



INK2J00053_GCH1_G201E_C08_BB
1285 bp

AAAGCTGGTGTGCTTTGGCTCTTAAATCTCACAGAAGTCTGATTTTTAAGATTTCAAATGTTCTAGAGACAGAAAAAGCTTCCAG
TTTCGACCACACAGAACCGAGAATTTAGAGTGTCTTCAGACTAAAAATTCTAAAGTTTACAAGATCTCTGTCTTTTTTCGAAGGTC

850

GCH1

GCH1-202

Donor Template WT -> SNV

CCACAGTTCAGGAGCGCCTTACAAAACAAATTGCTGTAGCAATCA

CTGTTTGTGTGTCAGACTCTCAAAGTCTTATCACATCCACAGTTCAGGAGCGCCTTACAAAACAAATTGCTGTAGCAATCA
GACAAACACAGTCTGAGAGTTTGACTCGAGGAATAGTGTAGGTGTCAAGTCTCGCGGAATGTTTTGTTTAAACGACATCGTTAGT

935

GCH1

GCH1-202

Donor Template WT -> SNV

Q E R L T K Q I A V A I
ENSE00003472475
GCH1-202

Donor Template WT -> SNV

CGGAAGCCTTGCGGCCTGCTGAGTCTGGGGTAGTGGTTGAAGCAACGTAAGTCTG

CGGAAGCCTTGCGGCCTGCTGAGTCTGGGGTAGTGGTTGAAGCAACGTAAGTCTGCATCTGCCTTTAGTAACGTCATAATGGTGC
GCCTTCGGAACGCCGGACGACCTCAGCCCCATCACCAACTTCGTTGCATTTCAGACGTAGACGGAAATCATTGCAGTATTACCACG

1020

GCH1

GCH1-202

Donor Template WT -> SNV

T E A L R P A G V G V V E A T
ENSE00003472475
GCH1-202

PAM
gRNA Protospacer

SNV

CGACCTCAGCCCCATCACCA
gRNA Protospacer

ACTAGAAGTGATCTTGCTATTTAGTGTCTTCATATTTTGTAGCACCAGGTGATGCCACACAACCTGATATGATAACTGTAGATTT
TGATCTTCACTAGAACGATAAATCACGAAGAGTATAAAACATCGTGGTCCACTACGGTGTGTTGACTATACTATTGACATCTAAA

1105

GCH1

GCH1-202

CCACTACGGTGTGTTGACTA
Sanger Sequencing Primer

CCATCCCTGAGCCTAAAGCTCTTTACCACTTTCATTTACTGTTACTGATATAGGAACAGAATATGGGAGAAGTATTTTTTGGAGG
GGTAGGGACTCGGATTTTCGAGAAAATGGTGAAAGTAAATGACAATGACTATATCCTTGTCTTATACCCTCTTCATAAAAAAAGTCC

1190

GCH1

GCH1-202

GTAGGATGGGGCTTGTGGAGGCATAGGGAGTTAAAAGCACAGGTGTAGAGATTTGCATAATCAATAGCCTTTTTTTTTTTTGGAGA
CATCCTACCCCGAACACCTCCGTATCCCTCAATTTTCGTGTCCACATCTCTAAACGTATTAGTTATCGGAAAAAAAAAAAAAAGTCT

1275

GCH1

GCH1-202

CCCTCAATTTTCGTGTCCACATCTC
PCR Reverse

TGGAGCCTCA 3'
1285
ACCTCGGAGT 5'

GCH1

GCH1-202

Feature	Location	Size	Start	End	Type
✓ GCH1	1 .. 1285	1285 bp	■	➔	gene
/note = gene ENSG00000131979 Protein coding					
GCH1-201	1 .. 1285	1285 bp	■	➔	prim_transcript
/note = primary transcript ENST00000254299 protein_coding_CDS_not_defined					
✓ GCH1-202	1 .. 1285	1285 bp	■	➔	prim_transcript
/note = primary transcript ENST00000395514					
GCH1-203	1 .. 1285	1285 bp	■	➔	prim_transcript
/note = primary transcript ENST00000395521 protein_coding_CDS_not_defined					
GCH1-204	1 .. 1285	1285 bp	■	➔	prim_transcript
/note = primary transcript ENST00000491895					
GCH1-205	1 .. 1285	1285 bp	■	➔	prim_transcript
/note = primary transcript ENST00000536224					
GCH1-206	1 .. 1285	1285 bp	■	➔	prim_transcript
/note = primary transcript ENST00000543643					
✓ Donor Template WT -> SNV	891 .. 990	100 bp	■	⌊	misc_feature
✓ GCH1-202	897 .. 981	85 bp	■	➔	CDS
/codon_start = 1					
/note = coding sequence ENSP00000378890					
/translation = QERLTKQIAVAITEALRPAGVGVVVEA 28 amino acids = 2.8 kDa					
GCH1-204	897 .. 981	85 bp	■	➔	CDS
/codon_start = 1					
/note = coding sequence ENSP00000419045					
/translation = QERLTKQIAVAITEALRPAGVGVVVEA 28 amino acids = 2.8 kDa					
GCH1-205	897 .. 981	85 bp	■	➔	CDS
/codon_start = 1					
/note = coding sequence ENSP00000445246					
/translation = QERLTKQIAVAITEALRPAGVGVVVEA 28 amino acids = 2.8 kDa					
GCH1-206	897 .. 981	85 bp	■	➔	CDS
/codon_start = 1					
/note = coding sequence ENSP00000444011					
/translation = QERLTKQIAVAITEALRPAGVGVVVEA 28 amino acids = 2.8 kDa					
✓ PAM	950 .. 952	3 bp	■	⌊	misc_feature
✓ gRNA Protospacer	953 .. 972	20 bp	■	⌊	misc_feature
✓ SNV	957 .. 957	1 bp	■	⌊	misc_feature
/note = WT = G SNV = A					

Primer	Length		Binding Sites	↕	Tm	Date Added
✓ PCR Forward	25-mer		424 .. 448	→	55°C	Jul 18, 2023
/sequence = GACAAGTCATTTTATTCAGGACAGG 40% GC / 7705.1 Da						
✓ Donor Template WT -> SNV	100-mer		891 .. 990	→	78°C	Jul 18, 2023
/sequence = CCACAGTTCAGGAGCGCCTTACAAAACAATTGCTGTAGCAATCACGGAAGCCTTGCGGCCTGCTGAAGTCGGGGTAGTGGTTGAAGCAACGTAAGTCTG 52% GC / 30,981.1 Da						
✓ gRNA Protospacer	20-mer		953 .. 972	←	63°C	Jul 18, 2023
/sequence = ACCACTACCCCGACTCCAGC 65% GC / 5951.9 Da						
✓ Sanger Sequencing Primer	20-mer		1069 .. 1088	←	58°C	Jul 18, 2023
/sequence = ATCAGTTGTGTGGCATCACC 50% GC / 6108.0 Da						
✓ PCR Reverse	25-mer		1216 .. 1240	←	60°C	Jul 18, 2023
/sequence = CTCTACACCTGTGCTTTTAACTCCC 48% GC / 7478.9 Da						