

**Table S2.** Summary of BLASTX analyses of contigs *de novo* assembled from reads generated by high-throughput sequencing (HTS) of the *Wisteria sinensis* tree affected by Wisteria mosaic disease (WMD).

<b>Virus genes</b>	<b>Contig number</b>	<b>Average length (nt)</b>	<b>Min length (nt)</b>	<b>Max length (nt)</b>	<b>Average identity (%)</b>
<i>Potyvirus</i>	133	250.17	101	9,694	91.4
<i>Badnavirus</i>	2	371.5	333	410	82.7
<i>Deltapartitivirus</i>	1	397.0	397	397	97.6
<i>Alphaendornavirus</i>	2	165.0	130	200	51.1

The *de novo* assembly was built with MEGAHIT v. 1.2.9 assembler. The average identity values refer to the local BLASTX alignment on RefSeq viral proteins, performed with the NCBI BLAST+ search tool. The expected value (E-value) cutoff was set at 0.001. Contigs showing alignment hits shorter than 100 nt in BLASTN search against RefSeq nucleotides were preliminarily excluded from this analysis.