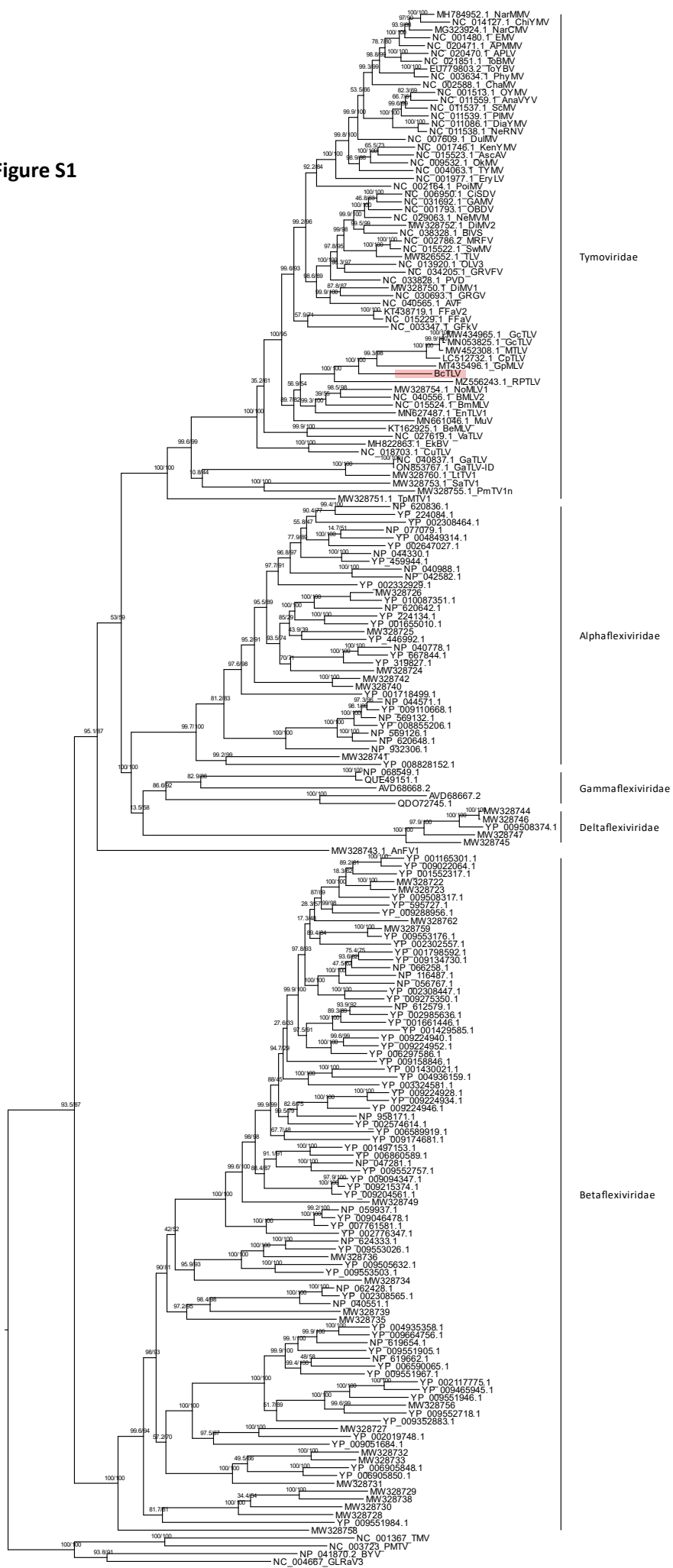


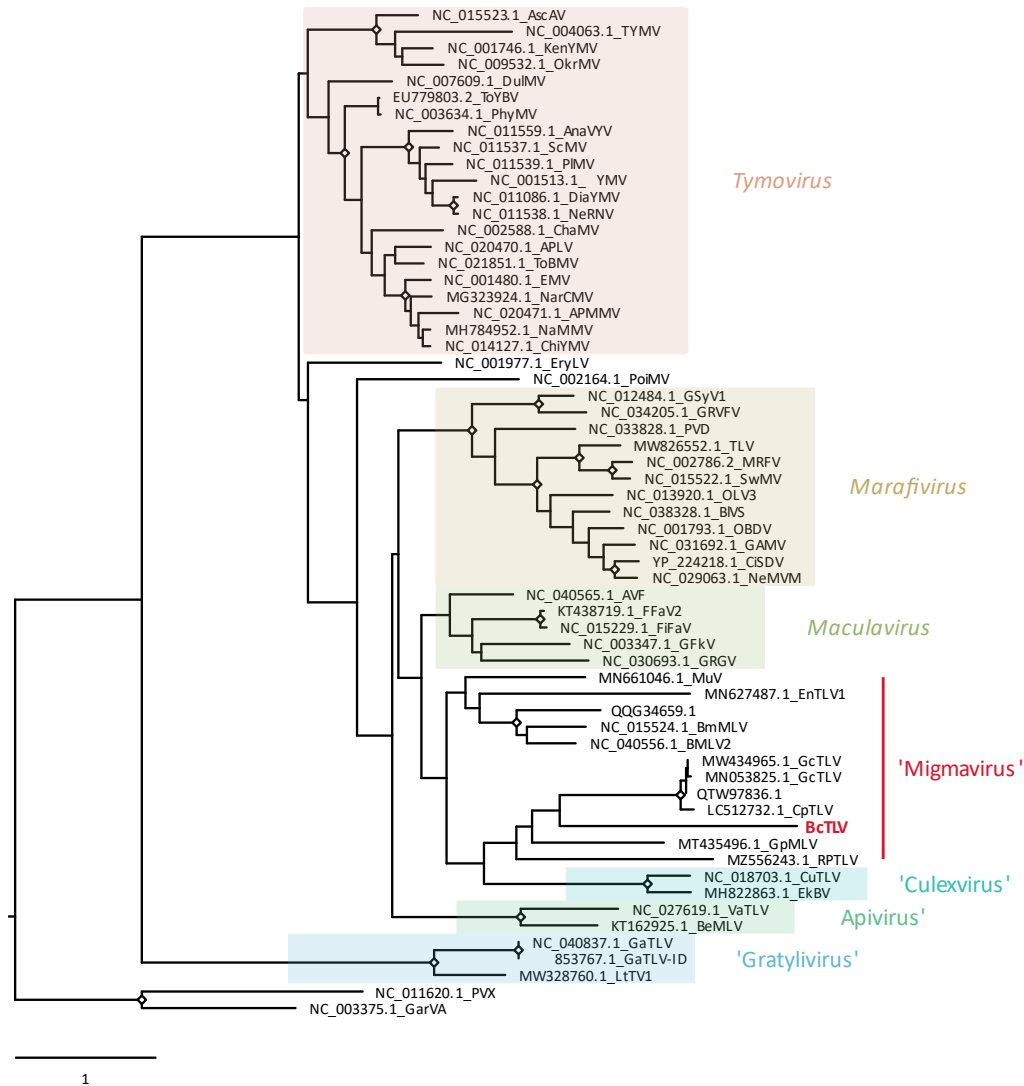
Supplemental Table S1. List of primer pairs used in this study. The sequences for all primer pairs used for RT-PCR testing of each virus (BcTLV, BcSLV-1 and BcSLV-2) are given in the table, with start and end positions based on the corresponding contig assembled from HTS data as described in main text, T_m for each primer as calculated by Primer3 implemented in Geneious Prime with default parameters, and length of predicted PCR product.

Name	Start	End	Sequence	T _m (°C)	Length (bp)
BcTLV_A_F	982	1001	TTCGAACTCTTCGCGTCACA	60.0	702
BcTLV_A_R	1664	1683	CACACTCGGGTTCCGAAGAA	60.0	
BcTLV_B_F	4507	4526	CCGAGCATCTCATCCAGGTC	60.0	421
BcTLV_B_R	4908	4927	GAATGGCCGACGCTGAATTC	60.0	
BcTLV_C_F	6171	6190	CCTCGGAGGAAGTCCCTACA	60.0	516
BcTLV_C_R	6667	6686	CGTGTTTGTACGCGGGTTTT	60.0	
BcSLV1_A_F	1573	1592	GCCCTTCAAGTGCCAACTTG	60.0	467
BcSLV1_A_R	2020	2039	CGTGCTTTCGATAACGGCTG	60.0	
BcSLV1_B_F	4023	4042	CGAGGCTCGTATGGAGAACC	60	975
BcSLV1_B_R	4978	4997	TATGTTGCCCCCATAGGGGA	60.0	
BcSLV2_A_F	274	293	AATGGGCAGCATTGTTTGGG	59.7	766
BcSLV2_A_R	1020	1039	TGCCTGAAACCATACCCAC	60.0	
BcSLV2_B_F	1189	1208	AGACAACGTGGACCAAGCTC	60.3	760
BcSLV2_B_R	1929	1948	CAGCCGTA CTCAACAGGAGG	60.1	
BcSLV2_C_F	2849	2868	GGCTGGGATTGGACAGTACA	59.4	581
BcSLV2_C_R	3407	3429	GTGAGTTTTGCTCCCATCTTAGC	59.9	

Supplemental Figure S1



Supplemental Figure S1. Phylogenetic analysis of the replicase proteins of members of the order *Tymovirales*. maximum-likelihood phylogenetic tree was inferred from the alignment of the replicase aminoacid sequences from representative viruses of the *Tymovirales* order, using IQtree2 with ModelFinder to choose the best fit model and branch support estimated using SH-like approximate-ratio test (SH-aLRT) and UltraFast bootstrapping (UFbootstrap), with 1000 replicates. Both bootstrap values are indicated at the nodes (SH-aLRT/UFbootstrap). The branch for BcTLV is highlighted in light red. The tree was rooted using an outgroup comprising replicase domains of viruses from the *Martellivirales* and *Hepellivirales* orders, with the root placed on the edge connecting the ingroup and outgroup. The scale bar shows the number of substitutions per site.



Supplemental Figure S2. Phylogenetic analysis of the coat proteins of members of the family *Tymoviridae*. maximum-likelihood phylogenetic tree was constructed from the alignment of the coat protein aminoacid sequences from representative viruses of the *Tymoviridae* family, using IQtree2 with ModelFinder to choose the best fit model, and branch support estimated using UltraFast bootstrapping (UFbootstrap) and SH-like approximate-ratio test (SH-aLRT). The tree was rooted using outgroup sequences of coat proteins of viruses from the *Alphaflexiviridae* family, with the root placed on the edge connecting the ingroup and outgroup. Significant bootstrap support, as estimated by SH-aLRT and UFbootstrap values, is indicated by a diamond shape at the concerned internal nodes (SH- LRT > 0% and UFbootstrap > %). The scale bar shows the number of substitutions per site.