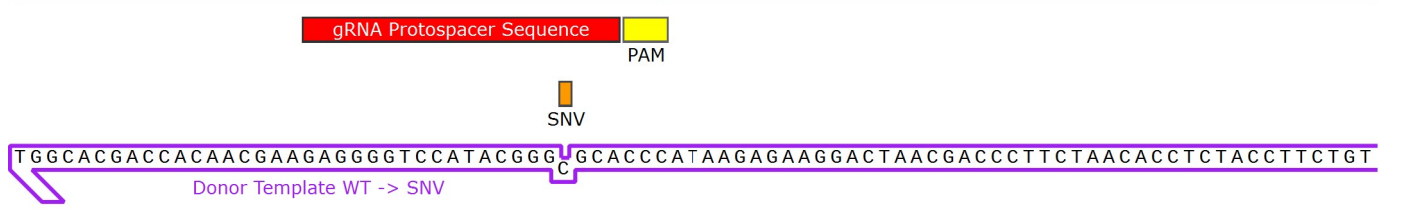
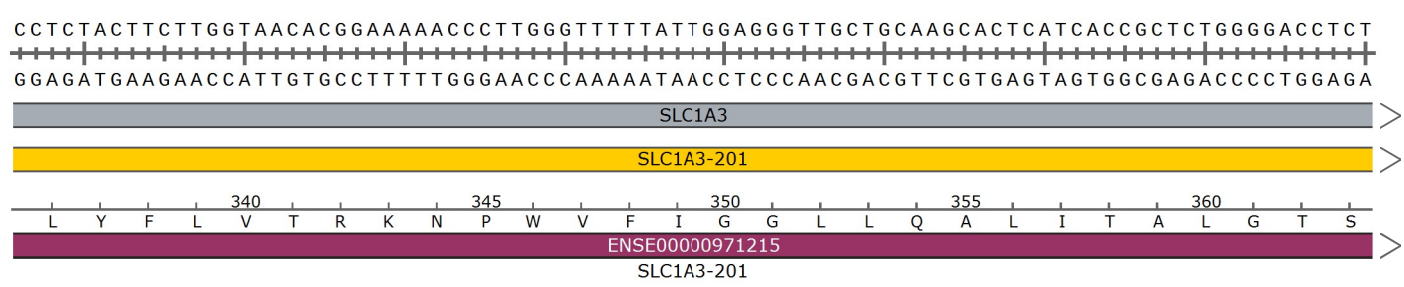
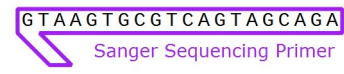
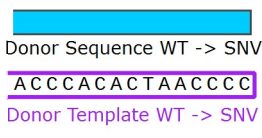
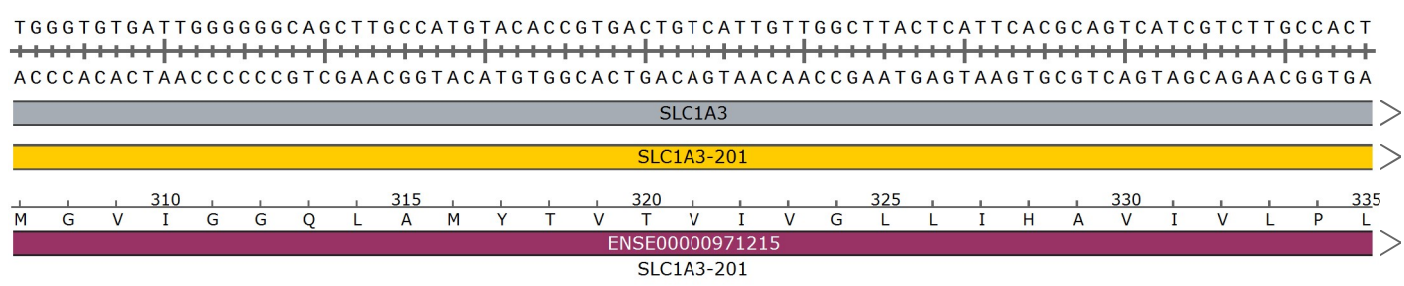


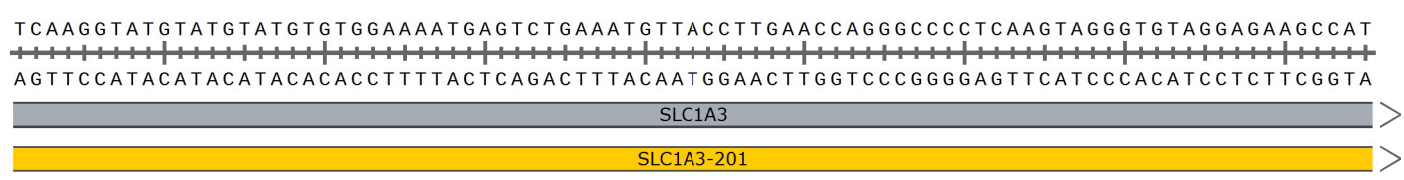
680



765



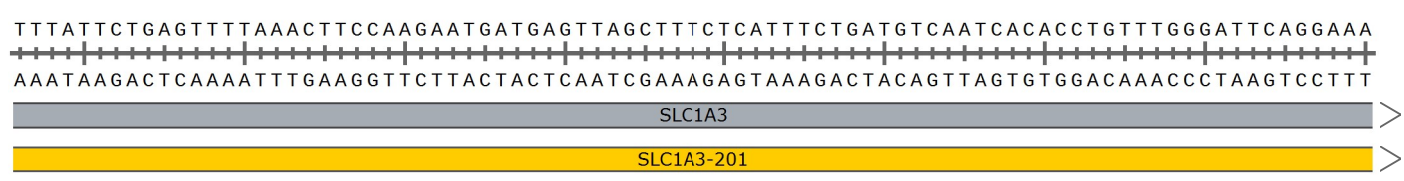
850



935



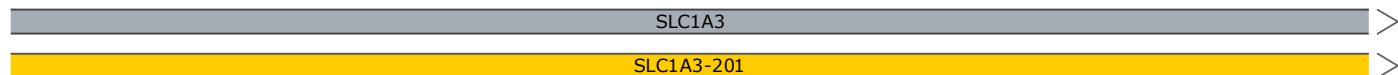
SLC1A3-201



1020

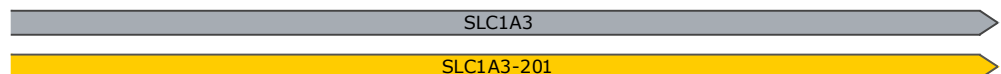


TGCCTGGCTACATATCTTTTGTGGGGACAAATTGGAAATCAACTATCCTTTCCCGTCCACTTCATCTCTCTTTAGTTGACATTTG
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 ACGGACCGATGTATAGAAAACACCCCTGTTTAACTTTAGTTGATAGGAAAGGGCAGGTGAAGTAGAGAGAAAATCAACTGTAAAC



ACGGACCGATGTATAGAAAAC
 PCR Reverse

CCTGAGGGAGAAGAGGCAGAGTGACTTGGCACAGGCTGTCGTGATGAGGGCATGATCACAAG 3 '
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1167
 GGACTCCCTCTTCTCCGTCTCACTGAACCGTGTCCGACAGCACTACTCCCGTACTAGTGTTT 5 '



Feature	Location	Size	Start	End	Type
SLC1A3-AS1	1 .38,037	38,037 bp	█	←	gene
/note = gene ENSG00000250155 lncRNA					
SLC1A3-AS1-202	1 .38,006	38,006 bp	█	←	prim_transcript
/note = primary transcript ENST00000510740 lncRNA					
✓ SLC1A3	1 .. 1167	1167 bp	█	→	gene
/note = gene ENSG00000079215 Protein coding					
✓ SLC1A3-201	1 .. 1167	1167 bp	█	→	prim_transcript
/note = primary transcript ENST00000265113					
SLC1A3-202	1 .. 1167	1167 bp	█	→	prim_transcript
/note = primary transcript ENST00000381918					
SLC1A3-215	1 .. 1167	1167 bp	█	→	prim_transcript
/note = primary transcript ENST00000612708					
SLC1A3-216	1 .. 1167	1167 bp	█	→	prim_transcript
/note = primary transcript ENST00000613445					
SLC1A3-217	1 .. 1167	1167 bp	█	→	prim_transcript
/note = primary transcript ENST00000624112 Retained intron					
SLC1A3-220	1 .. 1167	1167 bp	█	→	prim_transcript
/note = primary transcript ENST00000679487 Nonsense mediated decay					
SLC1A3-221	1 .. 1167	1167 bp	█	→	prim_transcript
/note = primary transcript ENST00000679784 Nonsense mediated decay					
SLC1A3-223	1 .. 1167	1167 bp	█	→	prim_transcript
/note = primary transcript ENST00000679958					
SLC1A3-224	1 .. 1167	1167 bp	█	→	prim_transcript
/note = primary transcript ENST00000679983					
SLC1A3-225	1 .. 1167	1167 bp	█	→	prim_transcript
/note = primary transcript ENST00000679992					
SLC1A3-227	1 .. 1167	1167 bp	█	→	prim_transcript
/note = primary transcript ENST00000680048 Nonsense mediated decay					
SLC1A3-228	1 .. 1167	1167 bp	█	→	prim_transcript
/note = primary transcript ENST00000680064 Retained intron					
SLC1A3-229	1 .. 1167	1167 bp	█	→	prim_transcript
/note = primary transcript ENST00000680125					
SLC1A3-232	1 .. 1167	1167 bp	█	→	prim_transcript
/note = primary transcript ENST00000680232					
SLC1A3-233	1 .. 1167	1167 bp	█	→	prim_transcript
/note = primary transcript ENST00000680318					
SLC1A3-237	1 .. 1167	1167 bp	█	→	prim_transcript
/note = primary transcript ENST00000680655 Nonsense mediated decay					
SLC1A3-239	1 .. 1167	1167 bp	█	→	prim_transcript
/note = primary transcript ENST00000680835 Nonsense mediated decay					
SLC1A3-240	1 .. 1167	1167 bp	█	→	prim_transcript
/note = primary transcript ENST00000680876 Retained intron					

Feature	Location	Size	Start	End	Type
SLC1A3-241	1 .. 1167	1167 bp	■	→	prim_transcript
/note = primary transcript ENST00000680878 Retained intron					
SLC1A3-242	1 .. 1167	1167 bp	■	→	prim_transcript
/note = primary transcript ENST00000680890					
SLC1A3-246	1 .. 1167	1167 bp	■	→	prim_transcript
/note = primary transcript ENST00000681440					
SLC1A3-247	1 .. 1167	1167 bp	■	→	prim_transcript
/note = primary transcript ENST00000681480 Nonsense mediated decay					
SLC1A3-249	1 .. 1167	1167 bp	■	→	prim_transcript
/note = primary transcript ENST00000681633 Retained intron					
SLC1A3-256	1 .. 1167	1167 bp	■	→	prim_transcript
/note = primary transcript ENST00000681814 Retained intron					
SLC1A3-259	1 .. 1167	1167 bp	■	→	prim_transcript
/note = primary transcript ENST00000681909					
SLC1A3-260	1 .. 1167	1167 bp	■	→	prim_transcript
/note = primary transcript ENST00000681926					
SLC1A3-251	1 .. 855	855 bp	■	→	prim_transcript
/note = primary transcript ENST00000681701 Nonsense mediated decay					
SLC1A3-258	1 .. 855	855 bp	■	→	prim_transcript
/note = primary transcript ENST00000681854					
SLC1A3-232	345 .. 855	511 bp	■	→	CDS
▶ 2 segments = 375 bp					
/codon_start = 1					
/note = coding sequence ENSP00000506207					
/translation = SKRKTLCPRAILSEGKARFCKNQGKFIFTKEKKEVHSFCKKRSPQFL, YAPVGILFLIAGKIVEMEDMGVIGGQLAMYTVTIVIVGLLIHAVIVLPLLYFLVTRKNPWVFIGG LLQALITALGTSS 125 amino acids = 13.7 kDa					
SLC1A3-258	575 .. 855	281 bp	■	→	CDS
▶ 2 segments = 153 bp					
/codon_start = 1					
/note = coding sequence ENSP00000504899					
/translation = LVETRLQPCWCCFSP, VIVLPLLYFLVTRKNPWVFIGGLLQALITALGTSS 51 amino acids = 5.6 kDa					
✓ Donor Sequence WT -> SNV	596 .. 695	100 bp	■		misc_feature
✓ gRNA Protospacer Sequence	614 .. 633	20 bp	■		misc_feature
SLC1A3-222	622 .. 1167	546 bp	■	→	prim_transcript
/note = primary transcript ENST00000679852					
SLC1A3-234	622 .. 1167	546 bp	■	→	prim_transcript
/note = primary transcript ENST00000680369					
SLC1A3-218	622 .. 1125	504 bp	■	→	prim_transcript
/note = primary transcript ENST00000679384 protein_coding_CDS_not_defined					
✓ SLC1A3-201	622 .. 855	234 bp	■	→	CDS
/codon_start = 1					
/note = coding sequence ENSP00000265113					
/translation = YAPVGILFLIAGKIVEMEDMGVIGGQLAMYTVTIVIVGLLIHAVIVLPLLYFLVTRKNPWVFIGGLLQALITALGTSS 78 amino acids = 8.2 kDa					

Feature	Location	Size	±	Type
SLC1A3-202	622 .. 855	234 bp	■ →	CDS
/codon_start = 1				
/note = coding sequence ENSP00000371343				
/translation = YAPVGILFLIAGKIVEMEDMGVIGGQLAMYTVTIVIGLLIHAVIVLPLLYFLVTRKNPWVFIGGLLQALITALGTSS 78 amino acids = 8.2 kDa				
SLC1A3-215	622 .. 855	234 bp	■ →	CDS
/codon_start = 1				
/note = coding sequence ENSP00000483657				
/translation = YAPVGILFLIAGKIVEMEDMGVIGGQLAMYTVTIVIGLLIHAVIVLPLLYFLVTRKNPWVFIGGLLQALITALGTSS 78 amino acids = 8.2 kDa				
SLC1A3-216	622 .. 855	234 bp	■ →	CDS
/codon_start = 1				
/note = coding sequence ENSP00000477672				
/translation = YAPVGILFLIAGKIVEMEDMGVIGGQLAMYTVTIVIGLLIHAVIVLPLLYFLVTRKNPWVFIGGLLQALITALGTSS 78 amino acids = 8.2 kDa				
SLC1A3-222	622 .. 855	234 bp	■ →	CDS
/note = coding sequence ENSP00000506649				
/translation = VCPRGYSLPDCWEDCGDGRHGCDWGAACHVHRDCHCWLTHSRSHRLATPLLLGNTEKPLGFYWRVAASTHHRSGDLFK 78 amino acids = 8.9 kDa				
SLC1A3-224	622 .. 855	234 bp	■ →	CDS
/codon_start = 1				
/note = coding sequence ENSP00000505238				
/translation = YAPVGILFLIAGKIVEMEDMGVIGGQLAMYTVTIVIGLLIHAVIVLPLLYFLVTRKNPWVFIGGLLQALITALGTSS 78 amino acids = 8.2 kDa				
SLC1A3-225	622 .. 855	234 bp	■ →	CDS
/codon_start = 1				
/note = coding sequence ENSP00000506585				
/translation = YAPVGILFLIAGKIVEMEDMGVIGGQLAMYTVTIVIGLLIHAVIVLPLLYFLVTRKNPWVFIGGLLQALITALGTSS 78 amino acids = 8.2 kDa				
SLC1A3-229	622 .. 855	234 bp	■ →	CDS
/codon_start = 1				
/note = coding sequence ENSP00000506424				
/translation = YAPVGILFLIAGKIVEMEDMGVIGGQLAMYTVTIVIGLLIHAVIVLPLLYFLVTRKNPWVFIGGLLQALITALGTSS 78 amino acids = 8.2 kDa				
SLC1A3-233	622 .. 855	234 bp	■ →	CDS
/codon_start = 1				
/note = coding sequence ENSP00000505057				
/translation = YAPVGILFLIAGKIVEMEDMGVIGGQLAMYTVTIVIGLLIHAVIVLPLLYFLVTRKNPWVFIGGLLQALITALGTSS 78 amino acids = 8.2 kDa				
SLC1A3-234	622 .. 855	234 bp	■ →	CDS
/note = coding sequence ENSP00000505836				
/translation = VCPRGYSLPDCWEDCGDGRHGCDWGAACHVHRDCHCWLTHSRSHRLATPLLLGNTEKPLGFYWRVAASTHHRSGDLFK 78 amino acids = 8.9 kDa				
SLC1A3-259	622 .. 855	234 bp	■ →	CDS
/codon_start = 1				
/note = coding sequence ENSP00000506599				
/translation = YAPVGILFLIAGKIVEMEDMGVIGGQLAMYTVTIVIGLLIHAVIVLPLLYFLVTRKNPWVFIGGLLQALITALGTSS 78 amino acids = 8.2 kDa				
SLC1A3-260	622 .. 855	234 bp	■ →	CDS
/codon_start = 1				
/note = coding sequence ENSP00000505850				
/translation = YAPVGILFLIAGKIVEMEDMGVIGGQLAMYTVTIVIGLLIHAVIVLPLLYFLVTRKNPWVFIGGLLQALITALGTSS 78 amino acids = 8.2 kDa				
✓ SNV	630 .. 630	1 bp	■	misc_feature
/note = WT = C SNV = G				
✓ PAM	634 .. 636	3 bp	■	misc_feature

Primer	Length	Binding Sites	Tm	Date Added
✓ PCR Forward /sequence = CTCTTGCTTTAACTTGGGAATCAGG 44% GC / 7663.0 Da	25-mer	118 .. 142	58°C	Aug 18, 2023
✓ Donor Template WT -> SNV /sequence = CCCC AATCACACCCATGTCTTCCATCTCCACAATCTTCCCAGCAATCAGGAAGAGAATACCCACGCGGGCATACTGGGGAGAAGCAACACCAGCACGGT 55% GC / 30,562.8 Da	100-mer	596 .. 695	78°C	Aug 18, 2023
✓ gRNA Protospacer /sequence = CTCCCCAGGTATGCCCCCGT 70% GC / 5989.9 Da	20-mer	614 .. 633	66°C	Aug 18, 2023
✓ Sanger Sequencing Primer /sequence = AGACGATGACTGCGTGAATG 50% GC / 6206.1 Da	20-mer	739 .. 758	57°C	Aug 18, 2023
✓ PCR Reverse /sequence = CAAAAGATATGTAGCCAGGCATTTTC 40% GC / 7674.1 Da	25-mer	1017 .. 1041	56°C	Aug 18, 2023