

5'

3'

CGCTTGCCTCTCGGGTAGCCGCGGGACCTAGCTGGGTGACAGACGGGAAGTTGCGGGCTGCCAGCGAAGCGGACCGGGCCGGGTGGAG
GCGAACGGAGAGCCCATCGGCGCCCTGGATCGACCCACGTCTGCCCTTCAACGCCGACGGTTCGCTTCGCCTGGCCGGCCACCTC

85

POLG

POLG-201

GCCACACGCTACCCCGAGGCTGCGTAGGCCGCGCGAAGGGGGACGCCGTGCCGTGGGCCTGGGGTTCGGGGAGCAGCAGACCGGG
CGGTGTGCGATGGGGCTCCGACGCATCCGGCGCGCTTCCCCCTGCGGCACGGCACCCGGACCCAGCCCCCTCGTCTGTCTGGCCC

170

POLG

POLG-201

AAGCACCGTGAGGACCGAGGTTTCCGGCGGGGTCGGCGGGGGAGGCCGGGTCGCTGAGCGACGGCGCGGCCCTCCCTCTCCA
TTCGTGGCACTCCTGGCTCCAAAGGCCGCCAGCCGCGCCCTCCGGCCAGCGACTCGCTGCCGCGCCGGGGAGGGAGAGGT

255

POLG

POLG-201

GTCAGGGAGCGAGGCCCGGAGCAGGGCGGGCTAGTCCAGGGCGCACCCGCGGCCTCTGCCGGGCGCAGGGCGGGCGGGGG
CAGTCCCTCGCTCCGGGCTCGTCCC GCCGCGATCAGGGTCCCGCGTGGCGCCGCGGAGACGGCCCGCTCCGCCCGCCGCC

340

POLG

POLG-201

CGCACGGGGGTGGCCGCCGACTCCTCCTGCAGGACGCTCTCGGCCGGGTGGGCCGTGGTCCGGGTGTGGGTGTGGGTCCCGGGGG
GCGTGGCCCCACCGGGCGGCTGAGGAGGACGTCTGCGAGAGCCGGCCACCCGGCACCAGGGCCACACCCACACCCAGGGGCCCCC

425

POLG

POLG-201

ACGGCGGGCCACCCTGCGGGTTTGAATCCGGGCGCTGGCACCTCTCGACGCTAGGCCCGCGCCGGTTCGCGGTAATGGCAGCCACC
TGCCGCGGGGTGGGACGCCAAGCTTAGGCCCGCGACCGTGGAGAGCTGCGATCCGGGCGCGGCCAGCGCCATTACCGTCTGGTGG

510

POLG

POLG-201

ATTTGCCGAGCGCTTGCCAAGAGCAGGGCCGACGACATAGGCCGCCCTGTGTCCCCCAGACAGCAGCCCGGTGTGACAGGCAGAA
TAAACGGCTCGCGAACGGTTCTCGTCCCGGCGTGTGTATCCGCGGGACACAGGGGGTCTGTCTCGGTCGAGCTCTTCCGTTCTT

595

POLG

POLG-201

TCCGTAATCCCATTTTACAGAATAGGATATCAGGGCCTAAGGAGCTTTGCCAAGGTCACACAGCTCGAGAGAGCCAGAAGCGGG
AGGCATTAGGGTAAAATGTCTTATCCTATAGTCCCAGGATTCTCGAAACGGGTTCCAGTGTGTCTGAGCTCTCTCGGTCTTCGCCC

680

POLG

POLG-201

GTTCAAAACCGCGTCGCCCTACTCCAGATACTGCTCTTACTCGCTGCCCTCGGCTTCCCACGTGGGTTCACTGACGAAAGTTG
CAAGTTTTGGCGCAGCGGGATGAGGTCTATGACGAGAGAATGAGCGACGGGAGCCGAAGGGGTGCACCCAAGTGACTGCTTCAAC

765

POLG

POLG-201

CGTGGACCCCGGTTCCCCAGGAGGGGATTGACGTTTTCCAAGTTTTGAGGCTTAACGGAAAATGCAACTGAAGCGCCTGGCAC
GCACCTGGGGCCAAAGGGGTCCTCCCATAACTGCAAAGGGTTCAAACTCCGAATTGCCTTTTACGTTGACTTCGCGGACCGTG

850

POLG

POLG-201

AGTGTGGGGACGCGAGTAAATGCTCAAGGAATGATGATTATGGATACACCTATTACATATATGGTAAAAATAACGCTTTATATCAT
TCACAACCCCTGCGTCATTTACGAGTTCCCTTACTACTAATACTATGTGGATAATGTATATACCATTTTATTGCGAAATATAGTA

935

POLG >

POLG-201 >

CTGTCTCCTTTAGGATTTGGGGTGGAAGGCAGGCATGGTCAAACCCATTTCACTGACAGGAGAGCAGAGACAGGACGTGTCTCTC
GACAGAGGAAATCCTAAACCCACCTTCCGTCCGTACCAGTTTGGGTAAGTGACTGTCCCTCTCGTCTCTGTCTCTGCACAGAGAG

1020

POLG >

POLG-201 >

TCCACGTCTTCCAGCCAGTAAAGAAGCCAAGCTGGAGCCCAAAGCCAGGTGTTTCTGACTCCCAGCGTGGGGGTCCCTGCACCAA
AGGTGCAGAAGGTCGGTCATTTTCTTCGGTTCGACCTCGGGTTTCGGTCCACAAGACTGAGGGTCGCACCCCAAGGGACGTGGTT

1105

POLG >

POLG-201 >

CCATGAGCCGCCTGCTCTGGAGGAAGGTGGCCGGCGCCACCGTCGGGCCAGGGCCGGTTCCAGCTCCGGGGCGCTGGGTCTCCAG
GGTACTCGGGCGACGAGACCTCCTTCCACCGGCCGCGGTGGCAGCCCGGTCCCGCCAAGGTCGAGGGCCCCGCGACCCAGAGGTC

1190

POLG >

POLG-201 >

1 5 10 15 20 25
M S R L L W R K V A G A T V G P G P V P A P G R W V S S

ENSE00000943530 >

POLG-201

CTCCGTCCCCGCGTCCGACCCACGCGACGGGCGGCGGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAACAGCAGCCT
GAGGCAAGGGGCGCAGGCTGGGGTCTGCTGCCCGTCCGCGGCGCGCGTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTTGTCTGTCGGA

1275

POLG >

POLG-201 >

30 35 40 45 50 55
S V P A S D P S D G Q R R Q Q Q Q Q Q Q Q Q Q P

ENSE00000943530 >

POLG-201

CAGCAGCCGCAAGTGCTATCCTCGGAGGGCGGGCAGCTGCGGCACAACCCATTGGACATCCAGATGCTCTCGAGAGGGCTGCACG
GTCGTCGGCGTTCACGATAGGAGCTCCCGCCCGTTCGACGCGCGTTGGGTAACCTGTAGGTTCTACGAGAGCTCTCCCGACGTC

1360

POLG >

POLG-201 >

60 65 70 75 80
Q Q P Q V L S S E G G Q L R H N P L D I Q M L S R G L H

ENSE00000943530 >

POLG-201

AGCAAATCTTCCGGCAAGGAGGGGAGATGCCTGGCGAGGCGCGGTCGCGCCGACGCTCGAGCACCTGCAGAAGCACGGGCTCTG
TCGTTTAGAAGCCCGTTCTCCCTCTACGGACCGCTCCGGCGCCACGCGGCGTCGACGCTCGTGGACGTCTTCTGTGCCCCGAGAC

1445

POLG >

POLG-201 >

85 90 95 100 105 110
E Q I F G Q G G E M P G E A A V R R S V E H L Q K H G L W

ENSE00000943530 >

POLG-201

GGGGCAGCCAGCCGTGCCCTTGCCCGACGTGGAGCTGCGCCTGCCGCCCTCTACGGGGACAACCTGGACCAGCACTTCCGCCTC

CCCCGTCGGTCGGCACGGGAACGGGCTGCACCTCGACGCGGACGGCGGGGAGATGCCCTGTTGGACCTGGTTCGTGAAGGCGGAG

1530

POLG

POLG-201

115 120 125 130 135 140
G Q P A V P L P D V E L R L P P L Y G D N L D Q H F R L

ENSE00000943530

POLG-201

CTGGCCCAAGAAGCAGAGCCTGCCCTACCTGGAGGCGGCCAACTTGCTGTTGACAGGCCAGCTGCCCCCGAAGCCCCCGGCTTGGG

GACCGGGTCTTCGTCTCGGACGGGATGGACCTCCGCCGGTTGAACGACAACGTCCGGGTCGACGGGGGCTTCGGGGGCGCAACCC

1615

POLG

POLG-201

145 150 155 160 165
L A Q K Q S L P Y L E A A N L L L Q A Q L P P K P P A W

ENSE00000943530

POLG-201

CCTGGGCGGAGGGCTGGACCCGGTACGGCCCCGAGGGGGAGGCCGTACCCGTGGCCATCCCCGAGGAGCGGGCCCTGGTGTTCGA

GGACCCGCCTCCCGACCTGGGCCATGCCGGGGCTCCCCCTCCGGCATGGGCACCGGTAGGGGCTCCTCGCCCGGGACCAAGCT

1700

POLG

POLG-201

170 175 180 185 190 195
A W A E G W T R Y G P E G E A V P V A I P E E R A L V F D

ENSE00000943530

POLG-201

CGTGGAGGTCTGCTTGGCAGAGGGAACTTGCCCCACATTGGCGGTGGCCATATCCCCCTCGGCCTGGTAAGTAGGGGCAGGGTTG

GCACCTCCAGACGAACCGTCTCCCTTGAACGGGGTGTAAACGCCACCGGTATAGGGGGAGCCGGACCATTTCATCCCCGTCCCAAC

1785

POLG

POLG-201

200 205 210 215 220
V E V C L A E G T C P T L A V A I S P S A W

ENSE00000943530

POLG-201

GGGACATAAGCAGGCATGGGGGCCAGCTTAATAGTTTGTTCAGTGAACATTTTCTGAGGTCCTGTTACGGGCTGGGTGCTCAC

CCCTGTATTTCGTCCGTACCCCCGGGTCGAATTATCAAACAAAGTCACTTGTAAAAGACTCCAGGACAATGCCCGACCCACGAGTG

1870

POLG

POLG-201

POLG-201

GTAGGGAGCGCTGATGTGTTGAATTAGGACTAGACCCCTGTTTATGTGGGACTCACTTTCTGGTGGGAAGATCACAGGCAGTAAG

CATCCCTCGCGACTACACAACCTTAATCCTGATCTGGGGACAAATACACCCTGAGTGAAAGACCACCTTCTAGTGTCCGTCATTC

1955

POLG

POLG-201

POLG-201

CAAATACCCAAGTAAATGTCAGGCAGTAAAGGCCACGCAGAGAATCACAGTAGAGCGCTGTACATGAGACCTTCGGGAGGCCACT

GTTTATGGGTTTCAATTTACAGTCCGTCATTTCCGGTGCCTCTTCTAGTGTCTCTCGCGACATGTAATCTGGAAGCCCTCCGGTGA

2040

POLG

POLG-201

POLG-201

TAAGATCACGGTGATTTGGTGCCTTTACCCCTCTCCTAATAGCGTCATGAGAAAGTTAGTCTGAAAAGTCATTTGAACAGTGTTT
ATTCTAGTGCCACTAAACCACGGAAATGGGGGAGAGGATTATCGCAGTACTCTTCAATCAGACTTTTTCAGTAAACTTGTCAAAA

2125

POLG

POLG-201

POLG-201

CTATTTGGGGAGCTATTAATTATTTTGGGCGGTAGAAAGCTCCCTTTTGTGGGACTGTCCCAGGCAGTATAGGACATTTAGCATC
GATAAACCCCTCGATAATTAATAAAACCCGCCATCTTTCGAGGGAAAAACACCCTGACAGGGTCCGTCATATCCTGTAAATCGTAG

2210

POLG

POLG-201

POLG-201

CCCAGCCTTTCCCATAAACGCCAGACCAACACCCCCCGCCCCCTGCCCCCGCCGGCAACGTTTCCAGACGCCCCCTTGAGGTG
GGGTCGAAAGGGTATTTGCGGTCTGGTTGTGGGGGGGCGGGGGGACGGGGGCGGCCGTTGCAAAGGTCTGCGGGGAACTCCAC

2295

POLG

POLG-201

POLG-201

GCATCTGGTTGACCACCCCTAGTTGAGAAACATTGCTTCCTTCCCCAGCCTTCCAAGCAGGCATTTTGGTCCCAAACAAGTATA
CGTAGACCAACTGGTGGGGATCAACTCTTTGTAACGAAGGAAGGGGGTCGGAAGGTTTCGTCCGTAAAACAGGGTTTGTTCATAT

2380

POLG

POLG-201

POLG-201

TCCAATCTCTCTTTTCTTTTAAATAACTTTCTAAGTGCTACCCAAGTTTCTTTTTCAAACAATGATGGCAGTACTGTTTCTCCC
AGGTTAGAGAGAAAAGAAAAATTTATTGAAAGATTACGATGGGTTCAAAGAAAAAGTTTGTACTACCGTCATGACAAAAGAGGG

2465

POLG

POLG-201

POLG-201

CTTTTTTATTCTTCATTCCAGGATTAATACTATTTACAACCTTAATGCTTTTCAGGCATGGCCAGCAAAAAAGTTGGCAGTTT
GAAAAAATAAGAAGTAAGGTCCTAATTTTATGATAAATGTTGGAATTACGAAAAGTCCGTACCGGTCGTTTTTTCAACCGTCAAA

2550

POLG

POLG-201

POLG-201

CTTTATTCCTATTGGAAGCTACATCTTTGTAAAGAAAGCTGCGAAATGTTAAATATGCAGTTGAAAATGGTGAAAACATGGCTAA
GAAATAAGGATAACCTTCGATGTAGAAACATTTCTTTCGACGCTTACAATTTATACGTCAACTTTTACCACTTTTGTACCGATT

2635

POLG

POLG-201

POLG-201

ATAGATAAGGTAGGCATTAATGGCTGAAAAGAGCAAACTAGATGATTCTGCATTGATTGAGTTCCAGTTACAATGAGAATCACA
TATCTATTCCATCCGTAATTACCGACTTTTCTCGTTTTGATCTACTAAGACGTAACCTCAAGGTCAATGTTACTCTTAGTGT

2720

POLG

POLG-201

POLG-201

CTACTTAGAATATGTAACCTTGATGGTCAAAGTAAAGGGGAATATCGGCCATCATTGAAAAGATAAAGTAGGCTTTGGTGGCTGA
GATGAATCTTATACATTGAACTACCAGTTTCATTTCCCTTATAGCCGGTAGTAACTTTTCTATTTTCATCCGAAACCACCGACT

2805

POLG

POLG-201

POLG-201

AAGAAAATTAGGAAACCAGTGACAAGAAAGATTTGTTTTTGTCTGTCGGTCATTTTAGGCCAAATTACCTCAAGTCCCCTTTT
TTCTTTTAATCCTTTGGTCACTGTTCTTTCTAAACAAAAAACTAGACAGCCAGTAAAATCCGGTTAATGGAGTTCAGGGGAAAA

2890

POLG

POLG-201

POLG-201

CTTTTCTCTTTCTCCTTCTTTCTCTCTTTTTACCTCTCCTTTCCCTCCCTGTCCTTCCCTGCTCTGCCCTCATTCTCATTCCATT
GAAAAGAGAAAGAGGAAGAAAGAGAGAAAAATGGAGAGGAAAGGGAGGGACAGGAAGGGACGAGACGGGAGTAAGAGTAAGGTAA

2975

POLG

POLG-201

POLG-201

CTTGCCAGTGGTACTCGGGGCATTGCTTAGTTGACCTGATGGCAGAAAGTCACTGTTAAGGCCTGGGCTCATGCTGGGACCTTCCCT
GAACGGTCACCATGAGCCCCGTAACGAATCAACTGGACTACCGTCTTCAGTGACAATTCCGGACCCGAGTACGACCCTGGAAGGA

3060

POLG

POLG-201

POLG-201

CCTGGGAGTCTGACTGGTGGGTGGGGGTGGGTGCCACATGGTGCCTAATAGCGGTCCACTTTGAACCTGGGCATGCCCTGCC
GGACCCTCAGACTGACCACCCACCCACCCACGGTGTACCACGGGATTATCGCCAGGTGAAACTTGGACCCGTACGGGGACGGG

3145

POLG

POLG-201

POLG-201

CTTAGCTGAGTAACATTAGGTACCTGACCAGCCCACAATTTACAATGGGAGGAGAAGCGGTAGTCAGCTATGAGCCTCCCACAGG
GAATCGACTCATTGTAATCCATGGACTGGTGGGTGTTAAATGTTACCTCCTCTTCGCCATCAGTCGATACTCGGAGGGTGTCC

3230

POLG

POLG-201

POLG-201

GCAGCTTCTTCCCAAAGGGTGTGGTAAGGGCTTCGGCCATCAGGCTAGAGGGACGTCTCTCTGGCCATCAGCATTCTTTCTAAGA
CGTCGAAGAAGGGTTTCCCAACACCATTCCCGAAGCCGGTAGTCCGATCTCCCTGCAGAGAGACCCGGTAGTCGTAAAAAGATTCT

3315

POLG

POLG-201

POLG-201

TTCACAGTAAACTAGTATTAATGGCATGGATCCCTACTCATCTTAAATTTGGCTTGTCTTTTAAATCACTAGTTTATAATAT
AAGTGTCAATTTGATCATAATTACCGTACCTAGGGATGAGTAGAATTTAAACCGAACAAAGAAAAATTAGTGATCAAATATTATA

3400

POLG

POLG-201

POLG-201

GGCTTCATGCACAGCTGCAGAGCTGCATCTTGACACCCAGTGTGGCTTTTTACTGTAACCAAAGTTCCTGTTACCACCATGGCCTC
CCGAAGTACGTGTGACGCTCTCGACGTAGAACTGTGGTCACACCGAAAAATGACATTGGTTTTCAAGGACAATGGTGGTACCGGAG

3485

POLG

POLG-201

POLG-201

AAAGATTTGGCATTCTTTAGCCTTTTTGTCTGCGTTGTTTTAAGGGCTTTGACATGCTGAATTAANAATGTGGGGGGGTGGGGATT
TTTTCTAAACCGTAAGAAATCGGAAAAACAGACGCAACAAAATTCCCGAAACTGTACGACTTAATTTTACACCCCCCACCCTAA

3570

POLG

POLG-201

POLG-201

TCTTTCAGTCCCTTGGCTTATTTTCACCATTTGGAGTATGAGTTTCGATTTTGTGAGGTTTAAAACTAGGAACCTCTTTTTGCTTT
AGAAAAGTCAGGGAAACCGAATAAAAAGTGGTAAACCTCATACTCAAGCTAAAACAGTCCAAATTTTATCCTTGGAGAAAAACGAAA

3655

POLG

POLG-201

POLG-201

CTCTTTGAAAGAAGTTAGTTTTATGTGTGTTGAATCTGTTGAGGCAGATACTCCCTTTTTCCCTTCCATAAAGGTTGCAAGGAGC
GAGAAACTTTCTTCAATCAAAAATACACACAACCTTAGACAACCTCCGTCTATGAGGGAAAAAGGGAAGGTATTTCCAACGTTCCCTCG

3740

POLG

POLG-201

POLG-201

TCCTTCGCAGCTGTGTTGTCCACACGTGGCCTCGTCACTCACTTTGATGCTGAGTGGGCCTTGATTGTTTAGAATAATCTGTGGC
AGGAAGCGTCGACACAACAGGTGTGCACCCGGAGCAGTGAGTGAACCTACGACTCACCCGGAACCTAACAAATCTTATTAGACACCG

3825

POLG

POLG-201

POLG-201

TTGCAACAGGCATTTTCCTCAGTGGCCATTCCCCTACACCTAGCCTTGTGGATCTTGAGCAAACCTGCAGCCTTTTCCTGAATCAGT
AACGTTGTCCGTAAAGGAGTCACCGGTAAGGGGATGTGGATCGGAACACCTAGAACTCGTTTGACGTCGGAAAAGGACTTAGTCA

3910

POLG

POLG-201

POLG-201

GTCGGGCCCCAACAGGCAGCACTCATCCCCTATCCCTCCCACCCCAACCCTGTCACATACACATACATTTTCTCATTCTGGCAC
CAGCCCGGGGTTGTCCGTCGTGAGTAGGGGATAGGGAGGGTGGGGTTGGGACAGTGTATGTGTATGTAAAAGAGTAAGACCGTG

3995

POLG

POLG-201

POLG-201

TTTCCCTGGTTCTCACTGAGGGTGGTTGCTTCTCCAAGGTGTGTGATTTGCTCTTTGTCCCCCAGAATCTTTTCAGCCGTGAGAT
AAAGGGACCAAGAGTGACTIONCCACCAACGAAGAGGTTCCACACACTAAACGAGAAACAGGGGGTCTTAGAAAAGTCGGCACTCTA

4080

POLG

POLG-201

POLG-201

GATTCATCCTGTACATGTGTGCAGCAGCATTGTCATTTTTTTTTTTTTTTGCCAATTCAATTAATCTCCACCTTGGGTTCTGTT
CTAAGTAGGACATGTACACACGTCGTCGTAACAGTAAAAAAAAAAAAAAAAACGGTTAAGTTAATTTAGAGGTGGAACCCAAGACAA

4165

POLG

POLG-201

POLG-201

ATTGTCTATCTCCTTTACTAGTACTTTGAACAGTAGCTGGTTTGTGCCTGTAGACGTGAGGGGTTGATAATGTTTCATAAAACCTC
TAACAGATAGAGGAAATGATCATGAAACTTGTGTCGACCAAACACGGACATCTGCACTCCCCAACTATTACAAGTATTTTTGGAG

4250

POLG

POLG-201

POLG-201

AGAGCTAGATGCAGACTCAGTGAACGCTGGGCCTAGCAAACACCTTGATAGCCCAGGCTGTAATAGAATACCTGCACGTAGGTCT
TCTCGATCTACGTCTGAGTCACTTGCAGACCCGGATCGTTTGTGGAACATCGGGTCCGACATTATCTTATGGACGTGCATCCAGA

4335

POLG

POLG-201

POLG-201

AATAGCCCAGTAGTTCCATTTTTATGTGCAGAAGTTTAAAGAAGCTTTTGTAGCTCTTGCCCGCCAGCACACACACCCACCCTGC
TTATCGGGTCATCAAGGTAAAAATACACGTCTTCAAATTTCTTCGAAAACATCGAGAACGGGCGGTGCTGTGTGTGGGTGGGACG

4420

POLG

POLG-201

POLG-201

CACACCTGACCTGTAGCTGTTTGGAGTTAGGAGCACCCCTTTGGTCTCACTTGTGTCCCCAGCTGCCAATGCACCATCTGGCATGTG
GTGTGGACTGGACATCGACAAACTCAATCCTCGTGGGAAACCAGAGTGAACACAGGGGTCGACGGTTACGTGGTAGACCGTACAC

4505

POLG

POLG-201

POLG-201

GCGGTAGGTGTGCAGTGGTTGTTGTGGAGTGGAAAGTTTAATGTCTCCATGGTGAACCTGCCTGCCTCTCACCTCCCTCAGGTATT
CGCCATCCACACGTCACCAACAACACCTCACCTTCAAATTACAGAGGTACCACTTGGACGGACGGAGAGTGGAGGGGAGTCCATAA

4590

POLG

POLG-201

Y
ENSE...

POLG-201

CCTGGTGCAGCCAGCGGCTGGTGGAAAGAGCGTTACTCTTGGACCAGCCAGCTGTCGCCGGCTGACCTCATCCCCCTGGAGGTCCC
GGACCACGTCGGTCGCCGACCACCTTCTCGCAATGAGAACCCTGGTCGGTCGACAGCGGCCGACTGGAGTAGGGGGACCTCCAGGG

4675

POLG

POLG-201

S W C S Q R L V E E R Y S W T S Q L S P A D L I P L E V P

ENSE00003993906

POLG-201

TACTGGTGCCAGCAGCCCCACCCAGAGAGACTGGCAGGAGCAGTTAGTGGTGGGGCACAATGTTTCTTTGACCGAGCTCATATC
ATGACCACGGTCGTCGGGGTGGGTCTCTCTGACCGTCTCGTCAATCACCACCCCGTGTACAAAGGAAACTGGCTCGAGTATAG

4760

POLG

POLG-201

T G A S S P T Q R D W Q E Q L V V G H N V S F D R A H I

ENSE00003993906

POLG-201

AGGGAGCAGTACCTGATCCAGGTAAGGTTCTGGGGCCAACCTGCAGGTTCTGGCATGGGATGGGCCAGGAGCCCTAATCTCAGTG
TCCCTCGTCATGGACTAGGTCCATTCCAAGGACCCCGGTTGACGTCCAAGACCGTACCCTACCCGGTCTCGGGATTAGAGTCAC

4845

POLG

POLG-201

R E Q Y L I Q

ENSE00003993906

POLG-201

GTTAGGGGAGGTAICTCTTTCTGGCACGTGTCTCTGTTGCCTTTGCTGAAGCCGCAAGGCGCATCTGTTGACCAGCTGTGCCTC
CAATCCCCTCCATGAGGAAAGGACCGTGCACAGAGACAACCGAAACGACTTCGGCGTTCGCGTAGACAACCTGGTCGACACGGAG

4930

POLG

POLG-201

POLG-201

TGGTCTCTGTGCCTAGCTGTTGTATGTCCCCGGGAAAGCCTGGTATAGGACCTAAGTTGTCACAAAGTAATAATGGCCTTCGTCT
ACCAGAGACACGGATCGACAACATACAGGGGGCCCTTTCGGACCATATCCTGGATTCAACAGTGTTCATTATTACCGGAAGCAGA

5015

POLG

POLG-201

POLG-201

CTGTGGCATT...TAGAGCTTAGCATGGGTCTTGAAGGTTTTGAGCCACAGCCTGGGCTCACTTCCTGCCTTAACCACCGATGACTA
GACACCGTAAAATCTCGAATCGTACCCAGAACTTCCAAAACCTCGGTGTCTGGACCCGAGTGAAGGACGGAATTGGTGGCTACTGAT

5100

POLG

POLG-201

POLG-201

CTGTGAGCGCCTTAACATCTCTAAGTCTTAGTTTTCTTTTTATAAAAAGGCAGACATAACAGAAATCTCATAGGATTAATAGGA
GACACTCGCGGAATTGTAGAGATTCAGAATCAAAGGAAAAAATATTTTTCCGTCTGTATTGTCTTTAGAGTATCCTAATTATCCT

5185

POLG

POLG-201

POLG-201

GGGTTGGAACAATGCCTGCATGTCAAACACTCAGCACTCTGCCTGGTGTATAGTAGTGGCAATTCTTAATTTTATGAAAAGTGTT
CCCAACCTTGTTACGGACGTACAGTTTGTGAGTCGTGAGACGGACCACATATCATCACCGTTAAGAATTAATAACTTTTTCACAA

5270

POLG

POLG-201

POLG-201

TTTTCACTGGATCTTCACAACAGCCCTAGAAGATAGGCCAGGCAGGGGAGAGCAACCTTACCCTATAGCTGAGGGTGCTGAGGCT
AAAAGTGACCTAGAAGTGTTGTCGGGATCTTCTATCCGGTCCGTCCCTCTCGTTGGAATGGGATATCGACTCCCACGACTCCGA

5355

POLG

POLG-201

POLG-201

CAGACAGCCTTGTTGACATGCTCAGGGCCACAGAGCTTTTGAGTGGCAGGGTTGGGGCCAGACCAGATAGCCCTGAAGGCTTTAT
GTCTGTCTGGAAACAACCTGTACGAGTCCCAGGTGCTCGAAAACCTCACCGTCCCAACCCCGGTCTGGTCTATCGGGACTTCCGAAATA

5440

POLG

POLG-201

POLG-201

TTTGGCCACTCTGTATCTACGTTGCTCAGAGCTATTGTTGGAAGCTGAGAAGGACTTGCACATTGGGATTGAGCCAGGCCTGCAT
AAACCGGTGAGACATAGATGCAACGAGTCTCGATAACAACCTTCGACTCTTCTGAAACGTGTAACCCCTAACTCGGTCCGGACGTA

5525

POLG

POLG-201

POLG-201

CTTAAAGGGTGGCTAGGATTTGGGAAGGCAGGCCCTTACAGGTGATGGGGCAAGCATGAACAAGCATGAGGATTCTGTATTTGG
GAATTTCCACCGATCCTAAACCTTCCGTCCGGGGAATGTCCACTACCCCGTTTCGTACTTGTTCGTACTCCTAAGACATAAACCC

5610

POLG

POLG-201

POLG-201

TGTTGAAGGCTGTGTGCTGGGAGGGGAGGCTGTTTGGAGGAGCTGAGGTGGGGCTGGAGGTCCACACCACCAAGCAGTGGTGGGCT
ACAACCTCCGACACACGACCCTCCCCTCCGACAAACTCCTCGACTCCACCCCGACCTCCAGGTGTGGTGGTTTCGTCAACCACCCGA

5695

POLG

POLG-201

POLG-201

GGCCCCACAGTTGCAGCCTCCCTCCTTCCCTTCCCTTTTTCTCCTCCTCCTCCTCAGGGTTCCCGCATGCGTTTTCTGGACACCAT
CCGGGGTGTCAACGTCGGAGGGAGGAAGGGAAAGGGAAAAGAGGAGGAGGAGGAGTCCCAAGGGCGTACGCAAAGGACCTGTGGTA

5780

POLG

POLG-201

POLG-201

290 295
G S R M R F L D T M
ENSE00003993911

GAGCATGCACATGGCCATCTCAGGGCTAAGCAGCTTCCAGCGCAGTCTGTGGATAGCAGCCAAGCAGGGCAAACACAAGGTCCAG
CTCGTACGTGTACCGGTAGAGTCCCATTGTCGAAGGTCGCGTCAGACACCTATCGTCGGTTCGTCCCGTTTTGTGTTCCAGGTC

5865

POLG

POLG-201

POLG-201

300 305 310 315 320
S M H M A I S G L S S F Q R S L W I A A K Q G K H K V Q
ENSE00003993911

CCCCCACAAAGCAAGGCCAGAAGTCCAGAGGAAAGCCAGAAGAGGGCCAGCGGTGAGAGCACACTGCCGGTGGGCAGGAGCAT
GGGGGGTGTTCGTTCCGGTCTTCAGGGTCTCCTTTCGGTCTTCTCCGGGTCGCCACTCTCGTGTGACGGCCACCCGTCCTCGTA

5950

POLG

POLG-201

POLG-201

325 330 335 340
P P T K Q G Q K S Q R K A R R G P A
ENSE00003993911

AGTGCTTGGGACCCCTCTCACCAGCCCGTCTGGCCCGAGGCCAGGCTGATCTGCCATGTCCCTTGCTCTGGTTCCCCAGATCTC
TCACGAACCCTGGGGGAGAGTGGTCGGGCAGACCGGGCTCCGGTCCGACTAGACGGTACAGGGAACGAGACCAAGGGGTCTAGAG

6035

POLG

POLG-201

POLG-201

I S
ENSE...

ATCCTGGGACTGGCTGGACATCAGCAGTGTCAACAGTCTGGCAGAGGTGCACAGACTTTATGTAGGGGGGCTCCCTTAGAGAAG
TAGGACCCTGACCGACCTGTAGTCGTCACAGTTGTTCAGACCGTCTCCACGTGTCTGAAATACATCCCCCGGAGGGAATCTCTTC

6120

POLG

POLG-201

POLG-201

345 350 355 360 365 370
S W D W L D I S S V N S L A E V H R L Y V G G P P L E K
ENSE00003993913

GAGCCTCGAGAAGTGTGTTGTAAGGGCACCATGAAGGACATTCGTGAGAAGTTCAGGTATGGTGCTGGAGGGGGCTCTGGGGAC
CTCGGAGCTCTTGACAAACACTTCCCGTGGTACTTCTGTAAAGCACTCTTGAAGGTCCATACCACGACCTCCCCCGAGACCCCTG

6205

POLG

POLG-201

E P R E L F V K G T M K D I R E N F Q

ENSE00003993913

POLG-201

ATGGGCTGTGGCACACCCCTAGCTGCACCTTGGGGAGATGCAGCTGCCAGGCCTGACCCTGAGAGCTGGTGGTGGTAATGGGATGG
TACCCGACACCGTGTGGGGATCGACGTGAACCCCTCTACGTCGACGGTCCGGACTGGGACTCTCGACCACCACATTACCCCTACC

6290

POLG

POLG-201

POLG-201

CTGCCACCTTGGCGCTTCTGTACCTTGTGCCAGGACCTGATGCAGTACTGTGCCAGGACGTGTGGGCCACCCATGAGGTTT
GACGGGTGGAACGCGGAAGGACAGTGAACACGGTCTGGACTACGTCATGACACGGGTCTGCACACCCGGTGGGTACTCCAAA

6375

POLG

POLG-201

D L M Q Y C A Q D V W A T H E V

ENSE00003993915

POLG-201

TCCAGCAGCAGCTACCGCTCTTCTTGGAGAGGTGAGGGGGAGCCCATGTGGGAATCTCTGGGGTCAAGTGTGTTCTGGTACCCG
AGGTGTCGTCGATGGCGAGAAGAACCCTCTCCACTCCCCCTCGGGTACACCCTTAGAGACCCCCAGTACACAAGGACCATGGGC

6460

POLG

POLG-201

F Q Q Q L P L F L E R

ENSE00003993915

POLG-201

GGCCACTGTAATCAGGTGGCGCTGGTTCTATCTCAGGTTGGGGACCTTAGCTTTTCTAGGCTGAAAAGTGGAGCCCTTCTGTT
CCGGGTGACATTAGTCCACCGCGACCAAGATAGAGTCCAACCCCTGGAATCGAAAAGATCCGACTTTCTTACCTCGGGAAGACAA

6545

POLG

POLG-201

POLG-201

CAGTGGTGTCCATCTGGGCCCTGGACTCTGGATTTGACAGAGGCCCTGAAGGGGAGGGCCATGGAGTTGTGCTTGTGTGCATGT
GTCACCACAGGTAGACCCGGGACCTGAGACCTAAACTGTCTCCGGGACTTCCCCTCCCGGTACCTCAACACGAACACACAGTACA

6630

POLG

POLG-201

POLG-201

GCACGGTCTCTGGTTTACTGTGCACCTTCTCTAACTAGATCCTTAGCCAAGGGCTTCACATACAGCGTGGTTATGTTTATTAATGA
CGTGCCAGGACCAAATGACACGTGGAAGAGATTGATCTAGGAATCGGTTCCCGAAGTGTATGTCGCACCAATACAAATAATTACT

6715

POLG

POLG-201

POLG-201

GTCTGTCTTATGAAGTGACCCTTGTATGCTGAAAATTCAGGTATATTTGTACCAAAGATATGGAAAGAAAAAGAAGGGAGGAAA
CAGACAGAATACTTCACTGGGAACATACGACTTTTAAAGTCCATATAAACATGGTTTTCTATACCTTTCTTTTTTCTTCCCTCCTTT

6800

POLG

POLG-201

POLG-201

ATTTGGGTGTAACCTTTTACTCCCTCAGAGCTTAACTACTAATAGCTTGCTGTTGGCTAGAAGCTTTACTGATAACATAATACAT
TAAACCCACATTGAAAACCTGAGGGAGTCTCGAATTGATGATTATCGAACGACAACCGATCTTCGAAATGACTATTGTATTATGTA

6885

POLG

POLG-201

POLG-201

ATTTTTTATGTTATACGTATTATATACTGTATTCTTAAAGTAAGCTAGATAAAAGAAAATGTATTAAGAAAATCATGAGGAGAAA
TAAAAAATACAATATGCATAATATATGACATAAGAATTTCAATTCGATCTATTTTCTTTTACATAAATCTTTTAGTACTCCTCTTT

6970

POLG

POLG-201

POLG-201

ATATGTTTACTATTTCATTAGGTGGAAGTGGATCATCATAAAGATATCTATCCTTCACGTTGAGTAGGCTGAGGGCGGGGGTTGGG
TATACAAATGATAAGTAATCCACCTTCACCTAGTAGTATTTCTATAGATAGGAAGTGCAACTCATCCGACTCCCGCCCCAACCC

7055

POLG

POLG-201

POLG-201

CTTGCTGTCTCGGGTGGCTAAGGCTGAAGAAAATAAATGTGTAAGTGAACCTTGACAGATCCAGACATGTGTTGTTTAAATGTCAG
GAACGACAGAGCCACCGATTCCGACTTCTTTTATTTACACATTCACCTTGAACGTGCTAGGTCTGTACACAACAAATTTACAGTC

7140

POLG

POLG-201

POLG-201

CTGTATTTTACCACCCAAGTTGTGAGGTTTCAAGCATGATGTTTTTTCATGTATGGGATTATTAGCACAGTGCCTGGCACAGAGTCA
GACATAAAATGGTGGGTTCAACACTCCAAGTCCGTAATAAAGTACATAACCCTAATAATCGTGTCACGGACCGTGTCTCAGT

7225

POLG

POLG-201

POLG-201

TTACTCCACGTGTGGCAGCCATTTTCACTTTTGCCATCTATATTTCCACATTACCCCTGAGGATGGGATGATATTGTTCCCAT
AATGAGGTGCACACCGTTCGGTAAAAGTGAAAACGGTAGATATAAAGGGTGAATGGGGACTCCTACCCTACTATAACAAGGGTAA

7310

POLG

POLG-201

POLG-201

TTATAGATGAAAGAAGCTGAGGCTCCGAGAGATGGGGTTGCTTACCCAGGGATGAGTAACAGTAGAGCTGGGATTTAATGCCGTCT
AATATCTACTTTCTTGACTCCGAGGCTCTCTACCCCAACGAATGGGTCCCTACTCATTGTTCATCTCGACCCTAAATTACGGCAGA

7395

POLG

POLG-201

POLG-201

GACTTTTGAGCTGTGCCATGTCAGTGGCTGGGTTGAGGCTTGTCTAAACCAGCTCAGGGATTGGGCCAGTCTTGCCTCCTGTGGTC
CTGAAAACCTCGACACGGTACAGTCAACGACCCAACTCCGAACGATTTGGTCGAGTCCCTAACCCGGTCAGAACGGAGGACACCAG

7480

POLG

POLG-201

POLG-201

ATTTATGGCAGCTCCTGGTGTGTTGCCTCCAAGGTGTCCCCACCCAGTACTCTGGCCGGCATGCTGGAGATGGGTGTCTCTACC
TAAATACCGTCGAGGACCACAAACGGAGGTTCCACAGGGGTGGGTCACTGAGACCGGCCGTACGACCTCTACCCACAGAGGATGG

7565

POLG

POLG-201

C P H P V T L A G M L E M G V S Y
ENSE00003993901

POLG-201

TGCCTGTCAACCAGAAGCTGGGAGCGTTACCTGGCAGAGGCACAGGGCACTTATGAGGAGCTCCAGCGGGAGATGAAGAAGTCGTT
ACGGACAGTTGGTCTTGACCCTCGCAATGGACCGTCTCCGTGTCCCGTGAATACTCCTCGAGGTGCGCCCTCTACTTCTTCAGCAA

7650

POLG

POLG-201

L P V N Q N W E R Y L A E A Q G T Y E E L Q R E M K K S L
ENSE00003993901

POLG-201

GATGGATCTGGCCAATGATGCCTGCCAGCTGCTCTCAGGAGAGAGGTAGCCAGGCCTTGGGTGGGCAGGATCTAGGCAGGGGACT
CTACCTAGACCGGTTACTACGGACGGTCGACGAGAGTCTCTCTCCATCGGTCCGGAACCCACCCGTCTAGATCCGTCCCCTGA

7735

POLG

POLG-201

M D L A N D A C Q L L S G E R
ENSE00003993901

POLG-201

GGCAGGTGGGCAGGCTAGCCTTTCGGCTTAGCCTTAGCCCTGCCCTAGTGGACTGGCTCTGTAGGTACAAAGAAGACCCCTGGCTC
CCGTCCACCCGCCGGATCGGAAGCCGAATCGGAATCGGGACGGGATCACCTGACCGAGACATCCATGTTTCTTCTGGGGACCGAG

7820

POLG

POLG-201

Y K E D P W L
ENSE00003993904

POLG-201

TGGGACCTGGAGTGGGACCTGCAAGAATTTAAGCAGAAGAAAGCTAAGAAGGTGAAGAAGGAACCCAGCCACAGCCAGCAAGTTGC
ACCCTGGACCTCACCCCTGGACGTTCTTAAATTCGTCTTCTTTTCGATTCTTCCACTTCTTCTTGGTTCGGTGTTCGGTTCGTTCAACG

7905

POLG

POLG-201

W D L E W D L Q E F K Q K K A K K V K K E P A T S K L
ENSE00003993904

POLG-201

CCATCGAGGGGGCTGGGGCCCTGGTGATCCCATGGATCAGGAAGGTGGGGAGCATGGGTGGGAGGTAGGGTAGGGTAGGGGTTG
GGTAGCTCCCCGACCCCGGGGACCACTAGGGTACCTAGTCTTCCACCCCTCGTACCCACCCCTCCATCCCATCCCATCCCCAAC

7990

POLG

POLG-201

515 520 525
P I E G A G A P G D P M D Q E

ENSE00003993904

POLG-201

TCTCTGGGAAGGTCTGTGATTGAGGGGGTCTTTCGAAAGGATTGCTCCAGCCTTCTGGAGATGAGCGGGTGGGAGCAGATCTTA
AGAGACCCTTCCAGGACACTAACTCCCCAGGAAGCTTTCTAACGAGGTCGGAAGACCTCTACTCGCCACCCCTCGTCTAGAAT

8075

POLG

POLG-201

POLG-201

TTGAGAGTTCCTTCTCCTGCTCCTGATTGTCTTCCCCACCCCTCACAGACCTCGGCCCTGCAGTGAGGAGGAGGAGTTTCAACA
AACTCTCAAGGAAGAGGACGAGGACTAACAGAAGGGGGTGGGAGTGTCTGGAGCCGGGGACGTCACTCCTCCTCCTCAAAGTTGT

8160

POLG

POLG-201

530 535 540
D L G P C S E E E E F Q Q

ENSE00003993909

POLG-201

AGATGTCATGGCCCGCGCCTGCTTGCAGAAGCTGAAGGGGACCACAGAGCTCCTGCCAAGCGGCCCCAGCACCTTCTGGACAC
TCTACAGTACCGGGCGCGGACGAACGTCTTCGACTTCCCCTGGTGTCTCGAGGACGGGTTTCGCCGGGGTTCGTGGAAGGACCTGTG

8245

POLG

POLG-201

545 550 555 560 565
D V M A R A C L Q K L K G T T E L L P K R P Q H L P G H

ENSE00003993909

POLG-201

CCTGGGTGAGCCCTGCCACCCCCAGCAGTGTATCTAGAGTCTACCCCTTGTCTCATTCTCAGGACAGCCCTGGTCTGGGTTCTGG
GGACCCACTCGGGACGGGTGGGGTTCGTACATAGATCTCAGATGGGAACGAGGTAAGAGTCTGTCTGGGACCAGACCCAAGACC

8330

POLG

POLG-201

570
P G

ENSE...

POLG-201

CACAGAGGCATCATGCACATGTATACTTATTGACCTGCTGCCATTCAGTCACACTGTCTTCCAGTCCTATTCTCATTTGCTCACT
GTGTCTCCGTAGTACGTGTACATATGAATAACTGGACGACGGTAAGTCAGTGTGACAGAAGGTCAGGATAAGAGTAAACGAGTGA

8415

POLG

POLG-201

POLG-201

CTGGACCGGCTCACTGGACTCATTACGACAGTGTGTGAGCACCTGCTGTGCAATGGCCCGTGGCAGCCACCGGGTGTACACAC
GACCTGGCCGAGTGACCTGAGTAAGTCGTGTCAACAACACTCGTGGACGACACGTTACCGGGCACCGTCTGGTGGCCCATGTGTG

8500

POLG

POLG-201

POLG-201

TGGAGCATAGCTCCTCCTTTCCAGTAGTTCTTTTTCTAGGAGGAGCCAGGCACGTAGACCAGCCAGTGCAGCTAGTGTCCATAG
ACCTCGTATCGAGGAGGAAAGGTCATCAAGAAAAAGGATCCTCCTCGGTCCGTGCATCTGGTCGGTCACGTCGATCACAGGTATC

8585

POLG

POLG-201

POLG-201

GTAGAGTTCTGACTCTGCCTCGGGAAATAAATCAAGAAGGCTTCTTTGAGAAGGTGCCCTTCTTTTGGAGCCTCATAGGGTGGCA
CATCTCAAGACTGAGACGGAGCCCTTATTTAGTTCTTCCGAAGGAACTCTTCCACGGGGAAGGAAACTCGGAGTATCCCACCGT

8670

POLG

POLG-201

POLG-201

GAGATGAGAAAAAGGGCAGCCAGGGTGAGCAGCAGGGTGCCAGCTTTGCACCTGCAAGACCCTGAGAGCAAGTGTCTTGAGTGCC
CTCTACTCTTTTTCCCGTCGGTCCCCTCGTCCGTCGACGGTGCAGAACGTTGGACGTTCTGGGACTCTCGTTCACAGGACTCACGG

8755

POLG

POLG-201

POLG-201

TTGCTAGTCTCACCTGGGCTCAACTCTGGTGAACAGCCTGCAAGAGAGCACCCAGAAGGACTGGTGTCTCTAGAGGGGTGGG
AACGATCAGAGTGGGACCCGAGTTGAGACCACTTGTTCGGACGTTCTCTCGTGGGTCTTCTGACCACAAAGAGATCTCCCCACCC

8840

POLG

POLG-201

POLG-201

GAGGGCAGATCTGCTCCCTCCTCTGGTCAAGTACCCTGGATGAAATGGAGCTTGGGAAGGAGCCCTGCCCTGGGTCAAGGATATGC
CTCCCGTCTAGACGAGGGAGGAGACCAGTCAATGGGACCTACTTTACCTCGAACCTTCTCCTCGGGACGGGACCCAGTCCCATAACG

8925

POLG

POLG-201

POLG-201

TTTTGTGTCCTGGCTTCTGACTAGTCCAGTGGGACTGACTTAGTGCTTTGCTTTTGAATATTCTTCTAGAGGATTCCATGGGG
AAAAACACAGGACCGAAGACTGATCAGGTCACCCTGACTGAATCACAGAAACGAAAACCTTTATAAGAAGATCTCCTAAGGTACCCC

9010

POLG

POLG-201

POLG-201

GTCCTGGCTAAAGCATCCCAGAGGAGGGGATGGCGGCTGTAGGCTGGGGTCACCAGAAAGCCCCAGGGCTTTGGAGGGTGGGTGG
CAGGACCGATTTTCGTAGGGTCTCCTCCCCTACCGCCGACATCCGACCCAGTGGTCTTTCGGGGTCCCGAAACCTCCCACCCACC

9095

POLG

POLG-201

POLG-201

9180 GGACATTGTGAGAGAGAGAACCTTCCCCCAACAACACTGCCCTTACCATCGTGACACTGCTGCTTCTCCTGCTGGGACGTAGATGGT
CCTGTAACACTCTCTCTCTTTGGAAGGGGGTTGTTGACGGGAATGGTAGCACTGTGACGACAGAAGGACGACCCTGCATCTACCA

POLG >

POLG-201 >

W
ENSE...

POLG-201 >

9265 ACCGGAAGCTCTGCCCCGGCTAGACGACCCCTGCATGGACCCCGGGCCCGAGCCTCCTCAGCCTGCAGATGCGGGTCACACCTAA
TGCCCTTCGAGACGGGGCCGATCTGCTGGGACGTACCTGGGGCCCGGGGTCGGAGGAGTCGGACGTCTACGCCCAAGTGTGGATT

POLG >

POLG-201 >

575 580 585 590 595 600
Y R K L C P R L D D P A W T P G P S L L S L Q M R V T P K

ENSE00003993914 >

POLG-201 >

9350 ACTCATGGCACTTACCTGGGATGGCTTCCCTCTGCACTACTCAGAGCGTCATGGCTGGGGCTACTTGGTGCCTGGGCGGCGGGAC
TGAGTACCCTGAATGGACCCCTACCGAAGGGAGACGTGATGAGTCTCGCAGTACCGACCCCGATGAACCACGGACCCGCGCCCTG

POLG >

POLG-201 >

605 610 615 620 625
L M A L T W D G F P L H Y S E R H G W G Y L V P G R R D

ENSE00003993914 >

POLG-201 >

9435 AACCTGGCCAAGCTGCCGACAGGTACCACCCTGGAGTCAGCTGGGGTGGTCTGCCCTACAGGTAAGGCTTAGGCCCAAGGGAGG
TTGGACCGGTTTCGACGGCTGTCCATGGTGGGACCTCAGTCGACCCCAACAGACGGGGATGTCCATTCCGAATCCGGGTCCCTCC

POLG >

POLG-201 >

630 635 640 645 650
N L A K L P T G T T L E S A G V V C P Y R

ENSE00003993914 >

POLG-201 >

9520 AAGGGGCTGGAGCCTAGGGACCCCTTCCCCTGGCTGGTCAGCTCAGGCTAGTGGAAAGAGTTTTGGTTCAAGAGTCTGGGTTTCAG
TTCCCCGACCTCGGATCCCTGGGGAAAGGGACCGACCAAGTCCGATCACCTTTCTCAAACCCAAGTTCTCAGACCCAAGTC

POLG >

POLG-201 >

POLG-201 >

9605 AAGAAGGGAAAAACAGGAAAAAAATTAACACACACACACACACCCTCTCTCTCTCTTTCTCTCTCTCTCACTCACTCACTCACT
TTCTTCCCTTTTGTCTTTTTTAATTGTGTGTGTGTGGGAGAGAGAGAGAGAAAGAGAGAGAGAGAGAGTGTGAGTGTGAGTGA

POLG >

POLG-201 >

POLG-201 >

9690 CTCTCTCTCACTCACTCACTCTCTCACTCACTCTCTCACTCACTCACTCTCTCACTCACTCACTCTCTCTCACTC
GAGAGAGAGTGTGAGTGTGAGTGTGAGAGAGTGTGAGTGTGAGAGAGTGTGAGTGTGAGTGTGAGAGAGTGTGAGTGTGAGAGAGTGTGAG

POLG >

POLG-201 >

POLG-201 >

TCTCACTCACTCACTCACTCACTCACTCTCTCACTCACTCTCTCACTCACTCACTCACTCTCTCTCACTCTCTCACTCACTCACT
AGAGTGAGTGAGTGAGTGAGTGAGTGAGTGAGAGAGTGAGTGAGTGAGTGAGTGAGTGAGTGAGAGAGAGTGAGAGAGTGAGTGAGTGA

9775

POLG >

POLG-201 >

POLG-201 >

CTCTCACTCACTCACTCACTCACTCACTCTCTCACTCACTCACTCACTCTCTGGGTTTCAGGTTTTTCTTCCATGGCTACCCTTA
GAGAGTGAGTGAGTGAGTGAGTGAGTGAGAGAGTGAGTGAGTGAGTGAGAGACCCAAAGTCCAAAAAGAAGGTACCGATGGGAAT

9860

POLG >

POLG-201 >

POLG-201 >

CCCTCTGGATCTCAGAGCTCTGGGAGGGAGTATGTTGAGATGTTTCACAGTGGGGAGGACTAAAGGCCCTACTCTTGGGCCCAAGAA
GGGAGACCTAGAGTCTCGAGACCCTCCCTCATACAACCTTACAAGTGTACCCCTCCTGATTTCCGGGATGAGAACCCTGGGCTCTT

9945

POLG >

POLG-201 >

POLG-201 >

GCATAGCTGCCTTTCAGGGAACATGCGGAGGGCTGTTACAAGTAGCAGGGAGATGGGCTTTTAAAAAAGTGTGTGTATATAATTT
CGTATCGACGGAAGTGTCTTGTACGCCTCCCGACAATGTTTCATCGTCCCTCTACCCGAAAATTTTTTCACACACATATATTTAAA

10,030

POLG >

POLG-201 >

POLG-201 >

GAGTGATAATTATGGGCCAAGCAGTGCTTCCCTTATTTGTTCCCAAGGAGTCCCATGAGCTAGAATGGTTATCCCATGTTGTA
CTCACTATTAATACCCGGTTCGTACGAAGGGAATAAACAAAGGGGTTCTCAGGGTACTCGATCTTACCAATAGGGGTACAACAT

10,115

POLG >

POLG-201 >

POLG-201 >

GTTGACAAAGGCTTGGTTGACTTAAGATCACAGACCCTGAGCTTTAGGCAGGCAGGTGTTGGGGAGAACTTACAGTGGCCCAAGA
CAACTGTTTCCGAACCAACTGAATTCTAGTGTCTGGGACTCGAAATCCGTCCGTCCACAACCCTCTTTGAATGTACCAGGGTCT

10,200

POLG >

POLG-201 >

POLG-201 >

ATTAAGAGTCCTGGCTCTTCCAGGGCAGCCTGAGTCTCTTATGGGGCCATGGGACCAAAGGGGATAAACTGGCCTTGCTCCTTTG
TAATTCTCAGGACCGAGAAGTCCCGTCGGACTCAGAGAATACCCCGGTACCCTGGTTTCCCTATTGTGACCGGAACGAGGAAAC

10,285

POLG >

POLG-201 >

POLG-201 >

AGCCCGAGGGTAGGTGAGCGGACAGGAGCCAGCCTGCAGCTGGGCCTTGGGTCCTGTCTCCCGCTGCTGTGCTCTCAGAACTTC
TCGGGCTCCCATCCACTCGCCTGTCTCGGTGCGGACGTCGACCCGGAACCCAGGACAGGAGGGCGACGACACGAGAGTCTTGAAG

10,370

POLG

POLG-201

POLG-201

TCTTGAGACGGCAGCTCTGTAGTGTAAGAGGAACTTGGATTTGAGTGAGACAAGGCCTTGAACCCAGCCTGCTGCCAGGGTGCT
AGAACTCTGCCGTCGAGACATCACATTCTCCTTGAACCTAAACTCACTCTGTTCCGGAACCTTGGGGTCGGACGACGGTCCCACGA

10,455

POLG

POLG-201

POLG-201

GTCATTTTCAGTTTGTCAATCAATCCCTGTCTAAAACCCGGGAAAGTGCTATCTGGTTCTGCCTCAGAGCTGATTCTGAGGACTA
CAGTAAAAGTCAAACAGTTAGTTAGGGACAGATTTTGGGCCCTTTCACGATAGACCAAGACGGAGTCTCGACTAAGACTCCTGAT

10,540

POLG

POLG-201

POLG-201

AACAAAGGGGAATTGTGGAAGGCACTAGCAAGCTGCCTGGCCAGAGTGGGCATCTGGTAATCAGCGGCTGCTGCTGCTACTGTTC
TTGTTTCCCTTAACACCTTCCGTGATCGTTCGACGGACCGGGTCTCACCCGTAGACCATTAGTCGCCGACGACGACGATGACAAG

10,625

POLG

POLG-201

POLG-201

TCTGCCAGAGCCATCGAGTCCCTGTACAGGAAGCACTGTCTCGAACAGGGGAAGCAGCAGCTGATGCCCCAGGAGGGCCGGCCTG
AGACGGGTCTCGGTAGCTCAGGGACATGTCCTTCGTGACAGAGCTTGTCCCCTTCGTGTCGACTACGGGGTCTCCGGCCGGAC

10,710

POLG

POLG-201

A I E S L Y R K H C L E Q G K Q Q L M P Q E A G L

ENSE00003993918

POLG-201

GCGGAGGAGTTCCTGCTCACTGACAATAGTGCCATATGGCAAACGGTGAGGGCAGGCTCTGAACCTGAGCTTTGGGGAGGGGAGG
CGCCTCCTCAAGGACGAGTGACTGTTATCACGGTATACCGTTTGGCACTCCCGTCCGAGACTTGGACTCGAAACCCCTCCCTCC

10,795

POLG

POLG-201

A E E F L L T D N S A I W Q T

ENSE00003993918

POLG-201

TCTCTGTATTCCACCCAGGGAAGGGGACAGCCTTTGGGTGGGAGGCTGGCACTGGTGGCTCACCCCAGACTGGCCTGCAGTGTCTG
AGAGACATAAGGTGGGTCCCTTCCCGTTCGGAAACCCACCCTCCGACCGTGACCACCGAGTGGGGTCTGACCGGACGTCACAGAC

10,880

POLG

POLG-201

POLG-201

AGTACCATGCAGGGAGGGGGCTGGTGGATTGGGGCCTACCCAGTCCCCTGCTTCACTACTTTGGTCCTTGGACTGCTCCAGGTAGA
TCATGGTACGTCCCTCCCCGACCACCTAACCCCGGATGGGTGAGGGGACGAAGTGATGAAACCAGGAACCTGACGAGGTCCATCT

10,965

POLG

POLG-201

V E
ENSE...

POLG-201

PCR Forward

AACTGGATTACTTAGAAGTGGAGGC

AGAACTGGATTACTTAGAAGTGGAGGCTGAGGCCAAGATGGAGAACTTGCAGCTGCAGTGCCAGGTCAACCCCTAGCTCTGGTG
TCTTGACCTAATGAATCTTCACCTCCGACTCCGGTTCTACCTCTTGAACGCTCGACGTCACGGTCCAGTTGGGGATCGAGACCAC

11,050

POLG

POLG-201

E L D Y L E V E A E A K M E N L R A A V P G Q P L A L

ENSE00003993908

POLG-201

AGCAGTGCGCCGGCTTGGGTTCTCTAGGTGGGTGCTGGGTGGAAAGGGCTTCTCTTGCCACCTAGTTCTTCCCAGCCAGAGTT
TCGTACGCGGGCCGAACCCAAGAGATCCACCCACGACCCACCTTCCCGAAGGAGAACGGGTGGATCAAGAAGGGTCCGGTCTCAA

11,135

POLG

POLG-201

POLG-201

CCCTAGGTCTTAAGGGGGTTGGAGATGCCACCCTGCCCTGGGAGGCCCCACACGTGTTGGAGCAAGGAGAAAGCCTGGGTGAGA
GGGATCCAGAATTCGCCAACCTCTACGGTGGGACGGGGACCTCCGGGGTGTGCACAACCTCGTTTCTCTTTCGGACCCACTCT

11,220

POLG

POLG-201

POLG-201

CCTCATGGCCATCTTGTCAATTTCCAGCTGATGACGACAGTTTTAGGGCCCTTTTCCACCCCTACCCCATGGCCCTTGCTGAAT
GGAGTACCGGTAGAACAGTAAAGGGTGCAGTACTGCTGTCAAAGTCCGGGAAAAGGGTGGGGGATGGGGTACCGGGAACGACTTA

11,305

POLG

POLG-201

POLG-201

Donor Template WT -> SNV

GGTGTGTGGCCCTCACAGACTGCCCGTGGTGGCCCCAAGGACACCCAGCCCAGCTATC

GCAGGTGCTGGAGCAGGGCCTGATATAGGTGTGTGGCCCTCACAGACTGCCCGTGGTGGCCCCAAGGACACCCAGCCCAGCTATC
CGTCCACGACCTCGTCCCGGACTATATCCACACACCGGGAGTGTCTGACGGGCACCACCGGGGTTCTGTGGGTTCGGGTTCGATAG

11,390

POLG

POLG-201

T A R G G P K D T Q P S Y

ENSE00003993898

POLG-201

Donor Template WT -> SNV

Donor Template WT -> SNV

ACCATGGCAAT C GACCTTACAACGACGTGGACATCCCTGGCT

ACCATGGCAAT G GACCTTACAACGACGTGGACATCCCTGGCTGCTGGTTTTTCAAGCTGCCTCACAAGGTGTGTCTCTGGGTCATG
TGGTACCGTTA C CTGGAATGTTGCTGCACCTGTAGGGACCGACGACCAAAAAGTTTCGACGGAGTGTTCCACACAGGACCCAGTAC

11,475

POLG

POLG-201

H H G N G P Y N D V D I P G C W F F K L P H K

ENSE00003993898

POLG-201

Donor Template WT -> SNV

Protospacer Sequence

PAM

SNV

ACCGTTACCTGGAATGTTGC

gRNA Protospacer

GCCTGTCTGTGGTGTTCCTCATTCTGCTCAAGGCCACAGCAGGCCTTCAGAGTGACACACCTGAGACTTTCTTTTTGTGGG
CGGACAGGACACCACAAAAGGAGTAAGACGAGTTCCGGGTGTCGTCCGGAAGTCTCACTGTGTGGACTCTGAAAGGAAAAACACCC

11,560

POLG

POLG-201

POLG-201

GGACAGGACACCACAAAAGGA

Sanger Sequencing

AATGACTAGTAGTGGGACAGAGTGTGATTTTCAGGCACATACTGTCATCTCTCAGCTTTTTGTTTTTCTAATGAAAAGTCGGGTGGCA
TTACTGATCATCACCCCTGTCTCACACTAAAGTCCGTGTATGACAGTAGAGAGTCGAAAAACAAAAGATTACTTTTCAGCCACCCGT

11,645

POLG

POLG-201

POLG-201

AGGGGCATGGTGGTGGAAATTAATGACATGGGGCACGTCGTATGTTTGGTACGACATCTGGTACGTGATAGGTTTTTCCGATTTG
TCCCCGTACCACCACCTTAATTTACTGTACCCCGTGCAGCATACAAACCATGCTGTAGACCATGCACTATCCAAAAAGGCTAAAC

11,730

POLG

POLG-201

POLG-201

TTATTATGCAGGGAGCCAGGTTTGTCTGTGTCTGTGTCTTAGGGGGCATGTGTGTGCACGTGTGTGTGTGCGTGCGCGCGTGC
AATAATACGTCCCTCGGTCCAAACGAACACAGACACACAGAATCCCCGTACACACACGTGCACACACACACGCACGCGCGCACG

11,815

POLG

POLG-201

POLG-201

GCGCGTGCGTGATACAATCAGGGATTTGCCTCAGACTGCTGAGGTTCTGGGCTCAGTGTTGGGAGGAGTGCAGGTA CTACGTTG
C GCGCACGCACTATGTTAGTCCCTAAACGGAGTCTGACGACTCCAAGACCCGAGTCACAACCTCCTCACGTCCATGAGTGCAAC

11,900

POLG

POLG-201

POLG-201

GTTCCCCACCCAGGGGTCTGCCACCTGCCTCCAGCCCCTGCTTCTTTGCTCTGTCCAGGATGGTAATAGCTGTAATGTGGGAAG
CAAGGGGTGGGTCCCCAGACGGTGGACGGAGGTCGGGGACGAAGGAAACGAGACAGGTCCTACCATTATCGACATTACACCCCTTC

11,985

POLG

POLG-201

D G N S C N V G S
ENSE00003993910

POLG-201

CCTACCATTATCGACATTACACCT
PCR Reverse

CCCCTTTGCCAAGGACTTCTGCCCAAGATGGAGGATGGCACCCCTGCAGGCTGGCCCCAGGAGGTGCCAGTGGGCCCCGTGCTCTG
GGGGAAACGGTTCTGAAGGACGGGTTCTACCTCCTACCCTGGGACGTCCTGACCGGGTCTCCACGGTCACCCGGGGCACGAGAC

12,070

POLG

POLG-201

765 770 775 780 785 790
P F A K D F L P K M E D G T L Q A G P G G A S G P R A L
ENSE00003993910

POLG-201

GAAATCAACAAAATGATTTCTTTCTGGAGGAACGCCATAAACGTATCAGGTGGGCCACCATGGGAGGAGTCTCTGGGATGCCTTT
CTTTAGTTGTTTTACTAAAGAAAGACCTCCTTGCGGGTATTTGCATAGTCCACCCGGTGGTACCCTCCTCAGGACCTACGGAAA

12,155

POLG

POLG-201

795 800 805
E I N K M I S F W R N A H K R I S
ENSE00003993910

POLG-201

CCCCTCTCTCCACCCAGGGACCCCTGACTAACCCCTGGATTCCACAGAGGGCCAGCCTGACTATGGTCTAGAGGCCTGGCTAC
GGGGAGAGAAGGGTGGGTCCCTGGGGACTGATTGGGACCTAAGGGTGTCTCCCGGTGGGACTGATACCAGATCTCCGGACCGATG

12,240

POLG

POLG-201

POLG-201

TTTTGGTCTGGTGCCATGGACCTTGGGCAGGTCTCCCCTCTAGCTTCAGTTTCCCTGTTAATGTAAAAAGAATGGTGTGTAGG
AAAACCAGGACCACGGTACCTGGAACCCGTCCAGAGGGGAGATCGAAGTCAAAGGGACAATTACATTTTTCTTACCACGACATCC

12,325

POLG

POLG-201

POLG-201

ACCATGAGAGCCCTTCGTAGCTCCAACAGAACTTCTTGGTGTAACTGCTGGAGCCGTGGGCTATGGCTGAGGACCATGGAGAGCT
TGGTACTCTCGGGAAGCATCGAGGTTGTCTTGAAGAACCACATTGACGACCTCGGCACCCGATACCGACTCCTGGTACCTCTCGA

12,410

POLG

POLG-201

POLG-201

GGTGGCCTGTAAGCCCTGTTGGGGGCTGGGAGCTGGGTCTTCTAGTCTGGAATGGCAAATGTATTCATCTTGAAGGCCATTTCCA
CCACCGGACATTGCGGACAACCCCGACCCCTCGACCCAGAAGATCAGACCTTACCGTTTACATAAGTAGAACTCCGGTAAAGGT

12,495

POLG

POLG-201

POLG-201

AGGTGGTTGTGGCCATCAGCACACTGGCGAGCAGAGTGGGTGTTGGGATGGTGAAGTCTGCCTGTGTGTAGGAAGAGGCATTGGT
TCCACCAACACCGGTAGTCGTGTGACCGCTCGTCTCACCCACAACCTTACCCTTCAGACGGACACACATCCTTCTCCGTAACCA

12,580

POLG

POLG-201

POLG-201

GGAAGGAGCGCCTCATGGATGCCCCCGGAGAGGAGCGGAAGCTCGCTCGGAGGCCTGGCCGGTTCCAGATGGTTTATGCTCTT
CCTTCCTCGCGGAGTACCTACGGGGGGCCTCTCCTCGCCTTCGAGCGAGCCTCCGGACCGGCCAAGGGTCTACCAAATACGAGAA

12,665

POLG

POLG-201

POLG-201

GATTGGTGTATCATAGGGCCCCAGTTCTTGGCTGAGCCAGGGCTCACCTTGAGTCCAGTTAGTGAGGCTGGGTAATGGAGTATAG
CTAACACATAGTATCCCGGGGTCAAGAACC GACTCGGTCCCGAGTGGAACCTCAGGTCAATCACTCCGACCCATTACCTCATATC

12,750

POLG

POLG-201

POLG-201

CAGTCCTGGAGGTGGGCAGGTGAGGGCCATGGTGGGATGTGGGATAGATTCTGCTTCCCATGGCTGTGCTGAGCCTCACGTTGTC
GTCAGGACCTCCACCCGTCCACTCCCGGTACCACCCTACACCCTATCTAAGACGAAGGGTACC GACACGACTCGGAGTGCAACAG

12,835

POLG

POLG-201

POLG-201

TGTCCCACAGCTCCAGATGGTGGTGTGGCTGCCAGGTCAGCTCTGCCCCGTGCTGTGATCAGGTATGGTCTGCTGAGTGGTT
ACAGGGGTGTCGAGGGTCTACCACCACACCGACGGGTCCAGTCGAGACGGGGCACGACACTAGTCCATACCAGACGACTCACCAA

12,920

POLG

POLG-201

810 S Q M V V W L P R S A L P R A V I R 820 825

ENSE00003993903

POLG-201

GTAGGGATAGGAGAACTGAGGTGAGGTGGTAGGTCCTAAGGCCAAAGCACCCCTGCTAAGACCCATTTCTTCCCCTGCACCCAC
CATCCCTATCCTCTTGACTCCACTCCACCATCCAGGATTCCGGTTTCGTGGGACGATTCTGGGTAAAGGAAGGGGACGTGGGGTG

13,005

POLG

POLG-201

POLG-201

CAGGCACCCCGACTATGATGAGGAAGGCCTCTATGGGGCCATCCTGCCCAAGTGGTGACTGCCGGCACCATCACTCGCCGGGCT
GTCCGTGGGGCTGATACTACTCTTCCGGAGATACCCCGGTAGGACGGGGTTCACCACTGACGGCCGTGGTAGTGAGCGGCCCGA

13,090

POLG

POLG-201

H P D Y D E E G L Y G A I L P Q V V T A G T I T R R A 830 835 840 845 850

ENSE00003993917

POLG-201

GTGGAGCCCACATGGCTCACCGCCAGCAATGCCCGGGTATGTGACCTCTGTACCTCTGGCCCCTGCTCTTCCTCTCCAGGTCTG
CACCTCGGGTGTACCGAGTGGCGGTCGTTACGGGCCCATACACTGGAGACATGGAGACCAGGACGAGAAGGAGAGGGTCCAGAC

13,175

POLG

POLG-201

855 860 865
V E P T W L T A S N A R

ENSE00003993917

POLG-201

TAGAAACTGGGCTCTGAGGGCCTTTAGGTATTTAGTGAGGATCATGAAAAGGACCCTGTGATCTGGGTCAGGCAGGACTCTAGTC
ATCTTTGACCCGAGACTCCCGGAAATCCATAAATCACTCCTAGTACTTTTCTGGGACACTAGACCCAGTCCGTCCTGAGATCAG

13,260

POLG

POLG-201

POLG-201

AAATCTGGCTTCATGATTTCTGTCCACTCCTTCAGTAAATATGTTCTGGGCACCTGCTCCTGGCCAGACCGTGACAGGCCTAATA
TTTAGACCGAAGTACTAAAGACAGGTGAGGAAGTCATTTATACAAGACCCGTGGACGAGGACCGGTCTGGCACTGTCCGCATTAT

13,345

POLG

POLG-201

POLG-201

GCTACAGCTCTCATGGAATTTAGATAGGACCGTGTAGGTGAGGGGTCTGGCATAGCGCTAGGCATAGAGTAGATTCTTTACCTGT
CGATGTCGAGAGTACCTTAAATCTATCCTGGCACATCCACTCCCAGACCGTATCGCGATCCGTATCTCATCTAAGAAATGGACA

13,430

POLG

POLG-201

POLG-201

CACACCAATTGCTGATAGGTGGCCATCTCTGGAACCTGTGGAATTTGAGCAGTGCTGTCTGGCATTCTCTAAAGCCATCCCCTCAG
GTGTGGTTAACGACTATCCACCGGTAGAGACCTTGACACCTTAAAGTCGTCACGACAGACCCTAAGAGATTTCCGTTAGGGGAGTC

13,515

POLG

POLG-201

POLG-201

GAAAGGCTCTAGCTCTTTCTCAGTCAACTCTGGCTCCAGGAATGGGGTAGGAAGAGTCTCATTTGGGTATCTCACTCTTCCACA
CTTTCCGAGATCGAGAAAGAGTCAGTTGAGACCGAGGTCTTACCCCATCTTCTCAGAGTAAACCCATAGAGTGAGAAGGGTGT

13,600

POLG

POLG-201

POLG-201

GCCTGACCGAGTAGGCAGTGAGTTGAAAGCCATGGTGCAGGCCCCACCTGGCTACACCTTGTGGGTGCTGATGTGGACTCCCAA
CGGACTGGCTCATCCGTCACCTCAACTTTCCGTTACCACGTCCGGGGTGGACCGATGTGGGAACACCCACGACTACACCTGAGGGTT

13,685

POLG

POLG-201

870 875 880 885 890
P D R V G S E L K A M V Q A P P G Y T L V G A D V D S Q

ENSE00003993907

POLG-201

GAGCTGTGGATTGCAGCTGTGCTTGGAGACGCCCACTTTGCCGGCATGCATGGTGAGCAGGAGCCGGGGTTGGGGCAGCCCCAGCC
CTCGACACCTAACGTCGACACGAACCTCTGCGGGTGAAACGGCCGTACGTACCACTCGTCTCTCGGCCCAACCCCGTCGGGTCGG

13,770

POLG

POLG-201

895 L W I A A V L G D A H F A G M H 910

ENSE00003993907

POLG-201

CCTCAGCATATTGACAGTTCTGATGAACATTGGGCAGAATGTTCTGAGCTGCTTTTCTCACTCTGCTTTGCTTCCAGGCTGCA
GGAGTCGTATAACTGTCAAGACTACTTGTAAACCCGCTTACAAGGACTCGACGAAAAGAGTGAGGACGAACAGAAGGTCCGACGT

13,855

POLG

POLG-201

G C
ENSE0...

POLG-201

CAGCCTTTGGGTGGATGACACTGCAGGGCAGGAAGAGCAGGGGCACTGATCTACACAGTAAGACAGCCACTACTGTGGGCATCAG
GTCGGAAACCCACCTACTGTGACGTCCCGTCCTTCTCGTCCCCGTGACTAGATGTGTCATTCTGTGCGGTGATGACACCCGTAGTC

13,940

POLG

POLG-201

915 T A F G W M T L Q G R K S R G T D L H S K T A T T V G I S 940

ENSE00003993900

POLG-201

CCGTGAGCATGCCAAAATCTTCAACTACGGCCGCATCTATGGTGCTGGGCAGCCCTTTGCTGAGCGCTTACTAATGCAGTTTAAC
GGCACTCGTACGGTTTTAGAAAGTTGATGCCGGCGTAGATACCACGACCCGTCGGGAAACGACTCGCGAATGATTACGTCAAATTG

14,025

POLG

POLG-201

945 R E H A K I F N Y G R I Y G A G Q P F A E R L L M Q F N 970

ENSE00003993900

POLG-201

CACCGGCTCACACAGCAGGAGGCAGCTGAGAAGGCCAGCAGATGTACGCTGCCACCAAGGGCCTCCGCTGGTGAGGGTCCCTCT
GTGGCCGAGTGTGTCGTCTCCGTCGACTCTCCGGGTCGTCTACATGCGACGGTGGTTCCCGGAGGCGACCACTCCAGGGGAGA

14,110

POLG

POLG-201

H R L T Q Q E A A E K A Q Q M Y A A T K G L R W 980 985 990

ENSE00003993900

POLG-201

CCCATCCACTTTAACACCCAGGACCCGAGGCCTGCTTTACTGTCTTTAGTACTACCATCTGTTCTATCTCCTGCCCACTTACTTG
GGGTAGGTGAAATTGTGGGTCCTGGGCTCCGGACGAAATGACAGGAAATCATGATGGTAGACAAGATAGAGGACGGGTAATGAAC

14,195

POLG

POLG-201

POLG-201

AACTCTCACCTAGCCCTCTCCTTCCACACCTGTGTAACCTGGTTCCAGGATGATTTGTCTATTGTGACATTTGGTTGCTTTAT
TTGAGAGTGATCGGGGAGAGGAAGGTGTGGACACATTGGACCAAGGTCCTACTAAACAGGATAAACACTGTAAACCAACGAAATA

14,280

POLG

POLG-201

POLG-201

AGTCAGCCTTAAACAGTTTTTTCCTCATGGGAGTAAAGCTATACTTTTTGGTATACTGTTACCAAGTGGTAGCATCTTGACAATTCT
TCAGTCGGAATTTGTCAAAAAGGAGTACCCTCATTTCGATATGAAAACCATATGACAATGGTTCACCATCGTAGAACTGTTAAGA

14,365

POLG

POLG-201

POLG-201

GATTATGCTGCATAATCAATAATACAGGGGTTGCAAACCTCAGATGCCTACAGGGAATGAGAGCAAATGGAGTGGGTGGAAGACAG
CTAATACGACGTATTAGTTATTATGTCCCAACGTTTGAGTCTACGGATGTCCCTTACTCTCGTTTACCTCACCCACCTTCTGTC

14,450

POLG

POLG-201

POLG-201

GAGTTGACAGGAGGGCGCTGTGGCAAACCTGGAGCATGTAGGCTGATGTTGATACTGGAGAAAGCATTACCAGGCCTCCAGGTTAC
CTCAACTGTCCTCCC CGC GACACCGTTTGACCTCGTACATCCGACTACAACATATGACCTCTTTCGTAATGGTCCGGAGGTCCAATG

14,535

POLG

POLG-201

POLG-201

TTAGCCTAGCTCTCCAATTTGTTTCTCTGATCGTACTGCATACTGTGTGCTCAGGGCCTTAGCAGACTCTCTGCAGGGTTCCAA
AATCGGATCGAGAGGTTAAACAAAGGAGACTAGCATGACGTATGACACACGAGTCCC GGAATCGTCTGAGAGACGTCCCAAGGTT

14,620

POLG

POLG-201

POLG-201

AAACATTGAGGGAAGAGAGGTACAACCTCCTGAGGTACAGTACACTGTCCACATTTAATTAGCTGGCTCATTGTGGAAACTTCAC
TTTGTAACCTCCCTTCTCTCCATGTTGAAGGACTCCATGTGATGTGACAGGTGTAATAATCGACCGAGTAACACCTTTGAAGTG

14,705

POLG

POLG-201

POLG-201

TTTCTCGTCAACAACCTAAAAGTTAAGTATGTGATAAATGATATAGTGGTTGATGACTATAAATGCAGGGAAGGGGAGCTGAGTAT
AAAGAGCAGTTGTTGATTTTCAATTCATACACTATTTACTATATCACCAACTACTGATATTTACGTCCCTTCCCCTCGACTCATA

14,790

POLG

POLG-201

POLG-201

CGTCCAGTGGATAAAGTGAGGTCGGGTAAGGCTCATACCGTGAGCAGCGTGTGCTGGTGGAGGCGAGAAAGGTGGTGGGGCTTTA
GCAGGTCACCTATTTCACTCCAGCCATTCCGAGTATGGCACTCGTCGCACACGACCACCTCCGCTCTTTCCACCACCCCGAAAT

14,875

POLG

POLG-201

POLG-201

GTTGTGGACACCTTTGAAAAGTGTACACAGGAGTTTGGACTGTGGGTGCAGGTGGTGGGGAAGCCATTTATGCGAGTGACGTGTCTC
CAACACCTGTGGAAACTTTTACAGTGTCTCAAACCTGACACCCACGTCCACCACCCCTTCGGTAAATACGCTCACTGCACAGAG

14,960

POLG

POLG-201

POLG-201

TGGAGCCTTCAGGCGACAAGCCTTGTGAGGTCTGCAGGTTAGATGGAAGCTGGGAGTTGTCTAGGGTTGTGGCAGTTGAGAGGGG
ACCTCGGAAAGTCCGCTGTTTCGGAACACTCCAGACGTCCAATCTACCTTCGACCCTCAACAGATCCCAACACCGTCAACTCTCCCC

15,045

POLG

POLG-201

POLG-201

TAAGCCAGGCCTGGCTGTTGTGTTTTCTGCTTCAACAAATGCCCCCTCCCCTTCAGGGAGTAGCCTATTCTTACCCTATCCCC
ATTCGGTCCGGACCGACAACACAAAAGACGAAGTTGTTTACGGGGGAGGGGAAGTCCCTCATCGGATAAGAATGGGGATAGGGGG

15,130

POLG

POLG-201

POLG-201

CAAATCTAGAGTGATGGCCCTTGCTGCCTCCTGAATAAAAAGGCCCGTGTGGTTCATTGGGCAATTCAGTGTCTAAAGAAACAGGA
GTTTAGATCTCACTACCGGGAACGACGGAGGACTTATTTCCGGGCACAACCAGTAACCCGTTAAGTCACAGATTTCTTTGTCTT

15,215

POLG

POLG-201

POLG-201

CAGTAGGAATAGTGGTGCCTCCTGTGCTGGAGTCTTTGTCTTTATTGGGCTACCATGGGGTGGCCAGGCTTTGGGGCTACAAA
GTCATCCTTATCACCACGGAGGACACGACCTCAGAAACAGGAAATAACCCGATGGTACCCACCCGGGTCCGAAACCCCGATGTTT

15,300

POLG

POLG-201

POLG-201

AGCCTGGGCTGCATCTCTTTCTAGCTCCATGATCCTAGGCAAGGCACTTAGCCTCTCTGAGCCGTTTCTTCTCTGAATAAAAAGC
TCGGACCCGACGTAGAGAAAAGATCGAGGTAAGGATCCGTTCCGTGAATCGGAGAGACTCGGCAAGAAGGAGACTTATTTTCG

15,385

POLG

POLG-201

POLG-201

CTTTAGGGGACTGGCATGATGTCAGTGTTTTTAAAAGTTGAAGTGATATGTGAACATTCCTTGCCAAGGCACTAGCGTGGCACAG
GAAATCCCCTGACCGTACTACAGTCACAAAAATTTCAACTTCACTATACTTGTAAAGGAACGGTTCCGTGATCGCACCGTGTC

15,470

POLG

POLG-201

POLG-201

GAAGCACTCCCCTGGAATGATGGTGATAACACTGCCCCAGGTATCGGCTGTCGGATGAGGGCGAGTGGCTGGTGAGGGAGTTGA
CTTCGTGAGGGCACCTTACTACCACTATTGTGACGGGGGTCCATAGCCGACAGCCTACTCCCGCTCACCGACCACTCCCTCAACT

15,555

POLG

POLG-201

995 1000 1005
Y R L S D E G E W L V R E L

ENSE00003993899

POLG-201

ACCTCCCAGTGGACAGGACTGAGGGTGGCTGGATTTCCTTGCAGGATCTGCGCAAGGTCCAGAGAGAACTGCAAGGAAGTAAGA
TGGAGGGTCACCTGTCTGACTCCCACCGACCTAAAGGGACGTCTTAGACGCGTTCCAGGTCTCTCTTTGACGTTCTTCATTCT

15,640

POLG

POLG-201

1010 1015 1020 1025 1030 1035
N L P V D R T E G G W I S L Q D L R K V Q R E T A R K

ENSE00003993899

POLG-201

ACCTTCTTTGTGTTAAGGATGGAGGGAGGGGTCTGGGCTTGCCCCAGAAGAGCTTGGATGCTTTGTTTTTAGCTTTGAGATGCT
TGGAAAGAAACACAATTCTACCTCCCTCCCAGACCCGAACGGGGTCTTCTCGAACCTACGAAACAAAAAATCGAAACTCTACGA

15,725

POLG

POLG-201

POLG-201

GAAAGACAAAGTCTGCCCTCTGTTTCTGGTCCCTTAGGTACAGTGGGAAGAAGTGGGAGGTGGTTGCTGAACGGGCATGGAAGGG
CTTTCTGTTTCAGACGGGAGACAAAGACCAAGGAATCCAGTGTACCTTCTTCACCTCCACCAACGACTTGCCCGTACCTTCCC

15,810

POLG

POLG-201

POLG-201

1040 1045 1050
S Q W K K W E V V A E R A W K G

ENSE00003993916

GGGCACAGAGTCAGAAATGTTCAATAAGCTTGAGAGCATTGCTACGTCTGACATACCACGTACCCCGGTGCTGGGCTGCTGCATC
CCCGTGTCTCAGTCTTTACAAGTTATTGAACTCTCGTAACGATGCAGACTGTATGGTGCATGGGGCCACGACCCGACGACGTAG

15,895

POLG

POLG-201

POLG-201

1055 1060 1065 1070 1075
G T E S E M F N K L E S I A T S D I P R T P V L G C C I

ENSE00003993916

AGCCGAGCCCTGGAGCCCTCGGCTGTCCAGGAAGAGGTATCTTGCTACCTTTGGAGCATGGGCAGAGGGGCCCCAGGGAGGGCAG
TCGGCTCGGGACCTCGGGAGCCGACAGGTCTTCTCCATAGAACGATGGAACCTCGTACCCGCTCCCCGGGGTCCCTCCCGTC

15,980

POLG

POLG-201

POLG-201

1080 1085 1090
S R A L E P S A V Q E E

ENSE00003993916

GGCAGAGCTCCCTGTGGACCTTACCAATGTTTGTAGGTAGGGCCAGAGTGAAGCTTCTCTTGGGGCTTCTACCCTGGAGTTAATT
CCGTCTCGAGGGACACCTGGAATGGTTACAAACATCCATCCCGGTCTCACTTGAAGAGAACCCTGAAGATGGGACCTCAATTAA

16,065

POLG

POLG-201

POLG-201

GGTATGTAGCATAGCCCCTTTACCTCTGCCACCTTCCCTTCCCAGTTTATGACCAGCCGTGTGAATTGGGTGGTACAGAGCTC
CCATACATCGTATCGGGGAAAAGTGGAGACGGGTGGAAGGGAAGGGTCAAATACTGGTCGGCACACTTAACCCACCATGTCTCGAG

16,150

POLG

POLG-201

F M T S R V N W V V Q S S
ENSE00003993905

POLG-201

TGCTGTTGACTACTTACACCTCATGCTTGTGGCCATGAAGTGGCTGTTTGAAGAGTTTGCCATAGATGGGCGCTTCTGCATCAGC
ACGACAACCTGATGAATGTGGAGTACGAACACCGGTACTTACCCGACAACTTCTCAAACGGTATCTACCCGCGAAGACGTAGTCG

16,235

POLG

POLG-201

A V D Y L H L M L V A M K W L F E E F A I D G R F C I S
ENSE00003993905

POLG-201

ATCCATGACGAGGTTTCGCTACCTGGTGCGGGAGGAGGACCGCTACCCGCGCTGCCCTGGCCTTGACAGATCACCAACCTCTTGACCA
TAGGTAAGTCTCCAAGCGATGGACCACGCCCTCCTCCTGGCGATGGCGCGACGGGACCGGAACGTCTAGTGGTTGGAGAAGTGGT

16,320

POLG

POLG-201

I H D E V R Y L V R E E D R Y R A A L A L Q I T N L L T
ENSE00003993905

POLG-201

GGTATGCGGGGCCCCATGGCCTCTAGCCTGGCCATGTGCTCCTATGTGGGGCTTTGGGTGAGCGTTCCTTGGGCCAGACTGGTCAG
CCATACGCCCCGGGTACCGGAGATCGGACCGGTACACGAGGATACACCCCGAAACCCACTCGCAAGGAACCCGGTCTGACCAGTC

16,405

POLG

POLG-201

I
R

POLG-201

TTTTGACTTTTTCATCCCCCTAGAAGTGAATGTTTCAGCTTATTTATTTATTTCTAATTTTTAAAAAGTTGTAGAAGTCTAAAAA
AAAAGTGAAGTGGGGGATCTTCACTTACAAAGTGAATAAATAAATAAAGATTAAAAATTTTTCAACATCTTCAGGATTTTT

16,490

POLG

POLG-201

POLG-201

GACTAGCCTCAATTCGTAAGGAGTTATTGGGTTTGAAGTGTGAAATACCAAGACTGATCATTGAGGGGAAGCAGTGAGGTT
CTGATCGGAGTTAAGCATTTTTTCTCAATAACCCAAACTTTTACACTTTATGGTTCTGACTAGTAACCTCCCTTCGTCACCTCAA

16,575

POLG

POLG-201

POLG-201

AGGGGAATTGTTCCGAAGGGTGGTACTCACGCTTTTCTATTTGGAAAATCAAATGACAGAAGCCTTTTCTCATTTTCATAGAAAAT
TCCCCTTAACAAGGCTTCCCACCATGAGTGCGAAAAGATAAACCTTTTAGTTTACTGTCTTCGGAAAAGAGTAAAGTATCTTTTA

16,660

POLG

POLG-201

POLG-201

TGAGATGTTTGTCTTTCTTTCTCCATAAATGTTTTCTTTCTTAAGTAAGTGCCAAAAGTTTGTATTGACTGCTAACAGAAAA
ACTCTACAAACAAAAAGAAAGAGGGTATTTACAAAAGAAAGAATTCATTCACGGTTTTCAACAATAAACTGACGATTGTCTTTT

16,745

POLG

POLG-201

POLG-201

CACTGTTAATGGGGACACTCAAATGTGATTTTTAAAAATATCTTATATATTTTATATATTGAGTTGTATTTCTTGAGTAAAAT
GTGACAATTACCCCTGTGAGTTTACACTAAAAATTTTTATAGAATATATAAAATATATAACTCAACATAAAAAGAACATCATTTTA

16,830

POLG

POLG-201

POLG-201

TCCTAGTTCATATGGATGAATTAATATTACCGTTCATGTTGATCTGCCACTCAGAACCAGTTTGGGAACCATGATCTATCCTG
AGGATCAAGTATACCTACTTAATTTATAATGGCAAGGTACAACCTAGACGGTGAGTCTTGGTCAAACCCCTGGTACTAGATAGGAC

16,915

POLG

POLG-201

POLG-201

ATTATTGGGTAAATAACAGATGTTTACAATATTCAACATTGTTCCATTGCCCTCTTAATCATCATCTCCGGGAGGTTATGCTTA
TAATAACCCATTTATTGTCTACAAATGTTATAAGTTGTAACAAGGGTAACGGGAGAATTAGTAGTAGAGGCCCTCCAATACGAAT

17,000

POLG

POLG-201

POLG-201

ACAAAGCTAAAAGTCTCATTTATGCTTCAAACCTCTGGCCCAATTGGAAGTGATTTTCGTATATTAATTAATAAAGTGACCAAAC
TGTTCGATTTTCAGGAGTAAATACGAAGTTTGAGACCGGGTTAACCTTCACTAAAGCATATAATTAATTTTACATGGTTTTG

17,085

POLG

POLG-201

POLG-201

TGGGAAAAAAAAAAAAAGTATGTTGAGTCCATAATTGCATTTTCAGTATCTCAGTGGGAGGTTAGGCTGCTGGATGGAAAACAGTG
ACCCTTTTTTTTTTTTTCATACAACCTCAGGTATTAACGTAAAGTCATAGAGTCACCCTCCAATCCGACGACCTACCTTTTGTAC

17,170

POLG

POLG-201

POLG-201

CTGGACCTTACCTTTCTTGACTTAGCTAAGTGAACAGATGGGGTGTGGTCCAGGGGAAGCCCTGCTCTAAGGGGTGTGGGGTC
GACCTGGAAGTGGAAAGAAGTGAATCGATTCACTTGTCTACCCACAACAGGTCCTTCCGGGACGAGATTCCCCACACCCAG

17,255

POLG

POLG-201

POLG-201

ATTGCTCCAGGAGTGATGCATCTGTTTCACAGGAGGGGCATGACTGTGAGAGTAGATTGGGTCTCTTTTCAGGTGCATGTTTGCCTA
TAACGAGGTCTCTCACTACGTAGACAAGTGTCTCTCCCGTACTGACACTCTCATCTAACCCAGAGAAAAGTCCACGTACAAACGGAT

17,340

POLG

POLG-201

C M F A Y
ENSE00003993912

POLG-201

CAAGCTGGGTCTGAATGACTTGCCCCAGTCAGTCGCCTTTTTTCAGTGCAGTCGATATTGACCGGTGCCTCAGGAAGGAAGTGACC
GTTTCGACCCAGACTTACTGAACGGGGTCAGTCAGCGGAAAAAGTCACGTCAGCTATAACTGGCCACGGAGTCCCTTCCCTTCACTGG

17,425

POLG

POLG-201

K L G L N D L P Q S V A F S A V D I D R C L R K E V T

ENSE00003993912

POLG-201

ATGGATTGTAAAACCCCTTCCAACCCAACCTGGGATGGAAAGGAGATACGGGATTCCCCAGGGTGAGCACAACACATTTGTTTCTC
TACCTAACATTTTGGGGAAGGTTGGGTTGACCCTACCTTTCTCTATGCCCTAAGGGGTCCCACTCGTGTGTGTAAACAAGGAG

17,510

POLG

POLG-201

M D C K T P S N P T G M E R R Y G I P Q

ENSE00003993912

POLG-201

ATTACACATAGGATCTGAGGTGGACTAGAAAAGTGGGTCTTGGGAGAACAGGAAACTTGGGGCCCCAGAGAATCCACTCTTGACTCA
TAATGTGTATCCTAGACTCCACCTGATCTTTACCCAGAACCTCTTGTCTTTGAACCCGGGGTCTCTTAGGTGAGAACTGAGT

17,595

POLG

POLG-201

POLG-201

GGCTATATTCTAGGCTAATTTTCAGTTTATAAGGTGCCCTGTGTCCAGAGTGAATGTGATATGATGTTTCAGAAATGAAGGCAGCA
CCGATATAAGATCCGATTAAAGTCAAATATTCCACGGGACACAGGTCTCACTTACACTATACTACAAAGTCTTTACTTCCGTCGT

17,680

POLG

POLG-201

POLG-201

GAGCTTCAAATATTCTACCTGTACCTGTCCCCTACTTCAACCACAGAAGAAATGTTTAAAGATAATTTATTCTATAGAGTGCATT
CTCGAAGTTTATAAGATGGACATGGACAGGGGATGAAGTTGGTGTCTTCTTTACAAATTTCTATTAATAAGATATCTCACGTAA

17,765

POLG

POLG-201

POLG-201

CTTGCACTCTATAGGTGACAGAAAAACAACTGTGCTTTAAATACCAAACAAGTAAATCAGAAAGCTTATTTTCTATTTAAAATA
GAACGTGAGATATCCACTGTCTTTTTGTTTGACACGAAATTTATGGTTTGTTCATTTAGTCTTTTGAATAAAAGATAAATTTTAT

17,850

POLG

POLG-201

POLG-201

TATCTAAGACACACTTATATAAAAAAGAAAACAGACCCTCCTAACATGTAACATTACCGTTCGTGGCAATTGTTCTCAACCTTTCA
ATAGATTCTGTGTGAATATATTTTTCTTTTGTCTGGGAGGATTGTACATTGTAATGGCAAGCACCGTTAACAAGAGTTGGAAAAGT

17,935

POLG

POLG-201

POLG-201

CTCTCCTTTTGACCTTAGCATTAAAGCTCCTTTGCTCACTTCTGAGCTCTCAGTTACAGTTCTTGAGGTGGCATCCTAACCAATTT
GAGAGGAAAACTGGAATCGTAATTCGAGGAAAACGAGTGAAGACTCGAGAGTCAATGTCAAGAACTCCACCGTAGGATTGGTTAAA

18,020

POLG

POLG-201

POLG-201

GCACTATCTTTTCAGGTGAAGCGCTGGATATTTACCAGATAATTGAACTCACCAAAGGCTCCTTGGA AAAACGAAGCCAGCCTGGA
CGTGATAGAAAAGTCCACTTCGCGACCTATAAATGGTCTATTA ACTTGAGTGGTTTCCGAGGAACCTTTTTGCTTCGGTCGGACCT

18,105

POLG

POLG-201

1215 G E A L D I Y Q I I 1220 1225 E L T K G 1230 S L E K R S Q P G 1235
ENSE00003993902

POLG-201

CCATAGCACTGCCTGGAGGCTCTGTATTTGCTCCCGTGGAGCTTCATCGGGGTGGTGCAGGCTCCCAAACCTCAGGCTTTTCAGCTG
GGTATCGTGACGGACCTCCGAGACATAAACGAGGGGCACCTCGAAGTAGCCCCACCACGTCCGAGGGTTTGAGTCCGAAAAGTCGAC

18,190

POLG

POLG-201

1240
P
ENSE...
POLG-201

TGCTTTTTGCAAAAAGGGCTTGCCTAAGGCCAGCCATTTTTTCAGTAGCAGGACCTGCCAAGAAGATTCTTCTAACTGAAGGTGCA
ACGAAAAACGTTTTCCCGAACGGATTCCGGTCGGTAAAAAGTCATCGTCCTGGACGGTTCTTCTAAGGAAGATTGACTTCCACGT

18,275

POLG

POLG-201

GTTGAATTCAGTGGGTT CAGAACCAAGATGCCAACATCGGTGTGGACTACAGGACAAGGGGCATTGTTGCTTGTGGGTAAAAAT
CAACTTAAGTCACCCAAGTCTTGGTTCTACGGTTGTAGCCACACCTGATGTCCTGTTCCCGTAACAACGAACAACCCATTTTTTA

18,360

POLG

POLG-201

GAAGCAGAAGCCCCAAAGTTCACATTA ACTCAGGCATTTCA TTTATTTTTCTTTTCTTCTTG GCTGGTTCTTTGTTCTGTCCC
CTTCGTCTTCGGGGTTTCAAGTGTAATTGAGTCCGTAAAGTAAATAAAAAAGGAAAAAGAAGAACCGACCAAGAAAACAAGACAGGG

18,445

POLG

POLG-201

CCATGCTCTGATGCAGTGCCTTAGAAGGGGAAAGAATTAATGCTCTAACGTGATAAACCTGCTCCAAGGCAGTGGAAATAAAAAG
GGTACGAGACTACGTACGGGATCTTCCCCTTTCTTAATTACGAGATTGCACTATTTGGACGAGGTTCCGTCACCTTTATTTTTTC

18,530

POLG

POLG-201

AAGGAAAAAAAAAGACTCTATCTTCTCATCAAAGCCTTTGTTAGTCATGCTTTCCCACTTTCCCACTCACAGGAGGTAATTATGT
TTCCTTTTTTTTCTGAGATAGAAGAGTAGTTTCGGAAACAATCAGTACGAAAGGGGTGAAAGGGTGAGTGTCTCCATTAATACA

18,615

POLG

POLG-201

TGTTGAAGAAGAGGAAGGAGTCCTCCAAAGTGTAGAGTAATAAGACAGTGGCACCTCCTTTTAGGACTTTTGTATACTGAGGAT
ACAACCTCTTCTCCTCCTCAGGAGGTTTCACATCTCATTATTCTGTACCCTGGAGGAAAATCCTGAAAACGATATGACTCCTA

18,700

POLG

ACTTATGGGACAAAATGACAAGAGAAGAAGCCATTGACATCAAATGCTACATGACTCTCCTGAGTGCAGCTGCCAAGTGGGTAA
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18,785

POLG

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18,870

POLG

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18,955

POLG

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19,040

POLG

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19,125

POLG

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19,210

POLG

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19,295

POLG

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19,380

POLG

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19,465

POLG

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19,550

POLG

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POLG

19,635

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POLG

19,720

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POLG

19,805

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POLG

19,890

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POLG

19,975

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POLG

20,060

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POLG

20,145

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POLG

20,230

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POLG

20,315

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POLG

20,400

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POLG

20,485

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POLG

20,570

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POLG

20,655

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POLG >

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POLG >

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POLG >

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POLG >

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POLG >

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POLG >

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POLG >

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POLG >

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POLG >

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POLG >

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POLG >

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POLG >

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POLG >

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POLG

21,845

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POLG

21,930

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POLG

22,015

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POLG

22,100

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POLG

22,185

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POLG

22,270

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POLG

22,355

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POLG

22,440

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POLG

22,525

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POLG

22,610

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POLG

22,695

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POLG

22,780

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POLG

22,865

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POLG >

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POLG >

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POLG >

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POLG >

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POLG >

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POLG >

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POLG >

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POLG >

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POLG >

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POLG >

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POLG >

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POLG >

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POLG >

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POLG

24,055

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POLG

24,140

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POLG

24,225

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POLG

24,310

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POLG

24,395

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POLG

24,480

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POLG

24,565

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POLG

24,650

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POLG

24,735

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POLG

24,820

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POLG

24,905

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POLG

24,990

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POLG

25,075

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POLG

26,265

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POLG

26,350

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POLG

26,435

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POLG

26,520

TAAGGACAACCTGGCAATTTCTGGAGACATTTTTGGCTGTTAAACTAGGGGGCTGCTACTGGCATCTGGTAGGTGGAGGCCAGGG
ATTCCTGTTGACCGTTAAAGACCTCTGTAAAAACCGACAATTTTGATCCCCGACGATGACCGTAGACCATCCACCTCCGGTCCC
POLG

26,605

ATGCTACTCAACATCCAAAAATGCACAGAACAGGTCCCACAACAAGAATTATCTAGCGCAACATGTCAATAGTGGTGAGGTTAA
TACGATGAGTTGTAGGGTTTTACGTGTCTTGTCCAGGGTGTGTTTCTTAATAGATCGCGTTGTACAGTTATCACCCTCCAATT
POLG

26,690

AAAACCTGGTTTAAGCAAACAGTAAAGGAGATTCAAGTACTGCAGGAATCTGATGGTATTTAGGACCAAATGACACTTACAAAGCC
TTTTGACCAAATTCGTTTGTCAATTTCTCTAAGTTCATGACGTCTTAGACTACCATAAATCCTGGTTTTACTGTGAATGTTTCGG
POLG

26,775

ACGTCCTTCCACTTCCCTGAAAAGTGCCTCACTGCACTGCCGTCTCATCACAACCCTTCTTCATGTGCTTGCTGCTACTCTGCTC
TGCAGGAAGGTGAAGGGACTTTCACGGGAGTGACGTGACGGCAGAGTAGTGTTGGGAAGAAGTACACGAACGACGATGAGACGAG
POLG

26,860

ACATTCCCAGAGGATGCCTCATGGCATGGACTTTCAGTCAACCAGGAATAAACCAAGTCCTTGAGCCTGAGCATGCTTGTTTCCTT
TGTAAGGGTCTCCTACGGAGTACCGTACCTGAAAAGTCAGTGGGTCTTATTTGGTTTCAGGAACTCGGACTCGTACGAACAAGGAA
POLG

26,945

CCTTGCTCCAAATGCAAACATATATGCTTCCCTTCTCCAAATTAAGTGAAACAGTTTTCTTTACATAAAGATGTCCTTGCTGCAA
GGAACGAGGTTTACGTTTGTATATACGAAGGAAAGAGGTTTAATTCACCTTTGTCAAAGAAATGTATTTCTACAGGAACGACGTT
POLG

27,030

AGCCCTCAAGCCTTGGCTTGGTCTCTGATGGGTGCCTCCAGCTTGTGGTAAGCAGGGAAAAAAGTTTTATATATGCTCAGTTCAGG
TCGGGAGTTCGGAACCGAACCCAGAGACTACCCACGGAGGTGCAACACCATTTCGTCCCTTTTTTCAAATATATACGAGTCAAGTCC
POLG

27,115

TGATCAATAGTCCCCTGGGCATGTAAGAAATCCTTTCTTGAAGACCTATTGGGTACTGCCTCTGAATCTCTTACCTGTACGTAAG
ACTAGTTATCAGGGGACCCGTACATTCTTTAGGAAAGAACTTCTGGATAACCCATGACGGAGACTTAGAGAATGGACATGCATTC
POLG

27,200

AAATGAAAGAATAACACAGGGGGGTGAGATGAGAACCAGACAGCTTCACCTGCACAACAAGGGAGAAGGAAACCAATGTAACCAG
TTTACTTTCTTATTGTGTCACCCAGTCTACTCTTGGTCTGTGCAAGTGGACGTGTTGTTCCCTCTTCTTTGGTTACATTGGTC
POLG

27,285

CAGTAAAAGTGCTTCCCCATTCTAGGAAAGGCATTCTCAACTCACCAGCTTTTCCATATTTTTTGGAAATTCCTCCGGAGCTCT
GTCATTTTACGAAGGGGGTAAGGATCCTTTCCGTAAGAGTTGAGTGGTCGAAAAGGTATAAAAAACCTTAAGGAGGCCTCGAGA
POLG >

27,370

GACACACCTGGAGATACTAATAAAAAAAGATTCCCTAGATTTAGTAGACTGTCCTATGAAACTACAAGTGACTGCTGCAGTGAGCC
CTGTGTGGACCTCTATGATTATTTTTTTCTAAGGATCTAAATCATCTGACAGGATACTTTGATGTTCACTGACGACGTCACCTCGG
POLG >

27,455

TATGGAGTGTGACTCATCATTCTGACTGAAGAGGAAAAACAAAATTCACAGAGAAGCCAAGACACAAGCTTCCTTATTCCTCTCC
ATACCTCACACTGAGTAGTAAGACTGACTTCTCCTTTTTGTTTTAAGTGTCTCTTCGGTTCTGTGTTTGAAGGAATAAGGAGAGG
POLG >

27,540

TCCAAAGCTCCTAAGCTTCCCAGACAATAAGTAATGAAGGGTTTGTCTGATTTGCTCATTCTTTAAAAATTCCTCAGGCTGG
AGGTTTCGAGGATTCGAAGGGTCTGTTATTCATTACTTCCCAAACAAAGACTAAACGAGTAAAGAAATTTTTAAGGAGTCCGACC
POLG >

27,625

TAGTCCCTGCATGTAAAAAACCAACAACCTTTGCTGTTTTCTTTTTAAAGATGCCAATAAAGAGAAGAGGCTCTCAGTATTTCCA
ATCAGGGACGTACATTTTTTTGGTTGTTGAAACGACAAAAAGGAAAATTTCTACGGTTATTTCTCTTCTCCGAGAGTCATAAAGGT
POLG >

27,710

CTACAGCAGCTTAGCCACATGTAGCTAGAGCTACACATTCTGAGAGAGCCACACTGCTGTGATGCGGGGTGGTCCACATCTTTCT
GATGTCGTCGAATCGGTGTACATCGATCTCGATGTGTAAGACTCTCTCGGTGTGACGACACTACGCCCCACCAGGTGTAGAAAAGA
POLG >

27,795

TGGATTATCTGTGCCTTTCTAAGTATTTAATATGGATCATTGCTAGGAACATAAACAGTAAGGGCAGGGTATGCCTTGTATTTTT
ACCTAATAGACACGGAAAGATTTCATAAATTATACCTAGTAACGATCCTTGTATTTGTCATTCCCGTCCCATACGGAACATAAAAA
POLG >

27,880

ATAAAAAATAATTTTCTTCCCACCTTAGTATTTGATCTATAAGGCATTTAACACCTACATGTTAAAGGAATGAAAAAGGAATA
TATTTTTTTATTAAGAAGGGGTGGAATCATAAACTAGATATTCCGTAATTTGTGGATGTACAATTTCTTACTTTTTTCTTAT
POLG >

27,965

AACATCTCTTTAAGTGTCCAGACTGGTTAGAAATGGTATAATTTCTATGCATTATGGGCCAGATTTAATTCTAGGATAGTTATA
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POLG >

28,050

GTTTAGATTAAACCTTAGAAGGTATTTAAAAGAGGCATTCTCAATCAGGTGCCACATACATGCCAAAGAATTAAGGGCCTC
CAAATCTAATTTGGAATCTTCCATAAATTTCTCCGTAAGTAAGAGTTAGTCCACGGTGTATGTACGGTTTTCTTAATTTCCGGAG
POLG >

28,135

CAAAAGCAGATTTTTACTTTATTTTTTAAATTTTTGAGATGGAGTCTCACTCTATTGCCAACGCTGGAGTACAGTGGCACAATCT
GTTTTCGTCTAAAAATGAAATAAAAAAATTA AAAACTCTACCTCAGAGTGAGATAACGGTTGCGACCTCATGTACCCTGTTAGA
POLG >

28,220

CAGCTCACTGCAACCTCCGCCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCTGAGTAGCTGGGATTACAGGTGCCACCA
GTCGAGTGACGTTGGAGGCGGAGGACCCAAGTTCGCTAAGAGGACGGAGTCGGAGGACTCATCGACCCTAATGTCCACGGGTGGT
POLG >

28,305

CCACGCCAGCTACTTTTTGTATTTTTAGTAGAGACGGGGTTTACCATGTTGGCCAGGCTGGTCTCGAACTCCTGACCTCAGGT
GGTGC GGTCGATGAAAAACATAAAAAATCATCTCTGCCCAAAGTGGTACAACGGTCCGACCAGAGCTTGAGGACTGGAGTCCA
POLG >

28,390

GATCCGCCCCTCTCAGCCTACCAAAGTGCTGGGATTACAGGCATGAACCACCGTGACAGGCCCAAAAGCAGATTAGAATTATAAA
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POLG

28,475

CTGTTTTCCCTGGCCTGTGGAGATGCCTGCCACCTACTGACCAAATAAAATGAAACCATGACCTGCCAAGATGGAGGGCAAATG
GACAAAAAGGGACC GGACACCTCTACGGACGGTGGATGACTGGTTTTGATTTTACTTTGGTACTGGACGGTTCTACCTCCGTTTTAC
POLG

28,560

CTCTCTTGTTTAGGGGCATTCTGCAGCAGTGGGCTGCTGCCCATCCTCATCTCCTGGCTCACTGGGGTAGAATGGTGGGGCGAA
GAGAGAACAATCCCCGTAAGACGTCGTCACCCGACGACGGGGTAGGAGTAGAGGACCGAGTGACCCCATCTTACCACCCCGCTT
POLG

28,645

TCTGCTTGTCTCAAATACTCACATATCTGACAAGGGCTGTAAGTGTGGTGTACATTTTGACAAAGTCCTTTAACAAGGTGTCCAC
AGACGAACAGAGTTTATGAGTGTATAGACTGTTCCCGACATTCACACCACATGTA AACGTTGTT CAGGAAATTGTTCCACAGGTG
POLG

28,730

ACAGCTGCCTGATGGCAGAGCTGTCTGCACCAGCTCGTGGAAAAATGTAAGCAGAGTTC CAGTTGCATGATGATAGCTTTCTCA
TGTCGACGGACTACCGTCTCGACAGACGTGGTTCGAGCACCTTTTTACATTCGTCTCAAGGGTCAACGTA CTACTATCGAAAGAGT
POLG

28,815

ACAGGCTGATTTGGTAGGGTTGCCTGAGAAGAGGCCTCTTCTAAAGGGAAATAAAATTGGCACATTC AAACCCA ACTTCGTTTTTC
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POLG

28,900

TAATTAAGAGTAAAGGAGATTTAGAAATTGATTACTACTA ACTAGAAAAGTCTTTATGGAAAAACGAACATTCAATATGCAGAGTG
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POLG

28,985

AATTAATCGTGCTGTGATAAGACATATGATCTTCTACTTCTTTATCACATAGGAAAAAATCTAGCTTAAAGGCAAATAAGAAAT
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POLG

29,070

TTAGCTCAGGGGCTCCATTTTTATGCACCGACCCAATATGAATTTTGACCTTGCTCATGTCAATTCCTGGAATCC CAGTTGAACT
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POLG

29,155

TATCTTACCTGATAAGGTTTCTTGGCTCACTTGTCCCTTAAGCTTGGTGATTAGCCAGTCCACTTCTTCTAGAACCTTCTCGGCC
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POLG

29,240

TGACTCAGAACAAGTAACTGAAAAGAAAAGAGTGCCTGGTGTGATTCACTACACACAGCTGTGGGGGTAATATAATAACTGTGGTC
ACTGAGTCTTGTTCATTGACTTTCTTTTCTCACGGACCACACTAAGTGATGTGTGTGTCGACACCCCCATTATATTATTGACACCAG
POLG

29,325

ACCTGGCCACCTACAGGTGGGTTACAGGCCTCAGGACACAAGCCGCTATAGGACACAAGTCACTTACATGGAGTAGAATGGAAA
TGGACCGGTGGATGTCCACCCAATGTCCGGAGTCTGTGTTTCGGCGATATCCTGTGTTTCAGTGAAGTGTACCTCATCTTACCTTT
POLG

29,410

GAATGACAAAGCTATTTCCCATGGCTCAGGTACAACACTTACACAGACAGTGGGGGCAGCCGTTCTCAAATTCACTATTGCAAAG
CTTACTGTTTCGATAAGGGGTACCGAGTCCATGTTGTGAATGTGTCTGTCAACCCCGTCGGCAAGAGTTTAAAGTGATAACGTTTTC
POLG

29,495

TGGTTTGTTCCTCCACCTCTACATCCTGGGGAAAAGAAGAGAGGTTGAGACCTAATGACAGTAAGGTTGTTCCCTTGACCCCAT
ACCAAACAAAAGAGGTTGGAGATGTAGGACCCCTTTTCTTCTCTCCACTCTGGATTACTGTCATTCCAACAAGGGAAGTGGGGGTA

29,580

POLG



CCCCACACAGGGTATTGTAAGGCTCATTATAGTACCTGGTCTATATCTCCAGATGCCCGTGGATATCCTGGGACAAGTC
GGGGTGTGTCCATAACATGACTTCCGAGTAATATCATGGACCAGATATAGAGGGTCTACGGGCACCTATAGGACCCCTGTTTCAG

3'

29,664

5'

POLG













Feature	Location	Size	Start	End	Type
✓ POLG	1 .. 29,664	29,664 bp	■	→	gene
/note	= gene ENSG00000140521 Protein coding				
POLG-202	1 .. 18,542	18,542 bp	■	→	prim_transcript
/note	= primary transcript ENST00000442287				
✓ POLG-201	38 .. 18,542	18,505 bp	■	→	prim_transcript
/note	= primary transcript ENST00000268124				
POLG-217	38 .. 18,178	18,141 bp	■	→	prim_transcript
/note	= primary transcript ENST00000636774 Nonsense mediated decay				
POLG-219	43 .. 18,542	18,500 bp	■	→	prim_transcript
/note	= primary transcript ENST00000636937				
POLG-213	45 .. 18,557	18,513 bp	■	→	prim_transcript
/note	= primary transcript ENST00000631044 Nonsense mediated decay				
POLG-215	151 .. 18,523	18,373 bp	■	→	prim_transcript
/note	= primary transcript ENST00000635986 Nonsense mediated decay				
POLG-228	151 .. 18,507	18,357 bp	■	→	prim_transcript
/note	= primary transcript ENST00000672071 Retained intron				
POLG-224	418 .. 1012	595 bp	■	→	prim_transcript
/note	= primary transcript ENST00000637711 protein_coding_CDS_not_defined				
POLG-225	1053 .. 4654	3602 bp	■	→	CDS
▶ 2 segments = 783 bp					
/note	= coding sequence ENSP00000497242				
/translation	= LEPKARCSDSQRGGPCTNHEPPALEEGRRRHRARRAGSSSGALGLQLRPRVPRQRRRAAAAAAAAAAAAAAAAAAATAASAAASAILGGRAAAAQPI GHPDALERAAARANLRRRGDAWRGRGAPQRRAPAEARALGAA SRA LARRGAA PA APLRGQPGPALPPP GP EAE PALPGGGQLAVAGPAAPEA PGLGLGGGLDPVRRGGGRTRGHPRGAGPGVRRGGLLGRGNLPHIGGGHIPLGL,,VFLVQPAAGGRA LLLDQPAVAG* 260 amino acids = 25.5 kDa				
POLG-225	1053 .. 4654	3602 bp	■	→	prim_transcript
/note	= primary transcript ENST00000650303				
✓ POLG-201	1108 .. 18,111	17,004 bp	■	→	CDS
▶ 22 segments = 3720 bp					
/note	= coding sequence ENSP00000268124				
/translation	= MSRLLRKVGATVGGPVPVAPGRWVSSVPSADPSDGQRRRQQQQQQQQQQQPQQPQVLSSEGGQLRHNPLDIQMLSRGLHEQIFG QGGEMPGEAAVRRSVEHLQKHGLWGQPAVPLPDVELRLPPLYGDNLQHFRLLAQKQSLPYLEAANLLLQAQLPPKPPAWAWAEGWTRYGPEG EAVPVAIPEERALVFDVEVCLAEGTCPTLAVAISSPAW,,YSWCSQRLVEERYSWTSQLSPADLIPLVPTGASSPTQRDWEQQLVVGHNVSFDR AHIREQYLIQ,,GSRMRFLDTMSMHMAISGLSSFQRSLWIAAKQGKHKVQPPTKQGGKSRKARRGPA,,ISSWDWLDISSVNSLAEVHRLYVGGP PLEKEPRELFVKGTMKDIRENFQ,,DLMQYCAQDVWATHEVFQQQLPLFLER,,C PHPVTLAGMLEMGVSYLPVNQNWERYLAEAQGTYEELQRE MKKSLMDLANDACQLLSGER,,YKEDPWLDLEWDLQEFKQKKAKKVKKPATASKLPIEGA GAPGDPMDQE,,DLGPCSEEEEFQQDVMARACL QKLGTTTELLPKRPQHLPGHGP,,WYRKLCPRLDDPAWTPGPSLLSLQMRVTPKLMALTWDGFP LHYSERHGWGYLVPGRRDNLAKLPTGTTLESA GVVCPYR,,AIESLYRKHCLEQGKQLMPQEA GLAEFFLLDNSAIWQT,,VEELDYLEVEAEAKMENLRAAVPGQPLAL,,TARGGPKDTQPSYHH GNGPYNDVDIPGCWFFKLPKH,,DGNSCNVGSPFAKDFLPKMEDGTLQAGPGGASGPRALEINKMISFWRNAHKRIS,,SQMVVWLPRAALPRAVI R,,HPDYDEEGLYGAILPQVVTA GTITRRAVEPTWLTASNAR,,PDRV GSELKAMVQAPPGYTLVGADVDSQELWIAAVLGD AHFAGMH,,GCTAFG WMTLQGRKSRGTDLHSKTATTV GISREHAKIFNYGRIYGAQPFAERLLMQFNHRLTQEEAEKAQQMYAATKGLRW,,YRLSDEGEWLVRELNL PVDRTTEGGWISLQDLRKVQRETARK,,SQWKKWEVVAERAWKGGTESEM FNKLESIA TSDIPRTPV LGCCISRALEPSAVQEE,,FM TSRVNWV VQ SSAVDYLLHLLVA MKWLFEEFAIDGRFCISIHDEVRYLVREEDRYRAALALQITNLLTR,,CMFAYKLG LNDLPQSVAFFSAVDIDRCLRKEV TMDC KTPSNPTGMERRYGIPO,,GEALDIYQIIELTKGSLEKRSQPGP*				

Feature	Location	Size	Type
POLG-202	1108 .. 18,111	17,004 bp	CDS
▶ 22 segments = 3720 bp			
/note	= coding sequence ENSP00000399851		
/translation	= MSRLLRKLVAGATVGGPVPVAPGRWVSSVSPASDPSDQRRRQQQQQQQQQQQQQPQQPQVLSSEGGQLRHNPLDIQMLSRGLHEQIFGQGGEMPGEAAVRRSVEHLQKHGLWGQPAVPLPDVELRLPPLYGDNLDQHFRLLAQKQSLPYLEAANLLLQAQLPPKPPAWAWAEGWTRYGPEG EAVPVAIPEERLALVFDVEVCLAEGTCPTLAVAISSPAW,,YSWCSQRLVEERYSWTSQLSPALDIPLEVP TGASSPTQRDWQEQLVVGHNVSFDR AHIREQYLIQ,,GSRMFLDTMSMHMAISGLSSFQ RSLWIAAKQGKHKVQPPTKQGQKSQRKARRGPA,,ISSWDWLDISSVNSLAEVHRLVGGP PLEKEPRELFVKGTMKDIRENFQ,,DLMQYCAQDVWATHEVFQQQLPLFLER,,CPHPVTLA GMLEMVSYLPVNQN WERYLAEAQGTYEELQRE MKKSLMDLANDACQLLSGER,,YKEDPWLWDLWDLQEFKQKAKKVKKEPATASKLPIEGAGAPGDPMDQE,,DLGPCSEEEEFQ QDV MARACL QKLKGTTELLPKRPQHLP GHPG,,WYRKLCPRLDDPAWTPGPSLLSLQMRVTPKLMALTWDGFPLHYSERHGWGYLVPGRRDNLAKLPTGTTLESA GVVCPYR,,AIESLYRKHCCLEQGKQQLMPQEAAGLAEFFLLDNSAIWQT,,VEELDYLEVEAEAKMENLRAAVPGQPLAL,,TARGGPKDTPSYHH GNGPYNDVDIPGCWFFKLP HK,,DGNSCNVGSPFAKDFLPKMEDGTLQAGP GGASGPRALEINKMISFWRNAHKRIS,,SQMVVWLP RSALPRAVI R,,HPDYDEEGLYGAILPQVV TAGTITRRAVEPTWLTA SNAR,,PDRVSELKAMVQAPPGYTLVGADVDSQELWIAAVLGD AHFA GMH,,GCTAFG WMTLQGRKSRGTDLHSKTATTV GISREHAKIFNYGRIYGAAGQPFAERLLMQFNHRLTQQEAAEKAQQMYAATKGLRW,,YRLSDEGEWLVRELNL PVDRTTEGGWISLQDLR KVQRETARK,,SQWKKWEVVAERA WKG GTESEMFNKLESIA TSDIPRTPVLGCCISRAL EPSAVQEE,,FM TSVNWWVQ		
POLG-219	1108 .. 18,111	17,004 bp	CDS
▶ 22 segments = 3720 bp			
/note	= coding sequence ENSP00000516154		
/translation	= MSRLLRKLVAGATVGGPVPVAPGRWVSSVSPASDPSDQRRRQQQQQQQQQQQQQPQQPQVLSSEGGQLRHNPLDIQMLSRGLHEQIFGQGGEMPGEAAVRRSVEHLQKHGLWGQPAVPLPDVELRLPPLYGDNLDQHFRLLAQKQSLPYLEAANLLLQAQLPPKPPAWAWAEGWTRYGPEG EAVPVAIPEERLALVFDVEVCLAEGTCPTLAVAISSPAW,,YSWCSQRLVEERYSWTSQLSPALDIPLEVP TGASSPTQRDWQEQLVVGHNVSFDR AHIREQYLIQ,,GSRMFLDTMSMHMAISGLSSFQ RSLWIAAKQGKHKVQPPTKQGQKSQRKARRGPA,,ISSWDWLDISSVNSLAEVHRLVGGP PLEKEPRELFVKGTMKDIRENFQ,,DLMQYCAQDVWATHEVFQQQLPLFLER,,CPHPVTLA GMLEMVSYLPVNQN WERYLAEAQGTYEELQRE MKKSLMDLANDACQLLSGER,,YKEDPWLWDLWDLQEFKQKAKKVKKEPATASKLPIEGAGAPGDPMDQE,,DLGPCSEEEEFQ QDV MARACL QKLKGTTELLPKRPQHLP GHPG,,WYRKLCPRLDDPAWTPGPSLLSLQMRVTPKLMALTWDGFPLHYSERHGWGYLVPGRRDNLAKLPTGTTLESA GVVCPYR,,AIESLYRKHCCLEQGKQQLMPQEAAGLAEFFLLDNSAIWQT,,VEELDYLEVEAEAKMENLRAAVPGQPLAL,,TARGGPKDTPSYHH GNGPYNDVDIPGCWFFKLP HK,,DGNSCNVGSPFAKDFLPKMEDGTLQAGP GGASGPRALEINKMISFWRNAHKRIS,,SQMVVWLP RSALPRAVI R,,HPDYDEEGLYGAILPQVV TAGTITRRAVEPTWLTA SNAR,,PDRVSELKAMVQAPPGYTLVGADVDSQELWIAAVLGD AHFA GMH,,GCTAFG WMTLQGRKSRGTDLHSKTATTV GISREHAKIFNYGRIYGAAGQPFAERLLMQFNHRLTQQEAAEKAQQMYAATKGLRW,,YRLSDEGEWLVRELNL PVDRTTEGGWISLQDLR KVQRETARK,,SQWKKWEVVAERA WKG GTESEMFNKLESIA TSDIPRTPVLGCCISRAL EPSAVQEE,,FM TSVNWWVQ		
POLG-226	1451 .. 18,512	17,062 bp	prim_transcript
/note	= primary transcript ENST00000666746 Nonsense mediated decay		
POLG-208	1507 .. 18,534	17,028 bp	prim_transcript
/note	= primary transcript ENST00000530292 Nonsense mediated decay		
POLG-223	1718 .. 4651	2934 bp	CDS
▶ 2 segments = 100 bp			
/note	= coding sequence ENSP00000490427		
/translation	= QRELAPHWRWPYPPRP,,ASGWKSVTLGPASCRR 33 amino acids = 3.9 kDa		
POLG-223	1718 .. 4651	2934 bp	prim_transcript
/note	= primary transcript ENST00000637307		
POLG-222	5825 .. 18,532	12,708 bp	prim_transcript
/note	= primary transcript ENST00000637264		
POLG-222	5825 .. 18,111	12,287 bp	CDS
▶ 20 segments = 2732 bp			
/note	= coding sequence ENSP00000489844		
/translation	= VCG*QPSRANTRSSPPQSKARSPRGKPEEAQR,,SHPGTGWTSVAVSTVWQRCTDFM*GGLP*RRSLENCL*RAP*RTFVRTSR,,T*CSTVPRTCG PPMRFSSSYRSSWR,,GVP TQ*LWPACWRWV SPTCLSTR TG SVTWQRHRALMRSSSGR*RSR*WIWPMMPASCSQER,,GTKKTPGSGTWSGTC KNLSRRKLRR*RRNQ PQPASCPSRGLGPLVIPWIRK,,TSPA VRRRSFNKMSWPA PA CRS*RG PQSSCPSPGPTFLDTL,,DGTGSSAPG*TTLHG PRA PASACRCGSHLNSWHLPGMASLCTTQ SVMAGATWCLGGGTTWPSCRQVPPWSQLGWSAPT,,EPSSPCTGSTVSNRGSSS*CPRRP AWR RSSCSLTIVPYGKR,,*KNWIT*KWRLRPRWRTELCQCVNP*L*,,LPVVA PRTPSPA ITMAMDLTTTWSLAA GFSSCLTR,,MVIAMWEAPLPR TSCPRWRMAPCRLAQEV PVGPVLWKSTK*FLSGGTPINV S,,APRWWC GCPGQLCPVL*S,,GTP TMMRKASMGSPCKW*LPAPSLAGLWSPHG SPPAMPG,,LTE*AVS*KPWRPHLATPLWVLMWTPKSCGLQLCLETPTLPACM,,AAQPLGG*HCRAGRAGALIYTVRQPLLWASAVSMPKSSTT AASMVLGSPLLSAY*CSLTTGSHSRRQLRRPSRCTLPPRAS A,,GIGCRMRA SGW*GS*TSQ WTGLRVAGFPCRICARSREKLQ G,,SHSGRSGRW LLNGHGRGAQSQKCSISLRA LLRLTYHVPRCWAASA EPWSPRLSRKS,,L*PAV*IGWYRALLTTYT SCLWP*SGCLKSLP*MGASASASMTRF		
POLG-230	5900 .. 18,521	12,622 bp	prim_transcript
/note	= primary transcript ENST00000672923 Retained intron		
POLG-210	6150 .. 7849	1700 bp	prim_transcript
/note	= primary transcript ENST00000532363 Retained intron		

Feature	Location	Size	Type
POLG-221	7526 .. 18,505	10,980 bp	prim_transcript
/note	= primary transcript ENST00000637238 Nonsense mediated decay		
MIR6766	8052 .. 8123	72 bp	gene
/note	= gene ENSG00000275101 miRNA		
MIR6766-201	8052 .. 8123	72 bp	prim_transcript
/note	= primary transcript ENST00000622641 miRNA		
POLG-203	8157 .. 12,120	3964 bp	CDS
▶ 5 segments = 700 bp			
/note	= coding sequence ENSP00000432389		
/translation	= NKMSWPAPACRS*RGPPQSSCPSPGPFSTFLDTL,,DGTGSSAPG*TTLHGPRAPASSACRCGSHLNSWHLPGMASLCTTQSVMAGATWCLGGGTT WPSCRQVPPWSQLGWSAPT,,EPSSPCTGSTVSNRGSS*CPRRPAWRRSSCSLTIVPYGKR,,*KNWIT*KWRLRPRWRTCELQCQVNP*LW,,MV IAVMWEAPLPRTSCPRWRMAPCRLAQEVPVGPVLWKSTK*FLSGGTPINVS 233 codons (7 internal stop codons)		
POLG-203	8157 .. 12,120	3964 bp	prim_transcript
/note	= primary transcript ENST00000526314		
POLG-227	8219 .. 15,570	7352 bp	CDS
▶ 8 segments = 859 bp			
/note	= coding sequence ENSP00000499709		
/translation	= KRQHLPGHPG,,WYRKLCPRLDDPAWTPGSPILLSLQMRVTPKLMALTWDGFPPLHYSERHWGWLVPGRRDNLAKLPTGTTLESAGVVCPIR,,AIE SLYRKHCCLEQ GKQQLMPQEA GLAEFLDNDNSAIWQT,,VEELDYLEVEAEAKMENLRAAVPGQPLAL,,TARGGPKDTPSYHHGNGPYNDVDIP GCWFFKLPKH,,DGNSCNVGSPFAKDFLPKMEDGTLQAGPGGASGPRALEINKMISFWRNAHKRIS,,SQMVVWLPRAALPRAVIR,,YRLSDEGEWL YSELRV 285 codons = 32.1 kDa		
POLG-227	8219 .. 15,570	7352 bp	prim_transcript
/note	= primary transcript ENST00000670281		
POLG-211	9262 .. 13,087	3826 bp	prim_transcript
/note	= primary transcript ENST00000532584 Retained intron		
POLG-204	9275 .. 12,057	2783 bp	prim_transcript
/note	= primary transcript ENST00000526398 Nonsense mediated decay		
POLG-205	9378 .. 11,348	1971 bp	prim_transcript
/note	= primary transcript ENST00000526573 Retained intron		
POLG-212	10,571 .. 11,342	772 bp	prim_transcript
/note	= primary transcript ENST00000533857 Retained intron		
✓ Donor Template WT -> SNV	11,333 .. 11,432	100 bp	misc_feature
✓ PAM	11,392 .. 11,394	3 bp	misc_feature
✓ Protospacer Sequence	11,395 .. 11,414	20 bp	misc_feature
✓ SNV	11,402 .. 11,402	1 bp	misc_feature
/note	= WT = G SNV = C		
POLG-207	11,425 .. 14,042	2618 bp	prim_transcript
/note	= primary transcript ENST00000528881 Nonsense mediated decay		
POLG-209	11,435 .. 15,594	4160 bp	prim_transcript
/note	= primary transcript ENST00000530715 Nonsense mediated decay		
POLG-229	13,939 .. 18,542	4604 bp	prim_transcript
/note	= primary transcript ENST00000672695 protein_coding_CDS_not_defined		
POLG-218	14,061 .. 15,524	1464 bp	CDS
▶ 2 segments = 100 bp			
/note	= coding sequence ENSP00000490403		
/translation	= PADVRCHQGPPL,,RGTGSTPVE*W**HCPQVSAV 33 codons (3 internal stop codons)		

Feature	Location	Size		Type
POLG-218	14,061 .. 15,524	1464 bp	→	prim_transcript
/note = primary transcript	ENST00000636812			
POLG-216	15,483 .. 15,798	316 bp	→	prim_transcript
/note = primary transcript	ENST00000636530 protein_coding_CDS_not_defined			
POLG-220	16,853 .. 17,419	567 bp	→	prim_transcript
/note = primary transcript	ENST00000637042 protein_coding_CDS_not_defined			
POLG-206	17,034 .. 18,345	1312 bp	→	prim_transcript
/note = primary transcript	ENST00000526671 Retained intron			
FANCI	17,601 .. 90,917	73,317 bp	←	gene
/note = gene	ENSG00000140525 Protein coding			
FANCI-201	17,601 .. 90,913	73,313 bp	←	prim_transcript
/note = primary transcript	ENST00000300027 Protein coding			
FANCI-202	17,731 .. 90,883	73,153 bp	←	prim_transcript
/note = primary transcript	ENST00000310775 Protein coding			
FANCI-212	17,734 .. 56,175	38,442 bp	←	prim_transcript
/note = primary transcript	ENST00000566895 Retained intron			
FANCI-222	17,751 .. 90,882	73,132 bp	←	prim_transcript
/note = primary transcript	ENST00000696717 Protein coding			
FANCI-219	17,759 .. 25,939	8181 bp	←	prim_transcript
/note = primary transcript	ENST00000675352 Retained intron			
FANCI-223	17,760 .. 90,866	73,107 bp	←	prim_transcript
/note = primary transcript	ENST00000696718 Protein coding			
FANCI-224	17,782 .. 90,845	73,064 bp	←	prim_transcript
/note = primary transcript	ENST00000696719 Protein coding			
FANCI-221	17,888 .. 25,190	7303 bp	←	prim_transcript
/note = primary transcript	ENST00000676110 Retained intron			
FANCI-220	18,028 .. 90,879	72,852 bp	←	prim_transcript
/note = primary transcript	ENST00000676003 Protein coding			
POLG-214	18,084 .. 29,664	11,581 bp	→	prim_transcript
/note = primary transcript	ENST00000635831			
POLG-214	18,084 .. 18,111	28 bp	→	CDS
/note = coding sequence	ENSP00000490231			
/translation =	GKTKPAWTI 9 amino acids = 1.0 kDa			
FANCI-203	18,381 .. 90,858	72,478 bp	←	prim_transcript
/note = primary transcript	ENST00000447611 Nonsense mediated decay			
FANCI-218	18,391 .. 90,917	72,527 bp	←	prim_transcript
/note = primary transcript	ENST00000674831 Protein coding			
FANCI-226	18,393 .. 35,663	17,271 bp	←	prim_transcript
/note = primary transcript	ENST00000696721 Retained intron			

Feature	Location	Size			Type
FANCI-204	18,418 .. 71,425	53,008 bp			prim_transcript
/note	= primary transcript ENST00000561894 Protein coding				
FANCI-211	18,436 .. 27,003	8568 bp			prim_transcript
/note	= primary transcript ENST00000566615 protein_coding_CDS_not_defined				
FANCI-210	20,216 .. 90,612	70,397 bp			prim_transcript
/note	= primary transcript ENST00000565522 protein_coding_CDS_not_defined				
FANCI-227	26,133 .. 28,003	1871 bp			prim_transcript
/note	= primary transcript ENST00000696722 Retained intron				

Primer	Length	Binding Sites	T _m	Date Added
✓ PCR Forward	25-mer	10,968 .. 10,992	58°C	Jan 11, 2023
/sequence = AACTGGATTACTTAGAAGTGGAGGC 44% GC / 7770.1 Da				
✓ Donor Template WT -> SNV	100-mer	11,333 .. 11,432	82°C	Jan 11, 2023
/sequence = GGTGTGTGGCCCTCACAGACTGCCCGTGGTGGCCCAAGGACACCCAGCCCAGCTATCACCATGGCAATCGACCTTACAACGACGTGG 42% GC / 8656.8 Da				
✓ gRNA Protospacer	20-mer	11,395 .. 11,414	58°C	Jan 11, 2023
/sequence = CGTTGTAAGGTCCATTGCCA 50% GC / 6108.0 Da				
✓ Sanger Sequencing	20-mer	11,477 .. 11,496	59°C	Jan 11, 2023
/sequence = AGGAAACACCACAGGACAGG 55% GC / 6178.1 Da				
✓ PCR Reverse	25-mer	11,959 .. 11,983	58°C	Jan 11, 2023
/sequence = TCCCACATTACAGCTATTACCATCC 44% GC / 7480.9 Da				