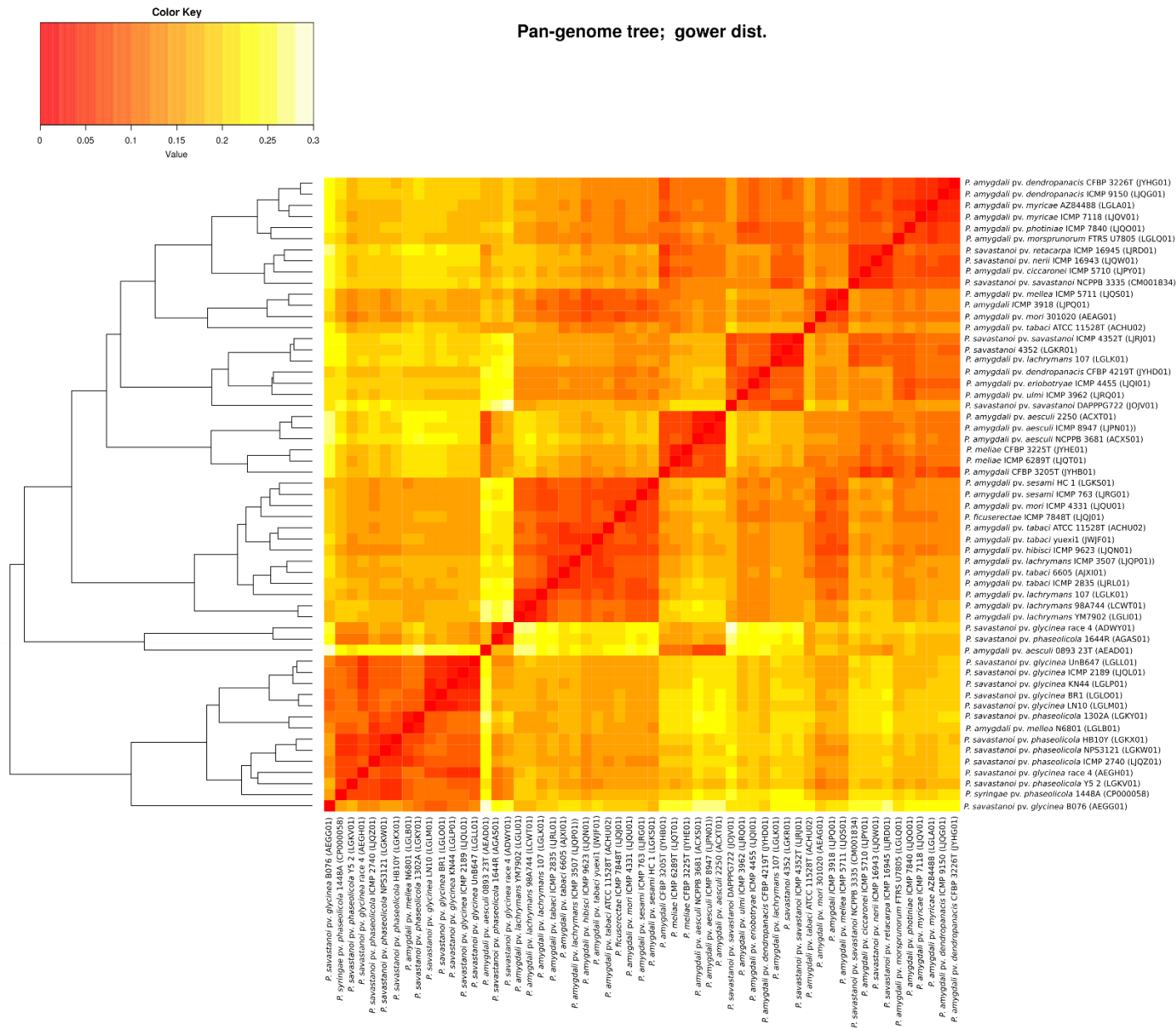**Supplemental Figure S8. Core and pangenome analysis of the 57 strains in the phylogenomic group IV (*P. amygdali, P. ficuserectae, P. meliae* and *P. savastanoi*).** (A) Venn diagram of core genomes generated by the BDBH, COG, and OMCL strategies. (B) Estimate of core genome size with the Tettelin (blue) and Willenbrock (red) fits. (C) Estimate of pangenome size with the Tettelin fit. (D) Venn analysis of pangenomes generated by COG and OMCL. (E and F) Partition of the OMCL pangenomic matrix into shell, cloud, soft-core, and core compartments.

(G)

Supplemental Figure S8. Core and pangenome analysis of the 57 strains in the phylogenomic group IV (*P. amygdali, P. ficuserectae, P. meliae* and *P. savastanoi*). (G) Heatmap representing the degree of similarity of the genomes based on the average amino acid identities of their protein coding genes. High similarities are indicated in red and low similarities in yellow.

Supplemental Figure S8. Core and pangenome analysis of the 57 strains in the phylogenomic group IV (*P. amygdali, P. ficuserectae, P. meliae* and *P. savastanoi*). (H) Phylogenetic tree of the concatenated amino acid sequences of 1,477 monocopy proteins of the core genome defined in the 57 genomes analyzed. 398,402 amino acid positions were used to construct the tree. Bootstrap values are indicated in the nodes.