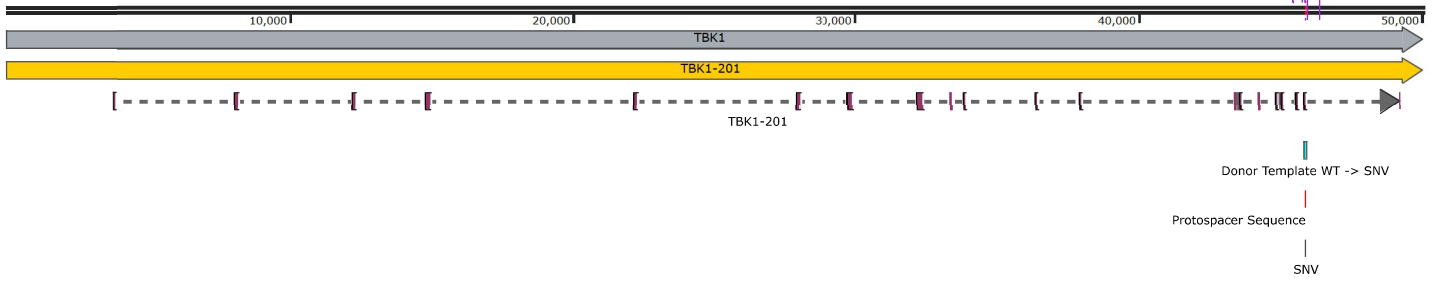


(45,888 .. 45,907) gRNA Protospacer
(45,778 .. 45,797) Sanger Sequencing Primer
(45,461 .. 45,485) PCR Forward
Donor Template (45,870 .. 45,969)
PCR Reverse (46,391 .. 46,415)



JIPSC1122_SnappeneDNA_INK2J00022_TBK1_E696K_SNVSNV
50,025 bp

Feature	Location	Size		Type
TBK1	1 .. 50,025	50,025 bp	■ →	gene
/note	= gene ENSG00000183735			Protein coding
TBK1-230	1 .. 50,011	50,011 bp	■ →	prim_transcript
/note	= primary transcript ENST00000676684			Retained intron
TBK1-242	1 .. 49,977	49,977 bp	■ →	prim_transcript
/note	= primary transcript ENST00000677499			Nonsense mediated decay
TBK1-246	1 .. 49,977	49,977 bp	■ →	prim_transcript
/note	= primary transcript ENST00000677641			
TBK1-229	1 .. 49,964	49,964 bp	■ →	prim_transcript
/note	= primary transcript ENST00000676654			Retained intron
TBK1-220	3 .. 49,959	49,957 bp	■ →	prim_transcript
/note	= primary transcript ENST00000652537			Nonsense mediated decay
TBK1-232	5 .. 50,025	50,021 bp	■ →	prim_transcript
/note	= primary transcript ENST00000676809			Nonsense mediated decay
TBK1-212	12 .. 49,966	49,955 bp	■ →	prim_transcript
/note	= primary transcript ENST00000650790			
TBK1-221	23 .. 50,011	49,989 bp	■ →	prim_transcript
/note	= primary transcript ENST00000652657			
TBK1-234	25 .. 50,011	49,987 bp	■ →	prim_transcript
/note	= primary transcript ENST00000676912			
TBK1-248	27 .. 49,977	49,951 bp	■ →	prim_transcript
/note	= primary transcript ENST00000677686			Retained intron
TBK1-219	28 .. 41,948	41,921 bp	■ →	prim_transcript
/note	= primary transcript ENST00000652389			Nonsense mediated decay
TBK1-201	31 .. 50,025	49,995 bp	■ →	prim_transcript
/note	= primary transcript ENST00000331710			
TBK1-215	31 .. 49,982	49,952 bp	■ →	prim_transcript
/note	= primary transcript ENST00000651262			Nonsense mediated decay
TBK1-245	31 .. 49,977	49,947 bp	■ →	prim_transcript
/note	= primary transcript ENST00000677632			
TBK1-213	31 .. 49,967	49,937 bp	■ →	prim_transcript
/note	= primary transcript ENST00000650997			Nonsense mediated decay
TBK1-226	31 .. 38,741	38,711 bp	■ →	prim_transcript
/note	= primary transcript ENST00000676551			Retained intron
TBK1-260	31 .. 13,178	13,148 bp	■ →	prim_transcript
/note	= primary transcript ENST00000678430			Retained intron
TBK1-243	31 .. 8240	8210 bp	■ →	prim_transcript
/note	= primary transcript ENST00000677545			
TBK1-256	34 .. 49,977	49,944 bp	■ →	prim_transcript
/note	= primary transcript ENST00000678180			
TBK1-270	40 .. 4766	4727 bp	■ →	prim_transcript
/note	= primary transcript ENST00000679065			Retained intron
TBK1-235	42 .. 50,011	49,970 bp	■ →	prim_transcript
/note	= primary transcript ENST00000676930			
TBK1-210	42 .. 49,652	49,611 bp	■ →	prim_transcript
/note	= primary transcript ENST00000650762			
TBK1-218	42 .. 38,287	38,246 bp	■ →	prim_transcript
/note	= primary transcript ENST00000651947			
TBK1-211	49 .. 49,997	49,949 bp	■ →	prim_transcript
/note	= primary transcript ENST00000650786			Nonsense mediated decay
TBK1-251	51 .. 49,977	49,927 bp	■ →	prim_transcript
/note	= primary transcript ENST00000677831			Nonsense mediated decay
TBK1-214	53 .. 49,960	49,908 bp	■ →	prim_transcript
/note	= primary transcript ENST00000651014			
TBK1-244	68 .. 33,146	33,079 bp	■ →	prim_transcript
/note	= primary transcript ENST00000677549			Retained intron
TBK1-203	101 .. 12,326	12,226 bp	■ →	prim_transcript
/note	= primary transcript ENST00000538890			
TBK1-216	251 .. 49,959	49,709 bp	■ →	prim_transcript
/note	= primary transcript ENST00000651878			Nonsense mediated decay

Feature	Location	Size	Type
TBK1-205	362 .. 12,310	11,949 bp	prim_transcript
/note	= primary transcript ENST00000540417		
TBK1-204	386 .. 12,317	11,932 bp	prim_transcript
/note	= primary transcript ENST00000539810		
TBK1-259	386 .. 3868	3483 bp	prim_transcript
/note	= primary transcript ENST00000678368		
	498 .. 812	315 bp	gene
/note	= gene ENSG00000277895 lncRNA		
	498 .. 812	315 bp	prim_transcript
/note	= primary transcript ENST00000610945 lncRNA		
TBK1-222	3751 .. 12,374	8624 bp	prim_transcript
/note	= primary transcript ENST00000676469		
TBK1-201	3782 .. 49,292	45,511 bp	CDS
▶ 20 segments = 2190 bp			
/note	= coding sequence ENSP00000329967		
/translation	= MQSTSNHLWLLSDILGQ GATANVFRGRHK,KTGDLFAIKVFNNISFLRPVDVQMRFEV LKLNHKNIVKLFAIEEE,TTTRHKVLIMEFCPCGSLYTVLEEPSNAYGLPESEFLIVLRDV,VGGMNLRENGIVHRDIKPGNIMR VIGEDGQSVYKLTDFGAARELEDDEQFVSLYGT E EYL,HPDMYERAVLRKDHQKKYGATVDLWSIGVTFYHAATGSLPFRPFEGPRRNKEVM,,YKIITGKPSGAISGVQKAENGPIDWSGDMPVSCSLSR,,GLQVLLTPVLANI LEADQEKCWGDFQFAAETSDILHRMVIHVFSLQ QMTAHKIYIHSYNT,,ATIFHELIVYKQTKIISNQ ELIYEGRRLLVLEPGRLAQHFPKTT EENPIFVVSREPLNTIGLIEK,,ISLPKVHPRYDLGDGASMAK,,AITGVV CYACRI ASTLLLYQELMRKGI RWLI,,ELIKDDYNETVHKTEVVITLDFCIRNIEKTVKV,,YEKLMKINLEAAELGEISDIHTKLLR,,LSSSQGTIETSLQDIDSR LSPGGSLADAWAHQEGTHPKDRN,,VEKLQVLLNCMTEIYYQFKDKA ER,,RLAYNEEQIHKFDK,,QKLYYHATKAMTHFTDECVKYEAFLNKSEEWIR,,KMLHLRQQLLSLTNQCFDIEEEVSKYQ EYTN E,,LQETLPQKMFTA SSGIKHTMTPIYSSNTLVEMTLG,,MKKLKEEMEGVV KELAENNHIL		
TBK1-212	3782 .. 49,292	45,511 bp	CDS
▶ 20 segments = 2190 bp			
/note	= coding sequence ENSP00000498995		
/translation	= MQSTSNHLWLLSDILGQ GATANVFRGRHK,KTGDLFAIKVFNNISFLRPVDVQMRFEV LKLNHKNIVKLFAIEEE,TTTRHKVLIMEFCPCGSLYTVLEEPSNAYGLPESEFLIVLRDV,VGGMNLRENGIVHRDIKPGNIMR VIGEDGQSVYKLTDFGAARELEDDEQFVSLYGT E EYL,HPDMYERAVLRKDHQKKYGATVDLWSIGVTFYHAATGSLPFRPFEGPRRNKEVM,,YKIITGKPSGAISGVQKAENGPIDWSGDMPVSCSLSR,,GLQVLLTPVLANI LEADQEKCWGDFQFAAETSDILHRMVIHVFSLQ QMTAHKIYIHSYNT,,ATIFHELIVYKQTKIISNQ ELIYEGRRLLVLEPGRLAQHFPKTT EENPIFVVSREPLNTIGLIEK,,ISLPKVHPRYDLGDGASMAK,,AITGVV CYACRI ASTLLLYQELMRKGI RWLI,,ELIKDDYNETVHKTEVVITLDFCIRNIEKTVKV,,YEKLMKINLEAAELGEISDIHTKLLR,,LSSSQGTIETSLQDIDSR LSPGGSLADAWAHQEGTHPKDRN,,VEKLQVLLNCMTEIYYQFKDKA ER,,RLAYNEEQIHKFDK,,QKLYYHATKAMTHFTDECVKYEAFLNKSEEWIR,,KMLHLRQQLLSLTNQCFDIEEEVSKYQ EYTN E,,LQETLPQKMFTA SSGIKHTMTPIYSSNTLVEMTLG,,MKKLKEEMEGVV KELAENNHIL		
TBK1-221	3782 .. 49,292	45,511 bp	CDS
▶ 19 segments = 2118 bp			
/note	= coding sequence ENSP00000498887		
/translation	= MQSTSNHLWLLSDILGQ GATANVFRGRHK,KTGDLFAIKVFNNISFLRPVDVQMRFEV LKLNHKNIVKLFAIEEE,TTTRHKVLIMEFCPCGSLYTVLEEPSNAYGLPESEFLIVLRDV,VGGMNLRENGIVHRDIKPGNIMR VIGEDGQSVYKLTDFGAARELEDDEQFVSLYGT E EYL,HPDMYERAVLRKDHQKKYGATVDLWSIGVTFYHAATGSLPFRPFEGPRRNKEVM,,YKIITGKPSGAISGVQKAENGPIDWSGDMPVSCSLSR,,GLQVLLTPVLANI LEADQEKCWGDFQFAAETSDILHRMVIHVFSLQ QMTAHKIYIHSYNT,,ATIFHELIVYKQTKIISNQ ELIYEGRRLLVLEPGRLAQHFPKTT EENPIFVVSREPLNTIGLIEK,,ISLPKVHPRYDLGDGASMAK,,AITGVV CYACRI ASTLLLYQELMRKGI RWLI,,ELIKDDYNETVHKTEVVITLDFCIRNIEKTVKV,,YEKLMKINLEAAELGEISDIHTKLLR,,LSSSQGTIETSLQDIDSR LSPGGSLADAWAHQEGTHPKDRN,,VEKLQVLLNCMTEIYYQFKDKA ER,,RLAYNEEQIHKFDK,,QKLYYHATKAMTHFTDECVKYEAFLNKSEEWIR,,KMLHLRQQLLSLTNQCFDIEEEVSKYQ EYTN E,,LQETLPQKMFTA SSGIKHTMTPIYSSNTLVEMTLG,,FGSLTMDGGLRNV DCL* 705 amino acids = 80.8 kDa		
TBK1-235	3782 .. 49,292	45,511 bp	CDS
▶ 17 segments = 1842 bp			
/note	= coding sequence ENSP00000502899		
/translation	= MQSTSNHLWLLSDILGQ GATANVFRGRHK,KTGDLFAIKVFNNISFLRPVDVQMRFEV LKLNHKNIVKLFAIEEE,TTTRHKVLIMEFCPCGSLYTVLEEPSNAYGLPESEFLIVLRDV,VGGMNLRENGIVHRDIKPGNIMR VIGEDGQSVYKLTDFGAARELEDDEQFVSLYGT E EYL,HPDMYERAVLRKDHQKKYGATVDLWSIGVTFYHAATGSLPFRPFEGPRRNKEVM,,YKIITGKPSGAISGVQKAENGPIDWSGDMPVSCSLSR,,GLQVLLTPVLANI LEADQEKCWGDFQFAAETSDILHRMVIHVFSLQ QMTAHKIYIHSYNT,,ELIKDDYNETVHKTEVVITLDFCIRNIEKTVKV,,YEKLMKINLEAAELGEISDIHTKLLR,,LSSSQGTIETSLQDIDSR LSPGGSLADAWAHQEGTH PKDRN,,VEKLQVLLNCMTEIYYQFKDKA ER,,RLAYNEEQIHKFDK,,QKLYYHATKAMTHFTDECVKYEAFLNKSEEWIR,,KMLHLRQQLLSLTNQCFDIEEEVSKYQ EYTN E,,LQETLPQKMFTA SSGIKHTMTPIYSSNTLVEMTLG,,FGSLTMDGGLRNV DCL* 705 amino acids = 80.8 kDa		
TBK1-245	3782 .. 49,292	45,511 bp	CDS
▶ 20 segments = 2175 bp			
/note	= coding sequence ENSP00000504586		
/translation	= MQSTSNHLWLLSDILGQ GATANVFRGRHK,KTGDLFAIKVFNNISFLRPVDVQMRFEV LKLNHKNIVKLFAIEEE,TTTRHKVLIMEFCPCGSLYTVLEEPSNAYGLPESEFLIVLRDV,VGGMNLRENGIVHRDIKPGNIMR VIGEDGQSVYKLTDFGAARELEDDEQFVSLYGT E EYL,HPDMYERAVLRKDHQKKYGATVDLWSIGVTFYHAATGSLPFRPFEGPRRNKEVM,,YKIITGKPSGAISGVQKAENGPIDWSGDMPVSCSLSR,,GLQVLLTPVLANI LEADQEKCWGDFQFAAETSDILHRMVIHVFSLQ QMTAHKIYIHSYNT,,ATIFHELIVYKQTKIISNQ ELIYEGRRLLVLEPGRLAQHFPKTT EENPIFVVSREPLNTIGLIEK,,ISLPKVHPRYDLGDGASMAK,,AITGVV CYACRI ASTLLLYQELMRKGI RWLI,,ELIKDDYNETVHKTEVVITLDFCIRNIEKTVKV,,YEKLMKINLEAAELGEISDIHTKLLR,,LSSSQGTIETSLQDIDSR LSPGGSLADAWAHQEGTH PKDRN,,VEKLQVLLNCMTEIYYQFKDKA ER,,RLAYNEEQIHKFDK,,QKLYYHATKAMTHFTDECVKYEAFLNKSEEWIR,,KMLHLRQQLLSLTNQCFDIEEEVSKYQ EYTN E,,LQETLPQKMFTA SSGIKHTMTPIYSSNTLVEMTLG,,MKKLKEEMEGVV KELAENNHILER,,FG		
TBK1-246	3782 .. 49,292	45,511 bp	CDS
▶ 20 segments = 2187 bp			
/note	= coding sequence ENSP00000504637		
/translation	= MQSTSNHLWLLSDILGQ GATANVFRGRHK,KTGDLFAIKVFNNISFLRPVDVQMRFEV LKLNHKNIVKLFAIEEE,TTTRHKVLIMEFCPCGSLYTVLEEPSNAYGLPESEFLIVLRDV,VGGMNLRENGIVHRDIKPGNIMR VIGEDGQSVYKLTDFGAARELEDDEQFVSLYGT E EYL,HPDMYERAVLRKDHQKKYGATVDLWSIGVTFYHAATGSLPFRPFEGPRRNKEVM,,YKIITGKPSGAISGVQKAENGPIDWSGDMPVSCSLSR,,GLQVLLTPVLANI LEADQEKCWGDFQFAAETSDILHRMVIHVFSLQ QMTAHKIYIHSYNT,,ATIFHELIVYKQTKIISNQ ELIYEGRRLLVLEPGRLAQHFPKTT EENPIFVVSREPLNTIGLIEK,,ISLPKVHPRYDLGDGASMAK,,AITGVV CYACRI ASTLLLYQELMRKGI RWLI,,ELIKDDYNETVHKTEVVITLDFCIRNIEKTVKV,,YEKLMKINLEAAELGEISDIHTKLLR,,LSSSQGTIETSLQDIDSR LSPGGSLADAWAHQEGTHPKDRN,,VEKLQVLLNCMTEIYYQFKDKA ER,,RLAYNEEQIHKFDK,,QKLYYHATKAMTHFTDECVKYEAFLNKSEEWIR,,KMLHLRQQLLSLTNQCFDIEEEVSKYQ EYTN E,,LQETLPQKMFTA SSGIKHTMTPIYSSNTLVEMTLG,,MKKLKEEMEGVV KELAENNHILE		
TBK1-256	3782 .. 49,292	45,511 bp	CDS
▶ 19 segments = 2088 bp			
/note	= coding sequence ENSP00000504132		
/translation	= MQSTSNHLWLLSDILGQ GATANVFRGRHK,KTGDLFAIKVFNNISFLRPVDVQMRFEV LKLNHKNIVKLFAIEEE,TTTRHKVLIMEFCPCGSLYTVLEEPSNAYGLPESEFLIVLRDV,VGGMNLRENGIVHRDIKPGNIMR VIGEDGQSVYKLTDFGAARELEDDEQFVSLYGT E EYL,HPDMYERAVLRKDHQKKYGATVDLWSIGVTFYHAATGSLPFRPFEGPRRNKEVM,,YKIITGKPSGAISGVQKAENGPIDWSGDMPVSCSLSR,,GLQVLLTPVLANI LEADQEKCWGDFQFAAETSDILHRMVIHVFSLQ QMTAHKIYIHSYNT,,ATIFHELIVYKQTKIISNQ ELIYEGRRLLVLEPGRLAQHFPKTT EENPIFVVSREPLNTIGLIEK,,ISLPKVHPRYDLGDGASMAK,,AITGVV CYACRI ASTLLLYQELMRKGI RWLI,,YEKLMKINLEAAELGEISDIHTKLLR,,LSSSQGTIETSLQDIDSR LSPGGSLADAWAHQEGTHPKDRN,,VEKLQVLLNCMTEIYYQFKDKA ER,,RLAYNEEQIHKFDK,,QKLYYHATKAMTHFTDECVKYEAFLNKSEEWIR,,KMLHLRQQLLSLTNQCFDIEEEVSKYQ EYTN E,,LQETLPQKMFTA SSGIKHTMTPIYSSNTLVEMTLG,,MKKLKEEMEGVV KELAENNHILER,,FGSLTMDGGLRNV DCL* 695 amino acids = 79.6 kDa		
TBK1-222	3782 .. 12,374	8593 bp	CDS
▶ 2 segments = 217 bp			
/note	= coding sequence ENSP00000503155		
/translation	= MQSTSNHLWLLSDILGQ GATANVFRGRHK,TTTRHKVLIMEFCPCGSLYTVLEEPSNAYGLPESEFLIVLRDV 72 amino acids = 8.1 kDa		
TBK1-203	3782 .. 12,326	8545 bp	CDS
▶ 3 segments = 310 bp			
/note	= coding sequence ENSP00000445834		
/translation	= MQSTSNHLWLLSDILGQ GATANVFRGRHK,KTGDLFAIKVFNNISFLRPVDVQMRFEV LKLNHKNIVKLFAIEEE,TTTRHKVLIMEFCPCGSLYTVLEEPSN 103 amino acids = 11.8 kDa		

Feature	Location	Size	Type
TBK1-205	3782 .. 12,310	8529 bp	CDS
▶ 3 segments = 294 bp			
/note	= coding sequence ENSP00000445628		
/translation	= MQSTSNHLWLLSDILGQ GATANVFRGRHK,,KTGDLFAIKVFNNSIFLRVVDVQMREFEV LKLNHNKIV KLFAIEEE,,TTTRHKVLIMEFCPCGSLYTVL 98 amino acids = 11.3 kDa		
TBK1-259	3782 .. 3868	87 bp	CDS
/note	= coding sequence ENSP00000504296		
/translation	= MQSTSNHLWLLSDILGQ GATANVFRGRHK 29 amino acids = 3.2 kDa		
TBK1-257	8029 .. 50,025	41,997 bp	prim_transcript
/note	= primary transcript ENST00000678197 Retained intron		
TBK1-269	8100 .. 14,993	6894 bp	prim_transcript
/note	= primary transcript ENST00000679050 Nonsense mediated decay		
TBK1-209	8137 .. 49,816	41,680 bp	prim_transcript
/note	= primary transcript ENST00000650708 Nonsense mediated decay		
TBK1-210	8169 .. 49,292	41,124 bp	CDS
▶ 18 segments = 1932 bp			
/note	= coding sequence ENSP00000498758		
/translation	= MREFEV LKLNHNKIV KLFAIEEE,,TTTRHKVLIMEFCPCGSLYTVLEEPSNAYGLPESEFLIVLRDV,,VGGMHNHRENGIVHRDIKPGNIMRVIGEDGQSVYKLTDFGAARELEDDEQFVSLYGTEEYL,,HPDMYERAVLRKDH QKKYGATVDLWSIGVTFYHAATGSLPFRPFEGPRRNKEVM,,YKIITGKPSGAISGVQKAENGPIDWSGDMPVSCSLSR,,GLQVLLTPVLANILEADQEKCWGFDQFFAETS DILHRMVIHV FSLQQMTA HKIYIHSYNT,,ATIFH ELVYKQTKIISNQELIYEGRRLLVLEPGRLAQHFPKTTTEENPIFVVSREPLNTIGLIYEK,,ISLPKVHPRYDLDDGASMAK,,AITGVVYACRIASTLLYQELMRKGIIRWLI,,YEKLMKINLEAAELGEISDIHTKLLR,,LSSSQGTI ETSLQDIDSR LSPGGSLADA WAHQEGTHPKDRN,,VEKLQVLLNCMTEIYYQFKDKAER,,RLAYNEEQIHKFDK,,QKLYYHATKAMTHFTDECVKKYEAFLNKSEEWIR,,KMLHLRQQLLSLTNQCFDIEEEVSKYQ EYTNE,,L QETLPQKMFATSSGKHTMTPIYSSNTLVEMTLG,,MKLKEEMEGVV KELAENNHILER,,FGSLTMDGGLRNV DCL*		
TBK1-214	8169 .. 49,292	41,124 bp	CDS
▶ 19 segments = 2034 bp			
/note	= coding sequence ENSP00000498885		
/translation	= MREFEV LKLNHNKIV KLFAIEEE,,TTTRHKVLIMEFCPCGSLYTVLEEPSNAYGLPESEFLIVLRDV,,VGGMHNHRENGIVHRDIKPGNIMRVIGEDGQSVYKLTDFGAARELEDDEQFVSLYGTEEYL,,HPDMYERAVLRKDH QKKYGATVDLWSIGVTFYHAATGSLPFRPFEGPRRNKEVM,,YKIITGKPSGAISGVQKAENGPIDWSGDMPVSCSLSR,,GLQVLLTPVLANILEADQEKCWGFDQFFAETS DILHRMVIHV FSLQQMTA HKIYIHSYNT,,ATIFH ELVYKQTKIISNQELIYEGRRLLVLEPGRLAQHFPKTTTEENPIFVVSREPLNTIGLIYEK,,ISLPKVHPRYDLDDGASMAK,,AITGVVYACRIASTLLYQELMRKGIIRWLI,,ELIKDDYNETVHKTEVITLDFCIRNIEKTVK, YEKLMKINLEAAELGEISDIHTKLLR,,LSSSQGTIETSLQDIDSR LSPGGSLADA WAHQEGTHPKDRN,,VEKLQVLLNCMTEIYYQFKDKAER,,RLAYNEEQIHKFDK,,QKLYYHATKAMTHFTDECVKKYEAFLNKSEEWIR,, KMLHLRQQLLSLTNQCFDIEEEVSKYQ EYTNE,,LQETLPQKMFATSSGKHTMTPIYSSNTLVEMTLG,,MKLKEEMEGVV KELAENNHILER,,FGSLTMDGGLRNV DCL*		
TBK1-234	8169 .. 49,292	41,124 bp	CDS
▶ 19 segments = 2034 bp			
/note	= coding sequence ENSP00000503567		
/translation	= MREFEV LKLNHNKIV KLFAIEEE,,TTTRHKVLIMEFCPCGSLYTVLEEPSNAYGLPESEFLIVLRDV,,VGGMHNHRENGIVHRDIKPGNIMRVIGEDGQSVYKLTDFGAARELEDDEQFVSLYGTEEYL,,HPDMYERAVLRKDH QKKYGATVDLWSIGVTFYHAATGSLPFRPFEGPRRNKEVM,,YKIITGKPSGAISGVQKAENGPIDWSGDMPVSCSLSR,,GLQVLLTPVLANILEADQEKCWGFDQFFAETS DILHRMVIHV FSLQQMTA HKIYIHSYNT,,ATIFH ELVYKQTKIISNQELIYEGRRLLVLEPGRLAQHFPKTTTEENPIFVVSREPLNTIGLIYEK,,ISLPKVHPRYDLDDGASMAK,,AITGVVYACRIASTLLYQELMRKGIIRWLI,,ELIKDDYNETVHKTEVITLDFCIRNIEKTVK, YEKLMKINLEAAELGEISDIHTKLLR,,LSSSQGTIETSLQDIDSR LSPGGSLADA WAHQEGTHPKDRN,,VEKLQVLLNCMTEIYYQFKDKAER,,RLAYNEEQIHKFDK,,QKLYYHATKAMTHFTDECVKKYEAFLNKSEEWIR,, KMLHLRQQLLSLTNQCFDIEEEVSKYQ EYTNE,,LQETLPQKMFATSSGKHTMTPIYSSNTLVEMTLG,,MKLKEEMEGVV KELAENNHILER,,FGSLTMDGGLRNV DCL*		
TBK1-204	8169 .. 12,317	4149 bp	CDS
▶ 2 segments = 145 bp			
/note	= coding sequence ENSP00000444428		
/translation	= MREFEV LKLNHNKIV KLFAIEEE,,TTTRHKVLIMEFCPCGSLYTVLEE 48 amino acids = 5.7 kDa		
TBK1-243	8169 .. 8240	72 bp	CDS
/note	= coding sequence ENSP00000504729		
/translation	= MREFEV LKLNHNKIV KLFAIEEE 24 amino acids = 3.0 kDa		
TBK1-233	10,977 .. 12,374	1398 bp	prim_transcript
/note	= primary transcript ENST00000676901		
TBK1-250	12,245 .. 22,301	10,057 bp	prim_transcript
/note	= primary transcript ENST00000677759 Nonsense mediated decay		
TBK1-271	12,245 .. 22,301	10,057 bp	prim_transcript
/note	= primary transcript ENST00000679302 Nonsense mediated decay		
TBK1-254	12,245 .. 14,993	2749 bp	CDS
▶ 2 segments = 234 bp			
/note	= coding sequence ENSP00000503613		
/translation	= TTTRHKVLIMEFCPCGSLYTVLEEPSNAYGLPESEFLIVLRDV,,GEDGQSVYKLTDFGAARELEDDEQFVSLYGTEEYL 78 amino acids = 8.8 kDa		
TBK1-254	12,245 .. 14,993	2749 bp	prim_transcript
/note	= primary transcript ENST00000678079		
TBK1-217	12,266 .. 38,363	26,098 bp	prim_transcript
/note	= primary transcript ENST00000651889 Retained intron		
TBK1-253	14,812 .. 29,932	15,121 bp	prim_transcript
/note	= primary transcript ENST00000677973 Nonsense mediated decay		
TBK1-237	14,812 .. 22,301	7490 bp	prim_transcript
/note	= primary transcript ENST00000677016 Nonsense mediated decay		
TBK1-238	14,812 .. 22,301	7490 bp	prim_transcript
/note	= primary transcript ENST00000677112 Nonsense mediated decay		
TBK1-264	14,812 .. 22,301	7490 bp	prim_transcript
/note	= primary transcript ENST00000678738 Nonsense mediated decay		

Feature	Location	Size	Start	End	Type
TBK1-265	14,812 .. 22,301	7490 bp	█	→	prim_transcript
/note	= primary transcript ENST00000678808 Nonsense mediated decay				
TBK1-239	21,836 .. 22,301	466 bp	█	→	prim_transcript
/note	= primary transcript ENST00000677242				
TBK1-263	22,141 .. 28,033	5893 bp	█	→	prim_transcript
/note	= primary transcript ENST00000678718 Nonsense mediated decay				
TBK1-236	27,923 .. 32,410	4488 bp	█	→	CDS
▶ 2 segments = 308 bp					
/note	= coding sequence ENSP00000503561				
/translation	= V*NNYRKAFWCNIWSTESRKWTN*LEWRHACFLQSFSS,,CYIIS*TGI*TNQNYFFKSRTYLRRATLSLRTWKAGTTFP*NY*GKPYICKSKPGTSEYHRINI*K 102 codons (7 internal stop codons)				
TBK1-236	27,923 .. 32,410	4488 bp	█	→	prim_transcript
/note	= primary transcript ENST00000676983				
TBK1-207	29,753 .. 33,424	3672 bp	█	→	prim_transcript
/note	= primary transcript ENST00000545025 Nonsense mediated decay				
TBK1-252	29,753 .. 33,424	3672 bp	█	→	prim_transcript
/note	= primary transcript ENST00000677858 Nonsense mediated decay				
TBK1-247	29,753 .. 30,921	1169 bp	█	→	prim_transcript
/note	= primary transcript ENST00000677670				
TBK1-258	29,753 .. 30,921	1169 bp	█	→	prim_transcript
/note	= primary transcript ENST00000678235				
TBK1-223	32,214 .. 38,030	5817 bp	█	→	prim_transcript
/note	= primary transcript ENST00000676490 Nonsense mediated decay				
TBK1-202	32,318 .. 36,497	4180 bp	█	→	prim_transcript
/note	= primary transcript ENST00000536906 Retained intron				
TBK1-225	33,366 .. 38,030	4665 bp	█	→	prim_transcript
/note	= primary transcript ENST00000676539 Nonsense mediated decay				
TBK1-231	33,734 .. 38,814	5081 bp	█	→	prim_transcript
/note	= primary transcript ENST00000676774 Retained intron				
TBK1-262	33,837 .. 36,499	2663 bp	█	→	prim_transcript
/note	= primary transcript ENST00000678582 Nonsense mediated decay				
TBK1-268	35,876 .. 38,284	2409 bp	█	→	prim_transcript
/note	= primary transcript ENST00000679010 Retained intron				
TBK1-241	36,398 .. 43,686	7289 bp	█	→	prim_transcript
/note	= primary transcript ENST00000677435 Nonsense mediated decay				
TBK1-227	37,952 .. 50,025	12,074 bp	█	→	prim_transcript
/note	= primary transcript ENST00000676587				
TBK1-227	37,952 .. 49,282	11,331 bp	█	→	CDS
▶ 2 segments = 121 bp					
/note	= coding sequence ENSP00000504858				
/translation	= I*KVDEQPGSGRVR*NFRHTHQIVE,,SLAL*PMMVAFATL 40 codons (3 internal stop codons)				
TBK1-261	37,952 .. 45,170	7219 bp	█	→	prim_transcript
/note	= primary transcript ENST00000678567 Nonsense mediated decay				
TBK1-249	38,538 .. 40,524	1987 bp	█	→	prim_transcript
/note	= primary transcript ENST00000677714				
TBK1-206	42,840 .. 44,313	1474 bp	█	→	prim_transcript
/note	= primary transcript ENST00000541805 Retained intron				
TBK1-208	42,967 .. 49,977	7011 bp	█	→	prim_transcript
/note	= primary transcript ENST00000545392 Retained intron				
TBK1-224	43,394 .. 45,170	1777 bp	█	→	prim_transcript
/note	= primary transcript ENST00000676521 Nonsense mediated decay				
TBK1-267	43,394 .. 44,317	924 bp	█	→	prim_transcript
/note	= primary transcript ENST00000678996 Nonsense mediated decay				
TBK1-255	43,610 .. 44,317	708 bp	█	→	CDS
▶ 2 segments = 111 bp					
/note	= coding sequence ENSP00000504253				
/translation	= CRKTTSPVKLHDRDLLSVQKRQSRTY,,L**RTNPQI** 37 codons (3 internal stop codons)				
TBK1-255	43,610 .. 44,317	708 bp	█	→	prim_transcript
/note	= primary transcript ENST00000678125				
Donor Template WT -> SNV	45,870 .. 45,969	100 bp	█	↔	misc_feature

Feature	Location	Size			Type
	45,879 .. 55,240	9362 bp		→	gene
/note	= gene ENSG00000288665 lncRNA				
	45,879 .. 55,240	9362 bp		→	prim_transcript
/note	= primary transcript ENST00000677093 lncRNA				
TBK1-228	45,879 .. 49,967	4089 bp		→	prim_transcript
/note	= primary transcript ENST00000676593				
TBK1-240	45,879 .. 49,967	4089 bp		→	prim_transcript
/note	= primary transcript ENST00000677313 Nonsense mediated decay				
TBK1-228	45,879 .. 47,035	1157 bp		→	CDS
▶ 2 segments = 130 bp					
/note	= coding sequence ENSP00000503458				
/translation	= YEEIKGRDGRGG*RTC*K*PHFRK,,TEFRCCPGWSPMA*SQLTV 43 codons (4 internal stop codons)				
✓ Protospacer Sequence	45,888 .. 45,907	20 bp		⊢	misc_feature
✓ SNV	45,898 .. 45,898	1 bp		⊢	misc_feature
/note	= WT = G SNV = A				
✓ PAM	45,908 .. 45,910	3 bp		⊢	misc_feature
TBK1-266	48,741 .. 49,966	1226 bp		→	prim_transcript
/note	= primary transcript ENST00000678992				

Primer	Length	Binding Sites	Tm	Date Added
✓ PCR Forward	25-mer	45,461 .. 45,485	→ 56°C	Jun 30, 2022
/sequence = TAAAAGCTGTAAACACTTGATGTCAG 36% GC / 7689.1 Da				
✓ Sanger Sequencing Primer	20-mer	45,778 .. 45,797	→ 49°C	Jul 1, 2022
/sequence = TAAGGTTATCTATTGACCAG 35% GC / 6131.1 Da				
✓ Donor Template	100-mer	45,870 .. 45,969	← 68°C	Jun 30, 2022
/sequence = TTATTTTGCATTACTCACCTTCTAAAATGTGGTTATTTTCAGCAAGTCTTTAACCCACCCCTTCCATCTTTTCCTTTAATTTCTTCATACTAATAAAA 29% GC / 30,396.9 Da				
✓ gRNA Protospacer	20-mer	45,888 .. 45,907	→ 49°C	Jun 30, 2022
/sequence = ATTAAA GGAAGAGATGGAAG 35% GC / 6287.2 Da				
✓ PCR Reverse	25-mer	46,391 .. 46,415	← 56°C	Jul 1, 2022
/sequence = GCTTCAAATCTCTTTGGCCTTATC 40% GC / 7549.0 Da				