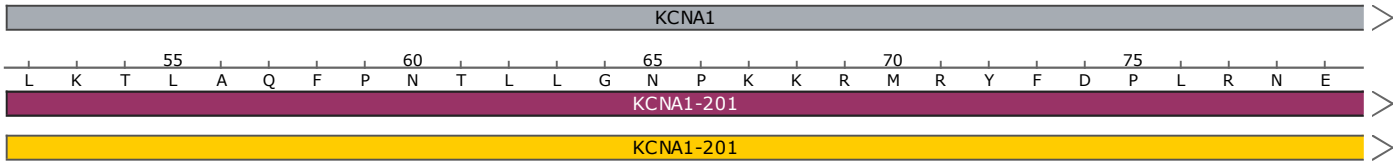


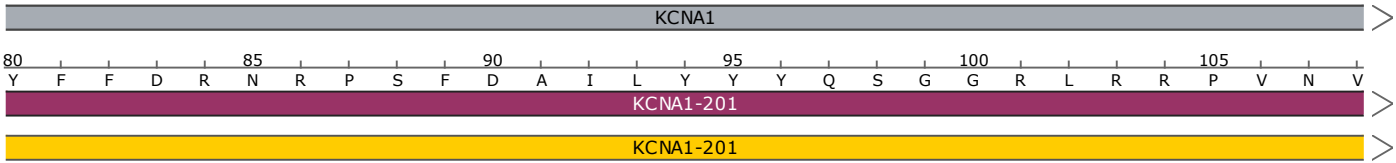
PCR Forward

CCTAAGAAACGCATGCGCTACTTCG

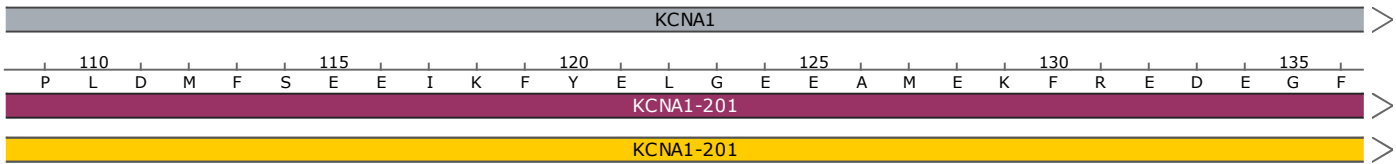
5' CTCAAGACCCTGGCGCAGTTC... 3' GAGTTCTGGGACCGCGTCAAGGGGT...



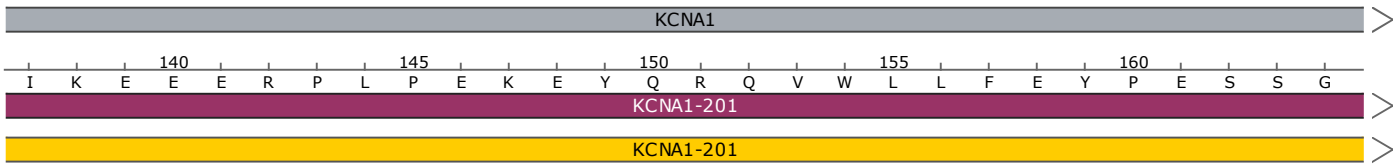
ACTTCTTCGACCGCAACCGGCCAGCTTCGACGCCATCCTCTACTACTACCAGTCCGGCGGCCGCTGCGGAGGCCGGTCAACGT...



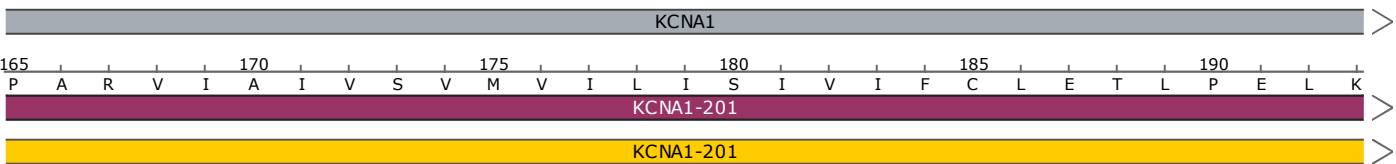
GCCCCTGGACATGTTCTCCGAGGAGATCAAGTTTTACGAGTTGGGCGAGGAGGCCATGGAGAAGTTCGGGAGGACGAGGGCTTC...



ATCAAGGAGGAGGAGCGCCCTCTGCCGAGAAGGAGTACCAGCGCCAGGTGTGGCTGCTCTTCGAGTACCCCGAGAGCTCGGGGC...



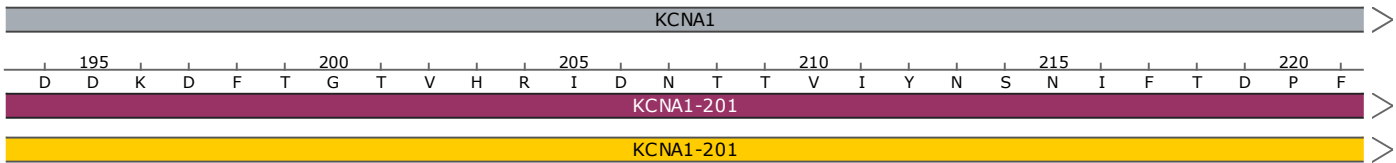
CCGCCAGGGTCATCGCCATCGTCTCCGTCATGGTCATCCTCATCTCCATCGTCATCTTTGCCTGGAGACGCTCCCCGAGCTGAA...



Donor Template SNV -> REV

TTCCAACATCTTCACAGACCCCTTC

GGATGACAAGGACTTCACGGGCACCGTCCACCGCATCGACAACACCACGGTCATCTACAATTCACAGACCCCTTC...

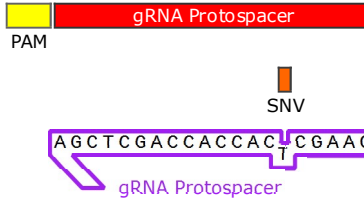
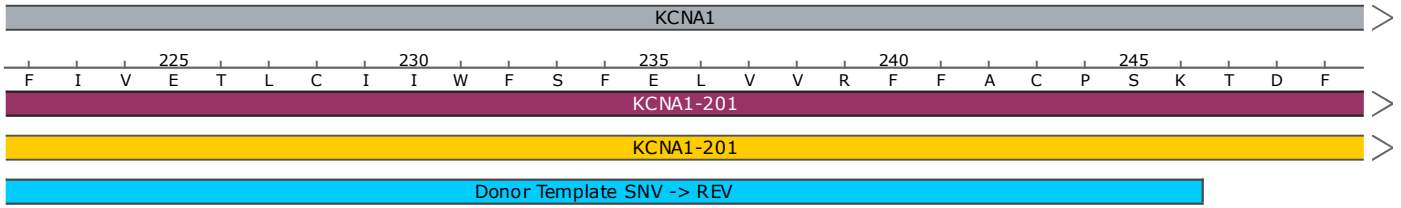


Donor Template SNV -> REV

Donor Template SNV -> REV

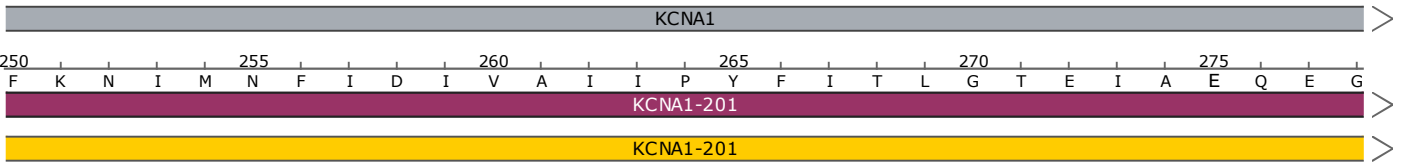
TTCATCGTGGAAACGCTGTGTATCATCTGGTTCTCCTTCGAGCTGGTGGTGCCTTCTTCGCCTGCCCCAGCAAG
 TTCATCGTGGAAACGCTGTGTATCATCTGGTTCTCCTTCGAGCTGGTGGTGCCTTCTTCGCCTGCCCCAGCAAGACGGACTTCT
 AAGTAGCACCTTTGCGACACATAGTAGACCAAGAGGAAGCTCGACCACCACGCGAAGAAGCGGACGGGGTCGTTCTGCCTGAAGA

595



TCAAAAACATCATGAACCTTCATAGACATTGTGGCCATCATTCTTATTTTCATCACGCTGGGCACCGAGATAGCTGAGCAGGAAGG
 AGTTTTTGTAGTACTTGAAGTATCTGTAACACCGGTAGTAAGGAATAAAGTAGTGCGACCCGTGGCTCTATCGACTCGTCCTTCC

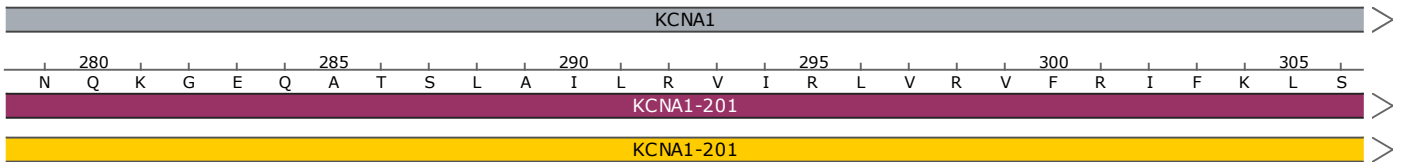
680



GGAATAAAGTAGTGCGACCC
 Sanger Sequencing Primer

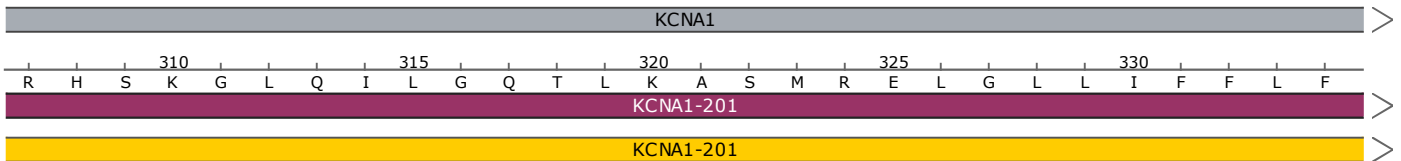
AAACCAGAAGGGCGAGCAGGCCACCTCCCTGGCCATCCTCAGGGTCATCCGCTTGGTAAGGGTTTTTGAATCTTCAAGCTCTCC
 TTTGGTCTTCCCGCTCGTCCGGTGGAGGGACCGGTAGGAGTCCCAGTAGGCGAACCATTCCCAAAAATCTTAGAAGTTCGAGAGG

765



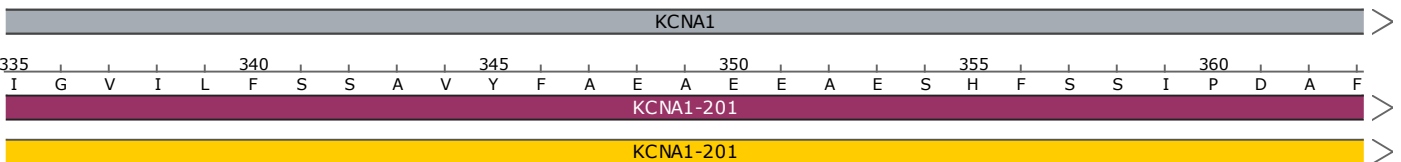
CGCCACTCTAAGGGCTCCAGATCCTGGGCCAGACCCTCAAAGCTAGTATGAGAGAGCTAGGGCTGCTCATCTTTTTCTCTTCA
 GCGGTGAGATTCGGGAGGTCTAGGACCCGGTCTGGGAGTTTCGATCATACTCTCTCGATCCCGACGAGTAGAAAAAGGAGAAGT

850



TCGGGGTCATCCTGTTTTCTAGTGCAGTGTACTTTGCCGAGGCGGAAGAAGCTGAGTCGCACTTCTCCAGTATCCCCGATGCTTT
 AGCCCCAGTAGGACAAAAGATCACGTACATGAAACGGCTCCGCCTTCTTCGACTCAGCGTGAAGAGGTTCATAGGGGCTACGAAA

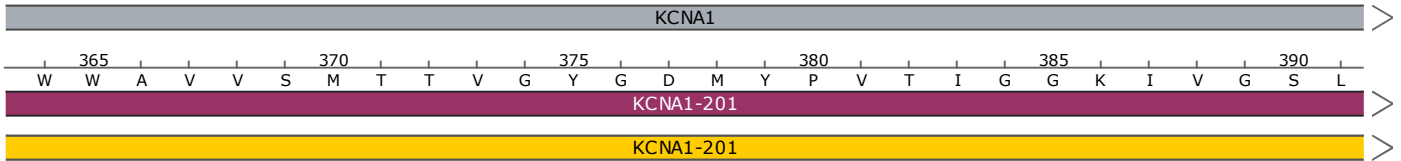
935



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 P D A F

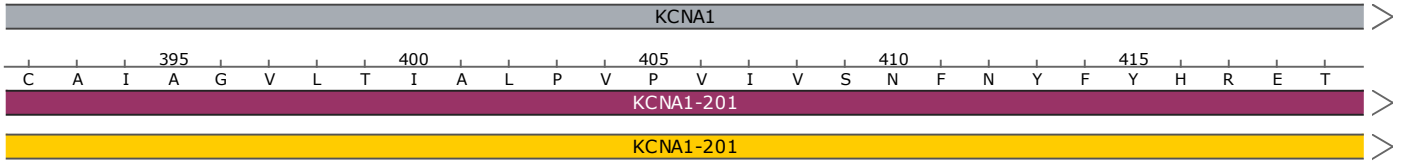
CTGGTGGGCGGTGGTGTCCATGACCACTGTAGGATACGGTGACATGTACCCTGTGACAATTGGAGGCAAGATCGTGGGCTCCTTG
 GACCACCCGCCACCACAGGTACTGGTGACATCCTATGCCACTGTACATGGGACACTGTAACTCCGTTCTAGCACCCGAGGAAC

1020



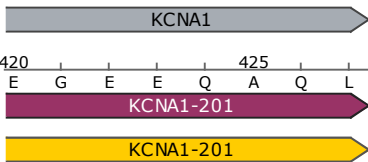
TGTGCCATCGCTGGTGTGCTAACAATTGCCCTGCCCGTACCTGTCATTGTGTCCAATTTCAACTATTTCTACCACCGAGAACTG
 ACACGGTAGCGACCACACGATTGTTAACGGGACGGGCATGGACAGTAACACAGGTTAAAGTTGATAAAGATGGTGGCTCTTTGAC

1105



GATTGTTAACGGGACGGGCATGGAC
 PCR Reverse

AGGGGGAAGAGCAGGCTCAGTTG 3'
 TCCCCCTTCTCGTCCGAGTCAAC 5'



Feature	Location	Size	Start	End	Type
	1 108,884	108,884 bp	█	➔	gene
/note = gene ENSG00000256654 lncRNA					
	1 108,884	108,884 bp	█	➔	prim_transcript
/note = primary transcript ENST00000640877 lncRNA					
	1 108,862	108,862 bp	█	➔	prim_transcript
/note = primary transcript ENST00000640962 lncRNA					
	1 .94,617	94,617 bp	█	➔	prim_transcript
/note = primary transcript ENST00000638821 lncRNA					
	1 .14,233	14,233 bp	█	➔	prim_transcript
/note = primary transcript ENST00000541095 lncRNA					
✓ KCNA1-201	1 .. 1128	1128 bp	█	➔	CDS
/note = coding sequence ENSP00000371985					
/translation = LKTLAQFPNTLLGNPKKRMRYFDPLRNEYFFDRNRPSFDAILYYQSGGRLRRPVNPLDMFSEEIKFYELGEEAMEKFREDEGFIKEEERPLPEKEYQRQVWLLFEYPESG PARVIAIVSVMVILISIVIFCLELPELKDDKDFGTVHRIDNTTVIYNSNIFTDPFFIVETLCIIWFSFELVVRFFACPSKTDFFKNIMNFIDIVAIIPYFITLGTIEAEQE GNQKGEQATSLAILRVIRLVRFRIKLSRHSKGLQILGQTLKASMRGLLIFLFIQVILFSSAVYFAEAEAEASHFSSIPDAFWAVVSMSTTVGYGDMYPVTIGGKIVGS LCAIAGVLTIALPVPVIVSNFNFYHRETEGEEQQL 376 amino acids = 43.3 kDa					
✓ KCNA1	1 .. 1128	1128 bp	█	➔	gene
/note = gene ENSG00000111262 Protein coding					
✓ KCNA1-201	1 .. 1128	1128 bp	█	➔	prim_transcript
/note = primary transcript ENST00000382545					
KCNA1-202	1 .. 1128	1128 bp	█	➔	prim_transcript
/note = primary transcript ENST00000543874 protein_coding_CDS_not_defined					
KCNA1-203	10 .. 1128	1119 bp	█	➔	prim_transcript
/note = primary transcript ENST00000639306 Nonsense mediated decay					
✓ Donor Template SNV -> REV	486 .. 585	100 bp	█	⌊	misc_feature
✓ PAM	545 .. 547	3 bp	█	⌊	misc_feature
✓ gRNA Protospacer	548 .. 567	20 bp	█	⌊	misc_feature
✓ SNV	562 .. 562	1 bp	█	⌊	misc_feature
/note = SNV = A REV = C					
KCNA1-204	660 .. 1128	469 bp	█	➔	prim_transcript
/note = primary transcript ENST00000639680					
KCNA1-204	660 .. 735	76 bp	█	➔	CDS
/note = coding sequence ENSP00000492218					
/translation = RDS*AGRKPEGRAGHLPGHPQGHL 25 codons (1 internal stop codon)					

Primer	Length	Binding Sites	Tm	Date Added
✓ PCR Forward /sequence = CCTAAGAAACGCATGCGCTACTTCG 52% GC / 7611.0 Da	25-mer	43 .. 67	62°C	Nov 7, 2023
✓ Donor Template SNV -> REV /sequence = TTCCAACATCTTCACAGACCCCTTCTTCATCGTGGAAACGCTGTGTATCATCTGGTTCTCCTTCGAGCTGGTGGTGGCGCTTCTTCGCCTGCCCCAGCAAG 54% GC / 30,531.8 Da	100-mer	486 .. 585	80°C	Nov 7, 2023
✓ gRNA Protospacer /sequence = GAAGCTCACCACCAGCTCGA 60% GC / 6056.0 Da	20-mer	548 .. 567	54°C	Nov 7, 2023
✓ Sanger Sequencing Primer /sequence = CCCAGCGTGATGAAATAAGG 50% GC / 6175.1 Da	20-mer	637 .. 656	55°C	Nov 7, 2023
✓ PCR Reverse /sequence = CAGGTACGGGCAGGGCAATTGTTAG 56% GC / 7787.1 Da	25-mer	1039 .. 1063	63°C	Nov 7, 2023