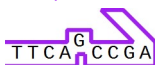


gRNA Protospacer



TTCAACCGAAGGTAAAGAACAAGAAGAGAAGTCCGGTGAAGATGGTGAGAAAGACACAAAGGATGACCAGACAGAGCAGGAACCT
 AAGTTGGCTTCCATTTCTTGTCTTCTTTCAGGCCACTTCTACCACCTTTTCTGTGTTTCCTACTGGTCTGTCTCGTCTCTTGGAA

595

MATR3

MATR3-201

S T E G K E Q E E K S G E D G E K D T K D D Q T E Q E P

ENSE00003768022

MATR3-201

Donor Template SNV -> REV



gRNA Protospacer



SNV

AAGTTGGCTTCCATTTCTTGTCTTCTTTCAGGCCACTTCTACCACCTTTTCTGTGTTTCCTACTGGTCT

Donor Template SNV -> REV

AATATGCTTCTTGAATCTGAAGATGAGCTACTTGTAGATGAAGAAGAAGCAGCAGCACTGCTAGAAAGTGGCAGTTCAGTGGGAG
 TTATACGAAGAAGCTTAGACTTCTACTCGATGAACATCTACTTCTTCTCGTCTGTCGTGACGATCTTTCACCGTCAAGTCACCCCTC

680

MATR3

MATR3-201

N M L L E S E D E L L V D E E E A A A L L E S G S S V G

ENSE00003768022

MATR3-201



Sanger Sequencing Primer

ACGAGACCGATCTTGCTAATTTAGGTGATGTGGCTTCTGATGGGAAAAAGGAACCATCAGATAAAGCTGTGAAAAAAGATGGAAG
 TGCTCTGGCTAGAACGATTAAATCCACTACACCGAAGACTACCCTTTTTCTTGGTAGTCTATTTTCGACACTTTTTTCTACCTTC

765

MATR3

MATR3-201

D E T D L A N L G D V A S D G K K E P S D K A V K K D G S

ENSE00003768022

MATR3-201

TGCTTCAGCAGCAGCAAAGAAAAAGCTTAAAAAGGTAAAGAAAGATACATTGATTTGTTTTAATAGAACATTAGATCAGATCAGT
 ACGAAGTCGTCGTCGTTTCTTTTCGAATTTTCCATTTCTTCTATGTAACATAACAAAATTATCTTGTAATCTAGTCTAGTCA

850

MATR3

MATR3-201

A S A A A K K K L K K V K K D T L I C F N R T L D Q I S

ENSE00003768022

MATR3-201

(in frame with MATR3-201)

ATTTCAAGTTATTTACCTAAGCAGGATCAGATAGAATTATATGATTTAAATCAGAAAATAAATCAGATATGAACCAGAATATAAA
 TAAAGTTCAATAAATGGATTTCGTCCTAGTCTATCTTAATATACTAAATTTAGTCTTTTATTTAGTCTATACTTGGTCTTATATT

935

MATR3

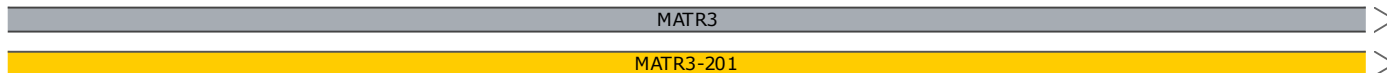
MATR3-201

I S S Y L P K Q D Q I E L Y D L N Q K I N Q I *

(in frame with MATR3-201)

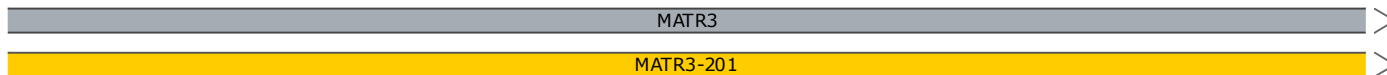
CATTTAAATCTAAACTCTGCAATAAATAATTAATAAGACATTTTATTATAGTTGGCAAAAAACATCAGCTCAAAGAGGAAACTT
 GTAAATTTAGATTTGAGACGTTATTTATTAATTTATTCTGTAAAATAATATCAACCGTTTTTTGTAGTCGAGTTTCTCCTTTGAA

1020



TTCAGTAAAAATGAGGGGAGAAAGACTCAAATATATGTGCTTCTGTATTGTAGTGGTGTAGTGGTAGCATATAGGTAGGCAGCCT
 AAGTCATTTTTACTCCCTCTTTCTGAGTTTTATATACACGAAGACATAACATCACCACATCACCATCGTATATCCATCCGTCGGA

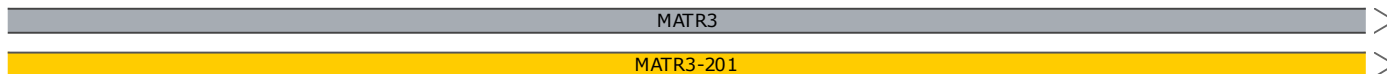
1105



CCATCGTATATCCATCCGTCGGA
 PCR Reverse

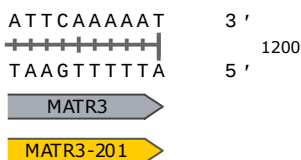
TATAGTGTAGCTTTGAAAAAAAAAATACAGGACGTGAGTTTGCAGTAAGTTAACTGACCCAACATAGTTAAAACTTTTGCCACTC
 ATATCACATCGAAACTTTTTTTTTTATGTCCTGCACTCAAACGTCATTCAATTGACTGGGTTGTATCAATTTGAAAACGGTGAG

1190



AT

PCR Reverse



Feature	Location	Size	Start	End	Type
✓ MATR3	1 .. 1200	1200 bp	■	→	gene
/note = gene ENSG00000015479 Protein coding					
MATR3	1 .. 1200	1200 bp	■	→	gene
/note = gene ENSG000000280987 Protein coding					
✓ MATR3-201	1 .. 1200	1200 bp	■	→	prim_transcript
/note = primary transcript ENST000000394805					
MATR3-202	1 .. 1200	1200 bp	■	→	prim_transcript
/note = primary transcript ENST000000502422 Retained intron					
MATR3-203	1 .. 1200	1200 bp	■	→	prim_transcript
/note = primary transcript ENST000000502499					
MATR3-206	1 .. 1200	1200 bp	■	→	prim_transcript
/note = primary transcript ENST000000503811					
MATR3-211	1 .. 1200	1200 bp	■	→	prim_transcript
/note = primary transcript ENST000000505625 Retained intron					
MATR3-215	1 .. 1200	1200 bp	■	→	prim_transcript
/note = primary transcript ENST000000510056					
MATR3-227	1 .. 1200	1200 bp	■	→	prim_transcript
/note = primary transcript ENST000000618441					
MATR3-228	1 .. 1200	1200 bp	■	→	prim_transcript
/note = primary transcript ENST000000361059 Protein coding					
MATR3-229	1 .. 1200	1200 bp	■	→	prim_transcript
/note = primary transcript ENST000000394800 Protein coding					
MATR3-230	1 .. 1200	1200 bp	■	→	prim_transcript
/note = primary transcript ENST000000502394 Protein coding					
MATR3-231	1 .. 1200	1200 bp	■	→	prim_transcript
/note = primary transcript ENST000000502929 Protein coding					
MATR3-232	1 .. 1200	1200 bp	■	→	prim_transcript
/note = primary transcript ENST000000504203 Protein coding					
MATR3-233	1 .. 1200	1200 bp	■	→	prim_transcript
/note = primary transcript ENST000000505016 Protein coding					
MATR3-236	1 .. 1200	1200 bp	■	→	prim_transcript
/note = primary transcript ENST000000509990 Protein coding					
MATR3-238	1 .. 1200	1200 bp	■	→	prim_transcript
/note = primary transcript ENST000000514694 Protein coding					
MATR3-210	1 .. 780	780 bp	■	→	prim_transcript
/note = primary transcript ENST000000504643 Retained intron					
MATR3-204	1 .. 522	522 bp	■	→	prim_transcript
/note = primary transcript ENST000000502944 Retained intron					

Feature	Location	Size	Start	End	Type
✓ MATR3-201	295 .. 799	505 bp	■	→	CDS
▶ 2 segments = 414 bp					
/note = coding sequence ENSP00000378284					
/translation = IPNRGIDLLKKDKSR, , KRSYSPDGKESPSDKKSKTDGSGQKTESSTEGKEQEEKSGEDGEKDKDDQTEQEPNMLLESEDELLVDEEEAAALLES GSSVGD ETDLANLG DVAS DGKKEPSDKAVKKDGSASAAAKKLLK 138 amino acids = 14.9 kDa					
MATR3-203	295 .. 799	505 bp	■	→	CDS
▶ 2 segments = 414 bp					
/note = coding sequence ENSP00000426030					
/translation = IPNRGIDLLKKDKSR, , KRSYSPDGKESPSDKKSKTDGSGQKTESSTEGKEQEEKSGEDGEKDKDDQTEQEPNMLLESEDELLVDEEEAAALLES GSSVGD ETDLANLG DVAS DGKKEPSDKAVKKDGSASAAAKKLLK 138 amino acids = 14.9 kDa					
MATR3-206	295 .. 799	505 bp	■	→	CDS
▶ 2 segments = 414 bp					
/note = coding sequence ENSP00000423587					
/translation = IPNRGIDLLKKDKSR, , KRSYSPDGKESPSDKKSKTDGSGQKTESSTEGKEQEEKSGEDGEKDKDDQTEQEPNMLLESEDELLVDEEEAAALLES GSSVGD ETDLANLG DVAS DGKKEPSDKAVKKDGSASAAAKKLLK 138 amino acids = 14.9 kDa					
MATR3-215	295 .. 799	505 bp	■	→	CDS
▶ 2 segments = 414 bp					
/note = coding sequence ENSP00000426743					
/translation = IPNRGIDLLKKDKSR, , KRSYSPDGKESPSDKKSKTDGSGQKTESSTEGKEQEEKSGEDGEKDKDDQTEQEPNMLLESEDELLVDEEEAAALLES GSSVGD ETDLANLG DVAS DGKKEPSDKAVKKDGSASAAAKKLLK 138 amino acids = 14.9 kDa					
MATR3-227	295 .. 799	505 bp	■	→	CDS
▶ 2 segments = 414 bp					
/note = coding sequence ENSP00000482895					
/translation = IPNRGIDLLKKDKSR, , KRSYSPDGKESPSDKKSKTDGSGQKTESSTEGKEQEEKSGEDGEKDKDDQTEQEPNMLLESEDELLVDEEEAAALLES GSSVGD ETDLANLG DVAS DGKKEPSDKAVKKDGSASAAAKKLLK 138 amino acids = 14.9 kDa					
✓ Donor Template SNV -> REV	482 .. 581	100 bp	■		misc_feature
✓ gRNA Protospacer	500 .. 519	20 bp	■		misc_feature
✓ SNV	515 .. 515	1 bp	■		misc_feature
/note = SNV = G REV = A					
✓ PAM	520 .. 522	3 bp	■		misc_feature
MATR3-219	578 .. 1200	623 bp	■	→	prim_transcript
/note = primary transcript ENST00000512040 protein_coding_CDS_not_defined					

Primer	Length	Binding Sites	Tm	Date Added
✓ PCR Forward /sequence = ATGGTCATGATGAATGTCTGTAGGC 44% GC / 7752.1 Da	25-mer	135 .. 159 →	59°C	Jul 19, 2023
✓ Donor Template SNV -> REV /sequence = TCTGGTCATCCTTTGTGTCTTTCTCACCATCTTCACCGGACTTCTCTTCTTGTCTTTACCTTCGGTTGAACTCTCAGTCTTCTGGGAACCATCAGTTTT 44% GC / 30,414.7 Da	100-mer	482 .. 581 ←	75°C	Jul 19, 2023
✓ gRNA Protospacer /sequence = AAGACTGAGAGTTCAGCCGA 50% GC / 6175.1 Da	20-mer	500 .. 519 →	50°C	Jul 19, 2023
✓ Sanger Sequencing Primer /sequence = TCTAGCAGTGCTGCTGCTTC 55% GC / 6075.0 Da	20-mer	641 .. 660 ←	59°C	Jul 19, 2023
✓ PCR Reverse /sequence = TAAGGCTGCCTACCTATATGCTACC 48% GC / 7577.0 Da	25-mer	1083 .. 1107 ←	59°C	Jul 19, 2023