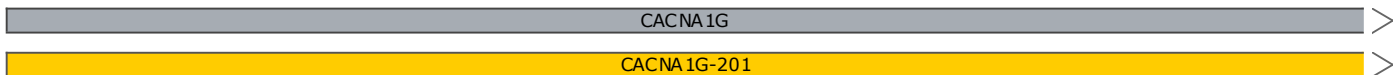
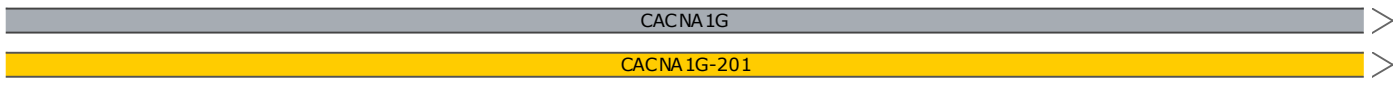


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1937 bp

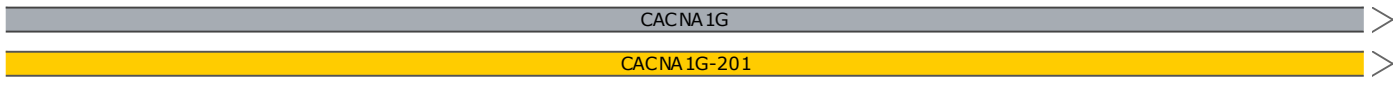
5' ATACAAGCCATGACTTCCCCTCTATCCATACCCATGTGCCCTGCCAGCCCCTCATCACCACCATCCCCCTGGGGATGGG
3' TAGTGTTCGGTACTGAAGGGTGAGATAGGTATGGGTACACGGGGACGGGGTCTGGGGAGTAGTGGTGGTAAGGGGGACCCCTACCC



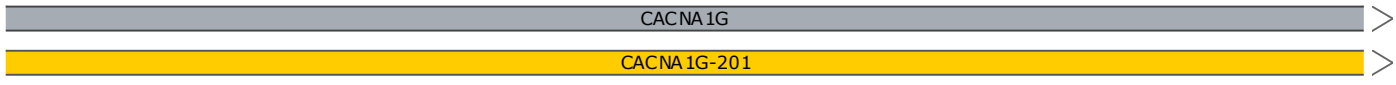
GTGCAGTGACCTCAGGGTTAGCATGTGAAGAGCAGGGCCAGTGTCTCCTCAGCTGAGGTGTGTCTCTGAACAGACAGCTGTGTGG
CACGTCCTGAGTCCCAATCGTACACTTCTCGTCCCGGTCACAGAGGAGTGCAGTCCACACAGAGACTTGTCTGTCTCGACACACC



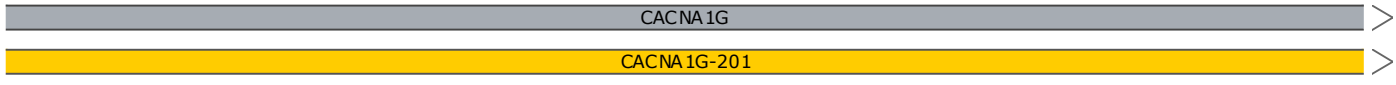
GGCCAGTGTGGATAACTGATGCTGCTTCCCAGCTCAGCAGGGAGGACAGGCAGGGGGCTGGGCTGGAGGCAGGGGTGGGGAGAG
CCGGTCACAAACTATTGACTACGACGAAGGGTCGAGTCGTCCCTCCTGTCCGTCCCCGACCCGACCTCCGTCCCCACCCCTCTC



GGGAGAGCGGGGTTGGGGATGCAGGGGAGGAGAGGGAGGAGGTGGAGAGGCAAGGGTCTCAGGGATGGGGAGGGGGCTGGCA
CCCTCTCGCCCCAACCCCTACGTCCCCTCCTCTCCCTCCTCCACTCTCCGTTCCCCAGGAGTCCCTACCCCTCCCCCGGACCGT

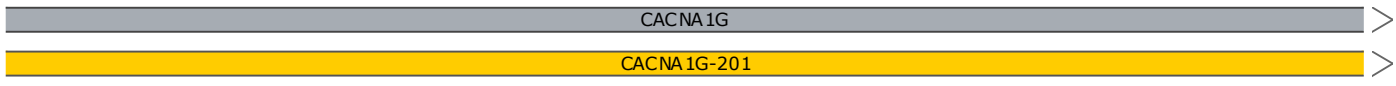


AGGTTGACAGGGAGATGAGGAGGTGGCTTTAGGAATAAAGGAAGAGAGGCAGGGCAGAGCTTGGGCCCCAGGTGGGAGAGGGTAG
TCCAAGTGTCCCTCTACTCCTCCACCGAAATCCTTATTTCTTCTCCTCGTCCCGTCTCGAACCAGGGGTCCACCCTCTCCCATC



PCR Forward
tgctcactactccagtggtt

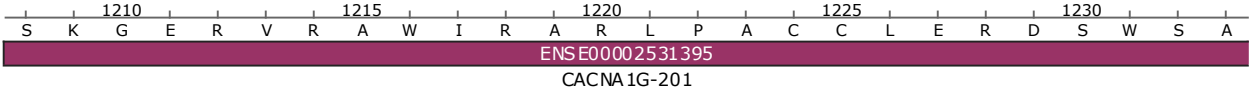
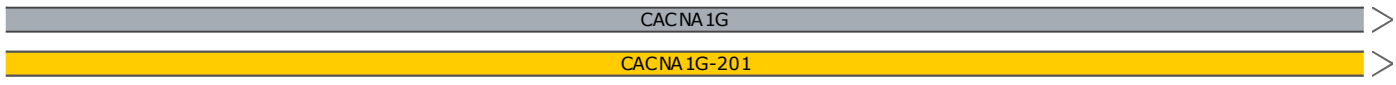
ACAAGGAGTGAGGCTCGTGAAGTCTGCTGAGGAGCCAGGAGCCGGGAACCTGGAGGCCTGGTCTGCTCATACTCCAGTGTGGT
TGTTCTCACTCCGAGCACTGAGACGACTCCTCGGTCTCGGCCCTTGGACCTCCGGACCAGGACGAGTATGAGGTACAAACA



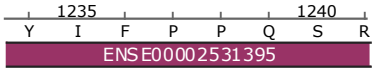
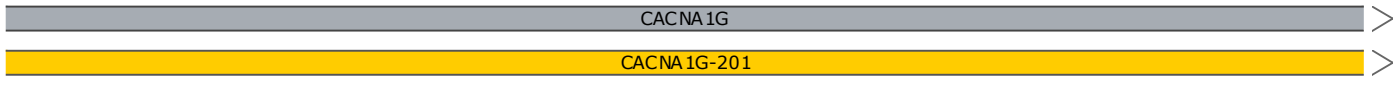
PCR Forward

tctg

TCTGCAGAGCAAAGGGGAACGGGTCGCGCGTGGATCCGAGCCCGACTCCCTGCCTGCTGCCTCGAGCGAGACTCCTGGTCAGCC
AGACGTCTCGTTTCCCCTTGCCAGGCGCGCACCTAGGCTCGGGCTGAGGGACGGACGACGGAGCTCGCTCTGAGGACCAGTCGG



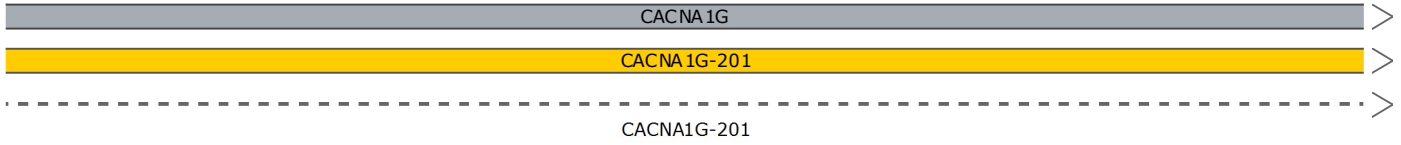
TACATCTTCCCTCCTCAGTCCAGGTAAGTGACAGGGCAGGGTCTGACCTGTGTCCCGACCTCTTCTTCTCACGGGAAATTACCG
ATGTAGAAGGGAGGAGTCAGGTCCATTCACTGTCCCGTCCCAGACTGGACACAGGGCTGGAGAAGAAGAGTGCCCTTTAATGGC



CACNA1G-201

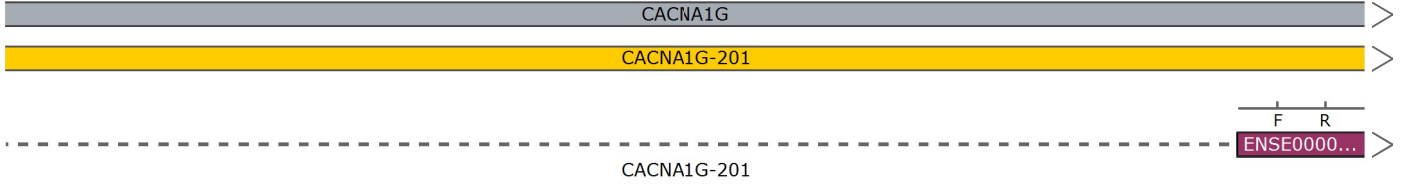
CTGGTGTGCTGTCAGGGATTTGAGAAGTGGCACCCCTGCCTGGGGTGTGAGCAGGGTGGCCTCAGCTGGGAGGGCACTGGAGGGG
GACCACTACGACAGTCCCTAAACTCTTACCCTGGGACGGACCCACACTCGTCCCACCGGAGTCGACCCTCCCGTGACCTCCCC

765



CAGGGGCTGCGGGCGGTGCCTCTCGTTGCCACCTGCCCTGCCTCCCCCTCTCAGCCGTTGCCTCCATGCCTGGGCAGGTTCCGCC
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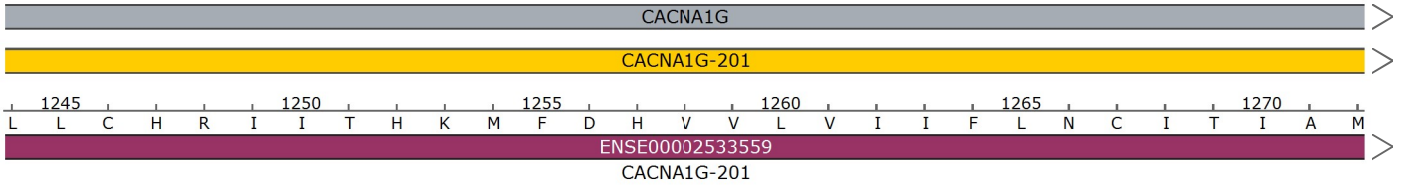
850



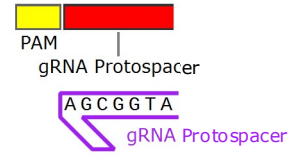
Donor Template WT -> SNV

CATCACCCACAAGATGTTTCGACCACGTGGTCTTGTGCATCATCTTCTTAAGTGCATCACCATCGCCAT
TCCTGTGTACACGGATCATCACCCACAAGATGTTTCGACCACGTGGTCTTGTGCATCATCTTCTTAAGTGCATCACCATCGCCAT
AGGACACAGTGGCCTAGTAGTGGGTGTTCTACAAGCTGGTGCACCAGGAACAGTAGTAGAAGGAATTGACGTAGTGGTAGCGGTA

935



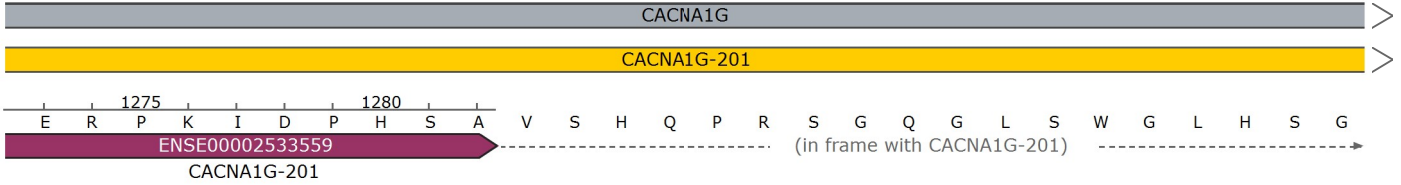
Donor Template WT -> SNV



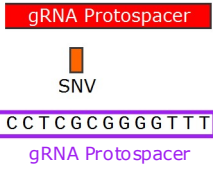
Donor Template WT -> SNV

GGAGAGCCCCAAAATTGACCCACAGCGCT
GGAGAGCCCCAAAATTGACCCACAGCGCTGTGAGTCACCAAGCCCGCTCAGGGCAAGGCCTCTCCTGGGGTTTGCACCTCAGGA
CCTCAGCGGGGTTTAACTGGGGGTGTCGCGACACTCAGTGGTGGGGCGAGTCCCGTCCGGAGAGGACCCCAAACGTGAGTCCT

1020



Donor Template WT -> SNV



CCAGTGAGGGAGGCCAAGGAGGCCACAGTTGCTGACCTGCAAGTCACACAGCAGGGAAACGAGGGGGCCAGGACTCTCCTTTAGGTC
GGTCACTCCCTCCGTTCCTCCGGTGTCAACGACTGGACGTTTCAGTGTGTCGTCCCTTGCTCCCCGGTCTGAGAGGAAATCCAG

1105

CACNA1G

CACNA1G-201

P V R E A R R P Q L L T C K S H S R E R G G Q D S P L G
(in frame with CACNA1G-201)

g

Sanger Sequencing Primer

TCTCACCAGATCCTGGTCCCCGGGATGCCCCCTGTGTCCTCTCCTGCCTCAGTTTCCCTTCTATGATACATCAGCCCAGCTGGGT
AGAGTGGTCTAGGACCAGGGGCCCTACGGGGGACACAGGAGAGGACGGAGTCAAAGGGAAGATACTATGTAGTCGGGTTCGACCCA

1190

CACNA1G

CACNA1G-201

L S P D P G P R D A P C V L S C L S F P S M I H Q P S W V
(in frame with CACNA1G-201)

agagtggcttaggaccagg

Sanger Sequencing Primer

GCTTTGTCTCATTCCAGGCTATTTCTCATGAGCCAGAGCCTTGTGGGGCACACGCGTGAGTCGGGGAGTGCTGGGGCGGTGCAGG
CGAAACAGAGTAAGGTCCGATAAAGAGTACTCGGTCTCGGAACACCCCGTGTGCGCACTCAGCCCCCTCACGACCCCGCCACGTCC

1275

CACNA1G

CACNA1G-201

L C L I P G Y F S *
(in frame with CACNA1G-201)

GGCTGTGTGCAGATGGGGAGGCATCTTGCCAGTCTGCCTCAGGGCCTCGGGGGCATGCAGAGTGGCCATGGAAGCCGTTCTTTG
CCGACACACGTCTACCCTCCGTAGAAGCGGTTCAGACGGAGTCCGGAGCCCCCGTACGTCTCACCAGTACCTTCGGCAAGAAAC

1360

CACNA1G

CACNA1G-201

CTCCTGGTCACTCCTTCCAGGTCAAACAAGTAGATTTTCAGGGGCCATAGTGGGGACATGGGTCACCTCTGCTTGGCTGCGAAC
GAGGACCAGTAGGAAGGTCCAGTTTGGTTCATCTAAAAGTCCCCGGTATCACCCCTGTACCCAGTGAAGACGAACCGACGCTTG

1445

CACNA1G

CACNA1G-201

gggccagttttggttcatctaaaag

PCR Reverse

CTGTCAGTCCTTCTCAGAAGGAGAGCCAGAGGCCCTGGACATACCGCCCCAGGGTTCGAACCCCTTCAGGGTGGGCCCAGCTCACC
GACAGTCAGGAAGAGTCTTCTCCTCCTCGGTCTCCGGGACCTGTATGGCGGGGTCCCAGCTTGGGGAAAGTCCCACCCGGGTTCGAGTGG

1530

CACNA1G

CACNA1G-201

CTGGGAGCTGTCTCTTCTAGCCTGGCATTATAGCCCTTTCGCTGTGCGGAGCAATTCTGGTTCCAGAAGGATGGGTGGGGGGTGG
GACCCTCGACAGAGAAGGATCGGACCGTAATATCGGGAAGCGACAGCCGTCGTTAAGACCAAGGTCTTCTACCCACCCCCACC

1615

CACNA1G

CACNA1G-201

TTGTGTTTCCGCTCACGGCATCCTGCACCACTTGCCTTAGAGGTGGCCAGGGTTTGCCTCTCATCCCTCTTTGCCATCTCCCACAC
AACACAAAGGCGAGTGCCTGAGGACGTGGTGAACGAATCTCCACCGGTCCCAAACGGAGAGTAGGGAGAAACGGTAGAGGGTGTG

1700

CACNA1G

CACNA1G-201

CATTGTTTAGATTTTCAGCGCTGCTGGGGCTTCTGTTTTCTATTAGGGTCGGGGTGGAGGGAGCCTGAGGAATGGCGGGAGCAGCC
GTAACAAATCTAAAGTCGCGACGACCCCGAAGACAAAAGATAATCCAGCCCCACCTCCCTCGGACTCCTTACCGCCCTCGTCGG

1785

CACNA1G

CACNA1G-201

CAAGACTAGGCGGGTGAGAGAGCACCCGCACTGGGGACCTCACACCCGGAGTCACAGGGTAAGGCAGGGGCGCTGGCTGCACTCC
GTTCTGATCCGCCCACTCTCTCGTGGGCGTGACCCCTGGAGTGTGGGCCTCAGTGTCCCATTCGGTCCCCGCGACCGACGTGAGG

1870

CACNA1G

CACNA1G-201

AGCCTTGGCTGCCTCCCGCCTGAGGCCCTGCTGTAGAGCTCTCTGTACCATGTCACTGTCTCCACG
TCGGAACCGACGGAGGGCGGACTCCGGGACGACATCTCGAGAGACAGTGGTACAGTGACAGAGGTGC

3'

1937

5'

CACNA1G









CACNA1G-201

Feature	Location	Size	Start	End	Type
✓ CACNA1G	1 .. 1937	1937 bp	■	➔	gene
/note = gene ENSG00000006283 Protein coding					
CACNA1G-AS1	1 .. 1937	1937 bp	■	←	gene
/note = gene ENSG00000250107 lncRNA					
✓ CACNA1G-201	1 .. 1937	1937 bp	■	➔	prim_transcript
/note = primary transcript ENST00000352832					
CACNA1G-202	1 .. 1937	1937 bp	■	➔	prim_transcript
/note = primary transcript ENST00000354983					
CACNA1G-203	1 .. 1937	1937 bp	■	➔	prim_transcript
/note = primary transcript ENST00000358244					
CACNA1G-204	1 .. 1937	1937 bp	■	➔	prim_transcript
/note = primary transcript ENST00000359106					
CACNA1G-205	1 .. 1937	1937 bp	■	➔	prim_transcript
/note = primary transcript ENST00000360761					
CACNA1G-206	1 .. 1937	1937 bp	■	➔	prim_transcript
/note = primary transcript ENST00000416767					
CACNA1G-207	1 .. 1937	1937 bp	■	➔	prim_transcript
/note = primary transcript ENST00000429973					
CACNA1G-208	1 .. 1937	1937 bp	■	➔	prim_transcript
/note = primary transcript ENST00000442258					
CACNA1G-209	1 .. 1937	1937 bp	■	➔	prim_transcript
/note = primary transcript ENST00000502264					
CACNA1G-210	1 .. 1937	1937 bp	■	➔	prim_transcript
/note = primary transcript ENST00000503436 Nonsense mediated decay					
CACNA1G-211	1 .. 1937	1937 bp	■	➔	prim_transcript
/note = primary transcript ENST00000503485					
CACNA1G-212	1 .. 1937	1937 bp	■	➔	prim_transcript
/note = primary transcript ENST00000503607 Nonsense mediated decay					
CACNA1G-213	1 .. 1937	1937 bp	■	➔	prim_transcript
/note = primary transcript ENST00000504076 Nonsense mediated decay					
CACNA1G-214	1 .. 1937	1937 bp	■	➔	prim_transcript
/note = primary transcript ENST00000505165					
CACNA1G-215	1 .. 1937	1937 bp	■	➔	prim_transcript
/note = primary transcript ENST00000506406 Nonsense mediated decay					
CACNA1G-216	1 .. 1937	1937 bp	■	➔	prim_transcript
/note = primary transcript ENST00000506520					
CACNA1G-217	1 .. 1937	1937 bp	■	➔	prim_transcript
/note = primary transcript ENST00000507336					
CACNA1G-218	1 .. 1937	1937 bp	■	➔	prim_transcript
/note = primary transcript ENST00000507510					
CACNA1G-219	1 .. 1937	1937 bp	■	➔	prim_transcript
/note = primary transcript ENST00000507609					
CACNA1G-220	1 .. 1937	1937 bp	■	➔	prim_transcript
/note = primary transcript ENST00000507896					
CACNA1G-221	1 .. 1937	1937 bp	■	➔	prim_transcript
/note = primary transcript ENST00000510115					
CACNA1G-222	1 .. 1937	1937 bp	■	➔	prim_transcript
/note = primary transcript ENST00000510366					

Feature	Location	Size	Start	End	Type
CACNA1G-223	1 .. 1937	1937 bp	■	→	prim_transcript
/note = primary transcript ENST00000511765 Nonsense mediated decay					
CACNA1G-224	1 .. 1937	1937 bp	■	→	prim_transcript
/note = primary transcript ENST00000511768 Nonsense mediated decay					
CACNA1G-225	1 .. 1937	1937 bp	■	→	prim_transcript
/note = primary transcript ENST00000512389					
CACNA1G-226	1 .. 1937	1937 bp	■	→	prim_transcript
/note = primary transcript ENST00000513689					
CACNA1G-227	1 .. 1937	1937 bp	■	→	prim_transcript
/note = primary transcript ENST00000513964					
CACNA1G-228	1 .. 1937	1937 bp	■	→	prim_transcript
/note = primary transcript ENST00000514079					
CACNA1G-229	1 .. 1937	1937 bp	■	→	prim_transcript
/note = primary transcript ENST00000514181					
CACNA1G-230	1 .. 1937	1937 bp	■	→	prim_transcript
/note = primary transcript ENST00000514717					
CACNA1G-231	1 .. 1937	1937 bp	■	→	prim_transcript
/note = primary transcript ENST00000515165					
CACNA1G-232	1 .. 1937	1937 bp	■	→	prim_transcript
/note = primary transcript ENST00000515411					
CACNA1G-233	1 .. 1937	1937 bp	■	→	prim_transcript
/note = primary transcript ENST00000515765					
CACNA1G-AS1-202	1 .. 1937	1937 bp	■	←	prim_transcript
/note = primary transcript ENST00000505793 lncRNA					
CACNA1G-201	518 .. 966	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000339302					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-202	518 .. 966	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000347078					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-203	518 .. 966	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000350979					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-204	518 .. 966	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000352011					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-205	518 .. 966	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000353990					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					

Feature	Location	Size	Start	End	Type
CACNA1G-206	518 .. 966	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000392390					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-207	518 .. 966	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000414388					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-208	518 .. 966	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000409759					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-209	518 .. 966	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000425522					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-211	518 .. 966	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000427238					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-214	518 .. 966	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000422268					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-216	518 .. 966	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000427697					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-217	518 .. 966	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000420918					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-218	518 .. 966	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000423112					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-219	518 .. 966	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000423045					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-220	518 .. 966	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000421518					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					

Feature	Location	Size	Start	End	Type
CACNA1G-221	518 .. 966	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000427173					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-222	518 .. 966	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000426814					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-225	518 .. 966	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000426261					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-226	518 .. 966	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000426172					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-227	518 .. 966	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000425451					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-228	518 .. 966	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000423317					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-229	518 .. 966	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000425698					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-230	518 .. 966	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000422407					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-231	518 .. 966	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000426098					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-232	518 .. 966	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000423155					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-233	518 .. 966	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000426232					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
✓ Donor Template WT -> SNV	867 .. 966	100 bp	■		misc_feature
✓ PAM	926 .. 928	3 bp	■		misc_feature
✓ gRNA Protospacer	929 .. 948	20 bp	■		misc_feature

Feature		Location	Size			Type
✓ SNV		940 .. 940	1 bp			misc_feature
/note	= WT = C SNV = A					
		1938 .. 6403	4466 bp			gene
/note	= gene ENSG00000251239 lncRNA					
		1938 .. 6403	4466 bp			prim_transcript
/note	= primary transcript ENST00000502435 lncRNA					

Primer	Length		Binding Sites	↕	Tm	Date Added
✓ PCR Forward /sequence = tgctcatactccagtgtttggttctg 44% GC / 7605.0 Da	25-mer		490 .. 514	→	59°C	Oct 5, 2023
✓ Donor Template WT -> SNV /sequence = CATCACCCACAAGATGTTTCGACCACGTGGTCCTTGTCATCATCTTCCTTAAGTGCATCACCATCGCCATGGAGAGCCCCAAAATTGACCCCCACAGCGCT 53% GC / 30,427.7 Da	100-mer		867 .. 966	→	79°C	Oct 5, 2023
✓ gRNA Protospacer /sequence = TTTGGGGCGCTCCATGGCGA 65% GC / 6165.0 Da	20-mer		929 .. 948	←	66°C	Oct 5, 2023
✓ Sanger Sequencing Primer /sequence = ggaccaggatctggtgagag 60% GC / 6247.1 Da	20-mer		1105 .. 1124	←	57°C	Oct 5, 2023
✓ PCR Reverse /sequence = gaaaatctacttggttttgacctgg 40% GC / 7687.1 Da	25-mer		1376 .. 1400	←	57°C	Oct 5, 2023