A

Y = C or T

K = G or T

R = A or G

B

```
    AY265456(It-Pi1)          TCC---GGGGAAAGAGATTATCCTGAGCTCGAAAAGTGTATCAGGCAGGCATGCAAGATAAAAGTTCGAGTCAGAGGGGAGCACTTGACAGAAGGAAATTGTTTGTGGTGCCTCAAAACCTTAGATTGTA
B2  FJ195346(Ov496)           TCCGGGGGGAAAAGAGATTATCCTGAGCTCGAAAAATGTATTAAGCAGGCATGCAAAATAAAAGTTCGAGTCAGAGGGGAGCACTTGACAGAAGGAAATTGTTTGTGGTGCCTCAAGACACTAGATTATA
    DQ190014                  TCCGGGGGAAAAAGGGATTATCCTGAGCTCGAAAAATGTCTCAAGCAGGCATGCAAGATAAAAGTTCGAGTCAGAGGGGAGCACTTGACAGAAGGAAATTGCTTATGGTGCCTTAAAACATTAGATTACA
    DQ190019                  TCCGGGGGAAAAAGGGATTATCCTGAGCTCGAAAAATGTATCAAGCTAGCATGCAAGATAAAAGTTCGAGCCAGAGGGGAGCACTTGACAGAAGGAAATTGTTTATGGTGCCTTAAAACATTAGATTATA
    DQ190028                  TCCGGGGGAAAAGGGAATATCCTGAGCTCGACAAATGCATCAAGCATGCGTGCAGGATAAGAGTTCGGCTCAGAGGGGAGCACTTGACAGAAGGAAATTGTTTATGGTGCCTCAAAACATTAGATTACA
    DQ190016                  TCCGGGGGAAAAGGGATTATCCTGAGCTCGAAAAATGTATCAAGCTAGCATGCAAGATAAGAGTTCGAGACAGAGGGGAGCACTTGACAGAAGGAAATTGTTTATGGTGCCTTAAAACATTAGATTATA
    DQ190020                  TCCGGGGGAAAAAGGGATTATCCTGAGCTCGAAAAATGTATCAAGCTAGCATGCAAGATAAAAGTTCGAGCCAGAGGGGAGCACTTGACAGAAGGAAATTGTTTATGGTGCCTTAAAACATTAGATTATA
    DQ190033                  TCCGGGGGGAAAAAGAGTTTATCCTGAGCTCGAAAAATGTATCAAGCTAGCATGCAAGATAAGAGTTCGAGACAGAGGGGAGCACTTGACAGAAGGAAATTGTTTATGGTGCCTTAAAACATTAGATTATA
    DQ190044                  TCCGGGGGGAAAAGAGATTATCCTGAGCTCGAAAAATGTATCAGGCAGGCATGCAAGATAAAAGTTCGAGTCAGAGGGGAGCACTTGACAGAAGGAAATTGCTTATGGTGCCTTAAAACATTAGATTACA
    AY900630(CAEVstraingansu) TCCGGGGGGAAAAGAGATTATCCTGAGCTCGAAAAATGTATCAAGCAGGCATGCAAGATAAAAGTTCGGCTCAGAGGGGAGCACTTGACAGAAGGAAATTGTTTATGGTGCCTTAAAACATTAGATTACA
    M33677(CAEVCo)            TCCGGGGGGAAAAGAGATTATCCTGAGCTCGAAAAATGTATCAAGCATGCATGCAAGATAAAAGTTCGACTCAGAGGGGAGCACTTGACAGAAGGAAATTGTTTGTGGTGCCTTAAAACATTAGATTACA
    JQ610955(37-18g)          TCCGGGGGGAAAAGGGATTATCCTGAGCTCGAAAAATGTCTCAAGAAGGCATGCAAAATAAGGGTTCGGCTCAGAGGGGAGCACTTGACAGAAGGAAATTGTTTGTGGTGCCTTAAAACATTAGACTACA
    JQ610942(37-20g)          TCCGGGGGGAAAAGGGATTATCCTGAGCTCGAAAAATGTCTCAAGAAGGCATGTAAAATAAGGGTTCGGCTCAGAGGGGAGCACTTGACAGAAGGAAATTGTTTGTGGTGCCTTAAAACATTAGACTACA
    JQ610943(37-25g)          TCCGGGGGGAAAAGGGATTATCCTGAGCTCGAAAAATGTCTCAAGAAGGCATGTAAAATGAGGGTTCGGCTCAGAGGGGAGCACTTGACAGAAGGAAATTGTTTGTGGTGCCTTAAAACATTAGACTACA
    JQ610944(37-31g)          TCCGGGGGGAAAAGGGATTATCCTGAGCTCGAAAAATGTCTCAAGAAGGCAGGGAGAATAAGGGTTCGGCTCAGAGGGGAGCACTTGACAGAAGGAAATTGTTTGTGGTGCCTTAAAACATTAGACTACA
    JQ610945(37-43g)          TCCGGGGGGAAAAGGGATTATCCTGAGCTCGAAAAATGTCTCAAAAAGGCGTGCAAAATAAGGGTTCGGCTCAGAGGGGAGCACTTGACAGAAGGAAATTGTTTGTGGTGCCTTAAAACATTAGACTACA
    JQ610946(37-53g)          TCCGGGGGGAAAAGGGATTATCCTGAGCTCGAAAAATGTCTCAAGAAGGCATGCAAAATAAGGGTTCGGCTCAGAGGGGAGCACTTGACAGAAGGAAATTGTTTGTGGTGCCTTAAAACATTAGACTACA
    JQ610947(37-59g)          TCCGGGGGGAAAAGGGATTATCCTGAGCTCGAAAAATGTCTCAAGAAGGCATGCAGAATAAGGGTTCGGCTCAGAGGGGAGCACTTGACAGAAGGAAATTGTTTGTGGTGCCTTAAAACATTAGACTACA
    JQ610948(37-61g)          TCCGGGGGGAAAAGGGATTATCCTGAGCTCGAAAAATGTCTCAAGAAGGCATGTAGAATAAGGGTTCGGCTCAGAGGGGAGCACTTGACAGAAGGAAATTGTTTGTGGTGCCTTAAAACATTAGACTACA
    JQ610949(37-63g)          TCCGGGGGGAAAAGGGATTATCCTGAGCTCGAAAAATGTCTCAAGAAGGCATGCAAAATAAAGGTTCGGCTCAGAGGGGAGCACTTGACAGAAGGAAATTGTTTGTGGTGCCTTAAAACATTAGACTACA
    JQ610950(37-65g)          TCCGGGGGGAAAAGGGATTATCCTGAGCTCGAAAAATGTCTCAAAAAAGCATGCAAAATAAGGGTTCGGCTCAGAGGGGAGCACTTGACAGAAGGAAATTGTTTGTGGTGCCTTAAAACATTAGACTACA
    JQ610951(37-66g)          TCCGGGGGGAAAAGGGATTATCCTGAGCTCGAAAAATGTCTCAAGAAGGCAAGCAGAATAAGGGTTCGGCTCAGAGGGGAGCACTTGACAGAAGGAAATTGTTTGTGGTGCCTTAAAACATTAGACTACA
    JQ610952(37-70g)          TCCGGGGGGAAAAGGGATTATCCTGAGCTCGAAAAATGTCTCAAGAAGGCATGCAAAATAAGGGTTCGGCTCAGAGGGGAGCACTTGACAGAAGGAAATTGTTTGTGGTGCCTTAAAACATTAGATTACA
    JQ610953(37-78g)          TCCGGGGGGAAAAGGGATTATCCTGAGCTCGAAAAATGTCTCAAGAAGGCATGCAAAATAAGGGTTCGGCTCAGAGGGGAGCACTTGACAGAAGGAAATTGCTTGTGGTGCCTTAAAACATTAGACTACA
B1  JQ610954(37-85g)          TCCGGGGGGAAAAGGGATTATCCTGAGCTCGAAAAATGTCTCAAGAAGGCATGCAAAATAAGGGTTCGGCTCAGAGGGGAGCACTTGACAGAAGGAAATTGTTTGTGGTGCCTTAAAACATTAGACTACA
    HQ910472(1-24g)           TCCGGGGGGAAAAGGGATTATCCTGAGCTCGAGAAATGTATCAAGCTAGCATGCAAGATAAAAGTTCGAGCCAGAGGGGAGAACTTGACAGAAGGAAATTGTTTATGGTGCCTTAAAACATTAGATTACA
    HQ910473(1-32g)           TCCGGGGGGAAAAGGGATTATCCTGAGCTCGAGAAATGTATCAAGCTAGCATGCAAGATAAAAGTTCGAGCCAGAGGGGAGCACTTGACAGAAGGAAATTGTTTATGGTGCCTTAAAACATTAGATTACA
    HQ910474(1-38g)           TCCGGGGGGAAAAGGGATTATCCTGAGCTCGAGAAATGTATCAAGCTAGCATGCAAGATAAAAGTTCGAGCCAGAGGGGAGAACTTGACAGAAGGAAATTGTTTATGGTGCCTTAAAACATTAGATTACA
    HQ910475(1-43g)           TCCGGGGGGAAAAGGGATTATCCTGAGCTCGAGAAATGTATCAAGCTAGCATGCAAGATAAAAGTTCGAGCCAGAGGGGAGAACTTGACAGAAGGAAATTGTTTATGGTGCCTTAAAACATTAGATTACA
    HQ910476(1-65g)           TCCGGGGGGAAAAGGGATTATCCTGAGCTCGAGAAATGTATCAAGCTAGCATGCAAGATGAAGTTCGAGCCAGAGGGGAGAACTTGACAGAAGGAAATTGTTTATGGTGCCTTAAAACATTAGATTACA
    HQ910477(1-66g)           TCCGGGGGGAAAAGGGATTATCCTGAGCTCGAGAAATGTATCAAGCTAGCATGCAAGATAAAAGTTCGAGCCAGAGGGGAGAACTTGACAGAAGGAAATTGTTTATGGTGCCTTAAAACATTAGATTACA
    HQ910478(1-77g)           TCCGGGGGGAAAAGGGATTATCCTGAGCTCGAGAAATGTATCAAGCTAGCATGCAAGATAAAAGTTCGAGCCAGAGGGGAGAACTTGACAGAAGGAAATTGTTTATGGTGCCTTAAAACATTAGATTACA
    HQ910479(1-86g)           TCCGGGGGGAAAAGGGATTATCCTGAGCTCGAGAAATGTATCAAGCTAGCATGCAAGATAAAAGTTCGAGCCAGAGGGGAGAACTTGACAGAAGGAAATTGTTTATGGTGCCTTAAAACATTAGATTACA
    HQ910480(1-87g)           TCCGGGGGGAAAAGGGATTATCCTGAGCTCGCGAAATGTATCAAGCTAGCATGCAAGATGAAAGTTCGAGCCAGAGGGGAGAACTTGACAGAAGGAAATTGTTTATGGTGCCTTAAAACATTAGATTATA
    HQ910481(1-90g)           TCCGGGGGGAAAAGGGATTATCCTGAGCTCGAGAAATGTATCAAGCTAGCATGCAAGATAAAAGTTCGAGCCAGAGGGGAGAACTTGACAGAAGGAAATTGTTTATGGTGCCTTAAAACATTAGATTACA
    HQ910482(1-96g)           TCCGGGGGGAAAAGGGATTATCCTGAGCTCGAGAAATGTATCAAGCTAGCATGCAAGATAAAAGTTCGAGCCAGAGGGGAGAACTTGACAGAAGGAAATTGTTTATGGTGCCTTAAAACATTAGATTACA
    HQ910483(1-99g)           TCCGGGGGGAAAAGGGATTATCCTGAGCTCGAGAAATGTATCAAGCTAGCATGCAAGATAAAAGTTCGAGCCAGAGGGGAGAACTTGACAGAAGGAAATTGTTTATGGTGCCTTAAAACATTAGATTACA
    HQ910484(1-106g)          TCCGGGGGGAAAAGGGATTATCCTGAGCTCGAGAAATGTATCAAGCTAGCATGCAAGATAAAAGTTCGAGCCAGAGGGGAGAACTTGACAGAAGGAAATTGTTTATGGTGCCTTAAAACATTAGATTACA
    HQ910485(1-108g)          TCCGGGGGGAAAAGGGATTATCCTGAGCTCGAGAAATGTATCAAGCTAGCATGCAAGATAAAAGTTCGAGCCAGAGGGGAGAACTTGACAGAAGGAAATTGTTTATGGTGCCTTAAAACATTAGATTACA
    HQ910486(1-110g)          TCCGGGGGGAAAAGGGATTATCCTGAGCTCGAGAAATGTATCAAGCTAGCATGCAAGATAAAAGTTCGAGCCAGAGGGGAGAACTTGACAGAAGGAAATTGTTTATGGTGCCTTAAAACGTTAGATTACA
    HQ910487(1-112g)          TCCGGGGGGAAAAGGGATTATCCTGAGCTCGAGAAATGTATCAAGCTAGCATGCAAGATAAAAGTTCGAGCCAGAGGGGAGAACTTGACAGAAGGAAATTGTTTATGGTGCCTTAAAACATTAGATTACA
    HQ910488(1-113g)          TCCGGGGGGAAAAGGGATTATCCTGAGCTCGAGAAATGTATCAAGCTAGCATGCAAGATAAAAGTTCGAGCCAGAGGGGAGAACTTGACAGAAGGAAATTGTTTATGGTGCCTTAAAACATTAGATTACA
    HQ910489(1-114g)          TCCGGGGGGAAAAGGGATTATCCTGAGCTCGAGAAATGTATCAAGCTAGCATGCAAGATAAAAGTTCGAGCCAGAGGGGAGAACTTGACAGAAGGAAATTGTTTATGGTGCCTTAAAACATTAGATTACA
    HQ910490(2-3g)            TCCGGGGGGAAAAGGGATTATCCTGAGCTCGAGAAATGTATCAAGCTAGCATGCAAGATAAAAGTTCGAGCCAGAGGGGAGAACTTGACAGAAGGAAATTGTTTATGGTGCCTTAAAACATTAGATTACA
    HQ910491(2-90g)           TCCGGGGGGAAAAGGGATTATCCTGAGCTCGAGAAATGTATCAAGCTAGCATGCAAGATAAAAGTTCGAGCCAGAGGGGAGAACTTGACAGAAGGAAATTGTTTATGGTGCCTTAAAACATTAGATTACA
    HQ910492(3-8g)            TCCGGGGGGAAAAGGGATTATCCTGAGCTCGAAAAATGTCTCAAGAAGGCATGCAAAATAAGGGTTCGGCTCAGAGGGGAGCACTTGACAGAAGGAAATTGTTTGTGGTGCCTTAAAACATTAGACTACA
    HQ910493(3-10g)           TCCGGGGGGAAAAGGGATTATCCTGAGCTCGAAAAATGTCTCAAGAAGGCATGCAAAATAAGGGTTCGGCTCAGAGGGGAGCACTTGACAGAAGGAAATTGTTTGTGGTGCCTTAAAACATTAGACTACA
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CAEVMA F
5'GGGAAAAGGGATTATCCTGAG 3'

CAEVMA R(reverse complement)
5'GTTTTAAGGCACCAYAAACAATTTC 3'

CAEVMA(reverse complement)
5'FAM-TCTGTCAAGTKCTCCCCTCTG-3'TAMRA

Y = C or T
K = G or T
R = A or G

C

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                                          10        20        30
                                  ....|....|....|....|....|....|....|....|...
AF322109(CAEV1GA)genotypeC        TCCGGAAGGGGAAAGGAGTACCCCGAGCTAAAAGAATG
primer MVVMA F1                   ---------------GGATACCCCGAGCTCAAAG----

EU293538(Roccaverano)genotypeE    TCAGATGGGAGAAAGGGATACCCCGAACTCAAAGAATT
primer MVVMA F1                   ---------------GGATACCCCGAGCTCAAAG----
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                                          10        20        30        40        50
                                  ....|....|....|....|....|....|....|....|....|....|..
AF322109(CAEV1GA)genotypeC        TTTTTATACACCAGAGACAATTTCCTTCTGTCAGGCGCTCCCCCCCAGCCCT
probe MVVMA                       ------------------------------TCTGTCAAGGTCTCCTTCCCG-----
primer MVVMA R3                   --TTYAAKGCCCAYAGACARTT-------------------------------

EU293538(Roccaverano)genotypeE    TTTTTATACACCAAAGACAATTGCCTTCTGTCAAGGTCTCCTTCCCGACTCC
probe MVVMA                       ------------------------------TCTGTCAAGGTCTCCTTCCCG-----
primer MVVMA R3                   --TTYAAKGCCCAYAGACARTT-------------------------------
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R = A or G