

Electronic supplementary information

Comparative transcriptomics reveals the mechanism of antibacterial activity of fruit-derived dihydrochalcone against *Porphyromonas gingivalis*

Desheng Wu ^a, Lisha Hao ^a, Xiaohan Liu ^a, Xiaofeng Li ^{a*}, Guanglei Zhao ^{b**}

^a School of Food Science and Engineering, South China University of Technology, Wushan Road 381,

Guangzhou, Guangdong, 510640, China

^b State Key Laboratory of Pulp and Paper Engineering, South China University of Technology, Guangzhou, Guangdong, 510641, China

Corresponding authors :

*Dr. Xiaofeng Li,

**Dr. Guanglei Zhao

School of Food Science and Engineering,

South China University of Technology,

Wushan Road 381, Guangzhou, Guangdong, 510640, China.

Tel: +86-20-2223-6819.

Fax: +86-20-8711-2853.

E-mail: xflibio@scut.edu.cn; glzhao@scut.edu.cn

Table S1. Genome mapping statistics

Sample	Total Reads	Unmapped Reads	Unique Reads	Mapped	Multiple reads	Mapped	Mapping Ratio
Blank1	6840522	82807(1.21%)	6475870(94.67%)		281845(4.12%)		98.79%
Blank2	6579550	90733(1.38%)	6235356(94.77%)		253461(3.85%)		98.62%
Phlorizin1	6467260	100719(1.56%)	6165198(95.33%)		201343(3.11%)		98.44%
Phlorizin2	7202516	89286(1.24%)	6876416(95.47%)		236814(3.29%)		98.76%
Naringenin1	7173432	95787(1.34%)	6851267(95.51%)		226378(3.16%)		98.66%
Naringenin2	6451988	107465(1.67%)	6136792(95.11%)		207731(3.22%)		98.33%
Phloretin1	6125130	95122(1.55%)	5855034(95.59%)		174974(2.86%)		98.45%
Phloretin2	6026522	108180(1.80%)	5753859(95.48%)		164483(2.73%)		98.20%

Table S2. Statistics on the number of genes detected in the samples

Sample Name	Known Gene Num	Group Name	Known Gene Num
Blank1	1829 (95.76%)	Blank	1851 (96.91%)
Blank2	1837 (96.18%)		
Phlorizin1	1830 (95.81%)	Naringenin	1852 (96.96%)
Phlorizin2	1841 (96.39%)		
Naringenin1	1839 (96.28%)	Phloretin	1842 (96.44%)
Naringenin2	1823 (95.45%)		
Phloretin1	1824 (95.50%)	Phlorizin	1855 (97.12%)
Phloretin2	1827 (95.65%)		
Reference Genes 1910		All Known Gene Num 1875 (98.17%)	

Table S3. Gene coverage statistics

Coverage range	Blank1 (%)	Blank2 (%)	Naringenin1 (%)	Naringenin2 (%)	Phloretin1 (%)	Phloretin2 (%)	Phlorizin1 (%)	Phlorizin2 (%)
00-20%	0 (0.0%)	2 (0.1085%)	1 (0.054%)	5 (0.2722%)	3 (0.1635%)	8 (0.4348%)	1 (0.05444%)	1 (0.05408%)
20-40%	10 (0.5438%)	13 (0.705%)	10 (0.54%)	8 (0.4355%)	12 (0.654%)	8 (0.4348%)	9 (0.4899%)	6 (0.3245%)
40-60%	30 (1.631%)	18 (0.9761%)	29 (1.566%)	21 (1.143%)	33 (1.798%)	32 (1.739%)	21 (1.143%)	20 (1.082%)
60-80%	51 (2.773%)	40 (2.169%)	51 (2.754%)	45 (2.45%)	32 (1.744%)	45 (2.446%)	41 (2.232%)	45 (2.434%)
80-100%	1748 (95.05%)	1771 (96.04%)	1761 (95.09%)	1758 (95.7%)	1755 (95.64%)	1747 (94.95%)	1765 (96.08%)	1777 (96.11%)

Table S4. The results of RNA-seq and qPCR of the treatment group.

Gene\Group	Blank vs Phlorizin		Blank vs Naringenin		Blank vs Phloretin	
	RNA-seq	QPCR	RNA-seq	QPCR	RNA-seq	QPCR
AhpC	0.51	0.38	0.38	0.33	0.33	0.33
FabF	0.97	1.16	1.22	1.39	2.20	3.12
HagA	0.60	0.78	0.60	0.78	0.40	0.80
PG_RS01230	2.60	2.75	2.04	1.74	1.41	1.52
PG_RS06630	0.73	0.82	0.47	0.55	0.28	0.31
RibH	0.62	0.56	0.60	0.55	0.38	0.41
RplX	0.56	0.60	0.47	0.55	0.54	0.80
Tpx	3.86	3.81	3.15	3.62	3.34	3.89
trxA	3.79	2.84	4.69	3.68	5.48	6.62

The RNA-seq results calculated as FPKM and qPCR results calculated as \log_2 FC.

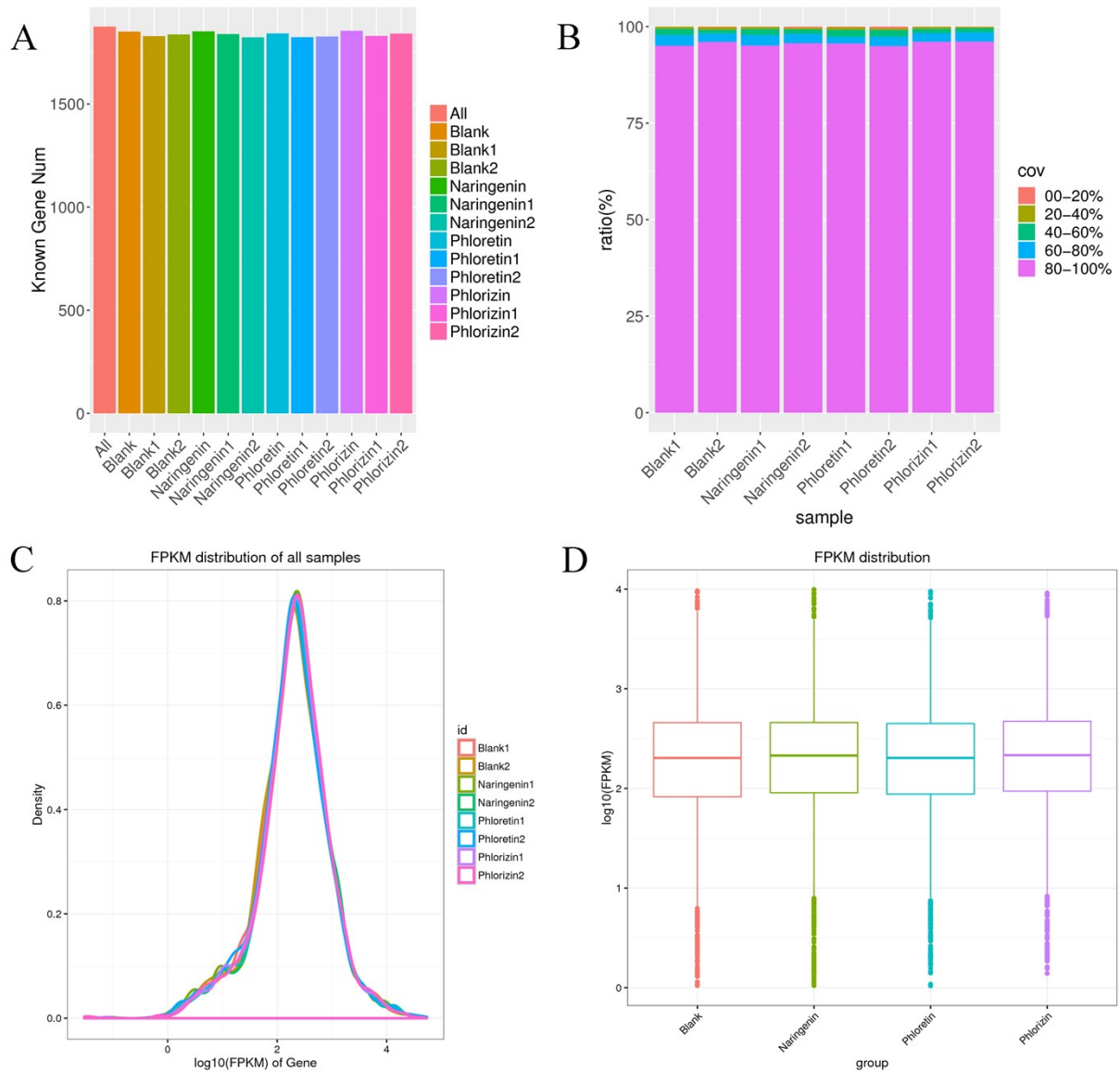


Fig. S1 Statistics on comparison between sequencing results and reference genome and comparison between groups, including statistics on the number of known genes (A), gene coverage distribution (B), sample expression abundance distribution (C) and comparison of expression levels between groups (D).

Significant Differential Gene Heatmap

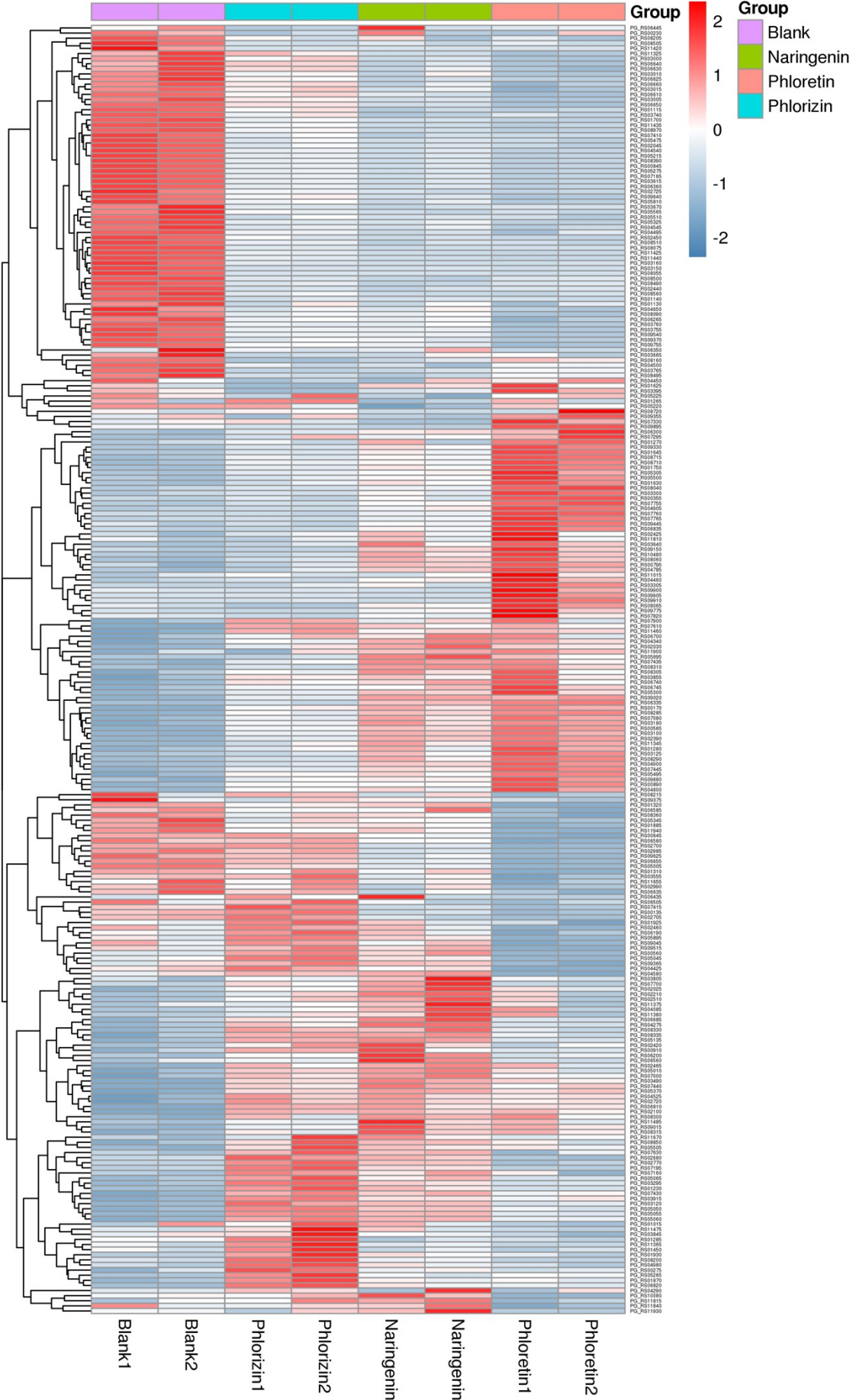


Fig. S2 Cluster diagram of differential expression patterns between groups.