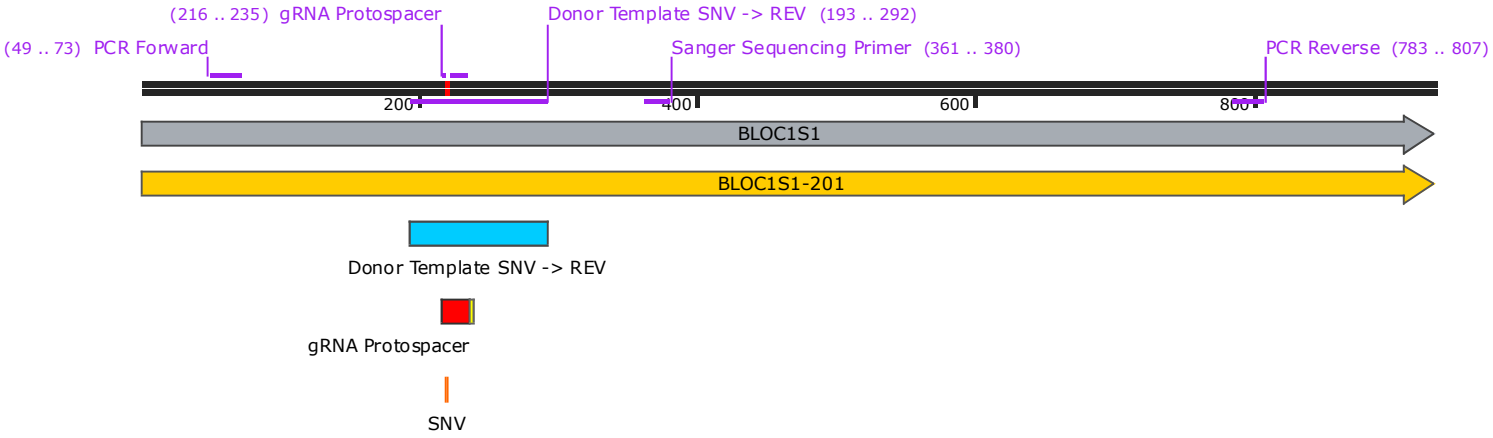
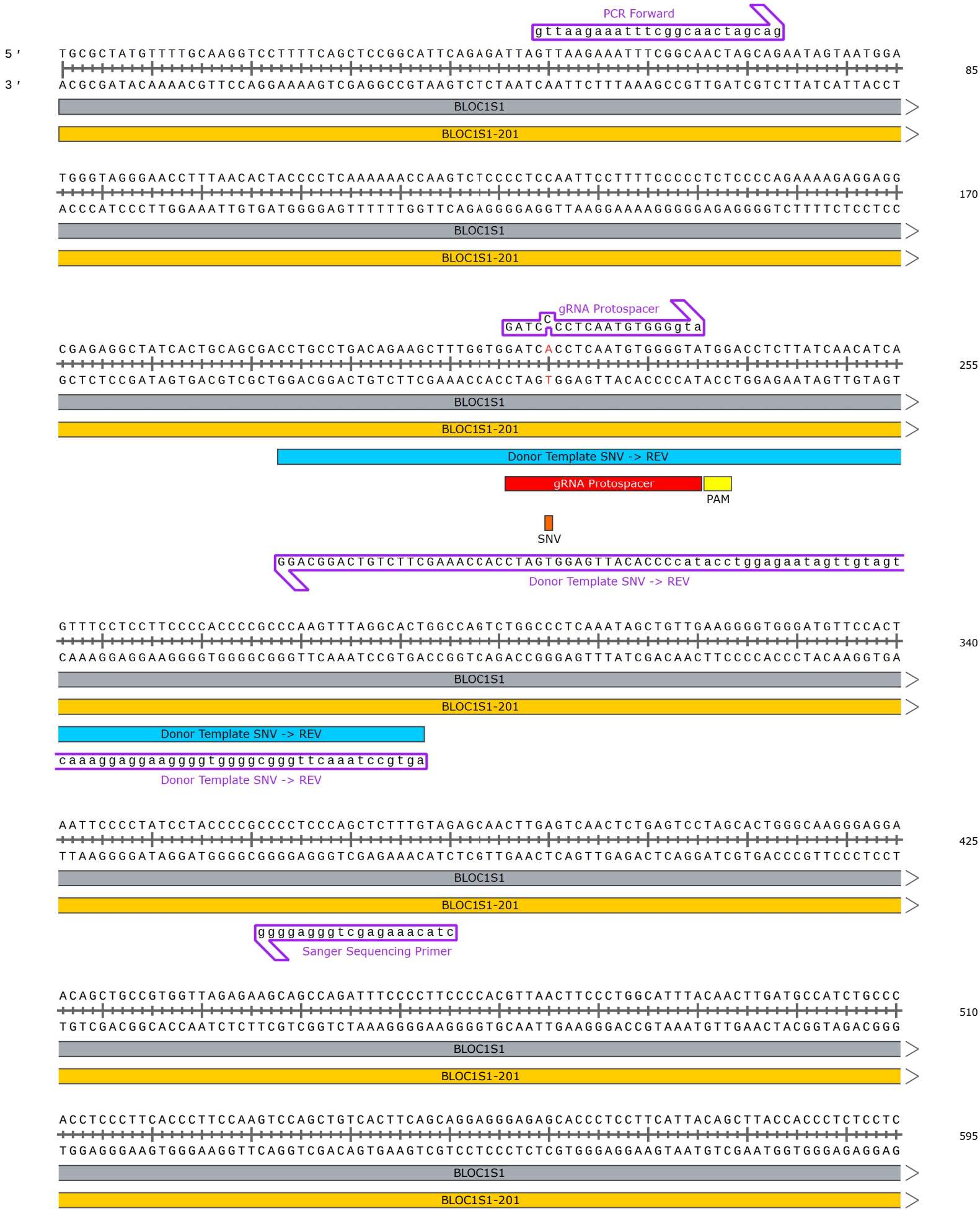


CZK2J00185R_BLOC1S1_H69P_F09_AA

928 bp


PCR Forward
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5'
TGCGCTATGTTTTGCAAGGTCCTTTTCAGCTCCGGCATTCAGAGATTAGTTAAGAAATTTCGGCAACTAGCAGAATAGTAATGGA
3'
ACGCGATACAAAACGTTCCAGGAAAAGTCGAGGCCGTAAGTCTCTAATCAATTCTTTAAAGCCGTTGATCGTCTTATCATTACCT
85
BLOC1S1
BLOC1S1-201
TGGGTAGGGAACCTTTAACACTACCCCTCAAAAAACCAAGTCTCCCCTCCAATTCCTTTTCCCCCTCTCCCCAGAAAAGAGGAGG
ACCCATCCCTTGGAAATTGTGATGGGGAGTTTTTTGGTTCAGAGGGGAGGTTAAGGAAAAGGGGGAGAGGGGTCTTTTCTCCTCC
170
BLOC1S1
BLOC1S1-201
gRNA Protospacer
GATCCCCTCAATGTGGGgta
CGAGAGGCTATCACTGCAGCGACCTGCCTGACAGAAGCTTTGGTGGATCACCTCAATGTGGGGTATGGACCTCTTATCAACATCA
GCTCTCCGATAGTGACGTCGCTGGACGGACTGTCTTCGAAACCACCTAGTGGAGTTACACCCCATACCTGGAGAATAGTTGTAGT
255
BLOC1S1
BLOC1S1-201
Donor Template SNV -> REV
gRNA Protospacer
PAM
SNV
GGACGGACTGTCTTCGAAACCACCTAGTGGAGTTACACCCcatacctggagaatagttgtagt
Donor Template SNV -> REV
GTTTCCTCCTTCCCCACCCCGCCCAAGTTTAGGCACTGGCCAGTCTGGCCCTCAAATAGCTGTTGAAGGGGTGGGATGTTCCACT
CAAAGGAGGAAGGGGTGGGGCGGGTTCAAATCCGTGACCGGTCAGACCGGGAGTTTATCGACAACTTCCCCACCCTACAAGGTGA
340
BLOC1S1
BLOC1S1-201
Donor Template SNV -> REV
caaaggaggaaggggtggggcgggttcaaatccgtga
Donor Template SNV -> REV
AATTCCCCTATCCTACCCCGCCCCTCCCAGCTCTTTGTAGAGCAACTTGAGTCAACTCTGAGTCCTAGCACTGGGCAAGGGAGGA
TTAAGGGGATAGGATGGGGCGGGGAGGGTCGAGAAACATCTCGTTGAACTCAGTTGAGACTCAGGATCGTGACCCGTTCCCTCCT
425
BLOC1S1
BLOC1S1-201
ggggagggtcgagaaacatc
Sanger Sequencing Primer
ACAGCTGCCGTGGTTAGAGAAGCAGCCAGATTTCCCCTTCCCCACGTTAACTTCCCTGGCATTTACAACTTGATGCCATCTGCCC
TGTCGACGGCACCAATCTCTTCGTCGGTCTAAAGGGGAAGGGGTGCAATTGAAGGGACCGTAAATGTTGAACTACGGTAGACGGG
510
BLOC1S1
BLOC1S1-201
ACCTCCCTTCACCCTTCCAAGTCCAGCTGTCACTTCAGCAGGAGGGAGAGCACCCTCCTTCATTACAGCTTACCACCCTCTCCTC
TGGAGGGAAGTGGGAAGGTTCAGGTCGACAGTGAAGTCGTCCTCCCTCTCGTGGGAGGAAGTAATGTCGAATGGTGGGAGAGGAG
595
BLOC1S1
BLOC1S1-201


TGCCTCCCACCCTCTGGCAAGCCTGGGGAGCAGCTGGCAGGAAAGAGATGGCAGAGCTGGTGGTGGTGAGAGTAGAACCTGTTCC
680
ACGGAGGGTGGGAGACCGTTCGGACCCCTCGTCGACCGTCCTTTCTCTACCGTCTCGACCACCACCACTCTCATCTTGGACAAGG
BLOC1S1
BLOC1S1-201
GGGAGCTATGGCAGAGCCAGGCTGTCTCTTACCTTCCTATTGGGTCTCTAGGGACCACACCCTGCCCCAGCCCTAAATGAGAATG
765
CCCTCGATACCGTCTCGGTCCGACAGAGAATGGAAGGATAACCCAGAGATCCCTGGTGTGGGACGGGGTCGGGATTTACTCTTAC
BLOC1S1
BLOC1S1-201
CAAGTAACAGCCAAAGACTTGGGAAAAAGCAAAGAACATTGTCTCTTGACCCTAAGTGACCCAGAAGCGTGCAGAGATGATGATT
850
GTTCATTGTCGGTTTCTGAACCCTTTTTCGTTTCTTGTAACAGAGAACTGGGATTCACTGGGTCTTCGCACGTCTCTACTACTAA
BLOC1S1
BLOC1S1-201
gaacccttttcgtttcttgtaaca
PCR Reverse
TGCTAGTCTGCCTATTGGAAGAAAGGCAGTATGGTACCTTCCACCCCAGGTCAAGTAGAACAGCTCGGTGTGAATCCA
3′
928
ACGATCAGACGGATAACCTTCTTTCCGTCATACCATGGAAGGTGGGGTCCAGTTCATCTTGTCGAGCCACACTTAGGT
5′
BLOC1S1
BLOC1S1-201

	Feature			Location	Size			Type
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	/note	=	gene ENSG00000258311 Protein coding					
				1 ..5544	5544 bp		→	prim_transcript
	/note	=	primary transcript ENST00000550412 Protein coding					
				1 ..5532	5532 bp		→	prim_transcript
	/note	=	primary transcript ENST00000257899 Nonsense mediated decay					
				1 ..3259	3259 bp		→	prim_transcript
	/note	=	primary transcript ENST00000551946 Nonsense mediated decay					
				1 ..2635	2635 bp		→	prim_transcript
	/note	=	primary transcript ENST00000549424 Protein coding					
✓	**BLOC1S1**			1 .. 928	928 bp		→	gene
	/note	=	gene ENSG00000135441 Protein coding					
✓	**BLOC1S1-201**			1 .. 928	928 bp		→	prim_transcript
	/note	=	primary transcript ENST00000547076					
	BLOC1S1-202			1 .. 928	928 bp		→	prim_transcript
	/note	=	primary transcript ENST00000548556					
	BLOC1S1-203			1 .. 928	928 bp		→	prim_transcript
	/note	=	primary transcript ENST00000548925					
	BLOC1S1-204			1 .. 928	928 bp		→	prim_transcript
	/note	=	primary transcript ENST00000549147					
	BLOC1S1-205			1 .. 928	928 bp		→	prim_transcript
	/note	=	primary transcript ENST00000551926					
	BLOC1S1-206			1 .. 928	928 bp		→	prim_transcript
	/note	=	primary transcript ENST00000553100 Nonsense mediated decay					
	BLOC1S1-203			160 .. 232	73 bp		→	CDS
	/codon_start	=	1					
	/note	=	coding sequence ENSP00000447537					
	/translation	=	KRRREAITAATCLTEALVDHLNV 24 amino acids = 2.6 kDa					
	BLOC1S1-204			160 .. 232	73 bp		→	CDS
	/codon_start	=	1					
	/note	=	coding sequence ENSP00000450328					
	/translation	=	KRRREAITAATCLTEALVDHLNV 24 amino acids = 2.6 kDa					
✓	**Donor Template SNV -> REV**			193 .. 292	100 bp		⊢	misc_feature
✓	**gRNA Protospacer**			216 .. 235	20 bp		⊢	misc_feature
✓	**SNV**			220 .. 220	1 bp		⊢	misc_feature
	/note	=	SNV = C REV = A					
✓	**PAM**			236 .. 238	3 bp		⊢	misc_feature
	ITGA7-215			15,156 ..4,953,997 bp			←	prim_transcript
	/note	=	primary transcript ENST00000556273 Nonsense mediated decay					
	ITGA7-221			28,330 ..4,940,823 bp			←	prim_transcript
	/note	=	primary transcript ENST00000686981 Nonsense mediated decay					
	ITGA7			28,347 ..4,940,806 bp			←	gene
	/note	=	gene ENSG00000135424 Protein coding					

	Primer	Length	Binding Sites		Tm	Date Added
✓	**PCR Forward**	25-mer	49 .. 73	→	56°C	Nov 6, 2023

/sequence = gttaagaaatttcggcaactagcag
40% GC / 7714.1 Da

✓	**Donor Template SNV -> REV**	100-mer	193 .. 292	←	79°C	Nov 6, 2023

/sequence = agtgcctaaacttgggcggggtggggaaggaggaaactgatgttgataagaggtccatacCCCACATTGAGGTGATCCACCAAAGCTTCTGTCAGGCAGG
53% GC / 31,126.2 Da

✓	**gRNA Protospacer**	20-mer	216 .. 235	→	47°C	Nov 6, 2023

/sequence = GATCCCCTCAATGTGGGgta
55% GC / 6133.0 Da

✓	**Sanger Sequencing Primer**	20-mer	361 .. 380	←	59°C	Nov 6, 2023

/sequence = ctacaaagagctgggagggg
60% GC / 6256.1 Da

✓	**PCR Reverse**	25-mer	783 .. 807	←	58°C	Nov 6, 2023

/sequence = acaatgttctttgctttttcccaag
36% GC / 7573.0 Da