

**INK2J00082R\_FUS\_R521H\_A04\_AA**  
 11,468 bp

5'

TGCTCAGTCCTCCAGGCGTCCGGTACTCAGCGGTGTTGGAACCTTCGTTGCTTGCCTGTGCGCGCGTGC CGCGGACATGGCCTC  
ACGAGTCAGGAGGTCCGCGAGCCATGAGTCGCCACAACCTTGAAGCAACGAACGAACGGACACGCGCGCACGCGCCTGTACCGGAG

85

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AAACGGTAGGTAAGGGCGCGAGGCGACGGCGGCGGCGCACCCGGCCGAGGCCTCCAGCTGGGCTTTTCGTTTTTCAGTGGGACCG  
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170

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255

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340

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425

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GCTCGAGCCCGCTTTGTCGCAGTGCTGCATCCGGGCACTCGCGGCGCGCACGCGCTCTGCGGGCCCTCCCCCTTCGCGGCGCGG  
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510

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GTACCCCTTCCCCGCTCGTGTGGTTGAGCTTTCTGTGCGGAGACCCTTCGCGGAAGACTCGGCGGCGCGCTCCGGTGTGAGC  
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595

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CTTGTCCCTCAGTGGTCTTCGCGAATGGGCGGGATCGCTCCGTTCCCGCCTGGGTTGCCACGCGGCTGGGGGCGGAGGCTCGGG  
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680

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ATCGGGGCGCCCTCTAGCTTAACGGTTTTGGCGGGCGGTGGTCAAGGTTTCGACCAACGGACTTGGGGACGGCCCGAGAGTTTTTCC  
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765

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CGCCTAAATTTCTTTCTTTTTTTTTTTGGAGACACGGTCTTCTCTGTGCGCCAGGCTGGAGTGCAGTGGTGCATCTCAGATCA  
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850

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935

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1020

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1105

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GGAGAAGAACGGCCGCCCGAGGCCACACCCTCTCCTGGTCTCTTTCCCTTTTCTGCGGGGGAAGCGCCGCGTTTTCTGTGCTG  
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1190

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1275

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1360

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1445

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1530

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1615

FUS

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1700

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ACCTTGGTTTTTCCAATGGTTAAGGCTTCTGGGACTCTGTAGAAACTTGCATTTTCTTCACTTTTTCTTTATTGTAAGAACACTT  
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1785

FUS

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1870

FUS

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1955

FUS

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2040

FUS

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ATGGGGCTTCACCATGTTGGTCAGGCCAGTCTCGAATTCCTGACCTCAAGTGATCCACCCACCTCGGCCTCCCAAACCTGCTGGGA  
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2125

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2210

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2295

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5 10  
D Y T Q Q A T Q S  
ENSE00003475065

TTTTTGGGCTTCCAGAGTTTGTAGAGGGCAAGGGTGGTCCACGCCATGTTTTCTGATCACGCTGGTTTTCTTTTATTTAGCTATG  
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2380

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2465

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15 G A Y P T Q P G Q G Y S Q Q S Q P Y G Q Q S Y S G Y S Q

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2550

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45 S T D T S G Y G Q S S Y S S Y G 60 S Q N

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CTCTTCCTACTCTTTCTGAATATTGCTTTTCTTTTTCTTGTTTTTTGGAGACGGAGTCTGGTCCTGTTGCCAGGCTGGAGTGCA  
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2635

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GTGGTGCTGTCTCAGCTCACTGCAACATCAGCCTACCGGGTTCAAACGATTCTCCTGCCTCAGCCTCCTGAGTAGCTGGGATTAC  
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2720

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2805

FUS

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2890

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GAGCAGCACTGAGATGTTGAAACTGTTCCATATTTCTTTTCCGTGAAACAGTGTATAAGTCTTAAACTTTTTGGGATCTGAGTC  
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2975

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3060

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3145

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3230

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3315

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3400

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3485

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TGGTGTGGGATTGGCGGGGTGAAATTGGAAC TGTACTAAAGAGTTGGTAGAAGTTGAAGCATTAAATTTAGGCTTTGAAAGGAG  
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3570

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3655

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3740

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65 70  
T G Y G T Q S  
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ACTCCCAGGGATATGGCTCGACTGGCGGCTATGGCAGTAGCCAGAGCTCCCAATCGTCTTACGGGCAGCAGTCCTCCTACCCTG  
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3825

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T P Q G Y G S T G G Y G S S Q S S Q S S Y G Q Q S S Y P  
ENSE00003599547

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3910

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100 105 110  
G Y G Q Q P A P S S T G S  
ENSE00003599547

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3995

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4080

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115  
Y G S  
ENSE000035...

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4165

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S S Q S 120 S S Y G Q 125 P Q S G S Y S Q Q P 135 Y G G Q 140 Q Q S Y  
ENSE00003537617



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4250

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145 150 155 160 165 170  
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4335

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TGTCTCTGTTGCTGAGGCTGGAGTGCAGTGGCACAATCTCGGCTCACTGCAAGCTCCGCCTTCCGGGTTTCGCGCCAGTCTCCTGC  
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4420

FUS

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4505

FUS

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4590

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4675

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4760

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4845

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175 N Y G Q 180 Q S S M 185 S S G G G  
G N Y G Q D Q S S M S S G G G

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4930

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190 S G G G Y 195 G N Q D Q 200 S G G G G 205 S G G Y G 210 Q Q D R G 215 G R G

ENSE00001791812

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5015

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220 R G G S G G G 225 G G G G G 230 G G Y N R 235 S S G G Y 240 E P R G R 245 G G

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5100

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250 G R G G R G G M 255 G

ENSE00001791812

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TCTCCCTGAAGCCAGTCCCTAGTGCATGGTTAGTATTCTTGTGTCTAGGGATCTGTGAGGGCTTTGATTTGGGGGCAGTGA  
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5185

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5270

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5355

FUS

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5440

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5525

FUS

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GAGCTTGATTTGCACTAATTTGACCGACATTGATTTTGTGTGTGACTTGGTTTTATGGGGCCAGCTGACTGAAGTAAGCAGACCTT  
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5610

FUS

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TTGGGCAAAAATATGCTTTGACAGTGGTCTCCACCTATTTGTTCCACTGTCTGCCTTCCCCTGGTTACTTAAAATTCATCAGCT  
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5695

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TGTCCAACCTGGACCTTCTTTCCTTCTGCTGAAGTTGATTTGAAGTAAAACCTTAGATTTGATGTTAAAACAGTTGTCAAATCTG  
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5780

FUS

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TTGGTAAATAAGATTTGAAGGACCCTACTCTGTCTCCCTTGAAAAAGGGGAGGAATGTCAGTGTTACTGTTTTTGGAAAAAGTAG  
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5865

FUS

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ATTTTTAAACCGAGTTTGGAAATGGTAAGTATGCAGAGGTGGGTGGGGGCAATCTCAAAAACGTGCAAAAATGAGGAAAAACAAA  
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5950

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ATGAGGAAATGTGTGCGTGTGTTTAAATGCAAAACTTTAAAAAGAAAAACAACCTGTTATGTGACTGTTAACTTGCTCTGCATTTTA  
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6035

FUS

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TGTGCCACAGGTATGAAAGGTGACATTGCAAAATACTCCGCTCTTCTCGCAGTGTAGAAGGGGTGACCCCGGGGGTTGGGGGAGA  
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6120

FUS

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TCAAAAACAGCTCAGTAGTTAGGACAGAGCTTAGCTAAGTTTGTCTTGCTTTAAGGGGAAGTTGCCTTTGGTTTTGACTTTTTAT  
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6205

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GGAATGGGGTTGGGTCTGCTTGCTGCTTTCAAAGCAAAAACCACAAAAATGTGTTCAAGGCTACCCCAGCCTGGTGTGAAATGTC  
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6290

FUS

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6375

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FUS-201

ATCGGAAGAACGACCAAGGAAAATGGGTTATTTTTTTCCAGAGGAAATAGATAACGTAACCTTTTAAAGCAAAATCTTTATAAA  
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6460

FUS

FUS-201

FUS-201

CTGTGTCTGAGAAATTGCACACGTGTGTGTGACATGCTCAAAGGTCAGACAAGGGGTGGTCAGGAAGGGATGTATTTTAGTAGCC  
GACACAGACTCTTTAACGTGTGCACACACACTGTACGAGTTTCCAGTCTGTTCCCACCAAGTCTTCCCTACATAAAATCATCGG

6545

FUS

FUS-201

FUS-201

ACTTGTATCTTTTTCCAAAAACACCTACCCATGTTTGGGGAATGTTAAACAAAATCAAAAAACAACCTTTTGTAGCCGTTGGAAG  
TGAACATAGAAAAAGGTTTTTGTGGATGGGTACAAACCCCTTACAATTTGTTTTAGTTTTTTGTTGGAAAAACATCGGCAACCTTC

6630

FUS

FUS-201

FUS-201

CTTCATGTCCTTTCTTCTAACTTGTCTTCTCCAGCGGAAGTGACCGTGGTGGCTTCAATAAATTTGGTGGTAAGTGAACAGAGTT  
GAAGTACAGGAAAAGAAGATTGAACAGAAGAGGTCGCCTTCACTGGCACCACCGAAGTTATTTAAACCACCATTCACTTGTCTCAA

6715

FUS

FUS-201

G S D R G G F N K F G  
260 265

ENSE00003521089

FUS-201

TCCAAAATCCCAACTCCCAGCAATGCTTTGTCTGATTGTTTCAATTTGCAGATGTCTTAGCGTGTTAATTTAAATGTCAAAGGTTT  
AGGTTTTAAGGGTTGAGGGTCGTTACGAAACAGACTAACAAGTAAACGTCTACAGAATCGCACAATTAATTTACAGTTTCCAAA

6800

FUS

FUS-201

FUS-201

TGAGGTGTCCAGAACCACCTCCAGAAAAGGGGTAGGGTAGAATGCCACCTGTTGCCTGGTGTGTGCTAACCTGGAGCAGGTAGGGG  
ACTCCACAGGTCTTGGTGGAGGTCTTTCCCATCCCATCTTACGGTGGACAACGGACCACACACGATTGGACCTCGTCCATCCCC

6885

FUS

FUS-201

FUS-201

TAAGACTCAATAGTCATCTTTTACCAAATGGGTTTGCCCAGGTTAATAAGAGGGGTCTAGTAGGCCTTGGACTGGGCCGTTGCC  
ATTCTGAGTTATCAGTAGAAAATGGTTTACCCAAACGGGGTCCAATTATTCTCCCCAGATCATCCGGAACCTGACCCGGCAACGG

6970

FUS

FUS-201

FUS-201

ACACCTGGCACTTAGTGACCATCATCATGAGAACTGGAGAGTGCGTGCTGGAACACGTGGTGCCATCTTGGCTTTAGGATCCTT  
TGTGGACCGTGAATCACTGGTAGTAGTACTCTTTGACCTCTCACGCACGACCTTGTGCACCACGGTAGAACCGAAATCCTAGGAA

7055

FUS

FUS-201

FUS-201

TTGATCGTTGTGTCCAAGGCTTGTGTGTGTGTGAGTGTGTGGGAGACAACTCCGAATGTTTAAATCTGGAAGAGGGATGTAACAT  
AACTAGCAACACAGGTTCCGAACACACACACACTCACACACCTCTGTTGAGGCTTACAAATTAAGACCTTCTCCCTACATTGTA

7140

FUS

FUS-201

FUS-201

TGCCCTGAGGATGGTGAAGTTGGTATACATTTATAAAGTACGGAATGGTGTCAATGAATGCAATTCTATGTATATGGACTTAACT  
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7225

FUS

FUS-201

FUS-201

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7310

FUS

FUS-201

FUS-201

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7395

FUS

FUS-201

FUS-201

ATTTGAGAAGTCTCCAGTAAGCTGGAACTTTTCTGGTTTTGGTTAACAAAAGTTTTCTTGATTTGTTTCAAGATTTAAAGCCAAA  
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7480

FUS

FUS-201

FUS-201

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7565

FUS

FUS-201

FUS-201

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7650

FUS

FUS-201

FUS-201

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7735

FUS

FUS-201

FUS-201

TTCCACAAGGGTTAAGTGTCTGGTGGTAAAGTTGGGAGAAACTGGATGGATGCACATCGCATGGCTGGTGGCGAGCCCATCTCTC  
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7820

FUS

FUS-201

FUS-201

TTCTCTCGGGTGAGAGAACCAGGGCCAAGCTGAGTTGGTTTGTTCACCTTAATGGGTCTCCGTTTCCCCTGCCACCTGTGCTGAGG  
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7905

FUS

FUS-201

FUS-201

ACATTTCCCAGCCTGAGCTGGGGGAGGCAGCATTGCTGAAGTGTGGAGTTGTCTCTGTGGAGACTCAAGTTACAGATCTTAAGG  
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7990

FUS

FUS-201

FUS-201

GGCCTGCCTAGAATTTTCTCCTCTGGGCAGGCGACCCAGGAAAGGGTTTGGAGTGAGGCTGTGAGCACTTACTTGATATTTTACA  
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8075

FUS

FUS-201

FUS-201

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8160

FUS

FUS-201

FUS-201

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8245

FUS

FUS-201

G P R D Q G S R H D S  
ENSE00003535451

FUS-201

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8330

FUS

FUS-201

FUS-201

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8415

FUS

FUS-201

FUS-201

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8500

FUS

FUS-201

FUS-201

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8585

FUS

FUS-201

FUS-201

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8670

FUS

FUS-201

FUS-201

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8755

FUS

FUS-201

FUS-201

ATACTGTATACTGGGTGTTAACATGTTTCAAAGGATAATTGTCAAAGTGAATCTGAAATTTATCAGCATGGCTGGCATATAGGGAATATGACATATGACCCACAATTGTACAAAGTTTCTTATTAACAGTTTACTTAGACTTTAAATAGTCGTACCGACCGTATATCCCT

8840

FUS

FUS-201

FUS-201

CTCAAAGGGATGTGGATTTCTTTTTAGTTGCTTCCATAAACCAAATGATACCAGTTGCTTGATGGATACTAGGTGCTTTAGGTGAGTTTTCCCTACACCTAAAGAAAAATCAACAGAAGGTATTTGGTTTACTATGGTCAACGAACCTACCTATGATCCACGAAATCCA

8925

FUS

FUS-201

FUS-201



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AAAAAGGACACAAAAAATAAAATGGAAAAGTGTAACGTAAGAGACAAAGTTGTTTCGTCTTGTCTATTAAGTCTGTTGTTGTG

9010

FUS

FUS-201

E Q D N S D N N T  
ENSE00003524436

FUS-201

CATCTTTGTGCAAGGCCTGGGTGAGAATGTTACAATTGAGTCTGTGGCTGATTACTTCAAGCAGATTGGTATTATTAAGGTACTT  
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9095

FUS

FUS-201

I F V Q G L G E N V T I E S V A D Y F K Q I G I I K

ENSE00003524436

FUS-201

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9180

FUS

FUS-201

FUS-201

CAGTAAAAACAAGTCTTAGTGGTTGTTGCCAGCTTAATTTGTTGAGGAAAGAGCCTTAGTACTGTTTTCTAAAAGAGAAGTTCT  
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9265

FUS

FUS-201

FUS-201

ATCTTAACACAAAAAGTATAACTTATCAGAGTACCCTAAACTCTTGAGATTTGTAAGTACTCTATAGTAACTTTTAGTTTTATCTTTCA  
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9350

FUS

FUS-201

FUS-201

ATATTGGAGTGAGAGACAGTTTTCTTTAATGGAGGTTTACATGTGAGGTAGGAAGAAGTAACTGGGAAGAGGGGAGCTGAAGTTT  
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9435

FUS

FUS-201

FUS-201

GGGAATTATAAACCTCATGTTCTAGAGGAAGAAGATGGAAAGGGAGTACTGTAGCCTTTAAAATTGATGTTACCTCATTTTTGCTT  
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9520

FUS

FUS-201

FUS-201

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9605

FUS

FUS-201

315 320 325 330 335  
T N K K T G Q P M I N L Y T D R E T G K L K G E A T

ENSE00003534484

FUS-201

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CAGAGAAAACCTACTGGGTGGAAGTCGATTTTCGTCGATAACTGACCAAACCTACCATACATACTCTTCCGACCGTCTCCACCCCGAC

9690

FUS

FUS-201

340 345 350 355  
V S F D D P P S A K A A I D W F D

ENSE00003534484

FUS-201

GGGATATAGGGCAGCAAGCCTTAGGAAACAAGCCATAGTTTTGAGGGTTCTTTTGTAGTCTTCCAACACTTACTTTAGCTGCGGTTT  
CCCTATATCCCGTCGTTTCGGAATCCTTTGTTCGGTATCAAACCTCCAAGAAAACCTCAGAAGGTTGTGAATGAAATCGACGCCAAA

9775

FUS

FUS-201

FUS-201

CAGGTAGTCTCATTTTTGCTTATGTGTCAGCAGATTATAAACCATTTGAGAAAAGGCACGCTTCTTGTATTTTTCGGATTAATGT  
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9860

FUS

FUS-201

FUS-201

GTCTTGCATTTAAAGTCTGTTGATGATTTTTGTTTCTCTAGGTAAGAATTCTCCGGAAATCCTATCAAGGTCTCATTTGCTAC  
CAGAACGTAAATTTAGACAACTACTAAAAAACAAAGAGATCCATTTCTTAAGAGGCCTTTAGGATAGTTCCAGAGTAAACGATG

9945

FUS

FUS-201

360 365 370  
G K E F S G N P I K V S F A T

ENSE00003653971

FUS-201

TCGCCGGGCAGACTTTAATCGGGGTGGTGGCAATGGTCGTGGAGGCCGAGGGCGAGGAGGTGAGGAGCTACCTGCTAGTGGTGCA  
AGCGGCCCGTCTGAAATTAGCCCCACCACCGTTACCAGCACCTCCGGCTCCCGCTCCTCCACTCCTCGATGGACGATCACCACGT

10,030

FUS

FUS-201

375 380 385  
R R A D F N R G G G N G R G G R G R G

ENSE00003653971

FUS-201

GAGGGGTAATGGGGAGAGTGCAGAAGATGGTAAAGGCTTGCATGGAATGGGTTAGATTTACCAAACCTGGAGAGGGAGCAGACCC  
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10,115

FUS

FUS-201

FUS-201

ATACCTTGGTCTATCTGCATTAGGACCCATGGGCCGTGGAGGCTATGGAGGTGGTGGCAGTGGTGGTGGTGGCCGAGGAGGATTTCT  
TATGAACCAGATAGACGTAATCCTGGGTACCCGGCACCTCCGATACCTCCACCACCGTCACCACCACCACCGGCTCCTCCTAAAG

10,200

FUS

FUS-201

390 P M G R G G Y G G G S G G G R G G F  
400 405 410

ENSE00003604625

FUS-201

CCAGTGGAGGTGGTGGCGGTGGAGGACAGCAGCGAGCTGGTGAAGTGTCTAATCCGTGAGTGAACTTAATTTTTTTCT  
GGTCACTCCACCACCGCCACCTCCTGTCGTCGCTCGACCACTGACCTTCACAGGATTAGGCACTCACTTTGAATTAATAAAGA

10,285

FUS

FUS-201

115 120 125 130  
P S G G G G G G Q Q R A G D W K C P N P

ENSE00003604625

FUS-201

TAGTTCTCTTGCATGCGTGCTCTTTGATATATTGGTACTGAGGTATGTGCGTGTTTTCCAAAGAAGTAAATGTCAAGGCCACACT  
ATCAAGAGAACGTACGCACGAGAACTATATAACCATGACTCCATACACGCACAAAAGGTTTCTTCATTTACAGTTCCGGTGTGA

10,370

FUS

FUS-201

FUS-201

GTTGGGGTCAGATTTAGCCAAAAGCTTACCTAGGTAAGGTTGATGTAATGGGAAAGGTAATGGATTGGGTTTCAGTAATACTGATT  
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10,455

FUS

FUS-201

FUS-201

TTTGTTCCTGACTCTGAGAAGCAAGCCGTTTTGTCTTTCTGAAGCTTCAGTTTTCTCACTGTATCTCTAAAGTCACCGTAGTTTC  
AAACAAGGACTGAGACTCTTCGTTTCGGCAAAACAGAAAGACTTCGAAGTCAAAGGAGTGACATAGAGATTTTCAGTGGCATCAAAG

10,540

FUS

FUS-201

FUS-201

TTCTAGTTCTAGGTCTTGCCATTCCCCATCGCTCCAGACTGATTGTCTTCTTTCTCCTTAGCACCTGTGAGAATATGAACTT  
AAGGATCAAGATCCAGAACGGATAAGGGGTAGCGAGGTCTGACTAACAGAAGGAAAGAGGAATCGTGGACACTCTTATACTTGAA

10,625

FUS

FUS-201

435  
T C E N M N F

ENSE00003494295

FUS-201

CTCTTGGAGGAATGAATGCAACCAGTGTAAGGCCCTAAACCAGATGGCCCAAGGAGGGGGACCAGGTGGCTCTCACATGGGTAAG  
GAGAACCCTCCTTACTTACGTTGGTCACATTCCGGGGATTGGTCTACCGGGTCTCCCCCTGGTCCACCGAGAGTGTACCCATTCT

10,710

FUS

FUS-201

440 445 450 455 460  
S W R N E C N Q C K A P K P D G P G G G P G G S H M

ENSE00003494295

FUS-201

PCR Forward

GGGAACATAGGGGAATGGGA

AAAGGCAGACCTGGTGCTAGGGAGCTGGGACCAAAGAATCCTTAATTTTTTCAGCGGGGAGGCTCGGGGAACATAGGGGAATGGGA  
TTTCCGTCTGGACCACGATCCCTCGACCCTGGTTTTCTTAGGAATTA AAAAAGTCGCCCTCCGAGCCCTTGTATCCCCTTACCCT

10,795

FUS

FUS-201

FUS-201

PCR Forward

ATATG

ATATGATAGATCTTGTTCCTTAGGGGGTAACCTACGGGGATGATCGTCGTGGTGGCAGAGGAGGCTATGATCGAGGCGG  
TATACTATCTAGAACAAGAAAACAGGATCCCCATTGATGCCCTACTAGCAGCACCACCGTCTCCTCCGATACTAGCTCCGCC

10,880

FUS

FUS-201

465 470 475 480  
G G N Y G D D R R G G R G G Y D R G G  
ENSE00003637572

FUS-201

CTACCGGGCCGCGGGGACCGTGGAGGCTTCCGAGGGGGCCGGGGTGGTGGGGACAGAGGTGGCTTTGGCCCTGGCAAGATG  
GATGGCCCCGGCGCCGCCCTGGCACCTCCGAAGGCTCCCCGGCCCCACCACCCTGTCTCCACCGAAACGGGACCGTTCTAC

10,965

FUS

FUS-201

485 490 495 500 505 510  
Y R G R G G D R G G F R G G R G G D R G G F G P G K M  
ENSE00003637572

FUS-201

GATTCAGGTAAGACTTTAAATCAGAATAAAAAAGTAGAGCAGTTGAACAGAGGCCATAGGATAACAGGGTTTTGTTGAGAAAAGT  
CTAAGGTCCATTCTGAAATTTAGTCTTATTTTTTCATCTCGTCAACTTGTCTCCGGTATCCTATTGTCCAAAACAACCTCTTTCA

11,050

FUS

FUS-201

D S R  
ENSE0000...

FUS-201

GGTTTCATTTTGGAGGGCTAGGTGGAAAGACCTGAGGTTGTAACCAGTAGTGGAGAGGGAAGGAAAATTAACCTCAGGGGGAGTGAA  
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11,135

FUS

FUS-201

FUS-201

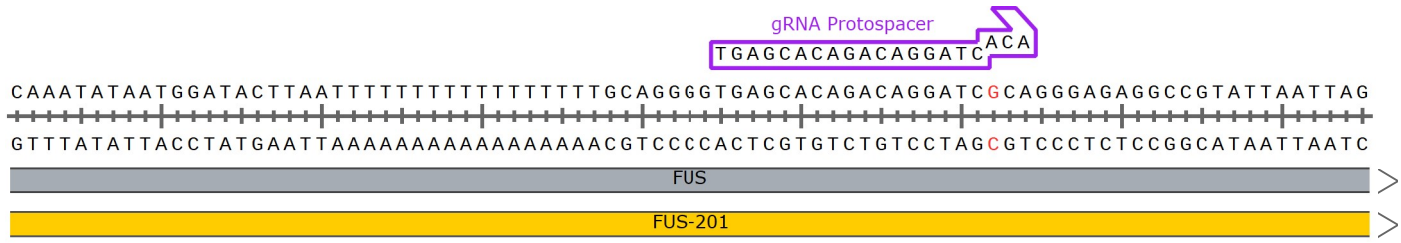
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11,220

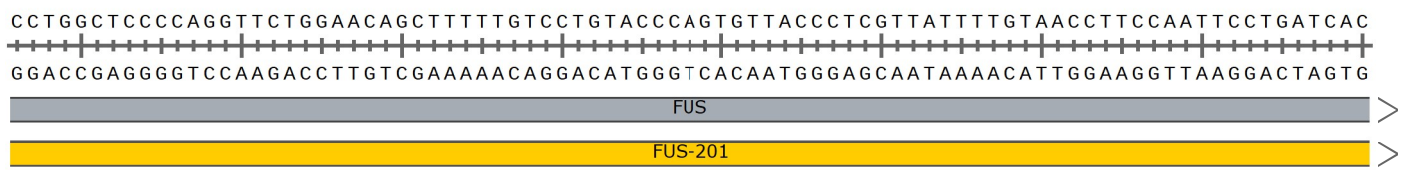
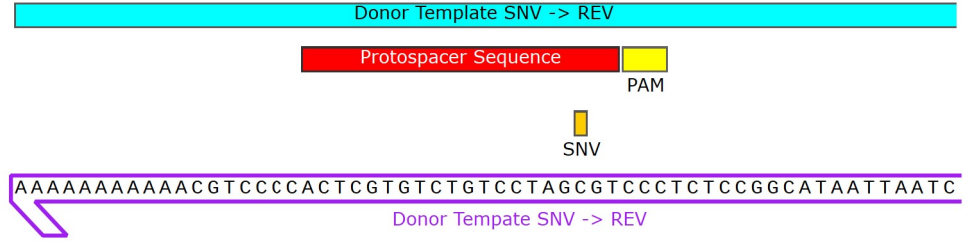
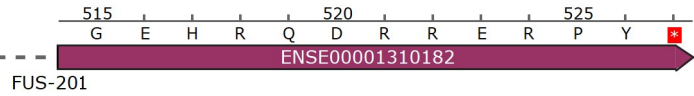
FUS

FUS-201

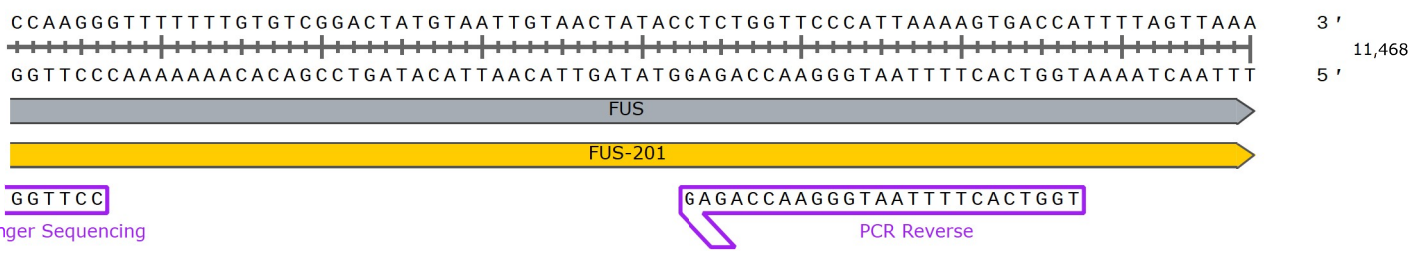
FUS-201



11,305





















11,390



11,468

Feature	Location	Size	Type
✓ <b>FUS</b>	1 .. 11,468	11,468 bp	gene
/note	= gene <a href="#">ENSG0000089280</a> Protein coding		
<b>FUS-209</b>	1 .. 11,465	11,465 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000566605</a> Nonsense mediated decay		
✓ <b>FUS-201</b>	2 .. 11,468	11,467 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000254108</a>		
<b>FUS-202</b>	2 .. 11,465	11,464 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000380244</a>		
<b>FUS-205</b>	2 .. 3213	3212 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000487045</a> Retained intron		
<b>FUS-206</b>	13 .. 11,465	11,453 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000487509</a> Retained intron		
<b>FUS-210</b>	14 .. 11,438	11,425 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000568685</a>		
✓ <b>FUS-201</b>	78 .. 11,301	11,224 bp	CDS
▶ 15 segments = 1581 bp			
/note	= coding sequence <a href="#">ENSP00000254108</a>		
/translation	= MASN,,DYTQ QATQS,,YGAYPTQPGQGYSQQSSQPYGQQSYSGYSQSTDTSGYGQSSYSSYGQSQN,,TGYGTQSTPQGYGSTGGYGSSQSS QSSYGQQSSYPGYGQQPAPSSTSGS,,YGSSSQSSSYGQPQSGYSYQQPSYGGQQQSYGQQQSYNPPQGYGQQNQYNSSSSGGGGGGGGGG, ,GNYGQDQSSMSSGGGSGGGYGNQDQSGGGGSGGYGQQDRGGRGRGGSGGGGGGGGGGYNRSSGGYEPGRGRGGRRGGRMG,,GSDRG GFNKF,,GPRDQGSRHDS,,EQDNSDNNTIFVQGLGENTVIESVADYFKQIGIIK,,TNKKTGQPMINLYTDRETGKLKGEATVSFDDPPSAKAAI DWFD,,GKEFSGNPIKV SFATRRADFNRGGGNGRGGRRGR,,GPMGRGGYGGGGSGGGRRGFPSSGGGGGGGQQRAGDWKCPNP,,TCENMNF SWRNFNCQCKAPKBDGSGGPGSSHM,,GGNYGDDRRGGRRGGYDRGGYRGRGGDRGGFRGGRRGGDRGGFGPGKMDSR,,GEHRQDRRERPY*		
<b>FUS-202</b>	78 .. 11,301	11,224 bp	CDS
▶ 15 segments = 1578 bp			
/note	= coding sequence <a href="#">ENSP00000369594</a>		
/translation	= MASN,,DYTQ QATQS,,YGAYPTQPGQGYSQQSSQPYGQQSYSGYSQSTDTSGYGQSSYSSYGQSQN,,SYGTQSTPQGYGSTGGYGSSQSSQ SSYGQQSSYPGYGQQPAPSSTSGS,,YGSSSQSSSYGQPQSGYSYQQPSYGGQQQSYGQQQSYNPPQGYGQQNQYNSSSSGGGGGGGGGG,,G NYGQDQSSMSSGGGSGGGYGNQDQSGGGGSGGYGQQDRGGRGRGGSGGGGGGGGGGYNRSSGGYEPGRGRGGRRGGRMG,,GSDRG GFNKF,,GPRDQGSRHDS,,EQDNSDNNTIFVQGLGENTVIESVADYFKQIGIIK,,TNKKTGQPMINLYTDRETGKLKGEATVSFDDPPSAKAAIDW FD,,GKEFSGNPIKV SFATRRADFNRGGGNGRGGRRGR,,GPMGRGGYGGGGSGGGRRGFPSSGGGGGGGQQRAGDWKCPNP,,TCENMNF SWRNFNCQCKAPKBDGSGGPGSSHM,,GGNYGDDRRGGRRGGYDRGGYRGRGGDRGGFRGGRRGGDRGGFGPGKMDSR,,GEHRQDRRERPY*		
<b>FUS-210</b>	78 .. 11,301	11,224 bp	CDS
▶ 15 segments = 1584 bp			
/note	= coding sequence <a href="#">ENSP00000455282</a>		
/translation	= MASN,,DYTQ QATQS,,YGAYPTQPGQGYSQQSSQPYGQQSYSGYSQSTDTSGYGQSSYSSYGQSQN,,TGYGTQSTPQGYGSTGGYGSSQSS QSSYGQQSSYPGYGQQPAPSSTSGS,,YGSSSQSSSYGQPQSGYSYQQPSYGGQQQSYGQQQSYNPPQGYGQQNQYNSSSSGGGGGGGGGG, ,GNYGQDQSSMSSGGGSGGGYGNQDQSGGGGSGGYGQQDRGGRGRGGSGGGGGGGGGGYNRSSGGYEPGRGRGGRRGGRMG,,GSDRG GFNKF,,GPRDQGSRHDS,,AEQDNSDNNTIFVQGLGENTVIESVADYFKQIGIIK,,TNKKTGQPMINLYTDRETGKLKGEATVSFDDPPSAKAA IDWFD,,GKEFSGNPIKV SFATRRADFNRGGGNGRGGRRGR,,GPMGRGGYGGGGSGGGRRGFPSSGGGGGGGQQRAGDWKCPNP,,TCENMNF SWRNFNCQCKAPKBDGSGGPGSSHM,,GGNYGDDRRGGRRGGYDRGGYRGRGGDRGGFRGGRRGGDRGGFGPGKMDSR,,GEHRQDRRERPY*		
	2374 .. 3148	775 bp	gene
/note	= gene <a href="#">ENSG00000260304</a> lncRNA		
	2374 .. 3148	775 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000564743</a> lncRNA		
<b>FUS-207</b>	3413 .. 4261	849 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000487974</a> Retained intron		
<b>FUS-213</b>	4943 .. 7108	2166 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000570090</a> Retained intron		
<b>FUS-203</b>	5362 .. 10,965	5604 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000474990</a> protein_coding_CDS_not_defined		

Feature		Location	Size			Type
<b>FUS-211</b>		8015 .. 9983	1969 bp			prim_transcript
/note	=	primary transcript <a href="#">ENST00000568901</a> Retained intron				
<b>FUS-208</b>		8330 .. 9558	1229 bp			prim_transcript
/note	=	primary transcript <a href="#">ENST00000564766</a> Retained intron				
<b>FUS-212</b>		10,079 .. 11,468	1390 bp			prim_transcript
/note	=	primary transcript <a href="#">ENST00000569760</a> Retained intron				
<b>FUS-204</b>		10,236 .. 11,421	1186 bp			prim_transcript
/note	=	primary transcript <a href="#">ENST00000483853</a> Retained intron				
✓	<b>Donor Template SNV -&gt; REV</b>	11,247 .. 11,346	100 bp			misc_feature
✓	<b>Protospacer Sequence</b>	11,265 .. 11,284	20 bp			misc_feature
✓	<b>SNV</b>	11,282 .. 11,282	1 bp			misc_feature
/note	=	REV = G SNV = A				
✓	<b>PAM</b>	11,285 .. 11,287	3 bp			misc_feature

Primer	Length	Binding Sites	Tm	Date Added
✓ <b>PCR Forward</b>	25-mer	10,776 .. 10,800	58°C	Jan 11, 2023
/sequence = GGGAACATAGGGGAATGGGAATATG 48% GC / 7884.2 Da				
✓ <b>Donor Template SNV -&gt; REV</b>	100-mer	11,247 .. 11,346	78°C	Jan 11, 2023
/sequence = GGTACAGGACAAAAAGCTGTTCCAGAACCTGGGGAGCCAGGCTAATTAATACGGCCTCTCCCTGCGATCCTGTCTGTGCTCACCCCTG 50% GC / 30769.0 Da				
✓ <b>gRNA Protospacer</b>	20-mer	11,265 .. 11,281	54°C	Jan 11, 2023
/sequence = TGAGCACAGACAGGATCACA 50% GC / 6144.1 Da				
✓ <b>Sanger Sequencing</b>	20-mer	11,377 .. 11,396	55°C	Jan 11, 2023
/sequence = CCTTGGGTGATCAGGAATTG 50% GC / 6188.1 Da				
✓ <b>PCR Reverse</b>	25-mer	11,433 .. 11,457	59°C	Jan 11, 2023
/sequence = TGGTCACTTTTAATGGGAACCCAGAG 44% GC / 7721.1 Da				