



**INK2J00034\_CACNA1A\_R583Q\_C05\_BB**  
 20,614 bp

5'

3'

CCTGGGCAACAAAGCAAGATCCTGTCTCAAAAAAAAAAAAAAAAAAAGATGTATTTTAGAAGGTAAATTCATCTGTCCAAAACTGAG  
GGACCCGTTGTTTCGTTCTAGGACAGAGTTTTTTTTTTTTTTTTTCTACATAAAATCTTCCATTTAAGTTAGACAGGTTTTGACTC

85

CACNA1A

CACNA1A-201

CTCTGACCTTCCCCTAAACCTGTGCCCATTCAGTGGATGAGAGCTCCATCCCTTAAGGGGTTACCAATTCATCCATTCCCTTTGT  
GAGACTGGAAGGGGATTTGGACACGGGTAAGTCACCTACTCTCGAGGTAGGGAATCCCCAAGTGTTAAGTAGGTAAGGAAACA

170

CACNA1A

CACNA1A-201

ATGTACATCATTCAATTCACCTTGGCTCATCCCTCTCTCTTACATCCACACCGTTCCATCAGCAAATGTTGAATCTGTCTTAAATG  
TACATGTAGTAAGTAAGTGAACCGAGTAGGGAGAGAGAATGTAGGTGTGGCAAGGTAGTCGTTTACAACCTTAGACAGAATTTAC

255

CACNA1A

CACNA1A-201

ATTCATCCCAAATCCTCCCCGCTTAACTACCACCCAACCTCCAGCCCCATCCATCATCATCACTTGCCTGGATGGGTTCAAGT  
TAAGTAGGGTTTAGGAGGGGCGAATTGATGGTGGGTTGAGGTCGGGGGTAGGTAGTAGTAGTAGTGAACGGACCTACCCAAGTCA

340

CACNA1A

CACNA1A-201

CACCTCCAGCCTGGTCTCCAGCTCCCGTCTCACCTCTCACTGTCTACTCTCCCACTCGGCAGCCAGAGGGTGCCTGTGAACAC  
GTGGAGGTCCGACCAGAGGGTTCGAGGGCAGGAGTGGAGAGTGACAGATGAGAGGGTGAGCCGTCGGTCTCCACGGACACTTGTG

425

CACNA1A

CACNA1A-201

CCAAATCAGGTTCCATCCCTCCTCTACTCAGAACCCTCCACGGCTCCCCCTCACTCAGGGTAAAAGCCAAAGTCTCTCTTGTGG  
GGTTTAGTCCAAGGTAGGGAGGAGATGAGTCTTGGGAGGTGCCGAGGGGGGAGTGAGTCCCATTTTCGGTTTCAGGAGGAACACC

510

CACNA1A

CACNA1A-201

TCCACCAGGCCATGCATGATCTGCCTGTCACCTCCCTGCCTTACCACCTTCCCTCTTTTCCCCTCAACCACTCCACTCCAGCCAC  
AGGTGGTCCGGTACGTACTAGACGGACAGTGGAGGGACGGAAGTGGTGGAAAGGAGAAAAGGGGAGTTGGTGAGGTGAGGTCCGGTG

595

CACNA1A

CACNA1A-201

ACTGACTTCCTTGTGCTCTTCCCCAAAAATGTCGGGCAGACACATTCATGCTTCAGGACCTTAAATTTGCTGTTTTCTCTACCTA  
TGACTGAAGGAACACGAGAAGGGTTTTTACAGCCCGTCTGTGTAAGTACGAAGTCTTGAATTTAAACGACAAAGGAGATGGAT

680

CACNA1A

CACNA1A-201

AGATACTAAAGTGACAAGTCAACACACTCACCTTGACCATGCAATTTAATGTTGCAGCCTACCCTGTGGACTCTCCAAGGGCTCC  
TCTATGATTTCACTGTTCAAGTTGTGTGAGTGGAACTGGTACGTTAAATTACAACGTCGGATGGGACACCTGAGAGGTTCCCGAGG

765

CACNA1A

CACNA1A-201

CAGTCCCTCTGTGATGCTTTACTTTTTCTCTTAAAAAAAAAATGTTATTTAAAAGAACTTGTCTCGCTGTGTTGCCAGGCTGG  
GTCAGGGGAGACACTACGAAATGAAAAAGAGAATTTTTTTTTTAAACAATAAATTTCTTGAACAGAGCGACACAACGGGTCCGACC

850

CACNA1A

CACNA1A-201

TGTCAAAACCTCCTGGCCTCATACAGTCTCCCATTCAGCTTCCCAAAGTACTGGGATTAGAGGCATGTGCCACTGCACCCATCCC  
ACAGTTTGGAGACCGGAGTATGTCAGGAGGGTAAGGTCGAAGGGTTTCATGACCCCTAATCTCCGTACACGGTGACGTGGGTAGGG

935

CACNA1A

CACNA1A-201

AACTTTTTTTTTTCCCATAGCACTTTTCATTTTCCATCCCCTGTTAATTTACTTATTACGTCCACTGTCTGTCTCCTCCCCTTAG  
TTGAAAAAAAAAAGGGTATCGTGAAAAGTAAAAGGTAGGGTGACAATTAATGAATAATGCAGGTGACAGACAGAGGGAGGGGAATC

1020

CACNA1A

CACNA1A-201

AGGGTCAGACCCCGGAAGTCCAGGCTCTGTTGCCTAATGTATCCTGAGCCCCTGGAACAGAGCCTGGCACAAAATAGGTA CTCAA  
TCCAGTCTGGGGCCTTCAGGTCCGAGACAACGGATTACATAGGACTCGGGGACCTTGTCTCGGACCGTGTTTTATCCATGAGTT

1105

CACNA1A

CACNA1A-201

TAAATGCATAAGAGCAAAACTATATGTAGGCAGAGGACACACCCAGCTTATTCCTCAGTGATCACTTCTAAAGTTAAATGTCCAT  
ATTTACGTATTCTCGTTTTGATATACATCCGTCTCCTGTGTGGGTCGAATAAGGAGTCACTAGTGAAGATTTCAATTTACAGGTA

1190

CACNA1A

CACNA1A-201

GGAAAAACAGTCTCATCCACATCTCTTTCTGGAGGCCTTCCAAGCGTGCTCCATGCAGCTCTGTTGCCTGCCCTGCATCAGGGAA  
CCTTTTGTGAGAGTAGGTGTAGAGAAAAGACCTCCGGAAGGTTTCGCACGAGGTACGTGAGACAACGGACGGGGACGTAGTCCCTT

1275

CACNA1A

CACNA1A-201

TGGAGGCTCTGCTTTATCCTGCCCTGTGGTGTGACTCCCAGAGGCATCAGATGTGGCTGGGAGTGGGAGACATGGAAAATTGGCT  
ACCTCCGAGACGAAAATAGGACGGGACACCACACTGAGGGTCTCCGTAGTCTACACCGACCTCACCTCTGTACCTTTTAACCGA

1360

CACNA1A

CACNA1A-201

CCTGCAACAGAGAACTATCAGCCTTCCCATCAATTGGTFACTTCTAATTCTGTTATTTTTTCAGGGGCACTGTCTTCTCATAAGCT  
GGACGTTGTCTTTGATAGTCCGGAAGGGTAGTTAACCAATGAAGATTAAGACAATAAAAAGTCCCCGTGACAGAAGAGTATTCTGA

1445

CACNA1A

CACNA1A-201

CCATCTATGCAAAAAC TAAGCCATGGGTCATGATGGTTCCCTCAGGCCAGAGGCTTGCTGGAGAGACTAATGGATCCCCTGGCTA  
GGTAGATACGTTTTGATTCGGGTACCCAGTACTACCAAGGGAGTCCGGTCTCCGAACGACCTCTCTGATTACCTAGGGGACCGAT

1530

CACNA1A

CACNA1A-201

AAATCTGTGCTTGGGCTGCACATTGGTTAATTTCTTCTGAAGGAACAGCCTGAGCCTGACATTCTCCATCTTTTCCCTGGCAGGT  
TTTAGACACGAACCCGACGTGTAACCAATTAAGAAGACTTCTTGTGCGGACTCGGACTGTAAGAGGTAGAAAAAGGGACCGTCCA

1615

CACNA1A

CACNA1A-201

CACNA1A-201

TCTCCCTTCGCCCAGCCAGCATTAAAAAGTGCCAAGCTGGAGAAGCTCGACCTTTTTTTCACAAAAAGGAGAGGGAGGATGCGTTTTCT  
AGAGGGAAGCGGGCTCGGTCGTAATTTTACCGGTTTCGACCTCTTGAGCTGGAAAAAAGTGTTTTTCTCTCCTCCTACGCAAAGA

1700

CACNA1A

CACNA1A-201

450 P F A R A S I K S A K L E N S T F F H K K E R R M R F

ENSE00001247111

CACNA1A-201

ACATCCGCCGCATGGTCAAAAAGCTCAGGCCTTCTACTGGACTGTACTCAGTTTGGTAGCTCTCAACACGCTGTGTGTTGCTATTGT  
TGTAGGCGGGCTACCAAGTTTTGAGTCCGGAAGATGACCTGACATGAGTCAAACCATCGAGAGTTGTGCGACACACAACGATAACA

1785

CACNA1A

CACNA1A-201

480 R M V K T Q A F Y W T V L S L V A L N T L C V A I V

ENSE00001247111

CACNA1A-201

TCACTACAACCAGCCCGAGTGGCTCTCCGACTTCCTTTGTGAGTATCACCCAGCCCCACCCCTGCCAACTCCCTGATCCCTCCCT  
AGTGATGTTGGTCGGGCTCACCGAGAGGCTGAAGGAAACACTCATAGTGGGTTCGGGGTGGGGACGGTTGAGGGACTAGGGAGGGA

1870

CACNA1A

CACNA1A-201

510 N Q P E W L S D F L

ENSE00001247111

CACNA1A-201

CACACCCTTTTTCCAATTCTCTTTCTCTGGTAGTATGTGTATCTTCTTTGGTCCTCATTGAATCTGCCCTTTCTTTAGCCATTT  
GTGTGGGAAAAAGGTGAAGAGAAAGAGACCATACACATAGAAGAAACCAGGAGTAACCTTAGACGGGAAAGGAAATCGGTAATA

1955

CACNA1A

CACNA1A-201

CACNA1A-201

CTATAACTGTCACTGGGGCCAATGTTACTGTTGCTATGACAATGGAACCCATCTCCCTTAGACCTGAGAGCTGGAAGCTGGAATT  
GATATTGACAGTGACCCCGGTTACAATGACAACGATACTGTTACCTTGGGTAGAGGGAATCTGGACTCTCGACCTTCGACCTTAA

2040

CACNA1A

CACNA1A-201

CACNA1A-201

CAGACCAACAAATGCTCCTGTGATTCTTTCTAAGAGAGAGGGACAGAGGGGTGCTGGTGAAGGGGATGTTGGAAGAGAGACAGA  
GTCTGGTTGTTTACGAGGACACTAAGGAAAGATTCTCTCCTGTCTCCACGACCACTTCCCCTACAACCTTCTCTCTGTCT

2125

CACNA1A

CACNA1A-201

CACNA1A-201

GAAAGACGGAGCTCATAAGATAGACAGATAGAAACAGAAACATACATGTATTAATAATTTTTATGTACATCTCTGGAAATGTTCA  
CTTTCTGCCTCGAGTATTCTATCTGTCTATCTTTGTCTTTGTATGTACATAATTATTAATAATACATGTAGAGACCTTTACAAGT

2210

CACNA1A

CACNA1A-201

CACNA1A-201

TAACCTTATGGTTAAGAGAGGATGCCTTAGAAATAAGGAGTGGCTTATATGTTGCCCTCATTTTTCTCTACTTATTTCTGACTCTAC  
ATTGAATACCAATTCTCTCCTACGGAATCTTTATTCTCACCGAATATACAACGGGAGTAAAAGAGATGAATAAAGACTGAGATG

2295

CACNA1A

CACNA1A-201

CACNA1A-201

TTCTCTCTTCTTTCAAACCTTCTGCTTCTTTCTGTTAGGTTGGTGCAAAATTAATTGCGTTTTTTGCCTTTTTTTTTTTTTTTTT  
AAGAGAGAAGAAAAGTTTGGAAAGACGAAGAAAAGGACAATCCAACCACGTTTTAATTAACGCAAAAAACGGAAAAAAAAAAAAAAAA

2380

CACNA1A

CACNA1A-201

CACNA1A-201

TTAACCCACAGTTACTTTTTGCACCAACCTAATACTTCTCCCTGCCCTTTTTGGCTTCTTATTTCATTCATAGAACATCCCCTCC  
AATTGGTGTCAATGAAAACGTGGTTGGATTATGAAGGAGGGGACGGGAAAAACCGAAGGAATAAGTAAGTATCTTGTAGGGGAGG

2465

CACNA1A

CACNA1A-201

CACNA1A-201

AGTATCTGCGAGAGCGTTTTGCTCCCTCAAGGTACAAGGCCCACTAAGGCTTTGCCCTCTGGGCCTATTCCCAGATTCTATGTGA  
TCATAGACGCTCTCGCAAAACGAGGGAGTTCCATGTTCCGGGTGATTCCGAAACGGGAGACCCGGATAAGGGTCTAAGATACACT

2550

CACNA1A

CACNA1A-201

CACNA1A-201

GTTAGCATGAGATAGTATCAAAATTGAGGGCCAAGTGAGGGTGAGGAAAAGCAGCAAAAGATGGGGAGATGTCTGAGCAGGATTT  
CAATCGTACTCTATCATAGTTTTAACTCCCGGTTCACTCCCCTCCTTTTTCGTCGTTTTCTACCCCTCTACAGACTCGTCTCTAAA

2635

CACNA1A

CACNA1A-201

CACNA1A-201

AAAAAGTAAAGAGCTCGAGGAATCAACAAGAGCAGCGACTGGGGCCAGGCATGGTGGCTCACACCTGTAATCCCAGCATTTTTGGG  
TTTTTCATTTCTCGAGCTCCTTAGTTGTTCTCGTCGCTGACCCCGGTCCGTACCACCGAGTGTGGACATTAGGGTCTGTA AAAACCC

2720

CACNA1A

CACNA1A-201

CACNA1A-201

AGGCTGAGGTGGGTGGATCACTTGAGGCCAGGAGTTCAAGACCAGCCTGGCCAATATGGTGAAACCCTGTCTTTACAAAAATAC  
TCCGACTCCACCCACCTAGTGA ACTCCGGTCTCAAGTTCTGGTCGGACCGGTTATACCCTTTGGGACAGAAATGTTTTTTATG

2805

CACNA1A

CACNA1A-201

CACNA1A-201

AAAAATTAGCCAGATGTGATGGTGCACACCTGTAATCCCAGCTACTCAGGAGGCTGAGGCACTAGAACTGCTTGAATCCAGGAGG  
TTTTTAATCGGTCTACACTACCACGTGTGGACATTAGGGTCGATGAGTCCTCCGACTCCGTGATCTTGACGAACTTAGGGTCCTCC

2890

CACNA1A

CACNA1A-201

CACNA1A-201

CAGAGGTTGCAGTGAGCCAAGATCATGCCACTGCACTCCAGCCTGAGCAACAGAGAGAGTGTCTGTCTCAAAAAATAAAGTAAAA  
GTCTCCAACGTCACCTCGGTTCTAGTACGGTGACGTGAGGTCGGACTCGTTGTCTCTCTCACAGACAGAGTTTTTTATTTTCATTTT

2975

CACNA1A

CACNA1A-201

CACNA1A-201

TAAAATAAAATAAAATAAAGAGTAGTGATTGGGCAGTGAGGGGGGCGAGGTGGATGCCCTGGCTTTGGCTCACAGGCCCAAGTAA  
ATTTTATTTTATTTTATTTTCTCATCACTAACCCTGTCACCTACGGGACCGAAACCGAGTGTCCGGGGTTTCATT

3060

CACNA1A

CACNA1A-201

CACNA1A-201

GGACTTCTCAAAACGTCTTTTGCCTACTGGCTGTCTAATTTATTTCACTGACCTTCTGACCTGGTTTCAGAATTGACTTAGGACAGC  
CCTGAAGAGTTTTGCAGAAAACGGATGACCGACAGATTAATAAGTGACTGGAAGACTGGACCAAGTCTTAACCTGAATCCTGTCTG

3145

CACNA1A

CACNA1A-201

CACNA1A-201

AAGAAGAGACAGTCTAGTCTTTGACCTAGAAAAGGCCCGTGAGCCTAGTCCAGGCCATTGTCTTCTTATAACCCTCCTTGTTCCCA  
TTCTTCTCTGTCAGATCAGAAACTGGATCTTTCCGGGCACTCGGATCAGGTCCGGTAACAGAAGAATATTGGGAGGAACAAGGGT

3230

CACNA1A

CACNA1A-201

CACNA1A-201

GTCACGTTGGCTGACCCCCAGGACACCCCTCAGGAACCAAGTTCTCCTTCCCAGGGCCCTGACCTAGTTTCAAACCTTAGTAATTG  
CAGTGCAACCGACTGGGGGGTCTGTGGGGAGTCTTGGTCAAGAGGAAGGGTCCCGGGACTGGATCAAAGTTTGAATCATTAAAC

3315

CACNA1A

CACNA1A-201

CACNA1A-201

TTTTTAGTCCCTCTGGAGTCTCTTATAAATGAGGACTCTACTTCGTGTTTTAACTTCCCTCTAATACTCTATTTTTAATCTCCTAT  
AAAAATCAGGGAGACCTCAGAGAATATTTACTCCTGAGATGAAGCACAAAATTGAAGGAGATTATGAGATAAAAAATTAGAGGATA

3400

CACNA1A

CACNA1A-201

CACNA1A-201

ATTCTCTCTACTAATCATCTTGTACAGTCTGTCCTGGTTCAGGAACAAGGGACTGAGACTTCCTGCCTGGGTCCTCAGTGTCTAT  
TAAGAGAGATGATTAGTAGAACATGTCAGACAGGACCAAGTCTTGTTCCTGACTCTGAAGGACGGACCCAGGAGTCCACAGATA

3485

CACNA1A

CACNA1A-201

CACNA1A-201

AAAGGTCCTTTACTCATTCCCACTTTCCCTTTGAGAAAACCTGAGACACAGAGAGGTTAAGTAGATTGCCAGGATCACACATTAG  
TTTCCAGGAAATGAGTAAGGGTGAAAGGGAAACTCTTTTGACTCTGTGTCTCTCCAATTCATCTAACGGGTCCTAGTGTGTAATC

3570

CACNA1A

CACNA1A-201

CACNA1A-201

CTTGGCATGATGGCGGGCGCCTGTAATCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCTGGGAGGCAGAGGTTG  
GAACCGTACTACCGCCCGCGGACATTAGGGTCGATGAACCTCCGACTCCGTCTCTTAGCGAACTTGGACCTCCGTCTCCAAC

3655

CACNA1A

CACNA1A-201

CACNA1A-201

CAGTGAGCCAGATCATGCCACTGCACTCTAGCCTGGGCAACAGAGCTAGACGCCATCTCAAAAAAAAAAAAAAAAAAAAAAGA  
GTCCTCGGGTCTAGTACGGTGACGTGAGATCGGACCCGTTGTCTCGATCTGCGGTAGAGTTTTTTTTTTTTTTTTTTTTTTCT

3740

CACNA1A

CACNA1A-201

CACNA1A-201

TACACATTAATTTAGAGATGTCAAAATATAAAACAAAAATGTATATCTTGGCATCAGTGAAGTGTAAGTTGTTTCTCTGGATCTCA  
ATGTGTAATTAAGTCTCTACAGTTTTATATTTGTTTTTACATATAGAACCCTAGTCACTTCACATCAACAAAGAGACCTAGAGT

3825

CACNA1A

CACNA1A-201

CACNA1A-201

GACTCCACATCTATGTGGTAGAAACCGGATTTGATGGTCCTGAAAGTTCTTCCAGATGCAACAATGCTAAGGATAAGTAATTCTT  
CTGAGGTGTAGATACACCATCTTTGGCCTAAACTACCAGGACTTTCAAGAAGGTCTACGTTGTTACGATTCTTATTCATTAAGAA

3910

CACNA1A

CACNA1A-201

CACNA1A-201

TCAAGTCTTGTGCATCACCTGCTATCATGTTTCCATGGTAACTGAGGAACAAGATCTCAGAAACTCTTCAAGTCTCCAGAGTTA  
AGTTCAGAACACGTAGTGGACGATAGTACAAAGGTACCATTTGACTCCTTGTCTAGAGTCTTTGAGAAGTCAAGGAGGGTCTCAAT

3995

CACNA1A

CACNA1A-201

CACNA1A-201

CTTCTGGTGGGTCTAGGAATGTGTCAGATGTTACAAACAGACTTCTCTGCTGATATTTTGGTCCTAGGAACCCCTAGAGTTCCCC  
GAAGACCACCCAGATCCTTACACAGTCTACAATGTTTGTCTGAAGGAGACGACTATAAAACCAGGATCCTTGGGATCTCAAGGGG

4080

CACNA1A

CACNA1A-201

CACNA1A-201

TCAGACACTAAGATCTCCTTAGCGTCCTATAAATAAGGAGAAATTTTGGTGATAAATACTGTGAAGGACTTTGACGGTCAGTTCA  
AGTCTGTGATTCTAGAGGAATCGCAGGATATTTATTCCTCTTTAAACCCTATTTATGACACTTCTGAAACTGCCAGTCAAGT

4165

CACNA1A

CACNA1A-201

CACNA1A-201

AAACACCTCTTAAAAGCATGACATAGCAAACACCCCTTGGCAAATATCTTAGTTCATTTGTAAGTCTATAACAAATTACCCGAGAC  
TTTGTGGAGAATTTTCGTACTGTATCGTTTGTGGGAACCGTTTATAGAATCAAGTAAACATGACGATATTGTTAATGGGCTCTG

4250

CACNA1A

CACNA1A-201

CACNA1A-201

TGGGTAATTTGATAAGAACAGAAATTTATTTTCTCACAGTTCTGGAGGCTGGGAAGCCCAAGATCAAGGCATTGGCAGGTTTCCC  
ACCCATTAAACTATTCTTGTCTTTAAATAAAAGAGTGTCAAGACCTCCGACCCCTTCGGGTTCTAGTTCGGTAACCGTCCAAAGGG

4335

CACNA1A

CACNA1A-201

CACNA1A-201

TGTCTGGCGAAAGCTACTCTCTGCTTCCAAGATTGCACCTTGAACACTGTATCCTCTGGAAGGGAGGAACACTGGGTCTTACAT  
ACAGACCGCTTTTCGATGAGAGACGAAGGTTCTAACGTGGAACCTTGTGACATAGGAGACCTTCCCTCCTTGTGACCCAGGAATGTA

4420

CACNA1A

CACNA1A-201

CACNA1A-201

GGCAGAAGGTGGAGGAGCAAGAGGGACAACTTCTCTGTCAACCTCTTTTATAAGGGCACCTAATCCCATTTCATGAGAGCTCTA  
CCGTCTTCCACCTCCTCGTTCTCCCTGTTTGAAGGAGACAGTTGGAGAAAATATTCCCGTGGATTAGGGTAAGTACTCTCGAGAT

4505

CACNA1A

CACNA1A-201

CACNA1A-201

CCGTAATGACTTAATCACCTCCTGAAGGCCCCACCTCTTAATACTGTTACATTGGCAATTAAGTTTCAACGTGAATTTTGGAGGG  
GGCATTACTGAATTAGTGGAGGACTTCCGGGGTGGAGAATTATGACAATGTAACCGTTAATTCAAAGTTGCACTTAAACCTCCC

4590

CACNA1A

CACNA1A-201

CACNA1A-201



GACACAAACATTTAAACCATCACAAACCACCAAAACACAATTAGCTTTGTGGCCTTAATTAGCTATATGAAATTCATGGAAGTTAGT  
CTGTGTTTGTAAATTTGGTAGTGTTGGTGGTTTGTGTTAATCGAAACACCGGAATTAATCGATATACTTTAAGTACCTTCAATCA

4675

CACNA1A

CACNA1A-201

CACNA1A-201

TTCAGTCCTCTGTCTCTTTCTTTCTGTATGCTTTCTGCTCCTCAGAAACCCTCCTCATCTCTCCTTTCTATCCATTAAGTACCC  
AAGTCAGGAGACAGAGAAAAGGAAAAGACATACGAAAGACGAGGAGTCTTTGGGAGGAGTAGAGAGGAAAAGATAGGTAATTCATGGG

4760

CACNA1A

CACNA1A-201

CACNA1A-201

ACGCCCTTCCCTAACTCCTCATCTTCCCTACCCCTACCAAGAAAGCCCTCTCAGAAAAGGATCTGATGTCAGCCATTTATTTGCTGGA  
TGCGGGAAGGATTGAGGAGTAGAAGGATGGGATGGTTCTTTTCGGGAGAGTCTTTTCTAGACTACAGTCGGTAAATAAACGACCT

4845

CACNA1A

CACNA1A-201

CACNA1A-201

GCAAAATGCATATCCATGTTTTACCCCTCCCTGAGGCATTTGCAATTTTATGCTTGCTCATCAAAGAACAAAAGGCTTTGTCTTAC  
CGTTTACGTATAGGTACAAAATGGGGAGGGACTCCGTAAACGTTAAAATACGAACGAGTAGTTTCTTGTTTTCCGAAACAGAATG

4930

CACNA1A

CACNA1A-201

CACNA1A-201

TCAAGACTTTTTAGGTCACACACAGGATTTCTAGGGGACATAAGACAAGTTTTCTGAGTTAGGAGAAAAGCCATACCTTA  
AGTTCTGAAAAATCCAGTGAGTGTTGTGTCCTAAAGATCCCCTGTATTCTGTTCAAAGACTCAATCCTCTTTTTCGGTATGGAAT

5015

CACNA1A

CACNA1A-201

CACNA1A-201

GGTGGGTTGCCTGTGTCGCTCCAACCTAAGTACTTAACTTCAGGATTACAAATAGGATATCATTATGATTTCTATTTCTTTTATC  
CCACCCAACGGACACAGCGAGGTTGATTCATGAATTGAAGTCTAATGTTTATCCTATAGTAATACTAAAGATAAAGGAAAATAG

5100

CACNA1A

CACNA1A-201

CACNA1A-201

CTTTGGAGCTCAGTCACGTAGAAGTAGATTAATATAATTGTTAGATCACAGCACCCCTGGCATTATGGGGCCGTTATGGTCCATT  
GAAACCTCGAGTCAGTGCATCTTCATCTAATTTATATTAACAATCTAGTGTCGTGGGACCGTAATACCCCGCAATACCAGGTAA

5185

CACNA1A

CACNA1A-201

CACNA1A-201

GTTATTATGTGAATTATTCAGTTAATTAGTTTATTTTTTAAATGTGATAAACACCCAGGAACCCACCAGTCAACACAAAAGTCCT  
CAATAATACACTTAATAAGTCAATTAATCAAATAAAAAATTTACACTATTTGTGGGTCCCTTGGGTGGTCAGTTGTGTTTTTCAGGA

5270

CACNA1A

CACNA1A-201

CACNA1A-201

TGGCAATAATCTATATCCGATCCTTCTCATCGAACCCAGGGCAAAAACCTACAAGATGGAGACCCACTGATATTTTTTCTCATTTCCTT  
ACCGTTATTAGATATAGGCTAGGAAGAGTAGCTTGGTCCCCTTTTTGATGTTCTACCTCTGGGTGACTATAAAAAGAGTAAGGAA

5355

CACNA1A

CACNA1A-201

CACNA1A-201

TTAAAATCGGCCTAAGGTTGGTTAGCTTGGTTGGTTGGAGGGTAGGGCATAATTGTTGCTTTTTTTTTTTTTTTTTTTTTTTAGAC  
AATTTTAGCCGGATTCCAACCAATCGAACAACCAACCTCCCATCCCGTATTAACAACGAAAAAAAAAAAAAAAAAAAAAAAAAATCTG

5440

CACNA1A

CACNA1A-201

CACNA1A-201

AAGGTCTTGCTCTGTCACCCAGGCTACAGTAGGGTGGCCCAATCTTGGCTCACTGCAACCTCCACCTCCCAGGTTTAAGTGATTC  
TTCCAGAACGAGACAGTGGGTCCGATGTCATCCCACCGGGTTAGAACCGAGTGACGTTGGAGGTGGAGGGTCCAAATTCACTAAG

5525

CACNA1A

CACNA1A-201

CACNA1A-201

TCATGCCTCAGCCTCCCAAGTAGCTGGGTTTACAGGCATGTGTCACCACACTGGCTAATTTTTGTATTTTTAGTAGAGGCGGGGT  
AGTACGGAGTCGGAGGGTTTCATCGACCCAAATGTCCGTACACAGTGGTGTGACCGATTAAAAACATAAAAAATCATCTCCGCCCCA

5610

CACNA1A

CACNA1A-201

CACNA1A-201

TTGCCATGTTAGCCAGGCTGGTCTCAAACCTCCTGACCTCAGTTGATCTGACCGCCTAGGCCTCCCAAAGTGCTGGGATTACAGAC  
AACGGTACAATCGGTCCGACCAGAGTTTGAGGACTGGAGTCAACTAGACTGGCGGATCCGGAGGGTTTCACGACCCTAATGTCTG

5695

CACNA1A

CACNA1A-201

CACNA1A-201

GTGAGCCACCATGCCCAGCCAGCTCTTCCTTTTTAACAGAGGGGAAACTGAGGCCCATGGGAAGGACACCTTGGACAGGGCGTG  
CACTCGGTGGTACGGGTCGGTCGAGAAGGAAAAATTGTCTCCCTTTGACTCCGGGTACCCTTCTGTGGAACCTGTCCCGCACC

5780

CACNA1A

CACNA1A-201

CACNA1A-201

CCACAGTGGGTCATGTATATAATCCCAGCACTTTGGGAGGCTGTGCTGGGAGGATCACTTGAGGCCAGGAGTTCAAGACCAGCCA  
GGTGTCACCAGTACATATATTAGGGTCGTGAAACCTCCGACACGACCCTCCTAGTGAAGTCCGGTCTCAAGTTCTGGTCGGT

5865

CACNA1A

CACNA1A-201

CACNA1A-201

GGGCAACATAGTGAGACCCCATCTCCACATAAAAATTTTAAAAAGAAAAAAGATAAGTCAGAAGTTGGGTGTGGTGACACATGC  
CCCGTTGTATCACTCTGGGGGTAGAGGTGTATTTTTAAAATTTTTCTTTTTCTATTTCAGTCTTCAACCCACACCACTGTGTACG

5950

CACNA1A

CACNA1A-201

CACNA1A-201

CTGTAGTTCTAGCATGTTGGAGGCCAAATCAGGGAAACTGTTTTGAGGCCAGGAGTTTGAACCAGCCTAACAGCATAGCAAGACC  
GACATCAAGATCGTACAACCTCCGGTTTAGTCCCTTTGACAAACTCCGGTCTCAAACCTTTGGTCGGATTGTCGTATCGTTCTGG

6035

CACNA1A

CACNA1A-201

CACNA1A-201

TCATCTCTACAAAAATAAAAAAGTTTAAAAATGATAATAAAAGGAAAGTCAGAGCCACCTGGAACCCCTACCCTCAGCAAGCCTA  
AGTAGAGATGTTTTTTATTTTTCAAATTTTTACTATTATTTCTTTTCAGTCTCGGTGGACCTTGGGGATGGGAGTCGTTCCGGAT

6120

CACNA1A

CACNA1A-201

CACNA1A-201

ACCTCCTCTCTGTTTCCTCCTTCTCCCTTCTAGACTATGCAGAATTCATTTTCTTAGGACTCTTTATGTCCGAAATGTTTATAAA  
TGGAGGAGAGACAAAGGAGGAAGAGGGGAAGATCTGATACGTCTTAAGTAAAAGAATCCTGAGAAATACAGGCTTTACAAATATTT

6205

CACNA1A

CACNA1A-201

Y Y A E F I F L G L F M S E M F I K  
ENSE00001247106

CACNA1A-201

AATGTACGGGCTTGGGACGCGGCCTTACTTCCACTCTTCTTCAACTGCTTTGACTGTGGGGTAAGTGCTCTTGTCTTCTAAGAGT  
TTACATGCCCGAACCTGCGCCGGAATGAAGGTGAGAAGGAAGTTGACGAAACTGACACCCCATTCACGAGAACAAGATTCTCA

6290

CACNA1A

CACNA1A-201

M Y G L G T R P Y F H S S F N C F D C G  
ENSE00001247106

CACNA1A-201

TCATTTCTCCAGCTCTTGCCTGGAATGACAGATACCTGGACACATTAAGGGGAGAAAGGTAAAGTCACCCCTGAATATGAGAGAC  
AGTAAAGAGGTGAGAACGGACCTTACTGTCTATGGACCTGTGTAATTTCCCTCTTTCCATTTTCAGTGGGGACTTATACTCTCTG

6375

CACNA1A

CACNA1A-201

CACNA1A-201

TCAGATGGATGCAGAAGGAATGAGAAAAACAATCCCAAACACTGGCAAGGATACAGTGTACCCAGAACCCTCAACCACCGCCAGTG  
AGTCTACCTACGTCTTCCTTACTCTTTTGTAGGGTTTGTGACCGTTCTATGTGCACATGGGTCTTGGGAGTTGGTGGCGGTCAC

6460

CACNA1A

CACNA1A-201

CACNA1A-201

GGAGGAAAACGTATAGACCCCCTTTGGAAAGCTAAGTGGGGGACATAAGACAAGTTTTTCCAAGTTGGGAGAAAAGCCATGCCTTA  
CCTCCTTTTGCATATCTGGGGGAAAACCTTTCGATTCACCCCCTGTATTCTGTTCAAAAAGGTTCAACCCTCTTTTCGGTACGGAAT

6545

CACNA1A

CACNA1A-201

CACNA1A-201

GGTGGGTTGCCTGTGTCGCTCCAACCTAAGTACCCAACCTTCAGGATTACAAACAGGACATCAATATGATTTCATTTCTTCTTTTC  
CCACCCAACGGACACAGCGAGGTTGATTTCATGGGTTGAAGTCTAATGTTTGTCTGTAGTTATACTAAAGATAAAGAAGAAAAG

6630

CACNA1A

CACNA1A-201

CACNA1A-201

CTTTGTAGCTCAGTCATGTGGAGGTAGATGAAGTATAATTGTTAGATTACAACACCCTGGCATTATGGAGCCATTATGGTCCTTT  
GAAACATCGAGTCAGTACACCTCCATCTACTTCATATTAACAATCTAATGTTTGTGGGACCGTAATACCTCGGTAATACCAGGAAA

6715

CACNA1A

CACNA1A-201

CACNA1A-201

GTTATTTTGTGAATTACTCAGTTAATTAATTTATTTTTTAAATGTGATTAACACCCAGTAACCCACTAGTCCACACAAAACCTAA  
CAATAAAACACTTAATGAGTCAATTAATTAATAAAAAATTTACACTAATTGTGGGTCAATTGGGTGATCAGGTGTGTTTTGGATT

6800

CACNA1A

CACNA1A-201

CACNA1A-201

GTCCTGGAGAATAATCTACGTCCAATCCTTCTCATCGAACCCAGGGCAAAAACCTACAAGATGGAGATATGACCCAGCATTCCATTG  
CAGGACCTCTTATTAGATGCAGGTTAGGAAGAGTAGCTTGGTCCCCTTTTTGATGTTCTACCTCTATACTGGGTGTAAGGTAAC

6885

CACNA1A

CACNA1A-201

CACNA1A-201

CTAGGAATTCATCCTAGAAAATCTCACCCAGATACCTAGGAGACACAGGCCAGAATGTCCCTGCAGCTGGAAGTGAAATTAAGGT  
GATCCTTAAGTAGGATCTTTTAGAGTGGGTCTATGGATCCTCTGTGTCCGGTCTTACAGGGACGTGACCTTCACTTTAATTCCA

6970

CACNA1A

CACNA1A-201

CACNA1A-201

TGTTTCGCAAATAAGTGGAGAATGCCTGGCCAGGGCAGCCCTAATCATTTACCATAGTCCTGTTGGTCTCAGAAAAGGCTTAATAA  
ACAAGCGTTTATTACCTCTTACGGACCGGGTCCCGTCGGGATTAGTAAATGGTATCAGGACAACCAGAGTCTTTCCGAATTATT

7055

CACNA1A

CACNA1A-201

CACNA1A-201

TTTATTTATTTTTTTTTTATTTTTTGTTTTTATTTTTTGTTTTTGAGATGGAGTCTCGTTCTGTACCCAGGCTGGAGTGCGGTGG  
AAATAAATAAAAAAAAAAATAAAAAACAAAAATAAAAAACAAAAACTCTACCTCAGAGCAAGACAGTGGGTCCGACCTCACGCCACC

7140

CACNA1A

CACNA1A-201

CACNA1A-201

CGCCATCTCGGCTCACTGCAAGCTCCGCCTCCAGGTTCACTCCATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGT  
GCGGTAGAGCCGAGTGACGTTTCGAGGCGGAGGGTCCAAGTGAGGTAAGAGGACGGAGTCGGAGGGCTCATCGACCCTGATGTCCA

7225

CACNA1A

CACNA1A-201

CACNA1A-201

GCCCGCCATCATACTGGCTAATTTTTTGTATTTTTAGTAGAGATGGGGTTTCACCGTGTTAGCCAGGATGGTCTTGATCTCCTG  
CGGGCGGTAGTATGGACCGATTAAAAACATAAAAAATCATCTCTACCCCAAAGTGGCACAATCGGTCTTACCAGAACTAGAGGAC

7310

CACNA1A

CACNA1A-201

CACNA1A-201

ACCTCGTGATCCACCCGCCTTGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCACACCCAGCCAGCTTAATAATTTATA  
TGGAGCACTAGGTGGGCGGAACCGGAGGGTTTCACGACCCTAATGTCCGCACTCGGTGGTGTGGGTCGGTTCGAATTATTAATAT

7395

CACNA1A

CACNA1A-201

CACNA1A-201

ATAACTGAATGTTGTACTGTTTTCTGCCATTATAGAAAATTATGTTGTTGGAGAAAACAAAATACATACAAACAAGCAAACCTTC  
TATTGACTTACAACATGACAAAAGACGGTAATATCTTTTAATACAACAACCTCTTTTGTTTTATGTATGTTTGTTCGTTTGGAAAG

7480

CACNA1A

CACNA1A-201

CACNA1A-201

CCTACATAAATGACCCAAGTAGTTAAAGAATAAAACCAATTTCTTTCCATTAAAAAGAAAAGAAAGCCGGGTGTGATGCCTCATG  
GGATGTATTTACTGGGTTTCATCAATTTCTTATTTTTGGTTAAAGAAAGGTAATTTTTCTTTTCTTTTCGGCCACACTACGGAGTAC

7565

CACNA1A

CACNA1A-201

CACNA1A-201

CCTATAGCCTCAGCTATTCAGGAGGCTGAGGCAGCAGAATTGCTTGAGCCCAGGAGTTGAAAAACCAGCCCAGGGCAACATAGCAAG  
GGATATCGGAGTCGATAAGTCCTCCGACTCCGTCGTCTTAACGAACTCGGGTCCTCAACTTTTTGGTCGGGTCCGTTGTATCGTTC

7650

CACNA1A

CACNA1A-201

CACNA1A-201

ACCCTGTCTCTACAAAAATTAATAATAATTAGCCAGGTGTGGTGGTGCACACCTGTAGCCCCAGCTACTCAGAAGGCTAAGGTGG  
TGGGACAGAGATGTTTTTAATTATTATTAATCGGTCCACACCACCACGTGTGGACATCGGGGTCGATGAGTCTTCCGATTCCACC

7735

CACNA1A

CACNA1A-201

CACNA1A-201

GAGGATTGCTTGAGCCCAGCAGTTTTGAGGCTGCAGTGAGCTATGATCACACCACTGCCCTCCAGCCTGGACAAGAGAGTGAGACC  
CTCCTAACGAACTCGGGTCGTCAAACCTCCGACGTCACCTCGATACTAGTGTGGTGACGGGAGGTCGGACCTGTTCTCTCACTCTGG

7820

CACNA1A

CACNA1A-201

CACNA1A-201

CCATCTCTAAGAAATAAAAAGTAGGCCAGGCACAGTGGCTCACACCTATAATCCCAGCACTTTGAGAGGCGGAGGCAGGTGGATCA  
GGTAGAGATTCTTTATTTTCATCCGGTCCGTCACCGAGTGTGGATATTAGGGTCGTGAAACTCTCCGCCTCCGTCCACCTAGT

7905

CACNA1A

CACNA1A-201

CACNA1A-201

CCTGAAGTCAGGAGTTCAAGACCAGCCTGGCCAACATGGCGAAACCCGTCATACTAAAAAATACAAAAATTAGCCAGGCGTC  
GGACTTCAGTCCTCAAGTTCTGGTCGGACCGGTTGTACCGCTTTGGGGCAGATATGATTTTTTTATGTTTTTAATCGGTCCGCAG

7990

CACNA1A

CACNA1A-201

CACNA1A-201

GTGGCACATGCCTGTAATCCCAGCTACTTGGGAGGCTGAGGAAGGAGAATCACTTGAAGTGGGGAGGCAGAGGTTGCAGTAAGCT  
CACCGTGACGGACATTAGGGTCGATGAACCCTCCGACTCCTTCTCTTAGTGAAGTTGACCCCTCCGTCTCCAACGTCATTCTGA

8075

CACNA1A

CACNA1A-201

CACNA1A-201

GAGATTGCACCACTGCACTCCAGCCTGGGTGACAGAATGAGACTCCGTCTCAAAAAAAAAAAGAAAAATTTTAAAATGTCCTG  
CTCTAACGTGGTGACGTGAGGTCGGACCCACTGTCTTACTCTGAGGCAGAGTTTTTTTTTTTTCTTTTTAAAATTTTACAGGAC

8160

CACNA1A

CACNA1A-201

CACNA1A-201

AGCAACCTTGTTTGTAAATAGTTCCAAGTCTCAATATCCGTGTATCCCTTTGCTGTAGAACAGATAAAATATTTTGTGGCATATCTA  
TCGTTGGAACAAACATTATCAAGGTTTCAGAGTTATAGGCACATAGGGAAACGACATCTTGTCTATTTATAAAAACACCGTATAGAT

8245

CACNA1A

CACNA1A-201

CACNA1A-201

TATAATGAAATACTCTGTGACAATCAAAGTCCACCAACAGCAGCCACATGCCCAACAACAGGAATGAATCTCACCCATGTAACAT  
ATATTACTTTATGAGACACTGTTAGTTTCAGGTGGTTGTCGTCGGTGTACGGGTTGTTGTCCTTACTTAGAGTGGGTACATTGTA

8330

CACNA1A

CACNA1A-201

CACNA1A-201

GGCACAGAAGGAGGCAGGAGCTAGCAACGTAAGTCCATACAGTTTCATGCAAAGTTC AAGTGGACAAAATTA AACTCTCTCTCTCT  
CCGTGTCTTCTCCGTCCTCGATCGTTGCATT CAGGTATGTCAAGTACGTTTCAAGTTCACCTGTTTTAATTTGAGAGAGAGAGA

8415

CACNA1A

CACNA1A-201

CACNA1A-201

CTCTACATATATATATATATATATATATATATATTTGAGACAGAGTCTCACTCTAT  
GAGATGTATATATATATATATATATATATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACTCTGTCTCAGAGTGAGATA

8500

CACNA1A

CACNA1A-201

CACNA1A-201

TGCCCAGGCTGGAGTGCAGTGGCGCAATCTTGGCTCACTACAACCTCCACCTCCCGGGTTCAAGCCATTCTCCCGCCTCAGCCTC  
ACGGGTCCGACCTCACGTCAACCGCTTAGAACCGAGTGATGTTGGAGGTGGAGGGCCCAAGTTCGGTAAGAGGGCGGAGTCGGAG

8585

CACNA1A

CACNA1A-201

CACNA1A-201

CCAAGTAGCTGGGATTAGAGGCATGCACCACCACCCCGGCTAATTTTGTATTTTTTTGTAGAGACCGGGATT CAGCAATTTGCC  
GGTTCATCGACCCTAATCTCCGTACGTGGTGGTGGGGCCGATTAAAACATAAAAAACATCTCTGGCCCTAAGTCGTTAAACGGG

8670

CACNA1A

CACNA1A-201

CACNA1A-201

AGGCTGGTCTCGAAATCCTGATCTCAGGTGATCCACCTGCCCTGGCCTCCCAAAGTGCTGGGATTACAAGCGTGAGCCACCACGC  
TCCGACCAGAGCTTTAGGACTAGAGTCCACTAGGTGGACGGGACCGGAGGGTTTCACGACCCTAATGTTTCGCACTCGGTGGTGCG

8755

CACNA1A

CACNA1A-201

CACNA1A-201

CCCGCCTTAAACTGTATTTTTTAAGGATGATACTTGAATACGTTAAAAAGGCGAGGACCTTGAAAACACAACGCTCGGTAAAAAGA  
GGGC GGAATTTGACATAAAAAATTCTACTATGAACTTATGCAATTTTTCCGCTCCTGGAACCTTTTGTGTTGCGAGCCATTTTCT

8840

CACNA1A

CACNA1A-201

CACNA1A-201

AACCAAACACAAAAGGTCAAGTATTGCATAATTCCATTTGTATGAAATGTCCAGAGCAGGCAAATCCATAGAGACAGAAAGTAGA  
TTGGTTTGTGTTTTCCAGTTCATAACGTATTAAGGTAAACATACTTTACAGGTCTCGTCCGTTTAGGTATCTCTGTCTTTTCATCT

8925

CACNA1A

CACNA1A-201

CACNA1A-201

TTAGTGGTTGCTAGGGTCTGGGTGAGGGAGAGTGGGGAGTAACTGCTCATGGGGACAGGGCCTCCTTTGGGGGTGATGAAAATGT  
AATCACCAACGATCCCAGACCCACTCCCTCTCACCCCTCATTGACGAGTACCCCTGTCCCGGAGGAAACCCCCACTACTTTTACA

9010

CACNA1A

CACNA1A-201

CACNA1A-201

TTTGGAACTTGATAGAGGTGATAGTTGCAGAATATTGTGCATGTACCTAAAGGCACTGAATTGTGTAATTCAAAGTGTGAATTTT  
AAACCTTGAACCTATCTCCACTATCAACGTCTTATAACACGTACATGGATTTCCGTGACTTAACACATTAAGTTTCACACTTAAAA

9095

CACNA1A

CACNA1A-201

CACNA1A-201

ATGTTATGTGAATTTACCTCAGTTTTTTTTAAGGTAAGAAAATGGTTATTACAAAATTCAGGATGGTAGTTATATCACAGTGTC  
TACAATACACTTAAAGTGGAGTCAAAAAAAATTCATTCTTTTACCAATAATGTTTTAAGTCTACCATCAATATAGTGTCACAG

9180

CACNA1A

CACNA1A-201

CACNA1A-201

TCTGGAAACTTCCAGGGTATCCACATGTCCCTTTTTATTTATTTTATTTTATTTTATTTTATTTTATTTGAGATAGGGTCTTGCTCTGTTGC  
AGACCTTTGAAGGTCCCATAGGTGTACAGGGAAAAATAAAAATAAAAATAAAAATAAAAATAAACTCTATCCCAGAACGAGACAACG

9265

CACNA1A

CACNA1A-201

CACNA1A-201

CCAGGCTAGAGTGCAGTGGCAGGATCATGACCCTCTCCTGTCTCAAATTCCTAGGCTCAAGCTATCCTCCCTCCTCAGCCTCCTA  
GGTCCGATCTCACGTACCGTCTTAGTACTGGGAGAGGACAGAGTTTAAAGGATCCGAGTTCGATAGGAGGGAGGAGTCGGAGGAT

9350

CACNA1A

CACNA1A-201

CACNA1A-201



AGTAGCTGGGACTATAGGCACATGCCACCATGCTTGACTAATTTTTTTTTTTTTTTTGTAAAGTCAGGGTTTCCCTGTGTTACCCAG  
TCATCGACCCTGATATCCGTGTACGGTGGTACGAACTGATTAACAAAAAAAAAAAAACATTTTCAGTCCCAAAGGGACACAATGGGTC

9435

CACNA1A

CACNA1A-201

CACNA1A-201

GCTGGTCTTGAACCTCCTGGGCTCAAGTGATCTGCCACCTCGGCCTCCCAAAGTTCCAGAATTACAGGCATGAGCCACTGCCCTA  
CGACCAGAACTTGAGGACCCGAGTTCCTAGACGGGTGGAGCCGGAGGGTTTCAAGGTCTTAATGTCCGTAICTGGTGACGGGAT

9520

CACNA1A

CACNA1A-201

CACNA1A-201

GCCTTCTCCTAATTGTTGACATAGGTAGTAGTTGCATGACATTCACCTTTGTAATTATGTGTTTTAGGAATTCTCAGGCCTGTGGG  
CGGAAGAGGATTAACAACCTGTATCCATCATCAACGTACTGTAAGTGAAACATTAATACACAAAGTCCCTTAAGAGTCCGGACACCC

9605

CACNA1A

CACNA1A-201

CACNA1A-201

AGCTCTTAATAAATAAAAAAGAGGCCAGGTGTGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCAGGCCGGATCA  
TCGAGAATTATTTATTTTTCTCCGGTCCACACCACCGAGTGCGGACATTAGGGTCGTGAAACCTCCGGCTCCGTCCGCCTAGT

9690

CACNA1A

CACNA1A-201

CACNA1A-201

CGAGGTCAGGAGTTTCGAGACTAGCCTGGCCAACACAGTGAAACCCCGTCTCTACTAAAAATACAAAAAATTAGCCGGGCGTGGTG  
GCTCCAGTCCTCAAGCTCTGATCGGACCGGTTGTGTCACCTTTGGGGCAGAGATGATTTTTATGTTTTTTAATCGGCCCGCACCCAC

9775

CACNA1A

CACNA1A-201

CACNA1A-201

GCGGGTGCCTGTAATCCCAGTTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCTGGGAGGCCGAGGTTGCAGTAAGCTGAG  
CGCCACGGACATTAGGGTCAATGAACCTCCGACTCCGTCTCTTAGCGAACTTGGACCCTCCGCCTCCAACGTCATTCGACTC

9860

CACNA1A

CACNA1A-201

CACNA1A-201

ATCGCGCCACTGCACACCAGCCTGGGTGATAAGAGCAAGACTCCATCTCAAAATAAATGAATAAATAAAAAATAAATAAATAAATA  
TAGCGCGGTGACGTGTGGTCCGACCCACTATTCTCGTTCTGAGGTAGAGTTTTATTTACTTATTTATTTTTATTTATTTATTTAT

9945

CACNA1A

CACNA1A-201

CACNA1A-201

AGAGGCCGGGTGCAGTGGCTCAATGCTTTGGAAAAGTGGAGGCCAACAGTTGGAGAGACCAAAGCAGGAGGATGGCTTCAGCCCAAG  
TCTCCGGCCACGTCACCGAGTTACGAAACCTTTACCTCCGGTTGTCAACCTCTCTGGTTTCGTCTCTACCGAAGTCGGGTC

10,030

CACNA1A

CACNA1A-201

CACNA1A-201

AAGTTTGAGGCCAGCCTGGGCAATACTAGCGAGACACTATCTCTATAAAAATGTTTTAAAATTAGCCAGATGTGGTGGGGCACAC  
TTCAAACCTCCGGTCGGACCCGTTATGATCGCTCTGTGATAGAGATATTTTTACAAAATTTAATCGGTCTACACCACCCCGTGTG

10,115

CACNA1A

CACNA1A-201

CACNA1A-201

CTGTAATCCCAGCTACTCAAGAGGCTGAGGTGGGAGGATCACTTAAGCCAGGAGGACAGTGCTGCAGTGAGCTATGATTGCGCC  
GACATTAGGGTCGATGAGTTCTCCGACTCCACCCTCCTAGTGAATTCGGGTCCTCTGTACAGACGTCACCTCGATACTAACGCGG

10,200

CACNA1A

CACNA1A-201

CACNA1A-201

PCR Forward

G A A T G G A T G A A T G A G G G G G T C A A G G

ACTGCACTCCAGCCTGGGTGACACAGTGAGACCCGGTCTCTATAGATAAATGAATGGATGAATGAGGGGGTCAAGGATCCTCACC  
TGACGTGAGGTCGGACCCACTGTGTCACTCTGGGCCAGAGATATCTATTTACTTACCTACTTACTCCCCAGTTTCTAGGAGTGG

10,285

CACNA1A

CACNA1A-201

CACNA1A-201

Sanger Sequencing

A A T G C T T G C C A G T T C T G G A G

CGGCTTCCATTTGGAGGGAGGAGTTTGGTTGAGTTCTTGCAAGGTTGGTACCTAGGAAATGCTTGCCAGTTCTGGAGCCAGACA  
GCCGAAGGTAAACCTCCCTCCTCAAACCAACTCAAGAACGTTCCAACCATGGATCCTTTACGAACGGTCAAGACCTCGGGTCTGT

10,370

CACNA1A

CACNA1A-201

CACNA1A-201

CTGTCCCTGGACATGAGACCAGGTTCTCTGCCCTAGGTTATCATTGGGAGCATCTTCGAGGTCATCTGGGCTGTCATAAACCTG  
GACAGGGACCTGTACTCTGGTCCAAGAGACGGGATCCAATAGTAACCCTCGTAGAAGCTCCAGTAGACCCGACAGTATTTTGGAC

10,455

CACNA1A

CACNA1A-201

CACNA1A-201

V I I G S I F E V I W A V I K P  
ENSE00001247101

Donor Template WT -> SNV

G A C

Donor Template WT -> SNV

gRNA Protospacer

TCAGCGTGTTACGAGCCCTC

GCACATCCTTTGGAATCAGCGTGTTACGAGCCCTCAGGTTATTGCGTATTTTCAAAGTCACAAAGTAAGTCTTTGGGGTTCTCTGG  
CGTGTAGGAAACCTTAGTTCGCACAATGCTCGGGAGTCCAATAACGCATAAAAAGTTTCAGTGTTCATTTCAGAAACCCCAAGGACC

10,540

CACNA1A

CACNA1A-201

G T S F G I S V L R A L R L R I F K V T K

ENSE00001247101

CACNA1A-201

Donor Template WT -> SNV

Protospacer Sequence

PAM

SNV

CGTGTAGGAAACCTTAGTTCGCACAATGCTCGGGAGTCCAATAACGCATAAAAAGTTTCAGTGTTCATTTCAGAAACCCCAAGGACC

Donor Template WT -> SNV

ACATTTGTACAGGGGGTGGGGATGGGGGACATGGTGGGGCCGCCTCCAGAAAGTTGGGAAAGTGAGCCTCGTGTTCGAGGGCTG  
TGTA AACATGTCCCCACCCCTACCCCTGTACCACCCCGGGCAGAGGCTTTCAACCCCTTCACTCGGAGCACAAAGCTCCCGAC

10,625

CACNA1A

CACNA1A-201

CACNA1A-201

Donor Template WT -> SNV

TGTA AACATGTC

Donor Template WT -> SNV

ACTCCGGGGCCCTGCCTCCCCCGCCTGGCCTGAGTCCCTCGCCTGGCCTCTGTTCGGCAGGTAAGTGGGCATCTCTCAGAAACCTGGT  
TGAGGGCCCCGGGACGGAGGGGGCGGACCGGACTCAGGAGCGGACCGGAGACAGCCGTCCATGACCCGTAGAGAGTCTTTGGACCA

10,710

CACNA1A

CACNA1A-201

595 Y W A S L 600 R N L V  
ENSE00001697204

CACNA1A-201

CGTCTCTCTCCTCAACTCCATGAAGTCCATCATCAGCCTGTTGTTTCTCCTTTTCTGTTTCATTGTCGTCTTCGCCCTTTTGGGA  
GCAGAGAGAGGAGTTGAGGTACTTCAGGTAGTAGTCGGACAACAAAGAGGAAAAGGACAAGTAACAGCAGAAGCGGGAAAACCT

10,795

CACNA1A

CACNA1A-201

V S L L N S M K S I I S L L F L L F I V V F A L L G

ENSE00001697204

CACNA1A-201

ATGCAACTCTTCGGCGGCCAGTAAGTCCCTTCACAGGAATTCAACTCCTGGTTCCCTGGGGTCAGGCTCAGGGAACACACAGTCC  
TACGTTGAGAAGCCCGGTCATTTCAGGAAGTGTCTTAAGGTTGAGGACCAAGGGACCCAGTCCGAGTCCCTTGTGTGTCAGG

10,880

CACNA1A

CACNA1A-201

M Q L F G G Q

ENSE00001697204

CACNA1A-201

CCTCCACCGTGCAGGCTGCCTTCCTCGTAGCCACAGACACCCATTGCGGTACCCCAAATGGGCAGGGCCCTGGGTACCACTCAGGG  
GGAGGTGGCACGTCCGACGGAAGGAGCATCGGGTCTGTGGGTAACGCCAGTGGGTTTACCCGTCCCGGGACCCATGGTGAGTCCC

10,965

CACNA1A

CACNA1A-201

CACNA1A-201

TTTCCTGGGGACAGAGATGATGGAGACGTTTCGTTTCCTTGGAGATGAGATACTGAGCCACACCCCTCAGAGCACCCCGGGTGGGGC  
AAAGGACCCCTGTCTCTACTACCTCTGCAAGCAAAGGAACCTCTACTCTATGACTCGGTGTGGGAGTCTCGTGGGGGCCACCCCG

11,050

CACNA1A

CACNA1A-201

CACNA1A-201

CAACGTGAAATGTCTGTGTCTCCCTGCAGGTTTAATTTTCGATGAAGGGACTCCTCCACCAACTTCGATACTTTTCCAGCAGCA  
GTTGCACTTTACAGACACAGGAGGGACGTCCAAATTAAGCTACTTCCCTGAGGAGGGTGGTTGAAGCTATGAAAAGGTCGTCGT

11,135

CACNA1A

CACNA1A-201

F N F D E G P P T N F D T F P A A  
ENSE00001247082

CACNA1A-201

ATAATGACGGTGTTCAGGTACAGCCTCCACCTGGCCCCACGGGCCAACACCTCTCAGTGTACAGATGAAAGTGCCTGCTCCAC  
TATTACTGCCACAAAGTCCATGTTCGGAGGTGGACCGGGGTGCCCGTTGTGGAGAGTACAGTGTCTACTTTTACGGACGAGGGTG

11,220

CACNA1A

CACNA1A-201

I M T V F Q  
ENSE00001247082

CACNA1A-201

GCCACAAAGTCCATGTTCGGAGGTGG  
PCR Reverse

ATCCAAGGGGCTTCCCTGAACTCCTCCTTCTCTACCTGGCCTTTTTCACACCACTTTGAAACACAGATTTTATGGTTATCATTATT  
TAGGTTCCCCGAAGGGACTTGAGGAGGAAGAGATGGACCGGAAAAGTGTGGTGAACTTTGTGTCTAAAATACCAATAGTAATAA

11,305

CACNA1A

CACNA1A-201

CACNA1A-201

CAATTATGGTGAGGCCAACAGATCAGGAGATGAATGTCATTGGAAAGATAGTTTGTGGCTGGGCACGGTGGCTCACACCCATAAT  
GTTAATACCACTCCGGTTGTCTAGTCTCTACTTACAGTAACCTTTCTATCAAACACCGACCCGTGCCACCGAGTGTGGGTATTA

11,390

CACNA1A

CACNA1A-201

CACNA1A-201

CCCAGCACTTTGGCCAGGTACGGTGGCTCACACCTGTAATCCCAACGCTTTGGGAAGCCAGGTGGGCGGATCACTTGAGATCAG  
GGGTCGTGAAAACCGGTCCATGCCACCGAGTGTGGACATTAGGGTTGCGAAAACCTTCGGGTCCACCCGCCTAGTGAACCTCTAGTC

11,475

CACNA1A

CACNA1A-201

CACNA1A-201

GAATTCGAGACCAGCCTGGCCAACATGGTGAAACCCCATCTCTACTAAAAATACAAAAATTAGCCGGGCGTGTTAGCACATGCCT  
CTTAAGCTCTGGTCGGACCGGTTGTACCACTTTGGGGTAGAGATGATTTTTATGTTTTTAATCGGCCCGCACCATCGTGTTACGGA

11,560

CACNA1A

CACNA1A-201

CACNA1A-201

GTAATCCCAGCTACTCGGGAGATGAGGCACAAGAATTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCAAGATCGCGCCACT  
CATTAGGGTCGATGAGCCCTCTACTCCGTGTTCTTAACGAACTTGGACCCCTCCGTCTCCAACGTCACCTCGGTTCTAGCGCGGTGA

11,645

CACNA1A

CACNA1A-201

CACNA1A-201

GCACTCCAGCCTGGGCAACAGAGTGAGACTCCATCTCAAAAAAGAAAAAGAAAAAACCACCTTTGGGAGGTCAAGATGGGAG  
CGTGAGGTCGGACCCGTTGTCTCACTCTGAGGTAGAGTTTTTCTTTTTCTTTTTTTTTTGGTGAAACCCCTCCAGTTCTACCCTC

11,730

CACNA1A

CACNA1A-201

CACNA1A-201

GACTACTTGAGGCCAGGAGTTTGAGACAAGTCTGGGCAACATAGTGAGACTCCGTCTCTGCAAAAAATAATAATAATAATTAGC  
CTGATGAACTCCGGTCCTCAAACCTCTGTTTCAGACCCGTTGTATCACTCTGAGGCAGAGACGTTTTTTTTATTATTATTATAATCG

11,815

CACNA1A

CACNA1A-201

CACNA1A-201

TGGGCATGGTGATACATACCTCCTAGCTACTAGGGCAGCTGAAGTGGAAGGATTGCTTGAGCCAGGAGGTTGAGGCTGCAGTAA  
ACCCGTACCACTATGTATGGAGGATCGATGATCCCCTCGACTTCACCTTCCTAACGAACTCGGGTCCTCCAACCTCCGACGTCATT

11,900

CACNA1A

CACNA1A-201

CACNA1A-201

GCTACAATCACACCACTATACTCCAGCCTGGGCGAGAGAGCAAAGCCCTGTCTCAAAAACGAAAAGAAAGTTTGTATACTCACA  
CGATGTTAGTGTGGTGATATGAGGTCGGACCCGCTCTCTCGTTTCGGGACAGAGTTTTTGTCTTTCTTTCAAACAATATGAGTGT

11,985

CACNA1A

CACNA1A-201

CACNA1A-201

GATCCTCAGAGAAGGAGCACACCATGCAGGACCAAGCAGAGAAGCAACAGGGTCAAGCAGGAAGAGAAGGAAAATGTGGGCAAGA  
CTAGGAGTCTTCTCCTCGTGTGGTACGTCTGTTTCGTTCTTTCGTTGTCCAGTTCGTCTTCTTCTTTTACACCCGTTCT

12,070

CACNA1A

CACNA1A-201

CACNA1A-201

GGCTTGATTGTGGTTTCCATGGGACGGAATGGGTGAGGCAGAGTAAACAGCTCGAGACTGGCTAGTTTGGATCATTTCAGTGGGC  
CCGAACTAACACCAAAGGTACCCTGCCTTACCCACTCCGTCTCATTTGTGCGAGCTCTGACCGATCAAACCTAGTAAAGTCACCCG

12,155

CACNA1A

CACNA1A-201

CACNA1A-201

TCTGGGGCAGAGGAGCTGTTTCTACTTGTCTAGGACCTGGCCTTGGGGTGATTAGGGCAGGTGGATAGTGCTGGGAAGATAAAGG  
AGACCCCGTCTCCTCGACAAGGATGAACAGATCCTGGACCGGAACCCCACTAATCCCGTCCACCTATCACGACCCCTTCTATTTCC

12,240

CACNA1A

CACNA1A-201

CACNA1A-201

AGGTGGTTGGGATATGGGCTGGTTGGGATATTGTTTGGTTTGTCTTTTAAAAAGCCTGCTCAGGGCTAAATTGTTTACTACCTCTA  
TCCACCAACCCTATACCCGACCAACCCTATAACAAACCAAACGAAAATTTTTCGGACGAGTCCCGATTTAACAAATGATGGAGAT

12,325

CACNA1A

CACNA1A-201

CACNA1A-201

GGGACTGGCTAGTGCTGGACCGGGCAGTCCCTCCAGAGTCAGCAAGACCCCAGATGCATCAGAATAAAGAAAAATAAAATGCGTG  
CCCTGACCGATCACGACCTGGCCCGTCAGGGAGGTCTCAGTCGTTCTGGGGTCTACGTAGTCTTATTTCTTTTATTTTACGCACC

12,410

CACNA1A

CACNA1A-201

CACNA1A-201

CCAGGCCAATGAGGTGGTTCATGCCTGTAATCTCAGCACTTTGGGAGACCAAGGCGGGAGGATTGCTTGAGCCAGGAGTTCAAG  
GGTCCGGTTACTCCACCAAGTACGGACATTAGAGTCGTGAAACCCTCTGGTTCCGCCCTCCTAACGAACTCGGGTCTCTCAAGTTC

12,495

CACNA1A

CACNA1A-201

CACNA1A-201

GCTGCCGTGAGCTCCAGCCTGCACCACAGAGCAAGGCCCTGTCTCTTAAAAAAGGCAGAGAAAAAATGGCTAATACACCCA  
CGACGGCACTCGAGGTCGGACGTGGTGTCTCGTTCCGGGACAGAGAATTTTTTTTCCGTCTCTTTTTTTTACCATTATGTGGGT

12,580

CACNA1A

CACNA1A-201

CACNA1A-201

TCAAATCTGAAGATACCTTGGTCTCATATTCCAGGGTGATCAACCCAAAGCAACTTCTGCACCCATGTGGGCGCATTCCCTGAGG  
AGTTTAGACTTCTATGGAACCAGAGTATAAGGTCCCACTAGTTGGGTTTCGTTGAAGACGTGGGTACACCCGCGTAAGGGACTCC

12,665

CACNA1A

CACNA1A-201

CACNA1A-201

CTTGGGACTGGCCACGCCGGGACCTTCAGAGCATCTTTGGTGGATTCTTTCTCTTTGAGGGACTGAGAGTGTATAGAAAATGTGA  
GAACCCTGACCGGGTCGGCCCTGGAAGTCTCGTAGAAACCACCTAAGAAAGAGAAACTCCCTGACTCTCACATATCTTTTACACT

12,750

CACNA1A

CACNA1A-201

CACNA1A-201

CTTCACTCTCTCCTTCTCCTGGGGAGGTAGTTTCTAAATGAGACCCCAAGACAGGGAGTTGAAGAGGAAACCTTCCATGAAGGGA  
GAAGTGAGAGAGGAAGAGGACCCCTCCATCAAAGATTTACTCTGGGGTTCTGTCCCTCAACTTCTCCTTTGGAAGGTA

12,835

CACNA1A

CACNA1A-201

CACNA1A-201

AGTTCTGAGCCCCACATAAGCGATTTTTTTTTTTTTTTTTTGGAGATGGAGTCTCGCTCTGTTGCCAGGCTGGAGTGCGACGGCAC  
TCAAGACTCGGGGGTGTATTTCGCTAAAAAAAAAAAAAAAAA

12,920

CACNA1A

CACNA1A-201

CACNA1A-201

GTTCTTGGCTCACTACAACCTCTGCCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCCGAGTAGCTGAGACTACAGGTGCA  
CAAGAACCGAGTGATGTTGGAGACGGAGGACCCAAGTTCGCTAAGAGGACGGAGTCGGAGGGCTCATCGACTCTGATGTCCACGT

13,005

CACNA1A

CACNA1A-201

CACNA1A-201

TACTACCATGCCTGGCTAATTTTTGTATTTTTAGTAGAGACAGGGTTTCACTATGTTGGCCAGGCTGGTCTCGAACTCCTGGCCT  
ATGATGGTACGGACCGATTAAAAACATAAAAAATCATCTCTGTCCCAAAGTGATACAACCGGTCCGACCAGAGCTTGAGGACCGGA

13,090

CACNA1A

CACNA1A-201

CACNA1A-201

CGTGATCTGCCTGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCACACCTGGCCATAAGCGATTATTAATAGC  
GCACTAGACGGACGGAGCCGGAGGGTTTACGACCCTAATGTCCGTA

13,175

CACNA1A

CACNA1A-201

CACNA1A-201

ACTGATCGCTAGTCATGTATCTTTAGCTCAGAGGTTCTCACCCAAGGACAAGTCTGTCCTCCAAGGACATGTAGCAATGTCTGCA  
TGACTAGCGATCAGTACATAGAAATCGAGTCTCCAAGAGTGGGTTCTGTTT

13,260

CACNA1A

CACNA1A-201

CACNA1A-201

AGCATTGTTGGTTGTCACAGCTAGGGAGAGGGGTGCTACTGGCATCTGGTGGGTGGAGACTAGGAATGCTGCTCAATATCCTACAA  
TCGTAACAACCAACAGTGTGATCCCTCTCCACGATGACCGTAGACCACCCACCTCTGATCCTTACGACGAGTTATAGGATGTT

13,345

CACNA1A

CACNA1A-201

CACNA1A-201

TGCACAGGACAGCCCCAAATAGAATAATCTGGCCCCAAATATCAGCAGTGCTGAGGCTTAGAAACCCCTGTTTTAGCAGATTCATG  
ACGTGTCCTGTGCGGGGTTTATCTTATTAGACCGGGGTTTATAGTCGTACGACTCCGAATCTTTGGGACAAAATCGTCTAAGTAC

13,430

CACNA1A

CACNA1A-201

CACNA1A-201

TTTTTGGAGTCTTTAACATTTACTTTATCCTCATGGGGATATGGATAGAAGGAAGGAAGTTGGATCTTTTTTAAAGGAGCATGT  
AAAAACCTCAAGAAATTGTAAATGAAATAGGAGTACCCCTATACCTATCTTCTTCTTCAACCTAGAAAAAATTTCTCGTACA

13,515

CACNA1A

CACNA1A-201

CACNA1A-201

AGGTGCTGTTTGAATATCCCCTTGGTTCTTTTCAGTATGCATCAGCACAACCTTGCCTGTGCAACACCTAATCCTTTGCCTTGGTC  
TCCACGACAAACTTATAGGGGAACCAAGAAAGTCATACGTAGTCGTGTTGAACGCAGACAGTTGTGGATTAGGAAACGGAACCAG

13,600

CACNA1A

CACNA1A-201

CACNA1A-201

TTTCTCTGGTCCCCTGCTCTGCCCCCAAGGAACTGCAGTCCAGCAGTACTGTGAATTTTTTGTGCCACACCTTAAAAGGAGCAGC  
AAAGAGACCAGGGGACGAGACGGGGGTTTCTTGACGTGAGGTCGTGATGACACTTAAAAAACACGGTGTGGAATTTTCTCGTCG

13,685

CACNA1A

CACNA1A-201

CACNA1A-201

CGTTGGTGGATAAATACCCAGCTCCCTCACCTCAGGTGGGATGACCCCTAGAGCTCCCCAGCAAGACCAAGCCCCGGTTACCT  
GCAACCACCTATTTATGGGGTCGAGGGAGTGGGAGTCCACCCTACTGGGGATCTCGAGGGGTCGTTCTGGTTCCGGGGCCAATGGA

13,770

CACNA1A

CACNA1A-201

CACNA1A-201

ACAGTGGAAACTCGCTTGATCACATACTGTTTACGTTCCACCCTCTTTTCCCTTTTCTCACTTCTCCTCTCCCCTACTGGTGCTT  
TGTCACCTTTGAGCGAACTAGTGTATGACAAATGCAAGGTGGGAGAAAAGGGAAAAGAGTGAAGAGGAGAGGGGATGACCACGAA

13,855

CACNA1A

CACNA1A-201

CACNA1A-201



CCTGAGATCACCTCCCAGACAAACCACTTGCACCCGAACCCCTTGTTCAGGGTCTGCCTCAGGCAGGGGGACCCCAAACGTGTCC  
GGACTCTAGTGGAGGGTCTGTTTGGTGAACGTGGGCTTGGGAACAAGGTCCCAGACGGAGTCCGTCCCCCTGGGGTTTGCACAGG

13,940

CACNA1A

CACNA1A-201

CACNA1A-201

TTGTGCTACATTTGTGCTATCCACGTAGTAGCTTGTTTAATCATCACCATGACCACATGAGGAACACAGGTAAATATTTAAATCC  
AACACGATGTAAACACGATAGGTGCATCATCGAACAAATTAGTAGTGGTACTGGTGTACTCCTTGTGTCCATTTATAATTTTAGG

14,025

CACNA1A

CACNA1A-201

CACNA1A-201

TGTCTTAGTCTGCTCAGGCAGCCATAACAAAATACCACACACTGGGTGGCTTATACAGGAAACATTTATTCTCTCATAGTTCTGG  
ACAGAATCAGACGAGTCCGTCCGGTATTGTTTTATGGTGTGTGACCCACCGAATATGTCTTTGTAAATAAGAGAGTATCAAGACC

14,110

CACNA1A

CACNA1A-201

CACNA1A-201

AGGCCGGGAAGTCCAAGATCAAAGTGTTAGCAGGGTTAGTTAGTTCCTGGTGAGGGCCCTCTTCCTAGCTTGCAGATAGCCACCT  
TCCGGCCCTTCAGGTTCTAGTTTCACAATCGTCCCAATCAATCAAGGACCACTCCCGGGAGAAGGATCGAACGTCTATCGGTGGA

14,195

CACNA1A

CACNA1A-201

CACNA1A-201

TCTTGCTGTGTCTCATATGTCAAAGAGAGAGAGAGAGAGATTGTGATGTTTCTTCTGTTCTTTTTTTTTTTTTTTTTTTTGGAGAC  
AGAACGACACAGGAGTATACAGTTTCTCTCTCTCTCTCAACACTACAAAGAAGGACAAGAAAAAAAAAAAAAAAAAAAACTCTG

14,280

CACNA1A

CACNA1A-201

CACNA1A-201

AAAAATCTCAAAAAAAAAATCTATTTTTTTTTTAGGCAAATCACATTTTTTTTGTACCCAGCCTGGAGTGCAGTGGCACAATCATA  
TTTTTAGAGTTTTTTTTTTAGATAAAAAAAAAAATCCGTTTAGTGTAACAAAAACAGTGGGTCCGACCTCACGTACCCTGTTAGTAT

14,365

CACNA1A

CACNA1A-201

CACNA1A-201

GCTCACTGCAGCCTCAAACCTCCTAGGTTCAAACGATCCTCCACCTCAGCCCTTGGAGTAGCTGGGACTACAGATGGGCACCAGC  
CGAGTGACGTCCGAGTTTGGAGATCCAAGTTTGTAGGAGGGTGGAGTCCGGGAACCTCATCGACCCTGATGTCTACCCGTGGTCCG

14,450

CACNA1A

CACNA1A-201

CACNA1A-201

TAATTTTTTTAAATTTTTTGTAAAGATGGGGTCTTGCTATATTGCCAGGCTAATCTTGAACCTCTGGGCTCAAGTGATCCTCCC  
ATTAATAAATTTAAAAAACATTTCTACCCAGAACGATATAACGGGTCCGATTAGAACTTGAGGACCCGAGTTCACTAGGAGGG

14,535

CACNA1A

CACNA1A-201

CACNA1A-201

ACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCATGGCATGCGGTCTCTTCCTGTTCTTATAAGGGCACTAATACCAT  
TGGAACCGGAGGGTTTCACGACCCTAATGTCCGTA CT CGGTACCGTACGCCAGAGAAGGACAAGAATATTCCCCTGATTATGGTA

14,620

CACNA1A

CACNA1A-201

CACNA1A-201

CATGAAGTCCCCCATGACCTCATCTAACCCCTAGTTACCTCTTAAAGGCCCCATCTCCAAATACCATCCCATCATAGGTTAGGGCT  
GTACTTCAGGGGGTACTGGAGTAGATTGGGATCAATGGAGAATTTCCGGGGTAGAGGTTTATGGTAGGGTAGTATCCAATCCCGA

14,705

CACNA1A

CACNA1A-201

CACNA1A-201

TCAACTCATGAATTTGGAGGCGGGCACAATTTAGTCCATAACAAATCCCCTTAATCACATCAAGTAAGACAGAGTTACAGGAGGG  
AGTTGAGTACTTAAACCTCCGCCCGTGTAAATCAGGTATTGTTTAGGGGAATTAGTGTAGTTTATTCTGTCTCAATGTCTCCC

14,790

CACNA1A

CACNA1A-201

CACNA1A-201

TCTGTGACTCCTCCAGGGTCCCATTTTCTAGAAAGCCAGGCTAAGAGCCCCACGACGCAGGAACGGCCCTTTCTACTCGCAAACA  
AGACACTGAGGAGGTCCCAGGGTAAAAGGATCTTCGGTCCGATTCTCGGGGTGCTGCGTCTTGCCGGGAAAGATGAGCGTTTTGT

14,875

CACNA1A

CACNA1A-201

CACNA1A-201

AAGAGAAAAGCCAAGGAGAAGCCAACACGGAGTCTGGCTCTGCAAACCGGGCAGGATTGTTAAAGACCTCCTGGGCTCGGGGATG  
TTCTCTTTTCGGTTCTCTCGGTTGTGCCTCAGACCGAGACGTTTGGCCCGTCTAACAATTTCTGGAGGACCCGAGCCCTAC

14,960

CACNA1A

CACNA1A-201

CACNA1A-201

GGGTGGGCGGATTCCGGCTCCACAGCTGCATCTCCAAGGGGCCCGTGGCTGAGAGGGGGTTGGCTGTGTGTTTCTTCTCCCT  
CCCACCCGCCTAAGGCCGAGGTGTGACGTAGAGGTTCCCAGGGCACCGACTCTCCCCCAACCGACACACAAAGAAGGAGGGGA

15,045

CACNA1A

CACNA1A-201

CACNA1A-201

TTCAGATCCTGACGGGGCGAAGACTGGAACGAGGTCATGTACGACGGGATCAAGTCTCAGGGGGGCGTGCAGGGCGGCATGGTGTT  
AAGTCTAGGACTGCCCGCTTCTGACCTTGCTCCAGTACATGCTGCCCTAGTTTCAGAGTCCCCCGCACGTCGCCGCGTACCACAA

15,130

CACNA1A

CACNA1A-201

I L T G E D W N E V M Y D G I K S Q G G V Q G G M V F  
ENSE00000951011

CACNA1A-201

CTCCATCTATTTTCATTGTA CTGACTGACGCTCTTTGGGAAC TGTATCCTTCATGGAGAGAGAGAAGGGGACAGGCCTGGACCTCTGGCA  
GAGGTAGATAAAGTAACATGACTGCGAGAAACCCCTTGACATAGGAAGTACCTCTCTCTCTTCCCTGTCCGGACCTGGAGACCGT

15,215

CACNA1A

CACNA1A-201

690 S I Y F I V L T L F 700  
ENSE00000951011

CACNA1A-201

GAGGAGAGGTTGCAGGGGCTCAAGGGAGGGTACTGAGAGACCCAGATACCCAGGGCCCAAGTGGTGTCCCACCAAGTGGTTGCTTT  
CTCCTCTCCAACGTCCCCGAGTTCCTCCCATGACTCTCTGGGTCTATGGGTCCC GGTTTACCACAGGGTGGTACCAACGAAA

15,300

CACNA1A

CACNA1A-201

CACNA1A-201

TCCTGACTCAGACATTTGCAGACACCCCTCCTGAATGTGTTCTTGGCCATCGCTGTGGACAATCTGGCCAACGCCCAAGGAGCTCAC  
AGGACTGAGTCTGTAAACGTCTGTGGGAGGACTTACACAAGAACCGGTAGCGACACCTGTTAGACCGGTTGCGGGTCTCGAGTG

15,385

CACNA1A

CACNA1A-201

Y T L L N V F L A I A V D N L A N A Q E L T  
ENSE00001660630

CACNA1A-201

CAAGGTGGAGGCGGTGGGAGAATGTTTCTCTGGCAAAGTTACCACCTGCCCATGGCAGATCAGGACGGGGGTGGGGGTGGGGGTG  
GTTCCACCTCCGCCACCCTCTTACAAAGAGACCGTTC AATGGTGGACGGGTACCGTCTAGTCCTGCCCCACCCCAACCCCAAC

15,470

CACNA1A

CACNA1A-201

K

EN...

CACNA1A-201

GGGGTGGGGGTGGGGGCATGGGAACAGGGTTAGAACTTTTGCCGGGGATGCACCATGCAAAGAGAAGGCGCCTCTCCCCCACTC  
CCCCACCCCAACCCCGTACCCTTGTCCTCAATCTTGAAAACGGCCCTACGTGGTACGTTTCTCTTCCGCGGAGAGGGGGGTGAG

15,555

CACNA1A

CACNA1A-201

CACNA1A-201

CCAGAAACAGACTGTCCCTCATCAAGCAAATTCTACAGCCAAGAGGGTGGGAAGGGGGAAGGCAGTGAGGTCGCTGCAGGAAACG  
GGTCTTTGTCTGACAGGGAGTAGTTTCGTTTAAGATGTCGGTTCTCCACCCCTTCCCCCTTCCGTC ACTCCAGCGACGTCCTTTGC

15,640

CACNA1A

CACNA1A-201

CACNA1A-201

GATGGCAAACCTCAACCAAAAAGGCCGTTTACAGGGAGTAAGCAGGGTTCCTCAAGGAATGGTGTAGCCCCCAGGCTAGTGGATGGGA  
CTACCGTTTGAGTTGGTTTTCCGGCAAATGTCCCTCATTTCGTCCCAAAGGTTCTTACCACATCGGGGGTCCGATCACCTACCCT

15,725

CACNA1A

CACNA1A-201

CACNA1A-201

GAGGGAGTGCTGTTATGGGGACCCAGTCAGAGCTGGGGCCAAGGAAAAAGGGCTGCCACCAGCCCTGGGACCTTAGAGAACCCAG  
CTCCCTCACGACAATACCCCTGGGTCAAGTCTCGACCCCGGTTCTTTTTCCCGACGGTGGTTCGGGACCCCTGGAATCTCTTGGGTC

15,810

CACNA1A

CACNA1A-201

CACNA1A-201

AACCATGGCAAGGCACAGATGGAGTGGCCAATAAATGTCCCCACCTTCTCTCTTCCCTCTGGCTTCCCGCTGGAGCCTCCCCCTTAG  
TTGGTACCGTTCGGTGTCTACCTCACCGGTTATTTACAGGGGTGGAAGAGAGAAGGAGACCGAAGGGCGACCTCGGAGGGGAATC

15,895

CACNA1A

CACNA1A-201

CACNA1A-201

CCAAACGCAGCATGTTAAGAGCTAGCCTCCGTCCAGCCTAAGCCTCTCCCCAAGGACCCTATTAAGTTAAGATTACATGTAACAG  
GGTTTGCCTCGTACAATTCTCGATCGGAGGCAGGTCGGATTTCGGAGAGGGGTTCTGGGATAATTCAATTCTAATGTACATTGTC

15,980

CACNA1A

CACNA1A-201

CACNA1A-201

GTACAGGGTCTTCCCTCTCAGCCCTGGGGTCTCCCTCAGCATTGCAGCCCCACCTCCAGTGCCTCGAGGTATTCAGGACATGTTTG  
CATGTCCCAGAAGGAGAGTCCGGGACCCAGAGGGAGTTCGTAACGTTCGGGGTGGAGGTCACGGAGCTCCATAAGTCTGTACAAAC

16,065

CACNA1A

CACNA1A-201

CACNA1A-201

TGAAATTGAACCAAAACCAAGCAGACGTTGCCAACGCTCCATCTGCCGGCCCTGGCAGGAGGGAGAGAGATTTCCCGGCCCCAGC  
ACTTTAACTTGGTTTGGTTCGTCTGCAACGGTTGCGAGGTAGACGGCCGGGACCGTCTCCTCTCTCTCAAAGGGCCGGGGTTCG

16,150

CACNA1A

CACNA1A-201

CACNA1A-201

TCCCAGTGGAGGGGAAGCGGAAGTCTCTGCCATCCCAAGCACACGGCCACAAGCCTGGCCACTGTGGAGCTGGCTGGCATGGCTGA  
AGGGTCACCTCCCTTCGCCTTCAGAGACGGTAGGGTTCGTGTGCCGGTGTTCGGACCGGTGACACCTCGACCGACCGTACCGACT

16,235

CACNA1A

CACNA1A-201

CACNA1A-201

GCCGAGGGGCTGATCCAGCCATGAGCTCATCCAAGTTCCAAGAGTCCATCCTTAGGGGGCTGGTGCAGGAGGGGTAGCAGAAGGGGGAG  
CGGCTCCCGACTAGGTCGGTACTCGAGTAGGTTCAAGGTTTCTCAGGTAGGAATCCCCGACCACGTCTCTCCCATCGTCTTCCCCTC

16,320

CACNA1A

CACNA1A-201

CACNA1A-201

GGAGAAAAGGCCAGTTCGTTTTATCTCCTGGGAGGTGTGGACATTCTCTCCAGATCCACATTCTTTCTTTTCATTGATCCTACAAGC  
CCTCTTTCCGGTCAAGCAAATAGAGGACCCTCCACACCTGTAAGGAGAGGGTCTAGGTGTAAGAAAAGAAAAGTAACTAGGATGTTTCG

16,405

CACNA1A

CACNA1A-201

CACNA1A-201

ATTTCTTGGGTCATTTAATACGTGTTTTAATCCTATTTCAGTCTCATGGAAACCTTAGGAGCCAAGTTCTCTGAGCCCCATTTTA  
TAAAGAACCAGTAAATTATGCACAAAAATTAGGATAAGTCAGGAGTACCTTTGGAATCCTCGGTTCAAGAGACTCGGGGTAAAAT

16,490

CACNA1A

CACNA1A-201

CACNA1A-201

CAGATTTTCATCATTTCAGTAAGCACTTAATGAGCACCTACTGTGTGACCAAGGCCCTGGTCTAGGACTTAGGGATTAAGCAGTGAA  
GTCTAAAGTAGTAAGTCATTTCGTGAATTAATCGTGGATGACACACTGGTTCCGGGACCAGATCCTGAATCCCTAATTCGTCACTT

16,575

CACNA1A

CACNA1A-201

CACNA1A-201

CAAAAAAAGGCCAAAAATCCCTGCCTCCGTGGAGCAGGGATTCAAGAGGGGAGACAGACAAGAAAACAAGATAAATTTGTAAACATA  
GTTTTTTTTCCGTTTTTTAGGGACGGAGGCACCTCGTCCCTAAGTTCTCCCCTCTGTCTGTTCTTTGTTCTATTTAAACATTTGTAT

16,660

CACNA1A

CACNA1A-201

CACNA1A-201

CGTAGCTTGTGAGTTGGTGATAAACACAACAGAGAAAAATTCAGTAGGGAAAGTCAGGGAGAGTTGGAATTTTAGATGAGATGTG  
GCATCGAACAGTCAACCACTATTTGTGTTGTCTCTTTTTAAGTCATCCCTTTTCAGTCCCTCTCAACCTTAAAATCTACTCTACAC

16,745

CACNA1A

CACNA1A-201

CACNA1A-201

TGTCGCACAGAGAGGTTGAGAGACTTGCCCAAGGCCACACAGCAGTAAGTTGTGGAGCTGGGATTTGAACCCAGGCCGTCTGGGT  
ACAGCGTGTCTCTCCAACCTCTCTGAACGGGTTCCGGTGTGTGTCGTCATTCAACACCTCGACCCTAAACTTGGGTCCGGCAGACCCA

16,830

CACNA1A

CACNA1A-201

CACNA1A-201

CTGCAGCTTGTGCTCTTAACTGCTGTGTACCAAGTTGCTTGAATTTGGGCATGTTTTATGCTCACTTGGGAACCTGTGGGAAATGC  
GACGTCGAACACGAGAATTGACGACACATGGTCAACGAACTTAAACCCGTACAAAATACGAGTGAACCCCTTGGACACCCCTTTACG

16,915

CACNA1A

CACNA1A-201

CACNA1A-201

AGATTCCAGGGCCCAGCACTGGTTCTATAGATTATTTGGGGAGCCTGAGGATCTGCATTTTAGGTGTTTCTGAGGCAGATGGTCC  
TCTAAGGTCCCAGGTCGTGACCAAGATATCTAATAAACCCCTCGGACTCCTAGACGTAATAATCCACAAAGACTCCGTCTACCAGG

17,000

CACNA1A

CACNA1A-201

CACNA1A-201

AGAGACCTAGCTCTGAAAAATGCTGGGAATGGTGCCAGGAGGGGTGGGGGTGGCCCTATGAGAGCAGGGTGGCCAGCCAGATCCC  
TCTCTGGATCGAGACTTTTTACGACCCTTACCACGGTCTCCCCACCCACCACGGGATACTCTCGTCCCACCGGTCGGTCTAGGG

17,085

CACNA1A

CACNA1A-201

CACNA1A-201

ATCTCCATGTTGTCTCTGACAGTGTCTGATCTGACCATTTCCAAGGTGGTAAGGTTGCTCCCCGTTCCAGTGATTCCGGAGCACA  
TAGAGGTACAACAGAGACTGTACAGGACTAGACTGGTAAAGGTTCCACCATTCCAACGAGGGGCAAGGTCACTAAGCCTCGTGT

17,170

CACNA1A

CACNA1A-201

CACNA1A-201

GCGGGAGAGCTGCCTGCAATGGCATGACTTTTCTTATGGGCGGGTTCATTTCTGGCCATTTCTTTCTCGTTGCCTTTTCTTTGCT  
CGCCCTCTCGACGGACGTTACCGTACTGAAAAGAATACCCGCCAAGTAAAGACCGGTAAAGAAAGAGCAACGGAAAAAGAAACGA

17,255

CACNA1A

CACNA1A-201

CACNA1A-201

TTTTCTTTGTTGGCTTTTCTGTTTTACGAATGAGGCCCTGCATGAAGGCTGAAGAAGGATTTAAAGTCCAAAAACGTCTTTTTCT  
AAAAGAAACAACCGAAAAAGACAAAATGCTTACTCCGGGACGTACTTCCGACTTCTTCTAAATTTTCAGGTTTTTGCAGAAAAAGA

17,340

CACNA1A

CACNA1A-201

CACNA1A-201

GTATGTATTTTTAAACCTCTTCCCCATTCTCCTCCTCTCTGAACCTAACCCACAGTGAGCAGCAGCACCCCTGGGCAGTTGGCT  
CATACATAAAAAATTTGGAGAAGGGGGTAAGAGGAGGAGAGACTTGGATTGGTGGTCACTCGTCTCGTGGGACCCGTC AACCGA

17,425

CACNA1A

CACNA1A-201

CACNA1A-201

GTAGCCCAAGTGCCCTGCTCTCCTCTCCCCACCGCCTTCTGTGTCATGGGGGCTGGGAATATAAAATTCCTCTCCTCATTCTCCTTC  
CATCGGGTTCACGGGACGAGAGGAGAGGGGTGGCGGAAGGACAGTACCCCCGACCCTTATATTTAAGGAGAGGAGTAAGAGGAAG 17,510

CACNA1A >

CACNA1A-201 >

----- >  
CACNA1A-201

TGGGGGCTGTTGACAGTGCATGGCAGGGGCCATCGGATGCCAGGCTCTTCTGTGTGTGAGGGTAGTTGGTGTTTTTTGAAGTTG  
ACCCCCGACAACACTGTCACGTACCGTCCCCGGTAGCCTACGGTCCGAGAAGACACACACTCCCATCAACCACAAAAAACTTTCAAC 17,595

CACNA1A >

CACNA1A-201 >

----- >  
CACNA1A-201

GTTTCAGAGAGTTTCACATGGCTCAGAAAGCCTAGTGAGAGGAAAATCTTTGCACTGCTTTCCAGCTCATTAAAGACAGGATGCAGGG  
CAAGTCTCTCAAGTGTACCGAGTCTTTTCGGATCACTCTCCTTTTAGAAAACGTGACGAAAGGTCGAGTAATTCTGTCTACGTCCC 17,680

CACNA1A >

CACNA1A-201 >

----- >  
CACNA1A-201

GCCAGGCATGGTGGCACATGCCTGGAATCCCAGCACTTTGGGAGGCCGAAATGGGAGGATCATTGAGGCCAGAAGTTCAAGACC  
CGGTCCGTACCACCGTGTACGGACCTTAGGGTCGTGAAACCTCCGGCTTTACCCTCCTAGTAAACTCCGGTCTTCAAGTTCTGG 17,765

CACNA1A >

CACNA1A-201 >

----- >  
CACNA1A-201

AGCCTGGGCAACATAGTGAGACCCTGTCTCTACAAAAAAAAAAAAAAAAAATTAATGTATACAGGCATAGTGGCATGCACCTGTAG  
TCGGACCCGTTGTATCACTCTGGGACAGAGATGTTTTTTTTTTTTTTTTTAATTTACATATGTCCGTATCACCGTACGTGGACATC 17,850

CACNA1A >

CACNA1A-201 >

----- >  
CACNA1A-201

TCCCAGTTGCTTGGGAGGCTGAGGTGGGAGGATTGCTTGAGCCCAGGAGTTCAAGGTTACAGTGAGCTATGATTGTGCCACTGCA  
AGGGTCAACGAACCCTCCGACTCCACCCTCCTAACGAACTCGGGTCTCAAGTTCCAATGTCACTCGATACTAACACGGTGACGT 17,935

CACNA1A >

CACNA1A-201 >

----- >  
CACNA1A-201

CTCCAGGCTGGGCAACCAAGGGGAGACTCTGTCTCTGAAAACAAACAAAAGAAAAAAAAAATAGGCTGCAGGAAAGTCTTCATTGTA  
GAGGTCCGACCCGTTGGTTCCTCTGAGACAGAGACTTTGTTGTTTTCTTTTTTTATCCGACGTCCTTTCAGAAGTAACAT 18,020

CACNA1A >

CACNA1A-201 >

----- >  
CACNA1A-201

GGAAGAGAAGGGACATTTTTATTTTTTGTATCTGGCTGTGTGTTAAAAATAGGCTTCATAATGAGTTAGATGTCAAACCTTATACA  
CCTTCTCTTCCCTGTAAAAATAAAAAACAATAGACCGACACACAATTTTATCCGAAGTATTACTCAATCTACAGTTTGAATATGT

18,105

CACNA1A

CACNA1A-201

CACNA1A-201

CAGAGGGGATAGCAATACACTTAACCAATAGCAGGTACCCATTCCAATTGGGGAGCCTTGGTTCTGATTGGTTCGAAATATTTCAA  
GTCTCCCCTATCGTTATGTGAATTGGTTATCGTCCATGGGTAAGGTTAACCCCTCGGAACCAAGACTAACCCAGCTTTATAAAGTT

18,190

CACNA1A

CACNA1A-201

CACNA1A-201

ATGTTGCCCTGGTCAGCAACAGGGTCAGAAGTGAGTCCCAAGGCCTAGTTTCATGTTTTGTGAACAAAGATTCCACGTGCCTTT  
TACAACGGGGACCAGTCGTTGTCCCAGTCTTCACTCAGGGGTTCCGGATCAAGTACAAAACACTTGTTCCTAAGGTGCACGGAAA

18,275

CACNA1A

CACNA1A-201

CACNA1A-201

TAGGACGAGCAAGAGGAAGAAGAAGCAGCGAACCCAGAAACTTGCCCTACAGAAAGCCAAGGAGGTGGCAGAAGTGAGTCCTCTGT  
ATCCTGCTCGTTCTCCTTCTTCTTTCGTCGCTTGGTCTTTGAACGGGATGTCCTTTCGGTTCCTCCACCGTCTTCACTCAGGAGACA

18,360

CACNA1A

CACNA1A-201

ENSE00000951013  
CACNA1A-201

725 D E Q E E E A A N Q 730 735 K L A L Q 740 K A K E V A E V S P L 750

CCGCGGCCAACATGTCTATAGCTGTGTAAGTGCCCTAATCCCTGGGATGCTACCCTGGCTCCTGAACGTCCACACTATCCCAAG  
GGCGCCGGTTGTACAGATATCGACACATTCACGGGGATTAGGGACCTACGATGGGACCGAGGACTTGCAGGTGTGATAGGGTCC

18,445

CACNA1A

CACNA1A-201

ENSE00000951013  
CACNA1A-201

755 S A A N M S I A V 760

CACAGATTTGGGAAGCAGTGGGGGTGGTCTTGACAGAAGTGGCTTTAGGAAGAGACACTTCTTGTCTTCCACCCACTTTTAC  
GTGTCTAAACCCTTCGTCAACCCACCAGGAAGTGTCTTGAAGTTCGAAATCCTTCTCTGTGAAGAACAGGAAGGTGGGTGAAAGTG

18,530

CACNA1A

CACNA1A-201

CACNA1A-201

TCAATAAATATTTGGTTAGCAGCTGTTATGTACCCAGCACTGTTCTAACTTCTGGGGATACAGCATTAAACAAGGAGGAAAAAAA  
AGTTATTTATAAACCAATCGTCGACAATACATGGGTGCTGACAAGATTGAAGACCCCTATGTCGTAATTGTTCTCTCTTTTTTTT

18,615

CACNA1A

CACNA1A-201

CACNA1A-201



AATCCCACCTGTGTGTAGCCATTCTAGCAAGGGAAGGAGTCAATAAATTAGATAAATAAGTAAATTATATATTGTGTTAGAAGGC  
TTAGGGTGGACACACATCGGTAAGATCGTTCCTTCCCTCAGTTATTTAATCTATTTATTCATTTAATATATAACACAATCTTCCG

18,700

CACNA1A

CACNA1A-201

CACNA1A-201

GATGGAACACTACAGAGAAAGTAGGGGAGGGAAATAGCAAATGCTGGGAGTGAAGAGAGTTGTGATTTTTAAACGAAGTTGTCAGGGA  
CTACCTTGATGTCTCTTTCATCCCCTCCCTTTATCGTTTACGACCCTCACTTCTCTCAACACTAAAATTTGCTTCAACAGTCCCT

18,785

CACNA1A

CACNA1A-201

CACNA1A-201

AGGCATCACCTAGAAATAGGGGTCCCCAGTCCCAGGGGCTGTGGACTGGTACCAGGCCGAGGCCTATTAGGAACGGGGCTGCACAGC  
TCCGTAGTGGATCTTATCCCCAGGGGTCAGGGCCCCGACACCTGACCATGGTCCGGCTCCGGATAATCCTTGCCCCGACGTGTCG

18,870

CACNA1A

CACNA1A-201

CACNA1A-201

AGGAGGTGAACAGTGAGCAAGCAAGCATTACCGCCTGAGCTCCACCTGCCGTGATCAGATCAGCAGGCAGCATTAGATTCTCATAGGA  
TCCTCCACTTGTCACTCGTTCGTTTCGTAATGGCGGACTCGAGGTGGACGGCAGTCTAGTCCGTCGTAATCTAAGAGTATCCT

18,955

CACNA1A

CACNA1A-201

CACNA1A-201

ACACAAACACTATTGTGAACGGTGCATCTGAGGGATCTAGGTTGCGTGCTCCTTTAAGAATCGAATGCCTGATGATCTCAGGTG  
TGTGTTTGTGATAACACTTGCCACGTAGACTCCCTAGATCCAACGCACGAGGAAAATTCTTAGCTTACGGACTACTAGAGTCCAC

19,040

CACNA1A

CACNA1A-201

CACNA1A-201

AAACAGTTTCATCCCAAACACCCCCACACCTAGGTCTGTGGAAAACTGTCTTCCACAAAACCTGGCCCTGGTGCCAAAAG  
TTTGTCAAAGTAGGGTTTTGGTGGGGGGTGTGGATCCAGACACCTTTTTGACAGAAGGTGTTTTGACCGGGGACCACGGTTTTTC

19,125

CACNA1A

CACNA1A-201

CACNA1A-201

GTTGGGGACTGCTCACCTAGAAGGTTACATGGCCTGAAGGAGGTGAGGGAGGAGCCACTGGGGGGCCTGGGGAAGGGCATCCCAG  
CAACCCCTGACGAGTGGATCTTCCAATGTACCGGACTTCCCTCCACTCCCTCCTCGGTGACCCCCGGACCCCTTCCCGTAGGGTC

19,210

CACNA1A

CACNA1A-201

CACNA1A-201

GCAGAGGGAAACAGCATAGGCAATGGCCCTGAGGCAGGAACATGCCTGATGTGAAGGAGGCCTGTGTGACTAGAATCGAATAGTAA  
CGTCTCCCTTGTCTGATCCGTTACCGGGACTCCGTCTTGTACGGACTACACTTCCCTCCGGACACACTGATCTTAGCTTATCATT

19,295

CACNA1A

CACNA1A-201

CACNA1A-201

GTGTGAGGAGGTGAAGGCAAGGAGGTGACAAGCAGATTACACAGGGCCTTCTGGGTCAGGGGGGAGGACTTGGGCTTTTGGCCCT  
CACACTCCTCCACTTCCGTTCCCTCCACTGTTTCGTCTAATGTGTCCCGAAGACCCAGTCCCCCTCCTGAACCCGAAAACGGGGA

19,380

CACNA1A

CACNA1A-201

CACNA1A-201

AGCCAGGTGGGAGCCATGGAGGGTCTTGAGCAGAGGAGGCTGGGACCTGACTCAGATGCTCACAGACTCCTAGCATTCAAGTGGG  
TCGGTCCACCCTCGGTACCTCCCAAGAAGTTCGTCTCCTCCGACCTGGACTGAGTCTACGAGTGTCTGAGGATCGTAAGTCACCC

19,465

CACNA1A

CACNA1A-201

CACNA1A-201

GAGTAGAGGGTGGAGAGCAGGAGTGGGAGGCTGAGATGTGGGTTGGTTCGCCTGGGTCATCCATCCAAGCTACAGTGCCTAGCAA  
CTCATCTCCACCTCTCGTCTCACCTCCGACTCTACACCCAACCAAGCGGACCCAGTAGGTAGGTTTCGATGTCACGGATCGTT

19,550

CACNA1A

CACNA1A-201

CACNA1A-201

TGCTCTAAGTCTGTGACCATGCCACTGCAGGAAAGAGCAACAGAAGAATCAAAAAGCCAGCCAAGTCCGTGTGGGAGCAGCGGAC  
ACGAGATTCAGGACACTGGTACGGTGACGTCCTTTCTCGTTGTCTTCTTAGTTTTTCGGTTCGGTTCAGGCACACCCTCGTCGCCTG

19,635

CACNA1A

CACNA1A-201

K E Q Q 765 K N Q K P A 770 K S V W 775 E Q R T

ENSE00001247059

CACNA1A-201

CAGTGAGATGCGAAAAGCAGAACTTGCTGGCCAGCCGGGAGGCCCTGTATAACGAAATGGACCCGGACGAGCGCTGGAAGGCTGCC  
GTCACTCTACGCTTTCGTCTTGAACGACCGGTCGGCCCTCCGGGACATATTGCTTTACCTGGGCTGCTCGCGACCTTCCGACGG

19,720

CACNA1A

CACNA1A-201

S E M R K Q 780 N L L A S 785 R E A L Y 790 N E M D P 795 D E R W K A A 800 805

ENSE00001247059

CACNA1A-201

TACACGGGCACCTGCGGCCAGACATGAAGACGCACTTGGACCGGCCGCTGGTGGTGGACCCGAGGAGAACC GCAACAACA  
ATGTGCGCCGTGGACGCGGTCTGTACTTCTGCGTGAACCTGGCCGGCGACCACCACTGGGCGTCTCTTGGCGTTGTTGTTGT

19,805

CACNA1A

CACNA1A-201

Y T R H L R P D 810 M K T H L 815 D R P L V 820 V D P Q E 825 N R N N N 830

ENSE00001247059

CACNA1A-201

CCAACAAGAGCCGGGCGGCCGAGCCACCGTGGACCAAGCGCCTCGGCCAGCAGCGCGCCGAGGACTTCTCAGGAAACAGGCCCG  
GGTTGTTCTCGGCCCGCCGGCTCGGGTGGCACCTGGTCGCGGAGCCGGTCTGTCGCGCGGCTCCTGAAGGAGTCTTTGTCCGGGC

19,890

CACNA1A

CACNA1A-201

835 T N K S R A A E P T V D Q R L G Q Q R A E D F L R K Q A R 860

ENSE00001247059

CACNA1A-201

CTACCACGATCGGGCCCGGGACCCAGCGGCTCGGCGGGCCTGGACGCACGGAGGCCCTGGGCGGGAAGCCAGGAGGCCGAGCTG  
GATGGTGCTAGCCCGGGCCCTGGGGTCGCCGAGCCGCCCGGACCTGCGTGCCCTCCGGGACCCGCCCTTCGGTCTCCGGCTCGAC

19,975

CACNA1A

CACNA1A-201

865 Y H D R A R D P S G S 870 875 A G L D A 880 R R P W A G S Q E A E L 890

ENSE00001247059

CACNA1A-201

AGCCGGGAGGGACCCCTACGGCCGCGAGTCGGACCACCACGCCCGGGAGGGCAGCCTGGAGCAACCCGGGTTCTGGGAGGGCGAGG  
TCGGCCCTCCCTGGGATGCCGGCGCTCAGCCTGGTGGTGGCGGGCCCTCCCGTCGGACCTCGTTGGGCCCAAGACCCCTCCCGCTCC

20,060

CACNA1A

CACNA1A-201

895 S R E G P Y G R E S D H H A R E G S L E Q P G F W E G E 915

ENSE00001247059

CACNA1A-201

CCGAGCGAGGCAAGGCCGGGGACCCACCGGAGGCACGTGCACCGGCAGGGGGGCGAGCGGGAGAGCCGCAGCGGGTCCCCGCG  
GGCTCGCTCCGTTCCGGCCCTGGGGGTGGCCTCCGTGCACGTGGCCGTCCCCCGTCGTCCTCTCGGCGTCGCCCAAGGGGCGC

20,145

CACNA1A

CACNA1A-201

920 A E R G K A G D P H R R H V H R Q G G S R E S R S G S P R 945

ENSE00001247059

CACNA1A-201

CACGGGCGCGGACGGGGAGCATCGACGTCATCGCGCGCACCCGCAGGCCCGGGGAGGAGGGTCCGGAGGACAAGGCCGGAGCGGAGG  
GTGCCCGCGCCTGCCCTCGTAGCTGCAGTAGCGCGCGTGGCGTCCGGGCCCTCCTCCAGGCCCTCCTGTTCCGCCCTCGCCTCC

20,230

CACNA1A

CACNA1A-201

950 T G A D G E H R R H R A H R R P 965 G E E G P E D K A E R R 975

ENSE00001247059

CACNA1A-201

CGCGCCGACCGGAGGGCAGCCGGCCGGCCCGGGGCGGCGAGGGCGAGGGCGAGGGCCCGACGGGGGCGAGCGCAGGAGAAGGC  
CGCGCCGTGGCGCTCCCGTCGGCCGGCCGGGCCCGCCGCTCCCGCTCCCGCTCCCGGGGCTGCCCGGCTCGCGTCTCTTCCG

20,315

CACNA1A

CACNA1A-201

980 A R H R E G S R P A R G G E G E G E G P D G G 1000 E R R R R

ENSE00001247059

CACNA1A-201

ACCGGCATGGCGCTCCAGCCACGTACGAGGGGGACGCGCGGAGGGAGGACAAGGAGCGGAGGCATCGGAGGAGGAAGTAAGTGGATGGCCTACCGCGAGGTCGGTGCATGCTCCCCCTGCGCGCCTCCCTCCTGTTCTCGCCTCCGTTAGCCTCCTCCTTCATTCACCT

20,400

CACNA1A

CACNA1A-201

1005 H R H G A P A T Y E G D A R R E D K E R R H R R R K 1030

ENSE00001247059

CACNA1A-201

GGTGACCTCGAATCCGCAGAATGACGGTAACATTAATAATGACAACAGCCAAAAGTAGCACGTGCTGTGTATTTGTTTATAAAAATCCACTGGAGCTTAGGGCGTCTTACTGCCATTGTAATTACTGTTGTGCGGTTTCATCGTGCACGACACATAAACAAATATTTTTA

20,485

CACNA1A

CACNA1A-201

ATATTATAAAATGCTGTATTTGGCCAGGCGCAGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGATGGATCAC TATAATATTTTACGACATAAACCGGTCCGCGTCACCGAGTGC GGACATTAGGGTCGTGAAACCTCCGGCTCCGCCTACCTAGTG

20,570

CACNA1A

CACNA1A-201

GAGGTCAGGAGTTCAAGACCAGCCTGGCCAAGATGGTGAAACCCCTCCAGTCCTCAAGTTCTGGTCCGGACCGGTTCTACCACTTTGGG

3'

20,614

5'

CACNA1A

CACNA1A-201

Feature	Location	Size	Color	Symbol	Type
✓ <b>CACNA1A</b>	1 .. 20,614	20,614 bp	Grey	→	gene
/note	= gene <a href="#">ENSG00000141837</a> Protein coding				
✓ <b>CACNA1A-201</b>	1 .. 20,614	20,614 bp	Yellow	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000360228</a>				
<b>CACNA1A-202</b>	1 .. 20,614	20,614 bp	Grey	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000573710</a>				
<b>CACNA1A-214</b>	1 .. 20,614	20,614 bp	Grey	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000635727</a>				
<b>CACNA1A-217</b>	1 .. 20,614	20,614 bp	Grey	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000635895</a>				
<b>CACNA1A-220</b>	1 .. 20,614	20,614 bp	Grey	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000636012</a>				
<b>CACNA1A-224</b>	1 .. 20,614	20,614 bp	Grey	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000636389</a>				
<b>CACNA1A-226</b>	1 .. 20,614	20,614 bp	Grey	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000636549</a>				
<b>CACNA1A-237</b>	1 .. 20,614	20,614 bp	Grey	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000637276</a>				
<b>CACNA1A-239</b>	1 .. 20,614	20,614 bp	Grey	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000637432</a>				
<b>CACNA1A-245</b>	1 .. 20,614	20,614 bp	Grey	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000637736</a>				
<b>CACNA1A-246</b>	1 .. 20,614	20,614 bp	Grey	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000637769</a>				
<b>CACNA1A-252</b>	1 .. 20,614	20,614 bp	Grey	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000637927</a>				
<b>CACNA1A-256</b>	1 .. 20,614	20,614 bp	Grey	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000638009</a>				
<b>CACNA1A-257</b>	1 .. 20,614	20,614 bp	Grey	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000638029</a>				
<b>CACNA1A-259</b>	1 .. 20,614	20,614 bp	Grey	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000664864</a>				
<b>CACNA1A-254</b>	1 .. 12,371	12,371 bp	Grey	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000637966</a> protein_coding_CDS_not_defined				
<b>CACNA1A-232</b>	1 .. 11,588	11,588 bp	Grey	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000636974</a> Retained intron				
<b>CACNA1A-221</b>	1 .. 6283	6283 bp	Grey	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000636022</a> Retained intron				
✓ <b>CACNA1A-201</b>	1614 .. 20,391	18,778 bp	Red	→	CDS
↳ 9 segments	= 1744 bp				
/codon_start	= 1				
/note	= coding sequence <a href="#">ENSP00000353362</a>				
/translation	= SPFARASIKSAKLENSTFFHKKERRMRFYIRRMVKTQAFYWTVLSLVALNLTLCVAIVHYNQPEWLSDFL,,YYAEFIFLGLFMSEMFIMKMYGLGTRP YFHSSFNCFDCG,,VIIGSIFEVIWAVIKPGTSFGISVLRALRLLRIFKVTK,,YWASLRNLVV SLLNSMKSII SLLFLLFLFIVV FALLGMQLFGGQ,,FN FDEGTPPTNFDTFPAAIMTVFQ,,ILTEDWNEVMYDGIKSQGGVQGGMVFSIYFIVLTLFGN,,YTLLNVFLAIAVDNLANAQELTK,,DEQEEEEEA ANQKLA LQ KAKEVAEV SPLSAANMSIAV,,KEQ QKNQ KPAKSVWEQRTSEMRKQ NLLASREALYNEMDPDERWKAAYTRHLRPDMKTHLDRPL VVDPQENRNNNTNKSRAAEPTVDQRLGQRAEDFLRKQARYHRDRAPSGSAGLDARRPWAGSQEA ELSREGPYGREGSDHHAREGSLEQPG FWEGEA ERGKA GDPHRRHVHRQ GGSRESRSGSPRTGADGHEHRRHRAHRRPGEEGPEDKAERRA RHREGSRPARGGEGEGEGPDGGERRRRHR SGAATYEGDA REEDKERRR 561 amino acids & 664 bp				

Feature	Location	Size	Type
<b>CACNA1A-202</b>	1614 .. 20,391	18,778 bp	CDS
▶ 9 segments = 1744 bp			
/codon_start = 1			
/note = coding sequence <a href="#">ENSP00000460092</a>			
/translation =	<pre> SPFARASIKSAKLENSTFFHKERRRMRFYIRRMVKTQAFYWTVLSLVALNTLCVAIVHYNQPEWLSDFL,,YYAEFIFLGLFMSEMFIKMYGLGTRP YFHSSFNCFDCG,,VIIGSIFEVIWAVIKPGTSFGISVLRALRLLRIFKVTK,,YWASLRNLVVSLLNSMKSIISLLFLLFLFIVV FALLGMQLFGGQ,,FN FDEGTPPTNFDTFPAAIMTVFQ,,ILTGEDWNEVMYDGIKSQGGVQGGMVFSIYFIVLTLFGN,,YTLLNVFLAIAVDNLANAQELTK,,DEQEEEEEA ANQKLA LQ KAKEVA EV SPLSAA NMSIAV,,KEQ QKNQ KPAKSV WEQRTSEMRKQ NLLA SREALYNEMDPDERWKAAYTRHLRPDMKTHLDRPL VVDPQENRNNNTNKSRAAEPTVDQRLGQ QRAEDFLRKQARYHDRA RDP SGSA GLDARRP WAGSQ EA ELSREGPYGRESDDHHA REGSLEQPG FWEGEA ERGKA GDPHRRHVHRQ GGSRESRSGSPRTGADGEHRRHRA HRRP GEEGPEDKAERRARHREGSRPARGGEGEGEGEPDGGERRRRHR HGAATYEGDARRBEOKRRRR </pre>		
<b>CACNA1A-214</b>	1614 .. 20,391	18,778 bp	CDS
▶ 9 segments = 1744 bp			
/codon_start = 1			
/note = coding sequence <a href="#">ENSP00000490001</a>			
/translation =	<pre> SPFARASIKSAKLENSTFFHKERRRMRFYIRRMVKTQAFYWTVLSLVALNTLCVAIVHYNQPEWLSDFL,,YYAEFIFLGLFMSEMFIKMYGLGTRP YFHSSFNCFDCG,,VIIGSIFEVIWAVIKPGTSFGISVLRALRLLRIFKVTK,,YWASLRNLVVSLLNSMKSIISLLFLLFLFIVV FALLGMQLFGGQ,,FN FDEGTPPTNFDTFPAAIMTVFQ,,ILTGEDWNEVMYDGIKSQGGVQGGMVFSIYFIVLTLFGN,,YTLLNVFLAIAVDNLANAQELTK,,DEQEEEEEA ANQKLA LQ KAKEVA EV SPLSAA NMSIAV,,KEQ QKNQ KPAKSV WEQRTSEMRKQ NLLA SREALYNEMDPDERWKAAYTRHLRPDMKTHLDRPL VVDPQENRNNNTNKSRAAEPTVDQRLGQ QRAEDFLRKQARYHDRA RDP SGSA GLDARRP WAGSQ EA ELSREGPYGRESDDHHA REGSLEQPG FWEGEA ERGKA GDPHRRHVHRQ GGSRESRSGSPRTGADGEHRRHRA HRRP GEEGPEDKAERRARHREGSRPARGGEGEGEGEPDGGERRRRHR HGAATYEGDARRBEOKRRRR </pre>		
<b>CACNA1A-217</b>	1614 .. 20,391	18,778 bp	CDS
▶ 9 segments = 1744 bp			
/codon_start = 1			
/note = coding sequence <a href="#">ENSP00000490323</a>			
/translation =	<pre> SPFARASIKSAKLENSTFFHKERRRMRFYIRRMVKTQAFYWTVLSLVALNTLCVAIVHYNQPEWLSDFL,,YYAEFIFLGLFMSEMFIKMYGLGTRP YFHSSFNCFDCG,,VIIGSIFEVIWAVIKPGTSFGISVLRALRLLRIFKVTK,,YWASLRNLVVSLLNSMKSIISLLFLLFLFIVV FALLGMQLFGGQ,,FN FDEGTPPTNFDTFPAAIMTVFQ,,ILTGEDWNEVMYDGIKSQGGVQGGMVFSIYFIVLTLFGN,,YTLLNVFLAIAVDNLANAQELTK,,DEQEEEEEA ANQKLA LQ KAKEVA EV SPLSAA NMSIAV,,KEQ QKNQ KPAKSV WEQRTSEMRKQ NLLA SREALYNEMDPDERWKAAYTRHLRPDMKTHLDRPL VVDPQENRNNNTNKSRAAEPTVDQRLGQ QRAEDFLRKQARYHDRA RDP SGSA GLDARRP WAGSQ EA ELSREGPYGRESDDHHA REGSLEQPG FWEGEA ERGKA GDPHRRHVHRQ GGSRESRSGSPRTGADGEHRRHRA HRRP GEEGPEDKAERRARHREGSRPARGGEGEGEGEPDGGERRRRHR HGAATYEGDARRBEOKRRRR </pre>		
<b>CACNA1A-220</b>	1614 .. 20,391	18,778 bp	CDS
▶ 9 segments = 1744 bp			
/codon_start = 1			
/note = coding sequence <a href="#">ENSP00000490223</a>			
/translation =	<pre> SPFARASIKSAKLENSTFFHKERRRMRFYIRRMVKTQAFYWTVLSLVALNTLCVAIVHYNQPEWLSDFL,,YYAEFIFLGLFMSEMFIKMYGLGTRP YFHSSFNCFDCG,,VIIGSIFEVIWAVIKPGTSFGISVLRALRLLRIFKVTK,,YWASLRNLVVSLLNSMKSIISLLFLLFLFIVV FALLGMQLFGGQ,,FN FDEGTPPTNFDTFPAAIMTVFQ,,ILTGEDWNEVMYDGIKSQGGVQGGMVFSIYFIVLTLFGN,,YTLLNVFLAIAVDNLANAQELTK,,DEQEEEEEA ANQKLA LQ KAKEVA EV SPLSAA NMSIAV,,KEQ QKNQ KPAKSV WEQRTSEMRKQ NLLA SREALYNEMDPDERWKAAYTRHLRPDMKTHLDRPL VVDPQENRNNNTNKSRAAEPTVDQRLGQ QRAEDFLRKQARYHDRA RDP SGSA GLDARRP WAGSQ EA ELSREGPYGRESDDHHA REGSLEQPG FWEGEA ERGKA GDPHRRHVHRQ GGSRESRSGSPRTGADGEHRRHRA HRRP GEEGPEDKAERRARHREGSRPARGGEGEGEGEPDGGERRRRHR HGAATYEGDARRBEOKRRRR </pre>		
<b>CACNA1A-224</b>	1614 .. 20,391	18,778 bp	CDS
▶ 9 segments = 1744 bp			
/codon_start = 1			
/note = coding sequence <a href="#">ENSP00000489992</a>			
/translation =	<pre> SPFARASIKSAKLENSTFFHKERRRMRFYIRRMVKTQAFYWTVLSLVALNTLCVAIVHYNQPEWLSDFL,,YYAEFIFLGLFMSEMFIKMYGLGTRP YFHSSFNCFDCG,,VIIGSIFEVIWAVIKPGTSFGISVLRALRLLRIFKVTK,,YWASLRNLVVSLLNSMKSIISLLFLLFLFIVV FALLGMQLFGGQ,,FN FDEGTPPTNFDTFPAAIMTVFQ,,ILTGEDWNEVMYDGIKSQGGVQGGMVFSIYFIVLTLFGN,,YTLLNVFLAIAVDNLANAQELTK,,DEQEEEEEA ANQKLA LQ KAKEVA EV SPLSAA NMSIAV,,KEQ QKNQ KPAKSV WEQRTSEMRKQ NLLA SREALYNEMDPDERWKAAYTRHLRPDMKTHLDRPL VVDPQENRNNNTNKSRAAEPTVDQRLGQ QRAEDFLRKQARYHDRA RDP SGSA GLDARRP WAGSQ EA ELSREGPYGRESDDHHA REGSLEQPG FWEGEA ERGKA GDPHRRHVHRQ GGSRESRSGSPRTGADGEHRRHRA HRRP GEEGPEDKAERRARHREGSRPARGGEGEGEGEPDGGERRRRHR HGAATYEGDARRBEOKRRRR </pre>		
<b>CACNA1A-226</b>	1614 .. 20,391	18,778 bp	CDS
▶ 9 segments = 1744 bp			
/codon_start = 1			
/note = coding sequence <a href="#">ENSP00000490578</a>			
/translation =	<pre> SPFARASIKSAKLENSTFFHKERRRMRFYIRRMVKTQAFYWTVLSLVALNTLCVAIVHYNQPEWLSDFL,,YYAEFIFLGLFMSEMFIKMYGLGTRP YFHSSFNCFDCG,,VIIGSIFEVIWAVIKPGTSFGISVLRALRLLRIFKVTK,,YWASLRNLVVSLLNSMKSIISLLFLLFLFIVV FALLGMQLFGGQ,,FN FDEGTPPTNFDTFPAAIMTVFQ,,ILTGEDWNEVMYDGIKSQGGVQGGMVFSIYFIVLTLFGN,,YTLLNVFLAIAVDNLANAQELTK,,DEQEEEEEA ANQKLA LQ KAKEVA EV SPLSAA NMSIAV,,KEQ QKNQ KPAKSV WEQRTSEMRKQ NLLA SREALYNEMDPDERWKAAYTRHLRPDMKTHLDRPL VVDPQENRNNNTNKSRAAEPTVDQRLGQ QRAEDFLRKQARYHDRA RDP SGSA GLDARRP WAGSQ EA ELSREGPYGRESDDHHA REGSLEQPG FWEGEA ERGKA GDPHRRHVHRQ GGSRESRSGSPRTGADGEHRRHRA HRRP GEEGPEDKAERRARHREGSRPARGGEGEGEGEPDGGERRRRHR HGAATYEGDARRBEOKRRRR </pre>		

Feature Location Size Type

**CACNA1A-237** 1614 .. 20,391 18,778 bp CDS  
9 segments = 1744 bp  
/codon\_start = 1  
/note = coding sequence [ENSP00000489777](#)  
/translation = SPFARASIKSAKLENSTFFHKERRMRFYIRRMVKTQAFYWTVLSLVALNTLCVAIVHYNQPEWLSDFL,,YYAEFIFLGLFMSEMFIKMYGLGTRP  
YFHSSFNCFDCG,,VIIGSIFEVIWAVIKPGTSFGISVLRALRLLRIFKVTK,,YWASLRNLVVSLLNSMKSIISLLFLLFLFIVV FALLGMQLFGGQ,,FN  
FDEGTPPTNFDTFPAAIMTVFQ,,ILTGEDWNEVMYDGIKSQGGVQGGMVFSIYFIVLTLFGN,,YTLLNVFLAIAVDNLANAQELTK,,DEQEEEEEA  
ANQKLA LQ KAKEVA EV SPLSAA NMSIAV,,KEQ QKNQ KPAKSV WEQRTSEMRKQ NLLA SREALYNEMDPDERWKAAYTRHLRPMKTHLDRPL  
VVDPQENRNNNTNKSRAAEPTVDQRLGQ QRAEDFLRKQARYHDRA RDP SGSA GLDARRP WAGSQ EA ELSREGPYGRESDDHHA REGSLEQPG  
FWEGEA ERGKA GDPHRRHVHRQ GGSRESRSGSPRTGADGEHRRHRAHRRP GEEGPEDKAERRARHREGSRPARGGEGEGEGPDGGERRRRHR  
HGATATYEGDARRBEQKRRHRR

**CACNA1A-239** 1614 .. 20,391 18,778 bp CDS  
9 segments = 1753 bp  
/codon\_start = 1  
/note = coding sequence [ENSP00000490617](#)  
/translation = SPFARASIKSAKLENSTFFHKERRMRFYIRRMVKTQAFYWTVLSLVALNTLCVAIVHYNQPEWLSDFL,,YYAEFIFLGLFMSEMFIKMYGLGTRP  
YFHSSFNCFDCG,,VIIGSIFEVIWAVIKPGTSFGISVLRALRLLRIFKVTK,,YWASLRNLVVSLLNSMKSIISLLFLLFLFIVV FALLGMQLFGGQ,,FN  
FDEGTPPTNFDTFPAAIMTVFQ,,ILTGEDWNEVMYDGIKSQGGVQGGMVFSIYFIVLTLFGN,,YTLLNVFLAIAVDNLANAQELTKVEA,,DEQEE  
EEAANQKLA LQ KAKEVA EV SPLSAA NMSIAV,,KEQ QKNQ KPAKSV WEQRTSEMRKQ NLLA SREALYNEMDPDERWKAAYTRHLRPMKTHLDRPL  
RPLVVDPQENRNNNTNKSRAAEPTVDQRLGQ QRAEDFLRKQARYHDRA RDP SGSA GLDARRP WAGSQ EA ELSREGPYGRESDDHHA REGSLE  
QPGFWEGEA ERGKA GDPHRRHVHRQ GGSRESRSGSPRTGADGEHRRHRAHRRP GEEGPEDKAERRARHREGSRPARGGEGEGEGPDGGERR  
RHRHGATATYEGDARRBEQKRRHRR

**CACNA1A-245** 1614 .. 20,391 18,778 bp CDS  
9 segments = 1744 bp  
/codon\_start = 1  
/note = coding sequence [ENSP00000489861](#)  
/translation = SPFARASIKSAKLENSTFFHKERRMRFYIRRMVKTQAFYWTVLSLVALNTLCVAIVHYNQPEWLSDFL,,YYAEFIFLGLFMSEMFIKMYGLGTRP  
YFHSSFNCFDCG,,VIIGSIFEVIWAVIKPGTSFGISVLRALRLLRIFKVTK,,YWASLRNLVVSLLNSMKSIISLLFLLFLFIVV FALLGMQLFGGQ,,FN  
FDEGTPPTNFDTFPAAIMTVFQ,,ILTGEDWNEVMYDGIKSQGGVQGGMVFSIYFIVLTLFGN,,YTLLNVFLAIAVDNLANAQELTK,,DEQEEEEEA  
ANQKLA LQ KAKEVA EV SPLSAA NMSIAV,,KEQ QKNQ KPAKSV WEQRTSEMRKQ NLLA SREALYNEMDPDERWKAAYTRHLRPMKTHLDRPL  
VVDPQENRNNNTNKSRAAEPTVDQRLGQ QRAEDFLRKQARYHDRA RDP SGSA GLDARRP WAGSQ EA ELSREGPYGRESDDHHA REGSLEQPG  
FWEGEA ERGKA GDPHRRHVHRQ GGSRESRSGSPRTGADGEHRRHRAHRRP GEEGPEDKAERRARHREGSRPARGGEGEGEGPDGGERRRRHR  
HGATATYEGDARRBEQKRRHRR

**CACNA1A-246** 1614 .. 20,391 18,778 bp CDS  
9 segments = 1744 bp  
/codon\_start = 1  
/note = coding sequence [ENSP00000489778](#)  
/translation = SPFARASIKSAKLENSTFFHKERRMRFYIRRMVKTQAFYWTVLSLVALNTLCVAIVHYNQPEWLSDFL,,YYAEFIFLGLFMSEMFIKMYGLGTRP  
YFHSSFNCFDCG,,VIIGSIFEVIWAVIKPGTSFGISVLRALRLLRIFKVTK,,YWASLRNLVVSLLNSMKSIISLLFLLFLFIVV FALLGMQLFGGQ,,FN  
FDEGTPPTNFDTFPAAIMTVFQ,,ILTGEDWNEVMYDGIKSQGGVQGGMVFSIYFIVLTLFGN,,YTLLNVFLAIAVDNLANAQELTK,,DEQEEEEEA  
ANQKLA LQ KAKEVA EV SPLSAA NMSIAV,,KEQ QKNQ KPAKSV WEQRTSEMRKQ NLLA SREALYNEMDPDERWKAAYTRHLRPMKTHLDRPL  
VVDPQENRNNNTNKSRAAEPTVDQRLGQ QRAEDFLRKQARYHDRA RDP SGSA GLDARRP WAGSQ EA ELSREGPYGRESDDHHA REGSLEQPG  
FWEGEA ERGKA GDPHRRHVHRQ GGSRESRSGSPRTGADGEHRRHRAHRRP GEEGPEDKAERRARHREGSRPARGGEGEGEGPDGGERRRRHR  
HGATATYEGDARRBEQKRRHRR

**CACNA1A-252** 1614 .. 20,391 18,778 bp CDS  
9 segments = 1744 bp  
/codon\_start = 1  
/note = coding sequence [ENSP00000489715](#)  
/translation = SPFARASIKSAKLENSTFFHKERRMRFYIRRMVKTQAFYWTVLSLVALNTLCVAIVHYNQPEWLSDFL,,YYAEFIFLGLFMSEMFIKMYGLGTRP  
YFHSSFNCFDCG,,VIIGSIFEVIWAVIKPGTSFGISVLRALRLLRIFKVTK,,YWASLRNLVVSLLNSMKSIISLLFLLFLFIVV FALLGMQLFGGQ,,FN  
FDEGTPPTNFDTFPAAIMTVFQ,,ILTGEDWNEVMYDGIKSQGGVQGGMVFSIYFIVLTLFGN,,YTLLNVFLAIAVDNLANAQELTK,,DEQEEEEEA  
ANQKLA LQ KAKEVA EV SPLSAA NMSIAV,,KEQ QKNQ KPAKSV WEQRTSEMRKQ NLLA SREALYNEMDPDERWKAAYTRHLRPMKTHLDRPL  
VVDPQENRNNNTNKSRAAEPTVDQRLGQ QRAEDFLRKQARYHDRA RDP SGSA GLDARRP WAGSQ EA ELSREGPYGRESDDHHA REGSLEQPG  
FWEGEA ERGKA GDPHRRHVHRQ GGSRESRSGSPRTGADGEHRRHRAHRRP GEEGPEDKAERRARHREGSRPARGGEGEGEGPDGGERRRRHR  
HGATATYEGDARRBEQKRRHRR

**CACNA1A-256** 1614 .. 20,391 18,778 bp CDS  
9 segments = 1744 bp  
/codon\_start = 1  
/note = coding sequence [ENSP00000489913](#)  
/translation = SPFARASIKSAKLENSTFFHKERRMRFYIRRMVKTQAFYWTVLSLVALNTLCVAIVHYNQPEWLSDFL,,YYAEFIFLGLFMSEMFIKMYGLGTRP  
YFHSSFNCFDCG,,VIIGSIFEVIWAVIKPGTSFGISVLRALRLLRIFKVTK,,YWASLRNLVVSLLNSMKSIISLLFLLFLFIVV FALLGMQLFGGQ,,FN  
FDEGTPPTNFDTFPAAIMTVFQ,,ILTGEDWNEVMYDGIKSQGGVQGGMVFSIYFIVLTLFGN,,YTLLNVFLAIAVDNLANAQELTK,,DEQEEEEEA  
ANQKLA LQ KAKEVA EV SPLSAA NMSIAV,,KEQ QKNQ KPAKSV WEQRTSEMRKQ NLLA SREALYNEMDPDERWKAAYTRHLRPMKTHLDRPL  
VVDPQENRNNNTNKSRAAEPTVDQRLGQ QRAEDFLRKQARYHDRA RDP SGSA GLDARRP WAGSQ EA ELSREGPYGRESDDHHA REGSLEQPG  
FWEGEA ERGKA GDPHRRHVHRQ GGSRESRSGSPRTGADGEHRRHRAHRRP GEEGPEDKAERRARHREGSRPARGGEGEGEGPDGGERRRRHR  
HGATATYEGDARRBEQKRRHRR

Feature	Location	Size	Color	Symbol	Type
<b>CACNA1A-257</b>	1614 .. 20,391	18,778 bp	■	→	CDS
▶ 9 segments = 1753 bp					
/codon_start	= 1				
/note	= coding sequence <a href="#">ENSP00000489829</a>				
/translation	= SPFARASIKSAKLENSTFFHKERRMRFYIRRMVKTQAFYWTVLSLVALNTLCVAIVHYNQPEWLSDFL,,YYAEFIFLGLFMSEMFIKMYGLGTRP YFHSSFNCFDCG,,VIIGSIFEVIWAVIKPGTSFGISVLRALRLLRIFKVTK,,YWASLRNLVVSLNLSMKSIIISLLFLLFLFIVV FALLGMQLFGGQ,,FN FDEGTPPTNFDTFPAAIMTVFQ,,ILTGEDWNEVMYDGIKSQGGVQGGMVFSIYFIVLTLFGN,,YTLLNVFLAIAVDNLANAQELTKVEA,,DEQEE EEAANQKALQKAKEVAEVSPLSAANMSIAV,,KEQQKNQKPAKSVWEQRTSEMRQNLLASREALYNEMDPDERWKAAYTRHLRPMKTHLD RPLVVDPQENRNNNTNKSRAAEPTVDQRLGQQRAEDFLRKQARYHDRARDPSGSAGLDARRPWAGSQEAELSREGPYGRESDDHAREGSLE QPGFWEGEAERGA GPDHRRHVHRQGGRESRSRSGSPRTGADGEHRRHRAHRRPGEEGPEDKAERRARHREGSRPARGGEGEGEGPDDGGERR RHHHHPATYEGDARRRDRR				
<b>CACNA1A-259</b>	1614 .. 20,391	18,778 bp	■	→	CDS
▶ 9 segments = 1744 bp					
/codon_start	= 1				
/note	= coding sequence <a href="#">ENSP00000499449</a>				
/translation	= SPFARASIKSAKLENSTFFHKERRMRFYIRRMVKTQAFYWTVLSLVALNTLCVAIVHYNQPEWLSDFL,,YYAEFIFLGLFMSEMFIKMYGLGTRP YFHSSFNCFDCG,,VIIGSIFEVIWAVIKPGTSFGISVLRALRLLRIFKVTK,,YWASLRNLVVSLNLSMKSIIISLLFLLFLFIVV FALLGMQLFGGQ,,FN FDEGTPPTNFDTFPAAIMTVFQ,,ILTGEDWNEVMYDGIKSQGGVQGGMVFSIYFIVLTLFGN,,YTLLNVFLAIAVDNLANAQELTK,,DEQEEEA ANQKALQKAKEVAEVSPLSAANMSIAV,,KEQQKNQKPAKSVWEQRTSEMRQNLLASREALYNEMDPDERWKAAYTRHLRPMKTHLDRPL VVDPQENRNNNTNKSRAAEPTVDQRLGQQRAEDFLRKQARYHDRARDPSGSAGLDARRPWAGSQEAELSREGPYGRESDDHAREGSLEQPG FWEGEAERGA GPDHRRHVHRQGGRESRSRSGSPRTGADGEHRRHRAHRRPGEEGPEDKAERRARHREGSRPARGGEGEGEGPDDGGERRRRR HCAATYEGDARRRDRR				
<b>CACNA1A-243</b>	1808 .. 3697	1890 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000637625</a> Retained intron				
<b>CACNA1A-235</b>	10,104 .. 11,656	1553 bp	■	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000637117</a> Retained intron				
✓ <b>Donor Template WT -&gt; SNV</b>	10,453 .. 10,552	100 bp	■	⇌	misc_feature
✓ <b>Protospacer Sequence</b>	10,471 .. 10,490	20 bp	■	⇌	misc_feature
✓ <b>SNV</b>	10,483 .. 10,483	1 bp	■	⇌	misc_feature
/note	= WT = G SNV = A				
✓ <b>PAM</b>	10,491 .. 10,492	2 bp	■	⇌	misc_feature



Primer	Length	Binding Sites	Tm	Date Added
✓ <b>PCR Forward</b> /sequence = GAATGGATGAATGAGGGGGTCAAGG 52% GC / 7900.2 Da	25-mer	10,252 .. 10,276	62°C	Jan 18, 2023
✓ <b>Sanger Sequencing</b> /sequence = AATGCTTGCCAGTTCTGGAG 50% GC / 6148.1 Da	20-mer	10,343 .. 10,362	58°C	Jan 18, 2023
✓ <b>Donor Template WT -&gt; SNV</b> /sequence = CTGTACAAATGTCCAGGAACCCCAAAGACTTACTTTGTGACTTTGAAAATACGCAATAACCTGAGGGCTTGTAACACGCTGATTCCAAA 66% GC / 10,426.1 Da	100-mer	10,453 .. 10,552	74°C	Jan 18, 2023
✓ <b>gRNA Protospacer</b> /sequence = TCAGCGTGTTACGAGCCCTC 60% GC / 6069.0 Da	20-mer	10,471 .. 10,490	61°C	Jan 18, 2023
✓ <b>PCR Reverse</b> /sequence = GGTGGAGGCTGTACCTGAAACACCG 60% GC / 7732.1 Da	25-mer	11,143 .. 11,167	64°C	Jan 18, 2023