



JIPSC1030_SnappeneDNA_INK2100074R_SNCB_P123H_REVWT
10,475 bp

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1755

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1890

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2025

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2160

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2295

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2430

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2700

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2835

SNCB

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3105

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T G C A A A A G A G A G G C A G G T T C A G C C T G T C A G C C C A G G C T G T G A T G G G T G T T T G C A C A G A A C A T T T C T C T G T G T C A C C T T T C T C C T A C T G G T G C T T G T T G A C G C C T C A A G G C T A C C C T C C C A A G G G A G C C C A A G A C G T T T T C T C C G T C C A A G T C G G A C A G T C G G G G T C C G A C A C T A C C C A A A C G T G T C T T G G T A A A G A G A G A C C A G T G G A A A G A G G A T G A C C A C A A A C T G C G G A G T T C C G A T G G G A G G T T C C C T C G G G T T C

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T T C T G A C T T T T T T T T A G A C G G A G T C T C G C C T G T T G C C A G G C T G G A G T G C A G T G C C A C A A T C T A G C T C A C T G A A A C C T T C A C C T C C T G G G T T C A A G C A A T G C T T T G C C T A G C C T C C T G A G T A A C T G A G A C A A G A C T G A A A A A A A A T C T G C C T C A G A G C G G A C A A C G G G T C C G A C C T C A C G T C A C G G T T A G A G T C G A G T G A C T T T G G A A G T G G A G A C C A A G T T C G T T A C G A G A A C G G A G T C G G A G G A C T A T T G A C T C T G

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7830

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7965

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8100

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8235

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8370

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8505

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8775

PCR Forward
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8910

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9045

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PCR Forward
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9180

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Sanger Sequencing Primer
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9315

SNCB

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95 100 105 110 115
P E E V A Q E A A E E P L I E P L M E P E
ENSE00003602811

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Donor Template SNV -> REV

CGGTCT

Donor Template SNV -> REV

gRNA Protospacer
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9450

SNCB

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120
G E S Y E D P P Q
ENSE00003602811

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Donor Template SNV -> REV

Protospacer Sequence PAM

SNV

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Donor Template SNV -> REV

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9585

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SNCB-202

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9720

SNCB

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125
E E
ENSE0000...

SNCB-202

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9855

SNCB

SNCB-202

130 135
Y Q E Y E P E A
ENSE00001196517

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9990

SNCB

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10,125

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10,260

SNCB

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SNCB-202

CACGTGGCGGGGAGTCTTCCAGGTCCAGCCTACCCCTCTGTGCTCTTTGGGGTCTGGCACACACAGCCAGGTACAAGA
GTGCACCGCCGCTCAGAAAGTCCAGGGTCGGATGGGGAGACACGAGAAACCCAGACCGTGTGTGTCGGGTCCATGTTCT

3'
10,475
5'

SNCB

SNCB-202

Feature	Location	Size	Color	Symbol	Type
SNCB	1 .. 10,475	10,475 bp	■	→	gene
/note	= gene ENSG00000074317 Protein coding				
SNCB-206	1 .. 10,347	10,347 bp	■	→	prim_transcript
/note	= primary transcript ENST00000614675				
SNCB-202	23 .. 10,475	10,453 bp	■	→	prim_transcript
/note	= primary transcript ENST00000393693				
SNCB-201	193 .. 10,473	10,281 bp	■	→	prim_transcript
/note	= primary transcript ENST00000310112				
SNCB-204	509 .. 9343	8835 bp	■	→	prim_transcript
/note	= primary transcript ENST00000508006 Retained intron				
SNCB-203	557 .. 9772	9216 bp	■	→	prim_transcript
/note	= primary transcript ENST00000506696				
SNCB-205	563 .. 9876	9314 bp	■	→	prim_transcript
/note	= primary transcript ENST00000510387				
SNCB-201	903 .. 9746	8844 bp	■	→	CDS
▶ 5 segments = 405 bp					
/note	= coding sequence ENSP00000308057				
/translation	= MDVFMKGLSMAKEGVVAAAEKTKQGVTEAAEKTKEGVLYV,,GSKTREGVVQGVAS,,VAEKTKEQASHLGGAVFSGAGNIAAATGLVKREEFPTDLK,,PEEVAQEAAEEPLIEPLMEPEGESYEDPPQ,,EEYQEYEP EA *				
134 amino acids = 14.3 kDa					
SNCB-202	903 .. 9746	8844 bp	■	→	CDS
▶ 5 segments = 405 bp					
/note	= coding sequence ENSP00000377296				
/translation	= MDVFMKGLSMAKEGVVAAAEKTKQGVTEAAEKTKEGVLYV,,GSKTREGVVQGVAS,,VAEKTKEQASHLGGAVFSGAGNIAAATGLVKREEFPTDLK,,PEEVAQEAAEEPLIEPLMEPEGESYEDPPQ,,EEYQEYEP EA *				
134 amino acids = 14.3 kDa					
SNCB-203	903 .. 9746	8844 bp	■	→	CDS
▶ 5 segments = 405 bp					
/note	= coding sequence ENSP00000422223				
/translation	= MDVFMKGLSMAKEGVVAAAEKTKQGVTEAAEKTKEGVLYV,,GSKTREGVVQGVAS,,VAEKTKEQASHLGGAVFSGAGNIAAATGLVKREEFPTDLK,,PEEVAQEAAEEPLIEPLMEPEGESYEDPPQ,,EEYQEYEP EA *				
134 amino acids = 14.3 kDa					
SNCB-205	903 .. 9746	8844 bp	■	→	CDS
▶ 5 segments = 405 bp					
/note	= coding sequence ENSP00000424073				
/translation	= MDVFMKGLSMAKEGVVAAAEKTKQGVTEAAEKTKEGVLYV,,GSKTREGVVQGVAS,,VAEKTKEQASHLGGAVFSGAGNIAAATGLVKREEFPTDLK,,PEEVAQEAAEEPLIEPLMEPEGESYEDPPQ,,EEYQEYEP EA *				
134 amino acids = 14.3 kDa					
SNCB-206	903 .. 9746	8844 bp	■	→	CDS
▶ 4 segments = 363 bp					
/note	= coding sequence ENSP00000479489				
/translation	= MDVFMKGLSMAKEGVVAAAEKTKQGVTEAAEKTKEGVLYV,,VAEKTKEQASHLGGAVFSGAGNIAAATGLVKREEFPTDLK,,PEEVAQEAAEEPLIEPLMEPEGESYEDPPQ,,EEYQEYEP EA *				
120 amino acids = 12.9 kDa					
MIR4281	1057 .. 1118	62 bp	■	→	gene
/note	= gene ENSG00000266329 miRNA				
MIR4281-201	1057 .. 1118	62 bp	■	→	prim_transcript
/note	= primary transcript ENST00000580852 miRNA				
Donor Template SNV -> REV	9310 .. 9409	100 bp	■	⇌	misc_feature
Protospacer Sequence	9328 .. 9347	20 bp	■	⇌	misc_feature
SNV	9339 .. 9339	1 bp	■	⇌	misc_feature
/note	= REV = C SNV = A				
PAM	9348 .. 9350	3 bp	■	⇌	misc_feature

Primer	Length	Binding Sites	Tm	Date Added
✓ PCR Forward	25-mer	8760 .. 8784 →	56°C	Jun 14, 2022
/sequence = TAAAATAGCAACAGCTGAAGAAACG 36% GC / 7725.1 Da				
✓ Sanger Sequencing Primer	20-mer	9228 .. 9247 →	57°C	Jun 14, 2022
/sequence = CGAGTCCTGACCTTTTCTGC 55% GC / 6035.0 Da				
✓ Donor Template SNV -> REV	100-mer	9310 .. 9409 ←	83°C	Jun 14, 2022
/sequence = CCAGCTAGGGACGGCAGCAATCATCCTGGATTCCCAAAGTCCCGCCAGCCCTGCTGCCCTCACCTGGGGTGGGTCTCATAACTCTCCCCTTCTGGC 64% GC / 30,461.6 Da				
✓ gRNA Protospacer	20-mer	9328 .. 9347 →	57°C	Jun 14, 2022
/sequence = TGAGGACCCACACCAGGTGA 60% GC / 6136.0 Da				
✓ PCR Reverse	25-mer	9883 .. 9907 ←	58°C	Jun 14, 2022
/sequence = GACAGATGGACAGACACTAACACAG 48% GC / 7702.1 Da				