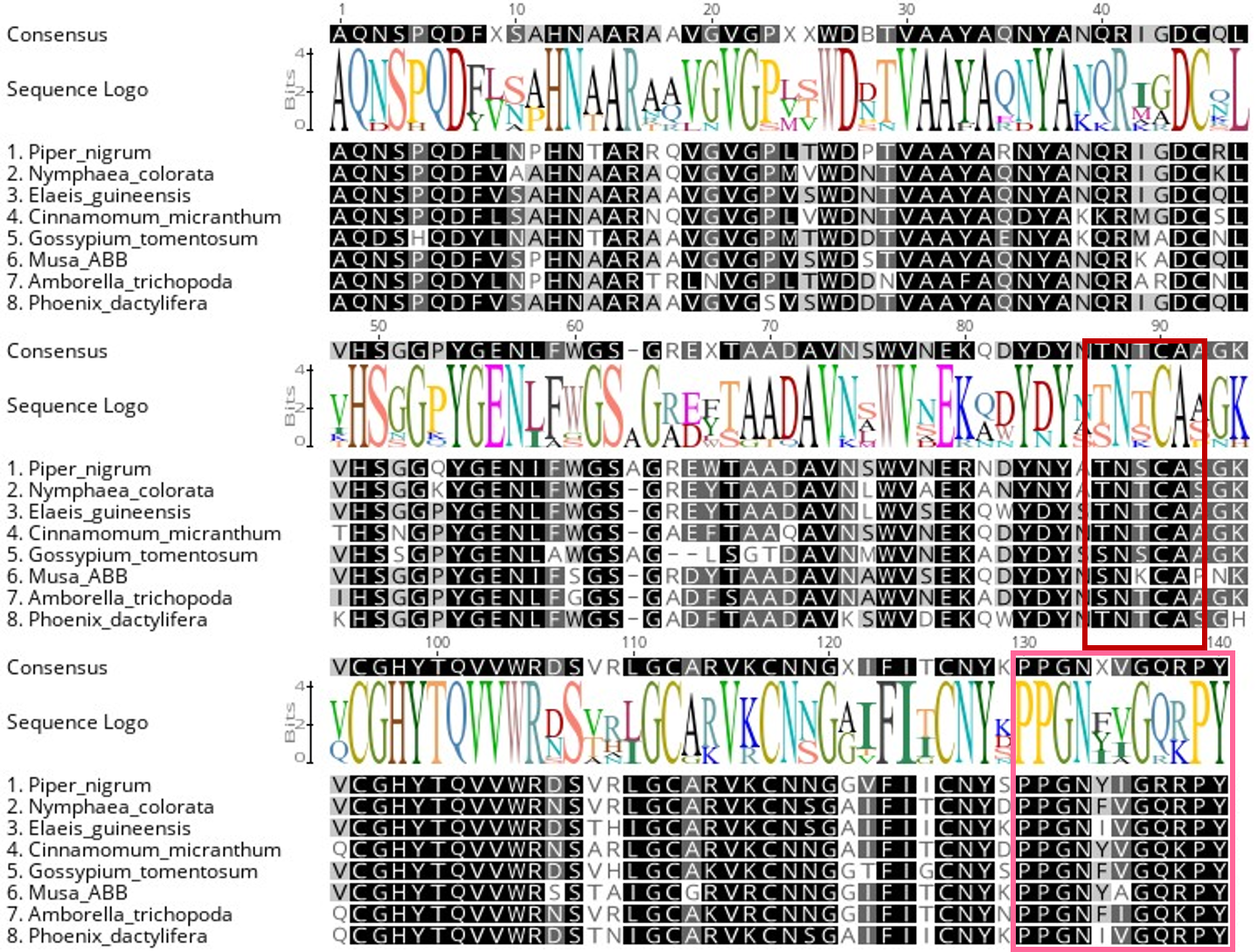
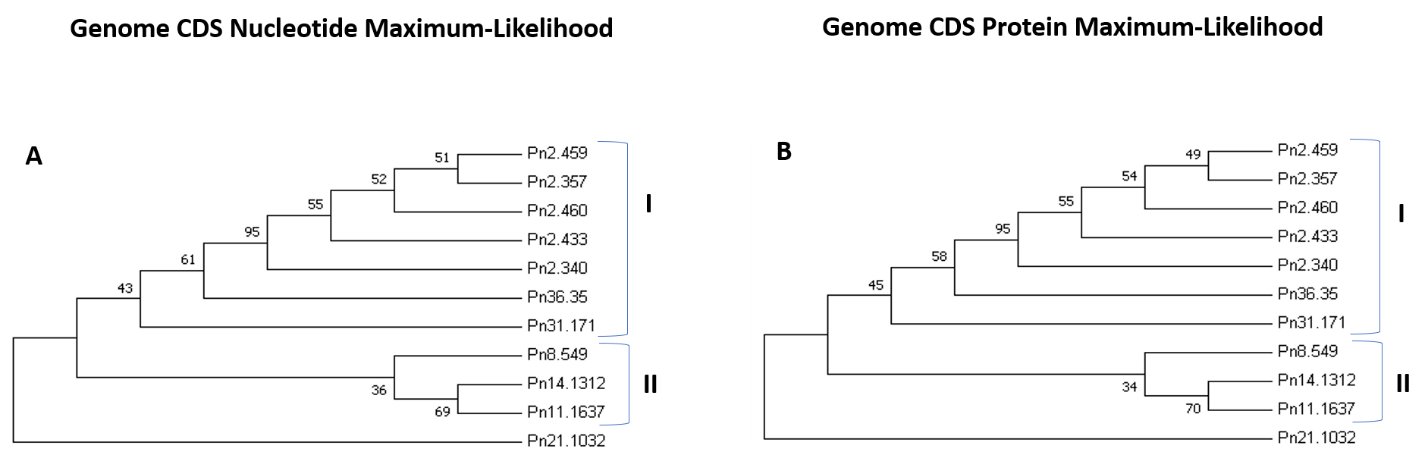
**Genome-wide analysis of *PR-1* genes from *Piper nigrum* reveals critical role in defense response during *Phytophthora capsici* infection**

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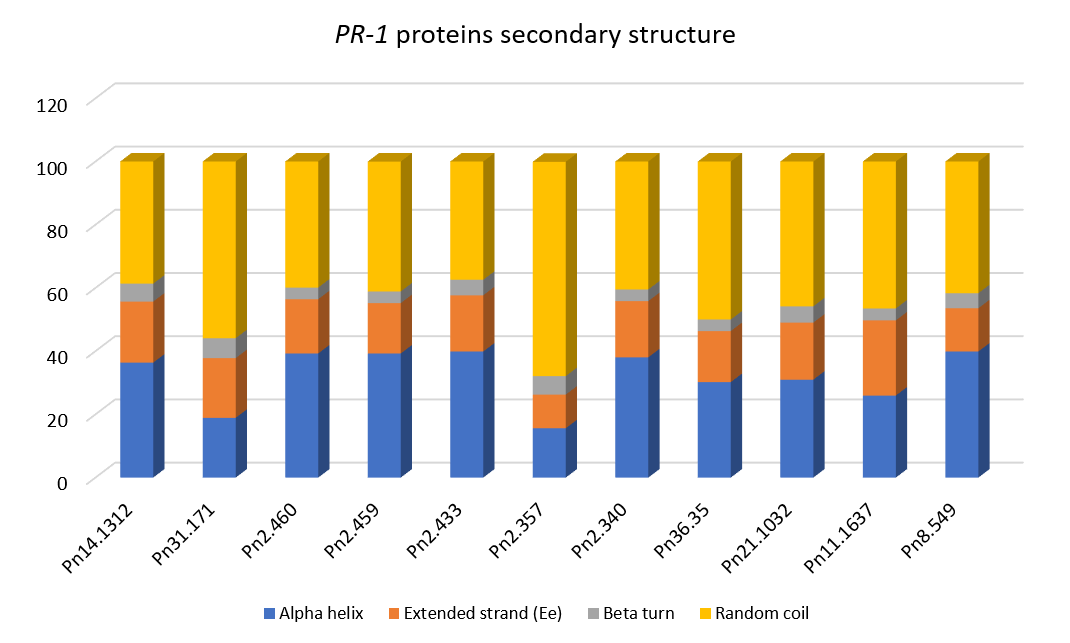
**Supplementary Figures**



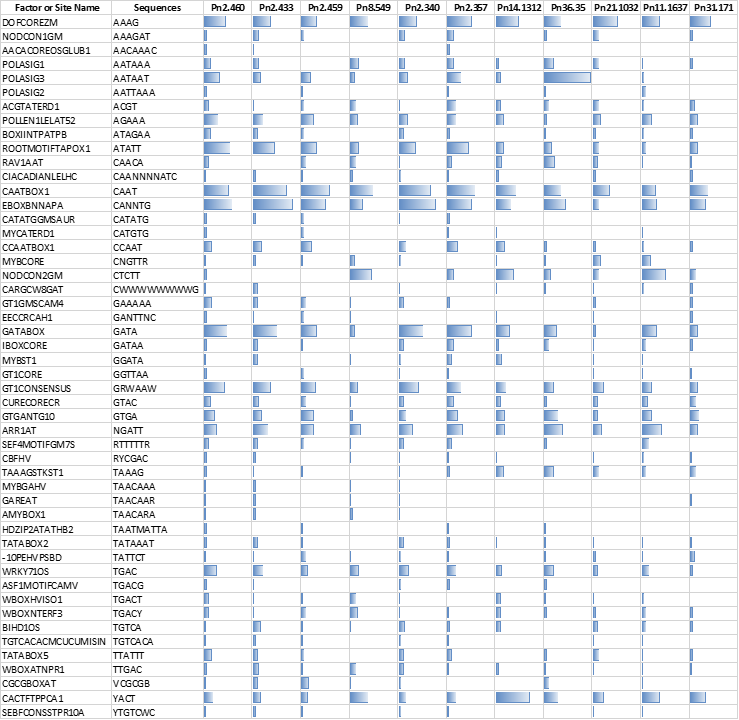
**Fig. S1:** The amino acid sequences from *Piper nigrum, Nymphaea colorata, Elaeis guineensis, Cinnamomum micranthum, Gossypium tomentosum, Musa ABB, Amborella trichopoda and Phoenix dactylifera* were aligned using Geneious bioinformatic software (https://www.geneious.com/) with default settings. The conserved domains are highlighted in different colours. CAP domain structure with caveolin-binding motif (CBM) and CAP-derived peptide (CAPE) are shown in red and pink boxes.



**Fig. S2: (A&B)** Phylogenetic analyses of *Piper nigrum PR-1* nucleotide and protein sequences. The phylogenetic tree was constructed using MEGA 7.0. by the maximum-likelihood (ML) method with 1000 bootstrap replicates and default parameters. The *PnPR-1* family genes were divided into two major groups, groups I and II.



**Fig. S3:** Details of predicted **s**econdary structure of *PnPR-1* proteins.



**Fig. S4**: Analysis of *cis*-acting elements in *PnPR-1* promoters using the NewPlace online server. The number of elements in each gene were represented in data bars.