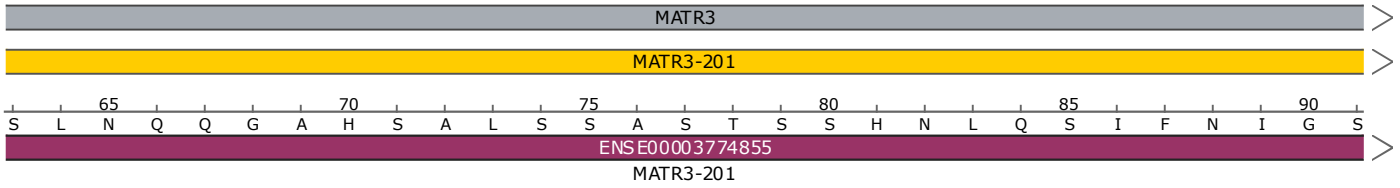


CATTGAATCAACAAGGAGCTCATAGTGCAGTCTTCTGCTAGTACTTCTTCCATAAATTTGCAGTCTATATTTAACATTGGAAG
 GTAACCTTAGTTGTTCTCGAGTATCACGTGACAGAAGACGATCATGAAGAAGGGTATTAACGTCAGATATAAATTGTAACCTTC

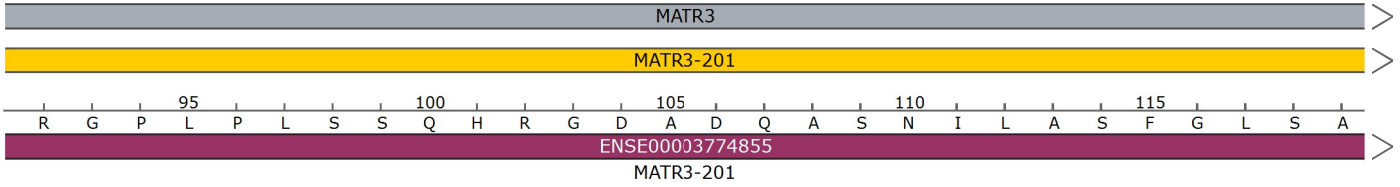
680



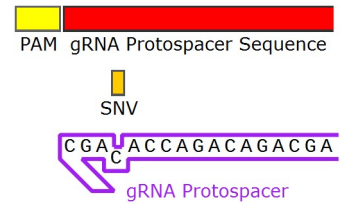
Donor Template SNV -> Rev

TCCACTCCCTTTATCTTCTCAACACCGTGGAGATGCAGACCAGGCCAGTAACATTTTGGCCAGCTTTGGTCTGTCTGCT
 TAGAGGTCCACTCCCTTTATCTTCTCAACACCGTGGAGATGCAGACCAGGCCAGTAACATTTTGGCCAGCTTTGGTCTGTCTGCT
 ATCTCCAGGTGAGGGAAATAGAAGAGTTGTGGCACCTCTACGTCTGGTCCGGTCATTGTAACACCGGTCGAACCAGACAGACGA

765



Donor Template Sequence SNV -> Rev

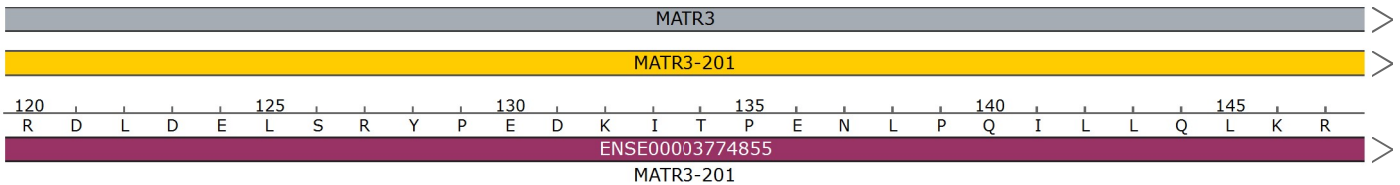


Donor Template SNV -> Rev

AGAGACTTAGATGAACTGAGT

AGAGACTTAGATGAACTGAGTCTGTTATCCAGAGGACAAGATTACTCCTGAGAATTTGCCCAAATCCTTCTACAGCTTAAAAGGA
 TCTCTGAATCTACTTGACTCAGCAATAGGTCTCCTGTTCTAATGAGGACTCTTAAACGGGGTTTAGGAAGATGTCGAATTTTCTC

850



Donor Template Sequence SNV -> Rev

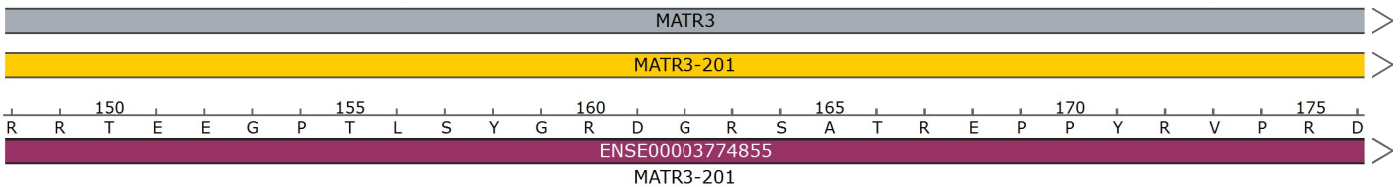
gRNA Protospacer Sequence

TCT

gRNA Protospacer

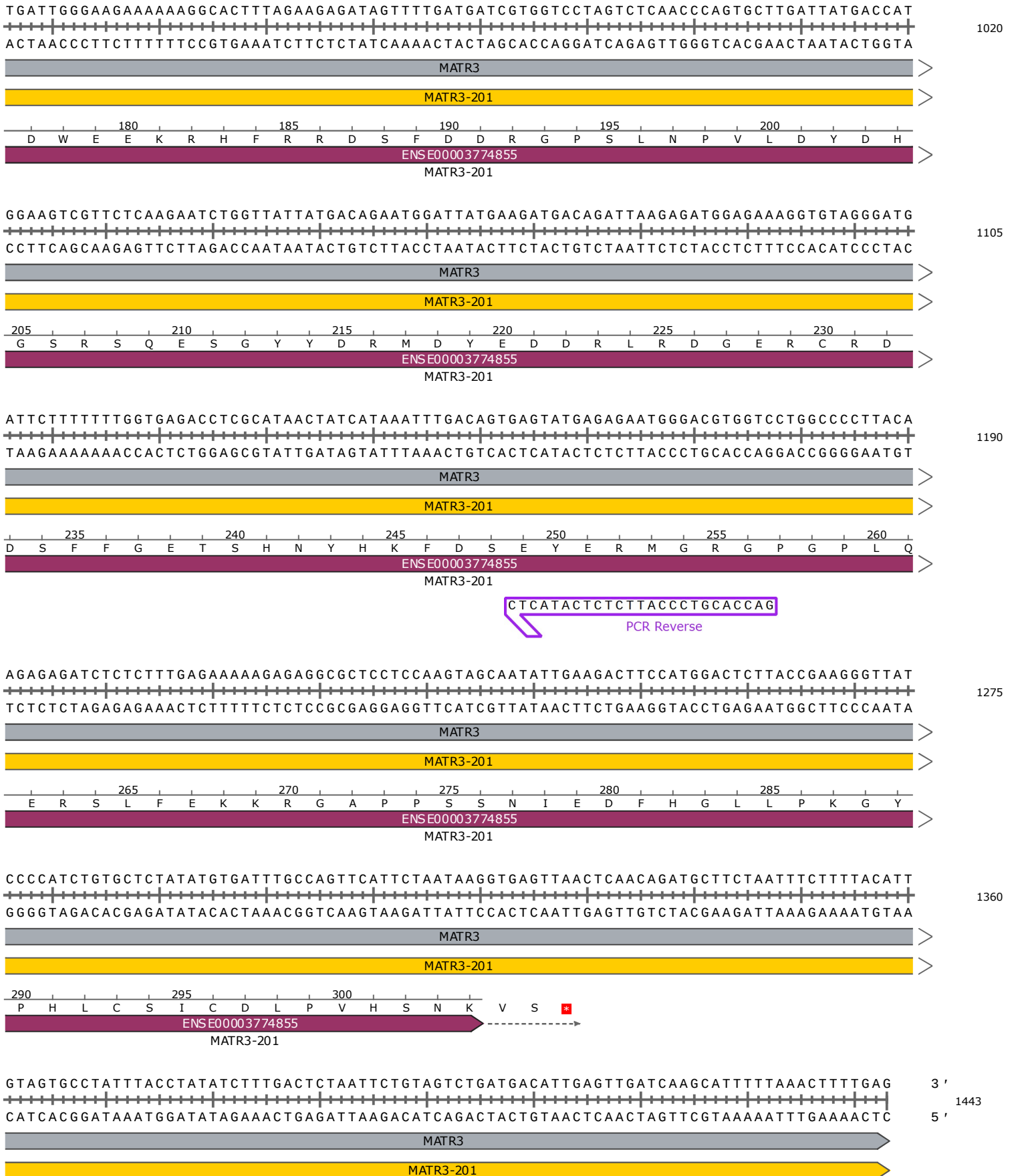
GGAGAACTGAAGAAGGCCCTACCTTGAGTTATGGTAGAGATGGCAGATCTGCTACACGGGAGCCACCATAACAGAGTACCTAGGGA
 CCTCTTGACTTCTTCCGGGATGGAACCTCAATACCATCTCTACCGTCTAGACGATGTGCCCTCGGTGGTATGTCTCATGGATCCCT

935



CCTCTTGACTTCTTCCGGGA

Sanger Sequencing Primer



Feature	Location	Size	Start	End	Type
✓ MATR3	1 .. 1443	1443 bp	■	➔	gene
/note = gene ENSG00000015479 Protein coding					
✓ MATR3-201	1 .. 1443	1443 bp	■	➔	prim_transcript
/note = primary transcript ENST00000394805					
MATR3-203	1 .. 1443	1443 bp	■	➔	prim_transcript
/note = primary transcript ENST00000502499					
MATR3-206	1 .. 1443	1443 bp	■	➔	prim_transcript
/note = primary transcript ENST00000503811					
MATR3-208	1 .. 1443	1443 bp	■	➔	prim_transcript
/note = primary transcript ENST00000504045					
MATR3-209	1 .. 1443	1443 bp	■	➔	prim_transcript
/note = primary transcript ENST00000504311					
MATR3-210	1 .. 1443	1443 bp	■	➔	prim_transcript
/note = primary transcript ENST00000504643 Retained intron					
MATR3-212	1 .. 1443	1443 bp	■	➔	prim_transcript
/note = primary transcript ENST00000507860 Retained intron					
MATR3-214	1 .. 1443	1443 bp	■	➔	prim_transcript
/note = primary transcript ENST00000509918 protein_coding_CDS_not_defined					
MATR3-215	1 .. 1443	1443 bp	■	➔	prim_transcript
/note = primary transcript ENST00000510056					
MATR3-216	1 .. 1443	1443 bp	■	➔	prim_transcript
/note = primary transcript ENST00000511249					
MATR3-218	1 .. 1443	1443 bp	■	➔	prim_transcript
/note = primary transcript ENST00000511978 protein_coding_CDS_not_defined					
MATR3-220	1 .. 1443	1443 bp	■	➔	prim_transcript
/note = primary transcript ENST00000512876					
MATR3-221	1 .. 1443	1443 bp	■	➔	prim_transcript
/note = primary transcript ENST00000513121 Retained intron					
MATR3-222	1 .. 1443	1443 bp	■	➔	prim_transcript
/note = primary transcript ENST00000513678					
MATR3-225	1 .. 1443	1443 bp	■	➔	prim_transcript
/note = primary transcript ENST00000514528					
MATR3-227	1 .. 1443	1443 bp	■	➔	prim_transcript
/note = primary transcript ENST00000618441					
MATR3-238	1 .. 730	730 bp	■	➔	prim_transcript
/note = primary transcript ENST00000514694 Protein coding					
MATR3-224	1 .. 708	708 bp	■	➔	prim_transcript
/note = primary transcript ENST00000514488					
MATR3-230	1 .. 707	707 bp	■	➔	prim_transcript
/note = primary transcript ENST00000502394 Protein coding					
MATR3-205	1 .. 670	670 bp	■	➔	prim_transcript
/note = primary transcript ENST00000503340					
MATR3-213	1 .. 643	643 bp	■	➔	prim_transcript
/note = primary transcript ENST00000508689					

Feature	Location	Size	Start	End	Type
MATR3-207	1 .. 641	641 bp	■	→	prim_transcript
/note	= primary transcript ENST00000504023				
MATR3-233	1 .. 549	549 bp	■	→	prim_transcript
/note	= primary transcript ENST00000505016 Protein coding				
✓ MATR3-201	409 .. 1320	912 bp	■	→	CDS
/note	= coding sequence ENSP00000378284				
/translation	= MSKSFQQSSLSRDSQGHGRDLSAAGIGLLAAATQSLMPASLGRMNQGTARLASLMNLGMSSSLNQQGAHSALSSASTSSHNLQSFNIGSRGPLPLSSQHRGDADQASNILA SFGLSARDLDELSPYEDKIPENLPQILLQLKRRRTEEGPTLSYGRDGRSATREPPYRVPRDDWEEKRHFRRDSFDDRGPSLNPVLDYDHGSRSQESGYDRMDYEDDLRLD GERCRDSSFFGETSHNYHKFDSEYERMGRGPGPLQERSLFEKRRGAPSSNIEDFHGLLPKGYPHLCSICDLPVHSNK 304 amino acids = 33.9 kDa				
MATR3-208	409 .. 1320	912 bp	■	→	CDS
/note	= coding sequence ENSP00000423290				
/translation	= MSKSFQQSSLSRDSQGHGRDLSAAGIGLLAAATQSLMPASLGRMNQGTARLASLMNLGMSSSLNQQGAHSALSSASTSSHNLQSFNIGSRGPLPLSSQHRGDADQASNILA SFGLSARDLDELSPYEDKIPENLPQILLQLKRRRTEEGPTLSYGRDGRSATREPPYRVPRDDWEEKRHFRRDSFDDRGPSLNPVLDYDHGSRSQESGYDRMDYEDDLRLD GERCRDSSFFGETSHNYHKFDSEYERMGRGPGPLQERSLFEKRRGAPSSNIEDFHGLLPKGYPHLCSICDLPVHSNK 304 amino acids = 33.9 kDa				
MATR3-215	409 .. 1320	912 bp	■	→	CDS
/note	= coding sequence ENSP00000426743				
/translation	= MSKSFQQSSLSRDSQGHGRDLSAAGIGLLAAATQSLMPASLGRMNQGTARLASLMNLGMSSSLNQQGAHSALSSASTSSHNLQSFNIGSRGPLPLSSQHRGDADQASNILA SFGLSARDLDELSPYEDKIPENLPQILLQLKRRRTEEGPTLSYGRDGRSATREPPYRVPRDDWEEKRHFRRDSFDDRGPSLNPVLDYDHGSRSQESGYDRMDYEDDLRLD GERCRDSSFFGETSHNYHKFDSEYERMGRGPGPLQERSLFEKRRGAPSSNIEDFHGLLPKGYPHLCSICDLPVHSNK 304 amino acids = 33.9 kDa				
MATR3-227	409 .. 1320	912 bp	■	→	CDS
/note	= coding sequence ENSP00000482895				
/translation	= MSKSFQQSSLSRDSQGHGRDLSAAGIGLLAAATQSLMPASLGRMNQGTARLASLMNLGMSSSLNQQGAHSALSSASTSSHNLQSFNIGSRGPLPLSSQHRGDADQASNILA SFGLSARDLDELSPYEDKIPENLPQILLQLKRRRTEEGPTLSYGRDGRSATREPPYRVPRDDWEEKRHFRRDSFDDRGPSLNPVLDYDHGSRSQESGYDRMDYEDDLRLD GERCRDSSFFGETSHNYHKFDSEYERMGRGPGPLQERSLFEKRRGAPSSNIEDFHGLLPKGYPHLCSICDLPVHSNK 304 amino acids = 33.9 kDa				
MATR3-224	409 .. 708	300 bp	■	→	CDS
/note	= coding sequence ENSP00000426801				
/translation	= MSKSFQQSSLSRDSQGHGRDLSAAGIGLLAAATQSLMPASLGRMNQGTARLASLMNLGMSSSLNQQGAHSALSSASTSSHNLQSFNIGSRGPLPLSSQ 100 amino acids = 10.2 kDa				
MATR3-205	409 .. 670	262 bp	■	→	CDS
/note	= coding sequence ENSP00000422590				
/translation	= MSKSFQQSSLSRDSQGHGRDLSAAGIGLLAAATQSLMPASLGRMNQGTARLASLMNLGMSSSLNQQGAHSALSSASTSSHNLQSFIF 87 amino acids = 8.9 kDa				
MATR3-213	409 .. 643	235 bp	■	→	CDS
/note	= coding sequence ENSP00000422137				
/translation	= MSKSFQQSSLSRDSQGHGRDLSAAGIGLLAAATQSLMPASLGRMNQGTARLASLMNLGMSSSLNQQGAHSALSSAST 78 amino acids = 7.9 kDa				
MATR3-207	409 .. 641	233 bp	■	→	CDS
/note	= coding sequence ENSP00000421145				
/translation	= MSKSFQQSSLSRDSQGHGRDLSAAGIGLLAAATQSLMPASLGRMNQGTARLASLMNLGMSSSLNQQGAHSALSSAS 77 amino acids = 7.8 kDa				
✓ Donor Template Sequence SNV -> Rev	687 .. 786	100 bp	■		misc_feature
✓ PAM	746 .. 748	3 bp	■		misc_feature
✓ gRNA Protospacer Sequence	749 .. 768	20 bp	■		misc_feature
✓ SNV	752 .. 752	1 bp	■		misc_feature
/note	= SNV = G WT = T				
MATR3-226	1088 .. 1443	356 bp	■	→	prim_transcript
/note	= primary transcript ENST00000515833				
MATR3-226	1088 .. 1320	233 bp	■	→	CDS
/note	= coding sequence ENSP00000422054				
/translation	= EKGVGMILFLVRPRITIIINLTVSMREWVVLAPYKRDLSLRKREALLQVAILKTSMDSYRRVIPICALYVICQFILI 77 amino acids = 9.0 kDa				

Feature	Location	Size		Type
MATR3-223	1236 .. 1443	208 bp	■ →	prim_transcript

/note = primary transcript [ENST00000514402](#)
Retained intron

Primer	Length	Binding Sites	Tm	Date Added
✓ PCR Forward /sequence = ATTTTCTACAGAGTTGTCTGCTGG 40% GC / 7669.1 Da	25-mer	220 .. 244	58°C	Aug 15, 2023
✓ Donor Template SNV -> Rev /sequence = TCCACTCCCTTTATCTTCTCAACACCGTGGAGATGCAGACCAGGCCAGTAACATTTTGGCCAGCTTTGGTCTGTCTGCTAGAGACTTAGATGAACTGAGT 48% GC / 30,725.0 Da	100-mer	687 .. 786	77°C	Aug 15, 2023
✓ gRNA Protospacer /sequence = TCTAGCAGACAGACCACAGC 55% GC / 6080.0 Da	20-mer	749 .. 768	50°C	Aug 15, 2023
✓ Sanger Sequencing Primer /sequence = AGGGCCTTCTTCAGTTCTCC 55% GC / 6035.0 Da	20-mer	851 .. 870	58°C	Aug 15, 2023
✓ PCR Reverse /sequence = GACCACGTCCCATTCTCTCATACTC 52% GC / 7472.9 Da	25-mer	1153 .. 1177	60°C	Aug 15, 2023