



**Figure S1.** Validation of viral sequences in the original RNAs. M) 1Kb plus DNA ladder; A) WSMV and the samples are as follows (1-17): FO19, NS02, RP19, EL19, RA02, NE01, SM19, SH02, ST19, SA19, KM19, KW19, DC19, FW40, ME19, NT 19, and KE19; B) TriMV and the samples are as follows (1-7): EL19, NS02, RA02, DC19, NT19, SM19, and SH02; C) the only positive HPWMoV sample: RA02; D1) BYDV RdRp: KE19 and LE01; D2) BYDV CP: KE19 and LE01; E1) CYDV RdRp: EL19; E2) CYDV CP: EL19; F) *Mitovirus* sp. for the following samples (1-7): GL01\_19, KM19, NT19, ME19, LE01, KW19, and SA19; G) WULV for the following (1-4): GL20, KW19, FO19, and KE19; H) WaVPV RNA1 for the following samples (1-6): GL01\_19, ME19, KW19, EL19, FO19, and NS02; I) WaVPV RNA2 for the following samples (1-6): GL01\_19, ME19, EL19, KW19, NS02, and FO19. RNA extracted from a healthy wheat plant (no symptoms) was used as a negative control (-) for screenings.

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5' WaVPV RNA 2 AGTTTGTGCTGCGTCCTTGAGACGTGACGAAAATCGTACATTAGGTACTTCCCGACAC 60
5' WaVPV RNA 1 AGTTTGTGCTGCGTCCTTGAGACGTGACGAAAATCGTACTATAAGTACTTCCCGAACC 60

5' WaVPV RNA 2 CACAACAAACGAACCGACCCACACACGACACGACCACAAAT----- 100
5' WaVPV RNA 1 GACCACAAACCAAACACCACACCCGACC CGACCACACAACACCGTA 107

3' WaVPV RNA 2 GTCACCAATTATATGCAATCCCTTACCAATTTATTCT-GTCCGTTGTGGACAATATGCT 58
3' WaVPV RNA 1 GTTGCT-GTCGTTTAGTTTAGTTTATTTATTTACTTTTAGATCATTGTGATCAA----- 53

3' WaVPV RNA 2 ATATGTTATGCGCGTGAGTTATCACGTATTGAAATTTTCCTTAAAAACACGAAGGAG--- 114
3' WaVPV RNA 1 -----ACCTTTAAGTTGT-----TATT-----TTTTTCCAAAAACACGAGGAGAAAAG 95

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**Figure S2.** The alignment of the 5' and 3' UTRs of WaVPV RNA1 and RNA2. The sequence alignments showed a high percentage of similarity in the 5' end highlighted in yellow.