

Table S1 Statistics of the transcriptome sequencing data

| Group | Sample | Clean Reads | HQ Clean Reads | Q20 (%) | Q30 (%) | GC Content (%) | Reads mapped to genome (%) |
|-------------------------------|--------|-------------|----------------|---------|---------|----------------|----------------------------|
| ZJ-T | 1 | 25602240 | 25389872 | 98.30 | 94.77 | 46.58 | 95.04% |
| | 2 | 21682388 | 21541760 | 98.52 | 95.22 | 46.90 | 96.42% |
| | 3 | 16938122 | 16807610 | 98.47 | 95.11 | 46.88 | 96.51% |
| ZJ-T- Δ <i>gcvB</i> | 1 | 21670674 | 21521282 | 98.46 | 95.10 | 46.99 | 96.44% |
| | 2 | 17402972 | 17260668 | 98.45 | 95.08 | 46.74 | 96.40% |
| | 3 | 25841482 | 25552878 | 98.47 | 95.12 | 47.03 | 96.03% |

Table S2 Nucleotide sequences of primers used in this study

| Primers | Sequence (5'-3') |
|---|---|
| For <i>gcvB</i> mutant strain construction | |
| pSW7848_F | GTCTGATTTCGTTACCAATTATGACAAC |
| pSW7848_R | GAATTCGATATCAAGCTTATCGATAC |
| <i>gcvB</i> -UP_F | ataagcttgatatacgaattcTAAGCAGGTTTCTCACTAC |
| <i>gcvB</i> -UP_R | tatttcacccTCTATCAAAAATCTCATCCG |
| <i>gcvB</i> -DOWN_F | tttgatagaGGGTGAAATATAGAATTTATCTG |
| <i>gcvB</i> -DOWN_R | taattggaacgaatcagacAGTGATTCATCCAATACTTC |
| Del-check-pSW7848-F | TCACTGTCCCTTATTCGCACC |
| Del-check-pSW7848-R | CTGCTTTTGAGCACTACCCG |
| Δ - <i>gcvB</i> -F | AGTATCCTTGAGCAAGTGGTTC |
| Δ - <i>gcvB</i> -R | CTACGTTCCAACACCTTATCTGTC |
| For <i>gcvB</i> complementary strain construction | |
| pMMB207_F | AGAAGCGGTCTGATAAAACAGAATTTGC |
| pMMB207_R | GCGCAACGCAATTAATGTAAGTTAG |
| <i>gcvB</i> -F | ttacattaattgcgttgcgcaAAATACGTTAAAAGGCGCAAATTG |
| <i>gcvB</i> -R | tgttttatcagaccgttctTGTCGTTGTGCAACAGC |
| pMMB207-check-F | ATGCTCTTCTGCTCCCGAAC |
| pMMB207-check-R | ACGGCGTTTCACTTCTGAGT |
| For translational fusions | |
| pSCT32-gfp_F | GTGAGCAAGGGCGAGGAGCT |
| pSCT32-gfp_R | TAAATGCATGCCGCTTCGCCTT |
| pSCT32-gfp-check-F | CGCTATCGCTACGTGACTGG |
| pSCT32-gfp-check-R | GTTTCACTTCTGAGTTCCGGCATG |
| <i>cysK</i> -TL_fwd | GGCGAAGCGGCATGCATTTAAAGACGTCATTTGTCAGG |
| <i>cysK</i> -TL_rev | AGCTCCTCGCCCTTGCTCACGTAGATTTTGCTCATAGTGATG |
| <i>cysN</i> -TL_fwd | GGCGAAGCGGCATGCATTTACCCCTGGTTGTTATCCATTG |
| <i>cysN</i> -TL_rev | GCCAAGCTTGGTACCAGATCAACTGCACTGTTCATTATC |
| <i>ilvG</i> -TL_fwd | GGCGAAGCGGCATGCATTTACCTACTAAGGTAAACCCCTGG |
| <i>ilvG</i> -TL_rev | AGCTCCTCGCCCTTGCTCACTTGTGCACCAGTCATCGTAAAC |
| For T7 in <i>vitro</i> transcription | |
| T7- <i>gcvB</i> -F | TAATACGACTCACTATAGGGCGCAACACGGGCCTGAAC |
| T7- <i>gcvB</i> -R | TAAAAAAACACCGCCTAATTTAGGCG |
| For Hfq recombinant protein construction | |
| pET28b_F | CACCACCACCACCACCAC |
| pET28b_R | GGTATATCTCCTTCTTAAAGTTAAACAAAATTATTTTC |
| Hfq-ORF_fwd | ttaagaaggagatataccATGGCTAAGGGGCAATCTC |
| Hfq-ORF_rev | tcagtgggtgggtgggtgATCTTCAGATTTCTCTTGTGGAC |
| pET28b-check-F | aagtggcgagcccgatcttc |
| pET28b-check-R | CTAGGGCGCTGGCAAGTGTA |

For qPCR

| | |
|-------------------|------------------------|
| q- <i>gcvB</i> -F | CAGGGAGTGTGGACAAAACA |
| q- <i>gcvB</i> -R | TGAACGGCTTGATTTCTTTGGA |
| q- <i>ilvC</i> -F | ACCGGTCACTTCTCTAGCAC |
| q- <i>ilvC</i> -R | GAATGCTAGCTCAACACCCG |
| q- <i>ilvD</i> -F | TGCAACGGGTGTGAAAGAAG |
| q- <i>ilvD</i> -R | TTCTTTCGCAATACCGCCAG |
| q- <i>ilvE</i> -F | CACTGCGCCAAAACAACTC |
| q- <i>ilvE</i> -R | TCCAGCTTGAAATCATCGCG |
| q- <i>cysM</i> -F | ACGACACTAAGCTTTGCGTG |
| q- <i>cysM</i> -R | CCGACTTTACGCCCAATCAG |
| q- <i>cysK</i> -F | ATGAGCCTAGAACGCCGTAA |
| q- <i>cysK</i> -R | CGTCGATTTACCGTCTGTC |
| q- <i>cysD</i> -F | GGGCTGTAGTCCGTTTGTTT |
| q- <i>cysD</i> -R | TGAATACACGCGCTCTTTTCG |
| q- <i>cysN</i> -F | AAGCACTTTGTTGTCGCGAT |
| q- <i>cysN</i> -R | ATCCACCACATTGTCCCCTT |
| q- <i>cysH</i> -F | TAGTTACTCGCGCCAAAACG |
| q- <i>cysH</i> -R | TCAATTCCCTCTACGCCCTG |
| q- <i>cysI</i> -F | GCTTAATGGATGACGGCGTT |
| q- <i>cysI</i> -R | GACACCCAGTTACACGCAAA |
| q- <i>cysJ</i> -F | TTGGTTTGCTTCGTCGTCTG |
| q- <i>cysJ</i> -R | TCTTCGAGACGCTGTGCTAA |
| q- <i>hutU</i> -F | TAAACGCGCTACTCAACACG |
| q- <i>hutU</i> -R | ATGACGCATGACACCAGTTG |
| q- <i>hutG</i> -F | TGGCGTCTCATTACTCGGTT |
| q- <i>hutG</i> -R | GCTTGAAATGGTTGCTGCAC |
| q- <i>hutI</i> -F | GCACGCTATTTTCGCCTTACA |
| q- <i>hutI</i> -R | CTACCAGACGTTTTGCTCCG |
| q-16S-F | CTGGAAGTGAAGACACGGTCC |
| q-16S-R | CTCGCACCCCTCCGTATTACC |

Table S3 *Vibrio alginolyticus* genes and/or proteins are up/down regulated significantly in *gcvB* knockout strain

| id | Symbol | Description | T-FC | T-FDR | P-FC | P-FDR |
|--------------------------|----------------|--|-------|--------|-------|--------|
| <u>Metabolism</u> | | | | | | |
| BAU10_18365 | <i>VC_1589</i> | alpha-acetolactate decarboxylase | -2.29 | 0.0107 | / | / |
| BAU10_00850 | <i>mtlD</i> | mannitol-1-phosphate 5-dehydrogenase | 5.72 | 0.0000 | 2.48 | 0.0003 |
| BAU10_00855 | <i>mtlA</i> | PTS mannitol transporter subunit II | 2.47 | 0.0429 | 1.82 | 0.0171 |
| BAU10_21550 | <i>otnI</i> | hydroxypyruvate isomerase family protein | / | / | 1.52 | 0.0001 |
| BAU10_18845 | -- | NADH:ubiquinone oxidoreductase | -2.76 | 0.0225 | / | / |
| BAU10_20290 | <i>prkC</i> | serine/threonine protein kinase | -2.04 | 0.0207 | / | / |
| BAU10_13125 | <i>argF</i> | Ornithine carbamoyltransferase | 4.58 | 0.0147 | / | / |
| BAU10_13135 | <i>pyrB</i> | aspartate carbamoyltransferase catalytic subunit | -2.69 | 0.0044 | / | / |
| BAU10_13665 | <i>argB</i> | acetylglutamate kinase | 6.70 | 0.0347 | / | / |
| BAU10_13670 | <i>argC</i> | N-acetyl-gamma-glutamyl-phosphate reductase | 5.66 | 0.0107 | / | / |
| BAU10_09145 | <i>metE</i> | methionine synthase | -3.14 | 0.0004 | / | / |
| BAU10_05660 | <i>hutU</i> | urocanate hydratase | 2.14 | 0.0083 | / | / |
| BAU10_05665 | <i>hutG</i> | formimidoylglutamase | 2.72 | 0.0000 | / | / |
| BAU10_05670 | <i>hutI</i> | imidazolonepropionase | 2.32 | 0.0024 | / | / |
| BAU10_03770 | <i>cysM</i> | cysteine synthase/cystathionine beta-synthase family protein | 5.56 | 0.0007 | -1.68 | 0.0097 |
| BAU10_03130 | -- | putative nitrogen regulatory protein P-II family protein | 2.80 | 0.0207 | / | / |
| BAU10_00735 | <i>leuB</i> | 3-isopropylmalate dehydrogenase | / | / | 1.99 | 0.0000 |
| BAU10_13495 | <i>cysI</i> | assimilatory sulfite reductase (NADPH) hemoprotein subunit | / | / | -2.36 | 0.0000 |
| BAU10_15025 | <i>ilvG</i> | acetolactate synthase II large subunit | / | / | 3.86 | 0.0000 |
| BAU10_13500 | <i>cysJ</i> | sulfite reductase [NADPH] flavoprotein, alpha-component | / | / | -2.43 | 0.0000 |
| BAU10_13490 | <i>cysH</i> | phosphoadenosine phosphosulfate reductase | / | / | -2.30 | 0.0000 |
| BAU10_22370 | <i>tdh</i> | L-threonine 3-dehydrogenase | / | / | 2.16 | 0.0000 |

| | | | | | | |
|-------------------------|-------------------|--|-------|--------|-------|--------|
| BAU10_00495 | <i>cysN</i> | sulfate adenylyltransferase subunit CysN | / | / | -2.27 | 0.0000 |
| BAU10_15045 | <i>ilvA</i> | threonine ammonia-lyase, biosynthetic | / | / | 1.79 | 0.0000 |
| BAU10_00490 | <i>cysD</i> | sulfate adenylyltransferase subunit 2 | / | / | -2.36 | 0.0001 |
| BAU10_00730 | <i>leuC</i> | 3-isopropylmalate dehydratase large subunit | / | / | 2.17 | 0.0003 |
| BAU10_22375 | <i>kbl</i> | glycine C-acetyltransferase | / | / | 2.07 | 0.0000 |
| BAU10_00725 | <i>leuD</i> | 3-isopropylmalate dehydratase small subunit | / | / | 2.26 | 0.0000 |
| BAU10_17915 | <i>aroG</i> | 3-deoxy-7-phosphoheptulonate synthase AroG | / | / | 1.81 | 0.0000 |
| BAU10_17355 | <i>OCC_04335</i> | aminotransferase, classes I and II superfamily | / | / | 2.01 | 0.0000 |
| BAU10_23920 | -- | lactoylglutathione lyase | / | / | 1.59 | 0.0443 |
| BAU10_05890 | -- | peptidase S41 | / | / | -1.75 | 0.0316 |
| BAU10_22890 | <i>MGYG_04702</i> | putative carboxypeptidase G2 | / | / | -1.53 | 0.0006 |
| BAU10_17520 | <i>dgkA</i> | diacylglycerol kinase | 3.80 | 0.0153 | / | / |
| BAU10_09900 | -- | aryl-sulfate sulfotransferase | 3.15 | 0.0083 | / | / |
| BAU10_18320 | <i>HI_0002</i> | putative long-chain-fatty-acid-CoA ligase | / | / | 1.51 | 0.0000 |
| BAU10_11015 | <i>glpF</i> | glycerol uptake facilitator protein GlpF | / | / | 1.60 | 0.0160 |
| <u>Transport</u> | | | | | | |
| BAU10_20535 | <i>artP</i> | arginine ABC transporter ATP-binding protein ArtP | 5.52 | 0.0249 | / | / |
| BAU10_17740 | <i>mdtN</i> | HlyD family secretion protein | 2.21 | 0.0327 | / | / |
| BAU10_07410 | <i>aapJ</i> | amino acid ABC transporter, periplasmic amino acid-binding protein | / | / | 2.69 | 0.0000 |
| BAU10_15175 | <i>patH</i> | amino acid ABC transporter, periplasmic amino acid-binding portion | / | / | -1.59 | 0.0000 |
| BAU10_02555 | <i>metN</i> | methionine ABC transporter ATP-binding protein MetN | / | / | 1.57 | 0.0001 |
| BAU10_20240 | <i>tssC</i> | type VI secretion system contractile sheath large subunit | -2.06 | 0.0072 | / | / |
| BAU10_20245 | <i>tssB</i> | type VI secretion system contractile sheath small subunit | -2.09 | 0.0078 | / | / |
| BAU10_20285 | <i>tagH</i> | type VI secretion system-associated FHA domain protein | -2.81 | 0.0083 | / | / |
| BAU10_07935 | <i>yscB</i> | type III secretion system chaperone | / | / | 1.99 | 0.0000 |
| BAU10_07880 | -- | type III chaperone | / | / | 2.44 | 0.0002 |

| | | | | | | |
|--|----------------|---|---------|--------|-------|--------|
| BAU10_07820 | <i>yscP</i> | type III secretion system needle length determinant | / | / | 1.94 | 0.0017 |
| BAU10_07915 | <i>yscF</i> | type III export protein YscF | / | / | 2.22 | 0.0038 |
| BAU10_07960 | <i>exsE2</i> | Type III secretion regulator | / | / | 2.30 | 0.0457 |
| BAU10_17790 | <i>secF</i> | putative protein-export membrane protein | / | / | 1.94 | 0.0316 |
| BAU10_07780 | <i>yscV</i> | type III secretion protein V | / | / | 2.75 | 0.0282 |
| BAU10_22965 | <i>sstT</i> | sodium/dicarboxylate symporter | / | / | 4.70 | 0.0000 |
| BAU10_18025 | <i>iutA</i> | TonB-dependent receptor | / | / | 1.59 | 0.0000 |
| BAU10_07860 | -- | cation transporter | / | / | 2.92 | 0.0316 |
| BAU10_19990 | <i>dcbB</i> | aerobic C4-dicarboxylate transporter | / | / | -1.92 | 0.0020 |
| Cellular process | | | | | | |
| BAU10_17000 | <i>ompV</i> | MipA/OmpV family protein | 3.00 | 0.0042 | / | / |
| BAU10_22900 | <i>yjiH</i> | membrane protein | / | / | -1.88 | 0.0017 |
| BAU10_09875 | <i>bdlA</i> | methyl-accepting chemotaxis protein | / | / | 1.69 | 0.0000 |
| BAU10_21265 | <i>pctA</i> | methyl-accepting chemotaxis protein | / | / | 3.27 | 0.0001 |
| BAU10_19335 | <i>tcpI</i> | methyl-accepting chemotaxis protein | / | / | -1.52 | 0.0078 |
| Genetic information processing | | | | | | |
| BAU10_16040 | <i>VP0184</i> | DNA repair protein RadC | 2.18 | 0.0068 | / | / |
| BAU10_14995 | -- | ribonuclease H | 3.19 | 0.0074 | / | / |
| BAU10_00990 | -- | HNH endonuclease | 2.00 | 0.0251 | / | / |
| BAU10_04605 | <i>ssb</i> | Single-stranded DNA-binding protein | 1986.67 | 0.0327 | / | / |
| BAU10_20810 | <i>SAR0107</i> | putative AraC-type regulatory protein | -2.03 | 0.0078 | / | / |
| BAU10_13685 | -- | predicted transcriptional regulator | 2.19 | 0.0005 | / | / |
| BAU10_08050 | <i>rbcR</i> | LysR family transcriptional regulator | / | / | 4.63 | 0.0000 |
| BAU10_14150 | <i>groL1</i> | chaperonin GroEL | -2.10 | 0.0007 | / | / |
| BAU10_14155 | <i>groS1</i> | 10 kDa chaperonin GroES protein | -2.86 | 0.0078 | / | / |
| Unknown function and hypothetical protein | | | | | | |

| | | | | | | |
|-------------|------------------|--|-------|--------|-------|--------|
| BAU10_21320 | -- | hypothetical protein | 4.31 | 0.0000 | / | / |
| BAU10_17525 | -- | hypothetical protein | 3.23 | 0.0182 | / | / |
| BAU10_00805 | -- | DUF3316 domain-containing protein | 2.62 | 0.0424 | / | / |
| BAU10_07600 | -- | DUF3316 domain-containing protein | 2.27 | 0.0300 | / | / |
| BAU10_08055 | -- | hypothetical protein | 5.70 | 0.0016 | / | / |
| BAU10_10975 | -- | TDT family transporter | 2.30 | 0.0078 | / | / |
| BAU10_13100 | -- | DUF2061 domain-containing protein | -2.65 | 0.0015 | / | / |
| BAU10_09150 | -- | DUF1852 domain-containing protein | -4.28 | 0.0000 | / | / |
| BAU10_06490 | <i>HI_1246</i> | LTA synthase family protein | 2.67 | 0.0207 | 4.01 | 0.0006 |
| BAU10_21320 | -- | hypothetical protein | / | / | 7.72 | 0.0003 |
| BAU10_08435 | -- | hypothetical protein | / | / | -1.74 | 0.0004 |
| BAU10_07875 | <i>vopS</i> | Va1686 | / | / | 2.52 | 0.0000 |
| BAU10_07920 | -- | VseE | / | / | 1.89 | 0.0000 |
| BAU10_06625 | <i>Ping_1243</i> | heme-degrading domain-containing protein | / | / | 1.69 | 0.0029 |
| BAU10_18215 | -- | hypothetical protein | / | / | -1.61 | 0.0145 |
| BAU10_07765 | <i>lcrV</i> | VcrV | / | / | 2.10 | 0.0043 |

Table S4 Twenty identified differentially expressed proteins for PPI network construction
(STRING score > 700)

| protein1 | protein2 | combined_score |
|-------------|-------------|----------------|
| <i>leuD</i> | <i>leuC</i> | 999 |
| <i>leuD</i> | <i>leuB</i> | 999 |
| <i>leuD</i> | <i>ilvG</i> | 982 |
| <i>leuD</i> | <i>ilvA</i> | 885 |
| <i>leuC</i> | <i>leuB</i> | 999 |
| <i>leuC</i> | <i>ilvG</i> | 982 |
| <i>leuC</i> | <i>ilvA</i> | 889 |
| <i>leuB</i> | <i>ilvG</i> | 998 |
| <i>leuB</i> | <i>ilvA</i> | 990 |
| <i>lcrD</i> | <i>bdlA</i> | 703 |
| <i>bdlA</i> | <i>tcpI</i> | 995 |
| <i>bdlA</i> | <i>pctA</i> | 839 |
| <i>tcpI</i> | <i>pctA</i> | 805 |
| <i>patH</i> | <i>cysK</i> | 815 |
| <i>cysK</i> | <i>cysN</i> | 987 |
| <i>cysK</i> | <i>cysD</i> | 987 |
| <i>cysK</i> | <i>cysH</i> | 993 |
| <i>cysK</i> | <i>cysI</i> | 998 |
| <i>cysK</i> | <i>cysJ</i> | 998 |
| <i>cysN</i> | <i>cysD</i> | 999 |
| <i>cysN</i> | <i>cysH</i> | 999 |
| <i>cysN</i> | <i>cysI</i> | 999 |
| <i>cysN</i> | <i>cysJ</i> | 999 |
| <i>cysD</i> | <i>cysH</i> | 988 |
| <i>cysD</i> | <i>cysI</i> | 999 |
| <i>cysD</i> | <i>cysJ</i> | 999 |
| <i>cysH</i> | <i>cysI</i> | 999 |
| <i>cysH</i> | <i>cysJ</i> | 999 |
| <i>cysI</i> | <i>cysJ</i> | 999 |
| <i>mtlA</i> | <i>mtlD</i> | 999 |
| <i>tdh</i> | <i>kbl</i> | 999 |
| <i>tdh</i> | <i>ilvA</i> | 900 |
| <i>ilvG</i> | <i>ilvA</i> | 997 |