



ASK2J00173_PINK1_A217D_E03_AB
 18,054 bp

5'

3'

85

170

255

340

425

510

595

AGAGGGCACCGCCCAAGTTTGTGTGACCGGGCGGGGACGCCGGTGGTGGCGGGCAGCGGGCGGCTGCGGGGGCACCGGGCCGCGGC
TCTCCGTGGCGGGTTCAAACAACACTGGCCGCCCCCTGCGGCCACCACCGCCGTCGCCGCCGACGCCCCCGTGGCCCGCGCCG

PINK1

PINK1-201

GCCACCATGGCGGTGCGACAGGCGCTGGGCGCGGGCCTGCAGCTGGGTGCGAGCGCTGCTGCTGCGCTTCACGGGCAAGCCCGGCC
CGGTGGTACCGCCACGCTGTCCGCGACCCGGCGCCGGACGTCGACCCAGCTCGCGACGACGACGCGAAAGTGCCCGTTCGGGCGCGG

PINK1

PINK1-201

1 5 10 15 20 25
M A V R Q A L G R G L Q L G R A L L L R F T G K P G

ENSE00001465660
PINK1-201

GGGCCTACGGCTTGGGGCGGCCGGGCCCCGGCGGGCGGGCTGTGTCCGCGGGGAGCGTCCAGGCTGGGCGCAGGACCGGGCGCGGA
CCCGGATGCCGAACCCCGCCGGGCCGGGCCGCCGCCGACACAGGCGCCCTCGCAGGTCCGACCCGGCGTCTCTGGCCCGCGCCT

PINK1

PINK1-201

30 35 40 45 50 55
R A Y G L G R P G P A A G C V R G E R P G W A A G P G A E

ENSE00001465660
PINK1-201

GCCTCGCAGGGTCGGGCTCGGGCTCCCTAACCGTCTCCGCTTCTTCCGCCAGTCGGTGGCCGGGCTGGCGGGCGCGTTGACAGCGG
CGGAGCGTCCCAGCCGAGCCGAGGGATTGGCAGAGGCGAAGAAGGCGGTACGCCACCGGCCCGACCGCCGCGCCAACGTCGCC

PINK1

PINK1-201

60 65 70 75 80
P R R V G L G L P N R L R F R Q S V A G L A A R L Q R

ENSE00001465660
PINK1-201

CAGTTCGTGGTGCGGGCTGGGGCTGCGCGGGCCCTTGCGGCCGGGACGTCCTTCTGGCCTTCGGGCTAGGGCTGGGCCTCATCG
GTCAAGCACCACGCCCGGACCCCGACGCGCCCGGGAACGCCGGCCCGTCCAGAAAGACCGGAAGCCCGATCCCGACCCGGAGTAGC

PINK1

PINK1-201

85 90 95 100 105 110
Q F V V R A W G C A G P C G R A V F L A F G L G L G L I

ENSE00001465660
PINK1-201

AGGAAAAACAGGCGGAGAGCCGGCGGGCGGTCTCGGCCTGTGAGGAGATCCAGGTGAGCGGGGCGGGTCCCTAAGCCGAGCGGAG
TCCTTTTTGTCCGCTCTCGGCCGCCCGCCAGAGCCGGACAGTCTCTAGGTCCACTCGCCCCGGCCAGGATTCGGCTCGCCTC

PINK1

PINK1-201

115 120 125
E E K Q A E S R R A V S A C Q E I Q

ENSE00001465660
PINK1-201

GACGGAGCTAAGCGCGGGGGCGGGTCCCTCAGCTGGGTGGGGGCGGGGCTAGGTGTGGAGGCGGGGCTCTGAGCAGATCGAGGGCC
CTGCCCTCGATTGCGGCCCGCCAGGAGTCGACCCACCCCGCCCGATCCACACCTCCGCCCGGAGACTCGTCTAGCTCCC

PINK1

PINK1-201

PINK1-201

GAGGCGAGGGTCTTAAAGCTCATCTATTTACCCATTACTGATCGGCTGCTATAAATAAAGCCAGCACCTCCCATTTGTTTTAAT
CTCCGCTCCAGGAATTTGAGTAGATAAAGTGGAATGACTAGCCGACGATATTTATTTTCGGTCGTGGAGGGTAAACAAAATTA

680

PINK1

PINK1-201

PINK1-201

GTTTCCCTTCCTCAAATGAAGACATGTTGCCGATTACAGCTCCTGTCGCAGCACAGCAAAGGCTTTGTGTAAATTTTCTAAAAT
CAAAGGGAAGGAGTTTACTTCTGTACAACGGCTAATGTGCGAGGACAGCGTCGTGTCGTTTTCCGAAACACATTTAAAAGATTTTA

765

PINK1

PINK1-201

PINK1-201

GTACGGACAACATAAATCATAACATTCCTATCCCTTTGAGGTAGTTGCCGTCCCTAATTTATGGAGAAGGAAAGTCCTCAGGTGAA
CATGCCTGTTGATTTAGTATTGTAAGGATAGGGAAACTCCATCAACGGCAGGGATTAAATACCTCTTCTTTTCAGGAGTCCACTT

850

PINK1

PINK1-201

PINK1-201

GGGACTTGCTCGAAGTCACACAGCTAATAAAATGCAGTGCCCTTAACCACTGAGCCAGGCTGCCTCCGCCGTTTAACCAAAGGAT
CCCTGAACGAGCTTCAGTGTGTCGATTATTTTACGTACGGGAATTGGTGACTCGGTCCGACGGAGGCGGCAAATTGGTTTCCTA

935

PINK1

PINK1-201

PINK1-201

TAGTAGTGACAGAGCTGAAACCGCAGTAAAACTATGAACGGCGAGAAAAACAGTCCTAACATTTTAGTTACCTGTGTAGAGTTA
ATCATCACTGTCTCGACTTTGGCGTCAATTTTGTACTTTGCCGCTCTTTTTGTGAGGATTGTAATAATCAATGGACACATCTCAAT

1020

PINK1

PINK1-201

PINK1-201

TCCCTGCTGACTGGATACACAAGGGTTCTTAGGGTTTTTAAATGCTTAAATAGCACAAGACTTCTCTTTTTGCCCAACCAAAGT
AGGGACGACTGACCTATGTGTTCCCAAGAATCCCAAAAAATTACGAATTTTATCGTGTTCTGAAGAGAAAAACGGGTTGGTTTCA

1105

PINK1

PINK1-201

PINK1-201

CTGTATTAGGGTTCTCAAATGGAATCAATAGGATGTGTCTATATAGAGGCAGGTTTATTTTGGAGACCTGGCTCCCTATGGGGA
GACATAATCCCAAGAGGTTTACCTTAGTTATCCTACACAGATATATCTCCGTCCAAATAAACTCCTGGACCGAGGGATACCCCT

1190

PINK1

PINK1-201

PINK1-201

TTGGCAAAGTCTTAAAAGCCGCAGAGTAGGCCGGGCAGGCTGGAGAGCCAGGGAGGAGCCAGCGGTGCAGTTTCAGGTTTGAAGCCT
AACCgTTTCAGAAATTTTCGGCGTCTCATCCGCCCGTCCGACCTCTCGGTCCCTCCTCGGTTCGCCACGTCAAGTCCAAACTTCGGA

1275

PINK1

PINK1-201

PINK1-201

GGCCGCTGGCAGAATTCCATCTTCTTCCAGGGAGGTCACCTCTTCTTCTCGGGGGTGTAGAACCCTCACTAAATTAGCATAGCCC
CCGGCGACCGTCTTAAGGTAGAAGAAGGTCCCTCCAGTGAGAAGAAGGACCCCCACATCTTGGTGAGTGATTTAATCGTATCGGG

1360

PINK1

PINK1-201

PINK1-201

CTGCATTTTACAGGTTAGGGCTGAGGTGGTGGAAAGAGGGAGTGACTTGCCCAAGGACACAGCTGTTAGGGCCAAGCAGTGGCTCC
GACGTAAAATGTCCAATCCCGACTCCACCACCTTCTCCCTCACTGAACGGGTTCTGTGTGCGACAATCCCGGTTTCGTACCCGAGG

1445

PINK1

PINK1-201

PINK1-201

TGGGTTTTCTGGTTTTCCATCCCAGTTCTTATTGCTCATCACCCTGTCTCATGTTTGAGCTCTGGCCAGTTTGGGGTGACAGGTG
ACCCAAAGGACCAAAGGTAGGGTCAAGAATAACGAGTAGTGGTGACAGAGTACAACTCGAGACCGGTCAAACCCCACTGTCCAC

1530

PINK1

PINK1-201

PINK1-201

ACATCTGGCCTAGTCCCCAGCCCCTGACCTTGTCTTTTGCCACAGCTTAACTGGCAGAAGCTAAGGATGGGAAATTTGACTAATC
TG TAGACCGGATCAGGGGTCTGGGGACTGGAACAGAAAACGGTGTGCAATTGACCGTCTTCGATTCTTACCCTTTAACTGATTAG

1615

PINK1

PINK1-201

PINK1-201

CTGCTTAAACTAAAGAGGCTTTTTTAACTGAGGAGATTGATCCTCCTAACTTACCATTACACACACCTTCTTCGCACACTTC
GACGAATTTTGATTTCTCCGAAAAAATTGACTCCTCTAACTAGGAGGATTTGAATGGTAAGTGTGTGTGGAAGAAGCGTGTGAAG

1700

PINK1

PINK1-201

PINK1-201

ACCCTCCTATGCCTGAAAATGTTATTAGTTATCAATTAATTTACATTAATAAATTTTGGTCAGGCACTGTGGCTCATGC
TGGGAGGATACGGACTTTTACAATAATCAATAGTTAATTAAGTGTAATTTTTTAAAAAACCAGTCCGTGACACCGAGTACG

1785

PINK1

PINK1-201

PINK1-201

CTGTAATCCCAGCACTTTGGGAGGCTGAGGCGGGCGGATCACGAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATGGTGGAAACC
GACATTAGGGTCGTGAAACCCCTCCGACTCCGCCCGCCTAGTGCTCCAGTCTCTCAAACCTCTGGTTCGGACCGGTTGTACCACCTTGG

1870

PINK1

PINK1-201

PINK1-201

CTGTCTCTACTAAAAATACAAAAATTACCCGGGCGCAGTGTTGGGCGCCTGTAATCCCAGCTACTTGGGAGACTGAGGCAGGAGA
GACAGAGATGATTTTTATGTTTTTAATGGGCCCGCGTCAACCACCCGCGGACATTAGGGTCGATGAACCCCTCTGACTCCGTCTCTCT

1955

PINK1

PINK1-201

PINK1-201

ATTCTTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGCCACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCTGA
TAAGGAACTTGGGCCCTCCGCCTCCAACGTCCTCGACTCTAGTGCGGTGACGTGAGGTCGGACCCACTGTCTCGTTCTGAGACT

2040

PINK1

PINK1-201

PINK1-201

CTGGGGGGAGAAAAAGTTGTTTTCACTGGCTACTTTTTGCTGGAATTAATTTACATTTAAAAAATTCTGGGCCGGGCGGGGTGGC
GACCCCCCTCTTTTTCAACAAAAGTGACCGATGAAAACGACCTTAATTAAGTGTAATTTTTTAAGACCCGGGCCCGCCCCACCG

2125

PINK1

PINK1-201

PINK1-201

TCATGCCTGTAATCTCAGCACTTTGGGAGGCCAAGGCGGGCGGATCATGAGGTCAGGAGATCGAGACCATCCTGGCTAACATGGT
AGTACGGACATTAGAGTCGTGAAACCCCTCCGGTTCCGCCCGCCTAGTACTCCAGTCTCTAGCTCTGGTAGGACCGATTGTACCA

2210

PINK1

PINK1-201

PINK1-201

GAAACCCCGCCTCTACTAAAAATACAAAAAATTAGCCAGGCATGGTGGCAGGCGCCTGTAGTCCCAGCTACTCGGGAGGCTGAG
CTTTGGGGCGGAGATGATTTTTATGTTTTTTAATCGGTCCGTACCACCGTCCGCGGACATCAGGGTCGATGAGCCCTCCGACTC

2295

PINK1

PINK1-201

PINK1-201

GCAGGAGAATGGCGTGAACCCGGGAGGCAGGGCTTGCAGTGAGCCAAGATCGCGCCACTGCACTCCAGCCTAGAGGACAGAGTGA
CGTCTCTTACCGCACTTGGGCCCTCCGTCCCGAACGTCCTCGGTTCTAGCGCGGTGACGTGAGGTCGGATCTCCTGTCTCACT

2380

PINK1

PINK1-201

PINK1-201

GACTCCGTCTCAAAAAAAAAATAAAAAAAAAAAAAAAAAATAAAAAAAAAATTCTGAAGCCAGGCATGGTGACTCATGCCTATAATCCTGGTGCT
CTGAGGCAGAGTTTTTTTTTATTTTTTATTTTTTATTTTTTAAAGACTTCGGTCCGTACCACTGAGTACGGATATTAGGACCACGA

2465

PINK1

PINK1-201

PINK1-201

TTGGGAGGCCAAGGTGAGAGAATCTCTTGAGCCCAGGAGTTGAAGACCAGCTGGGACAACATAGTGAGACCTTGTTCCACAAAA
AACCTCCGGTTCCTACTCTCTTAGAGAACTCGGGTCTCAACTTCTGGTTCGACCCTGTTGTATCACTCTGGAACAAGGGTGT

2550

PINK1

PINK1-201

PINK1-201

TATTA AAAAGTTAGCTAGGCATGGTGGCACATGCCGATAGTCCAGCTACTTAGGAGGCTGAGGTGGGTGGATTGCTTGAGCCCA
ATAATTTTTCAATCGATCCGTACCACTGACGGCTATCAGGGTCGATGAATCCTCCGACTCCACCCACCTAACGAACCTCGGGT

2635

PINK1

PINK1-201

PINK1-201

GGAGTTTGAGGCTGCAGTGAGCTGTAGTTGCAACACTGCACCCCATCCTGGGCAACTAGCAGGAGTGTGCTAGTAGCAAGCTCTA
CCTCAAACCTCCGACGTCCTCGACATCAACGTTGTGACGTGGGGTAGGACCCGTTGATCGTCTCACACGATCATCGTTCGAGAT

2720

PINK1

PINK1-201

PINK1-201

AAAATTTATATTATAAAAAATATATATAATGTGTATATATGTATATGTGTATATATGTTGTGTATACTATAATATGTATGTT
TTTTAAATATAATTTTTTATATATATATTACACATATATATACATATACACATATATACAACACATATGATATTATACATACAA

2805

PINK1

PINK1-201

PINK1-201

CCATATAATAGTATATAGTATATTTTTATATATATACACACACACGTTGCTTCTGCTCCATGAAGTTTATAAGGGAAGTTGGATTT
GGTATATTATCATATATCATATAAAATATATATATGTGTGTGTGCAACGAAGACGAGGTA CTTC AAATATTCCTTCAACCTAAA

2890

PINK1

PINK1-201

PINK1-201

TCCTTTTTTTTTTTTTGATACGGAGTCTCACACCGTCGCCCAGGCTGTGCAATGGCACGATCTCAGCTCACTGCAACCTCCACCTC
AGGAAAAAAAAAAAACTATGCCTCAGAGTGTGGCAGCGGGTCCGACACGTTACCGTGCTAGAGTCGAGTGACGTTGGAGGTGGAG

2975

PINK1

PINK1-201

PINK1-201

CCAGATTCACGCAATTCTTCTGCCTCAGCCTCCTGAGTAGCTGGGATTACATGTGCACACCACCACACCCGGCTAATTTTTTTGTA
GGTCTAAGTGCGTTAAGAAGACGGAGTCGGAGGACTCATCGACCTAATGTACACGTGTGGTGGTGTGGGCCGATTAAAAAACAT

3060

PINK1

PINK1-201

PINK1-201

TTTTTTAGTAGAGACGGGGTTTCACTATGTTGGCCAGGCTGGTCTTGAACCTCCTGACTTCATGATCCGCCTCCCTCGGCCTCCCA
AAAAAATCATCTCTGCCCAAAGTGATACAACCGGTCCGACCAGAACTTGAGGACTGAAGTACTAGGCGGAGGGAGCCGGAGGGT

3145

PINK1

PINK1-201

PINK1-201

AAGTGCTGGGATTACAGGCATGAGCCACCACGCCCGGCCTGGACTTTTCATTTTTTTAAAAGTTCAAAGTTATAGTGCAAGGTTA
TTCACGACCCTAATGTCCGTACTCGGTGGTGCGGGCCGGACCTGAAAGTAAAAAATTTTCCAAGTTTCAATATCACGTTCCAAT

3230

PINK1

PINK1-201

PINK1-201

AGTTGCTTACAGATAGCAGGTGCTTTAGGAACCCTCTAGAAGGAAAGTTGCCATGGGCTGGGTTCATCAGGGCTGGTCACAGAGGA
TCAACGAATGTCTATCGTCCACGAAATCCTTGGGAGATCTTCTTTCAACGGTACCCGACCCAGTAGTCCCAGCAGTGTCTCCT

3315

PINK1

PINK1-201

PINK1-201

AGGAGGAGCTTGAGTTGGGCTTGATGGCTGAGCAGGGATGAGCCAGACAGAGCAATACTATAGAAACAGGGGCTGGAAGGATGCT
TCCTCCTCGAACTCAACCCGAACTACCGACTCGTCCCTACTCGGTCTGTCTCGTTATGATATCTTTGTCCCCGACCTTCTTACGA

3400

PINK1

PINK1-201

PINK1-201

GTGAGCAGCTTTTCAGAGGGAGGCGTCCAAAGGATGAGTGCAGGCAGCGTGCAGACCAGCCTGGCAGCAGCCAGAACACAGATAAC
CACTCGTCGAAAAGTCTCCCTCCGCAGGTTTCTACTCACGTCCGTGCGACGTCTGGTCCGACCGTCTGTCGGTCTTGTGTCTATTG

3485

PINK1

PINK1-201

PINK1-201

CTCCTGGGCAGTCTGATGGACAGCCGAGTGACACATGAAAGCAACATATTTTGATGTGGCTCAGAGCAGGGGAAGGCACGGCACTG
GAGGACCCGTCAGACTACCTGTCGGCTCACTGTGTACTTTTCGTTGTATAAACTACACCGAGTCTCGTCCCTTCCGTGCCGTGAC

3570

PINK1

PINK1-201

PINK1-201

AGAGTGGGGTAGTCTAGAGATGGTGCCTGGTAGGCTATGGCCAAGGGGCATATGCAGAGCTGTGCCTGGCACCCAGGGGTGACTA
TCTCACCCCATCAGATCTCTACCACGGACCATCCGATACCGGTTCCCGTATACGTCTCGACACGGACCGTGGGTCCCCACTGAT

3655

PINK1

PINK1-201

PINK1-201

ACCTTGGAAAGGAAGAGCTCAGCAGATCAGACCATTTGAGAGGGAAAGCGGAGCCTGGGTGACTGGAAGAGTGACGTCACCGCTG
TGGAACCTTTCCTTCTCGAGTCGTCTAGTCTGGTAAACTCTCCCTTTCGCCTCGGACCCACTGACCTTCTCACTGCAGTGGCGAC

3740

PINK1

PINK1-201

PINK1-201

CCTGAAGCAGGGGAAGACCCACCAGATTTTTGTCACATGGCCTCTTTCCAGTGCAGCACTGCCCCAGCACCTGCACCTCCATC
GGACTTCGTCCCTTCTGGGTGGTCTAAAAACAGTGTACCGGAGAAAGGGTACGTCGTGACGGGGGTCGTGGACGTGGAGGTAG

3825

PINK1

PINK1-201

PINK1-201

TATTTCTGTCTGAACTCTTGTACTCTTGCTACCTTTCTGGACAGAGTAGCCTCATCGGGGCCCTAAGAGGCAGAGAGAGAAAGAC
ATAAAGACAGACTTGAGAACATGAGAACGATGGAAGACCTGTCTCATCGGAGTAGCCCCGGGATTCTCCGTCTCTCTTTCTG

3910

PINK1

PINK1-201

PINK1-201

AGTACTGAATCCCTCTGCTCTGGGGATGCGCCTGATGTCACCCACTTGCCTGAGAGACCCTCTGAGATCACTGTGGATCACACAC
TCATGACTTAGGGAGACGAGACCCCTACGCGGACTACAGTGGGTGAACGGACTCTCTGGGAGACTCTAGTGACACCTAGTGTGTG

3995

PINK1

PINK1-201

PINK1-201

TCCTGCTAGTTGCCAGGAGCCGTCAGCCAAGGTCTTTGCAGAGCGAGCTGTCTCCATAATCAGACACCTCCAGAACTCTGCTGG
AGGACGATCAACGGGTCTCGGCAGTCGGTTCAGAAACGTCTCGCTCGACAGAGGTATTAGTCTGTGGAGGTCTTGAGACGACC

4080

PINK1

PINK1-201

PINK1-201

AGAGTGAAGGCAGCAAGGAGAGGTGCACTGGCTGCGGGACGTGGGGTTTCTGACCTCTCAGATCATTGAGTATTGTGATCCCAGT
TCTCACTTCCGTCGTTCTCTCCACGTGACCGACGCCCTGCACCCAAAGACTGGAGAGTCTAGTAACTCATAACACTAGGGTCA

4165

PINK1

PINK1-201

PINK1-201

GAAGCAACAGAGTTTGGAGAAAAATCATTCTGAATAATGAGAAAAGAAGATGGCCTGGACCCAGGCTGAGCAGTAGAACCTGGTTGG
CTTCGTTGTCTCAAACCTCTTTTTAGTAAGACTTATTACTCTTTCTTCTACCGGACCTGGGTCCGACTCGTCATCTTGGACCAACC

4250

PINK1

PINK1-201

PINK1-201

GTTGTGTTTTTCTGGTTTATTGATCTGGTTCGACGTGGACCACGCCTTGCTGCACCTCTCTCTGCCTCCCCTGTTTCCCTTTTCTT
CAACACAAAAAGACCAAATAACTAGACCAGCTGCACCTGGTGCAGAACGACGTGGAGAGAGACGGAGGGGACAAAGGGAAAAAGAA

4335

PINK1

PINK1-201

PINK1-201

PCR Forward

CAATTTTACCCAGAAAAGCAAGCC

GGGCCTTCCTAGGCTCCCTGGCTCACGGTGCATTCTTTTCTCATCACAGGCAATTTTACCCAGAAAAGCAAGCCGGGGCCTGAC
CCCGGAAGGATCCGAGGGACCGAGTGCCACGTAAGAAAAGAGTAGTGTCCGTTAAAAATGGGTCTTTTCGTTCCGGCCCCGGACTG

4420

PINK1

PINK1-201

PINK1-201

130 135 140
A I F T Q K S K P G P D
ENSE00001041274

Sanger Sequencing Primer

TCTGATAGGGCAGTCCATTG

CCGTTGGACACGAGACGCTTGCAGGGCTTTTCGGCTGGAGGAGTATCTGATAGGGCAGTCCATTGGTAAGGGCTGCAGTGCTGCTG
GGCAACCTGTGCTCTGCGAACGTCCCGAAAAGCCGACCTCCTCATAGACTATCCCGTCAGGTAACCATTCCCGACGTCACGACGAC

4505

PINK1

PINK1-201

PINK1-201

145 150 155 160 165
P L D T R R L Q G F R L E E Y L I G Q S I G K G C S A A
ENSE00001041274

Donor Template WT -> SNV

CCCAGGTAC

TGTATGAAGCCACCATGCCTACATTGCCCCAGAACCTGGAGGTGACAAAAGACACCGGGTTGCTTCCAGGGAGAGGCCAGGTAC
ACATACTTCGGTGGTACGGATGTAACGGGGTCTTGGACCTCCACTGTTTCTCGTGGCCCAACGAAGGTCCCTCTCCGGGTCCATG

4590

PINK1

PINK1-201

PINK1-201

170 175 180 185 190 195
V Y E A T M P T L P Q N L E V T K S T G L L P G R G P G T
ENSE00001041274

Donor Sequence WT -> SNV

Donor Template WT -> SNV

CAGTGCACCAGGAGAAGGGCAGGAGCGAGCTCCGGGGGCCCTGCCTTCCCCTTGG^ACATCAAGATGATGTGGAACATCTCGgta
CAGTGCACCAGGAGAAGGGCAGGAGCGAGCTCCGGGGGCCCTGCCTTCCCCTTGG^CCATCAAGATGATGTGGAACATCTCGGTA
GTCACGTGGTCTCTTCCCCTCCTCGCTCGAGGGCCCCGGGGACGGAAGGGGAACC^GGTAGTTCTACTACACCTTGTAGAGCCAT

4675

PINK1

PINK1-201

S A P G E G Q E R A P G A P A F P L A I K M M W N I S

ENSE00001041274

PINK1-201

Donor Sequence WT -> SNV

gRNA Protospacer Sequence
PAM

SNV

ACCGGTAGTTCTACTACACC
gRNA Protospacer

Donor Template WT -> SNV

agcacc

AGCACCAGGCCTTTCATCTTTAAAGGAGATGTTCTCAAAATGCCATCTTAGTGGGCCTGGTGAGGATTTTTTCCAGGAAGTAGG
TCGTGGTCCGGAAAGTAGAAATTTCTCTACAAGAGTTTTACGGGTAGAATCACCCGGACCACTCCTAAAAAAGGTCCTTTCATCC

4760

PINK1

PINK1-201

PINK1-201

Donor Sequence WT -> SNV

TAGGAAAAGACAGATTATCCACAGGAAAGGTGCCTGTATAGTCAGGTTACCTCCCCTGTTACACAGAAGTCTAAACCAGAATGT
ATCCTTTTCTGTCTAATAGGTGTCTTTCCACGGACATATCA6TCCAATGGAGGGGACAATGTGTCTTCAGATTTGGTCTTACA

4845

PINK1

PINK1-201

PINK1-201

TTGAAATTGTATTCTGCCCACAGATCACCCAGAGATCAGGTTCAAAGGTAGATTTTGGCCAGGCCTGGTGGACCATGCCTGTAAT
AACTTTAACATAAGACGGGTGTCTAGTGGGTCTCTAGTCCAAGTTTCCATCTAAAACCGGTCCGGACCACTGGTACGGACATTA

4930

PINK1

PINK1-201

PINK1-201

CCCAGCACTTTGGGAGGCCAATCACTTGAGCTCAGGAGTTTGGAGACCAGCCTGGGCAACATGATGAAACCCCATCTCTATGAAAA
GGGTCTGTAAACCCCTCCGGTTAGTGAACCTCGAGTCTCAAACCTCTGGTCTGGACCCGTTGTAATACTTTGGGGTAGAGATACTTTT

5015

PINK1

PINK1-201

PINK1-201

ATACAAAAATTAGCCGGGTGTGACAGCTTGCACCTGTATGTAGTCTTAGCTACTTGGGTGGCTGGTGGCTGAAAGTGGGAGGATCA
TATGTTTTTAATCGGCCACACTGTCGAACGTGGACATACATCAGAATCGATGAACCCACCGACCACCGACTTCACCCTCCTAGT

5100

PINK1

PINK1-201

PINK1-201

CTTGAGTGCAAGAGGCAGAGGCTGCAGTGATCCAAGATTGTGGCACTGCACTCCAGCCTGGGTAAACAGAGTAAGACCCTGTCTCA
GAACTCACGTTCTCCGTCTCCGACGTCAGTGGTTCTAACACCGTGACGTGAGGTCGGACCCATTGTCTCATTCTGGGACAGAGT

5185

PINK1

PINK1-201

PINK1-201

AAACAAACAAACAAACAAACAAACAAACAAACAAACAAAGGTAGATTCTGATTCAGCAGGTCAGGGATGGGGCCTAAGATTGTGCCTTCCCAA
TTTGTGTTTGTGTTGTTGTTTTTTTTGGGTTTCCATCTAAGACTAAGTCGTCCAGTCCCTACCCCGGATTCTAACACGGAAGGGTT

5270

PINK1

PINK1-201

PINK1-201

TAAGCTCCCACGTGATACCAATGCCACTGCTCTGTCAACCACACTTTGAGTAACAAGTGCCTAAACCACTGATTTCTACCTTGAT
ATTCGAGGGTGCAGTATGGTTACGGTGACGAGACAGTTGGTGTGAAACTCATTGTTTACGGATTTGGTGACTAAAGATGGAACCTA

5355

PINK1

PINK1-201

PINK1-201

TGGTTAGTTCACCATCCCCTCCTTCCCTGCAACCTGCCTCACTGGAGAGGGGGAACTGGATCTCTTTCCCTTAAGCTCACTCTGCA
ACCAATCAAGTGGTAGGGGAGGAAGGACGTTGGACGGAGTGACCTCTCCCCCTTGACCTAGAGAAAGGAAATTCGAGTGAGACGT

5440

PINK1

PINK1-201

PINK1-201

ccccttgacctagagaaggaaatt

PCR Reverse

AGCCACCTCCAGCTCAGAGGCTTGCATGTCAACTCCCTACTCTCAACTCTTGGAAAGGACTCAAGACTTTGGGAAATTGAAGAGT
TCGGGTGGAGGTCGAGTCTCCGAACGTACAGTTGAGGGATGAGAGTTGAGAACCTTCCCTGAGTTCTGAAACCTTTAACTTCTCA

5525

PINK1

PINK1-201

PINK1-201

ATTTTTCCCCCACGAAACAATTTCTGTCCACTTAATTTATTTACCTTGCCATTGCTAGGTAGGTTTTAAAAATGTATTAAGACC
TAAAAAGGGGTGCTTTTGTAAAGACAGGTGAATTAATAAATGGAACGGTAACGATCCATCCAAAATTTTACATAATTCTGG

5610

PINK1

PINK1-201

PINK1-201

CGATGCTCTGTCTCCTGCCCATCCCTGGGCCCATCCATTCAAGGCCGAGTGGGAAGTGGCCACAGCCGTTTCATGGTGGGCCCTA
GCTACGAGACAGAGGACGGGTAGGGACCCGGGTAGGTAAGTTCCGGCGTCAACCCTTCACCGGTGTCGGCAAGTACCACCCGGGAT

5695

PINK1

PINK1-201

PINK1-201

GAGGATGCAGTTTCTTGTCTGATTTGGGGAATGAAGGTTATTAGACTGTTGCACTCCAAGCTGGGTTAATAGCTAACAAGTAGC
CTCCTACGTCAAAGAACAAGACTAAACCCCTTACTTCCAATAATCTGACAACGTGAGGTTTCGACCCAATTATCGATTGTTTCATCG

5780

PINK1

PINK1-201

PINK1-201

CAAATCCTTTGCCTGTGAAACATCCAGTCTTAGCATCAAACATGCCCTGGTTGGGGCATGACAGCTGTTGCATTACAGCAGCT
GTTTAGGAAACGGACACTTTGTAGGTCAGAATCGTAGTTTTGTACGGGACCAACCCCGTACTGTCGACAACGTAAGTGTCTCGTCGA

5865

PINK1

PINK1-201

PINK1-201

ACAAGATTGTTGATTCTTACCAGATCTTCTTGATACAGGTTTCATATGTCCTGAGAGCCCTTCCCAATACAATGAGGACAATAAG
TGTTCTAACAACTAAGAATGGTCTAGAAGAACTATGTCCAAAGTATACAGGACTCTCGGGAAGGGTTATGTTACTCTGTTATTC

5950

PINK1

PINK1-201

PINK1-201

GTGCTTTCCCACTCTTTGGTTTTTGTCTGTTTGTCTGTTGGGGGATGGAGGAAGGCTGTTCTGTGATTCAGTACAACCTTCACCCAG
CACGAAAGGGGTGAGAAACAAAAACAGACAAACAGCACCCCTACCTCCTTCCGACAAGACACTAAGTCATGTTGAAGTGGGTC

6035

PINK1

PINK1-201

PINK1-201

GGTGGAGCATGTCAGGCTCTGGCCTGGCTGCTGAAGGGAGCCTGCAGAATGAGTTAGTGATCCAGTGGTCAATTTTGAAGTGGTG
CCACCTCGTACAGTCCGAGACCGGACCGACGACTTCCCTCGGACGTCTTACTCAATCACTAGGTCACCAGTTAAAACTTGACCAC

6120

PINK1

PINK1-201

PINK1-201

GGGACCAGAGGCACCGATGGCAGGAAGCAGCACCCCATATCCTGATCACCTTGGCATCTCCTCCAGCCCTGGCATCTAGGCTGCA
CCCTGGTCTCCGTGGCTACCGTCCCTCGTCTGGGGTATAGGACTAGTGGAAACCGTAGAGGAGGTCGGGACCGTAGATCCGACGT

6205

PINK1

PINK1-201

PINK1-201

AGAGTTTGAGGAGTGTGAAGAATCCTCTGAGTTGGCATGGATGGTACCTCTGTCTGCCTCCCAGGAGTAACTAGTCTCAGCCTGC
TCTCAAACCTCCTCACACTTCTTAGGAGACTCAACCGTACCTACCATGGAGACAGACGGAGGGTCTCATTGATCAGAGTCGGACG

6290

PINK1

PINK1-201

PINK1-201

CAGTTAAGACAGGTCATCTTATCTCGAAGGTCAGAGCCAATTCTAGGCAGTAGCTGCCCTGCTCCAGGTTACAGGCAGGGCTTAC
GTCAATTCTGTCCAGTAGAATAGAGCTTCCAGTCTCGGTTAAGATCCGTTCATCGACGGGACGAGGTCCAATGTCCGTCCCGAATG

6375

PINK1

PINK1-201

PINK1-201

AAGGAACTTACCATTCTGCTCCGGCCTGTGTAACCCTGGGTTCTTGTGGGTGTTCCAGGCAGGTTCTCCAGCGAAGCCATCTT
TTCCTTGAATGGTAAGACGAGGCCGGACACATTGGGACCCAAGGAACACCCACAAGGTCCGTCCAAGGAGGTCGCTTCGGTAGAA

6460

PINK1

PINK1-201

PINK1-201

A G S S S E A I L
ENSE00001041273

GAACACAATGAGCCAGGAGCTGGTCCCAGCGAGCCGAGTGGCCTTGGCTGGGGAGTATGGAGCAGTCACTTACAGGTAAGTGCCC
CTTGTGTTACTCGGTCCTCGACCAGGGTTCGCTCGGCTCACCGGAACCGACCCCTCATACCTCGTCAGTGAATGTCCATTCACGGG

6545

PINK1

PINK1-201

PINK1-201

235 N T M S Q E L V P A S R V A L A G E Y G A V T Y R
240 245 250 255

ENSE00001041273

TCTGCCTGCCAGACTGACTGGGACTTCTTTGAGAGCAACTTCATCCATCACTTATGTCCTCAGCACCTGGTACAGTGTCTGATAT
AGACGGACGGTCTGACTGACCCTGAAGAACTCTCGTTGAAGTAGGTAGTGAATACAGGAGTCGTGGACCATGTCACAGACTATA

6630

PINK1

PINK1-201

PINK1-201

GACAGTAGATAATAAAGGCTTAATGTTGGTGATGGATTTTCAGTTAGTGGATAATTTCACTTGGGAAAGATTGCAGGTAATCTGA
CTGTCATCTATTATTTCCGAATTACAACCACTACCTAAAAGTCAATCACCTATTAAAGTGAACCCTTTCTAACGTCCATTAGACT

6715

PINK1

PINK1-201

PINK1-201

CCCCAAATGATGATGCACTTTCGTAATTCACATTGGAGCAGGGGAGAGGAGGCCCCCAAAAATGCCAGTTCACAGTGTTCAT
GGGGTTTACTACTACGTGAACGCATTAAGTGTAACCTCGTCCCCTCTCCTCCGGGGGGTTTTTACGGGTCAAGTGTACACAACGTA

6800

PINK1

PINK1-201

PINK1-201

GATTGACTGGGGTTCTCAGATTCCTCCTAAGAAATGCACGGGTAGAGCGCCACCTATCGGAATAAACTGAACTCTGTCCCCACCA
CTAACTGACCCCAAGAGTCTAAGGAGGATTCTTTACGTGCCCATCTCGCGGTGGATAGCCTTATTTGACTTGAGACAGGGGTGGT

6885

PINK1

PINK1-201

PINK1-201

GAGGGAACACTCATTTCACTAATAGTTATGTGCACTGATGGTGCCAAGAGATTTTTAAAAAACA AAAAGTGGTCTGTTGGCCCA
CTCCCTTGTGAGTAAAGTGATTATCAATACACGTGACTACCACGGTTCTCTAAAATTTTTTTTGT TTTTCCACCAGACAACCGGGT

6970

PINK1

PINK1-201

PINK1-201

GAGGTCTCAGTGTGGCAGCAGAGAGCCAGGGTGTAAAGTGCTAGAATCGAGTATGCTTGGGCTGAGGGAGCCCAAGGGGAGGCGTG
CTCCAGAGTACACCGTCGTCTCTCGGGTCCACATTCACGATCTTAGCTCATACGAACCCGACTCCCTCGGGTCCCCTCCGCAC

7055

PINK1

PINK1-201

PINK1-201

TGCTGCAGAGGAGGGGCTGCTCAGAAAAGCCTTCTCAAAGGGACAGTTTGTGCCACCTTGTGAAGGATGAATTGGCATTACTTGGG
ACGACGTCTCCTCCCCGACGAGTCTTTCGGAAGAGTTTCCCTGTCAAACACGGTGGAACACTTCTACTTAACCGTAATGAACCC

7140

PINK1

PINK1-201

PINK1-201

CAGAGGAGTAGGGAAGTGGCATTCCAGCAGAGGGAAGAGCAAGTGAACAGCAGCTACGCTTTCAGCTCAGAAAAGCCCATGTCC
GTCTCCTCATCCCTTACCCTAAGGGTTCGTCTCCCTTCTCGTTCACTTGTCTCGTATGCGAAAAGTCGAGTCTTTTTCGGGTACAGG

7225

PINK1

PINK1-201

PINK1-201

ACCACCAGCCTCACCACAGGTGGTGAGGACTGACGCGCAGGCTATGACAGAGGAGATACTTGTGCCACCTCAATATTTACAGCC
TGGTGGTCGGAGTGGTGTCCACCACTCCTGACTGCGCGTCCGATACTGTCTCCTCTATGAACACGGGTGGAGTTATAAATGTCGG

7310

PINK1

PINK1-201

PINK1-201

TGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCTGAGGTAGGCAGATCACTTGAGCCCAGGAGTTCAAGAGCAGCCTGGGCAA
ACCGAGTACGGACATTAGGGTCGTGAAACCCCTCCGACTCCATCCGTCTAGTGAACCTCGGGTCCCTCAAGTTCTCGTCCGACCCGTT

7395

PINK1

PINK1-201

PINK1-201

CATGGTGAAACCCCGCCTTTACAAAAAATAAATTTTAGCCGGGCATGGGGGCAAATGCCTGTGATCCCAGCTACTCAGGAGGCTG
GTACCACTTTGGGGCGGAAATGTTTTTTTATTTAAAAATCGGCCCGTACCCCGTTTACGGACACTAGGGTCGATGAGTCTCCGAC

7480

PINK1

PINK1-201

PINK1-201

AGGCGGGAGGATCATTTGAGTCCAGGGAGGTTGAGGCTGCAGTGAGCCAAGATCATGCCACTGCACTCCAGCCTGGGCGACCCTG
TCCGCCCTCCTAGTAAACTCAGGTCCCTCCAACCTCCGACGTCACCTCGGTTCTAGTACGGTGACGTGAGGTCTGGACCCGCTGGGAC

7565

PINK1

PINK1-201

PINK1-201

GAGTGAGACCCTGTCTCTCATTTGTAGACCCACCAAGAAGAGGTGGGTCTGCTGCATTTTTGGTGATTTACTGGAGGGCTGGTTT
CTCACTCTGGGACAGAGAGTAAACATCTGGGTGGTTCTTCTCCACCCAGACGACGTAAAAACCACTAAATGACCTCCCGACCAA

7650

PINK1

PINK1-201

PINK1-201

ATAGATCTTCATTCTGTCAGAAGCAGGGAGGGCAAAAGTATGAAATTAAGGGAGTGGTTGTGGAAAACCCCTTCCATGGTTTTGGAG
TATCTAGAAGTAAGACAGTCTTCGTCCCTCCGTTTTTCACTACTTTAATTCCCTCACCAACACCTTTTTGGGGAAGGTACCAAACCTC

7735

PINK1

PINK1-201

PINK1-201

GTTTCCAATGTGACTGGGAGTCCCTGCAGGCCGGTGGAGGTAGCTGCTCAAGTGGCTGCTGCTTCTCCTGAGGCCTTTTTGGAGA
CAAAGGTTACTACTGACCCTCAGGGACGTCCGGCCACCTCCATCGACGAGTTCACCGACGACGAAGAGGACTCCGGAAAAACCTCT

7820

PINK1

PINK1-201

PINK1-201

AAGTGGACACCTGAATGTCAGCTGCTTTGGGGCTAACATGATCCTTGATGCCTCCTTTTTGTGGCATGAGTGGCAGCCGGCCGACG
TTCACCTGTGGACTTACAGTCGACGAAACCCGATTGTAAGGAACTACGGAGGAAAAACCGTACTCACCGTCGGCCGGCTGC

7905

PINK1

PINK1-201

PINK1-201

TGGTGCTGTCCTGCTGCCGGAGCACCATGATGTCTGCTGCTGAGACCTCCCATCTGACATAGTCCCTGTCCCTCTTCAGGGACTT
ACCACGACAGGACGACGGCCTCGTGGTACTACAGACGACGACTCTGGAGGGTAGACTGTATCAGGGACAGGGAGAAGTCCCTGAA

7990

PINK1

PINK1-201

PINK1-201

TGTTCCCTTTAGCAGTTCTCACTGTCTGGCCTCAAATAACACGTCTTTTTCTGTTGGTTCCTTTTTGCTCCAGCTGTACTGTAAAC
ACAAGGAAATCGTCAAGAGTGACAGACCGGAGTTTATTGTGCAGAAAAAGACAACCAAGGAAAAACGAGGTCGACATGACATTTG

8075

PINK1

PINK1-201

PINK1-201

ACTCTTTGTTTACTGCATACCCTCAGTAAATACCTGTTGAATGACCGGATAGATGTGGCAGCAGGTACATTACCTCAACTTCTGG
TGAGAAACAAATGACGTATGGGAGTCATTTATGGACAACCTACTGGCCTATCTACACCGTCGTCCATGTAATGGAGTTGAAGACC

8160

PINK1

PINK1-201

PINK1-201

TACACCTTGGGAGAAGCTTTCCCAAGAACACCCTGGGTTCAATTCCTCCTAGCCTCTGCTCTCCTGGGGCCAGAGATTGAAGGC
ATGTGGAACCTCTTCGAAAGGGTTCTTGTGGGACCCAAGTAAAGGAGGATCGGAGACGAGAGGACCCCGGGTCTCTAACTCCG

8245

PINK1

PINK1-201

PINK1-201

GCTTAACCTGCTCATCTCACCACGTCTCCCGCCTTATCTCTCACCTTCTCATCAGCACCTTACACTCCACCACGCTGGCTTCAT
CGAATTGGACGAGTAGAGTGGTGCAGAGGGCGGAATAGAGAGTGGGAAGAGTAGTCGTGGGATGTGAGGTGGTGCACCGAAGTA

8330

PINK1

PINK1-201

PINK1-201

AGCTCCTTCCCGAATGTGCCAGGCTTCTCTGTGACCATCTCTTGAGCGTACAGCTGGCTATACCTGGGCTGCCCTCCTCCACA
TCGAGGAAGGGGCTTACACGGTCCGAAGAGACACTGGTAGAGAACTCGCATGTGACCGATATGGACCCGACGGGAGGAGGGTGT

8415

PINK1

PINK1-201

PINK1-201

TTTCAGGTCTCAGTTCAGACACCCGCAACCCACCATGTATCTCCCCAGTACAGCCATACTCCTCTGCCCTGAGCTCCCATGAC
AAAGTCCAGAGTCAAGTCTGTGGGCGTTGGGGTGGTACATAGAGGGGTCATGTGCGGTATGAGGAGACGGGGACTCGAGGGTACTG

8500

PINK1

PINK1-201

PINK1-201

ACCTGCTGGGGCCCTGACAGCCTGGGGCTGTGATCATGACTTGCCAGGGGCCCCGAGGGTGGAAACGATGCTCTGGCTCCTTTGA
TGGACGACCCCGGGACTGTGCGACCCCGACACTAGTACTGAACGGGTCCCGGGCTCCACCTTTGCTACGAGACCGAGGAAACT

8585

PINK1

PINK1-201

PINK1-201

TTGCATAGAACAGGGGGCCACTCAGGTTGACTCAAGAGCAGGAGCAGCGCGTGGGCACACGTGGACTGCAGCCACACAGCCTGGGG
AACGTATCTTGTCCCGGTGAGTCCAACCTGAGTTCTCGTCTCGTCGCGCACCCGTGTGCACCTGACGTGCGGTGTGTGCGGACCCC

8670

PINK1

PINK1-201

PINK1-201

ACCATGCAGTGCTGGGAGAGGGCCGGTGCCTGCTCTCTCCCCAGCACCGTCTAGGCTCTGCCCCATTTCGCTTCCCTCCACCATTG
TGGTACGTCACGACCCTCTCCGGCCACGGGACGAGAGAGGGGTCTGTGGCAGATCCGAGACGGGGTAAGCGAAGGGAGGTGGTAAC

8755

PINK1

PINK1-201

PINK1-201

TTATGCAGCAAAGGGGGCTCTAGCCTGATGTGCTAGAAGCAGTCAACTGGATTTTTGAGAAAAGCCAAGCTTTCTATTGTGAGT
AATACGTCGTTTTCCCGGAGATCGGACTACACGATCTTCGTCAGTGTGACCTAAAACTCTTTTCGGTTCGAAAGATAACACTCA

8840

PINK1

PINK1-201

PINK1-201

CGACTCATATGGAGACAGGAGTTGAATTC AACCCCTGTCTCCCTGTGCTAGCTTTAAGGCGGTAATTTTATTAGAGGAGGTTTAAG
GCTGAGTATACCTCTGTCTCAACTTAAGTTGGGACAGAGGGACACGATCGAAATTCGCCATTAAAATAATCTCCTCCAAATTC

8925

PINK1

PINK1-201

PINK1-201

GGGTGGATTCTAAGATTAGCAGGTGATTGATGGAAGGAAAGGAGAAGTCTGGACAGTCCCTGGACATGCACAGTTATCTGTTTCAT
CCCACCTAAGATTCTAATCGTCCACTAACTACCTTCCTTTCTCCTCCTCAGACCTGTCAGGAACCTGTACGTGTCAATAGACAAGTA

9010

PINK1

PINK1-201

PINK1-201

GCCAACTCATGGGTCCCCTGTGCAGATTTGGGAGGAGTGAGTATGAAACGTGCAGTGGCAATTCAGGCTTTGACATCAGCAAAC
CGGTTGAGTACCCAGGGGACACGTCTAAACCCTCCTCACTCATACTTTGCACGTCACCGTTAAGTCCGAAACTGTAGTCGTTTGA

9095

PINK1

PINK1-201

PINK1-201

TGTTCTGTGCAAGCTGCAATTGGCCTTATTGGTTCCAACCAATTTAGCCAGTTCTTTTATCTCATAAGCAGAGGGAGTTTCAGC
ACAAGACACGTTTCGACGTTAACCGGAATAACCAAGGTTGGTTAAAGTCGGTCAAGAAAATAGAGTATTTCGTCTCCCTCAAAGTCG

9180

PINK1

PINK1-201

PINK1-201

CTTTCAGAAAAGTGGTTTCTGCAAACCTCAAATTTTCTTTTATTTTTCTGAGACAGGGTCTTACTCTGTTGCCAGGGCTGGAGAGCA
GAAAGTCTTTCACCAAAGACGTTTGTAGTTTAAAAGAAAAATAAAAAGACTCTGTCCCAGAATGAGACAACGGGTCCGACCTCTCGT

9265

PINK1

PINK1-201

PINK1-201

GTGGCGTGATCTTGGCTCACTGCAGCCTCAACCTCCCTGGGCTCAAGTGATCCTCCCACCTCAGCCTCCCAAGTAGCTGGGTCTG
CACCGCACTAGAACCAGTGTACGTCGGAGTTGGAGGGACCCGAGTTCACTAGGAGGGTGGAGTCTGGAGGGTTTCATCGACCCAGAC

9350

PINK1

PINK1-201

PINK1-201

CAGGCACATGCCACCATGCCAGCTAATTTTTGTAGTTTTGTAGAGACAGAGTTTCTCCATGTTGCCCGGGCTGGCCTCGAACT
GTCCGTGTACGGTGGTACGGGTCGATTA AAAACATCAAAAACATCTCTGTCTCAAAGAGGTACAACGGGCCCCGACCGGAGCTTGA

9435

PINK1

PINK1-201

PINK1-201

CCTGGGCTCAAGCAATTGCCTGCCTCAGCCTCCCAAATTGCTGGGATTACAGGAGTGAGCCACGGGAATTTCCATCAGTTACTGA
GGACCCGAGTTCGTTAACGGACGGAGTCGGAGGGTTTAAACGACCTAATGTCTCACTCGGTGCCCTTAAAGGTAGTCAATGACT

9520

PINK1

PINK1-201

PINK1-201

TTCTTGAAC TTGTAGGAACGTGGTTCCACTGTCCACATGCTGTTCTTCTCCTCGCATCTCCTGTTTCTGCTTCCCTTTGGCCTGCT
AAGA ACTTGAACATCCTTGCACCAAGGTGACAGGTGTACGACAAGAAAGGAGCGTAGAGGACAAGGACGAAGGGAAACCGGACGA

9605

PINK1

PINK1-201

PINK1-201

CACCTCTGGCTCCTCATGGCCCCAGTGAAGTATCGTGGCTTCTCTCCACTGCAGACTGGCAGATTTCTTCACTCACACTCCCAA
GTGGAGACCGAGGAGTACCGGGGTCACTTCATAGCACCGAAGGAGAGGTGACGTCTGACCGTCTAAAGAAGTGAGTGTGAGGGTT

9690

PINK1

PINK1-201

PINK1-201

AAAGAGAATCTACTTCCCTCCCTTCCCTTCGTCCAACCATCTGGGTCTCGAGTGTCACTGTAGGTTCACTGCCGTTGGGGCAGGT
TTTCTCTTAGATGAAGGGAGGGAAAGGGAAGCAGGTTGGTAGACCCAGAGCTCACAGTGACATCCAAGTGACGGCAACCCCGTCCA

9775

PINK1

PINK1-201

PINK1-201

TAGGTTATTCTTTCCAGGTGTTGTATCTGATGCTGGCCTCATATGTTTGTCTCACTTGGCTGACTAGAAAATCCAAGAGAGGTCC
ATCCAATAAGAAAAGGTCCACAACATAGACTACGACCGGAGTATACAAACAGAGTGAACCGACTGATCTTTTTAGGTTCTCTCCAGG

11,050

PINK1

PINK1-201

260 K S K R G P 265

ENSE00003577628

PINK1-201

CAAGCAACTAGCCCCACCCCAACATCATCCGGGTTCTCCGCGCCTTACCTCTTCCGTGCCGCTGCTGCCAGGGGGCCCTGGTC
GTTTCGTTGATCGGGGAGTGGGGTTGTAGTAGGCCCAAGAGGCGCGGAAGTGGAGAAGGCACGGCGACGACGGTCCCCGGGACCAG

11,135

PINK1

PINK1-201

270 K Q L A P H P N I I R V L R A F T S S 285 290

ENSE00003577628

PINK1-201

GACTACCCTGATGTGCTGCCCTCACGCCTCCACCCTGAAGGCCTGGGCCATGGCCGGACGCTGTTTCCTCGTTATGAAGAAGTAAG
CTGATGGGACTACACGACGGGAGTGC GGAGGTGGGACTTCCGGACCCGGTACCGGCCTGCGACAAGGAGCAATACTTCTTCATTC

11,220

PINK1

PINK1-201

295 D Y P D V L P S R L H P E G L G H G R T L F L V M K N 320

ENSE00003577628

PINK1-201

TGACAGCAGCGCGGCAGGGCCTGGAGCTGATACATCTCCCAAGGGGAGCTGGTTTCCTGCCCTCCATGTGCACCTTGATCAGGGGG
ACTGTCGTCGCGCCGTCCC GGACCTCGACTATGTAGAGGGTTCCCTCGACCAAGGACGGGAGGTACACGTGGAAGTACTAGTCCCC

11,305

PINK1

PINK1-201

PINK1-201

TTTTGGAGAACAGGGTCATCACCTTCCGGAGAAGAAAGCCATGCAAAGGGAACATATCTGCCCTGGAGAGCATTTTCCCTGTAG
AAAACCTCTTGTCCCAGTAGTGGGAAGGCCTCTTCTTTCGGTACGTTTCCCTTGTATAGACGGGACCTCTCGTAAAAGGGACATC

11,390

PINK1

PINK1-201

PINK1-201

GACGATTTTTTCATGGAAACAAACTCTCATCTTCATCCAGAACATACTTGTACCTAGTCCTTTTGGTCCATTTGACTGTTAACCT
CTGCTAAAAAGTACCTTTGTTTGAGAGTAGAAGTAGGTCTTGTATGAACAGTGGATCAGGAAAACCAGGTAAACTGACAATTGGA

11,475

PINK1

PINK1-201

PINK1-201

TTTCTGTGGCTGGACTTATCTGTTTTTAACATAAAAACCGTTCTCCTTCCCTCACCTCTGTATCCCCTAACTTTGCTATAGTGGG
AAAGACACCGACCTGAATAGACAAAAATTGTATTTTTGGCAAGAGGAAGGAGTGGGAGACATAGGGGATTGAAACGATATCACCC

11,560

PINK1

PINK1-201

PINK1-201

TATTTTATTTTAAGGAAATAATTATCTGCACCATTACTTTGAATATAGGGAGCCCCAACTCTTACTTCCTAATTTGAGGATGGTG
ATAAAATAAAATTCCTTTATTAATAGACGTGGTAATGAAACTTATATCCCTCGGGGTTGAGAATGAAGGATTAAACTCCTACCAC

11,645

PINK1

PINK1-201

PINK1-201

AGTGGGAGGGAAACAGAAAGGATGCTGGGGAAAAGTGGGAATCAAAGTGCTCCTGGAAGGGGAAGAGGAACGGCCTAACCCCTAACA
TCACCCTCCCTTGTCTTTCCTACGACCCCTTTTCACCCTTAGTTTCACGAGGACCTTCCCTTCTCCTTGCCGGATTGGGATTGT

11,730

PINK1

PINK1-201

PINK1-201

GTGATTAAGGTTATTAGGAGGCCGGGAATGGTGGCTGACGCCTGTAATCCCAGCACTTTGGAAGGCGGAGGTGGGTAGATCACTT
CACTAATTCCAATAATCCTCCGGCCCTTACCACCGACTGCGGACATTAGGGTCGTGAAACCTTCCGCCTCCACCCATCTAGTGAA

11,815

PINK1

PINK1-201

PINK1-201

GAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATGATGAAACCCTGTATCTACTAAACATACAAAAATTAGCCTGGTGTGGTGGC
CTCCAGTCTCAAACCTCTGGTCGGACCGGTTGTACTACTTTGGGACATAGATGATTTGTATGTTTTTAATCGGACCACACCACCG

11,900

PINK1

PINK1-201

PINK1-201

GGGCACCTATAATCCCAGCTACTCGGGAGGCTGAGGTAGGAGAATTGCTTGAACCTGGAAGGTGGAGGTTGCAGTGAGCCAAGAT
CCCGTGGATATTAGGGTCGATGAGCCCTCCGACTCCATCCTCTTAACGAACTTGGACCTTCCACCTCCAACGTCACTCGGTTCTA

11,985

PINK1

PINK1-201

PINK1-201

CGTGCTACTGCACTCCAGCTTGGCGACAGAGTGAGACTCCATCTCAAAAAAAAAAAAAAAAAACGTATTGGGAGTCGTCGATGTGT
GCACGATGACGTGAGGTCGAACCGCTGTCTCACTCTGAGGTAGAGTTTTTTTTTTTTTTTTTGCATAACCCTCAGCAGCTACACA

12,070

PINK1

PINK1-201

PINK1-201

GGTAGCCAGAGGCCCTCTCCCCTCTCCGCCAGCTATCCCTGTACCCTGCGCCAGTACCTTTGTGTGAACACACCCAGCCCCCGCC
CCATCGGTCTCCGGGAGAGGGGAGAGGCGGTCGATAGGGACATGGGACGCGGTCATGGAAACACACTTGTGTGGGTCGGGGGCGG

12,155

PINK1

PINK1-201

Y P C T L R Q Y L C V N T P S P R

ENSE00003693654

PINK1-201

TCGCCGCATGATGCTGCTGTCAGCTGCTGGAAGGCGTGGACCATCTGGTTCAACAGGGGCATCGCGCACAGAGACCTGAAATCCGA
AGCGGCGGTTACTACGACGACGTCGACGACCTTCCGCACCTGGTAGACCAAGTTGTCCCGTAGCGCGTGTCTCTGGACTTTAGGCT

12,240

PINK1

PINK1-201

L A A M M L L Q L L E G V D H L V Q Q G I A H R D L K S D

ENSE00003693654

PINK1-201

CAACATCCTTGTGGAGCTGGACCCAGGTAGGAACCTGCTGCACCATCAGAGCTCTCCAGGGGCACTAGAGGGTGGGTCAGGAGCA
GTTGTAGGAACACCTCGACCTGGGTCCATCCTTGGACGACGTGGTAGTCTCGAGAGGTTCCCGTGATCTCCACCCAGTCTCTCGT

12,325

PINK1

PINK1-201

N I L V E L D P

ENSE00003693654

PINK1-201

TTTAGGACTGACTCTTCAGGTCCTCTCTGGTTTTGTGTTCTAAGTCATGTCTTTATTTAGCTCCGCACACAAGAGGTTAGCAATC
AAATCCTGACTGAGAAGTCCAGGAGAGACCAAAACACAAGATTCAGTACAGAAATAAATCGAGGCGTGTGTTCTCCAATCGTTAG

12,410

PINK1

PINK1-201

PINK1-201

TCTCCCTTAGAACGGGGTTTTTTTTTCTCTCTTTGCAGAGAGACAGCACTTCCCAAGTTCCTTTCTCTAGCCCACTTAAAGAACA
AGAGGGAATCTTGCCCCAAAAAAGAGAGAAACGTCTCTCTGTGCGTGAAGGGTTCAAGGAAAGAGATCGGGTGAATTTCTTGT

12,495

PINK1

PINK1-201

PINK1-201

AGGACCTCAGTGCTGCAAGTTTTCTTAGGTAATAAAGAGGCCCGGCACAGTGGCTGACACCTGTAATCCCAACACTTTGGGAGG
TCCTGGAGTCACGACGTTCAAAGGATCCATTTATTTCTCCGGGCCGTGTCAACCGACTGTGGACATTAGGGTTGTGAAACCTCC

12,580

PINK1

PINK1-201

PINK1-201

CTTGCTTGAGGATTGCTTGAGGCCAGCAGTTTGAGACCAGCCTGGGAAACAGAGTGAGATCCCTTCTCTACAAAAAATATG
GAACGAACTCCTAACGAACTCCGGTCGTCAAACTCTGGTCGGACCCCTTTGTCTCACTCTAGGGAAGAGATGTTTTTTTTTATAC

12,665

PINK1

PINK1-201

PINK1-201

TTTTAAATTAGCCGAAAAAAGTTAGCCAGGCATGGTGGCATGCACCTGTAGCCCCAGCTACTTGGGAGGCTGAGGTCGGAGGA
AAAATTTAATCGGCCTTTTTTTCAATCGGTCCGTACCACCGTACGTGGACATCGGGGTCGATGAACCTCCGACTCCAGCCTCCT

12,750

PINK1

PINK1-201

PINK1-201

TCACCTTGAGCCTAGGAGTTAAGAGTCTGCAATGAGCTATGAATGTGCCACTGTACTCCAGCCTGGGCAGCAGAGTGAGATCCTAT
AGTGAACCTCGGATCCTCAATTCTCAGACGTTACTCGATACTTACACGGTGACATGAGGTCGGACCCGTCGTCTCACTCTAGGATA

12,835

PINK1

PINK1-201

PINK1-201

CTCAAAAAATAATAAAAAATAATAAAGTAAAAGAGAAGTAGACTTTAGCTCATTATAAAAAATAACTTTTCGGCCGGGGGTAGTG
GAGTTTTTTTATTATTTTTTATTATTTTCATTTTCTCTTCATCTGAAATCGAGTAATATTTTTTATTGAAAGCCGGCCCCATCAC

12,920

PINK1

PINK1-201

PINK1-201

GCTCACGCCTGTAATCCCAGCACTTTGAGAGGCTGAGGCGGGCAGATCATGAGGTCAAGAGATCGAGACCATCCTGGCCAACATG
CGAGTGCGGACATTAGGGTCGTGAAACTCTCCGACTCCGCCGTCAGTACTCCAGTTCTCTAGCTCTGGTAGGACCGGTTGTAC

13,005

PINK1

PINK1-201

PINK1-201

GTGAAACCCCATCTCTACTAAAAATACAAAAATTAGCTGGGCATGGTGGCGGGCGCCTGTAATCTCAGCTACTTGGGAAGCTGAG
CACTTTGGGGTAGAGATGATTTTTATGTTTTAATCGACCCGTACCACCGCCCGCGGACATTAGAGTCGATGAACCCCTTCGACTC

13,090

PINK1

PINK1-201

PINK1-201

GCAGGAGAATTGCTTGAACCCGGGAGGCGGAGGTTGTAGTGAGCCGAGATTGTGCCACTGCATTCCAGCCTGGCGACAGAGTGAG
CGTCCTCTTAACGAACTTGGGCCCTCCGCCTCCAACATCACTCGGCTCTAACACGGTGACGTAAGGTCGGACCGCTGTCTCACTC

13,175

PINK1

PINK1-201

PINK1-201

AGTCCATCTCAAAATAAATTAATTAATTAATTAATTTTTCAAACAATGAAAGCTGTCCAAATGTAAGCCCAGTTGCCTCTGGAA
TCAGGTAGAGTTTTATTTAATTAATTAATTAATTTAAAAAGTTTGTACTTTTCGACAGGTTTACATTTCGGGTCAACGGAGACCTT

13,260

PINK1

PINK1-201

PINK1-201

ATGAGTTGCCTACCACTGGAAGCATTCAAGTAGAAGCTGAATGGCCACTTGCCTAGGAAAATTGTAAGGAGATTCATACATCTGA
TACTCAACGGATGGTGACCTTCGTAAGTTCATCTTCGACTTACCGGTGAACGGATCCTTTTAAACATTCTAAGTATGTAGACT

13,345

PINK1

PINK1-201

PINK1-201

TAAATTTTGAAGTAGAAGATTTAAAAATAATTGACTAGAGGAACTGGCTTTTATTATTCTTTATTACTTATTTATTTAT
ATTTAAAAAATTGATCTTCTAAATTTTATTAAGTATCTCCTTGACCGAAAAATAATAAGAAAAATAATAAATGAATAAATAAATA

13,430

PINK1

PINK1-201

PINK1-201

TTATTTATTTGAGACAGAATCTTGCTTTGTTGCCAGGCTGGAGTGCAGTGGCGCCATCTCAGCTCACTGCAACCTCTGCTTCCC
AATAAATAAACTCTGTCTTAGAACGAAACAACGGGTCCGACCTCACGTACC CGGTTAGAGTCGAGTGACGTTGGAGACGAAGGG

13,515

PINK1

PINK1-201

PINK1-201

AGGTTCAAGCAATTCCTCGTGCCTCCGCCTCCTGAGTAGCTAGGATTACAGGCAGGTGCCACCACGCCTAGCTAATTTTTGATTTT
TCCAAGTTCGTTAAGAGCACGGAGGCGGAGGACTCATCGATCCTAATGTCCGTCCACGGTGGTGC GGATCGATTA AAAACTAAAA

13,600

PINK1

PINK1-201

PINK1-201

TTTTTTTTTTTTTTTTTTGAGACTGAGTCTCGCTCTGTCAACCAGGCTGGAGTGCAATGGCATGATCTCGGCTCACTGCAAGCTCT
AAAAAAAAAAAAAAAAAACTCTGACTCAGAGCGAGACAGTGGGTCCGACCTCACGTTACCGTACTAGAGCCGAGTGACGTTTCGAGA

13,685

PINK1

PINK1-201

PINK1-201

ACCTCCCAGGTTACACCATTCTCCTGCTTCAGCCTCCCGAGTAGCTGGGACTACAGGCGCCACCACCACGCCCGGCTAATTTT
TGGAGGGTCCAAGTGTGGTAAGAGGACGAAGTCGGAGGGCTCATCGACCCTGATGTCCGCGGGTGGTGGTGC GGCCGATTAAAA

13,770

PINK1

PINK1-201

PINK1-201

TTTGTATTTTAGTACAGACGGGGTTTACCATTGTTAGCCAGGATGGTCTCTATCTCCTGACTTCGTGATCCACCTGCTTCGGCC
AAACATAAAAATCATGTCTGCCCAAAGTGGTACAATCGGTCTACCAGAGATAGAGGACTGAAGCACTAGGTGGACGAAGCCGG

13,855

PINK1

PINK1-201

PINK1-201

TCCCAAAGCGCTGGGATTATTATTTTGTGGAGATGGGGTTTCACTGTTGGCCAGGCTGGTCTCAAACCTCCTGGCCTCAAGTGA
AGGGTTTCGCGACCCTAATAATAAAAATCACCTCTACCCCAAAGTGACAACCGGTCCGACCAGAGTTTGAGGACCGGAGTTCAC

13,940

PINK1

PINK1-201

PINK1-201

TCCACCCACCTCAGCCTCCAAAATGTTGGGATTACAGGTATGAGCCACCACGCCAGCTGGGAGTTGGCTTTTTTTTTTTTTTTTT
AGGTGGGTGGAGTCGGAGGTTTTTACAACCCCTAATGTCCATACTCGGTGGTGCGGGTCGACCCTCAACCGAAAAAAAAAAAAAA

14,025

PINK1

PINK1-201

PINK1-201

TTTTTTGAGACGGAGTCTCACTCTGTCGCCAGGCTGGAGTGCAGTGGCATGATCTTGGCTCACTGCAACCCCTGCCTATCGGGT
AAAAAACTCTGCCTCAGAGTGAGACAGCGGGTCCGACCTCACGTACCCTACTAGAACCAGGTGACGTTGGGGACGGATAGCCCA

14,110

PINK1

PINK1-201

PINK1-201

TCAAGCAATTCTCCCGCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCACACGCCACTACACCTGGCTGATTTTTTGTATTTTTAG
AGTTCGTTAAGAGGGCGGAGTCGGAGGACTCATCGACCCTAATGTCCGTGTGCGGTGATGTGGACCGACTAAAAACATAAAAAATC

14,195

PINK1

PINK1-201

PINK1-201

TAGAGACGGGGTTTTACCATGTTGGTCAGGCTGATCTGGAACCTCTGACTTCGTGATCCGCCTGCCTCGGCCTCCCAAAGTTCTG
ATCTCTGCCCAAAGTGGTACAACCAAGTCCGACTAGACCTTGAGGACTGAAGCACTAGGCGGACGGAGCCGGAGGGTTTTCAAGAC

14,280

PINK1

PINK1-201

PINK1-201

GGATTACAGGCGTGAGCCACTGCGCCCAGCCAGGAACTGGCTTTTTAAAGGAATTTTGTGTGGACCCTTTTACAAATAACCAATT
CCTAATGTCCGCACTCGGTGACGCGGGTCGGTCCTTGACCGAAAAATTTCTTAAACACACCTGGGAAAAATGTTTATTGGTTAA

14,365

PINK1

PINK1-201

PINK1-201

CTTTTTTATTTTTCTGAGACAGAGTCTCGCTGTGTTGCTCAGGCTGAAGTGATTCTCCTGTCTCAGCCTCCTTCACCTCCCAG
GAAAAAATAAAAAAGACTCTGTCTCAGAGCGACACAACGAGTCCGACTTCACTAAGAGGACAGAGTCGGAGGAAGTGGAGGGTC

14,450

PINK1

PINK1-201

PINK1-201

GTTCAAGTAATTCTCCTGTCTCAGCCTCCCGAGTAGCTGGGATACAGGCACACACCACCATGCCTGGCTAGTTTTTTTTGTATTTT
CAAGTTCATTAAGAGGACAGAGTCGGAGGGCTCATCGACCCTATGTCCGTGTGTTGGTGGTACGGACCGATCAAAAAACATAAAA

14,535

PINK1

PINK1-201

PINK1-201

TAGTAGAGACAGGGGTTTCACCATGTTGGCCAGGCTGGTCTTGAACCTCCTGACCTCAGGTGATCTACCCGCCTCGGCCTCCCAA
ATCATCTCTGTCCCAAAGTGGTACAACCGGTCCGACCAGAACTTGAGGACTGGAGTCCACTAGATGGGCGGAGCCGGAGGGTTT

14,620

PINK1

PINK1-201

PINK1-201

ATGTTGGCATTACAGGCCACCACACCCGGCAATAACTGATTCTTAATGCACCTGGTTCTTAGGTTTGGATTTGGGGTTTTCAAATT
TACAACCGTAATGTCCGGTGGTGTGGGCCGTTATTGACTAAGAATTACGTGGACCAAGAATCCAAACCTAAACCCCAAAGTTTAA

14,705

PINK1

PINK1-201

PINK1-201

CAAATCAAAGTCTCCTGGGGTATAAGGGCCCTTGGAGATCATTGAACCAAGCTCTAGCTCCTTTGGTCTTGGGGACAGCTCCAA
GTTTAGTTTCAGAGGACCCCATATTCCCGGGAACCTCTAGTAAACTTGGTTCGAGATCGAGGAAACCAGAACCCTGTTCGAGGTT

14,790

PINK1

PINK1-201

PINK1-201

TTACTAGAACATGATTTAAATTGAGCCACACAGTCCTTTGCCTGGGGATTTTGCAGCCTGTACTTACTGGAGGCATTTCCGTGTT
AATGATCTTGTACTAAATTTAACTCGGTGTGTCAGGAAACGGACCCCTAAAACGTCGGACATGAATGACCTCCGTAAAGGCACAA

14,875

PINK1

PINK1-201

PINK1-201

CGCACAGCAGGCCCTTCTGATCAGCTCTCAGGCCTTGCTGACCTCCTGGGCCAACACTGAGCCATTAGCCCCTGTCAGCTATGTC
GCGTGTGTCGTCGGGAAGACTAGTCGAGAGTCCGGAACGACTGGAGGACCCGGTTGTGACTCGGTAATCGGGGACAGTCGATACAG

14,960

PINK1

PINK1-201

PINK1-201

TTGCTGGTGGCTTTAGTAGGGACATAGGAGGGCCTCTCAGAGGGAAGGAGGGGAGGAGAAATGGTCACTTTGCTTGTCTCTTCCC
AACGACCACCGAAATCATCCCTGTATCCTCCCGGAGAGTCTCCCTTCCCTCCCTCCTCTTTACCAGTGAAACGAACGAGGAAAGGG

15,045

PINK1

PINK1-201

PINK1-201

AGACGGCTGCCCCCTGGCTGGTGATCGCAGATTTTGGCTGCTGCCTGGCTGATGAGAGCATCGGCCTGCAGTTGCCCTTCAGCAGC
TCTGCCGACGGGGACCGACCACTAGCGTCTAAAACCGACGACGGACCGACTACTCTCGTAGCCGGACGTCAACGGGAAGTCGTCTG

15,130

PINK1

PINK1-201

375 D G C P W L V I A D F G C C L A D E S I G L Q L P F S S 400

ENSE00003662034

PINK1-201

TGGTACGTGGATCGGGGCGGAAACGGCTGTCTGATGGCCCCAGAGGTGAGTCCCGAGTGTGTCATGCGCCATCGGCAGCCCTTCC
ACCATGCACCTAGCCCCGCCTTTGCCGACAGACTACCGGGGTCTCCTACTCAGGGCTCACACAGTACGCGGTAGCCGTGCGGGAAGG

15,215

PINK1

PINK1-201

W Y V D R G G N G C L M A P E

ENSE00003662034

PINK1-201

CCCACATGTCCACTGAATGCAGGAGACTCGATGCCTTGTGATAACCCAACACCTCCATCTTTTTCTGACCCATAATTTGGCACAAG
GGGTGTACAGGTGACTTACGTCTCTGAGCTACGGAACACTATTGGGTTGTGGAGGTAGAAAAGACTGGGTATTAAACCGTGTTTC

15,300

PINK1

PINK1-201

PINK1-201

TTCTTCCCTGCCACTTTGCTTTCTCCGGCGTTCCTCATGTTCCAGGAGAATGCAAGTCTGTACATAAACCAGGTGGTCTA
AAGGAAGGGACGGTGAAACGAAAGGAGGCCGCAAGGGAGTACAAGGTCTCTTACGTTTCAGGACAGTGTATTTGGTCCACCAGAT

15,385

PINK1

PINK1-201

PINK1-201

AGCAGACCCCTTCTGGGTCTGAGCCACAGCTCAAGCTCTGGGTTCTTGGGACAGAGTTCAGATTAGCCCATGGATCAGGT
TCGTCTGGGGAAGACCCAGACTCGGTGTGAGTTCGAGACCCAAGGAACCTGTCTCAAGTCTAATCGGGTACCTAGTCCA

15,470

PINK1

PINK1-201

PINK1-201

GATGTGCAGGACATGAAAAGGTTAGATGGGCGGGCAGCGTGATGTCTCACCCACTGCTTCTGAGCAGGTGTCCACGGCCCGTCTCT
CTACACGTCCTGTACTTTTCCAATCTACCCGCCCGTGCCTACAGAGTGGGTGACGAAGACTCGTCCACAGGTGCCGGGCAGGA

15,555

PINK1

PINK1-201

V S T A R P
ENSE00003524815

PINK1-201

GGCCCCAGGGCAGTGATTGACTACAGCAAGGCTGATGCCTGGGCAGTGGGAGCCATCGCCTATGAAATCTTCGGGCTTGTCAATC
CCGGGGTCCCGTCACTAACTGATGTGCGTTCCGACTACGGACCCGTCAACCTCGGTAGCGGATACTTTAGAAGCCCGAACAGTTAG

15,640

PINK1

PINK1-201

G P R A V I D Y S K A D A W A V G A I A Y E I F G L V N

ENSE00003524815

PINK1-201

CCTTCTACGGCCAGGGCAAGGCCACCTTGAAAGCCGCGAGCTACCAAGAGGCTCAGCTACCTGCACTGCCCGAGTCAGTGCCTCC
GGAAGATGCCGGTCCCGTTCGGGTGGAACCTTCGGCGTCGATGGTTCTCCGAGTCGATGGACGTGACGGGCTCAGTCACGGAGG

15,725

PINK1

PINK1-201

P F Y G Q G K A H L E S R S Y Q E A Q L P A L P E S V P P

ENSE00003524815

PINK1-201

AGACGTGAGACAGTTGGTGAGGGGCACTGCTCCAGCGAGAGGGCCAGCAAGGTGAGGGCTGTCCCCGGCTTCGAGGGGGACGGTGTGGG
TCTGCACTCTGTCAACCACTCCCCTGACGAGGTCGCTCTCCGGTCGTTCCACTCCGACAGGGGGCCGAAGCTCCCCTGCCACACCC

15,810

PINK1

PINK1-201

D V R Q L V R A L L Q R E A S K
485 490 495

ENSE00003524815

PINK1-201

TAGAAACCTCTGTTCTCGTTCAGAGTGAAGGTCAGGTTTGGGCCAGAGCCACAGTGACAGATCCTCTGTGTTAGGAAGGTAAAG
ATCTTTGGAGACAAGAGCAAGGTCCTCACTTCCAGTCCAAACCCGGTCTCGGTGTCAGTGTCTAGGAGACACAATCCTTCCATTTC

15,895

PINK1

PINK1-201

PINK1-201

GCTAGTTACAAGAGAACAAAAACAGATTTTAATGTAGGTAGGAGTAGGAGCACTAGCCACCACAGCATAGTCAGAATCCTAGCA
CGATCAATGTTCTCTTGTGTTTTGTCTAAAATTACATCCATCCTCATCCTCGTGATCGGTGGTGTGATCAGTCTTAGGATCGT

15,980

PINK1

PINK1-201

PINK1-201

GTTCAACTCCTGTGGCTTTTTTAGTTGCTGAAAAAGTTGTTTCAGAGGCCAGACACGGTGGCTTACACCTATAATCACAGCACTTT
CAAGTTGAGGACACCGAAAAAATCAACGACTTTTTCAACAAGTCTCCGGTCTGTGCCACCGAATGTGGATATTAGTGTGCTGAAA

16,065

PINK1

PINK1-201

PINK1-201

GGGAGGCTGAGGCGGGTGGATCACTTGGGACCAGGAGTTCCAGTCCAGCCTGGCCAACATGGTAAAACCCCGTCTGTACTAAAAA
CCCTCCGACTCCGCCACCTAGTGAACCCTGGTCTCAAGGTCAGGTCGGACCGGTTGTACCATTTTGGGGCAGACATGATTTTT

16,150

PINK1

PINK1-201

PINK1-201

TACAAAAATTAGCTGAGTGTGCTGGCACACGCCTGTAATTCCAGGTAICTGGGAGGCTGAAGCAGGAGAATCGTTTGAACCCTGG
ATGTTTTTAATCGACTCACAGCACCGTGTGCGGACATTAAGGTCCATGAGCCCTCCGACTTCGTCTCTTAGCAAACCTTGGGACC

16,235

PINK1

PINK1-201

PINK1-201

AGGCAGAGGTTGCAGTGAGCCAAGATCGCGCCACTGCACTCTGGCCTAGGTGACAGTGCAAGTCTTTGTCTCAAAAAAAAAAAAA
TCCGTCTCCAACGTCAGTCCGGTCTAGCGCGGTGACGTGAGACCGGATCCACTGTACAGTTCAGAAACAGAGTTTTTTTTTTTTT

16,320

PINK1

PINK1-201

PINK1-201

AAAAAAAAAGGCTATTCAGAGAGAGAAAAAGGAGGCATTTTTTGAGAAATGTTTAATGGAGATGTAGCTCATGGAAGCAGCTGAGAA
TTTTTTTTTCCGATAAGTCTCTCTCTTTTTCTCCGTA AAAACTCTTTACAAATTACCTCTACATCGAGTACCTTCGTCGACTCTT

16,405

PINK1

PINK1-201

PINK1-201

CTGATCAGAGAGAGATGGAAAACATCTCCTGAGAGCAGATCTGGACATTGTGAAATTAATATAAAGGAATGCAAAGGCAGACCTA
GACTAGTCTCTCTCTACCTTTTGTAGAGGACTCTCGTCTAGACCTGTAACACTTTAATTATATTTCTTACGTTTCCGTCCTGGAT

16,490

PINK1

PINK1-201

PINK1-201

TCCGAAGCCATAATTGGAGTGGCAGCTGGCTCAGGGGCAGGCTTAGTGCAAAGAGCTGAGCCATACCTGCACCCCAAGCACTGTTC
AGGCTTCGGTATTAACCTCACCGTCGACCGAGTCCCGTCCGAATCACGTTTCTCGACTCGGTATGGACGTGGGGTCGTGACAAG

16,575

PINK1

PINK1-201

PINK1-201

TGCCACTCCGTTAACTGCTCTCTGTACGTGGCCTGCTATCTTGGTGCGCAGTGAAGGTTAGAACAACAGCTGCAACCAGTTATGA
ACGGTGAGGCAATTGACGAGAGACATGCACCGGACGATAGAACCACGCGTCACTTCCAATCTTGTGTGTCGACGTTGGTCAATACT

16,660

PINK1

PINK1-201

PINK1-201

AATGATAGAGGAGACTACTTACCTGGTTCAAGGGACCAGATAGCTGTGCACAAGAGGCCACTAGGCTTTCCACCCAGGGGGAAAAGG
TTACTATCTCCTCTGATGAATGGACCAAGTTCCTGGTCTATCGACACGTGTTCTCCGTGATCCGAAAAGGTGGGTCCCCCTTTCC

16,745

PINK1

PINK1-201

PINK1-201

CTATTTCAACAATGCATGCTGCCCATGCAGAGGTGTACACATGGAAAAGCTTGGAGCACGGGCAGGGGACAGGCAGTATTTGTC
GATAAAGTTGTTACGTACGACGGGTACGTCTCCACATGTGTACCTTTTCGAACCTCGTGCCCGTCCCCTGTCCGTCATAAACAG

16,830

PINK1

PINK1-201

PINK1-201

ACCTGAGTGAAGGGCATCAGTAGGAGATAGGGTAGAGGAAGAATTGGGTTGGGACCAGAGAAGGGGAAGACCCTCACTAACAAAGC
TGGACTCACTTCCCGTAGTCATCCTCTATCCCATCTCCTTCTTAACCCAACCCTGGTCTCTTCCCTTCTGGGAGTGATTGTTTCG

16,915

PINK1

PINK1-201

PINK1-201

AGGCTTTGGGTTGAGACTGTGTTAACAGATGTTCTAGCTACAGCTTCCCTTCTGTTGCAGAGACCATCTGCCCGAGTAGCCGCA
TCCGAAACCCAACCTCTGACACAATTGTCTACAAGATCGATGTCGAAGGGAAGGACAACGTCTCTGGTAGACGGGCTCATCGGCCT
PINK1
PINK1-201
R P S A R V A A
ENSE00001543152
PINK1-201

AATGTGCTTCATCTAAGCCTCTGGGGTGAACATATTCTAGCCCTGAAGAATCTGAAGTTAGACAAGATGGTTGGCTGGCTCCTCC
TTACACGAAGTAGATTTCGGAGACCCCACTTGTATAAGATCGGGACTTCTTAGACTTCAATCTGTTCTACCAACCGACCGAGGAGG
PINK1
PINK1-201
505 510 515 520 525 530
N V L H L S L W G E H I L A L K N L K L D K M V G W L L
ENSE00001543152
PINK1-201

AACAATCGGCCGCCACTTTGTTGGCCAACAGGCTCACAGAGAAGTGTGTTGTGGAAACAAAAATGAAGATGCTCTTTCTGGCTAA
TTGTTAGCCGGCGGTGAAACAACCGGTTGTCCGAGTGTCTCTTCAACAACACACCTTTGTTTTACTTCTACGAGAAAGACCGATT
PINK1
PINK1-201
535 540 545 550 555 560
Q Q S A A T L L A N R L T E K C C V E T K M K M L F L A N
ENSE00001543152
PINK1-201

CCTGGAGTGTGAAACGCTCTGCCAGGCAGCCCTCCTCCTCTGCTCATGGAGGGCAGCCCTGTGATGTCCCTGCATGGAGCTGGTG
GGACCTCACACTTTGCGAGACGGTCCGTCGGGAGGAGGAGACGAGTACCTCCCGTCCGGGACACTACAGGGACGTACCTCGACCAC
PINK1
PINK1-201
565 570 575 580
L E C E T L C Q A A L L C S W R A A L
ENSE00001543152
PINK1-201

AATTACTAAAAGAACATGGCATCCTCTGTGTCGTGATGGTCTGTGAATGGTGAGGGTGGGAGTCAGGAGACAAGACAGCGCAGAG
TTAATGATTTTCTTGTACCGTAGGAGACACAGCACTACCAGACACTTACCACTCCACCCCTCAGTCCCTCTGTTCTGTGCGCTCTC
PINK1
PINK1-201
AGGGCTGGTTAGCCGGAAAAGGCCTCGGGCTTGGCAAATGGAAGAACTTGAGTGAGAGTTCAGTCTGCAGTCCTCTGCTCACAGA
TCCCGACCAATCGGCCTTTTCCGGAGCCCGAACCGTTTACCTTCTTGAACTCACTCTCAAGTCAGACGTACAGGAGACGAGTGTCT
PINK1
PINK1-201

CATCTGAAAAGTGAATGGCCAAGCTGGTCTAGTAGATGAGGCTGGACTGAGGAGGGGTAGGCCTGCATCCACAGAGAGGATCCAG
GTAGACTTTTCACTTACCGGTTTCGACCAGATCATCTACTCCGACCTGACTCCTCCCATCCGGACGTAGGTGTCTCTCCTAGGTC
PINK1
PINK1-201

GCCAAGGCACTGGCTGTGTCAGTGGCAGAGTTTGGCTGTGACCTTTGCCCTAACACGAGGAACTCGTTTGAAGGGGGCAGCGTAGC
CGGTTCCGTGACCGACAGTCAACCGTCTCAAACCGACACTGGAAACGGGGATTGTGCTCCTTGAGCAAACCTTCCCCCGTCGCATCG
PINK1
PINK1-201

ATGTCTGATTTGCCACCTGGATGAAGGCAGACATCAACATGGGTCAGCACGTTTCAGTTACGGGAGTGGGAAATTACATGAGGCCT
TACAGACTAAACGGTGGACCTACTTCCGTCTGTAGTTGTACCCAGTCGTGCAAGTCAATGCCCTCACCCCTTAAATGTA CTCCGGA

17,680

PINK1

PINK1-201

GGGCCTCTGCGTTCCCAAGCTGTGCGTTCTGGACCAGCTACTGAATTATTAATCTCACTTAGCGAAAAGTGACGGATGAGCAGTAA
CCCGGAGACGCAAGGGTTCGACACGCAAGACCTGGTCGATGACTTAATAATTAGAGTGAATCGCTTTCCTACTGCCTACTCGTCATT

17,765

PINK1

PINK1-201

GTAAGTAAGTGTGGGGATTTAAACTTGAGGGTTTCCCTCCTGACTAGCCTCTCTTACAGGAATTGTGAAATATTAATGCAAATT
CATTTCATTACACCCCTAAATTTGAACTCCCAAAGGGAGGACTGATCGGAGAGAATGTCCTTAACACTTTATAATTTACGTTTAA

17,850

PINK1

PINK1-201

TACAACTGCAGATGACGTATGTGCCTTGAACCTGAATATTTGGCTTTAAGAATGATTCTTATACTCTGAAGGTGAGAATATTTTGT
ATGTTGACGTCTACTGCATACACGGAACCTTGACTTATAAACCGAAATTCCTACTAAGAATATGAGACTTCCACTCTTATAAAACA

17,935

PINK1

PINK1-201

GGGCAGGTATCAACATTGGGGAAGAGATTTTCATGTCTAACTAACTAACTTTATACATGATTTTTAGGAAGCTATTGCCTAAATCA
CCCGTCCATAGTTGTAACCCCTTCTCTAAAGTACAGATTGATTGATTGAAATATGTAATAAAAAATCCTTCGATAACGGATTTAGT

18,020

PINK1

PINK1-201

GCGTCAACATGCAGTAAAGGTTGTCTTCAACTGA
CGCAGTTGTACGTCATTTCCAACAGAAGTTGACT

3'

18,054

5'

PINK1

PINK1-201

Feature	Location	Size		Type
✓ PINK1	1 .. 18,054	18,054 bp	■ →	gene
/note	= gene ENSG00000158828 Protein coding			
✓ PINK1-201	1 .. 18,054	18,054 bp	■ →	prim_transcript
/note	= primary transcript ENST00000321556			
✓ PINK1-201	92 .. 17,234	17,143 bp	■ →	CDS
▶ 8 segments = 1746 bp				
/note	= coding sequence ENSP00000364204			
/translation	= MAVRQALGRGLQLGRALLLRF TGKPGRAYGLGRPGPAA GCVRGERPGWAA GPGAEP RRVGLGLPNLRRFFRQSVAGLAARLQRQFVVRAW GCAGPCGRAVFLAFGLGLG LIEEKQAESRRAVSACQEIQ,,AIFTQKSKPGDPDLTRRLQGFRLEEYLI GQSIGKGC SAAVYEATMPTLPQNL EVTKSTGLLPGRGPGTSA PEGEQERAPGAPAFPLAIKMMWNIS,,AGSSSEAILNTMSQELVPA SRVALAGEYGAVTYR,,KSKRGPQKLA PHP NIIRVLRA FTSSVPLLPGALVDY PDVLP SRLHPEGLGHGRTLFLVMKN,,YPC TLRQYLCVNT P SPRLAAMMLLQLLEGV DHLVQQGIAHRDLK SDNILVELDP,,DGCPWLVIADFGCCLADESIGLQLPFSSWYVDRGGNGCLMAPE,,VSTARPGPRAVIDYSKADA WAVGAIAYEIFGLV NPFY GQGKAHLESRSYQEAQLPALPESVPPDVRQLV RALLQREASK,,RPSARVAANV LHLSLWGEHILAKNLKLDKMGV GLLQQAATLLANRLT 5'CGTTCATKMLLADLLECFALCQAALLCSWRAAL*			
MIR6084	222 .. 331	110 bp	■ →	gene
/note	= gene ENSG00000284005 miRNA			
MIR6084-201	222 .. 331	110 bp	■ →	prim_transcript
/note	= primary transcript ENST00000622012 miRNA			
✓ Donor Sequence WT -> SNV	4582 .. 4681	100 bp	■ ⇌	misc_feature
✓ PAM	4641 .. 4643	3 bp	■ ⇌	misc_feature
✓ gRNA Protospacer Sequence	4644 .. 4663	20 bp	■ ⇌	misc_feature
✓ SNV	4647 .. 4647	1 bp	■ ⇌	misc_feature
/note	= WT = C SNV = A			
PINK1-203	4672 .. 17,859	13,188 bp	■ →	prim_transcript
/note	= primary transcript ENST00000492302 protein_coding_CDS_not_defined			
PINK1-AS	9200 .. 18,736	9537 bp	■ ←	gene
/note	= gene ENSG00000117242 lncRNA			
PINK1-AS-201	9200 .. 18,736	9537 bp	■ ←	prim_transcript
/note	= primary transcript ENST00000451424 lncRNA			
PINK1-202	12,051 .. 18,053	6003 bp	■ →	prim_transcript
/note	= primary transcript ENST00000400490 protein_coding_CDS_not_defined			

Primer	Length	Binding Sites	Tm	Date Added
✓ PCR Forward	25-mer	4386 .. 4410	57°C	May 5, 2023
/sequence	= CAATTTTACCCAGAAAAGCAAGCC			
	40% GC / 7603.0 Da			
✓ Sanger Sequencing Primer	20-mer	4465 .. 4484	56°C	May 5, 2023
/sequence	= TCTGATAGGGCAGTCCATTG			
	50% GC / 6148.1 Da			
✓ Donor Template WT -> SNV	100-mer	4582 .. 4681	82°C	May 5, 2023
/sequence	= CCCAGGTACCAAGTGCACCAGGAGAAGGGCAGGAGCGAGCTCCGGGGGCCCCCTGCCTTCCCCTTGGACATCAAGATGATGTGGAAC			
	57% GC / 7607.5 Da			
✓ gRNA Protospacer	20-mer	4644 .. 4663	57°C	May 5, 2023
/sequence	= CCACATCATCTTGATGGCCA			
	50% GC / 6037.0 Da			
✓ PCR Reverse	25-mer	5404 .. 5428	58°C	May 5, 2023
/sequence	= ttaaaggaagagatccagttcccc			
	44% GC / 7659.1 Da			