

Meav-1_RE-LJV-D-RNA1 D-RNA1_Sanger	ACATGCAATTCGATTTTGC GGTGGCCTTGGATCCTCTACATCTAAATGCTAACGAACGAA -----AATGCTAACGAACGAA *****	11813 61
Meav-1_RE-LJV-D-RNA1 D-RNA1_Sanger	GAGCTTTGACTTCATTGTTAGCTAGATTTAGAACAGGAGAACACCTGTCAGAGGGCAAG GAGCTTTGACTTCATTGTTAGCTAGATTTAGAACAGGAGAACACCTGTCAGAGGGCAAG *****	11873 121
Meav-1_RE-LJV-D-RNA1 D-RNA1_Sanger	CCTTAGGACAACGTGCTAGCAATCCACTAGATGATGTGGTTGAATCTATAGTTCCAGCGA CCTTAGGACAACGTGCTAGCAATCCACTAGATGATGTGGTTGAATCTATAGTTCCAGCGA *****	11933 181
Meav-1_RE-LJV-D-RNA1 D-RNA1_Sanger	CTTCTCGAGGAATGTTACGAGAGTTGACTGGCGGTGCCAGTACGCTTGGGTATAATAGAA CTTCTCGAGGAATGTTACGAGAGTTGACTGGCGGTGCCAGTACGCTTGGGTATAATAGAA *****	11993 241
Meav-1_RE-LJV-D-RNA1 D-RNA1_Sanger	GAAGACGCTACTAATTCAGCACCATGGCAACACCAACACCTGGAACACCAAACCTCTACTC GAAGACGCTACTAATTCAGCACCATGGCAACACCAACACCTGGAACACCAAACCTCTACTC *****	12053 301
Meav-1_RE-LJV-D-RNA1 D-RNA1_Sanger	CTCCTGATGCAAACAGTACTAATACCAACAGTCAAGTTGTGGCTGCTGTCGTACCTGGAG CTCCTGATGCAAACAGTACTAATACCAACAGTCAAGTTGTGGCTGCTGTCGTACCTGGAG *****	12113 361
Meav-1_RE-LJV-D-RNA1 D-RNA1_Sanger	GTCGTCAGACCGTTGDELETIONZONEAATAAACAAGAGTAGCACAAGTCGGTCCAACCC GTCGTCAGACCGTTG-----AATAAACAAGAGTAGCACAAGTCGGTCCAACCC *****	12173 409
Meav-1_RE-LJV-D-RNA1 D-RNA1_Sanger	TCACAATATGTACGAAGATTCTGGCGTTGCTCCAGAAATTTTCATGGGAGGACGACGTTG TCACAATATGTACGAAGATTCTGGCGTTG----- *****	12229 465

**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.

Meav-1_RE-LJV-D-RNA2 D-RNA2_Sanger	GAAGGAGCGTGCAGTAAACTCTAATGCGTGAAAAATGGGTGTCTTTCAATGACATTACT -----	8400 7
Meav-1_RE-LJV-D-RNA2 D-RNA2_Sanger	CAGGCTTTCGACAGTGAAGAAGTGTGTTCGCTAGCCGCGTTGTGTGAGGAGAAATAC -----TTCGACAGTGAAGAAGTGTGTTCGCTAGCCGCGTTGTGTGAGGAGAAATAC *****	8460 67
Meav-1_RE-LJV-D-RNA2 D-RNA2_Sanger	GGTCCTAGTCCGTGGTGGTACGCTGCGATAGCGACAATTCATTGTATCAGGGCCAATCCG GGTCCTAGTCCGTGGTGGTACGCTGCGATAGCGACAATTCATTGTATCAGGGCCAATCCG *****	8520 127
Meav-1_RE-LJV-D-RNA2 D-RNA2_Sanger	CAGCAATTTGAGAGGTGTTGGAGTGAATATCTTCTCCTAGTATAAATGAAGCAAAGAAG CAGCAATTTGAGAGGTGTTGGAGTGAATATCTTCTCCTAGTATAAATGAAGCAAAGAAG *****	8580 187
Meav-1_RE-LJV-D-RNA2 D-RNA2_Sanger	AGAAGCAAGGTCGTCTCCGAAGGAGGACCTGCGAGTTGTACAAATGACCAATTTATATTT AGAAGCAAGGTCGTCTCCGAAGGAGGACCTGCGAGTTGTACAAATGACCAATTTATATTT *****	8640 247
Meav-1_RE-LJV-D-RNA2 D-RNA2_Sanger	TGATTTTAAGTGGGCTATAACCGTTTDELETIONZONEACCTACAATTATGATGAAATAA TGATTTTAAGTGGGCTATAACCGTTT-----ACCTACAATTATGATGAAATAA *****	8700 295
Meav-1_RE-LJV-D-RNA2 D-RNA2_Sanger	AAACGACCATTGATAATGCTATCCTTCAGTATGGCTACGAAAACCCGTTCCGCAATTTCG AAACGACCATTGATAATGCTATCCTTCAGTATGGCTAC----- *****	8760 337
Meav-1_RE-LJV-D-RNA2 D-RNA2_Sanger	GGAGGAGTGCGACCAGTTTCATAATTCAAGCATTAGCAAATGGACTCATGGAACCCAATG -----	8820 337

**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.

Meav-2_RE-LJV-D-RNA3	CATTCCACTCCGTACTTCTGTTCTGAAGTTCCTGGTGGAAGCCGCTGGTAAACTACATTAC	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	GTCTGCATCAAGTTGGCCCATCTATGCGCTGAGAAATACGGTGCATCGAATTGGTGGTAC	8640
D_RNA3a-Sanger	GTCTGCATCAAGTTGGCCCATCTATGCGCTGAGAAATACGGTGCATCGAATTGGTGGTAC	190
D_RNA3b-Sanger	GTCTGCATCAAGTTGGCCCATCTATGCGCTGAGAAATACGGTGCATCGAATTGGTGGTAC	190
	*****	
Meav-2_RE-LJV-D-RNA3	GCTGCTATAGCTACAATCCATTGTATTCTGTGCAAACCAACACAATTTGCACGATGTTGG	8700
D_RNA3a-Sanger	GCTGCTATAGCTACAATCCATTGTATTCTGTGCAAACCAACACAATTTGCACGATGTTGG	250
D_RNA3b-Sanger	GCTGCTATAGCTACAATCCATTGTATTCTGTGCAAACCAACACAATTTGCACGATGTTGG	250
	*****	
Meav-2_RE-LJV-D-RNA3	GAGACAGTTGATTGTGAGAGCATACGTTCTCGTAAGTCGDELETIONZONECAAACAAAC	8760
D_RNA3a-Sanger	GAGACAGTTGATTGTGAGAGCATACGTTCTCGTAAGTCG-----CAAACAAAC	298
D_RNA3b-Sanger	GAGACAGTTGATTGTGAGAGCATACGTTCTCGTAAGTCG-----CAAACAAAC	298
	*****	
Meav-2_RE-LJV-D-RNA3	TAGTGTGGCAGTGGGGTGACAAAACCGTTACTACTACTTATAATAGTATTTCCGCTATGT	8820
D_RNA3a-Sanger	TAGTGTGGCAGTGGGGTGACAAAACCGTTACTACTACTTATAATAGTATTTCCGCTATGT	358
D_RNA3b-Sanger	TAGTGTGGCAGTGGGGTGACAAAACCGTTACTACTACTTATAATAGTATTTCCGCTATGT	358
	*****	
Meav-2_RE-LJV-D-RNA3	TTGCGAAACATGGAGGTACTATTCCTAATATTGAACGTGCTTGGTGCAATCCACTAGCTT	8880
D_RNA3a-Sanger	TTGCGAAACATGGAGGTACTATTCCTAATATTGAACGTGCTTGGTGCAATCCACTAGCTT	406
D_RNA3b-Sanger	TTGCGAAACATGGAGGTACTATTCCTAATATTGAACGTGCTTGGTGCAATCCACTAGCTT	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	ATCAAGCCCGCACAGACGAAGTCTTCACGAGCGCTCCACATAGATTAGTGGCTCTCACT -----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	CGAGATGTGCGAACTGATTGAGAAAATAACGGAACACGTCGCGAGGACTTTCTTAATTGAG CGAGATGTGCGAACTGATTGAGAAAATAACGGAACACGTCGCGAGGACTTTCTTAATTGAG *****	5280 173
Meav-2_MG-Mena-D-RNA-4 D-RNA4_Sanger	CAGTGTTCCTAACAATTATTACGTDELETIONZONETGATTTAGCAGAATGGACCATGTC CAGTGTTCCTAACAATTATTACGT-----TGATTTAGCAGAATGGACCATGTC *****	5340 221
Meav-2_MG-Mena-D-RNA-4 D-RNA4_Sanger	CAGAACGACATCGGGTAAGGCAGGTTTGTACAAAAACTGCAAATACCTTCACTTCCCCA CAGAACGACATCGGGTAAGGCAGGTTTGTACAAAAACTGCAAATACCTTCACTTCCCCA *****	5400 281
Meav-2_MG-Mena-D-RNA-4 D-RNA4_Sanger	TACTCAACTGGATGAATTCAAACCTATGGTGAAAGGGGATTTGAAACCAAACTAGATGA TACTCAACTGGATGAATTCAAACCTATGGTGAAAGGGGATTTGAAACCAAACTAGATGA *****	5460 341
Meav-2_MG-Mena-D-RNA-4 D-RNA4_Sanger	CAC TTGCTTATCCGACATTCGAGTGGTCAAAATATAGTTTATCACGAACGAGCAGTTTG CAC TTGCTTATCCGACATTCGAGTGGTCAAAATATAGTTTATCACGAACGAGCAGTTTG *****	5520 401
Meav-2_MG-Mena-D-RNA-4 D-RNA4_Sanger	TGCTTGTTTTCTGTCTGTTTCATCCAAATGACAAAAAGATTGAAAGCCATATTAAACAG TGCTTGTTTTCTGTCTGTTTCATCCAAATGACAAAAAGATTGAAAGCCATATTAAACAG *****	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.