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Phylogenetic and diversity analyses of *Garlic common latent virus* based on the TGB and CP gene sequence

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ELECTRONIC SUPPLEMENTARY MATERIAL (ESM)

The authors are fully responsible for both the content and the formal aspects of the electronic supplementary material. No editorial adjustments were made.

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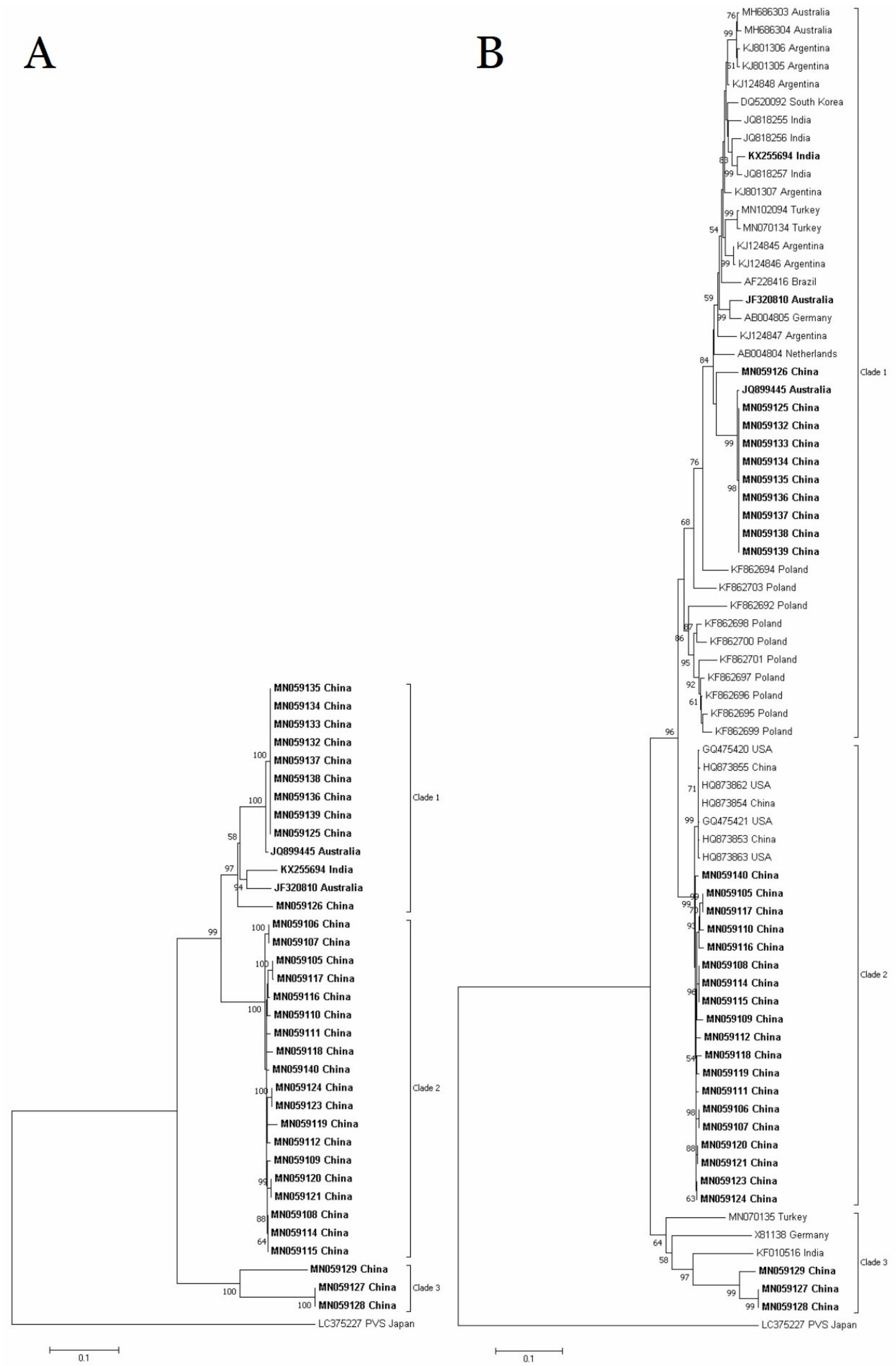

Figure S1. Neighbour-Joining phylogenetic tree of the nucleotide sequences of the GarCLV (A) TGB genes and (B) CP gene

The isolates printed in bold were used in both the TGB and CP comparisons; the bootstrap values on each branch were supported by 1 000 replicates; only values greater than 50% were shown; a Japanese *potato virus S* (PVS) isolate was used as the out-group; 35 and 73 isolates were included in TGB and CP comparison, respectively

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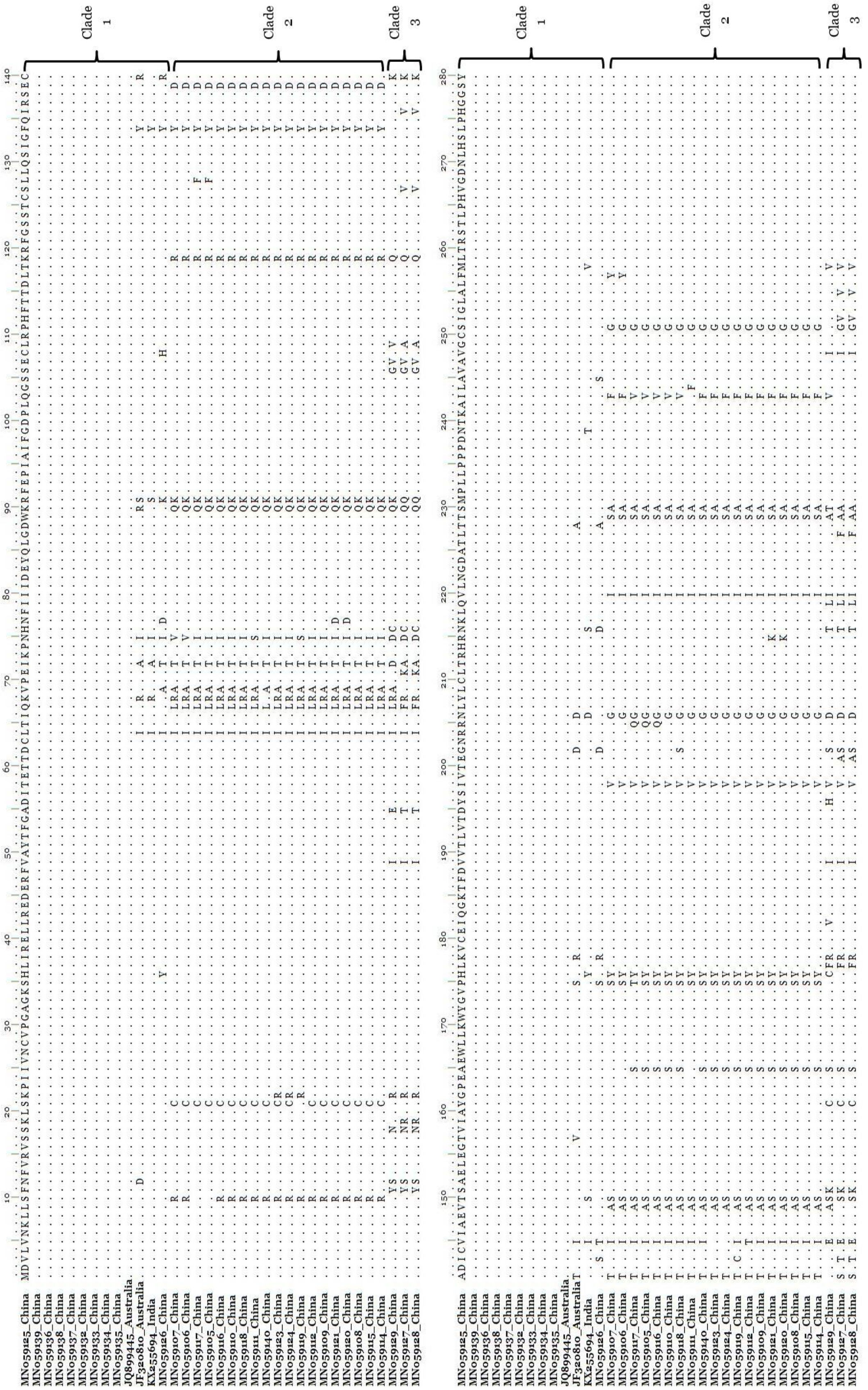

Figure S2. Multiple alignment of the amino acids of the TGB genes

TGB 1 – position 1–230; TGB 2 – position 231–338; TGB 3 – position 339–406

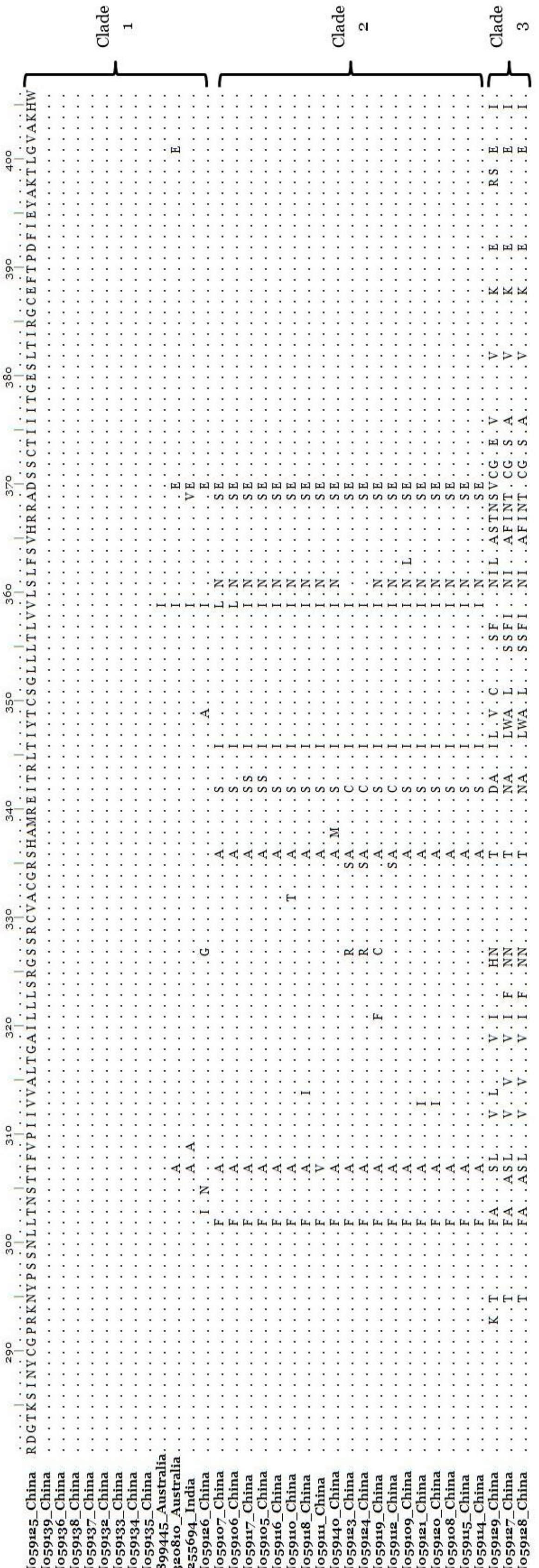

Figure S2.to be continued