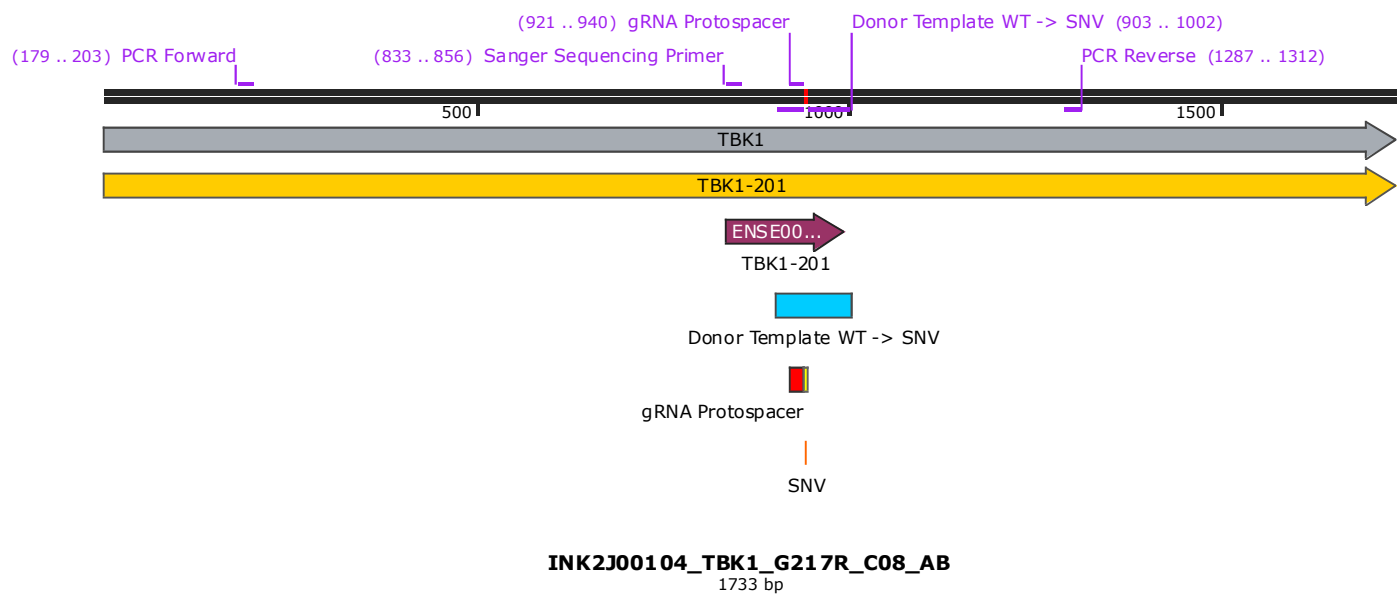


TANK binding kinase 1 [Source:HGNC Symbol;Acc:HGNC:11584]





Sanger Sequencing Primer

GCACCCTGATATGTATGA

TATCCATTTGTTTGTATAATGAAATGGGTCACAGTTTCATGATTTTTTTCTTTTTTTTTTAACTTTAGCACCCCTGATATGTATGA
ATAGGTAACAAACATATTACTTTACCCAGTGTCCAAGTACTAAAAAAGAAAAAAAAAATTAGAATCGTGGGACTATACATACT

850

TBK1

TBK1-201

H P D M Y E
ENSE00001317749

TBK1-201

Sanger Sequencing Primer

GAGAGC

gRNA Protospacer

ACATTTTACCATGCA

GAGAGCAGTGCTAAGAAAAGATCATCAGAAGAAATATGGAGCAACAGTTGATCTTTGGAGCATTGGGGTAACATTTTACCATGCA
CTCTCGTCACGATTCTTTTCTAGTAGTCTTCTTTATACCTCGTTGTCAACTAGAAACCTCGTAACCCCATTTGTAATAATGGTACGT

935

TBK1

TBK1-201

R A V L R K D H Q K K Y G A T V D L W S I G V T F Y H A

ENSE00001317749

TBK1-201

Donor Template WT -> SNV

gRNA Protospacer

GAAACCTCGTAACCCCATTTGTAATAATGGTACGT

Donor Template WT -> SNV

gRNA Protospacer

GCTAC

GCTACTGGATCACTGCCATTTAGACCCTTTGAAGGGCCTCGTAGGAATAAAGAAGTGATGTAAGTGGTTTTCCCGATCTAAAATCA
CGATGACCTAGTGACGGTAAATCTGGGAAACTTCCCGGAGCATCCTTATTTCTTCACTACATTCACCAAAGGGCTAGATTTTGT

1020

TBK1

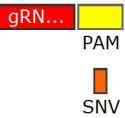
TBK1-201

215 220 225 230
A T G S L P F R P F E G P R R N K E V M

ENSE00001317749

TBK1-201

Donor Template WT -> SNV



CGATGACCTAGTGACGGTAAATCTGGGAAACTTCCCGGAGCATCCTTATTTCTTCACTACATTCACC

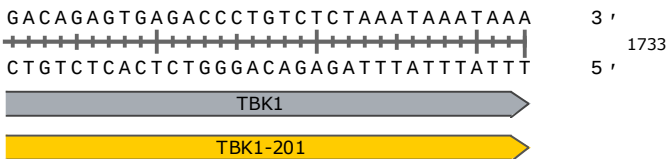
Donor Template WT -> SNV

GAGAAGCATTTAAAAAATGATTTCTGTCTTGGTTTCATCTTATTGTTAGTGGTTTATGCTAATAAAAAATTGATTTAACAATCATT
CTCTTCGTAAATTTTTTACTAAAGACAGAACCAAGTAGAATAACAATCACCAAATACGATTATTTTTAACTAAATTGTTAGTAA

1105

TBK1

TBK1-201



Feature	Location	Size	Start	End	Type
✓ TBK1	1 .. 1733	1733 bp	■	➔	gene
/note = gene ENSG00000183735 Protein coding					
✓ TBK1-201	1 .. 1733	1733 bp	■	➔	prim_transcript
/note = primary transcript ENST00000331710					
TBK1-209	1 .. 1733	1733 bp	■	➔	prim_transcript
/note = primary transcript ENST00000650708 Nonsense mediated decay					
TBK1-210	1 .. 1733	1733 bp	■	➔	prim_transcript
/note = primary transcript ENST00000650762					
TBK1-211	1 .. 1733	1733 bp	■	➔	prim_transcript
/note = primary transcript ENST00000650786 Nonsense mediated decay					
TBK1-212	1 .. 1733	1733 bp	■	➔	prim_transcript
/note = primary transcript ENST00000650790					
TBK1-213	1 .. 1733	1733 bp	■	➔	prim_transcript
/note = primary transcript ENST00000650997 Nonsense mediated decay					
TBK1-214	1 .. 1733	1733 bp	■	➔	prim_transcript
/note = primary transcript ENST00000651014					
TBK1-215	1 .. 1733	1733 bp	■	➔	prim_transcript
/note = primary transcript ENST00000651262 Nonsense mediated decay					
TBK1-216	1 .. 1733	1733 bp	■	➔	prim_transcript
/note = primary transcript ENST00000651878 Nonsense mediated decay					
TBK1-217	1 .. 1733	1733 bp	■	➔	prim_transcript
/note = primary transcript ENST00000651889 Retained intron					
TBK1-218	1 .. 1733	1733 bp	■	➔	prim_transcript
/note = primary transcript ENST00000651947 protein_coding_CDS_not_defined					
TBK1-219	1 .. 1733	1733 bp	■	➔	prim_transcript
/note = primary transcript ENST00000652389 Nonsense mediated decay					
TBK1-220	1 .. 1733	1733 bp	■	➔	prim_transcript
/note = primary transcript ENST00000652537 Nonsense mediated decay					
TBK1-221	1 .. 1733	1733 bp	■	➔	prim_transcript
/note = primary transcript ENST00000652657					
TBK1-226	1 .. 1733	1733 bp	■	➔	prim_transcript
/note = primary transcript ENST00000676551 Retained intron					
TBK1-229	1 .. 1733	1733 bp	■	➔	prim_transcript
/note = primary transcript ENST00000676654 Retained intron					
TBK1-230	1 .. 1733	1733 bp	■	➔	prim_transcript
/note = primary transcript ENST00000676684 Retained intron					
TBK1-232	1 .. 1733	1733 bp	■	➔	prim_transcript
/note = primary transcript ENST00000676809 Nonsense mediated decay					
TBK1-234	1 .. 1733	1733 bp	■	➔	prim_transcript
/note = primary transcript ENST00000676912					

Feature	Location	Size	Start	End	Type
TBK1-235	1 .. 1733	1733 bp	■	→	prim_transcript
/note = primary transcript ENST00000676930					
TBK1-242	1 .. 1733	1733 bp	■	→	prim_transcript
/note = primary transcript ENST00000677499 Nonsense mediated decay					
TBK1-244	1 .. 1733	1733 bp	■	→	prim_transcript
/note = primary transcript ENST00000677549 Retained intron					
TBK1-245	1 .. 1733	1733 bp	■	→	prim_transcript
/note = primary transcript ENST00000677632					
TBK1-246	1 .. 1733	1733 bp	■	→	prim_transcript
/note = primary transcript ENST00000677641					
TBK1-248	1 .. 1733	1733 bp	■	→	prim_transcript
/note = primary transcript ENST00000677686 Retained intron					
TBK1-251	1 .. 1733	1733 bp	■	→	prim_transcript
/note = primary transcript ENST00000677831 Nonsense mediated decay					
TBK1-253	1 .. 1733	1733 bp	■	→	prim_transcript
/note = primary transcript ENST00000677973 Nonsense mediated decay					
TBK1-256	1 .. 1733	1733 bp	■	→	prim_transcript
/note = primary transcript ENST00000678180					
TBK1-257	1 .. 1733	1733 bp	■	→	prim_transcript
/note = primary transcript ENST00000678197 Retained intron					
TBK1-237	1 .. 994	994 bp	■	→	prim_transcript
/note = primary transcript ENST00000677016 Nonsense mediated decay					
TBK1-238	1 .. 994	994 bp	■	→	prim_transcript
/note = primary transcript ENST00000677112 Nonsense mediated decay					
TBK1-250	1 .. 994	994 bp	■	→	prim_transcript
/note = primary transcript ENST00000677759 Nonsense mediated decay					
TBK1-264	1 .. 994	994 bp	■	→	prim_transcript
/note = primary transcript ENST00000678738 Nonsense mediated decay					
TBK1-265	1 .. 994	994 bp	■	→	prim_transcript
/note = primary transcript ENST00000678808 Nonsense mediated decay					
TBK1-271	1 .. 994	994 bp	■	→	prim_transcript
/note = primary transcript ENST00000679302 Nonsense mediated decay					
TBK1-239	529 .. 994	466 bp	■	→	prim_transcript
/note = primary transcript ENST00000677242 protein_coding_CDS_not_defined					
TBK1-263	834 .. 1733	900 bp	■	→	prim_transcript
/note = primary transcript ENST00000678718 Nonsense mediated decay					
✓ TBK1-201	834 .. 994	161 bp	■	→	CDS
/note = coding sequence ENSP00000329967					
/translation = HPDMYERAVLRKDHQKKYGATVDLWSIGVTFYHAATGSLPFRPFEGPRRKEV 53 amino acids = 6.2 kDa					

Feature	Location	Size	Start	End	Type
TBK1-210	834 .. 994	161 bp	■	→	CDS
/note	= coding sequence ENSP00000498758				
/translation	= HPDMYERAVLRKDHQKKYGATVDLWSIGVTFYHAATGSLPFRPFEGPRRNKEV 53 amino acids = 6.2 kDa				
TBK1-212	834 .. 994	161 bp	■	→	CDS
/note	= coding sequence ENSP00000498995				
/translation	= HPDMYERAVLRKDHQKKYGATVDLWSIGVTFYHAATGSLPFRPFEGPRRNKEV 53 amino acids = 6.2 kDa				
TBK1-214	834 .. 994	161 bp	■	→	CDS
/note	= coding sequence ENSP00000498885				
/translation	= HPDMYERAVLRKDHQKKYGATVDLWSIGVTFYHAATGSLPFRPFEGPRRNKEV 53 amino acids = 6.2 kDa				
TBK1-221	834 .. 994	161 bp	■	→	CDS
/note	= coding sequence ENSP00000498887				
/translation	= HPDMYERAVLRKDHQKKYGATVDLWSIGVTFYHAATGSLPFRPFEGPRRNKEV 53 amino acids = 6.2 kDa				
TBK1-234	834 .. 994	161 bp	■	→	CDS
/note	= coding sequence ENSP00000503567				
/translation	= HPDMYERAVLRKDHQKKYGATVDLWSIGVTFYHAATGSLPFRPFEGPRRNKEV 53 amino acids = 6.2 kDa				
TBK1-235	834 .. 994	161 bp	■	→	CDS
/note	= coding sequence ENSP00000502899				
/translation	= HPDMYERAVLRKDHQKKYGATVDLWSIGVTFYHAATGSLPFRPFEGPRRNKEV 53 amino acids = 6.2 kDa				
TBK1-245	834 .. 994	161 bp	■	→	CDS
/note	= coding sequence ENSP00000504586				
/translation	= HPDMYERAVLRKDHQKKYGATVDLWSIGVTFYHAATGSLPFRPFEGPRRNKEV 53 amino acids = 6.2 kDa				
TBK1-246	834 .. 994	161 bp	■	→	CDS
/note	= coding sequence ENSP00000504637				
/translation	= HPDMYERAVLRKDHQKKYGATVDLWSIGVTFYHAATGSLPFRPFEGPRRNKEV 53 amino acids = 6.2 kDa				
TBK1-256	834 .. 994	161 bp	■	→	CDS
/note	= coding sequence ENSP00000504132				
/translation	= HPDMYERAVLRKDHQKKYGATVDLWSIGVTFYHAATGSLPFRPFEGPRRNKEV 53 amino acids = 6.2 kDa				
✓ Donor Template WT -> SNV	903 .. 1002	100 bp	■		misc_feature
✓ gRNA Protospacer	921 .. 940	20 bp	■		misc_feature
✓ PAM	941 .. 943	3 bp	■		misc_feature
✓ SNV	942 .. 942	1 bp	■		misc_feature
/note	= WT = G SNV = A				
	1734 .. 6948	5215 bp	■	→	gene
/note	= gene ENSG00000288665 lncRNA				
	1734 .. 6948	5215 bp	■	→	prim_transcript
/note	= primary transcript ENST00000677093 lncRNA				

Primer	Length	Binding Sites	Tm	Date Added
✓ PCR Forward /sequence = AAAAGTTGGCCATGTATAGGTGCAG 44% GC / 7770.1 Da	25-mer	179 .. 203	60°C	Jun 14, 2023
✓ Sanger Sequencing Primer /sequence = GCACCCTGATATGTATGAGAGAGC 50% GC / 7401.9 Da	24-mer	833 .. 856	58°C	Jun 14, 2023
✓ Donor Template WT -> SNV /sequence = CCACTTACATCACTTCTTTATTCTACGAGGCCCTTCAAAGGGTCTAAATGGCAGTGATCTAGTAGCTGCATGGTAAAATGTTACCCCAATGCTCCAAG 44% GC / 30,670.0 Da	100-mer	903 .. 1002	74°C	Jun 14, 2023
✓ gRNA Protospacer /sequence = ACATTTTACCATGCAGCTAC 40% GC / 6036.0 Da	20-mer	921 .. 940	53°C	Jun 14, 2023
✓ PCR Reverse /sequence = GAAAGTGCTGACAAGTATGCAGAGTG 46% GC / 8108.4 Da	26-mer	1287 .. 1312	60°C	Jun 14, 2023