000407244					
/translation = SSPSPTPSPSPVLEPGSEPNLAVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEP 64 amino acids = 6.7 kDa					
EIF4G1-223	1 .. 194	194 bp	■	→	prim_transcript
/note = primary transcript ENST00000444134					
EIF4G1-236	1 .. 174	174 bp	■	→	prim_transcript
/note = primary transcript ENST00000484862 Retained intron					
EIF4G1-238	1 .. 147	147 bp	■	→	prim_transcript
/note = primary transcript ENST00000493299 Retained intron					
✓ Donor Template WT -> SNV	709 .. 808	100 bp	■		misc_feature
✓ gRNA Protospacer	727 .. 746	20 bp	■		misc_feature
✓ SNV	729 .. 729	1 bp	■		misc_feature
/note = WT = C SNV = T					
✓ PAM	747 .. 749	3 bp	■		misc_feature

Feature

Location

Size



Type

EIF4G1-233


1449 .. 1471

23 bp



prim_transcript

/note = primary transcript [ENST00000475721](#)
Retained intron

Primer	Length		Binding Sites	↕	Tm	Date Added
✓ PCR Forward	25-mer		230 .. 254	→	58°C	Jun 14, 2023
/sequence = CCAGAATCTGAGTTTTCTTCCAGTC 44% GC / 7583.0 Da						
✓ Donor Template WT -> SNV	100-mer		709 .. 808	←	79°C	Jun 14, 2023
/sequence = atcaaggagggcaaggaacgatatcccctagcccgcctacacctaccgtccaaccacaccttacCTTGAGTGGCTGCTACTGCCTCCAAATTCTGAGAC 55% GC / 30,517.8 Da						
✓ gRNA Protospacer	20-mer		727 .. 746	→	60°C	Jun 14, 2023
/sequence = AGCAGCAGCCACTCAAGGTA 55% GC / 6120.0 Da						
✓ Sanger Sequencing Primer	20-mer		887 .. 906	←	58°C	Jun 14, 2023
/sequence = atttcccctttgcatcacc 50% GC / 5938.9 Da						
✓ PCR Reverse	24-mer		1166 .. 1189	←	58°C	Jun 14, 2023
/sequence = GTTCGCctagaacaacagaacatc 46% GC / 7314.8 Da						