

5' TAGCTGATCCCAAAGAGAGAAACCAGAGATGTATTCATGAGTTCATGCATATGATGGATTTTCTTAGGTATTTATTCCTGACC  
 3' ATCGACTAGGGTTTTCTCTCTTTGGTCTCTACATAAGTACTCAAGGTACGTATACTACCTAAAAGAATCCATAAATAAGGACTGG  
 ITPR1  
 ITPR1-237

85

TTCTTATGCTACTCATTGACTTTAAAAAAGTATTTTTACCACAAATAAAGGAAATGAAACAGGGTAACATTGTTCCAGATCTCCA  
 AAGAATACGATGAGTAACTGAAATTTTTTCATAAAAATGGTGTTATTTCTTTACTTTGTCCCATTGTAACAAGGTCTAGAGGT  
 ITPR1  
 ITPR1-237  
 PCR Forward  
 AACATTGTTCCAGATCTCCA

170

GGTAG  
 GGTAGGCTTTATCTGTGTTTATTTAGCAGCACAGATCACTGGGGGCACAGTTAAGTCCTCTTGAATTAGGAATACGTTTAGAGCT  
 CCATCCGAAATAGACACAAATAAATCGTCGTGTCTAGTGACCCCGTGTCAATTCAGGAGAACTTAATCCTTATGCAAATCTCGA  
 ITPR1  
 ITPR1-237  
 PCR Forward

255

GAAAACCAGCTTTGGACCTTTTTGAAAAATAAATCACTAGATTAATAATTTATACTGTGCACCTTAATAAAATATCCACGTGTAAT  
 CTTTTGGTCGAAACCTGGAAAAACTTTTTATTTAGTGATCTAATTTAAATATGACACGTGAATTATTTATAGGTGCACATTTA  
 ITPR1  
 ITPR1-237

340

ACAGGCTATTTTGCTTAATTACATTTGTGTGGCAGGCTTAGAAAAGTAAAGGATGTGAAGGAGTTTGCAGCTGTTGCCCTAGGAT  
 TGTCGGATAAAACGAATTAATGTAAACACACCGTCCGAATCTTTTCATTTCTACACTTCTCAAACGTGCAACAGGGGATCCTA  
 ITPR1  
 ITPR1-237

425

AGAAAGTTGTAGGAAGACCTCCCTTATACTGTAATGTCTCTTAGGGGCAGTAGTTCTCATCAGGAAACATTGCTGCTTTCTTTA  
 TCTTTCAACATCCTTCTGGGAGGGAATATGACATTACAGAGAATCCCGTCATCAAGAGTAGTCCTTTGTAACGACGAAAGAAAT  
 ITPR1  
 ITPR1-237

510

GTCTACGCTTAACCATATTGTCATTTATCCTTCTACTGACGTCTTTTTCTCTCCTTATAAAGGAGTATATAGCCAAGCAGTTT  
 CAGATGCGAATTGGTATAACAGTAAATAGGAAGGATGACTGCAGAGAAAAGAGAGGAATATTTCTCATATATCGGTTCTGTCAAA  
 ITPR1  
 ITPR1-237

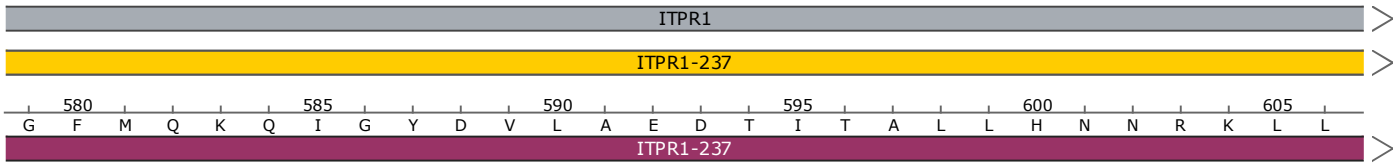
595

E Y I A K Q F  
 ITPR1-237

Donor Template WT -> SNV

TTCATGCAGAAGCAGATTGGCTATGATGTGTTGGCTGAAGACACTATCACTGCCCTGCTCCACAATGATCGGAAACTCCTGG  
GGCTTCATGCAGAAGCAGATTGGCTATGATGTGTTGGCTGAAGACACTATCACTGCCCTGCTCCACAATAATCGGAAACTCCTGG  
CCGAAGTACGTCTTCGTCTAACCGATACTACACAACCGACTTCTGTGATAGTGACGGGACGAGGTGTTATAGCCTTTGAGGACC

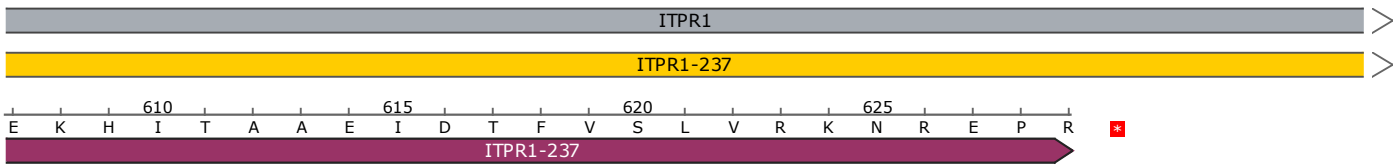
680



Donor Template WT -> SNV  
AAAAACACATTACCGCGG

AAAAACACATTACCGCGGCAGAGATTGACACATTTGTCAGCCTGGTGCGAAAGAACAGGGAGCCCAGGTGAGGCGGGAGTGGGGT  
TTTTTGTGTAATGGCGCCGTCTCTAACTGTGTAACAGTCGGACCACGCTTCTTGTCCCTCGGGTCCACTCCGCCCTCACCCCA

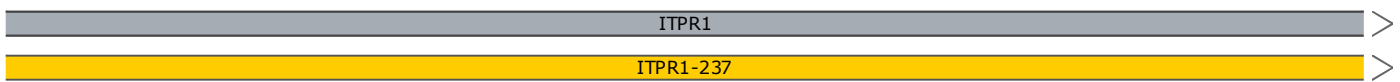
765



Donor Sequence WT -> SNV

CCATGCAGGATGGTGTCTCTGCCTGTAAGATGCAGGGACTTAGCTGGTGCTTTTTACTACGTTTCCTTGTGCTGCTAGTGACAAG  
GGTACGTCTACCACAGAGACGGACATTCTACGTCCCTGAATCGACCACGAAAAATGATGCAAAGGAACACGACGATCACTGTTC

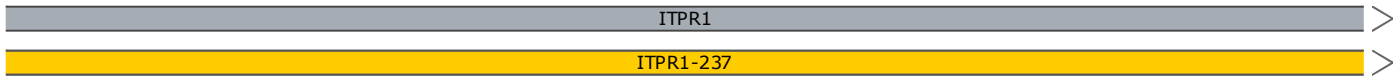
850



CTACGTCCCTGAATCGACCA  
Sanger Sequencing Primer

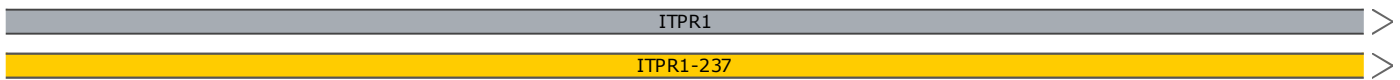
TTTTGATTAGTTAGGTCTGGAGAGGCTTTTTGATGAGTAGTGGCAAGAACTTGGTGTTAAAATGAGACCTGGGGGTGCATTCCCTA  
AAAACATAATCAATCCAGACCTCTCCGAAAAACTACTCATCACCGTCTTGAACCACAATTTTACTCTGGACCCCCACGTAAGGAT

935



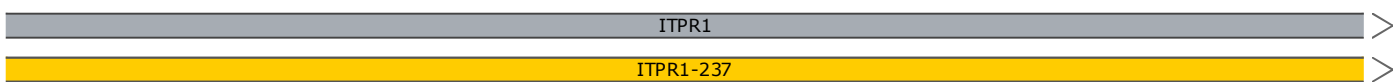
GCTCCAGTGTGTCACCTGGATGAGCTTGGGTTTTCTGAACTTTAATTTCTTATCTGCTAAATGGGTAGTTATGAAAATT  
CGAGGTCACACAGGGTGGACCTACTCGAACCCAAAAAGGACTTGAATTAAGGAATAGACGATTTACCCATCAATACTTTTAA

1020



AAATGAGAATAAACGCAGGTGACGTGCAGGCACCTTAGTGGATGCAGAGGAAATGACAAATTGTTGGCCACTCATTCACTTTTTAA  
TTTACTCTTATTTGCGTCCACTGCACGTCCGTGAATCACCTACGTCTCCTTACTGTTTAAACAACCGGTGAGTAAGTGAAAAATT

1105



PCR Reverse



Feature	Location	Size	Start	End	Type
✓ <b>ITPR1</b>	1 .. 1761	1761 bp	■	→	gene
/note = gene <a href="#">ENSG00000150995</a> Protein coding					
<b>ITPR1-201</b>	1 .. 1761	1761 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000302640</a> Nonsense mediated decay					
<b>ITPR1-202</b>	1 .. 1761	1761 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000354582</a>					
<b>ITPR1-203</b>	1 .. 1761	1761 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000357086</a>					
<b>ITPR1-204</b>	1 .. 1761	1761 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000443694</a>					
<b>ITPR1-205</b>	1 .. 1761	1761 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000456211</a>					
<b>ITPR1-210</b>	1 .. 1761	1761 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000477577</a> Retained intron					
<b>ITPR1-219</b>	1 .. 1761	1761 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000544951</a>					
<b>ITPR1-230</b>	1 .. 1761	1761 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000648266</a>					
<b>ITPR1-231</b>	1 .. 1761	1761 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000648309</a>					
✓ <b>ITPR1-237</b>	1 .. 1761	1761 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000649015</a>					
<b>ITPR1-238</b>	1 .. 1761	1761 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000649051</a> non_stop_decay					
<b>ITPR1-254</b>	1 .. 1761	1761 bp	■	→	prim_transcript
/note = primary transcript <a href="#">ENST00000650294</a>					
<b>ITPR1-202</b>	575 .. 747	173 bp	■	→	CDS
/note = coding sequence <a href="#">ENSP00000346595</a> /translation = EYIAKQFGFMQKQIGYDVLAEDTITALLHNNRKLLEKHITAAEIDTFVSLVRKNREP 57 amino acids = 6.6 kDa					
<b>ITPR1-203</b>	575 .. 747	173 bp	■	→	CDS
/note = coding sequence <a href="#">ENSP00000349597</a> /translation = EYIAKQFGFMQKQIGYDVLAEDTITALLHNNRKLLEKHITAAEIDTFVSLVRKNREP 57 amino acids = 6.6 kDa					
<b>ITPR1-204</b>	575 .. 747	173 bp	■	→	CDS
/note = coding sequence <a href="#">ENSP00000401671</a> /translation = EYIAKQFGFMQKQIGYDVLAEDTITALLHNNRKLLEKHITAAEIDTFVSLVRKNREP 57 amino acids = 6.6 kDa					
<b>ITPR1-205</b>	575 .. 747	173 bp	■	→	CDS
/note = coding sequence <a href="#">ENSP00000397885</a> /translation = EYIAKQFGFMQKQIGYDVLAEDTITALLHNNRKLLEKHITAAEIDTFVSLVRKNREP 57 amino acids = 6.6 kDa					
<b>ITPR1-230</b>	575 .. 747	173 bp	■	→	CDS
/note = coding sequence <a href="#">ENSP00000498014</a> /translation = EYIAKQFGFMQKQIGYDVLAEDTITALLHNNRKLLEKHITAAEIDTFVSLVRKNREP 57 amino acids = 6.6 kDa					
<b>ITPR1-231</b>	575 .. 747	173 bp	■	→	CDS
/note = coding sequence <a href="#">ENSP00000497026</a> /translation = EYIAKQFGFMQKQIGYDVLAEDTITALLHNNRKLLEKHITAAEIDTFVSLVRKNREP 57 amino acids = 6.6 kDa					

Feature	Location	Size	Start	End	Type
✓ <b>ITPR1-237</b>	575 .. 747	173 bp	■	→	CDS
/note = coding sequence <a href="#">ENSP00000497605</a>					
/translation = EYIAKQFGFMQKQIGYDVLAEDTITALLHNNRKLLEKHITAAEIDTFVSLVRKNREP 57 amino acids = 6.6 kDa					
<b>ITPR1-254</b>	575 .. 747	173 bp	■	→	CDS
/note = coding sequence <a href="#">ENSP00000498056</a>					
/translation = EYIAKQFGFMQKQIGYDVLAEDTITALLHNNRKLLEKHITAAEIDTFVSLVRKNREP 57 amino acids = 6.6 kDa					
✓ <b>Donor Sequence WT -&gt; SNV</b>	599 .. 698	100 bp	■		misc_feature
✓ <b>PAM</b>	658 .. 660	3 bp	■		misc_feature
✓ <b>gRNA Protospacer Sequence</b>	661 .. 680	20 bp	■		misc_feature
✓ <b>SNV</b>	665 .. 665	1 bp	■		misc_feature
/note = WT = A SNV = G					
	1762 ..41,548	39,787 bp	■	←	gene
/note = gene <a href="#">ENSG00000235978</a> lncRNA					
	1762 ..41,548	39,787 bp	■	←	prim_transcript
/note = primary transcript <a href="#">ENST00000441894</a> lncRNA					
	1762 ..40,043	38,282 bp	■	←	prim_transcript
/note = primary transcript <a href="#">ENST00000449914</a> lncRNA					
	1762 ..22,640	20,879 bp	■	←	prim_transcript
/note = primary transcript <a href="#">ENST00000687391</a> lncRNA					
	1762 ..22,556	20,795 bp	■	←	prim_transcript
/note = primary transcript <a href="#">ENST00000686919</a> lncRNA					
	1762 ..22,536	20,775 bp	■	←	prim_transcript
/note = primary transcript <a href="#">ENST00000693140</a> lncRNA					
	1762 ..11,010	9249 bp	■	←	prim_transcript
/note = primary transcript <a href="#">ENST00000465436</a> lncRNA					

Primer	Length	Binding Sites	Tm	Date Added
✓ <b>PCR Forward</b>  /sequence = AACATTGTTCCAGATCTCCAGGTAG 44% GC / 7641.0 Da	25-mer	151 .. 175	58°C	Aug 18, 2023
✓ <b>Donor Template WT -&gt; SNV</b>  /sequence = TTCATGCAGAAGCAGATTGGCTATGATGTGTTGGCTGAAGACACTATCACTGCCCTGCTCCACAATGATCGGAAACTCCTGGAAAAACACATTACCGCGG 48% GC / 30,819.1 Da	100-mer	599 .. 698	76°C	Aug 18, 2023
✓ <b>gRNA Protospacer</b>  /sequence = CCAGGAGTTTCCGATTATTG 45% GC / 6123.1 Da	20-mer	661 .. 680	54°C	Aug 18, 2023
✓ <b>Sanger Sequencing Primer</b>  /sequence = ACCAGCTAAGTCCCTGCATC 55% GC / 6022.0 Da	20-mer	794 .. 813	58°C	Aug 18, 2023
✓ <b>PCR Reverse</b>  /sequence = AATTTGTCATTTCTCTGCATCCAC 40% GC / 7518.0 Da	25-mer	1057 .. 1081	58°C	Aug 18, 2023