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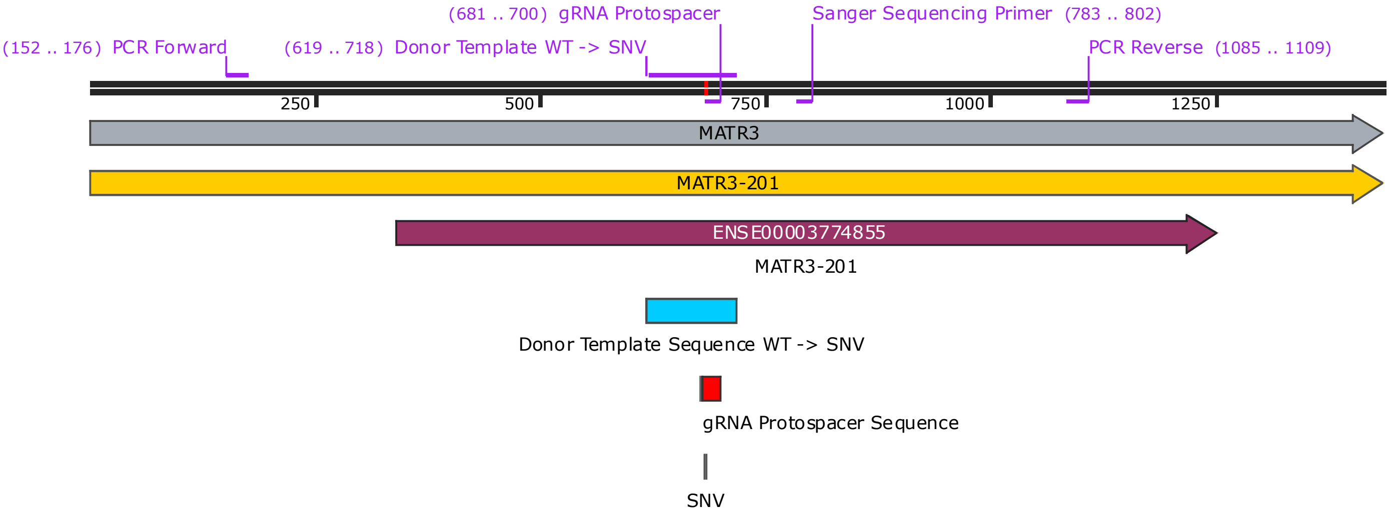
Features: 39 total
Primers: 5 total



INK2J00090_MATR3_F115C_A04_BB
1435 bp

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    MATR3
    MATR3-201
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                                                                PCR Forward
                                                                ATTTTTCTACAGAGTTGTC
    ATGCATAAGTTTTTTTTTCTTAAAAAAACGGCATCTGCTTAAAGGGATTTATGACTAAAATTGCTTATTTTTCTACAGAGTTGTC   170
    TACGTATTCAAAAAAAAAGAATTTTTTTGCCGTAGACGAATTTCCCTAAATACTGATTTTAACGAATAAAAAGATGTCTCAACAG
    MATR3
    MATR3-201
```

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PCR Forward
    TGCTGG
    TGCTGGTTCTCAGCTTGAAGAAGATTCTGCAGTCCTTATTGATCCTTTTTCTTGGCGTTACCATTTTTGAAGCAAAGTTAACCTA   255
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    MATR3
    MATR3-201
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    MATR3
    MATR3-201
```

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    ATGTCCAAGTCATTCCAGCAGTCATCTCTCAGTAGGGACTCACAGGGTCATGGGCGTGACCTGTCTGCGGCAGGAATAGGCCTTC   425
    TACAGGTTCAGTAAGGTCGTCAGTAGAGAGTCATCCCTGAGTGTCCCAGTACCCGCACTGGACAGACGCCGTCCTTATCCGGAAG
    MATR3
    MATR3-201
    1       5         10        15        20        25
    M S 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
    ENSE00003774855
    MATR3-201
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    AACGACGACGATGGGTCAGAAATTCATACGGTCGTAGAGAACCTTCCTACTTGGTCCCATGACGTGCGGAACGATCAAATTACTT
    MATR3
    MATR3-201
      30        35        40        45        50        55
    L A 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
    ENSE00003774855
    MATR3-201
```

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    MATR3
    MATR3-201
        60        65        70        75        80        85
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    ENSE00003774855
    MATR3-201
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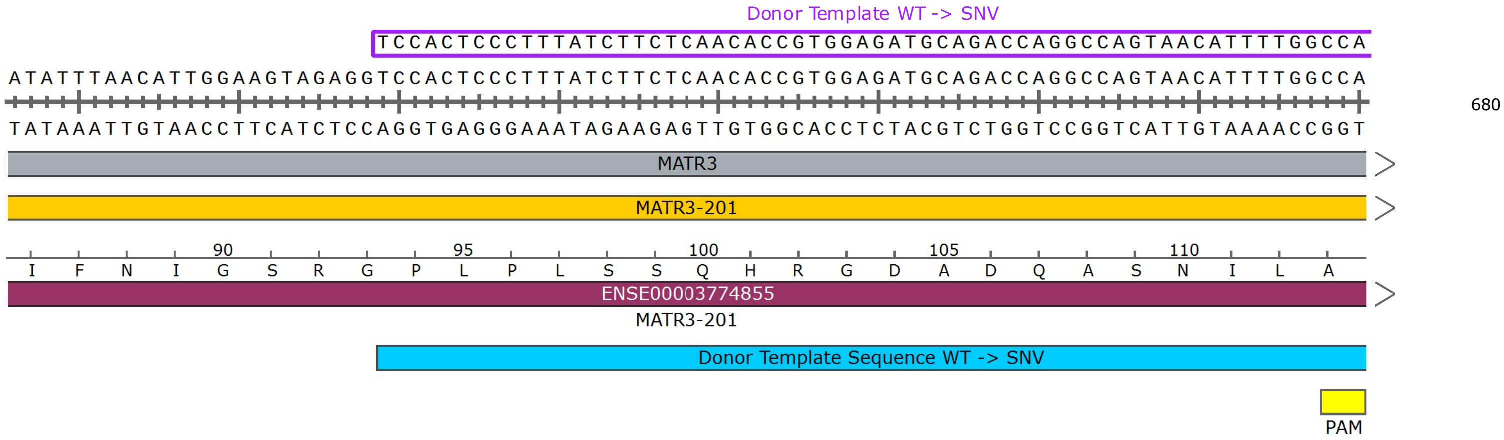
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680
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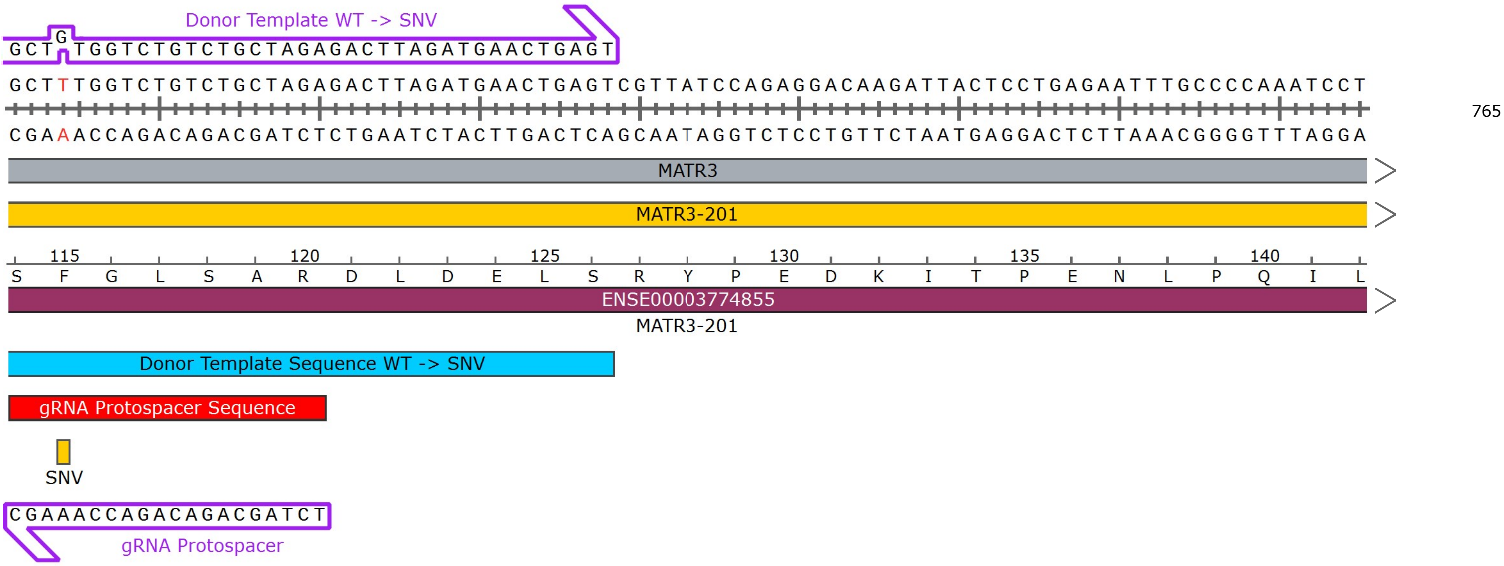
MATR3
MATR3-201
90
95
100
105
110
I F N I G S R G P L P L S S Q H R G D A D Q A S N I L A
ENSE00003774855
MATR3-201
Donor Template Sequence WT -> SNV
PAM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765
CGAAACCAGACAGACGATCTCTGAATCTACTTGACTCAGCAATAGGTCTCCTGTTCTAATGAGGACTCTTAAACGGGGTTTAGGA
MATR3
MATR3-201
115
120
125
130
135
140
S F 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
ENSE00003774855
MATR3-201
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gRNA Protospacer Sequence
SNV
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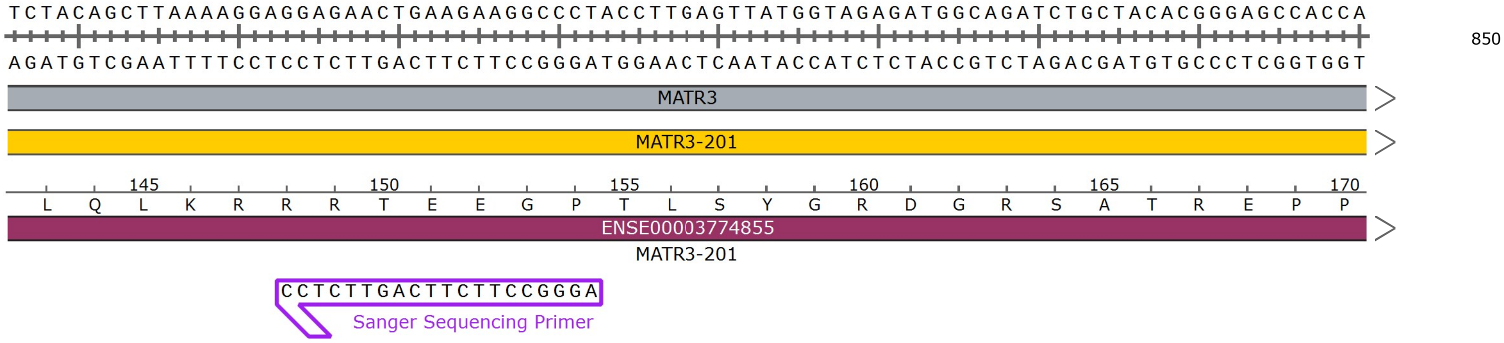
gRNA Protospacer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850
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MATR3
MATR3-201
145
150
155
160
165
170
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MATR3-201
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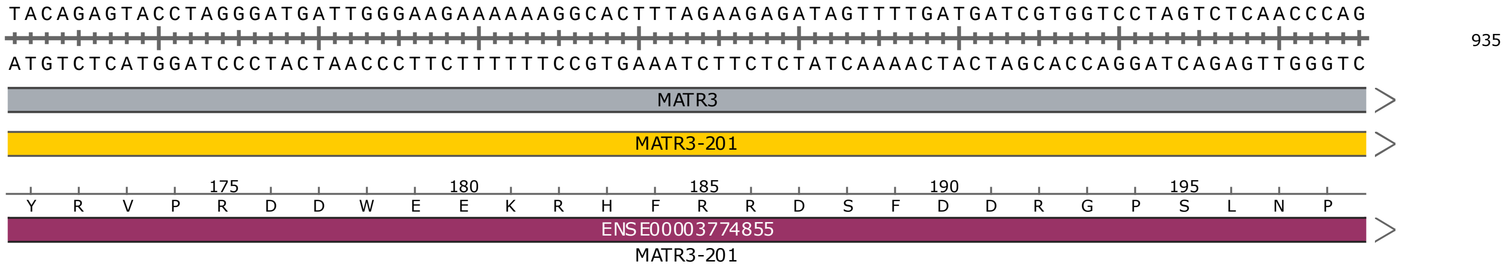
Sanger Sequencing Primer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935
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MATR3
MATR3-201
175
180
185
190
195
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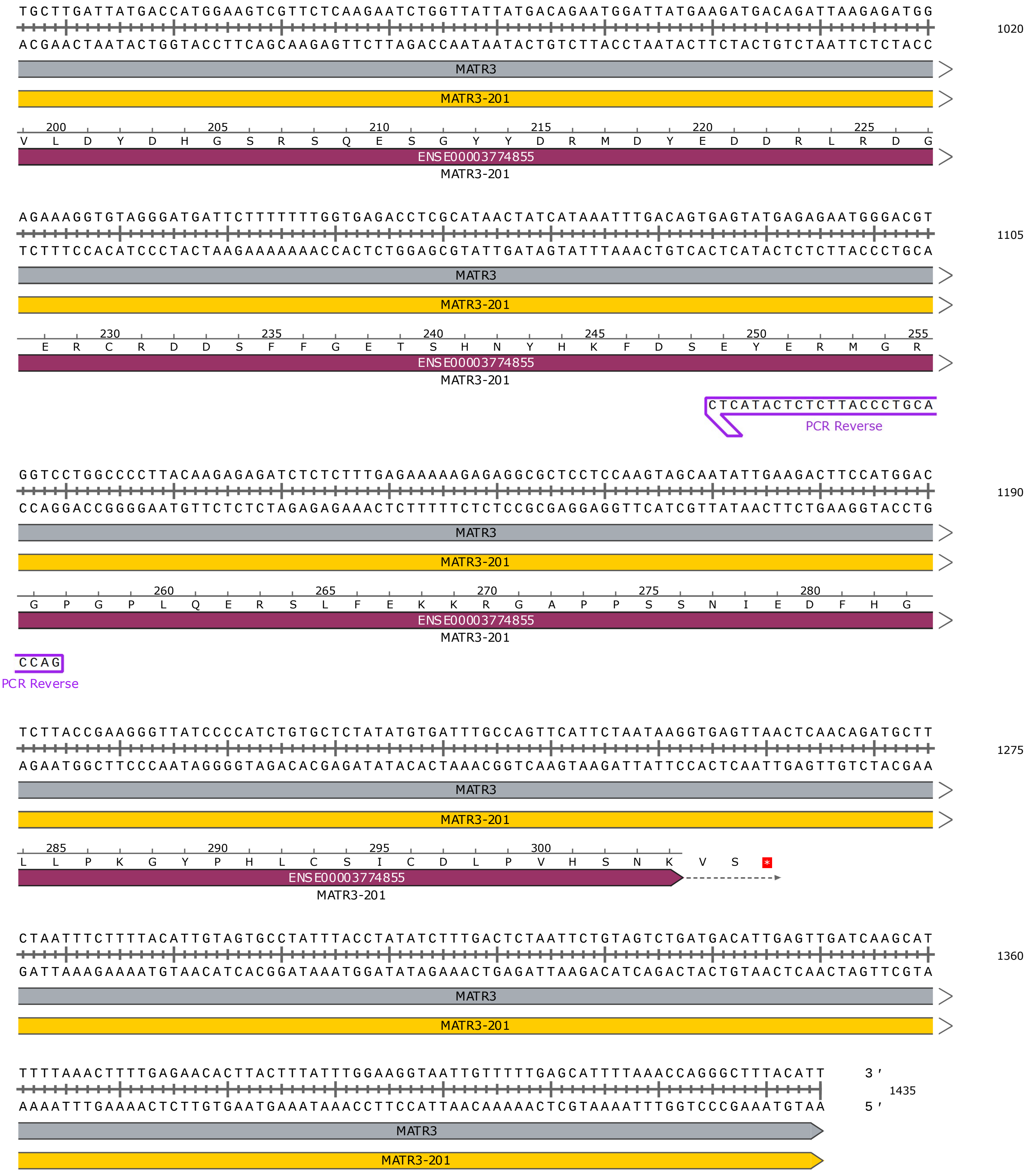
ENSE00003774855
MATR3-201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1020
MATR3
MATR3-201
200 205 210 215 220 225
V L D Y D H G S R S Q E S G Y Y D R M D Y E D D R L R D G
ENSE00003774855
MATR3-201
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1105
MATR3
MATR3-201
230 235 240 245 250 255
E 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
ENSE00003774855
MATR3-201
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PCR Reverse
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1190
MATR3
MATR3-201
260 265 270 275 280
G P 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
ENSE00003774855
MATR3-201
CCAG
PCR Reverse
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1275
MATR3
MATR3-201
285 290 295 300
L L P K G Y P H L C S I C D L P V H S N K V S *
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MATR3-201
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1360
MATR3
MATR3-201
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1435
MATR3
MATR3-201

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	MATR3-206	1 .. 1435	1435 bp	■	→	prim_transcript
	/note = primary transcript ENST00000503811					
	MATR3-208	1 .. 1435	1435 bp	■	→	prim_transcript
	/note = primary transcript ENST00000504045					
	MATR3-209	1 .. 1435	1435 bp	■	→	prim_transcript
	/note = primary transcript ENST00000504311					
	MATR3-210	1 .. 1435	1435 bp	■	→	prim_transcript
	/note = primary transcript ENST00000504643 Retained intron					
	MATR3-212	1 .. 1435	1435 bp	■	→	prim_transcript
	/note = primary transcript ENST00000507860 Retained intron					
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	MATR3-215	1 .. 1435	1435 bp	■	→	prim_transcript
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	MATR3-218	1 .. 1435	1435 bp	■	→	prim_transcript
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	MATR3-221	1 .. 1435	1435 bp	■	→	prim_transcript
	/note = primary transcript ENST00000513121 Retained intron					
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	/note = primary transcript ENST00000513678					
	MATR3-225	1 .. 1435	1435 bp	■	→	prim_transcript
	/note = primary transcript ENST00000514528					
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	MATR3-238	1 .. 662	662 bp	■	→	prim_transcript
	/note = primary transcript ENST00000514694 Protein coding					
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	/note = primary transcript ENST00000514488					
	MATR3-230	1 .. 639	639 bp	■	→	prim_transcript
	/note = primary transcript ENST00000502394 Protein coding					
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304 amino acids = 33.9 kDa</td></tr>
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304 amino acids = 33.9 kDa</td></tr>
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GERCRDDSFFGETSHNYHKFDSEYERMGRGPGPLQERSLFEKKRGAPPSSNIEDFHGLLPKGYPHLCSICDLPVHSNK
304 amino acids = 33.9 kDa</td></tr>
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SNV = G</td></tr>
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Feature	Location	Size		⇄	Type
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/note = primary transcript ENST00000514402
Retained intron

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✓	**Donor Template WT -> SNV**	100-mer		619 .. 718	→	76°C	Aug 15, 2023
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✓	**gRNA Protospacer**	20-mer		681 .. 700	←	56°C	Aug 15, 2023
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✓	**Sanger Sequencing Primer**	20-mer		783 .. 802	←	58°C	Aug 15, 2023
	/sequence = AGGGCCTTCTTCAGTTCTCC 55% GC / 6035.0 Da						
✓	**PCR Reverse**	25-mer		1085 .. 1109	←	60°C	Aug 15, 2023
	/sequence = GACCACGTCCCATTCTCTCATACTC 52% GC / 7472.9 Da						