

PCR Forward

**CGCCTGCCCCAGCAA**

5' CAGACCCCTTCTTCATCGTGGAAACGCTGTGTATCATCTGGTTCTCCTTCGAGCTGGTGGTGCCTTCTTCGCCTGCCCCAGCAA 85  
 3' GTCTGGGGAAGAAGTAGCACCTTTCGACACATAGTAGACCAAGAGGAAGCTCGACCACCACGCGAAGAAGCGGACGGGGTCTGT

KCNA1

KCNA1-201

220 225 230 235 240 245  
 D P F F I V E T L C I I W F S F E L V V R F A C P S K

KCNA1-201

PCR Forward

**GACGGACTTC**

GACGGACTTCTTCAAAAACATCATGAACCTTCATAGACATTGTGGCCATCATTCTTATTTTCATCACGCTGGGCACCGAGATAGCT 170  
 CTGCCTGAAGAAGTTTTGTAGTACTTGAAGTATCTGTAACACCGGTAGTAAGGAATAAAGTAGTGCGACCCGTGGCTCTATCGA

KCNA1

KCNA1-201

250 255 260 265 270  
 T D F F K N I M N F I D I V A I I P Y F I T L G T E I A

KCNA1-201

GAGCAGGAAGGAAACCAGAAGGGCGAGCAGGCCACCTCCCTGGCCATCCTCAGGGTCATCCGCTTGGAAGGGTTTTTAGAATCT 255  
 CTCGTCCTTCTTTGGTCTTCCCGCTCGTCCGGTGGAGGGACCGGTAGGAGTCCCAGTAGGCGAACCATTCCCAAAAATCTTAGA

KCNA1

KCNA1-201

275 280 285 290 295 300  
 E Q E G N Q K G E Q A T S L A I L R V I R L V R V F R I

KCNA1-201

TCAAGCTCTCCCGCCACTCTAAGGGCCTCCAGATCCTGGGCCAGACCCTCAAAGCTAGTATGAGAGAGCTAGGGCTGCTCATCTT 340  
 AGTTCGAGAGGGCGGTGAGATTCCTCGGAGGTCTAGGACCCGGTCTGGGAGTTTCGATCATACTCTCTCGATCCCGACGAGTAGAA

KCNA1

KCNA1-201

305 310 315 320 325 330  
 F K L S R H S K G L Q I L G Q T L K A S M R E L G L L I F

KCNA1-201

TTTCCTTTCATCGGGTCATCCTGTTTTCTAGTGCAGTGTACTTTGCCGAGGCGGAAGAAGCTGAGTCGCACTTCTCCAGTATC 425  
 AAAGGAGAAGTAGCCCCAGTAGGACAAAAGATCACGTACATGAAACGGCTCCGCCTTCTTCGACTCAGCGTGAAGAGGTCATAG

KCNA1

KCNA1-201

335 340 345 350 355  
 F L F I G V I L F S S A V Y F A E A E E A E S H F S S I

KCNA1-201

Sanger Sequencing Primer

**CCATGACCACTGTAGGATAC**

CCCGATGCTTTCTGGTGGGCGGTGGTGTCCATGACCACTGTAGGATACGGTGACATGTACCCTGTGACAATTGGAGGCAAGATCG 510  
 GGGCTACGAAAGACCACCCGCCACCACAGGTAAGTGGTGACATCCTATGCCACTGTACATGGGACACTGTTAACCTCCGTTCTAGC

KCNA1

KCNA1-201

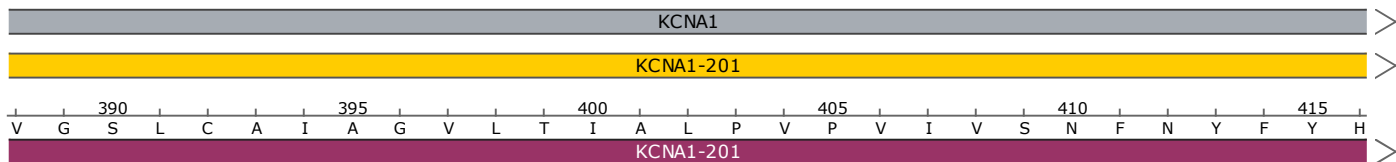
360 365 370 375 380 385  
 P D A F W W A V V S M T T V G Y G D M Y P V T I G G K I

KCNA1-201

Donor Template SNV -> REV

GGTGTGCTAACAAATTGCCCTGCCCGTACCTGTCATTGTGTCCAATTTCAACTATTTCTACCA  
TGGGCTCCTTGTGTGCCATCGCTGGTGTGCTAACAAATTGCCCTGCCCGTACCTGTCATTGTGTCCAATTTCAACTATTTCTACCA  
ACCCGAGGAACACACGGTAGCGACCACACGATTGTTAACGGGACGGGCATGGACAGTAACACAGGTTAAAGTTGATAAAGATGGT

595

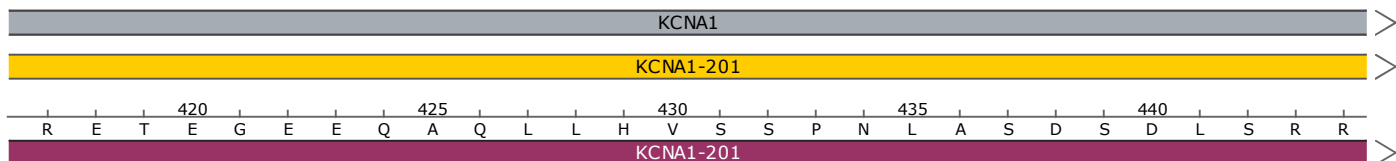


V G S L C A I A G V L T I A L P V V I V S N F N Y F Y H

Donor Template SNV -> REV

CCGAGAAACTGAGGGGGAAGAGCAGGCTCAGTTGCTCC  
CCGAGAAACTGAGGGGGAAGAGCAGGCTCAGTTGCTCCACGTGTCAGTTCCCCTAACTTAGCCTCTGACAGTGACCTCAGTCGCCGC  
GGCTCTTTGACTCCCCCTTCTCGTCCGAGTCAACGAGGTGCAGTCAAGGGGATTGAATCGGAGACTGTCACTGGAGTCAGCGGGC

680



R E T E G E E Q A Q L L H V S S P N L A S D S D L S R R

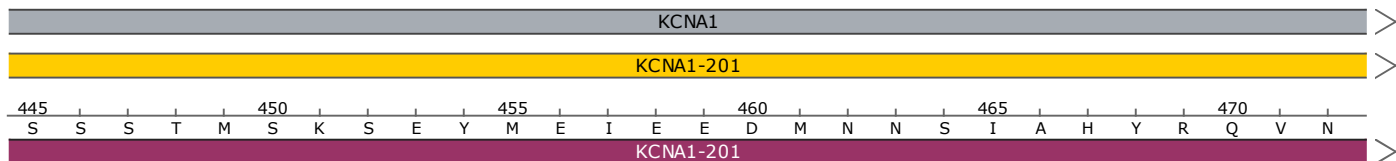
gRNA Protospacer

SNV

GA CTCTTTGACTCCCCCTTC  
gRNA Protospacer

AGTTCCTCTACTATGAGCAAGTCTGAGTACATGGAGATCGAAGAGGATATGAATAATAGCATAGCCATTATAGACAGGTCAATA  
TCAAGGAGATGATACTCGTTCAGACTCATGTACCTCTAGCTTCTCCTATACTTATTATCGTATCGGGTAATATCTGTCCAGTTAT

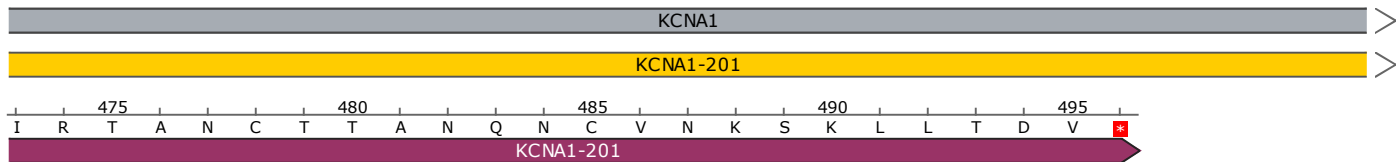
765



S S S T M S K S E Y M E I E E D M N N S I A H Y R Q V N

TCAGAACTGCCAATTGCACCACTGCTAACCAAACTGCGTTAATAAGAGCAAGCTACTGACCGATGTTAAAAAACAAGGCAAG  
AGTCTTGACGGTTAACGTGGTGACGATTGGTTTTGACGCAATTATTCTCGTTCGATGACTGGCTACAAATTTTTGTTTCCGTTT

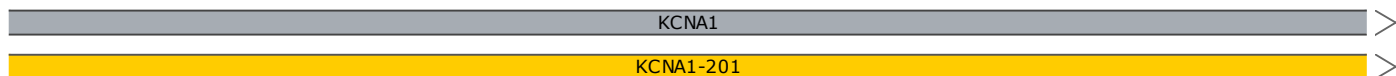
850



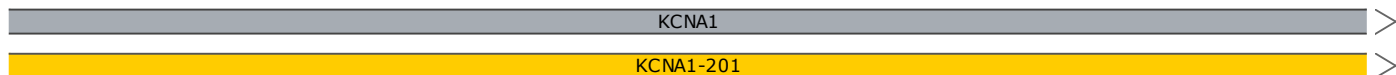
I R T A N C T T A N Q N C V N K S K L L T D V \*

CAAACAAAAAGCCCCACTTAGCAGCTCAAAGACTTAAAAACAACAGAAAACCTAGTGACTCATGTCACGCTTTGTAGATA  
GTTTGTTTTTTCGGGGTGAATCGTCGAGTTTTCTGAATTTTTGTTTTGCTTTTGGATCACTGAGTACAGTGCAGAACATCTAT

935

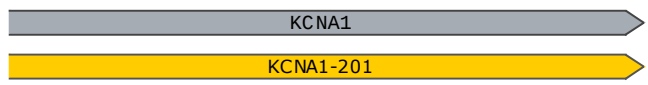


CTTTACTAAGTAGACTTGGAAATGCTCTATTTAACTGTCAATGCGTTGTTGCATTGAGGATTTTGGGGGTGGTGAACCAGAAGCTT  
GAAATGATTCATCTGAACCTTACGAGATAAATTGACAGTTACGCAACAACGTAACTCCTAAAACCCCCACCACTTGGTCTTCGAA



G T A A C T C C T A A A A C C C C C A C C A C T T  
PCR Reverse

TCAAGATCCATGACAAAATAAACTATTTTCCTTTTATTAA 3'  
AGTTCTAGGTACTGTTTTATTTGATAAAAAGGAAAATAATT 5' 1060



Feature	Location	Size	Start	End	Type
	1 108,816	108,816 bp	█	→	gene
/note = gene <a href="#">ENSG00000256654</a> lncRNA					
	1 108,816	108,816 bp	█	→	prim_transcript
/note = primary transcript <a href="#">ENST00000640877</a> lncRNA					
	1 108,794	108,794 bp	█	→	prim_transcript
/note = primary transcript <a href="#">ENST00000640962</a> lncRNA					
	1 .94,549	94,549 bp	█	→	prim_transcript
/note = primary transcript <a href="#">ENST00000638821</a> lncRNA					
	1 .14,165	14,165 bp	█	→	prim_transcript
/note = primary transcript <a href="#">ENST00000541095</a> lncRNA					
✓ <b>KCNA1</b>	1 .. 1060	1060 bp	█	→	gene
/note = gene <a href="#">ENSG00000111262</a> Protein coding					
✓ <b>KCNA1-201</b>	1 .. 1060	1060 bp	█	→	prim_transcript
/note = primary transcript <a href="#">ENST00000382545</a>					
<b>KCNA1-202</b>	1 .. 1060	1060 bp	█	→	prim_transcript
/note = primary transcript <a href="#">ENST00000543874</a> protein_coding_CDS_not_defined					
<b>KCNA1-203</b>	1 .. 1060	1060 bp	█	→	prim_transcript
/note = primary transcript <a href="#">ENST00000639306</a> Nonsense mediated decay					
✓ <b>KCNA1-201</b>	1 .. 836	836 bp	█	→	CDS
/codon_start = 1					
/note = coding sequence <a href="#">ENSP00000371985</a>					
/translation = DPFFIVETLCIIWFSFELVVRFFACPSKTDFFKNIMNFIDIVAIIPYFITLGTEIAEQEGNQKGEQATSLAILRVIRLVRFRIKLSRHSKGLQILGQTLKASMRELGLLIF FLFIGVILFSSAVYFAEAEAEESHFSSIPDAFWAVVSMTTVGYGDMYPVTIGGKIVGSLCAIAGVLTIALPVPVIVSNFNFYFHRETEGEEQAQLLHVSSPNLASDLSRR SSSTMSKSEYMEIEEDMNNSIAHYRQVNIIRTANCTTANQNCVNKSKLLTDV* 277 amino acids = 31.1 kDa					
<b>KCNA1-204</b>	161 .. 1060	900 bp	█	→	prim_transcript
/note = primary transcript <a href="#">ENST00000639680</a>					
<b>KCNA1-204</b>	161 .. 236	76 bp	█	→	CDS
/note = coding sequence <a href="#">ENSP00000492218</a>					
/translation = RDS*AGRKPEGRAGHLPGHPQGHPL 25 codons (1 internal stop codon)					
✓ <b>Donor Template SNV -&gt; REV</b>	534 .. 633	100 bp	█		misc_feature
✓ <b>PAM</b>	593 .. 595	3 bp	█		misc_feature
✓ <b>gRNA Protospacer</b>	596 .. 615	20 bp	█		misc_feature
✓ <b>SNV</b>	597 .. 597	1 bp	█		misc_feature
/note = SNV = T REV = C					

Primer	Length	Binding Sites	Tm	Date Added
✓ <b>PCR Forward</b>  /sequence = CGCCTGCCCCAGCAAGACGGACTTC 68% GC / 7572.9 Da	25-mer	71 .. 95	70°C	Jun 13, 2023
✓ <b>Sanger Sequencing Primer</b>  /sequence = CCATGACCACTGTAGGATAC 50% GC / 6086.0 Da	20-mer	454 .. 473	54°C	Jun 13, 2023
✓ <b>Donor Template SNV -&gt; REV</b>  /sequence = GGTGTGCTAACAATTGCCCTGCCCGTACCTGTCTATTGTGTCCAATTTCAACTATTTCTACCACCGAGAACTGAGGGGGAAGAGCAGGCTCAGTTGCTCC 51% GC / 30,760.0 Da	100-mer	534 .. 633	78°C	Jun 13, 2023
✓ <b>gRNA Protospacer</b>  /sequence = CTTCCCCCTCAGTTTCTCAG 55% GC / 5954.9 Da	20-mer	598 .. 615	55°C	Jun 13, 2023
✓ <b>PCR Reverse</b>  /sequence = TTCACCACCCCAAAATCCTCAATG 48% GC / 7474.9 Da	25-mer	986 .. 1010	62°C	Jun 13, 2023