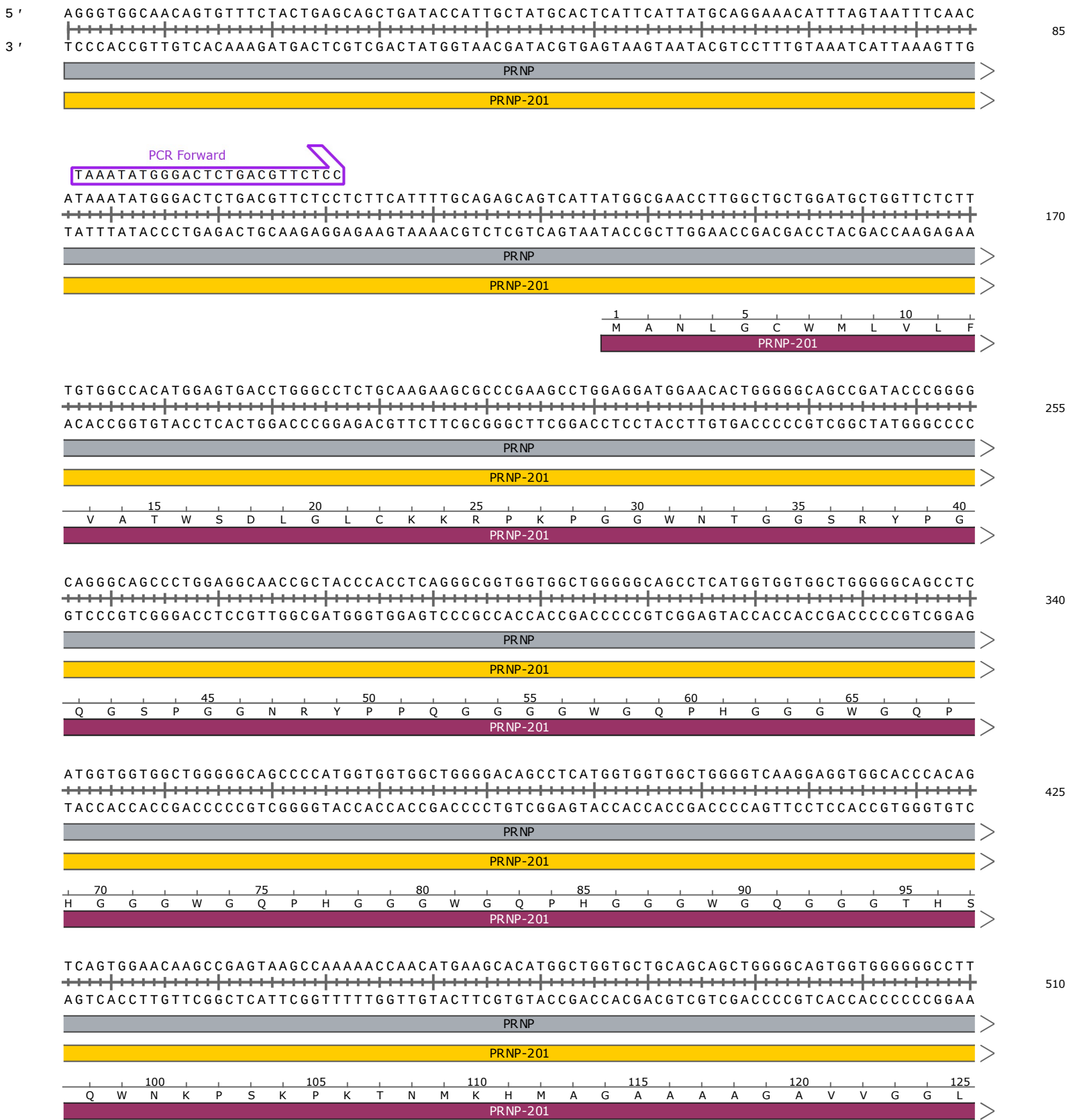


INK2J00068_PRNP_Q160X_A05_BB
1216 bp



Donor Template WT -> SNV

ATCATACATTTTCGGCAGTGACTATGAGGACCGTTACTATCGTGAAAACA

GGCGGCTACATGCTGGGAAGTGCCATGAGCAGGCCCATCATACATTTTCGGCAGTGACTATGAGGACCGTTACTATCGTGAAAACA
CCGCCGATGTACGACCCCTTACGGTACTCGTCCGGGTAGTATGTAAGCCGTCACCTGATACTCTGGCAATGATAGCACTTTTGT

595

PRNP

PRNP-201

G G Y M L G S A M S R P I I H F G S D Y E D R Y Y R E N

PRNP-201

Donor Template WT -> SNV

Donor Template WT -> SNV

TGCACCGTTACCCCAAC T AAGTGTACTACAGGCCCATGGATGAGTACAGCA

TGCACCGTTACCCCAAC CAAGTGTACTACAGGCCCATGGATGAGTACAGCAACCAGAACAACCTTTGTGCACGACTGCGTCAATAT
ACGTGGCAATGGGGTTG G TTCACATGATGTCCGGGTACCTACTCATGTGCGTTGGTCTTGTGAAACACGTGCTGACGCAGTTATA

680

PRNP

PRNP-201

M H R Y P N Q V Y Y R P M D E Y S N Q N N F V H D C V N I

PRNP-201

Donor Template WT -> SNV



CACAATCAAGCAGCACACGGTCACCACAACCACCAAGGGGGGGAAGTTCACCGAGACCGACGTTAAGATGATGGAGCGCGTGGTT
GTGTTAGTTTCGTGCTGTGCCAGTGGTGGTGGTGGTTCCTTCTTGAAGTGGCTCTGGCTGCAATTCTACTACCTCGCGCACCAA

765

PRNP

PRNP-201

T I K Q H T V T T T T K G E N F T E T D V K M M E R V V

PRNP-201



GAGCAGATGTGTATCACCCAGTACGAGAGGGAATCTCAGGCCTATTACCAGAGAGGATCGAGCATGGTCCTCTTCTCCTCTCCAC
CTCGTCTACACATAGTGGGTCATGCTCTCCCTTAGAGTCCGGATAATGGTCTCTCCTAGCTCGTACCAGGAGAAGAGGAGAGGTG

850

PRNP

PRNP-201

E Q M C I T Q Y E R E S Q A Y Y Q R G S S M V L F S S P

PRNP-201

CTGTGATCCTCCTGATCTCTTTCCTCATCTTCTGATAGTGGGATGAGGAAGGTCTTCTGTTTTACCATCTTTCTAATCTTT
GACACTAGGAGGACTAGAGAAAGGAGTAGAAGGACTATCACCTACTCCTTCCAGAAGGACAAAAGTGGTAGAAAGATTAGAAAA

935

PRNP

PRNP-201

P V I L L I S F L I F L I V G *

PRNP-201

TCCAGCTTGAGGGAGGCGGTATCCACCTGCAGCCCTTTTAGTGGTGGTGTCTCACTCTTTCTTCTCTTTGTCCC GGATAGGCT
 1020
 AGGTCGAACTCCCTCCGCCATAGGTGGACGTCGGGAAAATCACCACCACAGAGTGAGAAAGAAGAGAGAAACAGGGCCTATCCGA
 PRNP
 PRNP-201

PCR Reverse
 CCCCTTTGATTGAGTTCATC
 AATCAATACCCTTGGCACTGATGGGCACTGGAAAACATAGAGTAGACCTGAGATGCTGGTCAAGCCCCCTTTGATTGAGTTCATC
 1105
 TTAGTTATGGGAACCGTGACTACCCGTGACCTTTTGTATCTCATCTGGACTCTACGACCAGTTTCGGGGGAAACTAACTCAAGTAG
 PRNP
 PRNP-201

PCR Reverse
 ATGAG
 ATGAGCCGTTGCTAATGCCAGGCCAGTAAAAGTATAACAGCAAATAACCATTGGTTAATCTGGACTTATTTTTGGACTTAGTGCA
 1190
 TACTCGGCAACGATTACGGTCCGGTCATTTTCATATTGTCGTTTATTGGTAACCAATTAGACCTGAATAAAAACCTGAATCACGT
 PRNP
 PRNP-201

ACAGGTTGAGGCTAAAACAAATCTCA 3'
 1216
 TGTCCAACCTCCGATTTTGTAGAGT 5'
 PRNP
 PRNP-201

Feature	Location	Size	Start	End	Type
✓ PRNP	1 .. 1216	1216 bp	■	→	gene
/note	= gene ENSG00000171867 Protein coding				
✓ PRNP-201	1 .. 1216	1216 bp	■	→	prim_transcript
/note	= primary transcript ENST00000379440				
PRNP-202	1 .. 1216	1216 bp	■	→	prim_transcript
/note	= primary transcript ENST00000424424				
PRNP-203	1 .. 1216	1216 bp	■	→	prim_transcript
/note	= primary transcript ENST00000430350				
PRNP-204	1 .. 1216	1216 bp	■	→	prim_transcript
/note	= primary transcript ENST00000457586				
✓ PRNP-201	136 .. 897	762 bp	■	→	CDS
/note	= coding sequence ENSP00000368752				
/translation	= MANLGCWMLVLFVATWSDLGLCKKRPKPGGWNTGGSRYPGQGSPGGNRYPPQGGGGWGQPHGGGWGQPHGGGWGQPHGGGWGQPHGGGWGQGGGTHSQWNKPSKPKTNMKHMA GAAAAGAVVGGGLGGYMLGSAMSRPIIHFGSDYEDRYRENMHRYPNQVYYRPMDEYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYERESQAYY QRGSSMVLFSPPVILLISFLIFLIVG* 253 amino acids = 27.7 kDa				
PRNP-202	136 .. 897	762 bp	■	→	CDS
/note	= coding sequence ENSP00000411599				
/translation	= MANLGCWMLVLFVATWSDLGLCKKRPKPGGWNTGGSRYPGQGSPGGNRYPPQGGGGWGQPHGGGWGQPHGGGWGQPHGGGWGQPHGGGWGQGGGTHSQWNKPSKPKTNMKHMA GAAAAGAVVGGGLGGYMLGSAMSRPIIHFGSDYEDRYRENMHRYPNQVYYRPMDEYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYERESQAYY QRGSSMVLFSPPVILLISFLIFLIVG* 253 amino acids = 27.7 kDa				
PRNP-203	136 .. 897	762 bp	■	→	CDS
/note	= coding sequence ENSP00000399376				
/translation	= MANLGCWMLVLFVATWSDLGLCKKRPKPGGWNTGGSRYPGQGSPGGNRYPPQGGGGWGQPHGGGWGQPHGGGWGQPHGGGWGQPHGGGWGQGGGTHSQWNKPSKPKTNMKHMA GAAAAGAVVGGGLGGYMLGSAMSRPIIHFGSDYEDRYRENMHRYPNQVYYRPMDEYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYERESQAYY QRGSSMVLFSPPVILLISFLIFLIVG* 253 amino acids = 27.7 kDa				
PRNP-204	136 .. 897	762 bp	■	→	CDS
/note	= coding sequence ENSP00000415284				
/translation	= MANLGCWMLVLFVATWSDLGLCKKRPKPGGWNTGGSRYPGQGSPGGNRYPPQGGGGWGQPHGGGWGQPHGGGWGQPHGGGWGQPHGGGWGQGGGTHSQWNKPSKPKTNMKHMA GAAAAGAVVGGGLGGYMLGSAMSRPIIHFGSDYEDRYRENMHRYPNQVYYRPMDEYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYERESQAYY QRGSSMVLFSPPVILLISFLIFLIVG* 253 amino acids = 27.7 kDa				
✓ Donor Template WT -> SNV	547 .. 646	100 bp	■		misc_feature
✓ PAM	606 .. 608	3 bp	■		misc_feature
✓ gRNA Protospacer	609 .. 628	20 bp	■		misc_feature
✓ SNV	613 .. 613	1 bp	■		misc_feature
/note	= WT = C SNV = T				

Primer	Length	Binding Sites	Tm	Date Added
✓ PCR Forward /sequence = TAAATATGGGACTCTGACGTTCTCC 44% GC / 7632.0 Da	25-mer	87 .. 111	58°C	Jun 14, 2023
✓ Donor Template WT -> SNV /sequence = ATCATACATTTTCGGCAGTGACTATGAGGACCGTTACTATCGTGAAAACATGCACCGTTACCCCAACTAAGTGTACTACAGGCCCATGGATGAGTACAGCA 46% GC / 30,787.1 Da	100-mer	547 .. 646	75°C	Jun 14, 2023
✓ gRNA Protospacer /sequence = GCCTGTAGTACACTTGGTTG 50% GC / 6139.1 Da	20-mer	609 .. 628	54°C	Jun 14, 2023
✓ Sanger Sequencing Primer /sequence = ACGCGCTCCATCATCTTAAC 50% GC / 5997.0 Da	20-mer	742 .. 761	57°C	Jun 14, 2023
✓ PCR Reverse /sequence = CCCCTTTGATTGAGTTCATCATGAG 44% GC / 7623.0 Da	25-mer	1086 .. 1110	58°C	Jun 14, 2023