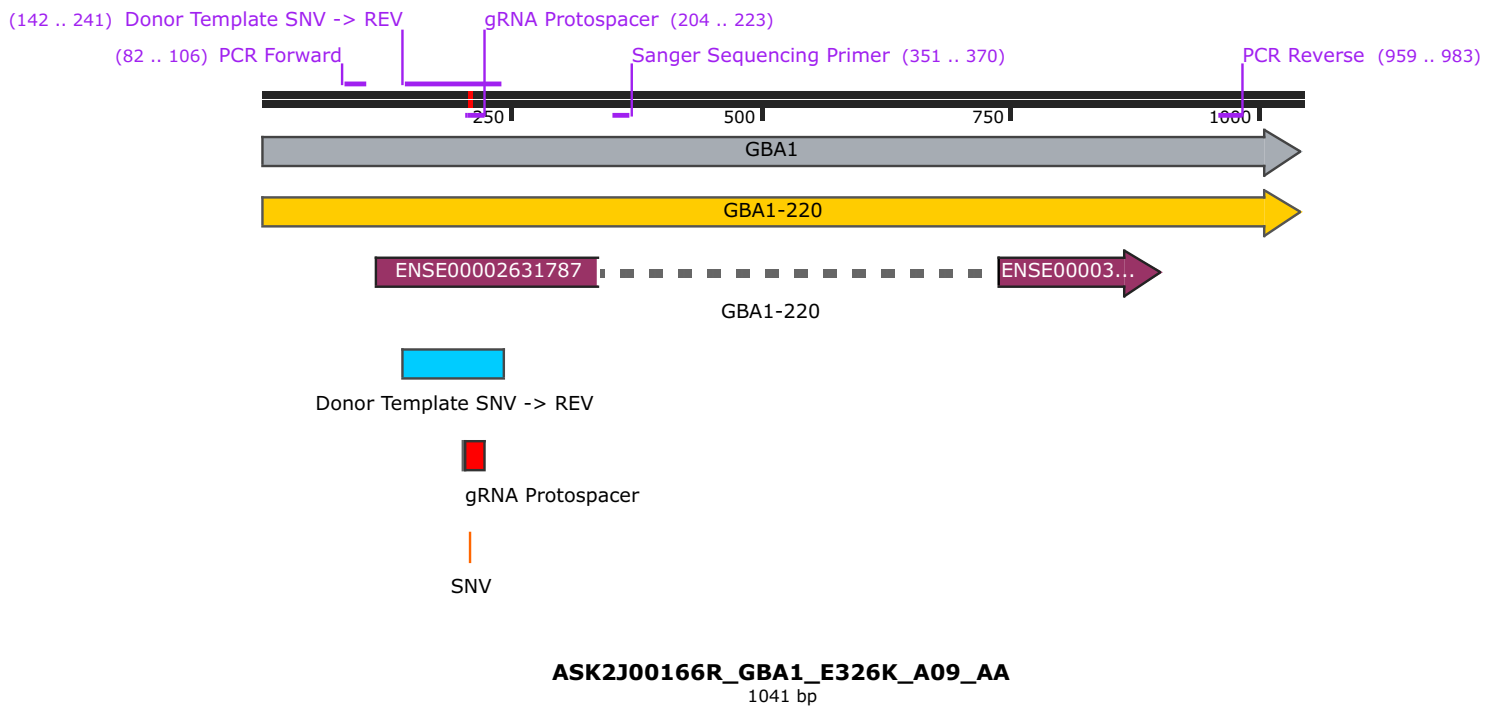
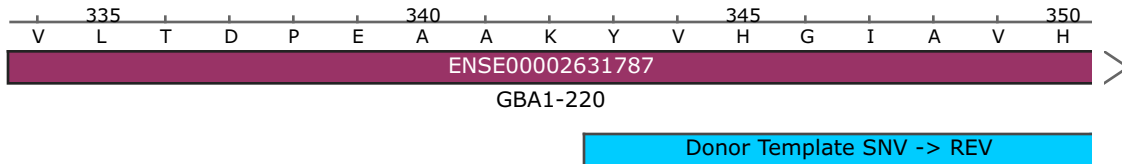
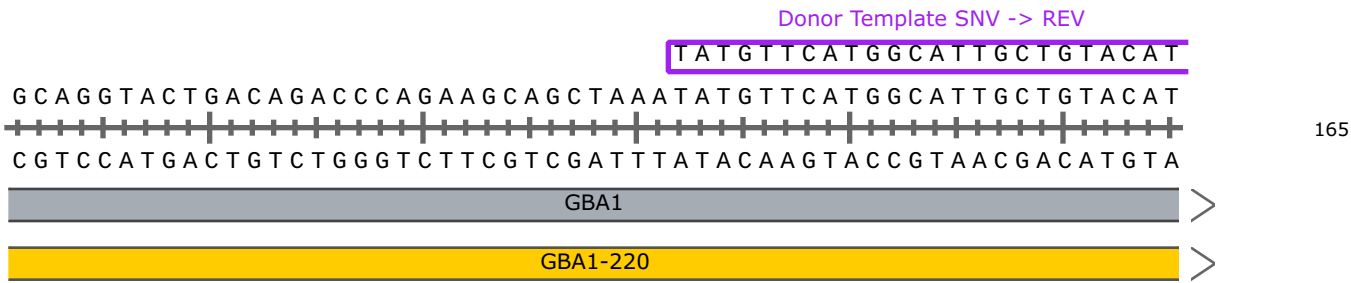
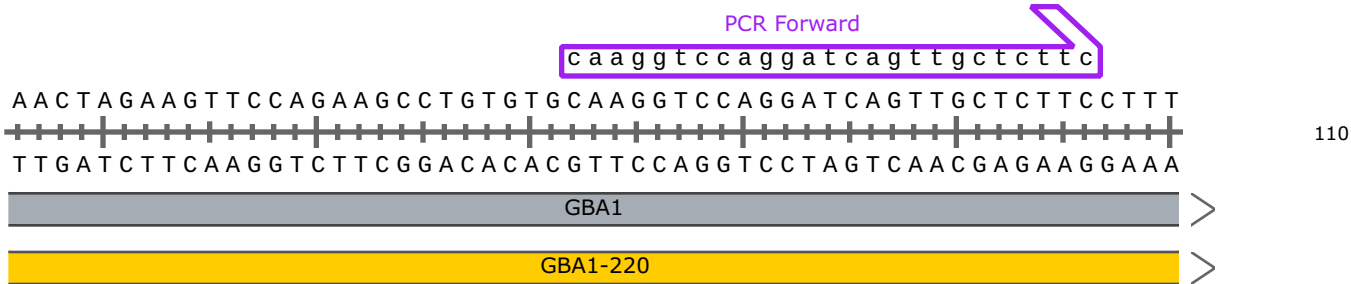
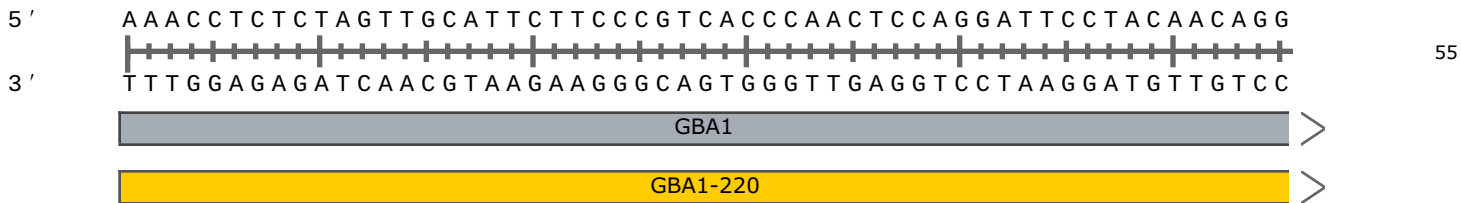


glucosylceramidase beta 1 [Source:HGNC Symbol;Acc:HGNC:4177]

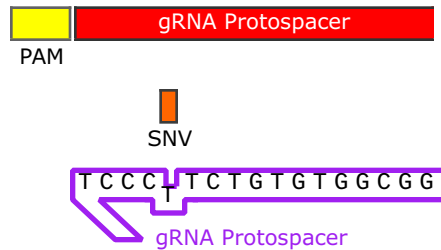
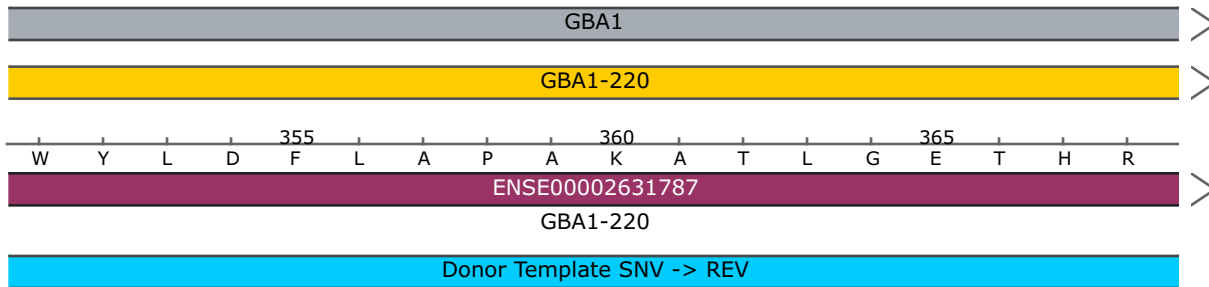




Donor Template SNV -> REV

TGGTACCTGGACTTTCTGGCTCCAGCCAAAGCCACCCTAGGGGAGACACACCGCC
 TGGTACCTGGACTTTCTGGCTCCAGCCAAAGCCACCCTAGGGGAGACACACCGCC
 ACCATGGACCTGAAAGACCGAGGTCGGTTTCGGTGGGATCCCCTCTGTGTGGCGG

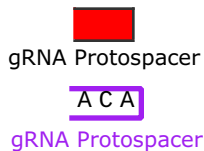
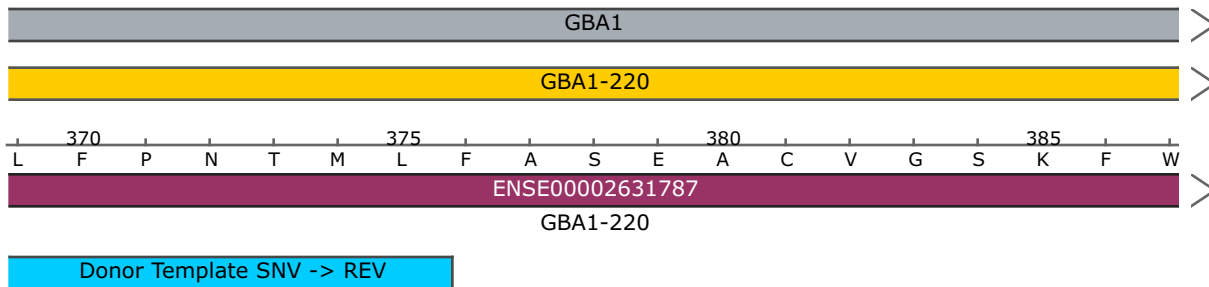
220



Donor Template SNV -> REV

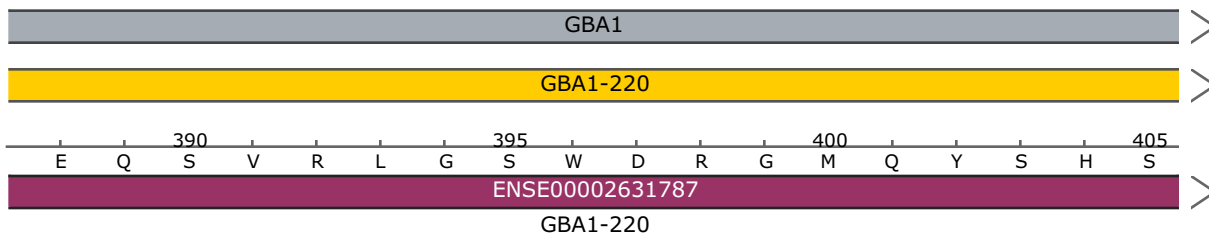
TGTTCCCAACACCATGCTCT
 TGTTCCCAACACCATGCTCTTTGCCTCAGAGGCCTGTGTGGGCTCCAAGTTCTG
 ACAAGGGGTTGTGGTACGAGAAACGGAGTCTCCGGACACACCCGAGGTTCAAGAC

275

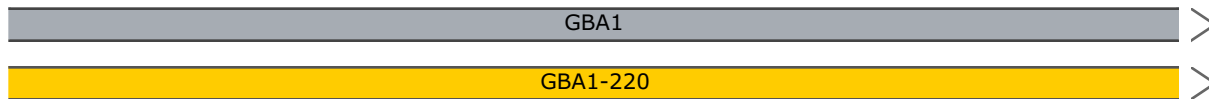


GGAGCAGAGTGTGCGGCTAGGCTCCTGGGATCGAGGGATGCAGTACAGCCACAGC
 CCTCGTCTCACACGCCGATCCGAGGACCCTAGCTCCCTACGTCAATGTGCGGTGTCG

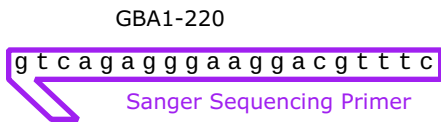
330



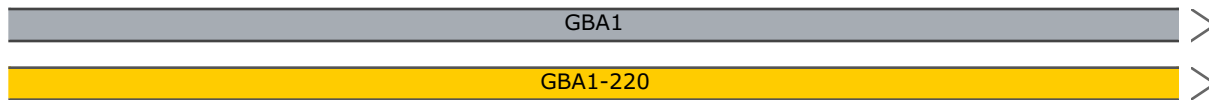
ATCATCACGGTAAGCCACCCCAGTCTCCCTTCCTGCAAAGCAGACCTCAGACCTC
 TAGTAGTGCCATTTCGGTGGGGTCAGAGGGAAGGACGTTTCGTCTGGAGTCTGGAG



I I T
 ENSE0000263...

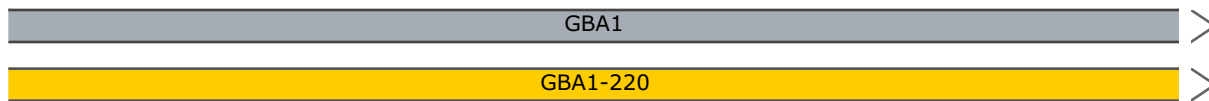


TTACTAGTTTCACCAAAGACTGACAGAAGCCCTTCCTGTCCAGCTTTCCCCAGCT
 AATGATCAAAGTGGTTTCTGACTGTCTTCGGGAAGGACAGGTCGAAAGGGGTCTGA



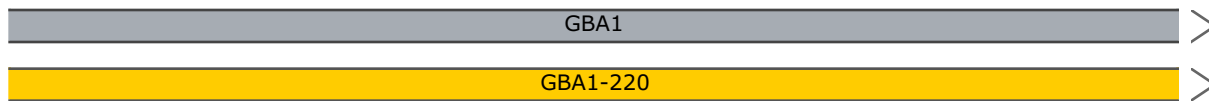
GBA1-220

AGCCTGCCCTTTTGAGCAACTCTGGGGAACCATGATTCCCTATCTTCCCTTTCCCT
 TCGGACGGGAAAACCTCGTTGAGACCCCTTGGTACTAAGGGATAGAAGGGAAAGGA



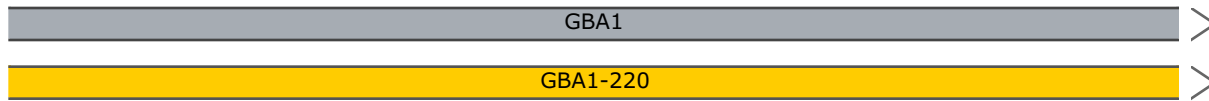
GBA1-220

TCACAGGTCTGCACACCTCATTGCCCTTTTGCAACTACTGAGGCACTTGCAGCT
 AGTGTCCAGACGTGTGGAGTAACGGGAAAACGTTGATGACTCCGTGAACGTCGA



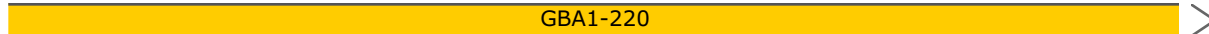
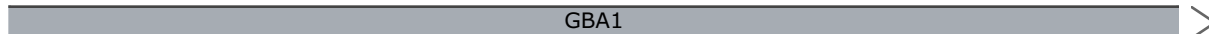
GBA1-220

GCCTCAGACTTCTCAGCTCCCCTTGAGATGCCTGGATCTTCACACCCCCAACTCC
 CGGAGTCTGAAGAGTTCGAGGGGAACTCTACGGACCTAGAAGTGTGGGGGTTGAGG



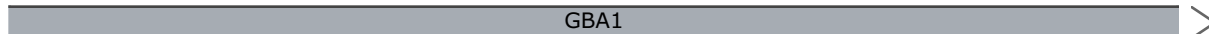
GBA1-220

TTAGCTACTAAGGAATGTGCCCTCACAGGGCTGACCTACCCACAGCTGCCTCTC
 AATCGATGATTCTTACACGGGGAGTGTCCCGACTGGATGGGTGTCGACGGAGAG



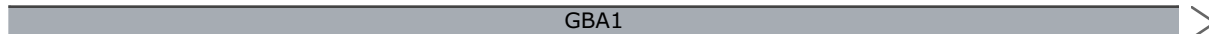
GBA1-220

CCACATGTGACCCTTACCTACACTCTCTGGGGACCCCAAGTGTGCGCCTTTGTC
 GGTGTACACTGGGAATGGATGTGAGAGACCCCTGGGGGTCAACGCGGAAACAG

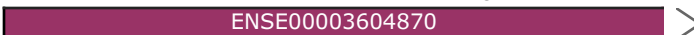


GBA1-220

TCTTTGCCTTTGTCCTTACCCTAGAACCTCCTGTACCATGTGGTTCGGCTGGACCG
 AGAAACGGAAACAGGAATGGGATCTTGGAGGACATGGTACACCAGCCGACCTGGC

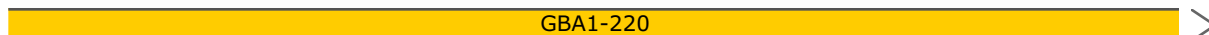
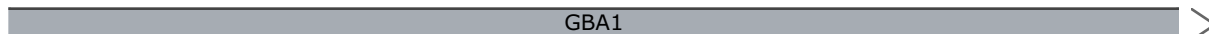


410 N L L Y H V V G W T 415

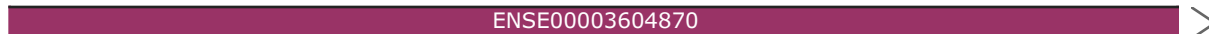


GBA1-220

ACTGGAACCTTGCCCTGAACCCCGAAGGAGGACCCAATTGGGTGCGTAACTTTGT
 TGACCTTGGAAACGGGACTTGGGGCTTCTCCTGGGTTAACCCACGCATTGAAACA

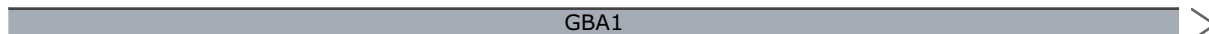


420 D W N L A L N P E G G P N W V R N F V 435

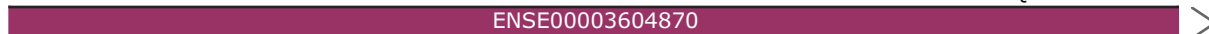


GBA1-220

CGACAGTCCCATCATTGTAGACATCACCAAGGACACGTTTTACAAACAGCCCATG
 GCTGTCAGGGTAGTAACATCTGTAGTGGTTCTGTGCAAAATGTTTGTGGGTAC

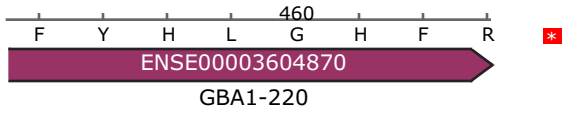
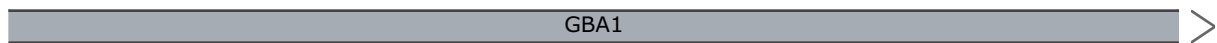


440 D S P I I V D I T K D T F Y K Q P M 455

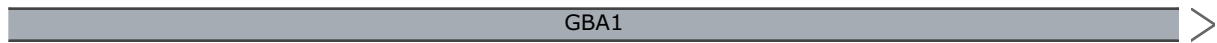


GBA1-220

TTCTACCACCTTGGCCACTTCAGGTGAGTGGAGGGCGGGCACCCCCATTCCATAC 935
 AAGATGGTGGAAACCGGTGAAGTCCA CT CACCTCCCGCCCGTGGGGGTAAGGTATG

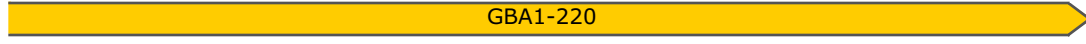


CAGGCCTATCATCTCCTACATCGGATGGCTTACATCACTCTACACCACGAGGGAG 990
 GTCCGGATAGTAGAGGATGTAGCCTACCGAATGTAGTGAGATGTGGTGCTCCCTC



ctaccgaatgtagtgagatgtggtg
 PCR Reverse

CAGGAAGGTGTT CAGGGTGGAAACCTCGGAAGAGGCACACCCATCCCTTTT 3'
 GTCCTTCCACAAGTCCACCTTGGAGCCTTCTCCGTGTGGGTAGGGGAAAA 5' 1041



Feature	Location	Size	Start	End	Type
✓ GBA1	1 .. 1041	1041 bp	■	→	gene
/note	= gene ENSG00000262446 Protein coding				
GBA1-215	1 .. 1041	1041 bp	■	→	prim_transcript
/note	= primary transcript ENST00000570340 protein_coding_CDS_not_defined				
✓ GBA1-220	1 .. 1041	1041 bp	■	→	prim_transcript
/note	= primary transcript ENST00000572338				
GBA1-224	1 .. 1041	1041 bp	■	→	prim_transcript
/note	= primary transcript ENST00000574670				
GBA1-227	1 .. 1041	1041 bp	■	→	prim_transcript
/note	= primary transcript ENST00000576421 protein_coding_CDS_not_defined				
GBA1-229	1 .. 1041	1041 bp	■	→	prim_transcript
/note	= primary transcript ENST00000613861				
GBA1-230	1 .. 1041	1041 bp	■	→	prim_transcript
/note	= primary transcript ENST00000618489				
GBA1-218	1 .. 402	402 bp	■	→	prim_transcript
/note	= primary transcript ENST00000571863 protein_coding_CDS_not_defined				
GBA1-222	1 .. 188	188 bp	■	→	prim_transcript
/note	= primary transcript ENST00000573812 protein_coding_CDS_not_defined				
✓ GBA1-220	115 .. 903	789 bp	■	→	CDS
▶ 2 segments = 389 bp					
/note	= coding sequence ENSP00000459642				
/translation	= VLTDPAAKYVHGI AVHWYLD FLAPAKATLGETHRLFPNTMLFASEACVGSKFWEQSVRLGSDRGMQYSHSIIT,, NLLYHVVGWTD WNLALNPEGPNWVRNFVDSPIIVDITKDTFYKQPMFYHLGHF 129 amino acids = 14.8 kDa				
GBA1-224	115 .. 903	789 bp	■	→	CDS
▶ 2 segments = 389 bp					
/note	= coding sequence ENSP00000458274				
/translation	= VLTDPAAKYVHGI AVHWYLD FLAPAKATLGETHRLFPNTMLFASEACVGSKFWEQSVRLGSDRGMQYSHSIIT,, NLLYHVVGWTD WNLALNPEGPNWVRNFVDSPIIVDITKDTFYKQPMFYHLGHF 129 amino acids = 14.8 kDa				
GBA1-229	115 .. 903	789 bp	■	→	CDS
▶ 2 segments = 389 bp					
/note	= coding sequence ENSP00000482397				
/translation	= VLTDPAAKYVHGI AVHWYLD FLAPAKATLGETHRLFPNTMLFASEACVGSKFWEQSVRLGSDRGMQYSHSIIT,, NLLYHVVGWTD WNLALNPEGPNWVRNFVDSPIIVDITKDTFYKQPMFYHLGHF 129 amino acids = 14.8 kDa				

Feature	Location	Size		→	Type
GBA1-230	115 .. 903	789 bp	■	→	CDS
▶ 2 segments = 389 bp					
/note	= coding sequence ENSP00000482419				
/translation	= VLTDPAAKYVHGIAVHWYLDLAPAKATLGETHRLFNPNTMLFASEACVGSKFWEQSVRLGSDRGMQYSHSIIT,,NLLYHVVGWTD WNLALNPEGPNWVRNFVDSPIIVDITKDTFYKQPMFYHLGHF 129 amino acids = 14.8 kDa				
GBA1-225	125 .. 1041	917 bp	■	→	prim_transcript
/note	= primary transcript ENST00000574935 protein_coding_CDS_not_defined				
✓ Donor Template SNV -> REV	142 .. 241	100 bp	■	⇄	misc_feature
✓ PAM	201 .. 203	3 bp	■	⇄	misc_feature
✓ gRNA Protospacer	204 .. 223	20 bp	■	⇄	misc_feature
✓ SNV	208 .. 208	1 bp	■	⇄	misc_feature
/note	= SNV = A REV = G				
GBA1-219	749 .. 1041	293 bp	■	→	prim_transcript
/note	= primary transcript ENST00000571897 protein_coding_CDS_not_defined				

Primer	Length	Binding Sites	Tm	Date Added
✓ PCR Forward	25-mer	82 .. 106	61°C	Apr 25, 2024
/sequence = caaggtccaggatcagttgctcttc 52% GC / 7633.0 Da				
✓ Donor Template SNV -> REV	100-mer	142 .. 241	80°C	Apr 25, 2024
/sequence = TATGTTTCATGGCATTGCTGTACATTGGTACCTGGACTTTCTGGCTCCAGCCAAAGCCACCCTAGGGGAGACACACCGCCTGTTCCCAA CACCATGCTCT 54% GC / 30,576.8 Da				
✓ gRNA Protospacer	20-mer	204 .. 223	59°C	Apr 25, 2024
/sequence = ACAGGCGGTGTGTCTTCCCT 60% GC / 6100.0 Da				
✓ Sanger Sequencing Primer	20-mer	351 .. 370	57°C	Apr 25, 2024
/sequence = ctttgaggaagggagactg 55% GC / 6222.1 Da				
✓ PCR Reverse	25-mer	959 .. 983	59°C	Apr 25, 2024
/sequence = gtggtgtagagtgatgtaagccatc 48% GC / 7777.1 Da				