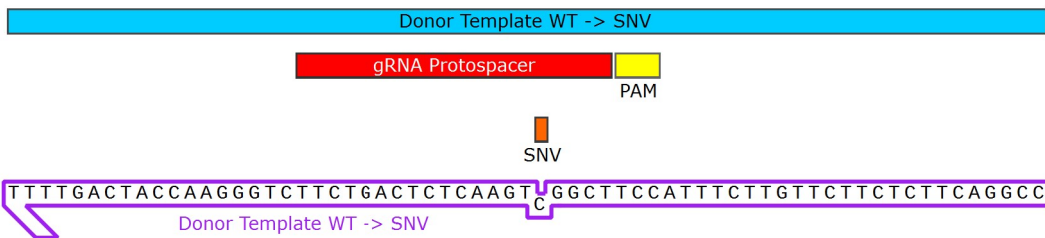
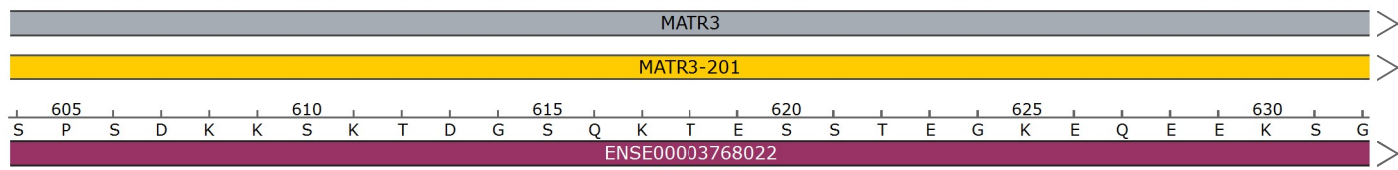


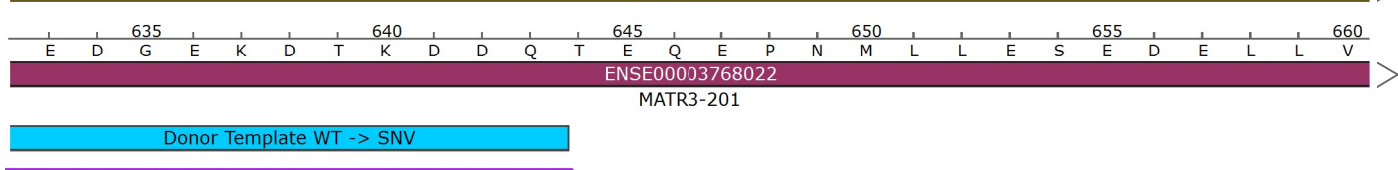


gRNA Protospacer
AAGACTGAGAGTTCAACCGA

CTCCAAGTGATAAGAAATCCAAAACCTGATGGTTCCCGAAGACTGAGAGTTCAACCGAAGGTAAGAACAAGAAGAGAAGTCCGG
 GAGGTTCACTATTCTTTAGGTTTTGACTACCAAGGGTCTTCTGACTCTCAAGTGGCTTCCATTTCTTGTCTTCTCTTCAGGCC



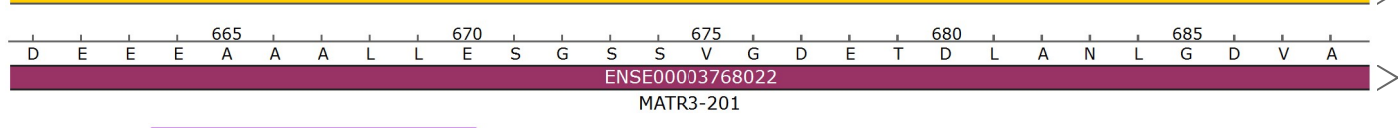
TGAAGATGGTGAGAAAGACACAAAGGATGACCAGACAGAGCAAGAACCTAATATGCTTCTTGAATCTGAAGATGAGCTACTTGT
 ACTTCTACCACTCTTTCTGTGTTTCTACTGGTCTGTCTCGTCTGGATTATACGAAGAAGCTTAGACTTCTACTCGATGAACAT



ACTTCTACCACTCTTTCTGTGTTTCTACTGGTCT

Donor Template WT -> SNV

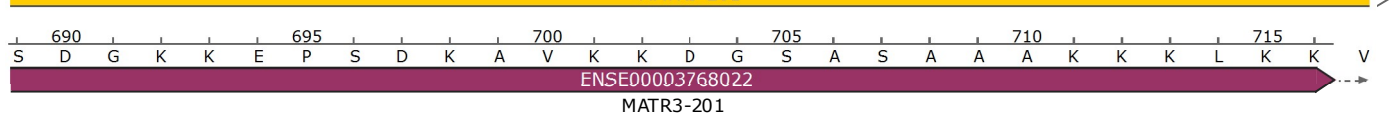
GATGAAGAAGAAGCAGCAGCACTGCTAGAAAAGTGGCAGTTCAGTGGGAGACGAGACCGATCTTGCTAATTTAGGTGATGTGGCTT
 CTACTTCTTCTTCGTCGTCGTGACGATCTTTCACCGTCAAGTACCCTCTGCTCTGGCTAGAACGATTAATCCACTACACCGAA



CTTCGTCGTCGTGACGATCT

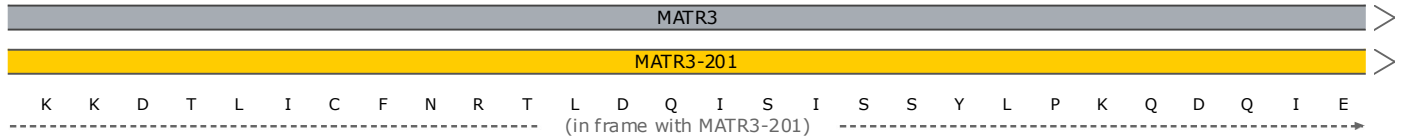
Sanger Sequencing Primer

CTGATGGGAAAAAGGAACCATCAGATAAAGCTGTGAAAAAAGATGGAAGTGCTTCAGCAGCAGCAAAGAAAAAGCTTAAAAAGGT
 GACTACCCTTTTTCTTGGTAGTCTATTTGACACTTTTTCTACCTTCACGAAGTCGTCGTCGTTTTCTTTTTCGAATTTTTCCA



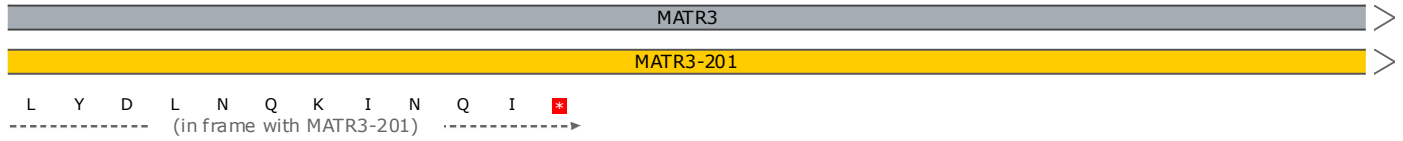
AAAGAAAGATACATTGATTTGTTTTAATAGAACATTAGATCAGATCAGTATTTCAGTTATTTACCTAAGCAGGATCAGATAGAA
 TTTCTTTCTATGTAACATAAACAAAATTATCTTGTAATCTAGTCTAGTCATAAAGTTCAATAAATGGATTCGTCCTAGTCTATCTT

935



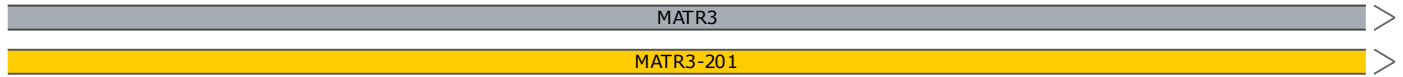
TTATATGATTTAAATCAGAAAATAAATCAGATATGAACCAGAATATAAACATTTAAATCTAAACTCTGCAATAAATAATTAATA
 AATATACTAAATTTAGTCTTTTTATTTAGTCTATACTTGGTCTTATATTTGTAAATTTAGATTTGAGACGTTATTTATTAATTTAT

1020



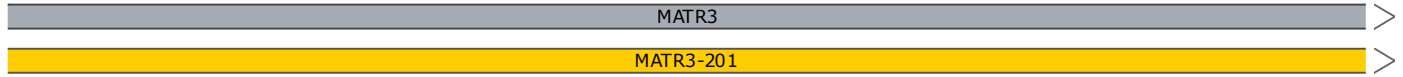
AGACATTTTATTATAGTTGGCAAAAAACATCAGCTCAAAGAGGAAACTTTTCAGTAAAAATGAGGGAGAAAGACTCAAAATATAT
 TCTGTAAAATAATATCAACCGTTTTTTGTAGTCGAGTTTCTCCTTTGAAAAGTCATTTTTACTCCCTCTTTCTGAGTTTTATATA

1105



GTGCTTCTGTATTGTAGTGGTGTAGTGGTAGCATATAGGTAGGCAGCCTTATAGTGTAGCTTTGAAAAAAAAAATACAGGACGTG
 CACGAAGACATAACATCACCACATCACCATCGTATATCCATCCGTCGGAATATCACATCGAAACTTTTTTTTTTATGTCCTGCAC

1190



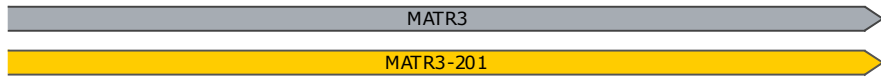
CCATCGTATATCCATCCGTCGGAAT
 PCR Reverse

AGTTTGCAGTAAGTTAACTGACCCAACATAGTTAAAACCTTTTGCCACTCATTCAA
 TCAAACGTCATTCAATTGACTGGGTTGTATCAATTTGAAAACGGTGAGTAAGTT

3'

1245

5'



Feature	Location	Size	Start	End	Type
✓ MATR3	1 .. 1245	1245 bp	■	➔	gene
/note = gene ENSG00000015479 Protein coding					
MATR3	1 .. 1245	1245 bp	■	➔	gene
/note = gene ENSG000000280987 Protein coding					
✓ MATR3-201	1 .. 1245	1245 bp	■	➔	prim_transcript
/note = primary transcript ENST000000394805					
MATR3-202	1 .. 1245	1245 bp	■	➔	prim_transcript
/note = primary transcript ENST000000502422 Retained intron					
MATR3-203	1 .. 1245	1245 bp	■	➔	prim_transcript
/note = primary transcript ENST000000502499					
MATR3-206	1 .. 1245	1245 bp	■	➔	prim_transcript
/note = primary transcript ENST000000503811					
MATR3-211	1 .. 1245	1245 bp	■	➔	prim_transcript
/note = primary transcript ENST000000505625 Retained intron					
MATR3-215	1 .. 1245	1245 bp	■	➔	prim_transcript
/note = primary transcript ENST000000510056					
MATR3-227	1 .. 1245	1245 bp	■	➔	prim_transcript
/note = primary transcript ENST000000618441					
MATR3-228	1 .. 1245	1245 bp	■	➔	prim_transcript
/note = primary transcript ENST000000361059 Protein coding					
MATR3-229	1 .. 1245	1245 bp	■	➔	prim_transcript
/note = primary transcript ENST000000394800 Protein coding					
MATR3-230	1 .. 1245	1245 bp	■	➔	prim_transcript
/note = primary transcript ENST000000502394 Protein coding					
MATR3-231	1 .. 1245	1245 bp	■	➔	prim_transcript
/note = primary transcript ENST000000502929 Protein coding					
MATR3-232	1 .. 1245	1245 bp	■	➔	prim_transcript
/note = primary transcript ENST000000504203 Protein coding					
MATR3-233	1 .. 1245	1245 bp	■	➔	prim_transcript
/note = primary transcript ENST000000505016 Protein coding					
MATR3-236	1 .. 1245	1245 bp	■	➔	prim_transcript
/note = primary transcript ENST000000509990 Protein coding					
MATR3-238	1 .. 1245	1245 bp	■	➔	prim_transcript
/note = primary transcript ENST000000514694 Protein coding					
MATR3-210	1 .. 829	829 bp	■	➔	prim_transcript
/note = primary transcript ENST000000504643 Retained intron					
MATR3-204	1 .. 571	571 bp	■	➔	prim_transcript
/note = primary transcript ENST000000502944 Retained intron					

Feature	Location	Size	Start	End	Type
✓ MATR3-201	344 .. 848	505 bp	■	→	CDS
▶ 2 segments = 414 bp					
/note = coding sequence ENSP00000378284					
/translation = IPNRGIDLLKKDKSR, ,KRSYSPDGKESPSDKKSKTDGSGQKTESSTEGKEQEEKSGEDGEKDKDDQTEQEPNMLLESEDELLVDEEEAAALLES GSSVGD ETDLANLGDVAS DGKKEPSDKAVKKDGSASAAAKKLLK 138 amino acids = 14.9 kDa					
MATR3-203	344 .. 848	505 bp	■	→	CDS
▶ 2 segments = 414 bp					
/note = coding sequence ENSP00000426030					
/translation = IPNRGIDLLKKDKSR, ,KRSYSPDGKESPSDKKSKTDGSGQKTESSTEGKEQEEKSGEDGEKDKDDQTEQEPNMLLESEDELLVDEEEAAALLES GSSVGD ETDLANLGDVAS DGKKEPSDKAVKKDGSASAAAKKLLK 138 amino acids = 14.9 kDa					
MATR3-206	344 .. 848	505 bp	■	→	CDS
▶ 2 segments = 414 bp					
/note = coding sequence ENSP00000423587					
/translation = IPNRGIDLLKKDKSR, ,KRSYSPDGKESPSDKKSKTDGSGQKTESSTEGKEQEEKSGEDGEKDKDDQTEQEPNMLLESEDELLVDEEEAAALLES GSSVGD ETDLANLGDVAS DGKKEPSDKAVKKDGSASAAAKKLLK 138 amino acids = 14.9 kDa					
MATR3-215	344 .. 848	505 bp	■	→	CDS
▶ 2 segments = 414 bp					
/note = coding sequence ENSP00000426743					
/translation = IPNRGIDLLKKDKSR, ,KRSYSPDGKESPSDKKSKTDGSGQKTESSTEGKEQEEKSGEDGEKDKDDQTEQEPNMLLESEDELLVDEEEAAALLES GSSVGD ETDLANLGDVAS DGKKEPSDKAVKKDGSASAAAKKLLK 138 amino acids = 14.9 kDa					
MATR3-227	344 .. 848	505 bp	■	→	CDS
▶ 2 segments = 414 bp					
/note = coding sequence ENSP00000482895					
/translation = IPNRGIDLLKKDKSR, ,KRSYSPDGKESPSDKKSKTDGSGQKTESSTEGKEQEEKSGEDGEKDKDDQTEQEPNMLLESEDELLVDEEEAAALLES GSSVGD ETDLANLGDVAS DGKKEPSDKAVKKDGSASAAAKKLLK 138 amino acids = 14.9 kDa					
✓ Donor Template WT -> SNV	531 .. 630	100 bp	■		misc_feature
✓ gRNA Protospacer	549 .. 568	20 bp	■		misc_feature
✓ SNV	564 .. 564	1 bp	■		misc_feature
/note = WT = A SNV = G					
✓ PAM	569 .. 571	3 bp	■		misc_feature
MATR3-219	627 .. 1245	619 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	184 .. 208	59°C	Jul 19, 2023
✓ Donor Template WT -> SNV /sequence = TCTGGTCATCCTTTGTGTCTTTCTCACCATCTTCACCGGACTTCTCTTCTTGTCTTTACCTTCGGCTGAACTCTCAGTCTTCTGGAACCATCAGTTTT 45% GC / 30,399.7 Da	100-mer	531 .. 630	74°C	Jul 19, 2023
✓ gRNA Protospacer /sequence = AAGACTGAGAGTTCAACCGA 45% GC / 6159.1 Da	20-mer	549 .. 568	54°C	Jul 19, 2023
✓ Sanger Sequencing Primer /sequence = TCTAGCAGTGCTGCTGCTTC 55% GC / 6075.0 Da	20-mer	690 .. 709	59°C	Jul 19, 2023
✓ PCR Reverse /sequence = TAAGGCTGCCTACCTATATGCTACC 48% GC / 7577.0 Da	25-mer	1132 .. 1156	59°C	Jul 19, 2023