

CZK2J00162_CACNA1G_R1274S_A09_AB
2346 bp

5'
3'

CAGAAAGACCCATCACTCATCTCTCCAAACTGATGCCCGCATCCCCCTTCTCGTCTCAACCTCATCACAAGCCATGACTTCCC
GTCTTTCTGGGTAGTGAGTAGAGAGGTTTGACTACGGGGCGTAGGGGAAAGAGCAGAGTTGGAGTAGTGTTCGGTACTGAAGGG

85

CACNA 1G >

CACNA 1G-201 >

ACTCTATCCATACCCATGTGCCCCCTGCCCCAGCCCCTCATCACCACCATTCCCCCTGGGGATGGGGTGCAGTGACCTCAGGGTTA
TGAGATAGGTATGGGTACACGGGGACGGGGTCGGGGAGTAGTGGTGGTAAGGGGGACCCCTACCCACGTCACTGGAGTCCCAAT

170

CACNA 1G >

CACNA 1G-201 >

GCATGTGAAGAGCAGGGCCAGTGTCTCCTCAGCTGAGGTGTGTCTCTGAACAGACAGCTGTGTGGGGCCAGTGTGATAACTGA
CGTACACTTCTCGTCCCGGTCACAGAGGAGTCGACTCCACACAGAGACTTGTCTGTGACACACCCCGGTCACAACTATTGACT

255

CACNA 1G >

CACNA 1G-201 >

TGCTGCTTCCCAGCTCAGCAGGGAGGACAGGCAGGGGGCTGGGCTGGAGGCAGGGGTGGGGAGAGGGGAGAGCGGGGTTGGGGAT
ACGACGAAGGGTCGAGTCGTCCCTCCTGTCCGTCCCCCGACCCGACCTCCGTCCCCACCCCTCTCCCCTCTCGCCCCAACCCCTA

340

CACNA 1G >

CACNA 1G-201 >

GCAGGGGAGGAGAGGGAGGAGGTGGAGAGGCAAGGGGTCCTCAGGGATGGGGAGGGGGCTGGCAAGGTTGACAGGGAGATGAGG
CGTCCCCTCCTCTCCCTCCTCACCTCTCCGTTCCCCAGGAGTCCCTACCCCTCCCCGGACCGTTCACACTGTCCCTCTACTCC

425

CACNA 1G >

CACNA 1G-201 >

AGGTGGCTTTAGGAATAAAGGAAGAGAGGCAGGGCAGAGCTTGGGCCCCAGGTGGGAGAGGGTAGACAAGGAGTGAGGGCTCGTGA
TCCACCGAAATCCTTATTTCTTCTCTCCGTCCCGTCTCGAACCCGGGGTCCACCCTCTCCCATCTGTTTCTCACTCCGAGCACT

510

CACNA 1G >

CACNA 1G-201 >

PCR Forward
tgctcataactccagtgtttgttctg

CTCTGCTGAGGAGCCAGGAGCCGGGGAACCTGGAGGCCTGGTCTGCTCATACTCCAGTGTGTTGTTCTGCAGAGCAAAGGGGAAC
GAGACGACTCCTCGGTCTCGGCCCTTGGACCTCCGGACCAGGACGAGTATGAGGTACAAACAAGACGTCTCGTTTCCCCTTG

595

CACNA 1G >

CACNA 1G-201 >

1210
S K G E
ENSE00002531395
CACNA 1G-201 >

GGGTCCGCGCGTGGATCCGAGCCCAGCTCCCTGCCTGCTGCCTCGAGCGAGACTCCTGGTCAGCCTACATCTTCCCTCCTCAGTC
CCCAGGCGCGCACCTAGGCTCGGGCTGAGGGACGGACGACGGAGCTCGCTCTGAGGACCAGTCGGATGTAGAAGGGAGGAGTCAG

680

CACNA 1G >

CACNA 1G-201 >

R V R A W I R A R L P A C C L E R D S W S A Y I F P P Q S
1215 1220 1225 1230 1235 1240
ENSE00002531395
CACNA 1G-201 >

CAGGTAAGTGACAGGGCAGGGGTCTGACCTGTGTCCCGACCTCTTCTTCTCACGGGAAATTACCGCTGGTGTGCTGTCAGGGAT
GTCCATTCACCTGTCCCCTCCCAGACTGGACACAGGGCTGGAGAAGAAGAGTGCCCTTTAATGGCGACCACTACGACAGTCCCTA

765

————— CACNA1G —————>

————— CACNA1G-201 —————>

—
R
|
————— CACNA1G-201 —————>

TTGAGAAGTGGCACCCCTGCCTGGGGTGTGAGCAGGGTGGCCTCAGCTGGGAGGGCACTGGAGGGGCAGGGGCTGCGGGCGGTGCC
AACTCTTCACCGTGGGACGGACCCACACTCGTCCCACCGGA6TGCACCCTCCCGTGACCTCCCCGTCCCCGACGCCCGCCACGG

850

————— CACNA1G —————>

————— CACNA1G-201 —————>

————— CACNA1G-201 —————>

Donor Template WT -> SNV

CATC

TCTCGTTGCCACCTGCCCTGCCTCCCCCTCTCAGCCGTTGCCTCCATGCCTGGGCAGGTTCCGCCTCCTGTGTACCCGGATCATC
AGAGCAACGGTGGACGGGACGGAGGGGGAGAGTCCGGCAACGGAGGTACGGACCCGTCCAAGGCGGAGGACACAGTGGCCTAGTAG

935

————— CACNA1G —————>

————— CACNA1G-201 —————>

————— CACNA1G-201 —————>
F R L L C H R I I
ENSE00002533559

Donor Template WT -> SNV

Donor Template WT -> SNV

ACCCACAAGATGTTTCGACCACGTGGTCCTTGTGCATCATCTTCTTAACTGCATCACCATCGCCATGGAGAGCCCCAAAATTGACC
ACCCACAAGATGTTTCGACCACGTGGTCCTTGTGCATCATCTTCTTAACTGCATCACCATCGCCATGGAGAGCCCCAAAATTGACC
TGGGTGTTCTACAAGCTGGTGCACCAGGAACAGTAGTAGAAGGAATTGACGTAGTGGTAGCGGTACCTCGCGGGTTTTAACTGG

1020

————— CACNA1G —————>

————— CACNA1G-201 —————>

T H K M F D H V V L V I I F L N C I T I A M E R P K I D
ENSE00002533559
————— CACNA1G-201 —————>

Donor Template WT -> SNV

PAM gRNA Protospacer

SNV

AGCGGTACCTCGCGGGTTT
gRNA Protospacer

Donor Template WT -> SNV

CCCACAGCGCT

CCCACAGCGCTGTGAGTCACCCAGCCCCGCTCAGGGCAAGGCCCTCTCCTGGGGTTTGCACCTCAGGACCAGTGAGGGGAGGCAAGGAG
GGGTGTCGCGACACTCAGTGGTCGGGGCGAGTCCCGTTCGGGAGAGGACCCCAAACGTGAGTCTGGTCACTCCCTCCGTTCTCT

1105

CACNA1G

CACNA1G-201

1280
P H S A V S H Q P R S G Q G L S W G L H S G P V R E A R R

ENSEF0000253... (in frame with CACNA1G-201)
CACNA1G-201

Donor Template WT -> SNV

GCCACAGTTGCTGACCTGCAAGTCACACAGCAGGGAACGAGGGGGCCAGGACTCTCCTTTAGGTCTCTCACCAGATCCTGGTCCC
CGGTGTC AACGACTGGACGTT CAGTGTGTCGTCCTTGTCTCCCGGTCCTGAGAGGAAATCCAGAGAGTGGTCTAGGACCAGGG

1190

CACNA1G

CACNA1G-201

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

gagagtggcttaggaccagg

Sanger Sequencing Primer

CGGGATGCCCCCTGTGTCCTCTCCTGCCTCAGTTTCCCTTCTATGATACATCAGCCCAGCTGGGTGCTTTGTCTCATTCCAGGCT
GCCCTACGGGGGACACAGGAGAGGACGGAGTCAAAGGGAAGATACTATGTAGTTCGGGTCGACCCACGAAACAGAGTAAGGTCCGA

1275

CACNA1G

CACNA1G-201

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

ATTTCTCATGAGCCAGAGCCTTGTGGGGCACACGCGTGAGTCGGGGAGTGTGGGGCGGTGCAGGGGCTGTGTGCAGATGGGGAG
TAAAGAGTACTCGGTCTCGGAACACCCCGTGTGCGCACTCAGCCCTCAGGACCCCGCCACGTCCCCGACACAGTCTACCCCTC

1360

CACNA1G

CACNA1G-201

Y F S *

GCATCTTGCCAGTCTGCCTCAGGGCCTCGGGGGCATGCAGAAGTGGCCATGGAAGCCGTTCTTTGCTCCTGGTCACTCTCCAGG
CGTAGAACGGGT CAGACGGAGTCCCGGAGCCCCCGTACGTCTCACCAGTACCTTCGGCAAGAAACGAGGACCAGTAGGAAGGTCC

1445

CACNA1G

CACNA1G-201

gggcc

PCR Reverse

TCAAACCAAGTAGATTTTCAGGGGCCATAGTGGGGACATGGGTCACTTCTGCTTGGCTGCGAACCTGTCAGTCTTCTCAGAAG
AGTTTTGGTTCATCTAAAAGTCCCCGGTATCACCCCTGTACCCAGTGAAGACGAACCGACGCTTGGACAGTCAGGAAGAGTCTTC

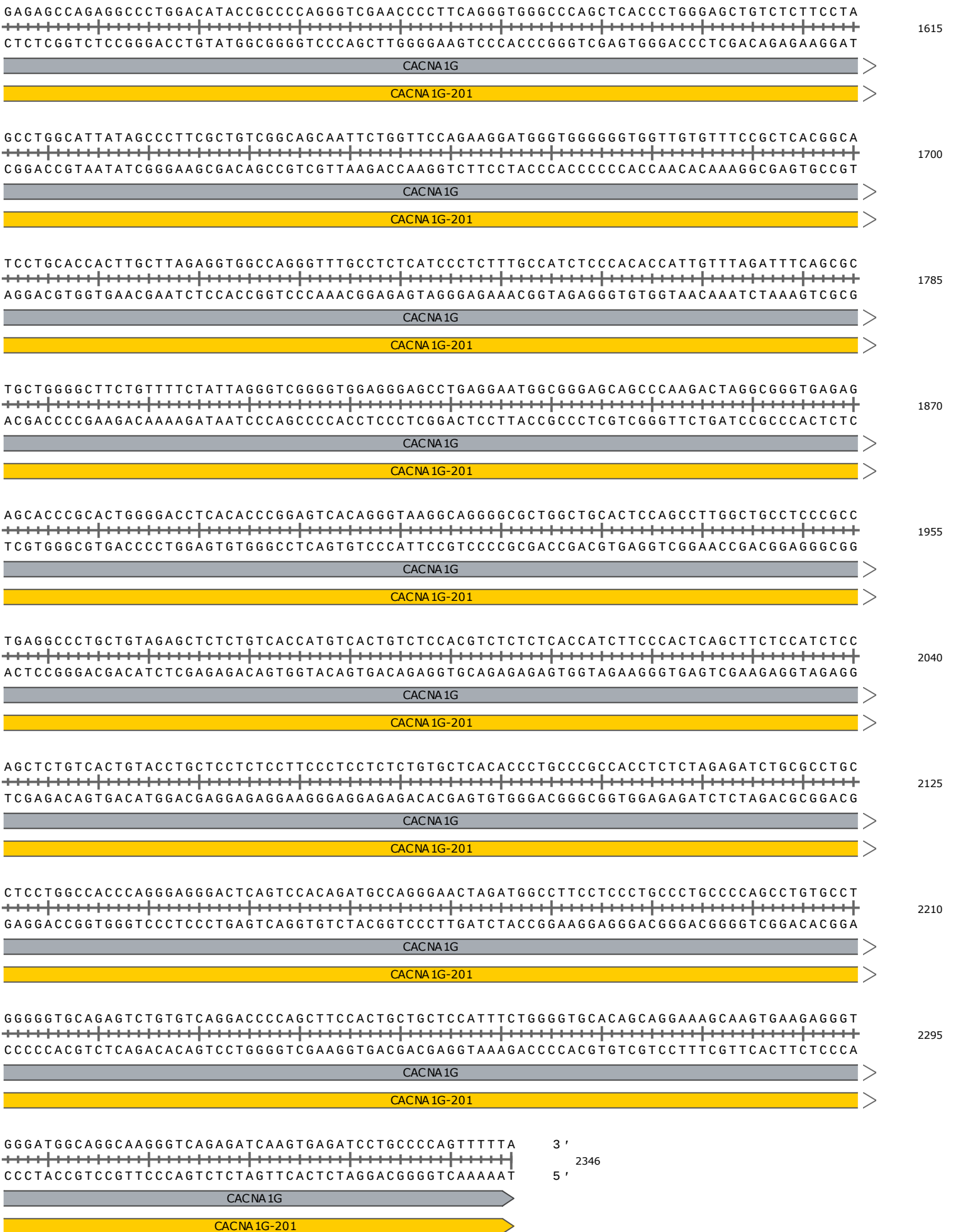
1530

CACNA1G

CACNA1G-201

agttttggttcatctaaaag

PCR Reverse











Feature	Location	Size	Start	End	Type
✓ CACNA1G	1 .. 2346	2346 bp	■	➔	gene
/note = gene ENSG00000006283 Protein coding					
CACNA1G-AS1	1 .. 2346	2346 bp	■	←	gene
/note = gene ENSG00000250107 lncRNA					
✓ CACNA1G-201	1 .. 2346	2346 bp	■	➔	prim_transcript
/note = primary transcript ENST00000352832					
CACNA1G-202	1 .. 2346	2346 bp	■	➔	prim_transcript
/note = primary transcript ENST00000354983					
CACNA1G-203	1 .. 2346	2346 bp	■	➔	prim_transcript
/note = primary transcript ENST00000358244					
CACNA1G-204	1 .. 2346	2346 bp	■	➔	prim_transcript
/note = primary transcript ENST00000359106					
CACNA1G-205	1 .. 2346	2346 bp	■	➔	prim_transcript
/note = primary transcript ENST00000360761					
CACNA1G-206	1 .. 2346	2346 bp	■	➔	prim_transcript
/note = primary transcript ENST00000416767					
CACNA1G-207	1 .. 2346	2346 bp	■	➔	prim_transcript
/note = primary transcript ENST00000429973					
CACNA1G-208	1 .. 2346	2346 bp	■	➔	prim_transcript
/note = primary transcript ENST00000442258					
CACNA1G-209	1 .. 2346	2346 bp	■	➔	prim_transcript
/note = primary transcript ENST00000502264					
CACNA1G-210	1 .. 2346	2346 bp	■	➔	prim_transcript
/note = primary transcript ENST00000503436 Nonsense mediated decay					
CACNA1G-211	1 .. 2346	2346 bp	■	➔	prim_transcript
/note = primary transcript ENST00000503485					
CACNA1G-212	1 .. 2346	2346 bp	■	➔	prim_transcript
/note = primary transcript ENST00000503607 Nonsense mediated decay					
CACNA1G-213	1 .. 2346	2346 bp	■	➔	prim_transcript
/note = primary transcript ENST00000504076 Nonsense mediated decay					
CACNA1G-214	1 .. 2346	2346 bp	■	➔	prim_transcript
/note = primary transcript ENST00000505165					
CACNA1G-215	1 .. 2346	2346 bp	■	➔	prim_transcript
/note = primary transcript ENST00000506406 Nonsense mediated decay					
CACNA1G-216	1 .. 2346	2346 bp	■	➔	prim_transcript
/note = primary transcript ENST00000506520					
CACNA1G-217	1 .. 2346	2346 bp	■	➔	prim_transcript
/note = primary transcript ENST00000507336					
CACNA1G-218	1 .. 2346	2346 bp	■	➔	prim_transcript
/note = primary transcript ENST00000507510					
CACNA1G-219	1 .. 2346	2346 bp	■	➔	prim_transcript
/note = primary transcript ENST00000507609					
CACNA1G-220	1 .. 2346	2346 bp	■	➔	prim_transcript
/note = primary transcript ENST00000507896					
CACNA1G-221	1 .. 2346	2346 bp	■	➔	prim_transcript
/note = primary transcript ENST00000510115					
CACNA1G-222	1 .. 2346	2346 bp	■	➔	prim_transcript
/note = primary transcript ENST00000510366					

Feature	Location	Size	Start	End	Type
CACNA1G-223	1 .. 2346	2346 bp	■	→	prim_transcript
/note = primary transcript ENST00000511765 Nonsense mediated decay					
CACNA1G-224	1 .. 2346	2346 bp	■	→	prim_transcript
/note = primary transcript ENST00000511768 Nonsense mediated decay					
CACNA1G-225	1 .. 2346	2346 bp	■	→	prim_transcript
/note = primary transcript ENST00000512389					
CACNA1G-226	1 .. 2346	2346 bp	■	→	prim_transcript
/note = primary transcript ENST00000513689					
CACNA1G-227	1 .. 2346	2346 bp	■	→	prim_transcript
/note = primary transcript ENST00000513964					
CACNA1G-228	1 .. 2346	2346 bp	■	→	prim_transcript
/note = primary transcript ENST00000514079					
CACNA1G-229	1 .. 2346	2346 bp	■	→	prim_transcript
/note = primary transcript ENST00000514181					
CACNA1G-230	1 .. 2346	2346 bp	■	→	prim_transcript
/note = primary transcript ENST00000514717					
CACNA1G-231	1 .. 2346	2346 bp	■	→	prim_transcript
/note = primary transcript ENST00000515165					
CACNA1G-232	1 .. 2346	2346 bp	■	→	prim_transcript
/note = primary transcript ENST00000515411					
CACNA1G-233	1 .. 2346	2346 bp	■	→	prim_transcript
/note = primary transcript ENST00000515765					
CACNA1G-AS1-202	1 .. 2346	2346 bp	■	←	prim_transcript
/note = primary transcript ENST00000505793 lncRNA					
CACNA1G-201	583 .. 1031	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000339302					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-202	583 .. 1031	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000347078					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-203	583 .. 1031	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000350979					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-204	583 .. 1031	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000352011					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-205	583 .. 1031	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	583 .. 1031	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000392390					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-207	583 .. 1031	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000414388					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-208	583 .. 1031	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000409759					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-209	583 .. 1031	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000425522					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-211	583 .. 1031	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000427238					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-214	583 .. 1031	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000422268					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-216	583 .. 1031	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000427697					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-217	583 .. 1031	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000420918					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-218	583 .. 1031	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000423112					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-219	583 .. 1031	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000423045					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-220	583 .. 1031	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	583 .. 1031	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000427173					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-222	583 .. 1031	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000426814					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-225	583 .. 1031	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000426261					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-226	583 .. 1031	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000426172					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-227	583 .. 1031	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000425451					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-228	583 .. 1031	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000423317					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-229	583 .. 1031	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000425698					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-230	583 .. 1031	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000422407					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-231	583 .. 1031	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000426098					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-232	583 .. 1031	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000423155					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
CACNA1G-233	583 .. 1031	449 bp	■	→	CDS
▶ 2 segments = 225 bp					
/note = coding sequence ENSP00000426232					
/translation = SKGERVRAWIRARLPACCLERDSWSAYIFPPQSR,,FRLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSA 75 amino acids = 8.8 kDa					
✓ Donor Template WT -> SNV	932 .. 1031	100 bp	■		misc_feature
✓ PAM	991 .. 993	3 bp	■		misc_feature
✓ gRNA Protospacer	994 .. 1013	20 bp	■		misc_feature

Feature		Location	Size			Type
✓ SNV		1005 .. 1005	1 bp			misc_feature
/note	= WT = C SNV = A					
		2347 .. 6812	4466 bp			gene
/note	= gene ENSG00000251239 lncRNA					
		2347 .. 6812	4466 bp			prim_transcript
/note	= primary transcript ENST00000502435 lncRNA					

Primer	Length	Binding Sites	Tm	Date Added
✓ PCR Forward /sequence = tgctcatactccagtggtttgttctg 44% GC / 7605.0 Da	25-mer	555 .. 579 →	59°C	Oct 5, 2023
✓ Donor Template WT -> SNV /sequence = CATCACCCACAAGATGTTTCGACCACGTGGTCCTTGTCATCATCTTCCTTAAGTGCATCACCATCGCCATGGAGAGCCCCAAAATTGACCCACAGCGCT 53% GC / 30,427.7 Da	100-mer	932 .. 1031 →	79°C	Oct 5, 2023
✓ gRNA Protospacer /sequence = TTTGGGGCGCTCCATGGCGA 65% GC / 6165.0 Da	20-mer	994 .. 1013 ←	66°C	Oct 5, 2023
✓ Sanger Sequencing Primer /sequence = ggaccaggatctggtgagag 60% GC / 6247.1 Da	20-mer	1170 .. 1189 ←	57°C	Oct 5, 2023
✓ PCR Reverse /sequence = gaaaatctacttggttttgacctgg 40% GC / 7687.1 Da	25-mer	1441 .. 1465 ←	57°C	Oct 5, 2023