

JIPSC1024_SnappeneDNA_INK2J00041R_ANG_K41I_REVWT
14,795 bp

Start (0)
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270
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405
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540
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4590

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ANG-202

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4725

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ANG-202

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4995

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ANG-202

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ANG-202

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ANG-202

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ANG-202

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ANG-202

5670
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ANG-202

6075
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ANG-202

6210
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6345
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ANG-202

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ANG-202

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ANG-202

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ANG
ANG-202

GCCTATTGTGAAGTGCAGATGTGCGGGATCCAGATTGTGCACCTTTATGAGAATCTAACTAATGCTTGTGATGATCTATCTGAACAGAAACAATTTATCTGAAACCATCCCCACCAATCCATAGAAATACTGT
CGGATAACACTTGACGCGTACACGCCCTAGGTCTAACACGTGAGAAATACTCTTAGATTGATTACGAACACTAGATAGACTTGGTCTTGTAAAGTAGGACTTTGGTAGGGGGTGGTTAGGTATCTTTATGACA
ANG
ANG-202

CTTCCAAAAATGATCCCTGGTGCCAAAAATGTTAGAGACCCTCCCTAAAACTCTTCTTAGCTCTCACCTCCTGATTACTATCTCATCTCAGTACATTGAAGCCCCATCTTTTCCCATGGATGCCTC
GAAGGTGTTTTACTAGGGACCACGGTTTTTACAATCTCTGGTGGGGGATTTTGGAGAGAAGAAATCGAGAGTGGAGGACATAATGATAGAGTAGAGTATGTAACCTCGGGGGTAGAAAAGGGGTACCTACGGAG
ANG
ANG-202

ATTTCTATTAGGGAGGCATTTTTTATTTTTTGTTTTTTATTTTTTCCGAGACGGAGTCTCGCTGTGTCGCAAGGCTGGAAGTGCAGTGGCGGATCTCGGCTACTGCAAGCTCCGCTCCCGGGTTCACGGC
TAAAGGATAATCCCTCCGTAAAAAATAAAAAACAAAAATAAAAAAAGGCTCTGCCTCAGAGCGGACAGCGGTTCCGACCTCACGTCACCGGCTAGAGCCGAGTGACGTTGAGGCGGAGGGCCCAAGTCCGG
ANG
ANG-202

ATTCTCTGCTCAGCCTCCCGAGTAGCTGGACTACAGGCGCCCGCCACTACGCCGGCTAATTTTTTGTATTTTTTAGTAGAGACGGGGTTTACCCTGGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGA
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ANG
ANG-202

TCCGCCCGCCTTGGCTCCCAAGTGTG66ATTACAGCGTGAAGCCACCGCGCCGGCGGTCATTTGGTATGCTTAAATGTGCTCAGGACCTAGCACAGTCCCTGGTACCAGTAGAGACCTATGTAATGTTT
AGGCGGGCGGAAACGGAGGGTTTTACGACCCTAATGTCCGCACTCGGTGGCGGGCCGGCAGTAAACATACAGAATTAACAGGAGTCTGGATCGTGTGAGGACCATGGGTCTCTGGATACATTACAAG
ANG
ANG-202

ATTATCAATTAATAACATGAATTAAGAGTGAAGTGGATTTTGAATGTTACGACTGATAGAGAATACTCAGTGATTCTAAGGGATGGGGAAGAACGGTTGGAGCTAGAGGTTGTGCTCAGGAACTAT
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ANG
ANG-202

PCR Forward
GATTCTAAGGGATGGGGAAGAACGG

TAAATAGACGTTCCGCCAGGAAGGGATTGACGAAGTGTGAGGTTAATGAGGAAGGGAAAAATAGAATATAAAAATTTGGTGGTGGAAAAAGATCTGATTCATGATGCCGTGCAGAGACAAAGCTCCTGTCCTTTTGG
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9315

ANG

ANG-202

Sanger Sequencing Primer

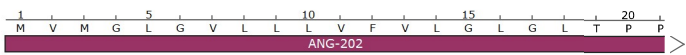
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9450

ANG

ANG-202



gRNA Protospacer

GCACTATGATGCCAACCAC

GACCTGGCTCAGGATAACTCCAGGTACACACACTTCTGACCCAGCACTATGATGCCAACCACAGGGCCGGGATGACAGATACTGTGAAAGCATCATGAGGAGACGGGGCTGACCTCACCTGCAAAGACAT
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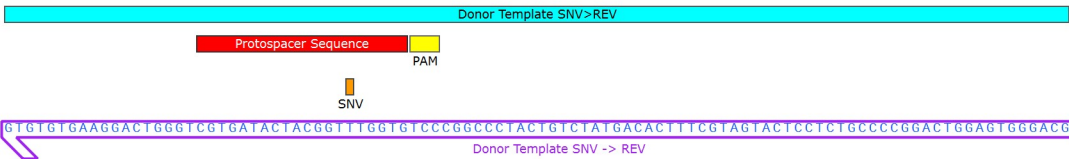
9585

ANG

ANG-202

T L A Q D N S R Y T H F L T Q H Y D A K P Q G R D D R Y C E S I M R R R G L T S P C K D I

ANG-202



CAACACATTTATTCATGGCAACAAGCCGAGCATCAAGGCCATCTGTGAAAAACAAGATGGAACCCCTCACAGAGAAAACTAAGAATAAGCAAGTCTTCTTCCAGGTCACCCTTGAAGCTACATGGAGTTCC
GTTGTGTAATAAGTACC6TTGTCGCGCTGATGTTCCGGTAGACACTTTTGTCTTACCTTTGGGAGTGTCTTTTGGATTCTTATTCGTTTCAAAGAAAGGTCAGGTTGTAACGTTTCATGTAACCTCCAAG

9720

ANG

ANG-202

N T F I H G N K R S I K A I C E N K N G N P H R E N L R I S K S S F Q V T T C K L H G G S

ANG-202

CCCCGGCCTCCATGCCAGTACCGAGCCACAGCGGGGTTCAAGAACGTTGTTGTTGCTTGTGAAAAATGGCTTACCTGTCCACTTGGATCAGTCAATTTCCGTCGTCGGTAACAGCGGGCCCTGGTCAAGTGC
GGGACCGGAGGTACGGTCATGGCTCGGTCGCCCCAAGTCTTTGCAACAACAACGAACTTTTACCGAATGGACAGGTGAACCTAGTCAGTAAAAGGACAGCAGGCATTTGGTCGCCCGGGGACCAAGTTACG

9855

ANG

ANG-202

P W P P C Q Y R A T A G F R N V V A C E N G L P V H L D Q S I F R R P

ANG-202

TGGCTCTGCTGCTTGCCTTCCATTTCCCTCTGCACCCAGAACAGTGGTGGCAACATTCATTGCCAAGGGCCCAAGAAAAGAGCTACCTGGACCTTTTGTCTGTTGACAACATGTTTAAATAAAAA
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9990

ANG

ANG-202

TGTCTTGATATCAGTAAGAATCAGAGTCTTCTCACTGATTTCTGGGCATATTGATCTTTCCCTATTTCTCTACTTGGCTGCTCCCTGAGAGGACTGCATAGGATAGAATGCCTTTTTCTTTCTTTTCGTTTT
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10,125

ANG

ANG-202

PCR Reverse
CAGAAAGTGTACTAAGACCCGTATA

TTTTTTTTTTTTTTTGGATGGAGTCTCACTCTGTCGCCAGGCTTAAAGTGCAATGGCACAATCTGGCTCACTGCAACCTCTCTCTCTGGTTCAAGTGATTCTCCTGCCTCAGCCTCCCAATAGCTGAGA
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10,260

ANG

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10,395

ANG

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AATGTCGCTACTCGGTGACTCGCCCGGTGAAAAAGGAATAGTCAGTCAAAAATGTTCAAGTAACTCCCTCATCTGAAATGGAGAGACACTTCTTTTCATACCATACAACCTAGATGCTCTCTCTACCTTTTTAAG

10,530

ANG

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10,665

ANG

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10,800

ANG

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10,935

ANG

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ANG

TAGCTGGCCGTGGTGGCACACACCTATAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCTAGGAGGGGAGGTTGCACTGAGCCGAGATCACGCCACTGCACTCCAGCCTGGCGACAGAGC 11,205
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ANG

GAGACTCCATCTCAAAAAAAAAAAAAAAAAAAGAAAGATCCCAGTTTATCCAGTTTATCCCTTATTCTTCTCAATCTCAAGATTTGTTTTTAAGTTAACATAACTTAGGTTAACACACTCTTTGTAAAAATACACT 11,340
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ANG

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ANG

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ANG

ACTGAAAGTATTCAAATTTAGGAATGGGTTTGAAGTAGGTAGCTGGTATGTGCTTAGCACAGAATCTCTCTTCTGGGTTAGTCTGTTTCAAACCTGAAAACACTGTCATTCTTAAAGAAAATAGGAAAAA 11,745
TGACTTTCATAAGTTAAATCCTTACCCAACTCTCATCCATCGACCATACCGAATCGTGTCTTAGAGAGAAGGAACCAATCAGACAAAGTTTGACTTTGTGACAGTAAGGAATCTTTTATCCTTTTT
ANG

GTATTCAAACCTCTGTCACTAGAAAAATTTGCCATATTACCAAATCTCAAAAACCTCTCAGGAAATGAGAAAGTCCAGTTTCTGGTAAACTATTTGGGCCCTTTTCTCAAGTTCTCCAACAGTGTATTTCTCT 11,880
CATAAGGTTTGGAGACAGTGATCTTTTAAACGGTATAATGGTTTAGAGTTTTTGGAGAGTCCCTTTACTCTTTCAGGGTCAAAGACATTGATAAACCCGGGAAAAGAGTTCAAGAGGTTGGTCACGATAAAGGA
ANG

TGAGGTGAGGCAAGTTACTCAAGATCATCGCTGCCACTCAAGGCCCTTGATAGGGCAAGTAAAAGGCATGGACATTATTTATTTGATCACAGCATAAGCTGTGAAAACCCACATCTTCTCCAACATCTGCTTG 12,015
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ANG

GAGCATTATCATCGCATAGTTTGTCTGGTGTTCAGGAAATCGCTGTTTATAGGAAATCACATGGCAGTGGGATGGGAGTGTTCCTGACCTGCCGATGGTACTGGCACCTGAGCAAGCATTCTAGTCTTTT 12,150
CTCGAATAGTAGCGTATCAAACGAGACCAAGTCCCTTAGCGACAAAGTATCCTTTAGTGTACCGTCACCTACCCTCACAAAGGACTGGACGGCTACCATGACCGTGGACTCGTTCGTAAGGATCAGGAAA
ANG

TTGGTCTGGGCCCTTTGTTCTATCACAAACCACAAGCTGTTTAAAAATAAAACGTCGAAGTACAGGCAAGTCAATTTTATCTGCGTGAATCAATTGAAGAATTGAAGTCTGGTCAAGTGTGATTGTTGGCTTTGCA 12,285
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ANG

AGGAAAAAGAAAGAACACTCCAAAATGCTAAATGCTTTGAAAGATAGTGACATGCAAGGAAGAAAATTCATGCAATTTGGAGAAGAAACATTTTCTAGGAATCTAGTAGCTGAGATTTTTATAGTTTAAAAA 12,420
TCCTTTTTCTCTCTGTGAGGTTTACGATTTACGAAACTCTTATCACTGTACGTTCCCTTTTAAAGTACGTTAAACCTCTCTTTGTA AAAAGATCCTTAGATCATCGACTCTATAAAATATCAAATTTTT
ANG

CAGACTTCCAATATCTTGAGAATACAGTTAGCTCTACGAAATAAAGAGGAGTCAATAATATATGCAACTCTGTAGTCATTCAATTTTTATCCAGATTGACAGAAAGCAGAGGAAAACCAAGAAAATGGAAGTGGT 12,555
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ANG

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TTTTTTTTTTTTTACGTCATTAAAGGTTATAAATGACTCGTAAATGGGACAGATCCGGAACAATATCCGGAATCTAACTAAAAGAAAAGTATTGTAGGGATTCTCCATCCATAATGTACGAGTAAACGAATA
ANG

GAGGAAATCTGCTGAGAGAGATTAAGTAAATTTCTCTAGTGCACAGCCTCAGTCTTTTAGACCAGGTTGCAAAAAGAGTCTTACTGTGAGTCAAGGTTGGTGCAGTGGAGAAAGCGTTTGGGAAAATCCTGAC 12,825
CTCCTTAGACGACTCTCTTAATTCATTAAGAGTACCAGTGTGGAGTGCAGAAAATCTGGTCCACAGTTTTCTTCAAGAAATGACACTCAGTCCACCACGTCACTCTTTGCAAAACCCCTTTTAGACTG
ANG

CCAAAAGTGTGCGTTGGGATGATGAGGATCATTCAATTTCTCTTGTAGCTACAGCTTGTAGATGCACCCATTGGTATCCACACTGGCCTGCTGCTCTCAAATATTTCTCTATGCTTGTACTTGAAGTGT 12,960
GGTTTTTACACAGCAACCCCTACTACACCTCTAGTAAGTTAAAAGAGAAACATCGATGTGAAAACCTCTAGTGGGTAACCATAGGTGTGACCGGACGACAGGAGTTATAAAGAGATACAGAAACAAATGAACATCA
ANG

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CGTTTTTGCAGTGCAGGACCCAGACGAGAGCGTACGTATCCACTCAA AAAAGAGACATCGATCAGTAGAAGCATTTGGTATAAAAACCAAGTGTCTTAGCTACTCTTTTCATCTATTTTGGTACCTTTGAG
ANG

GAGGTGCCACCGGAAGAGCAAACCAAGATATTTGATCTGCTGAAGCTATAATCCAAGTACTAAGTATACCTTCAGAAAGTTGATGCAATGTTCTTGGGCAAAAAGAAATCAAACATCTGCCCTTCTCCAC 13,230
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ANG

AACCTCTTACTTCCCTCTCTTCTAACACTGTATCTCACATCTACAGCTGCAGGCACACAGATATGACATACAGCTTGATATCTTTATGTGAAAAGGCAAAAAGATGGCTATGGATATAGGAGGTGGCATTAAAA 13,365
TTGGAGAAATGAAGGGAGAGAAGGATTTGACATAGAGTGTAGATGTGACGTCGGTGTCTATACTGTATGTGAACTATAGAAATACAGTTTCCGTTTTCTACCGATACCTATATCTCCACCGTAAATTT
ANG

AGAACAATATCCATGTTGATACTGCTTTTCATTATCAATAATGAAAAGGTAGCCTTTTCAGCAGAAACAAAGTAAAGTTACAGGTCGTTTGGAAAGCCATTTCACTCATTCACACAGTGTGATCCACCATTACGAAGCA 13,500
TCTTGTATAGGTACAAACTATGACGAAAGTAAATAGTTATTACTTTCCATCGGAAAAGTGTCTTGTTCATTCCATGTCAGCAAAACCTTCGGTAAAGTCAGTAAGTGTGTACACTAGGTGGTAAATGCTCTGT
ANG

GAATTTGAAATCAAAGACAATAGTACCCATATACATCAAACCTAGGAGTTCAACTGGGGTCAAGTCTTGGACTGCACATACAGAGTTGGGCTGCCTGACTCTCAAACATTTGCCCTTGTCAATTTGCGTTGCTCA 13,635
CTTAAACTTTAGTTTTCTGTTATCATGAGGTATATGATGTTGATCTCAAGTTGACCCAGTCAAGAACCTGACGTTGATGTCTCAACCCGACGGACTGAGAGTTTTGTAACGGGAACGATTAACGCAACGAGT
ANG

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13,770

ANG

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CACTCACTCAGGTGGAGGTCAGAATAATTTGAGACGACGCCCTTCATCGTTAAGACTCGTATTTACAGAACTATAGGACTTATAAAACCCACACCTACTCTCTCCGTCATCTATCACCTTTCTCGTGCCC

13,905

ANG

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14,040

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14,175

ANG

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14,310

ANG

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14,445

ANG

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14,580

ANG

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14,715

ANG

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TCAAACATTTGAAAGACACTGCATACGACTCAGATAGGTTTGACAGCCCTAACCTCGGAGGGCCCTTGGTTGTGAGGG

End (14,795)

3'

14,795

5'

ANG

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

Primer		Length		Binding Sites		Tm	Date Added
✓ PCR Forward		25-mer		9125 .. 9149	→	62°C	May 12, 2022
/sequence	= GATTCTAAGGGATGGGAAGAACGG 52% GC / 7860.2 Da						
✓ Sanger Sequencing Primer		20-mer		9369 .. 9388	→	58°C	May 12, 2022
/sequence	= AGGAGCCTGTGTTGGAAGAG 55% GC / 6262.1 Da						
✓ Donor Template SNV -> REV		100-mer		9478 .. 9577	←	80°C	May 12, 2022
/sequence	= GCAGGGTGAGGTCAGGCCCGTCTCCTCATGATGCTTTCACAGTATCTGTCATCCCGGCCCTGTGGTTGGCATCATAGTCTGGGTCAGGAAGTGTGTG 57% GC / 30,918.0 Da						
✓ gRNA Protospacer		20-mer		9496 .. 9515	→	50°C	May 12, 2022
/sequence	= GCACTATGATGCCATACCAC 50% GC / 6046.0 Da						
✓ PCR Reverse		25-mer		10,016 .. 10,040	←	58°C	May 12, 2022
/sequence	= ATATGCCCAATCAGTGAGAAGAC 44% GC / 7708.1 Da						