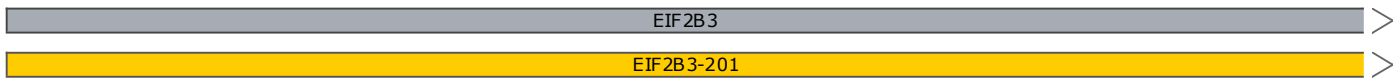


CZK2J00155 EIF2B3_I229M_A11_AB
 1750 bp

5'
3'

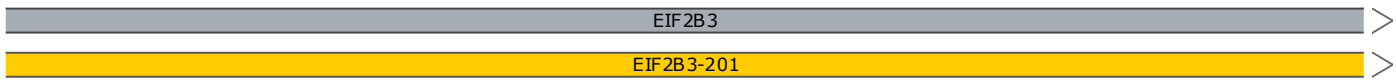
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85



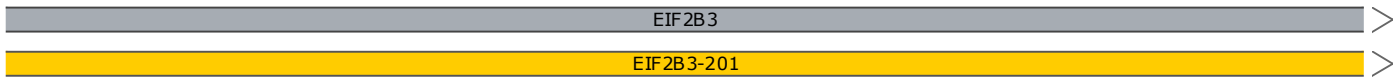
CACCTGTAATCCCAGCTTTCCAGCCACTCAGGAGGCTGAGGTGGGAGAATCACTTGAACCTGGGAGGCCAAAGGTTGCAGTGAGCT
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170



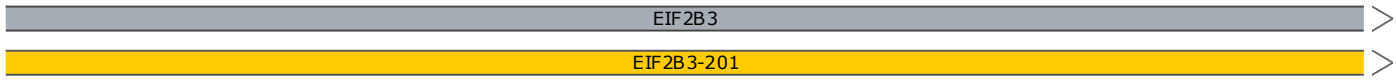
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255



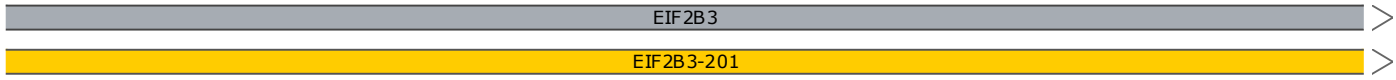
AGTTAGCTCAGCCTATGTCCAGGAATGAGCAAGAGCAATTTGGAGGTTAACAGCAAGATGGAGTTGATTAGGTCAGATTTCTTTCT
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340



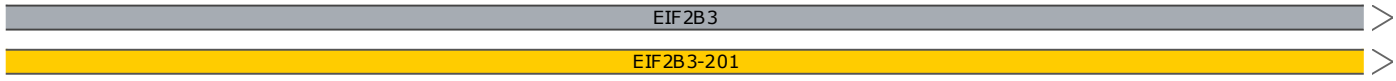
ACTGTCATAATTTTGTCACTGTTATTTTGTCAAAGGTGGTTTACCACAAAAAGCTTTCGTGATCTGGCCCCCTTGCTACCTGA
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425



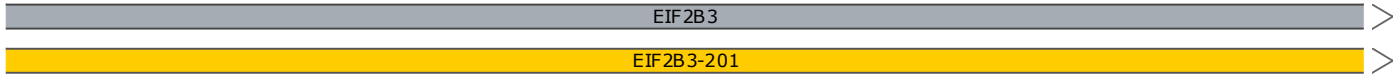
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510



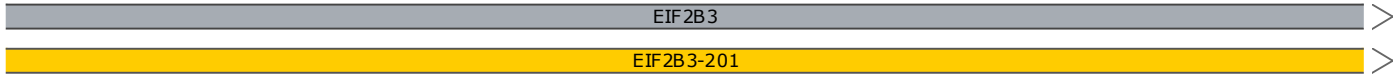
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595



CAGTGTGAGAGAACACTGAAAAACATGTGCTAGTTTCTCATCTCTCTGCTTTCCATTGCTAAGTATAAATAAAAAACATAAATAAA
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680

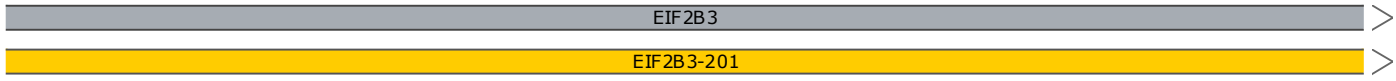


PCR Forward
ACTGAACTAAAGATCAGGTCCCTTC

Sanger Sequencing Primer
CCTGTCTCAGTAC

AAACACACACTGAACTAAAGATCAGGTCCCTTCTTCCCCTAGTACAGATTCCTGATCACTTAGACCCAACATCCTGTCTCAGTAC
TTTGTGTGTGACTTGATTTCTAGTCCAGGGAAGAAGGGGATCATGTCTAAGGACTAGTGAATCTGGGTTGTAGGACAGAGTCATG

765



CCACCAG

CCACCAGGAAGCACTCTGCTTCTCCGAAGTCCAAGTCAATGCCACATTTGATCTCTGACAGTCCCAAGGTGCCATGACAGGAAA
GGTGGTCCTTCGTGAGACGAAGAGGCTTGACGGTTCAGTTACGGTGTAAGTCTAGAGACTGTCAGGGTCCACGGTACTGTCCTTT

850

EIF2B3

EIF2B3-201

Donor Template WT -> SNV

CCAGACAGTCAGGTTTCTCATATTTGGCCATTCTTTCC

GGATTTGGCTTTTCTTGTATGCACAGAGCTTTTGTATCCGGGTATGTTCCAGACAGTCAGGTTTCTCATATTTGGCCATTCTTTCC
CCTAAACCGAAAAGGAACATACGTGTCTCGAAAAGTCCCATACAAGGTCTGTCAGTCCAAAGAGTATAAACCGGTAAGAAAAG

935

EIF2B3

EIF2B3-201

Donor Template WT -> SNV

Donor Template WT -> SNV

TTTCTAGGTCAATAACTTCTATCCGGAGTGAAGTGAATGTCATATTTAGTGAGAAAACAGTTTT

TTTCTAGGTCAATAACTTCTATCCGGAGTGAAGTGAATGTCATATTTAGTGAGAAAACAGTTTTTCTCAGCTTCTCACAACAGGG
AAAGATCCAGTTATTGAAGATAGGCCTCACTTGACTAAGGTATAAATCACTCTTTTGTCAAAGGAGTCAAGGAGTGTGTCC

1020

EIF2B3

EIF2B3-201

220 S I T S I R S E L I P Y L V R 235 K Q F S S A S S Q Q G 245
ENSE00001064945
EIF2B3-201

Donor Template WT -> SNV

PAM gRNA Protospacer

SNV

CTCACTTGACTAAGGTATAA
gRNA Protospacer

ACAAGAAGAAAAAGAGGAGGATCTAAAGAAAAAGGAGCTGAAATCCTTAGGTCAGTTCTTGGGTTGGTTTCAGTAAGAGGGGCAAG
TGTTCTTCTTTTTCTCCTCCTAGATTTCTTTTTCTCGACTTCAGGAATCCAGTCAAGAACCCAACCAAGTCAATTCTCCCCGTTCC

1105

EIF2B3

EIF2B3-201

250 Q E E K E E D L K K K E L K S L 260 G Q F L G W F S K R G K
EIF2B3-201 (in frame with EIF2B3-201)

GGTAGCAGCACCTTTGAAAAGAGTGGTTGGGCAGCTTAGCCCAGCCCAAGATGCCTGACTCAAGGCAGCAGACTATTTCTAGCCT
CCATCGTCGTGGAAACCTTCTCACCAACCCGTCGAATCGGGTCGGGTTCTACGGACTGAGTTCGTCGTCTGATAAAGATCGGA

1190

EIF2B3

EIF2B3-201

G S S T F G K S G W A A (in frame with EIF2B3-201)

ACGAGGCAAGACAGGCTTGCCAACCCACTGAGCTCTGGGTAAGCTTGCTCAGGCAGATTCTGCCACTGTGCTCTCGGCAACAGGC
TGCTCCGTTCTGTCCGAACGGTTGGGTGACTCGAGACCCATTGAAACGAGTCCGTCTAAGACGGTGACACGAGAGCCGTTGTCCG

1275

EIF2B3

EIF2B3-201

TAATCATGCCTCCAGCCCCATTCTCTGATTCATAGCTCTGGTTTGGCTGTGTTCCCTCACTAGACCATTTTGCCTTTAAACTCCAC
ATTAGTACGGAGGTCGGGGTAAGAGACTAAGTATCGAGACCAAACCGACACAAGGAGTGATCTGGTAAAACGGAAATTTGAGGTG

1360

EIF2B3

EIF2B3-201

CTGCCACTTCTTAGTTCCCTGTTCTCTAGGCTCTAGGCAGCCCCGTTCTGATTAAACTCAACCTCTTTTATCAAGGGAAGGAA
GACGGTGAAGAATCAAGGGGACAAGAGATCCGAGATCCGTCGGGGCAAGGACTAATTTGAGTTGGAGAAAATAGTTCCTTCCTT

1445

EIF2B3

EIF2B3-201

GTGAAGAATCAAGGGGACAAGAGAT

PCR Reverse

AGTGAAGGAATGTACAATTGCAGTCCAACCACAGGCCAACCCAGGTGTCTCCGTGCCAGGATCTGAAGATCGGATCTGTCTTGT
TCACTTCCTTACATGTTAACGTCAGGTTGGTGTCCGGTTGGGTCCACAGAGGCACGGTCCTAGACTTCTAGCCTAGACAGAACA

1530

EIF2B3

EIF2B3-201

TGCTGTCATATCCCTAATCCCCGGCCAGTCGTGGACTCATAGTAGATATTCTGAAAAAGTATTTATCAAATGAATACACTGACA
ACGACAGTATAGGGATTAGGGGCCGGGTCAGCACCTGAGTATCATCTATAAGACTTTTTTCATAAATAGTTTACTTATGTGACTGT

1615

EIF2B3

EIF2B3-201

GTACAGCATGATGATTAGGACTGTAGAACTGGGCATCAGACAGTTCTGGATTTGAAATCTGACTGCCTCTTACTAGCATTGTGTC
CATGTGCTACTACTAATCCTGACATCTTGACCCGTAGTCTGTCAAGACCTAAACTTTAGACTGACGGAGAATGATCGTAACACAG

1700

EIF2B3

EIF2B3-201

TTTTTTTTTTTTTATTTTTTTGAGACGGAGTCTCCCTCTGTGCGCCAGGC
AAAAAAAAAAAAAAAAATAAAAAAATCTGCCTCAGAGGGAGACAGCGGGTCCG

3'

1750

5'

EIF2B3

EIF2B3-201

Feature	Location	Size	Start	End	Type
✓ EIF2B3	1 .. 1750	1750 bp	■	→	gene
/note	= gene ENSG00000070785 Protein coding				
✓ EIF2B3-201	1 .. 1750	1750 bp	■	→	prim_transcript
/note	= primary transcript ENST00000360403				
EIF2B3-203	1 .. 1750	1750 bp	■	→	prim_transcript
/note	= primary transcript ENST00000372183				
EIF2B3-204	1 .. 1750	1750 bp	■	→	prim_transcript
/note	= primary transcript ENST00000439363				
EIF2B3-210	1 .. 1750	1750 bp	■	→	prim_transcript
/note	= primary transcript ENST00000620860				
✓ Donor Template WT -> SNV	899 .. 998	100 bp	■	⌊	misc_feature
✓ EIF2B3-201	943 .. 1070	128 bp	■	→	CDS
/codon_start	= 1				
/note	= coding sequence ENSP00000353575				
/translation	= SITSIRSELIPYLVRKQFSSASSQQGQEEKEEDLKKKELKSL 42 amino acids = 4.8 kDa				
EIF2B3-203	943 .. 1070	128 bp	■	→	CDS
/codon_start	= 1				
/note	= coding sequence ENSP00000361257				
/translation	= SITSIRSELIPYLVRKQFSSASSQQGQEEKEEDLKKKELKSL 42 amino acids = 4.8 kDa				
EIF2B3-204	943 .. 1070	128 bp	■	→	CDS
/codon_start	= 1				
/note	= coding sequence ENSP00000396985				
/translation	= Q*LLSGVN*FHI**ENSPQLPHNRDKKKKRRI*RKRS*SP* 42 codons (6 internal stop codons)				
EIF2B3-210	943 .. 1070	128 bp	■	→	CDS
/codon_start	= 1				
/note	= coding sequence ENSP00000483996				
/translation	= SITSIRSELIPYLVRKQFSSASSQQGQEEKEEDLKKKELKSL 42 amino acids = 4.8 kDa				
✓ PAM	958 .. 960	3 bp	■	⌊	misc_feature
✓ gRNA Protospacer	961 .. 980	20 bp	■	⌊	misc_feature
✓ SNV	973 .. 973	1 bp	■	⌊	misc_feature
/note	= WT = T SNV = G				

Primer	Length	Binding Sites	Tm	Date Added
✓ PCR Forward /sequence = ACTGAACTAAAGATCAGGTCCTTC 44% GC / 7610.0 Da	25-mer	689 .. 713 →	58°C	Sep 29, 2023
✓ Sanger Sequencing Primer /sequence = CCTGTCTCAGTACCCACCAG 60% GC / 5997.9 Da	20-mer	753 .. 772 →	59°C	Sep 29, 2023
✓ Donor Template WT -> SNV /sequence = CCAGACAGTCAGGTTTCTCATATTTGGCCATTCTTTCTTTCTAGGTCATAAATTCTATCCGGAGTGAAGTATGCCATATTTAGTGAGAAAACAGTTTT 38% GC / 30,742.1 Da	100-mer	899 .. 998 →	71°C	Sep 29, 2023
✓ gRNA Protospacer /sequence = AATATGGAATCAGTTCACTC 35% GC / 6100.1 Da	20-mer	961 .. 980 ←	49°C	Sep 29, 2023
✓ PCR Reverse /sequence = TAGAGAACAGGGGAAGTAAAGAGTG 44% GC / 7837.2 Da	25-mer	1365 .. 1389 ←	57°C	Sep 29, 2023