**Table S3. List of genes differentially expressed in *P. putida* DLL-△*pnpR* grown on glucose plus PNP compared to glucose. The fold changes are reported in log2-based format.**

|  |  |  |  |
| --- | --- | --- | --- |
| **Genes** | **Annotated functions** | **Fold changes**  **(log2)** | **Results** |
| DW66\_0004 | F0F1 ATP synthase subunit epsilon | 1.51 | up |
| DW66\_0005 | F0F1 ATP synthase subunit beta | 1.91 | up |
| DW66\_0010 | ATP synthase C chain | 1.18 | up |
| DW66\_0011 | F0F1 ATP synthase subunit A | -1.57 | down |
| DW66\_0012 | F0F1 ATP synthase subunit I | -1.57 | down |
| DW66\_0014 | cobyrinic acid ac-diamide synthase | -1.37 | down |
| DW66\_0017 | tRNA modification GTPase TrmE | 1.11 | up |
| DW66\_0018 | inner membrane protein translocase component YidC | -1.70 | down |
| DW66\_0019 | ribonuclease P | -4.16 | down |
| DW66\_0020 | 50S ribosomal protein L34 | -3.35 | down |
| DW66\_0021 | chromosomal replication initiation protein | -1.18 | down |
| DW66\_0025 | transmembrane protein | -1.83 | down |
| DW66\_0026 | *sigma*-54 dependent transcription regulator | -2.40 | down |
| DW66\_0027 | *beta*-lactamase domain-containing protein | 3.18 | up |
| DW66\_0028 | FAD-dependent pyridine nucleotide-disulfide oxidoreductase | 2.29 | up |
| DW66\_0030 | transcriptional regulator LysR | -2.52 | down |
| DW66\_0032 | transporter protein | 1.21 | up |
| DW66\_0036 | glycyl-tRNA synthetase subunit alpha | -1.36 | down |
| DW66\_0037 | DNA-3-methyladenine glycosylase I | -1.82 | down |
| DW66\_0038 | lipid A biosynthesis lauroyl acyltransferase | -1.79 | down |
| DW66\_0039 | Chaperone protein YscY (Yop proteins translocation protein Y) | 1.49 | up |
| DW66\_0042 | methionyl-tRNA formyltransferase | -1.15 | down |
| DW66\_0044 | DNA protecting protein DprA | -1.05 | down |
| DW66\_0045 | RimN | 1.26 | up |
| DW66\_0046 | hypothetical protein | 1.44 | up |
| DW66\_0047 | alcohol dehydrogenase | 1.26 | up |
| DW66\_0048 | coproporphyrinogen III oxidase | -1.21 | down |
| DW66\_0052 | choline-sulfatase | -2.42 | down |
| DW66\_0054 | NADH-flavin reductase | -1.12 | down |
| DW66\_0055 | DOPA 45-dioxygenase | -1.06 | down |
| DW66\_0056 | tryptophan synthase subunit alpha | 1.85 | up |
| DW66\_0058 | transcriptional regulator LysR | -1.86 | down |
| DW66\_0059 | hypothetical protein | -1.22 | down |
| DW66\_0060 | Dodecin Flavin-binding | 5.38 | up |
| DW66\_0061 | hypothetical protein | 2.77 | up |
| DW66\_0062 | luciferase-like monooxygenase | 1.48 | up |
| DW66\_0063 | protein OsmC | -2.30 | down |
| DW66\_0064 | hypothetical protein | 1.27 | up |
| DW66\_0065 | lipoprotein | 1.27 | up |
| DW66\_0066 | lipoprotein | -3.06 | down |
| DW66\_0067 | hypothetical protein | -1.46 | down |
| DW66\_0069 | carbonic anhydrase | -1.19 | down |
| DW66\_0071 | hypothetical protein | 1.70 | up |
| DW66\_0072 | peptidase M3A and M3B, thimet/oligopeptidase F | -3.49 | down |
| DW66\_0073 | radical SAM domain-containing protein | -1.29 | down |
| DW66\_0075 | sulfate transporter | -3.02 | down |
| DW66\_0077 | cytochrome c oxidase subunit II | 2.07 | up |
| DW66\_0078 | cytochrome c oxidase subunit I | 4.21 | up |
| DW66\_0079 | cytochrome C oxidase assembly protein | 4.18 | up |
| DW66\_0080 | cytochrome c oxidase subunit III | 4.48 | up |
| DW66\_0082 | Cytochrome oxidase biogenesis protein Surf1, facilitates heme A insertion | 1.98 | up |
| DW66\_0083 | transmembrane protein | 2.81 | up |
| DW66\_0084 | cytochrome oxidase assembly | 2.17 | up |
| DW66\_0085 | protoheme IX farnesyltransferase | 1.40 | up |
| DW66\_0087 | NLPA lipoprotein | 1.80 | up |
| DW66\_0088 | binding-protein-dependent transport system inner membrane protein | -1.04 | down |
| DW66\_0089 | DL-methionine transporter, ATP-binding subunit | -1.95 | down |
| DW66\_0090 | hydroperoxidase II | -2.14 | down |
| DW66\_0091 | lipoprotein | -2.71 | down |
| DW66\_0092 | zinc transporter | -1.58 | down |
| DW66\_0102 | DSBA oxidoreductase | -2.83 | down |
| DW66\_0103 | endonuclease/exonuclease/phosphatase | -3.17 | down |
| DW66\_0104 | diguanylate cyclase | -2.66 | down |
| DW66\_0105 | N-acetylmuramyl-L-alanine amidase, negative regulator of AmpC, AmpD | -1.11 | down |
| DW66\_0106 | EAL domain-containing protein | -2.39 | down |
| DW66\_0108 | two component sigma54 specific transcriptional regulator | -1.54 | down |
| DW66\_0109 | transport-associated protein | -2.73 | down |
| DW66\_0111 | hypothetical protein | 1.08 | up |
| DW66\_0112 | inhibitor of vertebrate lysozyme | -1.59 | down |
| DW66\_0113 | glutamate/aspartate:proton symporter | -5.26 | down |
| DW66\_0114 | nucleoside recognition domain-containing protein | -1.82 | down |
| DW66\_0115 | ABC transporter auxiliary component-like protein | 1.80 | up |
| DW66\_0118 | ABC-type transport system involved in resistance to organic solvents, permease component USSDB6A | -1.57 | down |
| DW66\_0123 | citrate/H+ symporter | -3.11 | down |
| DW66\_0124 | hypothetical protein | -2.53 | down |
| DW66\_0125 | aldehyde-activating protein | 1.20 | up |
| DW66\_0126 | hypothetical protein | -2.47 | down |
| DW66\_0129 | Outer membrane receptor proteins, mostly Fe transport | 2.02 | up |
| DW66\_0130 | hypothetical protein | 1.32 | up |
| DW66\_0132 | hypothetical protein | -3.70 | down |
| DW66\_0133 | NAD(P)(+) transhydrogenase | 1.40 | up |
| DW66\_0134 | pyridine proton-translocating NAD(P) transhydrogenase | 1.51 | up |
| DW66\_0135 | NAD(P) transhydrogenase subunit alpha | 1.27 | up |
| DW66\_0136 | transcriptional regulator LysR | -1.68 | down |
| DW66\_0137 | acyl-CoA dehydrogenase domain-containing protein | 1.88 | up |
| DW66\_0138 | L-carnitine dehydratase/bile acid-inducible protein F | 2.07 | up |
| DW66\_0140 | anti-FecI sigma factor FecR | -1.38 | down |
| DW66\_0141 | RNA polymerase sigma-24 factor | -1.52 | down |
| DW66\_0144 | hypothetical protein | -1.73 | down |
| DW66\_0146 | type I secretion membrane fusion protein HlyD | 1.32 | up |
| DW66\_0147 | type I secretion system ATPase | 1.32 | up |
| DW66\_0148 | hypothetical protein | -12.07 | down |
| DW66\_0150 | RTX toxin | 4.57 | up |
| DW66\_0151 | T1SS secreted agglutinin RTX | 4.50 | up |
| DW66\_0152 | RTX toxin | 4.52 | up |
| DW66\_0153 | transporter | 3.87 | up |
| DW66\_0155 | taurine dioxygenase | -7.81 | down |
| DW66\_0156 | ABC transporter substrate-binding protein | -5.13 | down |
| DW66\_0157 | ABC transporter ATP-binding protein | -2.76 | down |
| DW66\_0158 | binding-protein-dependent transport system inner membrane protein | -2.41 | down |
| DW66\_0159 | transcriptional regulator | -5.70 | down |
| DW66\_0160 | Sel1 domain-containing protein | -1.98 | down |
| DW66\_0161 | transcriptional regulator MarR | -7.29 | down |
| DW66\_0162 | fusaric acid resistance protein region | -6.05 | down |
| DW66\_0163 | membrane protein | -4.01 | down |
| DW66\_0164 | secretion protein HlyD | -3.51 | down |
| DW66\_0165 | RND efflux system outer membrane lipoprotein | -2.76 | down |
| DW66\_0167 | hypothetical protein | -1.44 | down |
| DW66\_0169 | cystathionine gamma-synthase | -1.79 | down |
| DW66\_0170 | DNA-binding protein inhibitor Id-2-related protein | 4.74 | up |
| DW66\_0171 | hypothetical protein | 1.46 | up |
| DW66\_0172 | glutathione S-transferase domain-containing protein | 1.07 | up |
| DW66\_0176 | uroporphyrinogen-III synthase | -1.04 | down |
| DW66\_0179 | disulfide bond formation protein DsbB | -5.87 | down |
| DW66\_0181 | FKBP-type peptidylprolyl isomerase | -2.53 | down |
| DW66\_0183 | hypothetical protein | 1.20 | up |
| DW66\_0184 | ABC transporter ATP-binding protein | -2.67 | down |
| DW66\_0185 | membrane protein | -3.94 | down |
| DW66\_0187 | membrane protease | 1.94 | up |
| DW66\_0188 | membrane-bound protease | 2.12 | up |
| DW66\_0189 | YbaK/prolyl-tRNA synthetase associated domain-containing protein | 5.29 | up |
| DW66\_0190 | hypothetical protein | 4.05 | up |
| DW66\_0191 | NADH:ubiquinone oxidoreductase subunit 2 (chain N) | 2.46 | up |
| DW66\_0192 | hypothetical protein | 4.81 | up |
| DW66\_0194 | hypothetical protein | -1.15 | down |
| DW66\_0195 | lipoprotein | 2.83 | up |
| DW66\_0196 | lipoprotein | 2.46 | up |
| DW66\_0197 | hypothetical protein | 2.18 | up |
| DW66\_0199 | ABC transporter ATP-binding protein | 2.27 | up |
| DW66\_0200 | ppkA-like protein | 3.97 | up |
| DW66\_0201 | hypothetical protein | 3.23 | up |
| DW66\_0202 | HopL1 protein | 3.16 | up |
| DW66\_0203 | SrfB | 2.58 | up |
| DW66\_0204 | virulence factor | -1.60 | down |
| DW66\_0205 | transcriptional regulator | -6.68 | down |
| DW66\_0206 | oxidoreductase | -5.09 | down |
| DW66\_0207 | 4Fe-4S ferredoxin | -5.32 | down |
| DW66\_0208 | nitrate ABC transporter periplasmic nitrate-binding protein | -5.86 | down |
| DW66\_0209 | nitrate ABC transporter permease | -7.10 | down |
| DW66\_0210 | nitrate ABC transporter ATP-binding protein | -4.15 | down |
| DW66\_0211 | phycobiliprotein | -2.27 | down |
| DW66\_0212 | hypothetical protein | -3.34 | down |
| DW66\_0213 | arylsulfotransferase | -2.16 | down |
| DW66\_0216 | type III effector HopAC1 | -3.22 | down |
| DW66\_0218 | PAS/PAC sensor-containing diguanylate cyclase | -2.00 | down |
| DW66\_0220 | GAF and PAS/PAC sensor-containing diguanylate cyclase/phosphodiesterase | -1.29 | down |
| DW66\_0221 | binding-protein-dependent transport system inner membrane protein | -3.72 | down |
| DW66\_0222 | ABC transporter ATP-binding protein | -4.02 | down |
| DW66\_0223 | NLPA lipoprotein | -2.72 | down |
| DW66\_0224 | DszA monooxygenase | -4.21 | down |
| DW66\_0225 | acyl-CoA dehydrogenase type 2 | -5.79 | down |
| DW66\_0226 | acyl-CoA dehydrogenase type 2 | -6.70 | down |
| DW66\_0227 | hypothetical protein | -12.03 | down |
| DW66\_0229 | polar amino acid ABC transporter inner membrane subunit | -1.86 | down |
| DW66\_0230 | cystine transporter subunit | -1.28 | down |
| DW66\_0231 | serine O-acetyltransferase | -1.37 | down |
| DW66\_0232 | choline/carnitine/betaine transporter | -1.99 | down |
| DW66\_0233 | taurine dioxygenase | -4.47 | down |
| DW66\_0234 | binding-protein-dependent transport system inner membrane protein | -5.84 | down |
| DW66\_0235 | taurine transporter, ATP-binding subunit | -6.05 | down |
| DW66\_0236 | taurine ABC transporter periplasmic taurine-binding protein | -7.73 | down |
| DW66\_0237 | outer membrane porin | -2.10 | down |
| DW66\_0238 | peroxidase | -3.88 | down |
| DW66\_0239 | NAD(P)H-dependent FMN reductase | -5.83 | down |
| DW66\_0240 | aliphatic sulfonates ABC transporter substrate-binding protein | -8.27 | down |
| DW66\_0241 | alkanesulfonate monooxygenase | -6.85 | down |
| DW66\_0242 | ABC-type transporter membrane permease | -8.96 | down |
| DW66\_0243 | aliphatic sulfonates transporter ATP-binding protein SsuB | -17.83 | down |
| DW66\_0244 | TOBE domain-containing protein | -7.66 | down |
| DW66\_0248 | RNA-binding S1 domain-containing protein | -1.55 | down |
| DW66\_0249 | hypothetical protein | -1.02 | down |
| DW66\_0251 | integral membrane sensor signal transduction histidine kinase | -1.94 | down |
| DW66\_0252 | *alpha*-L-glutamate ligase | 1.23 | up |
| DW66\_0253 | hypothetical protein | 1.05 | up |
| DW66\_0257 | phosphoenolpyruvate carboxykinase | -1.72 | down |
| DW66\_0259 | hypothetical protein | 1.24 | up |
| DW66\_0260 | oxidoreductase, alpha (molybdopterin) subunit | 1.17 | up |
| DW66\_0262 | LysM protein | 5.13 | up |
| DW66\_0264 | ADP-ribose diphosphatase NudE | -1.48 | down |
| DW66\_0265 | 3'(2'),5'-bisphosphate nucleotidase | -2.17 | down |
| DW66\_0269 | hypothetical protein | -6.48 | down |
| DW66\_0270 | dTDP-4-dehydrorhamnose 3,5-epimerase | 1.89 | up |
| DW66\_0271 | agmatine deiminase | -1.29 | down |
| DW66\_0272 | TonB-dependent siderophore receptor | -5.33 | down |
| DW66\_0274 | glutamate synthase | -2.64 | down |
| DW66\_0275 | integral membrane sensor signal transduction histidine kinase | -4.33 | down |
| DW66\_0276 | two component transcriptional regulator | -4.68 | down |
| DW66\_0277 | TonB-dependent siderophore receptor | -2.02 | down |
| DW66\_0278 | hypothetical protein | 4.87 | up |
| DW66\_0279 | hypothetical protein | -3.02 | down |
| DW66\_0280 | hypothetical protein | 1.58 | up |
| DW66\_0282 | polar amino acid ABC transporter inner membrane subunit | -1.38 | down |
| DW66\_0283 | polar amino acid ABC transporter inner membrane subunit | -2.46 | down |
| DW66\_0284 | amino acid ABC transporter periplasmic amino acid-binding protein | 1.19 | up |
| DW66\_0286 | GABA permease | 2.26 | up |
| DW66\_0288 | Polyphosphate kinase 2 | 2.00 | up |
| DW66\_0289 | hypothetical protein | 2.13 | up |
| DW66\_0290 | A/G-specific adenine glycosylase | 1.68 | up |
| DW66\_0292 | transporter protein | -2.77 | down |
| DW66\_0293 | hypothetical protein | -10.15 | down |
| DW66\_0299 | choline ABC transporter ATP-binding protein | 1.87 | up |
| DW66\_0301 | glycine betaine/L-proline ABC transporter periplasmic binding protein | 2.32 | up |
| DW66\_0302 | L-serine dehydratase | -1.23 | down |
| DW66\_0303 | transcriptional regulator AraC | 3.80 | up |
| DW66\_0304 | hypothetical protein | 1.98 | up |
| DW66\_0306 | 3-hydroxybutyryl-CoA dehydrogenase | -2.19 | down |
| DW66\_0307 | hypothetical protein | -2.88 | down |
| DW66\_0308 | choline ABC transporter periplasmic binding protein | -1.77 | down |
| DW66\_0309 | transcriptional regulator AraC | 1.17 | up |
| DW66\_0310 | hypothetical protein | -4.13 | down |
| DW66\_0311 | hypothetical protein | -3.58 | down |
| DW66\_0312 | hypothetical protein | -1.66 | down |
| DW66\_0314 | hypothetical protein | 1.81 | up |
| DW66\_0316 | iron-sulfur cluster-binding protein | -3.08 | down |
| DW66\_0317 | electron transfer flavoprotein subunit alpha | -2.62 | down |
| DW66\_0318 | electron transfer flavoprotein, alpha/beta-subunit-like protein | -1.26 | down |
| DW66\_0320 | oxidoreductase FAD-binding domain-containing protein | -1.24 | down |
| DW66\_0321 | methyl-accepting chemotaxis sensory transducer | -1.52 | down |
| DW66\_0322 | hypothetical protein | -2.15 | down |
| DW66\_0323 | hypothetical protein | -3.03 | down |
| DW66\_0324 | methyl-accepting chemotaxis sensory transducer | -3.26 | down |
| DW66\_0327 | sarcosine oxidase subunit beta | 1.30 | up |
| DW66\_0328 | sarcosine oxidase subunit delta | 1.68 | up |
| DW66\_0329 | sarcosine oxidase subunit alpha | 1.89 | up |
| DW66\_0332 | hypothetical protein | -1.15 | down |
| DW66\_0333 | formaldehyde dehydrogenase | 1.71 | up |
| DW66\_0335 | hypothetical protein | -2.42 | down |
| DW66\_0336 | amino acid permease-associated protein | -2.30 | down |
| DW66\_0337 | acyltransferase | -3.45 | down |
| DW66\_0338 | Ribosomal protein S6 glutaminyl transferase | -1.72 | down |
| DW66\_0339 | DNA-binding response regulator CreB | -3.89 | down |
| DW66\_0340 | sensory histidine kinase CreC | -4.44 | down |
| DW66\_0341 | Inner membrane protein CreD | -1.95 | down |
| DW66\_0345 | dihydrolipoamide acetyltransferase | 1.75 | up |
| DW66\_0346 | pyruvate dehydrogenase subunit E1 | 1.68 | up |
| DW66\_0347 | hypothetical protein | -2.59 | down |
| DW66\_0348 | (glutamate-ammonia-ligase) adenylyltransferase | 1.04 | up |
| DW66\_0349 | lipopolysaccharide heptosyltransferase II | -1.47 | down |
| DW66\_0350 | lipopolysaccharide heptosyltransferase I | -2.01 | down |
| DW66\_0352 | lipopolysaccharide kinase | -1.16 | down |
| DW66\_0356 | hypothetical protein | -3.87 | down |
| DW66\_0357 | hypothetical protein | -12.49 | down |
| DW66\_0358 | PepSY-associated TM helix domain-containing protein | -6.36 | down |
| DW66\_0359 | TonB-dependent siderophore receptor | -2.42 | down |
| DW66\_0361 | amino acid ABC transporter substrate-binding protein | -1.12 | down |
| DW66\_0362 | RNA polymerase sigma factor | -2.63 | down |
| DW66\_0363 | DNA polymerase III subunit epsilon | -1.65 | down |
| DW66\_0364 | signal-transduction protein containing cAMP-binding and CBS domains | -1.92 | down |
| DW66\_0365 | chemotaxis protein CheY | 2.11 | up |
| DW66\_0367 | ACT domain-containing protein | 1.66 | up |
| DW66\_0368 | transporter | -1.91 | down |
| DW66\_0372 | biotin synthase | 2.29 | up |
| DW66\_0374 | carboxylesterase | 2.20 | up |
| DW66\_0375 | biotin biosynthesis protein BioC | 2.10 | up |
| DW66\_0376 | dithiobiotin synthetase | 1.37 | up |
| DW66\_0377 | hypothetical protein | -1.27 | down |
| DW66\_0378 | acyl-CoA dehydrogenase domain-containing protein | -2.11 | down |
| DW66\_0379 | diguanylate cyclase | -1.16 | down |
| DW66\_0381 | transcriptional regulator LysR | -1.29 | down |
| DW66\_0382 | class III aminotransferase | -3.03 | down |
| DW66\_0383 | Stress induced hydrophobic peptide | 2.69 | up |
| DW66\_0385 | pyrroloquinoline quinone biosynthesis protein PqqE | -1.04 | down |
| DW66\_0388 | pyrroloquinoline quinone biosynthesis protein PqqB | -1.96 | down |
| DW66\_0389 | coenzyme PQQ biosynthesis protein PqqF | -1.38 | down |
| DW66\_0391 | amine oxidase | -1.32 | down |
| DW66\_0392 | hypothetical protein | -2.23 | down |
| DW66\_0393 | transcriptional regulator AsnC | -2.44 | down |
| DW66\_0394 | 6-hydroxy-3-succinoylpyridine hydroxylase | -2.25 | down |
| DW66\_0395 | PAS/PAC sensor-containing diguanylate cyclase/phosphodiesterase | 2.60 | up |
| DW66\_0398 | 30S ribosomal protein S21 | -1.18 | down |
| DW66\_0399 | DNA-binding/iron metalloprotein/AP endonuclease | -2.57 | down |
| DW66\_0400 | glycerol-3-phosphate acyltransferase PlsY | -1.56 | down |
| DW66\_0401 | dihydroneopterin aldolase | -2.26 | down |
| DW66\_0402 | 2-amino-4-hydroxy-6- hydroxymethyldihydropteridine pyrophosphokinase | -3.63 | down |
| DW66\_0403 | multifunctional tRNA nucleotidyl transferase/2'3'-cyclic phosphodiesterase/2'nucleotidase/phosphatase | 1.14 | up |
| DW66\_0404 | SpoVR protein | 5.95 | up |
| DW66\_0405 | hypothetical protein | 5.57 | up |
| DW66\_0406 | serine protein kinase PrkA | 6.50 | up |
| DW66\_0407 | thiosulfate sulfurtransferase | 2.34 | up |
| DW66\_0410 | dimethyladenosine transferase | 3.34 | up |
| DW66\_0411 | 4-hydroxythreonine-4-phosphate dehydrogenase | 1.93 | up |
| DW66\_0412 | SurA domain-containing protein | 2.16 | up |
| DW66\_0413 | LPS-assembly protein lptD | 1.34 | up |
| DW66\_0420 | spermidine/putrescine ABC transporter ATPase | -1.14 | down |
| DW66\_0423 | binding-protein-dependent transport system inner membrane protein | 1.25 | up |
| DW66\_0425 | phosphoglycolate phosphatase | -1.46 | down |
| DW66\_0426 | anthranilate synthase component I | -1.23 | down |
| DW66\_0427 | outer membrane autotransporter | 1.14 | up |
| DW66\_0428 | anthranilate synthase component II | -2.18 | down |
| DW66\_0431 | Lipoate-protein ligase A | -1.04 | down |
| DW66\_0432 | cAMP-regulatory protein | 1.08 | up |
| DW66\_0433 | protein OsmC | -2.81 | down |
| DW66\_0437 | short-chain dehydrogenase/reductase SDR | -1.11 | down |
| DW66\_0439 | Protoporphyrinogen IX oxidase | 1.21 | up |
| DW66\_0440 | N-acetyl-gamma-glutamyl-phosphate reductase | -1.34 | down |
| DW66\_0441 | iron-sulfur cluster insertion protein ErpA | -1.64 | down |
| DW66\_0444 | tyrosyl-tRNA synthetase | -1.63 | down |
| DW66\_0445 | hypothetical protein | 4.03 | up |
| DW66\_0446 | biotin-protein ligase | -1.69 | down |
| DW66\_0447 | pantothenate kinase | -1.33 | down |
| DW66\_0448 | hypothetical protein | -1.63 | down |
| DW66\_0450 | Preprotein translocase subunit SecE | -2.52 | down |
| DW66\_0451 | transcription antitermination protein NusG | -2.73 | down |
| DW66\_0452 | 50S ribosomal protein L11 | -3.12 | down |
| DW66\_0453 | 50S ribosomal protein L1 | -2.83 | down |
| DW66\_0454 | 50S ribosomal protein L10 | -3.54 | down |
| DW66\_0455 | 50S ribosomal protein L7/L12 | -1.63 | down |
| DW66\_0458 | 30S ribosomal protein S12 | -1.44 | down |
| DW66\_0459 | protein RpsG | -1.23 | down |
| DW66\_0462 | elongation factor Tu | 1.09 | up |
| DW66\_0463 | 30S ribosomal protein S10 | -2.52 | down |
| DW66\_0464 | ribosomal protein L3 | -3.15 | down |
| DW66\_0465 | 50S ribosomal protein L4 | -2.51 | down |
| DW66\_0466 | 50S ribosomal protein L23 | -1.94 | down |
| DW66\_0467 | 50S ribosomal protein L2 | -2.00 | down |
| DW66\_0468 | 30S ribosomal protein S19 | -1.62 | down |
| DW66\_0469 | 50S ribosomal protein L22 | -1.85 | down |
| DW66\_0470 | ribosomal protein S3 | -1.39 | down |
| DW66\_0471 | 50S ribosomal protein L16 | -1.61 | down |
| DW66\_0472 | 50S ribosomal protein L29 | -1.60 | down |
| DW66\_0478 | 30S ribosomal protein S8 | -2.92 | down |
| DW66\_0479 | 50S ribosomal protein L6 | -2.93 | down |
| DW66\_0480 | 50S ribosomal protein L18 | -2.61 | down |
| DW66\_0481 | 30S ribosomal protein S5 | -2.67 | down |
| DW66\_0482 | 50S ribosomal protein L30 | -2.39 | down |
| DW66\_0483 | 50S ribosomal protein L15 | -2.32 | down |
| DW66\_0484 | preprotein translocase subunit SecY | -2.57 | down |
| DW66\_0486 | 30S ribosomal protein S13 | -1.31 | down |
| DW66\_0487 | 30S ribosomal protein S11 | -1.24 | down |
| DW66\_0491 | catalase | 3.70 | up |
| DW66\_0492 | bacterioferritin | 4.51 | up |
| DW66\_0500 | formate dehydrogenase subunit beta | 3.43 | up |
| DW66\_0501 | formate dehydrogenase subunit gamma | 2.86 | up |
| DW66\_0502 | formate dehydrogenase accessory protein FdhE | 1.77 | up |
| DW66\_0503 | selenocysteine synthase | 1.41 | up |
| DW66\_0504 | selenocysteine-specific translation elongation factor | 1.87 | up |
| DW66\_0507 | hypothetical protein | -3.31 | down |
| DW66\_0509 | membrane protein YfcA | -2.53 | down |
| DW66\_0510 | hypothetical protein | -1.15 | down |
| DW66\_0511 | dTDP-4-dehydrorhamnose reductase | -1.36 | down |
| DW66\_0514 | transporter | -3.98 | down |
| DW66\_0515 | outer membrane protein W | 4.14 | up |
| DW66\_0516 | lipoprotein | -2.02 | down |
| DW66\_0517 | efflux ABC transporter permease | -3.86 | down |
| DW66\_0518 | efflux ABC transporter ATP-binding protein | -4.98 | down |
| DW66\_0519 | zinc-binding protein | -4.02 | down |
| DW66\_0520 | hypothetical protein | -1.24 | down |
| DW66\_0521 | thioredoxin | 1.28 | up |
| DW66\_0522 | type 12 methyltransferase | -1.58 | down |
| DW66\_0523 | lipoprotein | -1.08 | down |
| DW66\_0524 | ATP cone domain protein | -2.21 | down |
| DW66\_0525 | riboflavin biosynthesis protein RibD | -1.90 | down |
| DW66\_0526 | riboflavin synthase subunit alpha | -2.44 | down |
| DW66\_0527 | bifunctional 3,4-dihydroxy-2-butanone 4-phosphate synthase/GTP cyclohydrolase II-like protein | -1.12 | down |
| DW66\_0530 | thiamine monophosphate kinase | -1.64 | down |
| DW66\_0531 | phosphatidylglycerophosphatase A | -1.58 | down |
| DW66\_0532 | hypothetical protein | -2.23 | down |
| DW66\_0533 | GTP cyclohydrolase | -2.03 | down |
| DW66\_0534 | Permeases | -2.55 | down |
| DW66\_0535 | periplasmic binding protein | -3.96 | down |
| DW66\_0536 | 1-deoxy-D-xylulose-5-phosphate synthase | -1.16 | down |
| DW66\_0537 | polyprenyl synthetase | -3.40 | down |
| DW66\_0538 | exodeoxyribonuclease VII small subunit | -3.72 | down |
| DW66\_0539 | 3,4-dihydroxy-2-butanone 4-phosphate synthase | -3.32 | down |
| DW66\_0541 | hypothetical protein | -5.73 | down |
| DW66\_0543 | cytochrome c | -1.71 | down |
| DW66\_0545 | Multicopper oxidase | 1.41 | up |
| DW66\_0547 | transcriptional regulator | -5.36 | down |
| DW66\_0549 | Inner membrane protein | -2.23 | down |
| DW66\_0551 | N-acetyltransferase GCN5 | -1.02 | down |
| DW66\_0552 | ethanolamine ammonia-lyase, small subunit | 2.05 | up |
| DW66\_0554 | ethanolamine transporter | -1.62 | down |
| DW66\_0555 | aldehyde dehydrogenase | 3.22 | up |
| DW66\_0556 | hypothetical protein | -4.93 | down |
| DW66\_0558 | hypothetical protein | -3.01 | down |
| DW66\_0562 | Oxidoreductase | 3.48 | up |
| DW66\_0571 | ATP-NAD/AcoX kinase | -2.20 | down |
| DW66\_0573 | acetyl-CoA carboxylase biotin carboxylase subunit | 1.26 | up |
| DW66\_0576 | thiol:disulfide interchange protein | -1.40 | down |
| DW66\_0577 | methyl-accepting chemotaxis sensory transducer | -4.22 | down |
| DW66\_0578 | response regulator receiver modulated diguanylate cyclase | 1.82 | up |
| DW66\_0579 | hypothetical protein | -1.63 | down |
| DW66\_0580 | NUDIX hydrolase | -1.49 | down |
| DW66\_0581 | translation initiation factor SUI1 | -3.83 | down |
| DW66\_0583 | hypothetical protein | -1.89 | down |
| DW66\_0584 | MATE efflux protein | -3.50 | down |
| DW66\_0585 | alpha-2-macroglobulin domain-containing protein | 1.58 | up |
| DW66\_0586 | MFS transporter | -1.05 | down |
| DW66\_0587 | penicillin-binding protein 1C | -1.70 | down |
| DW66\_0588 | hypothetical protein | -3.94 | down |
| DW66\_0591 | peptidase A24A prepilin type IV | 1.57 | up |
| DW66\_0592 | sensory box protein | -11.12 | down |
| DW66\_0593 | lipoprotein | 1.97 | up |
| DW66\_0596 | hypothetical protein | -1.38 | down |
| DW66\_0597 | dehydratase | 1.90 | up |
| DW66\_0598 | 3-ketoacyl-ACP reductase | 1.62 | up |
| DW66\_0602 | transcriptional regulator MerR | 3.04 | up |
| DW66\_0603 | heavy metal translocating P-type ATPase | 1.84 | up |
| DW66\_0605 | heavy metal transport/detoxification protein | 5.22 | up |
| DW66\_0606 | multidrug resistance transporter | -1.11 | down |
| DW66\_0609 | short-chain dehydrogenase | 3.31 | up |
| DW66\_0614 | methylmalonate-semialdehyde dehydrogenase | 2.56 | up |
| DW66\_0615 | paraquat-inducible protein A | -1.11 | down |
| DW66\_0616 | paraquat-inducible protein A | -1.24 | down |
| DW66\_0618 | 30S ribosomal protein S20 | -2.34 | down |
| DW66\_0619 | integral membrane protein MviN | -1.70 | down |
| DW66\_0620 | hypothetical protein | -3.25 | down |
| DW66\_0621 | bifunctional riboflavin kinase/FMN adenylyltransferase | -1.68 | down |
| DW66\_0625 | 4-hydroxy-3-methylbut-2-enyl diphosphate reductase | -1.49 | down |
| DW66\_0628 | Type IV fimbrial biogenesis protein PilW | -2.20 | down |
| DW66\_0629 | Type IV fimbrial biogenesis protein PilX | -1.10 | down |
| DW66\_0630 | type IV pili biogenesis protein PilE | -2.44 | down |
| DW66\_0631 | FAD dependent oxidoreductase | -1.99 | down |
| DW66\_0634 | pseudouridine synthase RluA | -1.67 | down |
| DW66\_0635 | hypothetical protein | -2.34 | down |
| DW66\_0636 | ATPase | 3.61 | up |
| DW66\_0640 | hypothetical protein | -2.43 | down |
| DW66\_0645 | type II secretion system protein | 1.73 | up |
| DW66\_0647 | resolvase | 1.96 | up |
| DW66\_0650 | integrase | -4.26 | down |
| DW66\_0652 | ISPsy14, transposition helper protein | -5.57 | down |
| DW66\_0653 | ISPsy14, transposase | -2.38 | down |
| DW66\_0654 | hypothetical protein | -3.62 | down |
| DW66\_0655 | hypothetical protein | -2.35 | down |
| DW66\_0656 | transcriptional regulator | -2.59 | down |
| DW66\_0657 | arsenical pump membrane protein | -1.76 | down |
| DW66\_0658 | transporter protein | -3.73 | down |
| DW66\_0659 | hypothetical protein | -3.39 | down |
| DW66\_0660 | two component sigma54 specific transcriptional regulator | -1.42 | down |
| DW66\_0661 | histidine kinase | -2.56 | down |
| DW66\_0662 | malate dehydrogenase | 2.31 | up |
| DW66\_0663 | polar amino acid ABC transporter inner membrane subunit | -3.72 | down |
| DW66\_0664 | amino acid ABC transporter periplasmic amino acid-binding protein | -4.30 | down |
| DW66\_0666 | cystathionine *gamma*-synthase | -3.62 | down |
| DW66\_0667 | amino acid transporter | -3.07 | down |
| DW66\_0668 | transcriptional regulator LysR | -1.38 | down |
| DW66\_0669 | threonine synthase | -1.78 | down |
| DW66\_0670 | transcriptional regulator AsnC | -2.29 | down |
| DW66\_0672 | glyceraldehyde-3-phosphate dehydrogenase, NADP-dependent | -1.32 | down |
| DW66\_0673 | endoribonuclease L-PSP | -1.50 | down |
| DW66\_0674 | bile acid:sodium symporter | -2.08 | down |
| DW66\_0677 | hypothetical protein | -2.05 | down |
| DW66\_0679 | glutamate dehydrogenase | 1.94 | up |
| DW66\_0680 | elongation factor | -1.63 | down |
| DW66\_0683 | hypothetical protein | 4.54 | up |
| DW66\_0685 | hypothetical protein | 2.64 | up |
| DW66\_0686 | inner membrane protein | -2.56 | down |
| DW66\_0687 | hypothetical protein | 2.57 | up |
| DW66\_0689 | hypothetical protein | 3.02 | up |
| DW66\_0690 | alkylphosphonate utilization operon protein PhnA | 2.01 | up |
| DW66\_0691 | octaprenyl diphosphate synthase | -2.90 | down |
| DW66\_0692 | ribosomal protein L21 | -2.30 | down |
| DW66\_0693 | 50S ribosomal protein L27 | -1.46 | down |
| DW66\_0694 | GTPase ObgE | -3.64 | down |
| DW66\_0695 | gamma-glutamyl kinase | -1.39 | down |
| DW66\_0696 | CreA protein | -1.67 | down |
| DW66\_0698 | hypothetical protein | -2.66 | down |
| DW66\_0699 | hypothetical protein | -2.22 | down |
| DW66\_0701 | hypothetical protein | -1.46 | down |
| DW66\_0702 | ribosomal-protein-alanine acetyltransferase | -1.03 | down |
| DW66\_0703 | hypothetical protein | 1.05 | up |
| DW66\_0704 | transcriptional regulator LysR | -3.82 | down |
| DW66\_0705 | lysine exporter protein LysE/YggA | -7.61 | down |
| DW66\_0706 | anti-FecI sigma factor FecR | -5.49 | down |
| DW66\_0708 | hypothetical protein | -4.95 | down |
| DW66\_0709 | transporter protein | -5.91 | down |
| DW66\_0710 | DNA-3-methyladenine glycosylase II | -1.10 | down |
| DW66\_0711 | methylated-DNA--protein-cysteine methyltransferase | -2.25 | down |
| DW66\_0712 | mechanosensitive ion channel protein MscS | -1.21 | down |
| DW66\_0714 | hypothetical protein | 1.39 | up |
| DW66\_0715 | betaine-aldehyde dehydrogenase | -3.53 | down |
| DW66\_0716 | NCS1 nucleoside transporter | -4.73 | down |
| DW66\_0717 | Undecaprenyl pyrophosphate synthase | -4.82 | down |
| DW66\_0718 | Mg2 transporter protein CorA | -4.04 | down |
| DW66\_0719 | amino acid ABC transporter ATP-binding protein | -1.46 | down |
| DW66\_0720 | amino acid ABC transporter permease | -1.04 | down |
| DW66\_0721 | amino acid ABC transporter permease | -1.52 | down |
| DW66\_0722 | amino acid ABC transporter periplasmic amino acid-binding protein | -2.06 | down |
| DW66\_0723 | transcriptional regulator | -2.29 | down |
| DW66\_0724 | EutB ectoine utilization protein | -3.68 | down |
| DW66\_0725 | ectoine utilization protein EutC | -3.36 | down |
| DW66\_0726 | EutD ectoine utilization protein | -1.95 | down |
| DW66\_0727 | EutE ectoine utilization protein | -2.73 | down |
| DW66\_0730 | isochorismatase hydrolase | 5.45 | up |
| DW66\_0731 | hypothetical protein | 2.95 | up |
| DW66\_0732 | potassium efflux system protein | 2.95 | up |
| DW66\_0733 | permease | 4.03 | up |
| DW66\_0734 | RND efflux system outer membrane lipoprotein | 2.94 | up |
| DW66\_0735 | secretion protein HlyD | 2.97 | up |
| DW66\_0737 | sulfate transporter | 1.76 | up |
| DW66\_0738 | GTP-dependent nucleic acid-binding protein EngD | -2.17 | down |
| DW66\_0739 | peptidyl-tRNA hydrolase | -1.30 | down |
| DW66\_0741 | ribose-phosphate pyrophosphokinase | -2.95 | down |
| DW66\_0742 | 4-diphosphocytidyl-2-C-methyl-D-erythritol kinase | -4.92 | down |
| DW66\_0745 | hypothetical protein | -9.07 | down |
| DW66\_0747 | hypothetical protein | -1.26 | down |
| DW66\_0748 | Argininosuccinate lyase | -1.12 | down |
| DW66\_0749 | Phosphatidylserine synthase | -3.54 | down |
| DW66\_0750 | hypothetical protein | -2.82 | down |
| DW66\_0751 | glutamyl-tRNA reductase | -1.41 | down |
| DW66\_0752 | peptide chain release factor 1 | 1.56 | up |
| DW66\_0756 | Lipid A 3-O-deacylase | 1.19 | up |
| DW66\_0757 | short-chain dehydrogenase | 1.41 | up |
| DW66\_0758 | deoxyribodipyrimidine photo-lyase | 1.09 | up |
| DW66\_0762 | NAD-dependent epimerase/dehydratase | 1.08 | up |
| DW66\_0766 | hypoxanthine-guanine phosphoribosyltransferase | -3.03 | down |
| DW66\_0767 | Tryptophan synthase beta chain like | -1.61 | down |
| DW66\_0769 | Aminopeptidase N | -1.17 | down |
| DW66\_0770 | malate:quinone oxidoreductase | -1.33 | down |
| DW66\_0771 | hypothetical protein | -2.58 | down |
| DW66\_0773 | hypothetical protein | -2.75 | down |
| DW66\_0775 | Restriction endonuclease | 2.72 | up |
| DW66\_0778 | peptidase M48 Ste24p | -1.13 | down |
| DW66\_0779 | transmembrane protein | -5.04 | down |
| DW66\_0780 | rRNA (guanine-N(2)-)-methyltransferase | -2.90 | down |
| DW66\_0782 | long-chain fatty acid--CoA ligase | 1.56 | up |
| DW66\_0783 | hypothetical protein | 2.69 | up |
| DW66\_0784 | hypothetical protein | 3.96 | up |
| DW66\_0789 | toxin ChpB | -2.65 | down |
| DW66\_0790 | beta-lactamase domain-containing protein | -3.30 | down |
| DW66\_0791 | OmpA/MotB domain-containing protein | -2.14 | down |
| DW66\_0793 | hypothetical protein | 1.00 | up |
| DW66\_0795 | glutathione peroxidase | 2.30 | up |
| DW66\_0797 | methyl-accepting chemotaxis sensory transducer with Pas/Pac sensor | -2.18 | down |
| DW66\_0798 | hypothetical protein | -3.81 | down |
| DW66\_0799 | aspartyl-tRNA amidotransferase subunit B | -2.39 | down |
| DW66\_0801 | thioredoxin reductase | -1.33 | down |
| DW66\_0802 | nicotinate-nucleotide pyrophosphorylase | -1.02 | down |
| DW66\_0803 | Thymidine phosphorylase | 1.94 | up |
| DW66\_0804 | hypothetical protein | -4.29 | down |
| DW66\_0807 | TatD-related deoxyribonuclease | -3.20 | down |
| DW66\_0808 | DNA-binding transcriptional regulator FruR | -3.23 | down |
| DW66\_0809 | phosphoenolpyruvate-protein phosphotransferase | -2.30 | down |
| DW66\_0810 | 1-phosphofructokinase | -1.52 | down |
| DW66\_0811 | PTS system fructose | -1.25 | down |
| DW66\_0812 | hypothetical protein | -2.32 | down |
| DW66\_0814 | diguanylate cyclase | -1.76 | down |
| DW66\_0815 | outer membrane porin | -1.75 | down |
| DW66\_0820 | RND efflux transporter, MFP subunit | -2.32 | down |
| DW66\_0821 | cell division protein Fic | -3.92 | down |
| DW66\_0822 | hypothetical protein | -2.52 | down |
| DW66\_0823 | hypothetical protein | -2.16 | down |
| DW66\_0825 | anaerobic nitric oxide reductase transcriptional regulator | 4.92 | up |
| DW66\_0827 | disulfide bond formation protein B | -2.98 | down |
| DW66\_0828 | ubiquinol oxidase subunit II | -1.62 | down |
| DW66\_0834 | hypothetical protein | -3.66 | down |
| DW66\_0835 | Ferredoxin | -2.09 | down |
| DW66\_0836 | malate:quinone oxidoreductase | -1.37 | down |
| DW66\_0837 | hypothetical protein | -2.58 | down |
| DW66\_0839 | hypothetical protein | -2.77 | down |
| DW66\_0841 | Restriction endonuclease | 3.01 | up |
| DW66\_0842 | hypothetical protein | 2.93 | up |
| DW66\_0846 | phosphonates import ATP-binding protein phnC | -1.49 | down |
| DW66\_0847 | binding-protein-dependent transport system inner membrane protein | -2.01 | down |
| DW66\_0848 | phosphonate ABC transporter inner membrane subunit | -2.27 | down |
| DW66\_0849 | membrane protein | -2.30 | down |
| DW66\_0850 | acetyltransferase | -1.46 | down |
| DW66\_0852 | extracellular solute-binding protein | -1.62 | down |
| DW66\_0853 | ATP-binding component of ABC transporter | -3.26 | down |
| DW66\_0854 | amino acid ABC transporter permease | -2.74 | down |
| DW66\_0855 | amino acid ABC transporter permease | -2.34 | down |
| DW66\_0858 | endoribonuclease L-PSP | -1.63 | down |
| DW66\_0859 | D-amino-acid dehydrogenase | -2.30 | down |
| DW66\_0860 | transcriptional regulator LysR | -2.29 | down |
| DW66\_0861 | S-adenosylmethionine--tRNA ribosyltransferase-isomerase | -3.04 | down |
| DW66\_0864 | preprotein translocase subunit SecD | -1.20 | down |
| DW66\_0867 | protein SuhB | -1.42 | down |
| DW66\_0868 | RNA methyltransferase | -1.11 | down |
| DW66\_0870 | transcriptional regulator | -3.73 | down |
| DW66\_0871 | cysteine desulfurase | -2.81 | down |
| DW66\_0872 | scaffold protein | -1.71 | down |
| DW66\_0874 | co-chaperone HscB | -3.17 | down |
| DW66\_0875 | chaperone protein HscA | -2.95 | down |
| DW66\_0876 | ferredoxin, 2Fe-2S type, ISC system | -1.75 | down |
| DW66\_0878 | nucleoside diphosphate kinase | -1.15 | down |
| DW66\_0879 | radical SAM protein | -1.01 | down |
| DW66\_0880 | type IV pilus biogenesis/stability protein PilW | -1.37 | down |
| DW66\_0881 | transcriptional regulator XRE | -1.11 | down |
| DW66\_0888 | nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase | 1.03 | up |
| DW66\_0889 | flavodoxin/nitric oxide synthase | -2.08 | down |
| DW66\_0891 | TonB-dependent siderophore receptor | -2.69 | down |
| DW66\_0892 | hydroxylase | -3.39 | down |
| DW66\_0893 | Sel1 domain-containing protein | -3.07 | down |
| DW66\_0894 | ornithine decarboxylase | -2.55 | down |
| DW66\_0895 | RNA polymerase sigma-25 factor | -5.38 | down |
| DW66\_0896 | anti-FecI sigma factor FecR | -5.59 | down |
| DW66\_0897 | TonB-dependent siderophore receptor | -4.92 | down |
| DW66\_0898 | glycine betaine/L-proline ABC transporter ATPase | -2.78 | down |
| DW66\_0899 | binding-protein-dependent transport system inner membrane protein | -5.41 | down |
| DW66\_0900 | glycine betaine ABC transporter substrate-binding protein | -4.86 | down |
| DW66\_0901 | glycine/betaine ABC transporter permease | -6.47 | down |
| DW66\_0902 | peptide chain release factor 3 | -2.74 | down |
| DW66\_0903 | extracellular solute-binding protein | -2.63 | down |
| DW66\_0904 | hypothetical protein | -11.45 | down |
| DW66\_0905 | FAD dependent oxidoreductase | -3.43 | down |
| DW66\_0906 | transcriptional regulator AraC | -2.14 | down |
| DW66\_0907 | dipeptide transporter, ATP-binding subunit | 1.64 | up |
| DW66\_0908 | oligopeptide/dipeptide ABC transporter ATPase | 1.10 | up |
| DW66\_0910 | alkaline phosphatase | -1.68 | down |
| DW66\_0911 | peptide ABC transporter substrate-binding protein | 1.68 | up |
| DW66\_0912 | outer membrane porin | -2.21 | down |
| DW66\_0913 | extracellular solute-binding protein | -3.77 | down |
| DW66\_0914 | extracellular solute-binding protein | -2.42 | down |
| DW66\_0915 | hypothetical protein | -2.10 | down |
| DW66\_0917 | transcriptional regulator | 3.01 | up |
| DW66\_0918 | auxin efflux carrier | -1.62 | down |
| DW66\_0921 | conjugal transfer protein TraR | -2.04 | down |
| DW66\_0922 | rare lipoprotein A | -2.56 | down |
| DW66\_0923 | aspartyl/glutamyl-tRNA amidotransferase subunit B | 1.07 | up |
| DW66\_0925 | glutamyl-tRNA amidotransferase, C subunit | -1.12 | down |
| DW66\_0926 | rod shape-determining protein MreB | -2.49 | down |
| DW66\_0927 | rod shape-determining protein MreC | -4.05 | down |
| DW66\_0928 | rod shape-determining protein MreD | -2.64 | down |
| DW66\_0929 | Maf-like protein | -2.96 | down |
| DW66\_0931 | hypothetical protein | -1.16 | down |
| DW66\_0932 | nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase | 1.32 | up |
| DW66\_0933 | peptidase U62 modulator of DNA gyrase | 1.60 | up |
| DW66\_0936 | FagA protein | -1.48 | down |
| DW66\_0939 | phosphotransferase system, phosphocarrier protein HPr | -1.12 | down |
| DW66\_0942 | sigma 54 modulation protein/ribosomal protein S30EA | 2.95 | up |
| DW66\_0945 | lipopolysaccharide transport periplasmic protein LptA | 1.04 | up |
| DW66\_0948 | KpsF/GutQ protein | -1.31 | down |
| DW66\_0949 | hypothetical protein | -3.99 | down |
| DW66\_0950 | ABC transporter-like protein | -3.60 | down |
| DW66\_0951 | ABC transporter, permease component YrbE | -3.90 | down |
| DW66\_0952 | toluene tolerance protein Ttg2C | -2.12 | down |
| DW66\_0955 | BolA protein | -1.80 | down |
| DW66\_0956 | UDP-N-acetylglucosamine 1-carboxyvinyltransferase | -1.75 | down |
| DW66\_0957 | ATP phosphoribosyltransferase, catalytic subunit | -2.81 | down |
| DW66\_0958 | histidinol dehydrogenase | -1.89 | down |
| DW66\_0962 | Ketosteroid isomerase-related protein | -1.56 | down |
| DW66\_0963 | GIY-YIG nuclease | -1.94 | down |
| DW66\_0965 | DNA-binding protein | -2.11 | down |
| DW66\_0971 | YjgP permease | -1.36 | down |
| DW66\_0973 | transposase | -2.13 | down |
| DW66\_0974 | RDD domain-containing protein | -1.52 | down |
| DW66\_0976 | glycine cleavage system T protein | 1.28 | up |
| DW66\_0979 | glycine cleavage system protein H | -3.29 | down |
| DW66\_0981 | hypothetical protein | 2.07 | up |
| DW66\_0984 | sodium/glutamate symport carrier protein GltS | -2.64 | down |
| DW66\_0986 | Acetyl-CoA carboxylase alpha subunit | 3.06 | up |
| DW66\_0987 | carbamate kinase | 4.82 | up |
| DW66\_0988 | ornithine carbamoyltransferase | 6.52 | up |
| DW66\_0989 | arginine deiminase | 7.62 | up |
| DW66\_0990 | arginine/ornithine antiporter | 6.05 | up |
| DW66\_0992 | hypothetical protein | -2.04 | down |
| DW66\_0994 | TonB-dependent hemoglobin | 2.79 | up |
| DW66\_0995 | anti-FecI sigma factor FecR | -2.27 | down |
| DW66\_0996 | RNA polymerase sigma-26 factor | -4.74 | down |
| DW66\_1002 | N-acylglucosamine 2-epimerase | 1.66 | up |
| DW66\_1003 | extracellular solute-binding protein | 2.11 | up |
| DW66\_1004 | binding-protein-dependent transport system inner membrane protein | 1.29 | up |
| DW66\_1005 | binding-protein-dependent transport system inner membrane protein | 2.33 | up |
| DW66\_1006 | sugar ABC transporter ATP-binding protein | 3.81 | up |
| DW66\_1007 | carbohydrate-selective porin OprB | 4.05 | up |
| DW66\_1009 | DNA-binding transcriptional regulator HexR | -1.62 | down |
| DW66\_1011 | 6-phosphogluconolactonase | 1.75 | up |
| DW66\_1012 | keto-hydroxyglutarate-aldolase/keto-deoxy- phosphogluconate aldolase | 1.95 | up |
| DW66\_1014 | peptidase M23B | -2.49 | down |
| DW66\_1015 | exodeoxyribonuclease VII large subunit | -2.19 | down |
| DW66\_1016 | transcriptional regulator LysR | -1.36 | down |
| DW66\_1019 | inosine 5'-monophosphate dehydrogenase | -1.50 | down |
| DW66\_1021 | sulfatase | 1.17 | up |
| DW66\_1022 | hypothetical protein | -3.80 | down |
| DW66\_1023 | ADP-ribosyl-(dinitrogen reductase) hydrolase | -2.72 | down |
| DW66\_1024 | hypothetical protein | -3.30 | down |
| DW66\_1025 | multicopper oxidase type 3 | -1.55 | down |
| DW66\_1026 | CRISPR-associated protein Csn1 | -1.41 | down |
| DW66\_1027 | lytic transglycosylase | -1.08 | down |
| DW66\_1031 | sec-independent protein translocase, TatC subunit | -1.98 | down |
| DW66\_1032 | twin-arginine translocation protein subunit TatB | -8.65 | down |
| DW66\_1033 | twin arginine-targeting protein translocase | -4.49 | down |
| DW66\_1034 | general secretion pathway protein K | -2.23 | down |
| DW66\_1035 | phosphatase | -1.31 | down |
| DW66\_1036 | lipoprotein UxpA | -3.40 | down |
| DW66\_1037 | type II secretion protein C | -6.84 | down |
| DW66\_1038 | general secretion pathway protein D | -6.17 | down |
| DW66\_1039 | type II secretion system protein E | -4.12 | down |
| DW66\_1040 | general secretion pathway protein F | -4.72 | down |
| DW66\_1041 | general secretion pathway protein G | -3.16 | down |
| DW66\_1042 | general secretion pathway protein H | -3.35 | down |
| DW66\_1043 | type II secretion system protein I/J | -7.51 | down |
| DW66\_1044 | type II secretion system protein J | -5.45 | down |
| DW66\_1045 | general secretion pathway protein L | -3.31 | down |
| DW66\_1046 | type II secretion system protein M | -9.99 | down |
| DW66\_1047 | type II secretion pathway protein GspN | -3.92 | down |
| DW66\_1049 | filamentous hemagglutinin outer membrane protein | -2.41 | down |
| DW66\_1050 | secretion protein | -3.61 | down |
| DW66\_1054 | transferase | -1.84 | down |
| DW66\_1055 | hypothetical protein | -1.24 | down |
| DW66\_1056 | preQ0 transporter | -3.95 | down |
| DW66\_1057 | phosphoribosylglycinamide formyltransferase 2 | -2.49 | down |
| DW66\_1058 | metabolite-proton symporter | -1.32 | down |
| DW66\_1060 | cytochrome c assembly protein | -1.48 | down |
| DW66\_1061 | signal recognition particle protein | -1.53 | down |
| DW66\_1062 | 30S ribosomal protein S16 | -2.63 | down |
| DW66\_1063 | 16S rRNA-processing protein RimM | -3.37 | down |
| DW66\_1064 | tRNA (guanine-N1)-methyltransferase | -3.36 | down |
| DW66\_1065 | 50S ribosomal protein L19 | -1.50 | down |
| DW66\_1066 | thioesterase protein | -4.15 | down |
| DW66\_1067 | site-specific tyrosine recombinase XerD | -2.51 | down |
| DW66\_1068 | thiol:disulfide interchange protein DsbC | -1.11 | down |
| DW66\_1069 | homoserine dehydrogenase | -1.25 | down |
| DW66\_1071 | response regulator receiver protein | -5.90 | down |
| DW66\_1072 | hypothetical protein | -2.76 | down |
| DW66\_1075 | YaeQ protein | -2.74 | down |
| DW66\_1076 | single-stranded-DNA-specific exonuclease RecJ | -2.47 | down |
| DW66\_1077 | hypothetical protein | -2.86 | down |
| DW66\_1078 | NADH:flavin oxidoreductase | 4.67 | up |
| DW66\_1079 | HicB protein | -2.12 | down |
| DW66\_1080 | *gamma*-aminobutyraldehyde dehydrogenase | 3.40 | up |
| DW66\_1081 | binding-protein-dependent transport system inner membrane protein | 1.27 | up |
| DW66\_1082 | binding-protein-dependent transport system inner membrane protein | 1.73 | up |
| DW66\_1083 | spermidine/putrescine ABC transporter ATPase | 2.01 | up |
| DW66\_1084 | extracellular solute-binding protein | 2.83 | up |
| DW66\_1090 | CheA signal transduction histidine kinase | 1.32 | up |
| DW66\_1091 | chemotaxis-specific methylesterase | 1.71 | up |
| DW66\_1092 | response regulator receiver modulated diguanylate cyclase | 1.86 | up |
| DW66\_1093 | peptide chain release factor 2 | -1.52 | down |
| DW66\_1095 | transcriptional regulator TetR | -1.71 | down |
| DW66\_1100 | OmpA/MotB domain-containing protein | -1.09 | down |
| DW66\_1101 | hypothetical protein | -2.30 | down |
| DW66\_1102 | hypothetical protein | 2.03 | up |
| DW66\_1103 | phosphoenolpyruvate carboxylase | 1.65 | up |
| DW66\_1104 | adenylate kinase | -1.07 | down |
| DW66\_1105 | peptidase M22 glycoprotease | -2.41 | down |
| DW66\_1106 | hypothetical protein | -1.03 | down |
| DW66\_1107 | hypothetical protein | -2.03 | down |
| DW66\_1109 | extensin protein | -2.79 | down |
| DW66\_1111 | SAM-dependent methyltransferase | -1.30 | down |
| DW66\_1112 | hypothetical protein | -1.39 | down |
| DW66\_1113 | transcriptional regulator TetR | -1.90 | down |
| DW66\_1114 | RND efflux transporter, MFP subunit | -2.41 | down |
| DW66\_1115 | acriflavin resistance protein | -2.36 | down |
| DW66\_1118 | hypothetical protein | -2.99 | down |
| DW66\_1119 | lipoprotein | -1.21 | down |
| DW66\_1124 | rRNA (guanine-N(1)-)-methyltransferase | -1.22 | down |
| DW66\_1125 | succinyl-diaminopimelate desuccinylase | -2.43 | down |
| DW66\_1127 | UBA/THIF-type NAD/FAD binding protein | -3.30 | down |
| DW66\_1128 | Fe-S metabolism associated SufE | -1.39 | down |
| DW66\_1129 | class V aminotransferase | -1.31 | down |
| DW66\_1130 | 2,3,4,5-tetrahydropyridine-2,6-carboxylate N-succinyltransferase | -1.44 | down |
| DW66\_1131 | oxidoreductase, FAD-binding protein | -1.32 | down |
| DW66\_1132 | Na+/H+ antiporter | -2.35 | down |
| DW66\_1133 | succinyldiaminopimelate transaminase | 1.12 | up |
| DW66\_1137 | elongation factor Ts | -1.83 | down |
| DW66\_1138 | uridylate kinase | -1.22 | down |
| DW66\_1139 | ribosome recycling factor | -1.07 | down |
| DW66\_1140 | undecaprenyl diphosphate synthase | -2.27 | down |
| DW66\_1141 | phosphatidate cytidylyltransferase | -1.66 | down |
| DW66\_1144 | surface antigen | -1.09 | down |
| DW66\_1147 | (3R)-hydroxymyristoyl-ACP dehydratase | -1.00 | down |
| DW66\_1148 | UDP-N-acetylglucosamine acyltransferase | -1.03 | down |
| DW66\_1149 | lipid-A-disaccharide synthase | -2.34 | down |
| DW66\_1150 | ribonuclease HII | -1.91 | down |
| DW66\_1151 | hypothetical protein | -1.01 | down |
| DW66\_1154 | tRNA(Ile)-lysidine synthetase | -1.42 | down |
| DW66\_1156 | 2-dehydro-3-deoxyphosphooctonate aldolase | -1.17 | down |
| DW66\_1162 | S-formylglutathione hydrolase | 1.42 | up |
| DW66\_1163 | 2-C-methyl-D-erythritol 2,4-cyclo diphosphate synthase | -1.43 | down |
| DW66\_1164 | tRNA pseudouridine synthase D | -1.37 | down |
| DW66\_1167 | peptidase M23B | 1.14 | up |
| DW66\_1168 | RNA polymerase sigma factor RpoS | 2.68 | up |
| DW66\_1169 | 4Fe-4S ferredoxin | -2.04 | down |
| DW66\_1170 | DNA mismatch repair protein MutS | -1.41 | down |
| DW66\_1174 | Gamma-aminobutyrate:alpha-ketoglutarate aminotransferase | 1.98 | up |
| DW66\_1179 | hypothetical protein | -2.86 | down |
| DW66\_1182 | amino acid ABC transporter substrate-binding protein | 1.38 | up |
| DW66\_1184 | hypothetical protein | -2.77 | down |
| DW66\_1186 | amino acid MFS transporter | -2.43 | down |
| DW66\_1187 | ISPsy14, transposase | -2.62 | down |
| DW66\_1188 | ATPase AAA | -4.30 | down |
| DW66\_1189 | D-amino acid dehydrogenase small subunit | 1.66 | up |
| DW66\_1190 | Endoribonuclease L-PSP | 2.86 | up |
| DW66\_1191 | hypothetical protein | 1.35 | up |
| DW66\_1192 | N-acetyltransferase | -1.56 | down |
| DW66\_1194 | transcriptional regulator | 2.84 | up |
| DW66\_1196 | hypothetical protein | -3.28 | down |
| DW66\_1197 | hypothetical protein | -11.07 | down |
| DW66\_1198 | transcriptional regulator | -2.02 | down |
| DW66\_1201 | hypothetical protein | 5.53 | up |
| DW66\_1202 | hypothetical protein | 5.76 | up |
| DW66\_1203 | hypothetical protein | 3.28 | up |
| DW66\_1205 | recombination regulator RecX | -2.10 | down |
| DW66\_1206 | Decarboxylase | 2.56 | up |
| DW66\_1207 | hypothetical protein | 1.73 | up |
| DW66\_1208 | secreted protein | -2.67 | down |
| DW66\_1209 | DTW domain-containing protein | -2.67 | down |
| DW66\_1211 | diacylglycerol kinase | -2.12 | down |
| DW66\_1214 | Protein sprT | -1.17 | down |
| DW66\_1215 | membrane protein | 7.05 | up |
| DW66\_1217 | DNA-glycosylase | -1.26 | down |
| DW66\_1221 | alkyl hydroperoxide reductase/ thiol specific antioxidant/ Mal allergen | 1.71 | up |
| DW66\_1222 | Heat shock protein | -1.91 | down |
| DW66\_1223 | hypothetical protein | -1.20 | down |
| DW66\_1226 | two component transcriptional regulator | -3.73 | down |
| DW66\_1227 | integral membrane sensor signal transduction histidine kinase | -2.10 | down |
| DW66\_1228 | cysteine synthase B | -1.99 | down |
| DW66\_1233 | hypothetical protein | 1.48 | up |
| DW66\_1234 | hypothetical protein | -2.21 | down |
| DW66\_1235 | phosphoribosylglycinamide formyltransferase | -2.60 | down |
| DW66\_1236 | phosphoribosylaminoimidazole synthetase | -2.48 | down |
| DW66\_1237 | hypothetical protein | -1.04 | down |
| DW66\_1238 | hypothetical protein | -1.31 | down |
| DW66\_1239 | DNA replication initiation factor | -3.42 | down |
| DW66\_1240 | NLP/P60 protein | -3.38 | down |
| DW66\_1242 | L-sorbosone dehydrogenase | -2.11 | down |
| DW66\_1243 | hypothetical protein | -1.36 | down |
| DW66\_1244 | hypothetical protein | 3.08 | up |
| DW66\_1245 | cob(I)yrinic acid a,c-diamide adenosyltransferase | -3.68 | down |
| DW66\_1246 | cobyrinic acid a,c-diamide synthase | -2.99 | down |
| DW66\_1247 | cob(II)yrinic acid a,c-diamide reductase | -2.95 | down |
| DW66\_1248 | cobalamin biosynthesis protein | -1.56 | down |
| DW66\_1249 | threonine-phosphate decarboxylase | -1.50 | down |
| DW66\_1250 | cobyric acid synthase | -1.41 | down |
| DW66\_1251 | adenosylcobinamide kinase/adenosylcobinamide-phosphate guanylyltransferase | -2.09 | down |
| DW66\_1252 | nicotinate-nucleotide-dimethylbenzimidazole phosphoribosyltransferase | -1.44 | down |
| DW66\_1253 | *alpha*-ribazole phosphatase | -2.00 | down |
| DW66\_1254 | cobalamin synthase | -2.80 | down |
| DW66\_1255 | glycoside hydrolase | -3.74 | down |
| DW66\_1256 | transcriptional regulator MarR | -3.16 | down |
| DW66\_1257 | transporter protein | -2.03 | down |
| DW66\_1258 | hypothetical protein | -1.73 | down |
| DW66\_1261 | hypothetical protein | -3.09 | down |
| DW66\_1262 | transcriptional regulator LysR | -3.33 | down |
| DW66\_1263 | aromatic hydrocarbon degradation membrane protein | -1.54 | down |
| DW66\_1265 | hypothetical protein | -3.56 | down |
| DW66\_1266 | Sel1 domain-containing protein | -3.61 | down |
| DW66\_1269 | hypothetical protein | -2.44 | down |
| DW66\_1271 | hypothetical protein | -4.13 | down |
| DW66\_1273 | multidrug efflux pump | -2.04 | down |
| DW66\_1275 | recombination associated protein | -2.31 | down |
| DW66\_1276 | type II secretion system protein J | -1.74 | down |
| DW66\_1277 | methionine aminopeptidase | -1.43 | down |
| DW66\_1278 | hypothetical protein | -10.86 | down |
| DW66\_1279 | molybdopterin oxidoreductase | -2.96 | down |
| DW66\_1280 | nitrite reductase, (NAD(P)H) large subunit | -2.15 | down |
| DW66\_1281 | nitrite reductase, (NAD(P)H) small subunit | -2.48 | down |
| DW66\_1282 | transcriptional regulator LysR | -1.96 | down |
| DW66\_1283 | FKBP-type peptidylprolyl isomerase | -3.76 | down |
| DW66\_1284 | DUF1232 domain-containing protein | -4.00 | down |
| DW66\_1285 | transcriptional regulator Cro/CI | 1.78 | up |
| DW66\_1288 | carboxyl-terminal protease | 2.99 | up |
| DW66\_1289 | hypothetical protein | -1.97 | down |
| DW66\_1291 | hydrolase | 1.52 | up |
| DW66\_1293 | binding-protein-dependent transport system inner membrane protein | -1.10 | down |
| DW66\_1296 | ABC transporter substrate-binding protein | 2.45 | up |
| DW66\_1297 | transcriptional regulator | -1.33 | down |
| DW66\_1299 | hypothetical protein | 3.33 | up |
| DW66\_1301 | ribosomal large subunit pseudouridine synthase A | -2.63 | down |
| DW66\_1303 | septum site-determining protein MinD | -1.83 | down |
| DW66\_1304 | septum formation inhibitor | -3.85 | down |
| DW66\_1305 | lipid A biosynthesis lauroyl acyltransferase | -2.78 | down |
| DW66\_1306 | patatin | -1.88 | down |
| DW66\_1308 | serine protein kinase PrkA | -1.50 | down |
| DW66\_1670 | *beta* (1-6) glucans synthase | -1.03 | down |
| DW66\_1671 | glycine betaine ABC transporter substrate-binding protein | 3.33 | up |
| DW66\_1677 | hypothetical protein | -1.63 | down |
| DW66\_1678 | peptidase M42 | -1.82 | down |
| DW66\_1679 | acetyltransferase | -1.88 | down |
| DW66\_1680 | asparagine synthase amidotransferase | -3.04 | down |
| DW66\_1681 | 5-methylaminomethyl-2-thiouridine methyltransferase | -1.82 | down |
| DW66\_1682 | UDP-galactose-lipid carrier transferase | 1.14 | up |
| DW66\_1684 | membrane protein | -1.35 | down |
| DW66\_1686 | hypothetical protein | -2.37 | down |
| DW66\_1687 | BolA protein | -2.28 | down |
| DW66\_1691 | GAF and PAS/PAC sensor-containing diguanylate cyclase/phosphodiesterase | 2.45 | up |
| DW66\_1692 | Pyrroloquinoline quinone (Coenzyme PQQ) biosynthesis protein C | 4.11 | up |
| DW66\_1696 | methylthioribose-1-phosphate isomerase | -3.34 | down |
| DW66\_1698 | phosphoserine aminotransferase | -1.29 | down |
| DW66\_1702 | 30S ribosomal protein S1 | -1.26 | down |
| DW66\_1704 | integration host factor subunit beta | 2.69 | up |
| DW66\_1707 | *beta*-lactamase | -3.53 | down |
| DW66\_1710 | ISPsy14, transposase | -2.62 | down |
| DW66\_1711 | ATPase AAA | -4.30 | down |
| DW66\_1712 | hypothetical protein | -7.36 | down |
| DW66\_1713 | dTDP-4-dehydrorhamnose 3,5-epimerase | -1.39 | down |
| DW66\_1717 | hypothetical protein | -2.02 | down |
| DW66\_1718 | transposase IS66 | -2.16 | down |
| DW66\_1719 | Mobile element protein | -1.84 | down |
| DW66\_1722 | GDP-D-mannose dehydratase | -1.59 | down |
| DW66\_1723 | glycosyl transferase group 1 protein | -2.25 | down |
| DW66\_1724 | glycosyl transferase group 1 protein | -2.58 | down |
| DW66\_1725 | NAD-dependent dehydratase | -2.54 | down |
| DW66\_1728 | Mobile element protein | -1.83 | down |
| DW66\_1729 | transposase IS66 | -2.16 | down |
| DW66\_1731 | ATPase AAA | -4.30 | down |
| DW66\_1732 | ISPsy14, transposase | -2.62 | down |
| DW66\_1733 | hypothetical protein | 1.67 | up |
| DW66\_1736 | Helix-hairpin-helix repeat-containing competence protein ComEA | 1.12 | up |
| DW66\_1737 | hypothetical protein | 5.19 | up |
| DW66\_1738 | orotidine 5'-phosphate decarboxylase | -3.37 | down |
| DW66\_1739 | undecaprenyl pyrophosphate phosphatase | -2.24 | down |
| DW66\_1740 | hypothetical protein | -1.04 | down |
| DW66\_1742 | alcohol dehydrogenase | 1.07 | up |
| DW66\_1744 | MFS transporter | -3.78 | down |
| DW66\_1746 | methyl-accepting chemotaxis sensory transducer | 2.85 | up |
| DW66\_1747 | membrane protein | -1.21 | down |
| DW66\_1749 | glutaredoxin | -3.91 | down |
| DW66\_1750 | GTP cyclohydrolase I | -2.03 | down |
| DW66\_1751 | Smr protein/MutS2 | -3.03 | down |
| DW66\_1752 | hypothetical protein | -1.74 | down |
| DW66\_1753 | isochorismatase hydrolase | 2.15 | up |
| DW66\_1754 | N5-glutamine S-adenosyl-L-methionine-dependent methyltransferase | -1.36 | down |
| DW66\_1755 | hypothetical protein | -2.69 | down |
| DW66\_1756 | alpha/beta hydrolase fold protein | -3.25 | down |
| DW66\_1758 | transporter protein | -1.90 | down |
| DW66\_1759 | oxidase | -1.58 | down |
| DW66\_1760 | hypothetical protein | -3.79 | down |
| DW66\_1761 | hypothetical protein | -3.74 | down |
| DW66\_1762 | ankyrin | -1.42 | down |
| DW66\_1763 | hypothetical protein | -2.27 | down |
| DW66\_1764 | zinc/iron permease | -1.93 | down |
| DW66\_1765 | hypothetical protein | 2.03 | up |
| DW66\_1766 | sulfatase | -2.32 | down |
| DW66\_1767 | hypothetical protein | -2.13 | down |
| DW66\_1768 | DNA and RNA helicases | 1.97 | up |
| DW66\_1769 | cytochrome c | -1.58 | down |
| DW66\_1772 | 1-acyl-sn-glycerol-3-phosphate acyltransferase | -3.41 | down |
| DW66\_1773 | enoyl-CoA hydratase | -1.63 | down |
| DW66\_1774 | TonB-dependent siderophore receptor | -1.73 | down |
| DW66\_1775 | hypothetical protein | 1.38 | up |
| DW66\_1776 | transporter protein | -2.02 | down |
| DW66\_1777 | 3-ketoacyl-(acyl-carrier-protein) reductase | 1.59 | up |
| DW66\_1778 | transcriptional regulator LysR | -1.27 | down |
| DW66\_1780 | hypothetical protein | 1.18 | up |
| DW66\_1782 | elongation factor P | -1.03 | down |
| DW66\_1783 | protein OsmC | 4.18 | up |
| DW66\_1784 | transcriptional regulator MarR | -1.63 | down |
| DW66\_1785 | transcriptional regulator LysR | -2.06 | down |
| DW66\_1786 | membrane protein | -2.41 | down |
| DW66\_1787 | transcriptional regulator LysR | 1.63 | up |
| DW66\_1788 | hypothetical protein | -1.70 | down |
| DW66\_1791 | Spermidine synthase-like protein | -2.80 | down |
| DW66\_1792 | DEAD/DEAH box helicase | -4.17 | down |
| DW66\_1800 | ATP/GTP-binding protein | -2.66 | down |
| DW66\_1801 | GAF domain-containing protein | -1.05 | down |
| DW66\_1802 | hypothetical protein | 1.75 | up |
| DW66\_1803 | fimbrial protein | -2.42 | down |
| DW66\_1804 | ferrous iron transporter B | -1.83 | down |
| DW66\_1807 | Outer membrane autotransporter barrel | -4.09 | down |
| DW66\_1809 | pili assembly chaperone | -4.86 | down |
| DW66\_1810 | type I fimbrial protein FimA | -1.90 | down |
| DW66\_1812 | acyl-CoA dehydrogenase | 2.95 | up |
| DW66\_1814 | ABC transporter ATP-binding protein | -1.97 | down |
| DW66\_1815 | membrane protein | -1.59 | down |
| DW66\_1816 | acetyltransferase | -2.73 | down |
| DW66\_1817 | MotA/TolQ/ExbB proton channel | -2.25 | down |
| DW66\_1818 | biopolymer transport protein ExbD/TolR | -2.11 | down |
| DW66\_1819 | tetraacyldisaccharide 4'-kinase | -2.72 | down |
| DW66\_1823 | UDP-N-acetylenolpyruvoylglucosamine reductase | -1.09 | down |
| DW66\_1824 | ribonuclease E | -1.38 | down |
| DW66\_1825 | hypothetical protein | -1.67 | down |
| DW66\_1826 | pseudouridine synthase RluA | -2.67 | down |
| DW66\_1827 | hydrolase | -3.00 | down |
| DW66\_1828 | signal peptide peptidase SppA, 36K type | -2.75 | down |
| DW66\_1830 | hypothetical protein | -2.85 | down |
| DW66\_1831 | 50S ribosomal protein L32 | -2.93 | down |
| DW66\_1832 | phosphate acyltransferase | -4.82 | down |
| DW66\_1833 | malonyl CoA-acyl carrier protein transacylase | -1.20 | down |
| DW66\_1836 | 3-oxoacyl-(acyl carrier protein) synthase II | -1.62 | down |
| DW66\_1837 | 4-amino-4-deoxychorismate lyase | -1.91 | down |
| DW66\_1838 | aminodeoxychorismate lyase | -2.54 | down |
| DW66\_1842 | transcriptional regulator TetR | -1.26 | down |
| DW66\_1843 | molybdenum cofactor synthesis domain-containing protein | -3.81 | down |
| DW66\_1844 | lipoprotein | -2.96 | down |
| DW66\_1845 | hypothetical protein | -2.37 | down |
| DW66\_1846 | cupin | -4.24 | down |
| DW66\_1850 | hypothetical protein | 1.06 | up |
| DW66\_1851 | drug resistance transporter EmrB | -1.20 | down |
| DW66\_1852 | secretion protein HlyD | -1.18 | down |
| DW66\_1853 | glutamyl-tRNA synthetase | -1.53 | down |
| DW66\_1854 | transcriptional regulator TetR | -5.27 | down |
| DW66\_1855 | hydrolase | -4.19 | down |
| DW66\_1856 | hypothetical protein | -2.92 | down |
| DW66\_1857 | thioesterase protein | -3.83 | down |
| DW66\_1858 | dihydrouridine synthase DuS | -5.04 | down |
| DW66\_1859 | heat shock protein Hsp20 | 4.68 | up |
| DW66\_1860 | PAS/PAC sensor-containing diguanylate cyclase/phosphodiesterase | 3.43 | up |
| DW66\_1867 | hypothetical protein | -1.65 | down |
| DW66\_1868 | aspartate-semialdehyde dehydrogenase | -1.88 | down |
| DW66\_1869 | peptidoglycan-binding LysM | 1.65 | up |
| DW66\_1870 | tRNA pseudouridine synthase A | -1.73 | down |
| DW66\_1872 | acetyl-CoA carboxylase subunit beta | -1.23 | down |
| DW66\_1873 | bifunctional folylpolyglutamate synthase/ dihydrofolate synthase | -1.40 | down |
| DW66\_1874 | cell division protein | -1.58 | down |
| DW66\_1875 | colicin V production protein | -1.45 | down |
| DW66\_1879 | lipoprotein | -3.92 | down |
| DW66\_1882 | transcriptional regulator AraC | -2.19 | down |
| DW66\_1883 | nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase | -3.01 | down |
| DW66\_1884 | NADH:flavin oxidoreductase | -2.12 | down |
| DW66\_1885 | 1-aminocyclopropane-1-carboxylate deaminase | -2.75 | down |
| DW66\_1892 | hypothetical protein | -1.29 | down |
| DW66\_1893 | aminopeptidase N | 1.48 | up |
| DW66\_1897 | 3-carboxymuconate cyclase | 1.25 | up |
| DW66\_1898 | hypothetical protein | -4.57 | down |
| DW66\_1899 | glutathione S-transferase | -1.34 | down |
| DW66\_1900 | SMC domain-containing protein | -1.22 | down |
| DW66\_1901 | nuclease SbcCD subunit D | -3.45 | down |
| DW66\_1902 | type IV secretion protein Rhs | -1.89 | down |
| DW66\_1903 | membrane protein | -2.35 | down |
| DW66\_1904 | hypothetical protein | 2.00 | up |
| DW66\_1908 | hypothetical protein | -1.35 | down |
| DW66\_1909 | hypothetical protein | -1.26 | down |
| DW66\_1910 | ATPase | -1.11 | down |
| DW66\_1911 | hypothetical protein | -2.24 | down |
| DW66\_1912 | hypothetical protein | -2.68 | down |
| DW66\_1914 | benzoate transporter | -1.73 | down |
| DW66\_1916 | dihydrodipicolinate synthetase | 1.02 | up |
| DW66\_1917 | class II aldolase/adducin domain-containing protein | -2.60 | down |
| DW66\_1918 | transmembrane protein | -2.81 | down |
| DW66\_1919 | regulator domain-containing protein | -1.97 | down |
| DW66\_1920 | NmrA protein | 4.64 | up |
| DW66\_1921 | hypothetical protein | 4.56 | up |
| DW66\_1926 | transcriptional regulator | -2.95 | down |
| DW66\_1927 | N-acetyltransferase GCN5 | -2.26 | down |
| DW66\_1929 | diaminopimelate decarboxylase | -2.27 | down |
| DW66\_1932 | hypothetical protein | -1.40 | down |
| DW66\_1933 | hypothetical protein | -1.07 | down |
| DW66\_1934 | NAD-glutamate dehydrogenase | 2.99 | up |
| DW66\_1936 | hypothetical protein | -2.93 | down |
| DW66\_1938 | Alpha/beta hydrolase | -1.38 | down |
| DW66\_1941 | CrfX protein | 1.92 | up |
| DW66\_1942 | TM helix repeat-containing protein | 1.36 | up |
| DW66\_1943 | RNA polymerase sigma factor SigX | -1.46 | down |
| DW66\_1944 | OmpF protein | 1.10 | up |
| DW66\_1945 | uroporphyrin-III C-methyltransferase | -3.43 | down |
| DW66\_1946 | serine/threonine-protein kinase | -3.43 | down |
| DW66\_1947 | MFS transporter | -2.39 | down |
| DW66\_1948 | response regulator receiver/ANTAR domain-containing protein | -2.49 | down |
| DW66\_1949 | nitrate-binding protein NasS | -2.78 | down |
| DW66\_1950 | dihydroorotate dehydrogenase 2 | -2.33 | down |
| DW66\_1955 | PAS/PAC sensor hybrid histidine kinase | -4.03 | down |
| DW66\_1956 | transcriptional regulator | -4.17 | down |
| DW66\_1961 | ammonium transporter | -3.77 | down |
| DW66\_1963 | peptidase M15A | -3.59 | down |
| DW66\_1965 | pseudouridine synthase | -2.59 | down |
| DW66\_1968 | aconitate hydratase | 2.42 | up |
| DW66\_1969 | RNA 2'-O-ribose methyltransferase | -4.41 | down |
| DW66\_1971 | erythronate-4-phosphate dehydrogenase | -1.31 | down |
| DW66\_1972 | hypothetical protein | 4.39 | up |
| DW66\_1973 | hypothetical protein | 3.06 | up |
| DW66\_1974 | lipid ABC transporter ATPase/inner membrane protein | -3.41 | down |
| DW66\_1975 | hypothetical protein | -4.32 | down |
| DW66\_1976 | methyl-accepting chemotaxis sensory transducer | -4.49 | down |
| DW66\_1977 | malate:quinone oxidoreductase | -3.07 | down |
| DW66\_1981 | group 1 glycosyl transferase | 1.51 | up |
| DW66\_1982 | lipid kinase | -1.75 | down |
| DW66\_1983 | transcriptional regulator | -3.24 | down |
| DW66\_1984 | sensor histidine kinase | -3.59 | down |
| DW66\_1985 | CheA signal transduction histidine kinase | -3.15 | down |
| DW66\_1987 | MOSC domain-containing protein | -1.66 | down |
| DW66\_1988 | lytic transglycosylase | 2.20 | up |
| DW66\_1989 | ABC transporter ATP-binding protein | -2.49 | down |
| DW66\_1990 | UspA domain-containing protein | 2.86 | up |
| DW66\_1991 | hypothetical protein | -2.70 | down |
| DW66\_1992 | fatty acid oxidation complex subunit alpha | -2.99 | down |
| DW66\_2000 | transcriptional regulator TetR | -2.87 | down |
| DW66\_2001 | ErfK/YbiS/YcfS/YnhG protein | -3.91 | down |
| DW66\_2002 | *beta*-hexosaminidase | -3.83 | down |
| DW66\_2003 | *beta*-hexosaminidase | -4.55 | down |
| DW66\_2004 | non-specific serine/threonine protein kinase | 1.85 | up |
| DW66\_2005 | hypothetical protein | 1.12 | up |
| DW66\_2007 | glyceraldehyde-3-phosphate dehydrogenase | -1.20 | down |
| DW66\_2008 | lipoprotein ApbE | -1.29 | down |
| DW66\_2009 | soluble pyridine nucleotide transhydrogenase | -1.46 | down |
| DW66\_2010 | glycerophosphoryl diester phosphodiesterase | 1.14 | up |
| DW66\_2012 | lipoprotein releasing system, transmembrane protein | -2.95 | down |
| DW66\_2013 | lipoprotein releasing system ATP-binding protein | -1.16 | down |
| DW66\_2014 | lipoprotein releasing system, transmembrane protein | -2.20 | down |
| DW66\_2015 | sensory box protein | -6.19 | down |
| DW66\_2017 | two component heavy metal response transcriptional regulator | -1.91 | down |
| DW66\_2019 | chromosome segregation ATPase | 4.05 | up |
| DW66\_2020 | Phosphonoacetaldehyde phosphonohydrolase-related protein | -6.50 | down |
| DW66\_2025 | hypothetical protein | -2.89 | down |
| DW66\_2028 | transcriptional regulator AraC | -2.47 | down |
| DW66\_2029 | sterol desaturase | -3.70 | down |
| DW66\_2032 | 2-pyrone-4,6-dicarboxylic acid hydrolase | -1.62 | down |
| DW66\_2035 | Dimethylmenaquinone methyltransferase | 1.73 | up |
| DW66\_2036 | transport-related membrane protein | -2.90 | down |
| DW66\_2037 | permease | -1.82 | down |
| DW66\_2038 | SMP-30/gluconolaconase/LRE domain-containing protein | -1.11 | down |
| DW66\_2043 | formate dehydrogenase subunit alpha | 1.02 | up |
| DW66\_2045 | UspA domain-containing protein | 3.39 | up |
| DW66\_2046 | tRNA-hydroxylase | -2.37 | down |
| DW66\_2048 | hypothetical protein | -2.75 | down |
| DW66\_2050 | anti-FecI sigma factor FecR | -3.62 | down |
| DW66\_2051 | TonB-dependent siderophore receptor | -3.09 | down |
| DW66\_2052 | transcriptional regulator LysR | -2.03 | down |
| DW66\_2055 | hypothetical protein | -2.68 | down |
| DW66\_2056 | glucose sorbosone dehydrogenase | -2.17 | down |
| DW66\_2057 | ATPase AFG1 | -1.43 | down |
| DW66\_2058 | DinB protein | 2.32 | up |
| DW66\_2059 | alpha/beta hydrolase fold protein | -1.36 | down |
| DW66\_2060 | membrane protein | -1.20 | down |
| DW66\_2063 | hypothetical protein | -4.63 | down |
| DW66\_2064 | peptidase U32 | -1.81 | down |
| DW66\_2065 | membrane protein | -3.11 | down |
| DW66\_2067 | phosphonoacetaldehyde hydrolase | -1.41 | down |
| DW66\_2068 | 2-aminoethylphosphonate--pyruvate transaminase | -2.26 | down |
| DW66\_2069 | transcriptional regulator LysR | -1.62 | down |
| DW66\_2070 | transcriptional regulator AraC | -2.21 | down |
| DW66\_2071 | hypothetical protein | -3.52 | down |
| DW66\_2072 | Leucine-rich repeat domain protein | -3.00 | down |
| DW66\_2075 | acetyl-CoA acetyltransferase | 1.31 | up |
| DW66\_2078 | transcriptional regulator TraR | -2.48 | down |
| DW66\_2079 | hypothetical protein | -2.83 | down |
| DW66\_2080 | hypothetical protein | -3.32 | down |
| DW66\_2081 | hypothetical protein | -4.49 | down |
| DW66\_2082 | monovalent cation/H+ antiporter subunit G | 1.62 | up |
| DW66\_2087 | monovalent cation/H+ antiporter subunit A | -1.06 | down |
| DW66\_2088 | Permease of the drug/metabolite transporter | -1.90 | down |
| DW66\_2089 | transcriptional regulator XRE | -2.17 | down |
| DW66\_2090 | isochorismatase hydrolase | -2.00 | down |
| DW66\_2091 | transcriptional regulator AraC | -1.44 | down |
| DW66\_2092 | Chromosome segregation ATPases | -2.58 | down |
| DW66\_2093 | hydrolase | -3.00 | down |
| DW66\_2094 | Biotin carboxylase | -4.14 | down |
| DW66\_2098 | ABC transporter | -2.32 | down |
| DW66\_2100 | outer membrane receptor FepA | -5.06 | down |
| DW66\_2101 | phosphoglycerate mutase | -2.36 | down |
| DW66\_2102 | sulfate permease | -2.71 | down |
| DW66\_2103 | transcriptional regulator XRE | -1.44 | down |
| DW66\_2107 | membrane protein | -2.11 | down |
| DW66\_2108 | methyl-accepting chemotaxis sensory transducer | 2.45 | up |
| DW66\_2109 | hypothetical protein | -4.05 | down |
| DW66\_2111 | transmembrane pair domain-containing protein | -3.94 | down |
| DW66\_2115 | C4-dicarboxylate transporter DctA | -1.57 | down |
| DW66\_2116 | methyl-accepting chemotaxis sensory transducer with Pas/Pac sensor | -1.43 | down |
| DW66\_2117 | PAS/PAC sensor-containing diguanylate cyclase/phosphodiesterase | -2.05 | down |
| DW66\_2121 | GAF modulated sigma54 specific transcriptional regulator | 1.58 | up |
| DW66\_2122 | sugar ABC transporter ATP-binding protein | -2.15 | down |
| DW66\_2123 | sugar ABC transporter ATP-binding protein | -1.66 | down |
| DW66\_2124 | binding-protein-dependent transport system inner membrane protein | -2.27 | down |
| DW66\_2128 | hypothetical protein | -1.80 | down |
| DW66\_2131 | trigger factor | -1.92 | down |
| DW66\_2133 | ATP-dependent protease, ATP-binding subunit ClpX | 1.07 | up |
| DW66\_2134 | ATP-dependent protease La | 2.24 | up |
| DW66\_2136 | PpiC-type peptidyl-prolyl cis-trans isomerase | -1.75 | down |
| DW66\_2137 | patatin | 1.10 | up |
| DW66\_2140 | acyl-CoA thioesterase II | -2.72 | down |
| DW66\_2141 | Phage terminase, small subunit | 3.20 | up |
| DW66\_2142 | methyl-accepting chemotaxis sensory transducer | 3.41 | up |
| DW66\_2143 | preprotein translocase subunit TatD | -1.52 | down |
| DW66\_2144 | lytic transglycosylase | -3.56 | down |
| DW66\_2145 | DoxX protein | -5.06 | down |
| DW66\_2146 | hypothetical protein | -1.87 | down |
| DW66\_2147 | transcription elongation factor GreB | -1.48 | down |
| DW66\_2149 | ABC transporter ATP-binding protein | -2.13 | down |
| DW66\_2150 | arylesterase | -1.19 | down |
| DW66\_2151 | hypothetical protein | -4.39 | down |
| DW66\_2153 | outer membrane lipoprotein OprI | 5.57 | up |
| DW66\_2154 | hypothetical protein | 1.57 | up |
| DW66\_2156 | hypothetical protein | -11.55 | down |
| DW66\_2158 | UspA domain-containing protein | 3.21 | up |
| DW66\_2159 | transcriptional regulator CysB | 1.05 | up |
| DW66\_2161 | para-aminobenzoate synthase subunit I | -3.27 | down |
| DW66\_2164 | hypothetical protein | -2.51 | down |
| DW66\_2166 | 2-methylisocitrate lyase | 1.14 | up |
| DW66\_2167 | hypothetical protein | -3.67 | down |
| DW66\_2168 | methylcitrate synthase | 2.50 | up |
| DW66\_2169 | hypothetical protein | -1.21 | down |
| DW66\_2171 | aconitate hydratase | 1.81 | up |
| DW66\_2172 | AcnD-accessory protein PrpF | 1.48 | up |
| DW66\_2173 | 2-methylcitrate dehydratase | 1.48 | up |
| DW66\_2174 | bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase | 1.47 | up |
| DW66\_2176 | hypothetical protein | -1.93 | down |
| DW66\_2178 | hypothetical protein | -4.67 | down |
| DW66\_2181 | peptidase | -1.78 | down |
| DW66\_2182 | two component transcriptional regulator | -3.78 | down |
| DW66\_2183 | integral membrane sensor signal transduction histidine kinase | -2.82 | down |
| DW66\_2184 | hypothetical protein | -4.12 | down |
| DW66\_2185 | transcriptional regulator LysR | -1.49 | down |
| DW66\_2187 | ATPase AFG1 | -1.13 | down |
| DW66\_2189 | hypothetical protein | 1.35 | up |
| DW66\_2193 | spore coat U domain-containing protein | 1.80 | up |
| DW66\_2196 | spore coat U domain-containing protein | -1.13 | down |
| DW66\_2197 | type 1 pili usher pathway chaperone CsuC | -1.79 | down |
| DW66\_2198 | fimbrial biogenesis outer membrane usher protein | -2.19 | down |
| DW66\_2199 | spore coat U domain-containing protein | -2.50 | down |
| DW66\_2203 | integral membrane protein TerC | -3.05 | down |
| DW66\_2204 | hypothetical protein | -1.63 | down |
| DW66\_2205 | lipoprotein VacJ | -3.31 | down |
| DW66\_2206 | two component transcriptional regulator | -1.86 | down |
| DW66\_2207 | integral membrane sensor signal transduction histidine kinase | -3.36 | down |
| DW66\_2208 | hypothetical protein | 2.32 | up |
| DW66\_2209 | luciferase | -1.37 | down |
| DW66\_2212 | sulfite reductase (ferredoxin) | -1.17 | down |
| DW66\_2213 | hypothetical protein | -3.01 | down |
| DW66\_2214 | periplasmic binding protein/LacI transcriptional regulator | -2.66 | down |
| DW66\_2215 | hypothetical protein | 4.83 | up |
| DW66\_2216 | hypothetical protein | 3.22 | up |
| DW66\_2218 | fatty acid cistrans isomerase | -2.47 | down |
| DW66\_2219 | acyltransferase 3 | -2.97 | down |
| DW66\_2221 | photosynthetic protein synthase I | -1.29 | down |
| DW66\_2222 | Copper metallochaperone | -1.60 | down |
| DW66\_2223 | hypothetical protein | 4.58 | up |
| DW66\_2224 | coproporphyrinogen III oxidase | -2.09 | down |
| DW66\_2225 | transporter protein | -2.51 | down |
| DW66\_2226 | ornithine decarboxylase, constitutive | -1.96 | down |
| DW66\_2227 | transcriptional regulator AraC | -2.86 | down |
| DW66\_2228 | branched chain amino acid ABC transporter | -2.00 | down |
| DW66\_2229 | AzlC protein | -2.77 | down |
| DW66\_2230 | hypothetical protein | -1.70 | down |
| DW66\_2231 | hypothetical protein | 1.82 | up |
| DW66\_2233 | hypothetical protein | -2.45 | down |
| DW66\_2236 | Leucine-rich repeat containing protein | -1.16 | down |
| DW66\_2238 | hypothetical protein | -2.39 | down |
| DW66\_2239 | hypothetical protein | -3.98 | down |
| DW66\_2240 | hypothetical protein | -2.97 | down |
| DW66\_2241 | hypothetical protein | -4.81 | down |
| DW66\_2242 | ferric reductase domain-containing protein | -13.94 | down |
| DW66\_2244 | two component transcriptional regulator | -1.82 | down |
| DW66\_2245 | hypothetical protein | -2.43 | down |
| DW66\_2246 | redoxin domain-containing protein | -3.49 | down |
| DW66\_2249 | outer membrane efflux protein | -6.78 | down |
| DW66\_2250 | RND efflux transporter, MFP subunit | -6.29 | down |
| DW66\_2251 | heavy metal efflux protein | -4.36 | down |
| DW66\_2253 | TonB-dependent siderophore receptor | -4.09 | down |
| DW66\_2254 | hypothetical protein | -2.21 | down |
| DW66\_2255 | cobyrinic acid a,c-diamide synthase | -1.83 | down |
| DW66\_2256 | diguanylate cyclase | -2.02 | down |
| DW66\_2257 | hypothetical protein | -1.19 | down |
| DW66\_2258 | outer membrane porin | -4.13 | down |
| DW66\_2259 | iron ABC transporter ATP-binding protein | -5.80 | down |
| DW66\_2260 | transport system permease | -5.54 | down |
| DW66\_2261 | periplasmic binding protein | -5.00 | down |
| DW66\_2262 | membrane protein | -2.82 | down |
| DW66\_2263 | TonB-dependent siderophore receptor | -4.98 | down |
| DW66\_2264 | transcriptional regulator LysR | -4.10 | down |
| DW66\_2265 | lipoprotein | 1.10 | up |
| DW66\_2266 | integral membrane protein TerC | 1.53 | up |
| DW66\_2268 | hypothetical protein | -1.12 | down |
| DW66\_2269 | FAD dependent oxidoreductase | -2.81 | down |
| DW66\_2271 | Guanosine-3',5'-bis(Diphosphate) 3'-pyrophosphohydrolase | 1.77 | up |
| DW66\_2273 | glutaminase-asparaginase | -1.40 | down |
| DW66\_2280 | inosine/uridine-preferring nucleoside hydrolase | -1.34 | down |
| DW66\_2282 | lipoprotein | -1.29 | down |
| DW66\_2283 | cold shock protein CspA | 2.53 | up |
| DW66\_2284 | hypothetical protein | 1.08 | up |
| DW66\_2286 | translation initiation factor IF-3 | -2.44 | down |
| DW66\_2287 | ribosomal protein L35 | -2.14 | down |
| DW66\_2288 | 50S ribosomal protein L20 | -2.01 | down |
| DW66\_2289 | phenylalanyl-tRNA synthetase subunit alpha | -3.10 | down |
| DW66\_2293 | Transcriptional regulator | -1.56 | down |
| DW66\_2297 | diguanylate cyclase | 2.56 | up |
| DW66\_2298 | glutaminase | -1.09 | down |
| DW66\_2299 | transcriptional regulator | -2.09 | down |
| DW66\_2301 | transporter protein | -2.70 | down |
| DW66\_2302 | hypothetical protein | -1.13 | down |
| DW66\_2304 | hypothetical protein | 1.42 | up |
| DW66\_2305 | hypothetical protein | 3.49 | up |
| DW66\_2306 | hypothetical protein | -1.79 | down |
| DW66\_2307 | hypothetical protein | -2.42 | down |
| DW66\_2308 | hypothetical protein | -1.54 | down |
| DW66\_2309 | hypothetical protein | -2.77 | down |
| DW66\_2314 | oligopeptide transporter OPT | -2.42 | down |
| DW66\_2315 | hypothetical protein | -1.25 | down |
| DW66\_2317 | transcriptional regulator AraC | -1.25 | down |
| DW66\_2318 | metal dependent phosphohydrolase | -2.46 | down |
| DW66\_2319 | 5'-nucleotidase | -1.01 | down |
| DW66\_2320 | hypothetical protein | -3.43 | down |
| DW66\_2321 | transcriptional regulator LysR | -1.66 | down |
| DW66\_2322 | transporter protein | -2.09 | down |
| DW66\_2323 | glutathione S-transferase | -1.40 | down |
| DW66\_2324 | hypothetical protein | -3.73 | down |
| DW66\_2325 | hypothetical protein | -2.85 | down |
| DW66\_2326 | transcriptional regulator LysR | -3.07 | down |
| DW66\_2329 | iron-containing alcohol dehydrogenase | -4.29 | down |
| DW66\_2332 | short-chain dehydrogenase/reductase SDR | -2.32 | down |
| DW66\_2333 | transcriptional factor-like protein | -2.07 | down |
| DW66\_2334 | alcohol dehydrogenase | -2.70 | down |
| DW66\_2335 | transporter protein | -5.27 | down |
| DW66\_2336 | NADH:flavin oxidoreductase | -3.56 | down |
| DW66\_2339 | hypothetical protein | -1.19 | down |
| DW66\_2341 | transporter protein | -2.34 | down |
| DW66\_2342 | allantoate amidohydrolase | -1.48 | down |
| DW66\_2344 | hypothetical protein | 1.70 | up |
| DW66\_2345 | transcriptional regulator | -1.37 | down |
| DW66\_2346 | hypothetical protein | -1.23 | down |
| DW66\_2347 | amino acid permease-associated protein | -2.97 | down |
| DW66\_2348 | trans-aconitate 2-methyltransferase | 2.30 | up |
| DW66\_2349 | membrane protein | -1.45 | down |
| DW66\_2351 | transporter protein | -3.85 | down |
| DW66\_2352 | aminophosphonate oxidoreductase | -2.00 | down |
| DW66\_2353 | hypothetical protein | -2.39 | down |
| DW66\_2354 | transcriptional regulator LysR | -3.86 | down |
| DW66\_2356 | transporter protein | -1.94 | down |
| DW66\_2357 | hypothetical protein | -2.88 | down |
| DW66\_2358 | hypothetical protein | -5.94 | down |
| DW66\_2361 | chromate transporter | -2.08 | down |
| DW66\_2363 | type I secretion outer membrane protein TolC | 1.93 | up |
| DW66\_2364 | type I secretion membrane fusion protein HlyD | 2.25 | up |
| DW66\_2366 | heme peroxidase | -1.47 | down |
| DW66\_2367 | transcriptional regulator LysR | -1.35 | down |
| DW66\_2368 | hydrolase | -3.17 | down |
| DW66\_2370 | hypothetical protein | -10.59 | down |
| DW66\_2371 | UvrD/REP helicase | -2.89 | down |
| DW66\_2372 | Leucine-rich repeat domain protein | -1.53 | down |
| DW66\_2373 | alpha/beta hydrolase fold protein | -2.05 | down |
| DW66\_2374 | glyoxalase/bleomycin resistance protein/dioxygenase | -1.48 | down |
| DW66\_2375 | alpha/beta hydrolase fold protein | -1.22 | down |
| DW66\_2376 | transporter protein | 2.76 | up |
| DW66\_2377 | hypothetical protein | 1.48 | up |
| DW66\_2378 | Thermostable hemolysin delta-VPH | -3.86 | down |
| DW66\_2379 | long-chain-fatty-acid-CoA ligase | -3.64 | down |
| DW66\_2380 | long-chain acyl-CoA synthetase | -2.08 | down |
| DW66\_2381 | short-chain dehydrogenase | -1.55 | down |
| DW66\_2382 | hypothetical protein | -1.15 | down |
| DW66\_2385 | glyoxalase/bleomycin resistance protein/dioxygenase | 2.10 | up |
| DW66\_2387 | hypothetical protein | 4.57 | up |
| DW66\_2388 | paraquat-inducible protein A | 1.71 | up |
| DW66\_2389 | paraquat-inducible protein A | 2.26 | up |
| DW66\_2390 | Paraquat-inducible protein B | 2.75 | up |
| DW66\_2391 | hypothetical protein | 2.90 | up |
| DW66\_2392 | hypothetical protein | -5.84 | down |
| DW66\_2393 | hypothetical protein | 2.43 | up |
| DW66\_2395 | aldehyde dehydrogenase | -3.32 | down |
| DW66\_2396 | amino acid permease-associated protein | -2.49 | down |
| DW66\_2397 | transcriptional regulator | -1.23 | down |
| DW66\_2399 | aldehyde dehydrogenase | -1.14 | down |
| DW66\_2401 | FAD-binding dehydrogenase | -1.81 | down |
| DW66\_2402 | transcriptional regulator IclR | -1.36 | down |
| DW66\_2403 | oxidoreductase domain-containing protein | -2.65 | down |
| DW66\_2404 | xylose isomerase domain-containing protein | -1.85 | down |
| DW66\_2406 | fumarate reductase/succinate dehydrogenase flavoprotein domain-containing protein | -1.90 | down |
| DW66\_2412 | FAD dependent oxidoreductase | -2.63 | down |
| DW66\_2413 | BFD/(2Fe-2S)-binding domain-containing protein | -2.04 | down |
| DW66\_2415 | binding-protein-dependent transport system inner membrane protein | -3.63 | down |
| DW66\_2416 | binding-protein-dependent transport system inner membrane protein | -2.82 | down |
| DW66\_2417 | ABC transporter ATP-binding protein | -2.13 | down |
| DW66\_2418 | transcriptional regulator IclR | 2.42 | up |
| DW66\_2419 | ABC transporter ATP-binding protein | -1.51 | down |
| DW66\_2421 | Lactam utilization protein LamB | -1.52 | down |
| DW66\_2424 | Outer membrane protein ImpK/VasF, OmpA/MotB domain | -1.79 | down |
| DW66\_2426 | type VI secretion-associated protein ImpA | -1.89 | down |
| DW66\_2427 | hypothetical protein | -3.86 | down |
| DW66\_2428 | hypothetical protein | -2.38 | down |
| DW66\_2431 | hypothetical protein | -1.41 | down |
| DW66\_2432 | dihydrodipicolinate synthase | -1.82 | down |
| DW66\_2434 | transcriptional regulator | -2.00 | down |
| DW66\_2435 | hypothetical protein | -4.83 | down |
| DW66\_2436 | methyl-accepting chemotaxis sensory transducer | -3.08 | down |
| DW66\_2437 | hypothetical protein | -2.86 | down |
| DW66\_2439 | Kup system potassium uptake protein | -2.03 | down |
| DW66\_2440 | transporter protein | -2.71 | down |
| DW66\_2441 | universal stress protein | 4.18 | up |
| DW66\_2442 | hypothetical protein | 1.28 | up |
| DW66\_2443 | Plasmid stabilization system protein | -1.84 | down |
| DW66\_2444 | phosphate ABC transporter substrate-binding protein | -2.17 | down |
| DW66\_2445 | phosphate ABC transporter permease | -2.45 | down |
| DW66\_2446 | phosphate ABC transporter permease | -3.08 | down |
| DW66\_2449 | hypothetical protein | -2.28 | down |
| DW66\_2454 | transcriptional regulator XRE | -2.15 | down |
| DW66\_2455 | short-chain dehydrogenase/reductase SDR | 3.32 | up |
| DW66\_2456 | hypothetical protein | 1.28 | up |
| DW66\_2457 | deoxyribodipyrimidine photolyase-like protein | -1.66 | down |
| DW66\_2458 | hypothetical protein | -1.71 | down |
| DW66\_2462 | short-chain dehydrogenase/reductase | 1.07 | up |
| DW66\_2463 | hypothetical protein | 2.39 | up |
| DW66\_2464 | PAS/PAC sensor protein | 1.41 | up |
| DW66\_2465 | transcriptional regulator MerR | -3.19 | down |
| DW66\_2466 | Outer membrane protein (porin) | -3.72 | down |
| DW66\_2467 | hypothetical protein | -3.08 | down |
| DW66\_2468 | PAS/PAC sensor hybrid histidine kinase | -2.06 | down |
| DW66\_2469 | transcriptional regulator | -1.93 | down |
| DW66\_2470 | Rhodanese-related sulfurtransferase | -4.23 | down |
| DW66\_2471 | ABC transporter | -3.29 | down |
| DW66\_2472 | efflux ABC transporter ATP-binding protein | -2.47 | down |
| DW66\_2473 | outer membrane protein | -2.93 | down |
| DW66\_2474 | ABC-type branched-chain amino acid transport systems periplasmic compoment-like protein | -1.90 | down |
| DW66\_2475 | integral membrane sensor signal transduction histidine kinase | -3.73 | down |
| DW66\_2476 | transcriptional regulator | -3.73 | down |
| DW66\_2477 | pentapeptide repeat-containing protein | -4.74 | down |
| DW66\_2478 | quinoprotein ethanol dehydrogenase | -1.80 | down |
| DW66\_2480 | extracellular solute-binding protein | -1.65 | down |
| DW66\_2481 | hypothetical protein | -3.96 | down |
| DW66\_2482 | *beta*-lactamase domain-containing protein | -3.39 | down |
| DW66\_2486 | iron-containing alcohol dehydrogenase | -2.00 | down |
| DW66\_2487 | PAS/PAC sensor hybrid histidine kinase | -1.71 | down |
| DW66\_2488 | sulfate permease | 1.55 | up |
| DW66\_2489 | RND transporter | -4.41 | down |
| DW66\_2490 | RND efflux transporter, MFP subunit | -2.47 | down |
| DW66\_2491 | hydrophobe/amphiphile efflux-1 | -2.58 | down |
| DW66\_2492 | RND efflux system outer membrane lipoprotein | -1.40 | down |
| DW66\_2493 | transporter protein | -1.80 | down |
| DW66\_2496 | iron-containing alcohol dehydrogenase | 1.90 | up |
| DW66\_2498 | shikimate/quinate 5-dehydrogenase | 2.31 | up |
| DW66\_2500 | iron-containing alcohol dehydrogenase | -1.65 | down |
| DW66\_2501 | carbohydrate-selective porin OprB | -2.39 | down |
| DW66\_2502 | aldehyde dehydrogenase | -1.14 | down |
| DW66\_2503 | sugar ABC transporter periplasmic protein | -3.84 | down |
| DW66\_2504 | ribose ABC transporter ATP-binding protein | -3.73 | down |
| DW66\_2505 | monosaccharide-transporting ATPase | -1.53 | down |
| DW66\_2506 | transcriptional regulator | -1.06 | down |
| DW66\_2507 | transporter | -2.21 | down |
| DW66\_2508 | hypothetical protein | -2.40 | down |
| DW66\_2509 | hypothetical protein | -13.19 | down |
| DW66\_2510 | hypothetical protein | -1.51 | down |
| DW66\_2511 | exodeoxyribonuclease III | -3.11 | down |
| DW66\_2512 | hypothetical protein | -1.92 | down |
| DW66\_2513 | mechanosensitive ion channel protein MscS | -2.96 | down |
| DW66\_2514 | hypothetical protein | -1.57 | down |
| DW66\_2515 | Amino acid transporters | -3.68 | down |
| DW66\_2516 | hemerythrin HHE cation binding domain-containing protein | -2.83 | down |
| DW66\_2517 | membrane protein | -4.10 | down |
| DW66\_2518 | hypothetical protein | -3.73 | down |
| DW66\_2519 | CinA domain-containing protein | -3.74 | down |
| DW66\_2520 | hypothetical protein | -2.52 | down |
| DW66\_2521 | alcohol dehydrogenase | -3.50 | down |
| DW66\_2522 | integral membrane protein | -3.81 | down |
| DW66\_2523 | hypothetical protein | -1.05 | down |
| DW66\_2524 | transcriptional regulator AraC | -1.39 | down |
| DW66\_2527 | transcriptional regulator AraC | -3.15 | down |
| DW66\_2528 | *gamma*-aminobutyrate permease | -1.44 | down |
| DW66\_2529 | creatininase | -1.04 | down |
| DW66\_2530 | Transcriptional regulator | -3.04 | down |
| DW66\_2531 | creatinase | -1.80 | down |
| DW66\_2534 | transcriptional regulator LysR | -1.81 | down |
| DW66\_2535 | alcohol dehydrogenase | -2.73 | down |
| DW66\_2536 | transporter protein | -3.05 | down |
| DW66\_2537 | glyceraldehyde-3-phosphate dehydrogenase | -2.13 | down |
| DW66\_2539 | arsenical-resistance protein | -2.64 | down |
| DW66\_2540 | transcriptional regulator ArsR | -2.78 | down |
| DW66\_2541 | transcriptional regulator LysR | -1.54 | down |
| DW66\_2542 | tricarballylate dehydrogenase | -3.29 | down |
| DW66\_2543 | tricarballylate utilization protein B | -3.58 | down |
| DW66\_2544 | transcriptional regulator LysR | -2.55 | down |
| DW66\_2545 | hypothetical protein | -2.30 | down |
| DW66\_2546 | sodium:dicarboxylate symporter | -1.91 | down |
| DW66\_2547 | citrate transporter | -2.80 | down |
| DW66\_2548 | outer membrane porin | -1.75 | down |
| DW66\_2549 | permeases of the drug/metabolite transporter | -2.06 | down |
| DW66\_2550 | diguanylate cyclase | -2.33 | down |
| DW66\_2551 | NAD-dependent epimerase/dehydratase / Alpha/beta hydrolase | -4.53 | down |
| DW66\_2552 | transcriptional regulator MerR | -1.02 | down |
| DW66\_2553 | RNA polymerase | -2.44 | down |
| DW66\_2554 | transmembrane sensor | -3.29 | down |
| DW66\_2555 | Outer membrane receptor proteins, likely involved in siderophore uptake | -2.67 | down |
| DW66\_2556 | 2-isopropylmalate synthase | -2.65 | down |
| DW66\_2557 | short chain dehydrogenase/reductase oxidoreductase | -4.01 | down |
| DW66\_2558 | transcriptional activator FtrA | -1.73 | down |
| DW66\_2559 | rhodanese | -2.51 | down |
| DW66\_2560 | Chorismate mutase | -2.77 | down |
| DW66\_2561 | hypothetical protein | -11.92 | down |
| DW66\_2562 | hypothetical protein | -4.69 | down |
| DW66\_2563 | transcriptional regulator Cro/CI | -3.34 | down |
| DW66\_2564 | acetyltransferase | -3.46 | down |
| DW66\_2565 | transcriptional regulator LysR | -1.05 | down |
| DW66\_2566 | 2-dehydropantoate 2-reductase | -4.48 | down |
| DW66\_2567 | glyoxalase | -3.30 | down |
| DW66\_2568 | dehydratase | -3.62 | down |
| DW66\_2569 | L-carnitine dehydratase/bile acid-inducible protein F | -3.52 | down |
| DW66\_2570 | shikimate 5-dehydrogenase | -2.47 | down |
| DW66\_2573 | hypothetical protein | -2.79 | down |
| DW66\_2574 | hypothetical protein | -2.51 | down |
| DW66\_2575 | hypothetical protein | -3.88 | down |
| DW66\_2576 | major facilitator transporter | -2.75 | down |
| DW66\_2577 | sugar phosphate isomerase | -2.41 | down |
| DW66\_2578 | transcriptional regulator MocR | -1.87 | down |
| DW66\_2579 | hypothetical protein | -1.90 | down |
| DW66\_2580 | PAS/PAC sensor-containing diguanylate cyclase/phosphodiesterase | -1.65 | down |
| DW66\_2583 | glycine betaine ABC transporter permease | -2.41 | down |
| DW66\_2584 | glycine betaine ABC transporter ATP-binding protein | -2.62 | down |
| DW66\_2585 | histidine ammonia-lyase | -1.76 | down |
| DW66\_2586 | stress-induced protein | 1.71 | up |
| DW66\_2587 | short chain dehydrogenase | -1.42 | down |
| DW66\_2588 | mechanosensitive ion channel protein MscS | 1.25 | up |
| DW66\_2589 | membrane protein | -1.87 | down |
| DW66\_2592 | acetyltransferase | 1.55 | up |
| DW66\_2593 | hypothetical protein | -3.52 | down |
| DW66\_2597 | phosphoribosyl transferase | -2.14 | down |
| DW66\_2598 | hypothetical protein | -2.03 | down |
| DW66\_2600 | Acetyltransferase | 2.15 | up |
| DW66\_2601 | hypothetical protein | -3.91 | down |
| DW66\_2603 | heat-shock protein | 2.78 | up |
| DW66\_2605 | phosphoketolase | -1.13 | down |
| DW66\_2606 | ion transporter | -1.16 | down |
| DW66\_2608 | transport-associated protein | 2.59 | up |
| DW66\_2610 | ATPase P | -2.30 | down |
| DW66\_2612 | molecular chaperone GroEL | -3.58 | down |
| DW66\_2613 | universal stress protein | -3.61 | down |
| DW66\_2617 | universal stress protein | 1.35 | up |
| DW66\_2619 | sodium:proton antiporter | -2.06 | down |
| DW66\_2623 | hypothetical protein | 2.63 | up |
| DW66\_2624 | Mn2+/Fe2+ transporter | -1.81 | down |
| DW66\_2625 | short-chain dehydrogenase/reductase SDR | -3.09 | down |
| DW66\_2626 | oxidoreductase | -2.34 | down |
| DW66\_2628 | hypothetical protein | -1.43 | down |
| DW66\_2629 | hypothetical protein | -2.59 | down |
| DW66\_2630 | hypothetical protein | -2.81 | down |
| DW66\_2631 | transposase mutator type | -1.40 | down |
| DW66\_2632 | Mobile element protein | -1.62 | down |
| DW66\_2633 | ATP-dependent endonuclease | 1.03 | up |
| DW66\_2634 | transposase ISPs1 | -1.23 | down |
| DW66\_2635 | relaxase | -2.62 | down |
| DW66\_2636 | hypothetical protein | -4.21 | down |
| DW66\_2639 | hypothetical protein | 1.67 | up |
| DW66\_2641 | cobalamin synthesis protein P47K | -1.28 | down |
| DW66\_2642 | bifunctional 3,4-dihydroxy-2-butanone 4-phosphate synthase/GTP cyclohydrolase II protein | -1.65 | down |
| DW66\_2645 | reductase | -1.17 | down |
| DW66\_2657 | transposase IS66 | -2.15 | down |
| DW66\_2658 | Mobile element protein | -1.84 | down |
| DW66\_2662 | transposase IS66 | -2.16 | down |
| DW66\_2663 | Mobile element protein | -1.85 | down |
| DW66\_2667 | taurine:2-oxoglutarate aminotransferase | -2.54 | down |
| DW66\_2668 | demethylmenaquinone methyltransferase | -1.81 | down |
| DW66\_2669 | endoribonuclease | -1.99 | down |
| DW66\_2671 | MFS transporter | -1.65 | down |
| DW66\_2672 | allantoate amidohydrolase | -3.14 | down |
| DW66\_2673 | D-isomer specific 2-hydroxyacid dehydrogenase NAD-binding protein | -2.69 | down |
| DW66\_2674 | hypothetical protein | -4.70 | down |
| DW66\_2675 | aldolase II | -3.10 | down |
| DW66\_2676 | transporter | -3.59 | down |
| DW66\_2677 | transcriptional regulator LysR | -2.00 | down |
| DW66\_2678 | hypothetical protein | -3.01 | down |
| DW66\_2679 | amino acid permease-associated protein | -4.65 | down |
| DW66\_2680 | transcriptional regulator AsnC | -1.05 | down |
| DW66\_2682 | Amidinotransferase | -1.45 | down |
| DW66\_2683 | transporter | -1.43 | down |
| DW66\_2685 | transcriptional regulator LysR | -2.00 | down |
| DW66\_2686 | zinc-containing alcohol dehydrogenase | -1.14 | down |
| DW66\_2687 | hypothetical protein | -2.14 | down |
| DW66\_2688 | transcriptional regulator | -2.76 | down |
| DW66\_2689 | transporter protein | -3.58 | down |
| DW66\_2690 | mandelate racemase/muconate lactonizing protein | -2.94 | down |
| DW66\_2691 | transcriptional regulator LysR | -2.70 | down |
| DW66\_2694 | hypothetical protein | -1.19 | down |
| DW66\_2700 | hypothetical protein | 1.27 | up |
| DW66\_2701 | hypothetical protein | -2.22 | down |
| DW66\_2702 | hypothetical protein | -2.54 | down |
| DW66\_2705 | hypothetical protein | -1.30 | down |
| DW66\_2706 | hypothetical protein | -1.90 | down |
| DW66\_2709 | hypothetical protein | -2.36 | down |
| DW66\_2711 | Prophage PssSM-02 protein | -1.86 | down |
| DW66\_2713 | hypothetical protein | -3.91 | down |
| DW66\_2715 | hypothetical protein | -1.46 | down |
| DW66\_2716 | GAF sensor-containing diguanylate cyclase | -1.86 | down |
| DW66\_2718 | repressor | -1.59 | down |
| DW66\_2719 | hypothetical protein | -1.95 | down |
| DW66\_2720 | hypothetical protein | -2.33 | down |
| DW66\_2722 | DNA helicase | -2.21 | down |
| DW66\_2723 | hypothetical protein | -1.61 | down |
| DW66\_2726 | hypothetical protein | -11.25 | down |
| DW66\_2728 | Phage NinG rap recombination | -1.08 | down |
| DW66\_2732 | hypothetical protein | -3.99 | down |
| DW66\_2733 | membrane protein | -2.40 | down |
| DW66\_2734 | hypothetical protein | -1.66 | down |
| DW66\_2735 | Phage terminase, small subunit | -1.29 | down |
| DW66\_2736 | terminase | -5.13 | down |
| DW66\_2737 | hypothetical protein | -4.83 | down |
| DW66\_2738 | SPP1phage head morphogenesis protein | -3.57 | down |
| DW66\_2741 | phage-related hypothetical protein | -2.19 | down |
| DW66\_2742 | hypothetical protein | -4.72 | down |
| DW66\_2743 | hypothetical protein | -13.13 | down |
| DW66\_2744 | hypothetical protein | -9.98 | down |
| DW66\_2746 | hypothetical protein | -1.98 | down |
| DW66\_2747 | hypothetical protein | -2.19 | down |
| DW66\_2749 | tail length tape measure protein | -1.67 | down |
| DW66\_2750 | hypothetical protein | -1.45 | down |
| DW66\_2752 | hypothetical protein | -2.91 | down |
| DW66\_2755 | hypothetical protein | -4.55 | down |
| DW66\_2757 | hypothetical protein | -2.31 | down |
| DW66\_2758 | hypothetical protein | -2.06 | down |
| DW66\_2760 | transcriptional regulator LysR | -3.33 | down |
| DW66\_2761 | galactarate dehydratase | -2.64 | down |
| DW66\_2762 | malate/L-lactate dehydrogenase | -1.85 | down |
| DW66\_2763 | fumarylacetoacetate (FAA) hydrolase | -2.12 | down |
| DW66\_2764 | transporter protein | -1.64 | down |
| DW66\_2765 | VRR-NUC domain-containing protein | -2.13 | down |
| DW66\_2766 | DEAD/DEAH box helicase | -2.06 | down |
| DW66\_2767 | NnrS protein | -1.77 | down |
| DW66\_2768 | integrase | -6.31 | down |
| DW66\_2769 | hypothetical protein | -2.53 | down |
| DW66\_2770 | urease accessory protein UreD | -5.95 | down |
| DW66\_2771 | urease subunit gamma | -5.31 | down |
| DW66\_2772 | urease subunit beta | -3.47 | down |
| DW66\_2773 | urease subunit alpha | -2.68 | down |
| DW66\_2774 | urease accessory protein UreE | -2.32 | down |
| DW66\_2775 | HupE/UreJ protein | -1.29 | down |
| DW66\_2776 | urease accessory protein UreF | -1.27 | down |
| DW66\_2777 | urease accessory protein UreG | -2.87 | down |
| DW66\_2778 | hypothetical protein | 1.67 | up |
| DW66\_2779 | sulfatase | 2.01 | up |
| DW66\_2780 | Fap amyloid fiber secretin | 2.88 | up |
| DW66\_2781 | Fap system outer membrane protein | -1.30 | down |
| DW66\_2782 | peptidase C39, bacteriocin processing | -4.25 | down |
| DW66\_2783 | hypothetical protein | 2.58 | up |
| DW66\_2784 | Fap amyloid fibril minor component | -1.73 | down |
| DW66\_2785 | Fap unknown function protein | -2.68 | down |
| DW66\_2786 | Ribosylnicotinamide kinase | -3.74 | down |
| DW66\_2787 | nicotinamide mononucleotide transporter PnuC | -4.05 | down |
| DW66\_2789 | undecaprenyl pyrophosphate phosphatase | -2.15 | down |
| DW66\_2790 | Cold-shock DNA-binding domain | -1.16 | down |
| DW66\_2791 | hypothetical protein | -1.46 | down |
| DW66\_2792 | transcriptional regulator LysR | -1.46 | down |
| DW66\_2793 | azoreductase | -2.34 | down |
| DW66\_2794 | FAD-dependent pyridine nucleotide-disulfide oxidoreductase | 2.55 | up |
| DW66\_2795 | transcriptional regulator XRE | -2.10 | down |
| DW66\_2796 | NADH:flavin oxidoreductase | -1.58 | down |
| DW66\_2798 | aldolase II | 1.31 | up |
| DW66\_2801 | hypothetical protein | 8.48 | up |
| DW66\_2802 | hypothetical protein | 2.84 | up |
| DW66\_2803 | hypothetical protein | 5.88 | up |
| DW66\_2804 | beta-lactamase | -2.62 | down |
| DW66\_2806 | hypothetical protein | -2.30 | down |
| DW66\_2807 | transcriptional regulator TetR | -1.38 | down |
| DW66\_2808 | short-chain dehydrogenase | -1.23 | down |
| DW66\_2810 | transcriptional regulator XRE | -1.65 | down |
| DW66\_2811 | transporter protein | -2.43 | down |
| DW66\_2812 | cytochrome B561 | -1.86 | down |
| DW66\_2813 | catalase domain-containing protein | -2.45 | down |
| DW66\_2815 | transmembrane anti-sigma factor | -1.79 | down |
| DW66\_2819 | hypothetical protein | -1.91 | down |
| DW66\_2822 | hypothetical protein | -3.28 | down |
| DW66\_2823 | lipoprotein | -1.56 | down |
| DW66\_2825 | hypothetical protein | 3.30 | up |
| DW66\_2826 | hypothetical protein | 4.29 | up |
| DW66\_2827 | hypothetical protein | -2.04 | down |
| DW66\_2828 | hypothetical protein | -2.62 | down |
| DW66\_2829 | transcriptional regulator LysR | -1.89 | down |
| DW66\_2830 | transmembrane pair domain-containing protein | 7.01 | up |
| DW66\_2832 | ABC transporter-like protein | -2.67 | down |
| DW66\_2833 | hypothetical protein | -2.45 | down |
| DW66\_2834 | cobalamin biosynthesis protein CobW | -3.52 | down |
| DW66\_2835 | cobaltochelatase subunit CobN | -1.60 | down |
| DW66\_2837 | ChlD component of cobalt chelatase involved in B12 biosynthesis | -1.00 | down |
| DW66\_2838 | hypothetical protein | 1.26 | up |
| DW66\_2841 | lipoprotein signal peptide | -4.04 | down |
| DW66\_2843 | ABC transporte, ATP binding protein | -1.85 | down |
| DW66\_2845 | response regulator receiver domain-containing protein | 2.28 | up |
| DW66\_2850 | hypothetical protein | -2.16 | down |
| DW66\_2851 | secretion protein HlyD | -4.10 | down |
| DW66\_2853 | dioxygenase | -2.53 | down |
| DW66\_2854 | sodium:dicarboxylate symporter | -1.53 | down |
| DW66\_2855 | CigR (inner membrane protein) | 2.87 | up |
| DW66\_2856 | hypothetical protein | -1.34 | down |
| DW66\_2857 | hypothetical protein | -1.96 | down |
| DW66\_2859 | hypothetical protein | 4.23 | up |
| DW66\_2860 | alcohol dehydrogenase | -2.46 | down |
| DW66\_2861 | taurine dioxygenase | -3.33 | down |
| DW66\_2862 | Transposase | -2.73 | down |
| DW66\_2863 | transporter protein | -3.95 | down |
| DW66\_2864 | DSBA oxidoreductase | -4.51 | down |
| DW66\_2865 | (2Fe-2S)-binding protein | -3.13 | down |
| DW66\_2866 | membrane protein | -3.06 | down |
| DW66\_2868 | hypothetical protein | -1.90 | down |
| DW66\_2869 | hypothetical protein | -4.26 | down |
| DW66\_2870 | hypothetical protein | -2.95 | down |
| DW66\_2871 | glycosyl hydrolase | -1.69 | down |
| DW66\_2872 | transporter | -2.97 | down |
| DW66\_2873 | acyl-CoA dehydrogenase domain-containing protein | -1.36 | down |
| DW66\_2874 | acyl-CoA synthetase | -1.70 | down |
| DW66\_2876 | hypothetical protein | -4.93 | down |
| DW66\_2877 | nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase | -4.29 | down |
| DW66\_2880 | lysine exporter protein LysE/YggA | -4.55 | down |
| DW66\_2881 | transcriptional regulator AraC | -1.93 | down |
| DW66\_2882 | lysine exporter protein LysE/YggA | -1.02 | down |
| DW66\_2883 | outer membrane autotransporter | -2.30 | down |
| DW66\_2884 | PpiC-type peptidyl-prolyl cis-trans isomerase | -1.39 | down |
| DW66\_2885 | acetoacetyl-CoA synthetase | 1.82 | up |
| DW66\_2886 | ecotin | 1.39 | up |
| DW66\_2887 | *beta*-D-hydroxybutyrate dehydrogenase | 1.67 | up |
| DW66\_2888 | citrate transporter | -2.57 | down |
| DW66\_2890 | binding-protein-dependent transport system inner membrane protein | 1.29 | up |
| DW66\_2894 | phospho-2-dehydro-3-deoxyheptonate aldolase | -1.34 | down |
| DW66\_2895 | hypothetical protein | -4.39 | down |
| DW66\_2896 | hypothetical protein | 1.52 | up |
| DW66\_2899 | deoxyribonuclease I | -4.32 | down |
| DW66\_2900 | transporter protein | -2.83 | down |
| DW66\_2901 | transcriptional regulator LysR | -1.21 | down |
| DW66\_2903 | amino acid permease | -1.89 | down |
| DW66\_2904 | nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase | -3.22 | down |
| DW66\_2905 | transcriptional regulator | -2.21 | down |
| DW66\_2906 | Thymidylate kinase | -2.35 | down |
| DW66\_2907 | hypothetical protein | 6.38 | up |
| DW66\_2912 | transcriptional regulator LysR | -2.63 | down |
| DW66\_2913 | patatin | 1.63 | up |
| DW66\_2914 | thiamine pyrophosphate protein | -2.67 | down |
| DW66\_2915 | double-stranded beta helix domain-containing protein | -2.95 | down |
| DW66\_2916 | hypothetical protein | -3.26 | down |
| DW66\_2917 | hypothetical protein | -4.09 | down |
| DW66\_2919 | hypothetical protein | -7.42 | down |
| DW66\_2920 | hypothetical protein | 1.38 | up |
| DW66\_2921 | hypothetical protein | -2.38 | down |
| DW66\_2923 | hypothetical protein | -1.59 | down |
| DW66\_2925 | transcriptional regulator LysR | -2.45 | down |
| DW66\_2929 | transcriptional regulator | 1.99 | up |
| DW66\_2930 | DNA mismatch repair protein MutT | -1.64 | down |
| DW66\_2932 | Cytochrome c | -3.00 | down |
| DW66\_2933 | hypothetical protein | 1.23 | up |
| DW66\_2935 | transcriptional regulator AsnC | 1.80 | up |
| DW66\_2941 | hypothetical protein | -1.25 | down |
| DW66\_2943 | transcriptional regulator PaaX | -2.26 | down |
| DW66\_2944 | phenylacetic acid degradation protein PaaY | -1.62 | down |
| DW66\_2945 | enoyl-CoA hydratase-isomerase | -1.50 | down |
| DW66\_2947 | 3-hydroxyacyl-CoA dehydrogenase | -1.07 | down |
| DW66\_2950 | phenylacetate-CoA ligase | -2.27 | down |
| DW66\_2951 | phenylacetate-CoA oxygenase subunit PaaA | 1.16 | up |
| DW66\_2952 | phenylacetate-CoA oxygenase subunit PaaB | 4.60 | up |
| DW66\_2953 | phenylacetate-CoA oxygenase subunit PaaI | 1.49 | up |
| DW66\_2954 | phenylacetate-CoA oxygenase subunit PaaJ | 1.40 | up |
| DW66\_2955 | phenylacetate-CoA oxygenase/reductase subunit PaaK | 1.19 | up |
| DW66\_2959 | bifunctional aldehyde dehydrogenase/enoyl-CoA hydratase | 1.86 | up |
| DW66\_2961 | hypothetical protein | -1.38 | down |
| DW66\_2962 | Conidiation-specific protein | -2.62 | down |
| DW66\_2965 | Clp protease | -1.07 | down |
| DW66\_2966 | hypothetical protein | -2.74 | down |
| DW66\_2967 | hypothetical protein | -2.73 | down |
| DW66\_2968 | endonuclease/exonuclease/phosphatase | -5.50 | down |
| DW66\_2969 | cardiolipin synthase 2 | -1.98 | down |
| DW66\_2970 | Inner membrane protein YbhQ | -2.17 | down |
| DW66\_2973 | Phosphotransferase system, HPr-related protein | -1.93 | down |
| DW66\_2974 | ATP-dependent DNA ligase | -2.07 | down |
| DW66\_2975 | acyl-CoA dehydrogenase | -3.28 | down |
| DW66\_2976 | LmbE protein | -3.18 | down |
| DW66\_2977 | type 12 methyltransferase | -3.45 | down |
| DW66\_2978 | glycosyl transferase group 2 protein | -3.93 | down |
| DW66\_2979 | hypothetical protein | -2.79 | down |
| DW66\_2980 | oxidoreductase | -4.66 | down |
| DW66\_2981 | nucleoside phosphorylase-like protein | -4.22 | down |
| DW66\_2982 | carboxylate-amine ligase | -4.31 | down |
| DW66\_2983 | methyltransferase small | -3.15 | down |
| DW66\_2984 | hypothetical protein | -2.51 | down |
| DW66\_2985 | hypothetical protein | -2.82 | down |
| DW66\_2987 | transporter protein | -2.73 | down |
| DW66\_2988 | aldo/keto reductase | -1.15 | down |
| DW66\_2989 | peroxidase | -3.29 | down |
| DW66\_2991 | *beta*-carotene hydroxylase | -4.11 | down |
| DW66\_2992 | magnesium transporter MgtC | -6.04 | down |
| DW66\_2993 | N-acetyltransferase GCN5 | -4.67 | down |
| DW66\_2994 | diguanylate cyclase | 1.57 | up |
| DW66\_2995 | outer membrane protein | -1.47 | down |
| DW66\_2996 | Fructose-2,6-bisphosphatase | -2.15 | down |
| DW66\_2998 | N-isopropylammelide isopropylaminohydrolase | 1.69 | up |
| DW66\_3000 | transcription regulator TenA | -2.56 | down |
| DW66\_3001 | multicopper oxidase type 2 | -1.92 | down |
| DW66\_3002 | electron transport protein SCO1/SenC | -3.22 | down |
| DW66\_3003 | diguanylate cyclase/phosphodiesterase | -3.71 | down |
| DW66\_3004 | integrase | -2.90 | down |
| DW66\_3006 | glycerate kinase | -3.54 | down |
| DW66\_3007 | transcriptional regulator | -2.94 | down |
| DW66\_3008 | hypothetical protein | -4.55 | down |
| DW66\_3009 | transporter protein | -1.38 | down |
| DW66\_3010 | FAD-dependent pyridine nucleotide-disulfide oxidoreductase | -2.99 | down |
| DW66\_3012 | N-ethylmaleimide reductase | -2.03 | down |
| DW66\_3013 | luciferase | -2.83 | down |
| DW66\_3014 | transcriptional regulator LysR | -1.67 | down |
| DW66\_3015 | TraX protein | -2.50 | down |
| DW66\_3016 | membrane-bound metal-dependent hydrolase | -1.14 | down |
| DW66\_3017 | outer membrane porin | -3.79 | down |
| DW66\_3018 | membrane protein | -5.52 | down |
| DW66\_3019 | catechol 1,2-dioxygenase | -3.94 | down |
| DW66\_3020 | transporter protein | -4.40 | down |
| DW66\_3021 | 1,6-dihydroxycyclohexa-2,4-diene-1-carboxylate dehydrogenase | -4.43 | down |
| DW66\_3022 | hypothetical protein | -4.12 | down |
| DW66\_3024 | benzoate 1,2-dioxygenase small subunit | -4.27 | down |
| DW66\_3025 | benzoate dioxygenase subunit alpha | -2.82 | down |
| DW66\_3027 | lipoprotein | -3.81 | down |
| DW66\_3028 | histidinol-phosphate phosphatase | -3.41 | down |
| DW66\_3029 | UspA domain-containing protein | 3.40 | up |
| DW66\_3030 | TonB-dependent siderophore receptor | -1.82 | down |
| DW66\_3032 | hypothetical protein | 1.15 | up |
| DW66\_3033 | transcriptional regulator LysR | 1.16 | up |
| DW66\_3034 | aldehyde dehydrogenase | 3.91 | up |
| DW66\_3035 | helicase | -2.31 | down |
| DW66\_3036 | transcriptional regulator AraC | -2.29 | down |
| DW66\_3037 | glutamate-putrescine ligase | -1.79 | down |
| DW66\_3038 | extracellular solute-binding protein | -1.82 | down |
| DW66\_3039 | FAD dependent oxidoreductase | -2.71 | down |
| DW66\_3040 | outer membrane lipoprotein | 5.53 | up |
| DW66\_3041 | L-serine dehydratase | -3.73 | down |
| DW66\_3042 | transcriptional regulator LysR | -2.39 | down |
| DW66\_3043 | exopolysaccharide biosynthesis polyprenyl glycosylphosphotransferase | 1.70 | up |
| DW66\_3047 | VirK | 2.12 | up |
| DW66\_3048 | glycosyl transferase | 2.25 | up |
| DW66\_3049 | serine O-acetyltransferase | 2.79 | up |
| DW66\_3050 | glycosyl transferase | 3.09 | up |
| DW66\_3051 | hexapeptide repeat-containing transferase | 3.30 | up |
| DW66\_3052 | GMC oxidoreductase | 1.56 | up |
| DW66\_3053 | hypothetical protein | 1.36 | up |
| DW66\_3056 | hypothetical protein | 2.50 | up |
| DW66\_3058 | non-specific protein-tyrosine kinase | 4.14 | up |
| DW66\_3059 | lipopolysaccharide biosynthesis protein | 1.99 | up |
| DW66\_3061 | polysaccharide export protein | 1.32 | up |
| DW66\_3063 | short-chain fatty acid transporter | -1.33 | down |
| DW66\_3066 | transcriptional regulator LysR | -2.35 | down |
| DW66\_3067 | aldo/keto reductase | -2.87 | down |
| DW66\_3068 | error-prone DNA polymerase | -1.94 | down |
| DW66\_3069 | DNA polymerase-like protein | -2.70 | down |
| DW66\_3070 | RecA/RadA recombinase | -2.86 | down |
| DW66\_3071 | LexA repressor | -2.52 | down |
| DW66\_3072 | threonine efflux protein | -3.33 | down |
| DW66\_3077 | amidase | -4.10 | down |
| DW66\_3078 | transporter protein | -3.86 | down |
| DW66\_3079 | amidohydrolase | -3.27 | down |
| DW66\_3081 | YD repeat-containing protein | -1.78 | down |
| DW66\_3082 | hypothetical protein | -5.45 | down |
| DW66\_3083 | hypothetical protein | -3.18 | down |
| DW66\_3084 | Rhs element Vgr protein | -3.43 | down |
| DW66\_3085 | hypothetical protein | -1.87 | down |
| DW66\_3088 | hypothetical protein | -1.48 | down |
| DW66\_3089 | hypothetical protein | -1.21 | down |
| DW66\_3090 | hypothetical protein | -1.97 | down |
| DW66\_3091 | ADP-ribosyl-(dinitrogen reductase) hydrolase | -1.03 | down |
| DW66\_3092 | hypothetical protein | -5.49 | down |
| DW66\_3093 | type VI secretion protein | -5.07 | down |
| DW66\_3094 | type VI secretion protein EvpB | -5.15 | down |
| DW66\_3095 | type VI secretion system lysozyme-like protein | -6.38 | down |
| DW66\_3096 | type VI secretion protein | -5.50 | down |
| DW66\_3097 | hypothetical protein | -3.44 | down |
| DW66\_3098 | type VI secretion ATPase | -3.68 | down |
| DW66\_3099 | lipoprotein | -4.79 | down |
| DW66\_3100 | type VI secretion protein | -4.11 | down |
| DW66\_3101 | hypothetical protein | -3.09 | down |
| DW66\_3102 | ImcF domain-containing protein | -3.72 | down |
| DW66\_3103 | hypothetical protein | -3.05 | down |
| DW66\_3104 | OmpA/MotB domain-containing protein | -3.50 | down |
| DW66\_3105 | type VI secretion system effector | 1.82 | up |
| DW66\_3106 | type VI secretion-associated protein ImpA | -2.65 | down |
| DW66\_3108 | hypothetical protein | -3.09 | down |
| DW66\_3109 | auxin efflux carrier | -2.95 | down |
| DW66\_3110 | hypothetical protein | -7.92 | down |
| DW66\_3111 | MFS transporter | -4.11 | down |
| DW66\_3112 | gluconate 2-dehydrogenase | 4.54 | up |
| DW66\_3113 | transporter protein | 3.36 | up |
| DW66\_3114 | ribokinase-like domain-containing protein | 2.64 | up |
| DW66\_3115 | xylose isomerase domain-containing protein TIM barrel | 2.09 | up |
| DW66\_3116 | transcriptional regulator LacI | -1.06 | down |
| DW66\_3118 | gluconate 2-dehydrogenase | -1.04 | down |
| DW66\_3119 | Gluconate 2-dehydrogenase acceptor subunit | -2.79 | down |
| DW66\_3120 | hypothetical protein | -10.99 | down |
| DW66\_3121 | Outer membrane protein ImpK/VasF, OmpA/MotB domain | -2.18 | down |
| DW66\_3123 | hypothetical protein | -2.58 | down |
| DW66\_3125 | hypothetical protein | -4.77 | down |
| DW66\_3126 | Glycoprotein gp2 | -2.60 | down |
| DW66\_3127 | Glycoprotein gp2 | -1.89 | down |
| DW66\_3128 | curlin-associated protein | -2.56 | down |
| DW66\_3129 | curlin-associated protein | 1.09 | up |
| DW66\_3130 | 2OG-Fe(II) oxygenase | -2.77 | down |
| DW66\_3131 | hypothetical protein | -2.82 | down |
| DW66\_3132 | membrane protein | -3.14 | down |
| DW66\_3133 | hypothetical protein | 2.01 | up |
| DW66\_3134 | alcohol dehydrogenase | -2.11 | down |
| DW66\_3137 | hypothetical protein | -1.92 | down |
| DW66\_3138 | alpha/beta hydrolase fold protein | -2.80 | down |
| DW66\_3139 | lysine exporter protein LysE/YggA | -1.96 | down |
| DW66\_3141 | hypothetical protein | -6.83 | down |
| DW66\_3142 | cobalt transporter, CbtB subunit | -2.14 | down |
| DW66\_3143 | cobalt transporter, CbtA subunit | -2.63 | down |
| DW66\_3144 | cobalamin biosynthesis protein cobE | -3.28 | down |
| DW66\_3145 | precorrin-4 C(11)-methyltransferase | -2.64 | down |
| DW66\_3146 | hypothetical protein | -1.18 | down |
| DW66\_3147 | transcriptional regulator | 1.28 | up |
| DW66\_3149 | pili assembly chaperone | 1.24 | up |
| DW66\_3150 | transcriptional regulator LacI | -3.06 | down |
| DW66\_3152 | gluconate transporter | 1.75 | up |
| DW66\_3157 | integral membrane sensor signal transduction histidine kinase | 1.10 | up |
| DW66\_3158 | lytic transglycosylase | -2.62 | down |
| DW66\_3159 | general secretion pathway protein G | -3.20 | down |
| DW66\_3160 | type II secretion system protein | -3.39 | down |
| DW66\_3161 | RND efflux transporter, MFP subunit | -4.67 | down |
| DW66\_3162 | hydrophobe/amphiphile efflux-1 | -2.78 | down |
| DW66\_3163 | RND efflux system outer membrane lipoprotein | -1.15 | down |
| DW66\_3164 | TPR domain protein | -1.09 | down |
| DW66\_3165 | histidine kinase | -2.58 | down |
| DW66\_3167 | ThiJ/PfpI domain-containing protein | 2.34 | up |
| DW66\_3168 | Rtn protein | -1.07 | down |
| DW66\_3170 | hypothetical protein | 1.06 | up |
| DW66\_3172 | transporter | -1.87 | down |
| DW66\_3173 | membrane protein | -1.30 | down |
| DW66\_3174 | lysine exporter protein LysE/YggA | -2.57 | down |
| DW66\_3175 | transcriptional regulator AraC | -1.00 | down |
| DW66\_3178 | Leucine-rich repeat domain protein | -2.09 | down |
| DW66\_3179 | aldehyde dehydrogenase | -1.18 | down |
| DW66\_3180 | glyoxalase/bleomycin resistance protein/dioxygenase | 1.36 | up |
| DW66\_3182 | threonine dehydratase | -2.79 | down |
| DW66\_3183 | transmembrane pair domain-containing protein | -1.45 | down |
| DW66\_3184 | hypothetical protein | -4.07 | down |
| DW66\_3185 | bacteriophage N4 adsorption protein B | 2.89 | up |
| DW66\_3186 | bacteriophage N4 receptor, outer membrane subunit | 4.06 | up |
| DW66\_3187 | hypothetical protein | 4.32 | up |
| DW66\_3188 | diguanylate cyclase | 3.80 | up |
| DW66\_3189 | diguanylate cyclase | -1.04 | down |
| DW66\_3190 | integral membrane sensor signal transduction histidine kinase | -1.98 | down |
| DW66\_3191 | two component transcriptional regulator | -2.05 | down |
| DW66\_3194 | hydrophobe/amphiphile efflux-1 | -1.62 | down |
| DW66\_3195 | molybdopterin-guanine dinucleotide biosynthesis protein MobA | -2.43 | down |
| DW66\_3197 | Quinohemoprotein amine dehydrogenase beta subunit | 2.81 | up |
| DW66\_3200 | quinohemoprotein amine dehydrogenase, 60 kDa subunit | -1.82 | down |
| DW66\_3201 | hypothetical protein | -5.34 | down |
| DW66\_3203 | aldehyde dehydrogenase | -1.17 | down |
| DW66\_3204 | hypothetical protein | -3.79 | down |
| DW66\_3205 | monooxygenase FAD-binding protein | -1.21 | down |
| DW66\_3207 | efflux ABC transporter ATP-binding protein | -1.28 | down |
| DW66\_3208 | GAF modulated sigma54 specific transcriptional regulator | -1.46 | down |
| DW66\_3209 | hypothetical protein | -4.02 | down |
| DW66\_3210 | curli production assembly/transport component CsgG | -3.48 | down |
| DW66\_3211 | curli production assembly/transport component CsgF | -2.87 | down |
| DW66\_3212 | curli assembly protein CsgE | -4.09 | down |
| DW66\_3213 | secretion system X pseudopilin PulG-like protein | -4.11 | down |
| DW66\_3214 | type II secretion system protein G | -3.54 | down |
| DW66\_3215 | type II and III secretion system protein | -4.03 | down |
| DW66\_3216 | type II and III secretion system protein | -3.46 | down |
| DW66\_3217 | secretion system X translation initiation factor | -4.09 | down |
| DW66\_3218 | secretion system X transmembrane protein | -4.13 | down |
| DW66\_3219 | secretion system X transmembrane protein | -5.43 | down |
| DW66\_3220 | hypothetical protein | -3.26 | down |
| DW66\_3221 | type II secretion system protein E | -5.53 | down |
| DW66\_3222 | response regulator receiver protein | -2.56 | down |
| DW66\_3224 | cytochrome c | -2.37 | down |
| DW66\_3225 | electron transport protein SCO1/SenC | -1.76 | down |
| DW66\_3227 | Collagen triple helix repeat domain protein | -1.63 | down |
| DW66\_3228 | hypothetical protein | -2.54 | down |
| DW66\_3230 | malonate transporter subunit MadM | -2.09 | down |
| DW66\_3231 | malonate transporter subunit MadL | -1.46 | down |
| DW66\_3232 | malonate decarboxylase subunit epsilon | -1.57 | down |
| DW66\_3239 | hypothetical protein | -3.48 | down |
| DW66\_3240 | hypothetical protein | -12.35 | down |
| DW66\_3243 | transcriptional regulator LysR | -2.79 | down |
| DW66\_3245 | tRNA-m1A22 methylase | -3.83 | down |
| DW66\_3247 | hypothetical protein | -1.86 | down |
| DW66\_3252 | carboxynorspermidine decarboxylase | -3.28 | down |
| DW66\_3253 | saccharopine dehydrogenase | -1.46 | down |
| DW66\_3254 | ThiJ/PfpI domain-containing protein | -1.72 | down |
| DW66\_3256 | UDP-glucose 6-dehydrogenase | -3.61 | down |
| DW66\_3257 | malate:quinone oxidoreductase | 4.46 | up |
| DW66\_3258 | radical SAM domain-containing protein | -1.61 | down |
| DW66\_3259 | Domain often clustered or fused with uracil-DNA glycosylase | -1.45 | down |
| DW66\_3260 | trehalose synthase | -1.81 | down |
| DW66\_3261 | hypothetical protein | -3.55 | down |
| DW66\_3262 | riboflavin synthase subunit alpha | -2.63 | down |
| DW66\_3263 | hypothetical protein | -2.36 | down |
| DW66\_3264 | proline/glycine betaine transporter | -2.14 | down |
| DW66\_3265 | *delta*-aminolevulinic acid dehydratase | -2.40 | down |
| DW66\_3267 | GABA permease | -1.98 | down |
| DW66\_3269 | Carbon starvation induced protein CsiD | 2.47 | up |
| DW66\_3270 | DNA-binding transcriptional regulator CsiR | -1.20 | down |
| DW66\_3271 | two component transcriptional regulator | -4.29 | down |
| DW66\_3272 | integral membrane sensor signal transduction histidine kinase | -3.23 | down |
| DW66\_3277 | UDP-2,3-diacylglucosamine hydrolase | -1.16 | down |
| DW66\_3280 | Fe2+/Zn2+ uptake regulation proteins | 1.93 | up |
| DW66\_3282 | hypothetical protein | -2.81 | down |
| DW66\_3283 | hypothetical protein | -2.33 | down |
| DW66\_3284 | hypothetical protein | -2.17 | down |
| DW66\_3285 | hypothetical protein | -3.44 | down |
| DW66\_3286 | hypothetical protein | -2.10 | down |
| DW66\_3287 | surface antigen (D15) | -2.26 | down |
| DW66\_3288 | acetyltransferase | 2.14 | up |
| DW66\_3291 | aliphatic sulfonates ABC transporter substrate-binding protein | -5.22 | down |
| DW66\_3292 | monooxygenase | -3.74 | down |
| DW66\_3294 | lipid-binding START domain-containing protein | -1.98 | down |
| DW66\_3295 | transcriptional regulator LysR | -2.74 | down |
| DW66\_3296 | *gamma*-glutamyltransferase | -1.49 | down |
| DW66\_3298 | 4-hydroxybenzoate 3-monooxygenase | -4.51 | down |
| DW66\_3299 | transcriptional regulator AraC | -1.50 | down |
| DW66\_3302 | MgtC/SapB transporter | -2.78 | down |
| DW66\_3303 | hypothetical protein | -1.93 | down |
| DW66\_3304 | cytochrome c oxidase accessory protein CcoG | -1.09 | down |
| DW66\_3309 | ApbE-like lipoprotein | -1.34 | down |
| DW66\_3310 | electron transport complex protein RnfC | -2.47 | down |
| DW66\_3311 | RnfABCDGE type electron transport complex subunit D | -3.04 | down |
| DW66\_3312 | drug resistance transporter EmrB | -1.67 | down |
| DW66\_3313 | secretion protein HlyD | -3.00 | down |
| DW66\_3314 | transcriptional regulator MarR | -4.81 | down |
| DW66\_3315 | DNA-binding response regulator | -1.89 | down |
| DW66\_3316 | PAS/PAC sensor signal transduction histidine kinase | -2.63 | down |
| DW66\_3317 | acyl-CoA synthetase | -3.31 | down |
| DW66\_3318 | acyl-CoA dehydrogenase domain-containing protein | -2.03 | down |
| DW66\_3320 | Na+/H+ antiporter NhaC | -4.93 | down |
| DW66\_3322 | glycine betaine ABC transporter substrate-binding protein | 2.10 | up |
| DW66\_3323 | ABC transporter permease | 1.35 | up |
| DW66\_3324 | transcriptional regulator LysR | -1.47 | down |
| DW66\_3325 | hypothetical protein | -3.05 | down |
| DW66\_3327 | transmembrane protein | -2.83 | down |
| DW66\_3328 | transcriptional regulator AraC | -2.28 | down |
| DW66\_3329 | lysine exporter protein LysE/YggA | -7.18 | down |
| DW66\_3330 | transporter protein | -2.21 | down |
| DW66\_3331 | transcriptional regulator LysR | -2.66 | down |
| DW66\_3335 | carbohydrate-selective porin OprB | -1.47 | down |
| DW66\_3336 | acetylornithine deacetylase | -3.70 | down |
| DW66\_3337 | major pilin protein fimA | -3.31 | down |
| DW66\_3339 | monooxygenase | -1.90 | down |
| DW66\_3341 | TonB-dependent siderophore receptor | -1.84 | down |
| DW66\_3342 | anti-FecI sigma factor FecR | -2.82 | down |
| DW66\_3343 | RNA polymerase sigma-29 factor | -3.55 | down |
| DW66\_3346 | hypothetical protein | 2.68 | up |
| DW66\_3347 | diguanylate cyclase/phosphodiesterase | -3.68 | down |
| DW66\_3349 | acriflavin resistance protein | -1.25 | down |
| DW66\_3350 | acriflavin resistance protein | -2.05 | down |
| DW66\_3351 | RND efflux transporter, MFP subunit | -5.51 | down |
| DW66\_3352 | redoxin domain-containing protein | 2.83 | up |
| DW66\_3353 | aromatic amino acid permease | -1.98 | down |
| DW66\_3357 | transcriptional regulator RpiR | 2.77 | up |
| DW66\_3358 | amino acid ABC transporter periplasmic binding protein | 2.68 | up |
| DW66\_3363 | peptidase C26 | 2.00 | up |
| DW66\_3364 | 5-dehydro-4-deoxyglucarate dehydratase | -3.91 | down |
| DW66\_3365 | D-galactonate transporter | -2.21 | down |
| DW66\_3366 | galactarate dehydratase | -1.58 | down |
| DW66\_3369 | hypothetical protein | -3.36 | down |
| DW66\_3370 | Valyl-tRNA synthetase | -14.74 | down |
| DW66\_3371 | transcriptional regulator LysR | -3.12 | down |
| DW66\_3372 | alcohol dehydrogenase | -4.36 | down |
| DW66\_3374 | Integral membrane protein | -2.32 | down |
| DW66\_3375 | hypothetical protein | 2.45 | up |
| DW66\_3376 | TonB-dependent siderophore receptor | -3.64 | down |
| DW66\_3378 | type 11 methyltransferase | -4.84 | down |
| DW66\_3379 | hypothetical protein | -1.91 | down |
| DW66\_3380 | 2Fe-2S iron-sulfur cluster binding domain-containing protein | 1.60 | up |
| DW66\_3381 | aldehyde oxidase and xanthine dehydrogenase molybdopterin binding protein | 2.28 | up |
| DW66\_3382 | gluconate 2-dehydrogenase | 1.38 | up |
| DW66\_3385 | lysine exporter protein LysE/YggA | -1.36 | down |
| DW66\_3387 | hypothetical protein | 1.07 | up |
| DW66\_3388 | choline/carnitine/betaine transporter | -3.09 | down |
| DW66\_3389 | 3-demethylubiquinone-9 3-methyltransferase | 1.63 | up |
| DW66\_3390 | SH3 type 3 domain-containing protein | -3.72 | down |
| DW66\_3391 | hypothetical protein | 7.22 | up |
| DW66\_3392 | transcriptional regulator LysR | -2.63 | down |
| DW66\_3395 | transcriptional regulator LysR | -3.46 | down |
| DW66\_3396 | N-acetyl-gamma-glutamyl-phosphate reductase | -3.62 | down |
| DW66\_3397 | acetyltransferase | -1.47 | down |
| DW66\_3400 | sulfonate ABC transporter ATP-binding protein | -1.77 | down |
| DW66\_3403 | transcriptional regulator AraC | -1.33 | down |
| DW66\_3405 | FAD-dependent pyridine nucleotide-disulfide oxidoreductase | -2.30 | down |
| DW66\_3406 | cytosine/purines uracil thiamine allantoin permease | -2.47 | down |
| DW66\_3407 | flavin reductase domain-containing protein | -1.03 | down |
| DW66\_3408 | luciferase | 3.44 | up |
| DW66\_3409 | hypothetical protein | 1.87 | up |
| DW66\_3410 | alpha/beta hydrolase fold protein | 1.02 | up |
| DW66\_3412 | flavin reductase domain-containing protein | 2.42 | up |
| DW66\_3414 | transcriptional regulator | -1.52 | down |
| DW66\_3416 | transposase | -1.54 | down |
| DW66\_3417 | transposase | -2.69 | down |
| DW66\_3418 | GAF sensor hybrid histidine kinase | -1.50 | down |
| DW66\_3419 | lysine exporter protein LysE/YggA | -1.19 | down |
| DW66\_3421 | transcriptional regulator AsnC | -1.79 | down |
| DW66\_3422 | cytosine/purines uracil thiamine allantoin permease | -3.06 | down |
| DW66\_3423 | ammonium transporter | -2.36 | down |
| DW66\_3424 | ferredoxin-dependent glutamate synthase | -2.71 | down |
| DW66\_3425 | glutamate synthase subunit alpha | -2.79 | down |
| DW66\_3426 | glutamine amidotransferase | -1.88 | down |
| DW66\_3427 | glutamine synthetase | -3.54 | down |
| DW66\_3431 | nicotinamidase | 3.07 | up |
| DW66\_3432 | nicotinate phosphoribosyltransferase | 1.10 | up |
| DW66\_3433 | universal stress protein | -1.32 | down |
| DW66\_3435 | membrane protein YeiH | -2.89 | down |
| DW66\_3436 | Decarboxylase | 1.51 | up |
| DW66\_3437 | diguanylate cyclase | -1.25 | down |
| DW66\_3438 | hypothetical protein | -1.37 | down |
| DW66\_3441 | catalase/peroxidase HPI | 4.37 | up |
| DW66\_3442 | transcriptional regulator LysR | -2.26 | down |
| DW66\_3443 | hypothetical protein | -1.97 | down |
| DW66\_3444 | membrane protein | -2.59 | down |
| DW66\_3445 | transposase | -1.31 | down |
| DW66\_3446 | aldo/keto reductase | -1.84 | down |
| DW66\_3447 | lipoprotein UxpA | -10.84 | down |
| DW66\_3449 | hypothetical protein | -2.01 | down |
| DW66\_3453 | transcriptional regulator LysR | -1.71 | down |
| DW66\_3454 | D-serine dehydratase | -1.62 | down |
| DW66\_3455 | transcriptional regulator | -2.30 | down |
| DW66\_3456 | *Omega*-amino acid--pyruvate aminotransferase | -1.95 | down |
| DW66\_3457 | extracellular solute-binding protein | -2.37 | down |
| DW66\_3462 | Acetohydroxy acid synthase | -1.14 | down |
| DW66\_3463 | acyl-CoA synthetase | -3.24 | down |
| DW66\_3464 | acyl-CoA dehydrogenase domain-containing protein | -2.18 | down |
| DW66\_3465 | enoyl-CoA hydratase/isomerase | -2.20 | down |
| DW66\_3466 | amino acid permease-associated protein | -2.67 | down |
| DW66\_3467 | multi-sensor hybrid histidine kinase | -3.74 | down |
| DW66\_3468 | extracellular solute-binding protein | -5.93 | down |
| DW66\_3469 | two component transcriptional regulator | -3.27 | down |
| DW66\_3470 | transcriptional regulator TetR | -2.83 | down |
| DW66\_3471 | enoyl-CoA hydratase/isomerase | -2.79 | down |
| DW66\_3475 | hypothetical protein | -1.75 | down |
| DW66\_3478 | IcmF-related protein | -4.53 | down |
| DW66\_3479 | penicillin-binding protein 2 | -1.91 | down |
| DW66\_3480 | hypothetical protein | -10.49 | down |
| DW66\_3484 | glycolate oxidase subunit GlcD | -4.35 | down |
| DW66\_3485 | glycolate oxidase, FAD binding subunit | -3.20 | down |
| DW66\_3486 | glycolate oxidase, iron-sulfur subunit | -3.51 | down |
| DW66\_3487 | hypothetical protein | -2.18 | down |
| DW66\_3488 | malate synthase G | -1.80 | down |
| DW66\_3489 | hypothetical protein | -5.03 | down |
| DW66\_3490 | hypothetical protein | -2.25 | down |
| DW66\_3491 | transcriptional regulator | -1.41 | down |
| DW66\_3492 | transporter protein | -2.95 | down |
| DW66\_3493 | deaminase | -1.84 | down |
| DW66\_3495 | transcriptional regulator AraC | -2.90 | down |
| DW66\_3496 | *beta*-ketothiolase | 1.77 | up |
| DW66\_3497 | 3-hydroxybutyryl-CoA dehydrogenase | 2.18 | up |
| DW66\_3498 | transcriptional regulator TetR | 2.26 | up |
| DW66\_3499 | membrane protein | -1.73 | down |
| DW66\_3502 | MiaB-like tRNA modifying protein YliG | -3.89 | down |
| DW66\_3505 | hypothetical protein | -1.24 | down |
| DW66\_3506 | hypothetical protein | -4.38 | down |
| DW66\_3507 | acetyltransferase | 2.33 | up |
| DW66\_3512 | integral membrane sensor signal transduction histidine kinase | -6.36 | down |
| DW66\_3513 | two component transcriptional regulator | -6.74 | down |
| DW66\_3514 | outer membrane protein H1 | -5.80 | down |
| DW66\_3515 | dienelactone hydrolase | 5.20 | up |
| DW66\_3517 | integral membrane sensor signal transduction histidine kinase | -2.01 | down |
| DW66\_3518 | two component transcriptional regulator | -2.22 | down |
| DW66\_3519 | hypothetical protein | -2.42 | down |
| DW66\_3520 | ribonucleotide-diphosphate reductase subunit alpha | 2.21 | up |
| DW66\_3521 | hypothetical protein | -13.26 | down |
| DW66\_3522 | ribonucleotide-diphosphate reductase subunit beta | 1.97 | up |
| DW66\_3526 | hypothetical protein | 2.02 | up |
| DW66\_3527 | SMC domain-containing protein | 1.39 | up |
| DW66\_3528 | ISPpu14, transposase | -4.23 | down |
| DW66\_3529 | transposase | -6.63 | down |
| DW66\_3530 | transposase IS66 | -1.00 | down |
| DW66\_3532 | hypothetical protein | -1.70 | down |
| DW66\_3533 | hypothetical protein | -11.82 | down |
| DW66\_3534 | N-ethylmaleimide reductase | -1.42 | down |
| DW66\_3535 | hypothetical protein | -1.14 | down |
| DW66\_3536 | oxidoreductase | -1.81 | down |
| DW66\_3537 | MFS transporter | -5.53 | down |
| DW66\_3538 | transcriptional regulator LysR | -2.09 | down |
| DW66\_3539 | NAD binding domain protein | -1.24 | down |
| DW66\_3541 | hypothetical protein | -11.44 | down |
| DW66\_3545 | hypothetical protein | 1.55 | up |
| DW66\_3549 | transcriptional regulator CRP/FNR | -1.65 | down |
| DW66\_3551 | NADH:flavin oxidoreductase | -2.48 | down |
| DW66\_3552 | AttM/AiiB protein | -1.39 | down |
| DW66\_3553 | transport protein | -1.51 | down |
| DW66\_3554 | short-chain dehydrogenase | -3.05 | down |
| DW66\_3557 | Transcriptional regulator | 2.35 | up |
| DW66\_3559 | hypothetical protein | -4.02 | down |
| DW66\_3561 | RND efflux system outer membrane lipoprotein | 4.46 | up |
| DW66\_3562 | secretion protein HlyD | 4.67 | up |
| DW66\_3563 | MFS\_1 protein | 2.71 | up |
| DW66\_3564 | transcriptional regulator IclR | 3.75 | up |
| DW66\_3565 | monooxygenase, FAD-binding | 4.71 | up |
| DW66\_3566 | transcriptional regulator LysR | 3.76 | up |
| DW66\_3567 | RND transporter | -2.94 | down |
| DW66\_3568 | hypothetical protein | -3.01 | down |
| DW66\_3569 | hypothetical protein | -1.43 | down |
| DW66\_3570 | hypothetical protein | -6.94 | down |
| DW66\_3571 | hypothetical protein | -2.82 | down |
| DW66\_3572 | PnpA | 2.82 | up |
| DW66\_3573 | PnpB | 9.25 | up |
| DW66\_3574 | PnpX2 | 1.35 | up |
| DW66\_3575 | PnpX1 | 1.62 | up |
| DW66\_3576 | hydroxyquinol 1,2-dioxygenase | 2.29 | up |
| DW66\_3577 | PnpE | 3.67 | up |
| DW66\_3578 | PnpD | 3.66 | up |
| DW66\_3579 | PnpC2 | 4.94 | up |
| DW66\_3580 | PnpC1 | 4.43 | up |
| DW66\_3582 | hypothetical protein | -9.88 | down |
| DW66\_3583 | Mobile element protein | -1.59 | down |
| DW66\_3586 | hypothetical protein | 1.15 | up |
| DW66\_3590 | hypothetical protein | -10.92 | down |
| DW66\_3592 | hypothetical protein | 1.40 | up |
| DW66\_3593 | Dio1 protein | 1.71 | up |
| DW66\_3594 | maleylacetate reductase | 2.98 | up |
| DW66\_3595 | *gamma*-hydroxymuconic semialdehyde dehydrogenase | 3.51 | up |
| DW66\_3596 | hydroquinone dioxygenase large subunit | 5.45 | up |
| DW66\_3597 | hydroquinone dioxygenase small subunit | 6.03 | up |
| DW66\_3598 | transcriptional regulator LysR | -1.51 | down |
| DW66\_3599 | transcriptional regulator LysR | -1.48 | down |
| DW66\_3600 | double-stranded beta helix domain protein-containing protein | -2.12 | down |
| DW66\_3603 | resolvase protein | -1.05 | down |
| DW66\_3605 | SAM-dependent methyltransferase | -1.25 | down |
| DW66\_3606 | TnpA repressor protein | -1.94 | down |
| DW66\_3607 | hypothetical protein | -1.78 | down |
| DW66\_3608 | hypothetical protein | -1.52 | down |
| DW66\_3609 | major facilitator transporter | -4.38 | down |
| DW66\_3611 | transposase | 2.29 | up |
| DW66\_3612 | hypothetical protein | -5.18 | down |
| DW66\_3613 | pili assembly chaperone | 1.91 | up |
| DW66\_3615 | DNA-directed DNA polymerase | -1.48 | down |
| DW66\_3616 | transposase ISPs1 | -1.13 | down |
| DW66\_3617 | DNA-binding protein | -1.37 | down |
| DW66\_3618 | hypothetical protein | -1.04 | down |
| DW66\_3619 | permease | -1.77 | down |
| DW66\_3620 | permease | -3.14 | down |
| DW66\_3621 | hypothetical protein | -1.67 | down |
| DW66\_3622 | hypothetical protein | -1.73 | down |
| DW66\_3623 | metallophosphoesterase protein | -2.23 | down |
| DW66\_3627 | CTP:Inositol-1-phosphate cytidylyltransferase | -1.88 | down |
| DW66\_3628 | hypothetical protein | -4.07 | down |
| DW66\_3629 | Tn4653A-like resolvase protein | -4.35 | down |
| DW66\_3630 | hypothetical protein | -2.19 | down |
| DW66\_3631 | integrase for In2 | -2.04 | down |
| DW66\_3633 | TnpA protein | -1.72 | down |
| DW66\_3634 | RNA polymerase sigma-70 factor | -5.11 | down |
| DW66\_3636 | hypothetical protein | -3.88 | down |
| DW66\_3637 | TnpA protein | -1.67 | down |
| DW66\_3639 | integrase catalytic region | -1.34 | down |
| DW66\_3642 | hypothetical protein | -1.06 | down |
| DW66\_3643 | hypothetical protein | -1.39 | down |
| DW66\_3644 | lipoprotein | -1.18 | down |
| DW66\_3648 | transcriptional regulator LysR | -1.15 | down |
| DW66\_3650 | glutathione S-transferase domain-containing protein | -12.22 | down |
| DW66\_3651 | ISPpu14, transposase | -4.19 | down |
| DW66\_3652 | transposase | -6.63 | down |
| DW66\_3653 | transposase IS66 | -1.00 | down |
| DW66\_3654 | response regulator receiver protein | -1.56 | down |
| DW66\_3660 | precorrin 6A synthase | -3.61 | down |
| DW66\_3661 | outer membrane porin | -5.30 | down |
| DW66\_3662 | transcriptional regulator MvaT, P16 subunit | 2.02 | up |
| DW66\_3663 | lactoylglutathione lyase | -1.40 | down |
| DW66\_3664 | hypothetical protein | 1.21 | up |
| DW66\_3666 | hypothetical protein | -2.20 | down |
| DW66\_3667 | hypothetical protein | -3.65 | down |
| DW66\_3668 | endolysin | -2.70 | down |
| DW66\_3670 | phage repressor | -1.20 | down |
| DW66\_3671 | hypothetical protein | 1.45 | up |
| DW66\_3676 | L-ornithine N5-oxygenase PvdA | 3.14 | up |
| DW66\_3677 | peptidase | -1.94 | down |
| DW66\_3679 | hypothetical protein | 1.69 | up |
| DW66\_3680 | hypothetical protein | 1.03 | up |
| DW66\_3685 | lipoprotein | -2.67 | down |
| DW66\_3686 | isochorismatase hydrolase | -1.68 | down |
| DW66\_3687 | thioesterase | 2.03 | up |
| DW66\_3688 | balhimycin biosynthetic protein MbtH | 3.05 | up |
| DW66\_3689 | Ribosomal protein S3AE | -2.34 | down |
| DW66\_3691 | methylenetetrahydrofolate dehydrogenase | -2.12 | down |
| DW66\_3693 | sarcosine oxidase subunit delta heterotetrameric | -1.54 | down |
| DW66\_3702 | extracellular solute-binding protein | 1.62 | up |
| DW66\_3703 | binding-protein-dependent transport system inner membrane protein | 2.23 | up |
| DW66\_3704 | binding-protein-dependent transport system inner membrane protein | 1.64 | up |
| DW66\_3705 | Polyamine ABC transporter ATP-binding protein | 1.45 | up |
| DW66\_3706 | OmpA/MotB domain-containing protein | -2.78 | down |
| DW66\_3707 | integral membrane protein TerC | -1.17 | down |
| DW66\_3708 | acyl-CoA dehydrogenase domain-containing protein | -1.01 | down |
| DW66\_3709 | transcriptional regulator LysR | -1.61 | down |
| DW66\_3710 | class V aminotransferase | 5.62 | up |
| DW66\_3711 | RES domain-containing protein | -3.48 | down |
| DW66\_3712 | hypothetical protein | -1.97 | down |
| DW66\_3713 | dihydropteridine reductase | -1.56 | down |
| DW66\_3714 | transcriptional regulator LysR | -1.00 | down |
| DW66\_3715 | transcriptional regulator AraC | -1.80 | down |
| DW66\_3716 | lysine exporter protein LysE/YggA | -1.87 | down |
| DW66\_3717 | sugar efflux transporter | -2.84 | down |
| DW66\_3718 | hypothetical protein | -2.58 | down |
| DW66\_3719 | alcohol dehydrogenase | -2.74 | down |
| DW66\_3720 | transcriptional regulator AraC | -1.59 | down |
| DW66\_3721 | 2'-5' RNA ligase | -1.44 | down |
| DW66\_3722 | hypothetical protein | -1.88 | down |
| DW66\_3723 | aspartyl/asparaginyl beta-hydroxylase | -1.30 | down |
| DW66\_3724 | alkylhydroperoxidase | 3.93 | up |
| DW66\_3726 | serine/threonine transporter SstT | -1.55 | down |
| DW66\_3727 | Virulence factor mviM | -1.52 | down |
| DW66\_3728 | hypothetical protein | 2.26 | up |
| DW66\_3729 | alkyl hydroperoxide reductase subunit F | -1.65 | down |
| DW66\_3733 | cytochrome c class I | -1.98 | down |
| DW66\_3734 | cytochrome c-type protein | -2.43 | down |
| DW66\_3735 | hypothetical protein | -4.18 | down |
| DW66\_3740 | molybdate ABC transporter permease | -1.30 | down |
| DW66\_3742 | DNA topoisomerase | -2.41 | down |
| DW66\_3743 | carbon storage regulator | 1.29 | up |
| DW66\_3748 | DoxX protein | 4.00 | up |
| DW66\_3749 | hypothetical protein | 1.79 | up |
| DW66\_3750 | alcohol dehydrogenase | 1.79 | up |
| DW66\_3751 | hypothetical protein | -2.86 | down |
| DW66\_3752 | transcriptional regulator LysR | -2.80 | down |
| DW66\_3754 | retron-type reverse transcriptase | -3.04 | down |
| DW66\_3757 | ISPpu15, transposase | -4.45 | down |
| DW66\_3758 | ISPpu15, transposase | -1.19 | down |
| DW66\_3761 | copper-translocating P-type ATPase | 2.84 | up |
| DW66\_3762 | copper binding protein | 1.70 | up |
| DW66\_3765 | ISPs1, transposase | -1.07 | down |
| DW66\_3771 | transposase | 2.65 | up |
| DW66\_3772 | aerotaxis receptor Aer | 3.24 | up |
| DW66\_3773 | PAS/PAC sensor-containing diguanylate cyclase/phosphodiesterase | 3.46 | up |
| DW66\_3774 | DNA-binding protein | -1.37 | down |
| DW66\_3775 | hypothetical protein | -1.04 | down |
| DW66\_3776 | permease | -1.77 | down |
| DW66\_3777 | permease | -3.14 | down |
| DW66\_3778 | hypothetical protein | -1.67 | down |
| DW66\_3779 | hypothetical protein | -1.73 | down |
| DW66\_3780 | metallophosphoesterase protein | -2.23 | down |
| DW66\_3784 | CTP:Inositol-1-phosphate cytidylyltransferase | -1.88 | down |
| DW66\_3785 | hypothetical protein | -4.07 | down |
| DW66\_3786 | Tn4653A-like resolvase protein | -4.35 | down |
| DW66\_3787 | TniA transposase | -2.19 | down |
| DW66\_3788 | integrase for In2 | -2.04 | down |
| DW66\_3790 | TnpA protein | -1.72 | down |
| DW66\_3791 | RNA polymerase sigma-71 factor | -5.11 | down |
| DW66\_3793 | hypothetical protein | -3.88 | down |
| DW66\_3794 | TnpA protein | -1.67 | down |
| DW66\_3799 | hypothetical protein | -1.06 | down |
| DW66\_3800 | hypothetical protein | -1.39 | down |
| DW66\_3801 | lipoprotein | -1.18 | down |
| DW66\_3805 | transcriptional regulator LysR | -1.15 | down |
| DW66\_3807 | glutathione S-transferase domain-containing protein | -13.22 | down |
| DW66\_3808 | ATPase AAA | -4.29 | down |
| DW66\_3809 | ISPsy14, transposase | -2.60 | down |
| DW66\_3810 | TnpT protein | 2.71 | up |
| DW66\_3811 | Tn4652, cointegrate resolution protein S | 2.60 | up |
| DW66\_3812 | hypothetical protein | -3.74 | down |
| DW66\_3813 | hypothetical protein | -2.28 | down |
| DW66\_3814 | hypothetical protein | -2.40 | down |
| DW66\_3815 | hypothetical protein | -1.58 | down |
| DW66\_3816 | transposase for Tn21 | -1.12 | down |
| DW66\_3817 | resolvase for Tn21 | -1.33 | down |
| DW66\_3818 | transposase | -7.40 | down |
| DW66\_3820 | hypothetical protein | -1.67 | down |
| DW66\_3824 | D12 class N6 adenine-specific DNA methyltransferase | -2.21 | down |
| DW66\_3825 | hypothetical protein | -6.42 | down |
| DW66\_3826 | terminase, large subunit | -2.09 | down |
| DW66\_3827 | hypothetical protein | -3.87 | down |
| DW66\_3828 | integrase | -3.81 | down |
| DW66\_3830 | phosphoglycerate mutase | -2.35 | down |
| DW66\_3834 | type 12 methyltransferase | -1.60 | down |
| DW66\_3835 | phage-related lipoprotein | -1.25 | down |
| DW66\_3836 | hypothetical protein | -2.46 | down |
| DW66\_3837 | hypothetical protein | -2.25 | down |
| DW66\_3838 | hypothetical protein | -2.69 | down |
| DW66\_3839 | citrate transporter | -2.29 | down |
| DW66\_3840 | diguanylate cyclase | -3.00 | down |
| DW66\_3841 | membrane protein | -2.33 | down |
| DW66\_3842 | transcriptional regulator LysR | -2.52 | down |
| DW66\_3843 | isochorismatase hydrolase | -4.13 | down |
| DW66\_3844 | hypothetical protein | -3.52 | down |
| DW66\_3846 | site-specific recombinase | -1.01 | down |
| DW66\_3848 | xanthine permease | -3.74 | down |
| DW66\_3850 | sulfur relay protein TusC | -1.94 | down |
| DW66\_3851 | sulfur relay protein TusB/DsrH | -1.13 | down |
| DW66\_3852 | sulfur relay protein | -1.16 | down |
| DW66\_3857 | camphor resistance protein CrcB | -2.00 | down |
| DW66\_3858 | recombination factor protein RarA | -2.23 | down |
| DW66\_3859 | lipoprotein chaperone | -2.18 | down |
| DW66\_3860 | cell division protein FtsK | -1.47 | down |
| DW66\_3862 | leucyl/phenylalanyl-tRNA-protein transferase | -2.56 | down |
| DW66\_3863 | arginyl-tRNA-protein transferase | 3.11 | up |
| DW66\_3865 | ATP-dependent Clp protease ATP-binding protein ClpA | 2.18 | up |
| DW66\_3867 | cold-shock protein | 2.59 | up |
| DW66\_3868 | isocitrate dehydrogenase | 5.39 | up |
| DW66\_3870 | NUDIX hydrolase | -2.08 | down |
| DW66\_3873 | adenylosuccinate lyase | -1.54 | down |
| DW66\_3875 | acetyltransferase | 1.38 | up |
| DW66\_3876 | DNA topoisomerase III | -2.28 | down |
| DW66\_3878 | alpha/beta hydrolase fold protein | 5.78 | up |
| DW66\_3879 | hypothetical protein | -3.04 | down |
| DW66\_3880 | NADH pyrophosphatase | -2.79 | down |
| DW66\_3881 | enoyl-CoA hydratase | -1.21 | down |
| DW66\_3882 | sodium/proton antiporter | -2.72 | down |
| DW66\_3884 | lipocalin | -1.63 | down |
| DW66\_3885 | ribonuclease Z | -3.11 | down |
| DW66\_3886 | allantoate amidohydrolase | 1.67 | up |
| DW66\_3888 | phenylhydantoinase | 3.05 | up |
| DW66\_3889 | dihydropyrimidine dehydrogenase subunit A | 1.34 | up |
| DW66\_3890 | dihydropyrimidine dehydrogenase | 1.23 | up |
| DW66\_3891 | transcriptional regulator TetR | -1.78 | down |
| DW66\_3893 | acetyltransferase | -1.14 | down |
| DW66\_3894 | glucose-6-phosphate 1-dehydrogenase | -1.25 | down |
| DW66\_3896 | hypothetical protein | 5.45 | up |
| DW66\_3897 | DNA and RNA helicases | -1.80 | down |
| DW66\_3898 | hypothetical protein | -3.03 | down |
| DW66\_3899 | hypothetical protein | -4.74 | down |
| DW66\_3900 | VgrG protein | -4.65 | down |
| DW66\_3902 | malto-oligosyltrehalose trehalohydrolase | 1.68 | up |
| DW66\_3903 | 4-alpha-glucanotransferase | 1.12 | up |
| DW66\_3904 | maltooligosyl trehalose synthase | 1.94 | up |
| DW66\_3905 | hypothetical protein | 1.80 | up |
| DW66\_3906 | glycogen debranching protein GlgX | 1.91 | up |
| DW66\_3908 | outer membrane autotransporter | -2.82 | down |
| DW66\_3909 | glycogen branching enzyme | 2.35 | up |
| DW66\_3910 | trehalose synthase | 2.10 | up |
| DW66\_3912 | hypothetical protein | -1.53 | down |
| DW66\_3913 | AMP-binding domain protein | -1.15 | down |
| DW66\_3914 | hypothetical protein | -1.27 | down |
| DW66\_3919 | transcriptional regulator XRE | -3.60 | down |
| DW66\_3920 | transcriptional regulator XRE | -2.58 | down |
| DW66\_3921 | hypothetical protein | 1.49 | up |
| DW66\_3922 | *sigma*-70 region 4 type 2 | -3.26 | down |
| DW66\_3923 | transporter protein | -3.26 | down |
| DW66\_3924 | transcriptional regulator LysR | -1.79 | down |
| DW66\_3925 | short-chain type regulator | -2.18 | down |
| DW66\_3926 | MFS transporter | -3.09 | down |
| DW66\_3927 | transketolase | -2.87 | down |
| DW66\_3928 | transketolase, C-terminal subunit | -3.48 | down |
| DW66\_3929 | phosphate ABC transporter ATP-binding protein | -2.65 | down |
| DW66\_3930 | polar amino acid ABC transporter inner membrane subunit | -3.75 | down |
| DW66\_3931 | polar amino acid ABC transporter inner membrane subunit | -3.40 | down |
| DW66\_3932 | amino acid ABC transporter periplasmic amino acid-binding protein | -3.79 | down |
| DW66\_3933 | transcriptional regulator | -2.28 | down |
| DW66\_3934 | hypothetical protein | 1.69 | up |
| DW66\_3937 | Pas/Pac sensor-containing chemotaxis sensory transducer | -3.28 | down |
| DW66\_3938 | ImcF domain-containing protein | -3.41 | down |
| DW66\_3939 | hypothetical protein | -5.96 | down |
| DW66\_3940 | CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase | -1.07 | down |
| DW66\_3941 | excinuclease ABC subunit C | -1.51 | down |
| DW66\_3942 | DNA-binding response regulator GacA | -1.06 | down |
| DW66\_3945 | uroporphyrin-III c-methyltransferase | 1.86 | up |
| DW66\_3946 | phosphate transporter | 2.35 | up |
| DW66\_3951 | class III aminotransferase | 3.31 | up |
| DW66\_3952 | hypothetical protein | -2.12 | down |
| DW66\_3953 | hypothetical protein | -2.73 | down |
| DW66\_3954 | elongation factor G | 4.98 | up |
| DW66\_3955 | sulfate transporter | -3.95 | down |
| DW66\_3956 | NolW domain-containing protein | 1.32 | up |
| DW66\_3957 | hypothetical protein | -4.10 | down |
| DW66\_3958 | isocitrate lyase | 3.53 | up |
| DW66\_3959 | hypothetical protein | -1.66 | down |
| DW66\_3960 | hypothetical protein | 3.11 | up |
| DW66\_3962 | NADH dehydrogenase subunit A | 1.69 | up |
| DW66\_3963 | NADH dehydrogenase subunit B | 2.89 | up |
| DW66\_3964 | bifunctional NADH:ubiquinone oxidoreductase subunit C/D | 3.42 | up |
| DW66\_3965 | NADH dehydrogenase subunit E | 4.46 | up |
| DW66\_3966 | NADH dehydrogenase subunit F | 4.76 | up |
| DW66\_3967 | NADH dehydrogenase subunit G | 3.55 | up |
| DW66\_3968 | NADH:ubiquinone oxidoreductase subunit H | 3.51 | up |
| DW66\_3969 | NADH dehydrogenase subunit I | 4.47 | up |
| DW66\_3970 | NADH dehydrogenase subunit J | 3.18 | up |
| DW66\_3971 | NADH dehydrogenase subunit K | 3.38 | up |
| DW66\_3972 | NADH dehydrogenase subunit L | 2.49 | up |
| DW66\_3973 | NADH:ubiquinone oxidoreductase subunit M | 2.84 | up |
| DW66\_3974 | NADH dehydrogenase subunit N | 3.29 | up |
| DW66\_3975 | hypothetical protein | 1.37 | up |
| DW66\_3977 | hypothetical protein | -1.98 | down |
| DW66\_3978 | hypothetical protein | -3.41 | down |
| DW66\_3979 | transcriptional regulator | -1.76 | down |
| DW66\_3980 | hypothetical protein | -1.99 | down |
| DW66\_3981 | TonB-dependent receptor | -2.41 | down |
| DW66\_3982 | NADPH-dependent FMN reductase | 1.64 | up |
| DW66\_3983 | hypothetical protein | -2.64 | down |
| DW66\_3984 | lysine decarboxylase | 2.55 | up |
| DW66\_3985 | DNA polymerase III subunit epsilon | -1.89 | down |
| DW66\_3986 | ribonuclease H | -1.18 | down |
| DW66\_3989 | MltD domain-containing protein | -1.25 | down |
| DW66\_3990 | extracellular solute-binding protein | -2.42 | down |
| DW66\_3993 | ABC transporter permease | 1.27 | up |
| DW66\_3994 | peptide ABC transporter ATP-binding protein | 1.47 | up |
| DW66\_3995 | hypothetical protein | 1.15 | up |
| DW66\_3999 | transcriptional regulator LysR | -1.88 | down |
| DW66\_4000 | hypothetical protein | -4.11 | down |
| DW66\_4001 | hypothetical protein | -1.80 | down |
| DW66\_4003 | osmosensitive K+ channel signal transduction histidine kinase | -1.14 | down |
| DW66\_4004 | potassium-transporting, ATPase subunit C | -3.15 | down |
| DW66\_4005 | potassium-transporting, ATPase subunit B | -3.33 | down |
| DW66\_4006 | potassium-transporting ATPase subunit A | -4.02 | down |
| DW66\_4007 | membrane protein | -1.60 | down |
| DW66\_4008 | Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), A subunit | -1.37 | down |
| DW66\_4009 | alpha/beta hydrolase fold protein | -1.40 | down |
| DW66\_4010 | Alpha/beta hydrolase | -1.65 | down |
| DW66\_4011 | phosphohistidine phosphatase, SixA | -1.21 | down |
| DW66\_4014 | hypothetical protein | -3.06 | down |
| DW66\_4020 | amidohydrolase 2 | -2.55 | down |
| DW66\_4022 | dienelactone hydrolase | 2.87 | up |
| DW66\_4023 | heat shock protein 90 | 5.13 | up |
| DW66\_4027 | hypothetical protein | 1.69 | up |
| DW66\_4028 | branched-chain amino acid transport system II carrier protein | -1.82 | down |
| DW66\_4029 | succinyl-CoA synthetase subunit alpha | 1.97 | up |
| DW66\_4030 | succinyl-CoA synthetase subunit beta | 1.42 | up |
| DW66\_4031 | dihydrolipoamide dehydrogenase | 2.48 | up |
| DW66\_4032 | dihydrolipoamide succinyltransferase | 2.23 | up |
| DW66\_4033 | 2-oxoglutarate dehydrogenase E1 component | 2.73 | up |
| DW66\_4034 | succinate dehydrogenase iron-sulfur subunit | 2.15 | up |
| DW66\_4036 | succinate dehydrogenase, hydrophobic membrane anchor protein | -1.90 | down |
| DW66\_4037 | succinate dehydrogenase, cytochrome b556 subunit | -2.25 | down |
| DW66\_4039 | lipid-binding START domain-containing protein | -1.89 | down |
| DW66\_4040 | proteinase inhibitor | -2.10 | down |
| DW66\_4041 | Translation initiation factor 2 | -2.15 | down |
| DW66\_4043 | OmpA/MotB domain-containing protein | -1.10 | down |
| DW66\_4044 | lipoprotein | -1.56 | down |
| DW66\_4045 | Extracellular solute-binding protein | -1.38 | down |
| DW66\_4047 | electron transfer flavoprotein alpha/beta-subunit | -1.41 | down |
| DW66\_4048 | electron transfer flavoprotein-ubiquinone oxidoreductase | -2.85 | down |
| DW66\_4051 | RNA polymerase sigma factor | -3.53 | down |
| DW66\_4053 | efflux ABC transporter ATP-binding protein | 1.58 | up |
| DW66\_4057 | class V aminotransferase | 1.06 | up |
| DW66\_4060 | diaminobutyrate-2-oxoglutarate aminotransferase | 2.32 | up |
| DW66\_4061 | integral membrane sensor signal transduction histidine kinase | -1.25 | down |
| DW66\_4062 | two component transcriptional regulator | -1.65 | down |
| DW66\_4063 | hypothetical protein | -2.52 | down |
| DW66\_4066 | MobA-like protein | -1.66 | down |
| DW66\_4070 | aldehyde oxidase and xanthine dehydrogenase molybdopterin binding protein | -1.35 | down |
| DW66\_4071 | protein-disulfide reductase | -2.20 | down |
| DW66\_4072 | redoxin domain-containing protein | -1.04 | down |
| DW66\_4074 | peptide synthase | 2.83 | up |
| DW66\_4075 | extracytoplasmic-function sigma-70 factor | -3.61 | down |
| DW66\_4077 | extracellular solute-binding protein | -1.47 | down |
| DW66\_4079 | hypothetical protein | 1.05 | up |
| DW66\_4080 | hydrolase | 1.95 | up |
| DW66\_4081 | cbb3-type cytochrome c oxidase subunit I | 4.33 | up |
| DW66\_4082 | cbb3-type cytochrome c oxidase subunit II | 4.96 | up |
| DW66\_4083 | cbb3-type cytochrome c oxidase, CcoQ subunit | 5.07 | up |
| DW66\_4084 | cbb3-type cytochrome c oxidase subunit III | 4.31 | up |
| DW66\_4085 | cbb3-type cytochrome c oxidase subunit I | 2.06 | up |
| DW66\_4086 | cbb3-type cytochrome c oxidase subunit II | 4.16 | up |
| DW66\_4087 | cbb3-type cytochrome c oxidase, CcoQ subunit | 4.73 | up |
| DW66\_4088 | cbb3-type cytochrome c oxidase subunit III | 3.65 | up |
| DW66\_4089 | cbb3-type cytochrome c oxidase, accessory protein CcoG | 2.83 | up |
| DW66\_4090 | hypothetical protein | 1.75 | up |
| DW66\_4093 | membrane-bounded cytochrome biogenesis DsbD/cycZ-like domain | -1.81 | down |
| DW66\_4094 | coproporphyrinogen III oxidase | 3.42 | up |
| DW66\_4097 | recombination protein RecR | -4.15 | down |
| DW66\_4098 | hypothetical protein | 1.57 | up |
| DW66\_4099 | DNA polymerase III subunits gamma and tau | -1.37 | down |
| DW66\_4102 | membrane protein | -4.37 | down |
| DW66\_4103 | transcriptional regulator MerR | 1.89 | up |
| DW66\_4104 | NAD-dependent DNA ligase LigA | -1.98 | down |
| DW66\_4108 | transcriptional regulator | -2.09 | down |
| DW66\_4109 | xanthine dehydrogenase small subunit | 2.38 | up |
| DW66\_4110 | xanthine dehydrogenase molybdopterin binding subunit | 2.70 | up |
| DW66\_4115 | xanthine/uracil/vitamin C permease | -1.46 | down |
| DW66\_4116 | transposase | -1.29 | down |
| DW66\_4117 | hydroxyisourate hydrolase | 1.40 | up |
| DW66\_4119 | 2-oxo-4-hydroxy-4-carboxy--5-ureidoimidazoline (OHCU) decarboxylase | 1.05 | up |
| DW66\_4120 | ureidoglycolate hydrolase | 1.77 | up |
| DW66\_4122 | xanthine/uracil permease | -2.12 | down |
| DW66\_4123 | Nucleoside-binding outer membrane protein | -12.38 | down |
| DW66\_4124 | nucleoside-binding outer membrane protein-like protein | -2.29 | down |
| DW66\_4125 | membrane protein | -1.62 | down |
| DW66\_4126 | transcriptional regulator TetR | -1.42 | down |
| DW66\_4127 | GlcG protein | -3.01 | down |
| DW66\_4128 | hypothetical protein | -7.79 | down |
| DW66\_4129 | glyoxylate carboligase | 1.69 | up |
| DW66\_4131 | 2-hydroxy-3-oxopropionate reductase | 1.65 | up |
| DW66\_4132 | hydroxypyruvate reductase | -1.24 | down |
| DW66\_4133 | pyruvate kinase | -1.31 | down |
| DW66\_4134 | urea transporter | -2.18 | down |
| DW66\_4136 | sulfate ABC transporter substrate-binding protein | -3.00 | down |
| DW66\_4137 | Methyltransferase | -2.98 | down |
| DW66\_4138 | Permease of the drug/metabolite transporter | -2.07 | down |
| DW66\_4142 | type I hydrophobic transmembrane region and ATP/GTP binding motif protein | -3.58 | down |
| DW66\_4143 | hypothetical protein | -2.02 | down |
| DW66\_4144 | hypothetical protein | -1.89 | down |
| DW66\_4145 | FKBP-type peptidylprolyl isomerase | -1.91 | down |
| DW66\_4147 | phenazine biosynthesis protein | -3.13 | down |
| DW66\_4148 | D-isomer specific 2-hydroxyacid dehydrogenase NAD-binding protein | -3.33 | down |
| DW66\_4149 | Cytochrome c heme lyase subunit CcmH | -2.74 | down |
| DW66\_4151 | cytochrome c-type biogenesis protein CcmI | -1.73 | down |
| DW66\_4152 | cytochrome C biogenesis protein | -1.71 | down |
| DW66\_4158 | heme exporter protein CcmB | -2.10 | down |
| DW66\_4159 | cytochrome c biogenesis protein CcmA | -2.48 | down |
| DW66\_4160 | hypothetical protein | -10.64 | down |
| DW66\_4161 | hypothetical protein | -1.49 | down |
| DW66\_4162 | hypothetical protein | -4.81 | down |
| DW66\_4164 | hypothetical protein | -1.37 | down |
| DW66\_4165 | transcriptional regulator AraC | -1.47 | down |
| DW66\_4168 | O-succinylhomoserine sulfhydrylase | 1.76 | up |
| DW66\_4169 | transporter protein | 1.34 | up |
| DW66\_4171 | acetyl-transferase | -1.32 | down |
| DW66\_4172 | hypothetical protein | -1.50 | down |
| DW66\_4173 | hypothetical protein | -1.28 | down |
| DW66\_4174 | hypothetical protein | -2.42 | down |
| DW66\_4175 | purine-binding chemotaxis protein CheW | -1.79 | down |
| DW66\_4176 | CheW protein | -2.66 | down |
| DW66\_4177 | cobyrinic acid a,c-diamide synthase | -2.86 | down |
| DW66\_4179 | flagellar motor protein | -1.57 | down |
| DW66\_4182 | chemotaxis phosphatase, CheZ | -1.46 | down |
| DW66\_4186 | flagellar biosynthesis protein flhF | -1.28 | down |
| DW66\_4187 | flagellar biosynthesis protein FlhA | -1.23 | down |
| DW66\_4188 | flagellar biosynthesis protein FlhB | -3.98 | down |
| DW66\_4189 | flagellar biosynthesis protein FliR | -3.89 | down |
| DW66\_4190 | flagellar biosynthesis protein FliQ | -2.06 | down |
| DW66\_4191 | flagellar biosynthesis protein FliP | -2.93 | down |
| DW66\_4192 | flagellar biosynthesis protein FliO | -1.96 | down |
| DW66\_4193 | flagellar motor switch protein | -1.01 | down |
| DW66\_4194 | flagellar motor switch protein FliM | -1.83 | down |
| DW66\_4195 | flagellar basal body-associated protein FliL | -3.05 | down |
| DW66\_4196 | flagellar hook-length control protein | -2.05 | down |
| DW66\_4200 | flagellar biosynthesis chaperone | -2.23 | down |
| DW66\_4201 | flagellum-specific ATP synthase | -1.44 | down |
| DW66\_4202 | flagellar assembly protein H | -1.91 | down |
| DW66\_4204 | flagellar MS-ring protein | -1.97 | down |
| DW66\_4205 | flagellar hook-basal body protein FliE | -2.06 | down |
| DW66\_4207 | PAS/PAC sensor signal transduction histidine kinase | -1.72 | down |
| DW66\_4209 | flagellin FliC | 2.91 | up |
| DW66\_4210 | flagellin FlaG | 2.89 | up |
| DW66\_4212 | flagellar protein FliS | 1.27 | up |
| DW66\_4213 | hypothetical protein | 1.41 | up |
| DW66\_4218 | flagellar hook-associated protein FlgL | 2.42 | up |
| DW66\_4219 | flagellar hook-associated protein FlgK | 1.48 | up |
| DW66\_4220 | flagellar rod assembly protein/muramidase FlgJ | 1.55 | up |
| DW66\_4221 | flagellar basal body P-ring protein | 1.04 | up |
| DW66\_4224 | flagellar basal body rod protein FlgF | -1.09 | down |
| DW66\_4226 | flagellar hook protein FlgE | 2.58 | up |
| DW66\_4229 | flagellar basal body rod protein FlgB | -1.29 | down |
| DW66\_4232 | flagellar basal body P-ring biosynthesis protein FlgA | -2.76 | down |
| DW66\_4240 | branched-chain alpha-keto acid dehydrogenase subunit E2 | 1.09 | up |
| DW66\_4241 | dihydrolipoyl dehydrogenase | 1.75 | up |
| DW66\_4242 | PAS/PAC sensor-containing diguanylate cyclase | 2.10 | up |
| DW66\_4244 | branched-chain amino acid permease | -1.69 | down |
| DW66\_4245 | branched-chain amino acid transport | -2.64 | down |
| DW66\_4246 | phosphonate metabolism protein/1,5-bisphosphokinase PhnN | -1.68 | down |
| DW66\_4248 | magnesium transporter | -6.22 | down |
| DW66\_4249 | carbon storage regulator | -1.93 | down |
| DW66\_4251 | hypothetical protein | 1.45 | up |
| DW66\_4252 | alanyl-tRNA ligase | -1.62 | down |
| DW66\_4254 | succinylglutamate desuccinylase | 1.46 | up |
| DW66\_4255 | GTPases | 1.35 | up |
| DW66\_4256 | succinylarginine dihydrolase | 2.41 | up |
| DW66\_4259 | arginine/ornithine succinyltransferase | -1.31 | down |
| DW66\_4260 | bifunctional N-succinyldiaminopimelate-aminotransferase/acetylornithine transaminase protein | -1.70 | down |
| DW66\_4261 | hypothetical protein | -3.35 | down |
| DW66\_4265 | polar amino acid ABC transporter inner membrane subunit | -1.00 | down |
| DW66\_4266 | ABC transporter substrate-binding protein | -2.07 | down |
| DW66\_4267 | hypothetical protein | -2.38 | down |
| DW66\_4270 | PhhR | -2.23 | down |
| DW66\_4271 | phenylalanine 4-monooxygenase | 1.89 | up |
| DW66\_4272 | pterin-4-alpha-carbinolamine dehydratase | 3.01 | up |
| DW66\_4273 | MFS transporter | -2.55 | down |
| DW66\_4274 | FAD linked oxidase domain-containing protein | -2.29 | down |
| DW66\_4275 | transcriptional regulator LysR | -2.32 | down |
| DW66\_4276 | amino acid ABC transporter permease | -1.30 | down |
| DW66\_4277 | RNA-binding S4 domain-containing protein | -1.67 | down |
| DW66\_4279 | segregation and condensation protein B | -1.25 | down |
| DW66\_4283 | intracellular septation protein A | -1.52 | down |
| DW66\_4285 | two component transcriptional regulator | -1.68 | down |
| DW66\_4286 | hypothetical protein | -4.71 | down |
| DW66\_4287 | integral membrane sensor signal transduction histidine kinase | -5.83 | down |
| DW66\_4289 | potassium uptake protein TrkH | -4.47 | down |
| DW66\_4291 | transcriptional regulator AraC | 1.72 | up |
| DW66\_4292 | hypothetical protein | 2.57 | up |
| DW66\_4293 | metallophosphoesterase | -5.35 | down |
| DW66\_4294 | transcriptional regulator AraC | -4.01 | down |
| DW66\_4295 | membrane protein | -2.90 | down |
| DW66\_4296 | hypothetical protein | -1.58 | down |
| DW66\_4298 | patatin | -4.34 | down |
| DW66\_4302 | hypothetical protein | -1.41 | down |
| DW66\_4304 | DTW domain-containing protein | -1.56 | down |
| DW66\_4305 | methyl-accepting chemotaxis sensory transducer with Pas/Pac sensor | 3.06 | up |
| DW66\_4306 | transcriptional regulator LysR | -2.56 | down |
| DW66\_4307 | agmatinase | -4.64 | down |
| DW66\_4309 | hypothetical protein | 6.23 | up |
| DW66\_4311 | MFS precursor | -2.19 | down |
| DW66\_4312 | Permease of the drug/metabolite transporter | -3.37 | down |
| DW66\_4313 | hypothetical protein | -2.71 | down |
| DW66\_4316 | DEAD/DEAH box helicase | -1.87 | down |
| DW66\_4317 | hypothetical protein | -1.47 | down |
| DW66\_4318 | mechanosensitive ion channel protein MscS | -2.14 | down |
| DW66\_4319 | cytosine/purines uracil thiamine allantoin permease | -1.99 | down |
| DW66\_4320 | carboxylate/amino acid/amine transporter | -3.49 | down |
| DW66\_4321 | NAD(P)H dehydrogenase (quinone) | -2.67 | down |
| DW66\_4322 | 3-phosphoglycerate kinase | -1.34 | down |
| DW66\_4323 | transcriptional regulator LysR | -1.80 | down |
| DW66\_4327 | hypothetical protein | -1.85 | down |
| DW66\_4333 | acyl coenzyme A synthetase 1 | -1.49 | down |
| DW66\_4336 | dehydratase | -1.07 | down |
| DW66\_4337 | RNA polymerase | 1.14 | up |
| DW66\_4338 | activator of Hsp90 ATPase 1 | 1.33 | up |
| DW66\_4339 | DGPFAETKE protein | 2.50 | up |
| DW66\_4340 | Ketosteroid isomerase | 1.52 | up |
| DW66\_4342 | acetyltransferase | -2.73 | down |
| DW66\_4345 | CsbD protein | -1.70 | down |
| DW66\_4346 | hypothetical protein | -1.34 | down |
| DW66\_4347 | RNA-binding S1 domain-containing protein | -1.28 | down |
| DW66\_4349 | bifunctional isocitrate dehydrogenase kinase/phosphatase protein | 1.21 | up |
| DW66\_4351 | hypothetical protein | -1.86 | down |
| DW66\_4352 | Permease of the drug/metabolite transporter | -2.26 | down |
| DW66\_4353 | PvdO, pyoverdine responsive serine/threonine kinase (by OlgaV) | -1.17 | down |
| DW66\_4354 | TonB-dependent siderophore receptor | 1.07 | up |
| DW66\_4355 | amino acid adenylation domain-containing protein | 2.38 | up |
| DW66\_4356 | amino acid adenylation domain-containing protein | 2.84 | up |
| DW66\_4358 | amino acid adenylation domain-containing protein | 2.66 | up |
| DW66\_4359 | hypothetical protein | -2.09 | down |
| DW66\_4360 | hypothetical protein | -2.06 | down |
| DW66\_4364 | aspartyl/asparaginyl beta-hydroxylase | -1.98 | down |
| DW66\_4365 | cysteine synthase A | -1.05 | down |
| DW66\_4366 | hypothetical protein | -3.96 | down |
| DW66\_4367 | hypothetical protein | -3.86 | down |
| DW66\_4373 | transporter protein | -1.21 | down |
| DW66\_4375 | hypothetical protein | -3.03 | down |
| DW66\_4376 | glutamine amidotransferase | -2.24 | down |
| DW66\_4377 | Permeases | -2.04 | down |
| DW66\_4379 | hypothetical protein | 1.03 | up |
| DW66\_4384 | hypothetical protein | -3.08 | down |
| DW66\_4385 | hypothetical protein | -3.69 | down |
| DW66\_4387 | D-isomer specific 2-hydroxyacid dehydrogenase NAD-binding protein | -3.78 | down |
| DW66\_4388 | Protein YcgL | -3.30 | down |
| DW66\_4389 | ribonuclease D | -3.80 | down |
| DW66\_4390 | sulfatase | -8.19 | down |
| DW66\_4391 | 5-carboxymethyl-2-hydroxymuconate isomerase | -2.72 | down |
| DW66\_4392 | hypothetical protein | 4.48 | up |
| DW66\_4399 | molybdenum cofactor biosynthesis protein B | -2.94 | down |
| DW66\_4400 | transcriptional regulator LysR | -1.50 | down |
| DW66\_4401 | transcriptional regulator AraC | -4.16 | down |
| DW66\_4402 | amino acid permease-associated protein | -4.10 | down |
| DW66\_4403 | proline racemase | -1.92 | down |
| DW66\_4404 | dihydrodipicolinate synthetase | -2.30 | down |
| DW66\_4405 | ketoglutarate semialdehyde dehydrogenase | -1.29 | down |
| DW66\_4406 | FAD dependent oxidoreductase | -1.64 | down |
| DW66\_4407 | xenobiotic reductase A | -1.60 | down |
| DW66\_4408 | transcriptional regulator ArsR | -1.52 | down |
| DW66\_4411 | malate:quinone oxidoreductase | -2.01 | down |
| DW66\_4412 | proline racemase protein | -3.02 | down |
| DW66\_4413 | outer membrane lipoprotein | -1.29 | down |
| DW66\_4414 | potassium uptake protein TrkH | -1.83 | down |
| DW66\_4420 | glycine cleavage system transcriptional repressor | -2.41 | down |
| DW66\_4421 | alkyl hydroperoxide reductase/ thiol specific antioxidant/ Mal allergen | -1.87 | down |
| DW66\_4422 | permease PerM | -3.52 | down |
| DW66\_4423 | SirA protein | -3.57 | down |
| DW66\_4426 | GTP-binding protein | -1.32 | down |
| DW66\_4427 | amino acid ABC transporter permease | -5.31 | down |
| DW66\_4428 | methyl-accepting chemotaxis protein | -3.13 | down |
| DW66\_4430 | exsB protein | -1.67 | down |
| DW66\_4431 | radical SAM domain-containing protein | -3.03 | down |
| DW66\_4432 | tol-pal system protein YbgF | -2.09 | down |
| DW66\_4433 | peptidoglycan-associated lipoprotein OprL | -1.15 | down |
| DW66\_4434 | translocation protein TolB | -2.00 | down |
| DW66\_4435 | TolA protein | -2.64 | down |
| DW66\_4436 | biopolymer transport protein TolR | -1.87 | down |
| DW66\_4437 | TolQ | -2.52 | down |
| DW66\_4438 | 4-hydroxybenzoyl-CoA thioesterase | -1.76 | down |
| DW66\_4441 | Holliday junction resolvase | -3.85 | down |
| DW66\_4442 | hypothetical protein | -1.96 | down |
| DW66\_4443 | aspartyl-tRNA synthetase | -1.13 | down |
| DW66\_4444 | hypothetical protein | -1.27 | down |
| DW66\_4446 | ferritin Dps protein | 2.83 | up |
| DW66\_4448 | slyX protein | -1.07 | down |
| DW66\_4450 | outer membrane porin | 2.33 | up |
| DW66\_4451 | prolyl-tRNA synthetase | -1.09 | down |
| DW66\_4452 | lipoprotein | -1.17 | down |
| DW66\_4454 | membrane protein | -1.73 | down |
| DW66\_4457 | MiaB-like tRNA modifying protein YliG | -3.89 | down |
| DW66\_4460 | hypothetical protein | -1.24 | down |
| DW66\_4461 | hypothetical protein | -4.38 | down |
| DW66\_4462 | acetyltransferase | 2.33 | up |
| DW66\_4467 | integral membrane sensor signal transduction histidine kinase | -6.36 | down |
| DW66\_4468 | two component transcriptional regulator | -6.74 | down |
| DW66\_4469 | outer membrane protein H1 | -5.80 | down |
| DW66\_4470 | dienelactone hydrolase | 5.20 | up |
| DW66\_4472 | integral membrane sensor signal transduction histidine kinase | -2.01 | down |
| DW66\_4473 | two component transcriptional regulator | -2.22 | down |
| DW66\_4474 | hypothetical protein | -2.42 | down |
| DW66\_4475 | ribonucleotide-diphosphate reductase subunit alpha | 2.21 | up |
| DW66\_4476 | hypothetical protein | -13.26 | down |
| DW66\_4477 | ribonucleotide-diphosphate reductase subunit beta | 1.97 | up |
| DW66\_4479 | hypothetical protein | -1.06 | down |
| DW66\_4480 | hypothetical protein | -1.39 | down |
| DW66\_4481 | lipoprotein | -1.18 | down |
| DW66\_4485 | transcriptional regulator LysR | -1.15 | down |
| DW66\_4488 | metal-binding protein | -2.04 | down |
| DW66\_4489 | asparaginase/glutaminase | -2.60 | down |
| DW66\_4490 | hypothetical protein | -2.27 | down |
| DW66\_4491 | nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase | -3.83 | down |
| DW66\_4492 | amine oxidase | -3.06 | down |
| DW66\_4494 | acetolactate synthase | 1.68 | up |
| DW66\_4495 | formate/nitrate transporter | -1.31 | down |
| DW66\_4497 | diguanylate cyclase | 2.59 | up |
| DW66\_4501 | transcriptional regulator LysR | -2.65 | down |
| DW66\_4503 | secretion protein HlyD | -1.01 | down |
| DW66\_4505 | fusaric acid resistance protein region | -3.13 | down |
| DW66\_4506 | hypothetical protein | 9.01 | up |
| DW66\_4509 | hypothetical protein | -1.57 | down |
| DW66\_4510 | ATP-dependent helicase HepA | 1.44 | up |
| DW66\_4511 | diguanylate cyclase/phosphodiesterase | 3.58 | up |
| DW66\_4512 | hypothetical protein | -3.35 | down |
| DW66\_4515 | leucine/isoleucine/valine transporter, permease | 1.21 | up |
| DW66\_4516 | leucine/isoleucine/valine transporter, ATP-binding subunit | 2.13 | up |
| DW66\_4517 | branched chain amino acid ABC transporter ATP-binding protein | 2.13 | up |
| DW66\_4518 | lipoprotein | -1.38 | down |
| DW66\_4521 | 17 kDa surface antigen | -4.12 | down |
| DW66\_4522 | 30S ribosomal protein S3 | 3.28 | up |
| DW66\_4525 | beta-lactamase | -2.27 | down |
| DW66\_4527 | ATP-dependent DNA helicase DinG | -2.59 | down |
| DW66\_4528 | Phosphoribosylcarboxyaminoimidazole (NCAIR) mutase | -1.30 | down |
| DW66\_4530 | hypothetical protein | 1.15 | up |
| DW66\_4531 | OmpA/MotB domain-containing protein | 3.91 | up |
| DW66\_4532 | OmpA/MotB domain-containing protein | 7.13 | up |
| DW66\_4534 | hypothetical protein | 2.45 | up |
| DW66\_4535 | water stress/hypersensitive response domain-containing protein | 1.68 | up |
| DW66\_4537 | transporter protein | -3.06 | down |
| DW66\_4538 | transcriptional regulator | -2.19 | down |
| DW66\_4540 | exonuclease | -3.19 | down |
| DW66\_4541 | ATP-dependent DNA ligase | -2.29 | down |
| DW66\_4543 | DEAD/DEAH box helicase | -2.87 | down |
| DW66\_4544 | ICC-like protein phosphoesterase | -3.22 | down |
| DW66\_4546 | deoxycytidine triphosphate deaminase | -2.31 | down |
| DW66\_4553 | Electron transport complex protein RnfE | -1.15 | down |
| DW66\_4557 | hypothetical protein | -2.58 | down |
| DW66\_4558 | argininosuccinate synthase | 1.44 | up |
| DW66\_4560 | dihydroorotase | -1.16 | down |
| DW66\_4562 | anti-oxidant AhpCTSA | 3.75 | up |
| DW66\_4564 | bacterioferritin | 4.15 | up |
| DW66\_4567 | ornithine carbamoyltransferase | -2.61 | down |
| DW66\_4568 | ABC transporter ATP-binding protein | -2.97 | down |
| DW66\_4570 | channel protein | -5.15 | down |
| DW66\_4571 | glycerol kinase | -1.54 | down |
| DW66\_4573 | glycerol-3-phosphate dehydrogenase | -1.68 | down |
| DW66\_4574 | hypothetical protein | -3.88 | down |
| DW66\_4575 | extracellular solute-binding protein | 1.47 | up |
| DW66\_4576 | glutamate/aspartate ABC transporter permease | 2.24 | up |
| DW66\_4577 | polar amino acid ABC transporter inner membrane subunit | 2.34 | up |
| DW66\_4578 | glutamate-aspartate ABC transporter ATP-binding protein | 3.20 | up |
| DW66\_4582 | alpha/beta hydrolase | -2.06 | down |
| DW66\_4583 | transcriptional regulator MetR | -2.52 | down |
| DW66\_4584 | NUDIX hydrolase | -3.41 | down |
| DW66\_4587 | amino acid permease-associated protein | -2.04 | down |
| DW66\_4588 | membrane carboxypeptidase | 4.88 | up |
| DW66\_4590 | FAD-binding 9 siderophore-interacting domain-containing protein | 1.50 | up |
| DW66\_4591 | Integral membrane protein | -1.57 | down |
| DW66\_4593 | TonB-dependent receptor | -4.32 | down |
| DW66\_4594 | carbohydrate-selective porin OprB | -1.51 | down |
| DW66\_4595 | glucose dehydrogenase | 1.84 | up |
| DW66\_4596 | ATP-dependent protease La | 3.27 | up |
| DW66\_4598 | methyltransferase | -3.72 | down |
| DW66\_4599 | methyltransferase | -4.28 | down |
| DW66\_4600 | hypothetical protein | -2.99 | down |
| DW66\_4601 | two component heavy metal response transcriptional regulator | -7.22 | down |
| DW66\_4602 | heavy metal sensor signal transduction histidine kinase | -3.22 | down |
| DW66\_4603 | pyridoxine 5'-phosphate synthase | -2.25 | down |
| DW66\_4604 | DNA repair protein RecO | -4.91 | down |
| DW66\_4605 | GTP-binding protein Era | -1.48 | down |
| DW66\_4606 | ribonuclease III | -1.88 | down |
| DW66\_4607 | signal peptidase I | -2.48 | down |
| DW66\_4608 | GTP-binding protein LepA | -2.75 | down |
| DW66\_4609 | hypothetical protein | -1.08 | down |
| DW66\_4610 | protease Do | -1.47 | down |
| DW66\_4611 | sigma E regulatory protein MucB/RseB | -3.07 | down |
| DW66\_4612 | anti sigma-E protein, RseA | -2.93 | down |
| DW66\_4613 | RNA polymerase sigma factor AlgU | -2.56 | down |
| DW66\_4614 | L-aspartate oxidase | -1.78 | down |
| DW66\_4615 | hypothetical protein | -2.09 | down |
| DW66\_4618 | signal transduction protein | -1.13 | down |
| DW66\_4620 | two component transcriptional regulator | -1.29 | down |
| DW66\_4622 | tricarboxylate transport protein TctC | 1.08 | up |
| DW66\_4625 | ammonia monooxygenase | -1.94 | down |
| DW66\_4626 | uracil-DNA glycosylase | -3.67 | down |
| DW66\_4627 | enoyl-CoA hydratase/isomerase | 2.86 | up |
| DW66\_4630 | pseudouridine synthase | -2.41 | down |
| DW66\_4631 | (R)-3-hydroxydecanoyl-ACP:CoA transacylase | 2.49 | up |
| DW66\_4632 | sulfate transporter | -1.39 | down |
| DW66\_4633 | hypothetical protein | -2.61 | down |
| DW66\_4634 | Methyltransferase | -2.11 | down |
| DW66\_4635 | hypothetical protein | -3.96 | down |
| DW66\_4636 | glycoside hydrolase | -1.33 | down |
| DW66\_4637 | integral membrane sensor signal transduction histidine kinase | -1.70 | down |
| DW66\_4649 | NAD-dependent epimerase/dehydratase | 1.97 | up |
| DW66\_4650 | beta-lactamase domain-containing protein | -2.55 | down |
| DW66\_4651 | transcriptional regulator LysR | -1.58 | down |
| DW66\_4652 | carboxyphosphonoenolpyruvate phosphonomutase | -2.73 | down |
| DW66\_4653 | drug resistance transporter EmrB | -3.54 | down |
| DW66\_4654 | transcriptional regulator TetR | -2.36 | down |
| DW66\_4655 | RND efflux transporter, MFP subunit | -4.65 | down |
| DW66\_4656 | hydrophobe/amphiphile efflux-1 | -2.91 | down |
| DW66\_4658 | porin | -4.30 | down |
| DW66\_4659 | hypothetical protein | 2.48 | up |
| DW66\_4660 | 4-carboxymuconolactone decarboxylase | 3.09 | up |
| DW66\_4661 | 3-oxoadipate enol-lactonase | 2.51 | up |
| DW66\_4662 | 3-carboxy-cis,cis-muconate cycloisomerase | 1.95 | up |
| DW66\_4663 | metabolite/H(+) symporter | 2.12 | up |
| DW66\_4666 | 3-oxoadipate:succinyl-CoA transferase subunit A | -1.59 | down |
| DW66\_4667 | benzoate transporter | -1.61 | down |
| DW66\_4670 | phosphate transporter | -3.02 | down |
| DW66\_4673 | group 1 glycosyl transferase | 3.68 | up |
| DW66\_4674 | hypothetical protein | 2.69 | up |
| DW66\_4675 | hypothetical protein | 2.26 | up |
| DW66\_4676 | formyltetrahydrofolate deformylase | -1.56 | down |
| DW66\_4678 | exonuclease I | -1.33 | down |
| DW66\_4682 | 2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases | -1.17 | down |
| DW66\_4683 | hypothetical protein | -2.51 | down |
| DW66\_4684 | Fe-S type hydro-lyase subunit alpha | -1.84 | down |
| DW66\_4685 | nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase | -3.73 | down |
| DW66\_4686 | Histone acetyltransferase HPA2 and related acetyltransferases | -2.37 | down |
| DW66\_4687 | Isopropylmalate/homocitrate/citramalate synthases | -1.09 | down |
| DW66\_4688 | glutamine amidotransferase | 2.01 | up |
| DW66\_4689 | phospholipase | -2.64 | down |
| DW66\_4690 | hypothetical protein | -2.36 | down |
| DW66\_4691 | hypothetical protein | -2.20 | down |
| DW66\_4692 | *beta*-lactamase | -3.01 | down |
| DW66\_4694 | hemolysin | -2.12 | down |
| DW66\_4696 | Acyl carrier protein phosphodiesterase | -1.79 | down |
| DW66\_4697 | transcriptional regulator ArsR | -1.92 | down |
| DW66\_4698 | NADH:flavin oxidoreductase | -1.41 | down |
| DW66\_4699 | hypothetical protein | -2.46 | down |
| DW66\_4700 | NAD-dependent epimerase/dehydratase | -2.42 | down |
| DW66\_4701 | chromosome replication initiation inhibitor protein | -2.01 | down |
| DW66\_4702 | lysine exporter protein LysE/YggA | 1.76 | up |
| DW66\_4704 | hydroxypyruvate isomerase | -3.18 | down |
| DW66\_4705 | transcriptional regulator | -2.33 | down |
| DW66\_4706 | glucose dehydrogenase | -6.44 | down |
| DW66\_4707 | glucose dehydrogenase | -1.86 | down |
| DW66\_4709 | Iron-regulated protein A precursor | -1.85 | down |
| DW66\_4710 | thiol oxidoreductase with 2 cytochrome c heme-binding sites | -3.05 | down |
| DW66\_4715 | hypothetical protein | -1.58 | down |
| DW66\_4716 | lipopolysaccharide kinase | -5.43 | down |
| DW66\_4717 | type 11 methyltransferase | -5.52 | down |
| DW66\_4718 | integral membrane sensor signal transduction histidine kinase | -1.89 | down |
| DW66\_4719 | two component transcriptional regulator | -1.45 | down |
| DW66\_4720 | PAP2 protein | -6.79 | down |
| DW66\_4721 | chaperonin GroEL | 4.37 | up |
| DW66\_4722 | co-chaperonin GroES | 4.50 | up |
| DW66\_4724 | exclusion suppressor FxsA | 2.11 | up |
| DW66\_4726 | Peptide chain release factor RF-3 | -2.99 | down |
| DW66\_4727 | methylated-DNA-(protein)-cysteine S-methyltransferase DNA binding protein | 1.53 | up |
| DW66\_4728 | AmpG-related permease | -1.56 | down |
| DW66\_4729 | transporter protein | -4.59 | down |
| DW66\_4730 | mechanosensitive ion channel protein MscS | -1.90 | down |
| DW66\_4732 | 2-dehydropantoate 2-reductase | -1.28 | down |
| DW66\_4734 | ATP-cobalamin adenosyltransferase | 1.67 | up |
| DW66\_4735 | Mutator mutT protein (7,8-dihydro-8-oxoguanine-triphosphatase) | -1.03 | down |
| DW66\_4739 | hypothetical protein | -2.28 | down |
| DW66\_4740 | UDP-3-0-acyl N-acetylglucosamine deacetylase | 1.96 | up |
| DW66\_4741 | cell division protein FtsZ | 2.34 | up |
| DW66\_4744 | D-alanine--D-alanine ligase | 1.13 | up |
| DW66\_4745 | UDP-N-acetylmuramate--L-alanine ligase | 1.85 | up |
| DW66\_4746 | undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase | 2.00 | up |
| DW66\_4750 | UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D- alanine ligase | 1.65 | up |
| DW66\_4751 | UDP-N-acetylmuramoylalanyl-D-glutamate--2, 6-diaminopimelate ligase | 1.38 | up |
| DW66\_4753 | cell division protein FtsL | -1.48 | down |
| DW66\_4754 | S-adenosyl-methyltransferase MraW | -1.39 | down |
| DW66\_4756 | ribosomal RNA small subunit methyltransferase I | -1.17 | down |
| DW66\_4758 | endonuclease distantly related to archaeal Holliday junction resolvase | -1.42 | down |
| DW66\_4759 | phosphoheptose isomerase | -2.77 | down |
| DW66\_4760 | transport-associated protein | -2.41 | down |
| DW66\_4761 | lipoprotein | -1.56 | down |
| DW66\_4762 | ClpXP protease specificity-enhancing factor | -1.09 | down |
| DW66\_4764 | ubiquinol-cytochrome c reductase, cytochrome c1 | 3.73 | up |
| DW66\_4765 | cytochrome b/b6 domain-containing protein | 3.65 | up |
| DW66\_4766 | ubiquinol-cytochrome c reductase, iron-sulfur subunit | 2.43 | up |
| DW66\_4767 | 30S ribosomal protein S9 | -2.36 | down |
| DW66\_4768 | 50S ribosomal protein L13 | -2.68 | down |
| DW66\_4770 | transcriptional regulator AraC | -1.84 | down |
| DW66\_4771 | ATPase AFG1 | -1.69 | down |
| DW66\_4772 | tryptophanyl-tRNA synthetase | -1.36 | down |
| DW66\_4773 | Alpha/beta hydrolase | -2.27 | down |
| DW66\_4774 | hypothetical protein | 1.70 | up |
| DW66\_4776 | transcriptional regulator AsnC | -1.09 | down |
| DW66\_4778 | sulfate adenylyltransferase subunit 2 | -3.25 | down |
| DW66\_4779 | hypothetical protein | -1.37 | down |
| DW66\_4780 | 2-alkenal reductase | -1.67 | down |
| DW66\_4784 | amino acid ABC transporter periplasmic amino acid-binding protein | 2.09 | up |
| DW66\_4788 | molybdopterin biosynthesis protein MoaE | -1.83 | down |
| DW66\_4789 | molybdopterin converting factor subunit 1 | -1.38 | down |
| DW66\_4790 | molybdenum cofactor biosynthesis protein MoaC | -1.50 | down |
| DW66\_4791 | PhoH protein | 3.66 | up |
| DW66\_4792 | polysaccharide deacetylase | -1.35 | down |
| DW66\_4793 | hypothetical protein | -2.14 | down |
| DW66\_4794 | GDP-mannose 6-dehydrogenase | -1.63 | down |
| DW66\_4795 | glycosyl transferase Alg8 | -4.56 | down |
| DW66\_4796 | type IV pilus assembly PilZ | -3.92 | down |
| DW66\_4797 | Sel1 domain-containing protein | -3.84 | down |
| DW66\_4798 | outer membrane protein AlgE | -2.59 | down |
| DW66\_4799 | carbohydrate-binding and sugar hydrolysis protein | -2.25 | down |
| DW66\_4800 | alginate biosynthesis protein AlgX | -2.98 | down |
| DW66\_4801 | poly(beta-D-mannuronate) lyase | -1.65 | down |
| DW66\_4802 | alginate o-acetyltransferase AlgI | -3.05 | down |
| DW66\_4803 | protein AlgJ | -1.70 | down |
| DW66\_4804 | alginate O-acetyltransferase | 2.12 | up |
| DW66\_4805 | mannose-1-phosphate guanylyltransferase/mannose-6-phosphate isomerase | 1.70 | up |
| DW66\_4807 | short-chain dehydrogenase | -1.09 | down |
| DW66\_4808 | short-chain dehydrogenase/reductase | 5.68 | up |
| DW66\_4809 | RND efflux system outer membrane lipoprotein | 5.00 | up |
| DW66\_4810 | secretion protein HlyD | 4.75 | up |
| DW66\_4811 | transporter protein | 3.28 | up |
| DW66\_4812 | transcriptional regulator LysR | -1.78 | down |
| DW66\_4813 | UspA domain-containing protein | 1.91 | up |
| DW66\_4814 | secretion protein HlyD | -2.00 | down |
| DW66\_4815 | Na+-dependent transporters | -11.98 | down |
| DW66\_4816 | fusaric acid resistance protein region | -3.68 | down |
| DW66\_4817 | RND efflux system outer membrane lipoprotein | -4.46 | down |
| DW66\_4819 | D-isomer specific 2-hydroxyacid dehydrogenase NAD-binding protein | -2.50 | down |
| DW66\_4820 | Permease of the drug/metabolite transporter | 1.97 | up |
| DW66\_4822 | transcriptional regulator AraC | 1.31 | up |
| DW66\_4823 | TonB-dependent siderophore receptor | -3.22 | down |
| DW66\_4824 | anti-FecI sigma factor FecR | -4.35 | down |
| DW66\_4825 | RNA polymerase sigma-30 factor | -5.53 | down |
| DW66\_4826 | hypothetical protein | -4.68 | down |
| DW66\_4827 | PepSY-associated TM helix domain-containing protein | -4.13 | down |
| DW66\_4828 | hypothetical protein | -4.75 | down |
| DW66\_4829 | ribosomal subunit interface protein | 4.71 | up |
| DW66\_4831 | phosphate-starvation-inducible E | 1.58 | up |
| DW66\_4832 | hypothetical protein | 2.12 | up |
| DW66\_4833 | leucine dehydrogenase | 2.15 | up |
| DW66\_4835 | maleylacetoacetate isomerase | 1.50 | up |
| DW66\_4837 | homogentisate 1,2-dioxygenase | -1.31 | down |
| DW66\_4838 | transcriptional regulator IclR | -2.57 | down |
| DW66\_4839 | short-chain dehydrogenase/reductase SDR | -2.05 | down |
| DW66\_4840 | hypothetical protein | -2.95 | down |
| DW66\_4841 | alpha/beta hydrolase fold protein | 1.00 | up |
| DW66\_4842 | LrgB protein | -1.91 | down |
| DW66\_4843 | LrgA protein | -1.05 | down |
| DW66\_4845 | flavodoxin subunit alpha | -2.36 | down |
| DW66\_4846 | PAS/PAC sensor protein | -2.00 | down |
| DW66\_4847 | hypothetical protein | -1.04 | down |
| DW66\_4849 | membrane protein | -4.25 | down |
| DW66\_4851 | hypothetical protein | -1.26 | down |
| DW66\_4852 | HopJ type III effector protein | -1.36 | down |
| DW66\_4855 | cytochrome B561 | 2.90 | up |
| DW66\_4856 | signal peptide protein | 4.01 | up |
| DW66\_4857 | acetyl-CoA acetyltransferase | 1.14 | up |
| DW66\_4859 | methylenetetrahydrofolate reductase | -1.85 | down |
| DW66\_4862 | hypothetical protein | 3.02 | up |
| DW66\_4863 | carbon starvation protein CstA | 1.91 | up |
| DW66\_4864 | type IV pilus assembly PilZ | 1.61 | up |
| DW66\_4865 | uracil-xanthine permease | 1.60 | up |
| DW66\_4866 | DNA repair protein RadA | -2.38 | down |
| DW66\_4867 | large conductance mechanosensitive channel protein MscL | 1.52 | up |
| DW66\_4869 | transcriptional regulator | 1.26 | up |
| DW66\_4871 | Cyanide insensitive terminal oxidase, subunit III | 4.40 | up |
| DW66\_4872 | cytochrome d ubiquinol oxidase subunit II | 2.68 | up |
| DW66\_4873 | cytochrome bd ubiquinol oxidase subunit I | 2.20 | up |
| DW66\_4874 | major facilitator superfamily protein | -2.86 | down |
| DW66\_4877 | protocatechuate 3,4-dioxygenase subunit alpha | -1.08 | down |
| DW66\_4878 | protocatechuate 3,4-dioxygenase subunit beta | -1.29 | down |
| DW66\_4879 | metallopeptidase, zinc binding protein | 1.23 | up |
| DW66\_4881 | *gamma*-glutamyltransferase | 1.46 | up |
| DW66\_4883 | NAD(P)H dehydrogenase (quinone) | -2.25 | down |
| DW66\_4885 | membrane protein | -4.64 | down |
| DW66\_4886 | transcriptional regulator LysR | -1.30 | down |
| DW66\_4887 | CDP-alcohol phosphatidyltransferase | -1.78 | down |
| DW66\_4892 | hypothetical protein | -2.24 | down |
| DW66\_4895 | 3-hydroxyisobutyrate dehydrogenase | -1.04 | down |
| DW66\_4899 | 3-hydroxyisobutyrate dehydrogenase | 6.03 | up |
| DW66\_4900 | methylmalonate-semialdehyde dehydrogenase | 5.11 | up |
| DW66\_4901 | transcriptional regulator LysR | -2.63 | down |
| DW66\_4905 | exodeoxyribonuclease V subunit alpha | 2.28 | up |
| DW66\_4906 | exodeoxyribonuclease V subunit beta | 2.06 | up |
| DW66\_4907 | exodeoxyribonuclease V subunit gamma | 1.30 | up |
| DW66\_4908 | sulfite oxidase, YedZ subunit | -3.31 | down |
| DW66\_4909 | TMAO/DMSO reductase | -2.51 | down |
| DW66\_4910 | CDP-diacylglycerol--serine O-phosphatidyltransferase | -1.03 | down |
| DW66\_4911 | ketol-acid reductoisomerase | 1.46 | up |
| DW66\_4914 | hypothetical protein | -1.21 | down |
| DW66\_4916 | penicillin-binding protein 1B | -2.10 | down |
| DW66\_4917 | hypothetical protein | -3.89 | down |
| DW66\_4919 | TfoX domain-containing protein | 3.36 | up |
| DW66\_4920 | lipoprotein | -1.74 | down |
| DW66\_4921 | hemin importer, ATP-binding subunit | -1.23 | down |
| DW66\_4922 | transport system permease | -2.09 | down |
| DW66\_4923 | periplasmic binding protein | -3.09 | down |
| DW66\_4924 | Rieske (2Fe-2S) domain-containing protein | -3.49 | down |
| DW66\_4925 | sugar fermentation stimulation protein A | -2.67 | down |
| DW66\_4926 | Valine--pyruvate aminotransferase | -1.86 | down |
| DW66\_4928 | glutamyl-Q tRNA(Asp) synthetase | -2.66 | down |
| DW66\_4935 | 3-methyl-2-oxobutanoate hydroxymethyltransferase | -1.06 | down |
| DW66\_4937 | flagellar motor switch protein FliN | -3.36 | down |
| DW66\_4940 | hypothetical protein | -1.22 | down |
| DW66\_4943 | antibiotic biosynthesis monooxygenase | 1.41 | up |
| DW66\_4948 | tRNA pseudouridine synthase B | -1.41 | down |
| DW66\_4949 | ribosome-binding factor A | -2.72 | down |
| DW66\_4950 | translation initiation factor IF-2 | -1.00 | down |
| DW66\_4951 | transcription elongation factor NusA | -1.35 | down |
| DW66\_4952 | ribosome maturation factor rimP | -1.80 | down |
| DW66\_4953 | triosephosphate isomerase | -3.66 | down |
| DW66\_4959 | Permeases | -1.82 | down |
| DW66\_4960 | transcription elongation factor GreA | -1.22 | down |
| DW66\_4963 | dihydrodipicolinate reductase | 1.20 | up |
| DW66\_4965 | molecular chaperone DnaK | 4.51 | up |
| DW66\_4966 | heat shock protein GrpE | 3.66 | up |
| DW66\_4972 | transcriptional regulator | 1.01 | up |
| DW66\_4973 | L-lactate transport | 3.32 | up |
| DW66\_4974 | L-lactate dehydrogenase | 3.21 | up |
| DW66\_4975 | D-lactate dehydrogenase | 1.55 | up |
| DW66\_4981 | transporter protein | -1.29 | down |
| DW66\_4984 | glucarate dehydratase | -1.93 | down |
| DW66\_4985 | transporter protein | -4.49 | down |
| DW66\_4987 | alcohol dehydrogenase | 1.45 | up |
| DW66\_4992 | phosphohistidine phosphatase, SixA | -6.00 | down |
| DW66\_4993 | histone deacetylase protein | -1.86 | down |
| DW66\_4994 | NAD(FAD)-utilizing dehydrogenases | -2.56 | down |
| DW66\_4995 | DEAD/DEAH box helicase | -2.68 | down |
| DW66\_4996 | Permease of the drug/metabolite transporter | -3.66 | down |
| DW66\_4997 | transcriptional regulator AsnC | 1.17 | up |
| DW66\_4998 | DNA polymerase III subunit epsilon | -2.39 | down |
| DW66\_4999 | hypothetical protein | -2.14 | down |
| DW66\_5001 | hypothetical protein | -2.40 | down |
| DW66\_5003 | ATP-dependent helicase HrpB | -1.77 | down |
| DW66\_5005 | transporter | -2.10 | down |
| DW66\_5006 | hypothetical protein | -2.48 | down |
| DW66\_5008 | hypothetical protein | -1.12 | down |
| DW66\_5009 | pseudouridine synthase | -1.14 | down |
| DW66\_5011 | acyl-CoA dehydrogenase domain-containing protein | 1.38 | up |
| DW66\_5012 | hypothetical protein | -2.94 | down |
| DW66\_5013 | hypothetical protein | -2.33 | down |
| DW66\_5014 | integral membrane sensor signal transduction histidine kinase | -1.76 | down |
| DW66\_5015 | phosphomethylpyrimidine kinase | -1.63 | down |
| DW66\_5016 | thiamine-phosphate pyrophosphorylase | -1.51 | down |
| DW66\_5018 | Sel1 domain-containing protein | -1.37 | down |
| DW66\_5019 | hypothetical protein | -2.55 | down |
| DW66\_5023 | apolipoprotein N-acyltransferase | -1.50 | down |
| DW66\_5024 | membrane protein | -1.38 | down |
| DW66\_5025 | hypothetical protein | 5.84 | up |
| DW66\_5027 | rare lipoprotein B | 1.12 | up |
| DW66\_5028 | DNA polymerase III subunit delta | -1.35 | down |
| DW66\_5029 | D-isomer specific 2-hydroxyacid dehydrogenase, N | -1.56 | down |
| DW66\_5033 | lipoyltransferase | -1.23 | down |
| DW66\_5034 | lipoate regulatory protein YbeD | -1.23 | down |
| DW66\_5035 | serine-type D-Ala-D-Ala carboxypeptidase | -1.18 | down |
| DW66\_5037 | lytic murein transglycosylase B | -2.44 | down |
| DW66\_5038 | rod shape-determining protein RodA | -2.40 | down |
| DW66\_5039 | penicillin-binding protein 2 | -2.97 | down |
| DW66\_5040 | LSU m3Psi1915 methyltransferase RlmH | -1.86 | down |
| DW66\_5041 | iojap protein | -1.13 | down |
| DW66\_5043 | *gamma*-glutamyl phosphate reductase | -1.26 | down |
| DW66\_5044 | 3-methyladenine DNA glycosylase | -6.48 | down |
| DW66\_5045 | N-acetyltransferase GCN5 | -5.55 | down |
| DW66\_5048 | LrgA protein | -1.93 | down |
| DW66\_5050 | 50S ribosomal protein L11 methyltransferase | -1.96 | down |
| DW66\_5051 | CDGSH-type zinc finger protein | -1.71 | down |
| DW66\_5055 | hypothetical protein | -5.90 | down |
| DW66\_5058 | multiple antibiotic resistance (MarC)-like protein | -2.72 | down |
| DW66\_5059 | hypothetical protein | -4.54 | down |
| DW66\_5060 | hypothetical protein | -3.12 | down |
| DW66\_5064 | precorrin-3B synthase | -1.77 | down |
| DW66\_5065 | hypothetical protein | -2.41 | down |
| DW66\_5066 | precorrin-6y C5,15-methyltransferase (decarboxylating) CbiE subunit | -3.31 | down |
| DW66\_5067 | cobalt-precorrin-6A synthase | -2.02 | down |
| DW66\_5068 | cobalt-precorrin-6x reductase | -1.85 | down |
| DW66\_5069 | activity regulator of membrane protease YbbK | -2.14 | down |
| DW66\_5075 | TonB-dependent copper receptor | -1.28 | down |
| DW66\_5076 | peptidase | -1.71 | down |
| DW66\_5077 | D-alanine/D-serine/glycine permease | -1.85 | down |
| DW66\_5078 | urea ABC transporter urea binding protein | -2.36 | down |
| DW66\_5079 | urea ABC transporter permease UrtB | -6.19 | down |
| DW66\_5080 | urea ABC transporter permease UrtC | -5.20 | down |
| DW66\_5081 | branched-chain amino acid ABC transporter ATP-binding protein | -3.50 | down |
| DW66\_5082 | urea ABC transporter ATP-binding protein | -2.50 | down |
| DW66\_5083 | branched chain amino acid ABC transporter ATP-binding protein | 1.21 | up |
| DW66\_5084 | Chaperone-modulator protein CbpM | 1.46 | up |
| DW66\_5085 | chaperone DnaJ domain-containing protein | 1.14 | up |
| DW66\_5086 | molecular chaperone-like protein | -3.72 | down |
| DW66\_5088 | PsiF repeat-containing protein | 3.44 | up |
| DW66\_5090 | membrane protein | -1.73 | down |
| DW66\_5091 | alpha/beta hydrolase fold protein | -2.32 | down |
| DW66\_5092 | DNA-binding transcriptional activator OsmE | -1.95 | down |
| DW66\_5093 | ferritin Dps protein | -1.19 | down |
| DW66\_5094 | AsmA protein | -1.17 | down |
| DW66\_5095 | Phage infection protein | -3.51 | down |
| DW66\_5096 | transcriptional regulator TetR | -4.07 | down |
| DW66\_5097 | N-acylglucosamine 2-epimerase | -1.34 | down |
| DW66\_5099 | Branched chain amino acid ABC transporter ATP-binding protein | 1.59 | up |
| DW66\_5100 | branched chain amino acid ABC transporter ATP-binding protein | 2.07 | up |
| DW66\_5103 | extracellular ligand-binding receptor | 3.08 | up |
| DW66\_5104 | nicotinate phosphoribosyltransferase | -1.15 | down |
| DW66\_5106 | azurin | 4.74 | up |
| DW66\_5107 | Lysine decarboxylase | -1.63 | down |
| DW66\_5108 | oxidoreductase | -2.68 | down |
| DW66\_5109 | replicative DNA helicase | -2.17 | down |
| DW66\_5110 | 50S ribosomal protein L9 | -1.17 | down |
| DW66\_5111 | hypothetical protein | -1.49 | down |
| DW66\_5114 | 23S rRNA (guanosine-2'-O-)-methyltransferase | 1.22 | up |
| DW66\_5115 | ribonuclease R | 1.15 | up |
| DW66\_5116 | hypothetical protein | -1.29 | down |
| DW66\_5118 | binding-protein-dependent transport system inner membrane protein | -1.33 | down |
| DW66\_5119 | integral membrane protein | -3.36 | down |
| DW66\_5120 | type VI secretion system effector | -4.42 | down |
| DW66\_5123 | ATP phosphoribosyltransferase regulatory subunit | -2.59 | down |
| DW66\_5127 | RNA-binding protein Hfq | 1.42 | up |
| DW66\_5133 | iron-sulfur cluster binding protein | -1.70 | down |
| DW66\_5134 | membrane protein | -3.10 | down |
| DW66\_5136 | ribosome-associated GTPase | -1.13 | down |
| DW66\_5137 | flagellar motor protein MotB | -1.20 | down |
| DW66\_5138 | flagellar motor protein MotA | -1.22 | down |
| DW66\_5139 | hypothetical protein | -1.22 | down |
| DW66\_5143 | phosphoserine phosphatase SerB | -2.36 | down |
| DW66\_5147 | Transporter | -1.21 | down |
| DW66\_5150 | hypothetical protein | -2.45 | down |
| DW66\_5151 | Icc protein | -2.53 | down |
| DW66\_5153 | ADP-ribose pyrophosphatase NudF | 1.03 | up |
| DW66\_5154 | lipoprotein | -2.25 | down |
| DW66\_5155 | hydroxymethylpyrimidine transporter CytX | -1.00 | down |
| DW66\_5157 | type I secretion outer membrane protein TolC | 1.10 | up |
| DW66\_5159 | 3-deoxy-D-manno-octulosonic-acid transferase | -2.14 | down |
| DW66\_5160 | transcriptional regulator LysR | -2.46 | down |
| DW66\_5161 | small multidrug resistance protein | -2.02 | down |
| DW66\_5167 | O-antigen polymerase | -2.37 | down |
| DW66\_5168 | toluene tolerance protein Ttg8 | -1.34 | down |
| DW66\_5169 | group 1 glycosyl transferase | 1.34 | up |
| DW66\_5171 | Glycosyltransferase | -1.48 | down |
| DW66\_5172 | LmbE protein | -1.63 | down |
| DW66\_5173 | Mig-14 protein | -1.64 | down |
| DW66\_5174 | group 1 glycosyl transferase | -1.13 | down |
| DW66\_5175 | carbamoyltransferase | -1.04 | down |
| DW66\_5176 | hypothetical protein | -2.37 | down |
| DW66\_5178 | trifunctional transcriptional regulator/proline dehydrogenase/pyrroline-5-carboxylate dehydrogenase | 2.07 | up |
| DW66\_5181 | peptidase U62 modulator of DNA gyrase | 1.39 | up |
| DW66\_5182 | TldE/PmbA protein | 2.10 | up |
| DW66\_5184 | ATP-dependent RNA helicase DbpA | -2.05 | down |
| DW66\_5185 | hypothetical protein | -3.03 | down |
| DW66\_5186 | integral membrane protein YccS | -1.34 | down |
| DW66\_5187 | amino acid ABC transporter periplasmic amino acid-binding protein | -1.47 | down |
| DW66\_5188 | acetyltransferase | -1.19 | down |
| DW66\_5191 | response regulator receiver modulated diguanylate cyclase/phosphodiesterase with PAS/PAC sensor(s) | 3.43 | up |
| DW66\_5195 | phosphoglycerate kinase | -1.54 | down |
| DW66\_5196 | D-erythrose-4-phosphate dehydrogenase | -1.77 | down |
| DW66\_5198 | transcriptional regulator ArsR | 1.46 | up |
| DW66\_5199 | S-adenosylmethionine synthetase | 2.43 | up |
| DW66\_5202 | cytochrome c class II | -2.71 | down |
| DW66\_5203 | hypothetical protein | -2.21 | down |
| DW66\_5204 | MltA domain-containing protein | -1.32 | down |
| DW66\_5205 | membrane protein | -2.18 | down |
| DW66\_5207 | sodium/hydrogen exchanger | -1.21 | down |
| DW66\_5212 | extracellular solute-binding protein | -2.08 | down |
| DW66\_5213 | hypothetical protein | -3.80 | down |
| DW66\_5214 | DEAD/DEAH box helicase | -1.72 | down |
| DW66\_5215 | Protein yceI precursor | 1.25 | up |
| DW66\_5217 | amine oxidase | -1.76 | down |
| DW66\_5218 | hypothetical protein | -15.70 | down |
| DW66\_5220 | 16S ribosomal RNA methyltransferase RsmE | -1.07 | down |
| DW66\_5221 | hemolysin III channel protein | -2.77 | down |
| DW66\_5225 | CheW protein | -1.76 | down |
| DW66\_5227 | response regulator receiver protein | -1.14 | down |
| DW66\_5228 | glutathione synthetase | -1.63 | down |
| DW66\_5229 | TonB protein | -1.65 | down |
| DW66\_5231 | Holliday junction resolvase-like protein | -2.08 | down |
| DW66\_5232 | bifunctional protein pyrR | -1.10 | down |
| DW66\_5233 | aspartate carbamoyltransferase catalytic subunit | -1.14 | down |
| DW66\_5235 | ATP-dependent protease peptidase subunit | 4.41 | up |
| DW66\_5236 | ATP-dependent protease, ATP-binding subunit HslU | 5.04 | up |
| DW66\_5238 | poly(R)-hydroxyalkanoic acid synthase, class II | -1.51 | down |
| DW66\_5242 | poly(hydroxyalcanoate) granule associated protein GA2 | 2.26 | up |
| DW66\_5244 | hypothetical protein | -1.14 | down |
| DW66\_5246 | sterol-binding domain-containing protein | -1.27 | down |
| DW66\_5248 | phosphoribosyl-AMP cyclohydrolase | 1.71 | up |
| DW66\_5250 | twin arginine translocase protein A | -1.88 | down |
| DW66\_5251 | sec-independent translocase | -3.20 | down |
| DW66\_5252 | sec-independent protein translocase, TatC subunit | -2.61 | down |
| DW66\_5253 | 16S ribosomal RNA methyltransferase RsmE | -2.37 | down |
| DW66\_5255 | methyl-accepting chemotaxis sensory transducer | -2.92 | down |
| DW66\_5257 | polar amino acid ABC transporter inner membrane subunit | -1.36 | down |
| DW66\_5260 | glucan biosynthesis protein G | -2.56 | down |
| DW66\_5263 | hypothetical protein | -2.79 | down |
| DW66\_5264 | hypothetical protein | -3.28 | down |
| DW66\_5265 | hypothetical protein | -1.74 | down |
| DW66\_5266 | N-formylglutamate amidohydrolase | -1.16 | down |
| DW66\_5267 | imidazolonepropionase | -1.62 | down |
| DW66\_5268 | amino acid ABC transporter permease | -2.72 | down |
| DW66\_5271 | hypothetical protein | -2.32 | down |
| DW66\_5272 | histidine utilization repressor | -2.02 | down |
| DW66\_5273 | N-formimino-L-glutamate deiminase | 1.68 | up |
| DW66\_5274 | lipocalin | -3.17 | down |
| DW66\_5275 | lipoprotein | -2.57 | down |
| DW66\_5279 | Fe-S-oxidoreductase | -4.71 | down |
| DW66\_5280 | PhoP/Q-regulated protein PqaA | -1.85 | down |
| DW66\_5282 | thiamine biosynthesis protein ThiI | -2.97 | down |
| DW66\_5284 | chorismate mutase | -3.31 | down |
| DW66\_5287 | hypothetical protein | -1.60 | down |
| DW66\_5288 | RNA methyltransferase | -2.52 | down |
| DW66\_5290 | preprotein translocase subunit SecB | -2.22 | down |
| DW66\_5291 | glutaredoxin 3 | -1.90 | down |
| DW66\_5292 | rhodanese domain-containing protein | -1.12 | down |
| DW66\_5296 | divergent polysaccharide deacetylase | -1.02 | down |
| DW66\_5297 | hypothetical protein | -2.33 | down |
| DW66\_5298 | choline/carnitine/betaine transporter | -2.65 | down |
| DW66\_5299 | transcriptional regulator BetI | -1.44 | down |
| DW66\_5302 | potassium/proton antiporter | -2.02 | down |
| DW66\_5303 | potassium efflux protein KefA | -1.14 | down |
| DW66\_5307 | transcriptional regulator LysR | -2.53 | down |
| DW66\_5308 | transporter protein | -1.59 | down |
| DW66\_5309 | hypothetical protein | -2.45 | down |
| DW66\_5311 | hypothetical protein | -10.08 | down |
| DW66\_5314 | sporulation domain-containing protein | -2.00 | down |
| DW66\_5315 | 3-dehydroquinate synthase | -1.36 | down |
| DW66\_5317 | type IV pilus secretin PilQ | -3.01 | down |
| DW66\_5318 | type IV pili biogenesis protein PilP | -3.86 | down |
| DW66\_5319 | fimbrial assembly protein | -2.48 | down |
| DW66\_5320 | type IV pili biogenesis protein PilM | -1.30 | down |
| DW66\_5325 | primosome assembly protein PriA | -1.77 | down |
| DW66\_5326 | arginyl-tRNA synthetase | -1.41 | down |
| DW66\_5329 | NLP/P60 protein | -1.91 | down |
| DW66\_5330 | twitching motility protein | -1.88 | down |
| DW66\_5333 | Integral membrane protein YggT | 1.06 | up |
| DW66\_5334 | homoserine O-acetyltransferase | -1.90 | down |
| DW66\_5335 | methionine biosynthesis protein MetW | 1.29 | up |
| DW66\_5336 | hypothetical protein | 4.30 | up |
| DW66\_5337 | dITP/XTP pyrophosphatase | 3.68 | up |
| DW66\_5339 | Phosphotransferase system IIC components, glucose/maltose/N-acetylglucosamine-specific | -3.15 | down |
| DW66\_5340 | tRNA (guanine-N(7)-)-methyltransferase | -1.90 | down |
| DW66\_5341 | thiazole synthase | -2.24 | down |
| DW66\_5342 | sulfur carrier protein ThiS | -2.28 | down |
| DW66\_5343 | hypothetical protein | -2.75 | down |
| DW66\_5344 | peptidoglycan transglycosylase | -1.74 | down |
| DW66\_5345 | RNA polymerase factor sigma-32 | -1.56 | down |
| DW66\_5348 | signal recognition particle-docking protein FtsY | -1.70 | down |
| DW66\_5349 | hypothetical protein | -2.90 | down |
| DW66\_5350 | peptidase M16 domain-containing protein | -2.87 | down |
| DW66\_5353 | peptidase M16 domain-containing protein | -3.32 | down |
| DW66\_5354 | peptidase M16 domain-containing protein | -2.94 | down |
| DW66\_5355 | alpha/beta hydrolase fold protein | -1.34 | down |
| DW66\_5359 | hypothetical protein | 1.59 | up |
| DW66\_5361 | phosphopantetheine adenylyltransferase | -1.58 | down |
| DW66\_5362 | 4Fe-4S ferredoxin | -1.45 | down |
| DW66\_5363 | formamidopyrimidine-DNA glycosylase | -1.40 | down |
| DW66\_5364 | signal transduction protein | -2.85 | down |
| DW66\_5365 | intracellular peptidase | -1.37 | down |
| DW66\_5366 | LSU m5C1962 methyltransferase RlmI | -1.75 | down |
| DW66\_5368 | hypothetical protein | -2.75 | down |
| DW66\_5370 | Phosphoserine phosphatase | -1.49 | down |
| DW66\_5371 | sodium:dicarboxylate symporter | -4.50 | down |
| DW66\_5373 | integral membrane protein | -1.98 | down |
| DW66\_5375 | metal dependent phosphohydrolase | -2.82 | down |
| DW66\_5376 | ABC transporter substrate-binding protein | -1.43 | down |
| DW66\_5377 | 2-aminoethylphosphonate ABC transporter permease | -5.18 | down |
| DW66\_5378 | 2-aminoethylphosphonate ABC transporter ATP-binding protein | -5.51 | down |
| DW66\_5379 | transcriptional regulator LysR | -2.17 | down |
| DW66\_5383 | prolipoprotein diacylglyceryl transferase | -2.79 | down |
| DW66\_5384 | hypothetical protein | -3.66 | down |
| DW66\_5389 | integral membrane protein | 2.08 | up |
| DW66\_5390 | threonine dehydratase | -2.55 | down |
| DW66\_5392 | DNA-binding protein | -2.34 | down |
| DW66\_5394 | SdiA-regulated domain-containing protein | -3.38 | down |
| DW66\_5395 | fumarylacetoacetate (FAA) hydrolase | 1.28 | up |
| DW66\_5397 | hypothetical protein | -1.40 | down |
| DW66\_5400 | periplasmic binding protein from ABC-type transporter | -2.79 | down |
| DW66\_5401 | Purine nucleoside phosphorylase | -2.18 | down |
| DW66\_5402 | 2OG-Fe(II) oxygenase | -3.76 | down |
| DW66\_5403 | hypothetical protein | -1.58 | down |
| DW66\_5404 | lipase | -2.83 | down |
| DW66\_5405 | Thiol-disulfide isomerase and thioredoxins | -4.79 | down |
| DW66\_5407 | hexapeptide repeat-containing transferase | -2.54 | down |
| DW66\_5408 | peptidase S45 penicillin amidase | 1.12 | up |
| DW66\_5409 | hydrolase | 1.09 | up |
| DW66\_5410 | NLPA lipoprotein | -6.66 | down |
| DW66\_5411 | sigma-54 dependent transcriptional regulator | -6.29 | down |
| DW66\_5412 | hypothetical protein | -6.38 | down |
| DW66\_5413 | sulfate ABC transporter ATPase | -1.22 | down |
| DW66\_5414 | sulfate ABC transporter permease | -2.71 | down |
| DW66\_5415 | sulfate ABC transporter permease | -4.60 | down |
| DW66\_5416 | sulfate ABC transporter | -6.67 | down |
| DW66\_5417 | hypothetical protein | -6.88 | down |
| DW66\_5418 | acriflavin resistance protein | 1.70 | up |
| DW66\_5421 | hypothetical protein | -1.81 | down |
| DW66\_5423 | ornithine carbamoyltransferase | 2.03 | up |
| DW66\_5424 | binding-protein-dependent transport system inner membrane protein | 1.40 | up |
| DW66\_5427 | putrescine ABC transporter periplasmic putrescine-binding protein | 1.49 | up |
| DW66\_5435 | hypothetical protein | 1.12 | up |
| DW66\_5436 | type II secretion system protein E | -1.87 | down |
| DW66\_5437 | Ribonucleotide reductase, alpha subunit | -3.24 | down |
| DW66\_5438 | glycine dehydrogenase | 3.90 | up |
| DW66\_5561 | glycine cleavage system aminomethyltransferase T | -1.69 | down |
| DW66\_5562 | hypothetical protein | -5.64 | down |
| DW66\_5563 | binding-protein-dependent transport system inner membrane protein | -3.74 | down |
| DW66\_5564 | extracellular solute-binding protein | -2.76 | down |
| DW66\_5569 | hypothetical protein | -1.83 | down |
| DW66\_5571 | Z-ring-associated protein ZapA | -1.65 | down |
| DW66\_5573 | hypothetical protein | -1.00 | down |
| DW66\_5574 | hypothetical protein | -1.52 | down |
| DW66\_5575 | secretion protein HlyD | 2.19 | up |
| DW66\_5577 | ABC transporter | 1.40 | up |
| DW66\_5581 | CDP-6-deoxy-delta-3,4-glucoseen reductase | -1.70 | down |
| DW66\_5582 | decarboxylase UbiD | -1.81 | down |
| DW66\_5583 | transcription termination factor Rho | -2.81 | down |
| DW66\_5584 | thioredoxin | 1.27 | up |
| DW66\_5585 | Ppx/GppA phosphatase | 1.01 | up |
| DW66\_5591 | nucleoside diphosphate kinase regulator | 2.03 | up |
| DW66\_5595 | diaminopimelate decarboxylase | -1.01 | down |
| DW66\_5600 | hypothetical protein | 2.04 | up |
| DW66\_5601 | ammonium transporter | 1.14 | up |
| DW66\_5602 | nitrogen regulatory protein P-II 1 | 2.92 | up |
| DW66\_5605 | Mg chelatase, ChlI subunit | -3.45 | down |
| DW66\_5606 | recombinase-related protein | -2.18 | down |
| DW66\_5607 | hypothetical protein | -3.25 | down |
| DW66\_5608 | ISPpu15, transposase | -1.21 | down |
| DW66\_5609 | ISPpu15, transposase | -4.55 | down |
| DW66\_5610 | hypothetical protein | -5.18 | down |
| DW66\_5611 | hypothetical protein | -3.51 | down |
| DW66\_5612 | Mg chelatase, ChlI subunit | -2.00 | down |
| DW66\_5616 | sulfate transporter | -2.49 | down |
| DW66\_5617 | hypothetical protein | -1.04 | down |
| DW66\_5619 | hypothetical protein | -1.41 | down |
| DW66\_5621 | integrase | -1.89 | down |
| DW66\_5622 | hypothetical protein | -3.14 | down |
| DW66\_5623 | Transcriptional regulator | -14.99 | down |
| DW66\_5624 | hypothetical protein | -9.25 | down |
| DW66\_5625 | hypothetical protein | -7.24 | down |
| DW66\_5626 | Phage capsid and scaffold protein | -5.00 | down |
| DW66\_5627 | hypothetical protein | -6.18 | down |
| DW66\_5628 | hypothetical protein | -13.89 | down |
| DW66\_5629 | hypothetical protein | -2.35 | down |
| DW66\_5630 | hypothetical protein | -7.56 | down |
| DW66\_5631 | hypothetical protein | -3.53 | down |
| DW66\_5632 | Phage terminase, small subunit | -4.53 | down |
| DW66\_5633 | Phage terminase, large subunit | -4.40 | down |
| DW66\_5634 | Mu-like prophage FluMu protein gp29 | -2.27 | down |
| DW66\_5635 | virion morphogenesis protein | -3.14 | down |
| DW66\_5636 | phage virion morphogenesis protein | -5.59 | down |
| DW66\_5637 | Phage protein | -5.20 | down |
| DW66\_5638 | hypothetical protein | -4.48 | down |
| DW66\_5639 | hypothetical protein | -2.60 | down |
| DW66\_5640 | hypothetical protein | -2.20 | down |
| DW66\_5641 | membrane protein | -2.21 | down |
| DW66\_5642 | Mu-like prophage FluMu protein gp36 | -2.23 | down |
| DW66\_5643 | hypothetical protein | -2.33 | down |
| DW66\_5644 | tail protein | -2.13 | down |
| DW66\_5646 | hypothetical protein | -2.71 | down |
| DW66\_5647 | hypothetical protein | -1.74 | down |
| DW66\_5648 | hypothetical protein | -1.47 | down |
| DW66\_5652 | baseplate protein | -1.33 | down |
| DW66\_5653 | baseplate protein | -13.35 | down |
| DW66\_5654 | Phage-related baseplate assembly protein | -3.83 | down |
| DW66\_5655 | tail protein I | -6.72 | down |
| DW66\_5656 | hypothetical protein | -2.67 | down |
| DW66\_5657 | phage-related hypothetical protein | -2.67 | down |
| DW66\_5658 | hypothetical protein | -1.87 | down |
| DW66\_5660 | response regulator receiver protein | -1.79 | down |
| DW66\_5661 | DNA-binding response regulator | -1.58 | down |
| DW66\_5665 | transcriptional regulator AraC | -2.00 | down |
| DW66\_5666 | potassium efflux system protein | -2.30 | down |
| DW66\_5667 | hypothetical protein | 1.60 | up |
| DW66\_5668 | isochorismatase hydrolase | 3.36 | up |
| DW66\_5669 | transcriptional regulator LysR | -1.74 | down |
| DW66\_5670 | transcriptional regulator LysR | -1.73 | down |
| DW66\_5671 | outer membrane porin | -3.17 | down |
| DW66\_5672 | transporter | -1.64 | down |
| DW66\_5673 | amidohydrolase 3 | 1.68 | up |
| DW66\_5674 | hypothetical protein | -4.87 | down |
| DW66\_5675 | alpha/beta hydrolase fold protein | 1.63 | up |
| DW66\_5676 | membrane protein | 1.28 | up |
| DW66\_5677 | isochorismatase hydrolase | 4.61 | up |
| DW66\_5678 | cyclic nucleotide-regulated small mechanosensitive ion channel | -1.40 | down |
| DW66\_5679 | FAD dependent oxidoreductase | 1.28 | up |
| DW66\_5680 | aldehyde dehydrogenase | 3.73 | up |
| DW66\_5682 | hypothetical protein | 1.77 | up |
| DW66\_5683 | transcriptional regulator LysR | -1.19 | down |
| DW66\_5684 | multidrug efflux protein NorA | -2.71 | down |
| DW66\_5685 | diguanylate cyclase/phosphodiesterase | -3.26 | down |
| DW66\_5686 | ATP-dependent DNA helicase Rep | -2.93 | down |
| DW66\_5687 | xanthine phosphoribosyltransferase | -1.24 | down |
| DW66\_5688 | acetyl-CoA hydrolase-like protein | -1.30 | down |
| DW66\_5689 | cytochrome c5 | 3.05 | up |
| DW66\_5690 | transcriptional regulator XRE | -1.02 | down |
| DW66\_5691 | alanine racemase | 1.08 | up |
| DW66\_5692 | D-amino acid dehydrogenase small subunit | 1.18 | up |
| DW66\_5694 | hypothetical protein | -1.17 | down |
| DW66\_5695 | FAD dependent oxidoreductase | -1.99 | down |
| DW66\_5698 | phospholipase D/transphosphatidylase | -1.79 | down |
| DW66\_5699 | transporter protein | -2.66 | down |
| DW66\_5700 | aldehyde dehydrogenase | -1.15 | down |
| DW66\_5701 | hypothetical protein | 1.17 | up |
| DW66\_5703 | 50S ribosomal protein L28 | -1.67 | down |
| DW66\_5705 | DNA repair protein RadC | -1.49 | down |
| DW66\_5706 | bifunctional phosphopantothenoylcysteine decarboxylase/phosphopantothenate synthase | -1.93 | down |
| DW66\_5707 | deoxyuridine 5'-triphosphate nucleotidohydrolase | -1.54 | down |
| DW66\_5708 | phosphomannomutase | -1.90 | down |
| DW66\_5712 | hypothetical protein | -1.06 | down |
| DW66\_5714 | Protein YicC | -1.56 | down |
| DW66\_5715 | guanylate kinase | -1.12 | down |
| DW66\_5716 | amino acid permease-associated protein | -2.21 | down |
| DW66\_5717 | peptidase C26 | -1.08 | down |
| DW66\_5718 | glutamate--putrescine ligase | -1.86 | down |
| DW66\_5719 | transcriptional regulator LysR | -1.10 | down |
| DW66\_5720 | DNA-directed RNA polymerase subunit omega | -1.08 | down |
| DW66\_5722 | endoribonuclease | 1.97 | up |
| DW66\_5723 | lipoprotein | -2.02 | down |
| DW66\_5725 | TonB-system energizer ExbB type-1 | -3.58 | down |
| DW66\_5726 | biopolymer transport protein ExbD | -1.82 | down |
| DW66\_5727 | TonB protein | -2.69 | down |
| DW66\_5731 | DNA and RNA helicases | -1.69 | down |
| DW66\_5733 | FAD-dependent pyridine nucleotide-disulfide oxidoreductase | -1.60 | down |
| DW66\_5735 | chorismate lyase | -2.49 | down |
| DW66\_5736 | 4-hydroxybenzoate octaprenyltransferase | -2.37 | down |
| DW66\_5737 | hypothetical protein | 5.60 | up |
| DW66\_5738 | transcriptional regulator | 1.63 | up |
| DW66\_5739 | PAS/PAC sensor signal transduction histidine kinase | -1.71 | down |
| DW66\_5740 | metal ion transporter | -1.29 | down |
| DW66\_5741 | peptidase | 2.55 | up |
| DW66\_5742 | response regulator receiver protein | -1.64 | down |
| DW66\_5743 | phosphate uptake regulator PhoU | -1.38 | down |
| DW66\_5744 | phosphate ABC transporter ATP-binding protein | -1.09 | down |
| DW66\_5745 | phosphate ABC transporter permease | -1.35 | down |
| DW66\_5746 | binding-protein-dependent transport system inner membrane protein | -2.09 | down |
| DW66\_5747 | phosphate binding protein | -1.45 | down |
| DW66\_5748 | transporter protein | -2.27 | down |
| DW66\_5750 | aldose 1-epimerase | -1.05 | down |
| DW66\_5752 | transglycosylase-associated protein | 2.47 | up |
| DW66\_5753 | phosphoribosylaminoimidazole carboxylase ATPase subunit | -2.26 | down |
| DW66\_5754 | phosphoribosylaminoimidazole carboxylase catalytic subunit | -2.31 | down |
| DW66\_5755 | Ribosomal protein S8 | -1.88 | down |
| DW66\_5757 | hypothetical protein | -1.50 | down |
| DW66\_5758 | aspartate ammonia-lyase | 2.92 | up |
| DW66\_5760 | histone deacetylase protein | -1.45 | down |
| DW66\_5762 | transcriptional regulator | -1.07 | down |
| DW66\_5766 | pyruvate carboxylase subunit B | 3.30 | up |
| DW66\_5767 | pyruvate carboxylase subunit A | 4.00 | up |
| DW66\_5768 | transcriptional regulator LysR | -2.49 | down |
| DW66\_5773 | DNA-dependent helicase II | -1.13 | down |
| DW66\_5775 | hypothetical protein | 1.02 | up |
| DW66\_5776 | sodium/hydrogen exchanger | -2.36 | down |
| DW66\_5779 | pyridoxamine kinase | -1.13 | down |
| DW66\_5780 | hypothetical protein | 1.34 | up |
| DW66\_5781 | cobalamin synthesis protein P47K | -3.08 | down |
| DW66\_5782 | hypothetical protein | -5.28 | down |
| DW66\_5783 | cobalamin synthesis protein P47K | -4.64 | down |
| DW66\_5784 | GTP cyclohydrolase | -5.55 | down |
| DW66\_5785 | hypothetical protein | -1.39 | down |
| DW66\_5788 | dihydrolipoamide dehydrogenase | 2.27 | up |
| DW66\_5790 | copper resistance protein B | 1.34 | up |
| DW66\_5791 | Multicopper oxidase | 2.62 | up |
| DW66\_5793 | hypothetical protein | 2.04 | up |
| DW66\_5796 | cytochrome C | -2.24 | down |
| DW66\_5797 | cytochrome C biogenesis protein | -2.93 | down |
| DW66\_5799 | cation transporter | -4.06 | down |
| DW66\_5800 | Cation efflux system protein CusF precursor | -2.04 | down |
| DW66\_5801 | isoprenylcysteine carboxyl methyltransferase | 3.55 | up |
| DW66\_5802 | hypothetical protein | 4.61 | up |
| DW66\_5803 | hypothetical protein | 5.12 | up |
| DW66\_5804 | hypothetical protein | 5.10 | up |
| DW66\_5805 | heavy metal transport/detoxification protein | 3.45 | up |
| DW66\_5806 | cation-transporting ATPase transmembrane protein | 1.15 | up |
| DW66\_5807 | Mobile element protein | -2.87 | down |
| DW66\_5809 | sugar transferase | -1.74 | down |
| DW66\_5810 | ribonuclease III | -6.49 | down |
| DW66\_5811 | transcriptional regulator LysR | -2.32 | down |
| DW66\_5812 | phosphate-selective porin O and P | -1.81 | down |
| DW66\_5814 | hypothetical protein | -4.48 | down |
| DW66\_5815 | hypothetical protein | 1.03 | up |
| DW66\_5817 | hypothetical protein | 2.65 | up |
| DW66\_5818 | cobalt/zinc/cadmium efflux transporter permease | -2.74 | down |
| DW66\_5819 | cobalt/zinc/cadmium efflux transporter membrane fusion protein | -3.27 | down |
| DW66\_5820 | cobalt/zinc/cadmium efflux transporter outer membrane protein | -4.71 | down |
| DW66\_5821 | porin | -3.18 | down |
| DW66\_5822 | IS4, transposase | -1.39 | down |
| DW66\_5823 | porin | -3.06 | down |
| DW66\_5826 | ATPase AAA | -4.30 | down |
| DW66\_5827 | ISPsy14, transposase | -2.62 | down |
| DW66\_5828 | peptidase | -2.04 | down |
| DW66\_5829 | hypothetical protein | -1.75 | down |
| DW66\_5830 | chromate transport protein | -7.75 | down |
| DW66\_5832 | transposase | -2.77 | down |
| DW66\_5833 | transposase | 1.35 | up |
| DW66\_5834 | protein chain release factor B | 1.70 | up |
| DW66\_5836 | transcriptional regulator LysR | -1.59 | down |
| DW66\_5837 | endoribonuclease L-PSP | 3.62 | up |
| DW66\_5838 | transposase | 3.54 | up |
| DW66\_5840 | mercuric reductase | 1.55 | up |
| DW66\_5841 | mercury transporter MerC | 1.82 | up |
| DW66\_5842 | mercury transporter | 1.67 | up |
| DW66\_5845 | transposase | -3.81 | down |
| DW66\_5846 | Fe-S cluster assembly protein SufE | 2.90 | up |
| DW66\_5847 | Protein YidD | -1.80 | down |
| DW66\_5848 | MerD2 protein | -1.10 | down |
| DW66\_5850 | mercuric ion reductase | 2.81 | up |
| DW66\_5851 | mercury transporter | 3.27 | up |
| DW66\_5852 | mercuric ion transport protein | 2.23 | up |
| DW66\_5854 | addiction module antitoxin RelB | -2.48 | down |
| DW66\_5855 | ISPsy5, transposase | -4.09 | down |
| DW66\_5857 | transposase | -12.87 | down |
| DW66\_5860 | MerT | -2.89 | down |
| DW66\_5864 | Signal recognition particle receptor protein FtsY | -3.30 | down |
| DW66\_5865 | transcriptional regulator MerR | -2.36 | down |
| DW66\_5866 | Transposon Tn21 resolvase | -2.88 | down |
| DW66\_5867 | transposase for Tn21 | -1.15 | down |
| DW66\_5868 | TnpT protein | 2.81 | up |
| DW66\_5869 | Tn4652, cointegrate resolution protein S | 2.60 | up |
| DW66\_5870 | hypothetical protein | -3.74 | down |
| DW66\_5871 | hypothetical protein | -2.28 | down |
| DW66\_5872 | hypothetical protein | -2.35 | down |
| DW66\_5873 | hypothetical protein | -3.10 | down |
| DW66\_5874 | ISPsy14, transposase | -2.62 | down |
| DW66\_5875 | ATPase AAA | -4.31 | down |
| DW66\_5876 | hypothetical protein | -10.31 | down |
| DW66\_5877 | hypothetical protein | 1.84 | up |
| DW66\_5881 | signal transduction histidine kinase | -1.03 | down |
| DW66\_5884 | Ser/Thr protein phosphatase | -2.19 | down |
| DW66\_5885 | integrase | -1.92 | down |
| DW66\_5889 | glutathione S-transferase | 1.19 | up |
| DW66\_5890 | ThiJ/PfpI domain protein | 3.13 | up |
| DW66\_5891 | aldehyde dehydrogenase | 1.46 | up |
| DW66\_5893 | ATPase AAA | -4.31 | down |
| DW66\_5894 | ISPsy14, transposase | -2.62 | down |