

INK2J00034_CACNA1A_R583Q_B02_AB
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5'

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85

CACNA1A

CACNA1A-201

520 Y A E F I F L G L F 525

ENSE00001247106

CACNA1A-201

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170

CACNA1A

CACNA1A-201

530 M S E M F I K M Y G L G T R P Y F H S S F N C F D C G 555

ENSE00001247106

CACNA1A-201

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255

CACNA1A

CACNA1A-201

CACNA1A-201

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340

CACNA1A

CACNA1A-201

CACNA1A-201

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425

CACNA1A

CACNA1A-201

CACNA1A-201

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510

CACNA1A

CACNA1A-201

CACNA1A-201

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595

CACNA1A

CACNA1A-201

CACNA1A-201

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680

CACNA1A

CACNA1A-201

CACNA1A-201

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765

CACNA1A

CACNA1A-201

CACNA1A-201

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850

CACNA1A

CACNA1A-201

CACNA1A-201

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935

CACNA1A

CACNA1A-201

CACNA1A-201

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1020

CACNA1A

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1105

CACNA1A

CACNA1A-201

CACNA1A-201

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1190

CACNA1A

CACNA1A-201

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1275

CACNA1A

CACNA1A-201

CACNA1A-201

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1360

CACNA1A

CACNA1A-201

CACNA1A-201

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1445

CACNA1A

CACNA1A-201

CACNA1A-201

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1530

CACNA1A

CACNA1A-201

CACNA1A-201

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1615

CACNA1A

CACNA1A-201

CACNA1A-201

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1700

CACNA1A

CACNA1A-201

CACNA1A-201

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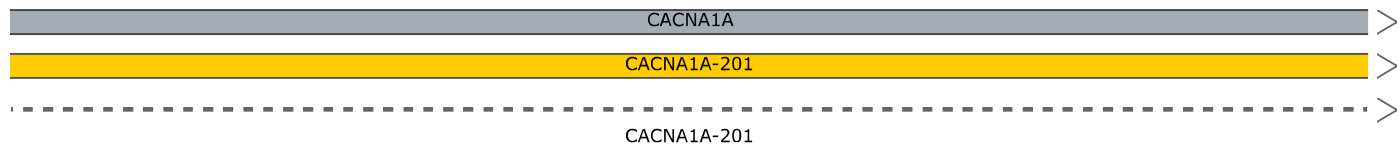
1785

CACNA1A

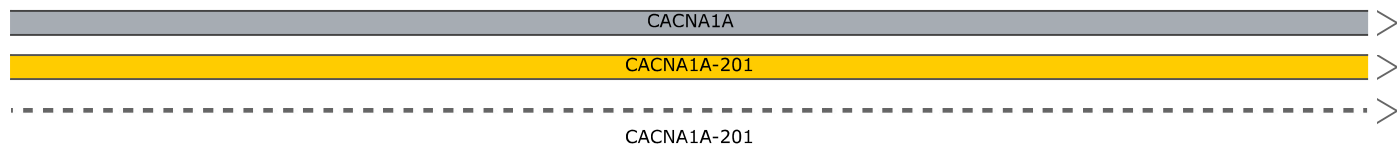
CACNA1A-201

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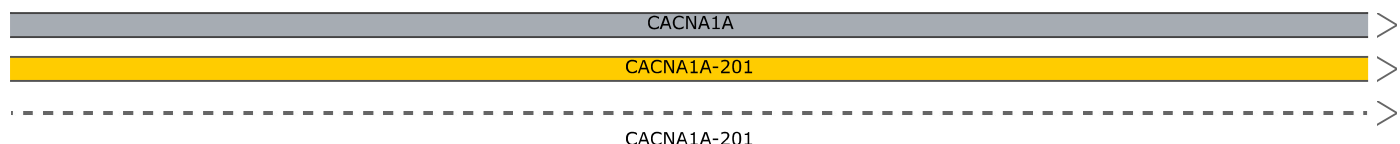
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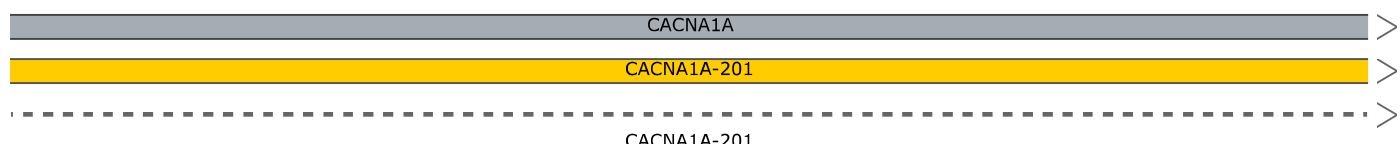
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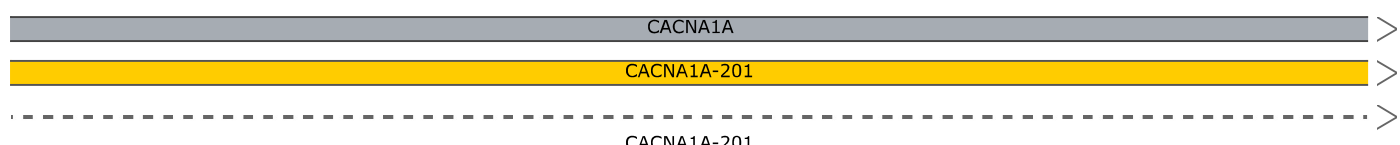
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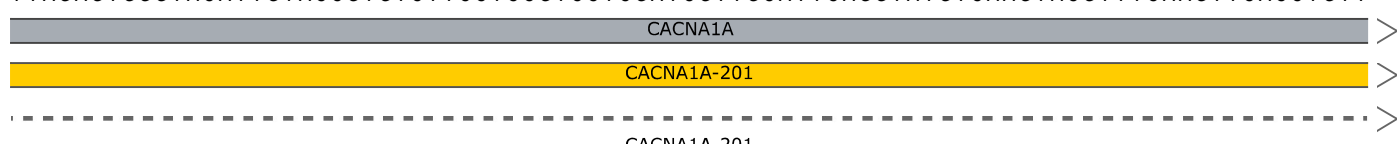
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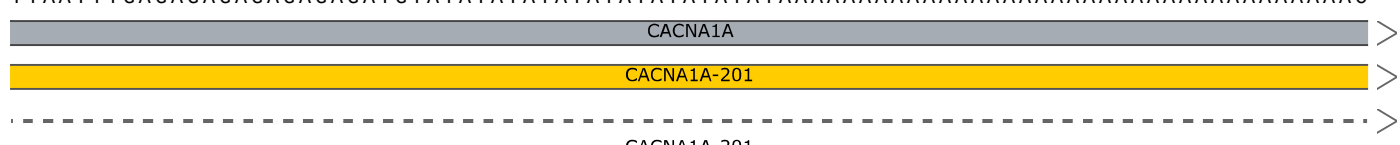
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2465

CACNA1A

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2550

CACNA1A

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2635

CACNA1A

CACNA1A-201

CACNA1A-201

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2720

CACNA1A

CACNA1A-201

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2805

CACNA1A

CACNA1A-201

CACNA1A-201

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2890

CACNA1A

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2975

CACNA1A

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3060

CACNA1A

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3145

CACNA1A

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3230

CACNA1A

CACNA1A-201

CACNA1A-201

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3315

CACNA1A

CACNA1A-201

CACNA1A-201

GTTTCCTGTGTTACCCAGGCTGGTCTTGAACCTCCTGGGCTCAAGTGATCTGCCACCTCGGCCTCCCAAAGTTCCAGAATTACA
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3400

CACNA1A

CACNA1A-201

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3485

CACNA1A

CACNA1A-201

CACNA1A-201

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CTTAAGAGTCCGGACACCCTCGAGAATTATTTATTTTCTCCGGTCCACACCACCGAGTGC GGACATTAGGGTCGTGAAACCT

3570

CACNA1A

CACNA1A-201

CACNA1A-201

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3655

CACNA1A

CACNA1A-201

CACNA1A-201

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3740

CACNA1A

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3825

CACNA1A

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3910

CACNA1A

CACNA1A-201

CACNA1A-201

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3995

CACNA1A

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4080

CACNA1A

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PCR Forward

GAATGGATGAATGAG

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4165

CACNA1A

CACNA1A-201

CACNA1A-201

PCR Forward

GGGGTCAAGG

Sanger Sequencing

AATGCTTGC

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CCCCAGTTTCTAGGAGTGGGCCGAAGGTAACCTCCCTCCTCAAACCAACTCAAGAACGTTCCAACCATGGATCCTTTACGAACG

4250

CACNA1A

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Sanger Sequencing

CAGTTCTGGAG

CAGTTCTGGAGCCCAGACACTGTCCCTGGACATGAGACCAGGTTCTCTGCCCTAGGTTATCATTGGGAGCATCTTCGAGGTCATC
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4335

CACNA1A

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V I I G S I F E V I
ENSE00001247101

gRNA Protospacer

TCAGCGTGTACGAGCCCTC

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4420

CACNA1A

CACNA1A-201

CACNA1A-201

ENSE00001247101

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

Donor Template WT -> SNV

Protospacer Sequence

PAM

SNV

GACCGTGTAGGAAACCTTAGTTCGCACAATGTCGGGAGTCCAATAACGCATAAAAAGTTTTCAGTGTTTCA

Donor Template WT -> SNV

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4505

CACNA1A

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CACNA1A-201

Donor Template WT -> SNV

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Donor Template WT -> SNV

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4590

CACNA1A

CACNA1A-201

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595
Y W

ENSE0000...

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4675

CACNA1A

CACNA1A-201

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

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CACNA1A-201

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4760

CACNA1A

CACNA1A-201

V F A L L G M Q L F G G Q

ENSE00001697204

CACNA1A-201

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4845

CACNA1A

CACNA1A-201

CACNA1A-201

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4930

CACNA1A

CACNA1A-201

CACNA1A-201

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5015

CACNA1A

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F N F D E G T P P T N F

ENSE00001247082

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5100

CACNA1A

CACNA1A-201

D T F P A A I M T V F Q

ENSE00001247082

CACNA1A-201

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PCR Reverse

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5185

CACNA1A

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CACNA1A-201

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5270

CACNA1A

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CACNA1A-201

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5355

CACNA1A

CACNA1A-201

CACNA1A-201

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5440

CACNA1A

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5525

CACNA1A

CACNA1A-201

CACNA1A-201

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5610

CACNA1A

CACNA1A-201

CACNA1A-201

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5695

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CACNA1A-201

CACNA1A-201

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5780

CACNA1A

CACNA1A-201

CACNA1A-201

GAGGTTGAGGCTGCAGTAAGCTACAATCACACCACTATACTCCAGCCTGGGCGAGAGAGCAAAGCCCTGTCTCAAAAACGAAAAG
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5865

CACNA1A

CACNA1A-201

CACNA1A-201

AAAGTTTGTATACTCACAGATCCTCAGAGAAGGAGCACACCATGCGAGGACCAAGCAGAGAAGCAACAGGGTCAAGCAGGAAGAG
TTTCAAACAATATGAGTGTCTAGGAGTCTCTTCTCGTGTGGTACGTCTCGTTTCGTCTCTTCGTTGTCCCAGTTCGTCTCTCTC

5950

CACNA1A

CACNA1A-201

CACNA1A-201

AAGGAAAATGTGGGCAAGAGGCTTGATTGTGGTTTTCCATGGGACGGAATGGGTGAGGCAGAGTAAACAGCTCGAGACTGGCTAGT
TTCCTTTTACACCCGTTCTCCGAACAAACACCAAAGGTACCCTGCCTTACCCACTCCGTCTCATTTGTGCGAGCTCTGACCGATCA

6035

CACNA1A

CACNA1A-201

CACNA1A-201

TTGGATCATTTCACTGAGTGGGCTCTGGGGCAGAGGAGCTGTTCTACTTGTCTAGGACCTGGCCTTGGGGTGATTAGGGCAGGTGGAT
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6120

CACNA1A

CACNA1A-201

CACNA1A-201

AGTGCTGGGAAGATAAAGGAGGTGGTTGGGATATGGGCTGGTTGGGATATTGTTTGGTTTGGCTTTTAAAAAGCCTGCTCAGGGCT
TCACGACCCTTCTATTTCTCCACCAACCCTATACCCGACCAACCCTATAACAAACCAAACGAAAATTTTTCGGACGAGTCCCGA

6205

CACNA1A

CACNA1A-201

CACNA1A-201

AAATTGTTTACTACCTCTAGGGACTGGCTAGTGCTGGACCGGGCAGTCCCTCCAGAGTCAGCAAGACCCCAAGATGCATCAGAATA
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6290

CACNA1A

CACNA1A-201

CACNA1A-201

AAGAAAATAAAATGCGTGGCCAGGCCAATGAGGTGGTTCATGCCTGTAATCTCAGCACTTTGGGAGACCAAGGCCGGGAGGATTGC
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6375

CACNA1A

CACNA1A-201

CACNA1A-201

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6460

CACNA1A

CACNA1A-201

CACNA1A-201

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6545

CACNA1A

CACNA1A-201

CACNA1A-201

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6630

CACNA1A

CACNA1A-201

CACNA1A-201

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6715

CACNA1A

CACNA1A-201

CACNA1A-201

GAAACCTTCCATGAAGGGAAGTTCTGAGCCCCACATAAGCGATTTTTTTTTTTTTTTTGGAGATGGAGTCTCGCTCTGTTGCCCA
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6800

CACNA1A

CACNA1A-201

CACNA1A-201

GGCTGGAGTGCGACGGCACGTTCTTGGCTCACTACAACCTCTGCCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCCGAGT
CCGACCTCACGCTGCCGTGCAAGAACCGAGTGATGTTGGAGACGGAGGACCCAAGTTCGCTAAGAGGACGGAGTCGGAGGGCTCA

6885

CACNA1A

CACNA1A-201

CACNA1A-201

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TCGACTCTGATGTCCACGTATGATGGTACGGACCGATTAAAAACATAAAAAATCATCTCTGTCCCAAAGTGATACAACCGGTCCGA

6970

CACNA1A

CACNA1A-201

CACNA1A-201

GGTCTCGAACTCCTGGCCTCGTGATCTGCCTGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCACACCTGGCCC
CCAGAGCTTGAGGACCGGAGCACTAGACGGACGGAGCCGGAGGGTTTTACGACCCTAATGTCCGTAICTCGGTGGTGTGGACCGGG

7055

CACNA1A

CACNA1A-201

CACNA1A-201

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7140

CACNA1A

CACNA1A-201

CACNA1A-201

ACATGTAGCAATGTCTGCAAGCATTGTTGGTTGTCACAGCTAGGGAGAGGGTGCTACTGGCATCTGGTGGGTGGAGACTAGGAAT
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7225

CACNA1A

CACNA1A-201

CACNA1A-201

GCTGCTCAATATCCTACAATGCACAGGACAGCCCCAAATAGAATAATCTGGCCCCAAATATCAGCAGTGCTGAGGCTTAGAAACC
CGACGAGTTATAGGATGTTACGTGTCTCTGTCGGGGTTTATCTTATTAGACCGGGGTTTATAGTCGTCACGACTCCGAATCTTTGG

7310

CACNA1A

CACNA1A-201

CACNA1A-201

CTGTTTTAGCAGATTCATGTTTTTGGAGTTCTTTAACATTTACTTTATCCTCATGGGGATATGGATAGAAGGAAGGAAGTTGGAT
GACAAAATCGTCTAAGTACAAAAACCTCAAGAAATTGTAAATGAAATAGGAGTACCCCTATACCTATCTTCCTTCCTTCAACCTA

7395

CACNA1A

CACNA1A-201

CACNA1A-201

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7480

CACNA1A

CACNA1A-201

CACNA1A-201

CTAATCCTTTGCCTTGGTCTTTCTCTGGTCCCCTGCTCTGCCCCCAAGGAACTGCAGTCCAGCAGTACTGTGAATTTTTTGTGCC
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7565

CACNA1A

CACNA1A-201

CACNA1A-201

ACACCTTAAAAGGAGCAGCCGTTGGTGGATAAATACCCCAGCTCCCTCACCCCTCAGGTGGGATGACCCCTAGAGCTCCCCAGCAA
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7650

CACNA1A

CACNA1A-201

CACNA1A-201

GACCAAGCCCCGGTTACCTACAGTGGAAACTCGCTTGATCACATACTGTTTACGTTCCACCCTCTTTTCCCTTTTCTCACTTCTC
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7735

CACNA1A

CACNA1A-201

CACNA1A-201

CTCTCCCCTACTGGTGCTTCCCTGAGATCACCTCCCAGACAAACCACTTGCACCCGAACCCTTGTTCCAGGGTCTGCCTCAGGCAG
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7820

CACNA1A

CACNA1A-201

CACNA1A-201

GGGGACCCCAAACGTGTCTTGTGCTACATTTGTGCTATCCACGTAGTAGCTTGTTTAAATCATCACCATGACCACATGAGGAAACA
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7905

CACNA1A

CACNA1A-201

CACNA1A-201

CAGGTAAATATTTAAATCCTGTCTTAGTCTGCTCAGGCAGCCATAACAAAATACCACACACTGGGTGGCTTATACAGGAAACATT
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7990

CACNA1A

CACNA1A-201

CACNA1A-201

TATTCTCTCATAGTTCTGGAGGCCGGGAAGTCCAAGATCAAAGTGTTAGCAGGGTTAGTTAGTTCCCTGGTGAGGGCCCTCTTCCT
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8075

CACNA1A

CACNA1A-201

CACNA1A-201

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8160

CACNA1A

CACNA1A-201

CACNA1A-201

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8245

CACNA1A

CACNA1A-201

CACNA1A-201

GTGCAGTGGCACAATCATAGCTCACTGCAGCCTCAAACCTCTAGGTTCAAACGATCCTCCCACCTCAGCCCCCTTGAGTAGCTGGG
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8330

CACNA1A

CACNA1A-201

CACNA1A-201

ACTACAGATGGGCACCAGCTAATTTTTTAAATTTTTGTAAAGATGGGGTCTTGCTATATTGCCCAGGCTAATCTTGAACCTCT
TGATGTCTACCCGTGGTCGATTAAAAAATTTAAAAAACATTTCTACCCAGAACGATATAACGGGTCCGATTAGAACCTTGAGGA

8415

CACNA1A

CACNA1A-201

CACNA1A-201

GGGCTCAAGTGATCCTCCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCATGGCATGCGGTCTCTTCTGTTCTT
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8500

CACNA1A

CACNA1A-201

CACNA1A-201

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8585

CACNA1A

CACNA1A-201

CACNA1A-201

CCCATCATAGGTTAGGGCTTCAACTCATGAATTTGGAGGCGGGCACAATTTAGTCCATAACAAATCCCCTTAATCACATCAAGTA
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8670

CACNA1A

CACNA1A-201

CACNA1A-201

AGACAGAGTTACAGGAGGGTCTGTGACTCCTCCAGGGTCCCATTTTCTAGAAAGCCAGGCTAAGAGCCCCACGACGCAGGAACGG
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8755

CACNA1A

CACNA1A-201

CACNA1A-201

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8840

CACNA1A

CACNA1A-201

CACNA1A-201

CCTCCTGGGCTCGGGGATGGGGTGGGCGGATTCCGGCTCCACAGCTGCATCTCCAAGGGGCCCGTGGCTGAGAGGGGGGTTGGCT
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8925

CACNA1A

CACNA1A-201

CACNA1A-201

GTGTGTTTCTTCTCCCTTTTCAGATCCTGACGGGCGAAGACTGGAACGAGGTCATGTACGACGGGATCAAGTCTCAGGGGGGCG
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9010

CACNA1A

CACNA1A-201

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

ENSE00000951011

CACNA1A-201

TGCAGGGCGGCATGGTGTCTCCATCTATTTTCACTGACTGACGCTCTTTGGGAACTGTATCCTTCATGGAGAGAGAGAAGGGGA
ACGTCCC GCGTACCACAAGAGGTAGATAAAGTAACATGACTGCGAGAAACCTTGACATAGGAAGTACCTCTCTCTCTTCCCCT

9095

CACNA1A

CACNA1A-201

V Q G G M V F S I Y F I V L T L F G N

ENSE00000951011

CACNA1A-201

CAGGCCTGGACCTCTGGCAGAGGAGAGGTTGCAGGGGCTCAAGGGAGGGTACTGAGAGACCCAGATACCCAGGGCCCAAGTGGTG
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9180

CACNA1A

CACNA1A-201

CACNA1A-201

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9265

CACNA1A

CACNA1A-201

Y T L L N V F L A I A V D N L

ENSE00001660630

CACNA1A-201

CCAACGCCAGGAGCTCACCAAGGTGGAGGCGGTGGGAGAATGTTTCTCTGGCAAAGTTACCACCTGCCCATGGCAGATCAGGAC
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9350

CACNA1A

CACNA1A-201

720
A N A Q E L T K
ENSE00001660630

CACNA1A-201

GGGGGTGGGGGTGGGGGTGGGGGTGGGGGTGGGGGCATGGGAACAGGGTTAGAACTTTTGGCGGGGATGCACCATGCAAAGAGAA
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9435

CACNA1A

CACNA1A-201

CACNA1A-201

GGCGCCTCTCCCCCACTCCCAGAAACAGACTGTCCCTCATCAAGCAAATTTCTACAGCCAAGAGGGTGGGAAGGGGGAAGGCAGT
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9520

CACNA1A

CACNA1A-201

CACNA1A-201

GAGGTCGCTGCAGGAAACGGATGGCAAACCTCAACCAAAAAGGCCGTTTACAGGGAGTAAGCAGGGTTTCCAAGGAATGGTGTAGCC
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9605

CACNA1A

CACNA1A-201

CACNA1A-201

CCCAGGCTAGTGGATGGGAGAGGGAGTGCTGTTATGGGGACCCAGTCAGAGCTGGGGCCAAGGAAAAAGGGCTGCCACCAGCCCT
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9690

CACNA1A

CACNA1A-201

CACNA1A-201

GGGACCTTAGAGAACCCAGAACCATGGCAAGGCACAGATGGAGTGGCCAATAAATGTCCCCACCTTCTCTCTTCTCTGGCTTCC
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9775

CACNA1A

CACNA1A-201

CACNA1A-201

CGCTGGAGCCTCCCTTAGCCAAACGCAGCATGTTAAGAGCTAGCCTCCGTCCAGCCTAAGCCTCTCCCAAGGACCCCTATTAAG
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9860

CACNA1A

CACNA1A-201

CACNA1A-201

TTAAGATTACATGTAACAGGTACAGGGTCTTCCTCTCAGCCCTGGGGTCTCCCTCAGCATTGCAGCCCCACCTCCAGTGCCTCGA
AATTCTAATGTACATTGTCCATGTCCCAGAAGGAGAGTCGGGACCCAGAGGGAGTCGTAACGTCGGGGTGGAGGTCACGGAGCT

9945

CACNA1A

CACNA1A-201

CACNA1A-201

GGTATTCAGGACATGTTTGTGAAATTGAACCAAACCAAGCAGACGTTGCCAACGCTCCATCTGCCGGCCCTGGCAGGAGGGAGAG
CCATAAGTCCTGTACAAACACTTTAACTTGGTTTGGTTTCGTCTGCAACGGTTGCGAGGTAGACGGCCGGGACCGTCTCTCCCTCTC

10,030

CACNA1A

CACNA1A-201

CACNA1A-201

AGAGTTTCCCGGCCCCAGCTCCCAGTGGAGGGAAGCGGAAGTCTCTGCCATCCCAAGCACACGGCCACAAGCCTGGCCACTGTGG
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10,115

CACNA1A

CACNA1A-201

CACNA1A-201

AGCTGGCTGGCATGGCTGAGCCGAGGGCTGATCCAGCCATGAGCTCATCCAAGTTCCAAGAGTCCATCCTTAGGGGCTGGTGCAG
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10,200

CACNA1A

CACNA1A-201

CACNA1A-201

GAGGGTAGCAGAAGGGGAGGGAGAAAGGCCAGTTCGTTTATCTCTGGGAGGTGTGGACATTCTCTCCAGATCCACATTCTTTC
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10,285

CACNA1A

CACNA1A-201

CACNA1A-201

TTTCATTGATCCTACAAGCATTCTTGGTCATTTAATACGTGTTTTTAATCCTATTTCAGTCCTCATGGAACCTTAGGAGCCAAG
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10,370

CACNA1A

CACNA1A-201

CACNA1A-201

TTCTCTGAGCCCCATTTTACAGATTTTCATCATTTCAGTAAGCACTTAATGAGCACCTACTGTGTGACCAAGGCCCTGGTCTAGGAC
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10,455

CACNA1A

CACNA1A-201

CACNA1A-201

TTAGGGATTAAGCAGTGAACAAAAAAGGCCAAAAATCCCTGCCTCCGTGGAGCAGGGATTCAAGAGGGGAGACAGACAAGAAACA
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10,540

CACNA1A

CACNA1A-201

CACNA1A-201

AGATAAATTTGTAAACATACGTAGCTTGTTCAGTTGGTGATAAACACAACAGAGAAAAATTCAGTAGGGAAAGTCAGGGAGAGTTG
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10,625

CACNA1A

CACNA1A-201

CACNA1A-201

GAATTTTAGATGAGATGTGTGTCGCACAGAGAGGTTGAGAGACTTGCCCAAGGCCACACAGCAGTAAGTTGTGGAGCTGGGATTT
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10,710

CACNA1A

CACNA1A-201

CACNA1A-201

GAACCCAGGCCGTCTGGGTCTGCAGCTTGTGCTCTTAACTGCTGTGTACCAGTTGCTTGAATTTGGGCATGTTTTATGCTCACTT
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10,795

CACNA1A

CACNA1A-201

CACNA1A-201

GGGAACCTGTGGGAAATGCAGATTCAGGGCCAGCACTGGTTCTATAGATTATTTGGGGAGCCTGAGGATCTGCATTTTAGGTG
CCCTTGGACACCCTTTACGTCTAAGGTCCCGGGTTCGTGACCAAGATATCTAATAAACCCCTCGGACTCCTAGACGTAAAATCCAC

10,880

CACNA1A

CACNA1A-201

CACNA1A-201

TTTCTGAGGCAGATGGTCCAGAGACCTAGCTCTGAAAAATGCTGGGAATGGTGCCAGGAGGGGTGGGGGTGGCCCTATGAGAGCA
AAAGACTCCGTCTACCAGGTCTCTGGATCGAGACTTTTTACGACCCTTACCACGGTCCTCCCCACCCCAACGGGATACTCTCGT

10,965

CACNA1A

CACNA1A-201

CACNA1A-201

GGGTGGCCAGCCAGATCCCATCTCCATGTTGTCTCTGACAGTGTCTGATCTGACCATTTCCAAGGTGGTAAGGTTGCTCCCCGT
CCCACCGGTCGGTCTAGGGTAGAGGTACAACAGAGACTGTACAGGACTAGACTGGTAAAGGTTCCACCATTCCAACGAGGGGCA

11,050

CACNA1A

CACNA1A-201

CACNA1A-201

TCCAGTGATTCGGAGCACAGCGGGAGAGCTGCCTGCAATGGCATGACTTTTTCTTATGGGCGGGTTCATTTCTGGCCATTTCTTTTC
AGGTCACTAAGCCTCGTGTCGCCCTCTCGACGGACGTTACCGTACTGAAAAGAATACCCGCCCAAGTAAAGACCGGTAAAGAAAAG

11,135

CACNA1A

CACNA1A-201

CACNA1A-201

TCGTTGCCTTTTCTTTGCTTTTTCTTTGTTGGCTTTTCTGTTTTACGAATGAGGCCCTGCATGAAGGCTGAAGAAGGATTTAAAG
AGCAACGGAAAAAGAAACGAAAAAGAAAACAACCGAAAAGACAAAATGCTTACTCCGGGACGTACTTCCGACTTCTTCTAAATTTTC

11,220

CACNA1A

CACNA1A-201

CACNA1A-201

TCCAAAAACGTCTTTTTCTGTATGTTTTTAAAACCTCTTCCCCCATTCTCCTCCTCTCTGAACCTAACCCACAGTGAGCAGCA
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11,305

CACNA1A

CACNA1A-201

CACNA1A-201

GCACCCTGGGCAGTTGGCTGTAGCCCAAGTGCCTGCTCTCCTCTCCCCACCGCCTTCTGTCATGGGGGCTGGGAATATAAATT
CGTGGGACCCGTCAACCGACATCGGGTTCACGGGACGAGAGGAGAGGGGTGGCGGAAGGACAGTACCCCCGACCTTATATTTAA

11,390

CACNA1A

CACNA1A-201

CACNA1A-201

CCTCTCCTCATTCTCCTTCTGGGGGCTGTTGACAGTGCATGGCAGGGGCCATCGGATGCCAGGCTCTTCTGTGTGTGAGGGTAGT
GGAGAGGAGTAAGAGGAAGACCCCCGACAACCTGTCACGTACCGTCCCCGGTAGCCTACGGTCCGAGAAGACACACACTCCCATCA

11,475

CACNA1A

CACNA1A-201

CACNA1A-201

TGGTGTTTTTTGAAGTTGGTTCAGAGAGTTCACATGGCTCAGAAAGCCTAGTGAGAGGAAAATCTTTGCACTGCTTTCCAGCTC
ACCACAAAAAATTTCAACCAAGTCTCTCAAGTGTACCGAGTCTTTCCGGATCACTCTCCTTTTAGAAACGTGACGAAAAGGTCGAG

11,560

CACNA1A

CACNA1A-201

CACNA1A-201

ATTAAGACAGGATGCAGGGGCCAGGCATGGTGGCACATGCCTGGAATCCCAGCACTTTGGGAGGCCGAAATGGGAGGATCATTTG
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11,645

CACNA1A

CACNA1A-201

CACNA1A-201

AGGCCAGAAAGTTCAAGACCAGCCTGGGCAACATAGTGAGACCCTGTCTCTACAAAAAAAAAAAAAAAAAATTAATGTATACAGGCA
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11,730

CACNA1A

CACNA1A-201

CACNA1A-201

TAGTGGCATGCACCTGTAGTCCCAGTTGCTTGGGAGGCTGAGGTGGGAGGATTGCTTGAGCCCAGGAGTTCAAGGTTACAGTGAG
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11,815

CACNA1A

CACNA1A-201

CACNA1A-201

CTATGATTGTGCCACTGCACTCCAGGCTGGGCAACCAAGGGAGACTCTGTCTCTGAAAACAAACAAAAGAAAAAAAAATAGGCTG
GATACTAACACGGTGACGTGAGGTCCGACCCGTTGGTTCCCTCTGAGACAGAGACTTTTGTGTTGTTTTCTTTTTTTTTATCCGAC

11,900

CACNA1A

CACNA1A-201

CACNA1A-201

CAGGAAAGTCTTCATTGTAGGAAGAGAAGGGACATTTTTATTTTTGTTATCTGGCTGTGTGTTAAAAATAGGCTTCATAATGAGT
GTCCTTTCAGAAGTAACATCCTTCTCTTCCCTGTAAAAATAAAAAACAATAGACCGACACACAATTTTATCCGAAGTATTACTCA

11,985

CACNA1A

CACNA1A-201

CACNA1A-201

TAGATGTCAAACCTTATACACAGAGGGGATAGCAATACACTTAACCAATAGCAGGTACCCATTCCAATTGGGGAGCCTTGTTCTG
ATCTACAGTTTGAATATGTGTCTCCCTATCGTTATGTGAATTGGTTATCGTCCATGGGTAAGGTTAACCCCTCGGAACCAAGAC

12,070

CACNA1A

CACNA1A-201

CACNA1A-201

ATTGGTCGAAATATTTCAAATGTTGCCCTGGTCAGCAACAGGGTCAGAAGTGAGTCCCAAGGCCTAGTTCATGTTTTGTGAAC
TAACCAGCTTTATAAAGTTTACAACGGGGACCAGTCGTTGTCCAGTCTTCACTCAGGGGTTCCGGATCAAGTACAAAACACTTG

12,155

CACNA1A

CACNA1A-201

CACNA1A-201

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TTTCTAAGGTGCACGGAAAATCCTGCTCGTTCTCTTCTTCTCGTCGTTGGTCTTTGAACGGGATGTCTTTCGGTTCCCTCCAC

12,240

CACNA1A

CACNA1A-201

725 730 735 740 745
D E Q E E E E A A N Q K L A L Q K A K E V

ENSE00000951013

CACNA1A-201

GCAGAAGTGAGTCTCTGTCCGCGGCCAACATGTCTATAGCTGTGTAAGTGCCCTAATCCCTGGGATGCTACCCTGGCTCCTGA
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12,325

CACNA1A

CACNA1A-201

A E V S P L S A A N M S I A V
750 755 760

ENSE00000951013

CACNA1A-201

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12,410

CACNA1A

CACNA1A-201

CACNA1A-201

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12,495

CACNA1A

CACNA1A-201

CACNA1A-201

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12,580

CACNA1A

CACNA1A-201

CACNA1A-201

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12,665

CACNA1A

CACNA1A-201

CACNA1A-201

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12,750

CACNA1A

CACNA1A-201

CACNA1A-201

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12,835

CACNA1A

CACNA1A-201

CACNA1A-201

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12,920

CACNA1A

CACNA1A-201

CACNA1A-201

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13,005

CACNA1A

CACNA1A-201

CACNA1A-201

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13,090

CACNA1A

CACNA1A-201

CACNA1A-201

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GACCCCTTCCCGTAGGGTCCGTCTCCCTTGTCTGATCCGTTACCGGACTCCGTCTTGTACGGACTACACTTCTCCGGACACA

13,175

CACNA1A

CACNA1A-201

CACNA1A-201

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13,260

CACNA1A

CACNA1A-201

CACNA1A-201

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13,345

CACNA1A

CACNA1A-201

CACNA1A-201

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13,430

CACNA1A

CACNA1A-201

CACNA1A-201

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13,515

CACNA1A

CACNA1A-201

765 770
K E Q Q K N Q K P A K
ENSE00001247059

CACNA1A-201

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13,600

CACNA1A

CACNA1A-201

S V W 775 Q R T S 780 E M R K Q 785 N L L A S 790 R E A L Y 795 N E M D P 800 D

ENSE00001247059

CACNA1A-201

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13,685

CACNA1A

CACNA1A-201

E R W 805 K A A Y T R 810 H L R P 815 D M K T H L 820 D R P L V 825 V D P Q

ENSE00001247059

CACNA1A-201

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13,770

CACNA1A

CACNA1A-201

E N R 830 N N N T N 835 K S R A 840 A E P T V 845 D Q R L G 850 Q Q R A E 855 D

ENSE00001247059

CACNA1A-201

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13,855

CACNA1A

CACNA1A-201

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ENSE00001247059

CACNA1A-201

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13,940

CACNA1A

CACNA1A-201

S Q E 890 A E L S R E G 895 P Y G R E S 900 D H H A 905 R E G S 910 L E Q P

ENSE00001247059

CACNA1A-201

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14,025

CACNA1A

CACNA1A-201

915 920 925 930 935 940
G F W E G E A E R G K A E H R R H V H R Q G G S R E

ENSE00001247059

CACNA1A-201

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14,110

CACNA1A

CACNA1A-201

945 950 955 960 965 970
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ENSE00001247059

CACNA1A-201

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14,195

CACNA1A

CACNA1A-201

975 980 985 990 995
D K A E R R A R H R E G S R P A R G G E G E G E G P D G

ENSE00001247059

CACNA1A-201

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14,280

CACNA1A

CACNA1A-201

1000 1005 1010 1015 1020 1025
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ENSE00001247059

CACNA1A-201

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14,365

CACNA1A

CACNA1A-201

1030
R R R K
ENSE00001...
CACNA1A-201

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14,450

CACNA1A

CACNA1A-201

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14,535

CACNA1A

CACNA1A-201

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14,620

CACNA1A

CACNA1A-201

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14,705

CACNA1A

CACNA1A-201

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14,790

CACNA1A

CACNA1A-201

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14,875

CACNA1A

CACNA1A-201

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14,960

CACNA1A

CACNA1A-201

GCCTGGGCAACAGAGCAA
CGGACCCGTTGTCTCGTT

3'

14,978

5'

CACNA1A

CACNA1A-201

Feature	Location	Size	Icons	Type
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	Protein coding			
✓ CACNA1A-201	1 .. 14,978	14,978 bp	☐ →	prim_transcript
/note =	primary transcript ENST00000360228			
CACNA1A-202	1 .. 14,978	14,978 bp	☐ →	prim_transcript
/note =	primary transcript ENST00000573710			
CACNA1A-214	1 .. 14,978	14,978 bp	☐ →	prim_transcript
/note =	primary transcript ENST00000635727			
CACNA1A-217	1 .. 14,978	14,978 bp	☐ →	prim_transcript
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CACNA1A-220	1 .. 14,978	14,978 bp	☐ →	prim_transcript
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CACNA1A-224	1 .. 14,978	14,978 bp	☐ →	prim_transcript
/note =	primary transcript ENST00000636389			
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/note =	primary transcript ENST00000636549			
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CACNA1A-232	1 .. 5487	5487 bp	☐ →	prim_transcript
/note =	primary transcript ENST00000636974			
	Retained intron			
CACNA1A-221	1 .. 182	182 bp	☐ →	prim_transcript
/note =	primary transcript ENST00000636022			
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✓ CACNA1A-201	53 .. 14,290	14,238 bp	☐ →	CDS
► 8 segments =	1534 bp			
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/note =	coding sequence ENSP00000353362			
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Feature	Location	Size	Type
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▶ 8 segments = 1534 bp			
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CACNA1A-214	53 .. 14,290	14,238 bp	CDS
▶ 8 segments = 1534 bp			
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CACNA1A-217	53 .. 14,290	14,238 bp	CDS
▶ 8 segments = 1534 bp			
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CACNA1A-220	53 .. 14,290	14,238 bp	CDS
▶ 8 segments = 1534 bp			
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/note	= coding sequence ENSP00000490223		
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CACNA1A-224	53 .. 14,290	14,238 bp	CDS
▶ 8 segments = 1534 bp			
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CACNA1A-226	53 .. 14,290	14,238 bp	CDS
▶ 8 segments = 1534 bp			
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Feature	Location	Size	Type
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▶ 8 segments = 1534 bp			
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/note	= coding sequence ENSP00000489777		
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/codon_start	= 1		
/note	= coding sequence ENSP00000490617		
/translation	= YAEFIFLGLFMSEFIKMYGLGTRPYFHSSFNCFDCG,,VIIGSIFEVIWAVIKPGTSFGISVLRALRLLRIFKVTK,,YWASLRNLVVSLNSMKSIIISL LFLLLFIVV FALLGMQLFGGQ,,FNFDEGTPPTNFDTFPAAIMTVFQ,,ILTGEDWNEV MYDGIKSQGGVQGGMVFSIYFIVLTLFGN,,YTLLNVFL AIAVDNLANAQELTK,,DEQEEEEANQKLA LQKAKEVAEVSPLSAANMSIAV,,KEQQKNQKPAKSVWEQRTSEMRKQNLLASREALYNEMDP MDPDERWKAAYTRHLRPPDMKTHLDRPLVVDPQENRNNNTNKSRAAEPTVDQRLGQ QRAEDFLRKQARYHDRARDPSGSA GLDARRPWAGSQEAE EAELSRGPGYGRESDDHAREGSLEQPGFWEGEAERGKAGDPHRRHVHRQGGRESRSRSGSPRTGADGEHRRHRAHRRPGEEGPEDKAERRARHREG SRPARGGEGEGEGPDSGERRRRHRHGAPATYEGDARREDKERRHRRR		
CACNA1A-245	53 .. 14,290	14,238 bp	CDS
▶ 8 segments = 1534 bp			
/codon_start	= 1		
/note	= coding sequence ENSP00000489861		
/translation	= YAEFIFLGLFMSEFIKMYGLGTRPYFHSSFNCFDCG,,VIIGSIFEVIWAVIKPGTSFGISVLRALRLLRIFKVTK,,YWASLRNLVVSLNSMKSIIISL LFLLLFIVV FALLGMQLFGGQ,,FNFDEGTPPTNFDTFPAAIMTVFQ,,ILTGEDWNEV MYDGIKSQGGVQGGMVFSIYFIVLTLFGN,,YTLLNVFL AIAVDNLANAQELTK,,DEQEEEEANQKLA LQKAKEVAEVSPLSAANMSIAV,,KEQQKNQKPAKSVWEQRTSEMRKQNLLASREALYNEMDP DERWKAAYTRHLRPPDMKTHLDRPLVVDPQENRNNNTNKSRAAEPTVDQRLGQ QRAEDFLRKQARYHDRARDPSGSA GLDARRPWAGSQEAE LSREGPYGRESDDHAREGSLEQPGFWEGEAERGKAGDPHRRHVHRQGGRESRSRSGSPRTGADGEHRRHRAHRRPGEEGPEDKAERRARHREG SRPARGGEGEGEGPDSGERRRRHRHGAPATYEGDARREDKERRHRRR		
CACNA1A-246	53 .. 14,290	14,238 bp	CDS
▶ 8 segments = 1534 bp			
/codon_start	= 1		
/note	= coding sequence ENSP00000489778		
/translation	= YAEFIFLGLFMSEFIKMYGLGTRPYFHSSFNCFDCG,,VIIGSIFEVIWAVIKPGTSFGISVLRALRLLRIFKVTK,,YWASLRNLVVSLNSMKSIIISL LFLLLFIVV FALLGMQLFGGQ,,FNFDEGTPPTNFDTFPAAIMTVFQ,,ILTGEDWNEV MYDGIKSQGGVQGGMVFSIYFIVLTLFGN,,YTLLNVFL AIAVDNLANAQELTK,,DEQEEEEANQKLA LQKAKEVAEVSPLSAANMSIAV,,KEQQKNQKPAKSVWEQRTSEMRKQNLLASREALYNEMDP DERWKAAYTRHLRPPDMKTHLDRPLVVDPQENRNNNTNKSRAAEPTVDQRLGQ QRAEDFLRKQARYHDRARDPSGSA GLDARRPWAGSQEAE LSREGPYGRESDDHAREGSLEQPGFWEGEAERGKAGDPHRRHVHRQGGRESRSRSGSPRTGADGEHRRHRAHRRPGEEGPEDKAERRARHREG SRPARGGEGEGEGPDSGERRRRHRHGAPATYEGDARREDKERRHRRR		
CACNA1A-252	53 .. 14,290	14,238 bp	CDS
▶ 8 segments = 1534 bp			
/codon_start	= 1		
/note	= coding sequence ENSP00000489715		
/translation	= YAEFIFLGLFMSEFIKMYGLGTRPYFHSSFNCFDCG,,VIIGSIFEVIWAVIKPGTSFGISVLRALRLLRIFKVTK,,YWASLRNLVVSLNSMKSIIISL LFLLLFIVV FALLGMQLFGGQ,,FNFDEGTPPTNFDTFPAAIMTVFQ,,ILTGEDWNEV MYDGIKSQGGVQGGMVFSIYFIVLTLFGN,,YTLLNVFL AIAVDNLANAQELTK,,DEQEEEEANQKLA LQKAKEVAEVSPLSAANMSIAV,,KEQQKNQKPAKSVWEQRTSEMRKQNLLASREALYNEMDP DERWKAAYTRHLRPPDMKTHLDRPLVVDPQENRNNNTNKSRAAEPTVDQRLGQ QRAEDFLRKQARYHDRARDPSGSA GLDARRPWAGSQEAE LSREGPYGRESDDHAREGSLEQPGFWEGEAERGKAGDPHRRHVHRQGGRESRSRSGSPRTGADGEHRRHRAHRRPGEEGPEDKAERRARHREG SRPARGGEGEGEGPDSGERRRRHRHGAPATYEGDARREDKERRHRRR		
CACNA1A-256	53 .. 14,290	14,238 bp	CDS
▶ 8 segments = 1534 bp			
/codon_start	= 1		
/note	= coding sequence ENSP00000489913		
/translation	= YAEFIFLGLFMSEFIKMYGLGTRPYFHSSFNCFDCG,,VIIGSIFEVIWAVIKPGTSFGISVLRALRLLRIFKVTK,,YWASLRNLVVSLNSMKSIIISL LFLLLFIVV FALLGMQLFGGQ,,FNFDEGTPPTNFDTFPAAIMTVFQ,,ILTGEDWNEV MYDGIKSQGGVQGGMVFSIYFIVLTLFGN,,YTLLNVFL AIAVDNLANAQELTK,,DEQEEEEANQKLA LQKAKEVAEVSPLSAANMSIAV,,KEQQKNQKPAKSVWEQRTSEMRKQNLLASREALYNEMDP DERWKAAYTRHLRPPDMKTHLDRPLVVDPQENRNNNTNKSRAAEPTVDQRLGQ QRAEDFLRKQARYHDRARDPSGSA GLDARRPWAGSQEAE LSREGPYGRESDDHAREGSLEQPGFWEGEAERGKAGDPHRRHVHRQGGRESRSRSGSPRTGADGEHRRHRAHRRPGEEGPEDKAERRARHREG SRPARGGEGEGEGPDSGERRRRHRHGAPATYEGDARREDKERRHRRR		

Feature	Location	Size		Type
CACNA1A-257	53 .. 14,290	14,238 bp		→ CDS
▶ 8 segments = 1543 bp				
/codon_start	= 1			
/note	= coding sequence ENSP00000489829			
/translation	= YAEFIFLGLFMSEMFIKMYGLGTRPYFHSSFNCFDCG,,VIIGSIFEVIWAVIKPGTSFGISVLRALRLLRIFKVTK,,YWASLRNLVV SLLNSMKSIIISL LFLLLFIVV FALLGMQLFGGQ,,FNFDEGTPPTNFDTFPAAIMTVFQ,,ILTGEDWNEV MYDGIKSQGGVQGGMVFSIYFIVLTLFGN,,YTLLNVFL AIAVDNLANAQELTKVEA,,DEQEEEEEAANQKLA LQKAKEVAEV SPLSAANMSIAV,,KEQQKNQKPAKSVWEQRTSEMRKQ NLLASREALYNE MDPDERWKAAYTRHLRPMKTHLDRPLVVDPQENRNNNTNKSRAA EPTVDQRLGQQRAEDFLRKQARYHDRARDP SG SAGLDARRPWAGSQ EAELSREGPYGRESDDHAREGSLEQPGFWEGEAERGKA GDPHRRHVHRQ GGSRESRSGSPRTGADGEHRRHRAHRRP GEEGPEDKAERRARH REGSRRAAPGGEGEGEGEDGGERRRRHRHGAPATYEGDARREDKERRHRRR 514 amino acids = 5130 bp			
CACNA1A-259	53 .. 14,290	14,238 bp		→ CDS
▶ 8 segments = 1534 bp				
/codon_start	= 1			
/note	= coding sequence ENSP00000499449			
/translation	= YAEFIFLGLFMSEMFIKMYGLGTRPYFHSSFNCFDCG,,VIIGSIFEVIWAVIKPGTSFGISVLRALRLLRIFKVTK,,YWASLRNLVV SLLNSMKSIIISL LFLLLFIVV FALLGMQLFGGQ,,FNFDEGTPPTNFDTFPAAIMTVFQ,,ILTGEDWNEV MYDGIKSQGGVQGGMVFSIYFIVLTLFGN,,YTLLNVFL AIAVDNLANAQELTK,,DEQEEEEEAANQKLA LQKAKEVAEV SPLSAANMSIAV,,KEQQKNQKPAKSVWEQRTSEMRKQ NLLASREALYNE MDPDERWKAAYTRHLRPMKTHLDRPLVVDPQENRNNNTNKSRAA EPTVDQRLGQQRAEDFLRKQARYHDRARDP SG SAGLDARRPWAGSQ EAE LSREGPYGRESDDHAREGSLEQPGFWEGEAERGKA GDPHRRHVHRQ GGSRESRSGSPRTGADGEHRRHRAHRRP GEEGPEDKAERRARHREG SRRAAPGGEGEGEGEDGGERRRRHRHGAPATYEGDARREDKERRHRRR 514 amino acids = 5130 bp			
CACNA1A-235	4003 .. 5555	1553 bp		→ prim_transcript
/note	= primary transcript ENST00000637117 Retained intron			
✓ Donor Template WT -> SNV	4352 .. 4451	100 bp		⇌ misc_feature
✓ Protospacer Sequence	4370 .. 4389	20 bp		⇌ misc_feature
✓ SNV	4382 .. 4382	1 bp		⇌ misc_feature
/note	= WT = G SNV = A			
✓ PAM	4390 .. 4391	2 bp		⇌ misc_feature

Primer	Length	Binding Sites	Tm	Date Added
✓ PCR Forward	25-mer	4151 .. 4175	62°C	Jan 18, 2023
/sequence = GAATGGATGAATGAGGGGGTCAAGG 52% GC / 7900.2 Da				
✓ Sanger Sequencing	20-mer	4242 .. 4261	58°C	Jan 18, 2023
/sequence = AATGCTTGCCAGTTCTGGAG 50% GC / 6148.1 Da				
✓ Donor Template WT -> SNV	100-mer	4352 .. 4451	74°C	Jan 18, 2023
/sequence = CTGTACAAATGTCCAGGAACCCCAAAGACTTACTTTGTGACTTTGAAAATACGCAATAACCTGAGGGCTTGTAACACGCTGATTCCAAA 64% GC / 12612.1 Da				
✓ gRNA Protospacer	20-mer	4370 .. 4389	61°C	Jan 18, 2023
/sequence = TCAGCGTGTTACGAGCCCTC 60% GC / 6069.0 Da				
✓ PCR Reverse	25-mer	5042 .. 5066	64°C	Jan 18, 2023
/sequence = GGTGGAGGCTGTACCTGAAACACCG 60% GC / 7732.1 Da				