

Supplementary Information

Pan-genomic and Transcriptomic Analyses of Marine *Pseudoalteromonas agarivorans* Hao 2018 Revealed Its Genomic and Metabolic Features

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Figure S1. A neighbor-joining tree based on 16S rRNA gene sequences, showing the phylogenetic relationships between strain Hao 2018 and closely related *Pseudoalteromonas* type strains by MEGA7. Bootstrap values are shown on branching nodes as percentages of 1000 replicates for values over 70%. *Pseudoalteromonas aestuariivivens* DB-2T (KT366926) was used as an outgroup. Bar, 0.002 changes per nucleotide position.

Figure S2. RPKM density discretization (**a**) and (**b**) statistical box plots of RPKM density distribution in the two groups of samples.

Figure S3. RPKM saturation in two samples of (**a**) 2h and (**b**) 24h.

Figure S4. Correlation test for two samples of 2h and 24h.

Figure S5. Principal component analysis.

Table S1. Statistics of data filtering results.

Table S2. Sequence mapping result statistics.

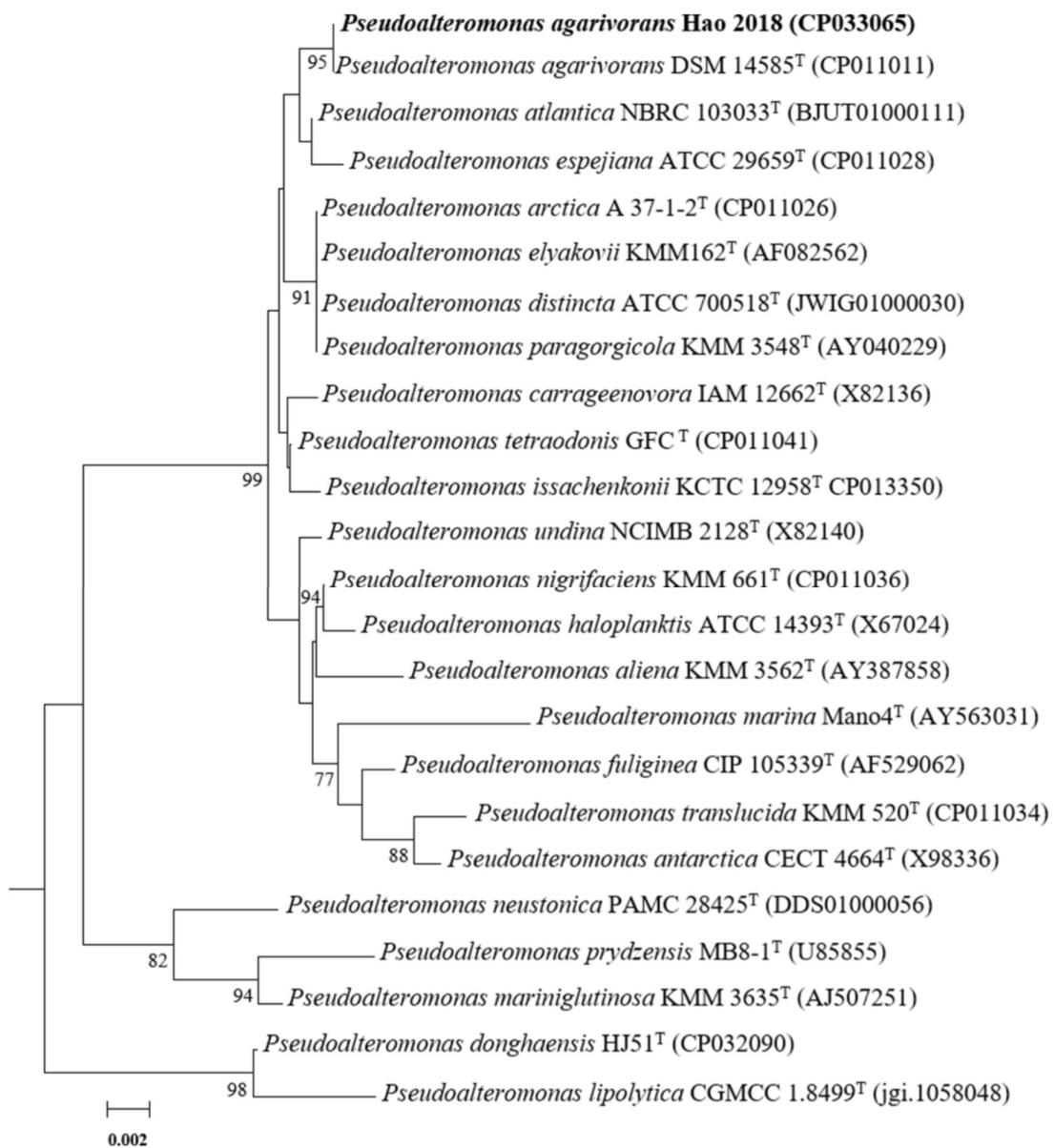


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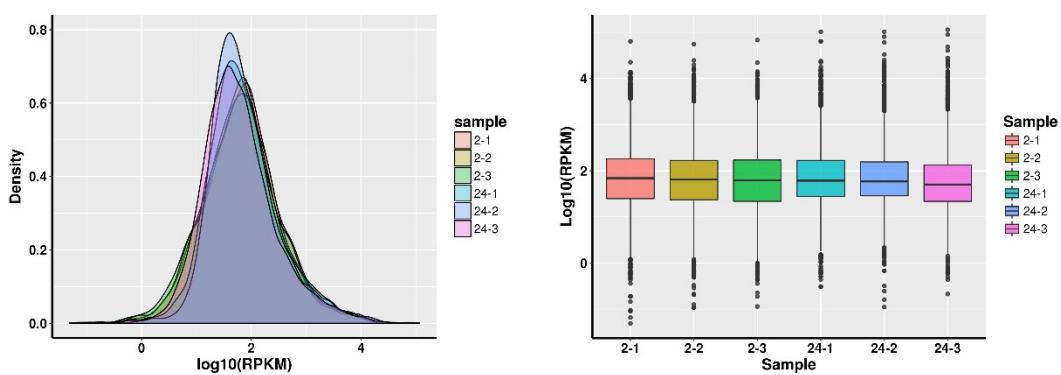


Figure S2. RPKM density discretization (a) and (b) statistical box plots of RPKM density distribution in the two groups of samples.

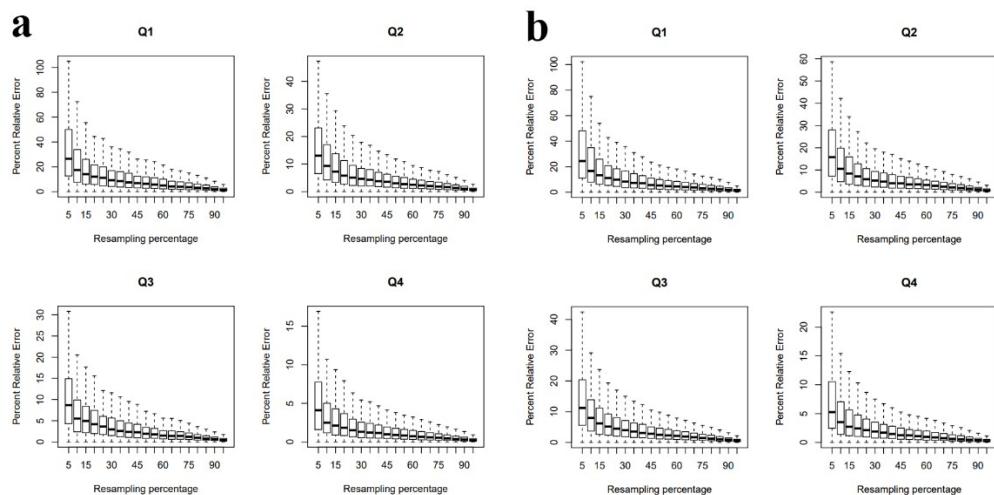


Figure S3. RPKM saturation in two samples of (a) 2h and (b) 24h.

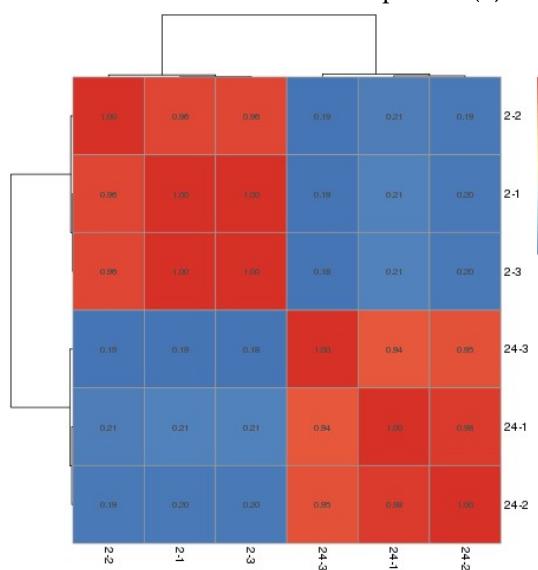


Figure S4. Correlation test for two samples of 2h and 24h.

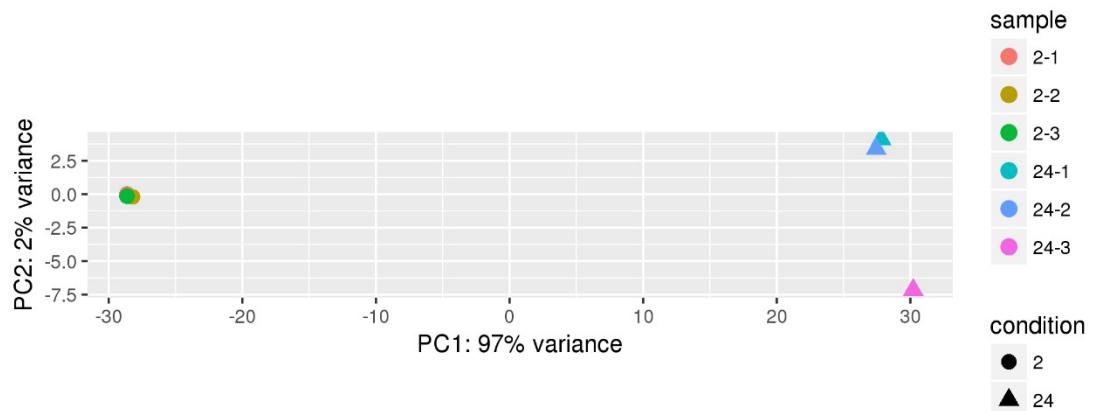


Figure S5. Principal component analysis.

Table S1. Statistics of data filtering results

Sample	Useful Reads	Total Mapped Reads number and percentage	Uniquely Mapped Reads number and percentage	Multiple Mapped Reads number and percentage
2-1	35,539,354	35,293,023 99.31%	34,100,616 96.62%	1,192,407 3.38%
2-2	32,827,394	32,562,294 99.19%	31,511,500 96.77%	1,050,794 3.23%
2-3	30,147,348	29,885,919 99.13%	28,776,927 96.29%	1,108,992 3.71%
24-1	36,407,882	36,102,399 99.16%	35,573,729 98.54%	528,670 1.46%
24-2	32,234,184	32,034,111 99.38%	31,667,698 98.86%	366,413 1.14%
24-3	36,228,242	35,964,709 99.27%	35,482,252 98.66%	482,457 1.34%

Table S2. Sequence mapping result statistics

Sample	Clean Reads No.	Clean Data (bp)	GC (%)	Clean Reads (%)	Clean Data (%)
2-1	35,539,354	5,315,365,568	42.93	99.74	99.45
2-2	32,827,394	4,911,816,504	43.26	99.72	99.47
2-3	30,147,348	4,510,663,522	43.03	99.71	99.45
24-1	36,407,882	5,448,102,540	44.49	99.36	99.12
24-2	32,234,184	4,824,059,398	43.86	99.70	99.47
24-3	36,228,242	5,419,476,838	44.34	99.69	99.42