

FIG S1 A Comparison of L-A-lus and L-A nucleotide sequences.

**Initiation**

L-A-lus	GAAAAATTGAATAATCATATAACTCCCC <b>ATG</b> CTTAGATTTCGTTACCAAAAACCTCTCAAG	60
L-A	GAAAAATTTTAAATTCATATAACTCCCC <b>ATG</b> CTAAGATTTGTTACTAAAAACCTCTCAAG	60
	***** ;*:*****:*****:***** ***** ***** *****	
L-A-lus	ACAAGTCTCCGATTTATTTCTATTTGCTCTGACAAAGGTACTTTTGTGCGCATAATA	120
L-A	ATAAATCGTCTGATCTATTTCTATTTGTTCTGATCGCGAACTTTTGTGCCATAATA	120
	* **.* ** ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** *	
L-A-lus	GGGTGAGGACTGACTTTAAATTTGACAACCTAGTTTTTAATCGAGTCTACGGCGTGTAC	180
L-A	GAGTTCGGACTGATTTCAAGTTTGAACAACCTAGTATTTCAACCGAGTTTATGGTGTTC	180
	* **.* ***** ** **.* *****:*** ** ***** ** ** * ** * ** * ** *	
L-A-lus	AAAAGTTCACCCTAGTCGGCAACCCGAAAGTCTGTTTCAATGAGGGAAGTTCGTACTTGG	240
L-A	AAAAATTTACGTTAGTCGGTAACCCGACAGTCTGCTTTAATGAAGGCAGTTCCTACCTAG	240
	****.* ** * ***** *****.* ***** ** *****.* ** ***** ** * ** *	
L-A-lus	AGGGTATTGCAAAGAAATATCTGACCTTGACGGTGGCCTGGCCATTGATAACATCCTCA	300
L-A	AAGGTATTGCTAAAAGTACCTAAGTTGGATGGAGGACTTGCATTGACAATGTCCTCA	300
	* .*****:* **.* ** * **.* ** ***** **:* **.* ***** ** * .*****	
L-A-lus	ATGAATTGAAATCAACATGTGGTATACCAGGTAATGCTGTCGCTTCTCATGCATACAACA	360
L-A	ATGAGTTGAGATCCACTTGGGATACCAGGTAATGCTGTTGCATCTCATGCGTATAATA	360
	****.* **.* **.* **.* **.* **.* *****.* *****.* **.* *****.* ** * *	
L-A-lus	TTACGCTCTGGAGATGGTACGATAATCAGTGGCATTACTCATGAATATGTTACGTGCGT	420
L-A	TTACATCTGGCGTTGGTATGACAATCAGTGGCAGTGTGATGAACATGTTGCGTGTCT	420
	****.* ** * **.* **.* ***** ** *****.* * . ***** *****.* ***** *	
L-A-lus	ACCATCTCAAGTGTATCTGAACAAGCCAGTATTCGCCGTTTCATACCCATGTACC	480
L-A	ACCATTACAAGTATTGACCGAACAGGCCAATATAGCGCTGGAGATATCCCTATGTACC	480
	**** * :*****.* **.* ** * *****.* *****.* ** :* ** :* .:::*****	
L-A-lus	ACGATGGGCATGTCAAATTAACCTTGACACTCCTATCAGTGAGGATGATGCTCCTGACT	540
L-A	ATGATGGACATGTCAAATCAAGCTACCAGTACTATCGATGACACGGCAGGCCAACAC	540
	* *****.* *****.* **.* ** :* . . . . *****.* ** * . * :* ** :* . . .	
L-A-lus	CATTTAAGTGGCCGAGTGACCGGACAACAGACTTACCAGACTGGGCTCAGTTCTCAG	600
L-A	AATTCGCTTGGCCTAGTGACAGGCTACTGATTCGTATCCTGATTGGGCACAGTTTTCTG	600
	.* ** . . ***** *****.* **:* **:* **:* **:* ** * ** * **:* ** * **:* ** * **:	
L-A-lus	AGTCCTTCCCGTCTATTGACGTCCTACTTAGATGTAGGCCACTTACTGTACCGAAG	660
L-A	AATCATTTCCATCAATCGACGTCCTTACCTAGATGTAGGCCATTGACCGTAACCGAAG	660
	* **.* ** * **.* **:* ** * *****.* ** * ***** ***** * ** * **:* ** * ** *	
L-A-lus	TTAATTTTGTGTTAATGATGATGAGTAAGTGGCACCGTCGGACTAACCTTGCTATTGACT	720
L-A	TCAATTTCTGTGCTTATGATGATGAGTAAGTGGCATAGACGTAACCTTAGCGATAGACT	720
	* ***** ** * :*****:*****.* **:* ** * ***** * ** * **:* ** * ** *	
L-A-lus	ATGAAGCGCCGGCGCTGGCAGACAAATTCGCCTACCGTCACGCCATTACGGTCCAGGATG	780
L-A	ACGAGGCACCCCACTAGCTGATAAGTTTCGCTTACCGCATGCGCTTACTGTTCAAGACG	780
	* **.* **.* ** . **.* **:* ** * **.* ***** ***** ** * ** * **.* ** * ** *	
L-A-lus	CAGATGAATGGATTGAAGGTGATAGGACAGATGATCAGTTAGACCACCTTCTTCTAAG	840
L-A	CTGACGAGTGGATAGAAGCGATAGAAGTACTGATGACAGTTCGGCCCCCTCGTCTAAG	840
	* **.* **.* *****.* *****.* *****.* **.* ***** ***** * **.* ** * **.* ** *	
L-A-lus	TAATGATGTCGGCATTGCGTAAGTATGTTAATCATAATCGACTTTACAACAGTTCCTATA	900
L-A	TAATGTTATCGGCCTTCGTAAGTACGTGAACCATAACAGGCTGTACAATCAGTTTTACA	900
	*****:* **.* ***** * *****.* ** * ***** . * ** * ***** ***** * ** *	
L-A-lus	CGCCGCTCAACTATTAGCTCAGATTATGATGAAACCAGTACCTAAGTTCGCTGAGGGT	960
L-A	CTGCAGCACAACTGTTAGCTCAAAATTAATGATGAAACCTGTCCTAAGTTCGCTGAGGGT	960
	* **.* **:* *****.* *****.* *****:*****.* **.* ***** *****.* ** *	
L-A-lus	ATGCATGGTTGATGCACGATGCTGCTGCAACTTGCAGGATTCGGGTTCGTTAGAGGGC	1020
L-A	ACGCTTGGCTGATGCATGACGCATTGGTCAATATACCAAAATTTGGTCTATTCGAGGAA	1020



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* .***** .**** .***** * .***** .**** .***** .** .** * .** *
L-A-lus TCCGATGAGATACATATGAACGAGCCAAATACATACCCCGCATGGATAAGGTTAGAAA 2160
L-A CCCTACAAGGTACATACATGACGGAACCAGGTACGTACCTGCGTGGATTAGATTAGAAA 2160
* * .** .***** * .** * .***** .**** .***** * .***** :** .***** **
L-A-lus TAGAGTACAGGCGGTATCTAGACAGAGGGCAACACATTTCTTATTTGATATAGTACCGGC 2220
L-A CAGAGTACAAGCTGTATCGCGTCAGAAAGCCACTCACTTCTTGTGTTGACATCGTACCTGC 2220
***** .** ***** .*:***** .** .** :** ***** .***** ** .***** **
L-A-lus CAGCAAAATTGCGGACTATACTACTTCCAAAACGGCTACTTTTGCATACAGGTCGCACAC 2280
L-A CGCAGTAATTAGTGATTTACTACGTCTGACACGTCTTCGTTTGCATACAAAATCGCACAC 2280
* . .:****. ** *:***** **: * .*** ** : ***** .*****
L-A-lus GTATGCATGCACGGTAACGGCACTACGCTTTGGAGATGACTACGGCTGTATGTCCAGGT 2340
L-A CTACGCTGTAATGTAACAGCATTTGAGGTTGAGTACACTTATGCCTTGTACGTACAGAC 2340
** **: .** .***** .*** * .** * .** :** .** * ***** ** .****.
L-A-lus AGAGGCTAACATGACATTTGTTAAGTCCGGCTGCACGGCGACAAGCTTCTGCTACGTACTC 2400
L-A TGATACCAACATGACAATTTTAAGCCAGCGGCGCGTCGCCAGGCTTCTGCGACGTACTC 2400
:** * ***** :* ***** ** .** * .** * .** .***** *****
L-A-lus TCAGGTTGAGGGTCTGTTTTAAACACACCTACGGTCATGGACACGCTAGCTAACATCTT 2460
L-A ACAGGTGGCAGGGTTTTGTTATAACACACCTACCGTTATGGATTGCTAGCGAATATCTT 2460
:***** * .***** *****:***** ** ***** :***** ** *****
L-A-lus GGATGTTGACCGCAATATTAGACCAAAGCACTTTAAAGGCTCGCTACTTATGAGAGGTC 2520
L-A GGACGTAGACCGCAATATACGACCCAAACACTTCAAGGTTTACGGCTATACACAAGGTC 2520
*** **:*****: .**** .** .***** ** .*** * .** . :** .** .*****
L-A-lus TAAGGTCACAGCACAAACACCACACTCACTTGGGCGCTGATGAAGTACTGGAAGCAGCGGC 2580
L-A TAAGGTCACTGCTCAACATCATACTCACTTGGGCGCAGACGAGCTAGTGAAGCGGCCGC 2580
*****:**:***** ** *****:*** ** .** ***** ** **
L-A-lus ACGTGTATCGCCTAGGCGAAAGTACTACTTATATGCGTCTGATAGACTATTAGCGGCATG 2640
L-A AAAGGTCFCGCCTAGACGTAATACTACTTAATGTGTGTAGTTGAGCTGCTCGCAACTT 2640
* . .** .***** .** :** .***** :* .** * .** :***** .** .***** .**
L-A-lus CGAGGTTAACATGGAAGCAGCAGTAGCTACAATAATGACGTACGTACTCACTTTGGACGA 2700
L-A ACAAGTAGATCTTGAAGCAGCAGTAGCTACTATTCTCGCATATGCTCAGACTAAGTGA 2700
. * .** :* .*****:**:** * .** * .** **: * .** **
L-A-lus AAAGTTCATACCTTTGTTTCTAGACTACGGACAATATGGCAGGGTAGTAAAGGACCTGA 2760
L-A AAAATTTGTACCAATTTCTTGGATTCTAGAGCAATATGGGTCGGTGAAGCTGGGCCTGA 2760
*** .** .****: ** * .** * .** :** .***** : *** . .:*****
L-A-lus AGAACTAACAGCCAGACTCAAGAAGGCGAGCGGCAGATTAAAAGTGTTCATACAGCTGA 2820
L-A TGCTCTGACTGCACGTCTCAAGGCCAGTAGTGGGCGAGATCAAGAGCATAACACAGGCTGA 2820
:*.**:**:**.**:*****. . ** ***** ** .** .** :** ** .*****
L-A-lus CTATGAGCCACTGACGGAAGTGTGTAATGGCTGTGCTCATGAACAGAGGCGTCGGGCA 2880
L-A TTACGAACCCTCACTGAACATTTGAGTTAGCAGTATTTGATGAACCGAGGTGTGGCCA 2880
** ** .***** ** ***** ** .** .** :** * ***** .**** ** ** **
L-A-lus TGTATCCTGGAAGACTGAAAGAGAACACAGAGAGAATCCGGATGTAGCAAACGTTAATCA 2940
L-A TGTCTCTGGCAAGCTGAAAAGGATCATCGCTTGAATCCCGACGTGGCTGTAGTTGATCA 2940
*** .** * .** .** .***** .** :** * .** :***** ** .** .** :** .** .*****
L-A-lus ACAAGCACTCTACGCGTGCCTACGTGACATGTTCCGAGGGGCAAGCAGACTTATGATTA 3000
L-A AGCAGCGCTATATTCGTGTGTGCGCGACATGTTCCGAGGATCAAAGCAGACGTATAAATA 3000
* .** * .** * .** * .** * .** * .** * .** * .** * .** * .** * .** * .** *
L-A-lus TCCTTACATGACATGGGATGACTATACGTCAAGTCGGTGGGAATGGGTGCCCTGGAGGAAG 3060
L-A TCCCTTTATGACGTGGGATGACTACACTGCAAACAGATGGGAGTGGGTTCCAGGTGGCAG 3060
*** *: ***** .***** ** * .** .** .***** .***** ** :** :** .**
L-A-lus TGTTCATTTCTCAGTACTCCGAGGATGATGAATATATATTTCCAGGACAATATACTAGGAA 3120
L-A TGTCCACTCTCAATACGAAGAAGACAACGATTATATCTATCCTGGTCACTACTAGGAA 3120
*** ** ***** .** .** .** * .** :***** :** :** :** .*****
L-A-lus CAAGTTTATTACAGTCAACAAAATGCCAAGCATAAGATCGCGGTATGATAGCATCTAC 3180
L-A CAAGTTCATAACTGTTAACAAAATGCCAAGCATAAGATATCTAGAATGATAGCATCAC 3180
***** **:**:** ***** ** .** * .** * .** :*****: .**

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L-A-lus      GTTTAAC AAGATTAAAGACGCTGTTTCAAAGGGCAGCAGAAACACGATAGCCTTGAAACG 4320
L-A          ATTTAATAAGATTAAAGATGCCGTAGCTAGAGGGAGTAGGAGCACTATAGCTCTGAAACG 4320
             .*****
L-A-lus      TAAGGCGAAGATTCTGCAGTCAAGAACGACTTCGTC AATAAATCTGAATGGGAGAGAAC 4380
L-A          TAAGGCTAGGATAACATCTAAGAAGAATGAATTCGCTAAC AAGTCGGAATGGGAAAGGAC 4380
             *****
L-A-lus      TATGTACAAAGCTTACAAAGGTTAGCAGTATCTTATATGCTAAC TTGAGCAAATTCAT 4440
L-A          AATGTACAAAGCTATAAGGGTTGGCAGTCTCATACTATGCTAAC CTGAGCAAATTCAT 4440
             ;*****
L-A-lus      GAGCATACCACCCATGGCAAACATAGAATTCGGACAAGCTAGATTTGCGATGCAGGCCGC 4500
L-A          GAGTATACCACCAATGGCGAACATTGAATTTGGGCAGGCTAGATATGCTATGCAAGCAGC 4500
             ***
L-A-lus      CTTAGATAGTTCGGATCCTTTAAGAGCACTACAAATATTCCTTA TGAAGTGCTCGAACGAT 4560
L-A          CCTTGATAGTTCGATCCACTCCGGGCATTACAGGTCATACTGT-AATTGCCAAAAGAT 4559
             *
L-A-lus      GAGGGTTTTTACCCATATGC 4580
L-A          AATGGGAATTACCCATATGC 4579
             .*

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**Termination**



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L-A-lus      NIKASVTEIEEQDRLRRVTSIFKVDREVVKAISTAHRVCGGISTDPWAPVTTKIKTDNEY 1380
L-A          RVQSAVTAIKEQLDKRVTKIFGVGDDVVRDIHTAHRVCGGISTDTWAPVETKIIITDNEY 1380
             .:>:::* *:*:*:*:*:*:* * . :*: * *****.*** ** *****

L-A-lus      EIPYEIDDPFSPWPGVNDYAYKVVQNFGERLEFNKIKDAVSKGSRNTIALKRKAKISAVKN 1440
L-A          EIPYEIDDPFSPWPGVNDYAYKVVQNFGERLEFNKIKDAVARGSRNTIALKRKARITSKKN 1440
             *****:*****:*****:*****:*****:*****:*****:*****:*****

L-A-lus      DFNKSEWERTMYKAYKGLAVSYANLSKFMSIPPMANIEFGQARFAMQAALDSSDPLRA 1500
L-A          EFANKSEWERTMYKAYKGLAVSYANLSKFMSIPPMANIEFGQARYAMQAALDSSDPLRA 1500
             :* .*****:*****:*****:*****:*****:*****:*****:*****

L-A-lus      LQIFL 1505
L-A          LQVIL 1505
             **::*

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**FIG S1** (A) ClustalW comparison between L-A-lus and L-A (+) strand nucleotide sequences, that are 73% identical. Since the sequencing was done on cDNA clones, T (tyminine) instead of U (uracil) is used. Initiation and termination codons are indicated in blue. Two regions are highlighted: in red the frameshifting region in which the *gag* and *pol* genes overlap, and in green the encapsidation signal, that is strictly conserved. These two sequences correspond to the secondary structures depicted in Fig. 1B. (B) A diagram of Gag (black) and Pol (blue) fusion protein is depicted on top of the clustalW comparison between the Gag-Pol encoded by L-A-lus or L-A dsRNA genomes. They are 86% identical. We used the same black or blue colors to indicate the Gag or Pol amino acids, respectively. Three stretches of amino acids deviate from the average conservation; they are boxed and indicated on the right of the sequences. 1. A stretch of 14 amino acids (out of 20) downstream of H154, the aa involved in cap-snatching. 2. A variable region of 43 amino acids that is likely to separate Gag and Pol domains, and 3) The central third of Pol that contains the 4 consensus motifs (A-D, highlighted in red) conserved in RNA-dependent RNA polymerases from totivirus (1).

(1) **Bruenn JA.** 2003 A structural and primary sequence comparison of the viral RNA-dependent RNA polymerases. *Nucleic Acids Res.* **31**:1821-829.

FIG S2

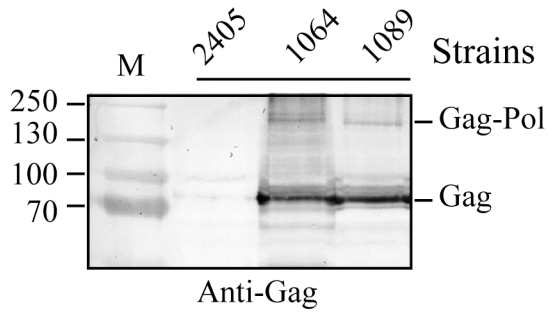


FIG S2 Western blot of lysates prepared from an L-A-o strain (2405), an L-A-containing strain (1064) or an L-A-lus-harboring strain (1089). Gag and Gag-Pol in the membrane are identified with L-A anti-Gag antibodies.

FIG S3

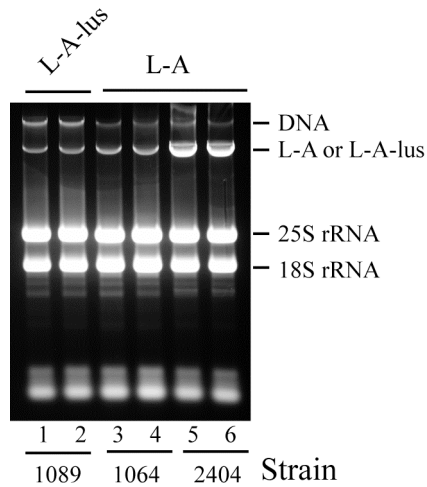


FIG S3 Different amounts of L-A or L-A-lus in yeast strains. Strains 1089, 1064 or 2404 are isogenic for nuclear markers ( $\alpha$  *kar1-1*, *his4-1*, Table 1) but carry different L-A viruses in their cytoplasm. Total RNAs (in duplicate) prepared after two days growth were separated in an agarose gel. The ethidium bromide-stained gel is shown. Note that strain 2404 (lanes 5 and 6) carries 5-10 fold more L-A than strain 1064 (lanes 3 and 4). The amount of L-A-lus in strain 1089 (lanes 1 and 2) and L-A in strain 1064 (lanes 3 and 4) is similar.



FIG S4. Clustalw comparison of L-A-lus, L-A-2 and L-A (sequences correspond to the 1.2 kb-RT-PCR fragments shown in Fig. 2B, spanning from nt 210 to 1454).

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L-A-lus      GTCTGTTTCAATGAGGGAAGTTCGTA CTTGGAGGGTATTGCAAAGAAATATCTGACCTTG 60
L-A-2       GTTTGTTTTAAATGAGGGGAGTTCCTACCTGGAAGGTATTGCGAAGAAGTACCTAACCCCTT 60
L-A         GTCTGCTTTAATGAAGGCAGTTCCTTACCTAGAAAGGTATTGCTAAAAAGTACCTAACTTTG 60
          ** ** * * *****.* * ***** ** * .*.***** ** .*.** * * .** *
L-A-lus      GACGGTGGCCTGGCCATTGATAACATCCTCAATGAATTGAAATCAACATGTGGTATACCA 120
L-A-2       GATGGTGGTTTGGCCATAGACAACATATTGAACGAGTTGAAGTCTACTTGTGGCATTCCCT 120
L-A         GATGGAGGACTTGCCATTGACAATGTCCCTCAATGAGTTGAGATCCACTTGGCGTATCCCA 120
          ** **:* * * *****:* * * .*. * * * ** .*****. ** **:* * * * * **:*
L-A-lus      GGTAATGCTGTCGCTTCTCATG CATAACAATTACGCTTGGAGATGGTACGATAATCAC 180
L-A-2       GGTAACGCTGTACCTCACATGCTTACAACATTACTTCGTGGAGATGGTATGATAATCAC 180
L-A         GGTAATGCTGTTGCGTCTCATGCGTATAATATTACATCCTGGCGTTGGTATGACAATCAC 180
          ***** ***** . * **:* ***** ** * * ***** ** * **.*:* ***** ** *****
L-A-lus      GTGGCATTACTCATGAATATGTTACGTGCGTACCATCTTCAAGTGTATCTGAACAAGGC 240
L-A-2       GTAGCATTACTTATGAATATGCTTCGCGCTTACCACCTGCAAGTGTGTCAGAACAGGGA 240
L-A         GTGGCACTGTTGATGAACATGTTGCGTGCCTACCACCTTACAAGTATTGACCGAACAGGGC 240
          ** .*** * . * ***** ** * * * * ***** * *****.*.*:* *****.*.
L-A-lus      CAGTATTCTGCCGGTTCATACCC TATGTACCACGATGGGCATGTCAAAATTA AACTTGAC 300
L-A-2       CAGTATTCTAGCAGGCTCTTACCCTATGTACCATGACGGACATGTCAAGATTAAGCTTGAT 300
L-A         CAATATAGCGCTGGAGATATCCCTATGTACCATGATGGACATGTCAAAATCAAGCTACCA 300
          ** .***:* * * * * .: :* ***** ***** ** * * .*****.* ** **.*:* .
L-A-lus      ACTCCTATCAGTGAGGATGATGCTCCTGACTCATTTAAGTGGCCGAGTGACCGGACAACA 360
L-A-2       GTGCCGATCGATGAGGATAATGCTCCTGATACTTTCAGATGGCCGAGTGACCGGGCAACA 360
L-A         GTGACTATCGATGACACGGCAGGCCAACACAATTCGCTTGGCCTAGTGACAGGTCTACT 360
          . . * ***.*** .. .:* **:. . .:* * . ***** *****.* ** **:*
L-A-lus      GACACTTACCCAGACTGGGCTCAGTTCTCAGAGTCTTCCCGTCTATTGACGTCCCATAC 420
L-A-2       GATACCTACCCGACTGGGCTCAGTTTTCAGAGTCTTCCCTCTATCGACGTGCCATAC 420
L-A         GATTTCGATCCTGATTGGGCACAGTTTCTGAATCATTTCATCAATCGACGTCCCGTAC 420
          ** :* * * * * * *****:* ***** **.*.* ** * * **:* * * ***** **.***
L-A-lus      TTAGATGTCAGGCCACTTACTGTTACCGAAGTTAATTTGTGTTAATGATGATGAGTAAG 480
L-A-2       CTAGATGTGAGACCGTTAACAGTCACGGAGGTTAACTTTGTCTGATGATGATGAGCAAA 480
L-A         CTAGATGTTAGCCATTGACCGTAACGGAAGTCAATTTCTGTGCTTATGATGATGAGTAAG 480
          ***** **.*. * * * * * * * * .** * * * * * * ***** ***** **
L-A-lus      TGGCACCGTCGGACTAACCTTGCTATTGACTATGAAGCGCCGGCGCTGGCAGACAAATTC 540
L-A-2       TGGCATCGCCGACTAATTTAGCGATCGACTATGAGGCACCTGCCCTGGCAGATAAATTC 540
L-A         TGGCATAGACGTACTAACTTAGCGATAGACTACGAGGCACCCAACTAGCTGATAAGTTC 540
          ***** . * * * ***** *:* * * ***** **.*.* * . **.*:* * * .***
L-A-lus      GCCTACCGTACGCCATTACGGTCCAGGATGCAGATGAATGGATTGAAGGTGATAGGACA 600
L-A-2       GCTTACAGACATGCCATAACTGTCCAAGATGCCGATGAGTGGATTGAGGGCGACAGGACT 600
L-A         GCTTACCGCCATGCGCTTACTGTTCAAGACGCTGACGAGTGGATAGAAGGCATAGAACT 600
          ** ***.* * * * * .:* * * * * .** * * * * .*****:* **.* ** **.***
L-A-lus      GATGATCAGTTTAGACCACCTTCTTCTAAGGTAATGATGTCGGCATTGCGTAAGTATGTT 660
L-A-2       GATGACCAATTTAGACCACCGACCGCTAAGGTCATGTTATCAGCACTACGTAAGTACGTT 660
L-A         GATGACCAGTTCGCCCCCCCTCGTCTAAAGTAATGTTATCGGCACTTCGTAAGTACGTTG 660
          ***** **.* * .*.*** ** :* *****.*.***:* **.*.* * ***** **
L-A-lus      AATCATAATCGACTTTACAACCA GTTCTATACGGCCGCTCAACTATTAGCTCAGATTATG 720
L-A-2       AACCACAATAGACTGTATAATCAGTTCTACACTGCTGCCAACTCTTGGCTCAGATAATG 720
L-A         AACCGTAACAGGCTGTACAATCAGTTTCTACACTGCAGCACA AACTGTTAGCTCAAATTATG 720
          ** * . * * .*.** * * * * ***** ** * * * * ***** **.******.***:*
L-A-lus      ATGAAACCAGTACCTA AACTGCGCTGAAGGGTATGCATGGTTGATGCACGATGCTCTGGTC 780
L-A-2       ATGAAACCTGTGCCTAATTGCGCAGAGGGATATGCCTGGTTGATGCACGACGCTTTGGTA 780

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L-A          ATGAAACCTGTCCCTAACTGCGCTGAGGGCTACGCTTGGCTGATGCATGACGCATTGGTC 780
*****: ** ***** *****: **. ** ** ** * ** * ** * ** * ** * ** * ** * ** * ** * ** *
L-A-lus     AACTTGCCGAAGTTCGGGTCCGTTAGAGGGCGTTACCCGTCTTACTTGCAGGTGACGCT 840
L-A-2       AACATACCTAAATTTGGGTCAATCAGAGGTCGCTACCCATTCTTATTGGCTGGCGACGCG 840
L-A         AATATACCAAATTTGGGTCTATTCGAGGAAGGTACCC'TTTT'TGTTATCAGGTGATGCA 840
** : **. ** ** . ** ***** . * . ***** . * ***** ** ** . * * . ** ** ** **
L-A-lus     GCCCTGATTCAGGCAACAGCACTTGAAGACTGGTCAGCAATTATGGCTAAGCCAGAACTG 900
L-A-2       GCTCTTATCCAAGCTACTGCTCTTGAGGATGGTCTGCTATATATGGCCAAACCCGAATTA 900
L-A         GCGTTGATTCAGGCTACAGCCCTAGAAGACTGGTCTGCTATCATGGCGAAACCCGAGCTG 900
** * ** ** . ** : ** : ** * ** : ** : ** * ** * ** * ** * ** * ** * ** * ** * ** *
L-A-lus     ATTTTTACCTACGCTATGCAGGTGCTGTCGCGTTGAACACTGGCTTATACTTACGGAGG 960
L-A-2       GTATTCAC'TTATGCAATGCAGGTAGCGGTAGCCCTGAACACTGGGCTTTACTTAAGGAGA 960
L-A         GTGTTAC'TTACGCGATGCAGGTGTCAGTAGCGTTAAACACCGGACTATACTTACGTCGC 960
. * ** ** ** ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** *
L-A-lus     GTCAAGAAAAC'TGGTTTCGGTACCCTGTTGACGATAGTTATGAAGACGGCGCATTTCTA 1020
L-A-2       GTTAAGAAGACTGGTTTCGGTACTACTATTGATGACAGCTACGAAGACGGCGCTTTCTTA 1020
L-A         GTTAAGAAAACAGGCTTCGGCACAAC'TATAGATGACAGCTATGAAGATGGAGCGTTTTTG 1020
** ***** . ** : ** ***** ** * ** . : ** * ** ** * ** * ** * ** * ** * ** * ** *
L-A-lus     CAACCTGAGACCTTCGTACAAGCTGCGATAGCTTGCTGCACTGGCCAAGATGCACCGCTT 1080
L-A-2       CAACCTGAGACGTTTGTACAGGCTGCTTTGGCTTGCTGCACTGGGCAGGACGCACCTTTG 1080
L-A         CAACCGGAGACGTTTCGTTACAGCCGCAC'TAGCATGTTGTACCGGACAAGATGCGCCCCTA 1080
***** ***** ** ** : **. ** ** * . ** : ** * ** ** * ** * ** * ** * ** * ** *
L-A-lus     AACGGTATGTCGATGTGTACGTGACATAACCAGATCTCCTTGAGTTCGATACTATAACA 1140
L-A-2       AACGGTATGTCAGATGTGTACGTTACATAACCTGATTTGCTAGAATTCGATACTATAACT 1140
L-A         AATGGGATGTCAGATGTGTATGTCAC'TTATCCAGATCTTCTAGAATTTGATGCTGTTACA 1140
** ** ***** : ***** ** ** : ** * ** : ** * ** * ** * ** * ** * ** * ** * ** *
L-A-lus     CGTGTCCCTGTTACGGTACTAGAACCTGAAGGCTATAATATACAGGATGGCGCCTTGGAA 1200
L-A-2       AGGGTGCCGGTCACTGTGCTAGAACCACAAGGATATAATATCGTTGACGGCGCTCTAGAA 1200
L-A         CAAGTACCCATCACGGTCATGAGCCCGCTGGCTATAACATGTTGATGATCATTTAGTG 1200
. . ** ** . * ** ** . : ** . ** . : ** . ***** ** : ** * . . * . : .
L-A-lus     GTGACAGGTGTTCCGATTGCC'TGCTCGCCTTACATGATTTCCCT 1245
L-A-2       GTGACGGGTGTTCCCAATAGCATGCTCGCCTATATGATATTCCCT 1245
L-A         GTTGTGGGTGTACCTGTGGCATGTTACCATACATGATATTCCA 1245
** . . ***** ** . * ** . ** * ** * ** * ** * ** * ** * ** * ** *

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**SeqA Name Length SeqB Name Length Score**

1	L-A	1245	2	L-A-lus	1245	73.0
1	L-A	1245	3	L-A-2	1245	74.0
2	L-A-lus	1245	3	L-A-2	1245	78.0

FIG S5.

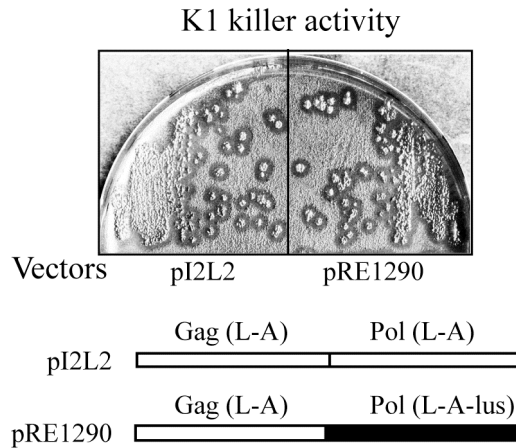


FIG S5 Hybrid virions made from Gag from L-A, and a hybrid Gag-Pol fusion protein have helper activity for M1 virus. Strain 2928 (L-A-o) was transformed with plasmids pI2L2 (expresses L-A capsid proteins) or pRE1290 (pI2L2 modified such as that the Pol part of L-A has been substituted by Pol from L-A-lus). Then M1 virions were introduced from strain 559 by cytoduction (strain 559 is L-A-o and M1 was maintained by proteins expressed from pI2L2). The K1 Killer activity of both types of cytoductants was tested on an MB plate seeded with sensitive strain 5X47. The size of halos surrounding the colonies is similar with both vectors, indicating a similar helper activity for M1 dsRNA by the virion proteins expressed from the plasmids. Under the killer assay a diagram of the Gag-Pol fusion protein in the virions is depicted. Pol part of L-A-lus in pRE1290 is indicated by black color.

Table S6. Oligonucleotides used

Name	Sequence (5' to 3' end)	Description
NR67	GACTCGAGTCGAGCGGCCGCTTTTTTTTTTTTTTTTTT	OligodT 3'RACE
NR68	GACTCGAGTCGAGCGGCCGC	Oligo 3'RACE
NR80	AATTAGCGGCCGCAGGGAAAATCATGTAAGG	L-A-lus (1437-1454)
NR81	AATTAGGATCCACTTGATCGAACAGACGG	L-A-lus (2035-2052)
NR86	AATTAGGATCCTCCCTCATTGAAACAGAC	L-A-lus (210-217)
NR87	AATTAGGATCCGATTATGCTTATAAAGTC	L-A-lus (4217-4234)
NR88	AATTAGGATCCGTCTGTTTCAATGAGGG	L-A-lus (210-226)
NR89	AATTAGATATCGATAAGTGTGCTCCGTAG	L-A-lus (3251-3268)
NR108	AATTAGCGGCCGCTAAACATAATAGAACCATC	L-A-lus (2070-2088)
NR109	AATTAGCGGCCGCGCATATGGGTAAAAACCC	L-A-lus (45634580)
NR112	AATTAGGATCCGTAATCCGGAGGCGCTCA	M2 (331-349)
NR113	AATTAGAATTCCATTCTCACCGTAGACCG	M2 (836-853)
RE548	AATTAGTCGACGAAAAATTTTAAATTCATATA	L-A (1-22)
RE549	AATTAGGATCCCGCAGCTACTGGAAATATCA	L-A (1444-1463)
RE587	<b>TTCGATTACGTTTAGCGGCCGCCCTCTACTAAAACAT</b>	L-A (2056-2083)
RE619	<b>TCTATTATGTTTACTCTACTAAAACATTG</b>	L-A (2054-2069), L-A-lus (2070-2082)

In bold specific sequences. The rest of nucleotides correspond to extensions (restriction sites and few extranucleotides).