

Figure S1. Top 12 enriched terms in three functional categories of DEGs in GO database. (A) DEGs of PT24 vs. PT102. (B) DEGs of PT24 vs. PT192. (C) DEGs of PT102 vs. PT192.

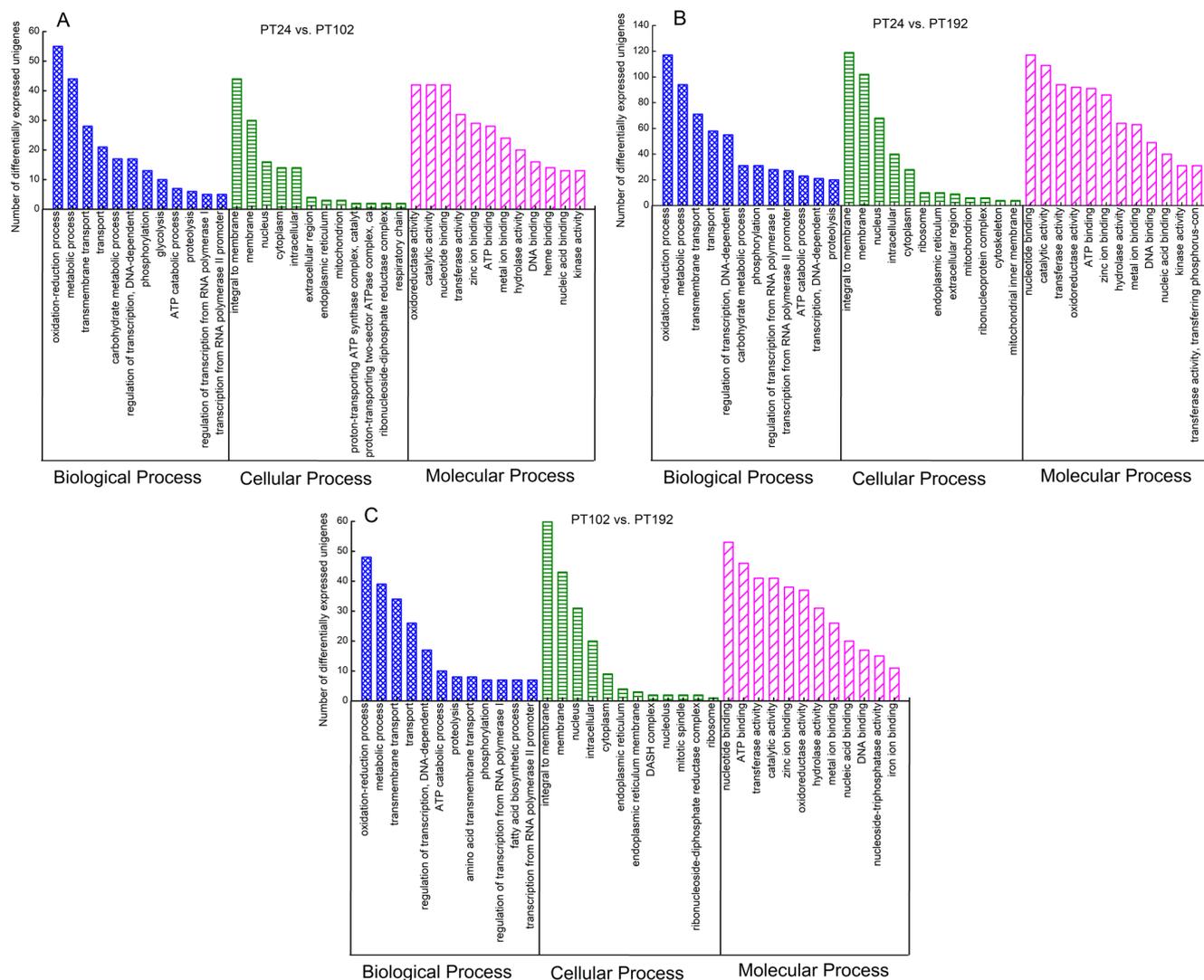


Figure S2. Top 12 pathways of DEGs in KEGG database. (A) DEGs of PT24 vs. PT102. (B) DEGs of PT24 vs. PT192. (C) DEGs of PT102 vs. PT192.

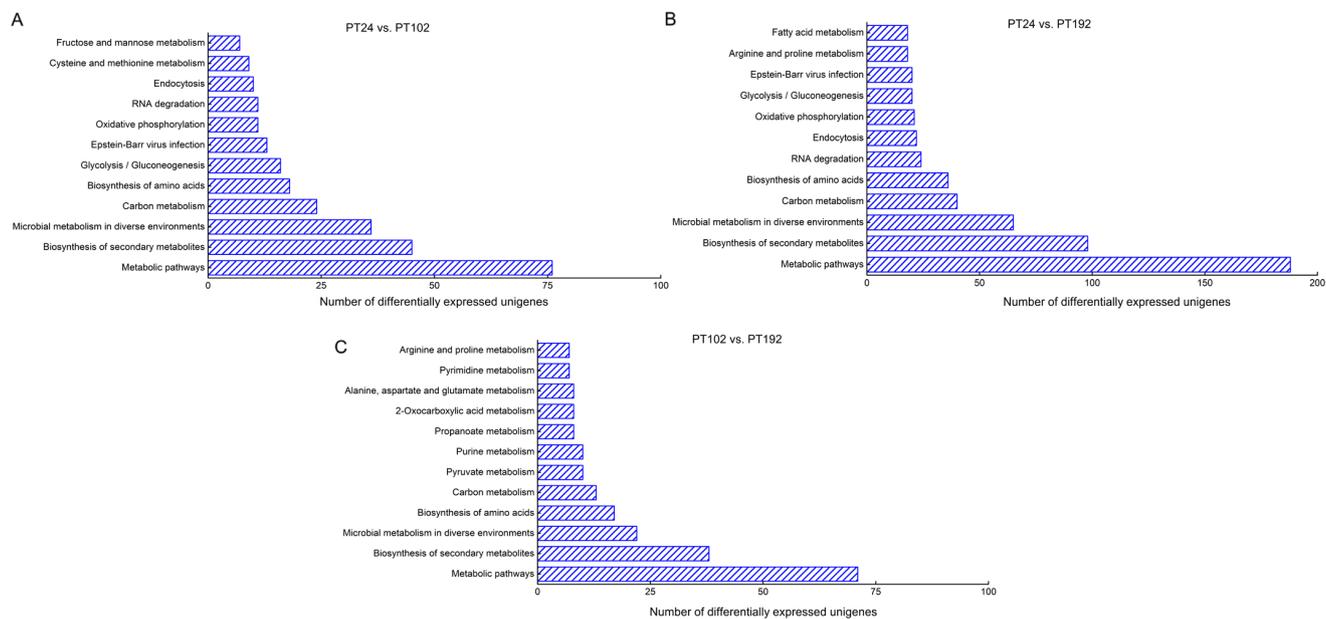


Table SI. Gene specific primers used in reverse transcription-quantitative PCR.

Unigene_ID	Primer sequences (5'→3')
<i>tefl-a</i>	F: CCTCCAACGTCACCACTGAAGT R: CGGAGACGTTCTTCACGTTGA
contig_114	F: TATTTCCACGCCAGGACTCCTT R: CCCTCCGTCATCTCTCCATCT
contig_1591	F: TCGTTTTAATGAACCGTCAGCC R: TGGCGTAGTGCATGCGAATA
contig_1606	F: GCAGCTGTCTTCCTGTTTCCTG R: CACCTGCCATCTTGGAGATCA
contig_2933	F: ACCCTGGTGTCAACAATGGCT R: ATAAGCGGCGCAGTGAAA
contig_3519	F: GAGTCAAGGTATGAATCGGCCT R: CCGCAGGAAGGAAAAAATTG
contig_1296	F: AAATGAAGTTTTTCGCGCGC R: CCGATACCATCGTGAAGCATG
contig_4264	F: GGAACGTAAGCCTCCACATCAG R: CAAGTTGGTCCATCCGTCAATT
contig_1707	F: ATCATGGATCAAGGCGGTCTT R: TCGAGAATGAAACCGCCCT
contig_5708	F: CGGAAATGTTTCATGGTGCG R: CAAGATGGTCGAGTTCCAGGAG
contig_571	F: GGACACGTAGTGTTGCAGTGCA R: CGTGCGCCAACCTTTTCAT
contig_753	F: ATGGCTCAAATCAACGGATCC R: CCATGAGCTCGTGGAGATCAA
contig_814	F: ACAACGTGACATGGTTTTTCG R: AATGATCTGGATGCCCCGA
contig_9544	F: CGTGGATGTCATTGACATGGAT R: CGACGACGTTCTCTACAGCAAA
contig_901	F: ATCATGGATCAAGGCGGTCTT R: TCGAGAATGAAACCGCCCT

F, forward; R, reverse; *tefl-a*, translation elongation factor 1a.

Table SII. Summary of clean reads for each sample.

Sample	Raw reads	Number of clean reads	Clean ratio
PT24	32,061,948	27,207,076	84.86%
PT102	37,531,698	31,708,556	84.48%
PT192	34,766,538	29,265,588	84.18%

Clean ratio, clean reads/raw reads.

Table III. Top 20 KEGG pathway enrichment of unigenes.

Pathway ID	KEGG categories	Number of unigenes
ko01100	Metabolic pathways	815
ko01110	Biosynthesis of secondary metabolites	329
ko01120	Microbial metabolism in diverse environments	225
ko01230	Biosynthesis of amino acids	126
ko01200	Carbon metabolism	114
ko05169	Epstein-Barr virus infection	93
ko00260	Glycine, serine and threonine metabolism	80
ko03018	RNA degradation	79
ko04144	Endocytosis	79
ko03010	Ribosome	75
ko03040	Spliceosome	74
ko03013	RNA transport	70
ko00230	Purine metabolism	69
ko04111	Cell cycle-yeast	69
ko04113	Meiosis-yeast	65
ko04141	Protein processing in endoplasmic reticulum	63
ko01212	Fatty acid metabolism	59
ko04011	MAPK signaling pathway-yeast	57
ko00520	Amino sugar and nucleotide sugar metabolism	55
ko04146	Peroxisome	55

KEGG, and Kyoto Encyclopedia of Genes and Genomes.