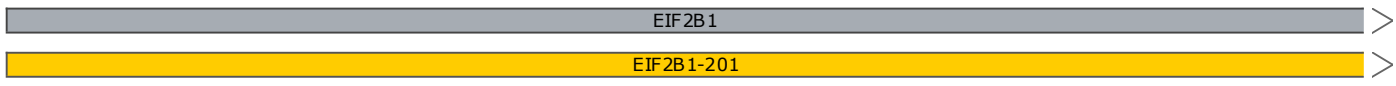


CZK2J00153 EIF2B1_V183F_G01_BB
846 bp

5'
3'

CCAGAATGTGCCCCAGCTTGCCAGCAGTCAGCACTGCCTTTTCATTGTACCTTTTCTGCCTTTGGAAGAAAAATCACTGAATTT
GGTCTTACACGGGGGTCGAACGGTCGTCAGTCGTGACGGAAAGTAACATGGAAAAGGACGGAAACCTTCTTTTAGTGACTTAAA

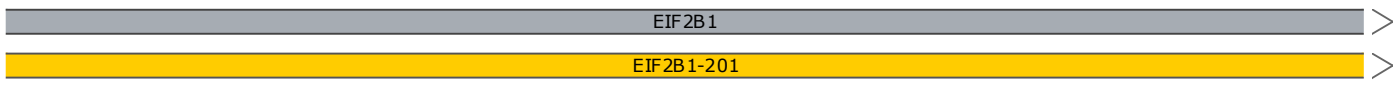
85



PCR Forward
TAAGTAGTTAACTCCGTGGAAGAGC

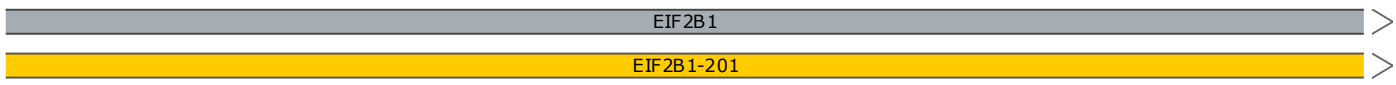
GCAGCAGGCCGCAGTATATGATCTAGGGGTTTCACTTAAGTAGTTAACTCCGTGGAAGAGCAGAGATTGTATTGATGAAGATTTT
CGTCGTCCGGCGTCATATACTAGATCCCCAAAGTGAATTCATCAATTGAGGCACCTTCTCGTCTCTAACATAACTACTTCTAAAA

170



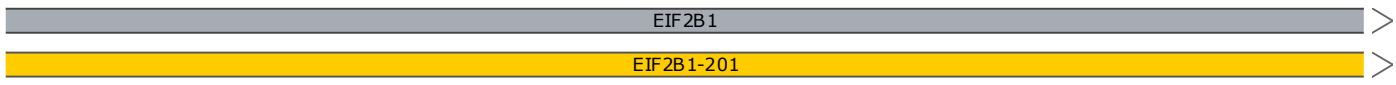
TATCAAGGAATAGGTAACCTTATATCTCCCTCTCTCTAGACGATAATCAAAGCAAACCTTCTCTTTTTCTGAATTTACATCT
ATAGTTCCTTATCCATTGAATATAGAGGGAGAGAGATCTGCTATTAGTTTCGTTTTGAAGGAGGAAAAAAGGACTTAAATGTAGA

255



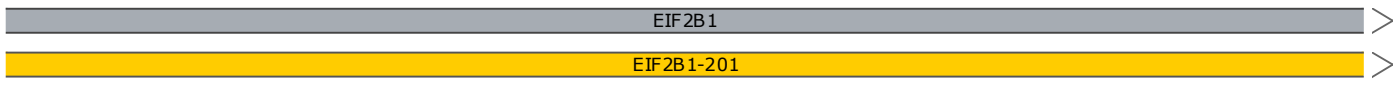
CTTACCCAGAGTCTAAGAGTATAGTTTTCCAAAAACTTCTTTCTAAAGAACTCAAATTCCTGTTTCCTTAGTCCAAAGTATTG
GAATGGGTCTCAGATTCTCATATCAAAGGTTTTATGAAGAAAGATTTCTTGAGTTTAAGAACAAGGAATCAGGTTTCATAAC

340



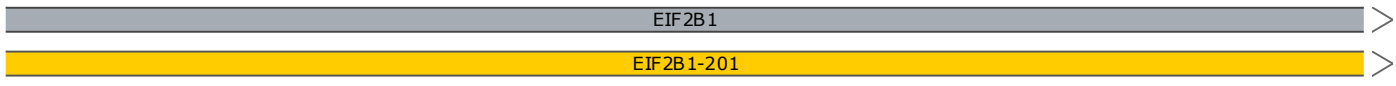
GGATCTGCCCTTAACCCATTAGTATTAATGTGAGTTTCAAGCAAACATCCACTGTCCACATTAGGTGACATACATCACTGTGGT
CCTAGACGGGGAATTGGGTAATCATAATTACACTCAAAGTTCGTTTGTAGGTGACAGGTGTAATCCACTGTATGTAGTGACACCA

425

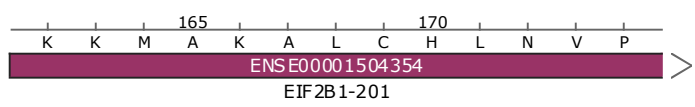


ACTGTCTTGACTTTCTCTAACGTTCTCAAATGTCATCTTCAGTAAGAAAATGGCCAAAGCCCTCTGCCACCTCAACGTCCCTG
TGACAGAACATGAAAGAGATTGCAAGAGTTTACAGTAGAAGTCATTCTTTTACCGTTTCGGGAGACGGTGGAGTTGCAGGGAC

510



Donor Template WT -> SNV



AGTTGCAGGGAC
Donor Template WT -> SNV

Feature	Location	Size	Start	End	Type
✓ EIF2B1	1 .. 846	846 bp	■	→	gene
/note	= gene ENSG00000111361 Protein coding				
✓ EIF2B1-201	1 .. 846	846 bp	■	→	prim_transcript
/note	= primary transcript ENST00000424014				
EIF2B1-203	1 .. 846	846 bp	■	→	prim_transcript
/note	= primary transcript ENST00000534960				
EIF2B1-204	1 .. 846	846 bp	■	→	prim_transcript
/note	= primary transcript ENST00000537073				
EIF2B1-205	1 .. 846	846 bp	■	→	prim_transcript
/note	= primary transcript ENST00000539951				
EIF2B1-204	1 .. 106	106 bp	■	→	CDS
/codon_start	= 1				
/note	= coding sequence ENSP00000444183				
/translation	= QNVPPACQQSALPFIVPFPAPFGRKITEFAAGRSI* 34 amino acids = 3.7 kDa				
✓ EIF2B1-201	470 .. 538	69 bp	■	→	CDS
/codon_start	= 1				
/note	= coding sequence ENSP00000416250				
/translation	= KKMAKALCHLNVPVTVLDAAV 23 amino acids = 2.3 kDa				
EIF2B1-205	470 .. 538	69 bp	■	→	CDS
/codon_start	= 1				
/note	= coding sequence ENSP00000438060				
/translation	= KKMAKALCHLNVPVTVLDAAV 23 amino acids = 2.3 kDa				
✓ Donor Template WT -> SNV	499 .. 598	100 bp	■		misc_feature
✓ gRNA Protospacer	517 .. 536	20 bp	■		misc_feature
✓ SNV	534 .. 534	1 bp	■		misc_feature
/note	= WT = G SNV = T				
✓ PAM	537 .. 539	3 bp	■		misc_feature
DDX55	847 19,175	18,329 bp	■	←	gene
/note	= gene ENSG00000111364 Protein coding				
DDX55-201	847 19,153	18,307 bp	■	←	prim_transcript
/note	= primary transcript ENST00000238146 Protein coding				
DDX55-203	847 ..3236	2390 bp	■	←	prim_transcript
/note	= primary transcript ENST00000421670 Protein coding				
GTF2H3-214	16,321 .. 8,254,952,668 bp		■	←	prim_transcript
/note	= primary transcript ENST00000618160 Protein coding				
GTF2H3	16,322 .. 8,254,952,667 bp		■	←	gene
/note	= gene ENSG00000111358 Protein coding				

Primer	Length	Binding Sites	Tm	Date Added
✓ PCR Forward /sequence = TAAGTAGTAACTCCGTGGAAGAGC 44% GC / 7730.1 Da	25-mer	122 .. 146	58°C	Sep 28, 2023
✓ Donor Template WT -> SNV /sequence = TTGCTGTAAGCCAGCATGGGGTGGGGGAGGTGATTATGGCTGGGGAAGATGGGCACTCACCCGAAAGCAGCATCTAGCACCACAGTGACAGGGACGTTGA 57% GC / 31,208.3 Da	100-mer	499 .. 598	81°C	Sep 28, 2023
✓ gRNA Protospacer /sequence = TGGTGCTAGATGCTGCTGTC 55% GC / 6155.1 Da	20-mer	517 .. 536	59°C	Sep 28, 2023
✓ Sanger Sequencing Primer /sequence = TCTCCCAACATCCTACAGC 55% GC / 5941.9 Da	20-mer	726 .. 745	58°C	Sep 28, 2023
✓ PCR Reverse /sequence = GCTATAGACACAACCTCCCACTCTC 50% GC / 7201.7 Da	24-mer	742 .. 765	58°C	Sep 28, 2023