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3'

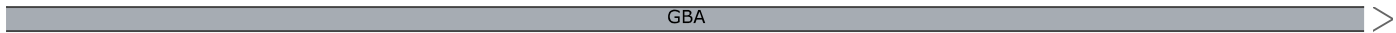
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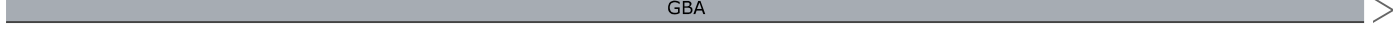
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170



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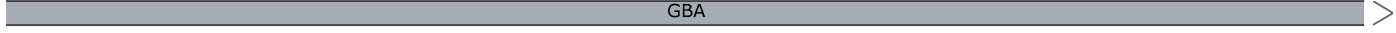
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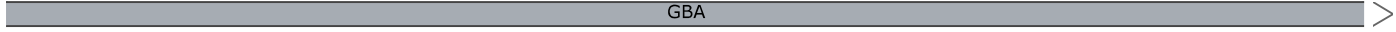
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595



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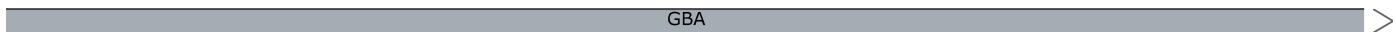
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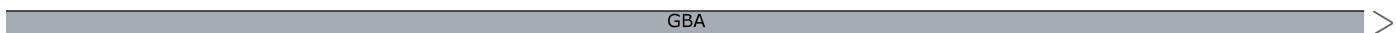
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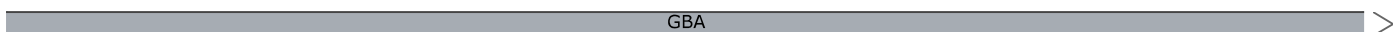
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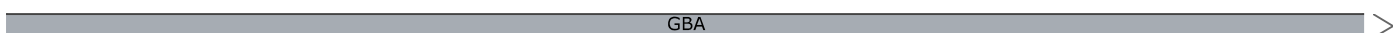
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1785

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1955

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2125

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3655

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GBA-202

1 5  
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GBA-202

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GBA-202

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GBA-202

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GBA-202

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5185

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GBA-202

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GBA-202

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GBA-202

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GBA

GBA-202

GBA-202

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GBA-202

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5695

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GBA-202

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5780

GBA

GBA-202

GBA-202



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5865

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GBA-202

GBA-202

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5950

GBA

GBA-202

GBA-202

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6035

GBA

GBA-202

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GBA-202

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GBA-202

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GBA

GBA-202

D T P D D F Q L H N F S L P E E D T K L K  
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GBA-202

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6290

GBA

GBA-202

GBA-202

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6375

GBA

GBA-202

GBA-202

CACTACCTTTGTCTCTAGATACCCCTGATTACCCGAGCCCTGCAGTTGGCCAGCGTCCCGTTTCACTCCTTGCCAGCCCTGGA  
GTGATGGAAACAGAGATCTATGGGGACTAAGTGGCTCGGGACGTCAACC GGTCGCAGGGCAAAGTGAGGAACGGTCGGGGACCT

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

CATCACCCACTTGGCTCAAGACCAATGGAGCGGTGAATGGGAAGGGGTCCTCAAGGGACAGCCCGGAGACATCTACCACCAGAC  
GTAGTGGGTGAACCGAGTTCTGGTTACCTCGCCACTTACCCTTCCCCAGTGAGTTCCCTGTCGGGCTCTGTAGATGGTGGTCTG

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

ENSE00003562842

GBA-202

CCAACCCTCAACCTAGTTCCACTTCCAGATCTGCCTGTCTCAGCTCACCTTTCTACCTTCTGGGCCTTTCAGCCTTGGGCCTGT  
GGTTGGGAGTTGGATCAAGGTGAAGGTCTAGACGGACAGGAGTCGAGTGAAAGATGGAAGACCCGGAAAGTCGGAACCCGGACA

6715

GBA

GBA-202

GBA-202

CAATCTTGCCCACTCCATCAGGCTTCTGTTCTCTCGGTCTGGCCACTTTCTTTTTATTTTTCTTCTTTTTTTTTTTTTTTGAGA  
GTTAGAACGGGTGAGGTAGTCCGAAGGACAAGAGAGCCAGACCGGGTGAAAGAAAAATAAAAAAGAAAAAAAAAAAAAAAAACTCT

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  
CGGTGGTGTGGGTCGACCAGACAGGTGAAAAGAACCAGGCTAGTAAGTACTGGAAAAGAGAACGGTCCAAGGACCTACGGATACGA

7140

GBA

GBA-202

255 F L D A Y A 260

ENSE00003488376

GBA-202

GAGCACAAGTTACAGTTCTGGGCAGTGACAGCTGAAAATGAGCCTTCTGCTGGGCTGTTGAGTGGATACCCCTTCCAGTGCCTGG  
CTCGTGTTC AATGTCAAGACCCGTCCTGTCGACTTTTACTCGGAAGACGACCCGACAACCTCACCTATGGGG AAGGTCACGGACC

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

GCTTCACCCCTGAACATCAGCGAGACTTCATTGCCCGTGACCTAGGTCTACCCCTCGCCAACAGTACTCACCACAATGTCCGCCT  
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

ACTCATGCTGGATGACCAACGCTTGCTGCTGCCCACTGGGCAAAGGTGGTAAGGCCTGGACCTCCATGGTGCTCCAGTGACCTT  
TGAGTACGACCTACTGGTTGCGAACGACGACGGGGTGACCCGTTTCCACCATTCCGGACCTGGAGGTACCACGAGGTCACTGGAA

7395

GBA

GBA-202

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

ENSE00003488376

GBA-202

CAAATCCAGCATCCAAATGACTGGCTCCCAAACCTTAGAGCGATTTCTCTACCCAACCTATGGATTCCCTAGAGCACCATTTCCCTGG  
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  
TGTTTTGTTTTGTTTTGATAGATCCGACCCCAACCAAGTACATACATACATATATGTATATATACACAAATATACATATA

7905

GBA

GBA-202

GBA-202

ATATATACACACACACATACATACACACACATACACACACAAATTAGCTGGGTGTGGCACCCGTGTAGTCCCAGCTACTCAGG  
TATATATGTGTGTGTGTGTATGTATGTGTGTGTATGTGTGTGTTTAAATCGACCCACACCCGTGGGCACATCAGGGTCGATGAGTCC

7990

GBA

GBA-202

GBA-202

AGGCTAATGTGGGAGGATCAGTTGACCCTAGGAAGTCAAGGCTGCAGTGAGTCGTGATTGCGCCACTGTACTCCAGCCCGAGTGA  
TCCGATTACACCCTCCTAGTCAACTGGGATCCTTCAGTTCAGTCCGACGTCCTCAGCACTAACGCGGTGACATGAGGTCGGGCTCACT

8075

GBA

GBA-202

GBA-202

CAGAGTGACATCCTGTCTCAAAAACAAAAAAAAAATCTCCCCAACCTCTCTAGTTGCATTCTTCCCGTCACCCAACTCCAGGATT  
GTCTCACTGTAGGACAGAGTTTTTTGTTTTTTTTTAGAGGGGTTTGGAGAGATCAACGTAAGAAGGGCAGTGGGTTGAGGTCCTAA

8160

GBA

GBA-202

GBA-202

CCTACAACAGGAACTAGAAAGTTCCAGAAGCCTGTGTGCAAGGTCCAGGATCAGTTGCTCTTCTCTTTCAGGTAAGTGCAGACACCA  
GGATGTTGTCTTGTATCTTCAAGGTCTTCGGACACACGTTCCAGGTCCTAGTCAACGAGAAGGAAACGTCATGACTGTCTGGGT

8245

GBA

GBA-202

335  
V L T D P  
ENSE00001231060

GBA-202

GAAGCAGCTAAATATGTTTCATGGCATTGCTGTACATTGGTACCTGGACTTTCTGGCTCCAGCCAAAGCCACCCCTAGGGGAGACAC  
CTTCGTCGATTTATACAAGTACCGTAACGACATGTAACCATGGACCTGAAAGACCCGAGGTCGGTTTTTCGGTGGGATCCCTCTGTG

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

ACCGCCTGTTCCCAACACCATGCTCTTTGCCTCAGAGGCCTGTGTGGGCTCCAAGTTCTGGGAGCAGAGTGTGCGGCTAGGCTC  
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  
GACCTTAGCTCCCTACGTCATGTCTGGTGTCTGCTAGTAGTGCCATTTCGGTGGGGTCAGAGGGAAGGACGTTTTCTGCTCTGGAGTCTGGA

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

CCATGATTCCCTATCTTCCCTTTCTTCCAGGTCGACACCTCATTGCCCTTTTTGCAACTACTGAGGCACTTGCAGCTGCCT  
GGTACTAAGGGATAGAAGGGAAAGGAAAGTGTCCAGACGTGTGGAGTAACGGGGAAAACGTTGATGACTCCGTGAACGTCGACGGA

8670

GBA

GBA-202

GBA-202

CAGACTTCTCAGCTCCCCTTGAGATGCCTGGATCTTCACACCCCAACTCCTTAGCTACTAAGGAATGTGCCCTCACAGGGCTG  
GTCTGAAGAGTTCGAGGGGAACCTCTACGGACCTAGAAGTGTGGGGGTTGAGGAATCGATGATTCTTACACGGGGAGTGTCCCGAC

8755

GBA

GBA-202

GBA-202

ACCTACCCACAGCTGCCTCTCCACATGTGACCCCTTACCTACACTCTCTGGGGACCCCAAGTGTGGCGCTTTGTCTCTTTGCCT  
TGGATGGGTGTTCGACGGAGAGGGTGTACACTGGGAATGGATGTGAGAGACCCCTGGGGGTCAACAACGCGGAAACAGAGAAACGGA

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  
CCCACGCATTGAAACAGCTGTCAGGGTAGTAACATCTGTAGTGGTTCCGTGCAAAAATGTTTGTTCGGGTACAAGATGGTGGAAAC

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

AAACAGCTGTCAGGGTAGTAACATCTGTAGTGGTTCCGTGCAAAAATGTTTGTTCGGGTACAAGATGGTGGAAAC  
Donor Template WT -> SNV

TCCTGTGCAAAAATGTTTGTGTC  
gRNA Protospacer

CCACTTCAGGTGAGTGGAGGGCGGGCACCCCATTCATACAGGCCTATCATCTCTACATCGGATGGCTTACATCACTCTACA  
GGTGAAGTCCACTCACCTCCCGCCCGTGGGGTAAGGTATGGTCCGGATAGTAGAGGATGTAGCCTACCGAATGTAGTGAGATGT

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  
ATCCATCGTTGTCTTTTGGGGTTACGGACTCCGACCTGACGCTACGTCTTTTCGTCCCAGTACACGGGTGCTCGTACCGAGGTCCG

9265

GBA

GBA-202

GBA-202

CTAGAGAGCCAGGGCAGAGCCTCTGCAGGAGTTATGGGGTGGGTCCGTGGGTGGGTGACTTCTTAGATGAGGGTTTCATGGGAGG  
GATCTCTCGGTCCCGTCTCGGAGACGTCTCAATACCCACCCAGGCACCCACCCACTGAAGAATCTACTCCCAAAGTACCTCC

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

TCTGTGACTAAAGAGGGCACAGCAGGGCCAGTGTGAGCTTACAGCGACGTAAGCCCAGGGGCAATGGTTTGGGTGACTCACTTTC  
AGACACTGATTTCTCCCGTGTCTCGTCCCGGTCACACTCGAATGTCGCTGCATTCCGGTCCCCGTTACCAAACCCACTGAGTGAAAG

9860

GBA

GBA-202

CCCTCTAGGTGGTGCCAGGGGCTGGAGGCCCTAGAAAAAGATCAGTAAGCCCCAGTGTCCCCCAGCCCCATGCTTATGTGAA  
GGGAGATCCACCACGGTCCCCGACCTCCGGGGATCTTTTTCTAGTCATTCGGGGTCACAGGGGGGTCTGGGGGTACGAATACACTT

9945

GBA

GBA-202

CATGCGCTGTGTGCTGCTTGTCTTTGGAAACTGGGCCTGGGTCCAGGCCTAGGGTGAGCTCACTGTCCGTACAAACACAAGATCAG  
GTACGCGACACACGACGAACGAAACCTTTGACCCGGACCCAGGTCCGGATCCCACTCGAGTGACAGGCATGTTTGTGTTCTAGTC

10,030

GBA

GBA-202

GGCTGAGGGTAAGGAAAAAGAAGAGACTAGGAAAGCTGGGCCAAAACCTGGAGACTGTTTGTCTTTCTGGAGATGCAGAACTGGG  
CCGACTCCCATTCTTTTCTTCTCTGATCCTTTGACCCGGGTTTTGACCTCTGACAAACAGAAAGGACCTCTACGTCTTGACCC

10,115

GBA

GBA-202

CCCGTGGAGCAGCAGTGTTCAGCATCAGGGCGGAAGCCTTAAAGCAGCAGCGGGTGTGCCAGGCACCCAGATGATTCCTATGGCA  
GGGCACCTCGTCTCACAGTCTAGTCCCCTTCGGAATTTTCGTCGTCGCCACACGGGTCCGTGGGTCTACTAAGGATACCGT

10,200

GBA

GBA-202

CCAGCCAGGAAAAATGGCAGCTCTTAAAGGAGAAAAATGTTTGTAGCCCA  
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,,ECPKPLSRVSIMAGSLTGLLLLQAVSWAS,,GARPCIPKSFYSSVVCVCNATYCDSDPPTFPALGTFSTRYESTRSGRRMELSM GPIQANHTGT,,GLLLTLPQEQKFQVKVKGFGGAMTDAALNILALSPPAQNLLKSYFSEE,,GIGYNIIRVPMASCDFSIRTYTYADTPDDFQLH NFSLPEEDTKLK,,IPLIHRAQLAQRPVSLASPWTSPWLKTNGAVNGKSLKGGQPGDIYHQTWARYFVK,,FLDAYAEHKLQFWAVTAENEP SAGLLSGYPFQCLGFTPEHQRFIARDLGPPTLANSTHNNVRLMLDDQRLLLPHWAKV,,VLTDPAAKYVHGIAVHWYLDLFLAPAKATLGETH RLFPNTMLFASEACVGSKFWEQSVRLGSWDRGMQYSHSIIT,,NLLYHVVGWTDWNLANPEGGPNWVRNFVDSPIIVDITKDTFYKQPMFYHL 536 SSKDVPLTIKDPVGFLETISP GYSIHTYLWRRQ*		
✓ <b>GBA-202</b>	3588 .. 9705	6118 bp	CDS
▶ 11 segments = 1611 bp			
/note	= coding sequence <a href="#">ENSP00000357357</a>		
/translation	= MEFSSPSRE,,ECPKPLSRVSIMAGSLTGLLLLQAVSWAS,,GARPCIPKSFYSSVVCVCNATYCDSDPPTFPALGTFSTRYESTRSGRRMELSM GPIQANHTGT,,GLLLTLPQEQKFQVKVKGFGGAMTDAALNILALSPPAQNLLKSYFSEE,,GIGYNIIRVPMASCDFSIRTYTYADTPDDFQLH NFSLPEEDTKLK,,IPLIHRAQLAQRPVSLASPWTSPWLKTNGAVNGKSLKGGQPGDIYHQTWARYFVK,,FLDAYAEHKLQFWAVTAENEP SAGLLSGYPFQCLGFTPEHQRFIARDLGPPTLANSTHNNVRLMLDDQRLLLPHWAKV,,VLTDPAAKYVHGIAVHWYLDLFLAPAKATLGETH RLFPNTMLFASEACVGSKFWEQSVRLGSWDRGMQYSHSIIT,,NLLYHVVGWTDWNLANPEGGPNWVRNFVDSPIIVDITKDTFYKQPMFYHL 536 SSKDVPLTIKDPVGFLETISP GYSIHTYLWRRQ*		
<b>GBA-203</b>	3588 .. 9705	6118 bp	CDS
▶ 10 segments = 1464 bp			
/note	= coding sequence <a href="#">ENSP00000402577</a>		
/translation	= MEFSSPSRE,,ECPKPLSRVSIMAGSLTGLLLLQAVSWAS,,GARPCIPKSFYSSVVCVCNATYCDSDPPTFPALGTFSTRYESTRSGRRMELSM GPIQANHTGT,,GIGYNIIRVPMASCDFSIRTYTYADTPDDFQLHNFSLPEEDTKLK,,IPLIHRAQLAQRPVSLASPWTSPWLKTNGAVNGK GSLKGGQPGDIYHQTWARYFVK,,FLDAYAEHKLQFWAVTAENEP SAGLLSGYPFQCLGFTPEHQRFIARDLGPPTLANSTHNNVRLMLDDQRL LLPHWAKV,,VLTDPAAKYVHGIAVHWYLDLFLAPAKATLGETHRLFPNTMLFASEACVGSKFWEQSVRLGSWDRGMQYSHSIIT,,NLLYHVV WTDWNLANPEGGPNWVRNFVDSPIIVDITKDTFYKQPMFYHLGHFS,,KFIPEGSQRVGLVASQKNDLDAVALMHPDGSVAVVVV LNR,,SSK 481 TIKDPAVGFLETISP 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 AENEPSAGLLSGYPFQCLGFTPEHQRFIARDLGPPLANSTHHNVRLMLDDQRLLLPHWAKV,,VLTDPAAKYVHGIAVHWYLDFLAPAKAT LGETHRLFPNTMLFASEACVGSKFWEQSVRLGSWDRGMQYSHSIT,,NLLYHVVGWTDWNLALNPEGGPNWVRNFVDSPIIVDITKDTFYKQP MFYHLGHFS,,KFIPEGSQRVGLVASQKNDLDAVALMHPDGSVVVVV LNR,,SSKDVP LTIKDP AVGFLETISP 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					