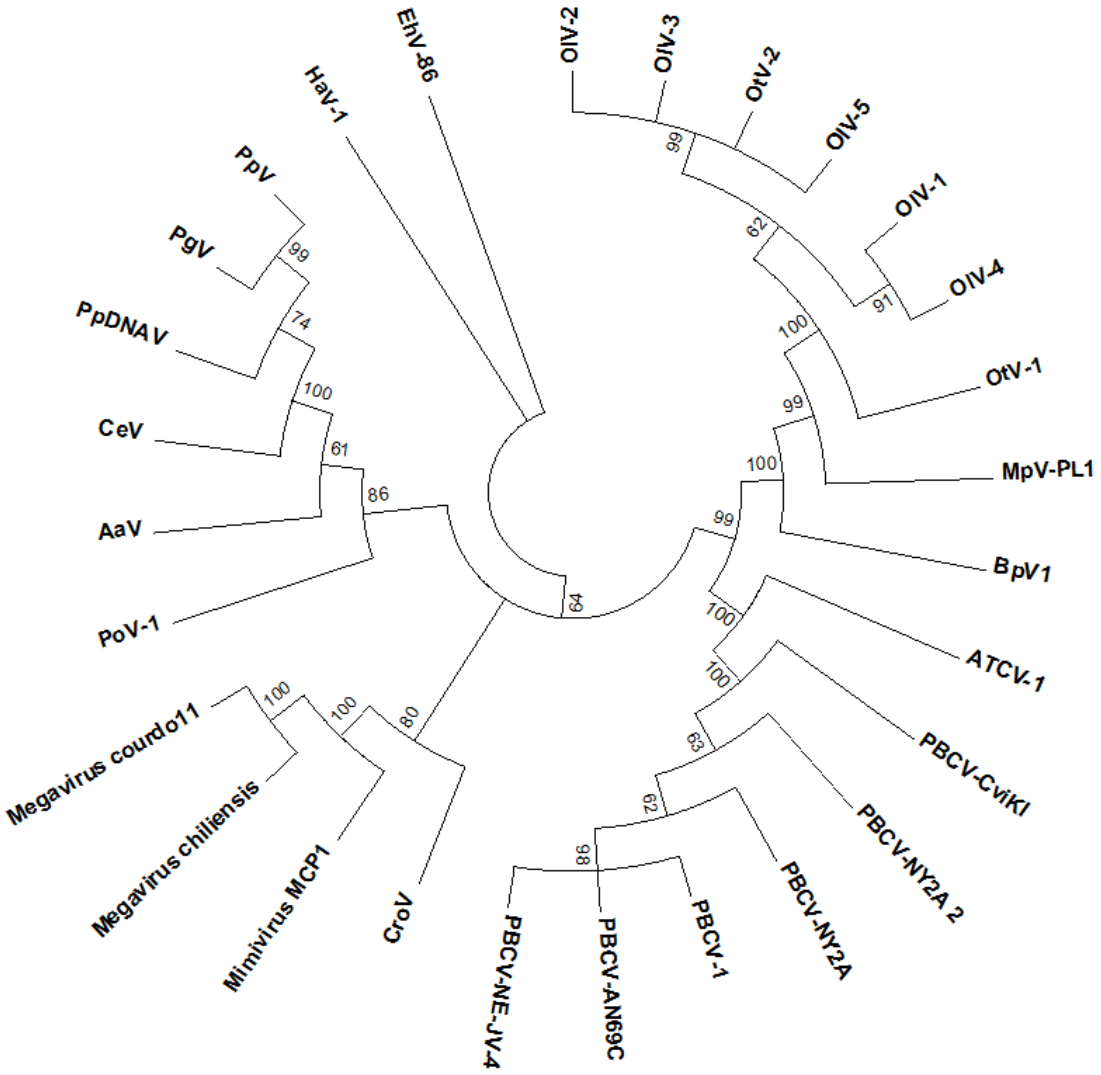

SI Figure 4. Phylogenetic clustering of PpDNAV with other large algal *Megaviridae*. Alignment was performed using the default settings of MAFFT [1], and the Neighbour-joining method (midpoint-rooted) [2] was used to construct a tree from 28 viral MCP sequences using MEGA7 [6]. The final tree was based on 336 ungapped positions, 500 resampling permutations, and was collapsed for bootstrap values <50. The tree shows that PpDNAV clusters with the algal-infecting *Megaviridae*, separate to the *Phycodnaviridae*.