

Dysbiosis in chronic periodontitis: Key microbial players and interactions with the human host

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Supplementary information

Figure S1. Clustering of the periodontal communities based on the abundance of total transcripts from the respective genomes from HOMD database. The Bray-Curtis was used for calculating the similarities between samples.

Figure S2. The microbial players contributing to the shifts of LPS biosynthesis, type II TA system, iron transport system. Only differentially expressed species specific genes with $\log_2\text{CPM} \geq 4.5$ and $p \leq 0.05$ are shown.

Figure S3. The bioinformatics pipeline. (A) Quality control and removal of primers and rRNA reads (B) Data processing (C) Enrichment analysis of KEGG pathways and functional modules.

Table S1. The mapping rate summary for the metatranscriptomes of each sample. The details of the mapping are described in Materials and methods.

Table S2. The composition of bacteria based on transcripts, HOMD was used as reference database

(sheet 1). The composition (% relative abundance) of bacteria based on transcript reads mapped onto all reference genomes

(sheet 2). The composition (% relative abundance) of bacterial species (genomes were grouped into species)

(Sheet 3). Differential expression analysis based on the total transcriptional abundance of each species

Table S3. KEGG enrichment analysis

(sheet 1). Differential expression analysis for KO genes

(sheet 2). KEGG Ortholog (KO) identifier, abbreviation for the KO genes and functional annotation used in this study

(sheet 3). Differential expression analysis for species specific genes

(sheet 4). Gene set of five extremely enriched KEGG pathways and modules

Table S4. The relative abundance (%) of viruses based on all reads mapped onto NCBI viral reference genomes

Table S5. The relative abundance (%) of archaea based on all reads mapped onto NCBI archaea reference genomes

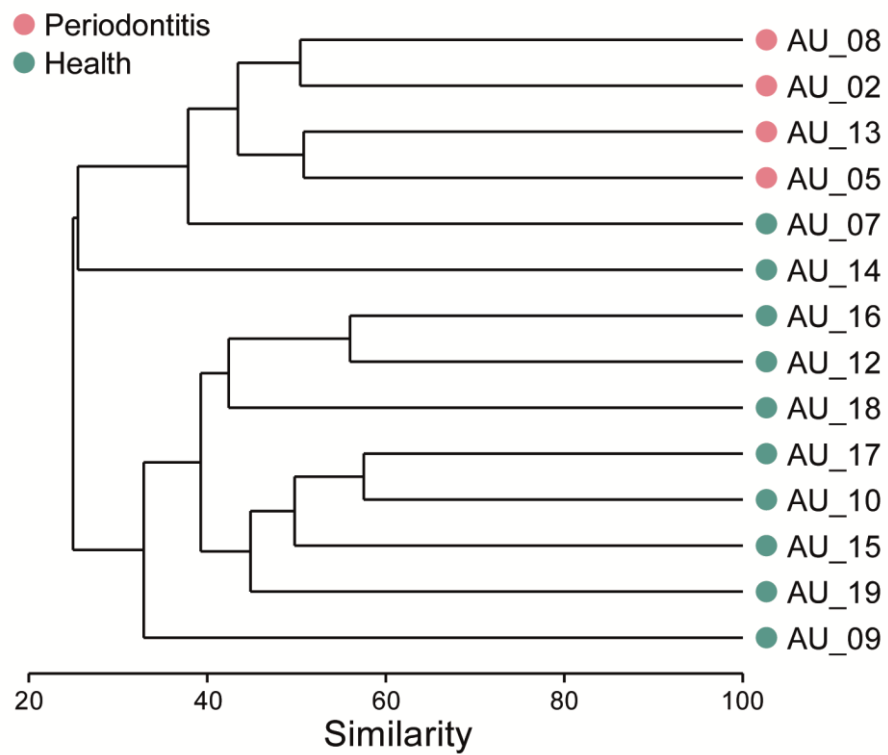


Figure S1. Clustering of the periodontal communities based on the abundance of total transcripts from the respective genomes from HOMB database

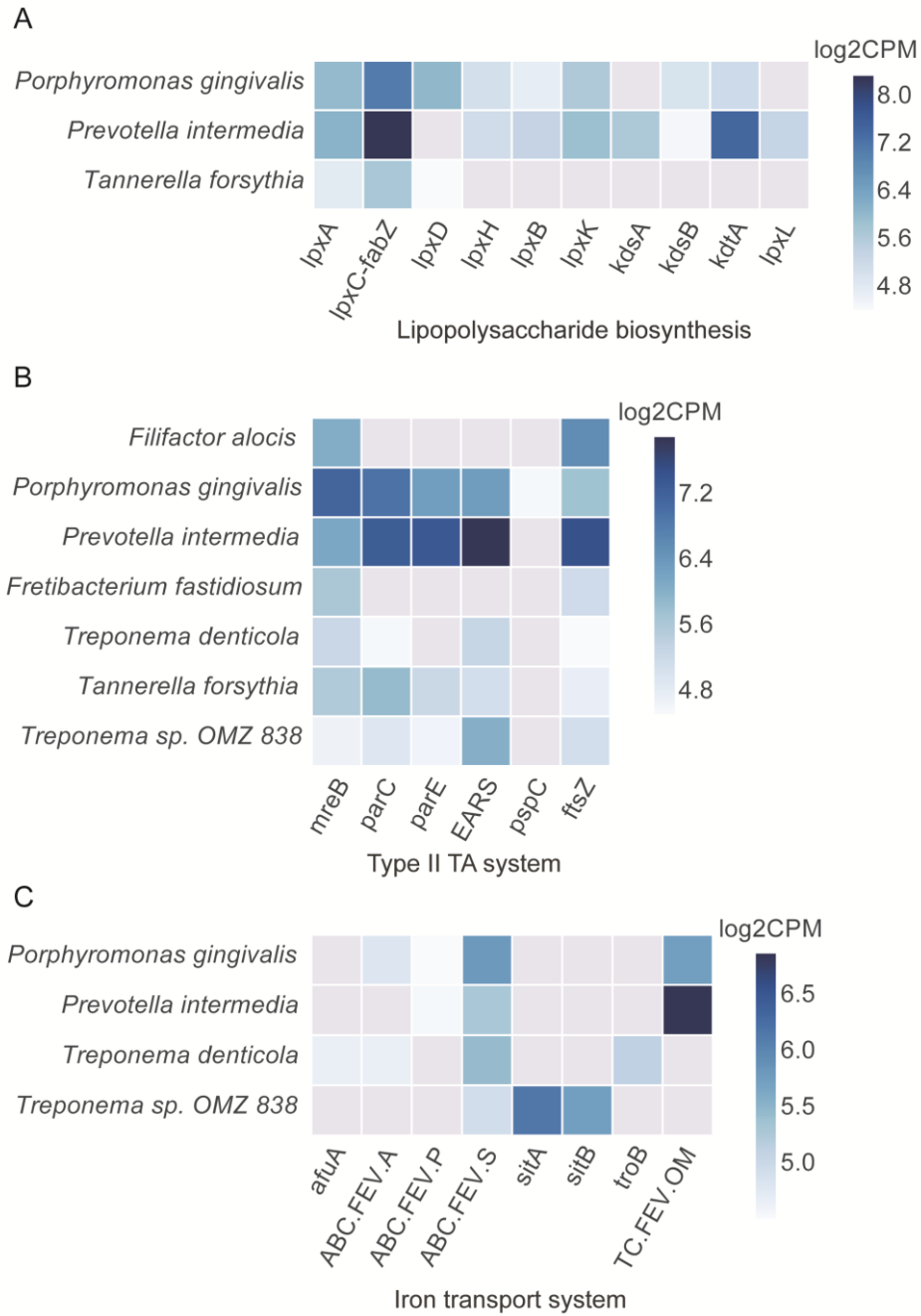


Figure S2. The microbial players contributing to the shifts of LPS biosynthesis, type II TA system, iron transport system

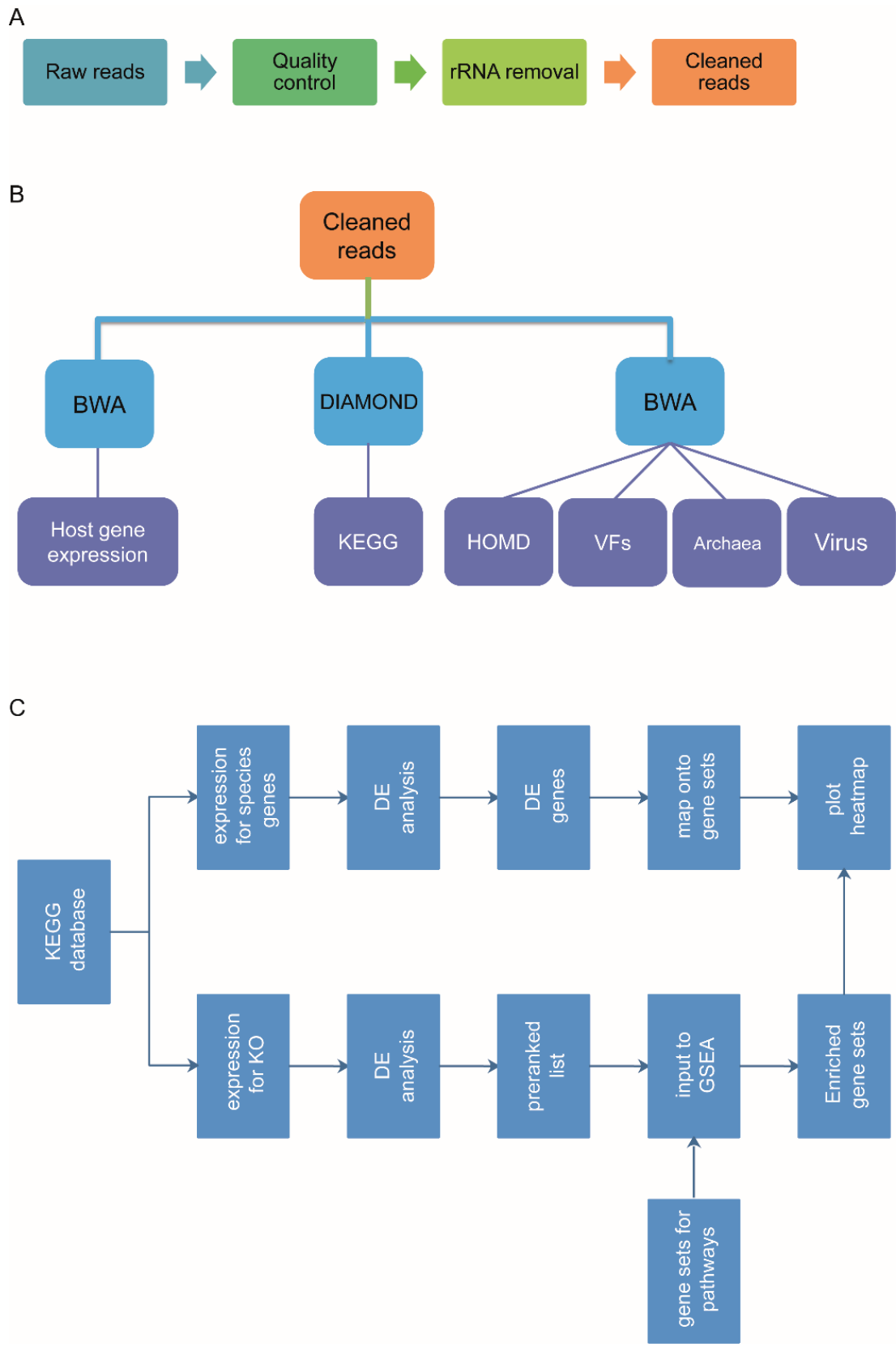


Figure S3. The bioinformatics pipeline