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') |
|------------|--------------------------|
| tef1-a     | F: CCTCCAACGTCACCACCTGAAGT<br>R: CCGAGACGTTCTTCAGTGTA |
| contig_114 | F: TATTTCCACCCAGGACTCTTT<br>R: CCCTCCGTCATCTCTCCATCT |
| contig_1591| F: TCGTTTTAATGAACCGTCAGCC<br>R: TGGCGTAGTCATGCGAATA |
| contig_1606| F: GCAGCTGTCTTCTCTGTCTCT<br>R: CACCTGCCATCTTGGAGATCA |
| contig_2933| F: ACCCTGGTGCAAAATGGCT<br>R: ATAAGCGGCGCAGTGGAATA |
| contig_3519| F: GAGTCAAGGTATGAACTCGGCT<br>R: CCGCAGGAAAGGAAAAATTG |
| contig_1296| F: AAATGAAGTTTCGCGCCT<br>R: CCGATACCACCTCGTGAAAGCATG |
| contig_4264| F: GGAACGTAAACCTCCCAATCGAG<br>R: CAATGGGTCCATCCGTCAGT |
| contig_1707| F: ATGATGGATCAACGGCCT<br>R: TCGAGAATGAAACGCGCT |
| contig_5708| F: CGGAAGGTTCCTGGGACGAG<br>R: CAAGATGGTCGCGCTGGAGAC |
| contig_571 | F: GGAACGTAAACCTCGAGTGGTTGCAAGTCA<br>R: CTGCGGCGCAACCTTTTCAT |
| contig_753 | F: ATGGCTCAAATACCCGACCT<br>R: CCAATAGCCTCGTGGGAGATCAA |
| contig_814 | F: ACAACGTCAGCATGTTTTCG<br>R: AATGATCTGATGATGCCCAG |
| contig_9544| F: CGTGATGTCATGGAGATGGAAT<br>R: CGACGAGTCCTGTACAGGAAAA |
| contig_901 | F: ATCATGGATCAAGGCGGCT<br>R: TCGAGAATGAAACCGCCCT |

F, forward; R, reverse; tef1-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 SIII. 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.