

3.8e-02 Carbohydrate transmembrane transport

- 3.8e-02 Organophosphate ester transport

1.6e-03 Glutamate catabolic process

1.6e-03 Dicarboxylic acid catabolic process

5.7e-03 Glutamine family amino acid catabolic process

6.5e-03 Glutamate metabolic process

3.8e-02 Dicarboxylic acid metabolic process

3.8e-02 Alpha-amino acid catabolic process

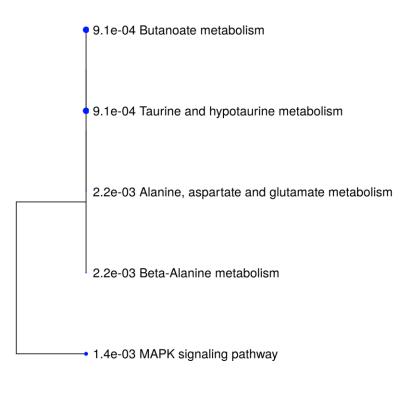
3.8e-02 Cellular amino acid catabolic process

3.8e-02 Glutamine family amino acid metabolic process

b 3.7e-02 Metal ion binding 3.7e-02 Cation binding 3.7e-02 Calcium ion binding 4.8e-02 Oxidoreductase activity, acting on peroxide as acceptor 4.8e-02 Peroxidase activity 4.0e-02 Protein serine/threonine phosphatase activity 3.7e-02 Magnesium-dependent protein serine/threonine phosphatase activity 4.1e-02 Ion transmembrane transporter activity 4.0e-02 Inorganic molecular entity transmembrane transporter activity 3.9e-02 Transporter activity 3.7e-02 Carbohydrate transmembrane transporter activity 4.8e-02 ATP binding 3.7e-02 Drug binding 3.7e-02 Carboxy-lyase activity 1.2e-03 Glutamate decarboxylase activity 3.9e-02 Carbon-carbon lyase activity 3.9e-02 Pyridoxal phosphate binding 3.9e-02 Vitamin B6 binding 4.8e-02 Vitamin binding

Supplemental Figure S1. Hierarchical trees summarizing significant gene ontology (GO) terms. The trees of GO categories, Biological Process (a) and Molecular Function (b), were generated by ShinyGO web site. GO Terms sharing more genes are grouped, and bigger dots at the end of branches correspond to more significant FDR values.

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Supplemental Figure S2 Hierarchical tree summarizing significant Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways. The details of tree are found in Fig. S1.

Table S1 Summary of transcriptome analysis

Sample name	Control-1	Control-2	Control-3	CO-1	CO-2	CO-3	CNF-1	CNF-2	CNF-3
Number of raw reads	5197979	6750046	9538029	8516607	7100973	5829062	7427079	7399271	6922205
Average read length (bp)	126	126	126	126	126	126	126	126	126
Uniquely mapped reads	92.54%	76.17%	93.00%	93.02%	92.77%	92.28%	92.34%	91.96%	91.14%
Average mapped length (bp)	125.04	123.45	124.89	125.07	124.95	125.01	124.9	124.99	125.04
Successfully assigned alignments	89.10%	85.10%	89.60%	89.20%	89.20%	89.60%	89.50%	89.70%	89.40%