



 SNCA-201


 Donor Template WT -> SNV


 gRNA Protospacer Sequence

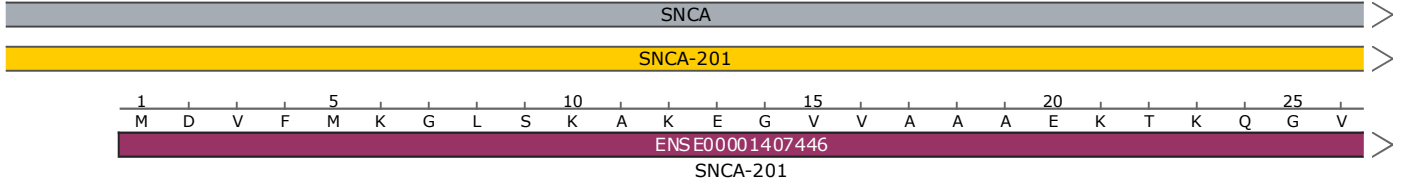

 SNV

ASK2J00178_SNCA_A30P_C01_BB
 3123 bp

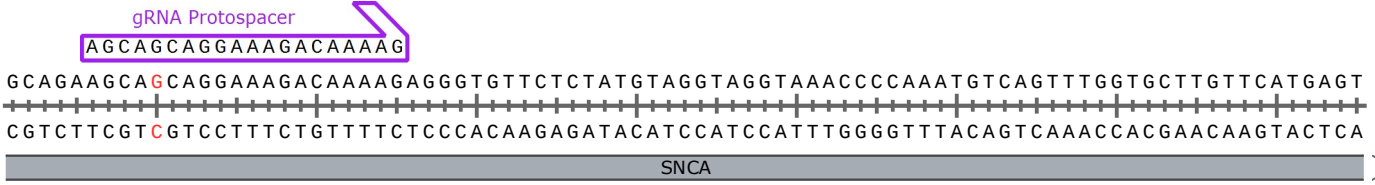


ATTAGCCATGGATGTATTCATGAAAGGACTTTCAAAGGCCAAGGAGGGAGTTGTGGCTGCTGCTGAGAAAACCAAACAGGGTGTG
TAATCGGTACCTACATAAGTACTTTCTGAAAGTTTCCGGTTCCTCCCTCAACACCGACGACGACTCTTTTGGTTTGTCCCACAC

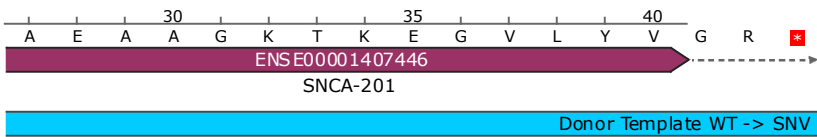
1700



Donor Template WT -> SNV
GTTTGTCCCACAC
Donor Template WT -> SNV



1785

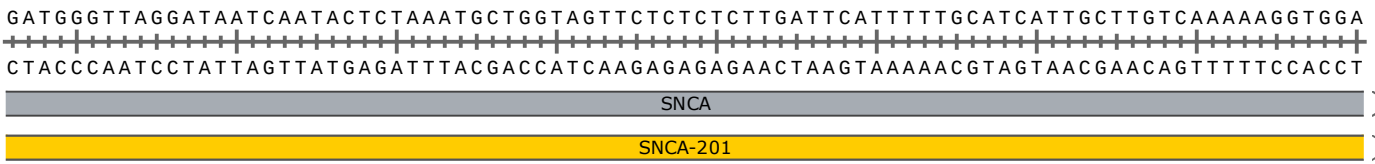


gRNA Protospacer Sequence PAM

SNV

CGTCTTCGTGTCCTTTCTGTTTTCTCCACAAGAGATACATccatccatttggggtttacagtcaaaccacgaacaagtactca

Donor Template WT -> SNV

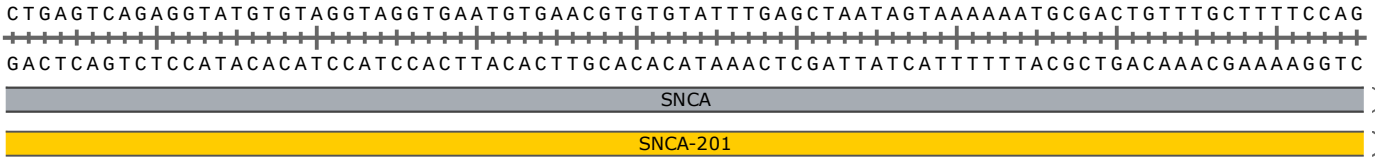


1870

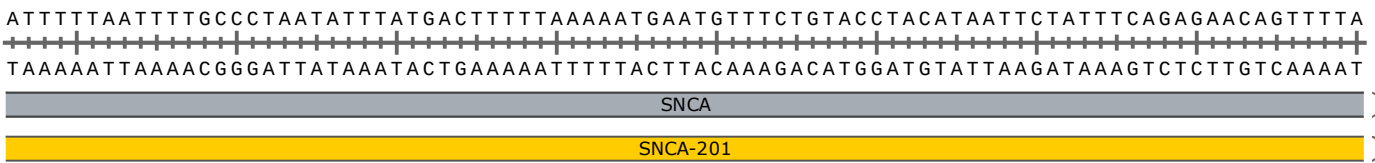
Donor Template WT -> SNV

ct

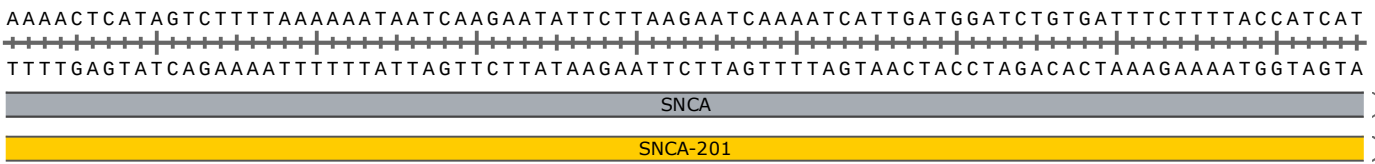
Donor Template WT -> SNV



1955



2040



2125

GAAAAATGTTTGTCAATTTTAAATCCATTCTGATTTTTAAAATATGACTTTGATATGCCCTGTGATGTGTATAAAGAGACCTATT
CTTTTTACAAACAGTTAAAATTAGGTAAGACTAAAAATTTTATACTGAAACTATACGGGGACACTACACATATTTCTCTGGATAA

2210

SNCA

SNCA-201

ctctggataa
PCR Reverse

TGTGGCCCTAAAATGGAAAGAACAGATTAGTCTTTGATAGAGTTACTTCATGTGATCATTGGTCTCTGTGAACACTGAGGACAG
ACACCGGGATTTTACCTTTCTTGCTAATCAGAAACTATCTCAATGAAGTACACTAGTAAACCAGAGACACTTGTGACTCCTGTC

2295

SNCA

SNCA-201

acaccgggattttac

PCR Reverse

AGAAAAGTGCTTGAGGGCTGCTACTAATCTCTCAGAAACATTTGTATAGTTCATCCATCAAATGACACACATACTAAAAGAATAA
TCTTTTCACGAACTCCCGACGATGATTAGAGAGTCTTTGTAACATATCAAGTAGGTAGTTTACTGTGTGTATGATTTTCTTATT

2380

SNCA

SNCA-201

AGAAATTGATGCTTATTACCTACTTGTTCCTAAAGTTCCACCTTGGGGTATACACCCAAACTCTGACTCTCTTTTCTGTAACCTG
TCTTTAACTACGAATAATGGATGAACAAGGATTTCAAGGTGGAACCCCATATGTGGGTTTGAGACTGAGAGAAAAGACATTGAAC

2465

SNCA

SNCA-201

AACTGTATTCAATTGAGTGTTATTTTACAAACCCTTTGAATTCCTTGGAAAAGAATAGACACACACTCTCATCCACAGGCATAG
TTGACATAAGTTAACTCACAATAAAATGTTTGGTGAACCTTAAGGAACCTTTTCTTATCTGTGTGTGAGAGTAGGTGTCCGTATC

2550

SNCA

SNCA-201

ACACACACACTCAACACAGACACATTGCCATTCTTCTCTCTTCTTCTCTCTGAGCTTTTTACATTCTCTGGTGGCAACTA
TGTGTGTGTGAGTTGTGTCTGTGTAACGGGTAAGAAGGAGAGAAGAAAGAGGAGACTCGAAAAAGTGAAGAGACCACCGTTGAT

2635

SNCA

SNCA-201

TAGCAGTAAGAGTCACAGGATGAACAGTCAGGTGGAGGATGACCACATTGAGTTGCCTAGCTGAAACATGTGCTCCGTCTATGTC
ATCGTCATTCTCAGTGTCTACTTGTCTCAGTCCACCTCCTACTGGTGTAACCTCAACGGATCGACTTTGTACACGAGGCAGATACAG

2720

SNCA

SNCA-201

TGCAAAGTGAAAGAAAGCTACACTATCTCTTCAACATAGATCAGTGGGGGAAATTTATACTTGGGATGATTTATATGAATGCAT
ACGTTTCACTTTCTTTTCGATGTGATAGAGAAGTTGTATCTAGTCACCCCTTTAAAATATGAACCCTACTAAATATACTTACGTA

2805

SNCA

SNCA-201

CTCATCAAAGTTCACAACACATTTTTTTTTTCAGTTTTTTATTTTCAGTTTTTTAGAGTCAGGGCCTTGCTCTGTGCGCCAGGCTGG
GAGTAGTTTCAAGTGTGTGTAATAAAAAAAGTCAAAAAATAAAAGTCAAAAAATCTCAGTCCCGGAACGAGACAGCGGGTCCGACC

2890

SNCA

SNCA-201

ACTGCAGTGATGCTATCATAGCTCACTGCATCCTTGAATTCCTGGGCTCAAGTCATGCCCCACCTCAGCCTCCTGAGTAGCCAG
TGACGTCACCTACGATAGTATCGAGTGACGTAGGAACTTAAGGACCCGAGTTCAGTACGGGGGTGGAGTCGGAGGACTCATCGGTC

2975

SNCA

SNCA-201

GATTATAGGCATGTGCCACTGCCTCATTATTTAGACTTTTTCTTATGTTGACTTAATCTTCCCACAAATCTTCAATTAATTACTT
CTAATATCCGTACACGGTGACGGAGTAATAAATCTGAAAAGAATACAACCTGAATTAGAAGGGTGTTTAGAAGTTAATTTAATGAA

3060

SNCA

SNCA-201

TTTTTCTACCTTAAACATATTTTCAGAAAGTCATTGAAATAGGGTGTTACAAGAGGAAAAAA
AAAAAGATGGAATTTTGTATAAAAAGTCTTTCAGTAACTTTATCCCACAATGTTCTCCTTTTTT

3'

3123



















5'

SNCA

SNCA-201

Feature	Location	Size	Start	End	Type
✓ SNCA	1 .. 3123	3123 bp	■	➔	gene
/note	= gene ENSG00000145335 Protein coding				
✓ SNCA-201	1 .. 3123	3123 bp	■	➔	prim_transcript
/note	= primary transcript ENST00000336904				
SNCA-216	1 .. 3123	3123 bp	■	➔	prim_transcript
/note	= primary transcript ENST00000673902				
SNCA-217	1 .. 3123	3123 bp	■	➔	prim_transcript
/note	= primary transcript ENST00000674129				
SNCA-204	91 .. 3123	3033 bp	■	➔	prim_transcript
/note	= primary transcript ENST00000394989				
SNCA-209	122 .. 3123	3002 bp	■	➔	prim_transcript
/note	= primary transcript ENST00000506244				
SNCA-205	129 .. 3123	2995 bp	■	➔	prim_transcript
/note	= primary transcript ENST00000394991				
SNCA-203	151 .. 3123	2973 bp	■	➔	prim_transcript
/note	= primary transcript ENST00000394986				
SNCA-210	214 .. 3123	2910 bp	■	➔	prim_transcript
/note	= primary transcript ENST00000506691				
SNCA-214	275 .. 3123	2849 bp	■	➔	prim_transcript
/note	= primary transcript ENST00000673718				
SNCA-206	314 .. 3123	2810 bp	■	➔	prim_transcript
/note	= primary transcript ENST00000420646				
SNCA-211	1077 .. 3123	2047 bp	■	➔	prim_transcript
/note	= primary transcript ENST00000508895				
SNCA-213	1077 .. 3123	2047 bp	■	➔	prim_transcript
/note	= primary transcript ENST00000618500				
SNCA-AS1-201	1253 .. 866	2737 bp	■	←	prim_transcript
/note	= primary transcript ENST00000501215 lncRNA				
SNCA-207	1595 .. 3123	1529 bp	■	➔	prim_transcript
/note	= primary transcript ENST00000502987				
SNCA-208	1605 .. 3123	1519 bp	■	➔	prim_transcript
/note	= primary transcript ENST00000505199				
SNCA-202	1610 .. 3123	1514 bp	■	➔	prim_transcript
/note	= primary transcript ENST00000345009				
SNCA-212	1623 .. 3123	1501 bp	■	➔	prim_transcript
/note	= primary transcript ENST00000611107				
✓ SNCA-201	1623 .. 1743	121 bp	■	➔	CDS
/note	= coding sequence ENSP00000338345				
/translation	= MDVFMKGLSKAKEGVVAAAETKQGVAAAGKTEGVLYV 40 amino acids = 4.1 kDa				
SNCA-202	1623 .. 1743	121 bp	■	➔	CDS
/note	= coding sequence ENSP00000343683				
/translation	= MDVFMKGLSKAKEGVVAAAETKQGVAAAGKTEGVLYV 40 amino acids = 4.1 kDa				
SNCA-203	1623 .. 1743	121 bp	■	➔	CDS
/note	= coding sequence ENSP00000378437				
/translation	= MDVFMKGLSKAKEGVVAAAETKQGVAAAGKTEGVLYV 40 amino acids = 4.1 kDa				
SNCA-204	1623 .. 1743	121 bp	■	➔	CDS
/note	= coding sequence ENSP00000378440				
/translation	= MDVFMKGLSKAKEGVVAAAETKQGVAAAGKTEGVLYV 40 amino acids = 4.1 kDa				

Feature	Location	Size	Start	End	Type
SNCA-205	1623 .. 1743	121 bp	■	→	CDS
/note	= coding sequence ENSP00000378442				
/translation	= MDVFMKGLSKAKEGVVAAAETKQGVAAEAGKTEGVLYV 40 amino acids = 4.1 kDa				
SNCA-206	1623 .. 1743	121 bp	■	→	CDS
/note	= coding sequence ENSP00000396241				
/translation	= MDVFMKGLSKAKEGVVAAAETKQGVAAEAGKTEGVLYV 40 amino acids = 4.1 kDa				
SNCA-207	1623 .. 1743	121 bp	■	→	CDS
/note	= coding sequence ENSP00000426034				
/translation	= MDVFMKGLSKAKEGVVAAAETKQGVAAEAGKTEGVLYV 40 amino acids = 4.1 kDa				
SNCA-208	1623 .. 1743	121 bp	■	→	CDS
/note	= coding sequence ENSP00000421485				
/translation	= MDVFMKGLSKAKEGVVAAAETKQGVAAEAGKTEGVLYV 40 amino acids = 4.1 kDa				
SNCA-209	1623 .. 1743	121 bp	■	→	CDS
/note	= coding sequence ENSP00000422238				
/translation	= MDVFMKGLSKAKEGVVAAAETKQGVAAEAGKTEGVLYV 40 amino acids = 4.1 kDa				
SNCA-210	1623 .. 1743	121 bp	■	→	CDS
/note	= coding sequence ENSP00000423445				
/translation	= MDVFMKGLSKAKEGVVAAAETKQGVAAEAGKTEGVLYV 40 amino acids = 4.1 kDa				
SNCA-211	1623 .. 1743	121 bp	■	→	CDS
/note	= coding sequence ENSP00000426955				
/translation	= MDVFMKGLSKAKEGVVAAAETKQGVAAEAGKTEGVLYV 40 amino acids = 4.1 kDa				
SNCA-212	1623 .. 1743	121 bp	■	→	CDS
/note	= coding sequence ENSP00000479604				
/translation	= MDVFMKGLSKAKEGVVAAAETKQGVAAEAGKTEGVLYV 40 amino acids = 4.1 kDa				
SNCA-213	1623 .. 1743	121 bp	■	→	CDS
/note	= coding sequence ENSP00000484044				
/translation	= MDVFMKGLSKAKEGVVAAAETKQGVAAEAGKTEGVLYV 40 amino acids = 4.1 kDa				
SNCA-214	1623 .. 1743	121 bp	■	→	CDS
/note	= coding sequence ENSP00000500990				
/translation	= MDVFMKGLSKAKEGVVAAAETKQGVAAEAGKTEGVLYV 40 amino acids = 4.1 kDa				
SNCA-216	1623 .. 1743	121 bp	■	→	CDS
/note	= coding sequence ENSP00000501102				
/translation	= MDVFMKGLSKAKEGVVAAAETKQGVAAEAGKTEGVLYV 40 amino acids = 4.1 kDa				
SNCA-217	1623 .. 1743	121 bp	■	→	CDS
/note	= coding sequence ENSP00000501269				
/translation	= MDVFMKGLSKAKEGVVAAAETKQGVAAEAGKTEGVLYV 40 amino acids = 4.1 kDa				
✓ Donor Template WT -> SNV	1688 .. 1787	100 bp	■	┌┐	misc_feature
✓ gRNA Protospacer Sequence	1706 .. 1725	20 bp	■	┌┐	misc_feature
✓ SNV	1710 .. 1710	1 bp	■	┌┐	misc_feature
/note	= WT = G SNV = C				
✓ PAM	1726 .. 1728	3 bp	■	┌┐	misc_feature
SNCA-AS1	2636 .. 882	1370 bp	■	←	gene
/note	= gene ENSG00000247775 lncRNA				
SNCA-AS1-202	2636 .. 882	1370 bp	■	←	prim_transcript
/note	= primary transcript ENST00000513653 lncRNA				

Feature		Location	Size			Type
		3124 292,508	289,385 bp			gene
/note	= gene ENSG00000251095 lncRNA					
		3124 292,508	289,385 bp			prim_transcript
/note	= primary transcript ENST00000659878 lncRNA					
		3124 152,078	148,955 bp			prim_transcript
/note	= primary transcript ENST00000508021 lncRNA					
		3124 120,961	117,838 bp			gene
/note	= gene ENSG00000288563 lncRNA					
		3124 120,961	117,838 bp			prim_transcript
/note	= primary transcript ENST00000673949 lncRNA					
		3124 .75,684	72,561 bp			prim_transcript
/note	= primary transcript ENST00000507916 lncRNA					
		3124 .21,963	18,840 bp			prim_transcript
/note	= primary transcript ENST00000689416 lncRNA					
		3124 .21,963	18,840 bp			prim_transcript
/note	= primary transcript ENST00000691837 lncRNA					

Primer	Length	Binding Sites	Tm	Date Added
✓ PCR Forward /sequence = atcttttcatgcaactccacttctg 40% GC / 7518.0 Da	25-mer	1323 .. 1347 →	58°C	Apr 24, 2023
✓ Sanger Sequencing Primer /sequence = cacactttggagggtttctc 50% GC / 6099.0 Da	20-mer	1507 .. 1526 →	56°C	Apr 24, 2023
✓ Donor Template WT ->SNV /sequence = tcactcatgaacaagcaccacaaactgacatttggggtttacctacCTACATAGAGAACCCTCTTTTGTCTTTCCTGGTGCTTCTGCCACACCTGTTTG 46% GC / 30,514.8 Da	100-mer	1688 .. 1787 ←	75°C	Apr 24, 2023
✓ gRNA Protospacer /sequence = AGCAGCAGGAAAGACAAAAG 45% GC / 6226.2 Da	20-mer	1706 .. 1725 →	56°C	Apr 24, 2023
✓ PCR Reverse /sequence = cattttagggccacaaataggtctc 44% GC / 7641.0 Da	25-mer	2201 .. 2225 ←	57°C	Apr 24, 2023