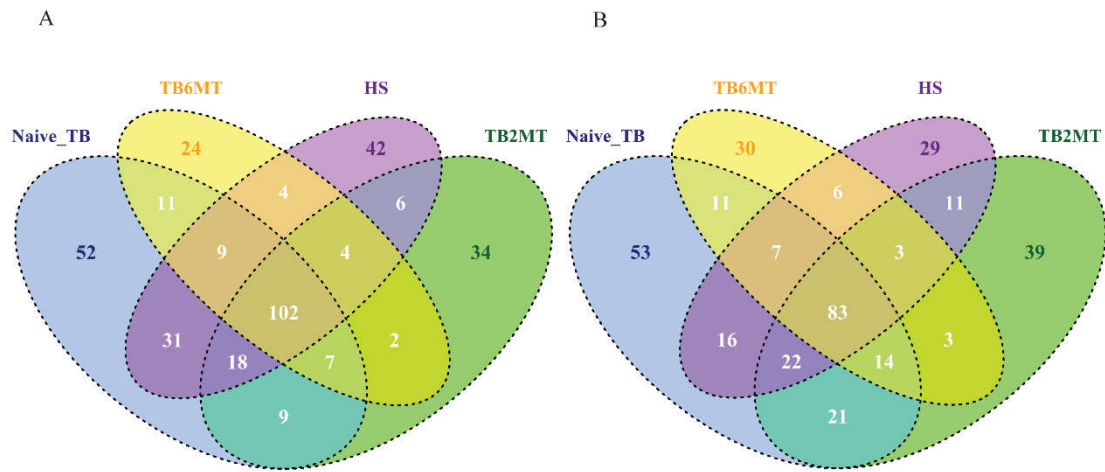


1 **Supplementary figures**

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4 **Figure S1 Genus composition analyses of the bacterial and fungal microbiota**

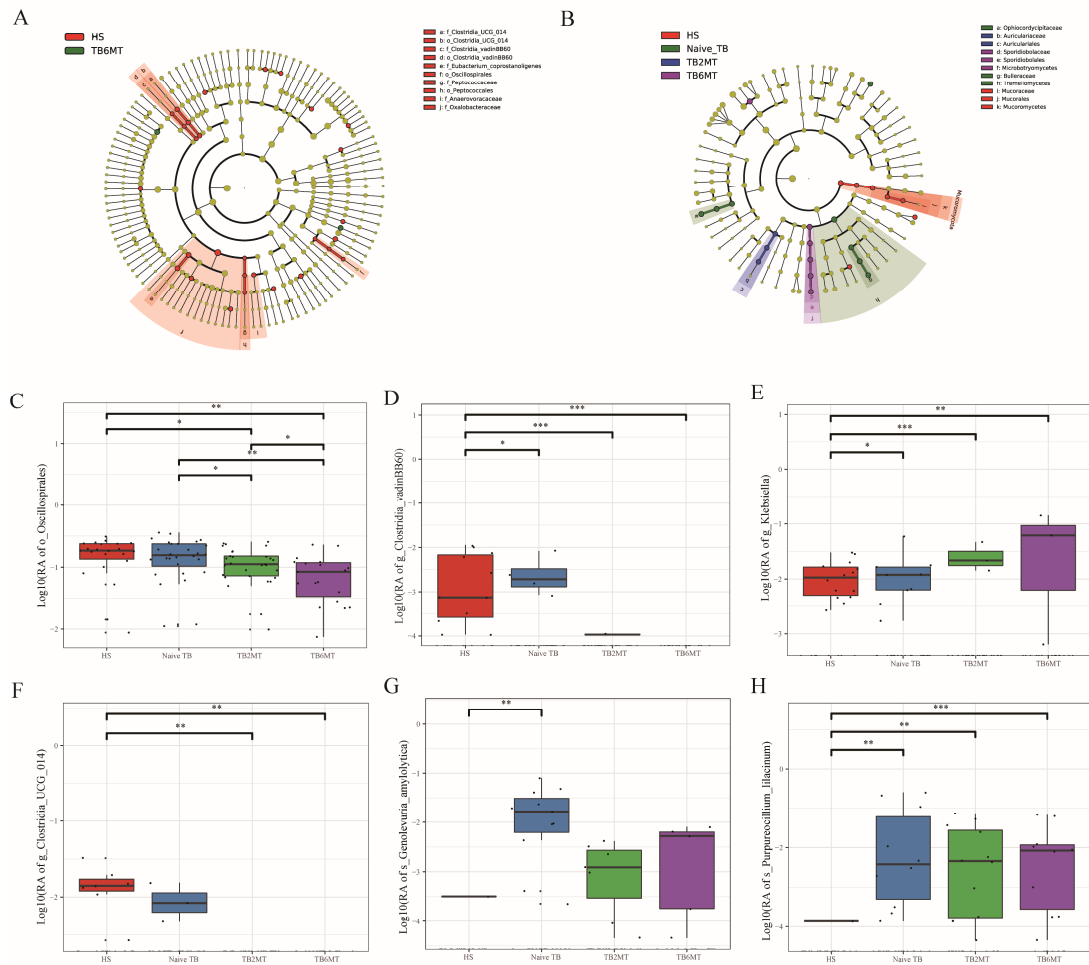
5 **among the four groups.** (A) Composition analysis of the bacterial genera within the

6 gut bacterial microbiota. (B) Composition analysis of the fungal genera within the gut

7 mycobiota. HS: healthy subjects; Naive TB: naive TB patients; TB2MT: TB patients

8 after 2 months of treatment; TB6MT: TB patients after 6 months of treatment.

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11 **Figure S2 Analysis of differential taxa abundances among the four groups.**

12 Significantly different taxa of bacteria (A) and fungi (B) shown in the cladogram

13 identified by LEfSe. The relative abundances (RAs) of *Eubacterium coprostanoligenes*

14 (C), *Clostridia vadinBB60* (D), *Klebsiella* (E), *Clostridia UCG_014* (F), *Genolevuria*

15 *amylytica* (G) and *Purpureocillium lilacinum* (H) were compared among the four
16 groups. HS: healthy subjects; Naive TB: naive TB patients; TB2MT: TB patients after
17 2 months of treatment; TB6MT: TB patients after 6 months of treatment (Wilcoxon
18 Rank Sum test, * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$)

