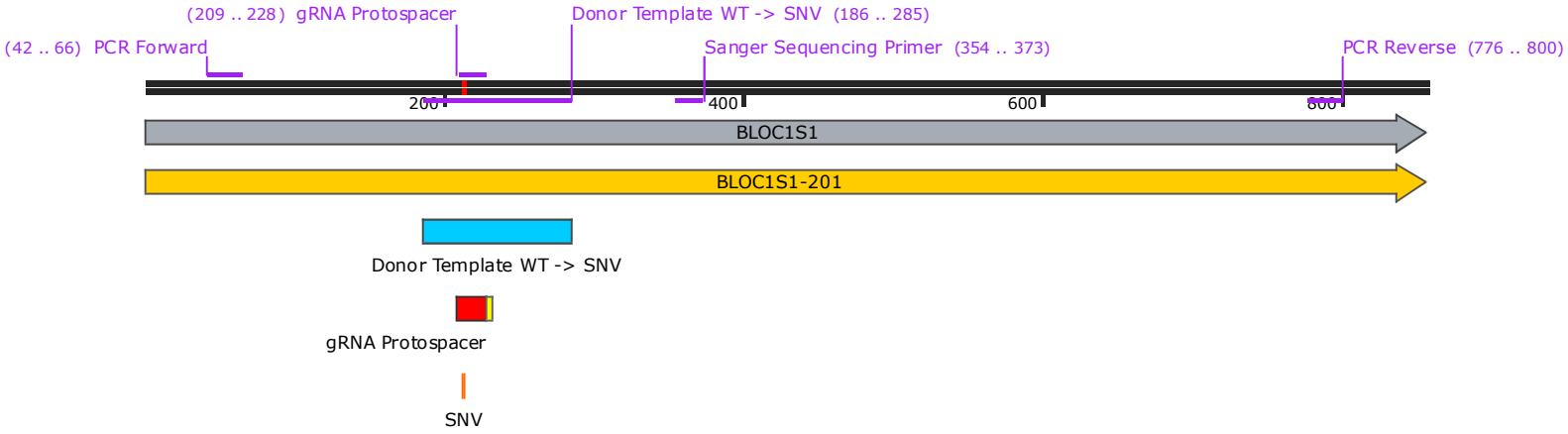
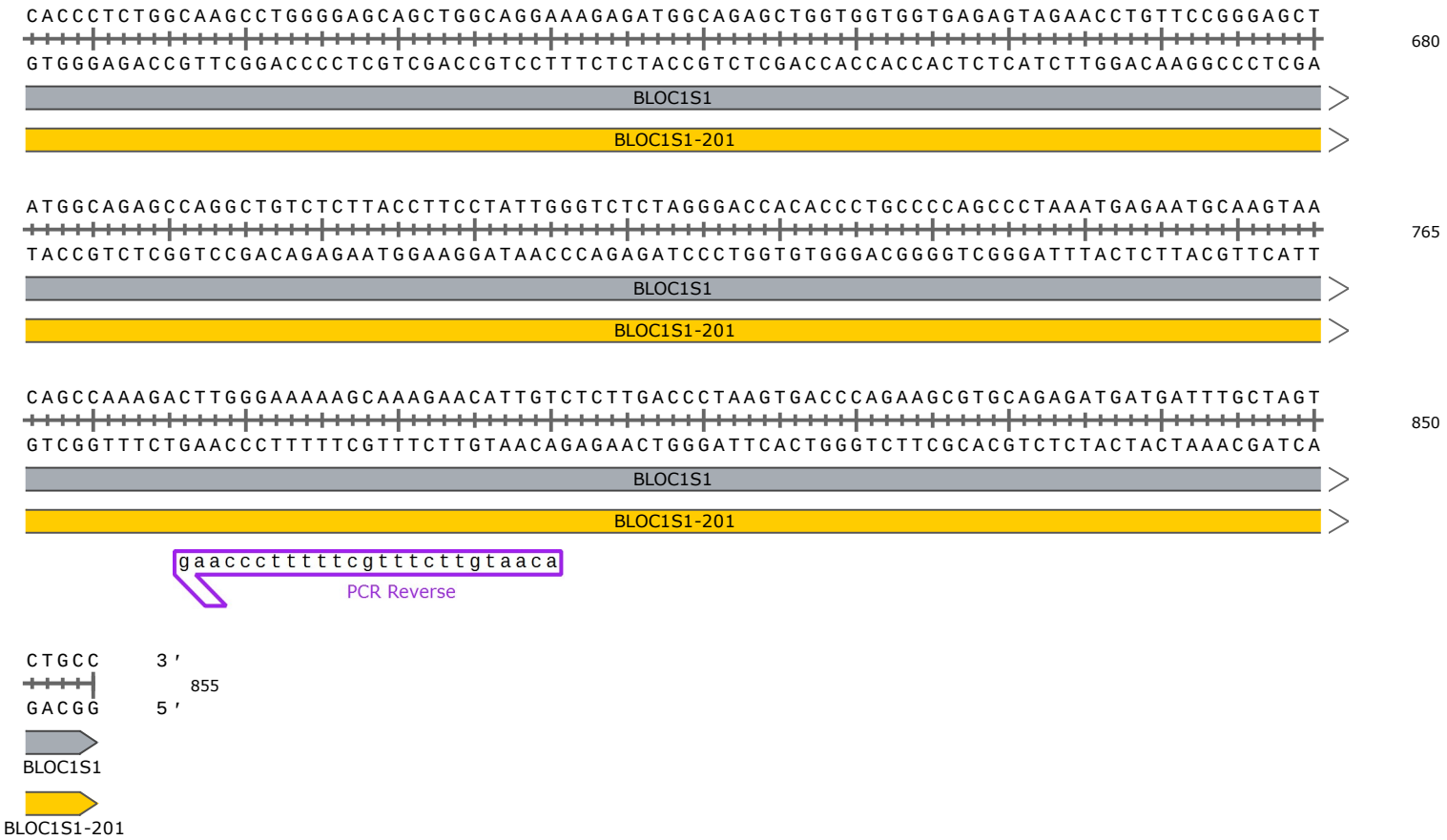


CZK2J00185_BLOC1S1_H69P_F01.2_AB

855 bp


PCR Forward
gttaagaaatttcggcaactagcag
5'
TGTTTTGCAAGGTCCTTTTCAGCTCCGGCATTCAGAGATTAGTTAAGAAATTTCGGCAACTAGCAGAATAGTAATGGATGGGTAG
3'
ACAAAACGTTCCAGGAAAAGTCGAGGCCGTAAGTCTCTAATCAATTCTTTAAAGCCGTTGATCGTCTTATCATTACCTACCCATC
85
BLOC1S1
BLOC1S1-201
GGAACCTTTAACACTACCCCTCAAAAAACCAAGTCTCCCCTCCAATTCCTTTTCCCCCCTCTCCCCAGAAAAGAGGAGGCGAGAGG
CCTTGGAAATTGTGATGGGGAGTTTTTTGGTTCAGAGGGGAGGTTAAGGAAAAGGGGGAGAGGGGTCTTTTCTCCTCCGCTCTCC
170
BLOC1S1
BLOC1S1-201
gRNA Protospacer
GATCACCTCAATGTGGGgta
CTATCACTGCAGCGACCTGCCTGACAGAAGCTTTGGTGGATCACCTCAATGTGGGGTATGGACCTCTTATCAACATCAGTTTCCT
GATAGTGACGTCGCTGGACGGACTGTCTTCGAAACCACCTAGTGGAGTTACACCCCATACCTGGAGAATAGTTGTAGTCAAAGGA
255
BLOC1S1
BLOC1S1-201
Donor Template WT -> SNV
gRNA Protospacer
PAM
SNV
GGACGGACTGTCTTCGAAACCACCTAGGGGAGTTACACCCcatacctggagaatagttgtagtcaaagga
Donor Template WT -> SNV
CCTTCCCCACCCCGCCCAAGTTTAGGCACTGGCCAGTCTGGCCCTCAAATAGCTGTTGAAGGGGTGGGATGTTCCACTAATTCCC
GGAAGGGGTGGGGCGGGTTCAAATCCGTGACCGGTCAGACCGGGAGTTTATCGACAACTTCCCCACCCTACAAGGTGATTAAGGG
340
BLOC1S1
BLOC1S1-201
Donor Template WT -> SNV
ggaaggggtggggcgggttcaaatccgtga
Donor Template WT -> SNV
CTATCCTACCCCGCCCCTCCCAGCTCTTTGTAGAGCAACTTGAGTCAACTCTGAGTCCTAGCACTGGGCAAGGGAGGAACAGCTG
GATAGGATGGGGCGGGGAGGGTCGAGAAACATCTCGTTGAACTCAGTTGAGACTCAGGATCGTGACCCGTTCCCTCCTTGTCGAC
425
BLOC1S1
BLOC1S1-201
ggggagggtcgagaaacatc
Sanger Sequencing Primer
CCGTGGTTAGAGAAGCAGCCAGATTTCCCCTTCCCCACGTTAACTTCCCTGGCATTTACAACTTGATGCCATCTGCCCACCTCCC
GGCACCAATCTCTTCGTCGGTCTAAAGGGGAAGGGGTGCAATTGAAGGGACCGTAAATGTTGAACTACGGTAGACGGGTGGAGGG
510
BLOC1S1
BLOC1S1-201
TTCACCCTTCCAAGTCCAGCTGTCACTTCAGCAGGAGGGAGAGCACCCTCCTTCATTACAGCTTACCACCCTCTCCTCTGCCTCC
AAGTGGGAAGGTTCAGGTCGACAGTGAAGTCGTCCTCCCTCTCGTGGGAGGAAGTAATGTCGAATGGTGGGAGAGGAGACGGAGG
595
BLOC1S1
BLOC1S1-201


CACCCTCTGGCAAGCCTGGGGAGCAGCTGGCAGGAAAGAGATGGCAGAGCTGGTGGTGGTGAGAGTAGAACCTGTTCCGGGAGCT
680
GTGGGAGACCGTTCGGACCCCTCGTCGACCGTCCTTTCTCTACCGTCTCGACCACCACCACTCTCATCTTGGACAAGGCCCTCGA
BLOC1S1
BLOC1S1-201
ATGGCAGAGCCAGGCTGTCTCTTACCTTCCTATTGGGTCTCTAGGGACCACACCCTGCCCCAGCCCTAAATGAGAATGCAAGTAA
765
TACCGTCTCGGTCCGACAGAGAATGGAAGGATAACCCAGAGATCCCTGGTGTGGGACGGGGTCGGGATTTACTCTTACGTTCATT
BLOC1S1
BLOC1S1-201
CAGCCAAAGACTTGGGAAAAAGCAAAGAACATTGTCTCTTGACCCTAAGTGACCCAGAAGCGTGCAGAGATGATGATTTGCTAGT
850
GTCGGTTTCTGAACCCTTTTTCGTTTCTTGTAACAGAGAACTGGGATTCACTGGGTCTTCGCACGTCTCTACTACTAAACGATCA
BLOC1S1
BLOC1S1-201
gaaccctttttcgtttcttgtaaca
PCR Reverse
CTGCC 3'
855
GACGG 5'
BLOC1S1
BLOC1S1-201

	Feature			Location	Size			Type
				1 ..5471	5471 bp		→	gene
	/note	=	gene ENSG00000258311 Protein coding					
				1 ..5471	5471 bp		→	prim_transcript
	/note	=	primary transcript ENST00000550412 Protein coding					
				1 ..5459	5459 bp		→	prim_transcript
	/note	=	primary transcript ENST00000257899 Nonsense mediated decay					
				1 ..3186	3186 bp		→	prim_transcript
	/note	=	primary transcript ENST00000551946 Nonsense mediated decay					
				1 ..2562	2562 bp		→	prim_transcript
	/note	=	primary transcript ENST00000549424 Protein coding					
✓	**BLOC1S1**			1 .. 855	855 bp		→	gene
	/note	=	gene ENSG00000135441 Protein coding					
✓	**BLOC1S1-201**			1 .. 855	855 bp		→	prim_transcript
	/note	=	primary transcript ENST00000547076					
	BLOC1S1-202			1 .. 855	855 bp		→	prim_transcript
	/note	=	primary transcript ENST00000548556					
	BLOC1S1-203			1 .. 855	855 bp		→	prim_transcript
	/note	=	primary transcript ENST00000548925					
	BLOC1S1-204			1 .. 855	855 bp		→	prim_transcript
	/note	=	primary transcript ENST00000549147					
	BLOC1S1-205			1 .. 855	855 bp		→	prim_transcript
	/note	=	primary transcript ENST00000551926					
	BLOC1S1-206			1 .. 855	855 bp		→	prim_transcript
	/note	=	primary transcript ENST00000553100 Nonsense mediated decay					
	BLOC1S1-203			153 .. 225	73 bp		→	CDS
	/codon_start	=	1					
	/note	=	coding sequence ENSP00000447537					
	/translation	=	KRRREAITAATCLTEALVDHLNV 24 amino acids = 2.6 kDa					
	BLOC1S1-204			153 .. 225	73 bp		→	CDS
	/codon_start	=	1					
	/note	=	coding sequence ENSP00000450328					
	/translation	=	KRRREAITAATCLTEALVDHLNV 24 amino acids = 2.6 kDa					
✓	**Donor Template WT -> SNV**			186 .. 285	100 bp		⊢	misc_feature
✓	**gRNA Protospacer**			209 .. 228	20 bp		⊢	misc_feature
✓	**SNV**			213 .. 213	1 bp		⊢	misc_feature
	/note	=	WT = A SNV = C					
✓	**PAM**			229 .. 231	3 bp		⊢	misc_feature
	ITGA7-215			15,083 ..4,968,953,924 bp			←	prim_transcript
	/note	=	primary transcript ENST00000556273 Nonsense mediated decay					
	ITGA7-221			28,257 ..4,968,940,750 bp			←	prim_transcript
	/note	=	primary transcript ENST00000686981 Nonsense mediated decay					
	ITGA7			28,274 ..4,968,940,733 bp			←	gene
	/note	=	gene ENSG00000135424 Protein coding					

	Primer	Length	Binding Sites		Tm	Date Added
✓	**PCR Forward**	25-mer	42 .. 66	→	56°C	Nov 6, 2023

/sequence = gttaagaaatttcggcaactagcag
40% GC / 7714.1 Da

✓	**Donor Template WT -> SNV**	100-mer	186 .. 285	←	79°C	Nov 6, 2023

/sequence = agtgcctaaacttgggcggggtggggaaggaggaaactgatgttgataagaggtccatacCCCACATTGAGGGGATCCACCAAAGCTTCTGTCAGGCAGG
54% GC / 31,151.3 Da

✓	**gRNA Protospacer**	20-mer	209 .. 228	→	55°C	Nov 6, 2023

/sequence = GATCACCTCAATGTGGGgta
50% GC / 6157.1 Da

✓	**Sanger Sequencing Primer**	20-mer	354 .. 373	←	59°C	Nov 6, 2023

/sequence = ctacaaagagctgggagggg
60% GC / 6256.1 Da

✓	**PCR Reverse**	25-mer	776 .. 800	←	58°C	Nov 6, 2023

/sequence = acaatgttctttgctttttcccaag
36% GC / 7573.0 Da