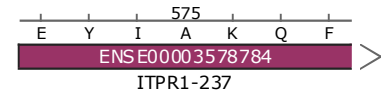
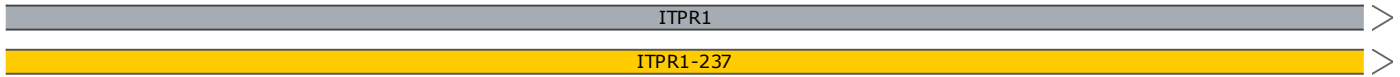


INK2J00055R_ITPR1_N602D_A03_AA
1501 bp



GTCTACGCTTAACCATATTGTCATTTATCCTTCCTACTGACGTCTCTTTTCTCTCCTTATAAAGGAGTATATAGCCAAGCAGTTT
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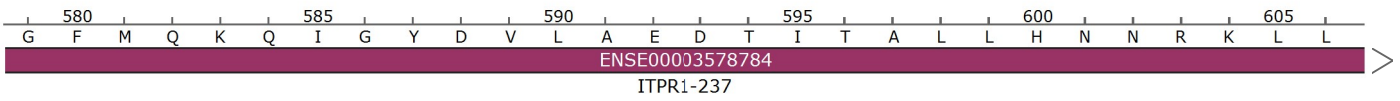
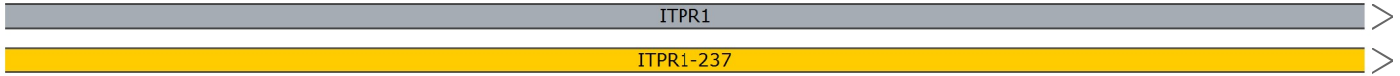
765



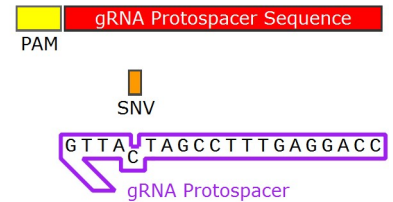
Donor Template SNV -> REV

TTCATGCAGAAGCAGATTGGCTATGATGTGTTGGCTGAAAGACACTATCACTGCCCTGCTCCACAATAATCGGAAACTCCTGG
 GGCTTCATGCAGAAGCAGATTGGCTATGATGTGTTGGCTGAAAGACACTATCACTGCCCTGCTCCACAATAATCGGAAACTCCTGG
 CCGAAGTACGTCTTCGTCTAACCATACTACACAACCGACTTCTGTGATAGTGACGGGACGAGGTGTTATAGCCTTTGAGGACC

850



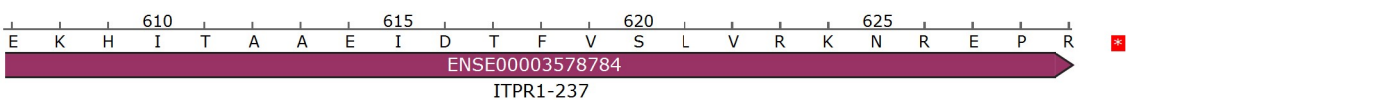
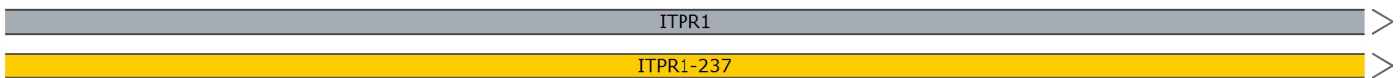
Donor Sequence SNV -> REV



Donor Template SNV -> REV

AAAAACACATTACCGCGG
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 TTTTGTGTAATGGCGCCGTCTCTAACTGTGTAACAGTCCGACCACGCTTTCTGTCCCTCGGGTCCACTCCGCCCTCACCCCA

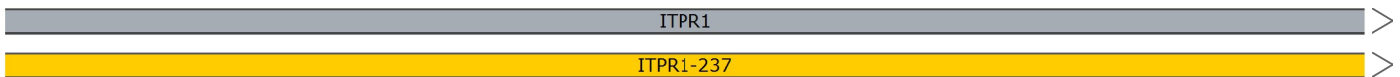
935



Donor Sequence SNV -> REV

CCATGCAGGATGGTGTCTCTGCCTGTAAGATGCAGGGACTTA6CTGGTGCTTTTTACTACGTTTCCTTGTGCTGCTAGTGACAAG
 GGTACGTCTTACCACAGAGACGGACATTCTACGTCCCTGAATCGACCACGAAAAATGATGCAAAGGAACACGACGATCACTGTTCC

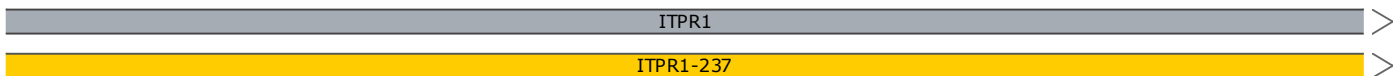
1020



CTACGTCCTGAATCGACCA
Sanger Sequencing Primer

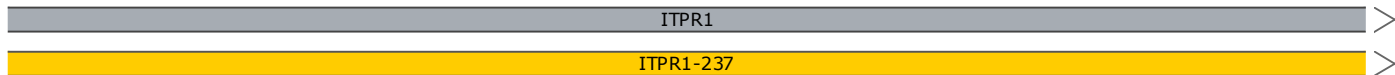
TTTTGATTAGTTAGGTCTGGAGAGGCTTTTTGATGAGTAGTGGAAGAAGCTGGTGTAAAATGAGACCTGGGGGTGCATTCTTA
 AAAACTAATCAATCCAGACCTCTCCGAAAAACTACTCATCACCGTCTTGAACCACAATTTACTCTGGACCCCCACGTAAGGAT

1105



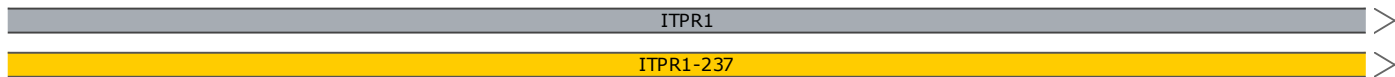
GCTCCAGTGTGTCACCTGGATGAGCTTGGGTTTTTCTGAACCTTAATTTCTTATCTGCTAAATGGGTAGTTATGAAAATT
 CGAGGTCACACAGGGTGGACCTACTCGAACCCAAAAAGGACTTGAAATTAAGGAATAGACGATTTACCCATCAATACTTTTAA

1190



AAATGAGAATAAACGCAGGTGACGTGCAGGCACTTAGTGGATGCAGAGGAAATGACAAATTGTTGGCCACTCATTCACTTTTAA
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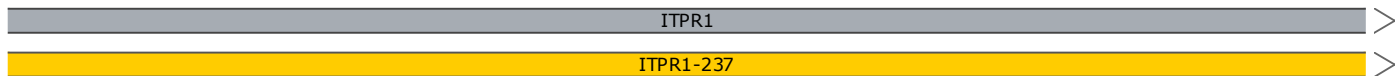
1275



CACCTACGTCTCCTTTACTGTTTAA
 PCR Reverse

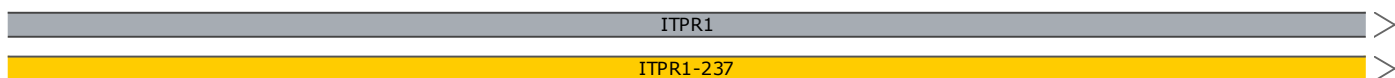
AAAATGTTCTTAATTTAATTTTAAATTTTGTGGGTACGTAGTAGGTGTATATATTTATGGGGTACATGAGATGTTTTGATGTA
 TTTTACAAGAATTTAAATTTAAAAATTTAAAAACACCCATGCATCATCCACATATATAAATACCCCATGTA CTCTACAAAAC TACAT

1360

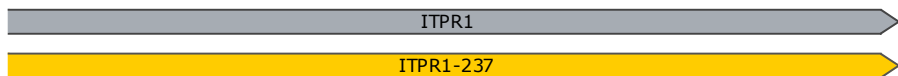


GGCATGCAATGTGTAATAATCACATTGTAGAGAATGGGGTATCCATCCCCTCAAACATTTATTTTTGTTACAAAGAATTCAGTT
 CCGTACGTTACACATTATTAGTGAACATCTTACCCCATAGGTAGGGGAGTTTGTAATAAAAAACAATGTTTCTTAAGTCAA

1445



CTATTCTTTTAGTTATTTTAAAATGTACAATTAATTTACTGTAATTACCCCA 3'
 GATAAGAAAATCAATAAAATTTTACATGTTAATTTAATAACTGACATTAATGGGGT 5' 1501



Feature	Location	Size	±	Type
✓ ITPR1	1 .. 1501	1501 bp	☐ →	gene
/note = gene ENSG00000150995 Protein coding				
ITPR1-201	1 .. 1501	1501 bp	☐ →	prim_transcript
/note = primary transcript ENST00000302640 Nonsense mediated decay				
ITPR1-202	1 .. 1501	1501 bp	☐ →	prim_transcript
/note = primary transcript ENST00000354582				
ITPR1-203	1 .. 1501	1501 bp	☐ →	prim_transcript
/note = primary transcript ENST00000357086				
ITPR1-204	1 .. 1501	1501 bp	☐ →	prim_transcript
/note = primary transcript ENST00000443694				
ITPR1-205	1 .. 1501	1501 bp	☐ →	prim_transcript
/note = primary transcript ENST00000456211				
ITPR1-210	1 .. 1501	1501 bp	☐ →	prim_transcript
/note = primary transcript ENST00000477577 Retained intron				
ITPR1-219	1 .. 1501	1501 bp	☐ →	prim_transcript
/note = primary transcript ENST00000544951				
ITPR1-230	1 .. 1501	1501 bp	☐ →	prim_transcript
/note = primary transcript ENST00000648266				
ITPR1-231	1 .. 1501	1501 bp	☐ →	prim_transcript
/note = primary transcript ENST00000648309				
✓ ITPR1-237	1 .. 1501	1501 bp	☐ →	prim_transcript
/note = primary transcript ENST00000649015				
ITPR1-238	1 .. 1501	1501 bp	☐ →	prim_transcript
/note = primary transcript ENST00000649051 non_stop_decay				
ITPR1-254	1 .. 1501	1501 bp	☐ →	prim_transcript
/note = primary transcript ENST00000650294				
ITPR1-202	745 .. 917	173 bp	■ →	CDS
/note = coding sequence ENSP00000346595				
/translation = EYIAKQFGFMQKQIGYDVLAEITITALLHNNRKLLEKHITAAEIDTFVSLVRKNREP 57 amino acids = 6.6 kDa				
ITPR1-203	745 .. 917	173 bp	■ →	CDS
/note = coding sequence ENSP00000349597				
/translation = EYIAKQFGFMQKQIGYDVLAEITITALLHNNRKLLEKHITAAEIDTFVSLVRKNREP 57 amino acids = 6.6 kDa				
ITPR1-204	745 .. 917	173 bp	■ →	CDS
/note = coding sequence ENSP00000401671				
/translation = EYIAKQFGFMQKQIGYDVLAEITITALLHNNRKLLEKHITAAEIDTFVSLVRKNREP 57 amino acids = 6.6 kDa				
ITPR1-205	745 .. 917	173 bp	■ →	CDS
/note = coding sequence ENSP00000397885				
/translation = EYIAKQFGFMQKQIGYDVLAEITITALLHNNRKLLEKHITAAEIDTFVSLVRKNREP 57 amino acids = 6.6 kDa				
ITPR1-230	745 .. 917	173 bp	■ →	CDS
/note = coding sequence ENSP00000498014				
/translation = EYIAKQFGFMQKQIGYDVLAEITITALLHNNRKLLEKHITAAEIDTFVSLVRKNREP 57 amino acids = 6.6 kDa				
ITPR1-231	745 .. 917	173 bp	■ →	CDS
/note = coding sequence ENSP00000497026				
/translation = EYIAKQFGFMQKQIGYDVLAEITITALLHNNRKLLEKHITAAEIDTFVSLVRKNREP 57 amino acids = 6.6 kDa				

Feature	Location	Size	Start	End	Type
✓ ITPR1-237	745 .. 917	173 bp	■	→	CDS
/note = coding sequence ENSP00000497605					
/translation = EYIAKQFGFMQKQIGYDVLAE D TITALLHNNRKLLEKHITAAEIDTFVSLVRKNREP 57 amino acids = 6.6 kDa					
ITPR1-254	745 .. 917	173 bp	■	→	CDS
/note = coding sequence ENSP00000498056					
/translation = EYIAKQFGFMQKQIGYDVLAE D TITALLHNNRKLLEKHITAAEIDTFVSLVRKNREP 57 amino acids = 6.6 kDa					
✓ Donor Sequence SNV -> REV	769 .. 868	100 bp	■	┌┐	misc_feature
✓ PAM	828 .. 830	3 bp	■	┌┐	misc_feature
✓ gRNA Protospacer Sequence	831 .. 850	20 bp	■	┌┐	misc_feature
✓ SNV	835 .. 835	1 bp	■	┌┐	misc_feature
/note = SNV = G REV = A					
	1502 ..41,288	39,787 bp	■	←	gene
/note = gene ENSG00000235978 lncRNA					
	1502 ..41,288	39,787 bp	■	←	prim_transcript
/note = primary transcript ENST00000441894 lncRNA					
	1502 ..39,783	38,282 bp	■	←	prim_transcript
/note = primary transcript ENST00000449914 lncRNA					
	1502 ..22,380	20,879 bp	■	←	prim_transcript
/note = primary transcript ENST00000687391 lncRNA					
	1502 ..22,296	20,795 bp	■	←	prim_transcript
/note = primary transcript ENST00000686919 lncRNA					
	1502 ..22,276	20,775 bp	■	←	prim_transcript
/note = primary transcript ENST00000693140 lncRNA					
	1502 ..10,750	9249 bp	■	←	prim_transcript
/note = primary transcript ENST00000465436 lncRNA					

Primer	Length	Binding Sites	Tm	Date Added
✓ PCR Forward /sequence = AACATTGTTCCAGATCTCCAGGTAG 44% GC / 7641.0 Da	25-mer	321 .. 345	58°C	Aug 18, 2023
✓ Donor Template SNV -> REV /sequence = TTCATGCAGAAGCAGATTGGCTATGATGTGTTGGCTGAAGACACTATCACTGCCCTGCTCCACAATAATCGGAAACTCCTGGAAAAACACATTACCGCGG 47% GC / 30,803.1 Da	100-mer	769 .. 868	77°C	Aug 18, 2023
✓ gRNA Protospacer /sequence = CCAGGAGTTTCCGATCATTG 50% GC / 6108.0 Da	20-mer	831 .. 850	48°C	Aug 18, 2023
✓ Sanger Sequencing Primer /sequence = ACCAGCTAAGTCCCTGCATC 55% GC / 6022.0 Da	20-mer	964 .. 983	58°C	Aug 18, 2023
✓ PCR Reverse /sequence = AATTTGTCATTTCTCTGCATCCAC 40% GC / 7518.0 Da	25-mer	1227 .. 1251	58°C	Aug 18, 2023