

INK2J00053R_GCH1_G201E_H01_AA
1160 bp

5'
3'

GCACATTCTTCACATTTTCATGCATATACCTGCATTTTCAAATCAATTTATTTGGATTATGTTTAAACAAAAATGGGCTCATT
CGTGTAAGGAAGTGTAAGTACGTATATGGACGTAAGTAAAGTTAGTTAAATAAACCTAATACAAATTTGTTTTACCCGAGTAAA

85

GCH1

GCH1-202

TATACATAATCAGCCTTGCTTTTTCCCTGCTTTTTTCATTTAACAAATCTTAAACATTTTTGCCACATCCATGTAACATCTC
ATATGTATTAGTCGGAACGAAAAAGGGACGAAAAAGTAAATTGTTTGAATTTGTAAAAACGGTGTAGGTACATTGATAGAG

170

GCH1

GCH1-202

ATTCATTCTGGTGGCTGTCTAGAATCCTACCGTATATGCCATGGCTTGGCGTAACCTATACCAGCTCTGATAGATACTGGGGGT
TAAGTAAGACCACCGACAGATCTTAGGATGGCATATACGGTACCGAACCGCATTGGATATGGTTCGAGACTATCTATGACCCCCA

255

GCH1

GCH1-202

PCR Forward
GACAAGTCATTTTATTCAGGACAGG

TTCATCAGTTTTCAAATAGATGCAGTGCTGCAATGAATATTCCTGTATGAATTTAAAGACAAGTCATTTTATTCAGGACAGGAAC
AAGTAGTCAAAAGTTTATCTACGTACGACGTTACTTATAAGGACATACTTAATTTCTGTTTCAGTAAAATAAGTCTGTCTCTTG

340

GCH1

GCH1-202

TATATTATTTAGGTTAAATTGTTGGTTTTCAACATTGCTCTAAGCACAATTCAATAATTGGACTGCAGCCCCCTTTGTTAACCTG
ATATAATAAATCCAATTTAAACAACCAAAGTTGTAACGAGATTCTGTGTTAAGTTATTAACCTGACGTCGGGGAAACAATTGGGAC

425

GCH1

GCH1-202

TTGCAGGCTATTTATTTGCTGCACTACTTTACCTCCATGGAGGTGCTTGGTAACCAGTACTGTGTTGTTCTAACTGCACAGGTAT
AACGTCCGATAAATAAACGACGTGATGAAATGGAGGTACCTCCACGAACCATTGGTCATGACACAACAAGATTGACGTGTCCATA

510

GCH1

GCH1-202

GAGATAATTGCTATTCTAATTCCTTCCCGCAGTGATGCTGGAGGGCTTCAGGGTGTCTGAGATCTCTTTAGCCCTGTACTTCAG
CTCTATTAACGATAAGATTAAGGAAGGGCGTCACTACGACCTCCGAAGTCCACAAGACTCTAGAGAAATCGGGACATGAAGTC

595

GCH1

GCH1-202

GTGAGGGAGTTGAATCCGGGCCTCTCTGTGGCCAGTCAGCAGACAAAGCAGTCTGGTAAAAGCTGGTGTGTCTTTGGCTCTTAAA
CACTCCCTCAACTTAGGCCCGGAGAGACACCGGGTCAGTCGTCTGTTTCGTCAGACCATTTTCGACCACACAGAACCAGAGAATTT

680

GCH1

GCH1-202

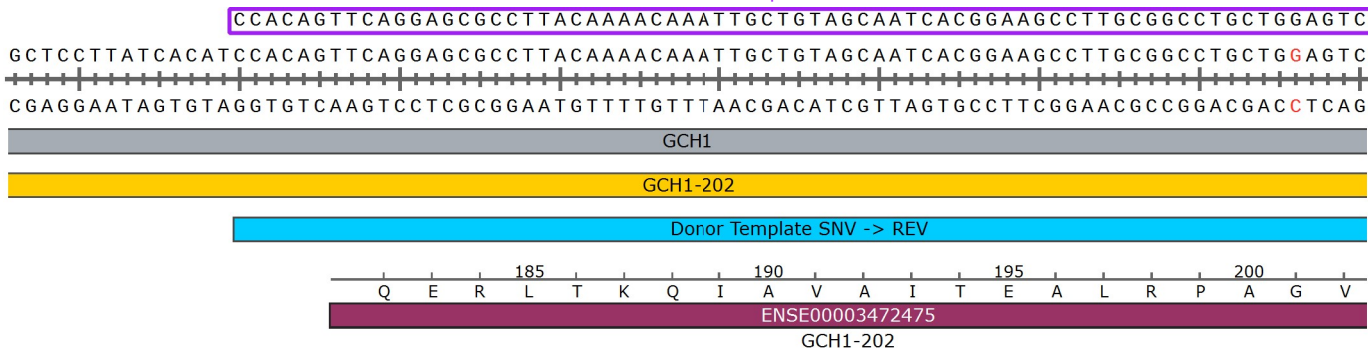
TCTCACAGAAGTCTGATTTTTAAGATTTCAAATGTTCTAGAGACAGAAAAAGCTTCCAGCTGTTTGTGTCAGACTCTCAAAGTGA
AGAGTGTCTTCAGACTAAAAATTCTAAAGTTTACAAGATCTCTGTCTTTTTCGAAGGTCGACAAACACAGTCTGAGAGTTTGACT

765

GCH1

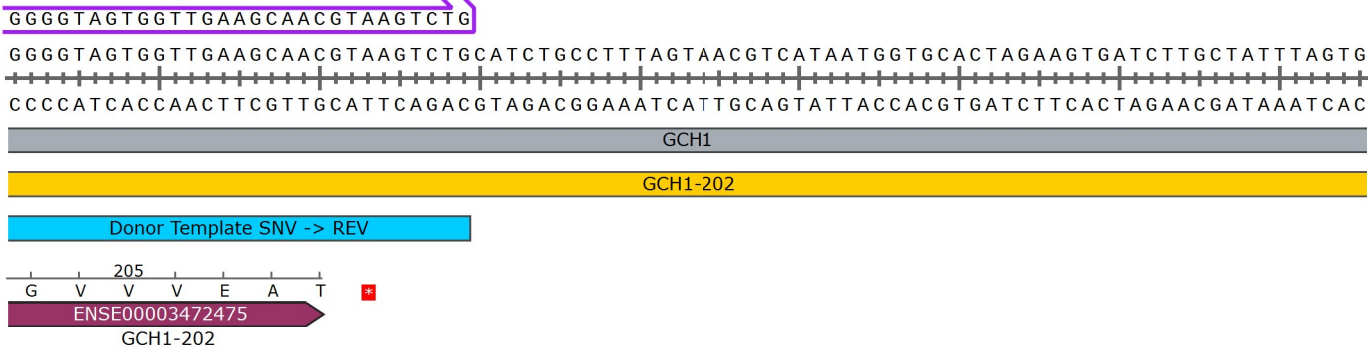
GCH1-202

Donor Template SNV -> REV

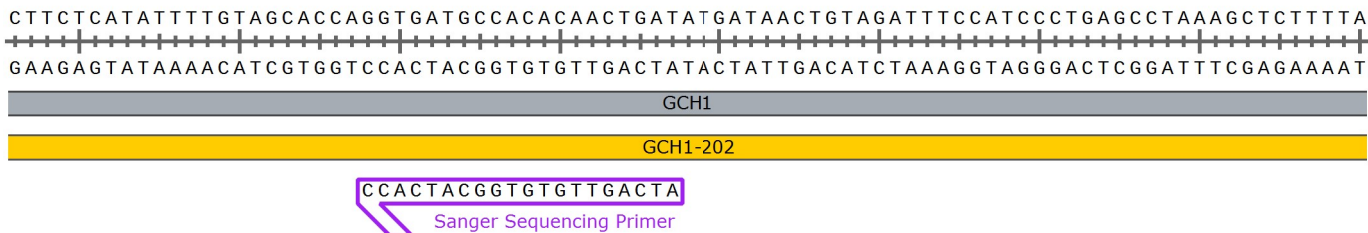


850

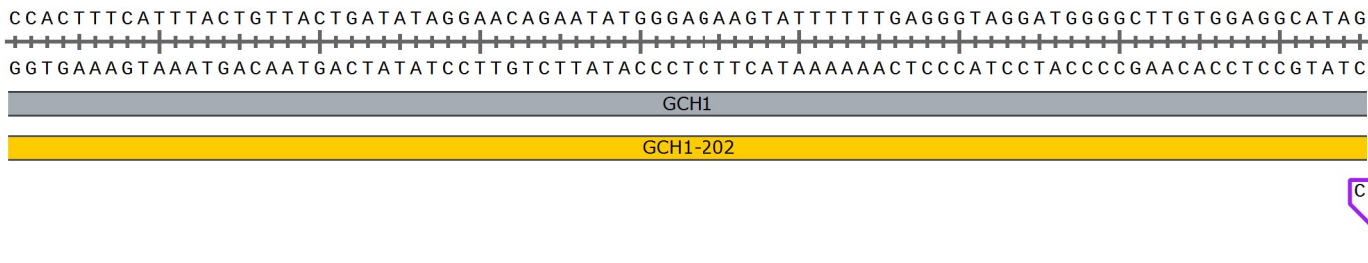
Donor Template SNV -> REV



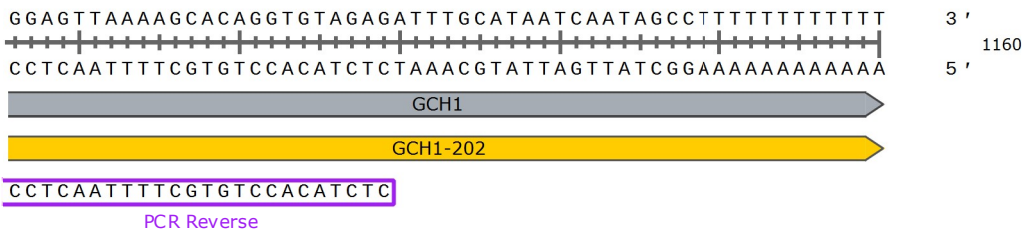
935



1020



1105



Feature	Location	Size	Start	End	Type
✓ GCH1	1 .. 1160	1160 bp	█	➔	gene
/note = gene ENSG00000131979 Protein coding					
GCH1-201	1 .. 1160	1160 bp	█	➔	prim_transcript
/note = primary transcript ENST00000254299 protein_coding_CDS_not_defined					
✓ GCH1-202	1 .. 1160	1160 bp	█	➔	prim_transcript
/note = primary transcript ENST00000395514					
GCH1-203	1 .. 1160	1160 bp	█	➔	prim_transcript
/note = primary transcript ENST00000395521 protein_coding_CDS_not_defined					
GCH1-204	1 .. 1160	1160 bp	█	➔	prim_transcript
/note = primary transcript ENST00000491895					
GCH1-205	1 .. 1160	1160 bp	█	➔	prim_transcript
/note = primary transcript ENST00000536224					
GCH1-206	1 .. 1160	1160 bp	█	➔	prim_transcript
/note = primary transcript ENST00000543643					
✓ Donor Template SNV -> REV	780 .. 879	100 bp	█	⌊	misc_feature
✓ GCH1-202	786 .. 870	85 bp	█	➔	CDS
/codon_start = 1					
/note = coding sequence ENSP00000378890					
/translation = QERLTKQIAVAITEALRPAGVGVVVEA 28 amino acids = 2.8 kDa					
GCH1-204	786 .. 870	85 bp	█	➔	CDS
/codon_start = 1					
/note = coding sequence ENSP00000419045					
/translation = QERLTKQIAVAITEALRPAGVGVVVEA 28 amino acids = 2.8 kDa					
GCH1-205	786 .. 870	85 bp	█	➔	CDS
/codon_start = 1					
/note = coding sequence ENSP00000445246					
/translation = QERLTKQIAVAITEALRPAGVGVVVEA 28 amino acids = 2.8 kDa					
GCH1-206	786 .. 870	85 bp	█	➔	CDS
/codon_start = 1					
/note = coding sequence ENSP00000444011					
/translation = QERLTKQIAVAITEALRPAGVGVVVEA 28 amino acids = 2.8 kDa					
✓ PAM	839 .. 841	3 bp	█	⌊	misc_feature
✓ gRNA Protospacer	842 .. 861	20 bp	█	⌊	misc_feature
✓ SNV	846 .. 846	1 bp	█	⌊	misc_feature
/note = SNV = A REV = G					

Primer	Length		Binding Sites	↕	Tm	Date Added
✓ PCR Forward	25-mer		313 .. 337	→	55°C	Jul 18, 2023
/sequence = GACAAGTCATTTTATTCAGGACAGG 40% GC / 7705.1 Da						
✓ Donor Template SNV -> REV	100-mer		780 .. 879	→	79°C	Jul 18, 2023
/sequence = CCACAGTTCAGGAGCGCCTTACAAAACAAATTGCTGTAGCAATCACGGAAGCCTTGCGGCCTGCTGGAGTCGGGGTAGTGGTTGAAGCAACGTAAGTCTG 53% GC / 30,997.1 Da						
✓ gRNA Protospacer	20-mer		842 .. 861	←	57°C	Jul 18, 2023
/sequence = ACCACTACCCCGACTTCAGC 60% GC / 5966.9 Da						
✓ Sanger Sequencing Primer	20-mer		958 .. 977	←	58°C	Jul 18, 2023
/sequence = ATCAGTTGTGTGGCATCACC 50% GC / 6108.0 Da						
✓ PCR Reverse	25-mer		1105 .. 1129	←	60°C	Jul 18, 2023
/sequence = CTCTACACCTGTGCTTTTAACTCCC 48% GC / 7478.9 Da						