Supplementary Materials

1. *Output of Transcriptome Sequencing Results and Quality Control*

A total of 38.5 Gb of clean data were obtained from this transcriptome sequencing, and the clean data of each sample reached 6.0 Gb, with the percentages of bases in Q20 and Q30 being over 96.76% and 91.75%, respectively. A total of 49.79% of the GC content of "Changjiang 2" and 47.85% of that of "Jianghai 21" were obtained on average. The average percentage of GC content was 49.79% for "Changjiang 2" and 47.85% for "Jianghai 21". Sequencing data for the samples are shown in Table S1.

Table S1. Summary of sample sequencing data quality.

Sample Number	Clean Reads	Clean Bases	GC/%	Q20/%	Q30/%
CJ_1	42540066	6.38G	52.00	97.12	92.77
CJ_2	43940748	6.59G	47.53	97.23	92.83
CJ_3	44391968	6.66G	49.86	97.3	93.11
JH_1	39995096	6.0G	46.26	96.76	91.75
JH_2	42751124	6.41G	46.34	97.26	92.87
JH_3	43099798	6.46G	50.96	97.16	92.8

Note: CJ: *E. sinensis* "Changjiang 2"; JH: *E. sinensis* "Jianghai 21". Clean reads: number of reads after filtering the raw data; clean bases: number of bases after filtering the raw data; GC/%: percentage of G vs. C in clean reads for all four bases; Q20/%: percentage of total bases with a value > 20; Q30/%: percentage of total bases with a value > 30.

2. *Comparison of Sequencing Data with Reference Genomes*

Comparison of the clean reads of the transcriptome of this experiment with the reference genome of *E. sinensis* revealed that (Table S2) the comparison efficiency of the reads of each sample with the reference genome of *E. sinensis* was in the range of 68.31%~86.8%, the proportion of the reads compared to a unique position in the genome was in the range of 62.88%~78.35%, and the proportion of the reads compared to multiple positions in the genome was in the range of 5.43%~8.45%.

Table S2. Statistics on the comparison of samples with the reference genome.

Sample Number	Total Reads	Total Map	Unique Map	Multi Map
CJ_1	42540066	36922732(86.8%)	33328538(78.35%)	3594194(8.45%)
CJ_2	43940748	32228169(73.34%)	29073845(66.17%)	3154324(7.18%)
CJ_3	44391968	35712788(80.45%)	32003418(72.09%)	3709370(8.36%)
JH_1	39995096	27319193(68.31%)	25148767(62.88%)	2170426(5.43%)
JH_2	42751124	29855954(69.84%)	27524505(64.38%)	2331449(5.45%)
JH_3	43099798	35885817(83.26%)	33033069(76.64%)	2852748(6.62%)

Note: CJ: *E. sinensis* "Changjiang 2"; JH: *E. sinensis* "Jianghai 21". Total reads: number of clean reads of sequencing data after quality control; total map: number of reads matched to the genome and their percentages; unique map: number and percentage of reads matched to a unique position in the reference genome; multi map: number and percentage of reads matched to multiple positions in the reference

genome.

3. *Sample Correlation Analysis*

The gene expression differences were visualized by FPKM, and the deviation of the three replicate samples within each group was confirmed by Pearson correlation coefficient and PCA (Figure S1). The correlation coefficients between the samples at each position were higher than 0.85, and the results of the principal component analysis were clearly clustered according to position (JH and CJ). Therefore, the above results determined the consistency between the replicate samples.

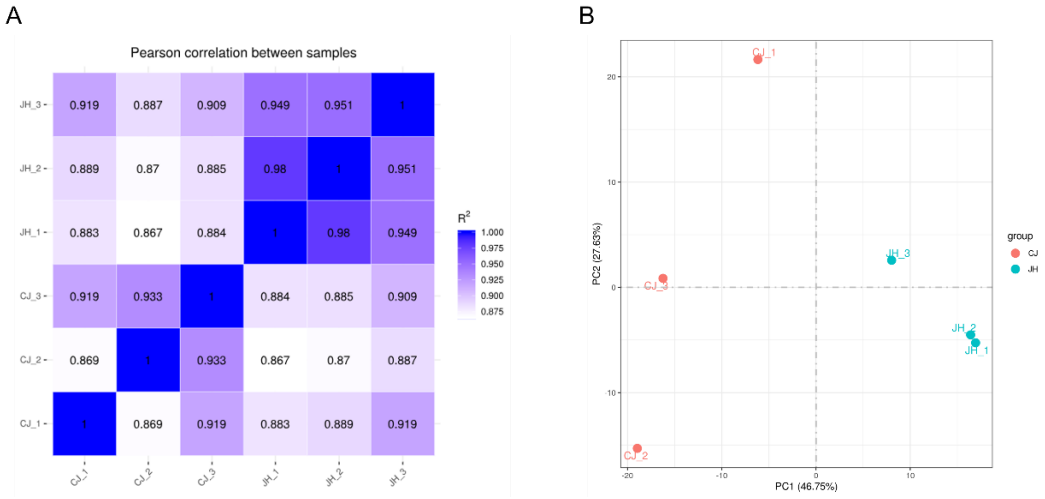

Figure S1. RNA-seq results: (A) Pearson correlation coefficient analysis between all biological replicated RNA-seq sample in *E. sinensis.* (B) Principal component plot of biological RNA-seq samples in *E. sinensis*.