

Supplementary information

Supplementary Figure S1. Differentially expressed genes in Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis.

Pathways highlighted in green, cyan, and light pink correspond to those with false discovery rate (FDR) < 0.05 and $\log_2$ (fold change [FC]) < -2, $-2 < \log_2$ (FC) < -1, and $1 < \log_2$ (FC) < 2, respectively.

Supplementary Figure S2. Hierarchical heat map plot and volcano plot of differential gene expression of *Porphyromonas gingivalis* treated with Gnetin-C using an alignment-free method.

(A) Heat map presenting the hierarchical clustering of mRNA expression profiles of *P. gingivalis* treated with Gnetin-C (test) at the minimum inhibitory concentration or untreated *P. gingivalis* (control). In the clustering analysis, downregulated and upregulated genes are colored green and red, respectively. (B) Volcano plot indicating upregulated and downregulated mRNAs. Green dots highlight the downregulated mRNAs significant at false discovery rate (FDR) < 0.05 and $\log_2$ (fold change [FC]) < -2. Red dots denote upregulated mRNAs significant at FDR < 0.05 and $\log_2$ (FC) > 2. Gray dots denote unchanged mRNAs.

Supplementary Table S1. Downregulated genes as analyzed using an alignment-based method. The gene numbers are consistent with the numbers on the volcano plot in Fig 3B. M, $\log_2$ (FC); FDR, false discovery rate.

Supplementary Table S2. Upregulated genes as analyzed using an alignment-based method. The gene numbers are consistent with the numbers on the volcano plot in Fig 3B. M, $\log_2$ (FC); FDR, false discovery rate.

Supplementary Table S3. Downregulated genes as analyzed using an alignment-free method. The gene numbers are consistent with the numbers on the volcano plot in Supplementary Figure S2B. M, $\log_2$ (FC); FDR, false discovery rate.

Supplementary Table S4. Upregulated genes as analyzed using an alignment-free method. The gene numbers are consistent with the numbers on the volcano plot in Supplementary Figure S2B. M, $\log_2$ (FC); FDR, false discovery rate.