

INK2J00077_SYNJ1_R219Q_G03_AB
2842 bp



AAATAAATAAATATTTTTTAAAAAGTAGAGCTTCATAAATTGGGGTGGGGACATGCATATGTATTCCTTTTTGGAACAAGTTAG
 TTTATTTATTTATAAAAAAATTTTTTCATCTCGAAGTATTTAACCCACCCCTGTACGTATACATAAGGAAAAACCTTGTTCAATC

935

SYNJ1
 SYNJ1-201

PCR Forward
 TAAAGACATAACAGAAATGGGCCAC

GTTATAAACACATTATATATAAAGACATAACAGAAATGGGCCACAGATACTAAAAACACAAAAATACTCCTTTTTCTGTGGATCAT
 CAATATTTGTGTAATATATATTTCTGTATTGCTTTACCCGGTGTCTATGATTTTTGTGTTTTTATGAGGAAAAGACACCTAGTA

1020

SYNJ1
 SYNJ1-201

AGATCACATGTTGAAGGATCTCGTTTTATAGCCCTATCTTCTGATCCCTAGCATAGTAAATGTAATGAATTGATTTGTTGTTTG
 TCTAGTGTACAACCTCCTAGAGCAAAATATCGGGATAGAAGACTAGGGATCGTATCATTACATTTACTTAACTAAACAACAAC

1105

SYNJ1
 SYNJ1-201

TGCCTTTAAATTTAATAATATTAATTAATTTTCCAGGAGATTATTTTAAAAGTCATACTTTGTTACTTAGTATTCATAAGCTA
 ACGGAAATTTAAATTATTATAATTTAATTAAGGTCCTCTAATAAAAATTTTCAGTATGAAACAATGAATCATAAAGGTATTCGAT

1190

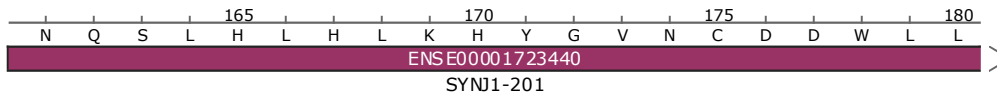
SYNJ1
 SYNJ1-201

Sanger Sequencing Primer
 GGC GTGAATTGTGATGACTG

ATCATTATTTCTTTTCTATTAGGAATCAGTCTTTGCATTTGCATCTCAAACACTATGGCGTGAATTGTGATGACTGGTTATTA
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1275

SYNJ1
 SYNJ1-201



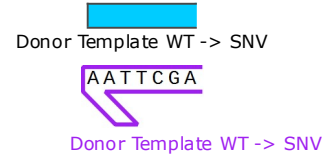
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1360

SYNJ1
 SYNJ1-201

R L M C G G V E I R T I Y A A H K Q A K A C L I S R L S

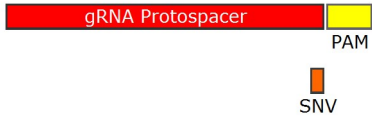
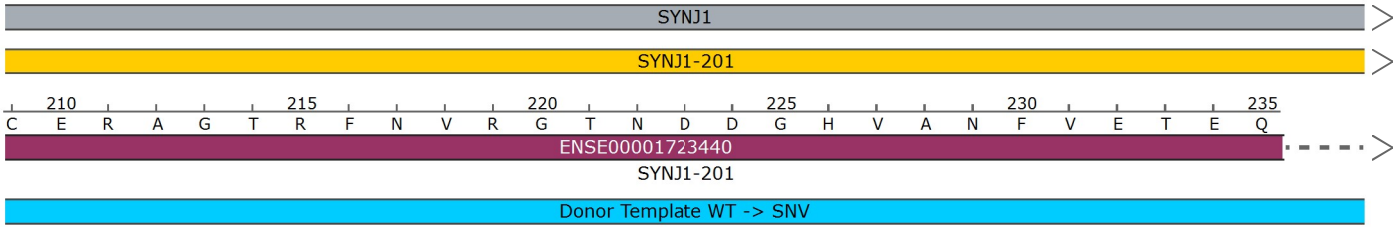
ENS E00001723440
 SYNJ1-201



gRNA Protospacer
GGGACCAGGTTTAATGTCCG

GTGAACGAGCTGGGACCAGGTTTAATGTCCGGGGAACAAATGATGATGGTCATGTTGCCAATTTTGTAGAAACAGAACAGGTATA
CACTTGCTCGACCCTGGTCCAAATTACAGGCCCTTGTCTTACTACTACCAGTACAACGGTTAAAACATCTTTGTCTTGTCCATAT

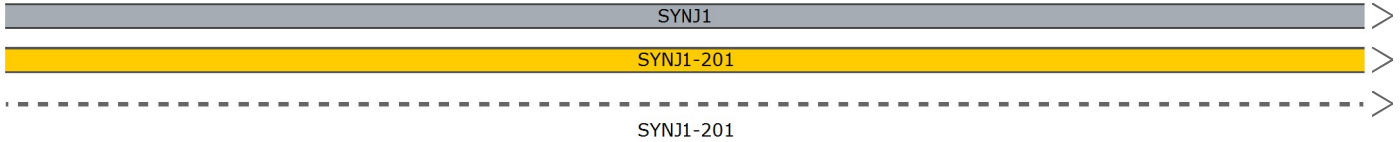
1445



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Donor Template WT -> SNV

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1530



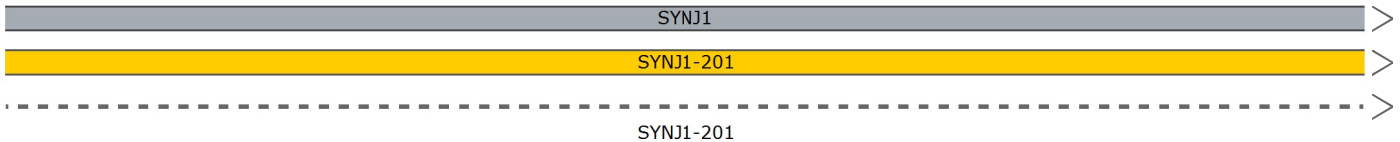
Donor Template WT -> SNV

ATATCACAA

Donor Template WT -> SNV

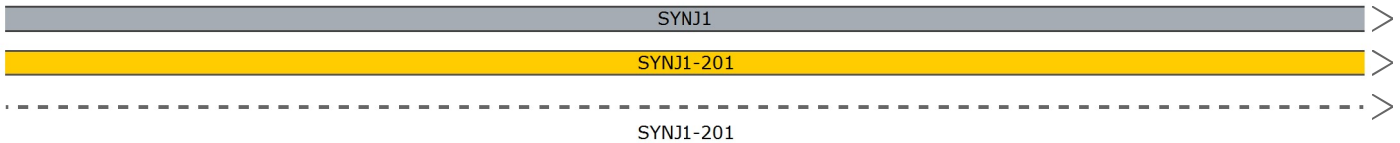
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1615



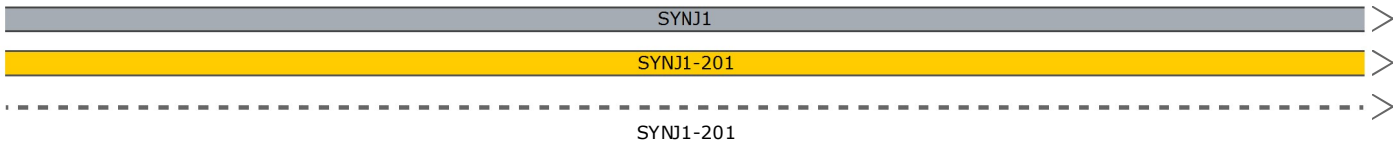
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1700



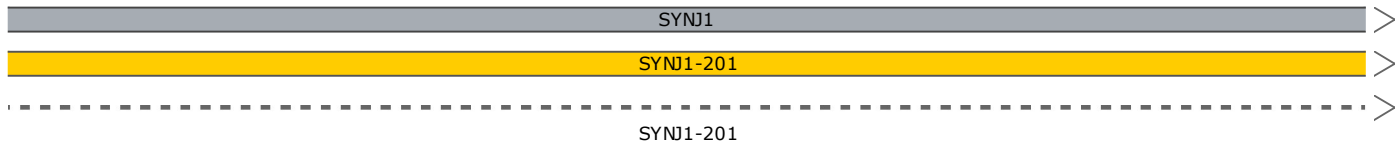
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1785



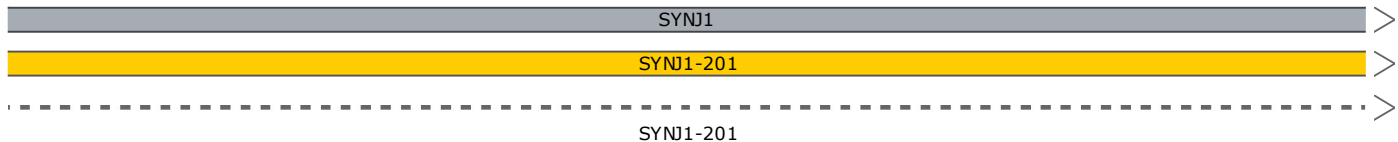
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1870



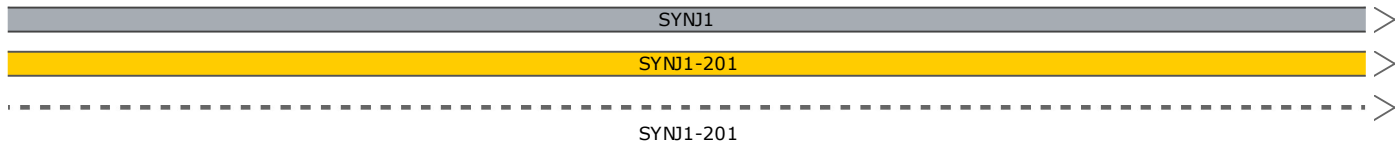
GATCTTCAAATTAGGTTATAAAGAGCTAAACAAAATGAAATATAAAGATATGTATGTAAAATATTAAGATTTAAAAGGAATTTAT
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1955



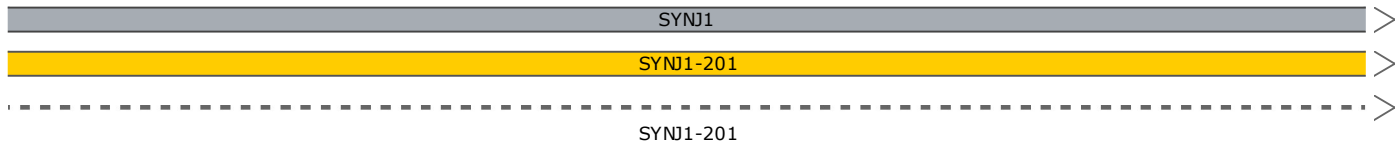
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2040



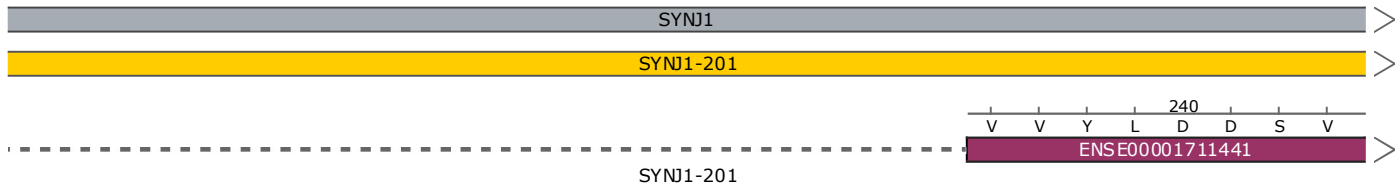
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2125



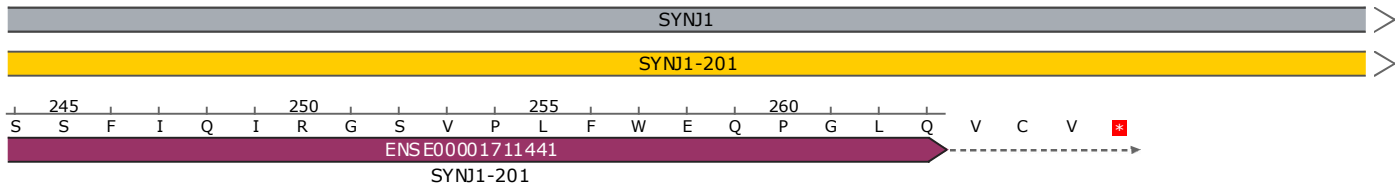
TAATGTAAGTGTAACAACCTTTCTGTGGAAATAGTTACATATTATTTTTTTTTCTGTAGGTTGTGTACTTAGATGACTCAGTTT
 ATTACATTCACATTGTTGAAAAGACACCTTTATCAAATGTATAATAAAAAAAGACATCCAACACATGAATCTACTGAGTCAAA

2210



CTTCCTTCATACAAATCCGAGGATCTGTTCCATTGTTCTGGGAGCAACCAGGGTTGCAAGTATGTGTTTGACATTCAGTTATTTT
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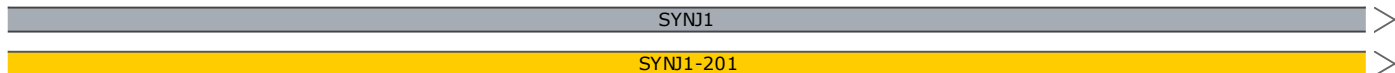
2295



245 S S F I Q I R G 250 S V P L F W E Q 255 P G L Q 260 V C V *

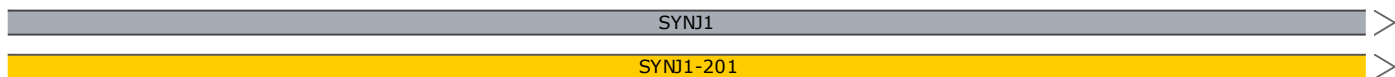
TGTTTTTGAACAATTTTCATATTTCTAAACTTTCTGGATAGTTTATTAATTAATTCATTGATGGTTCCATTATTCCATCTAAT
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 ACAAAAAAAGTGTAAAAGTATAAAAAGATTTGAAAGACCTATCAAATAATTAATTAAGTAACTACCAAGGTAATAAGGTAGATTA

2380



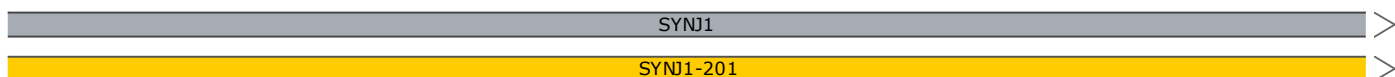
AATGTTAGCTGGATTTGCAAATAAGGGTCTAGACGAGTACAGAGTTTCTGGAATTATCTTAGATATTTTTCTTTTAAATGCTCTT
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 TTACAATCGACCTAAACGTTTATTCCCAGATCTGCTCATGTCTCAAAGACCTTAATAGAATCTATAAAAAAGAAAATTACGAGAA

2465



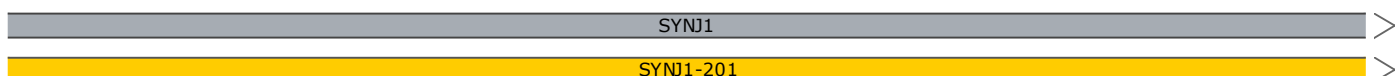
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2550



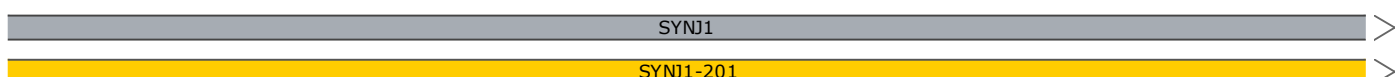
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2635



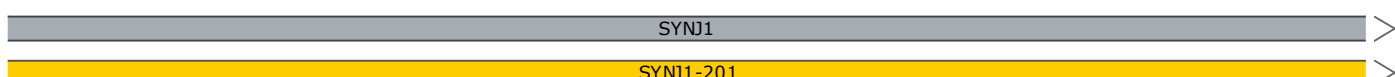
CCAGACTTCTTAATTGGGATCTTACTCTACCACTACTAGCTGTGTGATCTTGGGCAAATAATTTAACCCCTTGTGTGTCTCAGTT
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2720

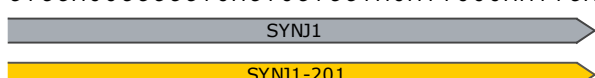


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 AGGAATAGACATATTACCCTTATTATAATTATCATGGATGAAATATCCCAACAACATTCCTAATTTAATTTTCGTGAATCTTATC

2805



CACCTGGCCCCCAGTCAGCACCATGTAAGGGTAACT 3 '
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 GTGGACCGGGGTTCAGTCGTGGTACATTCCCAATTGA 5 ' 2842



Feature	Location	Size	Start	End	Type
✓ SYNJ1	1 .. 2842	2842 bp	■	→	gene
/note = gene ENSG00000159082 Protein coding					
✓ SYNJ1-201	1 .. 2842	2842 bp	■	→	prim_transcript
/note = primary transcript ENST00000357345					
SYNJ1-202	1 .. 2842	2842 bp	■	→	prim_transcript
/note = primary transcript ENST00000382491					
SYNJ1-203	1 .. 2842	2842 bp	■	→	prim_transcript
/note = primary transcript ENST00000382499					
SYNJ1-205	1 .. 2842	2842 bp	■	→	prim_transcript
/note = primary transcript ENST00000429236					
SYNJ1-206	1 .. 2842	2842 bp	■	→	prim_transcript
/note = primary transcript ENST00000433931					
SYNJ1-211	1 .. 2842	2842 bp	■	→	prim_transcript
/note = primary transcript ENST00000630077					
SYNJ1-212	1 .. 2842	2842 bp	■	→	prim_transcript
/note = primary transcript ENST00000674204					
SYNJ1-213	1 .. 2842	2842 bp	■	→	prim_transcript
/note = primary transcript ENST00000674308					
SYNJ1-214	1 .. 2842	2842 bp	■	→	prim_transcript
/note = primary transcript ENST00000674351					
SYNJ1-208	1 .. 1271	1271 bp	■	→	prim_transcript
/note = primary transcript ENST00000456084					
✓ SYNJ1-201	1215 .. 2269	1055 bp	■	→	CDS
▶ 2 segments = 310 bp					
/codon_start = 1					
/note = coding sequence ENSP00000349903					
/translation = NQSLHLHLKHYGVNCDDWLLRLMCGGVEIRTIYAAHKQAKACLISRLSCERAGTRFNVRGTNDDGHVANFVETEQ, , VVYLDDSVSFSFIQIRGSVPLFWEQPLQ 103 amino acids = 11.6 kDa					
SYNJ1-202	1215 .. 2269	1055 bp	■	→	CDS
▶ 2 segments = 310 bp					
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/note = coding sequence ENSP00000371931					
/translation = NQSLHLHLKHYGVNCDDWLLRLMCGGVEIRTIYAAHKQAKACLISRLSCERAGTRFNVRGTNDDGHVANFVETEQ, , VVYLDDSVSFSFIQIRGSVPLFWEQPLQ 103 amino acids = 11.6 kDa					
SYNJ1-203	1215 .. 2269	1055 bp	■	→	CDS
▶ 2 segments = 310 bp					
/codon_start = 1					
/note = coding sequence ENSP00000371939					
/translation = NQSLHLHLKHYGVNCDDWLLRLMCGGVEIRTIYAAHKQAKACLISRLSCERAGTRFNVRGTNDDGHVANFVETEQ, , VVYLDDSVSFSFIQIRGSVPLFWEQPLQ 103 amino acids = 11.6 kDa					
SYNJ1-205	1215 .. 2269	1055 bp	■	→	CDS
▶ 2 segments = 310 bp					
/codon_start = 1					
/note = coding sequence ENSP00000413649					
/translation = NQSLHLHLKHYGVNCDDWLLRLMCGGVEIRTIYAAHKQAKACLISRLSCERAGTRFNVRGTNDDGHVANFVETEQ, , VVYLDDSVSFSFIQIRGSVPLFWEQPLQ 103 amino acids = 11.6 kDa					
SYNJ1-206	1215 .. 2269	1055 bp	■	→	CDS
▶ 2 segments = 310 bp					
/codon_start = 1					
/note = coding sequence ENSP00000409667					
/translation = NQSLHLHLKHYGVNCDDWLLRLMCGGVEIRTIYAAHKQAKACLISRLSCERAGTRFNVRGTNDDGHVANFVETEQ, , VVYLDDSVSFSFIQIRGSVPLFWEQPLQ 103 amino acids = 11.6 kDa					

Feature	Location	Size	Start	End	Type
SYNJ1-211	1215 .. 2269	1055 bp	■	→	CDS
▶ 2 segments = 310 bp					
/codon_start = 1					
/note = coding sequence ENSP00000487560					
/translation = NQSLHLHLKHYGVNCDDWLLRLMCGGVEIRTIYAAHKQAKACLISRLSCERAGTRFNVRGTNDDGHVANFVETEQ, , VVYLDDSVSSFIQIRGSVPLFWEQPGLQ 103 amino acids = 11.6 kDa					
SYNJ1-212	1215 .. 2269	1055 bp	■	→	CDS
▶ 2 segments = 310 bp					
/codon_start = 1					
/note = coding sequence ENSP00000501504					
/translation = NQSLHLHLKHYGVNCDDWLLRLMCGGVEIRTIYAAHKQAKACLISRLSCERAGTRFNVRGTNDDGHVANFVETEQ, , VVYLDDSVSSFIQIRGSVPLFWEQPGLQ 103 amino acids = 11.6 kDa					
SYNJ1-213	1215 .. 2269	1055 bp	■	→	CDS
▶ 2 segments = 310 bp					
/codon_start = 1					
/note = coding sequence ENSP00000501426					
/translation = NQSLHLHLKHYGVNCDDWLLRLMCGGVEIRTIYAAHKQAKACLISRLSCERAGTRFNVRGTNDDGHVANFVETEQ, , VVYLDDSVSSFIQIRGSVPLFWEQPGLQ 103 amino acids = 11.6 kDa					
SYNJ1-214	1215 .. 2269	1055 bp	■	→	CDS
▶ 2 segments = 310 bp					
/codon_start = 1					
/note = coding sequence ENSP00000501530					
/translation = NQSLHLHLKHYGVNCDDWLLRLMCGGVEIRTIYAAHKQAKACLISRLSCERAGTRFNVRGTNDDGHVANFVETEQ, , VVYLDDSVSSFIQIRGSVPLFWEQPGLQ 103 amino acids = 11.6 kDa					
SYNJ1-208	1215 .. 1271	57 bp	■	→	CDS
/codon_start = 1					
/note = coding sequence ENSP00000412707					
/translation = NQSLHLHLKHYGVNCDDW 19 amino acids = 2.2 kDa					
✓ Donor Template WT -> SNV	1354 .. 1453	100 bp	■		misc_feature
✓ gRNA Protospacer	1372 .. 1391	20 bp	■		misc_feature
✓ SNV	1391 .. 1391	1 bp	■		misc_feature
/note = WT = G SNV = A					
✓ PAM	1392 .. 1394	3 bp	■		misc_feature

Primer	Length	Binding Sites	Tm	Date Added
✓ PCR Forward /sequence = TAAAGACATAACAGAAATGGGCCAC 40% GC / 7701.1 Da	25-mer	955 .. 979	57°C	Sep 15, 2023
✓ Sanger Sequencing Primer /sequence = GCGTGAATTGTGATGACTG 50% GC / 6228.1 Da	20-mer	1249 .. 1268	57°C	Sep 15, 2023
✓ Donor Template WT -> SNV /sequence = ACACTATATACCTGTTCTGTTTCTACAAAATTGGCAACATGACCATCATCATTTGTTCCCTGGACATTAACCTGGTCCCAGCTCGTTCACAGCTTAA 40% GC / 30,529.9 Da	100-mer	1354 .. 1453	73°C	Sep 15, 2023
✓ gRNA Protospacer /sequence = GGGACCAGGTTTAATGTCCG 55% GC / 6173.1 Da	20-mer	1372 .. 1391	58°C	Sep 15, 2023
✓ PCR Reverse /sequence = AATTTGAAGATCTGTGTTGGGCTGG 44% GC / 7783.1 Da	25-mer	1858 .. 1882	60°C	Sep 15, 2023