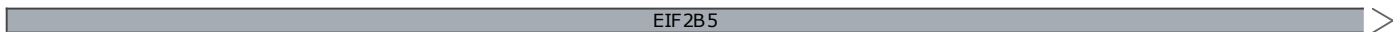


**CZK2J00157R EIF2B5\_R195H\_E07\_AA**  
1201 bp

5'  
3'

ACAGTTCCTAAATGTTATATGGATTGCAGAAGGGGAAAGCTGACGTGAAGCGTGTTCACAGGCTACTTTGTGTACCCCTAGGCTTC  
TGTCAAGGATTTACAATATACCTAACGTCTTCCCCTTTCGACTGCACCTTCGCACAAGGGTCCGATGAAACACATGGGATCCGAAG

85



PCR Forward

AGGAAATAACCATGTTTCCTAACCC

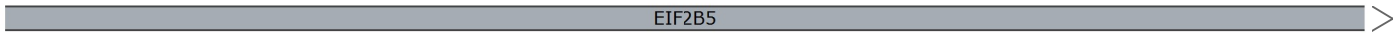
AGCAGGATTTGAGTTCAAATTGATGTTTAGGGACAAGGGTCAAGGTATGGAGAGGAAATAACCATGTTTCCTAACCCATAAAA  
TCGTCTCTAAAACCTCAAGTTTAACTACAAATCCCTGTTCCCAAGTTCATACCTCTCCTTTATTGGTACAAAGGATTGGGTATTT

170



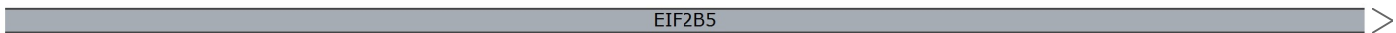
CAAGACTGGTGACACAGGATGCTGAAAGCATTATTATAGTTTCATAATACTCTTTGAAGTTGAAGACGCTGGCAAGAACCCAAAA  
GTTCTGACCACTGTGTCCTACGACTTTCGTAAGTAATATCAAATATTATGAGAACTTCAACTTCTGCGACCGTTCTTGGGTTTT

255



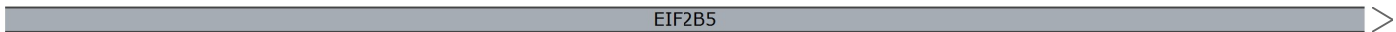
AAGCCATCGAGAAGGACTGTGAGTGTGAAAGGGGGTAAAAATGGGAAGGCTCAAATGATCTTTATGCTTGATACACTCATTTC  
TTCGGTAGCTCTTCTGACACTCACGACTTTCCTCCACTTTTACCCTTCCGAGTTTACTAGAAATACGAACATGTGAGTAAG

340



CCCTCACCTCCCTTCTTTAGGAAGTCAAAGTGGTGCCGCCCTACATCTCTCAATGTGGTTCGAATAATTACATCAGAGCTCTA  
GGGAGTGGGAGGGAAGGAAATCCTTCAGTTTACCACGGCGGGATGTAGAGAGTTACACCAAGCTTATTAATGTAGTCTCGAGAT

425

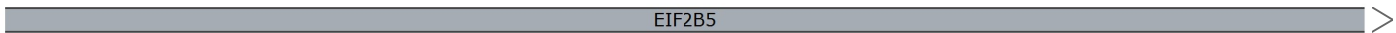


Sanger Sequencing Primer

TTTGGTGCGCTCTGACTTTC

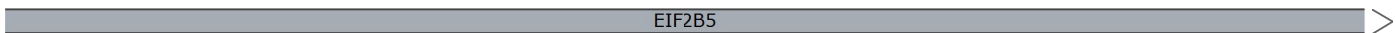
TCGATCACTGGGAGATGTCCTCCGTGATGTTGATGCCAAGGCTTTGGTGCGCTCTGACTTTCCTTCTGGTGTATGGGGATGTCATC  
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510



TCAAACATCAATATCACCAGAGCCCTTGAGGAACACAGGTCAGGATGGGAAAATGACAGGAACAAGGGTTAAAGACCAGCAGAGC  
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595

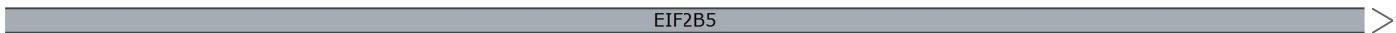


Donor Template SNV -> REV

CGGAAGCTAGAAAAAATGTTTCTGTGATGACG

CCTGAGACTGCTTTTTTGCAGTTCGTCCCTCCTGTCCTTTATAGGTTGAGACGGAAGCTAGAAAAAATGTTTCTGTGATGACG  
GGACTCTGACGAAAAAACGTCAAGACAGGGAGGACAGGAAATATCCTCAACTCTGCCTTCGATCTTTTTTTACAAAGACACTACTGC

680

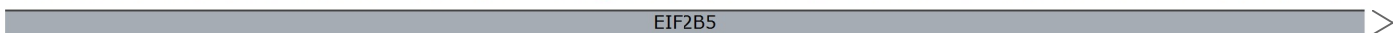


Donor Template SNV -> REV

ATGATCTTCAAGGAGTCATCCCCAGCCACCCAACCTCGTTGCCACGAAGACAATGTGGTAGTGGCTG

ATGATCTTCAAGGAGTCATCCCCAGCCACCCAACCTCGTTGCCACGAAGACAATGTGGTAGTGGCTGTGGATAGTACCACAAACA  
TACTAGAAGTTCTCAGTAGGGGTCGGTGGGTTGAGCAACG6TGCTTCTGTTACACCATCACCGACACCTATCATGGTGTGTTG

765





Feature	Location	Size	Start	End	Type
✓ <b>EIF2B5</b>	1 .. 1201	1201 bp	■	➔	gene
/note = gene <a href="#">ENSG00000145191</a> Protein coding					
<b>EIF2B5-DT</b>	1 .. 1201	1201 bp	■	←	gene
/note = gene <a href="#">ENSG00000272721</a> lncRNA					
<b>EIF2B5-202</b>	1 .. 1201	1201 bp	■	➔	prim_transcript
/note = primary transcript <a href="#">ENST00000432982</a> Nonsense mediated decay					
<b>EIF2B5-203</b>	1 .. 1201	1201 bp	■	➔	prim_transcript
/note = primary transcript <a href="#">ENST00000465218</a> Retained intron					
<b>EIF2B5-204</b>	1 .. 1201	1201 bp	■	➔	prim_transcript
/note = primary transcript <a href="#">ENST00000468748</a> Retained intron					
<b>EIF2B5-207</b>	1 .. 1201	1201 bp	■	➔	prim_transcript
/note = primary transcript <a href="#">ENST00000481054</a> Retained intron					
<b>EIF2B5-208</b>	1 .. 1201	1201 bp	■	➔	prim_transcript
/note = primary transcript <a href="#">ENST00000484154</a> Retained intron					
<b>EIF2B5-209</b>	1 .. 1201	1201 bp	■	➔	prim_transcript
/note = primary transcript <a href="#">ENST00000491008</a> Retained intron					
<b>EIF2B5-210</b>	1 .. 1201	1201 bp	■	➔	prim_transcript
/note = primary transcript <a href="#">ENST00000491144</a> Retained intron					
<b>EIF2B5-211</b>	1 .. 1201	1201 bp	■	➔	prim_transcript
/note = primary transcript <a href="#">ENST00000492226</a> Retained intron					
<b>EIF2B5-212</b>	1 .. 1201	1201 bp	■	➔	prim_transcript
/note = primary transcript <a href="#">ENST00000492773</a> Nonsense mediated decay					
<b>EIF2B5-215</b>	1 .. 1201	1201 bp	■	➔	prim_transcript
/note = primary transcript <a href="#">ENST00000647636</a> Nonsense mediated decay					
<b>EIF2B5-216</b>	1 .. 1201	1201 bp	■	➔	prim_transcript
/note = primary transcript <a href="#">ENST00000647909</a>					
<b>EIF2B5-217</b>	1 .. 1201	1201 bp	■	➔	prim_transcript
/note = primary transcript <a href="#">ENST00000648145</a> Nonsense mediated decay					
<b>EIF2B5-218</b>	1 .. 1201	1201 bp	■	➔	prim_transcript
/note = primary transcript <a href="#">ENST00000648189</a> Nonsense mediated decay					
<b>EIF2B5-219</b>	1 .. 1201	1201 bp	■	➔	prim_transcript
/note = primary transcript <a href="#">ENST00000648256</a> Nonsense mediated decay					
<b>EIF2B5-220</b>	1 .. 1201	1201 bp	■	➔	prim_transcript
/note = primary transcript <a href="#">ENST00000648314</a> Nonsense mediated decay					
<b>EIF2B5-221</b>	1 .. 1201	1201 bp	■	➔	prim_transcript
/note = primary transcript <a href="#">ENST00000648599</a> Nonsense mediated decay					
<b>EIF2B5-222</b>	1 .. 1201	1201 bp	■	➔	prim_transcript
/note = primary transcript <a href="#">ENST00000648630</a> Nonsense mediated decay					
<b>EIF2B5-223</b>	1 .. 1201	1201 bp	■	➔	prim_transcript
/note = primary transcript <a href="#">ENST00000648682</a> Nonsense mediated decay					

Feature	Location	Size	Start	End	Type
<b>EIF2B5-224</b>	1 .. 1201	1201 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000648882</a> Nonsense mediated decay				
<b>EIF2B5-225</b>	1 .. 1201	1201 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000648890</a> Nonsense mediated decay				
<b>EIF2B5-226</b>	1 .. 1201	1201 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000648915</a>				
<b>EIF2B5-227</b>	1 .. 1201	1201 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000649545</a> Nonsense mediated decay				
<b>EIF2B5-228</b>	1 .. 1201	1201 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000649688</a> Nonsense mediated decay				
<b>EIF2B5-229</b>	1 .. 1201	1201 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000649814</a> Retained intron				
<b>EIF2B5-231</b>	1 .. 1201	1201 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000650270</a> Nonsense mediated decay				
<b>EIF2B5-DT-201</b>	1 .. 1201	1201 bp	■	←	prim_transcript
/note	= primary transcript <a href="#">ENST00000608135</a> lncRNA				
<b>EIF2B5-DT-202</b>	1 .. 1201	1201 bp	■	←	prim_transcript
/note	= primary transcript <a href="#">ENST00000608232</a> lncRNA				
<b>EIF2B5-214</b>	1 .. 776	776 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000498831</a> protein_coding_CDS_not_defined				
<b>EIF2B5-230</b>	1 .. 685	685 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000650244</a> Nonsense mediated decay				
<b>EIF2B5-216</b>	363 .. 989	627 bp	■	→	CDS
▶ 3 segments	= 469 bp				
/codon_start	= 1				
/note	= coding sequence <a href="#">ENSP00000498164</a>				
/translation	= KSKWCRPTSLNVVRIITSELYRSLGDVLRDVKALVRSDFLLVYGDVISNITRALEEHS, , SVPPVLYRLRRKLEKNVSVMTMIFKESSPSHPTRCHEDNVVAVDSTTN RVLHFQKTQGLRRFAFPL, , SLFQGS SDGVEVRYDLLDCHISICSPQ 156 amino acids = 17.7 kDa				
<b>EIF2B5-226</b>	363 .. 989	627 bp	■	→	CDS
▶ 3 segments	= 445 bp				
/codon_start	= 1				
/note	= coding sequence <a href="#">ENSP00000497160</a>				
/translation	= KSKWCRPTSLNVVRIITSELYRSLGDVLRDVKALVRSDFLLVYGDVISNITRALEEHR, , LRRKLEKNVSVMTMIFKESSPSHPTRCHEDNVVAVDSTTNRVLHFQKT QGLRRFAFPL, , SLFQGS SDGVEVRYDLLDCHISICSPQ 148 amino acids = 16.9 kDa				
✓ <b>Donor Template SNV -&gt; REV</b>	648 .. 747	100 bp	■		misc_feature
✓ <b>PAM</b>	707 .. 709	3 bp	■		misc_feature
✓ <b>gRNA Protospacer</b>	710 .. 729	20 bp	■		misc_feature
✓ <b>SNV</b>	718 .. 718	1 bp	■		misc_feature
/note	= SNV = A REV = G				

Primer	Length	Binding Sites	Tm	Date Added
✓ <b>PCR Forward</b>  /sequence = AGGAAATAACCATGTTTCCTAACCC 40% GC / 7594.0 Da	25-mer	140 .. 164 →	57°C	Sep 29, 2023
✓ <b>Sanger Sequencing Primer</b>  /sequence = TTTGGTGGCTCTGACTTTC 50% GC / 6081.0 Da	20-mer	468 .. 487 →	58°C	Sep 29, 2023
✓ <b>Donor Template SNV -&gt; REV</b>  /sequence = CGGAAGCTAGAAAAAATGTTTCTGTGATGACGATGATCTTCAAGGAGTCATCCCCAGCCACCAACTCGTTGCCACGAAGACAATGTGGTAGTGGCTG 49% GC / 30,884.1 Da	100-mer	648 .. 747 →	77°C	Sep 29, 2023
✓ <b>gRNA Protospacer</b>  /sequence = CTTCGTGGCAATGAGTTGGG 55% GC / 6204.1 Da	20-mer	710 .. 729 ←	57°C	Sep 29, 2023
✓ <b>PCR Reverse</b>  /sequence = CAATAACAGACCCACAGAGTTCTAC 44% GC / 7588.0 Da	25-mer	1026 .. 1050 ←	56°C	Sep 29, 2023