

INK2J00090_MATR3_F115C_C05_AB
1536 bp

5' TTTAAACTCAGTATGAAAGTCCCTTTAATAGTTAAGCTTTAGCATGAAATACTACTTTTTAAATATCTATATGCAGGCTCTGCAT
 3' AAATTTGAGTCATACTTTTCAGGGAAATTATCAATTCGAAATCGTACTTTATGATGAAAAATTTATAGATATACGTCGGAGACGTA

MATR3
 MATR3-201

ACATCAGGAATCTGTTTAAGATATGTAATAAATTCCTTGTAAGTTTGAGATCTTAAATGTTTTTTTTTAAATCAACATGATGCA
 TGTAGTCCTTAGACAAATTCATACATTATTTAAGGAACATTCAAACTCTAGAATTTACAAAAAAAATTTAGTTGTACTIONGCT

MATR3
 MATR3-201

TAAGTTTTTTTTCTTAAAAAACGGCATCTGCTTAAAGGGATTTATGACTAAAATTGCTTATTTTTCTACAGAGTTGTCTGCTG
 ATTCAAAAAAAAGAATTTTTTTGCCGTAGACGAATTCCTAAATACTGATTTAACGAATAAAAAGATGTCTCAACAGACGAC

MATR3
 MATR3-201

PCR Forward
 ATTTTTCTACAGAGTTGTCTGCTG

PCR Forward
 G

GTTCTCAGCTTGAAGAAGATTCTGCAGTCCTTATTGATCCTTTTTCTTGCCGTTACCATTTTTGAAGCAAAGTTAACCTAGCTTT
 CAAGAGTCGAACCTCTTCTAAGACGTCAGGAATAACTAGGAAAAAGAACC GCAATGGTAAAAACTTCGTTCAATTGGATCGAAA

MATR3
 MATR3-201

CTAGTTTGAGCTTTCTTTTTGGCCGCTTTAAAAAATTTTTTTTTTAAATCTATAAAATAGACAAGAGCTAGTTCTACAATGTC
 GATCAAACCTCGAAAGAAAAACCGGCAGAAATTTTTTAAAAAAAATAATTAGATATTTTATCTGTTCTCGATCAAGATGTTACAG

MATR3
 MATR3-201

CAAGTCATTCCAGCAGTCATCTCTCAGTAGGGACTCACAGGGTCATGGGCGTGACCTGTCTGCGGCAGGAATAGGCCTTCTTGCT
 GTTCAGTAAGGTCGTCAGTAGAGAGTCATCCCTGAGTGTCCAGTACCCGCACTGGACAGACGCCGCTTATCCGGAAGAACGA

MATR3
 MATR3-201

K S F Q Q S S L S R D S Q G H G R D L S A A G I G L L A

ENSE E00003774855
 MATR3-201

GCTGCTACCCAGTCTTTAAGTATGCCAGCATCTCTTGAAGGATGAACCGGGTACTGCACGCCTTGCTAGTTTAAATGAATCTTG
 CGACGATGGGTCAGAAATTCATACGGTCGTAGAGAACCTTCTACTTGGTCCCATGACGTGCGGAACGATCAAATTACTIONGCT

MATR3
 MATR3-201

A A T Q S L S M P A S L G R M N Q G T A R L A S L M N L

ENSE E00003774855
 MATR3-201

1 M S
 ENSE...
 MATR3-201

GAATGAGTTCTTCATTGAATCAACAAGGAGCTCATAGTGCAGTCTTCTGCTAGTACTTCTCCATAATTTGCAGTCTATATT
 CTTACTCAAGAAGTAACTTAGTTGTTCTCGAGTATCACGTGACAGAAGACGATCATGAAGAAGGGTATTAACGTCAGATATAA

MATR3
 MATR3-201

60 65 70 75 80 85
 G M S S S L N Q Q G A H S A L S S A S T S S H N L Q S I F

ENSE00003774855
 MATR3-201

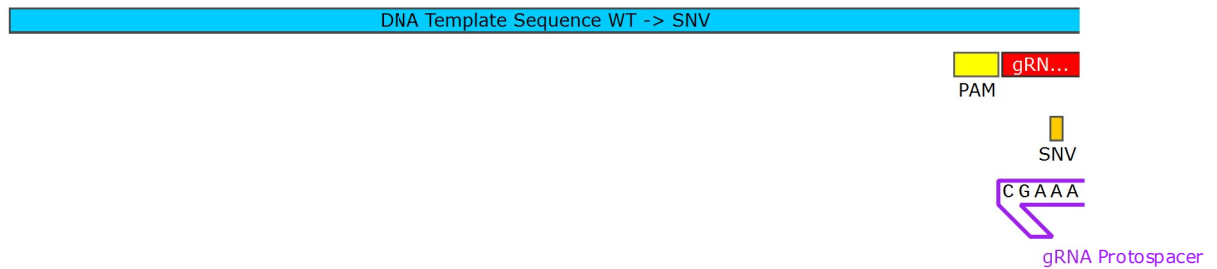
Donor Template WT -> SNV
 TCCACTCCCTTTATCTTCTCAACACCGTGGAGATGCAGACCAGGCCAGTAACATTTGGCCAGCTG

TAACATTGGAAGTAGAGGTCCACTCCCTTTATCTTCTCAACACCGTGGAGATGCAGACCAGGCCAGTAACATTTGGCCAGCTTT
 ATTGTAACCTTCATCTCCAGGTGAGGGAAATAGAAGAGTTGTGGCACCTCTACGTCTGGTCCGGTCATTGTAAAACCGGTCGAA

MATR3
 MATR3-201

90 95 100 105 110 115
 N I G S R G P L P L S S Q H R G D A D Q A S N I L A S F

ENSE00003774855
 MATR3-201



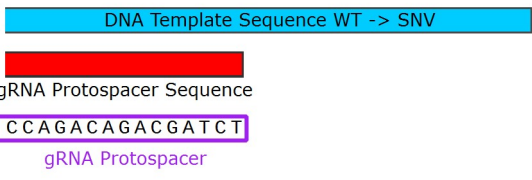
Donor Template WT -> SNV
 GGTCTGTCTGCTAGAGACTTAGATGAACTGAGT

GGTCTGTCTGCTAGAGACTTAGATGAACTGAGTCTGTTATCCAAGGACAAGATTACTCCTGAGAATTTGCCCAAATCCTTCTAC
 CCAGACAGACGATCTCTGAATCTACTTGACTCAGCAATAGGTCTCCTGTTCTAATGAGGACTCTTAAACGGGGTTTAGGAAGATG

MATR3
 MATR3-201

120 125 130 135 140
 G L S A R D L D E L S R Y P E D K I T P E N L P Q I L L

ENSE00003774855
 MATR3-201

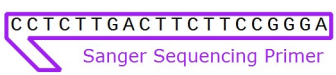


AGCTTAAAAGGAGGAGAAGTGAAGAAGGCCCTACCTTGAGTTATGGTAGAGATGGCAGATCTGCTACACGGGAGCCACCATAACAG
 TCGAATTTTCTCCTCTTGACTTCTTCCGGGATGGAAGTCAATACCATCTCTACCGTCTAGACGATGTGCCCTCGGTGGTATGTC

MATR3
 MATR3-201

145 150 155 160 165 170
 Q L K R R R T E E G P T L S Y G R D G R S A T R E P P Y R

ENSE00003774855
 MATR3-201



AGTACCTAGGGATGATTGGGAAGAAAAAGGCCACTTTAGAAGAGATAGTTTTGATGATCGTGGTCTAGTCTCAACCCAGTGCTT
 TCATGGATCCCTACTAACCCTTCTTTTTTCCGTGAAATCTTCTCTATCAAAACTACTAGCACCAGGATCAGAGTTGGGTACAGAA

MATR3
 MATR3-201

V P R D D W E E K R H F R R D S F D D R G P S L N P V L

ENSE00003774855
 MATR3-201

GATTATGACCATGGAAGTCGTTCTCAAGAATCTGGTTATTATGACAGAATGGATTATGAAGATGACAGATTAAGAGATGGAGAAA
 CTAATACTGGTACCTTCAGCAAGAGTTCTTAGACCAATAATACTGTCTTACCTAATACTTCTACTGTCTAATTCTCTACCTCTTT

MATR3
 MATR3-201

D Y D H G S R S Q E S G Y Y D R M D Y E D D R L R D G E

ENSE00003774855
 MATR3-201

GGTGTAGGGATGATTCTTTTTTTGGTGAGACCTCGCATAACTATCATAAATTTGACAGTGAGTATGAGAGAATGGGACGTGGTCC
 CCACATCCCTACTAAGAAAAAACCACCTCTGGAGCGTATTGATAGTATTTAAACTGTCACCTCATACTCTCTTACCCTGCACCAGG

MATR3
 MATR3-201

R C R D D S F F G E T S H N Y H K F D S E Y E R M G R G P

ENSE00003774855
 MATR3-201

CTCATACTCTCTTACCCTGCACCAG
 PCR Reverse

TGGCCCCTTACAAGAGAGATCTCTCTTTGAGAAAAAGAGAGGCGCTCCTCCAAGTAGCAATATTGAAGACTTCCATGGACTCTTA
 ACCGGGGAATGTTCTCTCTAGAGAGAACTCTTTTTCTCTCCGCGAGGAGTTTCATCGTTATAACTTCTGAAGGTACCTGAGAAT

MATR3
 MATR3-201

G P L Q E R S L F E K K R G A P P S S N I E D F H G L L

ENSE00003774855
 MATR3-201

CCGAAGGGTTATCCCCATCTGTGCTCTATATGTGATTTGCCAGTTCATTCTAATAAGGTGAGTTAACTCAACAGATGCTTCTAAT
 GGCTTCCCAATAGGGGTAGACACGAGATATACACTAAACGGTCAAGTAAGATTATTCCACTCAATTGAGTTGTCTACGAAGATTA

MATR3
 MATR3-201

P K G Y P H L C S I C D L P V H S N K V S *

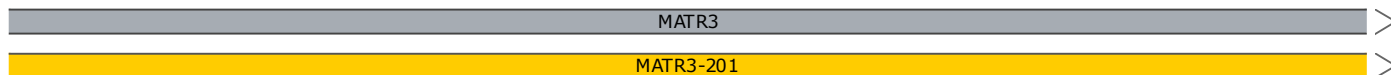
ENSE00003774855
 MATR3-201

TTCTTTTACATTGTAGTGCCTATTTACCTATATCTTTGACTCTAATTCTGTAGTCTGATGACATTGAGTTGATCAAGCATTTTTA
 AAGAAAATGTAACATCACGGATAAATGGATATAGAACTGAGATTAAGACATCAGACTACTGTAACCTCAACTAGTTCGTAAAAAT

MATR3
 MATR3-201

AACTTTTGAGAACACTTACTTTATTTGGAAGGTAATTGTTTTGAGCATTTTAAACCAGGGCTTTACATTAATATATTCTGCCTA
 TTGAAAACCTTTGTGAATGAAATAAACCTTCCATTAACAAAAACTCGTAAAATTTGGTCCCGAAATGTAATTATATAAGACGGAT

1530



GATTAC 3'
 +-----+ 1536
 CTAATG 5'

MATR3

MATR3-201

Feature	Location	Size	Start	End	Type
✓ MATR3	1 .. 1536	1536 bp	■	➔	gene
/note = gene ENSG00000015479 Protein coding					
✓ MATR3-201	1 .. 1536	1536 bp	■	➔	prim_transcript
/note = primary transcript ENST00000394805					
MATR3-203	1 .. 1536	1536 bp	■	➔	prim_transcript
/note = primary transcript ENST00000502499					
MATR3-206	1 .. 1536	1536 bp	■	➔	prim_transcript
/note = primary transcript ENST00000503811					
MATR3-208	1 .. 1536	1536 bp	■	➔	prim_transcript
/note = primary transcript ENST00000504045					
MATR3-209	1 .. 1536	1536 bp	■	➔	prim_transcript
/note = primary transcript ENST00000504311					
MATR3-210	1 .. 1536	1536 bp	■	➔	prim_transcript
/note = primary transcript ENST00000504643 Retained intron					
MATR3-212	1 .. 1536	1536 bp	■	➔	prim_transcript
/note = primary transcript ENST00000507860 Retained intron					
MATR3-214	1 .. 1536	1536 bp	■	➔	prim_transcript
/note = primary transcript ENST00000509918 protein_coding_CDS_not_defined					
MATR3-215	1 .. 1536	1536 bp	■	➔	prim_transcript
/note = primary transcript ENST00000510056					
MATR3-216	1 .. 1536	1536 bp	■	➔	prim_transcript
/note = primary transcript ENST00000511249					
MATR3-218	1 .. 1536	1536 bp	■	➔	prim_transcript
/note = primary transcript ENST00000511978 protein_coding_CDS_not_defined					
MATR3-220	1 .. 1536	1536 bp	■	➔	prim_transcript
/note = primary transcript ENST00000512876					
MATR3-221	1 .. 1536	1536 bp	■	➔	prim_transcript
/note = primary transcript ENST00000513121 Retained intron					
MATR3-222	1 .. 1536	1536 bp	■	➔	prim_transcript
/note = primary transcript ENST00000513678					
MATR3-225	1 .. 1536	1536 bp	■	➔	prim_transcript
/note = primary transcript ENST00000514528					
MATR3-227	1 .. 1536	1536 bp	■	➔	prim_transcript
/note = primary transcript ENST00000618441					
MATR3-238	1 .. 742	742 bp	■	➔	prim_transcript
/note = primary transcript ENST00000514694 Protein coding					
MATR3-224	1 .. 720	720 bp	■	➔	prim_transcript
/note = primary transcript ENST00000514488					
MATR3-230	1 .. 719	719 bp	■	➔	prim_transcript
/note = primary transcript ENST00000502394 Protein coding					
MATR3-205	1 .. 682	682 bp	■	➔	prim_transcript
/note = primary transcript ENST00000503340					
MATR3-213	1 .. 655	655 bp	■	➔	prim_transcript
/note = primary transcript ENST00000508689					

Feature	Location	Size	Start	End	Type
MATR3-207	1 .. 653	653 bp	■	→	prim_transcript
/note	= primary transcript ENST00000504023				
MATR3-233	1 .. 561	561 bp	■	→	prim_transcript
/note	= primary transcript ENST00000505016 Protein coding				
✓ MATR3-201	421 .. 1332	912 bp	■	→	CDS
/note	= coding sequence ENSP00000378284				
/translation	= MSKSFQQSSLSRDSQGHGRDLSAAGIGLLAAATQSLMPASLGRMNQGTARLASLMNLGMSSSLNQQGAHSALSSASTSSHNLQSFNIGSRGPLPLSSQHRGDADQASNILA SFGLSARDLDELSPYEDKIPENLPQILLQLKRRRTEEGPTLSYGRDGRSATREPPYRVPRDDWEEKRHFRRDSFDDRGPSLNPVLDYDHGSRSQESGYDRMDYEDDLRLD GERCRDSDFFGETSHNYHKFDSEYERMGRGPGPLQERSLFEKRRGAPSSNIEDFHGLLPKGYPHLCSICDLPVHSNK 304 amino acids = 33.9 kDa				
MATR3-208	421 .. 1332	912 bp	■	→	CDS
/note	= coding sequence ENSP00000423290				
/translation	= MSKSFQQSSLSRDSQGHGRDLSAAGIGLLAAATQSLMPASLGRMNQGTARLASLMNLGMSSSLNQQGAHSALSSASTSSHNLQSFNIGSRGPLPLSSQHRGDADQASNILA SFGLSARDLDELSPYEDKIPENLPQILLQLKRRRTEEGPTLSYGRDGRSATREPPYRVPRDDWEEKRHFRRDSFDDRGPSLNPVLDYDHGSRSQESGYDRMDYEDDLRLD GERCRDSDFFGETSHNYHKFDSEYERMGRGPGPLQERSLFEKRRGAPSSNIEDFHGLLPKGYPHLCSICDLPVHSNK 304 amino acids = 33.9 kDa				
MATR3-215	421 .. 1332	912 bp	■	→	CDS
/note	= coding sequence ENSP00000426743				
/translation	= MSKSFQQSSLSRDSQGHGRDLSAAGIGLLAAATQSLMPASLGRMNQGTARLASLMNLGMSSSLNQQGAHSALSSASTSSHNLQSFNIGSRGPLPLSSQHRGDADQASNILA SFGLSARDLDELSPYEDKIPENLPQILLQLKRRRTEEGPTLSYGRDGRSATREPPYRVPRDDWEEKRHFRRDSFDDRGPSLNPVLDYDHGSRSQESGYDRMDYEDDLRLD GERCRDSDFFGETSHNYHKFDSEYERMGRGPGPLQERSLFEKRRGAPSSNIEDFHGLLPKGYPHLCSICDLPVHSNK 304 amino acids = 33.9 kDa				
MATR3-227	421 .. 1332	912 bp	■	→	CDS
/note	= coding sequence ENSP00000482895				
/translation	= MSKSFQQSSLSRDSQGHGRDLSAAGIGLLAAATQSLMPASLGRMNQGTARLASLMNLGMSSSLNQQGAHSALSSASTSSHNLQSFNIGSRGPLPLSSQHRGDADQASNILA SFGLSARDLDELSPYEDKIPENLPQILLQLKRRRTEEGPTLSYGRDGRSATREPPYRVPRDDWEEKRHFRRDSFDDRGPSLNPVLDYDHGSRSQESGYDRMDYEDDLRLD GERCRDSDFFGETSHNYHKFDSEYERMGRGPGPLQERSLFEKRRGAPSSNIEDFHGLLPKGYPHLCSICDLPVHSNK 304 amino acids = 33.9 kDa				
MATR3-224	421 .. 720	300 bp	■	→	CDS
/note	= coding sequence ENSP00000426801				
/translation	= MSKSFQQSSLSRDSQGHGRDLSAAGIGLLAAATQSLMPASLGRMNQGTARLASLMNLGMSSSLNQQGAHSALSSASTSSHNLQSFNIGSRGPLPLSSQ 100 amino acids = 10.2 kDa				
MATR3-205	421 .. 682	262 bp	■	→	CDS
/note	= coding sequence ENSP00000422590				
/translation	= MSKSFQQSSLSRDSQGHGRDLSAAGIGLLAAATQSLMPASLGRMNQGTARLASLMNLGMSSSLNQQGAHSALSSASTSSHNLQSF 87 amino acids = 8.9 kDa				
MATR3-213	421 .. 655	235 bp	■	→	CDS
/note	= coding sequence ENSP00000422137				
/translation	= MSKSFQQSSLSRDSQGHGRDLSAAGIGLLAAATQSLMPASLGRMNQGTARLASLMNLGMSSSLNQQGAHSALSSAST 78 amino acids = 7.9 kDa				
MATR3-207	421 .. 653	233 bp	■	→	CDS
/note	= coding sequence ENSP00000421145				
/translation	= MSKSFQQSSLSRDSQGHGRDLSAAGIGLLAAATQSLMPASLGRMNQGTARLASLMNLGMSSSLNQQGAHSALSSAS 77 amino acids = 7.8 kDa				
✓ DNA Template Sequence WT -> SNV	699 .. 798	100 bp	■		misc_feature
✓ PAM	758 .. 760	3 bp	■		misc_feature
✓ gRNA Protospacer Sequence	761 .. 780	20 bp	■		misc_feature
✓ SNV	764 .. 764	1 bp	■		misc_feature
/note	= WT = T SNV = G				
MATR3-226	1100 .. 1536	437 bp	■	→	prim_transcript
/note	= primary transcript ENST00000515833				
MATR3-226	1100 .. 1332	233 bp	■	→	CDS
/note	= coding sequence ENSP00000422054				
/translation	= EKGVGMILFLVRPRITIIINLTVSMREWVVLAPYKRDLSLRKREALLQVAILKTSMDSYRRVIPICALYVICQFILI 77 amino acids = 9.0 kDa				

Feature	Location	Size		Type
MATR3-223	1248 .. 1536	289 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	232 .. 256	58°C	Aug 15, 2023
✓ Donor Template WT -> SNV /sequence = TCCACTCCCTTTATCTTCTCAACACCGTGGAGATGCAGACCAGGCCAGTAACATTTGGCCAGCTGTGGTCTGTCTGCTAGAGACTTAGATGAACTGAGT 49% GC / 30,750.0 Da	100-mer	699 .. 798	76°C	Aug 15, 2023
✓ gRNA Protospacer /sequence = TCTAGCAGACAGACCAAAGC 50% GC / 6104.0 Da	20-mer	761 .. 780	56°C	Aug 15, 2023
✓ Sanger Sequencing Primer /sequence = AGGGCCTTCTTCAGTTCTCC 55% GC / 6035.0 Da	20-mer	863 .. 882	58°C	Aug 15, 2023
✓ PCR Reverse /sequence = GACCACGTCCCATTCTCTCATACTC 52% GC / 7472.9 Da	25-mer	1165 .. 1189	60°C	Aug 15, 2023