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Meav-1_RE-LJV-D-RNA1      ACATGCAATTCGATTTTGC GGTGGCCTTGGATCCTCTACATCTAAATGCTAACGAACGAA 11813
D-RNA1_Sanger             -----AATGCTAACGAACGAA 61
                             *****

Meav-1_RE-LJV-D-RNA1      GAGCTTTGACTTCATTGTTAGCTAGATTTAGAACCAGGAGAACACCTGTCAGAGGGCAAG 11873
D-RNA1_Sanger             GAGCTTTGACTTCATTGTTAGCTAGATTTAGAACCAGGAGAACACCTGTCAGAGGGCAAG 121
                             *****

Meav-1_RE-LJV-D-RNA1      CCTTAGGACAACGTGCTAGCAATCCACTAGATGATGTGGTTGAATCTATAGTTCCAGCGA 11933
D-RNA1_Sanger             CCTTAGGACAACGTGCTAGCAATCCACTAGATGATGTGGTTGAATCTATAGTTCCAGCGA 181
                             *****

Meav-1_RE-LJV-D-RNA1      CTTCTCGAGGAATGTTACGAGAGTTGACTGGCGGTGCCAGTACGCTTGGGTATAATAGAA 11993
D-RNA1_Sanger             CTTCTCGAGGAATGTTACGAGAGTTGACTGGCGGTGCCAGTACGCTTGGGTATAATAGAA 241
                             *****

Meav-1_RE-LJV-D-RNA1      GAAGACGCTACTAATTCAGCACCATGGCAACACCAACACCTGGAACACCAAACCTACTC 12053
D-RNA1_Sanger             GAAGACGCTACTAATTCAGCACCATGGCAACACCAACACCTGGAACACCAAACCTACTC 301
                             *****

Meav-1_RE-LJV-D-RNA1      CTCCTGATGCAAACAGTACTAATACCAACAGTCAAGTTGTGGCTGCTGTCGTACCTGGAG 12113
D-RNA1_Sanger             CTCCTGATGCAAACAGTACTAATACCAACAGTCAAGTTGTGGCTGCTGTCGTACCTGGAG 361
                             *****

Meav-1_RE-LJV-D-RNA1      GTCGTCAGACCGTTGDELETIONZONEAATAAACAAGAGTAGCACAAGTCGGTCCAACCC 12173
D-RNA1_Sanger             GTCGTCAGACCGTTG-----AATAAACAAGAGTAGCACAAGTCGGTCCAACCC 409
                             *****

Meav-1_RE-LJV-D-RNA1      TCACAATATGTACGAAGATTCTGGCGTTGCTCCAGAAATTTTCATGGGAGGACGACGTTG 12229
D-RNA1_Sanger             TCACAATATGTACGAAGATTCTGGCGTTG----- 465
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Figure S1: Multiple sequence alignment of D-RNA1 clone (referred to in the figure as D-RNA1_Sanger) with the defective reference from HTS (MEaV-1_RE-LJV-D-RNA-1). The term “DELETIONZONE” has been inserted into the HTS defective reference to identify the zone where the deletion is located. This zone consists in 568 nucleotide sequences and is indicated by the rectangle.

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Meav-1_RE-LJV-D-RNA2      GAAGGAGCGTGACAGTAAACTCTAATGCGTGAAAAATGGGTGTCTTTCAATGACATTACT 8400
D-RNA2_Sanger             ----- 7

Meav-1_RE-LJV-D-RNA2      CAGGCTTTCGACAGTGAAGAAGTGTGTTGTCGTCTAGCCGCGTTGTGTGAGGAGAAATAC 8460
D-RNA2_Sanger             -----TTCGACAGTGAAGAAGTGTGTTGTCGTCTAGCCGCGTTGTGTGAGGAGAAATAC 67
                          *****

Meav-1_RE-LJV-D-RNA2      GGTCC TAGTCCGTGGTGGTACGCTGCGATAGCGACAATTCATTGTATCAGGGCCAATCCG 8520
D-RNA2_Sanger             GGTCC TAGTCCGTGGTGGTACGCTGCGATAGCGACAATTCATTGTATCAGGGCCAATCCG 127
                          *****

Meav-1_RE-LJV-D-RNA2      CAGCAATTTGAGAGGTGTTGGAGTGAATATCTTCTCCTAGTATAAATGAAGCAAAGAAG 8580
D-RNA2_Sanger             CAGCAATTTGAGAGGTGTTGGAGTGAATATCTTCTCCTAGTATAAATGAAGCAAAGAAG 187
                          *****

Meav-1_RE-LJV-D-RNA2      AGAAGCAAGGTCGTCTCCGAAGGAGGACCTGCGAGTTGTACAAATGACCAATTTATATTT 8640
D-RNA2_Sanger             AGAAGCAAGGTCGTCTCCGAAGGAGGACCTGCGAGTTGTACAAATGACCAATTTATATTT 247
                          *****

Meav-1_RE-LJV-D-RNA2      TGATTTTAAGTGGGCTATAACCGTTTDELETIONZONEACCTACAATTATGATGAAATAA 8700
D-RNA2_Sanger             TGATTTTAAGTGGGCTATAACCGTTT-----ACCTACAATTATGATGAAATAA 295
                          *****

Meav-1_RE-LJV-D-RNA2      AAACGACCATTGATAATGCTATCCTTCAGTATGGCTACGAAAACCCCGTTCGCCAATTCG 8760
D-RNA2_Sanger             AAACGACCATTGATAATGCTATCCTTCAGTATGGCTAC----- 337
                          *****

Meav-1_RE-LJV-D-RNA2      GGAGGAGTGCACAGTTTCATAATCAAGCATTAGCAAATGGACTCATGGAACCCAATG 8820
D-RNA2_Sanger             ----- 337

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Figure S2: Multiple sequence alignment of D-RNA2 clone (referred to in the figure as D-RNA2_Sanger) with the defective reference from HTS (MEaV-1_RE-LJV-D-RNA-2). The term “DELETIONZONE” has been inserted into the HTS defective reference to identify the zone where the deletion is located. This zone consists in 3761 nucleotide sequences and is indicated by the rectangle.

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Meav-2_RE-LJV-D-RNA3      CATTCCACTCCGTACTTCTGTTCTGAAGTTCTTGGTGGAAAGCCGCTGGTAAACTACATTAC 8460
D_RNA3a-Sanger            -----ACTACATTAC 10
D_RNA3b-Sanger            -----ACTACATTAC 10
                             *****

Meav-2_RE-LJV-D-RNA3      GTACCCGACCCCTTCAAATTTTTATAAAATTTGGAGCGGAAGGTGCACCGACAAAGCCA 8520
D_RNA3a-Sanger            GTACCCGACCCCTTCAAATTTTTATAAAATTTGGAGCGGAAGGTGCACCGACAAAGCCA 70
D_RNA3b-Sanger            GTACCCGACCCCTTCAAATTTTTATAAAATTTGGAGCGGAAGGTGCACCGACAAAGCCA 70
                             *****

Meav-2_RE-LJV-D-RNA3      TTATTTAAAGAGAAGTGGGCTTCATTTTACGACATAACAACCTGCTTATGACAGTGAGGAA 8580
D_RNA3a-Sanger            TTATTTAAAGAGAAGTGGGCTTCATTTTACGACATAACAACCTGCTTATGACAGTGAGGAA 130
D_RNA3b-Sanger            TTATTTAAAGAGAAGTGGGCTTCATTTTACGACATAACAACCTGCTTATGACAGTGAGGAA 130
                             *****

Meav-2_RE-LJV-D-RNA3      GCTGTCATCAAGTTGGCCCATCTATGCGCTGAGAAATACGGTGCATCGAATTGGTGGTAC 8640
D_RNA3a-Sanger            GCTGTCATCAAGTTGGCCCATCTATGCGCTGAGAAATACGGTGCATCGAATTGGTGGTAC 190
D_RNA3b-Sanger            GCTGTCATCAAGTTGGCCCATCTATGCGCTGAGAAATACGGTGCATCGAATTGGTGGTAC 190
                             *****

Meav-2_RE-LJV-D-RNA3      GCTGCTATAGCTACAATCCATTGTATTTCGTGCAAACCAACACAATTTGCACGATGTTGG 8700
D_RNA3a-Sanger            GCTGCTATAGCTACAATCCATTGTATTTCGTGCAAACCAACACAATTTGCACGATGTTGG 250
D_RNA3b-Sanger            GCTGCTATAGCTACAATCCATTGTATTTCGTGCAAACCAACACAATTTGCACGATGTTGG 250
                             *****

Meav-2_RE-LJV-D-RNA3      GAGACAGTTGATTGTGAGAGCATACGTTCTCGTAAGTCG-----CAACAAAC 8760
D_RNA3a-Sanger            GAGACAGTTGATTGTGAGAGCATACGTTCTCGTAAGTCG-----CAACAAAC 298
D_RNA3b-Sanger            GAGACAGTTGATTGTGAGAGCATACGTTCTCGTAAGTCG-----CAACAAAC 298
                             *****
                             DELETIONZONE
                             *****

Meav-2_RE-LJV-D-RNA3      TAGTGTGGCAGTGGGGTGACAAAACCGTTACTACTACTTATAATAGTATTTCCGCATATGT 8820
D_RNA3a-Sanger            TAGTGTGGCAGTGGGGTGACAAAACCGTTACTACTACTTATAATAGTATTTCCGCATATGT 358
D_RNA3b-Sanger            TAGTGTGGCAGTGGGGTGACAAAACCGTTACTACTACTTATAATAGTATTTCCGCATATGT 358
                             *****

Meav-2_RE-LJV-D-RNA3      TTGCGAAACATGGAGGTACTATTCTAATATTGAACGTGCTTGGTGCAATCCACTAGCTT 8880
D_RNA3a-Sanger            TTGCGAAACATGGAGGTACTATTCTAATATTGAACGTGCTTGGTGATCTT----- 406
D_RNA3b-Sanger            TTGCGAAACATGGAGGTACTATTCTAATATTGAACGTGCTTGGTGATCTT----- 406
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Figure S3: Multiple sequence alignment of D-RNA3 clones (two clones were sequenced and are referred to in the figure as D-RNA3a-Sanger and D-RNA3b-Sanger) with the defective reference from HTS (MEaV-2_RE-LJV-D-RNA3). The term “DELETIONZONE” has been inserted into the reference HTS defective to identify the zone where the deletion has been identified. This zone consists in 648 nucleotide sequences and is indicated by the rectangle.

Meav-2_MG-Mena-D-RNA-4 D-RNA4_Sanger	CGAGTGGCCACTGTGCATGAGTGTCAAGGGAAGACATATGAAAGAGTTGCATTGGTGCGA -----	5100 0
Meav-2_MG-Mena-D-RNA-4 D-RNA4_Sanger	ATCAAGCCCGCACAAAGACGAAGTCTTCACGAGCGCTCCACATAGATTAGTGGCTCTCACT -----AGCCGCAAGACGAAGTCTTCACGAGCGCTCCACATAGATTAGTGGCTCTCACT * *****	5160 53
Meav-2_MG-Mena-D-RNA-4 D-RNA4_Sanger	CGACACACTACGAGTTTAGACTTCTATTGCATAAGAAATCGAATGGACCAGGGGATTGGT CGACACACTACGAGTTTAGACTTCTATTGCATAAGAAATCGAATGGACCAGGGGATTGGT *****	5220 113
Meav-2_MG-Mena-D-RNA-4 D-RNA4_Sanger	CGAGATGTCGAACTGATTGAGAAAATAACGGAACACGTCGCGAGGACTTTCTTAATTGAG CGAGATGTCGAACTGATTGAGAAAATAACGGAACACGTCGCGAGGACTTTCTTAATTGAG *****	5280 173
Meav-2_MG-Mena-D-RNA-4 D-RNA4_Sanger	CAGTGTTCCTAACAATTATTACGTTDELETIONZONETGATTTAGCAGAATGGACCATGTC CAGTGTTCCTAACAATTATTACGTT-----TGATTTAGCAGAATGGACCATGTC *****	5340 221
Meav-2_MG-Mena-D-RNA-4 D-RNA4_Sanger	CAGAACGACATCGGGTAAGGCAGGTTTGTACAAAAACTGCAAAATACCTTCACTTCCCCA CAGAACGACATCGGGTAAGGCAGGTTTGTACAAAAACTGCAAAATACCTTCACTTCCCCA *****	5400 281
Meav-2_MG-Mena-D-RNA-4 D-RNA4_Sanger	TACTCAACTGGATGAATCAAACCTTATGGTGAAAGGGGATTTGAAACCAAACCTAGATGA TACTCAACTGGATGAATCAAACCTTATGGTGAAAGGGGATTTGAAACCAAACCTAGATGA *****	5460 341
Meav-2_MG-Mena-D-RNA-4 D-RNA4_Sanger	CACCTTGCTTATCCGACATTCAGTGGTCAAATATAGTTTATCAGAACGAGCAGTTTG CACCTTGCTTATCCGACATTCAGTGGTCAAATATAGTTTATCAGAACGAGCAGTTTG *****	5520 401
Meav-2_MG-Mena-D-RNA-4 D-RNA4_Sanger	TGCTTGTTTTCTGTCTGTTTCATCCAAATGACAAAAAGATTGAAAGCCATATTAACAG TGCTTGTTTTCTGTCTGTTTCATCCAAATGACAAAAAGATTGAAAGCCATATTAACAG *****	5580 461
Meav-2_MG-Mena-D-RNA-4 D-RNA4_Sanger	ACGAGCGAAATTATTTGTAGGTGTAGACCTCTCTGAATTTGCTCTCGATATTCAGCTCAC ACGAGCGAAATTATTTGTAGGTAA----- *****	5640 485

Figure S4: Multiple sequence alignment of D-RNA4 clone (referred to in the figure as D-RNA4-Sanger) with the defective reference from HTS (MEaV-2_MG-Mena-D-RNA-4). The term “DELETIONZONE” has been inserted into the reference HTS defective to identify the zone where the deletion is located. This zone consists in 444 nucleotide sequences and is indicated by the rectangle.