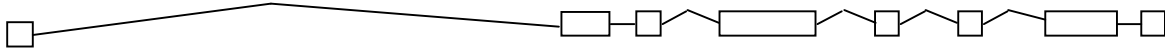
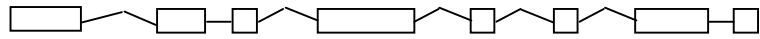


MTM-6A



MTM-6B



SL1 : GGTTTTAACCCAGTTAACCAAG

□□

aattttcatcgggttcggggggtttcaaaaATGCGATTTCGAGGACATTGGCATTTCGAAGgt-4250nt-ttc 4285
M...R...F...E...D...I...G...I...S...K...

SLn : GTTTAATTACCCAAGTTTGAG

□

ccacctaaatgccccaaaaatgctcgtaaacaccttcatcggtagcagacaccactgtcggcatggtggaataat 4359
M...S...S...T...P...S...S...V...T...T...P...L...S...A...W...W...N...N...

atgctcgctgtcgggtatctacccatcaatctccacctcaactccatcttctcctcatcctcgtggagctcgcat 4431
M...S...L...S...G...I...Y...P...S...I...S...T...S...T...P...S...S...S...S...W...S...S...H...

ttcgtatttggcggacatcatcatcatacgaacaacaacacggcgaacactccgcaatctacagtacccccg 4503
F...V...F...G...G...H...H...H...H...T...N...N...N...N...T...A...N...T...P...Q...S...T...V...P...P...

tcggcgtgctcgtcgggttatactgaagatattacgggtggcggatcactggtgaaggataaaattaatgga 4575
S...A...L...S...S...G...Y...T...E...D...I...T...V...A...G...S...L...L...K...D...K...I...N...G...

ttagttgattctctgatgggaagagagtcggttcattccgggtgtggttacgggggaagatggacgaattggc 4647
L...V...D...S...L...M...G...R...E...S...V...H...S...G...C...G...Y...G...E...D...G...R...I...A...

atgatggt-305nt-cagGTGGATAAAGTATGCCTTGTGCGATCGCTAGGGTGT CAGGAGAATCTAGTCGGC 5017
M...M ...V...D...K...V...C...L...V...D...R...L...G...C...Q...E...N...L...V...G 28(A)/134(B)

ACAGTCCATGTCAACTACACACATCATCTTCCGAGCTGAAAATGGATCAAAGAGTTATGGCTGGCGACT 5089
T...V...H...V...T...T...T...H...I...I...I...F...R...A...E...N...G...S...K...E...L...W...L...A...T... 52(A)/158(B)

GGGCTCATTCTTCAGTGGAAAAAGGACGCTAACAGCTGCCGGATGTATGCTAGTGTAGATGTAAACAT 5161
G...L...I...S...S...V...E...K...G...T...L...T...A...A...A...G...C...M...L...V...I...R...C...K...H... 76(A)/182(B)

TTTCAGgt-52nt-cagGTGATAACACTTCTGATCAGTAGAGATAAATCGTGTCAAGACCTATACGAGAGC 5278
F...Q ...I...T...L...L...I...S...R...D...K...S...C...Q...D...L...Y...E...T... 96(A)/202(B)

CTTCAACGTGCCGCAAAACCTGgt-206nt-cagTTTCAGTGAACGTGACGGAACGTGCTTGCCTTTGAGAAT 5549
L...Q...R...A...A...K...P...V ...S...V...N...V...T...E...L...L...A...F...E...N... 116(A)/222(B)

CGAGAACCCGTAGAAGACGTTTCGGGGATGGAGAAGATTGGATTGGAATTCAGAAATGACACGGCAAGGGATC 5621
R...E...P...V...E...D...V...R...G...W...R...R...L...D...W...N...S...E...M...T...R...Q...G...I... 140(A)/246(B)

ACAAAGTCACAATGGACAGAATCGAATATCAATGAAGGATACACGATCTGCGACACTTACCCCAATAAGCTG 5693
T...K...S...Q...W...T...E...S...N...I...N...E...G...Y...T...I...C...D...T...Y...P...N...K...L... 164(A)/270(B)

TGGTTTCCGACAGCGCCTCCACATCAGTTCTACTAGGATCCTGCAAATTCGAAGCCGTGGCCGCTTCCA 5765
W...F...P...T...A...A...S...T...S...V...L...L...G...S...C...K...F...R...S...R...G...R...L...P... 188(A)/294(B)

GTACTGACCTACTTCCATCAACAACTGAAGCCGCTTTGTGTAGATGTGCACAGCCTCTGACGGGATTCTCG 5837
V...L...T...Y...F...H...Q...Q...T...E...A...A...L...C...R...C...A...Q...P...L...T...G...F...S... 211(A)/318(B)

GCACGATGCGTAGAGGATGAGAAGCTTATGGAGTTGGTAGGAAAAGCGAATACAAACTCGGACAACCTGTTC 5909
A...R...C...V...E...D...E...K...L...M...E...L...V...G...K...A...N...T...N...S...D...N...L...F... 236(A)/342(B)

CTGGTAGATACTCGGCCGCGAGTCAACGCGATGGTGAATAAGTTTTCAGGAAAAGGATTGCAAGATGAGAGG 5981
L...V...D...T...R...P...R...V...N...A...M...V...N...K...V...Q...G...K...G...F...E...D...E...R... 260(A)/366(B)

AACTATTCAAATATGCGATTTCCTTTTTCGACATCGAGAATATTCATGTGATGCGGGCATCTCAGGCACGT 6053
N...Y...S...N...M...R...F...H...F...F...D...I...E...N...I...H...V...M...R...A...S...Q...A...R... 284(A)/390(B)

CTCCTCGACGCGGTGACCAAGTGTGTCGTGACGTCACAGAATACTGGAAAACGCTTGAGGCTTCTGGATGGTTG 6125
L...L...D...A...V...T...K...C...R...D...V...T...E...Y...W...K...T...L...E...A...S...G...W...L... 308(A)/414(B)

AAGCACGTGCGGAGTGTGTGCGAATGCTCACTTTTTTTGGCTGAATCCATCAGTCGAGGTACATCATGTGTC 6197
K H V R S V V E C S L F L A E S I S R G T S C V 332 (A) / 438 (B)
~~~~~  
A in ar515 (D N)  
GTTCAATTGTTTCGGATGGATGGGATCGGACTTCGCAAGTTGTGCGACTTTGTCAACTTCTTCTTGACCCATAC 6269  
V H C S D G W D R T S Q V V A L L C Q L L L L D P Y 356 (A) / 462 (B)  
~~~~~  
TACCGTACTATTACAGGATTTCAAGTTCTCATCGAGAAGGATTGGCTCGGTTTTGGACATAAATTCGATGAT 6341
Y R T I H G F Q V L I E K D W L G F G H K F D D 380 (A) / 486 (B)
~~~~~  
CGGTGTGGACATGTGGGGCGTTGAATGATGAAGCCGAAAAGAAGTTTCACCGATTTTCACTCAATGGTTG 6413  
R C G H V G A L N D E A G K E V S P I F T Q W L 404 (A) / 510 (B)  
~~~~~  
GATTGTATTTGGCAAATTATGCAACAAAACCACGAGCCTCCAGgt-525nt-cagTTC AACGAACGATAT 7003
D C I W Q I M Q Q K P R A F Q F N E R Y 424 (A) / 530 (B)
~~~~~  
CTGATTGAGATGCACGAGCAGCTCTATTCATGTCAATTTGGAAACATTTATTGGAAATTTGTGATAAAGATAGA 7075  
L I E M H E H V Y S C Q F G T F I G N C D K D R 448 (A) / 554 (B)  
~~~~~  
AGGgt-253nt-cagGATCTAAATCTGTCAAACGCACGAAATCTCTGTGGACTTGGATGGATGCGCGTCAT 7393
R D L N L S K R T K S L W T W M D A R H 468 (A) / 574 (B)
~~~~~  
GACGACTATATGAATCCATTTTATTCGgtaatttttaaatcttctgaaaattaaattctgaaaatgcgtatt 7465  
D D Y M N P F Y S 477 (A) / 583 (B)  
~~~~~  
gcacaacatgtttgacgcgcaaaatatctcaaacacagtaattctttaaataactgactactgtagtg-175nt- 7705
A in ar513 (W STOP)
cagCCTACCGCACAGTGTCTACTGGATCTTGACACTCGTGCAGCTCGTTCACAGTTTGGACTGCAATG 7777
P T A H V A L L D L D T R A A R F T V W T A M 500 (A) / 606 (B)
~~~~~  
TATAATCGATTGACAATGGTCTACAACCAAGAGAACGGCTTGAAGACCTAACTATGGCTGCGATGGAGCAC 7849  
Y N R F D N G L Q P R E R L E D L T M A A M E H 524 (A) / 630 (B)  
~~~~~  
GTTGGAGTACTAGAATCCCACGTGGCACAGTTGAGAACGAGACTAGCCGAACTGAAGACACAACAAAATCAA 7921
V G V L E S H V A Q L R T R L A E L K T Q Q N Q 548 (A) / 654 (B)
~~~~~  
CAGATAACTTCAACGAATACACCGCAATATGGTTGATAGTGAATGAGCAGTGAACCTGATGATTTGAAG 7993  
Q I T S T N T P T N M V D S G M S S A T D D D L K 572 (A) / 678 (B)  
~~~~~  
AATCTCAGTTTAAGCCATCCTTTGGATCCATTGAGCTCTACACTACCGATTCTGGAAAGAGCAACAAGTCAA 8065
N L S L S H P L D P L S S T L P I L E R A T S Q 596 (A) / 702 (B)
~~~~~  
GAAAGTGGAGTCAATGATTATCATCGTTTATACTATCCTGATGAGGCTCTGACCAAATATTCATAAAAATGGCAA 8137  
E S G V M D S S L Y Y P D E A L T K Y S L K W Q 620 (A) / 726 (B)  
~~~~~  
CCTCTTCGTGGAGCCGATAGATGCTCAAATCCAGCGTGCCGAGGGGAGTTCTCATCGACGATTGAGAGAAGA 8209
P L R G A D R C S N P A C R G E F S S T I E R R 644 (A) / 750 (B)
~~~~~  
ATTCATTGTCAATTTGTGTGGAATGgt-43nt-cagATTTTCTGCCGCCGTGCCTCAAAGTGTCTGCAGAC 8317  
I H C H L C G M I F C R R C L K V S A D 664 (A) / 770 (B)  
~~~~~  
GAACGTGAACGAGTATGTGACAAGTGCAAAACGATTGATTGATTTATTGATTTTCTTTTCATTCTTTCAATTTT 8389
E R E R V C D K C K T D * 676 (A) / 782 (B)
~~~~~  
TAATTTATTTCCCTACTTACCAATTTTTCTCTTTTTAATTTTACCTTGTATCAAATTTTATATATTTCCC 8461  
~~~~~  
CATGCCACCGAAATGCTTGTGATCACTTTTTGTATATTTTGCACGGTTTTAACACTTTTGAGCCACTTGA 8533
~~~~~  
GATTATATGCATAATTTATTTTCAGAAAAATAAACTCTTTGAAATTATATG 8584

..... -GRAM  
===== -RID  
~~~~~ -Phosphatase  
~~~~~ -SID  
===== -FYVE

overlined[]-Sequences deleted in ok330

## Figure 1 Supplementary