

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

GACGGACTTCTTCAAAAACATCATGAACCTTCATAGACATTGTGGCCATCATTCTTATTTTCATCAGCTGGGCACCGAGATAGCT 170
 CTGCCTGAAGAAGTTTTTGTAGTACTTGAAGTATCTGTAACACCGGTAGTAAGGAATAAAGTAGTGCGACCCGTGGCTCTATCGA

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
 CTCGTCCTTCTTTGGTCTTCCCGCTCGTCCGGTGGAGGGACCGGTAGGAGTCCAGTAGGCGAACCATTCCCAAAAATCTTAGA

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 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 WT -> SNV

GGTGTGCTAACAAATTGCCCTGCCCGTACCTGTCATTGTGTCCAATTTCAACTATTTCTACCA
TGGGCTCCTTGTGTGCCATCGCTGGTGTGCTAACAAATTGCCCTGCCCGTACCTGTCATTGTGTCCAATTTCAACTATTTCTACCA
ACCCGAGGAACACACGGTAGCGACCACACGATTGTTAACGGGACGGGCATGGACAGTAACACAGGTTAAAGTTGATAAAGATGGT

595

KCNA1

KCNA1-201

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

KCNA1-201

Donor Template WT -> SNV

PAM

Donor Template WT -> SNV

CTGAGAAACTGAGGGGGGAAGAGCAGGCTCAGTTGCTCC
CCGAGAAACTGAGGGGGGAAGAGCAGGCTCAGTTGCTCCACGTCAGTTCCCCTAAGTCTGACAGTGACCTCAGTCGCCGC
GGCTCTTTGACTCCCCCTTCTCGTCCGAGTCAACGAGGTGCAGTCAAGGGGATTGAATCGGAGACTGTCACTGGAGTCAGCGGGC

680

KCNA1

KCNA1-201

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

KCNA1-201

Donor Template WT -> SNV

gRNA Protospacer

SNV

GGCTCTTTGACTCCCCCTTC
gRNA Protospacer

AGTTCCTCTACTATGAGCAAGTCTGAGTACATGGAGATCGAAGAGGATATGAATAATAGCATAGCCATTATAGACAGGTCAATA
TCAAGGAGATGATACTCGTTCAGACTCATGTACCTCTAGCTTCTCCTATACTTATTATCGTATCGGGTAATATCTGTCCAGTTAT

765

KCNA1

KCNA1-201

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

KCNA1-201

TCAGAACTGCCAATTGCACCACTGCTAACCAAACTGCGTTAATAAGAGCAAGCTACTGACCGATGTTAAAAAACAAGGCAAG
AGTCTTGACGGTTAACGTGGTGACGATTGGTTTTGACGCAATTATTCTCGTTCGATGACTGGCTACAAATTTTTGTTTCCGTTT

850

KCNA1

KCNA1-201

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

KCNA1-201

CAAACAAAAAGCCCCACTTAGCAGCTCAAAGACTTAAAAAACAACAGAAAACCTAGTGACTCATGTCACGCTTTGTAGATA
GTTTGTTTTTTCGGGGTGAATCGTCGAGTTTTCTGAATTTTTGTTTTGCTTTTGGATCACTGAGTACAGTGCGAAACATCTAT

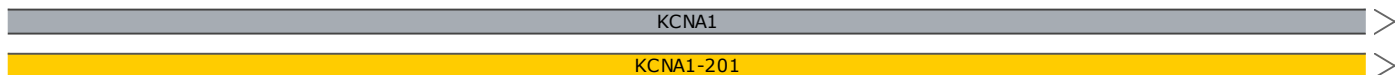
935

KCNA1

KCNA1-201

CTTTACTAAGTAGACTTGGAAATGCTCTATTTAACTGTCAATGCGTTGTTGCATTGAGGATTTTGGGGGTGGTGAACCAGAAGCTT
 GAAATGATTCATCTGAACCTTACGAGATAAATTGACAGTTACGCAACAACGTAACTCCTAAAACCCCACCACTTGGTCTTCGAA

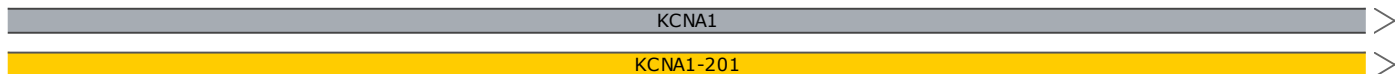
1020



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

TCAAGATCCATGACAAAATAAACTATTTTCCTTTTATTAATAAAATGGGAAAAGAGAGAGTATTTTCTAAAACCTGGCTTAAAAAGA
 AGTTCTAGGTACTGTTTTATTTGATAAAAGGAAAATAATTTTACCTTTTCTCTCTCATAAAAGATTTTGACCGAATTTTCT

1105



TTC 3'
 1108
 AAG 5'



Feature	Location	Size	Start	End	Type
	1 108,864	108,864 bp	█	→	gene
/note = gene ENSG00000256654 lncRNA					
	1 108,864	108,864 bp	█	→	prim_transcript
/note = primary transcript ENST00000640877 lncRNA					
	1 108,842	108,842 bp	█	→	prim_transcript
/note = primary transcript ENST00000640962 lncRNA					
	1 .94,597	94,597 bp	█	→	prim_transcript
/note = primary transcript ENST00000638821 lncRNA					
	1 .14,213	14,213 bp	█	→	prim_transcript
/note = primary transcript ENST00000541095 lncRNA					
✓ KCNA1	1 .. 1108	1108 bp	█	→	gene
/note = gene ENSG00000111262 Protein coding					
✓ KCNA1-201	1 .. 1108	1108 bp	█	→	prim_transcript
/note = primary transcript ENST00000382545					
KCNA1-202	1 .. 1108	1108 bp	█	→	prim_transcript
/note = primary transcript ENST00000543874 protein_coding_CDS_not_defined					
KCNA1-203	1 .. 1108	1108 bp	█	→	prim_transcript
/note = primary transcript ENST00000639306 Nonsense mediated decay					
✓ KCNA1-201	1 .. 836	836 bp	█	→	CDS
/codon_start = 1					
/note = coding sequence ENSP00000371985					
/translation = DPFFIVETLCIIWFSFELVVRFFACPSKTDFFKNIMNFIDIVAIIPYFITLGTEIAEQEGNQKGEQATSLAILRVIRLVRFRIKLSRHSKGLQILGQTLKASMRELGLLIFF FLFIGVILFSSAVYFAEAEAEESHFSSIPDAFWAVVSMTTVGYGDMYPVTIGGKIVGSLCAIAGVLTIALPVPVIVSNFNFYFHRETEGEEQQLLVHSSPNLASDLSRR SSSTMSKSEYMEIEEDMNSIAHYRQVNIIRTANCTTANQNCVNSKLLTDV* 277 amino acids = 31.1 kDa					
KCNA1-204	161 .. 1108	948 bp	█	→	prim_transcript
/note = primary transcript ENST00000639680					
KCNA1-204	161 .. 236	76 bp	█	→	CDS
/note = coding sequence ENSP00000492218					
/translation = RDS*AGRKPEGRAGHLPGHPQGHPL 25 codons (1 internal stop codon)					
✓ Donor Template WT -> SNV	534 .. 633	100 bp	█		misc_feature
✓ PAM	593 .. 595	3 bp	█		misc_feature
✓ gRNA Protospacer	596 .. 615	20 bp	█		misc_feature
✓ SNV	597 .. 597	1 bp	█		misc_feature
/note = WT = C SNV = T					

Primer	Length	Binding Sites	Tm	Date Added
✓ PCR Forward /sequence = CGCCTGCCCCAGCAAGACGGACTTC 68% GC / 7572.9 Da	25-mer	71 .. 95	70°C	Jun 13, 2023
✓ Sanger Sequencing Primer /sequence = CCATGACCACTGTAGGATAC 50% GC / 6086.0 Da	20-mer	454 .. 473	54°C	Jun 13, 2023
✓ Donor Template WT -> SNV /sequence = GGTGTGCTAACAATTGCCCTGCCCGTACCTGTCAATTGTGTCCAATTTCAACTATTTCTACCACTGAGAACTGAGGGGAAGAGCAGGCTCAGTTGCTCC 50% GC / 30,775.0 Da	100-mer	534 .. 633	77°C	Jun 13, 2023
✓ gRNA Protospacer /sequence = CTTCCCTCAGTTTCTCGG 60% GC / 5970.9 Da	20-mer	596 .. 615	60°C	Jun 13, 2023
✓ PCR Reverse /sequence = TTCACCACCCCAAAATCCTCAATG 48% GC / 7474.9 Da	25-mer	986 .. 1010	62°C	Jun 13, 2023