

5' AAGGAGTTTTGTGGTCAATTTAGAGATCTTTTAAAATGGGAGATATTAAGCATGTTTGTAAAGCAGAAAGTAATGAATCA 80
 3' TTCCTCAAACACCAGTTAAATCTCTAGAAAATTTACCCTCTATAATTTTCGTACAAACATTCGTCTTTCATTACTTAGT
 TBK1
 TBK1-201

GAACAGAGGGAAACATTGCTGCATTAATAAGTGGGATAATTACAAGAATTGATTTCTGGAATTGGCAAGATGATATGAT 160
 CTTGTCTCCCTTTGTAACGACGTAATTTATTCACCCTATTAATGTTCTTAACTAAAGACCTTAACCGTTCCTACTATACTA
 TBK1
 TBK1-201

PCR Forward
AAAAGTTGGCCATGTATAGGTGCAG

AGGCTCTACAGCACAGATGGAAAAGTTGGCCATGTATAGGTGCAGTTCATTGTGACTGGAAAAGTAGGCCTGGAAAATGG 240
 TCCGAGATGTCGTGTCTACCTTTCAACCGGTACATATCCACGTCAAGGTAACACTGACCTTTCATCCGGACCTTTTACC
 TBK1
 TBK1-201

ACACAGATTGGCCAGGTGCAGTGGCTCATGCCTGTAATCCCAGTACTTTGAAAGGCCAAGGCTCTTAAGGTCCTCAAGGA 320
 TGTGTCTAACCGGTCCACGTACCGAGTACGGACATTAGGGTCATGAAACTTCCGGTCCGAGAATTCCAGGAGTTCCT
 TBK1
 TBK1-201

TCACTTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAACCCTGTCTCTACTAAAAATACAAAAATTAGCTA 400
 AGTGAACCTAGTCTCAAGTTCTGGTCCGACCGGTTGTACCCTTTGGGACAGAGATGATTTTTATGTTTTTAATCGAT
 TBK1
 TBK1-201

GGCATCATGGCAAGCACTTGTAGTCCCAGCTACTCAGGAGGCTGATGCAGGAGAATCACTCGAACCCGGGAAGCAGAGGT 480
 CCGTAGTACCGTTCGTGAACATCAGGGTCGATGAGTCCTCCGACTACGTCTCTTAGTGAGCTTGGGCCCTTCGTCTCCA
 TBK1
 TBK1-201

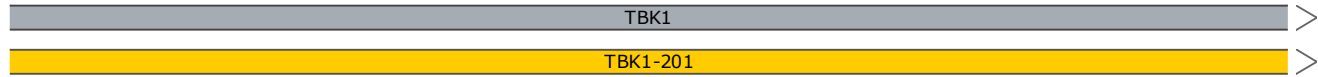
TGCAGTGAGCCGAGATCAAGCCACTGCACTCCACCCCATCTCAAAAAAAGAGAAAAAATAAAACGGACACAGATTCAG 560
 ACGTCACTCGGCTCTAGTTCGGTGACGTGAGGTGGGGTAGAGTTTTTTTTCTTTTTTTATTTTGCCTGTGTCTAAGTC
 TBK1
 TBK1-201

GTAGGTTGTATTTGGTAAAGGGCATAAGGGAGTCTGGTCTGATTCCTTCCATTTCCACATTAATTATGAAGCAGGGTC 640
 CATCCAACATAAACCATTTCCCGTATTCCTCACGACCAGACTAAGGAAGGTAAAGGTGTAATTTAATACTTCGTCCCAG
 TBK1
 TBK1-201

ATCAAACTGAGGATCAAAGGAGGTGGTGGAGGTTTGAGGAGGGAGGGGAAGATGTGAAATAGTCTTTTCAGATTGGGAA 720
 TAGTTTTGACTCCTAGTTTCTCCACCACCTCAAACCTCCTCCCTCCCTTCTACACTTTATCAGAAAAGTCTAACCTT
 TBK1
 TBK1-201

AGTGAAGTTATTAGGAAAACAAAATAGAATTTCTAAGCATTATTGAGTATCCATTTGTTTGTATAATGAAATGGGTCACA
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800



Sanger Sequencing Primer

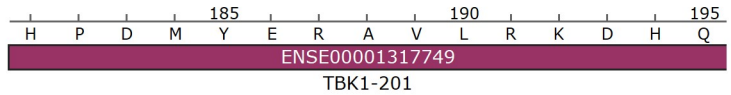
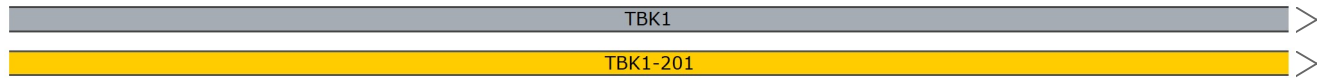
GCACCCTGATATGTATGAGAGAGC

Donor Template WT -> SNV

GATCATCAG

GGTTCATGATTTTTTCTTTTTTTTTTAATCTTAGCACCCCTGATATGTATGAGAGAGCAGTGCCTAAGAAAAGATCATCAG
CCAAGTACTAAAAAAGAAAAAATAATAGAATCGTGGGACTATACATACTCTCTCGTCACGATTCTTTTCTAGTAGTC

880

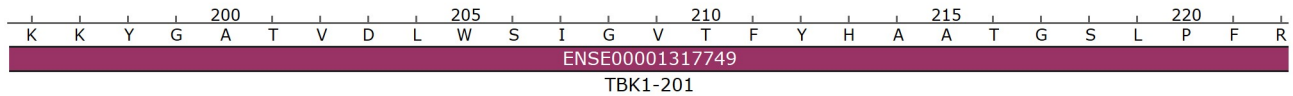


Donor Template WT -> SNV

Donor Template WT -> SNV

AAGAAATATGGAGCAACAGTTGATCTTTGGAGCATTGGGGTAACATTTTACCATGCAGCTACTGGATCAGTCCATTTAG
AAGAAATATGGAGCAACAGTTGATCTTTGGAGCATTGGGGTAACATTTTACCATGCAGCTACTGGATCAGTCCATTTAG
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960



Donor Template WT -> SNV



SNV

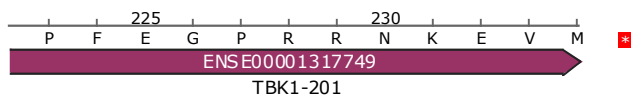


Donor Template WT -> SNV

ACCCTTTGAAG

ACCCTTTGAAGGGCCTCGTAGGAATAAAGAAGTGATGTAAGTGGTTTCCCGATCTAAAATCAGAGAAGCATTAAAAAAT
TGGGAAACTTCCGGAGCATCCTATTCTTCACTACATTCACCAAAGGGCTAGATTTAGTCTCTTCGTAAATTTTTTA

1040

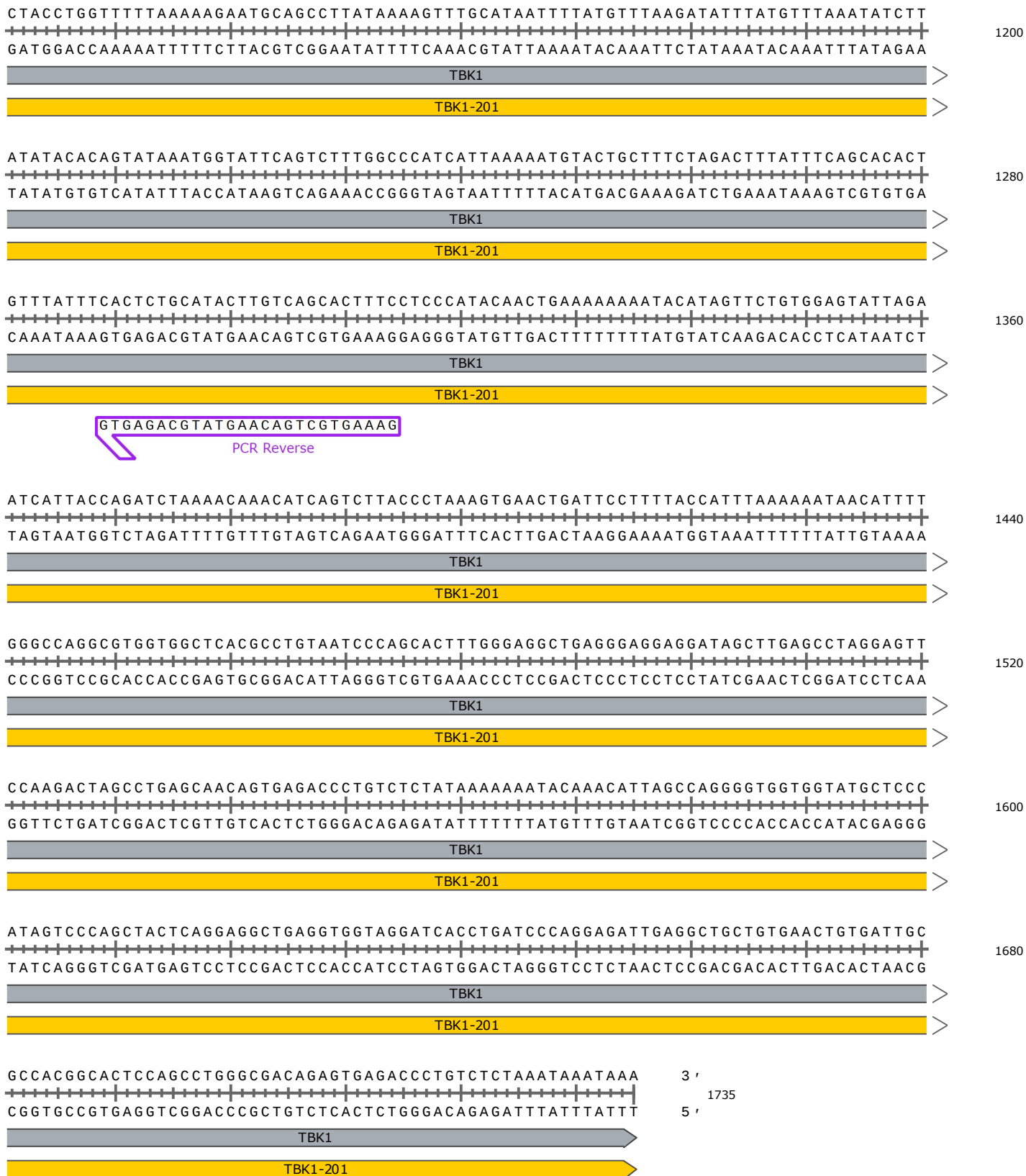


Donor Template WT -> SNV

GATTTCTGTCTTGGTTCATCTTATTGTTAGTGGTTATGCTAATAAAAATTGATTTAACAATCATTCTGATATTTAAG
CTAAAGACAGAACCAAGTAGAATAACAATCACCAAATACGATTATTTTAACTAAATTGTTAGTAAAGACTATAAAATTC

1120












Feature	Location	Size		Type
✓ TBK1	1 .. 1735	1735 bp	■ →	gene
/note = gene ENSG00000183735 Protein coding				
✓ TBK1-201	1 .. 1735	1735 bp	■ →	prim_transcript
/note = primary transcript ENST00000331710				
TBK1-209	1 .. 1735	1735 bp	■ →	prim_transcript
/note = primary transcript ENST00000650708 Nonsense mediated decay				
TBK1-210	1 .. 1735	1735 bp	■ →	prim_transcript
/note = primary transcript ENST00000650762				
TBK1-211	1 .. 1735	1735 bp	■ →	prim_transcript
/note = primary transcript ENST00000650786 Nonsense mediated decay				
TBK1-212	1 .. 1735	1735 bp	■ →	prim_transcript
/note = primary transcript ENST00000650790				
TBK1-213	1 .. 1735	1735 bp	■ →	prim_transcript
/note = primary transcript ENST00000650997 Nonsense mediated decay				
TBK1-214	1 .. 1735	1735 bp	■ →	prim_transcript
/note = primary transcript ENST00000651014				
TBK1-215	1 .. 1735	1735 bp	■ →	prim_transcript
/note = primary transcript ENST00000651262 Nonsense mediated decay				
TBK1-216	1 .. 1735	1735 bp	■ →	prim_transcript
/note = primary transcript ENST00000651878 Nonsense mediated decay				
TBK1-217	1 .. 1735	1735 bp	■ →	prim_transcript
/note = primary transcript ENST00000651889 Retained intron				
TBK1-218	1 .. 1735	1735 bp	■ →	prim_transcript
/note = primary transcript ENST00000651947 protein_coding_CDS_not_defined				
TBK1-219	1 .. 1735	1735 bp	■ →	prim_transcript
/note = primary transcript ENST00000652389 Nonsense mediated decay				
TBK1-220	1 .. 1735	1735 bp	■ →	prim_transcript
/note = primary transcript ENST00000652537 Nonsense mediated decay				
TBK1-221	1 .. 1735	1735 bp	■ →	prim_transcript
/note = primary transcript ENST00000652657				
TBK1-226	1 .. 1735	1735 bp	■ →	prim_transcript
/note = primary transcript ENST00000676551 Retained intron				
TBK1-229	1 .. 1735	1735 bp	■ →	prim_transcript
/note = primary transcript ENST00000676654 Retained intron				
TBK1-230	1 .. 1735	1735 bp	■ →	prim_transcript
/note = primary transcript ENST00000676684 Retained intron				
TBK1-232	1 .. 1735	1735 bp	■ →	prim_transcript
/note = primary transcript ENST00000676809 Nonsense mediated decay				
TBK1-234	1 .. 1735	1735 bp	■ →	prim_transcript
/note = primary transcript ENST00000676912				

Feature	Location	Size	▣	→	Type
TBK1-235	1 .. 1735	1735 bp	▣	→	prim_transcript
/note = primary transcript ENST00000676930					
TBK1-242	1 .. 1735	1735 bp	▣	→	prim_transcript
/note = primary transcript ENST00000677499 Nonsense mediated decay					
TBK1-244	1 .. 1735	1735 bp	▣	→	prim_transcript
/note = primary transcript ENST00000677549 Retained intron					
TBK1-245	1 .. 1735	1735 bp	▣	→	prim_transcript
/note = primary transcript ENST00000677632					
TBK1-246	1 .. 1735	1735 bp	▣	→	prim_transcript
/note = primary transcript ENST00000677641					
TBK1-248	1 .. 1735	1735 bp	▣	→	prim_transcript
/note = primary transcript ENST00000677686 Retained intron					
TBK1-251	1 .. 1735	1735 bp	▣	→	prim_transcript
/note = primary transcript ENST00000677831 Nonsense mediated decay					
TBK1-253	1 .. 1735	1735 bp	▣	→	prim_transcript
/note = primary transcript ENST00000677973 Nonsense mediated decay					
TBK1-256	1 .. 1735	1735 bp	▣	→	prim_transcript
/note = primary transcript ENST00000678180					
TBK1-257	1 .. 1735	1735 bp	▣	→	prim_transcript
/note = primary transcript ENST00000678197 Retained intron					
TBK1-237	1 .. 996	996 bp	▣	→	prim_transcript
/note = primary transcript ENST00000677016 Nonsense mediated decay					
TBK1-238	1 .. 996	996 bp	▣	→	prim_transcript
/note = primary transcript ENST00000677112 Nonsense mediated decay					
TBK1-250	1 .. 996	996 bp	▣	→	prim_transcript
/note = primary transcript ENST00000677759 Nonsense mediated decay					
TBK1-264	1 .. 996	996 bp	▣	→	prim_transcript
/note = primary transcript ENST00000678738 Nonsense mediated decay					
TBK1-265	1 .. 996	996 bp	▣	→	prim_transcript
/note = primary transcript ENST00000678808 Nonsense mediated decay					
TBK1-271	1 .. 996	996 bp	▣	→	prim_transcript
/note = primary transcript ENST00000679302 Nonsense mediated decay					
TBK1-239	531 .. 996	466 bp	▣	→	prim_transcript
/note = primary transcript ENST00000677242 protein_coding_CDS_not_defined					
TBK1-263	836 .. 1735	900 bp	▣	→	prim_transcript
/note = primary transcript ENST00000678718 Nonsense mediated decay					
✓ TBK1-201	836 .. 996	161 bp	▣	→	CDS
/note = coding sequence ENSP00000329967					
/translation = HPDMYERAVLRKDHQKKYGATVDLWSIGVTFYHAATGSLPFRPFEGPRRKEV 53 amino acids = 6.2 kDa					

Feature	Location	Size	Start	End	Type
TBK1-210	836 .. 996	161 bp	■	→	CDS
/note	= coding sequence ENSP00000498758				
/translation	= HPDMYERAVLRKDHQKKYGATVDLWSIGVTFYHAATGSLPFRPFEGPRRNKEV 53 amino acids = 6.2 kDa				
TBK1-212	836 .. 996	161 bp	■	→	CDS
/note	= coding sequence ENSP00000498995				
/translation	= HPDMYERAVLRKDHQKKYGATVDLWSIGVTFYHAATGSLPFRPFEGPRRNKEV 53 amino acids = 6.2 kDa				
TBK1-214	836 .. 996	161 bp	■	→	CDS
/note	= coding sequence ENSP00000498885				
/translation	= HPDMYERAVLRKDHQKKYGATVDLWSIGVTFYHAATGSLPFRPFEGPRRNKEV 53 amino acids = 6.2 kDa				
TBK1-221	836 .. 996	161 bp	■	→	CDS
/note	= coding sequence ENSP00000498887				
/translation	= HPDMYERAVLRKDHQKKYGATVDLWSIGVTFYHAATGSLPFRPFEGPRRNKEV 53 amino acids = 6.2 kDa				
TBK1-234	836 .. 996	161 bp	■	→	CDS
/note	= coding sequence ENSP00000503567				
/translation	= HPDMYERAVLRKDHQKKYGATVDLWSIGVTFYHAATGSLPFRPFEGPRRNKEV 53 amino acids = 6.2 kDa				
TBK1-235	836 .. 996	161 bp	■	→	CDS
/note	= coding sequence ENSP00000502899				
/translation	= HPDMYERAVLRKDHQKKYGATVDLWSIGVTFYHAATGSLPFRPFEGPRRNKEV 53 amino acids = 6.2 kDa				
TBK1-245	836 .. 996	161 bp	■	→	CDS
/note	= coding sequence ENSP00000504586				
/translation	= HPDMYERAVLRKDHQKKYGATVDLWSIGVTFYHAATGSLPFRPFEGPRRNKEV 53 amino acids = 6.2 kDa				
TBK1-246	836 .. 996	161 bp	■	→	CDS
/note	= coding sequence ENSP00000504637				
/translation	= HPDMYERAVLRKDHQKKYGATVDLWSIGVTFYHAATGSLPFRPFEGPRRNKEV 53 amino acids = 6.2 kDa				
TBK1-256	836 .. 996	161 bp	■	→	CDS
/note	= coding sequence ENSP00000504132				
/translation	= HPDMYERAVLRKDHQKKYGATVDLWSIGVTFYHAATGSLPFRPFEGPRRNKEV 53 amino acids = 6.2 kDa				
✓ Donor Template WT -> SNV	872 .. 971	100 bp	■		misc_feature
✓ PAM	931 .. 933	3 bp	■		misc_feature
✓ gRNA Protospacer	934 .. 953	20 bp	■		misc_feature
✓ SNV	944 .. 944	1 bp	■		misc_feature
/note	= SNV = A REV = G				
	1736 .. 6950	5215 bp	■	→	gene
/note	= gene ENSG00000288665 lncRNA				
	1736 .. 6950	5215 bp	■	→	prim_transcript
/note	= primary transcript ENST00000677093 lncRNA				

Primer	Length		Binding Sites		Tm	Date Added
✓ PCR Forward	25-mer		181 .. 205		60°C	Jun 14, 2023
/sequence = AAAAGTTGGCCATGTATAGGTGCAG 44% GC / 7770.1 Da						
✓ Sanger Sequencing Primer	24-mer		835 .. 858		58°C	Jun 14, 2023
/sequence = GCACCCTGATATGTATGAGAGAGC 50% GC / 7401.9 Da						
✓ Donor Template WT -> SNV	100-mer		872 .. 971		73°C	Jun 14, 2023
/sequence = GATCATCAGAAGAAATATGGAGCAACAGTTGATCTTTGGAGCATTGGGGTAACATTTTACCATGCAGCTACTGGATCACTGCCATTTAGACCCTTTGAAG 42% GC / 30,918.2 Da						
✓ gRNA Protospacer	20-mer		934 .. 953		53°C	Jun 14, 2023
/sequence = GCAGTGATCTAGTAGCTGCA 50% GC / 6157.1 Da						
✓ PCR Reverse	26-mer		1289 .. 1314		60°C	Jun 14, 2023
/sequence = GAAAGTGCTGACAAGTATGCAGAGTG 46% GC / 8108.4 Da						