

**INK2S00116\_GBA\_D448V\_A02\_AB**  
 10,248 bp

5'  
3'

CTCTTTTCCAATCCAGGTCCC GCCCGACTCCCCAGGGCTGCTTTTCTCGCGGCTGCGGGTGGTTCGGGCTGCATCCTGCCTTCAAG  
GAGAAAAGGTTAGGTCCAGGGCGGGGCTGAGGGGTCCCGACGAAAAGAGCGCCGACGCCACCAGCCGACGTAGGACGGAAAGTC

85

GBA >

AGTCTTACTGCGCGGGGCCCCAGTCTCCAAGTCCC GCCCAGGGCGCCTTTGCAGGGCTGCGGTGGGATTTTCGTTTTGCCTCCGGTTGG  
TCAGAATGACGCGCCCCGGGGTCAGAGGTCAAGGGCGGGTCCGCGGAAACGTCCGACGCCACCCTAAAGCAAAAACGGAGGGCCAACC

170

GBA >

GGCTGCTGTTTCTCTTCGCCGACGGTAGGGCGTAATGAATATTTTCGACCTTTGGATCTTAGCTGTCCCCTCCCTGCGTTTCGCACTT  
CCGACGACAAAAGAGAAGCGGCTGCCATCCGCATTACTTATAAAGCTGGAAAACCTAGAATCGACAGGGGAGGGACGCAAGCGTGAA

255

GBA >

AACCTTTTTACCATTATTATTATTATTGTTATTATTATTATTTTTGAGGGAGTCTCGCCCTGTCGCCCAGGGCTGGAGTGTAAAT  
TTGAAAAAGTGGTAATAATAATAACAATAATAATAAAAACTCCCTCAGAGCGGGACAGCGGGTCCGACCTCACATTA

340

GBA >

GGCGCCTTCTTGGCTCACTGCAACCTCCGCCTCCCGGGTTCAGGGCATTCTCCGACCTCAGCCTCCCAAGTACGTGGGATTACAG  
CCGCGGAAGAACCAGGTGACGTTGGAGGC GGAGGGCCCAAGTCCGCTAAGAGGCTGGAGTCGGAGGGTTCATGCACCCTAATGTC

425

GBA >

GCACCCGCCACCACGCACGGCTAATTTTTGTATCTTTTAGTAGAGACGGGGTTTTACCATGTTGGTCAGGCTGGTCTCCAATTC  
CGTGGGCGGTGGTGCCTGCGGATTAAAAAACATAGAAAATCATCTCTGCCCCAAAGTGGTACAACCAGTCCGACCAGAGGTTAAG

510

GBA >

CTGACCTCGTGATCCGCCCGCCTCGGCCTGCCAAACAGCTGTGATTATAGGCGTGAGCCACC GCGCCCGCCAACCATCATTATT  
GACTGGAGCACTAGGCGGGCGGAGCCGGACGGTTTTGTCGACACTAATATCCGCACTCGGTGGCGCGGGCCGGTTGGTAGTAATAA

595

GBA >

ATTTTTAACGGTAAGGATGGTCAGATTTTACTAATGAAGAAGAGATTATAAAATCTTCAAGTCTTTATATCCAATTGCTTTTTGA  
TAAAAATTGCCATTCTACCAGTCTAAAATGATTACTTCTTCTCTAATATTTTAGAAGTTCAGAAAATATAGGTGAACGAAAAACT

680

GBA >

GGGGTGGAGTGGGAAGAAGGTTATGTAATTCATACGTTCTTCAGACATGTGACAAACATTCACGGAGCCCGGCGACGAGCGTCGG  
CCCCACCTCACCTTCTTCCAATACATTAAGTATGCAAGAAGTCTGTACACTGTTTGTAAAGTGCTCGGGCCGCTGCTCGCAGCC

765

GBA >

GGTTGGGATTCGCACTGGAGCTGCAGATGGGTGCCAGGATGGACTGGTCCCTACCCTCCGCTTGAACCTAGGAGGCGGAGGTTGC  
CCAACCCTAAGCGTGACCTCGACGTCTACCCACGGTCTTACCTGACCAGGGATGGGAGGCGAACTTGGATCCTCCGCCTCCAACG

850

GBA >

AGTGAACCGAGATCGTGCCACTGCACTCCAGCCTGGGTGACAGAGATACTCCGTCTCAAAAAAAAAAACAAAAACAAGC  
TCACTTGGCTCTAGCACGGTGACGTGAGGTCGGACCCACTGTCTCTATGAGGCAGAGTTTTTTTTTTTTGTTTTGTTTTGTTTCG

935

GBA >

GGACTGGGCGCAGTGCCTCACCTGTAATCCAGCACTTTGCAAAGCCAAGGCGGGAGGATCCTTTGAGTTTAGGAGTTTGAGAC  
CCTGACCCGCGTCACGGAGTGGGACATTAGGGTCTGTGAAACGTTTCGGTTCCGCCCTCCTAGGAAACTCAAATCCTCAAACCTCTG

1020

GBA >

CAACCTGCGCAACACAGTAAGACCCCGTCTCTACAAAAAATACAGAAATTAGCCAGGTGTGGTGGTGTGCGCCTATAGTCCCAGC  
GTTGGACGCGTTGTGTCATTCTGGGGCAGAGATGTTTTTTATGTCTTTAATCGGTCCACACCACCACACGCGGATATCAGGGTTCG

1105

GBA >

TATTCTGGAGGCTGAGGTGGGAGGATTGCTTATTCTGGAGGCAGAGGTTGCACTGAGCCGAAATCAAGCTACTACACTCCATCCA  
ATAAGACCTCCGACTCCACCCTCTAACGAATAAGACCTCCGTCTCCAACGTGACTCGGCTTTAGTTCGATGATGTGAGGTAGGT  
GBA

1190

GGGCAACATACGGAGACCCTGTCTCAAACAAACAAACAAAAAATTGCTCAGTACCTGGCCAAAAAAGAAGAGGCTCACTATGCAG  
CCCCTTGTATGCCTCTGGGACAGAGTTTGTGTTTGTGTTTTTAACGAGTCATGGACCGTTTTTTTCTTCTCCGAGTGATACGTC  
GBA

1275

AGGGGAAGTGGAAAGGAGATGTTTGGACTTCTAAACTCAATAGAGCAGGAGAGGCCAAATGTAGAATGTGCTCAGGAAATATCTGTG  
TCCCCTTACACCTTCTCTACAAACCTGAAGATTTGAGTTATCTCGTCCTCTCCGTTTACATCTTACACGAGTCCTTTATAGACAC  
GBA

1360

AGATGAATGAACTTGAGGGGAAGTAAGGTACTAGATATTACCTGCCCTACCCAGAACAATCCTGTGCAATGTTTCCTTGAAAAGT  
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GBA

1445

GAGAAGTCTGGAAAGGGGTGGCTACTGACATAGTGAAGCAACTAGTTCAATTCTACAACCTTGACAGCTACCCCTGTGCCAGGCTAT  
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GBA

1530

CTACGAGGATACTTAGAATGCATAAGACATTCCTTCAAGGAACTCCAGGAACAGAGGCCTGACATGTTGCAATGTTTAGTGTCAA  
GATGCTCCTATGAATCTTACGTATTCTGTAAGGAAGTTCTTGGAGTCTTGTCTCCGGACTGTACAACGTTACAAATCACAGTT  
GBA

1615

GCAGTGTACTAGAGACACATTATCACACTCAAACCTCACAACAATTCTGTGAGGTAGGAGTTATCACTCCCCTTTTATAGATGAA  
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GBA

1700

ACAGAGGCTTAGAGTGATTGATTTATTGAAAAGTCAAACAGCCAGTAAATGGTGTAGCCAGGATTCCAAACTTGCTGTCTCACTGA  
TGTCTCCGAATCTCACTAACTAAATAACTTTTCAGTTTGTGCGGTCAATTAACACATCGGTCTAAGGTTTGAACGACAGAGTGACT  
GBA

1785

GACTGTACTTAATTACTGGAGGGACCGGGTGTGGTGGCTCATTGCTATAATCCCAACACCTTGGGAGGCTGAGGCTGGTGGATCA  
CTGACATGAATTAATGACCTCCCTGGCCACACCACCGAGTAACGATATTAGGGTTGTGGAACCTCCGACTCCGACCACCTAGT  
GBA

1870

CCTGAGGTCAGGGGTTTCGAGACCAGCCTGGCCAACATGGTGAAACCCCATCTCTACTAAAAATACAAAAATTAGCTGGGCATGGT  
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GBA

1955

GGTGGGCTCCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGGCAATTGCTTGAGCCGAGATCACACTGCACTCCAGCCTGGGC  
CCACCCGAGGACATTAGGGTTCGATGAGTCTCCGACTCCGTCCCGTTAACGAACCTCGGCTCTAGTGTGACGTGAGGTTCGGACCCG  
GBA

2040

AACAGGGCAAGACTCTGTCTCAAACCAAAAAAAAAAAAAAATTACTGGAGGAACCTAGAAGAAGAAATGATCAATTTTGCTTGGAG  
TTGTCCCCTTCTGAGACAGAGTTTTGGTTTTTTTTTTTTTAAATGACCTCCTTGGATCTTCTTCTTTACTAGTTAAACGAACCTC  
GBA

2125

TGTATCTAGAAAAGACTTCACTGAGATCATTTAAAGAACAAAAAGGATGGCTGGGGTCCAGCGCAGTGGCTCATGCCTGTAATCCC  
ACATAGATCTTTCTGAAGTGACTCTAGTAAATTTCTTGTTTTTCTACCGACCCAGGTCGCGTCACCGAGTACGGACATTAGGG  
GBA

2210

AGCACTTTCGGATACCAAGGCAGCAGATCACCTGAGGTCCAGAGTTTTCAGACCAGCCTGGCCAACATAGTGAAAACCCCATCTCTA  
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GBA

2295

CTAAAAATAAAAAAATTAGCTGAGCATGTTGGAGGGCACCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCACTCGA  
GATTTTTATTTTTTAAATCGACTCGTACAACCTCCCGTGGACATTAGGGTCGATGAACCCTCCGACTCCGTCTCTTAGTGAGCT  
GBA

2380

ACCCAGGAGGTGGAGGTTGCAGTGAGCCAAGATCACGCCACTGCACTCCAGCCTGGGCAACAGAGTGAGACTCTGTCTCAAAAAA  
TGGGTCTCCACCTCCAACGTCACTCGGTTCTAGTGCGGTGACGTGAGGTCGGACCCGTTGTCTCACTCTGAGACAGAGTTTTTTT  
GBA

2465

CAACAACAACAAAAAATACAAACAAGAGACAAGTAGTTCACAGGTGCCTACCAAGTGGTCAGGCACTGCACTTACCTCACTGACT  
GTTGTTGTTGTTTTTATGTTTGTCTCTGTTTCATCAAGGGTCCACGGATGGTTCACCAGTCCGTGACGTGAATGGAGTGACTGA  
GBA

2550

GCAGTAACCACCCTTTGAGGTTGTGGCATTGCCTCCATTTTCCAGGCAAGGAAATGGGCTGAGAGCTGGGATTAGTCAGGTCATG  
CGTCATTGGTGGGAAACTCCAACACCGTAACGGAGGTAAAAGGTCCGTTCTTTACCCGACTCTCGACCCTAATCAGTCCAGTAC  
GBA

2635

ACTGTGTGTGCCACTCCCGCTAAATCTCATTTGATGTGGTTCATGAGGCCACACCATGGACAGCTTCCTCCTTGTGTCCACTGAG  
TGACACACACGGTGAGGGCGATTTAGAGTAAACTACACCAAGTACTCCGGTGTGGTACCTGTGGAAGGAGGAACACAGGTGACTC  
GBA

2720

GATATGGCTTTGTACAACACTTTGGTTTTTGAACGACTTTACAAACCTCCCTGTCTTGTGAGGAAGGAAGAACAGTTATTACCAT  
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GBA

2805

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GACGTAGACTACTACTTTGTTCCCTGCGACGCTCTCCTCGGCCTGACTGGTGAGGGAGGGAGGTCAGGACAGTAGGGTGACGGTCA  
GBA

2890

GTCCCACCCTCTTGTGCCCTGCACTTCACTGGCTAATAACCCCCCTCACTTTTTCTCTGTGAAAGCCATCCTGGATAATTCCCA  
CAGGGTGGGAGAACACGGGACGTGAAGTGACCGATTATTGGGGGAGTGAAAAAGGAGACACTTCGGTAGGACCTATTAAGGGGT  
GBA

2975

CCCACGAATGGTCCCTCCTCATCTCAGAGAGCTCTCCATGCACACCTGTTACCGTTTCTGTCTTTATCTGTAATATCTGTGTGT  
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GBA

3060

CTGACTTCCATGCCTCACACACCTCTATAGGGCAAAGACTGTCTTAAACATCTTGGTAGTGTCAGTATTTTGCACAGTGAAGTTT  
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GBA

3145

TTTTTTTTAAATTATATCAGCTTTATTTGTACCTTTTTGACATTTCTATCAAAAAAGAAGTGTGCCTGCTGTGGTTCCCATCCTC  
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GBA

3230

TGGGATTTAGGAGCCTCTACCCATTCTCCATGCAAACTCTGTGTTCTAGGCTCTTCCTAAAGTTGTCACCCATACATGCCCTCCA  
ACCCTAAATCCTCGGAGATGGGGTAAGAGGTACGTTTAGACACAAGATCCGAGAAGGATTTCAACAGTGGGTATGTACGGGAGGT  
GBA

3315

GAGTTTTATAGGGCATATAATCTGTAACAGATGAGAGGAAGCCAATTGCCCTTTAGAAATATGGCTGTGATTGCCTCACTTCCTG  
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3400

GBA

TGTCATGTGACGCTCCTAGTCATCACATGACCCATCCACATCGGGAAGCCGGAATTACTTGCAGGGCTAACCTAGTGCCTATAGC  
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3485

GBA

GBA-202

TAAGGCAGGTACCTGCATCCTTGTTTTGTTTAGTGGATCCTCTATCCTTCAGAGACTCTGGAACCCCTGTGGTCTTCTCTTCAT  
ATTCCGTCCATGGACGTAGGAACAAAAACAAATCACCTAGGAGATAGGAAGTCTCTGAGACCTTGGGGACACCAGAAGAGAAGTA

3570

GBA

GBA-202

CTAATGACCCTGAGGGGATGGAGTTTTCAAGTCCTTCCAGAGAGGTAAGAGAGAGAGCTCCCAATCAGCATTGTCACAGTGCTTC  
GATTACTGGGACTCCCTACCTCAAAAGTTCAGGAAGGTCTCTCCATTCTCTCTCTCGAGGGTTAGTCGTAACAGTGTACGAAG

3655

GBA

GBA-202

1 M E F S S P S R E  
ENSE00001890492

GBA-202

TGGAATCCTGGCACTGGAATTTAATGAATGACAGACTCTCTTTGAATCCAGGGCCATCATGGCTCTTTGAGCAAGGCACAGATGG  
ACCTTAGGACCCTGACCTTAAATTACTTACTGTCTGAGAGAAACTTAGGTCCCAGGTAGTACCGAGAAACTCGTTCCGTGTCTACC

3740

GBA

GBA-202

GBA-202

AGGGAGGGGTCGAAGTTGAAATGGGTGGGAAGAGTGTTGGGGAGCATCCTGATTTGGGGTGGGCAGAGAGTTGTCATCAGAAGGG  
TCCCTCCCCAGCTTCAACTTTACCCACCCTTCTCACCACCCTCGTAGGACTAAACCCACCCGTCTCTCAACAGTAGTCTTCCC

3825

GBA

GBA-202

GBA-202

TTGCAGGGAGAGCTGCACCCAGGTTTCTGTGGGCCTTGTCTTAATGAATGTGGGAGACCGGGCCATGGGCACCCAAAGGCAGCTA  
AACGTCCCTCTCGACGTGGGTCCAAAGACACCCGGAACAGGATTACTTACACCTCTGGCCCGGTACCCGTGGGTTTCCGTCTGAT

3910

GBA

GBA-202

GBA-202

AGCCCTGCCAGGAGAGTAGTTGAGGGGTGGAGAGGGGCTTGCTTTTCAGTCATTCTCATTCTGTCTCAGGAATGTCCCAAGC  
TCGGGACGGGTCTCTCATCAACTCCCCACCTCTCCCCGAACGAAAAGTCAGTAAGGAGTAAGACAGGAGTCTTACAGGGTTCG

3995

GBA

GBA-202

10 E C P K  
ENSE00003469059

GBA-202

CTTTGAGTAGGGTAAGCATCATGGCTGGCAGCCTCACAGGATTGCTTCTACTTTCAGGCAGTGTCTGTTGGGCATCAGGTGAGTGAGT  
GAAACTCATCCCATTTCGTAGTAGTACCGACCGTCGGAGTGTCTTAACGAAGATGAAGTCCGTCACAGCACCCGTTAGTCCACTCACTCA

4080

GBA

GBA-202

15 20 25 30 35  
P L S R V S I M A G S L T G L L L L Q A V S W A S

ENSE00003469059

GBA-202

CAAGGCAGTGGGGAGGTAGCACAGAGCCTCCCTTCTGCCTCATAGTCCTTTGGTAGCCTTCCAGTAAGCTGGTGGTAGACTTTTA  
GTTCCGTCACCCCTCCATCGTGTCTCGGAGGGAAGACGGAGTATCAGGAAACCATCGGAAGGTCATTCGACCACCATCTGAAAAT

4165

GBA

GBA-202

GBA-202

GTAGGTGCTCAATAAATCCTTTTGAGTGACTGAGACCAACTTTGGGGTGAGGATTTTGTTTTTTTCTTTTGAAACAGAGTCTTA  
CATCCACGAGTTATTTAGGAAAACCTCACTGACTCTGGTTGAAACCCCACTCCTAAAAACAAAAAAGAAAACCTTTGTCTCAGAAT

4250

GBA

GBA-202

GBA-202

CTCTGTTGCCTGGGCTGGAGTGCAGTGGTGCATTTTGGCTCATTCCAACCTCTGCCTCCCAGATTCAAGCGATTCTCTTGCTTC  
GAGACAACGGACCCGACCTCACGTCACCACGTTAAAACCGAGTAAGGTTGGAGACGGAGGGTCTAAGTTCGCTAAGAGAACGAAG

4335

GBA

GBA-202

GBA-202

AGCTTCCAGGTAGCTGGGATTACAGGCGGCCACCACTACGCCAGCTAATTTTTGTATTTTTAGTAGAGACGGGGTTTTACCCAT  
TCGAAGGGTCCATCGACCCTAATGTCCGCCGGTGGTGTATGCGGGTTCGATTAAAAACATAAAAAATCATCTCTGCCCAAAGTGGA

4420

GBA

GBA-202

GBA-202

GCTGGCAAGGCAGGTCTCAAACCTCCTCACCTCAGGTGATCCGCCACCTCGGCCTCCTAAAGTGCTAGGATTACAGGTGTGAGCC  
CGACCGTTCCGTCCAGAGTTTGAGGAGTGGAGTCCACTAGGCGGGTGGAGCCGGAGGATTTACGATCCTAATGTCCACACTCGG

4505

GBA

GBA-202

GBA-202

CCTGCGCCCGGCCAAGGGGTGAGGAATTTGAAACCGTGTTCAGTCTCTCCTAGCAGATGTGTCCATTCTCCATGTCTTCATCAG  
GGACGCGGGCCGGTTCCTCAAACTTTGGCACAAGTCAGAGAGGATCGTCTACACAGGTAAGAGGTACAGAAGTAGTC

4590

GBA

GBA-202

GBA-202

ACCTCACTCTGCTTGTACTCCCTCCCTCCCAGGTGCCCGCCCTGCATCCCTAAAAAGCTTCGGCTACAGCTCGGTGGTGTGTGTC  
TGGAGTGAGACGAACATGAGGGGAGGGAGGGTCCACGGGCGGGGACGTAGGGATTTTCGAAGCCGATGTCGAGCCACCACACACAG

4675

GBA

GBA-202

G A R P C I P K S F G Y S S V V C V

ENSE00003675620

GBA-202

TGCAATGCCACATACTGTGACTCCTTTGACCCCCCGACCTTTCTGCCCTTGGTACCTTCAGCCGCTATGAGAGTACACGCAGTG  
ACGTTACGGTGTATGACACTGAGGAAACTGGGGGGCTGGAAAGGACGGGAACCATGGAAGTCGGCGATACTCTCATGTGCGTCAC

4760

GBA

GBA-202

C N A T Y C D S F D P P T F P A L G T F S R Y E S T R S

ENSE00003675620

GBA-202

GGCGACGGATGGAGCTGAGTATGGGGCCCATCCAGGCTAATCACACGGGCACAGGTAACCATTACACCCCTCACCCCTGGGCCA  
CCGCTGCCTACCTCGACTCATACCCGGGTAGGTCCGATTAGTGTGCCCGTGTCCATTGGTAATGTGGGGAGTGGGGGACCCGGT

4845

GBA

GBA-202

G R R M E L S M G P I Q A N H T G T

ENSE00003675620

GBA-202

GGCTGGGTCCCTCCTAGAGGTAAATGGTGTCAGTGATCACCATGGAGTTTCCCGCTGGGTACTGATACCCTTATTCCTGTGGATG  
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4930

GBA

GBA-202

GBA-202

TCCTCAGGCCTGCTACTGACCCTGCAGCCAGAACAGAAGTTCCAGAAAGTGAAGGGATTTGGAGGGGCCATGACAGATGCTGCTG  
AGGAGTCCGGACGATGACTGGGACGTCGGTCTTGTCTTCAAGGTCTTCACTTCCCTAAACCTCCCCGGTACTGTCTACGACGAC

5015

GBA

GBA-202

G L L L T L Q P E Q K F Q K V K G F G G A M T D A A

ENSE00003499798

GBA-202

CTCTCAACATCCTTGCCCTGTACCCCTGCCCAAAATTTGCTACTTAAATCGTACTTCTCTGAAGAAGGTGAGGAGGAAGGGGA  
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5100

GBA

GBA-202

A L N I L A L S P P A Q N L L K S Y F S E E

ENSE00003499798

GBA-202

CAAGATGACATAGAGCCATTGAAACTTTTTCGTTTTTCTTTTTTAAAAATTTTTTGGAGGCAGAATCTCACTCTGCCATT  
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5185

GBA

GBA-202

GBA-202

CTGTCGGCGAGACAGGAGTGCAGTGGTGTGATCTCCCCTCACAGCAACCTCTGCCTCCCAGGCTATAGTGATTCTCCTGCCTCAG  
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5270

GBA

GBA-202

GBA-202

CCTCCTGAGTAGCTGGAATTATAGGCGTGCGCCACTACCACCTGGCTAATTTTTGTATTTTTAGTAGAGACAGGGTTTTCATCATG  
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5355

GBA

GBA-202

GBA-202

TTGACCAGGCTAGTCTTAAACTCCTGACCTCAAATGATATACCTGCCTTGGCCTCCCGAAGTGCTGGAATTACAAGTGTGAGCCA  
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5440

GBA

GBA-202

GBA-202

CCGAGCCCAGCAGACACTTTTTCTTTTTCTTTTTTTTTTTTTTGGAGACAGAGTCTCGCACTGTCACCCAGGCTGGAGTGCAGTGGC  
GGCTCGGGTCTGTCTGTGAAAAGAAAAAAGAAAAAATAAACTCTGTCTCAGAGCGTGACAGTGGGTCCGACCTCACGTCACCG

5525

GBA

GBA-202

GBA-202

ACAATCTCAGCTCACTGCAACCTCCACCTCCCGGGTTCAGGTGATTCTCCTGTCTCAGCCTCTCGAGTACCTGGGATTACAGGTG  
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5610

GBA

GBA-202

GBA-202

CCTGCCACCACGCCCGGCTAATTTTTGTATTTTTAGTAGAGACAGGGTTTTCACTATGTTGGCCAGGATGATTGCGAACTCCTGA  
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5695

GBA

GBA-202

GBA-202

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5780

GBA

GBA-202

GBA-202



CCCTGACTTCTGCCCATCCCTGACATTTGGTTTCCTGTTTTAATGCCCTGTGAAATAAGATTTACCCGCCTATCATCTGCTAACTG  
GGGACTGAAGACGGGTAGGGACTGTAAACCAAGGACAAAATTACGGGACACTTTATTCTAAAGTGGCGGATAGTAGACGATTGAC

5865

GBA

GBA-202

GBA-202

CTACGGACTCAGGCTCAGAAAGGCCTGCGCTTCACCCAGGTGCCAGCCTCCACAGGTTCCAACCCAGGAGCCCAAGTTCCCTTTG  
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5950

GBA

GBA-202

GBA-202

GCCCTGACTCAGACACTATTAGGACTGGCAAGTGATAAGCAGAGTCCCATACTCTCTATTGACTCGGACTACCATATCTTGATC  
CGGGACTGAGTCTGTGATAATCCTGACCGTTCACTATTTCGTCTCAGGGTATGAGAGGATAACTGAGCCTGATGGTATAGAAGTAG

6035

GBA

GBA-202

GBA-202

ATCCTTTTCTGTAGGAATCGGATATAACATCATCCGGGTACCCATGGCCAGCTGTGACTTCTCCATCCGCACCTACACCTATGCA  
TAGGAAAAGACATCCTTAGCCTATATTGTAGTAGGCCCATGGGTACCGGTCGACACTGAAGAGGTAGGCCTGGATGTGGATACGT

6120

GBA

GBA-202

G I G Y N I I R V P M A S C D F S I R T Y T Y A  
ENSE00003618264

GBA-202

GACACCCCTGATGATTTCCAGTTGCACAACCTTCAGCCTCCCAGAGGAAGATACCAAGCTCAAGGTAGGCATTCTAGCTTTTTTCAG  
CTGTGGGGACTACTAAAGGTCAACGTGTTGAAGTCGGAGGGTCTCCTTCTATGGTTTCGAGTTCATCCGTAAGATCGAAAAAGTC

6205

GBA

GBA-202

D T P D D F Q L H N F S L P E E D T K L K  
ENSE00003618264

GBA-202

GCCCTGAGGGCCCTGATGTCTGGGGGTTGAGAACTGTAGGGTAGGTCTGCTTGTACAGACATTTTGTCCCCTGCTGTTTTGTCC  
CGGGACTCCCGGGACTACAGACCCCCAACTCTTTGACATCCCATCCAGACGAACATGTCTGTAAAACAGGGGACGACAAAACAGG

6290

GBA

GBA-202

GBA-202

TGGGGGTGGGAGGGTGGAGGCTAATGGCTGAACCGGATGCACTGGTTGGGCTAGTATGTGTTCCAACCTCTGGGTGCTTCTCTCTT  
ACCCCCACCCTCCACCTCCGATTACCGACTTGGCCTACGTGACCAACCCGATCATAACAAGGTTGAGACCCACGAAGAGAGAA

6375

GBA

GBA-202

GBA-202

CACTACCTTTGTCTCTAGATACCCCTGATTCACCGAGCCCTGCAGTTGGCCAGCGTCCCGTTTCACTCCTTGCCAGCCCCTGGA  
GTGATGGAAACAGAGATCTATGGGGACTAAGTGGCTCGGGACGTCAACCGGGTTCGCAGGGCAAAGTGAGGAACGGTCGGGGACCT

6460

GBA

GBA-202

I P L I H R A L Q L A Q R P V S L L A S P W

ENSE00003562842

GBA-202

CATCACCCACTTGGCTCAAGACCAATGGAGCGGTGAATGGGAAGGGGTCCTCAAGGGACAGCCCCGGAGACATCTACCACCAGAC  
GTAGTGGGTGAACCGAGTTCTGGTTACCTCGCCACTTACCCTTCCCCAGTGAGTTCCCTGTCGGGCCCTCTGTAGATGGTGGTCTG

6545

GBA

GBA-202

T S P T W L K T N G A V N G K G S L K G Q P G D I Y H Q T

ENSE00003562842

GBA-202

CTGGGCCAGATACTTTGTGAAGTAAGGGATCAGCAAGGATGTGGGATCAGGACTGGCCTCCCATTTAGCCATGCTGATCTGTGTC  
GACCCGGTCTATGAAACACTTCATTCCCTAGTCGTTCCCTACACCCTAGTCCTGACCGGAGGGTAAATCGGTACGACTAGACACAG

6630

GBA

GBA-202

W A R Y F V K

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GBA-202

CCAACCCTCAACCTAGTTCCACTTCCAGATCTGCCTGTCTCAGCTCACCTTTCTACCTTCTGGGCCTTTCAGCCTTGGGCCTGT  
GGTTGGGAGTTGGATCAAGGTGAAGGTCTAGACGGACAGGAGTCGAGTGAAAGATGGAAGACCCGGAAAGTCGGAACCCGGACA

6715

GBA

GBA-202

GBA-202

CAATCTTGCCCACTCCATCAGGCTTCTGTTCTCTCGGTCTGGCCCACTTTCTTTTTATTTTTCTTCTTTTTTTTTTTTTTTGAGA  
GTTAGAACGGGTGAGGTAGTCCGAAGGACAAGAGAGCCAGACCGGGTGAAAGAAAAATAAAAAAGAAAAAAAAAAAAAAAAAACTCT

6800

GBA

GBA-202

GBA-202

AGGAGTCTCTCTCTGTACCCAGGCTGGAGTGCTGTGGCGCCATTTCACTCACTGTAACCTCTGCCTCCTGAGTTCAAGCAA  
TCCTCAGAGAGAGACAGTGGGTCCGACCTCACGACACCGCGGTAGAAGTGAGTGACATTGGAGACGGAGGACTCAAGTTCGTT

6885

GBA

GBA-202

GBA-202

TTCTCCTGCCTCAGCCTTCCAAGTAGCTGGGATTATAGGCGCCTGCCACCAGGCCAGCTGATTTTTCTATTTTTAGTAGAGACG  
AAGAGGACGGAGTCGGAAGGTTTCATCGACCTAATATCCGCGGACGGTGGTCCGGGTCGACTAAAAAGATAAAAAATCATCTCTGC

6970

GBA

GBA-202

GBA-202

GGGTTTCGCCAGGCTGTTCTCGAACTCCTGAACTCAAGTGATCCACCTGCCTCGGCTTCCCAAAGTGCTGGGATTACAGGTGTGA  
-----  
CCCAAAGCGGTCCGACAAGAGCTTGAGGACTTGAGTTCAGTGGACGGAGCCGAAGGGTTTCACGACCCTAATGTCCCACT

7055

GBA

GBA-202

GBA-202

GCCACCACACCCAGCTGGTCTGGTCCACTTTCTTGCCGGATCATTTCATGACCTTTCTCTTGCCAGGTTCTGGATGCCTATGCT  
-----  
CGGTGGTGTGGGTCGACCAGACCAGGTGAAAAGAACCAGGCTAGTAAGTACTGGAAAAGAGAACGGTCCAAGGACCTACGGATACGA

7140

GBA

GBA-202

255 F L D A Y A 260

ENSE00003488376

GBA-202

GAGCACAAGTTACAGTTCTGGGCAGTGACAGCTGAAAATGAGCCTTCTGCTGGGCTGTTGAGTGGATACCCCTTCCAGTGCCTGG  
-----  
CTCGTGTTC AATGTCAAGACCCGTCCTGTCGACTTTTACTCGGAAGACGACCCGACAACCTCACCTATGGGGAAGGTCACGGACC

7225

GBA

GBA-202

E H K L Q F W A V T A E N E P S A G L L S G Y P F Q C L

ENSE00003488376

GBA-202

GCTTCACCCCTGAACATCAGCGAGACTTCATTGCCCGTGACCTAGGTCTACCCTCGCCAACAGTACTCACCACAATGTCCGCCT  
-----  
CGAAGTGGGGACTTGTAGTCGCTCTGAAGTAACGGGCACTGGATCCAGGATGGGAGCGGTTGTTCATGAGTGGTGTTCACAGGCGGA

7310

GBA

GBA-202

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

ENSE00003488376

GBA-202

ACTCATGCTGGATGACCAACGCTTGCTGCTGCCCACTGGGCAAAGGTGGTAAGGCCTGGACCTCCATGGTGTCTCCAGTGACCTT  
-----  
TGAGTACGACCTACTGGTTGCGAACGACGACGGGGTGACCCGTTTCCACCATTCCGGACCTGGAGGTACCACGAGGTCACTGGAA

7395

GBA

GBA-202

L M L D D Q R L L L P H W A K V

ENSE00003488376

GBA-202

CAAATCCAGCATCCAAATGACTGGCTCCCAAACCTTAGAGCGATTTCTCTACCCAACCTATGGATTCCCTAGAGCACCATTTCCCCTGG  
-----  
GTTTAGGTCGTAGGTTTACTGACCGAGGGTTTGAATCTCGCTAAAGAGATGGGTTGATACCTAAGGATCTCGTGGTAAGGGGACC

7480

GBA

GBA-202

GBA-202

ACCTCCAGGGTGCCATGGATCCCACAGTTGTCGCTTGAAACCTTTCTAGGGGCTGGGCGAGGTGGCTCACTCATGCAAACCCAGC  
-----  
TGGAGGTCCACGGTACCTAGGGTGTCAACAGCGAACTTTGGAAAGATCCCCGACCCGCTCCACCGAGTGAGTACGTTTGGGTCG

7565

GBA

GBA-202

GBA-202

ACTTTGGGAAGCCGAGGCGGGTGATCACCTGAGGTCAGGAGTTTAAGACCACCCTGGCCAACGTGTTGAAACCCTGTGTCTACTA  
TGA AACCCCTTCGGCTCCGCCCCTAGTGGACTCCAGTCCTCAAATTTCTGGTGGGACCGGTTGCACAACCTTTGGGACACAGATGAT

7650

GBA

GBA-202

GBA-202

AAATACAAAAAAAAAAAAATTATCTGGGCATGATGGTGGGTGTCTGTAATCCCAGCTACTCAGGAGGCTGAGAAGGGAGAATCAGT  
TTTATGTTTTTTTTTTTTAATAGACCCGTA CTACCACCCACAGACATTAGGGTTCGATGAGTCCTCCGACTCTTCCCTCTTAGTCA

7735

GBA

GBA-202

GBA-202

TGAACCCGGGAGATGGTGGTTGCGGTGAGCCGAGATCGCGCCACTGCACTCCAGCCTGGGAGGCTGAGCGAGACTCCATCTCGAA  
ACTTGGGCCCTCTACCACCAACGCCACTCGGCTCTAGCGCGGTGACGTGAGGTCGGACCCCTCCGACTCGCTCTGAGGTAGAGCTT

7820

GBA

GBA-202

GBA-202

ACAAAACAAAACAAAACACTATCTAGGCTGGGGGTGGTGGTTCATGTATGTATGTGTATATACATATATATGTGTTTTATATGTATAT  
TGTTTTGTTTTGTTTTGATAGATCCGACCCCCACCACCAAGTACATACATACATATATGTATATATACACAAATATACATATA

7905

GBA

GBA-202

GBA-202

ATATATACACACACACATACATACACACACATACACACACAAATTAGCTGGGTGTGGCACCCGTGTAGTCCCAGCTACTCAGG  
TATATATGTGTGTGTGTGTATGTATGTGTGTGTATGTGTGTGTTTAAATCGACCCACACCCGTGGGCACATCAGGGTCGATGAGTCC

7990

GBA

GBA-202

GBA-202

AGGCTAATGTGGGAGGATCAGTTGACCCTAGGAAGTCAAGGCTGCAGTGAGTCGTGATTGCGCCACTGTACTCCAGCCCGAGTGA  
TCCGATTACACCCTCCTAGTCAACTGGGATCCTTCAGTTCAGCAGTCACTCAGCACTAACGCGGTGACATGAGGTCGGGCTCACT

8075

GBA

GBA-202

GBA-202

CAGAGTGACATCCTGTCTCAAAAACAAAAAAAAAATCTCCCCAACCTCTCTAGTTGCATTCTTCCCGTCACCCAACTCCAGGATT  
GTCTCACTGTAGGACAGAGTTTTTTGTTTTTTTTTAGAGGGGTTTGGAGAGATCAACGTAAGAAGGGCAGTGGGTTGAGGTCCTAA

8160

GBA

GBA-202

GBA-202

CCTACAACAGGAACTAGAAAGTTCCAGAAGCCTGTGTGCAAGGTCCAGGATCAGTTGCTCTTCTCTTTCAGGTTACTGACAGACCCA  
GGATGTTGTCTTGTATCTTCAAGGTCTTCGGACACACGTTCCAGGTCCTAGTCAACGAGAAGGAAACGTCATGACTGTCTGGGT

8245

GBA

GBA-202

335  
V L T D P  
ENSE00001231060

GBA-202

GAAGCAGCTAAATATGTTTCATGGCATTGCTGTACATTGGTACCTGGACTTTCTGGCTCCAGCCAAAGCCACCCCTAGGGGAGACAC  
CTTCGTCGATTTATACAAGTACCGTAACGACATGTAACCATGGACCTGAAAGACCCGAGGTCGGTTTTCCGGTGGGATCCCTCTGTG

8330

GBA

GBA-202

340 345 350 355 360 365  
E A A K Y V H G I A V H W Y L D F L A P A K A T L G E T

ENSE00001231060

GBA-202

ACCGCCTGTTCCCAACACCCATGCTCTTTGCCTCAGAGGCCTGTGTGGGCTCCAAGTTCTGGGAGCAGAGTGTGCGGCTAGGCTC  
TGGCGGACAAGGGGTTGTGGTACGAGAAACGGAGTCTCCGGACACACCCGAGGTTCAAGACCCTCGTCTCACACGCCGATCCGAG

8415

GBA

GBA-202

370 375 380 385 390 395  
H R L F P N T M L F A S E A C V G S K F W E Q S V R L G S

ENSE00001231060

GBA-202

CTGGGATCGAGGGATGCAGTACAGCCACAGCATCATCACGGTAAGCCACCCAGTCTCCCTTCTGCAAAGCAGACCTCAGACCT  
GACCTTAGCTCCCTACGTCATGTCTGGTGTCTGCTAGTAGTGCCATTCCGGTGGGGTCAGAGGGAAGGACGTTTTCGTCTGGAGTCTGGA

8500

GBA

GBA-202

400 405  
W D R G M Q Y S H S I I T

ENSE00001231060

GBA-202

Sanger Sequencing

GGGGAA

PCR Reverse

GGGGAA

CTTACTAGTTTTACCAAAGACTGACAGAAGCCCTTCTGTCCAGCTTTCCCCAGCTAGCCTGCCCTTTTTGAGCAACTCTGGGGAA  
GAATGATCAAAGTGGTTTTCTGACTGTCTTCGGGAAGGACAGGTCGAAAGGGGTCGATCGGACGGGAAAACCTCGTTGAGACCCCTT

8585

GBA

GBA-202

GBA-202

Sanger Sequencing

CCATGATTCCCTATCTTC

PCR Reverse

CCATGATTCCCTATCTTC

CCATGATTCCCTATCTTCCCTTTCCTTTCACAGGCTGCACACCTCATTGCCCTTTTTGCAACTACTGAGGCACTTGCAGCTGCCT  
GGTACTAAGGGATAGAAGGGAAAGGAAAGTGTCCAGACGTGTGGAGTAACGGGGAAAACGTTGATGACTCCGTGAACGTCGACGGA

8670

GBA

GBA-202

GBA-202

CAGACTTCTCAGCTCCCCTTGAGATGCCTGGATCTTCACACCCCAACTCCTTAGCTACTAAGGAATGTGCCCTCACAGGGCTG  
GTCTGAAGAGTTCGAGGGGAACCTCTACGGACCTAGAAGTGTGGGGGTTGAGGAATCGATGATTCTTACACGGGGAGTGTCCCGAC

8755

GBA

GBA-202

GBA-202

ACCTACCCACAGCTGCCTCTCCCACATGTGACCCCTTACCTACACTCTCTGGGGACCCCCAGTGTGGCGCCTTTGTCTCTTTGCCT  
TGGATGGGTGTTCGACGGAGAGGGGTGTACACTGGGAATGGATGTGAGAGACCCCTGGGGGTCAACAACGCGGAAACAGAGAAACGGA

8840

GBA

GBA-202

GBA-202

TTGTCTTACCCTAGAACCCTCCTGTACCATGTGGTTCGGCTGGACCGACTGGAACCTTGCCTGAACCCCGAAGGAGGACCCAATT  
AACAGGAATGGGATCTTGGAGGACATGGTACACCAGCCGACCTGGCTGACCTTGAACGGGACTTGGGGCTTCTCTCTGGGTTAA

8925

GBA

GBA-202

GBA-202

410 415 420 425 430  
N L L Y H V V G W T D W N L A L N P E G G P N  
ENSE00003506590

GGGTGCGTAACTTTGTTCGACAGTCCCATCATTGTAGACATCACCAAGGACACGTTTTTACAAACAGCCCATGTTCTACCACCTTGG  
CCCACGCATTGAAACAGCTGTCAGGGTAGTAACATCTGTAGTGGTTCCGTGCAAAAATGTTTGTTCGGGTACAAGATGGTGGAAACC

9010

GBA

GBA-202

ENSE00003506590

GBA-202

435 440 445 450 455 460  
W V R N F V D S P I I V D I T K D T F Y K Q P M F Y H L G

Donor Template WT -> SNV

PAM Protospacer Sequence

SNV

AAACAGCTGTCAGGGTAGTAACATCTGTAGTGGTTCCGTGCAAAAATGTTTGTTCGGGTACAAGATGGTGGAAACC  
Donor Template WT -> SNV

TCCTGTGCAAAAATGTTTGTGTC  
gRNA Protospacer

CCACTTCAGGTGAGTGGAGGGCGGGCACCCCATTCATACCAGGCCTATCATCTCTACATCGGATGGCTTACATCACTCTACA  
GGTGAAGTCCACTCACCTCCCGCCCGTGGGGGTAAGGTATGGTCCGGATAGTAGAGGATGTAGCCTACCGAATGTAGTGAGATGT

9095

GBA

GBA-202

GBA-202

H F S  
ENSE00003...

Donor Template WT -> SNV

G

Donor Template WT -> SNV

CCACGAGGGAGCAGGAAGGTGTTTCAGGGTGGAACTCGGAAGAGGCACACCCATCCCCTTTTGCACCATGGAGGCAGGAAGTGAC  
GGTGCTCCCTCGTCTTCCACAAGTCCACCTTGGAGCCTTCTCCGTGTGGGTAGGGGAAAACGTGGTACCTCCGTCCTTCACTG

9180

GBA

GBA-202

GBA-202

TAGGTAGCAACAGAAAACCCCAATGCCTGAGGCTGGACTGCGATGCAGAAAAGCAGGGTTCAGTGCCCAGCAGCATGGCTCCAGGC  
ATCCATCGTTGTCTTTTGGGGTTACGGACTCCGACCTGACGCTACGTCTTTTCGTCCCAAGTCACGGGTCTGTCGTACCGAGGTCCG

9265

GBA

GBA-202

GBA-202

CTAGAGAGCCAGGGCAGAGCCTCTGCAGGAGTTATGGGGTGGGTCCGTGGGTGGGTGACTTCTTAGATGAGGGTTTCATGGGAGG  
GATCTCTCGGTCCCGTCTCGGAGACGTCTCAATACCCACCCAGGCACCCACCCACTGAAGAATCTACTCCCAAAGTACCCTCC

9350

GBA

GBA-202

GBA-202

CGGAGACGTCCTCAATACCC  
PCR Forward

TACCCCGAGGGACTCTGACCATCTGTTCCACATTCAGCAAGTTTCATTCTGAGGGCTCCCAGAGAGTGGGGCTGGTTGCCAGTC  
ATGGGGCTCCCTGAGACTGGTAGACAAGGGTGTAAAGTCGTTCAAGTAAGGACTCCCGAGGGTCTCTCACCCGACCAACGGTCAG

9435

GBA

GBA-202

GBA-202

K 465 I P E G 470 S Q R V G 475 L V A S  
ENSE00003644399

AGAAGAACGACCTGGACGCAGTGGCACTGATGCATCCCGATGGCTCTGCTGTTGTGGTCGTGCTAAACCGGTGAGGGCAATGGTG  
TCTTCTTGCTGGACCTGCGTCACCGTACTAGGGCTACCGAGACGACAACACCAGCACGATTTGGCCACTCCCGTTACCAC

9520

GBA

GBA-202

GBA-202

Q 480 K N D L D 485 A V A L M 490 H P D G S 495 A V V V V 500 L N R  
ENSE00003644399

AGGTCTGGGAAGTGGGCTGAAGACAGCGTTGGGGGCCTTGGCAGGATCACACTCTCAGCTTCTCCTCCCTGCTCCCTAGCTCCTC  
TCCAGACCTTACCCGACTTCTGTGCAACCCCGGAACCGTCTAGTGTGAGAGTCGAAGAGGAGGGACGAGGGATCGAGGAG

9605

GBA

GBA-202

GBA-202

S S  
ENSE0...

TAAGGATGTGCCTCTTACCATCAAGGATCCTGCTGTGGGCTTCTGGAGACAATCTCACCTGGCTACTCCATTACACCTACCTG  
ATTCCTACACGGAGAATGGTAGTTCCTAGGACGACACCCGAAGGACCTCTGTTAGAGTGGACCGATGAGGTAAGTGTGGATGGAC

9690

GBA

GBA-202

505 510 515 520 525 530  
K D V P L T I K D P A V G F L E T I S P G Y S I H T Y L

ENSE00001917720

GBA-202

TGGCGTCGCCAGTGATGGAGCAGATACTCAAGGAGGCACTGGGCTCAGCCTGGGCATTAAAGGGACAGAGTCAGCTCACACGCTG  
ACCGCAGCGGTCACCTACCTCGTCTATGAGTTCCTCCGTGACCCGAGTCGGACCCGTAATTTCCCTGTCTCAGTCGAGTGTGCGAC

9775

GBA

GBA-202

535  
W R R Q  
ENSE00001917720  
GBA-202

TCTGTGACTAAAGAGGGCACAGCAGGGCCAGTGTGAGCTTACAGCGCAGTAAGCCCAGGGGCAATGGTTTGGGTGACTCACTTTC  
AGACACTGATTTCTCCCGTGTCTCGTCCCGGTCACACTCGAATGTCGCTGCATTCCGGTCCCCGTTACCAAACCCACTGAGTGAAAG

9860

GBA

GBA-202

CCCTCTAGGTGGTGCCAGGGGCTGGAGGCCCTAGAAAAAGATCAGTAAGCCCCAGTGTCCCCCAGCCCCATGCTTATGTGAA  
GGGAGATCCACCACGGTCCCCGACCTCCGGGGATCTTTTTCTAGTCATTCGGGGTCACAGGGGGGTCGGGGGTACGAATACACTT

9945

GBA

GBA-202

CATGCGCTGTGTGCTGCTTGTCTTTGGAAACTGGGCCTGGGTCCAGGCCTAGGGTGAGCTCACTGTCCGTACAAACACAAGATCAG  
GTACGCGACACACGACGAACGAAACCTTTGACCCGGACCCAGGTCCGGATCCCCTCGAGTGACAGGCATGTTTGTGTTCTAGTC

10,030

GBA

GBA-202

GGCTGAGGGTAAGGAAAAAGAAGAGACTAGGAAAAGCTGGGCCAAAAGTGGAGACTGTTTGTCTTTCTGGAGATGCAGAAGTGGG  
CCGACTCCCATTCTTTTCTTCTCTGATCCTTTGACCCGGGTTTTGACCTCTGACAAACAGAAAGGACCTCTACGTCTTGACCC

10,115

GBA

GBA-202

CCCGTGGAGCAGCAGTGTGTCAGCATCAGGGCGGAAGCCTTAAAGCAGCAGCGGGTGTGCCAGGCACCCAGATGATTCCTATGGCA  
GGGCACCTCGTCTGTCACAGTCTGATGCCGCTTCGGAATTTCTGTCGTCGCCACACGGGTCCGTGGGTCTACTAAGGATACCGT

10,200

GBA

GBA-202

CCAGCCAGGAAAAATGGCAGCTCTTAAAGGAGAAAAATGTTTGGACCCA  
GGTCGGTCCCTTTTACCGTCGAGAATTTCTCTTTTACAAACTCGGGT

3'

10,248








5'

GBA

GBA-202



Feature	Location	Size	Type
✓ <b>GBA</b>	1 .. 10,248	10,248 bp	gene
/note	= gene <a href="#">ENSG00000177628</a> Protein coding		
<b>GBA-204</b>	1 .. 9832	9832 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000428024</a>		
<b>GBA-201</b>	30 .. 10,248	10,219 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000327247</a>		
<b>GBA-213</b>	64 .. 6487	6424 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000493842</a> protein_coding_CDS_not_defined		
<b>GBA-209</b>	78 .. 6136	6059 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000473570</a> protein_coding_CDS_not_defined		
<b>GBA-207</b>	94 .. 5065	4972 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000467918</a> protein_coding_CDS_not_defined		
<b>GBA-203</b>	3425 .. 10,141	6717 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000427500</a>		
✓ <b>GBA-202</b>	3451 .. 10,248	6798 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000368373</a>		
<b>GBA-208</b>	3457 .. 4740	1284 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000470104</a> protein_coding_CDS_not_defined		
<b>GBA-211</b>	3469 .. 9684	6216 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000484489</a> protein_coding_CDS_not_defined		
<b>GBA-201</b>	3588 .. 9705	6118 bp	CDS
▶ 11 segments = 1611 bp			
/note	= coding sequence <a href="#">ENSP00000314508</a>		
/translation	= MEFSSPSRE,,ECPKPLSRV SIMAGSLTG LLLLQAVSWAS,,GARPCIPKSFYSSVVCVCNATYCDSDPPTFPALGTFSTRYESTRSGRRMELSM GPIQANHTGT,,G LLLTLQPEQKFQVKVKGFGGAMTDA AALNILALSPPAQNLLLSYFSEE,,GIGYNIIRVPMASCDFSIRTYTYADTPDDFQLH NFSLPEEDTKLK,,IPLIHRA LQLAQRPVSLASPWTSPWLKTNGAVNGKGLKGP GDIIYHQTWARYFVK,,FLDAYAEHKLQFWAVTAENEP SAGLLSGYPFQCLGFTPEHQ RDFIARDLGPTLANSTH HNVRLMLDDQRLLLPHWAKV,,VLTDP EAAKYVHGIAVHWYLDFLAPAKATLGETH RLFPNTMLFASEA CVGSKFWEQSVRLGSWDRGMQYSHSIIT,,NLLYHVVGWTDWNLA LNPEGGPNWVRNFVDSPIIVDITKDTFYKQPMFYHL 536 SSKDVPLTIKDP AVGFLETISP GYSIHTYLWRRQ*		
✓ <b>GBA-202</b>	3588 .. 9705	6118 bp	CDS
▶ 11 segments = 1611 bp			
/note	= coding sequence <a href="#">ENSP00000357357</a>		
/translation	= MEFSSPSRE,,ECPKPLSRV SIMAGSLTG LLLLQAVSWAS,,GARPCIPKSFYSSVVCVCNATYCDSDPPTFPALGTFSTRYESTRSGRRMELSM GPIQANHTGT,,G LLLTLQPEQKFQVKVKGFGGAMTDA AALNILALSPPAQNLLLSYFSEE,,GIGYNIIRVPMASCDFSIRTYTYADTPDDFQLH NFSLPEEDTKLK,,IPLIHRA LQLAQRPVSLASPWTSPWLKTNGAVNGKGLKGP GDIIYHQTWARYFVK,,FLDAYAEHKLQFWAVTAENEP SAGLLSGYPFQCLGFTPEHQ RDFIARDLGPTLANSTH HNVRLMLDDQRLLLPHWAKV,,VLTDP EAAKYVHGIAVHWYLDFLAPAKATLGETH RLFPNTMLFASEA CVGSKFWEQSVRLGSWDRGMQYSHSIIT,,NLLYHVVGWTDWNLA LNPEGGPNWVRNFVDSPIIVDITKDTFYKQPMFYHL 536 SSKDVPLTIKDP AVGFLETISP GYSIHTYLWRRQ*		
<b>GBA-203</b>	3588 .. 9705	6118 bp	CDS
▶ 10 segments = 1464 bp			
/note	= coding sequence <a href="#">ENSP00000402577</a>		
/translation	= MEFSSPSRE,,ECPKPLSRV SIMAGSLTG LLLLQAVSWAS,,GARPCIPKSFYSSVVCVCNATYCDSDPPTFPALGTFSTRYESTRSGRRMELSM GPIQANHTGT,,GIGYNIIRVPMASCDFSIRTYTYADTPDDFQLH NFSLPEEDTKLK,,IPLIHRA LQLAQRPVSLASPWTSPWLKTNGAVNGK GSLKGP GDIIYHQTWARYFVK,,FLDAYAEHKLQFWAVTAENEP SAGLLSGYPFQCLGFTPEHQ RDFIARDLGPTLANSTH HNVRLMLDDQRL LLPHWAKV,,VLTDP EAAKYVHGIAVHWYLDFLAPAKATLGETH RLPNTMLFASEA CVGSKFWEQSVRLGSWDRGMQYSHSIIT,,NLLYHVV GWDWNLA LNPEGGPNWVRNFVDSPIIVDITKDTFYKQPMFYHLGHFS,,KFIPEGSQRVGLVASQKNDLDAVALMHPDGS AVVVV LNR,,SSK 481 IKDPAVGFLETISP GYSIHTYLWRRQ*		
<b>GBA-214</b>	4738 .. 8304	3567 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000497670</a> protein_coding_CDS_not_defined		

Feature	Location	Size		Type
<b>GBA-204</b>	4769 .. 9705	4937 bp	 →	CDS
▶ 9 segments = 1350 bp				
/note	= coding sequence <a href="#">ENSP00000397986</a>			
/translation	= MELSMGPIQANHTGT,,GLLLTLQPEQKFQKVKGFGGAMTDAAAALNILALSPPAQNLLLKSYFSEE,,GIGYNIIRVPMASCDIFSIRTYTYADTPD DFQLHNFSLPEEDTKLK,,IPLIHRALQLAQRVSLASPWTSPWLKTNGAVNGKGSKGGQPGDIYHQTWARYFVK,,FLDAYAEHKLQFWAVT AENEPSAGLLSGYPFQCLGFTPEHQRFIARDLGPTLANSTHHNVRLMLDDQRLLPHWAKV,,VLTDPAAKYVHGIAVHWYLDFLAPAKAT LGETHRLFPNTMLFASEACVGSKFWEQSVRLGSWDRGMQYSHSIT,,NLLYHVVGWTDWNLALNPEGGPNWVRNFVDSPIIVDITKDTFYKQP MFYHLGHFS,,KFIPEGSQRVGLVASQKNDLDAVALMHPDGSVVVVV LNR,,SSKDVP LTIKDPAVGFLETISP GYSIHTYLWRRQ * 449 amino acids = 50.3 kDa			
<b>GBA-205</b>	5809 .. 6768	960 bp	 →	prim_transcript
/note	= primary transcript <a href="#">ENST00000460156</a> protein_coding_CDS_not_defined			
<b>GBA-212</b>	5991 .. 8518	2528 bp	 →	prim_transcript
/note	= primary transcript <a href="#">ENST00000491081</a> protein_coding_CDS_not_defined			
<b>GBA-210</b>	8241 .. 9739	1499 bp	 →	prim_transcript
/note	= primary transcript <a href="#">ENST00000478472</a> protein_coding_CDS_not_defined			
<b>GBA-206</b>	8865 .. 10,247	1383 bp	 →	prim_transcript
/note	= primary transcript <a href="#">ENST00000464536</a> protein_coding_CDS_not_defined			
✓ <b>Donor Template WT -&gt; SNV</b>	8937 .. 9011	75 bp	 ⇌	misc_feature
✓ <b>PAM</b>	8968 .. 8970	3 bp	 ⇌	misc_feature
✓ <b>Protospacer Sequence</b>	8971 .. 8990	20 bp	 ⇌	misc_feature
✓ <b>SNV</b>	8974 .. 8974	1 bp	 ⇌	misc_feature
/note	= WT = A SNV = T			

Primer	Length		Binding Sites		Tm	Date Added
✓ <b>PCR Reverse</b>	24-mer		8580 .. 8603		59°C	Jan 10, 2023
/sequence	= GGGGAACCATGATTCCCTATCTTC 50% GC / 7303.8 Da					
✓ <b>Sanger Sequencing</b>	24-mer		8580 .. 8603		59°C	Jan 10, 2023
/sequence	= GGGGAACCATGATTCCCTATCTTC 50% GC / 7303.8 Da					
✓ <b>Donor Template WT -&gt; SNV</b>	75-mer		8937 .. 9011		73°C	Jan 10, 2023
/sequence	= GCCAAGGTGGTAGAACATGGGCTGTTTGTA AACGTGACCTTGGTGATGTCTACAATGATGGGACTGTCGACAAA 47% GC / 23,337.2 Da					
✓ <b>gRNA Protospacer</b>	20-mer		8971 .. 8990		53°C	Jan 10, 2023
/sequence	= CTGTTTGTA AACGTGTCCT 40% GC / 6098.0 Da					
✓ <b>PCR Forward</b>	20-mer		9284 .. 9303		59°C	Jan 10, 2023
/sequence	= CCCATAACTCCTGCAGAGGC 60% GC / 6047.0 Da					