



**JIPSC1020\_SnappeneDNA\_INK2J00041\_ANG\_K41I\_SNVSNV**  
14,795 bp

Start (0)

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135

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675

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810

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1215

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1485

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1620

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1755

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2700

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ANG-202 >

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ANG-202

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ANG-202

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ANG-202

PCR Forward  
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ANG

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ANG





Feature	Location	Size	Color	Strand	Type	
<b>ANG</b>	1 .. 14,795	14,795 bp	■	→	gene	
/note	= gene <a href="#">ENSG00000214274</a> Protein coding					
<b>ANG-201</b>	1 .. 10,010	10,010 bp	■	→	prim_transcript	
/note	= primary transcript <a href="#">ENST00000336811</a>					
<b>RNASE4</b>	384 .. 17,040	16,657 bp	■	→	gene	
/note	= gene <a href="#">ENSG00000258818</a> Protein coding					
<b>RNASE4-203</b>	384 .. 17,040	16,657 bp	■	→	prim_transcript	
/note	= primary transcript <a href="#">ENST00000555835</a> Protein coding					
<b>RNASE4-201</b>	407 .. 15,917	15,511 bp	■	→	prim_transcript	
/note	= primary transcript <a href="#">ENST00000397995</a> Protein coding					
/note	= gene <a href="#">ENSG00000259171</a> Protein coding	411 .. 16,400	15,990 bp	■	→	gene
/note	= primary transcript <a href="#">ENST00000553909</a> Protein coding	411 .. 16,400	15,990 bp	■	→	prim_transcript
<b>ANG-203</b>	438 .. 14,795	14,358 bp	■	→	prim_transcript	
/note	= primary transcript <a href="#">ENST00000554073</a>					
<b>ANG-202</b>	4588 .. 10,007	5420 bp	■	→	prim_transcript	
/note	= primary transcript <a href="#">ENST00000397990</a>					
<b>RNASE4-202</b>	4606 .. 16,426	11,821 bp	■	→	prim_transcript	
/note	= primary transcript <a href="#">ENST00000555597</a> Protein coding					
<b>EGILA</b>	9304 .. 22,944	13,641 bp	■	←	gene	
/note	= gene <a href="#">ENSG00000258451</a> lncRNA					
<b>EGILA-201</b>	9304 .. 22,944	13,641 bp	■	←	prim_transcript	
/note	= primary transcript <a href="#">ENST00000554286</a> lncRNA					
<b>ANG-201</b>	9389 .. 9832	444 bp	■	→	CDS	
/note	= coding sequence <a href="#">ENSP00000336762</a>					
/translation	= MVMGLGVLLLVFVLGLGLTPPTLAQDNSRYTHFLTQHYDAKPQGRDDRYCESIMRRRGLTSPCKDINTFIHGNKRSIKAICENKGNPHRENLRISKSSFQVTTCKLHGGSPWPPCQYRATAGFRNVVACENGLPVHLDQSFRRP* 147 amino acids = 16.6 kDa					
<b>ANG-202</b>	9389 .. 9832	444 bp	■	→	CDS	
/note	= coding sequence <a href="#">ENSP00000381077</a>					
/translation	= MVMGLGVLLLVFVLGLGLTPPTLAQDNSRYTHFLTQHYDAKPQGRDDRYCESIMRRRGLTSPCKDINTFIHGNKRSIKAICENKGNPHRENLRISKSSFQVTTCKLHGGSPWPPCQYRATAGFRNVVACENGLPVHLDQSFRRP* 147 amino acids = 16.6 kDa					
<b>Donor Template WT-&gt;SNV</b>	9478 .. 9577	100 bp	■	⇌	misc_feature	
<b>Protospacer Sequence</b>	9496 .. 9515	20 bp	■	⇌	misc_feature	
<b>SNV</b>	9510 .. 9510	1 bp	■	⇌	misc_feature	
/note	= WT = A SNV = T					
<b>PAM</b>	9516 .. 9518	3 bp	■	⇌	misc_feature	

Primer		Length		Binding Sites		Tm	Date Added
✓ <b>PCR Forward</b>		25-mer		9125 .. 9149	→	62°C	May 12, 2022
/sequence	= GATTCTAAGGGATGGGAAGAACGG 52% GC / 7860.2 Da						
✓ <b>Sanger Sequencing Primer</b>		20-mer		9369 .. 9388	→	58°C	May 12, 2022
/sequence	= AGGAGCCTGTGTGGAAGAG 55% GC / 6262.1 Da						
✓ <b>Donor Template WT-&gt; SNV</b>		100-mer		9478 .. 9577	←	80°C	May 12, 2022
/sequence	= GCAGGGTGAGGTCAGGCCCTCTCCTCATGATGCTTTCACAGTATCTGTCATCCCGCCCTGTGGTATGGCATCATAGTGCTGGGTCAGGAAGTGTGTG 57% GC / 30,927.0 Da						
✓ <b>gRNA Protospacer</b>		20-mer		9496 .. 9515	→	56°C	May 12, 2022
/sequence	= GCACTATGATGCCAAACCAC 50% GC / 6055.0 Da						
✓ <b>PCR Reverse</b>		25-mer		10,016 .. 10,040	←	58°C	May 12, 2022
/sequence	= ATATGCCCAAGATCAGTGAGAAGAC 44% GC / 7708.1 Da						