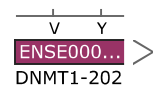
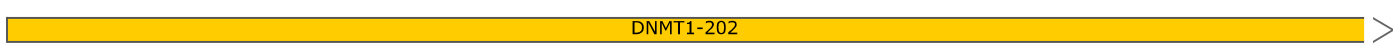
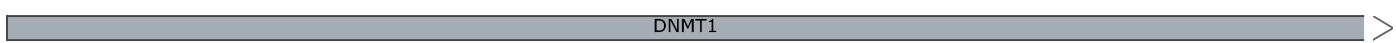


INK2J00048_DNMT1_Y511C_D05_AB
 5231 bp

5'
3'

85

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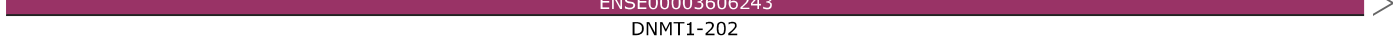


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170

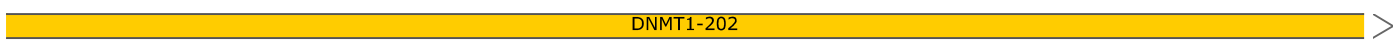


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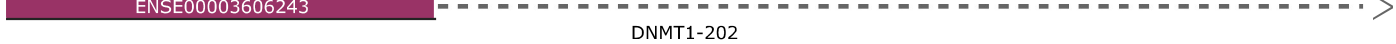


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255

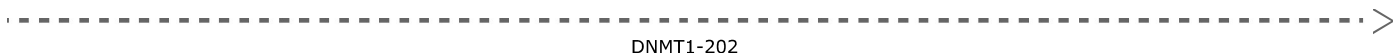
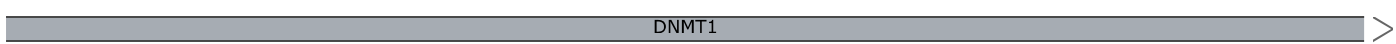


460 I Y D D D P S L E 465



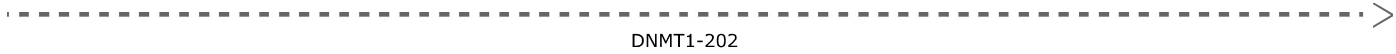
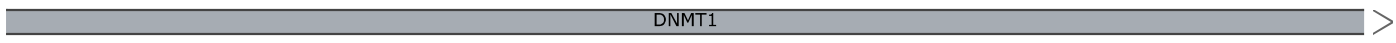
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340



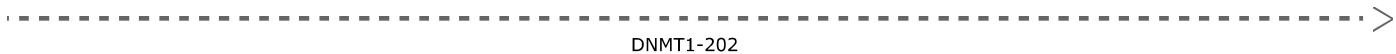
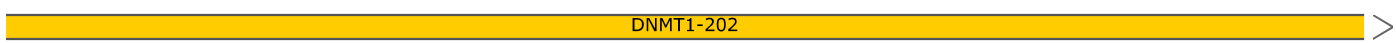
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425



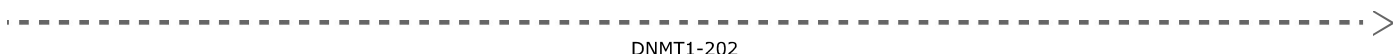
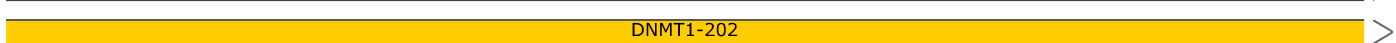
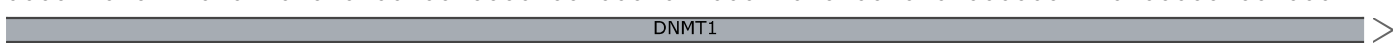
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510



GGCCAAGTCATTGTGATGACTGAGGAGCACCCGACCTGGCTGATGGGATGTCTGCTGAGTGGGCGCTTAGAGCGCCTCCTGGGTT
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595



TGGGATGTGAGTCAGAGCCTTTAGTCCATTTCTTTTTCTGCTCTAGGTGGTGTTAATGGCAAAAATCTTGGCCCCATAAATGAA
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680

DNMT1

DNMT1-202

G G V N G K N L G P I N E
ENSE00003538226

DNMT1-202

TGGTGGATCACTGGCTTTGATGGAGGTGAAAAGGCCCTCATCGGCTTCAGCACCTGTAAGTGTGTGGCCCATCATAGGCTGGCCG
ACCACCTAGTGACCGAAACTACCTCCACTTTTCCGGGAGTAGCCGAAGTCGTGGACATTCACACACCGGGTAGTATCCGACCGGC

765

DNMT1

DNMT1-202

480 W W I T G 485 F D G G E 490 A L I G 495 F S T
ENSE00003538226

DNMT1-202

GGGTCTGAAAGGGGCCTTCATGTTCTCCTTCTGGGGGCTGACGGGGCTCTGGTGGGAATTCTCAGCAGGCTTGCAGAAAGGCCAT
CCCAGACTTTCCCGAAAGTACAAGAGGAAGGACCCCGACTGCCCGAGACCACCTTAAGAGTCGTCCGAACGTCTTCCGGTA

850

DNMT1

DNMT1-202

DNMT1-202

PCR Forward

TTAGTTATGACTGGCTCTGGAAGT

GTGACTGGGAACCTTAGCAGGTTCAAGTTGGGGTAGCCTCTTGTGTTAGTTATGACTGGCTCTGGAAGTACTCTCCAGTTGTAAG
CACTGACCCTTGGAAATCGTCCAAGTCAACCCCATCGGAGAACACAATCAATACTGACCGAGACCTTGACTGAGAGGTCAACATTC

935

DNMT1

DNMT1-202

DNMT1-202

AGCAGGTCTTGGCCGGATATGGTGGCTCACACCTGTAATCCAGCACTTTGGGAGGCCGAGTTGGGGGGATCATTTGAGGCCAGG
TCGTCCAGAACC GGCCCTATACCACCGAGTGTGGACATTAGGGTCGTGAAACCTCCGGCTCAACCCCCCTAGTAAACTCCGGTCC

1020

DNMT1

DNMT1-202

DNMT1-202

AATTCGAGACCAGCCTAGCCTGGCCAACATGGTGAACCCCTCTCTACCAAAAATACAAAATAGCCACGCATGGTGGTGCAT
TTAAGCTCTGGTCCGATCGGACCGGTTGTACCCTTTGGGGGAGAGATGGTTTTTATGTTTTTAATCGGTGCGTACCACCACGTA

1105

DNMT1

DNMT1-202

DNMT1-202

ACCTGTAATCCCAGCTACTTGGGAGGCTATGGCAGGAGAATCACGTGAACCCAGCAGACAGAGTTGCAGTGAGCCGAGATCACG
TGGACATTAGGGTCGATGAACCCCTCCGATACCGTCTCTTAGTGCACTTGGGTCTGTCTGTCTCCAACGTCACTCGGCTCTAGTGC

1190

DNMT1

DNMT1-202

DNMT1-202

CCACTGCCCTCCAGCCTGGGTGACGGAGCAAGACTCTGTCTCCCCTGAAAAAAAAAAAAAGAGCAGGTCTTATTCTTGCAACCCA
GGTGACGGGAGGTCGGACCACTGCCTCGTTCTGAGACAGGAGGGGACTTTTTTTTTTTTCTCGTCCAGAATAAGAACGTTGGGT

1275

DNMT1

DNMT1-202

DNMT1-202

AACCCAGACTGAATTCCAAACACCAGAGATGAGCTCAATGAAAGCCTACTCAGCTAGTCTTCGCTCTCTGGCTGGCTCAGACAGG
TTGGGTCTGACTTAAGGTTTGTGGTCTCTACTCGAGTTACTTCCGGATGAGTCGATCAGAAGCGAGAGACCGACCGAGTCTGTCC

1360

DNMT1

DNMT1-202

DNMT1-202

Sanger Sequencing

ACATTTGGGTACGGGATGAC

CTTCTTCAGAACAAAGCCAGCTATGATGTGTTGTGCCCTATGTTTCTGACATTTGGGTACGGGATGACTTTTAGACTGTTGGGTGA
GAAGAAGTCTTGTTCGGTCGATACTACACAACACGGGATACAAAGACTGTAAACCCATGCCCTACTGAAAATCTGACAACCCACT

1445

DNMT1

DNMT1-202

DNMT1-202

Donor Template WT -> SNV

TTCCACACCTCCTCTGTTCAACCCCA

GTTTGGTAGACTCCTCCATGCCCTGTGGCCACTGTAGGCGCCATCAGATTCCAGCCCCTTTTCCACACCTCCTCTGTTCAACCCCA
CAAACCATCTGAGGAGGTACGGGACACCGGTGACATCCGCGGTAGTCTAAGGTCGGGGAAAAGGTGTGGAGGAGACAAGTGGGGT

1530

DNMT1

DNMT1-202

DNMT1-202

Donor Template WT -> SNV

Donor Template WT -> SNV

GCATTTGCCGAATACATTCTGATGGATCCCAGTCCCGAGT T GCGCCCATATTTGGGCTGATGCAGGAGAAGATC
GCATTTGCCGAATACATTCTGATGGATCCCAGTCCCGAGT A T GCGCCCATATTTGGGCTGATGCAGGAGAAGATCTACATCAGCA
CGTAAACGGCTTATGTAAGACTACCTAGGGTCAGGGCTCA T ACGCGGGTATAAACCCGACTACGTCTCTTCTAGATGTAGTCGT

1615

DNMT1

DNMT1-202

S F A E Y I L M D P S P E Y A P I F G L M Q E K I Y I S

ENSE00003601320

DNMT1-202

Donor Template WT -> SNV

PAM Protospacer Sequence

SNV

TCATACGCGGGTATAAACCC
gRNA Protospacer

AGATTGTGGTGGAGTTCCCTGCAGAGCAATTCCGACTCGACCTATGAGGACCTGATCAACAAGATCGAGGTAAGAGATCGAGGGTC
TCTAACACCACCTCAAGGACGTCTCGTTAAGGCTGAGCTGGATACTCCTGGACTAGTTGTTCTAGCTCCATTCTCTAGCTCCCAAG

1700

DNMT1

DNMT1-202

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

ENSE00003601320

DNMT1-202

CTCAGCATCCGGGATTCCCACTGGAAACTTGCCCTTCAGAACCAGCAGACACTGTTCTTCAGTTGGATTTAGGCCAGTTTGGCTTA
GAGTCGTAGGCCCTAAGGGTGACCTTTGAACGGAAGTCTTGGTCGTCTGTGACAAGAAGTCAACCTAAATCCGGTCAAACCGAAT

1785

DNMT1

DNMT1-202

DNMT1-202

AGCATGAGAGAAAACCTGTTCTCTTTCAAGACCACGGTTCCCTCCTTCTGGCCTCAACTTGAACCGCTTCACAGAGGACTCCCTCCT
TCGTA CTCTCTTTGGACAAGAGAAAAGTTCTGGTGCCAAGGAGGAAGACCGGAGTTGAACTTGGCGAAGTGCTCTCTGAGGGAGGA

1870

DNMT1

DNMT1-202

T T V P P S G L N L N R F T E D S L L

ENSE00003615043

DNMT1-202

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CGCTGTGCGCGTCAAACACCACCTCGTCCACCTCTCAATACTGCTCCGGCCCTGTCACTACTCGTCGGGTAGAAGGACTGTGGG

1955

DNMT1

DNMT1-202

R H A Q F V V E Q V E S Y D E A G S D S D E Q P I F L T P

ENSE00003615043

DNMT1-202

TGCATGCGGGACCTGATCAAGCTGGCTGGGGTCACGCTGGGACAGAGGTAAGGATGCGGCAGGGACCAGAGTGAAGACTGGAGAC
ACGTACGCCCTGGACTAGTTTCGACCCGACCCAGTGCACCTGTCTCCATTCTACGCCGTCCCTGGTCTCACTTCTGACCTCTG

2040

DNMT1

DNMT1-202

C M R D L I K L A G V T L G Q R

ENSE00003615043

DNMT1-202

CGGGGAGGGTAGAGCATGGCCACATCCTCTGTCCAGTCTCTGAGATGCTGGAACCTCTCCCGTAGGGCAGCCAGGGCAGGGC
GCCCTCCCATCTCGTACCGGGTGTAGGAGACAGGGTCAAGGACTCTACGACCTTGGAGAGGGCATCCGCTCGGGTCCGCTCCG

2125

DNMT1

DNMT1-202

R A Q A R

ENSE00003636455

DNMT1-202

GGCAGACCATCAGGCATTCTACCAGGGGAGAAGGACAGGGGACCCACGAAAGCCACCACCACCAAGCTGGTCTACCAGATCTTCGA
CCGTCTGGTAGTCCGTAAGATGGTCCCTCTTCTGTCCCTGGGTGCTTTCGGTGGTGGTGGTTCGACCAGATGGTCTAGAAGCT

2210

DNMT1

DNMT1-202

R Q T I R H S T R E K D R G P T K A T T T K L V Y Q I F D

ENSE00003636455

DNMT1-202

CT

PCR Reverse

TACTTTCTTCGCAGAGCAAATTGAAAAGGATGACAGAGAAGACAAGGAGAACGCCTTTAAGCGCCGGCGATGTGGCGTCTGTGAG
ATGAAAGAAGCGTCTCGTTTAACTTTTCTACTGTCTCTTCTGTTCCTCTTTCGGGAAATTCGCGGCCGCTACACCGCAGACACTC

2295

DNMT1

DNMT1-202

T F F A E Q I E K D D R E D K E N A F K R R R C G V C E

ENSE00003636455

DNMT1-202

ATGAAAGAAGCGTCTCGTTTAACT

PCR Reverse

GTAACCTCACCTGTGGGTGCTCCCGCTCCCTAAGGTGGCCAGCCTCTGGCCTGATCTGAGGACTGCTCCATCTTTCTCTCTGT
CATTGGAGTGGACACCCACGAGGGCGAGGGGATTCCACCGGGTCGGAGACCGGACTAGACTCCTGACGAGGTAGAAAAGAGAGACA

2380

DNMT1

DNMT1-202

DNMT1-202

GGCTTGAGACTCTGGCTGCTCAAATGTGACCCCTGAGACAGAAATTAGTTAGTGGTCTGGGAGGACCCTGCATACTTCATTGAAC
CCGAACCTCTGAGACCGACGAGTTTACACTGGGGACTCTGTCTTTAATCAATCACCAGACCCTCCTGGGACGTATGAAGTAACCTTG

2465

DNMT1

DNMT1-202

DNMT1-202

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CAGTTATCTGTCTACAGGTGTCTCCGTACGAACCCACGAAACGACTATTACGGTGACAGGAATTAACCTTCTCGGACCGAAGACC

2550

DNMT1

DNMT1-202

DNMT1-202

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CACCGAGACGACACGGACGTAGAGTGTCTCAGACTTCCGGGGACAACCTGACGATTTCCCCATAAGTGTAGATTACCCCGTGAAACA

2635

DNMT1

DNMT1-202

DNMT1-202

CCAGCTTAGATTTGAGGCCCTCAGGAGGCGTCCCTTTCTGTGAGTTTTTAAAAATATATGTTTACTTCACTCAGGAGGAACTAACT
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2720

DNMT1

DNMT1-202

DNMT1-202

TCCTAGTCCTATGACCCAAAGACCAGGACTATTTTTGATACCTATTACCTGACTTTTCTTTTGGATAAAGACTGGCTTCAGGGCTTT
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2805

DNMT1

DNMT1-202

DNMT1-202

GCTTTTGATCCCCGCTGGCATCTCTTAACAGGAGCCTGCATGTCTCACCATTGTTATTTTTGGTTTTATTTTTATTTTTCTTGGTT
CGAAAAC TAGGGGCGACCGTAGAGAATTGTCTCGGACGTACAGGAGTGGTAACAATAAAACCAAATAAAAATAAAAAGAACCAA

2890

DNMT1

DNMT1-202

DNMT1-202

AACACACGTGTGTCCAATGTTTTATAACTTCTAAAATCTTTTTTTTTTTTTTTTTAATTTTTTTGAGACAGTCTCTCTCTGTCACC
TTGTGTGCACACAGGTTACAAAATATTGAAGATTTTAGAAAAAAAAAAAAAAAAAATTAATAAACTCTGTCTCAGAGAGACAGTGG

2975

DNMT1

DNMT1-202

DNMT1-202

CAGGCTAGAGTGCAAGTGGCACCATCTCAGCTCACCGTAACCTCCGCCTCCCGGGTTCAATCAGTTCTCCACCTCAGCCTCCCGA
GTCCGATCTCACGTCACCGTGGTAGAGTCGAGTGGCATTGGAGGCGGAGGGCCCAAGTTAGTCAAGAGGGTGGAGTCTGGAGGGCT

3060

DNMT1

DNMT1-202

DNMT1-202

GTGGCTGGGATTATAGGCACCCGCCACCATACCCGGCTAATTTTTTTTTGTATTTTTAGTAGAGATGGGGTTTCACCATGTTGGCC
CACCGACCCTAATATCCGTGGGCGGTGGTATGGGCCGATTAATAAAACATAAAAATCATCTCTACCCCAAAGTGGTACAACCGG

3145

DNMT1

DNMT1-202

DNMT1-202

AGGCTGGTCTTAAACTCCTGACCTTAAGTGATCTACCTACCTCGGCCTCCCAAAGTGCTGGGATTACAGGTGTGAGCCACTGTGC
TCCGACCAGAATTTGAGGACTGGAATTCAGTAGATGGATGGAGCCGGAGGGTTTACGACCCTAATGTCCACACTCGGTGACACG

3230

DNMT1

DNMT1-202

DNMT1-202

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GGTCGGGATTTTAGTAAACAAAAATAAACACATTGACAATGCACAACATGACCATCTAGATCAATAAAGTAAAAATTTATAAGAC

3315

DNMT1

DNMT1-202

DNMT1-202

TAGTATTTTGTAAATGAATATCCTAACTTACTCCTCAATGATAGGCACCTCTTCAGTATTGTAAATATGTGGCAGCATCCTTGA
ATCATAAAAAAATTTACTTATAGGATTGAATGAGGAGTTACTATCCGTGGAGAAAGTCATAACATTTATACACCGTCGTAGGAACT

3400

DNMT1

DNMT1-202

DNMT1-202

GCAAAGCTTCTCGCGAGTGATCTGCTTAGAAGTAGCGTTGCTGGGTTGTGGGTGTGTATTCTTAACTTTGATCTAGAAGATTGC
CGTTTCGAAGAGCGCTCACATAGACGAATCTTCATCGCAACGACCCAACACCCACACATAAGAATTGAAACTAGATCTTCTAACG

3485

DNMT1

DNMT1-202

DNMT1-202

TCTCCAAAATGGTTCTACCAACTTACCATTTGAGCAGTGTGCGTTCTTCTTTTCTCACACCACCTATCTGGCTTCTTAACCCATC
AGAGGTTTTACCAAGATGGTTGAATGGTAAACTCGTCACACGCAAGAAGAAAGGAGTGTGGTGGATAGACCGAAGAATTGGGTAG

3570

DNMT1

DNMT1-202

DNMT1-202

TGGAGAATGGGAAGGGAATTTTATTTCTCTCACTTACCATATTTCTAATGAGGTTGAATATTGCTTTTTTTTTTTTTTTTTTTGTAG
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3655

DNMT1

DNMT1-202

DNMT1-202

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TCTGTCCAGGACGACACAACGGAACGGACCAGAGTTTGAGGACCGAAGTTCACCAGGAGGACAGAACCAGGAGGTTTGACGGCC

3740

DNMT1

DNMT1-202

DNMT1-202

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CTAATCTCCGTA CTCCGTGACGTGGGTCGGTTTATCCGTGTAAAAATTTT CAGAACCAAAAACAACAACAACAACAACAACAACA

3825

DNMT1

DNMT1-202

DNMT1-202

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CAACTCTACCCAGAGCAAGACAGTGGGTGACACCTTACGTCACCGTACTAACATCGAGTGACGTAAGAGTTGGATGACCCGAGTT

3910

DNMT1

DNMT1-202

DNMT1-202

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CACTAGAAGGGTGAATCGGAGGGTTCATCGACCCCTGGTGTCCACGTGCGGTGGTACGGGTCGATTAATTTTTTTTTTGTAAAAACA

3995

DNMT1

DNMT1-202

DNMT1-202

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TCTACCCTAAAACGGTACAACGGATCCGACCAGAACTTACGGACTTGAGTTCGTCAGGAGGGCGGAATCGTAGGACTCAACGGCC

4080

DNMT1

DNMT1-202

DNMT1-202

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CTGACGTCTTAAACAGTGTGCGGACCGATTAAAATTAACAAAAACATCTCAACCCCCAGAATTATACAACGGGTCCGACCAGAACT

4165

DNMT1

DNMT1-202

DNMT1-202

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TGAGAACCTGAGTTCAGTAGGTAGATGGAGACGAAGTCCGAGGGTTACATGACCAAGTCCATACTCGGTGGTACGGGTCCGATTT

4250

DNMT1

DNMT1-202

DNMT1-202

AGTCTTAATTCACCGTTTGTTCATTGTTGCTAAGGGCTGTGTGACTCACTTTTTTTTTTTTTTTTTTTTTTAAATTTTTTGAGACCTAAA
TCAGAATTAAGTGGCAAACAAAGTAACAACGATTCCCGACACACTGAGTGAAAAAAAAAAAAAAAAAATTAACAAAACTCTGGATTT

4335

DNMT1

DNMT1-202

DNMT1-202

AGTCTTAATGCATCATTGTTCTCATTGTTAGTAAGGGCTGTGTGATTTGCCCTTTTTTTTTTCTTTTTTTTTTTTTTTTTTTTTT
TCAGAATTACGTAGTAAACAGAGTAACAATCATTCCCGACACACTAAACGGGAAAAAAAAAAGGAAAAAAAAAAAAAAAAAAAA

4420

DNMT1

DNMT1-202

DNMT1-202

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AAAAAACTCTACCTCAAAATGAGAACAGCAGGTCCGACCTTATACCACCACACTAGAACCGATTGACATTAGAGGTGGAGGGTC

4505

DNMT1

DNMT1-202

DNMT1-202

G TTCAGGCAATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGATTACAGGCACACCCTACCATGCCTGGCTAATCTTTGTATTTTT
CAAGTCCGTTAAGAGGACGGAGTCCGAGGGTTCATCGACCCTAATGTCCGTGTGGGATGGTACGGACCGATTAGAAACATAAAAA

4590

DNMT1

DNMT1-202

DNMT1-202

AGTAGAGATGGGGTTTCACCACGTTGGCCAGGCTGGTCTGCAATTCTGACCTTAAGTGATCTGCCTGCCTCGGCCTTCTGAAAT
TCATCTCTACCCCAAAGTGGTGAACCGGTCCGACCAGACGTTAAGGACTGGAATTCACTAGACGGACGGAGCCGGAAGACTTTA

4675

DNMT1

DNMT1-202

DNMT1-202

ACTGGGATTACAGGCATGAACCACTGTGCCAGCCCTGATTTGCCTTTTTAATGCCATTTTTTAGGTGTGTCAGCAGCCTGAGTG
TGACCCTAATGTCCGTACTTGGTGACACGGGTCGGGACTAAACGGAAAAATTACGGTAAAAAATCCACACAGTCGTCGGACTCAC

4760

DNMT1

DNMT1-202

DNMT1-202

675 680
V C Q Q P E C
ENSE00003497876

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ACCCTTTACATTTCCGGACGTTCTGTACCAATTTAAACCACCGTCACCTGCCTCGTTCGTCGGAACGGTTCTCGCCTCCATCCAG

4845

DNMT1

DNMT1-202

DNMT1-202

G K C K 685 A C K D M V 690 K F G G 695 S G R S K Q 700 A C Q E 705 R R
ENSE00003497876

AGGCCGAGTCTTCTCCTGTGGCAGAGGACTTGCCAGCTGGTGGCAGATGCACTGTGGAGAAGGGCCTGCATGTGTGGGACAGCA
TCCGGCTCAGAAGGAGGACACCGTCTCCTGAACGGTCCGACCACCGTCTACGTGACACCTCTTCCCGGACGTACACACCCTGTCTGT

4930

DNMT1

DNMT1-202

DNMT1-202

CCAGGATTCTTCGTTAGGCATTGTCTCAGGACCTGTCCCTGTTATGAAGAAAACAGCCCCGGTTGGTCTTACTTAGAAAAGGGG
GGTCCCTAAGGAAGCAATCCGTAACAGAGTCTCGGACAGGGACAATACTTCTTTTGTGGGGCCAACCAGAATGAATCTTTTCCCC

5015

DNMT1

DNMT1-202

DNMT1-202

CCTTAGGTATAACCAGTGACATTGCAGGTGTCCCAATATGGCCATGAAGGAGGCAGATGACGATGAGGAAGTCGATGATAACATC
GGAATCCATATTGGTCACTGTAACGTCCACAGGGTTATACCGGTA CTTCTCCGTCTACTGCTACTCCTTCAGCTACTATTGTAG

5100

DNMT1

DNMT1-202

710 715 720 725
C P N M A M K E A D D D E E V D D N I

ENSE00003480315

DNMT1-202

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GGTCTCTACGGCAGTGGGTTTTTTTTACGTGGTCCCTTCTTCTTTGTCTTGTCTTAGCGTAGAGAACCCAGCCTCTTCGGC

5185

DNMT1

DNMT1-202

730 735 740 745 750
P E M P S P K K M H Q G K K K Q N K N R I S W V G E A

ENSE00003480315

DNMT1-202

TCAAGGTAACCCCTTGGAGCCCCTTGGTCAGCTCACTGCCATGTTCC
AGTTCCATTGGGAACCTCGGGGAACCAAGTCGAGTGACGGTACAAGG

3'

5231

5'

DNMT1





















DNMT1-202















755
V K V T L G A P W S A H C H V

EN... (in frame with DNMT1-202)

DNMT1-202

Feature		Location	Size			Type
✓ DNMT1		1 .. 5231	5231 bp			gene
/note	= gene ENSG00000130816 Protein coding					
DNMT1-201		1 .. 5231	5231 bp			prim_transcript
/note	= primary transcript ENST00000340748					
✓ DNMT1-202		1 .. 5231	5231 bp			prim_transcript
/note	= primary transcript ENST00000359526					
DNMT1-227		1 .. 5231	5231 bp			prim_transcript
/note	= primary transcript ENST00000592705 Nonsense mediated decay					
DNMT1-229		1 .. 5231	5231 bp			prim_transcript
/note	= primary transcript ENST00000676604 protein_coding_CDS_not_defined					
DNMT1-230		1 .. 5231	5231 bp			prim_transcript
/note	= primary transcript ENST00000676610					
DNMT1-231		1 .. 5231	5231 bp			prim_transcript
/note	= primary transcript ENST00000676820 Retained intron					
DNMT1-232		1 .. 5231	5231 bp			prim_transcript
/note	= primary transcript ENST00000676868 Retained intron					
DNMT1-233		1 .. 5231	5231 bp			prim_transcript
/note	= primary transcript ENST00000677013 Nonsense mediated decay					
DNMT1-236		1 .. 5231	5231 bp			prim_transcript
/note	= primary transcript ENST00000677250 Nonsense mediated decay					
DNMT1-237		1 .. 5231	5231 bp			prim_transcript
/note	= primary transcript ENST00000677616 Nonsense mediated decay					
DNMT1-238		1 .. 5231	5231 bp			prim_transcript
/note	= primary transcript ENST00000677634 Nonsense mediated decay					
DNMT1-239		1 .. 5231	5231 bp			prim_transcript
/note	= primary transcript ENST00000677685 Nonsense mediated decay					
DNMT1-240		1 .. 5231	5231 bp			prim_transcript
/note	= primary transcript ENST00000677783 Retained intron					
DNMT1-241		1 .. 5231	5231 bp			prim_transcript
/note	= primary transcript ENST00000677946					
DNMT1-242		1 .. 5231	5231 bp			prim_transcript
/note	= primary transcript ENST00000678024 Retained intron					
DNMT1-246		1 .. 5231	5231 bp			prim_transcript
/note	= primary transcript ENST00000678694 Retained intron					
DNMT1-247		1 .. 5231	5231 bp			prim_transcript
/note	= primary transcript ENST00000678804					
DNMT1-251		1 .. 5231	5231 bp			prim_transcript
/note	= primary transcript ENST00000679103					
DNMT1-252		1 .. 5231	5231 bp			prim_transcript
/note	= primary transcript ENST00000679313					
DNMT1-203		1 .. 1924	1924 bp			prim_transcript
/note	= primary transcript ENST00000585843 Retained intron					

Feature	Location	Size			Type
DNMT1-201	79 .. 5190	5112 bp			CDS
▶ 7 segments = 985 bp					
/codon_start	= 1				
/note	= coding sequence ENSP00000345739				
/translation	= VYCKHGHLCPIDTGLIEKNIELFFSGSAKPIYDDDP SLE,,GGVNGKNLGPINEWWITGFDGG EKALIGFST,,SFAEYILMDPSPEYAPIFGLMQE KIYISKIVVEFLQSNDSSTYEDLINKIE,,TTVPPSGLNLRFTEDSLLRHAQFVVEQVESYDEAGDSDEQPIFLTPCMRDLIKLAGVTLGQR,,R AQARRQTIRHSTREKDRGPTKATTTKL VYQIFDTFFAEQIEKDDREDKENAFKRRRCGVCE,,VCQQPEC GKCKACKDMVKFGGSGRSKQAC QERR,,CPNMAMKEADDDEEVDDNIPEMPSPKMMHQGKKKKQKNKRISWVGEAVK 328 amino acids = 37.1 kDa				
DNMT1-202	79 .. 5190	5112 bp			CDS
▶ 7 segments = 985 bp					
/codon_start	= 1				
/note	= coding sequence ENSP00000352516				
/translation	= VYCKHGHLCPIDTGLIEKNIELFFSGSAKPIYDDDP SLE,,GGVNGKNLGPINEWWITGFDGG EKALIGFST,,SFAEYILMDPSPEYAPIFGLMQE KIYISKIVVEFLQSNDSSTYEDLINKIE,,TTVPPSGLNLRFTEDSLLRHAQFVVEQVESYDEAGDSDEQPIFLTPCMRDLIKLAGVTLGQR,,R AQARRQTIRHSTREKDRGPTKATTTKL VYQIFDTFFAEQIEKDDREDKENAFKRRRCGVCE,,VCQQPEC GKCKACKDMVKFGGSGRSKQAC QERR,,CPNMAMKEADDDEEVDDNIPEMPSPKMMHQGKKKKQKNKRISWVGEAVK 328 amino acids = 37.1 kDa				
DNMT1-230	79 .. 5190	5112 bp			CDS
▶ 7 segments = 985 bp					
/codon_start	= 1				
/note	= coding sequence ENSP00000504236				
/translation	= VYCKHGHLCPIDTGLIEKNIELFFSGSAKPIYDDDP SLE,,GGVNGKNLGPINEWWITGFDGG EKALIGFST,,SFAEYILMDPSPEYAPIFGLMQE KIYISKIVVEFLQSNDSSTYEDLINKIE,,TTVPPSGLNLRFTEDSLLRHAQFVVEQVESYDEAGDSDEQPIFLTPCMRDLIKLAGVTLGQR,,R AQARRQTIRHSTREKDRGPTKATTTKL VYQIFDTFFAEQIEKDDREDKENAFKRRRCGVCE,,VCQQPEC GKCKACKDMVKFGGSGRSKQAC QERR,,CPNMAMKEADDDEEVDDNIPEMPSPKMMHQGKKKKQKNKRISWVGEAVK 328 amino acids = 37.1 kDa				
DNMT1-241	79 .. 5190	5112 bp			CDS
▶ 7 segments = 985 bp					
/codon_start	= 1				
/note	= coding sequence ENSP00000504202				
/translation	= VYCKHGHLCPIDTGLIEKNIELFFSGSAKPIYDDDP SLE,,GGVNGKNLGPINEWWITGFDGG EKALIGFST,,SFAEYILMDPSPEYAPIFGLMQE KIYISKIVVEFLQSNDSSTYEDLINKIE,,TTVPPSGLNLRFTEDSLLRHAQFVVEQVESYDEAGDSDEQPIFLTPCMRDLIKLAGVTLGQR,,R AQARRQTIRHSTREKDRGPTKATTTKL VYQIFDTFFAEQIEKDDREDKENAFKRRRCGVCE,,VCQQPEC GKCKACKDMVKFGGSGRSKQAC QERR,,CPNMAMKEADDDEEVDDNIPEMPSPKMMHQGKKKKQKNKRISWVGEAVK 328 amino acids = 37.1 kDa				
DNMT1-247	79 .. 5190	5112 bp			CDS
▶ 7 segments = 985 bp					
/codon_start	= 1				
/note	= coding sequence ENSP00000503853				
/translation	= VYCKHGHLCPIDTGLIEKNIELFFSGSAKPIYDDDP SLE,,GGVNGKNLGPINEWWITGFDGG EKALIGFST,,SFAEYILMDPSPEYAPIFGLMQE KIYISKIVVEFLQSNDSSTYEDLINKIE,,TTVPPSGLNLRFTEDSLLRHAQFVVEQVESYDEAGDSDEQPIFLTPCMRDLIKLAGVTLGQR,,R AQARRQTIRHSTREKDRGPTKATTTKL VYQIFDTFFAEQIEKDDREDKENAFKRRRCGVCE,,VCQQPEC GKCKACKDMVKFGGSGRSKQAC QERR,,CPNMAMKEADDDEEVDDNIPEMPSPKMMHQGKKKKQKNKRISWVGEAVK 328 amino acids = 37.1 kDa				
DNMT1-251	79 .. 5190	5112 bp			CDS
▶ 7 segments = 985 bp					
/codon_start	= 1				
/note	= coding sequence ENSP00000503151				
/translation	= VYCKHGHLCPIDTGLIEKNIELFFSGSAKPIYDDDP SLE,,GGVNGKNLGPINEWWITGFDGG EKALIGFST,,SFAEYILMDPSPEYAPIFGLMQE KIYISKIVVEFLQSNDSSTYEDLINKIE,,TTVPPSGLNLRFTEDSLLRHAQFVVEQVESYDEAGDSDEQPIFLTPCMRDLIKLAGVTLGQR,,R AQARRQTIRHSTREKDRGPTKATTTKL VYQIFDTFFAEQIEKDDREDKENAFKRRRCGVCE,,VCQQPEC GKCKACKDMVKFGGSGRSKQAC QERR,,CPNMAMKEADDDEEVDDNIPEMPSPKMMHQGKKKKQKNKRISWVGEAVK 328 amino acids = 37.1 kDa				
DNMT1-252	79 .. 5190	5112 bp			CDS
▶ 7 segments = 985 bp					
/codon_start	= 1				
/note	= coding sequence ENSP00000504512				
/translation	= VYCKHGHLCPIDTGLIEKNIELFFSGSAKPIYDDDP SLE,,GGVNGKNLGPINEWWITGFDGG EKALIGFST,,SFAEYILMDPSPEYAPIFGLMQE KIYISKIVVEFLQSNDSSTYEDLINKIE,,TTVPPSGLNLRFTEDSLLRHAQFVVEQVESYDEAGDSDEQPIFLTPCMRDLIKLAGVTLGQR,,R AQARRQTIRHSTREKDRGPTKATTTKL VYQIFDTFFAEQIEKDDREDKENAFKRRRCGVCE,,VCQQPEC GKCKACKDMVKFGGSGRSKQAC QERR,,CPNMAMKEADDDEEVDDNIPEMPSPKMMHQGKKKKQKNKRISWVGEAVK 328 amino acids = 37.1 kDa				
Donor Template WT -> SNV	1506 .. 1605	100 bp			misc_feature
PAM	1565 .. 1567	3 bp			misc_feature

Feature	Location	Size			Type
✓ Protospacer Sequence	1568 .. 1587	20 bp			misc_feature
✓ SNV	1571 .. 1571	1 bp			misc_feature
/note	= WT = A SNV = G				
DNMT1-208	1611 .. 5231	3621 bp			prim_transcript
/note	= primary transcript ENST00000586799 Nonsense mediated decay				
DNMT1-250	4583 .. 5231	649 bp			prim_transcript
/note	= primary transcript ENST00000679100 Retained intron				
DNMT1-245	4841 .. 5231	391 bp			prim_transcript
/note	= primary transcript ENST00000678647 Retained intron				
DNMT1-207	4891 .. 5231	341 bp			prim_transcript
/note	= primary transcript ENST00000586667 Retained intron				

Primer	Length	Binding Sites	Tm	Date Added
✓ PCR Forward	25-mer	895 .. 919	58°C	Nov 10, 2022
/sequence = TTAGTTATGACTGGCTCTGGAAGTCTG 44% GC / 7703.1 Da				
✓ Sanger Sequencing	20-mer	1408 .. 1427	57°C	Nov 10, 2022
/sequence = ACATTTGGGTACGGGATGAC 50% GC / 6197.1 Da				
✓ Donor Template WT -> SNV	100-mer	1506 .. 1605	78°C	Nov 10, 2022
/sequence = TTCCACACCTCCTCTGTTCAACCCAGCATTGCGGAATACATTCTGATGGATCCCAGTCCCGAGTGTGCGCCCATATTTGGGCTGATG 51% GC / 13047.1 Da				
✓ gRNA Protospacer	20-mer	1568 .. 1587	57°C	Nov 9, 2022
/sequence = CCCAAATATGGGCGCATACT 50% GC / 6086.0 Da				
✓ PCR Reverse	25-mer	2209 .. 2233	57°C	Nov 10, 2022
/sequence = CAATTTGCTCTGCGAAGAAAGTATC 40% GC / 7665.1 Da				