

Supplementary Figure 1 Genome-wide analysis results of taxa. The red line in Manhattan plot indicates the threshold of 5×10^{-8} and the blue line indicates the threshold of 5×10^{-5} . Quantile-quantile plot (QQ-plot) shows observed $-\log_{10}$ p-values with the expected $-\log_{10}$ p-values. Blue dots show all SNPs and the red line indicates null hypothesis of no association. (A). Manhattan plot of all SNPs from genome-wide analysis of *Saccharibacteria*. (B). QQ-plot of all SNPs genome-wide analysis of *Saccharibacteria*. (C). Manhattan plot of all SNPs from genome-wide analysis of *Clostridiaceae*. (D). QQ-plot of all SNPs genome-wide analysis of *Clostridiaceae*. (E). Manhattan plot of all SNPs from genome-wide analysis of *Comamonadaceae*. (F). QQ-plot of all SNPs genome-wide analysis of *Comamonadaceae*. (G). Manhattan plot of all SNPs from genome-wide analysis of *Klebsiella*. (H). QQ-plot of all SNPs genome-wide analysis of *Klebsiella*. (I). Manhattan plot of all SNPs from genome-wide analysis of *Desulfovibrio d168*. (J). QQ-plot of all SNPs genome-wide analysis of *Desulfovibrio d168*.

Supplementary Figure 2 Spearman's correlation of the relative abundance of AF-associated taxa with the relative level of diseases predicted by PICRUSt. The grey components show no significance of correlation with Bonferroni correction ($p > 0.05 / (5.6 \times 22)$, $p > 0.0004$).

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