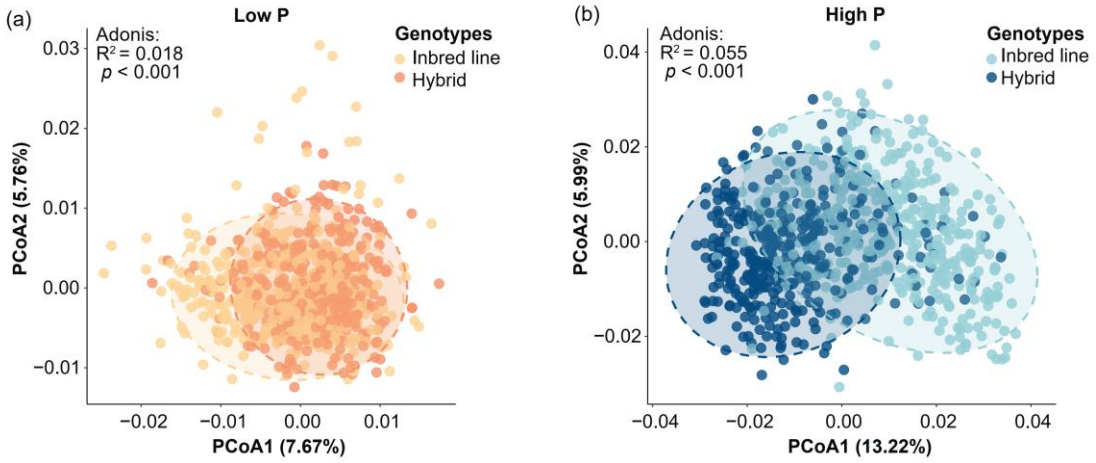
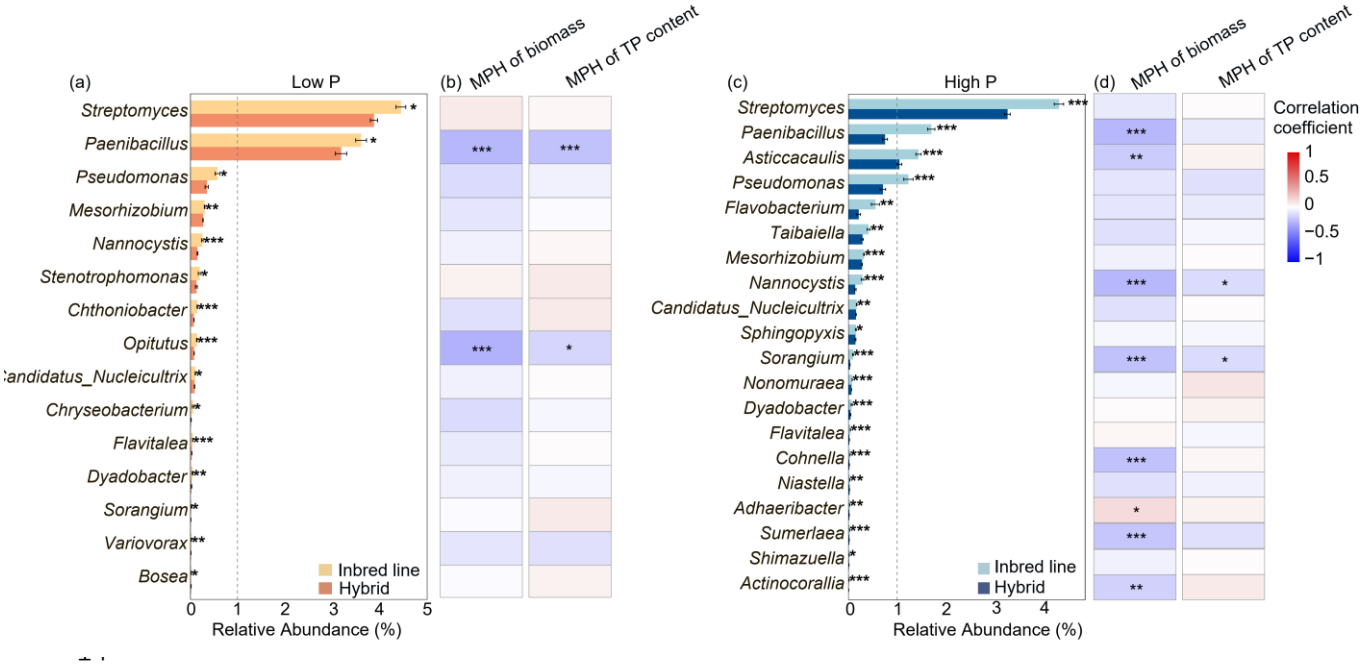
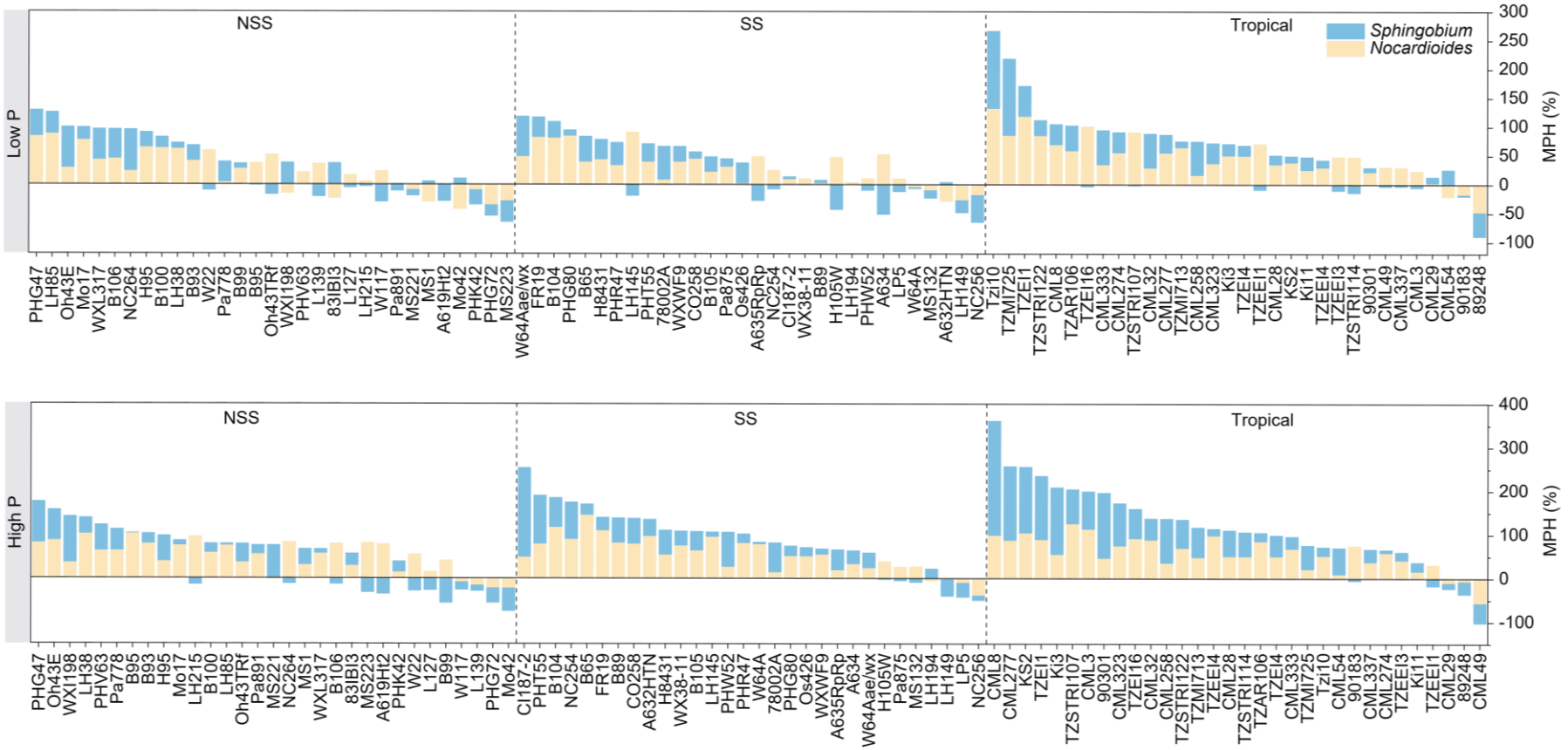
Supplementary Fig. 1 Principal coordinate analysis (PCoA) revealed the difference of the rhizobacterial composition at ASV level between inbred lines and hybrids under low P treatment and high P treatment respectively. Permutational multivariate analysis of variance (PERMANOVA) with Bray-Curtis distance was applied to assess statistical significance of differences of inbred lines and hybrids.



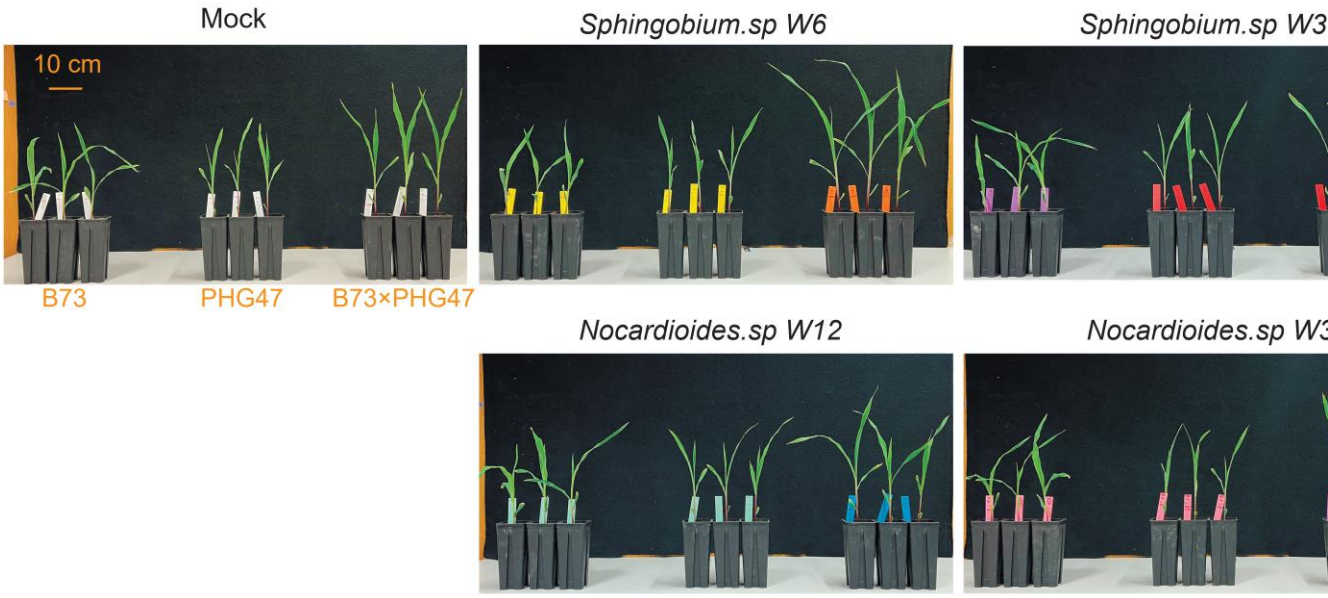
Supplementary Fig. 2 a, c Bar plots show significant differences in the relative abundance of rhizobacterial genera between hybrids and inbred lines under low and high P conditions. **b, d** Correlation heatmaps illustrates the relationships between the mid-parent heterosis (MPH) of rhizobacterial genera relative abundance and the MPH of biomass (shoot dry weight) and total P content in the shoots under low P and high P conditions.



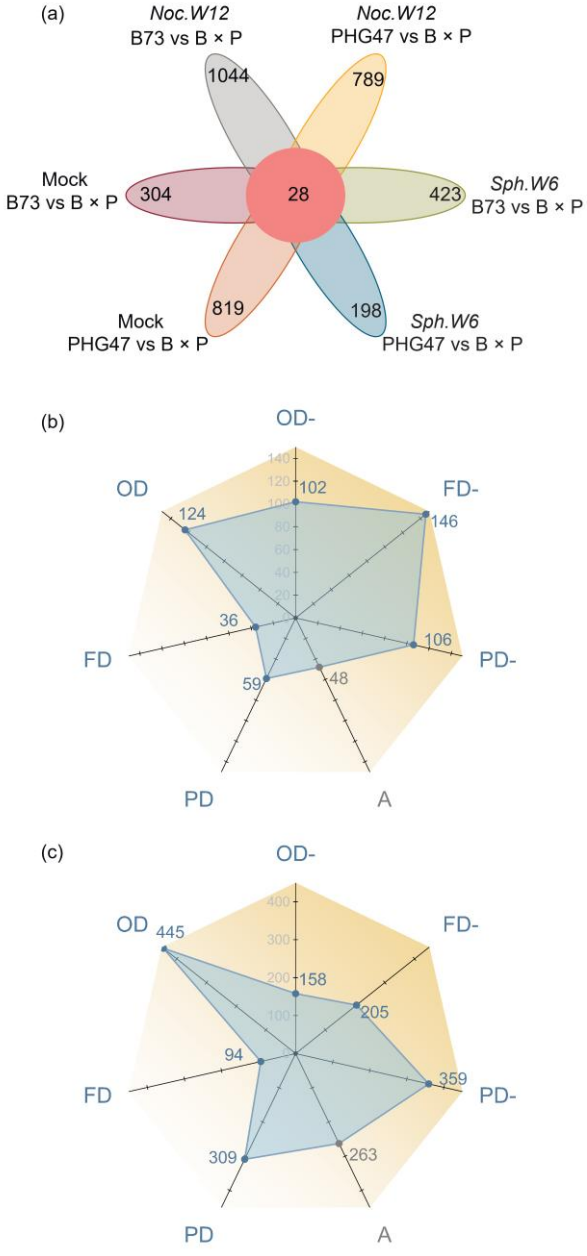
Supplementary Fig. 3 The bar plots illustrate the cumulative distribution of mid-parent heterosis (MPH) for *Nocardioides* (yellow) and *Sphingobium* (blue) across 93 maize crossing triplets. These triplets share the common maternal genotype B73, with paternal lines representing three heterotic groups, including non-stiff stalk (NSS), stiff stalk (SS), and tropical varieties, under low P and high P conditions.



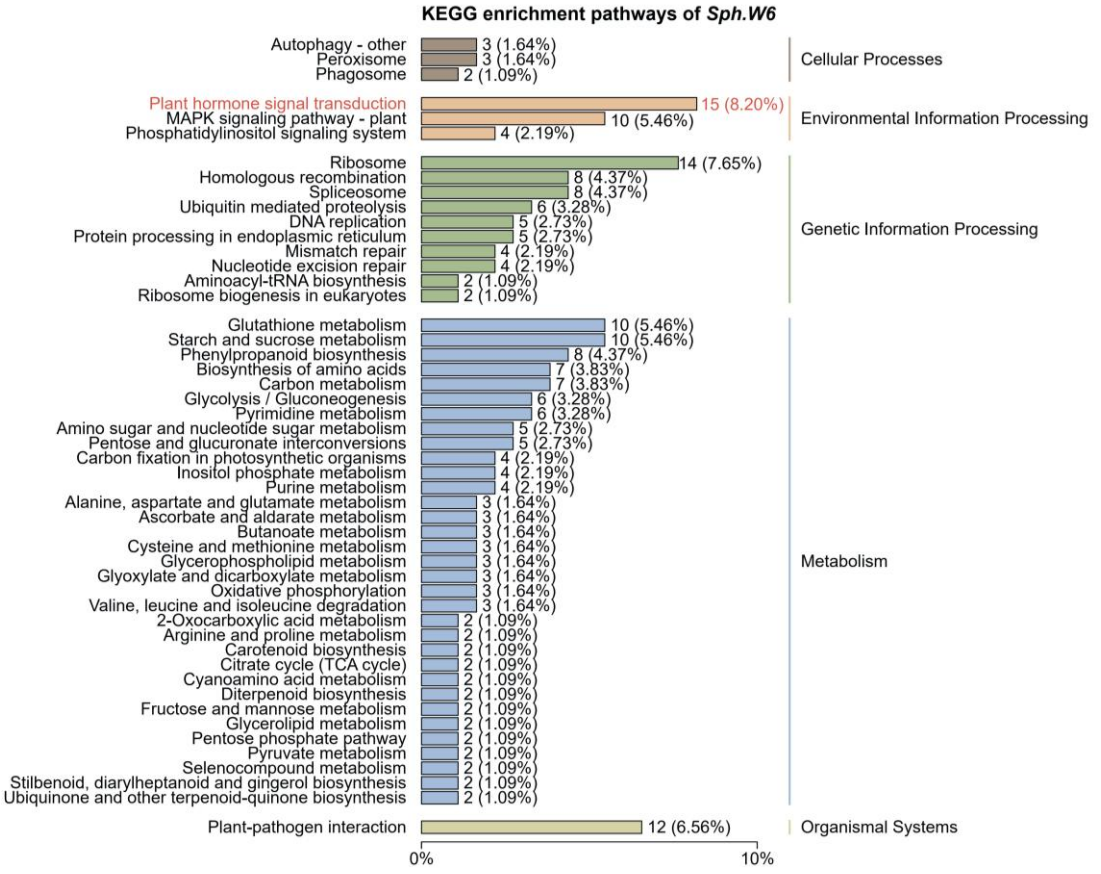
Supplementary Fig. 4 Two weeks plants of PHG47 (paternal inbred line), B73 (maternal inbred line), and corresponding hybrid (B × P) with inoculated *Sphingobium* and *Nocardioides* strains under low P treatment.



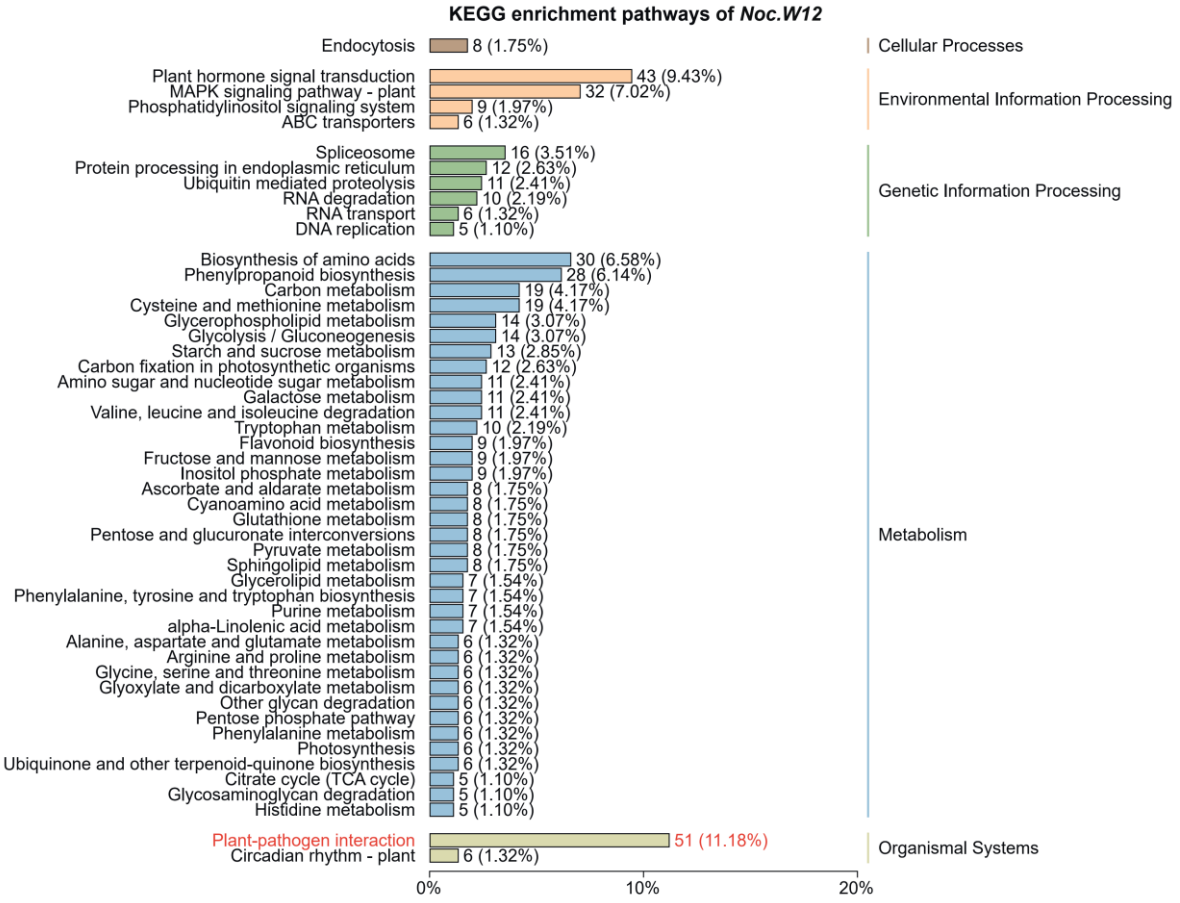
Supplementary Fig. 5 a Venn diagram was used to identify special differentially expressed genes (DEGs) between inbred lines and hybrid under different strains inoculation. **b, c** dominance patterns of DEGs of enriched in hybrid (compared with inbred lines) were further characterized under *Sphingobium* W6 (b) and *Nocardioides* W12 (c) inoculation. Note: *sph.W6* means *Sphingobium* W6; *Noc.W12* means *Nocardioides* W12. Dominance patterns: additive (A: D/|A| < 0.2), up-regulated partial-dominance (PD: 0.2 ≤ D/|A| < 0.8), down-regulated partial-dominance (PD-: -0.8 ≤ D/|A| < -0.2), up-regulated full-dominance (FD: 0.8 ≤ D/|A| < 1.2), down-regulated full-dominance (FD-: -1.2 ≤ D/|A| < -0.8), up-regulated overdominance (OD: D/|A| ≥ 1.2) and down-regulated overdominance (OD: D/|A| ≤ -1.2)



Supplementary Fig. 6 KEGG enrichment pathways of the differentially expressed genes with non-additively genes expression pattern that enriched in hybrid (compared with inbred lines) (NAE-DEGs) with *Sphingobium* W6 inoculation.

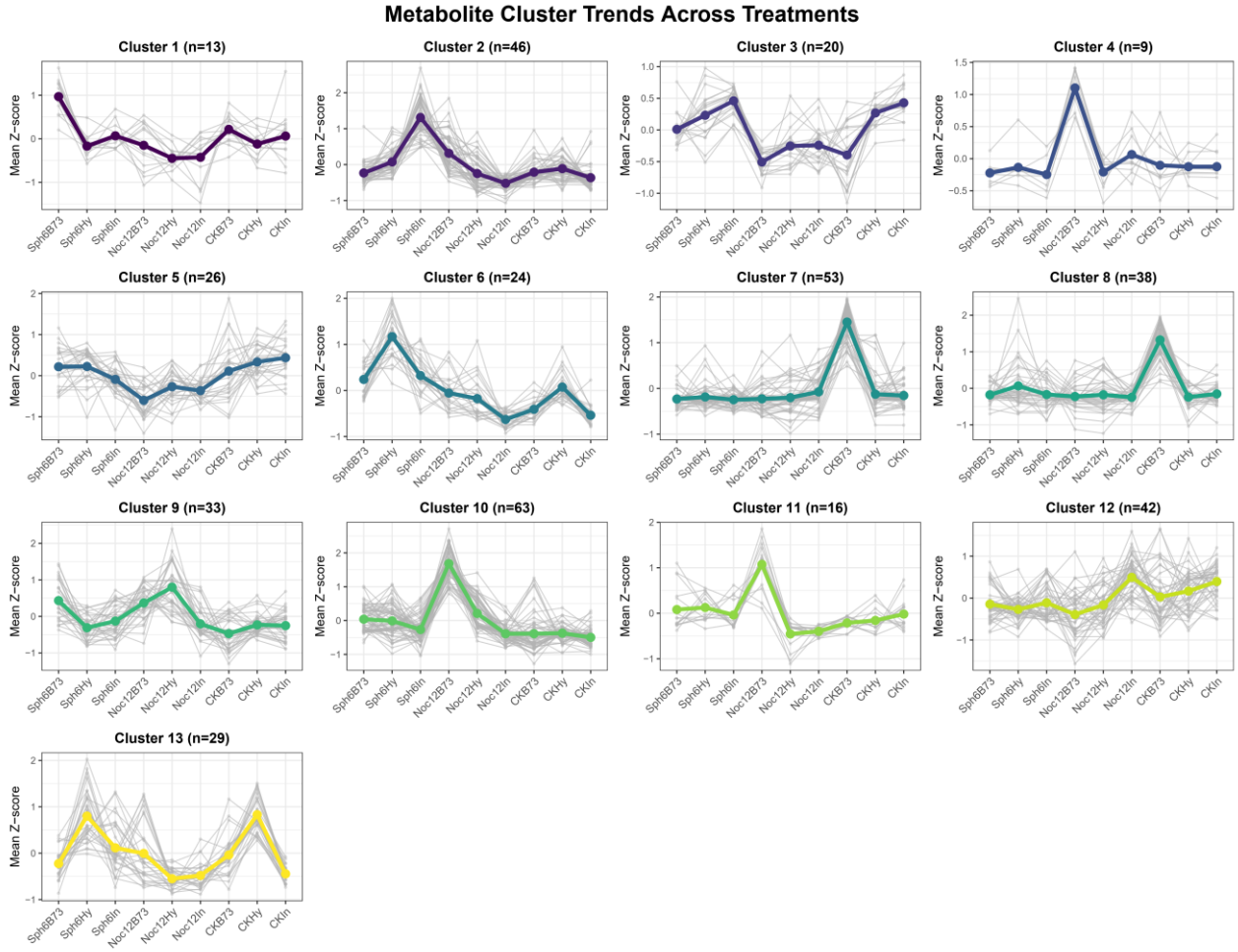


Supplementary Fig. 7 KEGG enrichment pathways of the differentially expressed genes with non-additively genes expression pattern that enriched in hybrid (compared with inbred lines) (NAE-DEGs) with *Nocardioides* W12 inoculation.

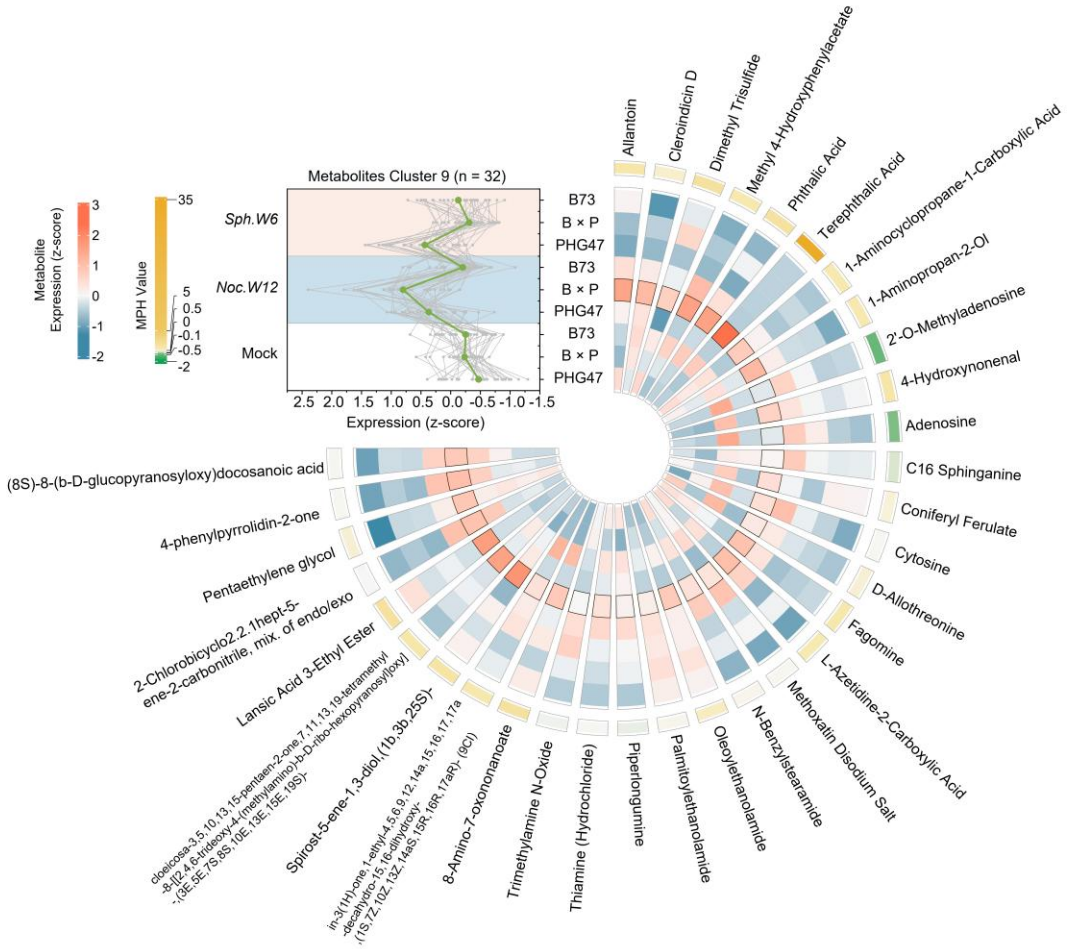


Supplementary Fig. 8 The GO classifications of the differentially expressed genes with non-additively genes expression pattern that enriched in hybrid (compared with inbred lines) (NAE-DEGs) on biological process were further identified in main plant-pathogen interaction pathways with *Nocardioides* W12 inoculation.

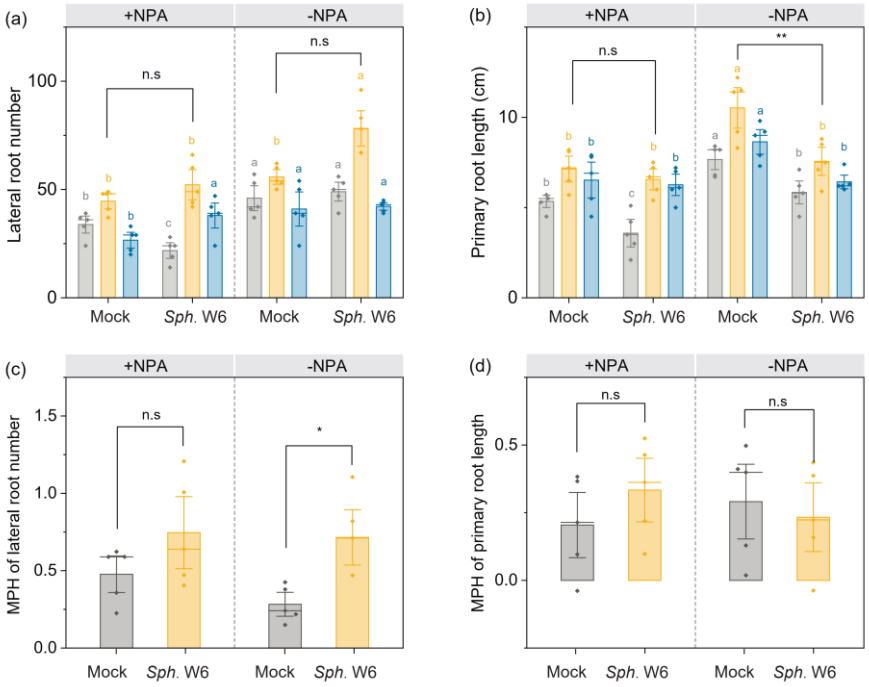
- **Supplementary Fig. 9 Treatment-specific metabolite clusters identified by k-means analysis.** K-means clustering partitioned the metabolites into distinct clusters, thereby delineating their treatment-specific accumulation profiles.



Supplementary Fig. 10 Metabolite cluster specifically enriched in the hybrid following *Nocardioides* W12 inoculation, identified by k-means clustering analysis. The inner ring shows z-score-normalized metabolite abundance across treatments, whereas the outer ring represents the corresponding mid-parent heterosis (MPH) values of individual metabolites.



Supplementary Fig. 11 The root traits and heterosis in response to bacterial inoculation under different NPA treatment. a,b, Lateral root number (**a**) and total root length (**b**) of the triplet under different combinations of *Sphingobium* W6 inoculation and NPA treatment. **c,d,** Mid-parent heterosis (MPH) for lateral root number (**c**) and total root length (**d**) under different combinations of *Sphingobium* W6 inoculation and NPA treatment. For all box plots (**a-b**), center lines indicate medians, box limits indicate the first and third quartiles, and whiskers represent the minimum and maximum values ($n = 5$ independent biological replicates). Statistical significance between inoculation treatments was assessed using two-sided Wilcoxon rank-sum tests ($P < 0.05$, $P < 0.01$, $P < 0.001$; n.s., not significant). Different lowercase letters indicate significant differences among inoculation treatments within the same genotype, as determined by one-way ANOVA followed by Duncan's multiple range test ($P < 0.05$).



Supplementary Fig. 12 The circularized genome map of *Sphingobium. W6.* The outermost ring represents the total genome size, with each tick marking 5 kb. The second and third rings show genes on the positive and negative strands, respectively, with colors indicating COG functional categories. The fourth ring displays the distribution of repetitive sequences. The fifth ring denotes tRNA (blue) and rRNA (purple). The sixth ring represents GC content: light yellow peaks indicate regions where GC content exceeds the genome-wide average, with taller peaks reflecting greater deviation; blue peaks indicate regions below the average. The innermost ring depicts GC skew, where dark grey marks regions with more G than C, and red shows regions with more C than G.