



Supplemental Material to:

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Brahma regulates a specific trans-splicing event at the
mod(mdg4) locus of *Drosophila melanogaster*

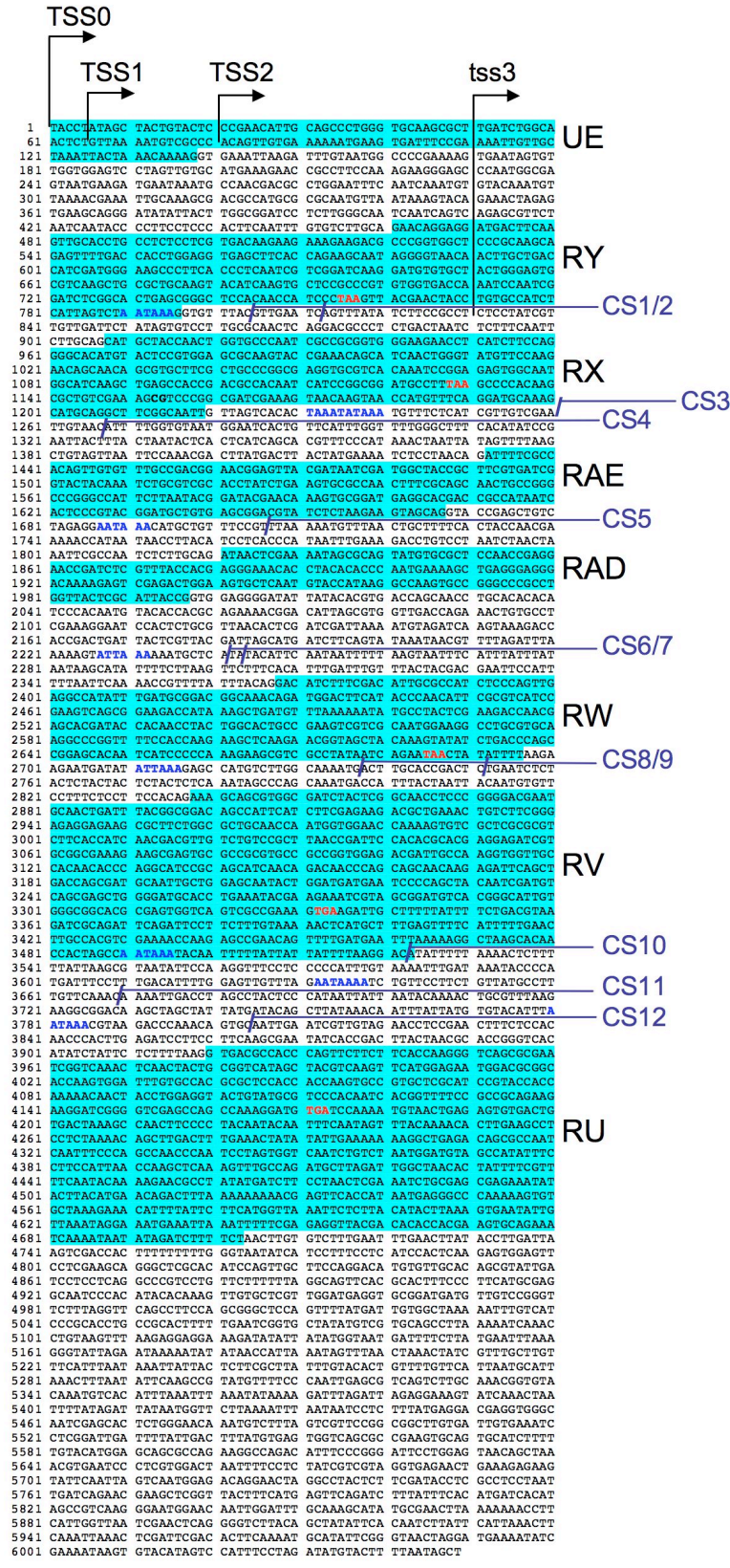
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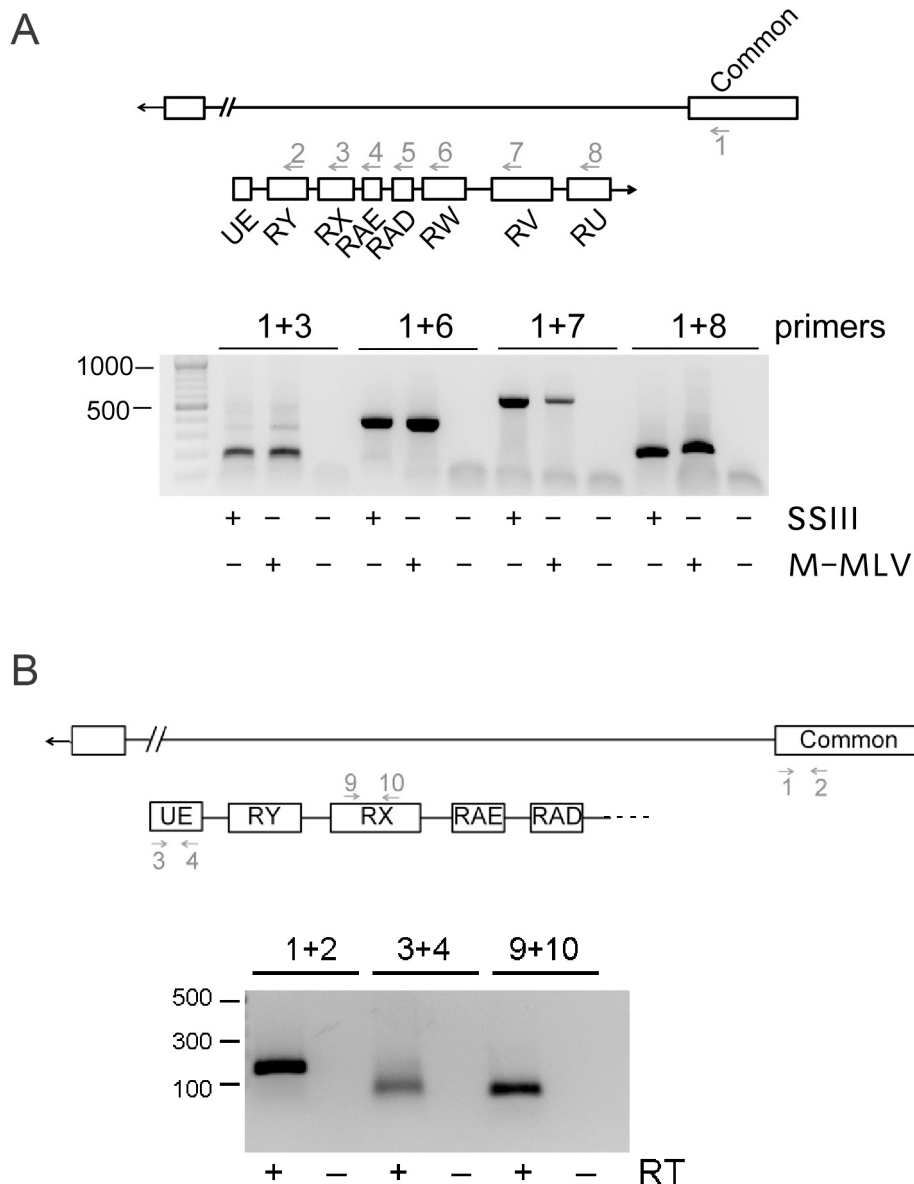
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Supplementary Materials

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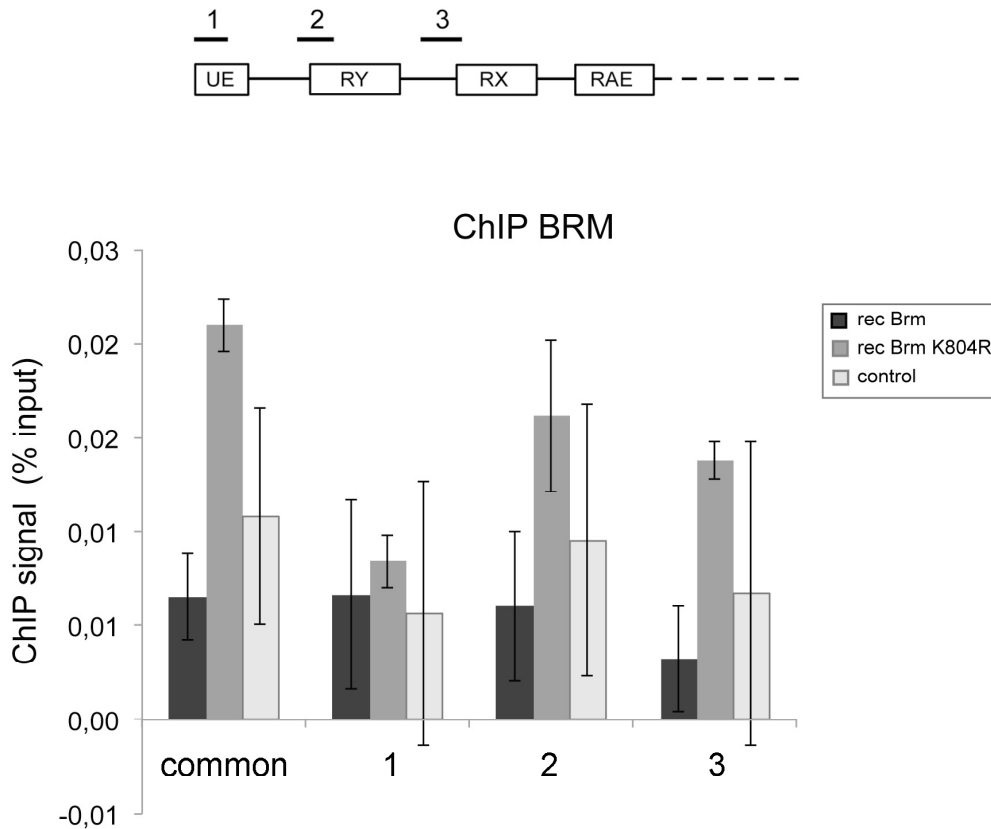
Supplementary Figure S1: The sequence features of the anti-sense 1 transcript
 The figure shows the sequence of the anti-sense region 1 based on the DGM2-chr 3R gene prediction and on our own data. The trans-spliced exons are shown as blue boxes. The TSS and CS sites are indicated in the figure. Polyadenylation signals are highlighted in blue, and stop codons in frame are highlighted in red.



Supplementary Figure S2. RT control reactions

A. *In vivo* analysis of the *mod(mdg4)* trans-splicing. The figure shows RT-PCR reactions in which the same trans-spliced products were amplified from *D. melanogaster* fly cDNA using two different reverse transcriptases, SuperScript III (SSIII) and Moloney Murine Leukemia Virus reverse transcriptase (M-MLV). The experiment also included control reactions without reverse transcriptase, as indicated. The primer-pairs used in each reaction and their positions are indicated in the figure.

B. RT(−) control reactions using total RNA purified from S2 cells. The purified RNA was treated with DNase (Turbo DNA-free kit) and reverse transcribed with Superscript III (Invitrogen) using random primers. Control reactions without reverse transcriptase (RT−) were carried out in parallel. The resulting cDNAs were used as templates in PCR reactions with the primer-pairs indicated in the figure.



Supplementary Figure S3. The association of BRM with the *mod(mdg4)* gene

The association of BRM with the *mod(mdg4)* gene was analyzed by ChIP. Chromatin was extracted from either S2 control cells or from S2 cells that over-expressed either recombinant recBRM or recBRM-K804R proteins, as in Figure 7. The cells were fixed with formaldehyde and immunoprecipitation reactions were carried out with an antibody against the human BRG1 protein that cross-reacts with the BRM of *D. melanogaster*. A negative control immunoprecipitation was carried out in parallel without primary antibody. The immunoprecipitated DNA was analyzed by qPCR using a standard curve for each primer pair. Primer pairs we designed to quantify the sense promoter region (*common*) and three genomic regions within the anti-sense region 1. The values obtained in no-antibody controls were subtracted, and the resulting signals were expressed relative to input. The histograms show average folds and the error bars represent standard deviations calculated from three independent experiments (n=3).

Supplementary Table S1.**The primer-pair combinations that were used in the different RACE reactions.**

RACE	1st PCR primers	2nd PCR primers	
TSS1	5RACE outer+RY1R	5RACE inner+RY1R	Clone nested PCR product
TSS2	5RACE outer+RY1R	5RACE inner+RY1R	Clone nested PCR product
TSS3	5RACE outer+RXR	5RACE inner+RXR	Clone nested PCR product
CS1	COMMON F+3RACE outer	RY F+3RACE inner	Purify gel band from nested PCR
CS2	COMMON F+3RACE outer	RY exon junc F+3RACE inner	Clone nested PCR product
CS3	COMMON F+3RACE outer	RX exon junc F+3RACE inner	Clone nested PCR product
CS4	COMMON F+3RACE outer	RX exon junc F+3RACE inner	Clone nested PCR product
CS5	COMMON F+3RACE outer	RAE F+3RACE inner	Clone nested PCR product
CS6	COMMON F+3RACE outer	RAE F+3RACE inner	Clone nested PCR product
CS7	COMMON F+3RACE outer	RAD or RAE F+3RACE inner	Purify gel band from nested PCR
CS8	COMMON F+3RACE outer	RW F+3RACE inner	Purify gel band from nested PCR
CS9	COMMON F+3RACE outer		Clone PCR product
CS10	COMMON F+3RACE outer	RV F+3RACE inner	Purify gel band from nested PCR
CS11	COMMON F+3RACE outer	RV F+3RACE inner	Purify gel band from nested PCR
CS12	COMMON F+3RACE outer	RV F+3RACE inner	Purify gel band from nested PCR

Supplementary Table S2.

The nucleotide sequences of the bands in Figure 4.

>Figure4B_a

CAGGCGCACATGTACTCCGTGGAACGCAAGTACCGAAACAGCATCAACTGGGTATGTTCC
AAGAACAGCAACAGTGTGTTACGCTGCCC GGCGAGGTGCGTCACAAATCCGGAGAGTGGC
AATGGCATCAAGCTGAGCCACCGACGCCACAATCATCCGGCGGATGCCTTTAAGCCCCAC
AAGCGCTGTTGAAAGCGTCCC GGCGATCGAAAAGTAACAAGTAACCATGT TTCAGGATGCA
AAGCATGCAGGCTTCGGCAATTATTTTCGCCACGATT

>Figure4B_b

AGGGCACATGTACTCCGTGGAACGCAAGTACCGAAACAGCATCAACTGGGTATGTTCCAA
GAACAGCAACAGTGTGTTACGCTGCCC GGCGAGGTGCGTCACAAATCCGGAGAGTGGCAA
TGGCATCAAGCTGAGCCACCGACGCCACAATCATCCGGCGGATGCCTTTAAGCCCCACAA
GCGCTGTTGAAAGCGTCCC GGCGATCGAAAAGTAACAAGTAACCATGT TTCAGGATGCAAA
GCATGCAGGCTTCGGCAATTATTTTCGCCACAGTTGTGTTTGCCGACGGAACGGAGTTAC
GATAATCGATGGCTACCGCTTCGTGATCGGTACTACAAATCTGCGTCGCACCTATCTGAA
GTGCGCCAACCTTTCGCAGCAACTGCCGGGCCCGGGCCATTCTTAATACGGACACGAACAA
AGTGC GGATGAGGCACGACCGCCATAATCACTCTCGTACGGATGCTGTGAGCGGACGTAT
CTCTAAGAAGTAGCAGATAACTCGAAAATAGCGCAGTATGTGCGCTCCAACCGAGGAACC
GATCTCGTTTACCACGAGGGAAACACCTACACACCCAATGAAAACCTTG

>Figure4B_c

AGGTGCACATGTACTCCGTGGAACGCAAGTACCGAAACAGCATCAACTGGGTATGTTCCA
AGAACAGCAACAGTGTGTTACGCTGCCC GGCGAGGTGCGTCACAAATCCGGAGAGTGGCA
ATGGCATCAAGCTGAGCCACCGACGCCACAATCATCCGGCGGATGCCTTTAAGCCCCACA
AGCGCTGTTGAAAGCGTCCC GGCGATCGAAAAGTAACAAGTAACCATGT TTCAGGATGCAA
AGCATGCAGGCTTCGGCAATTATTTTCGCCACAGTTGTGTTTGCCGACGGAACGGAGTTA
CGATAATCGATGGCTACCGCTTCGTGATCGGTACTACAAATCTGCGTCGCACCTATCTGA
AGTGC GGCAACTTTCGCAGCAACTGCCGGGCCCGGGCCATTCTTAATACGGACACGAACA
AAGTGC GGATGAGGCACGACCGCCATAATCACTCTCGTACGGATGCTGTGAGCGGACGTA
TCTCTAAGAAGTAGCAGATAACTCGAAAATAGCGCAGTATGTGCGCTCCAACCGAGGAA
CCGATCTCGTTTACCACGAGGGAAACACCTACACACCCAATGAAAAGCTGAGGGAGGGAC
AAAAGAGTCGAGACTGGAAGTGCTCAATGTACCATAAGGCCAAGTGCCGGGCCCGCCTGG
TTACTCGCATTACCGGTGGAGGGGATATTATACACGTGACCAGCAACCTGCACACACATC
CCACAATGTACACCACGCAGAAAACGGACATTAGCGTGGTTGACCAGAACTGTGCCTCG
AAAGGAATCCACTCTGCGTTAACACTCGATCGATTAATAATGTAGATCAAGACATCTTTCG
ACATTGCGCCATCTCCAGTTGAGGCCATATTTGATGCGGACGGCAAACAGATGGACTTC
ATACCAACATTCGCGTCATCCGAAGTCAGCGGAG

>Figure4B_d

CAGGGCACATGTACTCCGTGGAACGCAAGTACCGAAACAGCATCAACTGGGTATGTTCCA
AGAACAGCAACAGTGTGTTACGCTGCCC GGCGAGGTGCGTCACAAATCCGGAGAGTGGCA
ATGGCATCAAGCTGAGCCACCGACGCCACAATCATCCGGCGGATGCCTTTAAGCCCCACA
AGCGCTGTTGAAAGCGTCCC GGCGATCGAAAAGTAACAAGTAACCATGT TTCAGGATGCAA
AGCATGCAGGCTTCGGCAATTGACATCTTTTCGACATTGCGCCATCTCCAGTTGAGGCCA
TATTTGATGCGGACGGCAAACAGATGGACTTCATACCCAACATTCGCGTCATCCGAAGTC
AGCGGAAGACCATAAAGCTGATGTTTTAAAAAATATGCCTACTCGAAGACCAACGAGCAG
ATACCACAACCTACTGGCACTGCCGAAGTCGTGCGCAATGGAAGGCCTGCGTGCAAGGCC
GGTTTTCCACCAAGAAGCTCAAGAACGGTAGCTACAAAGTATATCTGACCCAGCCGGAAA
CTTCTGC

>Figure4B_e

CATCTTCAGGGGCACATGTACTCCGTGGAACGCAAGTACCGAAACAGCATCAACTGGGTA
TGTTC AAGAACAGCAACAGTGTGTTACGCTGCCC GGCGAGGTGCGTCACAAATCCGGAG
AGTGGCAATGGCATCAAGCTGAGCCACCGACGCCACAATCATCCGGCGGATGCCTTTAAG

CCCACAAGCGCTGTTGAAAGCGTCCCGGCGATCGAAAGTAACAAGTAACCATGTTTCAG
GATGCAAAGCATGCAGGCTTCGGCAATTATTTTCGCCACAGTTGTGTTTGCCGACGGAAC
GGAGTTACGATAATCGATGGCTACCGCTTCGTGATCGGTACTACAAATCTGCGTTCGCACC
TATCTGAAGTGCGCCAACTTTCGCAGCAACTGCCGGGCCCGGGCCATTCTTAATACGGAC
ACGAACAAAGTGC GGATGAGGCACGACCGCCATAATCACTCTCGTACGGATGCTGTGAGC
GGACGTATCTCTAAGAAGTAGCAGATAACTCGAAAATAGCGCAGTATGTGCGCTCCAACC
GAGGAACCGATCTCGTTTACCACGAGGAAACACCTACACACCCAATGAAAAGCTGAGGG
AGGGACAAAAGAGTTCGAGACTGGAAGTGCTCAATGTACCATAAGGCCAAGTGCCGGGCC
GCCTGGTTACTCGCATTACCGGTGGAGGGGATATTATACACGTGACCAGCAACCTGCACA
CACATCCCACAATGTACACCACGCAGAAAACGGACATTAGCGTGGTTGACCAGAACTGT
GCCTCGAAAGGAATCCACTCTGCGTTAACACTCGATCGATTAAAATGTAGATCAAGTGAC
GCCACCCAGTTCTTCTTACCAAGGGTCAGCGCAATCGGTCAAACCTAACTACTGCGGT
CATAGCTACGTCAGTCTG

>Figure4C_d

GTCGTCGCAATGGAAGGCCTGCGTGCAAGGCCCGGTTTTCCACCAAGAAGCTCAAGAACGAA
AGCAGCGTGGCGATCTACTCGGCAACCTCCCGGGACGAATGCAACTGATTTACGGCGGACA
GCCATTCATCTTCGAGAAGACGCTGAAACTGTCTTCGGGAGAGGAGAAGCGCTTCTGGCGCT
GCAACCAATGGTGGAAACCAAAAGTGTGCTCGCGCTTTCACCATCAACGACGTTGTCTGT
CCGCTTAACCGATTCCACACGCATGAGGAGATCGTGCGGCGAAAGAAGCGAGTGCGCCGCGT
GCCGCCGGTGGAGACGATTGCCAAGGTGGTTGCCACAACACCCAGGCATCCGCAGCATCAAC
AGACAACCCAGCAGCCACAAGAGATTCAGCTGCCAGAGATGCAATTGATGGAGCAATACTG
GACGATGAATCCCCAGCTACAATCGATGTCAGCGAGCTGGGGATGCATCTGAAATACGAAGA
AATCGTAGCGGATGTCACGGGCATTGTGGGCGGCACGCGAGTGGTCAGTCGCCGAAAGTGAA
TATTGCTTTTTTATTTTCTGACGTGACGCCACCCAGTTCTTCTTACCAAGGGTCAGCGCGAA
TCGGTCAAACCTAACTACTGCGTCATGCAC

>Figure4C_f

GAAAGAAGCGAGTGCGCCGCGTGCCGCCGGTGGAGACGATTGCCAAGGTGGTTGCCACAACA
CCCAGGCATCCGCAGCATCAACAGACAACCCAGCAGCAACAAGAGATTCAGCTGACCAGCGA
TGCAATTGCTGGAGCAATACTGGACGATGAATCCCCAGCTACAATCGATGTCAGCGAGCTGG
GGATGCATCTGAAATACGAAGAAATCGTAGCGGATGTCACGGCATTGTGGGCGGCACGCGA
GTGGTCAGTCGCCGAAAGTGAATATTGCTTTTTTATTTTCTGACGTGACGCCACCCAGTTCTT
CTTACCAAGGGTCAGCGCGAATCGGTCAAACCTAACTAC

Supplementary Table S3
Nucleotide sequences of PCR primers.

Primers used for RT-PCR and RT-qPCR

Actin 2 F GCACACCCACAAGCTTACACA
Actin 2 R TTGCGCTTTGGGAAATATCTTC
Mod(mdg4) Common F CACCCACGCTATCGTATTCC
Mod(mdg4) Common R CGTTAGCCCCTTGATTTGC
Mod(mdg4) UE F outer TGTACTCCCGAACATTGCAG
Mod(mdg4) UE R TGTGGGCGACATTTTAACAG
Mod(mdg4) RY intron F TTAAGTGGCGGATCCTCTTG
Mod(mdg4) RY F CCCGGTGGCTCCCGCAAGCAGAG
Mod(mdg4) RY middle R ATCCTTGATCCGACGATTGA
Mod(mdg4) RYRX junc F CTAATAAAGCATGCTACCAACTG
Mod(mdg4) RX intron F GGACGCCCTCTGACTAATCTC
Mod(mdg4) RX F CTACCAACTGGTGCCCAATC
Mod(mdg4) RX R AGTACATGTGCCCTGGAAG
Mod(mdg4) RAE F AATCTGCGTCGCACCTATCT
Mod(mdg4) RAE R CAAACACAACCTGTGGCGAAA
Mod(mdg4) RAD F GGAACCGATCTCGTTTACCA
Mod(mdg4) RAD R CTCCCTCAGCTTTTCATTGG
Mod(mdg4) RW F AGACCAACGAGCACGATAC
Mod(mdg4) RW R TCCGGCTGGGTCAGATATAC
Mod(mdg4) RV F GAAACTGTCTTCGGGAGAGG
Mod(mdg4) RV R ACAATGCCCGTGACATCC
Mod(mdg4) RU R GCGTCCATTCTCCATGAACT
Mod(mdg4)-prom F AACACTTCTAATTTTCACGTC
Mod(mdg4)-prom R ACTAACTAAAGCCAGAGTTTTT
Mod(mdg4) RY-RU nt 57 F GGCAACTCTGTAAAATGTC
Mod(mdg4) RY-RU nt 150 R TCTTAATTTACCTTTTGTTT
Mod(mdg4) RY-RU nt 829 F CTCTCCTATCGTTGTTGATT
Mod(mdg4) RY-RU nt 907 R CTGCAAGAATTGAAAGAGAT

Primers used for synthesis of dsRNA

Brm BKNT7 F taatacgaactcactatagggagaAAGCCCAATCGCATTACAAC
Brm BKNT7 R taatacgaactcactatagggagaTGAAGTGTATCAGCCGCTTG
Brm HFAT7 F TTAATACGACTCACTATAGGGAGAgtttcgctgtacaataacaat
Brm HFAT7 R TTAATACGACTCACTATAGGGAGAatgtggagcaggacttaag
GFP T7 F taatacgaactcactatagggagaATGGTGAGCAAGGGCGAGGAGCTG
GFP T7 R taatacgaactcactatagggagaGCGGTCACGAACTCCAGCAG

Primers used for Northern blot probe

Mod(mdg4) const probe 2 CTTGAGCCTCTGTGTTGCCCTGATC
Mod(mdg4) RX probe 2 CGATTGGGCACCCAGTTGGTAGCATG

Mod(mdg4) const+RX junction probe

CGATTGGGCACCAGTTGGTAGCATGCTTGAGCCTCTGTGTTGCCCTGATC

Primers for RACE

5'RACE adapter

GCUGAUGGCGAUGAAUGAACACUGCGUUUGCUGGCUUUGAUGAAA

5RACE outer GCTGATGGCGATGAATGAACACTG

5RACE inner CGCGGATCCGAACACTGCGTTTGCTGGCTTTGATG

3'RACE adapter GCGAGCACAGAATTAATACGACTCACTATAGGT12VN

3RACE outer GCGAGCACAGAATTAATACGACT

3RACE inner CGCGGATCCGAATTAATACGACTCACTATAGG

Mod(mdg4) RY F CCCGGTGGCTCCCGCAAGCAGAG

Mod(mdg4) RY exon junc F CAGAGGCTCAAGGAACAGGA

Mod(mdg4) RY 1R GGGATGGTTGTGGAGCCCGC

Mod(mdg4) RX F CTACCAACTGGTGCCCAATC

Mod(mdg4) RX exon junc F CAGAGGCTCAAGCATGCTACC

Mod(mdg4) RX R AGTACATGTGCCCTGGAAG

Mod(mdg4) RAE F AATCTGCGTCGCACCTATCT

Mod(mdg4) RAD F GGAACCGATCTCGTTTACCA

Mod(mdg4) RW F AGACCAACGAGCACGATAC

Mod(mdg4) RV F GAAACTGTCTTCGGGAGAGG

Primers used for cloning the Brm wide type and K804 mutant

Brm-K804R CCGATGAAATGGGTTTGGGTCGAACCATTCAAACCATTTCGC

Brm-K804R antisense

GCGAAATGGTTTGAATGGTTCGACCCAAACCCATTTTCATCGG

Brm-SpeI F GATAACTAGTAAGTCAAGAAAGGAGCTGCAA

Brm-SacII R GAATCCGCGGGTCCATGTCATCGTCGTCAT

Primers used for cloning the mod(mdg4) anti-sense strand

Mod(mdg4) AS 5UTR F SpeI GCACTAGTTGTACTCCCGAACATTGCAG

Mod(mdg4) RW intron R EcoRV ATCCGGATATCTTCCTTTCGAGGCACAGTTT

Supplementary Table S4.

The nucleotide sequences of the PCR products obtained in the RACE reactions.

>TSS1_RY1R_RY1R

CTTGCGCCTGAATTTTGTAAAATTCGCGTTAAATTTTTGTAAATCAGCTCATTTTTTAAC
CAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAGAATAGACCGAGATAGGGTTGAG
TGTTGTTCCAGTTTGGAAACAAGAGTCCACTATTAAGAACGTGGACTCCAACGTCAAAGGC
GAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCTAATCAAGTTTTTTG
GGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAGGGAGCCCCGATTTAGAGCTTG
ACGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGAAAGAAAGCGAAAGGAGCGGGCGCTA
GGGCGCTGGCAAGTGTAGCGGTCACGCTGCGCGTAACCACCACACCCGCCGCTTAATGCG
CCGCTACAGGGCGCGTCCATTCGCCATTAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTG
CGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTG
GGTAACGCCAGGGTTTTCCAGTACGACGTTGTAAAACGACGGCCAGTGAATTGTAATACG
ACTACTATAGGGCGAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCCGCAGTGTGATGGA
TATCTGCAGAATTCGCCCTTCGCGGATCCGAACACTGCGTTTGCTGGCTTTGATGAAAAGTTA
AAATGTCGCCACAGTTGTGAAAAAATGAAGTGATTTCCGAAAATTGTTGCTAAATTACTAA
ACAAAAGGAGGATGACTTCAAGTTGCACCTGCCTCTCCTCGTGACAAGGAGAAAGAAGACGC
CCGGTGGCTCCCAGCAAGCAGAGAAGGGCGAATTCAGCACACTGGCGGCCGTTACTAGTGGA
TCCGAGCTCGTA

>TSS2_RY1R_RY1R

TTGCGCCTGAATTTTGTAAAATTCGCGTTAAATTTTTGTAAATCAGCTCATTTTTTAACC
AATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAGAATAGACCGAGATAGGGTTGAG
TGTTGTTCCAGTTTGGAAACAAGAGTCCACTATTAAGAACGTGGACTCCAACGTCAAAGGC
GAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCTAATCAAGTTTTTTG
GGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAGGGAGCCCCGATTTAGAGCTTG
ACGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGAAAGAAAGCGAAAGGAGCGGGCGCTA
GGGCGCTGGCAAGTGTAGCGGTCACGCTGCGCGTAACCACCACACCCGCCGCTTAATGCG
CCGCTACAGGGCGCGTCCATTCGCCATTAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTG
CGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTG
GGTAACGCCAGGGTTTTCCAGTACGACGTTGTAAAACGACGGCCAGTGAATTGTAATACG
ACTACTATAGGGCGAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCCGCAGTGTGATGGA
TATCTGCAGAATTCGCCCTTCGCGGATCCGAACACTGCGTTTGCTGGCTTTGATGAAAACAG
TTGTGAAAAAATGAAGTGATTTCCGAAAATTGTTGCTAAATTACTAAAACAAAAGAAGCAGGAG
GATGACTTCAAGTTGCACCTGCCTCTCCTCGTGACAAGGAGAAAGAAGACGCCCGGTGGCTC
CCGCAAGCAGAGAAGGGCGAATTCAGCACACTGGCGGCCGTTACTAGTGGATCCGAGCTCG
TA

>TSS3_RXR_RXR

CTTGTCAGATAGCCAGTAGCTGACATTCATCCGGGGTCAGCACCGTTTCTGCGGACTGGC
TTTCTACGTGTTCCGCTTCTTTAGCAGCCCTTGCGCCCTGAATTTTGTAAAATTCGCGTT
AAATTTTTGTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATA
AATCAAAGAATAGACCGAGATAGGGTTGAGTGTGTTCCAGTTTGGAAACAAGAGTCCACTA
TTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAACCGTCTATCAGGGCGATGGCCCACT
ACGTGAACCATCACCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGA
ACCCTAAAGGGAGCCCCGATTTAGAGCTTGACGGGAAAGCCGGCGAACGTGGCGAGAAAG
GAAGGAAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCG
CGTAACCACCACACCCGCCGCTTAATGCGCCGCTACAGGGCGCGTCCATTCGCCATTAG
GCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGA
AAGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCAGTACGACGCT
TGTAACGACGCGCCAGTGAATTGTAATACGACTACTATAGGGCGAATGGGCCCTCTAGA
TGCATGCTCGAGCGGCCCGCAGTGTGATGGATATCTGCAGAATTCGCCCTTCGCGGATCCGA
ACACTGCGTTTTGCTGGCTTTGATGAAACTTCCGCTCTCCTATCGTTGTTGATTCTATAGTG
TCCTTGCAGCAACTCAGGACGCCCTCTGACTAATCTCTTTCAATTCCTTGCAGCATGCTACCAA

CTGGTGCCCAATCGCCGCGGTGGGAAGAACCTCATCTTCCAGGGGCACATGTACTAAGGGCG
AATTCAGCACACTGGCGGCCGTTACTAGTGAT

>CS1_Common F_RY F

GGTGAGCTTACCAGAAGCAATAGGGGTAACAACCTTGCTGACCATCGATGGGAAGCCCTTCA
CCCTCAATCGTCGGATCAAGGATGTGTGCTACTGGGAGTGCCTCAAGCTGCGCTGCAAGTAC
ATCAAGTGCTCCGCCCGTGTGGTGACCAAATCCAATCGGATCTCGGCACTGAGCGGGCTCCA
CAACCATCCCTAAGTTACGAACTACCTGTGCCATCTCATTAGTCTAATAAAGGTGTTTACGT
TGAATCAAAAAAAAAAAAAA

>CS2_Common F_RY exon junc F

TCACATGTTCTTTCCTGCGTTATCCCTGATTCTGTGGATAACCGTATTACCGCCTTTGAGTG
AGCTGATACCGCTCGCCGAGCCGAACGACCGAGCGCAGCGAGTCAGTGAGCGAGGAAGCGG
AAGAGCGCCCAATACGCAAACCGCCTCTCCCCGCGCTTGGCCGATTCAATTAATGCAGCTGG
CACGACAGGTTTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTAGCT
CACTCATTAGGCACCCAGGCTTTACACTTTATGCTTCCGGCTCGTATGTTGTGTGGAAATTG
TGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACGCCAAGCTTGGTACC
GAGCTCGGATCCACTAGTAACGGCCGCCAGTGCTGGAATTCGCCCTTTACGAGCGGTGGC
GGAGTGACGGCGACCACTTCCAAGGCTGTGGTCAAGCAACAGTCCCAGAACTACAGTGAATC
ATCGTTTGTGACACCAGCGGGGATCAGGGCAACACAGAGGCTCAAGAACAGGAGGATGACT
TCAAGTTGCACCTGCCTCTCCTCGTGACAAGGAGAAAGAACGCCCGGTGGCTCCCACAAG
CAGAGTTTTGACCACCTGGAGGTGAGCTTACCAGAAGCAACAGGGGTAACAACCTTGCTGAC
CATCGATGGGAAGCCCTTACCCTCAATCGTCGGATCAAGGATGTGTGCTACTGGGAGTGCG
TCAAGCTGCGCTGCAAGTACATCAAGTGCTCCGCCCGTGTGGTGACCAAATCCAATCGGATC
TCGGCACTGAGCGGGCTCCACAACCATCCCTAAGTTACGAACTACCTGTGCCATCTCATTAG
TCTAATAAAGGTGTTTACGCAAAAAAAAAAAAAAACCCTATAGTGAGTCGTATTAATTCTGTGCT
CGCAAGGGCGAATTCTGCAGATATCCATCACACTGGCGGCCGCTCGAGCATGCATC

>CS_3 Common F_RX exon junc F

TCGAGCGGCCCGCCAGTGTGATGGATATCTGCAGAATTCGCCCTTCAGAGGCTCAAGCATGCT
ACCAACTGGTGCCCAATCGCCGCGGTGGGAAGAACCTCATCTTCCAGGGGCACATGTACTCC
GTGGAACGCAAGTACCGAAACAGCATCAACTGGGTATGTTCCAAGAACAGCAACAGTGTGTT
ACGCTGCCCGGCGAGGTGCGTCACAAATCCGAGAGTGGCAATGGCATCAAGCTGAGCCACC
GACGCCACAATCATCCGGCGGATGCCTTTAAGCCCCACAAGCGCTGTTGAAAGCGTCCCAGC
GATCGAAAGTAACAAGTAACCATGTTTTCAGGATGCAAAGCATGCAGGCTTCGGCAATTGTTA
GTCACACTAAATATAAATGTTTCTCATCGTTGTCGAAAAAAAAAAAAAAAAACCTATAGTGAGTCG
TATTAATTCGGATCCGCGAAGGGCGAATTCCAGCACACTGGCGGCCGTTACTAGTGGATCCG
AGCTCGGTACCAAGCTTGGCGTAATCATGGTCATAGCTGTTTCCCTGTGTGAAATTGTTATCC
GCTCACAATTCACACAACATACGAGCCGGAAGCATAAAGTGTAAGCCTGGGGTGCCTAAT
GAGTGAGCTAACTCACATTAATGCGTTGCGTCACTGCCCGCTTTCAGTCCGGAAACCTG
TCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTGCGTATTGGGCG
CTCTTCCGCTTCCCTCGCTCACTGACTCGCTGCGTCCGGTCCGCTCGGCTCGCGCGAGCGGTAT
CAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCACGGGATAACGCACG

>CS4_Common F_RX exon junc F

CGAGCGGCCCGCCAGTGTGATGGATATCTGCAGAATTCGCCCTTCAGAGGCTCAAGCATGCTA
CCAACCTGGTGCCCAATCGCCGCGGTGGGAAGAACCTCATCTTCCAGGGGCACATGTACTCCG
TGGAACGCAAGTACCGAAACAGCATCAACTGGGTATGTTCCAAGAACAGCAACAGTGTGTTA
CGCTGCCCGGCGAGGTGCGTCACAAATCCGGAGAGTGGCAATGGCATCAAGCTGAGCCACC
ACGCCACAATCATCCGGCGGATGCCTTTAAGCCCCACAAGCGCTGTTGAAAGCGTCCCAGC
ATCGAAAGTAACAAGTAACCATGTTTTCAGGATGCAAAGCATGCAGGCTTCGGCAATTGTTAG
TCACACTAAATATAAATGTTTCTCATCGTTGTCGAAACAAAAAAAAAAAAAAAAACCTATAGTGAG
TCTATTAATTCGGATCCGCGAAGGGCGAATTCCAGCACACTGGCGGCCGTTACTAGTGGATC
CGAGCTCGGTACCAAGCTTGGCGTAATCATGGTCATAGCTGTTTCCCTGTGTGAAATTGTTAT
CCGCTCACAATTCACACAACATACGAGCCGGAAGCATAAAGTGTAAGCCTGGGGTGCCTA
ATGAGTGAGCTAACTCACATTAATGCGTTGCGTCACTGCCCGCTTTCAGTCCGGAAACCC
TGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCATATTGGG

CGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCCGGCTGCGGCGAGCGGT
ATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGGAAAG
AACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTT
TTCCATAGGCTC

>CS5_Common F_RAE F
GGGCTTCTTAATACGGACACGAACAAAGTGCGGATGAGGCACGACCGCCATAATCACTCTC
GTACGGATGCTGTGAGCGGACGTATCTCTAAGAAGTAGCAGGTACCGAGCTGTCTAGAGGAA
TAAACATGCTGTTCCGTTTAAAAAAAAAAAAA

>CS6_Common F_RAE F
GGCCTTCTTAATACGGACACGAACAAAGTGCGGATGAGGCACGACCGCCATAATCACTCTCG
TACGGATGCTGTGAGCGGACGTATCTCTAAGAAGTAGCAGATAACTCGAAAATAGCGCAGTA
TGTGCGCTCCAACCGAGGAACCGATCTCGTTTACCACGAGGGAAACACCTACACACCCAATG
AAAAGCTGAGGGAGGGACAAAAGAGTCGAGACTGGAAGTGCTCAATGTACCATAAGGCCAAG
TGCCGGGCCCGCCTGGTTACTCGCATTACCGGTGGAGGGGATATTATACACGTGACCAGCAA
CCTGCACACACATCCACAATGTACACCACGCAGAAAACGGACATTAGCGTGGTTGACCAGA
AACTGTGCCTCGAAAGGAATCCACTCTGCGTTAACACTCGATCGATTAAAATGTAGATCAAG
TAAAGACCACCGACTGATTACTCGTTACGATTAGCATGATCTTCAGTATAAATAACGTTTAA
GATTTAAAAAGTATTAAAAAATGCTCATATACATTTCAACAAAAAAAAAAAAA

>CS7_Common F_RAD F
GAAGCTGAGGGAGGGACAAAAGAGTCGAGACTGGAAGTGCTCAATGTACCATAAGGCCAAGT
GCCGGGCCCGCTGGTTACTCGCATTACCGGTGGAGGGGATATTATACACGTGACCAGCAAC
CTGCACACACATCCACAATGTACACCACGCAGAAAACGGACATTAGCGTGGTTGACCAGAA
ACTGTGCCTCGAAAGGAATCCACTCTGCGTTAACACTCGATCGATTAAAATGTAGATCAAGT
AAAGACCACCGACTGATTACTCGTTACGATTAGCATGATCTTCAGTATAAATAACGTTTAA
ATTTAAAAAGTATTAAAAAATGCTCATATACATTTCAATAAAAAAAAAAAAAA

>CS8_Common F
ACTAGTACGGCCGCGCAGTGTGCTGGAATTCGCCCTTTACGAGCGGTGGCGGAGTGACGGCGA
CCACTTCCAAGGCTGTGGTCAAGCAACAGTCCCAGAACTACAGTGAATCATCGTTTGTGAC
ACCAGCGGGGATCAGGGCAACACAGAGGCTCAAGGACATCTTTCGACATTGCGCCATCTCCC
AGTTGAGGCCATATTTGATGCGGACGGCAAACAGATGGACTTCATACCCAACATTCGCGTCA
TCCGAAGTCAGCGGAAGACCATAAAGCTGATGTTTTAAAAAATATGCCTACTCGAAGACCAAC
GAGCACGATACCACAACCTACTGGCACTGCCGAAGTCGTCGCAATGGAAGGCCTGCGTGCAA
GGCCCGTTTTCCACCAAGAAGCTCAAGAACGGTAGCTACAAAGTATATCTGACCCAGCCGG
AGCACAATCATCCCCAAAGAAGCGTCGCTATAATCAGAATAACTATATTTTTAAGAAGAAT
GATATATTAAGAGCCATGTCTTGCCAAAATGACTTGCACCGACTCCCCAAAAAAAAAAAAAAC
CTATAGTGAGTCGTATTAATCTGTGCTCGCAAGGGCGAATTCGTCAGATATCCATCACACT
GGCGCCGCTCGAGCATGCATCTAGAGGGCCCAATTCGCCCTATAGTGAGTCGTATTACAAT
TCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCTGGCGTTACCCAACCTAATCG
CCTTGACACATCCCCCTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCAGATCGCC
CTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGACGCGCCCTGTAGCGGCGCATTAAGCG
CGGCGGGTGTGGTGGTTACGCGCAGCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCT
CCTTCGCTTTCTTCCCTTCTTCTCGCACGTTTCGCGGGCTTTCCTCCCGTCAAGCTCTAATC
GGGGCTCCCTTA

>CS9_Common F_RW F
GGAGGCCTGCGTGCAAGGCCCGTTTTCCACCAAGAAGCTCAAGAACGGTAGCTACAAAGTA
TATCTGACCCAGCCGGAGCACAATCATCCCCAAAGAAGCGTCGCCTATAATCAGAATAACT
ATATTTAAGAAGAATGATATATTAAGAGCCATGTCTTGGCAAAATGAAAAAAAAAAAAA

>CS10_Common F_RV F
CTCACATGGTGGACAAAAGTGTCGCTCGCGCGTCTTACCATCAACGACGTTGTCTGTCCG
CTTAACCGATTCCACACGCATGAGGAGATCGTGGCGGAAAGAAGCGAGTGGCCCGCGTGGC
GCCGTTGGAGACGATTGCCAAGGTGGTTGCCACAACACCCAGGCATCCGCAGCATCAACAGA

CAACCCAGCAGCAACAAGAGATTCAGCTGACCAGCGATGCAATTGCTGGAGCAATACTGGAC
GATGAATCCCCAGCTACAATCGATGTCAGCGAGCTGGGGATGCATCTGAAATACGAAGAAAT
CGTAGCGGATGTCACGGGCATTGTGGGCGGCACGCGAGTGGTCAGTCGCCGAAAGTGAATAT
TGCTTTTTATTTCTGACGTAAGATCGCAGATTCAGATTCCCTTCTTTGTAAAACTCATGCT
TTGAGTTTTCATTTTTGAACTTGCCACGTCGAAAACCAAGAGCCGAACAGTTTTTGATGAATT
TAAAAAGGCTAAGCACAACCACTAGCCAATAAATACAATTTTTATTATTATTTAAGGACAAA
AAAAAAAAA

>CS11_Common F_RV F

GTGTCGCTCGCGCTCTTACCATCAACGACGTTGTCTGTCCGCTTAACCGATTCCACACGC
ATGAGGAGATCGTGCGGCGAAAGAAGCGAGTGCGCCGCTGCCGCCGGTGGAGACGATTGCC
AAGGTGGTTGCCACAACACCCAGGCATCCGCAGCATCAACAGACAACCCAGCAGCAACAAGA
GATTCAGCTGACCAGCGATGCAATTGCTGGAGCAATACTGGACGATGAATCCCCAGCTACAA
TCGATGTCAGCGAGCTGGGGATGCATCTGAAATACGAAGAAATCGTAGCGGATGTCACGGGC
ATTGTGGGCGGCACGCGAGTGGTCAGTCGCCGAAAGTGAATATTGCTTTTTATTTCTGACG
TAAGATCGCAGATTCAGATTCCCTTCTTTGTAAAACTCATGCTTTGAGTTTTCATTTTTGAA
CTTGCCACGTCGAAAACCAAGAGCCGAACAGTTTTTGATGAATTTAAAAAGGCTAAGCACAAC
CACTAGCCAATAAATACAATTTTTATTATTATTTAAGGACATTTTTTAAAACCTTTTTTAT
TAAGCGTAATATTCGAAGGTTCCCTCCCCATTTGTAAAAATTTGATAAATACCCCATGATTT
CCTTTGACATTTTGAGTTGTTTAGAATAAAATCTGTTCCCTTCTGTTATGCCTTTGTTCAA
CAAAAAAAAAA

>CS12_Common F_RV F

TGCACATGGTGGACCAAAGTGTGCTCGCGCTCTTACCATCAACGACGTTGTCTGTCCG
CTTAACCGATTCCACACGCATGAGGAGATCGTGCGGCGAAAGAAGCGAGTGCGCCGCTGCC
GCCGGTGGAGACGATTGCCAAGTGGTTGCCACAACACCCAGGCATCCGCAGCATCAACAGA
CAACCCAGCAGCAACAAGAGATTCAGCTGACCAGCGATGCAATTGCTGGAGCAATACTGGAC
GATGAATCCCCAGCTACAATCGATGTCAGCGAGCTGGGGATGCATCTGAAATACGAAGAAAT
CGTAGCGGATGTCACGGGCATTGTGGGCGGCACGCGAGTGGTCAGTCGCCGAAAGTGAATAT
TGCTTTTTATTTCTGACGTAAGATCGCAGATTCAGATTCCCTTCTTTGTAAAACTCATGCT
TTGAGTTTTCATTTTTGAACTTGCCACGTCGAAAACCAAGAGCCGAACAGTTTTTGATGAATT
TAAAAAGGCTAAGCACAACCACTAGCCAATAAATACAATTTTTATTATTATTTAAGGACATA
TTTTTAAAACCTTTTTTATTAAGCGTAATATTCGAAGGTTCCCTCCCCATTTGTAAAAATTT
GATAAATACCCCATGATTTCCCTTGACATTTTGAGTTGTTTAGAATAAAATCTGTTCCCTT
TGTTATGCCTTTGTTCAAACAAAATTGACCTAGCCTACTCCATAATTATTAATACAAAACCT
GCGTTTAAGAAGGCGGACAAGCTAGCTATTATGATACAGCTTACAACAATTTATTATGTGT
ACATTTAATAAACGTAAGACCCAAACAGTGCAAAAAAAAAA