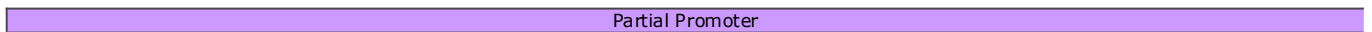


5'
3'

TAAC TAATGACATTTCTAGACAAAGTGACTTCAGATTTTCAAAGCGTACCTGTTTACATCATTTTGCCAATTTGCGGTACTGCA
ATTGATTACTGTAAAGATCTGTTTCACTGAAGTCTAAAAGTTTCGCATGGGACAAATGTAGTAAAACGGTTAAAGCGCATGACGT

85

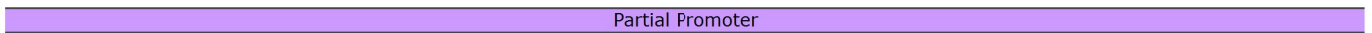


PCR Forward

agaaggttgTTTTCTCCacatttcg

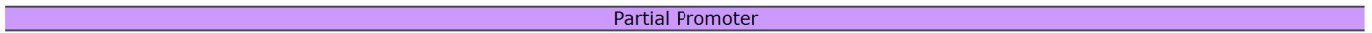
ACCGGCGGGCCACGCCCCCGTGAAAAGAAGGTTGTTTTCTCCACATTTGCGGGTTCTGGACGTTTCCCGGCTGCGGGGCGGGGGG
TGGCCGCCCGGTGCGGGGGCACTTTTCTTCCAACAAAAGAGGTGTAAAGCCCCAAGACCTGCAAAGGGCCGACGCCCCGCCCC

170



AGTCTCCGGCGCACGCGGGCCCTTGGCCCCGCCCCAGTCATTTCCCGGCCACTCGCGACCCGAGGCTGCCGACAGGGGGCGGGCTG
TCAGAGGCCGCGTGCGCCGGGAACCGGGGCGGGGTCAGTAAGGGCCGGTGAGCGCTGGGCTCCGACGGCGTCCCCGCCCGAC

255



Sanger Sequencing Primer

gtgCGaggcgattggTTTg

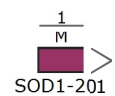
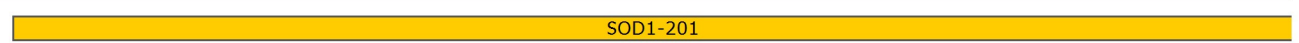
AGCGCGTGCAGGGCGATTGGTTTGGGGCCAGAGTGGGCGAGGCGCGGAGGCTGGCCTATAAAGTAGTCGCGGAGACGGGGTGCT
TCGCGCACGCTCCGCTAACCAAACCCCGGTCTCACCCGCTCCGCGCCTCCAGACCGGATATTTTCATCAGCGCCTCTGCCCCACGA

340



GGTTTGCCTCGTAGTCTCCTGCAGCGTCTGGGGTTTTCCGTTGCAGTCTCTCGGAACCAAGGACCTCGGCGTGGCCTAGCGAGTTATG
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425



Donor Template WT -> SNV

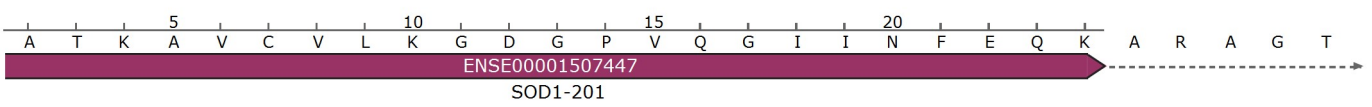
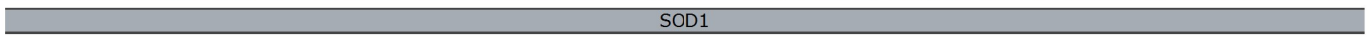
GATCGCTCAATAC
Donor Template WT -> SNV

gRNA Protospacer

GAAGGCCGTGTGCGTGCTGA

GCGACGAAGGCGTGTGCGTGCTGAAGGGCGACGGCCCAAGTGCAGGGCATCATCAATTTTCGAGCAGAAGGCAAGGGCTGGGACGG
CGCTGCTTCCGGCACACGCACGACTTCCCGCTGCCGGGTCACGTCCCGTAGTAGTTAAAGCTCGTCTTCCGTTCCCGACCCCTGCC

510



CGCTGCTTCCGCACACGCACGACTTCCCGCTGCCGGGTCACGTCCCGTAGTAGTTAAAGCTCGTCTTCCggttcccgaccctgcc

Donor Template WT -> SNV

AGGCTTGTTTTCGAGGGCCGCTCCCACCCGCTCGTCCCCCGCGCACCTTTGCTAGGAGCGGGTCGCCCGCCAGGCCTCGGGGGCCG
TCCGAACAAACGCTCCGGCGAGGGTGGGCGAGCAGGGGGGCGCGTGGAAACGATCCTCGCCAGCGGGCGGTCCGGAGCCCCGGC

595

SOD1

SOD1-201

E A C L R G R S H P L V P P R T F A R S G S P A R P R G R
(in frame with SOD1-201)

Donor Template WT -> SNV

TC
Donor Template WT -> SNV

CCCTGGTCCAGCGCCCGGTCCCGGCCGTCGCCCGCCGGTGGTGCCTTCGCCCCAGCGGTGCGGTGCCCAAGTGCTGAGTCACC
GGGACCAGGTGCGGGGCCAGGGCCGGGCACGGCGGGCCAGCCACGGAAGCGGGGGTTCGCCACGCCACGGGTTACAGACTCAGTGG

680

SOD1

SOD1-201

P G P A P G P G P C R P V G A F A P S G A V P K C *
(in frame with SOD1-201)

GGGCGGGCCCCGGGCGCGGGGCGTGGGACCGAGGCCGCCGCGGGGCTGGGCCTGCGCGTGGCGGGAGCGCGGGGAGGGATTGCCGC
CCCCGCCGGGCCCGCGCCCCGCACCCTGGCTCCGGCGGGCGCCCCGACCCGGACGCGCACCCGCCCTCGCGCCCCCTCCCTAACGGGC

765

SOD1

SOD1-201

GGGCGGGGAGGGGCGGGGCGGGCGTGCTGCCCTCTGTGGTCTTGGGCCGCCGCCGCGGGTCTGTCGTGGTGCCTGGAGCGGC
CCCCGGCCCCCTCCCCGCCCCCGCCCGCACGACGGGAGACACCAGGAACCCGGCGGGCGGCCAGACAGCACCCAGGACCTCGCCG

850

SOD1

SOD1-201

TGTGCTCGTCCCTTGCTTGGCCGTGTTCTCGTTCCTGAGGGTCCCGCGGACACCGAGTGGCGCAGTGCCAGGCCAGCCCCGGGA
ACACGAGCAGGGAACGAACCGGCACAAGAGCAAGGACTCCAGGGCGCCTGTGGCTCACCGCGTCACGGTCCGGGTCCGGGCCCT

935

SOD1

SOD1-201

TGGCGACTGCGCCTGGGCCCGCCTGGTGTCTTCGCATCCCTCTCCGCTTTCGGCTTCAGCGCTCTAGGTGAGGGAGTCTTCGCT
ACCGCTGACGCGGACCCGGGCGGACCACAGAAGCGTAGGGAGAGGCGAAAGGCCGAAGTGCAGGATCCAGTCCCTCAGAAGCGA

1020

SOD1

SOD1-201

TTTGTACAGCTCTAAGGCTAGGAATGGTTTTTATATTTTTAAAAGGCTTTGGAAAACAAAAATACGCAACAGAGACCGTTTGTGT
AAACATGTCGAGATTCCGATCCTTACAAAAATATAAAAATTTTCCGAAACCTTTTGTTTTTATGCGTTGTCTCTGGCAAACACA

1105

SOD1

SOD1-201

GACACTTTCAGGGAAGTTTGTGGCCTCTGTTCTAGGTGATGATTGGGCTGCAAGGGCAGAGAAGGTAGCCTTGAACAGAGGTC
CTGTGAAACGTCCCTTCAAACGACCGGAGACAAGATCCAGTACTAACCAGCGTTCCCGTCTCTTCCATCGGAACCTTGTCTCCAG

1190

SOD1

SOD1-201

gagacaagatccagtactaaccgga
PCR Reverse

CTTTTCCTCCTCCTAAGCTCCGGGAGCCAGAGGTTTAACTGACCC

GAAAAGGAGGAGGATTGAGGCCCTCGGTCTCCAAATTGACTGGG

3'

1235

5'



Feature	Location	Size	±	Type
✓ Partial Promoter	1 .. 318	318 bp		misc_feature
✓ SOD1	319 .. 1235	917 bp		gene
/note = gene ENSG00000142168 Protein coding				
SOD1-202	319 .. 1235	917 bp		prim_transcript
/note = primary transcript ENST00000389995				
✓ SOD1-201	346 .. 1235	890 bp		prim_transcript
/note = primary transcript ENST00000270142				
SOD1-204	346 .. 1235	890 bp		prim_transcript
/note = primary transcript ENST00000476106 protein_coding_CDS_not_defined				
SOD1-203	362 .. 1235	874 bp		prim_transcript
/note = primary transcript ENST00000470944 protein_coding_CDS_not_defined				
✓ Donor Template WT -> SNV	413 .. 512	100 bp		misc_feature
✓ SOD1-201	423 .. 494	72 bp		CDS
/note = coding sequence ENSP00000270142				
/translation = MATKAVCVLKGDGPVQGIINFEQK 24 amino acids = 2.5 kDa				
SOD1-202	423 .. 437	15 bp		CDS
/note = coding sequence ENSP00000374645				
/translation = MATKA 5 amino acids = 520.7 Da				
✓ gRNA Protospacer	431 .. 450	20 bp		misc_feature
✓ SNV	436 .. 436	1 bp		misc_feature
/note = WT = C SNV = T				
✓ PAM	451 .. 453	3 bp		misc_feature

Primer	Length	Binding Sites	Tm	Date Added
✓ PCR Forward /sequence = agaaggttgTTTTCTCCACATTTCG 40% GC / 7638.0 Da	25-mer	111 .. 135 →	58°C	Oct 6, 2023
✓ Sanger Sequencing Primer /sequence = gtgCGAGGCgattggTTTg 58% GC / 5930.9 Da	19-mer	261 .. 279 →	59°C	Oct 13, 2023
✓ Donor Template WT -> SNV /sequence = ctccgtcccagcccttgCCTTCTGCTCGAAATTGATGATGCCCTGCACTGGGCCGTGCCCTTCAGCACGCACACGACCTTCGTCGCCATAACTCGCTAG 61% GC / 30,426.6 Da	100-mer	413 .. 512 ←	82°C	Oct 5, 2023
✓ gRNA Protospacer /sequence = GAAGGCCGTGTGCGTGCTGA 65% GC / 6214.1 Da	20-mer	431 .. 450 →	64°C	Oct 5, 2023
✓ PCR Reverse /sequence = agcccaatcatgacctagaacagag 48% GC / 7653.1 Da	25-mer	1132 .. 1156 ←	60°C	Oct 13, 2023