

Fig. S8**a**

	H1 vs H2	G1 vs G2	DP1 vs DP2	RP1 cs RP2
NCBI nr	0.025	0.028	0.022	0.022
VFDB	0.002	0.01	0.049	0.085
MvirDB	0.143	0.227	0.029	0.016

b

Pre-treatment	H1 vs G1	H1 vs DP1	H1 vs RP1	G1 vs DP1	G1 vs RP1	DP1 vs RP1
NCBI nr	1	0.006	0.006	0.006	0.06	1
VFDB	1	0.03	0.006	0.03	0.018	1
MvirDB	0.174	0.006	0.006	0.006	0.012	1
Post-treatment	H2 vs G2	H2 vs DP2	H2 vs RP2	G2 vs DP2	G2 vs RP2	DP2 vs RP2
NCBI nr	1	0.216	1	0.096	1	1
VFDB	0.054	0.126	0.216	0.024	0.072	0.534
MvirDB	0.102	0.108	0.126	0.132	0.024	0.942

Supplementary Fig. S8 Summary of PERMANOVA using Bray-Curtis distance based on the functional gene abundance from each database. Values with p or adjusted p value < 0.01 are marked in dark orange, and those with $0.01 \leq p$ or adjusted p value < 0.05 are marked in light orange. (A) PERMANOVA (p value) for longitudinal comparisons by each database. (H) Bonferroni test (adjusted p value) for cross-sectional comparisons by each database.