

## Supplementary materials

### Changes in microbial community structure in response to gummosis in peach tree bark

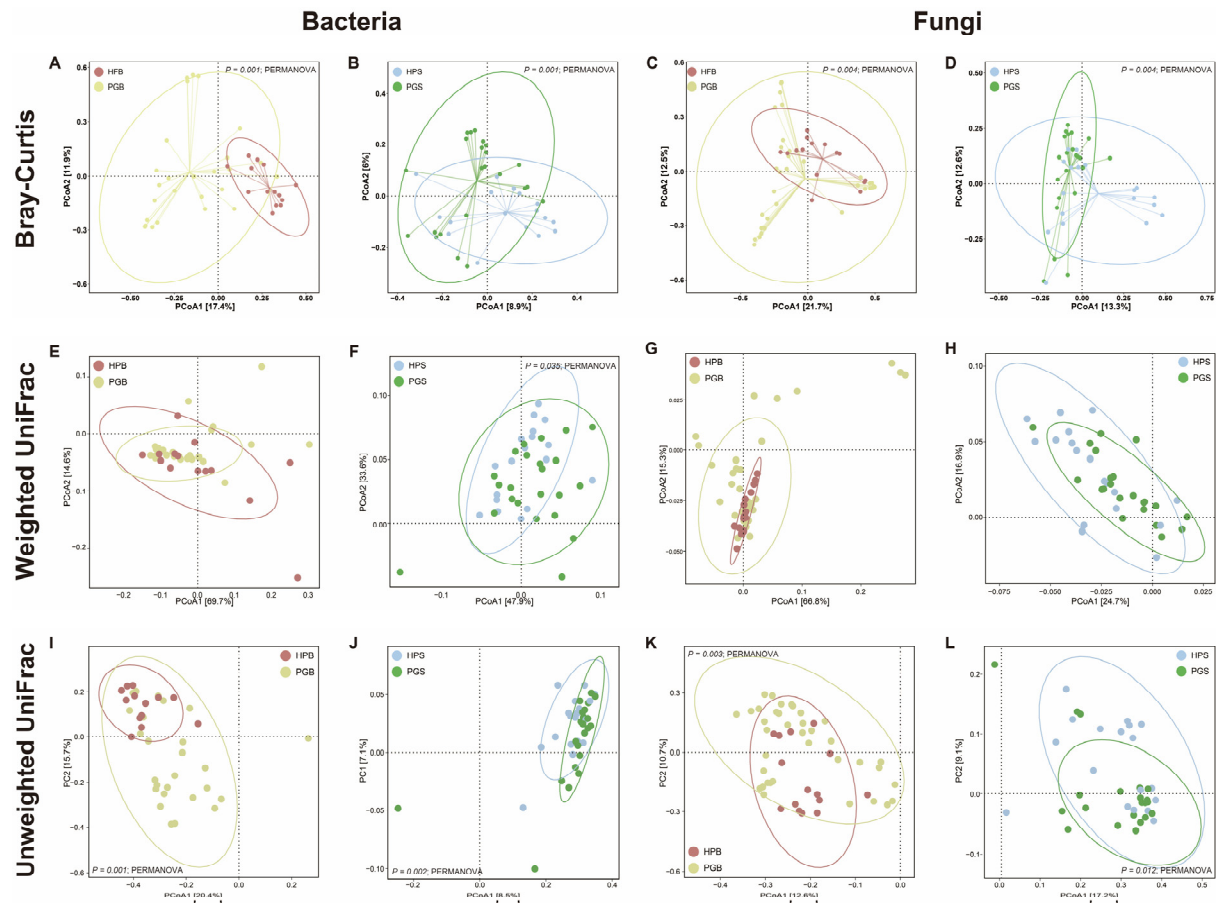
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**Figure S1.** Microbial dissimilarity within bark and soil according to gummosis. All dissimilarity was computed using three strategies including Bray-Curtis (A-D), weighted UniFrac (E-H) and unweighted UniFrac (I-L). Each Permanova values were displayed in the individual plots.

**Table S1.** Microbial composition (%) of HPB, PGB, HPS, PGS, at phylum and family level.**Bacteria**

Phylum	HPB	PGB	HPS	PGS
Acidobacteriota	2	3	12	16
Actionobacteriota	22	14	8	12
Crenarchaeota	2	3	10	7
Firmicutes	28	19	6	6
Proteobacteria	40	56	32	34
Other	6	5	24	25

**Fungi**

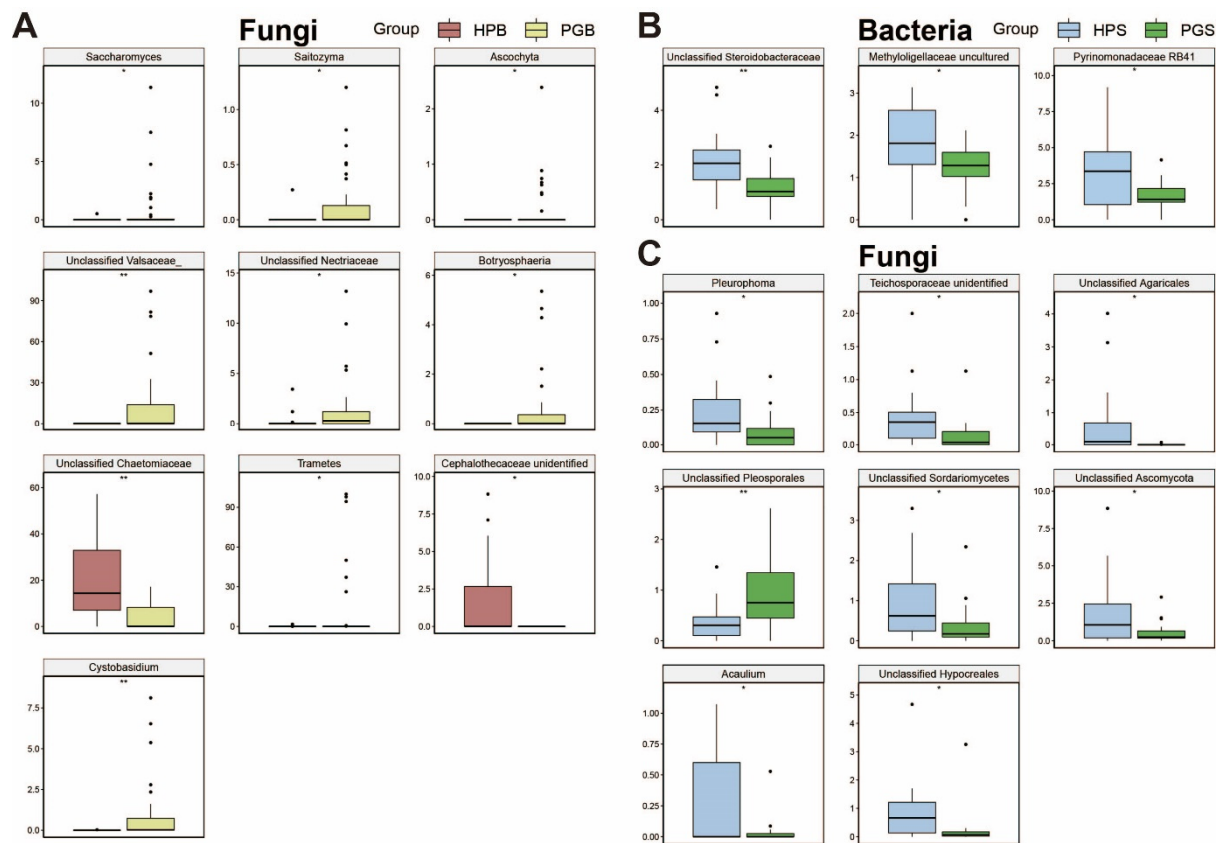
Phylum	HPB	PGB	HPS	PGS
Ascomycota	98	86	81	85
Basidiomycota	1	13	15	10
Kingdom_Fungi	1	1	2	2
Mortierellomycota	0	0	2	2
Other	0	0	0	1

**Bacteria**

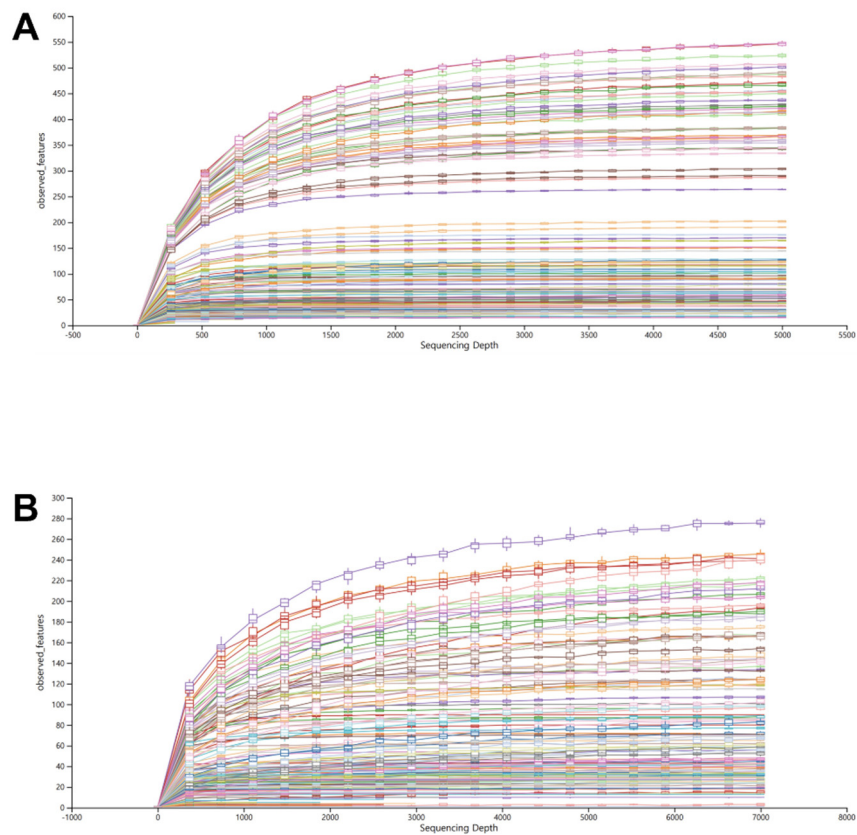
Family	HPB	PGB	HPS	PGS
Beijerinckiaceae	1	15	1	2
Chitinophagaceae	0	0	4	6
Nitrososphaeraceae	2	3	10	7
Other	39	47	69	70
Paenibacillaceae	9	7	1	1
Propionibacteriaceae	16	5	0	0
Pseudomonadaceae	1	11	0	0
Rhodobacteraceae	30	3	0	0
Sphingomonadaceae	0	8	3	4
uncultured	1	0	6	5
Vicinamibacteraceae	1	0	6	5

**Fungi**

Family	HPB	PGB	HPS	PGS
Chaetomiaceae	23	4	8	12
Cladosporiaceae	5	5	3	4
Helotiaceae	3	7	2	3
Nectriaceae	12	12	21	26
Order_Microascales	2	0	5	3
Order_Onygenales	5	4	0	0
Other	44	46	53	44
Phylum_Ascomycota	5	7	2	1
Pseudeurotiaceae	2	2	5	6
Valsaceae	0	13	0	0



**Figure S2.** Genera with statistical difference between HP and PG. (A) Fungal genera between HFB and PGB. (B) and (C) Bacterial and fungal genera between HPS and PGS, respectively. All displayed genera show less than 10% of prevalence and 1% relative abundance in each groups. Percent (%) was adopted for the unit of bacterial concentration. Mann-Whitney U test was applied to assess statistical significance. \*  $p < 0.05$ , \*\*  $p < 0.01$ .



**Figure S3.** Rarefaction curves of Illumina MiSeq sequencing. (A) Rarefaction curve of bacterial sequencing with 5000 of sequencing depth (B) Rarefaction curve of fungal sequencing with 7000 of sequencing depth.