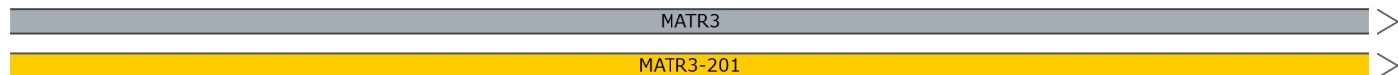


gRNA Protospacer
AAGACTGAGAGTTCAACCG
 AGATCTTACTCTCCAGATGGCAAAGAATCTCCAAGTGATAAGAAATCCAAAAGTGGTTCCCAAGAACTGATGGTTCCCAAGAACTGAGAGTTCAACCG
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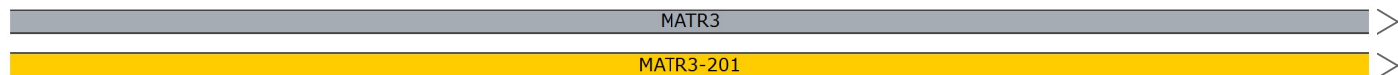


595 600 605 610 615 620
 R S Y S P D G K E S P S D K K S K T D G S Q K T E S S T
 ENSE00003768022
 MATR3-201

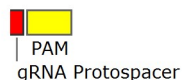


gRNA Protospacer

A
 AAGGTAAAGAACAAGAAGAGAAGTCCGGTGAAGATGGTGAGAAAGACACAAAGGATGACCAGACAGAGCAGGAACCTAATATGCT
 TTCCATTTCTTGTCTTCTCTTCAGGCCACTTCTACCACTCTTCTGTGTTTCCTACTGGTCTGTCTCGTCTTGGATTATACGA



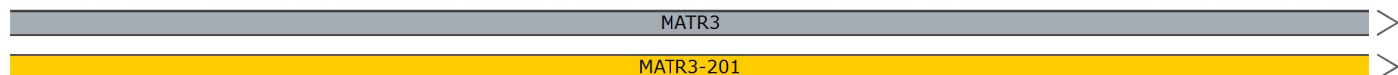
625 630 635 640 645 650
 E G K E Q E E K S G E D G E K D T K D D Q T E Q E P N M L
 ENSE00003768022
 MATR3-201



TTCCATTTCTTGTCTTCTCTTCAGGCCACTTCTACCACTCTTCTGTGTTTCCTACTGGTCT

Donor Template WT -> SNV

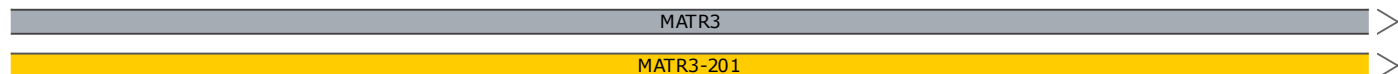
TCTTGAATCTGAAGATGAGCTACTTGTAGATGAAGAAGAAGCAGCAGCACTGCTAGAAAGTGGCAGTTCAGTGGGAGACGAGACC
 AGAAGTTAGACTTCTACTCGATGAACATCTACTTCTTCTCGTCTGTCGACGATCTTTCACCGTCAAGTCAACCTCTGCTCTGG



655 660 665 670 675
 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 D E T
 ENSE00003768022
 MATR3-201



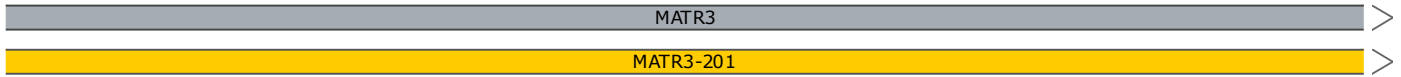
GATCTTGCTAATTTAGGTGATGTGGCTTCTGATGGGAAAAAGGAACCATCAGATAAAGCTGTGAAAAAAGATGGAAGTGCTTCAG
 CTAGAACGATTAAATCCACTACACCGAAGACTACCTTTTTCTTGGTAGTCTATTTTCGACACTTTTTTCTACCTTCACGAAGTC



680 685 690 695 700 705
 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 A S
 ENSE00003768022
 MATR3-201

CAGCAGCAAAGAAAAAGCTTAAAAAGGTAAAGAAAGATACATTGATTTGTTTTAATAGAACATTAGATCAGATCAGTATTTCAAG
 GTCGTCGTTTCTTTTTCGAATTTTCCATTTCTTTCTATGTAACATAACAAAATTATCTTGTAATCTAGTCTAGTCATAAAGTTC

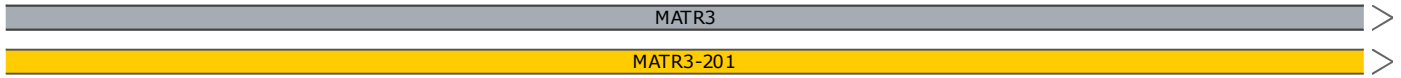
935



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 I S S
 ENS E00003768022 (in frame with MATR3-201)
 MATR3-201

TTATTTACCTAAGCAGGATCAGATAGAATTATATGATTTAAATCAGAAAATAAATCAGATATGAACCAGAATATAAACATTTAAA
 AATAAATGGATTTCGTCCTAGTCTATCTTAATATACTAAATTTAGTCTTTTATTTAGTCTATACTTGGTCTTATATTTGTAATTT

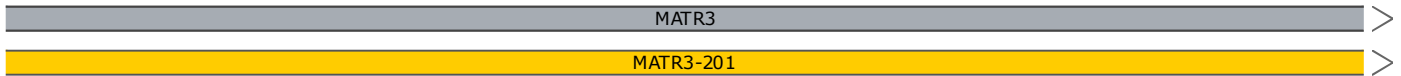
1020



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)

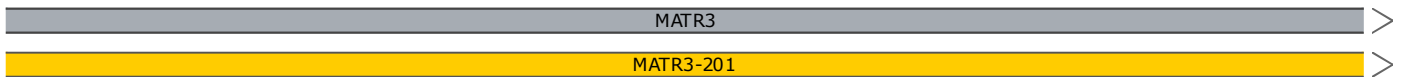
TCTAAACTCTGCAATAAATAATTAATAAGACATTTTATTATAGTTGGCAAAAAACATCAGCTCAAAGAGGAAACTTTTCAGTAA
 AGATTTGAGACGTTATTTATTAATTTATTCTGTAAAATAATATCAACCGTTTTTTGTAGTCGAGTTTCTCCTTTGAAAAGTCATT

1105



AAATGAGGGAGAAAGACTCAAATATATGTGCTTCTGTATTGTAGTGGTGTAGTGGTAGCATATAGGTAGGCAGCCTTATAGTGT
 TTTACTCCCTCTTTCTGAGTTTTATATACACGAAGACATAACATCACCACATCACCATCGTATATCCATCCGTCGGAATATCACA

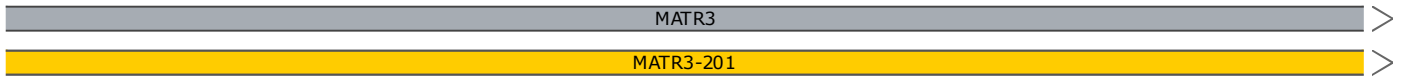
1190



CCATCGTATATCCATCCGTCGGAAT
 PCR Reverse

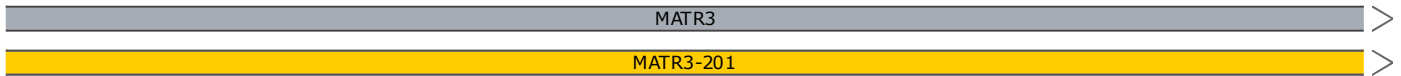
AGCTTTGAAAAAAAATACAGGACGTGAGTTTGCAGTAAGTTAACTGACCCAACATAGTTAAAACTTTTGCCACTCATTCAAAA
 TCGAAACTTTTTTTTTTATGTCCTGCACTCAAACGTCATTCAATTGACTGGGTTGTATCAATTTGAAAACGGTGAGTAAGTTTT

1275

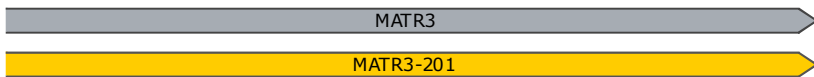


ATTATTGAATAATTTTCTATTTGAGAAATGTTGGCCTGGTCAGATACCTTAGTATCCTTTAAAACAATTTTATTGAACAAGT
 TAATAACTTATTA AAAAGGATAAACTCTTACAACCGGACCAGTCTATGGAATCATAGGAAATTTGTTAAAATAAACTTGTTCA

1360



AAGTCATTTAGAAGCCATGTATAAAGTGAATATAAATATAAAAATACACAC 3'
 TTCAGTAAATCTTCGGTACATATTTCACTTATATTTATATTTTATGTTG 5'
 1411



Feature	Location	Size	Start	End	Type
✓ MATR3	1 .. 1411	1411 bp	■	➔	gene
/note = gene ENSG00000015479 Protein coding					
MATR3	1 .. 1411	1411 bp	■	➔	gene
/note = gene ENSG000000280987 Protein coding					
✓ MATR3-201	1 .. 1411	1411 bp	■	➔	prim_transcript
/note = primary transcript ENST000000394805					
MATR3-202	1 .. 1411	1411 bp	■	➔	prim_transcript
/note = primary transcript ENST000000502422 Retained intron					
MATR3-203	1 .. 1411	1411 bp	■	➔	prim_transcript
/note = primary transcript ENST000000502499					
MATR3-206	1 .. 1411	1411 bp	■	➔	prim_transcript
/note = primary transcript ENST000000503811					
MATR3-211	1 .. 1411	1411 bp	■	➔	prim_transcript
/note = primary transcript ENST000000505625 Retained intron					
MATR3-215	1 .. 1411	1411 bp	■	➔	prim_transcript
/note = primary transcript ENST000000510056					
MATR3-227	1 .. 1411	1411 bp	■	➔	prim_transcript
/note = primary transcript ENST000000618441					
MATR3-228	1 .. 1411	1411 bp	■	➔	prim_transcript
/note = primary transcript ENST000000361059 Protein coding					
MATR3-229	1 .. 1411	1411 bp	■	➔	prim_transcript
/note = primary transcript ENST000000394800 Protein coding					
MATR3-230	1 .. 1411	1411 bp	■	➔	prim_transcript
/note = primary transcript ENST000000502394 Protein coding					
MATR3-231	1 .. 1411	1411 bp	■	➔	prim_transcript
/note = primary transcript ENST000000502929 Protein coding					
MATR3-232	1 .. 1411	1411 bp	■	➔	prim_transcript
/note = primary transcript ENST000000504203 Protein coding					
MATR3-233	1 .. 1411	1411 bp	■	➔	prim_transcript
/note = primary transcript ENST000000505016 Protein coding					
MATR3-236	1 .. 1411	1411 bp	■	➔	prim_transcript
/note = primary transcript ENST000000509990 Protein coding					
MATR3-238	1 .. 1411	1411 bp	■	➔	prim_transcript
/note = primary transcript ENST000000514694 Protein coding					
MATR3-210	1 .. 857	857 bp	■	➔	prim_transcript
/note = primary transcript ENST000000504643 Retained intron					
MATR3-204	1 .. 599	599 bp	■	➔	prim_transcript
/note = primary transcript ENST000000502944 Retained intron					

Feature	Location	Size	Start	End	Type
✓ MATR3-201	372 .. 876	505 bp	■	→	CDS
▶ 2 segments = 414 bp					
/note = coding sequence ENSP00000378284					
/translation = IPNRGIDLLKKDKSR, , KRSYSPDGKESPSDKKSKTDGSGQKTESSTEGKEQEEKSGEDGEKDTKDDQTEQEPNMLLESEDELLVDEEEAAALLES GSSVGD ETDLANLGDVAS DGKKEPSDKAVKKDGSASAAAKKLLK 138 amino acids = 14.9 kDa					
MATR3-203	372 .. 876	505 bp	■	→	CDS
▶ 2 segments = 414 bp					
/note = coding sequence ENSP00000426030					
/translation = IPNRGIDLLKKDKSR, , KRSYSPDGKESPSDKKSKTDGSGQKTESSTEGKEQEEKSGEDGEKDTKDDQTEQEPNMLLESEDELLVDEEEAAALLES GSSVGD ETDLANLGDVAS DGKKEPSDKAVKKDGSASAAAKKLLK 138 amino acids = 14.9 kDa					
MATR3-206	372 .. 876	505 bp	■	→	CDS
▶ 2 segments = 414 bp					
/note = coding sequence ENSP00000423587					
/translation = IPNRGIDLLKKDKSR, , KRSYSPDGKESPSDKKSKTDGSGQKTESSTEGKEQEEKSGEDGEKDTKDDQTEQEPNMLLESEDELLVDEEEAAALLES GSSVGD ETDLANLGDVAS DGKKEPSDKAVKKDGSASAAAKKLLK 138 amino acids = 14.9 kDa					
MATR3-215	372 .. 876	505 bp	■	→	CDS
▶ 2 segments = 414 bp					
/note = coding sequence ENSP00000426743					
/translation = IPNRGIDLLKKDKSR, , KRSYSPDGKESPSDKKSKTDGSGQKTESSTEGKEQEEKSGEDGEKDTKDDQTEQEPNMLLESEDELLVDEEEAAALLES GSSVGD ETDLANLGDVAS DGKKEPSDKAVKKDGSASAAAKKLLK 138 amino acids = 14.9 kDa					
MATR3-227	372 .. 876	505 bp	■	→	CDS
▶ 2 segments = 414 bp					
/note = coding sequence ENSP00000482895					
/translation = IPNRGIDLLKKDKSR, , KRSYSPDGKESPSDKKSKTDGSGQKTESSTEGKEQEEKSGEDGEKDTKDDQTEQEPNMLLESEDELLVDEEEAAALLES GSSVGD ETDLANLGDVAS DGKKEPSDKAVKKDGSASAAAKKLLK 138 amino acids = 14.9 kDa					
✓ Donor Template WT -> SNV	559 .. 658	100 bp	■		misc_feature
✓ gRNA Protospacer	577 .. 596	20 bp	■		misc_feature
✓ SNV	592 .. 592	1 bp	■		misc_feature
/note = WT = A SNV = G					
✓ PAM	597 .. 599	3 bp	■		misc_feature
MATR3-219	655 .. 1411	757 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	212 .. 236	59°C	Jul 19, 2023
✓ Donor Template WT -> SNV /sequence = TCTGGTCATCCTTTGTGTCTTTCTCACCATCTTCACCGGACTTCTCTTCTTGTCTTTACCTTCGGCTGAACTCTCAGTCTTCTGGGAACCATCAGTTTT 45% GC / 30,399.7 Da	100-mer	559 .. 658	74°C	Jul 19, 2023
✓ gRNA Protospacer /sequence = AAGACTGAGAGTTCAACCGA 45% GC / 6159.1 Da	20-mer	577 .. 596	54°C	Jul 19, 2023
✓ Sanger Sequencing Primer /sequence = TCTAGCAGTGCTGCTGCTTC 55% GC / 6075.0 Da	20-mer	718 .. 737	59°C	Jul 19, 2023
✓ PCR Reverse /sequence = TAAGGCTGCCTACCTATATGCTACC 48% GC / 7577.0 Da	25-mer	1160 .. 1184	59°C	Jul 19, 2023