Figure S1. NMDS plots on OTU level showing the distribution patterns of (**a**) bacteria and (**b**) fung. Abundance data were transformed for equal sampling depth prior to generation of the distance matrix used for the non-metric multidimensional scaling (NMDS) plot. The Bray–Curtis index was used as the distance matrix. Stress < 0.05 showing good representativeness. The distance matrix of Bray-Curtis: $D_{Bray-Curtis} = 1 - 2\frac{\sum \min(S_{A,i}, S_{B,i})}{\sum S_{A,i} + \sum S_{B,i}}$. $S_{A,i}$ means the number of sequences contained in the ith taxon in sample A, $S_{B,I}$ means the number of sequences contained in the ith taxon in sample B.