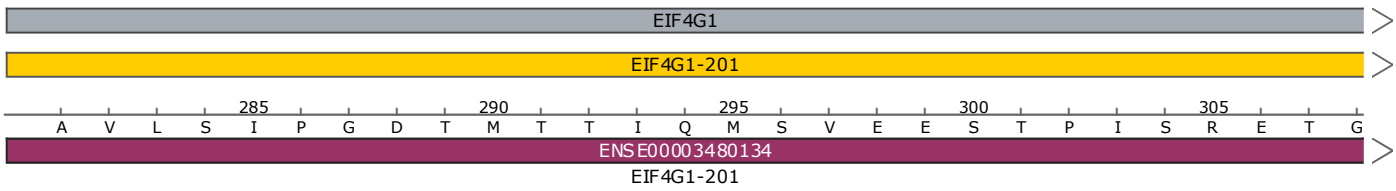


CZK2J00158 EIF4G1_A502V_G06_AB
1361 bp

5'
3'

TCGCAGTCCTCTCTATTCTGGGGACACTATGACAACATAACAAATGTCTGTAGAAGAATCAACCCCATCTCCCGTGAAACTGG
AGCGTCAGGAGAGATAAGGACCCCTGTGATACTGTTGATATGTTTACAGACATCTTCTTAGTTGGGGGTAGAGGGCACTTTGACC

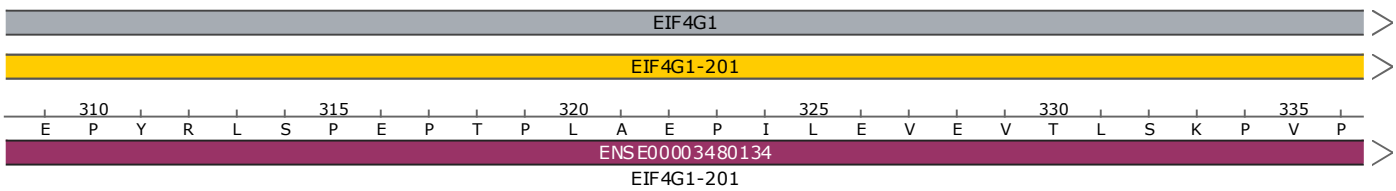
85



PCR Forward
CCA

GGAGCCATATCGCCTCTCTCCAGAACCCTCCTCTCGCCGAACCATACTGGAAGTAGAAGTGACACTTAGCAAACCGGTTCCA
CCTCGGTATAGCGGAGAGAGGTCTTGGGTGAGGAGAGCGGCTTGGGTATGACCTTCATCTTCACTGTGAATCGTTTGGCCAAGGT

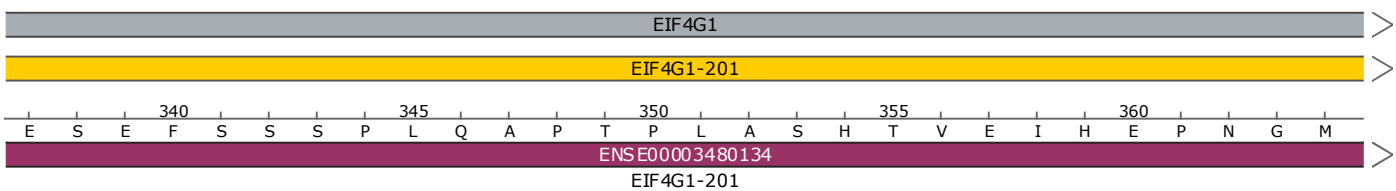
170



PCR Forward
GAATCTGAGTTTTCTTCCAGTC

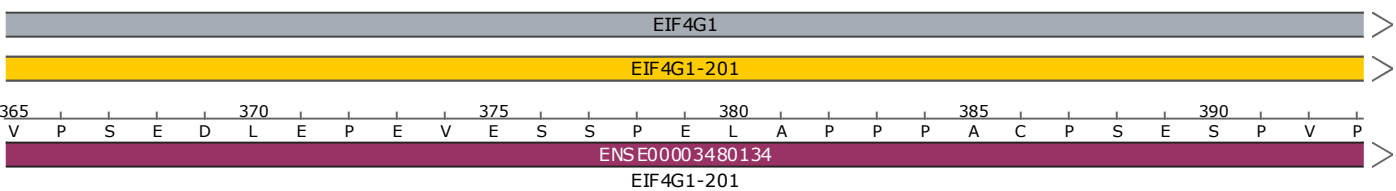
GAATCTGAGTTTTCTTCCAGTCCTCTCCAGGCTCCCACCCCTTTGGCATCTCACACAGTGGAAATTCATGAGCCTAATGGCATGG
CTTAGACTCAAAGAAGGTCAGGAGAGGTCGAGGGTGGGGAAACCGTAGAGTGTGTACCTTTAAGTACTCGGATTACCGTACC

255



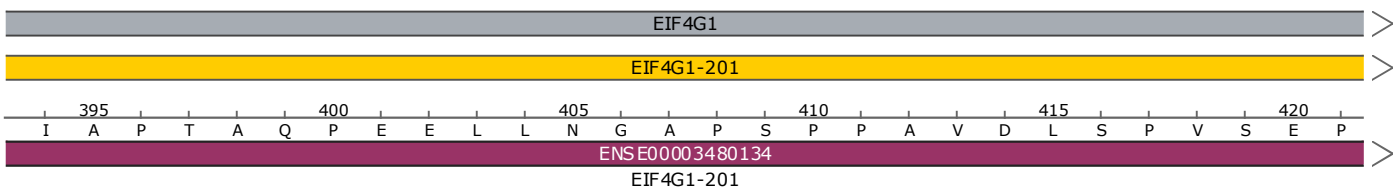
TCCCATCTGAAGATCTGGAACCAGAGGTGGAGTCAAGCCCAGAGCTTGCTCCTCCCCAGCTTGCCCTCCGAATCCCCTGTGCC
AGGGTAGACTTCTAGACCTTGGTCTCCACCTCAGTTCGGGTCTCGAACGAGGAGGGGGTGAACGGGGAGGCTTAGGGGACACGG

340



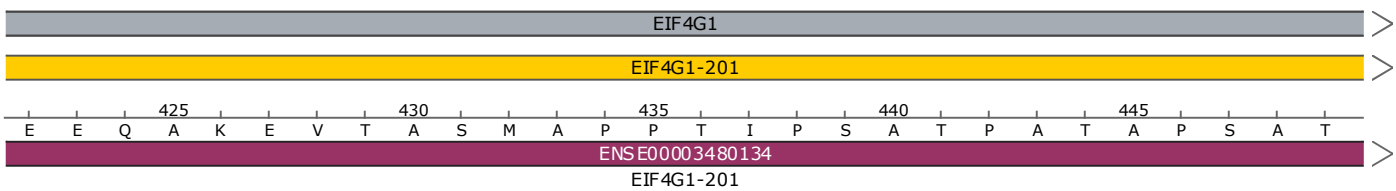
CATTGCTCCAAGTCCCAACCTGAGGAACTGCTCAACGGAGCCCCCTCGCCACCAGCTGTGGACTTAAGCCCAGTCAGTGAGCCA
GTAACGAGGTTGACGGGTTGGACTCCTTGACGAGTTGCCTCGGGGAGCGGTGGTGCACACCTGAATTCGGGTGAGTCACTCGGT

425



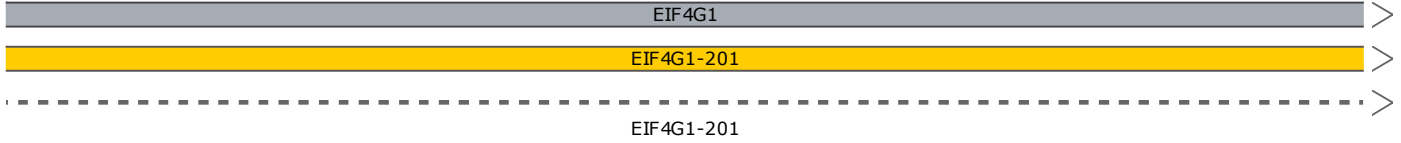
GAGGAGCAGGCCAAGGAGGTGACAGCATCAATGGCGCCCCCACCATCCCCTCTGCTACTCCAGCTACGGCTCCTTCAGCTACTT
CTCCTCGTCCGGTTCCTCCACTGTCGTAGTTACCGCGGGGGGTGGTAGGGGAGACGATGAGGTGCATGCCGAGGAAGTCGATGAA

510



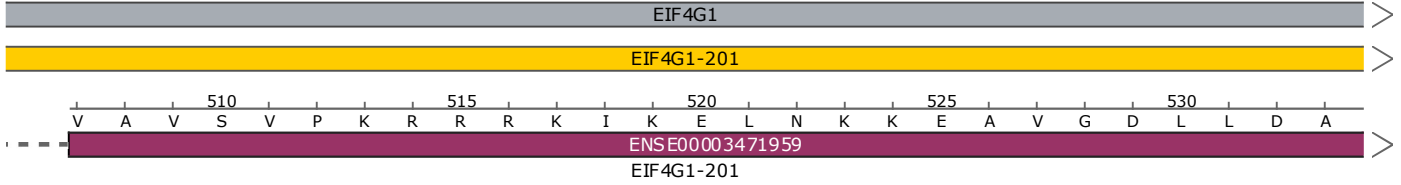
CTTTGGCTGCTTTCTATTTCCACGGGATTAAGGGTACTCCTTAAATTATTGGCAAAGATCCATGCTTTTATTTATTTATTTTAA
GAAACCGACGAAAGATAAAGGGTCCCTAATTTCCCATGAGGAATTTAATAACCGTTTCTAGGTACGAAAAATAAATAAAAAAATT

935



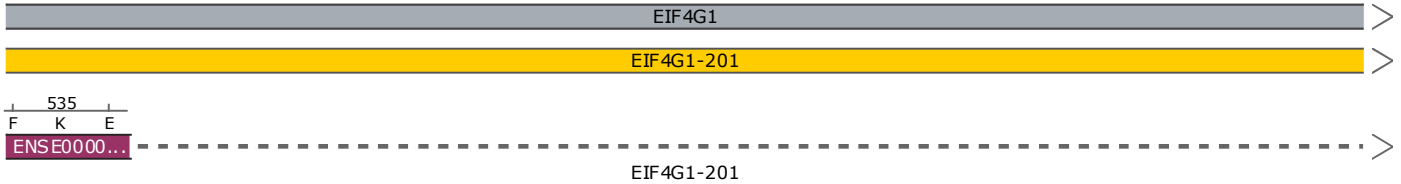
TTAGTGGCAGTATCTGTGCCAAAGAGGAGACGGAAAATTAAGGAGCTAAATAAGAAGGAGGCTGTTGGAGACCTTCTGGATGCCT
AATCACCGTCATAGACACGGTTTCTCCTCTGCCTTTTAATTCCTCGATTTATTCTTCTCCGACAACCTCTGGAAGACCTACGGA

1020



TCAAGGAGGTAAGGGAGCAGAAAATGGGAGGGGAGAGGGCCAAGTTGAGGTATGGAGCAGTGGTCATTCTGCAACCAAAACTGGA
AGTTCCTCCATTCCCTCGTCTTTTACCCTCCCCTCTCCCGTTCAACTCCATACCTCGTCACCAGTAAGACGTTGGTTTTGACCT

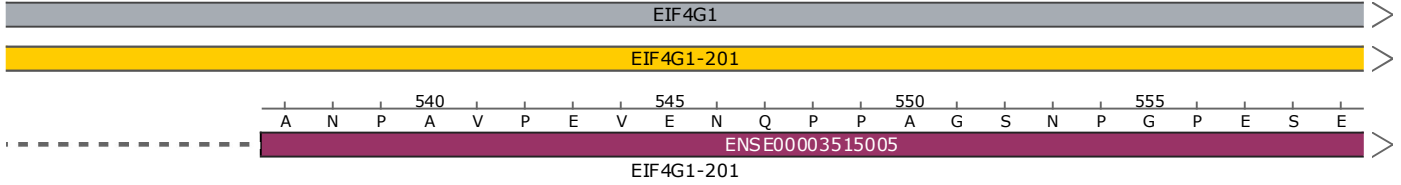
1105



ct
PCR Reverse

TGTTCTGTTGTTCTAGGCGAACCCGGCAGTACCAGAGGTGGAAAATCAGCCTCCTGCAGGCAGCAATCCAGGCCAGAGTCTGAG
ACAAGACAACAAGATCCGCTTGGGCCGTGTCATGGTCTCCACCTTTAGTCGGAGGACGTCCGTCGTTAGGTCCGGGTCTCAGACTC

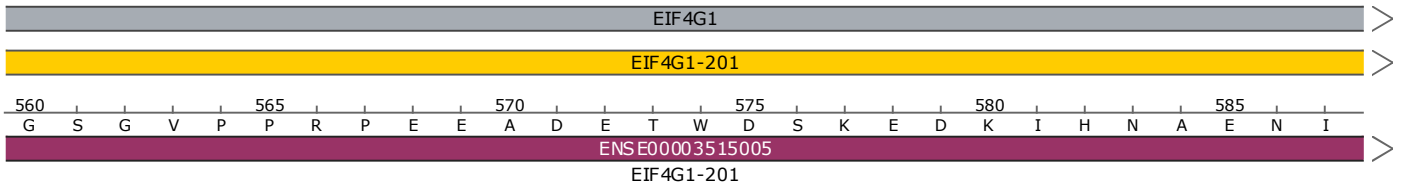
1190



acaagacaacaagatcCGCTTG
PCR Reverse

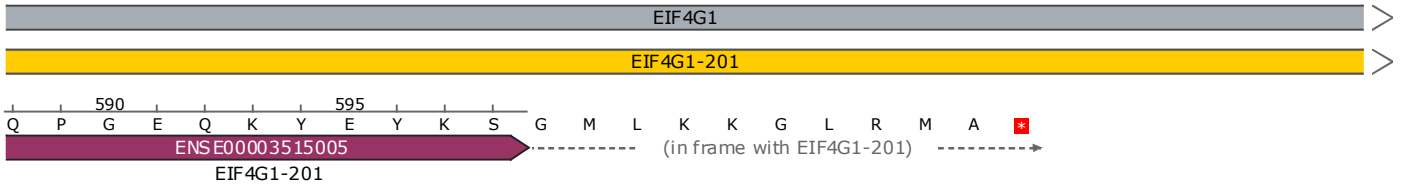
GGCAGTGGTGTGCCCCACGTCCTGAGGAAGCAGATGAGACCTGGGACTCAAAGGAAGACAAAATTCACAATGCTGAGAACATCC
CCGTCACCACACGGGGGTGCAGGACTCCTTCGTCTACTCTGGACCCTGAGTTTCTTCTGTTTTAAGTGTTACGACTCTTGTAGG

1275



AGCCCGGGGAACAGAAGTATGAATATAAGTCAGGTATGCTGAAGAAAGGGTTGAGAATGGCTTGAGTTTTCTTATTAGGGCCAGA
TCGGGCCCTTGTCTTCATACTTATATTCAGTCCATACGACTTCTTTCCAACTCTTACCGAACTCAAAGAATAATCCCGGTCT

1360



(in frame with EIF4G1-201)

G 3'
C 5' 1361

EIF4G1


EIF4G1-201

Feature	Location	Size	Start	End	Type
✓ EIF4G1	1 .. 1361	1361 bp	■	➔	gene
/note = gene ENSG00000114867 Protein coding					
✓ EIF4G1-201	1 .. 1361	1361 bp	■	➔	prim_transcript
/note = primary transcript ENST00000342981					
EIF4G1-202	1 .. 1361	1361 bp	■	➔	prim_transcript
/note = primary transcript ENST00000346169					
EIF4G1-203	1 .. 1361	1361 bp	■	➔	prim_transcript
/note = primary transcript ENST00000350481					
EIF4G1-204	1 .. 1361	1361 bp	■	➔	prim_transcript
/note = primary transcript ENST00000352767					
EIF4G1-205	1 .. 1361	1361 bp	■	➔	prim_transcript
/note = primary transcript ENST00000382330					
EIF4G1-206	1 .. 1361	1361 bp	■	➔	prim_transcript
/note = primary transcript ENST00000392537					
EIF4G1-207	1 .. 1361	1361 bp	■	➔	prim_transcript
/note = primary transcript ENST00000411531					
EIF4G1-208	1 .. 1361	1361 bp	■	➔	prim_transcript
/note = primary transcript ENST00000413967 Nonsense mediated decay					
EIF4G1-209	1 .. 1361	1361 bp	■	➔	prim_transcript
/note = primary transcript ENST00000414031					
EIF4G1-210	1 .. 1361	1361 bp	■	➔	prim_transcript
/note = primary transcript ENST00000421110					
EIF4G1-212	1 .. 1361	1361 bp	■	➔	prim_transcript
/note = primary transcript ENST00000424196					
EIF4G1-213	1 .. 1361	1361 bp	■	➔	prim_transcript
/note = primary transcript ENST00000426123					
EIF4G1-216	1 .. 1361	1361 bp	■	➔	prim_transcript
/note = primary transcript ENST00000427845					
EIF4G1-218	1 .. 1361	1361 bp	■	➔	prim_transcript
/note = primary transcript ENST00000434061					
EIF4G1-219	1 .. 1361	1361 bp	■	➔	prim_transcript
/note = primary transcript ENST00000435046					
EIF4G1-221	1 .. 1361	1361 bp	■	➔	prim_transcript
/note = primary transcript ENST00000441154					
EIF4G1-222	1 .. 1361	1361 bp	■	➔	prim_transcript
/note = primary transcript ENST00000442406 Nonsense mediated decay					
EIF4G1-224	1 .. 1361	1361 bp	■	➔	prim_transcript
/note = primary transcript ENST00000444861					
EIF4G1-226	1 .. 1361	1361 bp	■	➔	prim_transcript
/note = primary transcript ENST00000450424					
EIF4G1-240	1 .. 1361	1361 bp	■	➔	prim_transcript
/note = primary transcript ENST00000676453 Nonsense mediated decay					
✓ EIF4G1-201	1 .. 1308	1308 bp	■	➔	CDS
▶ 3 segments = 957 bp					
/codon_start = 1					
/note = coding sequence ENSP00000343450					
/translation = AVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEPILVEVTL SKVPPESEFSSSPLQAPTPLASHTVEIHEPNGMVPSLEPEVESSPELAPPPACPSESPVP IAPTAQPEELLLNGAPSPPAVDLSPVSEPEEQAKEVTASMAPPTIP SATPATAPSATSPAQEEEMEEEEEEEGEAGEAGEAESEKGG EELLPPPESTPIPANLSQNL EAAAATQ ,, VAVSVPKRRRKIKELNKKEAVGDLLDAFKE,, ANPAVPEVENQPPAGSNPGPESEGGVPPRPEEADETDWDSKEDIHNAENIQPGEQKYEYKS 319 amino acids = 33.6 kDa					

Feature	Location	Size	Start	End	Type
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▶ 3 segments = 957 bp					
/codon_start = 1					
/note = coding sequence ENSP00000316879					
/translation = AVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEPILVEVTL SKVPPESEFSSSPLQAPTPLASHTVEIHEPNGMVPSEDL EPEVESSPELAPPACPSESPVP IAPTAQPEELNNGAPSPPAVDLSPVSEPEEQAKEVTASMAPPTIPSATPATAPSATSPAQEEEMEEEEEEEEEGEAGEAGEAESEKGGGELL PPESTPIPANLSQNLEAAATQ ,, VAVSVPKRRRKIKELNKKEAVGDLLDAFKE,, ANPAVPEVENQPPAGSNPGPESESGVPPRPEEADETWDSKEDKIHNAENIQPGEQKYEYKS 319 amino acids = 33.6 kDa					
EIF4G1-203	1 .. 1308	1308 bp	■	→	CDS
▶ 3 segments = 957 bp					
/codon_start = 1					
/note = coding sequence ENSP00000317600					
/translation = AVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEPILVEVTL SKVPPESEFSSSPLQAPTPLASHTVEIHEPNGMVPSEDL EPEVESSPELAPPACPSESPVP IAPTAQPEELNNGAPSPPAVDLSPVSEPEEQAKEVTASMAPPTIPSATPATAPSATSPAQEEEMEEEEEEEEEGEAGEAGEAESEKGGGELL PPESTPIPANLSQNLEAAATQ ,, VAVSVPKRRRKIKELNKKEAVGDLLDAFKE,, ANPAVPEVENQPPAGSNPGPESESGVPPRPEEADETWDSKEDKIHNAENIQPGEQKYEYKS 319 amino acids = 33.6 kDa					
EIF4G1-204	1 .. 1308	1308 bp	■	→	CDS
▶ 3 segments = 957 bp					
/codon_start = 1					
/note = coding sequence ENSP00000338020					
/translation = AVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEPILVEVTL SKVPPESEFSSSPLQAPTPLASHTVEIHEPNGMVPSEDL EPEVESSPELAPPACPSESPVP IAPTAQPEELNNGAPSPPAVDLSPVSEPEEQAKEVTASMAPPTIPSATPATAPSATSPAQEEEMEEEEEEEEEGEAGEAGEAESEKGGGELL PPESTPIPANLSQNLEAAATQ ,, VAVSVPKRRRKIKELNKKEAVGDLLDAFKE,, ANPAVPEVENQPPAGSNPGPESESGVPPRPEEADETWDSKEDKIHNAENIQPGEQKYEYKS 319 amino acids = 33.6 kDa					
EIF4G1-205	1 .. 1308	1308 bp	■	→	CDS
▶ 3 segments = 957 bp					
/codon_start = 1					
/note = coding sequence ENSP00000371767					
/translation = AVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEPILVEVTL SKVPPESEFSSSPLQAPTPLASHTVEIHEPNGMVPSEDL EPEVESSPELAPPACPSESPVP IAPTAQPEELNNGAPSPPAVDLSPVSEPEEQAKEVTASMAPPTIPSATPATAPSATSPAQEEEMEEEEEEEEEGEAGEAGEAESEKGGGELL PPESTPIPANLSQNLEAAATQ ,, VAVSVPKRRRKIKELNKKEAVGDLLDAFKE,, ANPAVPEVENQPPAGSNPGPESESGVPPRPEEADETWDSKEDKIHNAENIQPGEQKYEYKS 319 amino acids = 33.6 kDa					
EIF4G1-206	1 .. 1308	1308 bp	■	→	CDS
▶ 3 segments = 957 bp					
/codon_start = 1					
/note = coding sequence ENSP00000376320					
/translation = AVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEPILVEVTL SKVPPESEFSSSPLQAPTPLASHTVEIHEPNGMVPSEDL EPEVESSPELAPPACPSESPVP IAPTAQPEELNNGAPSPPAVDLSPVSEPEEQAKEVTASMAPPTIPSATPATAPSATSPAQEEEMEEEEEEEEEGEAGEAGEAESEKGGGELL PPESTPIPANLSQNLEAAATQ ,, VAVSVPKRRRKIKELNKKEAVGDLLDAFKE,, ANPAVPEVENQPPAGSNPGPESESGVPPRPEEADETWDSKEDKIHNAENIQPGEQKYEYKS 319 amino acids = 33.6 kDa					
EIF4G1-207	1 .. 1308	1308 bp	■	→	CDS
▶ 3 segments = 957 bp					
/codon_start = 1					
/note = coding sequence ENSP00000395974					
/translation = AVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEPILVEVTL SKVPPESEFSSSPLQAPTPLASHTVEIHEPNGMVPSEDL EPEVESSPELAPPACPSESPVP IAPTAQPEELNNGAPSPPAVDLSPVSEPEEQAKEVTASMAPPTIPSATPATAPSATSPAQEEEMEEEEEEEEEGEAGEAGEAESEKGGGELL PPESTPIPANLSQNLEAAATQ ,, VAVSVPKRRRKIKELNKKEAVGDLLDAFKE,, ANPAVPEVENQPPAGSNPGPESESGVPPRPEEADETWDSKEDKIHNAENIQPGEQKYEYKS 319 amino acids = 33.6 kDa					
EIF4G1-209	1 .. 1308	1308 bp	■	→	CDS
▶ 3 segments = 957 bp					
/codon_start = 1					
/note = coding sequence ENSP00000391935					
/translation = AVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEPILVEVTL SKVPPESEFSSSPLQAPTPLASHTVEIHEPNGMVPSEDL EPEVESSPELAPPACPSESPVP IAPTAQPEELNNGAPSPPAVDLSPVSEPEEQAKEVTASMAPPTIPSATPATAPSATSPAQEEEMEEEEEEEEEGEAGEAGEAESEKGGGELL PPESTPIPANLSQNLEAAATQ ,, VAVSVPKRRRKIKELNKKEAVGDLLDAFKE,, ANPAVPEVENQPPAGSNPGPESESGVPPRPEEADETWDSKEDKIHNAENIQPGEQKYEYKS 319 amino acids = 33.6 kDa					
EIF4G1-210	1 .. 1308	1308 bp	■	→	CDS
▶ 3 segments = 957 bp					
/codon_start = 1					
/note = coding sequence ENSP00000413159					
/translation = AVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEPILVEVTL SKVPPESEFSSSPLQAPTPLASHTVEIHEPNGMVPSEDL EPEVESSPELAPPACPSESPVP IAPTAQPEELNNGAPSPPAVDLSPVSEPEEQAKEVTASMAPPTIPSATPATAPSATSPAQEEEMEEEEEEEEEGEAGEAGEAESEKGGGELL PPESTPIPANLSQNLEAAATQ ,, VAVSVPKRRRKIKELNKKEAVGDLLDAFKE,, ANPAVPEVENQPPAGSNPGPESESGVPPRPEEADETWDSKEDKIHNAENIQPGEQKYEYKS 319 amino acids = 33.6 kDa					

Feature	Location	Size	Start	End	Type
EIF4G1-212	1 .. 1308	1308 bp	■	→	CDS
▶ 3 segments = 957 bp					
/codon_start = 1					
/note = coding sequence ENSP00000416255					
/translation = AVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEPILVEVTL SKVPPESEFSSSPLQAPTPLASHTVEIHEPNGMVPSEDL EPEVESSPELAPPACPSESPVP IAPTAQPEELNNGAPSPPAVDLSPVSEPEEQAQEV TASMPTTIP SATPATAP SATSPAQEEEMEEEEEEEEEGEAGEAGEAESEKGG EELL PPESTPIPANLSQNLEAAATQ ,, VAVSVPKRRRKIKELNKKEAVGDLLDAFKE,, ANPAVPEVENQPPAGSNPGPESESGVPPRPEEAD ETWDSKEDKIHNAENIQPGEQKY EYKS 319 amino acids = 33.6 kDa					
EIF4G1-213	1 .. 1308	1308 bp	■	→	CDS
▶ 3 segments = 957 bp					
/codon_start = 1					
/note = coding sequence ENSP00000403269					
/translation = AVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEPILVEVTL SKVPPESEFSSSPLQAPTPLASHTVEIHEPNGMVPSEDL EPEVESSPELAPPACPSESPVP IAPTAQPEELNNGAPSPPAVDLSPVSEPEEQAQEV TASMPTTIP SATPATAP SATSPAQEEEMEEEEEEEEEGEAGEAGEAESEKGG EELL PPESTPIPANLSQNLEAAATQ ,, VAVSVPKRRRKIKELNKKEAVGDLLDAFKE,, ANPAVPEVENQPPAGSNPGPESESGVPPRPEEAD ETWDSKEDKIHNAENIQPGEQKY EYKS 319 amino acids = 33.6 kDa					
EIF4G1-216	1 .. 1308	1308 bp	■	→	CDS
▶ 3 segments = 957 bp					
/codon_start = 1					
/note = coding sequence ENSP00000407682					
/translation = AVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEPILVEVTL SKVPPESEFSSSPLQAPTPLASHTVEIHEPNGMVPSEDL EPEVESSPELAPPACPSESPVP IAPTAQPEELNNGAPSPPAVDLSPVSEPEEQAQEV TASMPTTIP SATPATAP SATSPAQEEEMEEEEEEEEEGEAGEAGEAESEKGG EELL PPESTPIPANLSQNLEAAATQ ,, VAVSVPKRRRKIKELNKKEAVGDLLDAFKE,, ANPAVPEVENQPPAGSNPGPESESGVPPRPEEAD ETWDSKEDKIHNAENIQPGEQKY EYKS 319 amino acids = 33.6 kDa					
EIF4G1-218	1 .. 1308	1308 bp	■	→	CDS
▶ 3 segments = 957 bp					
/codon_start = 1					
/note = coding sequence ENSP00000411826					
/translation = AVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEPILVEVTL SKVPPESEFSSSPLQAPTPLASHTVEIHEPNGMVPSEDL EPEVESSPELAPPACPSESPVP IAPTAQPEELNNGAPSPPAVDLSPVSEPEEQAQEV TASMPTTIP SATPATAP SATSPAQEEEMEEEEEEEEEGEAGEAGEAESEKGG EELL PPESTPIPANLSQNLEAAATQ ,, VAVSVPKRRRKIKELNKKEAVGDLLDAFKE,, ANPAVPEVENQPPAGSNPGPESESGVPPRPEEAD ETWDSKEDKIHNAENIQPGEQKY EYKS 319 amino acids = 33.6 kDa					
EIF4G1-219	1 .. 1308	1308 bp	■	→	CDS
▶ 3 segments = 957 bp					
/codon_start = 1					
/note = coding sequence ENSP00000404754					
/translation = AVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEPILVEVTL SKVPPESEFSSSPLQAPTPLASHTVEIHEPNGMVPSEDL EPEVESSPELAPPACPSESPVP IAPTAQPEELNNGAPSPPAVDLSPVSEPEEQAQEV TASMPTTIP SATPATAP SATSPAQEEEMEEEEEEEEEGEAGEAGEAESEKGG EELL PPESTPIPANLSQNLEAAATQ ,, VAVSVPKRRRKIKELNKKEAVGDLLDAFKE,, ANPAVPEVENQPPAGSNPGPESESGVPPRPEEAD ETWDSKEDKIHNAENIQPGEQKY EYKS 319 amino acids = 33.6 kDa					
EIF4G1-221	1 .. 1308	1308 bp	■	→	CDS
▶ 3 segments = 957 bp					
/codon_start = 1					
/note = coding sequence ENSP00000399858					
/translation = AVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEPILVEVTL SKVPPESEFSSSPLQAPTPLASHTVEIHEPNGMVPSEDL EPEVESSPELAPPACPSESPVP IAPTAQPEELNNGAPSPPAVDLSPVSEPEEQAQEV TASMPTTIP SATPATAP SATSPAQEEEMEEEEEEEEEGEAGEAGEAESEKGG EELL PPESTPIPANLSQNLEAAATQ ,, VAVSVPKRRRKIKELNKKEAVGDLLDAFKE,, ANPAVPEVENQPPAGSNPGPESESGVPPRPEEAD ETWDSKEDKIHNAENIQPGEQKY EYKS 319 amino acids = 33.6 kDa					
EIF4G1-224	1 .. 1308	1308 bp	■	→	CDS
▶ 3 segments = 957 bp					
/codon_start = 1					
/note = coding sequence ENSP00000398145					
/translation = AVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEPILVEVTL SKVPPESEFSSSPLQAPTPLASHTVEIHEPNGMVPSEDL EPEVESSPELAPPACPSESPVP IAPTAQPEELNNGAPSPPAVDLSPVSEPEEQAQEV TASMPTTIP SATPATAP SATSPAQEEEMEEEEEEEEEGEAGEAGEAESEKGG EELL PPESTPIPANLSQNLEAAATQ ,, VAVSVPKRRRKIKELNKKEAVGDLLDAFKE,, ANPAVPEVENQPPAGSNPGPESESGVPPRPEEAD ETWDSKEDKIHNAENIQPGEQKY EYKS 319 amino acids = 33.6 kDa					
EIF4G1-226	1 .. 1308	1308 bp	■	→	CDS
▶ 3 segments = 957 bp					
/codon_start = 1					
/note = coding sequence ENSP00000391412					
/translation = AVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEPILVEVTL SKVPPESEFSSSPLQAPTPLASHTVEIHEPNGMVPSEDL EPEVESSPELAPPACPSESPVP IAPTAQPEELNNGAPSPPAVDLSPVSEPEEQAQEV TASMPTTIP SATPATAP SATSPAQEEEMEEEEEEEEEGEAGEAGEAESEKGG EELL PPESTPIPANLSQNLEAAATQ ,, VAVSVPKRRRKIKELNKKEAVGDLLDAFKE,, ANPAVPEVENQPPAGSNPGPESESGVPPRPEEAD ETWDSKEDKIHNAENIQPGEQKY EYKS 319 amino acids = 33.6 kDa					

Feature	Location	Size	Start	End	Type
EIF4G1-229	1 .. 605	605 bp	■	➔	CDS
/codon_start = 1					
/note = coding sequence ENSP00000399969					
/translation = AVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEPILVEVTL SKVPPESEFSSSPLQAPTPLASHTVEIHEPNGMVPSEDL EPEVESSPELAPPPACPSSESPV IAPTAQPEELLNGAPSPPAVDLSPVSEPEEQAKEVTASMAPPTIP SATPATAPSATSPAQEEMEEEEEEEEEGEAGEAGEAESEKGG E 201 amino acids = 20.9 kDa					
EIF4G1-229	1 .. 605	605 bp	■	➔	prim_transcript
/note = primary transcript ENST00000457456					
EIF4G1-215	1 .. 239	239 bp	■	➔	CDS
/codon_start = 1					
/note = coding sequence ENSP00000409545					
/translation = AVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEPILVEVTL SKVPPESEFSSSPLQAPTPLASHTVEIH 79 amino acids = 8.5 kDa					
EIF4G1-215	1 .. 239	239 bp	■	➔	prim_transcript
/note = primary transcript ENST00000427607					
EIF4G1-217	1 .. 181	181 bp	■	➔	CDS
/codon_start = 1					
/note = coding sequence ENSP00000411707					
/translation = AVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEPILVEVTL SKVPPESE 60 amino acids = 6.4 kDa					
EIF4G1-217	1 .. 181	181 bp	■	➔	prim_transcript
/note = primary transcript ENST00000428387					
EIF4G1-223	1 .. 132	132 bp	■	➔	CDS
/codon_start = 1					
/note = coding sequence ENSP00000407244					
/translation = AVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEP 44 amino acids = 4.6 kDa					
EIF4G1-223	1 .. 132	132 bp	■	➔	prim_transcript
/note = primary transcript ENST00000444134					
EIF4G1-236	1 .. 112	112 bp	■	➔	prim_transcript
/note = primary transcript ENST00000484862 Retained intron					
EIF4G1-238	1 .. 85	85 bp	■	➔	prim_transcript
/note = primary transcript ENST00000493299 Retained intron					
✓ Donor Template WT -> SNV	647 .. 746	100 bp	■	⌊	misc_feature
✓ gRNA Protospacer	665 .. 684	20 bp	■	⌊	misc_feature
✓ SNV	667 .. 667	1 bp	■	⌊	misc_feature
/note = WT = C SNV = T					
✓ PAM	685 .. 687	3 bp	■	⌊	misc_feature

Primer	Length		Binding Sites	↕	Tm	Date Added
✓ PCR Forward	25-mer		168 .. 192	→	58°C	Jun 14, 2023
/sequence = CCAGAATCTGAGTTTTCTTCCAGTC 44% GC / 7583.0 Da						
✓ Donor Template WT -> SNV	100-mer		647 .. 746	←	79°C	Jun 14, 2023
/sequence = atcaaggagggaaggaacgatatcccctagcccgccctacacctaccgtccaaccacaccttacCTTGAGTGGCTGCTACTGCCTCCAAATTCTGAGAC 55% GC / 30,517.8 Da						
✓ gRNA Protospacer	20-mer		665 .. 684	→	60°C	Jun 14, 2023
/sequence = AGCAGCAGCCACTCAAGGTA 55% GC / 6120.0 Da						
✓ Sanger Sequencing Primer	20-mer		825 .. 844	←	58°C	Jun 14, 2023
/sequence = atttcccctttgcatcacc 50% GC / 5938.9 Da						
✓ PCR Reverse	24-mer		1104 .. 1127	←	58°C	Jun 14, 2023
/sequence = GTTCGCctagaacaacagaacatc 46% GC / 7314.8 Da						