**Supplementary Table 1**. Top 90 significant genes by 1-class SAM for evolved isolates grown individually.

| **ID** | **gene** | **$Log_2$ CV101/ JA122** | **$Log_2$ CV103/ JA122** | **$Log_2$ CV115/ JA122** | **$Log_2$ CV116/ JA122** | **gene product** | **Transcription Unit** | **MultiFun category** |
|---|---|---|---|---|---|---|---|---|
| b4036 | ***lamB*** | 3.6 | 5.1 | 2.9 | 2.2 | maltose outer membrane porin (maltoporin) | malK-lamB-malM (malKp) | transport; (The Outer Membrane Porin (OMP) Functional Superfamily); The Sugar Porin (SP) Family |
| b2148 | ***mglC*** | 3.5 | 3.1 | 2.6 | 2.5 | membrane component of an ABC superfamily methyl-galactoside transporter | mglBAC (mglBp) | metabolism; carbon utilization; transport; The ATP-binding Cassette (ABC) Superfamily |
| b3902 | ***rhaD*** | 3.4 | 3.4 | 2.7 | 2.7 | rhamnulose-1-phosphate aldolase | rhaBAD (rhaBp) | Metabolism; carbon utilization; |
| b2149 | ***mglA*** | 4.5 | 3.9 | 3.6 | 3.3 | fused methyl-galactoside transporter subunits of ABC superfamily: ATP-binding components | mglBAC (mglBp) | metabolism; carbon utilization; The ATP-binding Cassette (ABC) Superfamily |
| b2150 | ***mglB*** | 4.1 | 4.1 | 3.6 | 2.7 | periplasmic-binding component of an ABC superfamily methyl-galactoside transporter | mglBAC (mglBp) | Metabolism; carbon utilization; chaperoning, folding, transport; Primary Active Transporters; The ATP-binding Cassette (ABC) Superfamily |
| b1804 | ***rnd*** | 0.6 | 0.6 | 0.6 | 0.7 | ribonuclease D | rnd | metabolism; macromolecule degradation; information transfer; RNA modification |
| b0589 | ***fepG*** | 1.0 | 1.0 | 0.7 | 1.0 | membrane component of an ABC superfamily iron-enterobactin transporter | fepDGC (fepDp1) | transport; The ATP-binding Cassette (ABC) Superfamily |
| b3505 | ***insH-11*** | 0.7 | 1.0 | 1.2 | 1.2 | IS5 transposase | insH-11 | Extrachromosomal; transposon related |
| b3218 | ***insH-10*** | 0.7 | 0.9 | 1.1 | 1.1 | IS5 transposase | insH-10 | Extrachromosomal; transposon related |
| b0656 | ***insH-3*** | 0.6 | 0.9 | 1.0 | 1.0 | IS5 transposase | insH-3 | Extrachromosomal; transposon related |
| b0552 | ***insH-2*** | 0.7 | 0.8 | 1.0 | 1.1 | IS5 transposase | insH-2 | Extrachromosomal; prophage genes;transposon related |
| b2192 | ***insH-8*** | 0.6 | 0.9 | 1.0 | 1.1 | IS5 transposase | insH-8 | Extrachromosomal; transposon related |
| b1370 | ***insH-5*** | 0.7 | 0.9 | 1.0 | 1.1 | IS5 transposase | insH-5 | Extrachromosomal; prophage genes; transposon related |
| b1331 | ***insH-4*** | 0.6 | 0.9 | 1.0 | 1.1 | IS5 transposase | insH-4 | Extrachromosomal; transposon related |
| b2030 | ***insH-7*** | 0.6 | 0.9 | 1.1 | 1.1 | IS5 transposase | insH-7 | Extrachromosomal; transposon related |
| b2982 | ***insH-9*** | 0.6 | 0.9 | 1.1 | 1.2 | IS5 transposase | insH-9 | Extrachromosomal; transposon related |
| b0259 | ***insH-1*** | 0.7 | 0.9 | 1.1 | 1.1 | IS5 transposase | insH-1 | Extrachromosomal; prophage genes; transposon related |

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|---|---|---|---|---|---|---|---|---|
| b1994 | ***insH-6*** | 0.6 | 0.9 | 1.1 | 1.1 | IS5 transposase | insH-6 | Extrachromosomal; transposon related |
| b2289 | ***lrhA*** | 0.9 | 0.9 | 1.1 | 1.1 | DNA-binding transcriptional repressor of flagellar, motility and chemotaxis genes | lrhA | metabolism; energy metabolism, aerobic respiration, regulation; transcriptional level; repressor |
| b2147 | ***yeiA*** | 1.4 | 1.7 | 1.6 | 1.4 | predicted oxidoreductase | yeiAT (yeiTp) | metabolism; central intermediary metabolism; unassigned reversible reactions |
| b2151 | ***galS*** | 1.9 | 2.0 | 2.0 | 2.2 | DNA-binding transcriptional repressor | galS | metabolism; carbon utilization; regulation; transcriptional level; repressor |
| b1042 | ***csgA*** | -2.9 | -2.7 | -4.0 | -4.3 | cryptic curlin major subunit | csgBAC (csgBp) | metabolism; macromolecules (cellular constituent) biosynthesis; glycoprotein, cell structure; pilus, |
| b1923 | ***fliC*** | -2.6 | -2.7 | -3.5 | -3.8 | flagellar filament structural protein (flagellin) | fliC | metabolism; macromolecules (cellular constituent) biosynthesis; flagella |
| b0897 | ***ycaC*** | -2.9 | -1.8 | -3.6 | -3.6 | predicted hydrolase | ycaC | Metabolism; carbon utilization; amino acids |
| b1444 | ***ydcW*** | -1.4 | -2.6 | -3.3 | -3.3 | medium chain aldehyde dehydrogenase | ydcW | |
| b3555 | ***yiaG*** | -2.0 | -0.6 | -2.4 | -2.4 | predicted transcriptional regulator | yiaG | regulation; transcriptional level |
| b2665 | ***ygaU*** | -2.5 | -1.0 | -2.7 | -2.6 | predicted protein | ygaU | |
| b2080 | ***yegP*** | -2.4 | -1.1 | -2.6 | -2.4 | predicted protein | yegP | |
| b1896 | ***otsA*** | -2.4 | -0.7 | -2.6 | -2.4 | trehalose-6-phosphate synthase | otsBA (otsBp) | metabolism; central intermediary metabolism; glucose metabolism, |
| b1051 | ***msyB*** | -2.3 | -0.8 | -2.4 | -2.3 | predicted protein | msyB | transport; substrate; protein |
| b0812 | ***dps*** | -2.8 | -2.2 | -2.9 | -2.4 | Fe-binding and storage protein | dps | Information transfer; protein related; cell processes; adaptation to stress; starvation response |
| b4376 | ***osmY*** | -2.3 | -1.8 | -2.8 | -3.0 | periplasmic protein | osmY | Cell processes; adaptation to stress; osmotic pressure |
| b3447 | ***ggt*** | -2.2 | -1.9 | -2.9 | -2.9 | gamma-glutamyltranspeptidase | ggt | metabolism; macromolecules (cellular constituent) biosynthesis; thioredoxin, glutaredoxin |
| b1258 | ***yciF*** | -2.6 | -1.5 | -2.8 | -2.6 | conserved protein | yciGFE (yciGp) | |
| b1885 | ***tap*** | -1.5 | -2.0 | -2.8 | -2.9 | methyl-accepting protein IV | tar-tap-cheRBYZ (tarp) | regulation; posttranscriptional; cell processes; motility (incl. |
| b1443 | ***ydcV*** | -1.4 | -2.4 | -2.5 | -2.8 | membrane component of an ABC superfamily predicted spermidine/putrescine transporter | ydcSTUV | transport; The ATP-binding Cassette (ABC) Superfamily |
| b1040 | ***csgD*** | -1.7 | -1.8 | -2.3 | -2.6 | DNA-binding transcriptional regulator of adhesion determinants | csgDEFG (csgDp2) | Information transfer; RNA related; transcription related,activator |

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|---|---|---|---|---|---|---|---|---|
| b1967 | ***hchA*** | -1.9 | -1.9 | -2.8 | -2.0 | Hsp31 molecular chaperone | hchA | |
| b2924 | ***mscS*** | -2.0 | -1.7 | -1.9 | -2.1 | component of the MscS mechanosensitive channel | mscS | transport; Channel-type Transporters; The Small Conductance Mechanosensitive Ion Channel (MscS) Family |
| b1038 | ***csgF*** | -1.8 | -1.8 | -2.1 | -2.0 | predicted transport protein | csgDEFG (csgDp2) | transport; Putative uncharacterized transport protein, cell structure; pilus, curli subunit |
| b1480 | ***sra*** | -2.0 | -1.7 | -2.3 | -2.3 | 30S ribosomal subunit protein S22 | sraA (sraAp) | Information transfer; protein related; ribosomal proteins |
| b1482 | ***osmC*** | -2.1 | -1.9 | -2.2 | -2.1 | osmotically inducible, stress-inducible membrane protein | osmC | Cell processes; adaptation to stress; osmotic pressure |
| b2465 | ***tktB*** | -1.9 | -1.3 | -2.5 | -2.3 | transketolase 2, thiamin-binding | tktB | metabolism; carbon utilization; central intermediary metabolism; pentose phosphate shunt, non-oxidative branch,;nucleotide and nucleoside conversions |
| b2266 | ***elaB*** | -1.8 | -1.3 | -2.3 | -2.2 | conserved protein | elaB | |
| b2097 | ***fbaB*** | -1.8 | -1.2 | -2.3 | -2.1 | fructose-bisphosphate aldolase class I | fbaB | metabolism; energy metabolism, carbon; glycolysis |
| b1004 | ***wrbA*** | -2.0 | -1.4 | -2.3 | -2.0 | predicted flavoprotein in Trp regulation | wrbA-yccJ (wrbAp) | Metabolism; building block biosynthesis; amino acids; tryptophan |
| b1732 | ***katE*** | -1.9 | -1.5 | -2.2 | -2.1 | hydroperoxidase HPII(III) (catalase) | katE | Cell processes; protection; detoxification (xenobiotic metabolism) |
| b0871 | ***poxB*** | -1.6 | -2.7 | -2.0 | -1.9 | pyruvate dehydrogenase (pyruvate oxidase), thiamin-dependent, FAD-binding | ltaE-poxB-ybjT | metabolism; carbon utilization; central intermediary metabolism; pyruvate oxidation |
| b1478 | ***adhP*** | -1.3 | -2.2 | -1.8 | -1.7 | alcohol dehydrogenase, 1-propanol preferring | adhP | metabolism; energy metabolism, carbon; anaerobic respiration |
| b1037 | ***csgG*** | -1.6 | -1.9 | -1.7 | -1.4 | outer membrane channel lipoprotein | csgDEFG (csgDp2) | transport; Putative uncharacterized transport protein, cell structure; pilus, curli subunit |
| b1431 | ***ydcL*** | -1.5 | -1.5 | -1.6 | -1.8 | predicted lipoprotein | ydcL | |
| b1490 | ***yddV*** | -1.5 | -1.5 | -1.5 | -1.8 | predicted diguanylate cyclase | yddV-dos | |
| b1197 | ***treA*** | -1.6 | -1.3 | -1.8 | -1.9 | periplasmic trehalase | treA | metabolism; central intermediary metabolism; adaptation to stress; osmotic pressure |
| b1101 | ***ptsG*** | -1.8 | -1.4 | -1.7 | -1.4 | PTS system glucose-specific IICB component | ptsG | Metabolism; carbon utilization; regulation; type of regulation; posttranscriptional; transport |
| b1259 | ***yciG*** | -1.7 | -1.5 | -1.8 | -1.5 | predicted protein | yciGFE (yciGp) | |
| b0753 | ***ybgS*** | -1.9 | -1.2 | -1.9 | -1.7 | conserved protein | ybgS | |
| b3515 | ***gadW*** | -1.6 | -1.3 | -2.1 | -1.7 | DNA-binding transcriptional activator | gadXW (gadXp) | Information transfer; RNA related; transcription related, regulation; activator |
| b1710 | ***btuE*** | -1.5 | -1.1 | -2.0 | -1.8 | predicted glutathione | btuCED | Metabolism; building block biosynthesis; cobalamin (Vitamin |

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|---|---|---|---|---|---|---|---|---|
| | | | | | | peroxidase | | B12), transport; Primary Active Transporters; The ATP-binding Cassette (ABC) Superfamily |
| b1810 | ***yoaC*** | -1.8 | -0.9 | -1.8 | -2.1 | predicted protein | yoaC | |
| b1050 | ***yceK*** | -1.9 | -0.9 | -2.4 | -1.8 | predicted lipoprotein | yceK | |
| b2464 | ***talA*** | -1.9 | -1.0 | -2.1 | -1.8 | transaldolase A | talA | metabolism; central intermediary metabolism; pentose phosphate shunt, non-oxidative branch |
| b0453 | ***ybaY*** | -1.9 | -1.0 | -2.1 | -2.0 | predicted outer membrane lipoprotein | ybaY | metabolism; macromolecules biosynthesis; lipoprotein; glycoprotein |
| b1836 | ***yebV*** | -1.4 | -0.7 | -2.2 | -1.9 | predicted protein | yebV | |
| b1064 | ***grxB*** | -1.6 | -1.3 | -1.6 | -1.0 | glutaredoxin 2 (Grx2) | grxB | metabolism; macromolecules (cellular constituent) biosynthesis; large molecule carriers; thioredoxin, glutaredoxin |
| b1003 | ***yccJ*** | -1.3 | -1.1 | -1.7 | -1.4 | predicted protein | wrbA-yccJ (wrbAp) | |
| b1241 | ***adhE*** | -1.4 | -0.7 | -1.2 | -1.6 | fused acetaldehyde-CoA dehydrogenase and iron-dependent alcohol dehydrogenase and pyruvate-formate lyase deactivase | adhE | metabolism; energy metabolism, carbon; fermentation |
| b1709 | ***btuD*** | -1.1 | -0.6 | -1.7 | -1.3 | vitamin B12 transporter subunit : ATP-binding component of ABC superfamily | btuCED | Metabolism; building block biosynthesis; cobalamin (Vitamin B12), transport; The ATP-binding Cassette (ABC) Superfamily |
| b1661 | ***cfa*** | -1.5 | -0.6 | -1.6 | -1.3 | cyclopropane fatty acyl phospholipid synthase | cfa | Metabolism; building block biosynthesis; fatty acid and phosphatidic acid |
| b2594 | ***rluD*** | -0.4 | -0.5 | -0.6 | -0.6 | 23S rRNA pseudouridine synthase | rluD-yfiH | Information transfer; RNA related; RNA modification |
| b1049 | ***mdoH*** | -0.4 | -0.7 | -0.8 | -0.6 | glycosyl transferase | mdoGH (mdoGp1) | Cell processes; adaptation to stress; osmotic pressure |
| b1641 | ***slyB*** | -0.8 | -1.3 | -0.8 | -0.7 | outer membrane lipoprotein | slyB | Cell structure; membrane |
| b4384 | ***deoD*** | -0.7 | -0.9 | -0.9 | -0.7 | purine-nucleoside phosphorylase | deoCABD (deoCp1) | metabolism; central intermediary metabolism; nucleotide and nucleoside conversions |
| b0708 | ***phr*** | -0.8 | -0.9 | -0.9 | -0.8 | deoxyribodipyrimidine photolyase | ybgA-phr (ybgAp1) | Metabolism; building block biosynthesis; riboflavin (Vitamin B2), FAD, FMN, information transfer; DNA related; DNA repair |
| b3401 | ***hslO*** | -0.8 | -0.7 | -0.8 | -0.9 | heat shock protein Hsp33 | hslR-hslO (hslRp) | Information transfer; protein related; chaperoning, folding |
| b2415 | ***ptsH*** | -0.9 | -0.6 | -0.8 | -0.9 | phosphohistidinoprotein-hexose phosphotransferase component of PTS system (Hpr) | ptsHI-crr (ptsHp1) | metabolism; carbon utilization; Group Translocators; The Phosphotransferase System HPr (HPr) Family, transport; substrate; sugar |
| b3919 | ***tpiA*** | -0.9 | -0.9 | -1.0 | -1.1 | triosephosphate isomerase | tpiA | metabolism; energy metabolism, carbon; glycolysis |

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|---|---|---|---|---|---|---|---|---|
| b1380 | ***ldhA*** | -1.0 | -0.8 | -0.8 | -1.0 | fermentative D-lactate dehydrogenase, NAD-dependent | ldhA | metabolism; energy metabolism, carbon; fermentation |
| b4383 | ***deoB*** | -1.1 | -1.2 | -1.2 | -1.1 | phosphopentomutase | deoCABD (deoCp1) | metabolism; central intermediary metabolism; nucleotide and nucleoside conversions |
| b0903 | ***pflB*** | -0.6 | -0.9 | -1.1 | -1.1 | pyruvate formate lyase I | focA-pflB (focAp1) | metabolism; energy metabolism, carbon; anaerobic respiration, carbon utilization; central intermediary metabolism; threonine catabolism |
| b1039 | ***csgE*** | -1.0 | -0.8 | -1.5 | -1.4 | predicted transport protein | csgDEFG (csgDp2) | transport; Transporters of Unknown Classification; Putative uncharacterized transport protein, cell structure; pilus,curli |
| b1957 | ***yodC*** | -1.0 | -0.9 | -1.4 | -1.2 | predicted protein | yodC | |
| b0904 | ***focA*** | -1.0 | -0.7 | -1.4 | -1.2 | formate transporter | focA-pflB (focAp1) | metabolism; carbon utilization; transport; The Formate-Nitrite Transporter (FNT) Family |
| b2687 | ***luxS*** | -1.1 | -0.8 | -1.3 | -1.2 | S-ribosylhomocysteine lyase | luxS | regulation; transcriptional level; complex regulation; quorum sensing |
| b3024 | ***ygiW*** | -1.1 | -0.8 | -1.3 | -1.2 | conserved protein | ygiW | |
| b2779 | ***eno*** | -1.0 | -1.0 | -1.2 | -1.4 | enolase | eno-pyrG (pyrGp) | metabolism; energy metabolism, carbon; glycolysis; anaerobic respiration; gluconeogenesis |
| b1795 | ***yeaQ*** | -1.1 | -0.9 | -1.1 | -1.1 | conserved inner membrane protein | yeaQ | |
| b0707 | ***ybgA*** | -1.2 | -0.7 | -1.2 | -1.0 | conserved protein | ybgA-phr (ybgAp1) | |
| b3336 | ***bfr*** | -1.1 | -0.7 | -1.1 | -1.0 | bacterioferritin, iron storage and detoxification protein | bfd-bfr | Cell processes; adaptation to stress; Fe aquisition |
| b0965 | ***yccU*** | -0.9 | -0.6 | -1.3 | -1.0 | predicted CoA-binding protein | yccU | |
| b2417 | ***crr*** | -0.9 | -0.5 | -1.1 | -1.1 | glucose-specific enzyme IIA component of PTS | ptsHI-crr (ptsHp1) | metabolism; carbon utilization; The PTS Fructose-Mannitol (Fru) Family, transport; substrate; D-glucose/trehalose |