

INK2J00028.1_PSEN1_E276A_A03.2_BB
 26,923 bp

5'
3'

AAAAAAAAAGAGTAAATTAATTTAAAGGGAAGTATTAAATAAATAATAGCACAGTTGATATAGGTTATGGTAAAATTATAAAGGTGG
TTTTTTTTCTCATTTAATTAATTTCCCTTCATAATTTATTTATTATCGTGTCAACTATATCCAATACCATTTTAATATTTCCACC

85

PSEN1

PSEN1-201

GATATTAATATCTAATGTTTGGGAGCCATCACATTATTCTAAATAATGTTTTGGTGAAAATTATTGTACATCTTTTAAAATCTGT
CTATAATTATAGATTACAAAACCTCGGTAGTGTAATAAGATTTATTACAAAACCACTTTAATAACATGTAGAAAATTTTAGACA

170

PSEN1

PSEN1-201

GTAATTTTTTTTTCAGGGAAGTGTTTAAAACCTATAACGTTGCTGTGGACTACATTACTGTTGCACTCCTGATCTGGAATTTTGGT
CATTAAAAAAAAGTCCCTTCACAAATTTTGGATATTGCAACGACACCTGATGTAATGACAACGTGAGGACTAGACCTTAAAACCA

255

PSEN1

PSEN1-201

185 190 195 200 205
E V F K T Y N V A V D Y I T V A L L I W N F G
ENSE00003979383
PSEN1-201

GTGGTGGGAATGATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAGCAGGCATATCTCATTATGATTAGTGCCCTCATGGCCC
CACCACCCTTACTAAAGGTAAGTGACCTTTCCAGGTGAAGCTGAGGTGCGTCCGTATAGAGTAATACTAATCACGGGAGTACCGGG

340

PSEN1

PSEN1-201

210 215 220 225 230
V V G M I S I H W K G P L R L Q Q A Y L I M I S A L M A

ENSE00003979383

PSEN1-201

TGGTGTTTATCAAGTACCTCCCTGAATGGACTGCGTGGCTCATCTTGGCTGTGATTTTCAGTATATGGTAAAACCCAAGACTGATA
ACCACAAATAGTTCATGGAGGGACTTACCTGACGCACCGAGTAGAACCGACACTAAAGTCATATACCATTTTGGGTTCTGACTAT

425

PSEN1

PSEN1-201

235 240 245 250 255
L V F I K Y L P E W T A W L I L A V I S V Y

ENSE00003979383

PSEN1-201

ATTTGTTTGTACAGGAATGCCCCACTGGAGTGTTTTCTTTCTCATCTCTTTATCTTGATTTAGAGAAAATGGTAAACGTGTACA
TAAACAAACAGTGTCTTACGGGGTGACCTCACAAAAGAAAGGAGTAGAGAAAATAGAACTAAATCTCTTTTACCATTGCACATGT

510

PSEN1

PSEN1-201

PSEN1-201

TCCATAACTCTTCAGTAAATCATTAAATTAGCTATAGTAACTTTTTCATTTGAAGATTTTCGGCTGGGCATGGTAGCTCATGCCTG
AGGGTATTGAGAAGTCATTTAGTAATTAATCGATATCATTGAAAAAGTAAACTTCTAAAGCCGACCCGTACCATCGAGTACGGAC

595

PSEN1

PSEN1-201

PSEN1-201

TAATCTTAGCACTTTGGGAGGCTGAGGCGGGCAGATCACCTAAGCCCAGAGTTCAAGACCAGCCTGGGCAACATGGCAAAACCTC
ATTAGAATCGTGAAACCCTCCGACTCCGCCCGTCTAGTGATTTCGGGTCTCAAGTTCTGGTCTGGACCCGTTGTACCGTTTTGGAG

680

PSEN1

PSEN1-201

PSEN1-201

GTATCTACAGAAAATACAAAATTAGCCGGGCATGGTGGTGCACACCTGTAGTTCCAGCTACTTAGGAGGCTGAGGTGGGAGGAT
CATAGATGTCTTTTATGTTTTAATCGGCCCGTACCACCACGTGTGGACATCAAGGTCGATGAATCCTCCGACTCCACCCTCCTA

765

PSEN1

PSEN1-201

PSEN1-201

CGATTGAGCCCAGGAGGTCAAGGCTGCAGTGAGCCATGATTGCATCACTGTATTCCAGCCTGGGTGATAGAACAAGACCTTGTCT
GCTAACTCGGGTCTCCAGTTCGACGTCCTCGGTAACGTAAGGTCGGACCCACTATCTTGTCTGGAACAGA

850

PSEN1

PSEN1-201

PSEN1-201

CAAAAAAAAAATTTGGTTTTTCAAGCTTTTTGAGGTTTTGACAAGCTGGCCAATATGGTGAAACCCCGTCTCTACTAAAAATACAAA
GTTTTTTTTAAACCAAAAAGTTCGAAAACTCCAAAAGTTCGACCGGTTATACCACTTTGGGGCAGAGATGATTTTTATGTTT

935

PSEN1

PSEN1-201

PSEN1-201

AATTAGCTGGGTGTGGTGGCGTACCCTTGTATTCCAGCTACTTGAGAGGCTGAGGCAGGAGAATTATTTGAACCCAGGAAGTGA
TTAATCGACCCACACCACCGCATGGGAACATAAGGGTCGATGAACTCTCCGACTCCGTCCTCTTAATAAACTTTGGGTCTTCACT

1020

PSEN1

PSEN1-201

PSEN1-201

AGTGGAGGTTGCAGTGAGCCGAGATGGTGCCACTGCACTCTAGCCTGGGTGACAGAGCGAGACTCTGTCTCAAAAAAAAAAAAA
TCACCTCCAACGTCCTCGGCTCTACCACGGTGACGTGAGATCGGACCCACTGTCTCGCTCTGAGACAGAGTTTTTTTTTTTTTTT

1105

PSEN1

PSEN1-201

PSEN1-201

AGCAAAAAAAAAAAGCACAAAGCAGAGTGGTAGACACACAAAATGCTCAATTCATTTTTTAAACGATTTTTTCTTTTATATCTT
TCGTTTTTTTTTTTCGTGTTTCGTCTCACCATCTGTGTGTTTTACGAGTTAAGTAAAAAATTTGCTAAAAAAGGAAATATAGAA

1190

PSEN1

PSEN1-201

PSEN1-201

ACTGCAGAAGCTTTTTTCTTTTTTTTGGAGACAAAGTCTTGCTGTGTACCCAGGCTGGGGTGCAGTGGCACAGTCATAGCTCACT
TGACGTCTTCGAAAAAAGAAAAAAACTCTGTTTCAGAACGACACAGTGGGTCCGACCCACGTCACCGTGTTCAGTATCGAGTGA

1275

PSEN1

PSEN1-201

PSEN1-201

GCAACCTTGAACCTCCCTGGCTCATGCGATCCTCCCACTTCAGCCTCTCAAGTAGCTAGAACTACAGGTGTGCACCACCATGCCTG
CGTTGGAACCTTGAGGGACCGAGTACGCTAGGAGGGTGAAGTCGGAGAGTTCATCGATCTTGATGTCCACACGTGGTGGTACGGAC

1360

PSEN1

PSEN1-201

PSEN1-201

ACTAACTTGTTTATTTTTTGTAGAGAGAACGCTTGCTATATTGCCTAGGCTGGTCTTGAACCTCTGGGCTCAAGCAATCCTCCT
TGATTGAACAAATAAAAAACATCTCTCTTGCAGAACGATATAACGGATCCGACCAGAACCTTGAGAACCCGAGTTTCGTTAGGAGGA

1445

PSEN1

PSEN1-201

PSEN1-201

ACCTTGGCCTCTCAAGGTATTGGGATTATAGGTGTGAGCCACTGCATCTGGCCTCAATTCACTTTTAAAATCAAAATTAGGTTAC
TGGAACCGGAGAGTTCATAACCCCTAATATCCACACTCGGTGACGTAGACCGGAGTTAAGTGAAAATTTAGTTTTAATCCAATG

1530

PSEN1

PSEN1-201

PSEN1-201

CTACTTTTTATAAGGTAATGTATAGAATTATTCTTTTTAAAAATAAAACCGATTTGGACAGTGTGAGATTACATTCTGTAACCAC
GATGAAAAATATTCCATTACATATCTTAATAAGAAAATTTTTATTTTTGGCTAAACCTGTCCACACTCTAAGTGTAAAGACATTGGTG

1615

PSEN1

PSEN1-201

PSEN1-201

CAGTGTGACATGGGTCTTGAACAGTTAGAACATACTCCAGCCATTAACCCAGGCAGCTTTCAGGTACGTACTCTGTGGCTGTTGC
GTCACACTGTACCCAGGACTTGTCAATCTTGATGAGGTGCGTAATTGGGTCCGTCGAAAGTCCATGCATGAGACACCGACAACG

1700

PSEN1

PSEN1-201

PSEN1-201

CTTGATGAAAGCCAAAAAGAGATCCATTTTTAGAGATTAATATGTGACCCCTTCTATATTATAAGGCCATGGCCATACTCTTTT
GAACATACTTTTCGGTTTTTCTCTAGGTAAAAGTCTCTAATTATACACTGGGGAAGATATAATATTCCGGTACCGGTATGAGAAAA

1785

PSEN1

PSEN1-201

PSEN1-201

TTTTTCTTTTTGTTTTTTCTTCCAAAGACAGGATCTCTCTGTGCATCCACGCTAGAGTACAGTGGCATGAACGTGGCTTACT
AAAAAAGAAAAACAAAAAAGAAGGTTTCTGTCTTAGAGAGAGACAGTAGGTGCGATCTCATGTCCACCGTACTTGCACCGAATGA

1870

PSEN1

PSEN1-201

PSEN1-201

GCAGCCTCAAACCCCTTGTCTGTTGGGCTCAAACAATCCTCCCACCTCAGCCTTCAAAGTAGATAGAACTACAGGCATGCACTACCAT
CGTCGGAGTTTGGGAACAGGACCCGAGTTTGTAGGAGGGTGGAGTCGGAAGTTTCATCTATCTTGATGTCCGTACGTGATGGTA

1955

PSEN1

PSEN1-201

PSEN1-201

GCCTAATTTTTTAAAAAAAATTTTTTTTTCAGAGATGAGATCTCACTGTGTTTTCCAGGCTTGTCCGGAACCTCGGCCTCAAGC
CGGATTAATAAATTTTTTTTAAAAAAAAGTCTCTACTCTAGAGTGACACAAAGGGTCCGAACAGGCCTTGAGGACCCGGAGTTTCG

2040

PSEN1

PSEN1-201

PSEN1-201

GATCCTCCCACCTTGGCCTGCCAAAAGTGTGGGATTACAGGCATGAGCCACCATGCCTGGCCATACACTTTTTTTTTTTTTTTTTT
CTAGGAGGGTGAACCGGACGGTTTCACAACCCTAATGTCCGTACTCGGTGGTACGGACCGGTATGTGAAAAAAAAAAAAAAAAA

2125

PSEN1

PSEN1-201

PSEN1-201

TTCAAGACGGAGTCTGGCTCTGTGCCCCAGACTGGAGTGCAGTGGCGTGATCTTGGCTCACTGCAAGCTTCGCCTCCCAGGTTCA
AAGTTCTGCCTCAGACCGAGACAGCGGGTCTGACCTCACGTCAACCGACTAGAACCGAGTGACGTTTGAAGCGGAGGGTCCAAGT

2210

PSEN1

PSEN1-201

PSEN1-201

TGCCGTTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGACTACAGGCATCTGCCACCACGCCCGGCTATTTTTTTGTATTTGTAGTA
ACGGCAAGAGGACGGAGTCGGAGGGTTTCATCGACCCTGATGTCCGTAGACGGTGGTGCGGGCCGATAAAAAACATAAACATCAT

2295

PSEN1

PSEN1-201

PSEN1-201

GAGACGGGGTTTACCATGTTAGCCAGGATGATCTCGATCTCCTGACCTCATGATTCACCTGCCTCGGCCTCCCAAAGTGTGGG
CTCTGCCCAAAGTGGTACAATCGGTCTACTAGAGCTAGAGGACTGGAGTACTAAGTGGACGGAGCCGGAGGGTTTACAACCC

2380

PSEN1

PSEN1-201

PSEN1-201

ATTACAGGCATGAGCCACCGTGCCCGGCCTGGCCATACACTTTTGTTCATTATTTACATACTTACTAAAATGTTTGGTGGCCTGTA
TAATGTCCGTACTCGGTGGCACGGGCGGACCGGTATGTGAAAACAGTAATAAATGTATGAATGATTTTACAAACCACCGGACAT

2465

PSEN1

PSEN1-201

PSEN1-201

ATAGGAAACATCATCCTCATTGATTGACGAAGAAGTCTGTGGAATAGGATTGAACTGGTTCTGTTCTTGTATTTGAGTAATCA
TATCCTTTGTAGTAGGAGTAAACTAACTGCTTCTTCAGACACCTTTATCCTAACTTGACCAAGACAAGAACATAAACTCATTAGT

2550

PSEN1

PSEN1-201

PSEN1-201

GTTGTGGAACTATAGAAGTCATATACTCTCTGACTTTTCATAATTACCTTATGTTGTATAGTACTTGATGGTTTTGCAAAGTAAC
CAACACCTTGATATCTTCAGTATATGAGAGAGACTGAAAGTATTAATGGAATACAACATATCATGAACTACCAAACGTTTCATTG

2635

PSEN1

PSEN1-201

PSEN1-201

CATCTATTCTTGCTTAGCTGTGAGTAAGAATGCCAGGTCTGGAGACAGAATGTCTGGGTTCAAATTCTACTCATCACTTTTTATT
GTAGATAAGAACGAATCGACACTCATTCTTACGGTCCAGACCTCTGTCTTACAGACCCAAGTTTAAGATGAGTAGTGAAAAATAA

2720

PSEN1

PSEN1-201

PSEN1-201

TTTATTTTTTTGAGATAGAGTCTCGCTTTGTTGCCAGGCTGGAGTGCAAGTGGCGTGATCTCAGCTCACTACAACCTCTCCCTC
AAATAAAAAAACTCTATCTCAGAGCGAAACAACGGGTCCGACCTCACGTCAACCGCACTAGAGTCGAGTGATGTTGGAGAGGGAG

2805

PSEN1

PSEN1-201

PSEN1-201

CCGGGATCAAGCGATTCTCCTGCCTCAGCCTTCCGAGTAGCTGGGACTACAAGTGCGCACCACCACGCCAGCTAATTTTTGTAT
GGCCCTAGTTTCGCTAAGAGGACGGAGTCGGAAGGCTCATCGACCCTGATGTTACACGCGTGTTGGTGC GGTCGATTAAAAACATA

2890

PSEN1

PSEN1-201

PSEN1-201

TTTTAGTAGAGACGAGGTTTTGCCATGTTGGCCAGGCTGGTCTCAAACCTCCTGACCTCAAGTGATCTGCCTGCCTCAGCCTCCCA
AAAATCATCTCTGCTCCAAAACGGTACAACCGGTCCGACCAGAGTTTGAGGACTGGAGTTCACTAGACGGACGGAGTCGGAGGGT

2975

PSEN1

PSEN1-201

PSEN1-201

GAGTGCTGGGATTACAGGCTTGAACCACTGCGCCAGCCTACTCATCACTTACTAGCTATTTGACCACACAAGTTACTCAACTCC
CTCACGACCCTAATGTCCGAACCTTGGTGACGCGGGTCGGATGAGTAGTGAATGATCGATAAACTGGTGTGTTCAATGAGTTGAGG

3060

PSEN1

PSEN1-201

PSEN1-201

TATGTCAGTTATGAAGATTAAATTAATGATCCATTTAATACAATAATACACTTAGAACAATGTCTATCAGTAAATTTTTTCTG
ATACAGTCAATACTTCTAATTTAATTTACTAGGTAAATTATGTTATTATGTGAATCTTGTTACAGATAGTCATTTAAAAAAGAC

3145

PSEN1

PSEN1-201

PSEN1-201

TTTTAAGAAACAGGATCTCACTCTGTCTCCCAGGCTGGAGTGAAGTGGCACGATTATAGCTCACTGTAGCTTCAAAGCCTGGGC
AAAATTCTTTGTCTTAGAGTGAGACAGAGGGTCCGACCTCACTTCACCGTGCTAATATCGAGTGACATCGAAGTTTTTCGGACCCG

3230

PSEN1

PSEN1-201

PSEN1-201

TCAAGCAGTCCTCCTGTCTCAGCCTCCCGAGTAGATAAGACTACAGGCACAGGTTGGTGTGACCTCCTAGCTTCAAGCAGCCTC
AGTTCGTCAAGGAGACAGAGTCGGAGGGCTCATCTATTCTGATGTCCGTGTCCAACCACAACCTGGAGGATCGAAGTTCGTCTGGAG

3315

PSEN1

PSEN1-201

PSEN1-201

CCAAAGTGCTGAGATTACAGGTGTGAGCCACTATACCCAGCCCAGTGTATATTTTTGTATAATCCTATGAAGTATCAAGGCAGT
GGTTTTACGACTCTAATGTCCACACTCGGTGATATGGGTGCGGTGTTCAATATAAAAAACATATTAGGATACTTCATAGTTCCGTCA

3400

PSEN1

PSEN1-201

PSEN1-201

TATTATCCCTGTTTTACTGCTAAGAACTTGAAGTTTACAGAGGTAAATTTTTGCCTAAGCCTAAACTCTGATCTCGAATCTGA
ATAATAGGGACAAAATGACGATTCTTTGAACTTCAAATGTCTCCATTTAATAAACGGATTTCGGATTTGAGACTAGAGCTTAGACT

3485

PSEN1

PSEN1-201

PSEN1-201

ATCCCAAGTCCAATATTCTTTTACCGTATTACAATATTTTTACCATCAACCCTCCATTCTGTCTGCACATCATACAAATGAGTA
TAGGGTTCAGGTTATAAGAAAAGTGGCATAATGTTATAAAAATGGTAGTTGGGAGGTAAGACAGACGTGTAGTATGTTTACTCAT

3570

PSEN1

PSEN1-201

PSEN1-201

TCTCTACAGAGCTTTGAGTTGCTTTTAAACAAAAGAGATTTTTGTACCCAATGTTTAGAGTAGTGATTCTCGGCTCCATTTTAC
AGAGATGTCTCGAAACTCAACGAAAATTTGTTTTCTCTAAAAACATGGGTTACAAATCTCATCACTAAGAGCCGAGGTAAAAATG

3655

PSEN1

PSEN1-201

PSEN1-201

AAGATTTCAAGATTTAATTTGTCAAAAAAGTTCTGAAATTTTCAAAGCAAAGCAATTTTAATTTAATTGCTCTAAAAATAAGC
TTCTAAAGTTCTAAATTA AACAGTTTTTTCAAGACTTTAAAAGTTTCGTTTTCGTTAAAATTAATTAACGAGATTTTTTATTTCG

3740

PSEN1

PSEN1-201

PSEN1-201

AGATTTATCATTTAGCAATTCCTTAAGGGAGAGTGATCATAAAACCTGAAATAGTACTGAATGTGGCAGAATCAAACAAGTTGAA
TCTAAATAGTAAATCGTTAAGAAATTCCTCTCACATAGTATTTGACTTTATCATGACTTACACCGTCTTAGTTTGTTCAACTT

3825

PSEN1

PSEN1-201

PSEN1-201

AATCTCATCACTTCAGAGCAGGGCAGACTTCTCATTCAAACAAATTGAGGTAGAAGTGGTGAGAGTAGAGATTTCTTTGTGTATG
TTAGAGTAGTGAAGTCTCGTCCCCTCTGAAGAGTAAGTTTGTTAACTCCATCTTCACCACTCTCATCTCTAAAGAAACACATAC

3910

PSEN1

PSEN1-201

PSEN1-201

TGTGTTTTATTACTGTAATATATTATATTATAGTTCTATATATACTATATTATATTGTACATATATATTATTATATGAAGAGACA
ACACAAAATAATGACATGATATAATATAATATCAAGATATATATGATATAATATAACATGTATATATAATAATACTTCTCTGT

3995

PSEN1

PSEN1-201

PSEN1-201

TGACCACTTTGAGGCATGAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTGTGAGGCACGGTCTTACTTTGTACCTAGGCAGTGGCGCCA
ACTGGTGAAACTCCGTACTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAACTCCGTGCCAGAATGAAACAGTGGATCCGTACCCGCGGT

4080

PSEN1

PSEN1-201

PSEN1-201

TCTTGGCTCACTGCAGCCTCCACCTCCAGGGCTCAAGCAATCCTCCCACCTCAGCTTCTGAGTAGCTGGGACTATAGGCACCTG
AGAACCGAGTGACGTCCGAGGTGGAGGTCCCGAGTTTCGTTAGGAGGGTGGAGTCAAGGACTCATCGACCCTGATATCCGTGGAC

4165

PSEN1

PSEN1-201

PSEN1-201

CCACCATGAGCTGCTAATTTTTTGTATTTTTTGGTAGAGACGGGGTTTTGCCATCTTGGCCAGGCTGGTCTCAAACCTCCTGAGCAC
GGTGGTACTCGACGATTAACAAAAACATAAAAAACCATCTCTGCCCAAACGGTAGAACCGGTCCGACCAGAGTTTGAGGACTCGTG

4250

PSEN1

PSEN1-201

PSEN1-201

AAGTGATCTGCTGCCTCAGCCTCCCCAAAGTGCTGGAATTACAAGCATAAGCCACTGTGCCTGGCAAGACATGAAATTTTTAAAT
TTCAGTAGACGACGGAGTCGGAGGGGTTTCACGACCTTAATGTTTCGTATTCGGTGACACGGACCGTTCTGTACTTTAAAAATTTA

4335

PSEN1

PSEN1-201

PSEN1-201

GTAAATGCATTTAAGTGACAATAATGTGAATACAAGTTATCAATTCTTCCTTTACAAGTTTAGCTATACCTGTTTTATATTTTTTC
CATTTACGTAAATTCAGTGTATTACACTTATGTTCAATAGTTAAGAAGGAAATGTTCAAATCGATATGGACAAAAATATAAAAAAG

4420

PSEN1

PSEN1-201

PSEN1-201

AGTGTTTTAAATTTATTTTTATTTTTATATTCTGAATTTTCTTTCTTTCTTTCTTTTTTTTTTTTTTTTTTTTTTTTGGAGACGGAGTCTC
TCACAAATTTAATAAAAAATATAAAAAATATAAGACTTAAAAGAAAGAAAGAAAGAAAAAAAAAAAAAAAAAAAACTCTGCCTCAGAG

4505

PSEN1

PSEN1-201

PSEN1-201

GCTGTATTGCCAGGCTGGAGTGCAAGTGGCGCAATCTCGGCGCACTGCAAGCTCCGCTTCCCGGGTTCACGCCGTTCTCCTGCCT
CGACATAACGGGTCCGACCTCACGTCACCGCGTTAGAGCCGCGTGACGTTTCGAGGGCGAAGGGCCCAAGTGCGGGCAAGAGGACGGA

4590

PSEN1

PSEN1-201

PSEN1-201

CAGCCTCCCGAGTAGCTGGGACTACAGGCACGCGCCACCACACCCAGCTAATTTTTTGTATTTTTTAGTAGAGACAGGGTTTCAC
GTCGGAGGGCTCATCGACCCTGATGTCCGTGCGCGGTGGTGTGGGTGCGATTAAAAAACATAAAAAATCATCTCTGTGCCCAAAGTG

4675

PSEN1

PSEN1-201

PSEN1-201

CGTGTTAGCCAGGATGGTCTTGATCTCCTGACCTTGTGATCCGCCACCTCGGCCTCCCAAAGTGCTGGGATTGCAGGCCTGAGC
GCACAATCGGTCTTACCAGAACTAGAGGACTGGAACACTAGGCGGGTGGAGCCGGAGGGTTTCACGACCCTAACGTCCGCACTCG

4760

PSEN1

PSEN1-201

PSEN1-201

CACTGCGCCCGGCCTATATGCTGAATTTTCATGACAGAGAATGAAAGAAAAAGTGCAGTTGATCGAAAGAAATGGTGGTATAAAC
GTGACGCGGGCCGGATATACGACTTAAAAGTACTGTCTCTTACTTTCTTTTTTTCACGTCAACTAGCTTTTCTTTACCACCATATTTG

4845

PSEN1

PSEN1-201

PSEN1-201

AGGAATAACAGGCATGTTGTTTTCTCTCTGATTTATTATTTTTGTAAAATAAGCTACTTTTTCAGCACCACATACATATGTTCTGA
TCCTTATTGTCCGTACAACAAAGGAGAGACTAAATAATAAAAAACATTTTATTTCGATGAAAAGTCGTGGTGTATGTATACAAGACT

4930

PSEN1

PSEN1-201

PSEN1-201

GACCTGAATATTTGTGACCAAAGAGTAAAGAAGTAATAAACTTTATCTCGCAAAGAGTTATTATTGTGTTTTATTTAAATTTACT
CTGGACTTATAAACACTGGTTTCTCATTCTTCATTATTTGAAATAGAGCGTTTCTCAATAATAACACAAAATAAATTTAAATGA

5015

PSEN1

PSEN1-201

PSEN1-201

GCCCTCTTACTTCAAGTACTTCTCAGTAGTACGTAATACTGCTTTTTAAAAAGGAGAAGGGATGAATTTCTTCTACTCTGCTCTTC
CGGGAGAATGAAGTTCATGAAGAGTCATCATGCATTATGACGAAAATTTTTCTCTTCCCTACTTAAAGAAGATGAGACGAGAAG

5100

PSEN1

PSEN1-201

PSEN1-201

ATATTTTGAAAAGTTCAGTCAAATCCCCTTTATTAATTCATCTCAGAGTAATCTTTTTAATTTGTAGTTCATATCCGTGATTAG
TATAAACTTTTCAAGTCAGTTTAGGGGAAATAATTTAAGTAGAGTCTCATTAGAAAAATTAACATCAAGTATAGGCCTAATC

5185

PSEN1

PSEN1-201

PSEN1-201

PCR Forward

TTCTCCCTGTTTCTGCTCACTGTAG

TTTAGAAGTGACTTCTCCCTGTTTCTGCTCACTGTAGGTTGACAACCTGCTTAAAATAGTCTATCTCATCATTATCTCTGCAGCTT
AAATCTTCACTGAAGAGGGACAAAGACGAGTGACATCCAACCTGTTGACGAATTTTATCAGATAGAGTAGTAATAGAGACGTCGAA

5270

PSEN1

PSEN1-201

PSEN1-201

TCCTTTAACTAGGAAGACTTGTTCCCTATACCCAGTAACGATACACTGTACACTAAGCAAATAGCAGTCAAACCCAAATGAAAT
AGGAAATTTGATCCTTCTGAACAAGGATATGGGGTCATTGCTATGTGACATGTGATTTCGTTTATCGTCAGTTTGGGTTTACTTTA

5355

PSEN1

PSEN1-201

PSEN1-201

TTTTACAGATGTTCTGTGTCATTTTATTTTGTGTTATGTTGTCTCCCCACCCCCACCAGTTCACCTGCCATTTATTTTCATATTCA
AAAAATGCTCTACAAGACACAGTAAAAATAAAACAAATACAACAGAGGGGGTGGGGGTGGTCAAGTGGACGGTAAATAAAGTATAAGT

5440

PSEN1

PSEN1-201

PSEN1-201

TTCAACGTCTTTTTGTGTA AAAAGAGACAAAAACATTAAACTTTTTTCTTCGTTAATTCCTCCCTACCACCCATTTACAAGTT
AAGTTGCAGAAAAACACATTTTCTCTGTTTTTGTAAATTTGAAAAAAGGAAGCAATTAAGGAGGGATGGTGGGTAAATGTTCAA

5525

PSEN1

PSEN1-201

PSEN1-201

gRNA Protospacer

T

TAGCCCATACATTTTATTAGATGCTTTTTATGTTTTCTTTTTCTAGATTTAGTGGCTGTTTTGTGTCCGAAAGGTCCACTTCGT
ATCGGGTATGTA AAAATAATCTACAGAAAATACAAAAAGAAAAAGATCTAAATCACCGACAAAACACAGGCTTTCCAGGTGAAGCA

5610

PSEN1

PSEN1-201

260 265
D L V A V L C P K G P L R
ENSE00003979367

PSEN1-201

Donor Template WT -> SNV

Protospacer Sequence

AGGCTTTCCAGGTGAAGCA
Donor Template WT -> SNV

gRNA Protospacer

ATGCTGGTTGAAACAGCTC

ATGCTGGTTGAAACAGCTCAGGAGAGAAAATGA AACGCTTTTTTCCAGCTCTCATTACTCCTGTAAGTATTTGAGAAGGATATTGA
TACGACCAACTTTGTGCGAGTCCTCTCTTTACTTTGCGAAAAAAGGTCGAGAGTAAATGAGGACATTCATAAACTCTTCCTATAACT

5695

PSEN1

PSEN1-201

270 275 280 285
M L V E T A Q E R N E T L F P A L I Y S

ENSE00003979367

PSEN1-201

Donor Template WT -> SNV

Protospacer Sequence

PAM

SNV

Silent SNV

TACGACCAACTTTGTGCGAGTCCTCTCTTTACTTTGCGAAAAAAGGTCGAGAGTAAATGAGGACATTCATAAACTCTTCCTAT

Donor Template WT -> SNV

ATTAGTAATCAGTGTAGAAATTTATCGGAACTGAAGCACATGTAACATGTTTCATGGTACTTGTTCATCTTAAATGCA
TAATCATTAGTCACATCTTAAATAGCCTTGACTTCGTGTACATTGATACCAGTAAAAGTACCATGAACAAGAGTAGAATTTACGT

5780

PSEN1

PSEN1-201

PSEN1-201

CGT

Sanger Sequencing

CAGCATTCTGGAACCTCCTGCAGATCTCTTTGTTTCCTTGCAAGCAATTGTCTTCTACCTGATGTTGATTCAAGAGAGTTTTCAA
GTCGTAAGGACCTTGAGGACGTCTAGAGAAACAAAGGAACGTTGTTAACAGAAGATGGACTACAACCTAAGTTCTCTCAAAAGTT

5865

PSEN1

PSEN1-201

PSEN1-201

GTCGTAAGGACCTTGAG

Sanger Sequencing

TATGAATAGAAAAGAAAAGAAAATGTTTAGATATTGGGGAACCCAGCATTCCCATTTTTAAAACCTGTTAGGAGTTGTTGATTAGGGCA
ATACTTATCTTTCTTTCTTTTACAAATCTATAACCCCTTGGTCGTAAGGGTAAAATTTTGGACAATCCTCAACAACCTAATCCCGT

5950

PSEN1

PSEN1-201

PSEN1-201

AGCTCAAGGATTCCTTTGAGTGACTGGTTTTAGATGTCTTTCTGCTATTCGGTGACCACTGGGGAACCTGAGATTGTTGAGCAGAAG
TCGAGTTCCTAAGGAAACTCACTGACCAAATCTACAGAAAGACGATAAGCCACTGGTGACCCCTTGACTCTAACAACCTCGTCTTC

6035

PSEN1

PSEN1-201

PSEN1-201

GGTAATGTGAGCAGAGCCGTGCCTTTGTAAGCTGGCAGCACTGTGTGAGATGAATTGGTGGGTTGGATACTGAGATCATGAGAGG
CCATTACACTCGTCTCGGCACGGAAACATTCGACCGTCGTGACACACTCTACTTAACCACCCAACCTATGACTCTAGTACTCTCC

6120

PSEN1

PSEN1-201

PSEN1-201

CATACTAAGCATAATTAAGATGATATTGCCATGATCTAGGTGGAAAGTAATGGGGGTTTGAATTATGGTAGTGGCAGTAGCAATC
GTATGATTGATTAATTCTACTATAACGGTACTAGATCCACCTTTCATTACCCCCAAACTTAATACCATCACCGTCATCGTTAG

6205

PSEN1

PSEN1-201

PSEN1-201

CCACCTTTCATTACCCCCAACTTA

PCR Reverse

AAGGGAAAGAGTTGATCAGAGGATTCAGAGGTAGAATCAATAGTTCTAGCAACTGAGGAGAGAAGTTGTAAGCTTGAAGGAAAGG
TTCCCTTTCTCAACTAGTCTCCTAAGTCTCCATCTTAGTTATCAAGATCGTTGACTCCTCTCTTCAACATTCGAACCTTCTTTCC

6290

PSEN1

PSEN1-201

PSEN1-201

TGATGAAGAAAAAATGCTTTTCTGTGTTTTCTTGTGTTGTTGTTGAGATAGGGTCTCACTCCCATCCAGGATGGAGTACAGTAG
ACTACTTCTTTTTTACGAAAGGACACAAAAGAACAACAACAACAACTCTATCCCAGAGTGAGGGTAGGTCTTACCTCATGTCATC

6375

PSEN1

PSEN1-201

PSEN1-201

TGTGATCATGGCTCACTGCAGCCTCGACCTCCCAGGCTCAGGTGATCCACCCACCTCAGCCTCCCGAGTAGCTGTGACTACAGGC
ACACTAGTACCGAGTGACGTCGGAGCTGGAGGGTCCGAGTCCACTAGGTGGGTGGAGTCGGAGGGCTCATCGACACTGATGTCCG

6460

PSEN1

PSEN1-201

PSEN1-201

ACGCACTACCAGGCCTGGCTAATTTTTTTGTGTTGTGTGTAGAGACTGGGTTTTGCCATGTGCCCAGGCTGGTCTTGAACCTCCTC
TGCGTGATGGTCCGGACCGATTAAAAAACACAACACACATCTCTGACCCAAAACGGTACACGGGTCCGACCAGAACCTTGAGGAG

6545

PSEN1

PSEN1-201

PSEN1-201

GGCTTAAGCGATCCTCCTGCCTTGACTTCACAAAGTGCTTGAGTTACAGGTGTGAGCTACCACGCCTGGCCATGTTTTCTTGTGT
CCGAATTCGCTAGGAGGACGGAACCTGAAGTGTTTACGAACTCAATGTCCACACTCGATGGTGC GGACCGGTACAAAAGAACAACA

6630

PSEN1

PSEN1-201

PSEN1-201

GAAGGATCTGTTTAGTTTTATATCTTTCTGTGGCTCATATCTAATTTAGTTGACAGTACCTGTGGGTCCTAGGTAGACATTGCT
CTTCTAGACAAATCAAAATATAGAAAAGACACCGAGTATAGATTAAATCAACTGTCATGGACACCCAGTGATCCATCTGTAACGA

6715

PSEN1

PSEN1-201

PSEN1-201

AGCAGACGTTTAGAAATGAAATACTAGAGCTTGGGAAAAAGTTGATATTTGAGATAGAGACTTGAAGAACATTAGCAGAGAGTTG
TCGTCTGCAAACTTTACTTTATGATCTCGAACCTTTTTCAACTATAAACTCTATCTCTGAACTTCTTGTAAATCGTCTCTCAAC

6800

PSEN1

PSEN1-201

PSEN1-201

GTAGTTAAGGTCTGTGAGCTGGTGAGCAATTCAAATAAAAAGCAGAAGAGAAGAGGAAGACAAGGGTCAAACCTTTGTCAACTACTG
CATCAATTCAGACACTCGACCCTCGTTAAGTTTATTTTCGTCTTCTCTTCTCCTTCTGTTCCCAAGTTTGAAACAGTTGATGAC

6885

PSEN1

PSEN1-201

PSEN1-201

TGTTTAGAGAATGAGACAAGAGAGGATACTACAGGAAGTAGAGGAAAATAGTGGAAAATTGGGCAAGCCAGTATTTTTCACTTAA
ACAAATCTCTTACTCTGTTCTCTCCTATGATGTCCTTCATCTCCTTTTATCACCTTTTAACCCGTTTCGGTCATAAAAAAGTGAATT

6970

PSEN1

PSEN1-201

PSEN1-201

GAATATCATTACTGTTTTTTGATGTCAGCACATGAAATGGCTGCATAGTGTCTCTTACGTAGATATTCAGTGGTGGGTATCCTC
CTTATAGTAATGACAAAAAACTACAGTCGTGTACTTTACCGACGTATCACAAGAGAATGCATCTATAAGTCACCACCCATAGGAG

7055

PSEN1

PSEN1-201

PSEN1-201

ATTGATAGACATTTAGATCATTTCCATTTATTTTCTATCACAGACAGCACTTACAGAGTGCATCCATGAACTTATGAATATTATT
TAACTATCTGTAAATCTAGTAAAGGTAAATAAAAGATAGTGTCTGTCTGTAATGTCTCACGTAGGTACTTGAATACTTATAATAA

7140

PSEN1

PSEN1-201

PSEN1-201

ATAAAATGTATTCTTACAGTAGAATTGCTAAGTCAAAGGATGTATTTAAATTTTGATAGTTTGCCATATTGCCTCCTAAAAAGC
TATTTTACATAAGAATGTCATCTTAACGATTCAGTTTTCTACATAAATTTAAAACCTATCAAACGGTATAACGGAGGATTTTTTCG

7225

PSEN1

PSEN1-201

PSEN1-201

TGTGCCTGTTTACATTCCCTTCAGTAATATGAAAGTATCAATTTCTTACCCCTTTGGTGTGTTTGGTTTGTGTTTGGAGAC
ACACGGACAAATGTAAGGGAAGTCATTATACTTTCATAGTTAAAGGAATGGGGAAACCACAAAACCAAACAAAACCTCTG

7310

PSEN1

PSEN1-201

PSEN1-201

TGAGTCTCGCTCTGTCATGCAGGCTGGAGTGCAGTGGTGCATCTCGGCTCACTGCAACCTCCGCCTCCTGGGTTCAAGCAGTTC
ACTCAGAGCGAGACAGTACGTCCGACCTCACGTACCACGCTAGAGCCGAGTGACGTTGGAGGCGGAGGACCCAAGTTCGTCAAG

7395

PSEN1

PSEN1-201

PSEN1-201

TCCTGCCTCAGCCTCCGGAGTGGCTGGGATTACAGGCGTGTGCCACCACACCCAGCTAATTTTTTGTATTTTTAGTGGAGACACG
AGGACGGAGTCGGAGGCCTCACCGACCCTAATGTCCGCACACGGTGGTGTGGGTTCGATTAACAAAAACATAAAAAATCACCTCTGTGC

7480

PSEN1

PSEN1-201

PSEN1-201

GTTTCACCATGTTGACCAGGCTGGTCTCGAACTCCTGACTTCAGGTGATCCGCCTGCCTAGGCCTCCCAAAATGCCAGGATTATA
CAAAGTGGTACAACCTGGTCCGACCAGAGCTTGAGGACTGAAAGTCCACTAGGCGGACGGATCCGGAGGGTTTTACGGTCTTAATAT

7565

PSEN1

PSEN1-201

PSEN1-201

GCTGTGAGCCACCATGCCCGGCCACTGCTTTGTTAATGCTTGCCTGTGTCTGTGCATACATGCATGTGTGTGTGTCTGAGAGAGA
CGACACTCGGTGGTACGGGCGGGTGACGAAACAATTACGAACGGACACAGACACGTATGTACGTACACACACACAGACTCTCTCT

7650

PSEN1

PSEN1-201

PSEN1-201

AAGAGATCTAATAGGCCAAAAAATAACATCTTGTTTTATTTTTATTGTTTGTCTAATGCTTTGGGTGATTATTTGAACTTTTTT
TTCTCTAGATTATCCGTTTTTTTTATTGTAGAACAAAAATAAAAAATAACAAACAGATTACGAAACCCACTAATAAACCCTTGAAAAA

7735

PSEN1

PSEN1-201

PSEN1-201

TCATGTGTTTCTTAGTTACAGATCTGAATTTATTTTGTAACTGGCTTGGTATAATCTTTTTTCATATTTGTGAAATTAATCTTTTT
AGTACACAAAGAATCAATGTCTAGACTTAAATAAACATTGACCGAACCATATTAGAAAAAGTATAAACACTTTAATTAGAAAAA

7820

PSEN1

PSEN1-201

PSEN1-201

TGTGTGTGTGTGAGACAGTCTCTCTCTGTCACCCAAGCTGGAGTACAGTGGCGCAATCTCAACTCACTGCAACCTCCATCTCCCA
ACACACACACACTCTGTCAGAGAGAGACAGTGGGTTTCGACCTCATGTACCCGCGTTAGAGTTGAGTGACGTTGGAGGTTAGAGGGT

7905

PSEN1

PSEN1-201

PSEN1-201

GGTTCAAGCAATTCTCCTCTCTCAGCCTCCCAAGTAGCTGGAATTACAGGCGCATGCCACCACGCCTGGCTGATTTTTGTATTTT
CCAAGTTCGTTAAGAGGAGAGAGTCCGAGGGTTCATCGACCTTAATGTCCGCGTACGGTGGTGCAGGACCGACTAAAAACATAAAA

7990

PSEN1

PSEN1-201

PSEN1-201

TAGTAGAGACGGGATTTCCACCACGTTGGCCAGGCTGGTCTCAAGTGATCCAAGTGCCTCAGACTCCCAAAGCATTAGTATTACAG
ATCATCTCTGCCCTAAAGTGGTGCAACCGGTCCGACCAGAGTTCACTAGGTTGACGGAGTCTGAGGGTTTCGTAATCATAATGTC

8075

PSEN1

PSEN1-201

PSEN1-201

GTGTGAGCCACTGCTCCCAGCCCTGTAAAATTAATCTTAATTATACAAGTAATTCATTATCCTTGAAAAAGGATAAACATTACAG
CACACTCGGTGACGAGGGTCTGGGACATTTTAATTAGAATTAATATGTTTCATTAAGTAATAGGAACTTTTTCTATTGTAAATGTC

8160

PSEN1

PSEN1-201

PSEN1-201

ATAAAAAATAAATTTACCGTAACATCATCTCTAATCTTAATGCCTTATCAAGTACTTACCCCTGTTGTCAGTTTTGTTGTATATC
TATTTTTATTTAAAGTGCCATTGATAGTAGAGATTAGAATTACGGAATAGTTTCATGAATGGGGACAACAGTCAAACAACATATAG

8245

PSEN1

PSEN1-201

PSEN1-201

CTTGTAGATTTTTTTTGGCAATTTTTCTGTTGAGTTACTGGAAAAGCAGTTTCAAGAAGGAGAGAGGCTGGGCGTGGTGGCTAAC
GAACATCTAAAAAAAACGGTTAAAAAGACAACCTCAATGACCTTTTCGTCAAAGTCTTCTCTCTCCGACCCGCACCACCGATTG

8330

PSEN1

PSEN1-201

PSEN1-201

ACCTGTAATCCAGCACTTTGGGAGGCCTAGGTGGGCGGATCACTTGAGGTCAGGAGTTTGAAACCAGCCTGGCCAACATGGTGA
TGGACATTAGGGTCTGTGAAACCCTCCGGATCCACCCGCC TAGTGAACCTCCAGTCCTCAAACCTTTGGTCGGACCGGTTGTACCACT

8415

PSEN1

PSEN1-201

PSEN1-201

AACTCTGTCTTTACTAAAAATATAAAAAATCAGCTGGGTGTGGTGGTGCACACTTGTAATCCAGTTACTTGGGAGGCTGAGGTGG
TTGAGACAGAAATGATTTTTATATTTTTAGTCGACCCACACCACCGTGTGAACATTAGGGTCAATGAACCCTCCGACTCCACC

8500

PSEN1

PSEN1-201

PSEN1-201

GAGGATCACTTGAACCCAGGAGGCGGAGGTTACAGTGAGCCATGATCGTGCCACTGCACTCCAGCCTGAGTGACAGCAAGGCTTC
CTCCTAGTGAACCTTGGGTCTCCGCCTCCAATGTCACTCGGTACTAGCACGGTGACGTGAGGTCGGACTCACTGTCGTTCCGAAG

8585

PSEN1

PSEN1-201

PSEN1-201

ATCCCCACCCCTCCCAAAAAAAAAAGAGAATATCTTTTTGTTTGTGGCAGAGTCTTGCTGTGTCG
TAGGGGTGGGAGGGTTTTTTTTCTCTTATAGAAAAACAAACAAACAAACAAACAAACAAACACCGTCTCAGAACGACACAGC

8670

PSEN1

PSEN1-201

PSEN1-201

CCCAGGCTGGAGTTCAGTGGGGCGATCTCGGCTCACTGCAAGCTCCGCCTCCTGGGTTTCAGCCATTCTCCTGCCTCAGCCTCCCC
GGGTCCGACCTCAAGTCACCCCGCTAGAGCCGAGTGACGTTTCGAGGCGGAGGACCCAAGTCGGTAAGAGGACGGAGTTCGGAGGGG

8755

PSEN1

PSEN1-201

PSEN1-201

AGCAGCTGGGACTACAGGCACACGCCGCCACGCCCGGCTAATTTTTGTATTTTTAGTAGCAACGGGGTTTCACCATGTTAGCCAG
TCGTGACCCCTGATGTCCGTGTGCGGCGGTGCGGGCCGATTAACAAACATAAAAATCATCGTTGCCCAAAGTGGTACAATCGGTC

8840

PSEN1

PSEN1-201

PSEN1-201

GATGGTCTCGATCTCCTGACCTTGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCTGG
CTACCAGAGCTAGAGGACTGGAACACTAGGCGGGCGGAGCCGGAGGGTTTCACGACCCTAATGTCCGCACTCGGTGGCGCGGACC

8925

PSEN1

PSEN1-201

PSEN1-201

CCGAGAATATCATTTTTTATAAAGAAGTCAAAGGTAATGAGGACTAAGTAAAACCATACAGTATTTGCTGTCTAAGATGTCATTA
GGCTCTTATAGTAAAAAATATTTCTTCAGTTTCCATTACTCCTGATTCATTTTTGGTATGTCATAAACGACAGATTCTACAGTAAT

9010

PSEN1

PSEN1-201

PSEN1-201

GTGACATTGAAGAGAGCAGTTTTTCAGTAGAGTGATAGAACCAGAAGCAGTACTCCAAAGGGAAGGTGCGTATGTTGTCATGTCATGT
CACTGTAACCTTCTCTCGTCAAAGTCATCTCACTATCTTGGTCTTCGTCATGAGGTTTCCCTTCCACGCATACACACGTACGTACA

9095

PSEN1

PSEN1-201

PSEN1-201

CTCTGTGTTTTGCCAGTGCTGGCAGTGGAAAGTGATGGTGTAGGCAGAGAATGGGTGGTGAAGAAGGAGAGGTATAGTAAATGTCA
GAGACACAAAACGGTCACGACCGTCACCTTCACTACCACATCCGTCTCTTACCCACCACTTCTTCTCTCCATATCATTTACAGT

9180

PSEN1

PSEN1-201

PSEN1-201

TGTA CTACATCAAAGATTCCTGTCTCACAGGCAGAGCAGGTGGTGACCTGACAGGAGAACAGGTTTCAGGAAAAGGTGTTTCAAGG
ACATGATGTAGTTTCTAAGGACAGAGTGTCCGTCTCGTCCACCACTGGACTGTCTCTTGTCCAAAGTCCTTTCCACAAAGTTCC

9265

PSEN1

PSEN1-201

PSEN1-201

AGAGGGAAGGTTCCATTTTATTTTATTTATTTATTTTTTTTTGAAACAGAGTCTTGCTCTGTTGCTCGGGCTAGAGTGCAGTGGTG
TCTCCCTTCCAAGGTAAAAATAAAATAAAATAAAAAAACTTTGTCTCAGAACGAGACAACGAGCCCGATCTCACGTCAACCAC

9350

PSEN1

PSEN1-201

PSEN1-201

TGATCTTGGCTCACTGCAACCCCCGCCTCCCAAGTTCAAGCAATGGTCTGTCTCAGCCTCCGGAGTAGCTGGGATTATAGGCAC
ACTAGAACCAGAGTGACGTTGGGGGCGGAGGGTTCAAGTTCGTTACCAGGACAGAGTCGGAGGCCTCATCGACCCTAATATCCGTG

9435

PSEN1

PSEN1-201

PSEN1-201

CCACCACCACATCCGGCTAATGTTTGTATTTTGTAGTAGAGTTGGGGTTTTCGCCACATTGGCCAGGCTGGCCTTGAACCTCCCCACC
GGTGGTGGTGTAGGCCGATTACAAACATAAAAAATCATCTCAACCCCAAAGCGGTGTAACCGGTCCGACCGGAACCTTGAGGGGTGG

9520

PSEN1

PSEN1-201

PSEN1-201

TCAAGTGATCCACCTGCCTCGGCCTCCCAAAGTGCTGGGATTACAGACGTGAGCCACTGCACCCGACCTGTTTTATTTTATTTTT
AGTTCACTAGGTGGACGGAGCCGGAGGGTTTTACGACCTAATGTCTGCACTCGGTGACGTGGGCTGGACAAAAATAAAATAAAAA

9605

PSEN1

PSEN1-201

PSEN1-201

GAGGTAAGTCTTGCTCTGTTGCCAGGCTGGAGTGCAGTGGCGCAATCTCAGCTCACTGCAACCTCCATCTCTCTGGGTTTCAGGCA
CTCCATTCAGAACGAGACAACGGGTCCGACCTCACGTCACCGCGTTAGAGTCGAGTGACGTTGGAGGTAGAGGACCCAAGTCCGT

9690

PSEN1

PSEN1-201

PSEN1-201

ATTCTCCTGCCTCAGCCTCCCGAGTAGTTGAGATTACAAGCATGCGCCACTATACCTGGCTAATTTTTTTTTTCCATATTTTTAG
TAAGAGGACGGAGTCGGAGGGCTCATCAACTCTAATGTTTCGTACGCGGTGATATGGACCGATTAAAAAAAAGGTATAAAAATC

9775

PSEN1

PSEN1-201

PSEN1-201

TTGAGCCACAGGTTGGGAGAAGGGAAAAATACATTCTACTCAAAGTGAGTCCGTGGCAAAGTGTGAGTACAGAGATGGGTGAGGA
AACTCGGTGTCCAACCCCTCTTCCCTTTTATGTAAGATGAGTTTCACTCAGGCACCGTTTTTCACACTCATGTCTCTACCCACTCCT

9860

PSEN1

PSEN1-201

PSEN1-201

ATTAGGACCAGACTTTCAGTCTGCAGCAACATTAACATGTATGTTAATTTAATACTCAGAAAGAAGCATTACTCTGTTTTAAA
TAATCCTGGTCTGAAAGTCAGACGTCGTTGTAATTTGTACATAACAATTAATATGAGTCTTCTTCGTAATGAGACAAAATTT

9945

PSEN1

PSEN1-201

PSEN1-201

ATATCTATCACATACTATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
TATAGATAGTGTATGATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

10,030

PSEN1

PSEN1-201

PSEN1-201

TTTTGAGACAGTCTTGCTCTGTCCAGGCTGGAGTGCAGTAGCGTGATCTCGACTCACTGCAAGCTCCACCTCCCGGGTTTCCAC
AAAACCTCTGT CAGAACGAGACAGTGGGTCGACCTCACGT CATCGCACTAGAGCTGAGTGCAGTTCGAGGTGGAGGGCCCAAGTG

10,115

PSEN1

PSEN1-201

PSEN1-201

GCCATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGACTCTAGGCGCCCGCCACCATGCCTGGCTAATTTTTTTGTATTTTTAGTAG
CGGTAAAGAGGACGGAGTCGGAGGGCTCATCGACCTGAGATCCGCGGGCGGTGGTACGGACCGATTAAAAAACATAAAAAATCATC

10,200

PSEN1

PSEN1-201

PSEN1-201

AGACGGGGTTTTACCGTGTTAGCCAGGATTGTCTCGATCTCTTGACCTCGTAATCTGCCCTCCTCGGCCTCCCAAAGTGCTGGGA
TCTGCCCCAAAAGTGGCACAATCGGTCCTAACAGAGCTAGAGAAGTGGAGCATTAGACGGGAGGAGCCGGAGGGTTTTACGACCCCT

10,285

PSEN1

PSEN1-201

PSEN1-201

TTACAGGCGTGAGCCACCGTGCCCGAGCCTATCATATATAATTTTTAAAACTCAACGTCTGTGCTCGCTTTAGCAGCACATAAT
AATGTCCGCACTCGGTGGCAGCGGTCGGATAGTATATATAAAAAATTTTGAGTTGCAGACACGAGCGAAATCGTCTGTATTATA

10,370

PSEN1

PSEN1-201

PSEN1-201

AGTAAAAATTGGAATGATACAGATGATTTGCATGTATTTTTTAAAAAGTTCTCAAGTCTATTTAATAACCACAGAATATGAGACAT
TCATTTTAAACCTTACTATGTCTACTAAACGTACATAAAAAAATTTTCAAGAGTTTCAGATAAATTATTGGTGTCTTATACTCTGTA

10,455

PSEN1

PSEN1-201

PSEN1-201

TCTGAGATGTTTTAGAAACAGTTCAACATATGTGGGAAAATAGGAGTATAAACCCCTTACCTCCTGTGTAGATCAGGTAGGTTCAA
AGACTCTACAAAATCTTTGTCAAGTTGTATACACCCTTTTATCCTCATATTTGGGAATGGAGGACACATCTAGTCCATCCAAGTT

10,540

PSEN1

PSEN1-201

PSEN1-201

GATTGCATCTGTTCTTTTGTAACTAAATGTCTGGTGAAGATTTGAGGATTTTATATAAATCATTGAGTTTGAGAGGTTTTTTTT
CTAACGTAGACAAGAAAACATTATGATTTACAGACCCTTCTAAACTCCTAAAATATATTTAGTAACTCAAACCTCTCCAAAAAAA

10,625

PSEN1

PSEN1-201

PSEN1-201

GTTTTTGTTTTTGAGATGGAGTTTCACTCTTGTGGCCAGGCTGAAGTGCAATGGCACAATCTCGGCTCACTGCAACCTCCGCCT
CAAAAACAAAACCTCTACCTCAAAGTGAGAACAACGGGTCCGACTTCACGTTACCGTGTTAGAGCCGAGTGACGTTGGAGGCGGA

10,710

PSEN1

PSEN1-201

PSEN1-201

CCCAGGTTCAAGCGATTCTCCTGCCTCGGCCTCCTGAGTAGCTGGGATTACAGACGCCTGCCACCACGCCAGCTAATTTTTTGT
GGGTCCAAGTTCGCTAAGAGGACGGAGCCGGAGGACTCATCGACCCTAATGTCTGCGGACGGTGGTGCGGGTCGATTAAAAAACA

10,795

PSEN1

PSEN1-201

PSEN1-201

ATTTTTGTATTTTGTAGAGAGAGGGTTTTACCATGTTGGCCAGGCTGGTCTCAAACCTTGTGACCTCAGGTGATCTACCCGCCT
TAAAAACATAAAAAATCATCTCTCTCCCAAAGTGGTACAACCGGTCCGACCAGAGTTTGAACACTGGAGTCCACTAGATGGGCGGA

10,880

PSEN1

PSEN1-201

PSEN1-201

CACCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCGCACCTGGCCTTCGTTTTGTTTTTCAACAGAATGTAAGAATTTTT
GTGGGAGGGTTTACGACCCTAATGTCCGTACTCGGTGGCGTGGACCGGAAGCAAAAACAAAAAAGTTGTCTTACATTCTTAAAAA

10,965

PSEN1

PSEN1-201

PSEN1-201

TCTTACATTTTTCTTACATTTTTAACAGAATGTAAGAAAACCAACGCAATGCCGATGAGTACTTTTTCCCTGAAGTGGATATA
AGAATGTAAAAAGAATGTAAAAATTGTCTTACATTCTTTTGGTGTTCGCTTACGGCTACTCATGAAAAAGGGACTTCACCTATAT

11,050

PSEN1

PSEN1-201

PSEN1-201

AGCATGAATATAAAAAGTTTTAAATCAGTCATCCTGGCTATTTGTTCTCTAAAAATCAATAAATAATTCTTTCATGCATTTTAAT
TCGTACTIONATTTTTCAAAAATTTAGTCAGTAGGACCGATAAACAAGAGATTTTAGTTATTTATTAAGAAAAGTACGTAAAATTA

11,135

PSEN1

PSEN1-201

PSEN1-201

ACTGTCTCCAGTTAAGGGTATTCAGTTTTGCAAAATGCTCTTACTGACAGGAAATGTATGAGCATTTTTTGTTTTTACTTCTGTC
TGACAGAGGGTCAATTCCCATAAGTCAAACGTTTTACGAGAATGACTGTCTTTACATACTCGTAAAAACAAAAAATGAAGACAG

11,220

PSEN1

PSEN1-201

PSEN1-201

GTTTGACAGAAAAAATATACACCTACTCTTTGAGCTAATTTATTCTTACCTAGTGGTCATTAGTAGAAGTGGTTCACTCTGGGAG
CAAACGTCTTTTTTATATGTGGATGAGAACTCGATTAAATAAGAATGGATCACCAGTAATCATCTTCACCAAGTGAGACCCCTC

11,305

PSEN1

PSEN1-201

PSEN1-201

CTTAAGTAGAAGGGAAACTAACAATTCCTTGAGGTAGATCATTATCTAAAGCTTTTTGATTTTCATATCAGTTGGGGGCGGGTA
GAATTGATCTTCCCTTTGATTGTTAAGGAACTCCATCTAGTAAAAATAGATTTTCGAAAAACTAAAGTATAGTCAACCCCGCCCAT

11,390

PSEN1

PSEN1-201

PSEN1-201

TATTATGTTAATTTTTAAATCTGCATATTTCCAGCCAGGCATGACTATAATCCCAGGACTTTGGGAGGTAGAAGCAGGAGGATT
ATAATACAATTAATAATTTAGACGTATAAAAAGGTCGGTCCGTACTIONATTTAGGGTCTGAAACCCTCCATCTTCGTCTCTCTAA

11,475

PSEN1

PSEN1-201

PSEN1-201

GCTTGAGCCCAGGAATTCAGACCACCCTAGACTACATTAATAAACATATTTTTTTGATTTATTTTTTATTTTATTTTTTTGAG
CGAACTCGGGTCTTAAGTTCTGGTGGGATCTGATGTAATTTTTTTGTATAAAAAACATAAATAAAAAATAAAAAAATAAAAAACTC

11,560

PSEN1

PSEN1-201

PSEN1-201

ACAGAGTTTTCGCTCTCATTGCCAGGCTGGAGTGCAATGGCACGATCTCGGCTCACCACAGCCTCCGCCTCCTGGATTCAAGCAA
TGTCTCAAAGCGAGAGTAACGGGTCCGACCTCACGTTACCGTGCTAGAGCCGAGTGGTGTCTGGAGGCGGAGGACCTAAGTTCGTT

11,645

PSEN1

PSEN1-201

PSEN1-201

TTCTCCTGCCTCAGCCTCCCGAGTCGCCGGGATTATAGACATGCACCACCACACCGGGCTAATTTTGTATTTTTAGTAGAGACAG
AAGAGGACGGAGTCGGAGGGCTCAGCGGCCCTAATATCTGTACGTGGTGGTGTGGCCCGATTAAAAACATAAAAAATCATCTCTGTC

11,730

PSEN1

PSEN1-201

PSEN1-201

GGTTTCTCCATGTTGGTCAGGCTGGTCTTGAACCTCTGACCTCAGGTGATCCACCCACCTCCGACTCCCAAAGTGCTGGGATTAC
CCAAAGAGGTACAACCAGTCCGACCAGAACTTGAGGACTGGAGTCCACTAGGTGGGTGGAGGCTGAGGGTTTCACGACCCTAATG

11,815

PSEN1

PSEN1-201

PSEN1-201

AGGTGTGAGCCACCATGCCTGGCCTTTTTTTTTTTTTTAATTTAAACGAAATCTGCTTATTTTCTGTTGATGTAAGGTGTTTG
TCCCACTCGGTGGTACGGACCGGAAAAAAAAAAAAAAAAAATTAAATTTGCTTTAGACGAATAAAAGGACAACCTACATTCCACAAAC

11,900

PSEN1

PSEN1-201

PSEN1-201

TGTTAAGGTGAAATGAAAAGTGATTTTTAAAAAATATTATTTTAGGACTATTTAACAAATATACTATTTATGATAATTAACATG
ACAATTCCACTTTACTTTTTCACTAAAAATTTTTTATAATAAAATCCTGATAAATTGTTTATATGATAAAATACTATTAATTGTAC

11,985

PSEN1

PSEN1-201

PSEN1-201

GGGTTAGCAAACCTACTGCTTGAAGCCAAATATGGCCCATGGCTTGTTTTTGTACAGCTTATAAGCTAAAAATGCTTTTTTACATTT
CCCAATCGTTTGATGACGAACTTCGGTTTATACCGGTACCGAACAAAAACATGTCGAATATTCGATTTTTTACGAAAAATGTAAA

12,070

PSEN1

PSEN1-201

PSEN1-201

AAAAAAAAAAAAAAAAAAGAACAAAGGAAGAATATGTGACACACAAAACCTGAAATGTTTACTCCCTGGCCATTTACAGAAAAAGTTAG
TTTTTTTTTTTTTTCTTGTTCCTTCTTATACACTGTGTGTTTTGGACTTTACAAATGAGGGACCGGTAAATGTCTTTTTCAATC

12,155

PSEN1

PSEN1-201

PSEN1-201

CTGGACATTGATTTTCATGTTACTATTAAGTCTGCTAAAAACAAAGGAGCTTGTAGCTATATTTTTTCATACTTGCATAAAGAAAGAA
GACCTGTAACATAAAAGTACAATGATAATTGACGATTTTGTTCCTCGAACATCGATATAAAAAAGTATGAACGTATTTCTTTCTT

12,240

PSEN1

PSEN1-201

PSEN1-201

AACCTAATAAATCGCTGGTGGCTTCATTTCCAAAAGGCTATGGAAATCCATAAACAGGCTGGGTGCAGTGGCTCATGCCTGTAAT
TTGGATTATTTAGCGACCACCGAAGTAAAGGTTTTCCGATACCTTTAGGTATTTGTCCGACCCACGTCACCGAGTACGGACATTA

12,325

PSEN1

PSEN1-201

PSEN1-201

CCTAGCACTTTGGGAGGCTGAGGCGGGAGGATTGCTTGAGCCCAAGGAGTTTGTAGTCTGGCCTGGGCAACGTAGTGAGACCCTGTT
GGATCGTGAAACCCCTCCGACTCCGCCTCCTAACGAACTCGGGTCTCAAACCTCAGACCCGACCCGTTGCATCACTCTGGGACAA

12,410

PSEN1

PSEN1-201

PSEN1-201

TTTAGAAAAAATGAAGATAAAAAACTAATCCATAAACCTCATACTTGGTGGTTGCCCTTCAGTTTTTCTTCTTTAGATCTGGATT
AAATCTTTTTTACTTCTATTTTTTGATTAGGTATTTGGAGTATGAACCACCAACGGGAAGTCAAAAAGAAGAAATCTAGACCTAA

12,495

PSEN1

PSEN1-201

PSEN1-201

TAGTTAAACAGTGTATTGCCTGCCTGGTTTCTGTAACTTTTGATCATTGGTTGGGTTATCCTATAATGAAACTTGGTTGACCT
ATCAATTTGTACATAACGGACGGACCAAAGACAATTGAAAACCTAGTAAACCAACCCAATAGGATATTACTTTGAACCAACTGGA

12,580

PSEN1

PSEN1-201

PSEN1-201

CAGAAATAACAAGGTGGTCGTTTCAGCTTCTTTGATTGTGTGTTTCTTTCATAAGTTCTTCAAGAAGCCTGAGTATTAGAAACATG
GTCTTTATTGTTCCACCAGCAAGTCAAGAACTAACACACAAAGAAAGTATTCAAGAAGTTCTTCGGACTCATAATCTTTGTAC

12,665

PSEN1

PSEN1-201

PSEN1-201

GATAAAATTATTGTGATAAAAAGCCAGAGAGACATAAATGTCAAGTATCTTGTTTTAAATTACTGTGACCAGGCCGGGCGTGGTG
CTATTTTAATAACACTATTTTTCGGTCTCTCTGTATTTACAGTTTCATAGAACAAATTTAATGACACTGGTCCGGCCCGCACCAC

12,750

PSEN1

PSEN1-201

PSEN1-201

GCTCACGCCTGTAATCCCAGCACTTTGGGAGGGCTGAGGCGGGCGGATCACGAGGTCAGGAGATCGAGACCATCCTGGCTAACACA
CGAGTGCGGACATTAGGGTCGTGAAACCCCTCCGACTCCGCCCGCCTAGTGCTCCAGTCTCTAGCTCTGGTAGGACCGATTGTGT

12,835

PSEN1

PSEN1-201

PSEN1-201

GTGAAACCCACCTCTACTAAAAAATAACAAAAATTAGCCAGGCATGGTGGCGGGCGCCTGTAGTCCCAGCTACTCGGGAGGC
CACTTTGGGGTGGAGATGATTTTTTTTATGTTTTTAAATCGGTCCGTACCACCGCCCGCGGACATCAGGGTCGATGAGCCCTCCG

12,920

PSEN1

PSEN1-201

PSEN1-201

TGAGGCAGGAGAATGGCGTGAACCCAGGAGACGGAGCTTGCAGTGAGCCGAGATCATGCCACTGTACTCCAGCCTGGGTGACAGA
ACTCCGTCTCTTACCGCACTTGGGTCCTCTGCCTCGAACGTCCTCGGCTCTAGTACGGTGACATGAGGTCGGACCCACTGTCT

13,005

PSEN1

PSEN1-201

PSEN1-201

GCAAGACTCTGTCTCAAAAAAAAAAAAAAAAAAAAAAAAAAATTACTGTGACCAGATTGGACTCAGCTTGCTGCTGGCATTGGTTCCC
CGTTCTGAGACAGAGTTTTTTTTTTTTTTTTTTTTTTTTAATGACACTGGTCTAACCTGAGTCGAACGACGACCGTAAACCAAGGG

13,090

PSEN1

PSEN1-201

PSEN1-201

ACCATAACCTCATATGTCATGTGTTTGCTTATATGTACTTTTGTGTTATTGTTGGTGTATCTTCAGGATAAGTTCCAAAATGTAA
TGGTATTGGAGTATACAGTACACAAACGAATATACATGAAAACACAATAACAACCACATAGAAGTCCTATTCAAGGTTTTACATT

13,175

PSEN1

PSEN1-201

PSEN1-201

TATTGCTGGGTTAAAGGATTAATGCACATGTAGTTTTATTAGATGTTACCAAATTTCCCTCCAGTGGGGATTATACCATTTTTCA
ATAACGACCCAATTTCCCTAATTACGTGTACATCAAAAATAATCTACAATGGTTTTAAAGGGAGGTCACCCCTAATATGGTAAAAAGT

13,260

PSEN1

PSEN1-201

PSEN1-201

TTCCTGCCTGAAATATATGAGAGAAGCACCATTTTTAAAGTTTTTACAATGTCTCTGAACTAAAATGTGGTAGAGATGCACATGTG
AAGGACGGACTTTATATACTCTCTTCGTGGTAAAATTTCAAAGTGTTACAGAGACTTGATTTTACACCATCTCTACGTGTACAC

13,345

PSEN1

PSEN1-201

PSEN1-201

TATATCTAGATCTAGATTGATATATTGATATACATGTATTTTTGTAGAAAGGGGCACAGAGGAGGCCTCTTGACTATCCCTATTAT
ATATAGATCTAGATCTAACTATATAACTATATGTACATAAAAAACATCTTCCCGTGTCTCCTCCGGAGAAGCTGATAGGGATAATA

13,430

PSEN1

PSEN1-201

PSEN1-201

GTTTATTGCTTTTAAACGTTTTTCTCACGCCGGGTTTAAACATGGTTTTAGCATTATTGAACATTCTAAAAATGAGACATAATAT
CAAATAACGAAAATTGCAAAAAAGAGTGCGGCCCAAATTTGTACCAAATCGTAATAACTTGTAAGATTTTTACTCTGTATTATA

13,515

PSEN1

PSEN1-201

PSEN1-201

GAAGGAAATTTACTCTGTGCATCTTTTGAATTATAATCACCATCTGAGGCTTTTGTGAGCTCCAGTTTGTCTGGAATTTAGAAC
CTTCTTTAAATGAGACACGTAGAAAACCTTAATATTAGTGGTAGACTCCGAAAACACTCGAGGTCAAACAGGACCTTAAATCTTG

13,600

PSEN1

PSEN1-201

PSEN1-201

ATTCAACTAGTCCAGCTATTGTTTCAGTGGAAATCTTGCTGGCCTGAACAGTTTTCTTCTGGTTCCTTTTTCAGGGACTAAAAATG
TAAGTTGATCAGGTCGATAACAAAGTCACCTTAGAACGACCGGACTTGTCAAAAGGAAGACCAAGGAAAAGTCCCTGATTTTTAC

13,685

PSEN1

PSEN1-201

PSEN1-201

ATGAAGAGTTTTGTGATAGCAGGTGCAGTTTTGAGTACTACAGTAAACATTCAGTTTCAGAACTTCTTCTCTTACCTGCTAAAACC
TACTTCTCAAAACACTATCGTCCACGTCAAACCTCATGATGTCAATTTGTAAGTCAAAGTCTTGAAGAAGAGAATGGACGATTTTTGG

13,770

PSEN1

PSEN1-201

PSEN1-201

AAAGAGAACCTTTTTTTTATTTTTACTTCTGATTGTTGAACAGTCTTAAGGCAGCATTAGGAAGACTGGCGATTTGTGTGGAGAA
TTTCTCTTGGAATAAAAAATGAAGACTAACAACCTTGTCAGAATTCGTCGTAATCCTTCTGACCGCTAAACACACCTCTT

13,855

PSEN1

PSEN1-201

PSEN1-201

ATGATGGCTTGTTGTTGTCTATGCATACTTTGTGTGTCCAGTGCTTACCTGGAATTTTGTCTTTCCCAACAGCAACAATGGTGTG
TACTACCGAACAACAACAGATACGTATGAAACACACAGGTCACGAATGGACCTTAAAACAGAAAGGGTTGTCGTTGTTACCACAC

13,940

PSEN1

PSEN1-201

PSEN1-201

290
S T M V W
ENSE00003979370

GTTGGTGAATATGGCAGAAGGAGACCCGGAAGCTCAAAGGAGAGTATCCAAAAATTCCAAGTATAATGCAGAAAAGTAGGTAACCTT
CAACCACTTATACCGTCTTCTCTGGGCCCTTCGAGTTTCTCTCATAGGTTTTTAAGGTTTCATATTACGTCTTTTCATCCATTGAA

14,025

PSEN1

PSEN1-201

295 L V N M A E G D P E 300 305 A Q R R V S K N S K Y N A E 315

ENSE00003979370

PSEN1-201

TTATTAGATAATATCTTGATTTTTTCAGGGTCACTGTTATAAGCTAACAGTATAGCAATGTTTTTATCGTCTTTCTTTGGTCATAG
AATAATCTATTATAGAAGCTAAAAAGTCCCAGTGACAATATTCGATTGTCATATCGTTACAAAAATAGCAGAAAAGAAACCAGTATC

14,110

PSEN1

PSEN1-201

PSEN1-201

ACTCCTTTGAGAATCTCTTGAGAACTATGATAATGCCAGTAAATACACAGATAAGTATTTAAGGAGTTCAGATACTCAAAACCC
TGAGGAAACTCTTAGAGAAGCTCTTGATACTATTACGGGTCAATTTATGTGTCTATTATAAATTCCTCAAGTCTATGAGTTTTGGG

14,195

PSEN1

PSEN1-201

PSEN1-201

AACAATACAGTCAAAGCATCCTAGGTTAAGACACCTCCCATTAATACAGAATACCAGCATGGAAAGGTTTCAGGCTGAGGTTATG
TTGTTATGTCAGTTTTCGTAGGATCCAATTCTGTGGAGGGTAATTTATGTCTTATGGTCGTACCTTTCCAAGTCCGACTCCAATAC

14,280

PSEN1

PSEN1-201

PSEN1-201

ATTTTGTGTTTTGTTTTTTGTTTTTTGTTTTTTATAAGTCATGATTTTAAAAAGAAAAAATAAACTCTCTCCAACATGTAAAAGTAAG
TAAAACAAAAAACAAAAACAAAAAATATTCAGTACTAAAATTTTTCTTTTTTATTTGAGAGAGGTTTGTACATTTTCATTC

14,365

PSEN1

PSEN1-201

PSEN1-201

AATCTCCTAAAAGAAACAAAAAAGAAACAGACAATAAAGGAAAAATAAGTAAACAAAAAAGCAAAATATAAACAAACATAAAAAAT
TTAGAGGATTTTCTTTGTTTTTTCTTTGTCTGTTATTTCTTTTTTATTCATTTGTTTTTTTCGTTTTATATTTGTTGATTTTTTA

14,450

PSEN1

PSEN1-201

PSEN1-201

GAGAACCTCTTGCTAACATGGCCAGAATAACTGAAATATGATTTGAGATGTGCTGATGTGTATACTGAGAAGATCAAAATATTCT
CTCTTGAGAACAGATTGTACCGGTCTTATTGACTTTATACTAAACTCTACACGACTACACATATGACTCTTCTAGTTTTATAAGA

14,535

PSEN1

PSEN1-201

PSEN1-201

AGGTGGATATGACTTTTTAGAAAGAGGATAAGAATGACTTAGGATGAGCTGGGTGCAGTGATGTGTGCCTGTAGTCCCAGCTACAT
TCCACCTATACTGAAAAATCTTCTCCTATTCTTACTGAATCCTACTCGACCCACGTCCTACTACACACGGACATCAGGGTCGATGTA

14,620

PSEN1

PSEN1-201

PSEN1-201

GGCCAAGGCAAGAGGATCACTTGAGCTAAGGAGTTCCGGATTACCCTGGGCAACTTATACCTTACCTCAAAAAATAATAATAATA
CCGGTTCGGTTCCTAGTGAACCTCGATTCCCTCAAGGCCTAATGGGACCCGTTGAATATGGAATGGAGTTTTTATTATTATTATT

14,705

PSEN1

PSEN1-201

PSEN1-201

TGAATAATAATAATGACTTAGGATAAGAGAGTGAAAGGCCCTCTAAGGATACTACAGAACATATTAAGGAGAACACAAGTTAGAA
ACTTATTATTACTGAATCCTATTCTCTCACTTTCCGGGAGATTCCCTATGATGTCTTGTATAATTCTCTTGTGTTCAATCTT

14,790

PSEN1

PSEN1-201

PSEN1-201

GTTGTTATTAGATGGAGTTGAGGGGGAGCTTTCATTCAGTTTTCTGGAATGGAGGCTACCTTCCCACACACACTAAAAAAAAA
CAACAATAATCTACCTCAACTCCCCCTCGAAAGTAAGTCAAAGACCTTACCTCCGATGGAAGGGTGTGTGTGATTTTTTTTTTT

14,875

PSEN1

PSEN1-201

PSEN1-201

GAAAGGGTTGAGGAATAACAGCACAATATAAATAGTCTAAAAAAGGGCTAACTTTTATGAGGAATCTGAAAAACAACAGGCACA
CTTTCCCAACTCCTTATTGTCGTGTTATATTTATCAGATTTTTTCCCGATTGAAAAACTCCTTAGACTTTTTGTTGTCCGTGT

14,960

PSEN1

PSEN1-201

PSEN1-201

GTAAATATTGGTGAGGAAAAAAGGCCTTAATTGAGTTGCTGTTTGTGTCAGGAAAGGGAGAGTTTATGTTTTATAAAGCCAGGAAA
CATTTATAACCACTCCTTTTTTCCGGAATTAAGTCAACGACAAACAGTCCCTTCCCTCTCAAATACAAAATATTTCCGGTCCTTT

15,045

PSEN1

PSEN1-201

PSEN1-201

TCTACAGAGTTAGCATTTAGGCAACTGCAAGGAAGATACTTTCAACCAGGAATTCCTATTTGGAACCTCAGAGATGTGAGTCTTTA
AGATGTCTCAATCGTAAATCCGTTGACGTTCCCTTCTATGAAAGTTGGTCCTTAAGGATAAACCTTGAGTCTCTACTCAGAAAT

15,130

PSEN1

PSEN1-201

PSEN1-201

TTATACAGTAAGCAAGGCAGCAGAACAAGGTCATGTTAGACTCTCACGGGATCCTTAGGGTGTGACTTTTGTAGCCAGAAACCTC
AATATGTCATTCGTTCCGTCGTCTTGTTCAGTACAATCTGAGAGTGCCCTAGGAATCCACACTGAAACGATCGGTCTTTGGAG

15,215

PSEN1

PSEN1-201

PSEN1-201

TGTGGCTGGTGGCACCTTTTCCTGAGATTTGCTCAGGCCCACTGGGCTCATTCCACCTACTCAGCCTAGCTGGCTATGCTTGGCT
ACACCGACCACCGTGGAAAAAGGACTCTAAACGAGTCCGGGTGACCCGAGTAAGGTGGATGAGTCGGATCGACCGATACGAACCGA

15,300

PSEN1

PSEN1-201

PSEN1-201

TTCTCTACCAGCTGGACCCCATGCCTGCCAAAGGCAAGCCAGGCATGGAGCAGCGAGGAGTGCATGAGCAAGTGAGTGCAGGGTC
AAGAGATGGTCGACCTGGGGTACGGACGGTTCCGTTCCGGTCCGTACCTCGTCGCTCCTCACGTACTCGTTCACCTCACGTCCCAG

15,385

PSEN1

PSEN1-201

PSEN1-201

CAGCCACTGCACACAGCCAGGCATGCTGGCTGCAGCAGGGCAGGCAGCCTCAGGTACTAGCTCCCTGCTGCAGCTAGACCAGGCA
GTCGGTGACGTGTGTCGGTCCGTACGACCGACGTCGTCCCGTCCGTGCGAGTCCATGATCGAGGGACGACGTCGATCTGGTCCGT

15,470

PSEN1

PSEN1-201

PSEN1-201

TTACCTAAGCAGCTTTGACTACAGGCCACTACCACTAGTAAACCTGATAGAAAAGTAAGAAATATACTGGAAAAGAAATTGCCACAA
AATGGATTTCGTCGAAACTGATGTCCGGTGATGGTGATCATTTGGACTATCTTTTCATTCTTTATATGACCTTTCTTAACGGTGTT

15,555

PSEN1

PSEN1-201

PSEN1-201

GCCTGGCTCTTGTGTTAACCTTGTGTTAACCTGGGGAACACAGGGGCACCCAGAAGCTTGGAGATGCCAGGAACTGCAGAACCCC
CGGACCGAGAACACAATTGGAACACAATTGGACCCCTTGTGTCCCGTGGGTCTTCGAACCTCTACGGTCTTGACGTCTTGGGG

15,640

PSEN1

PSEN1-201

PSEN1-201

AAAGAGGGGGGTCATAGCCCTGGCTTAGGGAACTCCTGAGTCTGGACTCCCCGAAGGGCCACATCTTCACTCCTCTCTTCTCT
TTTCTCCCCCAGTATCGGGACCGAATCCCTTGAGGACTCAGACCTGAGGGGCTTCCCGGTGTAGAGAAGTGAGGAGAGAAGAGA

15,725

PSEN1

PSEN1-201

PSEN1-201

CCTTCTCGCCACCTGCAACGTGGCAAGTGGGGGGGCACGTTTTTCAGCCCTGTTTGTCTTACGGTTCTTTCAATCCTGCCATTCAATG
GGAAGAGCGGTGGACGTTGCACCGTTCACCCCCCGTGCAAAGTCGGGACAAACAGAATGCCAAGAAAAGTTAGGACGGTAAGTTAC

15,810

PSEN1

PSEN1-201

PSEN1-201

GGTCCCAAGTTCTTGTCTGCATCCAGGAAGAATGAAGTACGTGGACAGCTGGAGGGAGAGCAAGATGAAAAGGTGCTTTATTGA
CCAGGGTTCAAGAACAGGACGTAGGTCCTTCTTACTTCATGCACCTGTGACCTCCCTCTCGTTCTACTTTTCCACGAAATAACT

15,895

PSEN1

PSEN1-201

PSEN1-201

GCAACAGTACAGCTCTCAGGAGACCCTATCTGCAGGCAGGTCGTCCCATTGTCTCTGCAGCTCTCAGTGGAGAGGAGACCTGGAG
CGTTGTCATGTGAGAGTCCCTCTGGGATAGACGTCCGTCCAGCAGGGTAACAGAGACGTGAGAGTACCTCTCCTCTGGACCTC

15,980

PSEN1

PSEN1-201

PSEN1-201

TGGGTAGCTCCTGTCTGCAGGCAGGTCATCCTGATGTCTGTAATCCTCAGTGGAGAGGAGACCCGGAATGGGTATCTCCTATCCA
ACCCATCGAGGACAGACGTCCGTCCAGTAGGACTACAGACATTAGGAGTCACTCTCCTCTGGGCCTTACCCATAGAGGATAGGT

16,065

PSEN1

PSEN1-201

PSEN1-201

CAAGCAGGTCATCCCATCATCTCTGCAGCCCTCAGTGGAGAGGAGACCCGAGTGGGTAGCTTCTTTCTGCAGGCAGGTTGTCCC
GTTCTGTCAGTAGGGTAGTAGAGACGTGCGGAGTCACTCTCCTCTGGGCCTCACCCATCGAAGAAAAGACGTCCGTCCAACAGGG

16,150

PSEN1

PSEN1-201

PSEN1-201

TTCATCTGCCCAAGTCTGACTGAGTCTGGGGTTTTTATGGGCTTCAGAGGGGAGGAAGTACATGCTGATGGGTCCATGGGTGGCC
AAGTAGACGGGTTGAGACTGACTCAGACCCCAAAAATACCCGAAGTCTCCCTCCTTCATGTACGACTACCCAGGTACCCACCGG

16,235

PSEN1

PSEN1-201

PSEN1-201

ATGAGCAGGCCCCAGAAAATGCACCATAAGTTCTCACTGTGGTCTGTGGAAGTGGGAGCTTGGCCTCCAGGCTTCAGGCTTTCCCT
TACTCGTCCGGGTCTTTTACGTGGTATTCAAGAGTGACACCAGACACCTTGACCCTCGAACCAGGAGGTCGAAGTCCGAAAGGGA

16,320

PSEN1

PSEN1-201

PSEN1-201

GACTTGAGGGTGGTGCCTTCACCAGGGAACTTCCCCTTTCCGCCTAGGAGCCTGTCTGCCTCCTGCTGCCATCAACCTGCTGTCTAT
CTGAACTCCACCACGAAGTGGTCCCTTGAAGGGGAAAGGCGGATCCTCGGACAGACGGAGGACGACGGTAGTTGGACGACAGATA

16,405

PSEN1

PSEN1-201

PSEN1-201

AGCTCCCATGGCACCCAGGCTGTTTCATGCCAAAGGGTGCCTGCAGGCCACGGTAAGCTGCCTTCAGCCCCTCCTCAGTCTCCCT
TCGAGGGTACCGTGGGTCCGACAAGTACGGTTTCCACGGACGTCCGGGTGCCATTTCGACGGAAGTCGGGGAGGAGTCAGAGGGA

16,490

PSEN1

PSEN1-201

PSEN1-201

CCCATGCTTGTTCAGCACCCAAAGTCCAGAGGGGGCCAAGGTGGCAGGGGGCTGGCATGTTCAGTGTGCCCCAAGCGCCCCGCACAC
GGGTACGAACAGTCGTGGGTTCAGGTCTCCCCGGTTCCACCGTCCCCGACCGTACAGTACAGACGGGGTTCGCGGGCGTGTG

16,575

PSEN1

PSEN1-201

PSEN1-201

CCGGCCAGGTCATGACAGCACCCAGCCTCAGCCACAACCTTTGCTCTGAAATCGGAGCCTGCAGACGCAAGGGGCTTCTGGACCC
GGCCGGTCCAGTACTGTCGTGGGTCCGAGTCGGTGTGAAACGAGACTTTAGCCTCGGACGTCTGCGTTCCCCGAAGGACCTGGG

16,660

PSEN1

PSEN1-201

PSEN1-201

CTGAGAGCACAGGGATGCCAGGTCTACAGCCACAGCTGGGAAGCTGCAGCTGTGGGAGTGCGGGACTTCTGCCCCACCAACTCA
GACTCTCGTGTCCCTACGGGTCCAGATGTCGGTGTGCGACCTTCGACGTGACACCCTCACGCCCTGAAGACGGGGTGGTTGAGT

16,745

PSEN1

PSEN1-201

PSEN1-201

GAAGGGGGCAGGACTCCCGCCTGTTCTGCTCCTGCCAGCTCACAGAGCATGCTGCCCCAGCTGCACCTCCCCTGCTGCAGCTG
CTTCCCCGTCCTGAGGGCGGACAAGGACCGAGGACGGTCGAGTGTCTCGTACGACGGGGTCGACGTGGAGGGGACGACGTCGAC

16,830

PSEN1

PSEN1-201

PSEN1-201

CCATCTTTGCAGCAGCCACTCCAGATGGGCGCTGCTGCCATCAAGACCACTAGTAAACCTGATAGAAAAGTAAGAAATATACTG
GGTAGAAACGTCGTCGGTGAGGTCTACCCGGCGACGACGGTAGTTCTGGTGATCATTTGGACTATCTTTTCATTCTTTATATGAC

16,915

PSEN1

PSEN1-201

PSEN1-201

GAAAGAATTGCCACAAGCCTGGCTCTTGTGTTAACCTGTGTTAAGCTAAAGAAAATCAAATGATTGTCTGTGAGCATGTAGGTAT
CTTTCTTAACGGTGTTTCGGACCGAGAACAATTGGACACAATTCGATTCTTTTAGTTTACTAACAGACACTCGTACATCCATA

17,000

PSEN1

PSEN1-201

PSEN1-201

ATATGTATGTGAGTGAGTGATAACAACAGAATTTCAATTCATTTTACAGATGTTGACTGAGCACCTGACTATGTGCTAGGCCCTGGG
TATACATACTCACTCACTATGTTGTCTTAAAGTAAGTAAAATGTCTACAACCTGACTCGTGGACTGATACACGATCCGGGACCC

17,085

PSEN1

PSEN1-201

PSEN1-201

GATATAGCACTGAACAAGATTTCCCTGCCCTTGTGGAGCTTATAGTCTATTTGGAGAGATAGATGGTCAACAAATTATTACATA
CTATATCGTGACTTGTCTAAAGGGGACGGGAACACCTCGAATATCAGATAAACCTCTCTATCTACCAGTTGTTTAAATAATGTAT

17,170

PSEN1

PSEN1-201

PSEN1-201

AATAATTCATACAGTTGTGATAGGTACTACAAAGAAGACGTATAAGTTGCTATGAAAGTTTATAATAGGGGAATTTTACGTATCC
TTATTAAGTATGTCAACACTATCCATGATGTTTCTTCTGCATATTC AACGATACTTTCAAATATTATCCCTTAAATGCATAGG

17,255

PSEN1

PSEN1-201

PSEN1-201

TGGAAGTCAAGGGGTGCTTCCCTGAGGAAGTGGTAATAGGGGACGGCCGCTGAAGGATGGAGGAAGAGCTTTCCAAGAGAGGG
ACCTTTCAGTTCCCCACGAAGGGACTCCTTCACCAATTATCCCTGCCGGGCGACTTCTTACCTCCTTCTCGAAAGGTTCTCTCCC

17,340

PSEN1

PSEN1-201

PSEN1-201

ACAACATGAGCAAGGGCTTTGAAATGAGAAGGCTGGATGAACTGCAGGCTTCTCAGTGAGAATGCTGCTGGTATTTTGGGGGGC
TGTTGTA CTGTTCCCGAAACTTTACTCTTCCGACCTACTTGACGTCCGAAGGAGTCACTCTTACGACGACCATAAAAACCCCCG

17,425

PSEN1

PSEN1-201

PSEN1-201

ACAGTTCTTTGTGGGACTTTCCCTCATATTGCAAGATATTTAACATCCCTGGCCCTCACCCACTAAATGCCAATAATGGCTTTA
TGTC AAGAAACACCCTGAAAGGGAGTATAACGTTCTATAAATTGTAGGGACCGGGGAGTGGGTGATTTACGGTTATTACCGAAAT

17,510

PSEN1

PSEN1-201

PSEN1-201

AGGCTTTGCAATAATCAAAAACTCCTCCATCCTAGTTATTTCCAAACACTCCCCGGAAGGGAGGTGCTATCCCTAGTTGAAAAAT
TCCGAAACGTTATTAGTTTTTGGAGGAGGTAGGATCAATAAAGGTTTGTGAGGGGCCTTCCCTCCACGATAGGGATCAACTTTTTTA

17,595

PSEN1

PSEN1-201

PSEN1-201

CACTGTGTTAACGGAACTAGAAGTTACATTGGAACAAAAGGGCATAGGGCTCCAAGAGGGATATCTGTGTAAGGAAAAACAAC
GTGACACAATTGCCTTGATCTTCAATGTAACCTTGTTCCTCGTATCCCGAGGTTCTCCCTATAGACACATTCCTTTTTTGTGTTG

17,680

PSEN1

PSEN1-201

PSEN1-201

AAAAGAACTGAGAGATTACCTGATGTGGTTGAGCTCTGTGAGAGCATTTCAGGATAAATTAGTCATAGATAATAATATAAAATTC
TTTTCTTGACTCTCTAATGGACTACACCAACTCGAGACAGTCTCGTAAAGTCCATTTAATCAGTATCTATTATTATATTTAAG

17,765

PSEN1

PSEN1-201

PSEN1-201

ATCAGTGGAAAAAATGAGGCAGTTTTCCAAAGAAAAACAAAACTTGCTCAAAAAAGCAAATGTAATTATAGTATATTCTGGCTA
TAGTCACCTTTTTTACTCCGTCAAAGGTTTCTTTTGTGTTTGAACGAGTTTTTTCGTTTACATTAATATCATATAAGACCGAT

17,850

PSEN1

PSEN1-201

PSEN1-201

TAGCAAAGTAGTTTAGTTGTGAATATTATTTGCATAGTGAGAATATAAAGCTGAATTTAATATAAGGTTATGGCACTGGGAAGAC
ATCGTTTTATCAAATCAACACTTATAATAAACGTATCACTCTTATATTTTCGACTTAAATTATATTCCAATACCGTGACCCCTTCTG

17,935

PSEN1

PSEN1-201

PSEN1-201

AGGAAGAGTTACATTTGCGTGCACTAAAGGATGAGACCTAATGCTTTATCTTCTCTATAGGAGGTGAATAAGTACCTCAAATTAA
TCCTTCTCAATGTAAACGCACGTGATTTCTACTCTGGATTACGAAATAGAAGAGATATCCTCCACTTATTCATGGAGTTTAATT

18,020

PSEN1

PSEN1-201

PSEN1-201

AACATCAAGTTATGGCACAATGAGCATGCTACTTATAATTAATTATGGAGGTAAATACCAAAGGGATGGCTAAAAGAGTTTAAG
TTGTAGTTCAATACCGTGTTACTCGTACGATGAATATTAATTAATACCTCCATTTATGGTTTTCCCTACCGATTTTCTCAAATTC

18,105

PSEN1

PSEN1-201

PSEN1-201

GTAGGAATGAGTATCAGAAAGTGAGGAGGGGAGGGGGTAGAAAAAGGGACTGCTGTTTTTCATTTATAAATCTTATTCTTATATTATTT
CATCCTTACTCATAGTCTTCACTCCTCCCTCCCCCATCTTTTCCCTGACGACAAAAAGTAAATATTTAGAAATAAGAATATAATAAA

18,190

PSEN1

PSEN1-201

PSEN1-201

CATAAACTCCAAACCAGAGAAGATTCAGGTTTTTGGAGATCTGGATAATAAAAAAGAATACAAAACCTATCAATACAAAATTGTGAG
GTATTTGAGGTTTGGTCTCTTCTAAGTCCAAAAACCTCTAGACCTATTATTTTTCTTATGTTTTGATAGTTATGTTTTAACACTC

18,275

PSEN1

PSEN1-201

PSEN1-201

GGCTCTCCAGAGGAAGCCATGCAAGGAAGGGCCCTGAAGCTTACAAGCTTTACTTATTCATGGCAAATCTACTTCTGCTCTGAA
CCGAGAGGGTCTCCTTCGGTACGTTCTTCCCGGGACTTCGAATGTTCGAAATGAATAAGTACCGTTTAGATGAAGACGAGACTT

18,360

PSEN1

PSEN1-201

PSEN1-201

CATGTATTACTTTTATAAAAAATGAAGGAAGAATAAAAGTACTTTGAACTTCACTTATATATTTTAATTATTTTTAATGTATGGA
GTACATAATGAAAATATTTTTTACTTCTTCTTATTTTCATGAACTTGAAGTGAATATATAAAATTAATAAAAAATTACATACCT

18,445

PSEN1

PSEN1-201

PSEN1-201

AGTTTTTTAAGACTATCATGCTCACCATTTTTCAATGAGATTGATAGTCATTATAATGAAATGACTGGCCCATAAAGACATTCACT
TCAAAAAATTCTGATAGTACGAGTGGTAAAAGTTACTCTAACTATCAGTAATATTACTTTACTGACCGGGTATTTCTGTAAGTGA

18,530

PSEN1

PSEN1-201

PSEN1-201

CCCCGCTCCTTTCCCAATCCACCCTCCAGAATGAAGCCACTTTTATAATTTTGTACCAAATCCAGGGATGAGTGCCAACAGTTA
GGGGCGAGGAAAGGGTTAGGTGGGAGGTCTTACTTCGGTGAAAATATTA AACAGTGTTTAGGTCCCTACTCACGGTTGTCAAT

18,615

PSEN1

PSEN1-201

PSEN1-201

GGAAGCTTTTCAGTTGCAAAAAGATAAAAAGCCCAACTCAGTTGCCTTAAACAAAGAAGAAATTTATTCTTTTCACGTGACAGGAAGG
CCTTCGAAAGTCAACGTTTTCTATTTTTTCGGGTTGAGTCAACGGAATTTGTTTCTTCTTTAAATAAGAAAGTGCCTGCTTCC

18,700

PSEN1

PSEN1-201

PSEN1-201

CCTGAGGTGTAGGCATTTGAAATTTGTAGGGTTGGTTAATTTGGTGGCTCAGGGATGTTTTCAAGTAGCCCAACTTCCTACTCTA
GGACTCCACATCCGTA AACCTTTAAACATCCCAACCAATTA AACACCAGTCCCTACAAAAGTTCATCGGGTTGAAGGATGAGAT

18,785

PSEN1

PSEN1-201

PSEN1-201

CCATCACTAGTTTATAGGCTTGGTCTTCAGCCCACTGCTCTTCGTGGTCATGACAGCTGTAGTTCTAGGCATCATGTCTAGATAA
GGTAGTGATCAAATATCCGAACCAAGTCCGGGTGACGAGAAGCACCAGTACTGTGACATCAAGATCCGTTAGTACAGATCTATT

18,870

PSEN1

PSEN1-201

PSEN1-201

GGCAACATTCAGGGGTAGAAGGGGACTGTTTATTTTTCTTTAGTCTCTCTTAAAGAGTGAGAAAAATTTCCAGGAATCCCG
CCGTTGTAAGTCCCATCTTCCCTGACAAATAAAAAAGGAAATCAGAGAGAATTTCTCACTCTTTTTAAAAGGGTCTTAGGGC

18,955

PSEN1

PSEN1-201

PSEN1-201

GTGGACTTTGCTTCACCACTCATAGGTTTCATACCAAGTTACAACCCACAACTTAGAGCTTTTGTAGGAAGAGGCTTGGTGGG
CACCTGAAACGAAGTGGTGAGTATCCAAGTATGGTTCAATGTTGGGGTGTGGAAATCTCGAAAACAATCCTTCTCCGAACCAACC

19,040

PSEN1

PSEN1-201

PSEN1-201

ATTACCGTGCTTGGCTTGGCTTGGTCAGGATTCACCACCAGAGTCATGTGGGAGGGGGTGGGAACCCAAACAATTCAGGATTCTG
TAATGGCACGAACCGAACCGAACCAAGTCCTAAGTGGTGGTCTCAGTACACCCTCCCCACCCCTTGGGTTTGTAAAGTCCTAAGAC

19,125

PSEN1

PSEN1-201

PSEN1-201

CCCTCAGGAAATAAAGGAGAAAATAGCTGTTGGATAAACTACCAGCAGGCACTGCTACAGCCCATGCTTTGTGGTTTTAAGGGCCA
GGGAGTCTTTATTTCTCTTTTATCGACAACCTATTTGATGGTTCGTCGATGTCGGGTACGAAACACCAAAATTCCTGGT

19,210

PSEN1

PSEN1-201

PSEN1-201

GCTAGTTACAATGACAGCTAGTFACTGTTTCCATGTAATTTCTTAAAGGTATTAATTTTTCTAAATATTAGAGCTGTAACCTTC
CGATCAATGTTACTGTGATCAATGACAAAGGTACATTAAGAATTTCCATAATTTAAAAGATTTATAATCTCGACATTGAAG

19,295

PSEN1

PSEN1-201

PSEN1-201

CACTTTCTCTTGAAGGCACAGAAAGGGAGTCACAAGACACTGTTGCAGAGAATGATGATGGCGGGTTTCAGTGAGGAATGGGAAGC
GTGAAAGAGAACTTCCGTGTCTTTCCCTCAGTGTTCTGTGACAACGTCTCTTACTACTACCGCCCAAGTCACTCCTTACCCCTTCG

19,380

PSEN1

PSEN1-201

S T E R E S Q D T V A E N D D G G F S E E W E A
ENSE00003979376

PSEN1-201

CCAGAGGGACAGTCATCTAGGGCCTCATCGCTCTACACCTGAGTCACGAGCTGCTGTCCAGGAACTTTCCAGCAGTATCCTCGCT
GGTCTCCCTGTCAAGTAGATCCCGGAGTAGCGAGATGTGGACTCAGTGCTCGACGACAGGTCCTTGAAAGGTCGTCATAGGAGCGA

19,465

PSEN1

PSEN1-201

Q R D S H L G P H R S T P E S R A A V Q E L S S I L A
ENSE00003979376

PSEN1-201

GGTGAAGACCCAGAGGAAAGTATGTGCATTTCTCTATGTTGCAAAGTCATGGATTCTTTAGGTAGCTACATTATCAACCTTTTT
CCTTCTGGGTCTCCTTTCATACACGTAAAGAGATACAACGTTTCAGTACCTAAGGAAATCCATCGATGTAATAGTTGGAAAAA

19,550

PSEN1

PSEN1-201

G E D P E E
ENSE00003979376

PSEN1-201

GAGAATAAAATGAATTGAGAGTGTTACAGTCTAATTCTATATCACATGTAACCTTTTATTTGGATATATCAGTAATAGTGCTTTTT
CTCTTATTTTACTTAACTCTCACAAATGTCAGATTAAGATATAGTGACATTGAAAATAAACCTATATAGTCATTATCACGAAAAA

19,635

PSEN1

PSEN1-201

TTTGGAGACAGAGTCTCGCTCTGTCGCCAGGTTGGAGTGCAATGGTGCGATCT
AAACTCTGTCTCAGAGCGAGACAGCGGTCCAACCTCACGTTACCACGCTAGA

19,720

PSEN1

PSEN1-201

TGGCTCACTGCAAGCTCCACCTCCCAGGTTCAAGTGATTCTCTGCTCAGCCTCCCAAGTAGCTGGGACTACAGGCCTGCGCCA
ACCGAGTGACGTTGAGGTTGGAGGGCCCAAGTTCACCTAAGAGGACGGAGTCGGAGGGTTCATCGACCCTGATGTCCGCACGCGGT

19,805

PSEN1

PSEN1-201

CCACGCCTGGATAATTTTTGTATTTTTAGTAGAGATGGGGTTTTACCATCTTGGGCAGGCTGGTCTTGAACCTCCTGACATCATGA
GGTGCGGACCTATTA AAAACATA AAAATCATCTTACCCCAAAGTGGTAGAACCCGTCCGACCAGA AACTTGAGGACTGTAGTACT

19,890

PSEN1

PSEN1-201

PSEN1-201

TCTGCCTGCCTTAGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACTGTACCTGGCCTCCCTTCAGACTTTTTAAGTTGGCA
AGACGGACGGAATCGGAGGGTTTTACGACCCTAATGTCCGCACTCGGTGACATGGACCGGAGGGAAGTCTGAAAAATTCAACCGT

19,975

PSEN1

PSEN1-201

PSEN1-201

TTTTACAGCCTGACCTTTTTGGCATTATTTTTATAAAGTAAAAGATTTGTTTTTTTTAATTGTTCCAGTAAGCCTTCATGGCCGTAA
AAAATGTCGGACTGGAAAACCGTAAATAAAAATATTTTCATTTTCTAAACAAAAAAATTAACAAGGTCATTTCGGAAGTACCGGCATT

20,060

PSEN1

PSEN1-201

PSEN1-201

TACATTTGTCTACAAAAATTTTATTAATATGTCTCACTCTGCTGTAGAGAGATCTGTGGATTTGCATGATACAACCTTGTACATT
ATGTAACAGATGTTTTTAAAATAATTATACAGAGTGAGACGACATCTCTCTAGACACCTAAACGTACTATGTTGGAACATGTAA

20,145

PSEN1

PSEN1-201

PSEN1-201

ATTATTCCTTTTGTGACAAGTGCTATATTTTATTTTAAAGAAAATCAAAGGGATTTAGGATATTGGCAGAAATGCAAGTATTTTC
TAATAAGGAAAACAACCTGTTTCACGATATAAAAATAAAATTTCTTTTAGTTTCCCTAAATCCTATAACCGTCTTTACGTTTCATAAAG

20,230

PSEN1

PSEN1-201

PSEN1-201

TTCAGTGTCTAAGATGTGTTGCCACTTGATGGATTTAAGTTAACACTTAGGGCTTCTTAGGAACATTATCAGCCACTAAAGCCCT
AAGTCACAGATTCTACACAACGGTGAACCTAACCTAAATTCATTGTGAATCCCGAAGAATCCTTGTAATAGTCGGTGATTTTCGGGA

20,315

PSEN1

PSEN1-201

PSEN1-201

TTGGTTAGGGCTCAGTCATCTCTTCAGTTAGTCTTAGAGATGTGGTTTCATTGAATAAGACTTTAGCATATTTTCCAACCAAGTTA
AACCAATCCCGAGTCAGTAGAGAAGTCAATCAGAATCTCTACACCAAGTAACTTATTCTGAAATCGTATAAAAAGGTTGGTTCAAT

20,400

PSEN1

PSEN1-201

PSEN1-201

TTTTTGGTTGTCTTGTTTTTGCAAGAGTGAAACTTGATTAAAACATTACAACAAGAATATTAAGTAGTTTTAAGGAAACAAACAC
AAAAACCAACAGAACAAAAACGTTCTCACTTTGAACTAATTTGTAAATGTTGTTCTTATAATTCATCAAAATTCCTTTGTTTGTG

20,485

PSEN1

PSEN1-201

PSEN1-201

CTAGGTTCCCTTAGCATCTTTAATCATTAGTCACTAATTATTATGACCTTGACATATCCATCAGTTTGAGGAGAACACTTTTTTACA
GATCCAAGGAATCGTAGAAATTAGTAATCAGTGATTAATAATACTGGAAGTGTATAGGTAGTCAAACCTCTTGTGAAAAATGT

20,570

PSEN1

PSEN1-201

PSEN1-201

CCTTGTCCCTCAGTTTTTTAACTGAGTCAGAACTTTCACTGGGCATGTTTCATGACTTTACTGCTTGGCTGAGTTTTCCAGATATCA
GGAACAGGAGTCAAAAAATTGACTCAGTCTTGAAAAGTGACCCGTACAAGTACTGAAATGACGAACCGACTCAAAAAGGTCTATAGT

20,655

PSEN1

PSEN1-201

PSEN1-201

AAGCCAGCTGCAGCCTGTGACTTTACACTCCTGGAAAAGTAGACGTATCTGCCTGCTCTTACAGCAGGCTTTAGCTTGCCTTT
TTCGGGTCGACGTCGGACACTGAAAAGTGTGAGGACCTTTTCATCTGCATAGACGGACGAGAATGTCGTCCGAAATCGAACGGAAA

20,740

PSEN1

PSEN1-201

PSEN1-201

GCTGGGACTTTGTTCTGCCCTCAGTTACCACAGTAATTAGGTTGCCTCTTCTACTTTCTCTTTTCTCACAGGCACCAGGAGCCA
CGACCCTGAAACAAGACGGGAGTCAATGGTGTCAATTAATCCAACGGAGAAGATGAAAGGAGAAAAGAGTGTCCGTGGTCTCCTCGGT

20,825

PSEN1

PSEN1-201

PSEN1-201

GAGGAAATAACATAATAGTTGTTGACCAGAGCAGCAGCATAATTCTTTCATGACTGCCTTTTCTAATTTGACGATTCCCTCTCCT
CTCCTTTATTGTATTATCAACAACCTGGTCTCGTCTCGTATTAAAGAAAGTACTGACGGAAAAGATTAAACTGCTAAGGGAGAGGA

20,910

PSEN1

PSEN1-201

PSEN1-201

GAGAGGGCTCTTTGTGTCTCCTCCTCTTTCGTCTCCAACTTTTAAAAAAAAAAAAAGTGAAACTATCAAGTATTGCTCCTGCTAAC
CTCTCCCGAGAAAACACAGGAGGAGGAGAAGCAGAGGTTGAAAATTTTTTTTTTTTCACTTTGATAGTTTCATAACGAGGACGATTG

20,995

PSEN1

PSEN1-201

PSEN1-201

TTCAGATCAGTATTTTCTTCTCTGAAGCCAATGCAAAGTAATAACGGACGTGCTTCATCATCTTAGCATTTCAGCACACGTGTCA
AAGTCTAGTCATAAAAGAAAGAGACTTCGGTTACGTTTCATTATTGCCTGCACGAAGTAGTAGAATCGTAAGTCGTGTGCACAGT

21,080

PSEN1

PSEN1-201

PSEN1-201

CCATCTCTGATGGTGTGAGCATGTTAAACCAGACTTGTGGGTACTTACCAAAAAGGTTTCAGTTGACACTATAGGTCAGTTGCTAAA
GGTAGAGACTACCACACTCGTACAATTTGGTCTGAACACCCATGAATGGTTTTTCCAAGTCAACTGTGATATCCAGTCAACGATTT

21,165

PSEN1

PSEN1-201

PSEN1-201

AGGCACAAATGTCTTCTAAAGCAATCTGTTAAAAGTCAACATTTAACATTTAATTAGAAAAGTCAAGGATCTGAATGTTTA
TCCGTGTTTACAGAAGATTTTCGTTAGACAATTTTCAGTTGTAATTTGTAATTAATCTTTTGACTAGTTTCCCTAGACTTACAAAT

21,250

PSEN1

PSEN1-201

PSEN1-201

GTTCTCCCAAGAAAATGTAAAAATGATCTGTAAACACATAAAAAGATACTCAGCATCATTAGCCATCAAGGAAATGCAAATCAA
CAAGAGGGTTCTTTTACATTTTACTAGACATTTGTGTATTTTCTATGAGTCGTAGTAATCGGTAGTTCCCTTACGTTTAGTTT

21,335

PSEN1

PSEN1-201

PSEN1-201

ACCACTTCATACTCACTAGATTGGCTATAATAAAAAAGATAGACAATAACAGGTGTTGGTGAGGATGCGAAGAAAAGTGGAAATCCT
TGGTGAAGTATGAGTGATCTAACCGATATTATTTTTCTATCTGTTATTGTCCACAACCACTCCTACGCTTCTTTGACCTTAGGA

21,420

PSEN1

PSEN1-201

PSEN1-201

CATACACTGCTGGTGGGAATGTAAAAATAGTATAGTGATTTTTGGAAAACAGTTCGGTAGTTCTTTGAAAAGATTAAATATGACCCGG
GTATGTGACGACCACCTTACATTTTATCATATCACTAAAACCTTTTGTCAAGCCATCAAGAAAAGTTTCTAATTTATACTGGGCC

21,505

PSEN1

PSEN1-201

PSEN1-201

TAATTCTACTCCTAGGTATATACTCAAGAGAATTTTAAAACATATGTCAACACAAAGACACATATACAATGGTCATAGTAATATT
ATTAAGATGAGGATCCATATATGAGTTCTCTTAAAATTTTGTATACAGTTGTGTTTCTGTGTATATGTTACCAGTATCATTATAA

21,590

PSEN1

PSEN1-201

PSEN1-201

GTTCATAACAGGTAAAAACAGAAACAACCCACATGTCTATTAAGTATAAGTGGATAATAAATGTGGTATATTCATACAATGGAA
CAAGTATTGTCCATTTTGTCTTTGTTGGGTGTACAGATAATTGACTATTACCTATTATTTACACCATATAAGTATGTTACCTT

21,675

PSEN1

PSEN1-201

PSEN1-201

TATTACTTGGTTATAAAAAAGAAACAATCTATCATTAGTAGTACACTTAGGATGAGCTTGTTACTGGCATGTTGGCTGTGGGAAGTATA
ATAATGAACCAATATTTTTCTTTGTTAGATAGTAATCATGTGAATCCTACTCGAACAATGACCGTACAACCGACACCCCTTCATAT

21,760

PSEN1

PSEN1-201

PSEN1-201

TCTTGAAATTCACTAAAAGACCAACTATTGCTGGGCGCAGTGGCTCAAGCACCTGTAATCCCAGCACTTTGGAAGGCCAAGGCAG
AGAACTTTAAGTGATTTTTCTGGTTGATAACGACCCGCGTCACCGAGTTCGTGGACATTAGGGTCGTGAAACCTTCCGGTTCCGTC

21,845

PSEN1

PSEN1-201

PSEN1-201

GCGGACCACCTGAGATCAGGAGTTTCGAGACCAGCCCAACCAACATGGAGAAACCCACCTCTACTAAAAATACAAAATTAGCCCA
CGCCTGGTGGACTCTAGTCCTCAAGCTCTGGTCGGGTTGGTTGTACCTCTTTGGGGTGGAGATGATTTTTATGTTTTAATCGGGT

21,930

PSEN1

PSEN1-201

PSEN1-201

TTGTGGTGGCACATGCCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGTGGAGGTTGCAGT
AACACCACCGTGTACGGACATCAGGGTCGATGAGTCTCCGACTCCGTCCTCTTAGTGAACCTGGACCTCCACCTCCAACGTCA

22,015

PSEN1

PSEN1-201

PSEN1-201

GAGCTGAGATCATACCATTGCACTCCAGCCTGGGCAACAAGAGCGAACTCCATCTCAAAAAAAAAAAAAAAAAAGACCAACTACC
CTCGACTCTAGTATGGTAACGTGAGGTCGGACCCGTTGTTCTCGCTTTGAGGTAGAGTTTTTTTTTTTTTTTTTTTTCTGGTTGATGG

22,100

PSEN1

PSEN1-201

PSEN1-201

TTCACAATAAATAAAAAATGTCTTACATTTCTAATTAATAATTTTTGTTTCAGTTTTATTATTTCAGCTTTAAAAAGGAAGGGAATTCT
AAGTGTTATTTATTTTACAGAATGTAAAGATTAATTTTAAAAACAAGTCAAAAATAATAAGTCGAAATTTTTCTTCCCTTAAGA

22,185

PSEN1

PSEN1-201

PSEN1-201

GACATGTTACAACATGAATAAATCTTGAGTACTTTGTGCTAAGTGAAATAAGCTAGTTACAAAAAGAAAAATACTGTATGATTCC
CTGTACAATGTTGTACTTATTTAGAACTCATGAAACACGATTCACTTTATTCGATCAATGTTTTCTTTTTATGACATACTAAGG

22,270

PSEN1

PSEN1-201

PSEN1-201

ACTTACATCAGAGTAGTCAGAAAAGTAGACTGGTGGTTGCCAGGGGTTAAGGGGAGGGGAAATGAAGGGTCGTTTAATGGGTGTAG
TGAATGTAGTCTCATCAGTCTTTTCATCTGACCACCAACGGTCCCAATTCCCCTCCCCTTTACTTCCCAGCAAATTACCCACATC

22,355

PSEN1

PSEN1-201

PSEN1-201

AGTTTCAGTTTTTACAAGATGAAAAGAGTTCTGTGGATGGACGATGGTAATGGTAGCACAATGATACGATTATACCTAGTGTCTTT
TCAAAGTCAAATGTTCTACTTTTCTCAAGACACCTACCTGCTACCATTACCATCGTGTTACTATGCTAATATGGATCACAGAAA

22,440

PSEN1

PSEN1-201

PSEN1-201

GAACGGTGAACCTTAAAAAGGGTTAAGATGTTAACTTGATGGGTATCTTACCACAGTTAAATTTTTATTATTTTTTTATTTTTTG
CTTGCCACTTGAATTTTTCCCAATTCTACAATTTGAACTACCCATAGAATGGTGTCAATTTAAAAATAATAAAAAATAAAAAAC

22,525

PSEN1

PSEN1-201

PSEN1-201

AGACAATTTTCGCTCGTTGCCTAGGGTGGAGTGCAGTGCTGGGATCTCAGCTCACTGCAACTCTGCCTCCCAGGTTCAAGCGATAC
TCTGTTAAAGCGAGCAACGGATCCCACCTCACGTACGACCCCTAGAGTCGAGTGACGTTGAGACGGAGGGTCCAAGTTCGCTATG

22,610

PSEN1

PSEN1-201

PSEN1-201

TCCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGCACACATCACCATACCCGGCTAATTTTTATATTTTTTAGTAGAGACAAGG
AGGACGGAGTCGGAGGGGCTCATCGACCCTGATGTCCGTGTGTAGTGGTATGGGCGGATTAATAATAATAATAATCATCTCTGTTCC

22,695

PSEN1

PSEN1-201

PSEN1-201

TTTCACCATGTTGGCCAGGCTGGTCTTGAACCTCCTGACCTCAAGTGATCTGCCACCTCAGCCTCCCAGAGTGCTGGGATTACAG
AAAGTGGTACAACCGGTCCGACCAGAACTTGAGGACTGGAGTTCCTAGACGGGTGGAGTCGGAGGGTCTCACGACCCTAATGTC

22,780

PSEN1

PSEN1-201

PSEN1-201

GTGTGAGCCACTGTGCCCGGCCAAAAAATTTTTTTAAATACCGTTAAGAAGTGGAAAATAAGGCCAGGTGTGGTGGCTCACAC
CACACTCGGTGACACGGGCGGTTTTTTTTAAAAAATTTATGGCAATTCCTCACCTTTTATTCCGGTCCACACCACCGAGTGTG

22,865

PSEN1

PSEN1-201

PSEN1-201

CTGTAATCCCAGCACTTTGGGAGACCAAGGTTGGTGGATCACCTGAGGTTTGGAGTTTGAGACCAGCCTGGCCAACATGGTAAAA
GACATTAGGGTCGTGAAACCTCTGGTTCCAACCACCTAGTGGACTCCAACCTCAAACCTCTGGTCGGACCGGTTGTACCATTTT

22,950

PSEN1

PSEN1-201

PSEN1-201

CCTCATATCTACTAAAAATACAAAATTAGCCGGGCGTGGTGGCGCATGTCTGTAATCCCAGCTATTCGAGAGGCTGCGGCAGGAT
GGAGTATAGATGATTTTTATGTTTTAATCGGCCCGCACCACCGCGTACAGACATTAGGGTCGATAAGCTCTCCGACGCCGTCTTA

23,035

PSEN1

PSEN1-201

PSEN1-201

AATTGCTTGAAATCGGGAGGTGGAGGTTTCAGTGAGCCGAGATCACTTAAAAAAAAAAGGAAAAATAAGCTACCAGCTGAGAGAA
TTAACGAACTTTAGCCCTCCACCTCAAAGTCACTCGGCTCTAGTGAATTTTTTTTTTCTTTTATTTCGATGGTCGACTCTCTT

23,120

PSEN1

PSEN1-201

PSEN1-201

AATATATGCAAATCATATTGAAGTCCTGTTAAAGGACTTGTATTTAGGATATATAAAGGATGCTTACAACCTAATACGAAGACGA
TTATATACGTTTAGTATAACTTCAGGACAATTTCTGAACATAAATCCTATATATTTCTACGAATGTTGAATTATGCTTCTGCT

23,205

PSEN1

PSEN1-201

PSEN1-201

TAGCCCAAATTTAAGATAGGGAAATGCTTTGACTAGACATTCTACCAAAGAGATATATAATGGCTAAAAAGCACATGAAAAGAT
ATCGGGTTTTAAATTTCTATCCCTTTACGAAACTGATCTGTAAGATGGTTTTCTCTATATATTACCGATTTTTTCGTGTACTTTTCTA

23,290

PSEN1

PSEN1-201

PSEN1-201

GCTCAACATCATTAAATCAGAGTGGCTAGAATGAAAAAGGCTAACAATACCAAGAGCTGGTGAGGATGTGAAAAACTGGAACCTCT
CGAGTTGTAGTAATTAGTCTCACCGATCTTACTTTTTCCGATTGTTATGGTTCTCGACCACTCCTACACTTTTTTGACCTTGAGA

23,375

PSEN1

PSEN1-201

PSEN1-201

CAATTGTTGCTGGTGGAAATTCAGACTGGTACAGCCAGTGTGGAATGTGATTTGGCAGTTTATTAAAAAGCTAAAAACCTAACT
GTTAACAACGACCACCTTTAAGTCTGACCATGTCGGTCACACCTTACACTAAACCGTCAAATAATTTTTCGATTTTTGGATTTGA

23,460

PSEN1

PSEN1-201

PSEN1-201

TACATAGCCCAGCAATTGCACCCCCAGGAGTCTACCCAATGGAAATGAAAACAGTCCGTCCCCACAGAGACATGGACATAAATGT
ATGTATCGGGTCGTTAACGTGGGGGTCCTCAGATGGGTTACCTTTACTTTTTGTTCAGGCAGGGGTGTCTCTGTACCTGTATTTACA

23,545

PSEN1

PSEN1-201

PSEN1-201

TCATAGCAGCATTATTCAGAATAGCCCCAAATTGAAAACAATCCAGATGTCCATCAACTGGTAAATGGATAAGCAAACCATATAA
AGTATCGTTCGTAATAAGTCTTATCGGGGTTAACTTTTGTAGGTCTACAGGTAGTTGACCATTTACCTATTCGTTTGGTATATT

23,630

PSEN1

PSEN1-201

PSEN1-201

TGGAAAACCATTTCAGCTTCCAATAACTTCCAAGAACTGTAGACACATGCAGTATCATGGTTAAACCTCAAAAACATTATATTAA
ACCTTTTGGTAAGTCGAAGGTTATTGAAGGTTCTTTGACATCTGTGTACGTCATAGTACCAATTTGGAGTTTTTGTAAATATAATT

23,715

PSEN1

PSEN1-201

PSEN1-201

GTAAAATAGGCGAGGCATGTATTGTATGAGTCATATGAAATGTCTAGAAAAGGCCAAATTTATTGAGATAGAAAAGCAGATCACTGG
CATTTTATCCGCTCCGTACATAACATACTCAGTATACTTTACAGATCTTTTTCCGTTTAAATAACTCTATCTTTTCGTCTAGTGACC

23,800

PSEN1

PSEN1-201

PSEN1-201

TTGCTTAAGGCCTAGGGTAGGAGTGGGGATTAAGTAAACGGGTACAAGGTACCTGACTGGGGCAATGGACATGTGGATTGTGA
AACGAATTCCGGATCCCATCCTCACCCCTAATTGACATTTGCCCATGTTCCATGGACTGACCCCGTTACCTGTACACCTAACACT

23,885

PSEN1

PSEN1-201

PSEN1-201

TGATAGTTAAATTGTACAGCTCTCTCTATATATAGTTGTACAGCTCTATTAATTTCCACAATCATTGAATCATGTCTTCCAGTT
ACTATCAATTTAACATGTCGAGAGAGATATATATCAACATGTGCGAGATAATTAAGGTTAGTAACTTAGTACAGAAGGTCAA

23,970

PSEN1

PSEN1-201

PSEN1-201

TTATGAGGTAAATCATAGTCCAATGAAGCTTTTTTAAAAATAAGATGATAGGCCATGTGTGGTGGCTCACGTCTGTAATCCCAGC
AATACTCCATTTAGTATCAGGTTACTTCGAAAAAATTTTTATTCTACTATCCGGTACACACCACCGAGTGCAGACATTAGGGTCG

24,055

PSEN1

PSEN1-201

PSEN1-201

ACTTTGGGAGGCCAAGGTGGGTGGATCATGAGGTCAGGAGTTTCGAGACCAGCCTGACCAACATGGTGAAACCCTGTCTCCATCAA
TGA AAC CCTCCGGTTCCACCCACCTAGTACTCCAGTCCTCAAGCTCTGGTCGGACTGGTTGTACCACTTTGGGACAGAGGTAGTT

24,140

PSEN1

PSEN1-201

PSEN1-201

AAATAAAAAAATTAGCCAGGCATGGTGGCATGCGCCTGTAATCCCACCTACTCAGGAGGCTGAGACAGGAAAGTCGCTTGAACCT
TTTATTTTTTAAATCGGTCCGTACCACCGTACGCGGACATTAGGGTGGATGAGTCCTCCGACTCTGTCTTTTCAGCGAACTTGGGA

24,225

PSEN1

PSEN1-201

PSEN1-201

GGGCGGCAGAGTCTGCAGTGAGCCGAGATCATGCTGCTGTAATCCCACCTACTCAGGAGGCTGAGACAGGAAAGTCGCTTGAACCT
CCC GCCGTCTCAGACGTCACCTCGGCTCTAGTACGACGACATGAGGTCGGACCCGGTGTCTCGTTTTGAGGTAGAGTTTTTTTTTTT

24,310

PSEN1

PSEN1-201

PSEN1-201

AAAATATTAATTAATATGATAAAATGATGCCTATCTCAGAATTCTTGTAAGGATTTCTTAGTACAAGTGCTGGGTATAAACTATA
TTTTATAATTAATTATACTATTTTACTACGGATAGAGTCTTAAGAACATTCTAAAGAATCATGTTTCACGACCCATATTTGATAT

24,395

PSEN1

PSEN1-201

PSEN1-201

TATTCAATAGATGACGATTATTACTTATTATTGTTATTGATAAATAACAGCAGCATCTACAGTTAAGACTCCAGAGTCAGTCACA
ATAAGTTATCTACTGCTAATAATGAATAAATAACAATAACTATTTATTGTCGTCGTAGATGTCAATTCTGAGGTCTCAGTCAGTGT

24,480

PSEN1

PSEN1-201

PSEN1-201

TAGAATCTGGAACCTCTATTGTAGAAAACCAAAAAGAAAGAAAACACAGCTGAAGCCTAATTTTGTATATCATTTACTGACTTC
ATCTTAGACCTTGAGGATAACATCTTTTGGTTTTTTCTTTCTTTTGTGTCGACTTCGGATTA AAAACATATAGTAAATGACTGAAG

24,565

PSEN1

PSEN1-201

PSEN1-201

TCTCATTTCATTGTGGGGTTGAGTAGGGCAGTGATATTTTTGAATTGTGAAATCATAGCAAAGAGTGACCAACTTTTTAATATTTG
AGAGTAAGTAACACCCCAACTCATCCGTCACCTATAAAAACCTTAACACTTTAGTATCGTTTCTCACTGGTTGAAAAATTATAAAC

24,650

PSEN1

PSEN1-201

PSEN1-201

TAACCTTTTCCTTTTTAGGGGGAGTAAACTTGGATTGGGAGATTTTCATTTTCTACAGTGTCTGGTTGGTAAAGCCTCAGCAACA
ATTGGAAAGGAAAAATCCCCCTCATTTTGAACCTAACCTCTAAAGTAAAAGATGTCACAAGACCAACCATTTTCGGAGTCGTTGT

24,735

PSEN1

PSEN1-201

R G V K L G L G D F I F Y S V L V G K A S A T
ENSE00003979377

PSEN1-201

GCCAGTGGAGACTGGAACACAACCATAGCCTGTTTTCGTAGCCATATTAATTGTAAGTATACTAATAAGAATGTGTCAGAGCTC
CGGTCACCTCTGACCTTGTGTTGGTATCGGACAAAGCATCGGTATAATTAACATTCATATGTGATTATTCTTACACAGTCTCGAG

24,820

PSEN1

PSEN1-201

A S G D W N T T I A C F V A I L I
ENSE00003979377

PSEN1-201

TAAATGTCAAACTTTGATTACACAGTCCCTTTAAGGCAGTTCTGTTTTAACCCCAGGTGGGTTAAATATTCCAGCTATCTGAGG
AATTACAGTTTTGAAACTAATGTGTCAGGGAAATTCGTC AAGACAAAATTGGGGTCCACCCAATTTATAAGGTCGATAGACTCC

24,905

PSEN1

PSEN1-201

PSEN1-201

AGCTTTTTGATAATTGGACCTCACCTTAGTAGTTCTCTACCCTGGCCACACATTAGAATCACTTGGGAGCTTTTAAACTGTAAG
TCGAAAAACTATTAACCTGGAGTGGAATCATCAAGAGATGGGACCGGTGTGTAATCTTAGTGAACCCTCGAAAAATTTGACATTC

24,990

PSEN1

PSEN1-201

PSEN1-201

CTCTGCCCTGAGATATTCTTACTCAATTTAATTGTGTAGTTTTTAAAATTTCCCAGGAAATTTCTGGTATTTCTGTTTAGGAACCG
GAGACGGGACTCTATAAGAATGAGTTAAATTAACACATCAAAAATTTAAGGGTCTTTAAGACCATAAAGACAAAATCCTTGGC

25,075

PSEN1

PSEN1-201

PSEN1-201

CTGCCCTAAGCCTAGCAGCACAGATATGTAGGAAATTAGCTCTGTAAGGTTGGTCTTACAGGGATAAACAGATCCTTCCTTAGTC
GACGGAGTTCGGATCGTCTGTCTATACATCCTTTAATCGAGACATTCCAACCAGAATGTCCCTATTTGTCTAGGAAGGAATCAG

25,160

PSEN1

PSEN1-201

PSEN1-201

CCTGGACTTAATCACTGAGAGTTTGGTGGTGGTTTTGCATTTAATGACACAACCTGTAGCATGCAGTGTACTTAAGACAGCAAG
GGACCTGAATTAGTGACTCTCAAACCACCACAAAACGTAAATTAATGTTGGACATCGTACGTCACAATGAATTTCTGTCTGTTTC

25,245

PSEN1

PSEN1-201

PSEN1-201

CATCTAGTGAGAGGAGCTGGTGCCATGCATGACCCACATAGATCTTGCTGATAGTGCTACAGCATGAACCCTGAAGCTTTCAAA
GTAGATCACTCTCCTCGACCACGGTACGTA CTGGGGTGTATCTAGAACGACTATCACGATGTCGTA CTGGGACTTCGAAAAGTTT

25,330

PSEN1

PSEN1-201

PSEN1-201

ACTATGATTTTTTTTTTTTTTTTTTTTTTTGAGACGGAGTCTCTGTCA CCGAGGCTGGAGTGGTGCAATCTCGGCTCATTGCAACCTC
TGATACTAAAAAAAAAAAAAAAAAAAACTCTGCCTCAGAGACAGTGGGTCCGACCTCACCACGTTAGAGCCGAGTAACGTTGGAG

25,415

PSEN1

PSEN1-201

PSEN1-201

TGCCTCCCAGATTTAAGTGATTCTCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGTGCCTGCCACCACGCCCGGCTAATTTT
ACGGAGGGTCTAAATTCAC TAAGAGACGGAGTCGGAGGGCTCATCGACCCTAATGTCCACGGACGGTGGTGC GGGCCGATTAAAA

25,500

PSEN1

PSEN1-201

PSEN1-201

TGTATTTTTAGTAGAAACAGGGTTTTACCATGTTGGCCAGGCTCCTCTTGA ACTCCTGACCTCAAGTGATGTGCCTGCCTCGGCC
ACATAAAAATCATCTTTGTCCCAAAGTGGTACAACCGGTCCGAGGAGAACTTGAGGACTGGAGTTCACTACACGGACGGAGCCGG

25,585

PSEN1

PSEN1-201

PSEN1-201

TCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCACCTGGCTTTTTTTTTTTTTTTTTTTTTTTGGAGACAGAGTCTTGCTCTG
AGGGTTTTACGACCCTAATGTCCGCACTCGGTGGCGTGGACCGAAAAAAAAAAAAAAAAAAAAAAAAA CCTCTGTCTCAGAACGAGAC

25,670

PSEN1

PSEN1-201

PSEN1-201

TCGCCAAACTAGAGTGCA GTGACATTAGCTCACTGCAACTTCTGCCTCCTAGGTTCAAGCGATCCTCCTGTCTCAGCCTCCCAA
AGCGGGTTTGATCTCACGTCACTGTAATCGAGTGACGTTGAAGACGGAGGATCCAAGTTCGCTAGGAGGACAGAGTCGGAGGGTT

25,755

PSEN1

PSEN1-201

PSEN1-201

GTAGCTGGAATTACATGTGTGCACCACCATGCCTGGCTAATTTTTGTATTTTTAGTGGAGATGAGGTTTTGCCACATTGCCCAGG
CATCGACCTTAATGTACACACGTGGTGGTACGGACCGATTAAAAACATAAAAATCACCTCTACTCCAAAACGGTGTAAACGGGTCC

25,840

PSEN1

PSEN1-201

PSEN1-201

CTGGTCTCAAACCTTCTGACCTCAACTGATCTGCCTGCCTCAGCCGCATAAAGTGCTGGGATTACAGGCATGAGCCACTGTGCCCA
GACCAGAGTTTGAAGACTGGAGTTGACTAGACGGACGGAGTCGGCGTATTTTACGACCCCTAATGTCCGTA CT CGGTGACACGGGT

25,925

PSEN1

PSEN1-201

PSEN1-201

ACCTGAAAACCTATGATTTAAGTAAACAACCCATAAAATATTTCTTGCTATTTTTACTAAAGATGTGTTATCTTGGCCGGGTGAAG
TGGACTTTTGATACTAAATTCATTTGTTGGGTATTTTATAAAGAACGATAAAAAATGATTTCTACACAATAGAACC GGCCCACTTC

26,010

PSEN1

PSEN1-201

PSEN1-201

ACTTTCTAGTGTTCGTAAGTAAAGTAAACAACCCATAAAATATTTCTTGCTATTTTTACTAAAGATGTGTTATCTTGGCCGGGTGAAG
TGGACTTTTGATACTAAATTCATTTGTTGGGTATTTTATAAAGAACGATAAAAAATGATTTCTACACAATAGAACC GGCCCACTTC

26,095

PSEN1

PSEN1-201

PSEN1-201

TCATAAATAAACTTTTAGTTTTATTTTTATTTTTTAAACACTGCAGCCTCATCATGCTTCACGGAGGAGCCTGTGCGGGGAAGAATGC
AGTATTTATTTGAAAATCAAATAAAATAAAAAATTTGTGACGTCGGAGTAGTACGAAGTGCCTCCTCGGACACGCCCTTCTTACG

26,180

PSEN1

PSEN1-201

PSEN1-201

TCCACACAGCATAAAGAATGCTCCCGCACAGCATAGAGAATGCCCCGCACAGCATAGAGAAGCCCCGCACAGCATAGAGAAT
AGGGTGTGTCGTATTTCTTACGAGGGCGTGTGTCGTATCTCTTACGGGGGCGTGTGTCGTATCTCTTACGGGGGCGTGTGTCGTATCTCTTA

26,265

PSEN1

PSEN1-201

PSEN1-201

GCCCCGCACAGCATAGAGAAGCCCCGCACAGCATAGAGAATGCTCTTACCTCTGGGTTTTTAAACCAGCCAAACTAAAATCAC
CGGGGGCGTGTGTCGTATCTCTTACGAGAAAGTGGAGACCCAAAAATTGGTTCGGTTTTGATTTTAGTG

26,350

PSEN1

PSEN1-201

PSEN1-201

AGAGGCCAACACATCATTTAAGATAGAAATTTCTGTATCTTTTAAATTTTTTCAAAGTAGTTTTACTTATTTTCAGATTCTATTT
TCTCCGGTTGTGTCGTATCTCTTAAAGACATAGAAAATTAATAAAGTTTCATCAAAATGAATAAAGTCTAAGATAAA

26,435

PSEN1

PSEN1-201

PSEN1-201

CTTTACTAGAATTAAGGGATAAAAATAACAATGTGTGCATAATGAACCCTATGAAACAAACAAAAGCTAGGTTTTTTTCATAGCTC
GAAATGATCTTAATTCCTATTTTATTGTTACACACGTATTACTTGGGATACTTTGTTTGTTCGATCCAAAAAAGTATCGAG

26,520

PSEN1

PSEN1-201

PSEN1-201

TTCTTCCAGATTGAATGAACGTCTGTTCTAAAATTTAACCCAAAAGGAAAATATTCAGTTAACTATGTTAAAAACCAAGACTTG
AAGAAGGTCTAACTTACTTGCAGACAAGATTTTAAATTGGGGTTTTCTTTTATAAGTCAATTGATACAATTTTGGTTCTGAAC

26,605

PSEN1

PSEN1-201

PSEN1-201

TGATTGAGTTTTGCCTGAAAATGCTTTTCATAATTATGTGTGAATGTGTGTCTTTCCCATCTTCTCCACAGGGTTTTGTGCCTTACA
ACTAACTCAAAACGGACTTTTACGAAAGTATTAATACACACTTACACACAGAAAGGGTAGAAGAGGTGTCCCAAACACGGAATGT

26,690

PSEN1

PSEN1-201

G L C L T
420
ENSE00002555450

PSEN1-201

TTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAGCTCTTCCAATCTCCATCACCTTTGGGCTTGTCTTCTACTTTGCCACAG
AATAATGAGGAACGGTAAAAGTTCTTTTCGTAACGGTTCGAGAAGGTTAGAGGTAGTGGAAACCCGAACAAAAGATGAAACGGTGTCT

26,775

PSEN1

PSEN1-201

L L L L A I F K K A L P A L P I S I T F G L V F Y F A T
425 430 435 440 445
ENSE00002555450

PSEN1-201

ATTATCTTGACAGCCTTTTATGGACCAATTAGCATTCCATCAATTTTATATCTAGCATATTTGCGGTTAGAATCCCATGGATGT
TAATAGAACATGTCGGAAAATACCTGGTTAATCGTAAGGTAGTTAAAATATAGATCGTATAAACGCCAATCTTAGGGTACCTACA

26,860

PSEN1

PSEN1-201













































D Y L V Q P F M D Q L A F H Q F Y I
450 455 460 465
ENSE00002555450
PSEN1-201

TTCTTCTTTGACTATAACAAAATCTGGGGAGGACAAAGGTGATTTTCTGTGTCCACATCTAA
AAGAAGAACTGATATTGTTTTAGACCCCTCCTGTTTCCACTAAAAGGACACAGGTGTAGATT

3'
26,923
5'

PSEN1

















PSEN1-201

















Feature	Location	Size			Type
✓ PSEN1	1 .. 26,923	26,923 bp			gene
/note	= gene ENSG00000080815 Protein coding				
✓ PSEN1-201	1 .. 26,923	26,923 bp			prim_transcript
/note	= primary transcript ENST00000324501				
PSEN1-202	1 .. 26,923	26,923 bp			prim_transcript
/note	= primary transcript ENST00000357710				
PSEN1-204	1 .. 26,923	26,923 bp			prim_transcript
/note	= primary transcript ENST00000394164				
PSEN1-205	1 .. 26,923	26,923 bp			prim_transcript
/note	= primary transcript ENST00000406768 Retained intron				
PSEN1-207	1 .. 26,923	26,923 bp			prim_transcript
/note	= primary transcript ENST00000553599				
PSEN1-209	1 .. 26,923	26,923 bp			prim_transcript
/note	= primary transcript ENST00000554131				
PSEN1-215	1 .. 26,923	26,923 bp			prim_transcript
/note	= primary transcript ENST00000556066 Retained intron				
PSEN1-218	1 .. 26,923	26,923 bp			prim_transcript
/note	= primary transcript ENST00000556951				
PSEN1-220	1 .. 26,923	26,923 bp			prim_transcript
/note	= primary transcript ENST00000557293				
PSEN1-223	1 .. 26,923	26,923 bp			prim_transcript
/note	= primary transcript ENST00000559361 Nonsense mediated decay				
PSEN1-225	1 .. 26,923	26,923 bp			prim_transcript
/note	= primary transcript ENST00000697912 Nonsense mediated decay				
PSEN1-226	1 .. 26,923	26,923 bp			prim_transcript
/note	= primary transcript ENST00000697913 Retained intron				
PSEN1-229	1 .. 26,923	26,923 bp			prim_transcript
/note	= primary transcript ENST00000700265				
PSEN1-230	1 .. 26,923	26,923 bp			prim_transcript
/note	= primary transcript ENST00000700266 Nonsense mediated decay				
PSEN1-231	1 .. 26,923	26,923 bp			prim_transcript
/note	= primary transcript ENST00000700267				
PSEN1-232	1 .. 26,923	26,923 bp			prim_transcript
/note	= primary transcript ENST00000700268				
PSEN1-233	1 .. 26,923	26,923 bp			prim_transcript
/note	= primary transcript ENST00000700269				
PSEN1-235	1 .. 26,923	26,923 bp			prim_transcript
/note	= primary transcript ENST00000700271				
PSEN1-236	1 .. 26,923	26,923 bp			prim_transcript
/note	= primary transcript ENST00000700272 Nonsense mediated decay				
PSEN1-237	1 .. 26,923	26,923 bp			prim_transcript
/note	= primary transcript ENST00000700273				
PSEN1-238	1 .. 26,923	26,923 bp			prim_transcript
/note	= primary transcript ENST00000700302 Nonsense mediated decay				

















Feature	Location	Size			Type
PSEN1-239	1 .. 26,923	26,923 bp			prim_transcript
/note	= primary transcript ENST00000700303 Nonsense mediated decay				
PSEN1-240	1 .. 26,923	26,923 bp			prim_transcript
/note	= primary transcript ENST00000700304 Nonsense mediated decay				
PSEN1-241	1 .. 26,923	26,923 bp			prim_transcript
/note	= primary transcript ENST00000700305 Nonsense mediated decay				
PSEN1-242	1 .. 26,923	26,923 bp			prim_transcript
/note	= primary transcript ENST00000700306				
PSEN1-243	1 .. 26,923	26,923 bp			prim_transcript
/note	= primary transcript ENST00000700307				
PSEN1-244	1 .. 26,923	26,923 bp			prim_transcript
/note	= primary transcript ENST00000700308 Nonsense mediated decay				
PSEN1-245	1 .. 26,923	26,923 bp			prim_transcript
/note	= primary transcript ENST00000700309 Nonsense mediated decay				
PSEN1-246	1 .. 26,923	26,923 bp			prim_transcript
/note	= primary transcript ENST00000700310 Nonsense mediated decay				
PSEN1-247	1 .. 26,923	26,923 bp			prim_transcript
/note	= primary transcript ENST00000700311 Nonsense mediated decay				
PSEN1-248	1 .. 26,923	26,923 bp			prim_transcript
/note	= primary transcript ENST00000700312				
PSEN1-249	1 .. 26,923	26,923 bp			prim_transcript
/note	= primary transcript ENST00000700313				
PSEN1-250	1 .. 26,923	26,923 bp			prim_transcript
/note	= primary transcript ENST00000700314 Nonsense mediated decay				
PSEN1-251	1 .. 26,923	26,923 bp			prim_transcript
/note	= primary transcript ENST00000700315 Nonsense mediated decay				
PSEN1-252	1 .. 26,923	26,923 bp			prim_transcript
/note	= primary transcript ENST00000700316 Nonsense mediated decay				
PSEN1-253	1 .. 26,923	26,923 bp			prim_transcript
/note	= primary transcript ENST00000700317				
PSEN1-254	1 .. 26,923	26,923 bp			prim_transcript
/note	= primary transcript ENST00000700318 Nonsense mediated decay				
PSEN1-255	1 .. 26,923	26,923 bp			prim_transcript
/note	= primary transcript ENST00000700319 Nonsense mediated decay				
PSEN1-256	1 .. 26,923	26,923 bp			prim_transcript
/note	= primary transcript ENST00000700320				
PSEN1-257	1 .. 26,923	26,923 bp			prim_transcript
/note	= primary transcript ENST00000700321				
PSEN1-258	1 .. 26,923	26,923 bp			prim_transcript
/note	= primary transcript ENST00000700322				
PSEN1-259	1 .. 26,923	26,923 bp			prim_transcript
/note	= primary transcript ENST00000700323				

Feature	Location	Size			Type
PSEN1-260	1 .. 26,923	26,923 bp			prim_transcript
/note = primary transcript ENST00000700324					
PSEN1-262	1 .. 26,923	26,923 bp			prim_transcript
/note = primary transcript ENST00000700375					
PSEN1-264	1 .. 26,923	26,923 bp			prim_transcript
/note = primary transcript ENST00000700377 Nonsense mediated decay					
PSEN1-265	1 .. 26,923	26,923 bp			prim_transcript
/note = primary transcript ENST00000700378					
PSEN1-266	1 .. 26,923	26,923 bp			prim_transcript
/note = primary transcript ENST00000700379 protein_coding_CDS_not_defined					
PSEN1-268	1 .. 26,923	26,923 bp			prim_transcript
/note = primary transcript ENST00000700389					
PSEN1-269	1 .. 26,923	26,923 bp			prim_transcript
/note = primary transcript ENST00000700390 Retained intron					
PSEN1-271	1 .. 26,923	26,923 bp			prim_transcript
/note = primary transcript ENST00000700404 Retained intron					
PSEN1-284	1 .. 26,923	26,923 bp			prim_transcript
/note = primary transcript ENST00000700436 Nonsense mediated decay					
PSEN1-285	1 .. 26,923	26,923 bp			prim_transcript
/note = primary transcript ENST00000700437					
PSEN1-287	1 .. 26,923	26,923 bp			prim_transcript
/note = primary transcript ENST00000700468					
PSEN1-288	1 .. 26,923	26,923 bp			prim_transcript
/note = primary transcript ENST00000700469					
PSEN1-212	1 .. 26,831	26,831 bp			prim_transcript
/note = primary transcript ENST00000555386 Nonsense mediated decay					
PSEN1-222	1 .. 26,831	26,831 bp			prim_transcript
/note = primary transcript ENST00000557511					
PSEN1-208	1 .. 24,700	24,700 bp			prim_transcript
/note = primary transcript ENST00000553855 Nonsense mediated decay					
PSEN1-283	1 .. 20,965	20,965 bp			prim_transcript
/note = primary transcript ENST00000700435 protein_coding_CDS_not_defined					
PSEN1-286	1 .. 14,879	14,879 bp			prim_transcript
/note = primary transcript ENST00000700467 Retained intron					
PSEN1-234	1 .. 14,797	14,797 bp			prim_transcript
/note = primary transcript ENST00000700270 Retained intron					
PSEN1-282	1 .. 14,426	14,426 bp			prim_transcript
/note = primary transcript ENST00000700434 Retained intron					
PSEN1-281	1 .. 14,392	14,392 bp			prim_transcript
/note = primary transcript ENST00000700433 Retained intron					
PSEN1-280	1 .. 1121	1121 bp			prim_transcript
/note = primary transcript ENST00000700432 Retained intron					


Feature	Location	Size	Type
PSEN1-263	1 .. 674	674 bp	prim_transcript
/note	= primary transcript ENST00000700376 Retained intron		
PSEN1-267	1 .. 542	542 bp	prim_transcript
/note	= primary transcript ENST00000700388 Retained intron		
PSEN1-201	186 .. 26,831	26,646 bp	CDS
▶ 6 segments	= 856 bp		
/codon_start	= 1		
/note	= coding sequence ENSP00000326366		
/translation	= EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQA YLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQR RVSKNSKYNAE,,STERESQDTVAENDDGGFSEEW EAQRDShLGP HRSTPESRAAVQELSSSILA GEDPEE,,RGV KLGLGDFIFYSVLV GKASATASGDWNTTIACFVA ILI,,GLCLT LLLLAIFK KALPALPISITFGLV FYFATDYL VQPFMDQLAFHQ 284* amino acids = 31.7 kDa		
PSEN1-202	186 .. 26,831	26,646 bp	CDS
▶ 6 segments	= 856 bp		
/codon_start	= 1		
/note	= coding sequence ENSP00000350342		
/translation	= EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQA YLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQR RVSKNSKYNAE,,STERESQDTVAENDDGGFSEEW EAQRDShLGP HRSTPESRAAVQELSSSILA GEDPEE,,RGV KLGLGDFIFYSVLV GKASATASGDWNTTIACFVA ILI,,GLCLT LLLLAIFK KALPALPISITFGLV FYFATDYL VQPFMDQLAFHQ 284* amino acids = 31.7 kDa		
PSEN1-204	186 .. 26,831	26,646 bp	CDS
▶ 6 segments	= 856 bp		
/codon_start	= 1		
/note	= coding sequence ENSP00000377719		
/translation	= EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQA YLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQR RVSKNSKYNAE,,STERESQDTVAENDDGGFSEEW EAQRDShLGP HRSTPESRAAVQELSSSILA GEDPEE,,RGV KLGLGDFIFYSVLV GKASATASGDWNTTIACFVA ILI,,GLCLT LLLLAIFK KALPALPISITFGLV FYFATDYL VQPFMDQLAFHQ 284* amino acids = 31.7 kDa		
PSEN1-207	186 .. 26,831	26,646 bp	CDS
▶ 6 segments	= 856 bp		
/codon_start	= 1		
/note	= coding sequence ENSP00000452477		
/translation	= EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQA YLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQR RVSKNSKYNAE,,STERESQDTVAENDDGGFSEEW EAQRDShLGP HRSTPESRAAVQELSSSILA GEDPEE,,RGV KLGLGDFIFYSVLV GKASATASGDWNTTIACFVA ILI,,GLCLT LLLLAIFK KALPALPISITFGLV FYFATDYL VQPFMDQLAFHQ 284* amino acids = 31.7 kDa		
PSEN1-209	186 .. 26,831	26,646 bp	CDS
▶ 6 segments	= 856 bp		
/codon_start	= 1		
/note	= coding sequence ENSP00000451915		
/translation	= EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQA YLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQR RVSKNSKYNAE,,STERESQDTVAENDDGGFSEEW EAQRDShLGP HRSTPESRAAVQELSSSILA GEDPEE,,RGV KLGLGDFIFYSVLV GKASATASGDWNTTIACFVA ILI,,GLCLT LLLLAIFK KALPALPISITFGLV FYFATDYL VQPFMDQLAFHQ 284* amino acids = 31.7 kDa		
PSEN1-218	186 .. 26,831	26,646 bp	CDS
▶ 6 segments	= 856 bp		
/codon_start	= 1		
/note	= coding sequence ENSP00000450551		
/translation	= EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQA YLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQR RVSKNSKYNAE,,STERESQDTVAENDDGGFSEEW EAQRDShLGP HRSTPESRAAVQELSSSILA GEDPEE,,RGV KLGLGDFIFYSVLV GKASATASGDWNTTIACFVA ILI,,GLCLT LLLLAIFK KALPALPISITFGLV FYFATDYL VQPFMDQLAFHQ 284* amino acids = 31.7 kDa		
PSEN1-220	186 .. 26,831	26,646 bp	CDS
▶ 6 segments	= 736 bp		
/codon_start	= 1		
/note	= coding sequence ENSP00000451880		
/translation	= EVFKTYNVAVDYITVALLIWNFGVVGMISIHWK,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQR RVSKNSKYNAE,,STERESQDTVAENDDGGFSEEW EAQRDShLGP HRSTPESRAAVQELSSSILA GEDPEE,,RGV KLGLGDFIFYSVLV GKASATASGDWNTTIACFVA ILI,,GLCLT LLLLAIFK KALPALPISITFGLV FYFATDYL VQPFMDQLAFHQFYI* 244 amino acids = 27.1 kDa		

Feature	Location	Size			Type
PSEN1-222	186 .. 26,831	26,646 bp			CDS
▶ 5 segments = 682 bp					
/codon_start	= 1				
/note	= coding sequence ENSP00000451429				
/translation	= EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQRVSKNSKYNAE,,RGV KLGLGDFIFYSVLV GKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKALPALPISITFGLVYFATDYLVPFMDQLAFHQFYI* 226 amino acids = 25.4 kDa				
PSEN1-229	186 .. 26,831	26,646 bp			CDS
▶ 6 segments = 856 bp					
/codon_start	= 1				
/note	= coding sequence ENSP00000514901				
/translation	= EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQRVSKNSKYNAE,,STERESQDTVAENDDGGFSEWEAQRDShLGP HRSTPESRAAVQELSSSILAGEDPEE,,RGV KLGLGDFIFYSVLV GKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKALPALPISITFGLVYFATDYLVPFMDQLAFHQ 284* amino acids = 31.7 kDa				
PSEN1-231	186 .. 26,831	26,646 bp			CDS
▶ 6 segments = 856 bp					
/codon_start	= 1				
/note	= coding sequence ENSP00000514903				
/translation	= EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQRVSKNSKYNAE,,STERESQDTVAENDDGGFSEWEAQRDShLGP HRSTPESRAAVQELSSSILAGEDPEE,,RGV KLGLGDFIFYSVLV GKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKALPALPISITFGLVYFATDYLVPFMDQLAFHQ 284* amino acids = 31.7 kDa				
PSEN1-232	186 .. 26,831	26,646 bp			CDS
▶ 6 segments = 856 bp					
/codon_start	= 1				
/note	= coding sequence ENSP00000514904				
/translation	= EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQRVSKNSKYNAE,,STERESQDTVAENDDGGFSEWEAQRDShLGP HRSTPESRAAVQELSSSILAGEDPEE,,RGV KLGLGDFIFYSVLV GKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKALPALPISITFGLVYFATDYLVPFMDQLAFHQ 284* amino acids = 31.7 kDa				
PSEN1-233	186 .. 26,831	26,646 bp			CDS
▶ 6 segments = 856 bp					
/codon_start	= 1				
/note	= coding sequence ENSP00000514905				
/translation	= EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQRVSKNSKYNAE,,STERESQDTVAENDDGGFSEWEAQRDShLGP HRSTPESRAAVQELSSSILAGEDPEE,,RGV KLGLGDFIFYSVLV GKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKALPALPISITFGLVYFATDYLVPFMDQLAFHQ 284* amino acids = 31.7 kDa				
PSEN1-235	186 .. 26,831	26,646 bp			CDS
▶ 5 segments = 682 bp					
/codon_start	= 1				
/note	= coding sequence ENSP00000514906				
/translation	= EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQRVSKNSKYNAE,,RGV KLGLGDFIFYSVLV GKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKALPALPISITFGLVYFATDYLVPFMDQLAFHQFYI* 226 amino acids = 25.4 kDa				
PSEN1-237	186 .. 26,831	26,646 bp			CDS
▶ 6 segments = 856 bp					
/codon_start	= 1				
/note	= coding sequence ENSP00000514908				
/translation	= EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQRVSKNSKYNAE,,STERESQDTVAENDDGGFSEWEAQRDShLGP HRSTPESRAAVQELSSSILAGEDPEE,,RGV KLGLGDFIFYSVLV GKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKALPALPISITFGLVYFATDYLVPFMDQLAFHQ 284* amino acids = 31.7 kDa				

Feature	Location	Size			Type
PSEN1-242	186 .. 26,831	26,646 bp			CDS
▶ 6 segments = 856 bp					
/codon_start = 1					
/note = coding sequence ENSP00000514933					
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQRVSKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRDShLGP HRSTPESRAAVQELSSSILAGEDPEE,,RGVKLGLGDFIFYSVLV GKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVFFYFATDYL VQPFMDQLAFHQE84* amino acids = 31.7 kDa					
PSEN1-243	186 .. 26,831	26,646 bp			CDS
▶ 5 segments = 757 bp					
/codon_start = 1					
/note = coding sequence ENSP00000514934					
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,ATMVWLVNMAEGDPEAQRVSKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRDShLGP HRSTPESRAAVQELSSSILAGEDPEE,,RGVKLGLGDFIFYSVLV GKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVFFYFATDYL VQPFMDQLAFHQFYI* 251 amino acids = 28.0 kDa					
PSEN1-248	186 .. 26,831	26,646 bp			CDS
▶ 6 segments = 856 bp					
/codon_start = 1					
/note = coding sequence ENSP00000514939					
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQRVSKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRDShLGP HRSTPESRAAVQELSSSILAGEDPEE,,RGVKLGLGDFIFYSVLV GKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVFFYFATDYL VQPFMDQLAFHQE84* amino acids = 31.7 kDa					
PSEN1-249	186 .. 26,831	26,646 bp			CDS
▶ 6 segments = 856 bp					
/codon_start = 1					
/note = coding sequence ENSP00000514940					
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQRVSKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRDShLGP HRSTPESRAAVQELSSSILAGEDPEE,,RGVKLGLGDFIFYSVLV GKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVFFYFATDYL VQPFMDQLAFHQE84* amino acids = 31.7 kDa					
PSEN1-253	186 .. 26,831	26,646 bp			CDS
▶ 6 segments = 856 bp					
/codon_start = 1					
/note = coding sequence ENSP00000514944					
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQRVSKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRDShLGP HRSTPESRAAVQELSSSILAGEDPEE,,RGVKLGLGDFIFYSVLV GKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVFFYFATDYL VQPFMDQLAFHQE84* amino acids = 31.7 kDa					
PSEN1-256	186 .. 26,831	26,646 bp			CDS
▶ 6 segments = 883 bp					
/codon_start = 1					
/note = coding sequence ENSP00000514947					
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DVFYVFLDLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQRVSKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRDShLGP HRSTPESRAAVQELSSSILAGEDPEE,,RGVKLGLGDFIFYSVLV GKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVFFYFATDYL VQPFMDQLAFHQE84* amino acids = 32.8 kDa					
PSEN1-257	186 .. 26,831	26,646 bp			CDS
▶ 6 segments = 856 bp					
/codon_start = 1					
/note = coding sequence ENSP00000514948					
/translation = EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQRVSKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRDShLGP HRSTPESRAAVQELSSSILAGEDPEE,,RGVKLGLGDFIFYSVLV GKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVFFYFATDYL VQPFMDQLAFHQE84* amino acids = 31.7 kDa					

Feature	Location	Size			Type
PSEN1-258	186 .. 26,831	26,646 bp			CDS
▶ 6 segments = 856 bp					
/codon_start	= 1				
/note	= coding sequence ENSP00000514949				
/translation	= EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQRVSKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRDShLGP HRSTPESRAAVQELSSSILAGEDPEE,,RGVKLGLGDFIFYSVLV GKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVYFYFATDYL VQPFMDQLAFHQ				
	284* amino acids = 31.7 kDa				
PSEN1-259	186 .. 26,831	26,646 bp			CDS
▶ 6 segments = 856 bp					
/codon_start	= 1				
/note	= coding sequence ENSP00000514950				
/translation	= EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQRVSKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRDShLGP HRSTPESRAAVQELSSSILAGEDPEE,,RGVKLGLGDFIFYSVLV GKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVYFYFATDYL VQPFMDQLAFHQ				
	284* amino acids = 31.7 kDa				
PSEN1-260	186 .. 26,831	26,646 bp			CDS
▶ 6 segments = 856 bp					
/codon_start	= 1				
/note	= coding sequence ENSP00000514951				
/translation	= EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQRVSKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRDShLGP HRSTPESRAAVQELSSSILAGEDPEE,,RGVKLGLGDFIFYSVLV GKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVYFYFATDYL VQPFMDQLAFHQ				
	284* amino acids = 31.7 kDa				
PSEN1-262	186 .. 26,831	26,646 bp			CDS
▶ 6 segments = 856 bp					
/codon_start	= 1				
/note	= coding sequence ENSP00000514966				
/translation	= EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQRVSKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRDShLGP HRSTPESRAAVQELSSSILAGEDPEE,,RGVKLGLGDFIFYSVLV GKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVYFYFATDYL VQPFMDQLAFHQ				
	284* amino acids = 31.7 kDa				
PSEN1-265	186 .. 26,831	26,646 bp			CDS
▶ 6 segments = 856 bp					
/codon_start	= 1				
/note	= coding sequence ENSP00000514968				
/translation	= EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQRVSKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRDShLGP HRSTPESRAAVQELSSSILAGEDPEE,,RGVKLGLGDFIFYSVLV GKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVYFYFATDYL VQPFMDQLAFHQ				
	284* amino acids = 31.7 kDa				
PSEN1-268	186 .. 26,831	26,646 bp			CDS
▶ 6 segments = 856 bp					
/codon_start	= 1				
/note	= coding sequence ENSP00000514970				
/translation	= EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQRVSKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRDShLGP HRSTPESRAAVQELSSSILAGEDPEE,,RGVKLGLGDFIFYSVLV GKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVYFYFATDYL VQPFMDQLAFHQ				
	284* amino acids = 31.7 kDa				
PSEN1-285	186 .. 26,831	26,646 bp			CDS
▶ 6 segments = 856 bp					
/codon_start	= 1				
/note	= coding sequence ENSP00000514988				
/translation	= EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQRVSKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRDShLGP HRSTPESRAAVQELSSSILAGEDPEE,,RGVKLGLGDFIFYSVLV GKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLVYFYFATDYL VQPFMDQLAFHQ				
	284* amino acids = 31.7 kDa				

Feature	Location	Size			Type
PSEN1-287	186 .. 26,831	26,646 bp		→	CDS
▶ 5 segments = 757 bp					
/codon_start	= 1				
/note	= coding sequence ENSP00000515001				
/translation	= EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQA YLIMISALMALVFIKYLPEWTAWLILAVISVY,,ATMVWLVNMAEGDPEAQRRVSKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRD SHLGP HRSTPESRAAVQELSSSILAGEDPEE,,RGV KLGLGDFIFYSVLV GKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLV F YFATDYL VQPFMDQLAFHQFYI*				
	251 amino acids = 28.0 kDa				
PSEN1-288	186 .. 26,831	26,646 bp		→	CDS
▶ 6 segments = 856 bp					
/codon_start	= 1				
/note	= coding sequence ENSP00000515002				
/translation	= EVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQA YLIMISALMALVFIKYLPEWTAWLILAVISVY,,DLVAVLCPKGPLRMLVETAQERNETLFPALIYS,,STMVWLVNMAEGDPEAQRRVSKNSKYNAE,,STERESQDTVAENDDGGFSEEWEAQRD SHLGP HRSTPESRAAVQELSSSILAGEDPEE,,RGV KLGLGDFIFYSVLV GKASATASGDWNTTIACFVAILI,,GLCLTLLLLAIFKKALPALPISITFGLV F YFATDYL VQPFMDQLAFHQ				
	284* amino acids = 31.7 kDa				
PSEN1-210	4054 .. 26,923	22,870 bp		→	prim_transcript
/note	= primary transcript ENST00000554995 Retained intron				
✓ Donor Template WT -> SNV	5592 .. 5691	100 bp		⇌	misc_feature
✓ Protospacer Sequence	5610 .. 5629	20 bp		⇌	misc_feature
✓ Silent SNV	5628 .. 5628	1 bp		⇌	misc_feature
/note	= WT = T SNV = G				
✓ PAM	5630 .. 5632	3 bp		⇌	misc_feature
✓ SNV	5642 .. 5642	1 bp		⇌	misc_feature
/note	= WT = A SNV = C				
PSEN1-270	13,629 .. 26,923	13,295 bp		→	prim_transcript
/note	= primary transcript ENST00000700391 protein_coding_CDS_not_defined				
PSEN1-213	13,695 .. 26,923	13,229 bp		→	prim_transcript
/note	= primary transcript ENST00000555867 Retained intron				
PSEN1-228	24,182 .. 26,923	2742 bp		→	prim_transcript
/note	= primary transcript ENST00000697915 Retained intron				

Primer	Length		Binding Sites		Tm	Date Added
✓ PCR Forward	25-mer		5198 .. 5222		60°C	Jan 11, 2023
/sequence = TTCTCCCTGTTTCTGCTCACTGTAG 48% GC / 7540.9 Da						
✓ Donor Template WT -> SNV	100-mer		5592 .. 5691		72°C	Jan 11, 2023
/sequence = TATCCTTCTCAAATACTTACAGGAGTAAATGAGAGCTGGAAAAAGCGTTGCATTTCTCTCCTGCGCTGTTTCAACCAGCATACGAAGTG GATGCTTCGTA 64% GC / 8571.1 Da						
✓ gRNA Protospacer	20-mer		5610 .. 5629		55°C	Jan 11, 2023
/sequence = TATGCTGGTTGAAACAGCTC 45% GC / 6132.1 Da						
✓ Sanger Sequencing	20-mer		5778 .. 5797		58°C	Jan 11, 2023
/sequence = GAGTTCCAGGAATGCTGTGC 55% GC / 6173.1 Da						
✓ PCR Reverse	25-mer		6159 .. 6183		60°C	Jan 11, 2023
/sequence = ATTCAAACCCCCATTACTTTCCACC 44% GC / 7440.9 Da						