

Supplementary Tables

Table S1 Primers used in this study

| Primer name | Sequence (5'-3') |
|------------------|--|
| <i>VadhE2</i> -F | tctagagtcgacgtcacgcg |
| <i>Vpthl</i> -R | ACTATTTTCGCTGAATATTCAGccgggtaccgagctcgaattc |
| <i>pthl</i> -F | CTGAATATTCAGCGAAAATAGTATATTATATAATTATAA ATTG |
| <i>pthl</i> -R | CCTCCTAAATATTTATGGATCCAAATTTAAATTGATTAC AAACCTTTTTACCAAC |
| <i>adhE2</i> -F | GGATCCATAAATATTTAGGAGGAATAGTCatgaaagttacaaat caaaaagaactaaaacaaaagc |
| <i>adhE2</i> -R | cgcgtgacgtcgactctagattaaaatgattttatagatatacctaagttcactata |
| <i>catI</i> -FOR | CAGgaaacagctatgaccgcgGCCGCTCAATATTTACATCCAAA TCTTTTTTCAAATTC |
| <i>catI</i> -REV | AATATTCAGccgggtaccgagctCGTAGACTTTAAGGATGGA ACCTTTG |
| <i>VcatI</i> -F | agctcgggtaccggCTGAATATTCAGCGAAAATAG |
| <i>VcatI</i> -R | GCggtcatagctgtttcctg |

Table S2 The differentially expressed genes of the strains CtADGBC, which cultured in SSPM.

| Function | Gene | Fold change | Log ₂ ratio | Description |
|-----------------------|---------------|-------------|------------------------|---|
| Amino acid metabolism | GTH52_RS09035 | 14.0 | 3.8 | aspartate ammonia-lyase |
| | GTH52_RS03140 | 3.6 | 1.8 | histidinol phosphate phosphatase |
| | asnB | 3.5 | 1.8 | asparagine synthase B |
| | GTH52_RS08565 | 0.4 | -1.2 | aspartate 4-decarboxylase |
| | GTH52_RS00315 | 2.2 | 1.1 | homoserine dehydrogenase |
| | GTH52_RS07545 | 3.2 | 1.7 | Homoserine O-succinyltransferase |
| | GTH52_RS04585 | 3.2 | 1.7 | threonine synthase |
| | GTH52_RS05050 | 2.6 | 1.4 | aminotransferase class I/II-fold pyridoxal phosphate-dependent enzyme |
| | GTH52_RS05920 | 2.5 | 1.3 | pyridoxal phosphate-dependent |

| | | | | |
|-------------------------|---------------|-------|------|--|
| | | | | aminotransferase |
| | GTH52_RS01615 | 5.6 | 2.5 | hypothetical protein |
| | GTH52_RS01605 | 2.3 | 1.2 | pyridoxal phosphate-dependent aminotransferase |
| | GTH52_RS07560 | 82.4 | 6.4 | L-aspartate oxidase |
| | GTH52_RS08765 | 0.4 | -1.2 | argininosuccinate synthase |
| | GTH52_RS09035 | 14.0 | 3.8 | aspartate ammonia-lyase |
| | GTH52_RS02380 | 4.1 | 2.0 | transcription elongation factor GreA |
| | GTH52_RS05760 | 0.4 | -1.5 | threonine ammonia-lyase |
| Carbohydrate metabolism | GTH52_RS12365 | 72.4 | 6.2 | homocitrate synthase NifV |
| | GTH52_RS11725 | 3.8 | 1.9 | acyl-CoA dehydrogenase |
| | xylB | 3.2 | 1.7 | xylulokinase |
| | xylA | 2.6 | 1.4 | xylose isomerase |
| | GTH52_RS14450 | 2.1 | 1.1 | FAD-binding oxidoreductase |
| Nitrogen metabolism | GTH52_RS05005 | 5.6 | 2.5 | nitrogenase component 1 |
| | GTH52_RS05240 | 2.2 | 1.1 | nitrogenase component 1 |
| | GTH52_RS12345 | 146.7 | 7.2 | nitrogenase molybdenum-iron protein alpha chain |
| | GTH52_RS05235 | 2.1 | 1.1 | nitrogenase component 1 |
| | GTH52_RS12350 | 132.0 | 7.0 | nitrogenase molybdenum-iron protein subunit beta |
| | GTH52_RS04575 | 3.8 | 1.9 | nitrogenase iron protein NifH |
| | GTH52_RS12330 | 283.7 | 8.2 | nitrogenase iron protein |
| | GTH52_RS13620 | 4.1 | 2.0 | nitrite reductase (NADH) large subunit |
| | GTH52_RS14395 | 0.4 | -1.3 | NADPH-dependent glutamate synthase |
| | GTH52_RS09300 | 0.3 | -1.9 | NADP-specific glutamate dehydrogenase |
| | GTH52_RS04440 | 8.8 | 3.6 | glutamate synthase subunit beta |
| | glnA | 5.0 | 2.3 | NADPH-dependent glutamate synthase |
| | gltB | 7.1 | 2.8 | glutamate synthase large subunit |
| | gdhA | 0.3 | -1.9 | NADP-specific glutamate dehydrogenase |
| | glnA | 5.0 | 2.3 | glutamine synthetase |
| | gltD | 8.9 | 3.2 | glutamate synthase subunit |

| | | | | |
|----------------------|---------------|-------|-----|---|
| | | | | beta |
| Amino acid transport | GTH52_RS08220 | 128.7 | 7.0 | ABC transporter permease |
| | glnP | 117.0 | 6.9 | amino acid ABC transporter permease |
| | glnH | 41.7 | 5.4 | transporter substrate-binding domain-containing protein |
| | glnQ | 36.1 | 5.2 | amino acid ABC transporter ATP-binding protein |
| | peb1C | 2.2 | 1.1 | amino acid ABC transporter ATP-binding protein |

Supplementary Figures

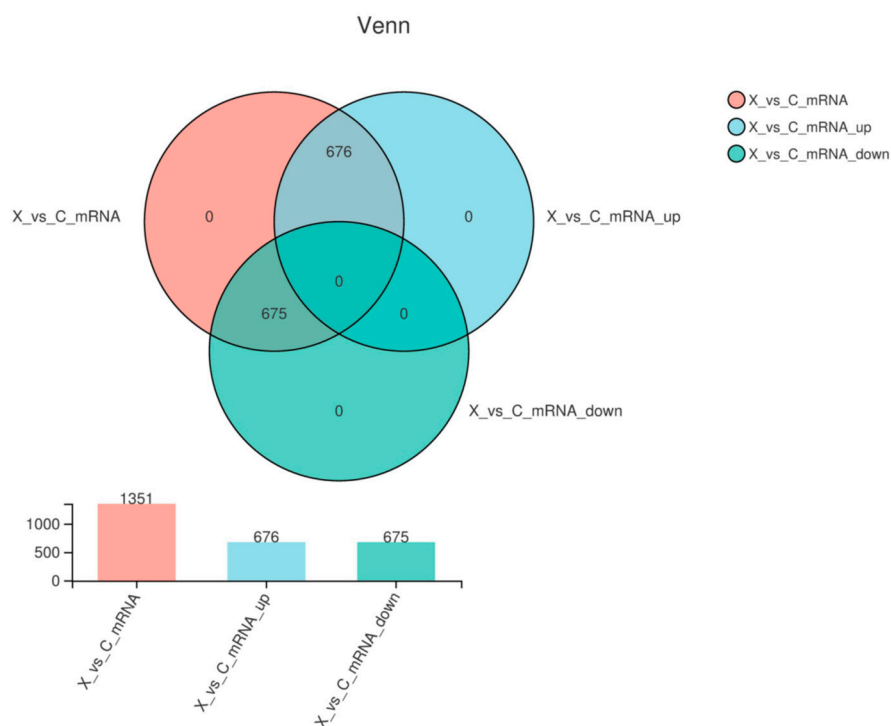


Figure S1 The Venn analysis showed the number of genes in each gene set and the overlapping relationship between gene sets.

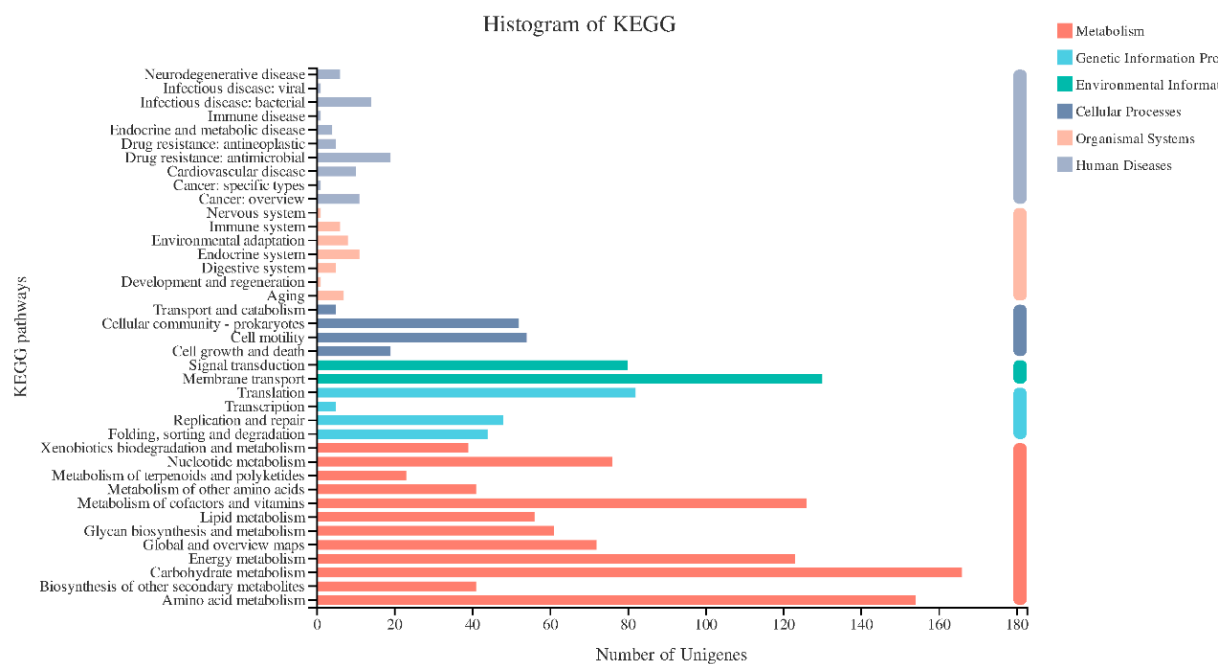


Figure S2 The KEGG annotation analysis of differentially expressed genes.