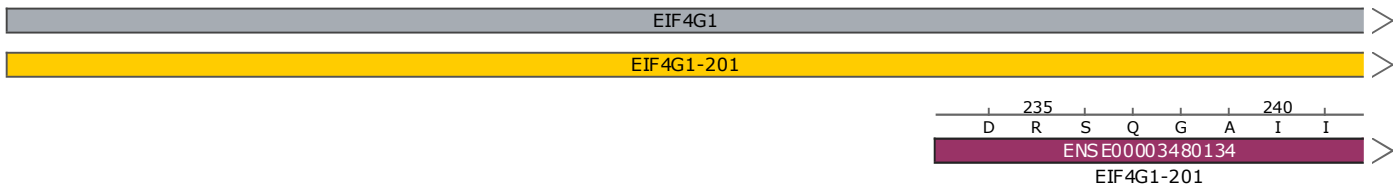


**CZK2J00158R EIF4G1\_A502V\_C01\_AA**  
 1446 bp

5'  
3'

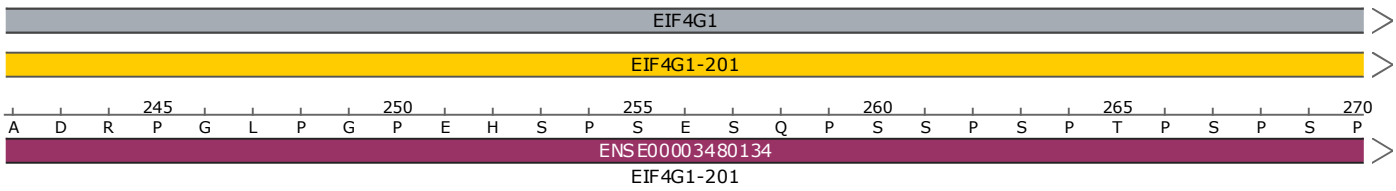
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85



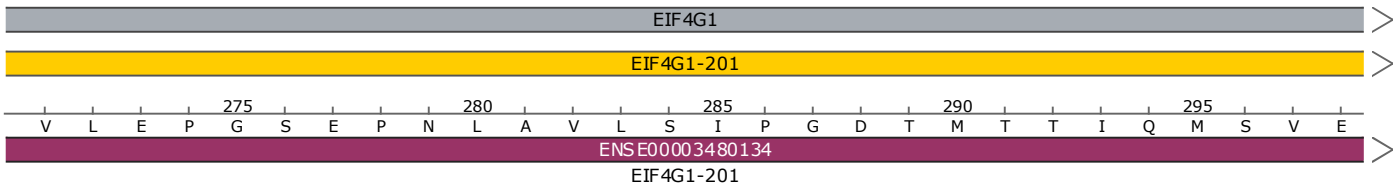
CTGACCGGCCAGGGCTGCCTGGCCAGAGCATAGCCCTTCCAGAATCCCAGCCTTCGTGCGCTTCTCCGACCCCATCACCATCCCC  
GACTGGCCGGTCCCAGCGGACCGGGTCTCGTATCGGGAAGTCTTAGGGTCCGAAGCAGCGGAAGAGGCTGGGGTAGTGGTAGGGG

170



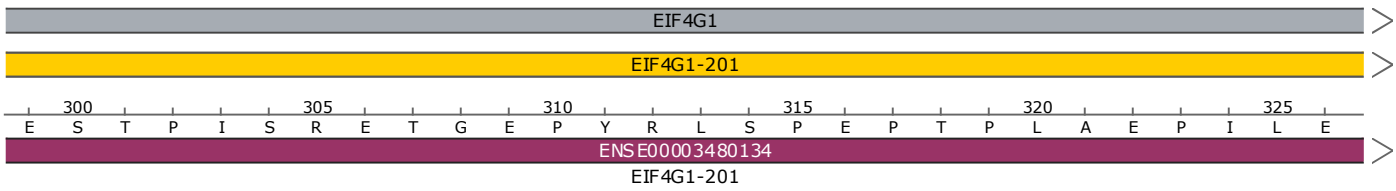
AGTCTTGAACCGGGGCTGAGCCTAATCTCGCAGTCTCTCTATTCTGGGGACACTATGACAACATATACAAATGTCTGTAGAA  
TCAGAACCTTGGCCCCAGACTCGGATTAGAGCGTCAGGAGAGATAAGGACCCCTGTGATACTGTTGATATGTTTACAGACATCTT

255



GAATCAACCCCATCTCCCGTGAAACTGGGGAGCCATATCGCCTCTCTCCAGAACCCTCTCTCGCCGAACCCATACTGGAAG  
CTTAGTTGGGGGTAGAGGGCACTTTGACCCCTCGGTATAGCGGAGAGAGGTCTTGGGTGAGGAGAGCGGCTTGGGTATGACCTTC

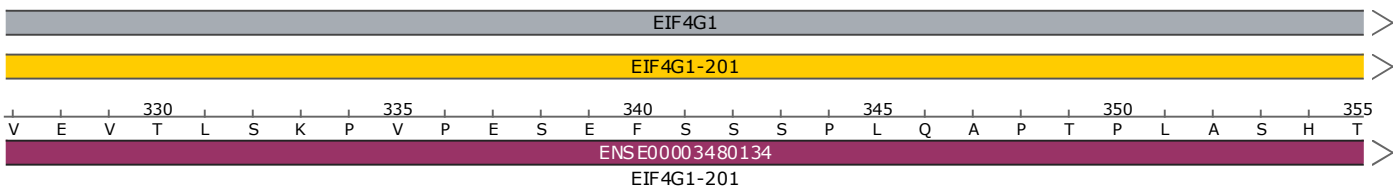
340



PCR Forward  
CCAGAATCTGAGTTTTCTTCCAGTC

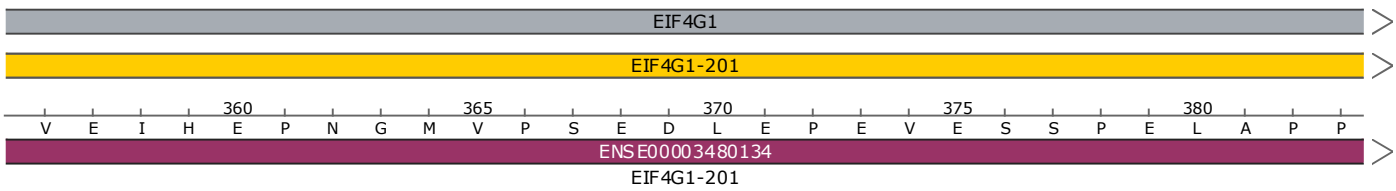
TAGAAGTGACACTTAGCAAACCGGTTCCAGAATCTGAGTTTTCTTCCAGTCTCTCCAGGCTCCCACCCCTTTGGCATCTCACAC  
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425



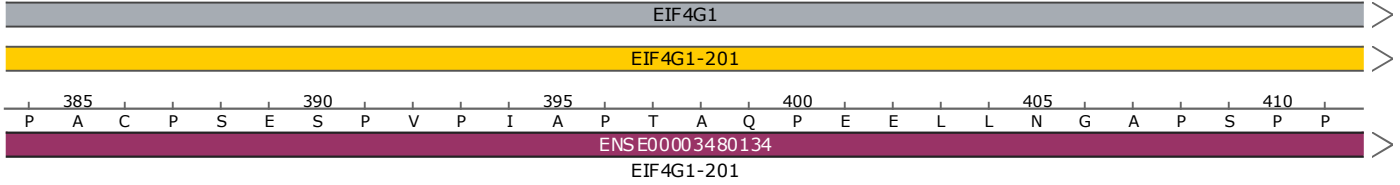
AGTGGAAATTCATGAGCCTAATGGCATGGTCCCATCTGAAGATCTGGAACCAGAGGTGGAGTCAAGCCCAGAGCTTGCTCCTCCC  
TCACCTTTAAGTACTCGGATTACCGTACCAGGGTAGACTTCTAGACCTTGGTCTCCACCTCAGTTCCGGTCTCGAACGAGGAGGG

510



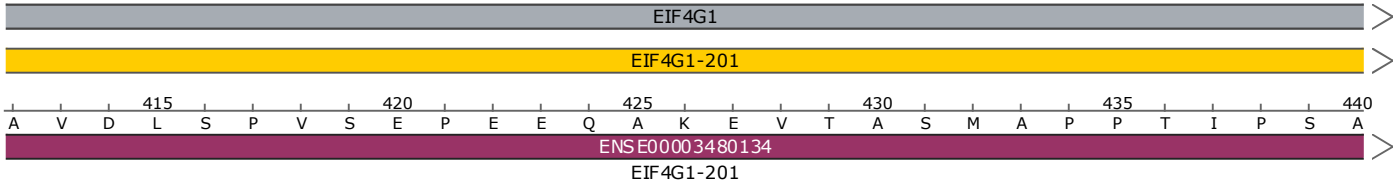
CCAGCTTGCCCCTCCGAATCCCCTGTGCCATTGCTCCAACCTGCCAACCTGAGGAACTGCTCAACGGAGCCCCCTCGCCACCAG  
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595



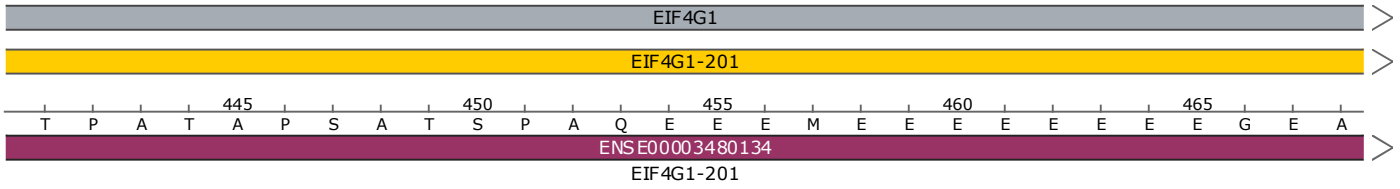
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680



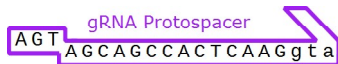
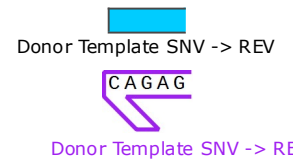
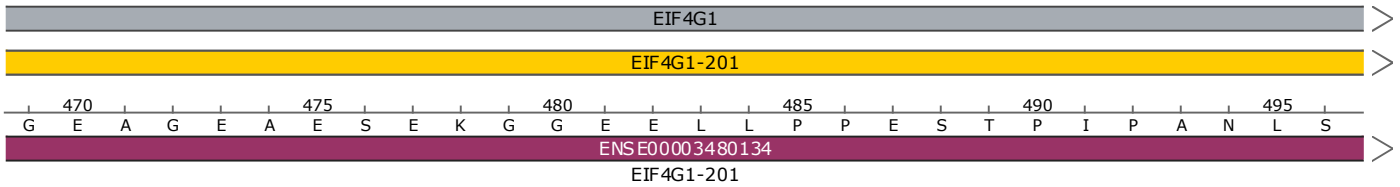
TACTCCAGCTACGGCTCCTTCAGCTACTTCCCCAGCTCAGGAGGAGGAAATGGAAGAAGAAGAAGAAGAGGAAGAAGGAGAAGCA  
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765



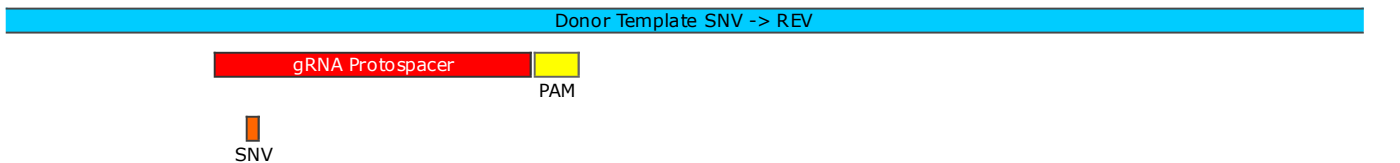
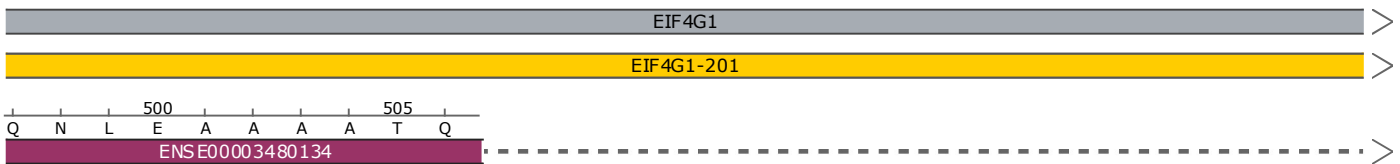
GGAGAAGCAGGAGAAGCTGAGAGTGAGAAAGGAGGAGAGGAAGTCTCCCCCAGAGAGTACCCTATTCCAGCCAACCTTGCTCTC  
 CCTTTCGTCCTTTCGACTCTCACTCTTCTCCTCCTTGCAGGGGGGGTCTCTCATGGGGATAAGGTTCGGTTGAACAGAG

850



AGAATTTGGAGGCAGCAGCAGCCACTCAAGGTAAGGTGTGGTTGGACGGTAGAGGTAGGGCGGGCTAGGGGATATCGTTCTTGC  
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935

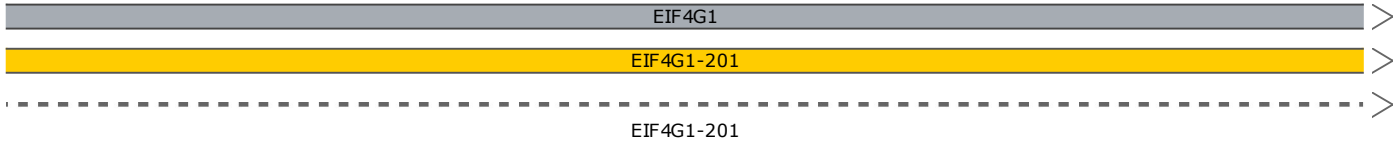


TCTTAAACCTCCGTCTCGTTCGGTTCATTCCACACCAACCTGCCATCTCCATCCCGCCGATCCCCTATAGCAAGGAACG

Donor Template SNV -> REV

CCTCCTTGATGACCGCCCATTTTTGACATGTTTCTGGGTCCCTGCAATGGAATCTAAGAAGTAAAGGACTTTTAAGCCTAA  
GGAGGAAGTACTGGCGGGTAAAAACTGTACAAAGACCCAGGGACGTTACCTTAGATTCTTGATCTAATTCCTGAAAATTCGGATT

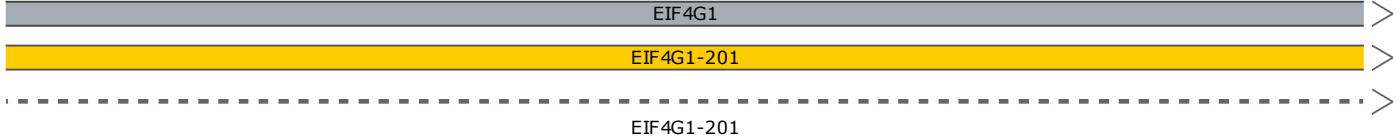
1020



Donor Template SNV -> REV  
**ggaggaacta**  
Donor Template SNV -> REV

AAAGGGTGATGCAAAGGGGAAATACTGTTCTTTGGCTGCTTTCTATTTCCAGGGATTAAGGGTACTCCTTAAATTATTGGCAA  
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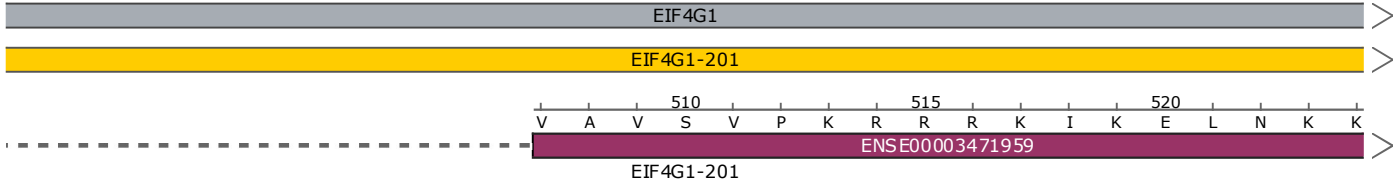
1105



**cccactacgtttccccttta**  
Sanger Sequencing Primer

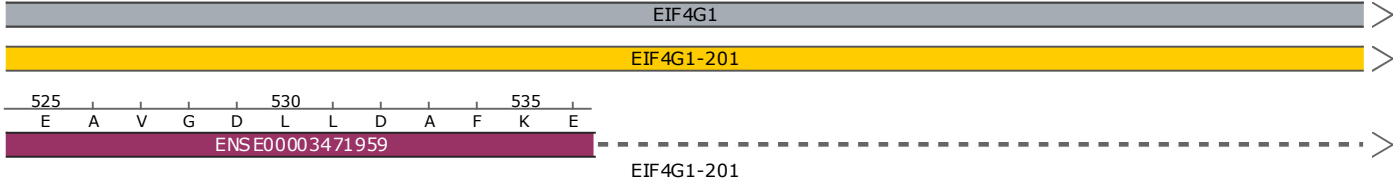
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1190



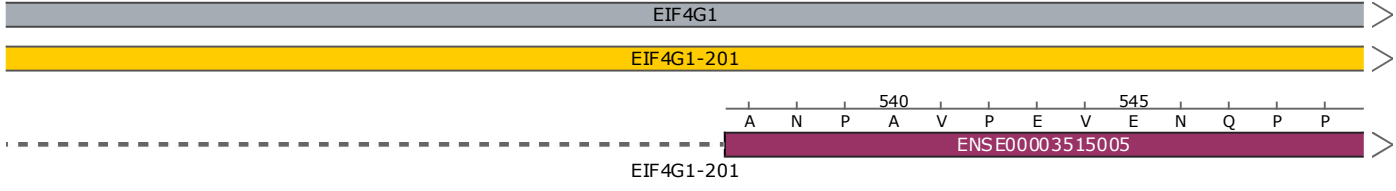
GGAGGCTGTTGGAGACCTTCTGGATGCCTTCAAGGAGGTAAGGGAGCAGAAAATGGGAGGGGAGAGGGCCAAGTTGAGGTATGGA  
CCTCCGACAACCTCTGGAAGACCTACGGAAGTTCTCCATTCCCTCGTCTTTACCCTCCCCTCTCCCGGTTCAACTCCATACCT

1275



GCAGTGGTCATTCTGCAACCAAAACTGGATGTTCTGTTGTTCTAGGCGAACCCGGCAGTACCAGAGGTGGAAAATCAGCCTCCTG  
CGTCACCAGTAAGACGTTGGTTTTGACCTACAAGACAACAAGATCCGCTTGGGCCGTCATGGTCTCCACCTTTTAGTCGGAGGAC

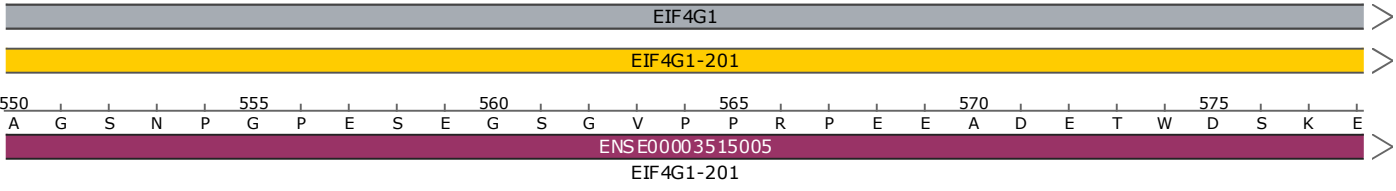
1360



**ctacaagacaacaagatcCGCTTG**  
PCR Reverse

CAGGCAGCAATCCAGGCCAGAGTCTGAGGGCAGTGGTGTGCCCCACGTCTGAGGAAGCAGATGAGACCTGGGACTCAAAGGA  
GTCCGTCGTTAGGTCCGGGTCTCAGACTCCCGTCACCACACGGGGGTGCAGGACTCCTTCGTCTACTCTGGACCCTGAGTTTCTT

1445



550 A G S N P G P E S E 560 G S G V P P R P E E 570 A D E T W D S K E

A 3'  
T 5' 1446



EIF4G1



EIF4G1-201



EIF4G1-201

Feature	Location	Size	⚡	→	Type
✓ <b>EIF4G1</b>	1 .. 1446	1446 bp	■	→	gene
/note = gene <a href="#">ENSG00000114867</a> Protein coding					
✓ <b>EIF4G1-201</b>	1 .. 1446	1446 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000342981</a>					
<b>EIF4G1-202</b>	1 .. 1446	1446 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000346169</a>					
<b>EIF4G1-203</b>	1 .. 1446	1446 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000350481</a>					
<b>EIF4G1-204</b>	1 .. 1446	1446 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000352767</a>					
<b>EIF4G1-205</b>	1 .. 1446	1446 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000382330</a>					
<b>EIF4G1-206</b>	1 .. 1446	1446 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000392537</a>					
<b>EIF4G1-207</b>	1 .. 1446	1446 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000411531</a>					
<b>EIF4G1-208</b>	1 .. 1446	1446 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000413967</a> Nonsense mediated decay					
<b>EIF4G1-209</b>	1 .. 1446	1446 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000414031</a>					
<b>EIF4G1-210</b>	1 .. 1446	1446 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000421110</a>					
<b>EIF4G1-212</b>	1 .. 1446	1446 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000424196</a>					
<b>EIF4G1-213</b>	1 .. 1446	1446 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000426123</a>					
<b>EIF4G1-216</b>	1 .. 1446	1446 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000427845</a>					
<b>EIF4G1-218</b>	1 .. 1446	1446 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000434061</a>					
<b>EIF4G1-219</b>	1 .. 1446	1446 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000435046</a>					
<b>EIF4G1-221</b>	1 .. 1446	1446 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000441154</a>					
<b>EIF4G1-222</b>	1 .. 1446	1446 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000442406</a> Nonsense mediated decay					
<b>EIF4G1-224</b>	1 .. 1446	1446 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000444861</a>					
<b>EIF4G1-226</b>	1 .. 1446	1446 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000450424</a>					
<b>EIF4G1-240</b>	1 .. 1446	1446 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000676453</a> Nonsense mediated decay					
<b>EIF4G1-229</b>	1 .. 804	804 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000457456</a>					
<b>EIF4G1-215</b>	1 .. 438	438 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000427607</a>					
<b>EIF4G1-217</b>	1 .. 380	380 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000428387</a>					

Feature	Location	Size	Start	End	Type
<b>EIF4G1-223</b>	1 .. 331	331 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000444134</a>					
<b>EIF4G1-236</b>	1 .. 311	311 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000484862</a> Retained intron					
<b>EIF4G1-238</b>	1 .. 284	284 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000493299</a> Retained intron					
<b>EIF4G1-201</b>	59 .. 1446	1388 bp	■	→	CDS
▶ 3 segments = 1037 bp					
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<b>EIF4G1-202</b>	59 .. 1446	1388 bp	■	→	CDS
▶ 3 segments = 1037 bp					
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<b>EIF4G1-203</b>	59 .. 1446	1388 bp	■	→	CDS
▶ 3 segments = 1037 bp					
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<b>EIF4G1-204</b>	59 .. 1446	1388 bp	■	→	CDS
▶ 3 segments = 1037 bp					
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/note = coding sequence <a href="#">ENSP00000338020</a>					
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<b>EIF4G1-205</b>	59 .. 1446	1388 bp	■	→	CDS
▶ 3 segments = 1037 bp					
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<b>EIF4G1-206</b>	59 .. 1446	1388 bp	■	→	CDS
▶ 3 segments = 1037 bp					
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/note = coding sequence <a href="#">ENSP00000376320</a>					
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Feature	Location	Size	Start	End	Type
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/note = coding sequence <a href="#">ENSP00000395974</a>					
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<b>EIF4G1-209</b>	59 .. 1446	1388 bp	■	→	CDS
▶ 3 segments = 1037 bp					
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/note = coding sequence <a href="#">ENSP00000391935</a>					
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<b>EIF4G1-210</b>	59 .. 1446	1388 bp	■	→	CDS
▶ 3 segments = 1037 bp					
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/note = coding sequence <a href="#">ENSP00000413159</a>					
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<b>EIF4G1-212</b>	59 .. 1446	1388 bp	■	→	CDS
▶ 3 segments = 1037 bp					
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/note = coding sequence <a href="#">ENSP00000416255</a>					
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<b>EIF4G1-213</b>	59 .. 1446	1388 bp	■	→	CDS
▶ 3 segments = 1037 bp					
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/note = coding sequence <a href="#">ENSP00000403269</a>					
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<b>EIF4G1-216</b>	59 .. 1446	1388 bp	■	→	CDS
▶ 3 segments = 1037 bp					
/codon_start = 1					
/note = coding sequence <a href="#">ENSP00000407682</a>					
/translation = DRSQGAIIADRPGLPGPEHSPSESQPSSPSTPSPSPVLEPGSEPNLAVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEPILEVEVTL SKVPPESEFSSSPLQ APTPLASHTVEIHEPNGMVPSEDLPEVESSPELAPPACPSESPVPIAPTAQPEELLNGAPSPPAVDLSPVSEPEEQAKEVTASMAPPTIP SATPATAPSATSPAQEEEMEE EEEEEEGEAGEAGEAESEKGG EELLPP ESTPIPANLSQNLEAAAATQ, , VAVSVPKRRRKIKELNKKEAVGDLLDAFKE, , ANPAVPEVENQPPAGSNPGPESEGSVPPRPE EADETWSKE 345 amino acids = 36.0 kDa					
<b>EIF4G1-218</b>	59 .. 1446	1388 bp	■	→	CDS
▶ 3 segments = 1037 bp					
/codon_start = 1					
/note = coding sequence <a href="#">ENSP00000411826</a>					
/translation = DRSQGAIIADRPGLPGPEHSPSESQPSSPSTPSPSPVLEPGSEPNLAVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEPILEVEVTL SKVPPESEFSSSPLQ APTPLASHTVEIHEPNGMVPSEDLPEVESSPELAPPACPSESPVPIAPTAQPEELLNGAPSPPAVDLSPVSEPEEQAKEVTASMAPPTIP SATPATAPSATSPAQEEEMEE EEEEEEGEAGEAGEAESEKGG EELLPP ESTPIPANLSQNLEAAAATQ, , VAVSVPKRRRKIKELNKKEAVGDLLDAFKE, , ANPAVPEVENQPPAGSNPGPESEGSVPPRPE EADETWSKE 345 amino acids = 36.0 kDa					



Feature	Location	Size	Start	End	Type
<b>EIF4G1-219</b>	59 .. 1446	1388 bp	■	→	CDS
▶ 3 segments = 1037 bp					
/codon_start = 1					
/note = coding sequence <a href="#">ENSP0000404754</a>					
/translation = DRSQGAIIDRPLPGPEHSPSEQPSSPSTPSPVLEPGSEPNLAVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEPILEVEVTLSKVPPESEFSSSPLQ APTPLASHTVEIHEPNGMVPSEDLPEVESSPELAPPACPSESVPPIAPTAQPEELLNGAPSPPAVDLSPVSEPEEQAKEVTASMAPPTIPSATPATAPSATSPAQEEEMEE EEEEEEGEAGEAGEAESEKGGEEELLPESTPIPANLSQNLEAAAATQ, , VAVSVPKRRRKIKELNKKEAVGDLDFAFKE, , ANPAVPEVENQPPAGSNPGPESEGSVPPRPE EADETWDSKE 345 amino acids = 36.0 kDa					
<b>EIF4G1-221</b>	59 .. 1446	1388 bp	■	→	CDS
▶ 3 segments = 1037 bp					
/codon_start = 1					
/note = coding sequence <a href="#">ENSP0000399858</a>					
/translation = DRSQGAIIDRPLPGPEHSPSEQPSSPSTPSPVLEPGSEPNLAVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEPILEVEVTLSKVPPESEFSSSPLQ APTPLASHTVEIHEPNGMVPSEDLPEVESSPELAPPACPSESVPPIAPTAQPEELLNGAPSPPAVDLSPVSEPEEQAKEVTASMAPPTIPSATPATAPSATSPAQEEEMEE EEEEEEGEAGEAGEAESEKGGEEELLPESTPIPANLSQNLEAAAATQ, , VAVSVPKRRRKIKELNKKEAVGDLDFAFKE, , ANPAVPEVENQPPAGSNPGPESEGSVPPRPE EADETWDSKE 345 amino acids = 36.0 kDa					
<b>EIF4G1-224</b>	59 .. 1446	1388 bp	■	→	CDS
▶ 3 segments = 1037 bp					
/codon_start = 1					
/note = coding sequence <a href="#">ENSP0000398145</a>					
/translation = DRSQGAIIDRPLPGPEHSPSEQPSSPSTPSPVLEPGSEPNLAVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEPILEVEVTLSKVPPESEFSSSPLQ APTPLASHTVEIHEPNGMVPSEDLPEVESSPELAPPACPSESVPPIAPTAQPEELLNGAPSPPAVDLSPVSEPEEQAKEVTASMAPPTIPSATPATAPSATSPAQEEEMEE EEEEEEGEAGEAGEAESEKGGEEELLPESTPIPANLSQNLEAAAATQ, , VAVSVPKRRRKIKELNKKEAVGDLDFAFKE, , ANPAVPEVENQPPAGSNPGPESEGSVPPRPE EADETWDSKE 345 amino acids = 36.0 kDa					
<b>EIF4G1-226</b>	59 .. 1446	1388 bp	■	→	CDS
▶ 3 segments = 1037 bp					
/codon_start = 1					
/note = coding sequence <a href="#">ENSP0000391412</a>					
/translation = DRSQGAIIDRPLPGPEHSPSEQPSSPSTPSPVLEPGSEPNLAVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEPILEVEVTLSKVPPESEFSSSPLQ APTPLASHTVEIHEPNGMVPSEDLPEVESSPELAPPACPSESVPPIAPTAQPEELLNGAPSPPAVDLSPVSEPEEQAKEVTASMAPPTIPSATPATAPSATSPAQEEEMEE EEEEEEGEAGEAGEAESEKGGEEELLPESTPIPANLSQNLEAAAATQ, , VAVSVPKRRRKIKELNKKEAVGDLDFAFKE, , ANPAVPEVENQPPAGSNPGPESEGSVPPRPE EADETWDSKE 345 amino acids = 36.0 kDa					
<b>EIF4G1-229</b>	59 .. 804	746 bp	■	→	CDS
/codon_start = 1					
/note = coding sequence <a href="#">ENSP0000399969</a>					
/translation = DRSQGAIIDRPLPGPEHSPSEQPSSPSTPSPVLEPGSEPNLAVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEPILEVEVTLSKVPPESEFSSSPLQ APTPLASHTVEIHEPNGMVPSEDLPEVESSPELAPPACPSESVPPIAPTAQPEELLNGAPSPPAVDLSPVSEPEEQAKEVTASMAPPTIPSATPATAPSATSPAQEEEMEE EEEEEEGEAGEAGEAESEKGGEE 248 amino acids = 25.7 kDa					
<b>EIF4G1-215</b>	59 .. 438	380 bp	■	→	CDS
/codon_start = 1					
/note = coding sequence <a href="#">ENSP0000409545</a>					
/translation = DRSQGAIIDRPLPGPEHSPSEQPSSPSTPSPVLEPGSEPNLAVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEPILEVEVTLSKVPPESEFSSSPLQ APTPLASHTVEIH 126 amino acids = 13.2 kDa					
<b>EIF4G1-217</b>	59 .. 380	322 bp	■	→	CDS
/codon_start = 1					
/note = coding sequence <a href="#">ENSP0000411707</a>					
/translation = DRSQGAIIDRPLPGPEHSPSEQPSSPSTPSPVLEPGSEPNLAVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEPILEVEVTLSKVPPESE 107 amino acids = 11.1 kDa					
<b>EIF4G1-223</b>	59 .. 331	273 bp	■	→	CDS
/codon_start = 1					
/note = coding sequence <a href="#">ENSP0000407244</a>					
/translation = DRSQGAIIDRPLPGPEHSPSEQPSSPSTPSPVLEPGSEPNLAVLSIPGDTMTTIQMSVEESTPISRETGEPYRLSPEPTPLAEP 91 amino acids = 9.4 kDa					
✓ <b>Donor Template SNV -&gt; REV</b>	846 .. 945	100 bp	■	⌊	misc_feature
✓ <b>gRNA Protospacer</b>	864 .. 883	20 bp	■	⌊	misc_feature
✓ <b>SNV</b>	866 .. 866	1 bp	■	⌊	misc_feature
/note = SNV = T REV = C					
✓ <b>PAM</b>	884 .. 886	3 bp	■	⌊	misc_feature

Primer	Length		Binding Sites	↕	Tm	Date Added
✓ <b>PCR Forward</b>	25-mer		367 .. 391	→	58°C	Jun 14, 2023
/sequence = CCAGAATCTGAGTTTTCTTCCAGTC 44% GC / 7583.0 Da						
✓ <b>Donor Template SNV -&gt; REV</b>	100-mer		846 .. 945	←	80°C	Jun 14, 2023
/sequence = atcaaggagggcaaggaacgatatcccctagcccgcctacacctaccgtccaaccacaccttacCTTGAGTGGCTGCTGCTGCCTCCAAATTCTGAGAC 56% GC / 30,533.8 Da						
✓ <b>gRNA Protospacer</b>	20-mer		867 .. 883	→	55°C	Jun 14, 2023
/sequence = AGTAGCAGCCACTCAAGgta 50% GC / 6135.1 Da						
✓ <b>Sanger Sequencing Primer</b>	20-mer		1024 .. 1043	←	58°C	Jun 14, 2023
/sequence = atttcccctttgcatcacc 50% GC / 5938.9 Da						
✓ <b>PCR Reverse</b>	24-mer		1303 .. 1326	←	58°C	Jun 14, 2023
/sequence = GTTCGCctagaacaacagaacatc 46% GC / 7314.8 Da						