



Figure S1. Sequence polymorphism within Wisteria vein mosaic virus (WVMV) haplotypes identified with DnaSP software, version 6.12.03, with the indication of amino acid substitutions within the N-terminal coding region of the capsid protein (amino acid residues 1-151). WVMV isolates corresponding to each haplotype are indicated in brackets. Detailed information on individual isolates can be found in Table S2. Analysis of codon amino acid polymorphism was conducted using Unipro UGENE software, version 44.0, and graphical output was generated with BioEdit Sequence Editor, version 7.0.9.