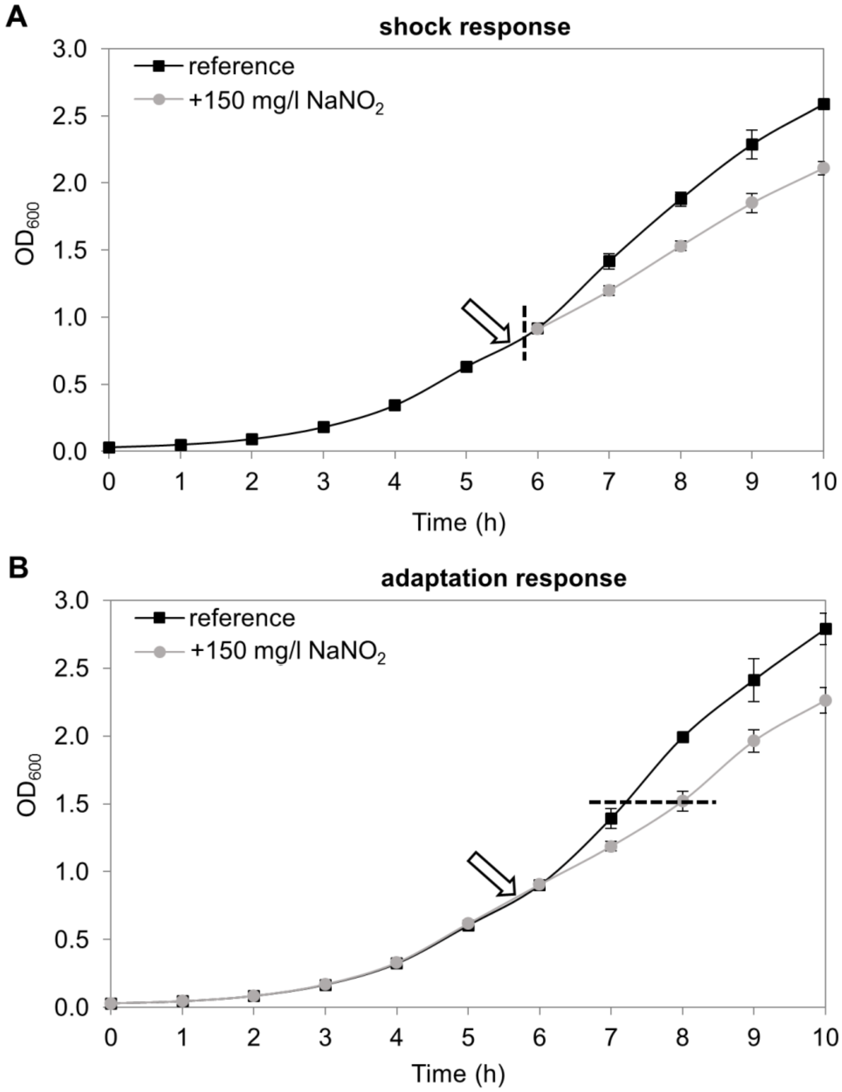

**FIG S1:** Growth curves of *S.* Typhimurium 14028 WT illustrating the experimental set-ups for the analysis of the transcriptional response to acidified $NaNO_2$ shock (A) and adaptation (B). Growth of shaken flask cultures of the reference culture without $NaNO_2$ (black square) and the culture to which 150 mg/l $NaNO_2$ was added (grey circle) at 24°C was recorded. Data represent mean values and standard deviations from three independent experiments. The arrow indicates the time-point ($OD_{600}$ = 0.80-0.85), at which 150 mg/l $NaNO_2$ was added. The time points of harvesting the cultures for RNA extraction (A: 10 min after addition of $NaNO_2$, B: $OD_{600}$ = 1.5) are indicated by the dashed line.

## Table S1: Gene-specific primer sets used for qPCR

| Gene name | 14028 identifier | Forward primer (5‘ to 3‘) | Reverse primer (5‘ to 3‘) | Amplicon size |
|---|---|---|---|---|
| 16S rDNA | | GTCTGTCAAGTCGGATGTG | AGATCTCTACGCATTTCACC | 122 bp |
| *ampD* | STM14_0175 | ATTATTCACCGGAACGATAG | ACATACTGGACGATTTCACC | 114 bp |
| *fhuA* | STM14_0228 | GCCTCTATGTTCAGGATCAG | AACTGGTGGTCATTACGTTC | 145 bp |
| *speF* | STM14_0818 | ACAATTTATTCCGATGATGG | TTATGGATCTGCGAGGTCT | 132 bp |
| *potB* | STM14_1402 | CGTGATTGATACACCGATT | TAGTGGTTTGTCGAGCTTCT | 127 bp |
| *purB* | STM14_1410 | ATCAGTTCAGCGAAGAGTTC | GATCAGGATGGTGTTAAAGC | 128 bp |
| *ttrC* | STM14_1678 | TATGCACACTGCTGTTCTGT | CGGTTTGTACCTGAATCAAC | 132 bp |
| *hdeB* | STM14_1885 | TTACGCCTAAAGGTATGAGC | ACTGCTGTCGTCTCAGTTTC | 145 bp |
| *fliF* | STM14_2390 | TGCTAATGATGTGGAAAGC | CTTTATTGGCAAAATCCAAC | 116 bp |
| *hmpA* | STM14_3135 | CCGAGATTTATCACGAGAAC | GACTGGTTCAAACTCAAAGC | 119 bp |
| *cadA* | STM14_3138 | TCATTTATGAAACCCAGTCC | TGGTGGTATGCATCATGTAG | 123 bp |
| *yfiA* | STM14_3266 | ATTAATACACCGAACGGACA | TTGTGCTGCACTTTATTGAG | 113 bp |
| *norV* | STM14_3431 | GCTACTACGCCAATATCCTG | GCCCATTTCAGATACAGTTC | 160 bp |
| *yhbU* | STM14_3956 | CGCTGCTATCTTTCTTCCTA | GTAACGGTCAATCAGGACAT | 138 bp |
| *rplM* | STM14_4037 | AATACACTCCGCACGTAGAT | AAAGGTCGCTTGTTTGATAC | 140 bp |
| *rpsH* | STM14_4129 | CCAGGGTAAAGCTGTTGTAG | TGCACGATCAGTCATAACAC | 148 bp |
| *feoB* | STM14_4222 | ATTCAATGGATTGGCTACAC | GGAGAGGAACAGGTACATCA | 132 bp |
| *pyrE* | STM14_4495 | GTACTGCTTTAACCGCAAAG | CGCCTGAATAATCTCCATT | 145 bp |
| *rnpA* | STM14_4635 | TCCCCGTATCGGTCTTAC | GAAATCCATTGCAGGAAGT | 124 bp |
| *nrfA* | STM14_5143 | CGGAATATGAAACCTGGAG | CGATTTTATGGTCGGTGTAG | 117 bp |
| *adi* | STM14_5169 | CACGCACAAACTACTGAATG | CATATAACGGAGAGGTGGTG | 128 bp |
| - | STM14_5179 | CTGTCGTTATTGTGAAATGC | AAGAATCCACACAAATAGGG | 131 bp |
| - | STM14_5361 | TGTTGATCGGTATGTCTGAA | GTGTCAAGGTGCATACAGG | 136 bp |

## Table S2: Up-regulated genes under acidified $NaNO_2$ shock in *S*. Typhimurium 14028 WT

| COG | 14028 identifier | LT2 identifier | Gene name | Product | $\log_2$ FC | p-value (BH-adjusted) |
|---|---|---|---|---|---|---|
| *Energy production & conversion (C)* | | | | | | |
| COG1151C | STM14_1052 | STM0937 | *hcp* | hydroxylamine reductase | 2.90 | 3.21E-03 |
| COG0247C | STM14_2821 | STM2286 | *glpC* | sn-glycerol-3-phosphate dehydrogenase subunit C | 2.06 | 4.85E-02 |
| COG1018C | STM14_3135 | STM2556 | *hmpA* | nitric oxide dioxygenase | 6.49 | 4.38E-12 |
| *COG1819GC | STM14_3344 | STM2773 | *iroB* | putative glycosyl transferase | 2.49 | 1.60E-02 |
| COG0426C | STM14_3431 | STM2840 | *norV*[1] | anaerobic nitric oxide reductase flavorubredoxin | 8.44 | 8.43E-17 |
| COG1902C | STM14_3898 | STM3219 | *fadH* | 2,4-dienoyl-CoA reductase | 2.99 | 1.69E-03 |
| *COG0604CR | STM14_5103 | STM4245 | *qor* | quinone oxidoreductase | 1.96 | 4.69E-02 |
| *Carbohydrate transport & metabolism (G)* | | | | | | |
| COG1440G | STM14_1594 | STM1312 | *celA* | PTS system N,N'-diacetylchitobiose-specific transporter subunit IIB | 2.06 | 3.47E-02 |
| COG1447G | STM14_1596 | STM1314 | *celC* | PTS system N,N'-diacetylchitobiose-specific transporter subunit IIA | 2.27 | 1.85E-02 |
| COG2814G | STM14_2686 | STM2179 | - | putative sugar transporter | 2.34 | 4.04E-02 |
| *COG1819GC | STM14_3344 | STM2773 | *iroB* | putative glycosyl transferase | 2.49 | 1.60E-02 |
| COG2271G | STM14_3791 | STM3134 | - | putative permease | 3.34 | 3.55E-04 |
| COG1312G | STM14_3795 | STM3135 | - | mannonate dehydratase | 2.17 | 2.45E-02 |
| COG0246G | STM14_3796 | STM3136 | - | putative D-mannonate oxidoreductase | 2.19 | 2.37E-02 |
| COG3836G | STM14_3931 | STM3249 | *garL* | alpha-dehydro-beta-deoxy-D-glucarate aldolase | 2.32 | 3.37E-02 |
| COG0524G | STM14_4272 | STM3547.Sc | - | putative transcriptional regulator | 2.13 | 3.43E-02 |
| COG3775G | STM14_4561 | STM3782 | - | putative PTS system galactitol-specific enzyme IIC component | 2.20 | 2.60E-02 |
| *COG1762GT | STM14_4563 | STM3784 | - | phosphotransferase system mannitol/fructose-specific IIA component | 2.34 | 1.36E-02 |
| COG2814G | STM14_5161 | STM4290 | *proP* | proline/glycine betaine transporter | 2.11 | 2.92E-02 |
| *COG2610GE | STM14_5378 | STM4482 | *idnT* | L-idonate transport protein | 3.12 | 3.33E-03 |
| *Amino acid transport & metabolism (E)* | | | | | | |
| COG1280E | STM14_0427 | STM0365 | *yahN* | putative transport protein | 2.04 | 4.39E-02 |
| COG3075E | STM14_2820 | STM2285 | *glpB* | anaerobic glycerol-3-phosphate dehydrogenase subunit B | 2.97 | 1.23E-02 |
| COG0531E | STM14_3137 | STM2558 | *cadB* | lysine/cadaverine antiporter | 4.81 | 6.92E-07 |
| COG1982E | STM14_3138 | STM2559 | *cadA* | lysine decarboxylase 1 | 4.17 | 9.28E-06 |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
| COG3104E | STM14_4321 | STM3592 | *yhiP* | inner membrane transporter YhiP | 2.80 | 2.74E-03 |
| COG0747E | STM14_4375 | STM3630 | *dppA* | dipeptide transport protein | 3.22 | 4.43E-04 |
| COG0002E | STM14_4956 | STM4121 | *argC* | N-acetyl-gamma-glutamyl-phosphate reductase | 2.92 | 6.11E-03 |
| COG0531E | STM14_5166 | STM4294 | *yjdE* | arginine:agmatin antiporter | 4.03 | 1.85E-05 |
| COG1982E | STM14_5169 | STM4296 | *adi* | catabolic arginine decarboxylase | 5.40 | 3.97E-09 |
| *COG2610GE | STM14_5378 | STM4482 | *idnT* | L-idonate transport protein | 3.12 | 3.33E-03 |
| *COG0601EP | STM14_4373 | STM3629 | *dppB* | dipeptide transporter permease DppB | 2.30 | 3.32E-02 |
| *Coenzyme transport & metabolism (H)* |  |  |  |  |  |  |
| COG0746H | STM14_4803 | STM3994 | *mobA* | molybdopterin-guanine dinucleotide biosynthesis protein MobA | 2.07 | 3.64E-02 |
| *Lipid transport & metabolism (I)* |  |  |  |  |  |  |
| COG1960I | STM14_0365 | STM0309 | *fadE* | acyl-CoA dehydrogenase | 2.11 | 3.03E-02 |
| COG1250I | STM14_2937 | STM2388 | *fadJ* | multifunctional fatty acid oxidation complex subunit alpha | 2.02 | 3.93E-02 |
| *Inorganic ion transport & metabolism (P)* |  |  |  |  |  |  |
| COG1464P | STM14_0600 | STM0510 | *sfbA* | ABC transporter ATP-binding protein | 3.00 | 1.63E-03 |
| COG1135P | STM14_0601 | STM0511 | *sfbB* | ABC transporter ATP-binding protein | 2.19 | 2.90E-02 |
| COG0783P | STM14_0966 | STM0831 | *dps* | DNA starvation/stationary phase protection protein Dps | 1.95 | 4.39E-02 |
| COG3615P | STM14_1534 | STM1271 | *yeaR* | putative cytoplasmic protein | 2.60 | 8.23E-03 |
| COG3615P | STM14_2185 | STM1808 | - | putative cytoplasmic protein | 6.67 | 4.38E-12 |
| COG4771P | STM14_3348 | STM2777 | *iroN* | outer membrane receptor FepA | 2.13 | 3.10E-02 |
| *COG0601EP | STM14_4373 | STM3629 | *dppB* | dipeptide transporter permease DppB | 2.30 | 3.32E-02 |
| *Secondary metabolites biosynthesis, transport & catabolism (Q)* |  |  |  |  |  |  |
| COG1228Q | STM14_0913 | STM0787 | *hutI* | imidazolonepropionase | 2.31 | 1.77E-02 |
| COG0412Q | STM14_4773 | STM3967 | *dlhH* | putative dienelactone hydrolase | 2.40 | 2.03E-02 |
| *Translation, ribosomal structure & biogenesis (J)* |  |  |  |  |  |  |
| COG1544J | STM14_3266 | STM2665 | *yfiA* | translation inhibitor protein RaiA | 3.58 | 7.63E-05 |
| COG1544J | STM14_4009 | STM3321 | *yhbH* | putative sigma(54) modulation protein | 2.02 | 3.64E-02 |
| *Transcription (K)* |  |  |  |  |  |  |
| COG2188K | STM14_0915 | STM0789 | *hutC* | histidine utilization repressor | 2.65 | 9.13E-03 |
| *COG2197TK | STM14_1526 | STM1265 | - | putative response regulator | 1.97 | 4.28E-02 |
| *COG2197TK | STM14_3463 | STM2866 | *sprB* | transcriptional regulator | 2.34 | 1.40E-02 |
| COG2207K | STM14_3465 | STM2867 | *hilC* | invasion regulatory protein | 1.92 | 4.73E-02 |
| COG2732K | STM14_4057 | STM3363 | *yhcO* | putative cytoplasmic protein | 2.11 | 3.37E-02 |
| COG2944K | STM14_4398 | STM3648 | *yiaG* | putative transcriptional regulator | 2.73 | 3.42E-03 |
| COG2944K | STM14_4557 | STM3778 | - | putative DNA-binding protein | 2.03 | 4.50E-02 |
| COG0583K | STM14_4693 | STM3897 | *yifA* | transcriptional regulator HdfR | 2.42 | 1.06E-02 |
| COG2207K | STM14_5314 | STM4423 | - | putative DNA-binding protein | 2.81 | 4.35E-03 |
| *Replication, recombination & repair (L)* |  |  |  |  |  |  |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
| COG0350L | STM14_2006 | STM1659 | *ogt* | O-6-alkylguanine-DNA:cysteine-protein methyltransferase | 2.21 | 2.21E-02 |
| *Cell cycle control, cell division, chromosome partitioning (D)* |  |  |  |  |  |  |
| COG2846D | STM14_5283 | STM4399 | *ytfE* | cell morphogenesis/cell wall metabolism regulator | 6.06 | 1.77E-10 |
| *Signal transduction mechanisms (T)* |  |  |  |  |  |  |
| COG0589T | STM14_0713 | STM0614 | *ybdQ* | putative universal stress protein | 1.99 | 3.89E-02 |
| *COG2197TK | STM14_1526 | STM1265 | - | putative response regulator | 1.97 | 4.28E-02 |
| COG2766T | STM14_1558 | STM1285 | *yeaG* | putative serine protein kinase | 2.16 | 2.45E-02 |
| COG0589T | STM14_2344 | STM1927 | *yecG* | universal stress protein UspC | 2.42 | 1.95E-02 |
| *COG2197TK | STM14_3463 | STM2866 | *sprB* | transcriptional regulator | 2.34 | 1.40E-02 |
| *COG0840NT | STM14_3893 | STM3216 | - | putative methyl-accepting chemotaxis protein | 1.92 | 4.85E-02 |
| *COG0840NT | STM14_4305 | STM3577 | *tcp* | methyl-accepting transmembrane citrate/phenol chemoreceptor | 2.45 | 9.17E-03 |
| *COG1762GT | STM14_4563 | STM3784 | - | phosphotransferase system mannitol/fructose-specific IIA component | 2.34 | 1.36E-02 |
| *Cell motility (N)* |  |  |  |  |  |  |
| *COG0840NT | STM14_3893 | STM3216 | - | putative methyl-accepting chemotaxis protein | 1.92 | 4.85E-02 |
| *COG0840NT | STM14_4305 | STM3577 | *tcp* | methyl-accepting transmembrane citrate/phenol chemoreceptor | 2.45 | 9.17E-03 |
| *Posttranslational modification, protein turnover, chaperones (O)* |  |  |  |  |  |  |
| COG0071O | STM14_1509 | STM1251 | - | putative molecular chaperone | 2.00 | 3.74E-02 |
| COG1764O | STM14_1886 | STM1563 | *osmC* | putative envelope protein | 2.96 | 1.78E-03 |
| COG0695O | STM14_3387 | STM2805 | *nrdH* | glutaredoxin-like protein | 3.10 | 1.56E-03 |
| *General function prediction only (R)* |  |  |  |  |  |  |
| COG0446R | STM14_3432 | STM2841 | *norW*[1] | nitric oxide reductase | 7.49 | 1.33E-13 |
| COG1203R | STM14_3548 | STM2944 | *ygcB* | putative helicase | 3.31 | 3.55E-04 |
| *COG0604CR | STM14_5103 | STM4245 | *qor* | quinone oxidoreductase | 1.96 | 4.69E-02 |
| *Function unknown (S)* |  |  |  |  |  |  |
| COG3123S | STM14_0462 | STM0391 | *yaiE* | hypothetical protein | 2.12 | 3.37E-02 |
| COG5464S | STM14_0564 | STM0479 | - | putative transposase | 2.07 | 4.63E-02 |
| COG3110S | STM14_1222 | STM1077 | *yccT* | hypothetical protein | 3.29 | 4.25E-03 |
| COG0316S | STM14_1663 | STM1369 | *sufA* | iron-sulfur cluster assembly scaffold protein | 2.36 | 1.90E-02 |
| COG2719S | STM14_2181 | STM1804.S | *ycgB* | hypothetical protein | 3.06 | 8.82E-04 |
| COG3157S | STM14_3785 | STM3131 | - | putative cytoplasmic protein | 2.59 | 1.62E-02 |
| COG3111S | STM14_3848 | STM3176 | *ygiW* | putative outer membrane protein | 2.03 | 3.66E-02 |
| COG3237S | STM14_5097 | STM4240 | *yjbJ* | putative stress-response protein | 1.97 | 4.14E-02 |

| | | | | | | |
|---|---|---|---|---|---|---|
| COG5464S | STM14_5428 | STM4518 | - | putative inner membrane protein | 2.37 | 2.54E-02 |
| *Not assigned* | | | | | | |
| | STM14_0135 | STM0114 | *leuL* | leu operon leader peptide | 3.79 | 3.60E-05 |
| | STM14_0193 | STM0161 | *kdgT* | 2-keto-3-deoxygluconate permease | 2.01 | 4.05E-02 |
| | STM14_0224 | - | - | hypothetical protein | 2.43 | 3.66E-02 |
| | STM14_0383 | STM0327 | - | putative cytoplasmic protein | 3.50 | 1.13E-04 |
| | STM14_0803 | STM0688 | *ybfN* | putative lipoprotein | 2.04 | 4.32E-02 |
| | STM14_958 | - | - | hypothetical protein | 2.22 | 3.48E-02 |
| | STM14_1060 | - | - | hypothetical protein | 2.53 | 2.47E-02 |
| | STM14_1273 | - | - | hypothetical protein | 2.09 | 3.98E-02 |
| | STM14_1275 | STM1121 | *ymdF* | putative cytoplasmic protein | 2.29 | 1.85E-02 |
| | STM14_1330 | STM1161.S | *bssS* | biofilm formation regulatory protein BssS | 2.95 | 1.35E-03 |
| | STM14_1535 | STM1272 | *yoaG* | putative cytoplasmic protein | 2.20 | 2.19E-02 |
| | STM14_1593 | - | - | hypothetical protein | 2.14 | 3.08E-02 |
| | STM14_1885 | STM1562 | *hdeB* | acid-resistance protein | 2.60 | 5.30E-03 |
| | STM14_2680 | - | - | hypothetical protein | 2.12 | 2.77E-02 |
| | STM14_3199 | - | - | hypothetical protein | 4.19 | 5.99E-06 |
| | STM14_3253 | STM2655 | - | putative cytoplasmic protein | 2.24 | 3.43E-02 |
| | STM14_3267 | - | - | hypothetical protein | 2.23 | 2.03E-02 |
| | STM14_3376 | - | - | hypothetical protein | 2.05 | 3.83E-02 |
| | STM14_3456 | STM2860 | *ygbA* | hypothetical protein | 5.29 | 7.64E-09 |
| | STM14_3630 | STM3007 | *ygdR* | putative peptide transport protein | 2.64 | 4.56E-03 |
| | STM14_3631 | - | - | hypothetical protein | 1.94 | 5.00E-02 |
| | STM14_3749 | STM3105 | *yggM* | hypothetical protein | 3.15 | 1.02E-03 |
| | STM14_3910 | STM3228 | *yqjC* | hypothetical protein | 1.98 | 4.02E-02 |
| | STM14_3919 | STM3237 | *yhaL* | putative cytoplasmic protein | 3.52 | 2.84E-03 |
| | STM14_4278 | STM3552 | *yhhA* | hypothetical protein | 2.52 | 1.67E-02 |
| | STM14_4319 | STM3590 | *uspB* | universal stress protein UspB | 2.26 | 2.03E-02 |
| | STM14_4446 | STM3688 | - | putative cytoplasmic protein | 3.74 | 4.16E-04 |
| | STM14_4697 | STM3900 | *ilvL* | ilvG operon leader peptide | 3.45 | 1.49E-04 |
| | STM14_5259 | STM4377 | *aidB* | isovaleryl CoA dehydrogenase | 2.64 | 9.13E-03 |
| | STM14_5469 | STM4552 | - | putative inner membrane protein | 3.80 | 4.19E-05 |

*****Genes assigned to more than one COG

[1] Gene names according to the *E. coli* homologues

## Table S3: Down-regulated genes under acidified $NaNO_2$ shock in *S.* Typhimurium 14028 WT

| COG | 14028 identifier | LT2 identifier | Gene name | Product | $\log_2$ FC | p-value (BH-adjusted) |
|---|---|---|---|---|---|---|
| *Energy production & conversion (C)* | | | | | | |
| COG4660C | STM14_1753 | STM1454 | *ydgQ* | SoxR-reducing system protein RsxE | -2.41 | 1.38E-02 |
| COG4659C | STM14_1754 | STM1455 | *ydgP* | electron transport complex protein RnfG | -2.09 | 3.37E-02 |
| COG4658C | STM14_1755 | STM1456 | *rnfD* | electron transport complex protein RnfD | -2.65 | 8.27E-03 |
| COG4656C | STM14_1756 | STM1457 | - | electron transport complex protein RnfC | -2.42 | 1.25E-02 |
| COG2878C | STM14_1757 | STM1458 | *ydgM* | electron transport complex protein RnfB | -2.01 | 4.50E-02 |
| COG0282C | STM14_2882 | STM2337 | *ackA* | acetate kinase | -2.26 | 1.78E-02 |
| COG1143C | STM14_3156 | STM2576 | *yfhL* | putative ferredoxin | -2.86 | 4.25E-03 |
| COG1032C | STM14_3839 | STM3168 | *ygiR* | hypothetical protein | -2.65 | 6.69E-03 |
| *Carbohydrate transport & metabolism (G)* | | | | | | |
| COG0524G | STM14_0578 | STM0491 | *gsk* | inosine-guanosine kinase | -2.79 | 3.58E-03 |
| COG2814G | STM14_1016 | STM0866 | *mdfA* | multidrug translocase | -2.00 | 4.92E-02 |
| COG2814G | STM14_1094 | STM0968 | *ycaD* | MFS family transporter | -4.06 | 6.79E-05 |
| COG0574G | STM14_1639 | STM1349 | *pps* | phosphoenolpyruvate synthase | -2.35 | 1.26E-02 |
| COG0483G | STM14_3124 | STM2546 | *suhB* | inositol monophosphatase | -3.34 | 2.81E-04 |
| COG2814G | STM14_4586 | STM3798 | *emrD* | multidrug resistance protein D | -2.05 | 3.89E-02 |
| *Amino acid transport & metabolism (E)* | | | | | | |
| *COG0505EF | STM14_0077 | STM0066 | *carA* | carbamoyl phosphate synthase small subunit | -4.78 | 1.82E-06 |
| COG1586E | STM14_0197 | STM0165 | *speD* | S-adenosylmethionine decarboxylase | -2.52 | 8.09E-03 |
| COG1177E | STM14_1398 | STM1223 | *potC* | spermidine/putrescine ABC transporter membrane protein | -2.24 | 2.03E-02 |
| COG1176E | STM14_1402 | STM1225 | *potB* | spermidine/putrescine ABC transporter membrane protein | -3.27 | 5.16E-04 |
| COG3842E | STM14_1403 | STM1226 | *potA* | putrescine/spermidine ABC transporter ATPase | -2.44 | 1.08E-02 |
| COG1605E | STM14_1531 | STM1269 | - | chorismate mutase | -2.79 | 4.10E-03 |
| *COG0252EJ | STM14_1571 | STM1294 | *ansA* | asparaginase | -2.15 | 3.14E-02 |
| *COG0462FE | STM14_2153 | STM1780 | *prsA* | ribose-phosphate pyrophosphokinase | -3.28 | 3.34E-04 |
| COG0814E | STM14_2355 | STM1937 | *tyrP* | tyrosine-specific transport protein | -2.70 | 9.13E-03 |
| COG0531E | STM14_2560 | STM2068 | *yeeF* | putative amino acid transport protein | -3.47 | 1.42E-04 |
| COG0436E | STM14_2874 | STM2331 | *yfbQ* | aminotransferase AlaT | -2.12 | 3.08E-02 |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
| COG0814E | STM14_3650 | STM3022 | - | putative transport protein | -2.18 | 2.55E-02 |
| COG1982E | STM14_3761 | STM3114 | *speC* | ornithine decarboxylase | -2.20 | 2.90E-02 |
| COG0814E | STM14_4369 | STM3625 | *yhjV* | putative transport protein | -2.43 | 1.92E-02 |
| COG0174E | STM14_4820 | STM4007 | *glnA* | glutamine synthetase | -2.02 | 3.66E-02 |
| *Nucleotide transport & metabolism (F)* |  |  |  |  |  |  |
| *COG0505EF | STM14_0077 | STM0066 | *carA* | carbamoyl phosphate synthase small subunit | -4.78 | 1.82E-06 |
| COG1051F | STM14_0163 | STM0137 | *mutT* | nucleoside triphosphate pyrophosphohydrolase | -2.26 | 3.15E-02 |
| COG0634F | STM14_0202 | STM0170 | *hpt* | hypoxanthine-guanine phosphoribosyltransferase | -2.46 | 9.13E-03 |
| COG0528F | STM14_0259 | STM0218 | *pyrH* | uridylate kinase | -2.14 | 2.64E-02 |
| COG0503F | STM14_0373 | STM0317 | *gpt* | xanthine-guanine phosphoribosyltransferase | -3.17 | 5.64E-04 |
| COG0563F | STM14_0574 | STM0488 | *adk* | adenylate kinase | -2.43 | 1.01E-02 |
| COG0167F | STM14_1200 | STM1058 | *pyrD* | dihydroorotate dehydrogenase 2 | -2.47 | 9.70E-03 |
| COG0418F | STM14_1332 | STM1163 | *pyrC* | dihydroorotase | -2.22 | 2.49E-02 |
| COG0015F | STM14_1410 | STM1232 | *purB* | adenylosuccinate lyase | -3.16 | 6.27E-04 |
| COG0284F | STM14_2064 | STM1707 | *pyrF* | orotidine 5'-phosphate decarboxylase | -2.94 | 2.40E-03 |
| *COG0462FE | STM14_2153 | STM1780 | *prsA* | ribose-phosphate pyrophosphokinase | -3.28 | 3.34E-04 |
| COG0572F | STM14_2618 | STM2122 | *udk* | uridine kinase | -2.68 | 4.56E-03 |
| COG0034F | STM14_2909 | STM2362 | *purF* | amidophosphoribosyltransferase | -2.06 | 3.46E-02 |
| COG2233F | STM14_3061 | STM2497 | *uraA* | uracil transporter | -3.94 | 3.88E-05 |
| COG0150F | STM14_3064 | STM2499.S | *purM* | phosphoribosylaminoimidazole synthetase | -2.13 | 3.15E-02 |
| COG0519F | STM14_3075 | STM2510 | *guaA* | bifunctional GMP synthase/glutamine amidotransferase protein | -2.26 | 1.83E-02 |
| COG0516F | STM14_3076 | STM2511 | *guaB* | inositol-5-monophosphate dehydrogenase | -3.80 | 4.19E-05 |
| COG0207F | STM14_3617 | STM3001 | *thyA* | thymidylate synthase | -1.96 | 4.96E-02 |
| COG1457F | STM14_4024 | STM3333 | *codB* | cytosine permease | -2.21 | 3.74E-02 |
| COG0461F | STM14_4495 | STM3733 | *pyrE* | orotate phosphoribosyltransferase | -3.33 | 4.43E-04 |
| COG0138F | STM14_5017 | STM4176 | *purH* | bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase | -2.63 | 9.13E-03 |
| *Coenzyme transport & metabolism (H)* |  |  |  |  |  |  |
| COG0262H | STM14_0106 | STM0087 | *folA* | dihydrofolate reductase | -2.99 | 3.21E-03 |
| COG0413H | STM14_0216 | STM0182 | *panB* | 3-methyl-2-oxobutanoate hydroxymethyltransferase | -3.18 | 2.97E-03 |

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|---|---|---|---|---|---|---|
| COG0301H | STM14_0503 | STM0425 | *thiI* | thiamine biosynthesis protein ThiI | -1.96 | 4.39E-02 |
| COG2240H | STM14_1748 | STM1450 | *pdxY* | pyridoxamine kinase | -2.11 | 2.90E-02 |
| COG2226H | STM14_2217 | STM1835 | *rrmA* | 23S rRNA methyltransferase A | -2.81 | 6.11E-03 |
| COG2227H | STM14_2318 | STM1906 | *yecP* | hypothetical protein | -2.13 | 3.15E-02 |
| COG1477H | STM14_2796 | STM2266 | *apbE* | thiamine biosynthesis lipoprotein ApbE | -2.00 | 4.39E-02 |
| COG0720H | STM14_3554 | STM2949 | *ptpS* | putative 6-pyruvoyl tetrahydrobiopterin synthase | -4.04 | 1.84E-04 |
| COG1072H | STM14_4975 | STM4139 | *coaA* | pantothenate kinase | -2.08 | 3.15E-02 |
| *Lipid transport & metabolism (I)* | | | | | | |
| COG0764I | STM14_1211 | STM1067 | *fabA* | 3-hydroxydecanoyl-ACP dehydratase | -2.71 | 3.86E-03 |
| COG1607I | STM14_2099 | STM1736 | *yciA* | acyl-CoA thioester hydrolase | -2.58 | 1.57E-02 |
| COG1835I | STM14_2758 | STM2232 | *oafA* | O-antigen acetylase | -3.04 | 8.65E-04 |
| *Inorganic ion transport & metabolism (P)* | | | | | | |
| COG0306P | STM14_4318 | STM3589 | *pitA* | low-affinity phosphate transporter | -2.41 | 1.13E-02 |
| *Secondary metabolites biosynthesis, transport & catabolism (Q)* | | | | | | |
| COG1021Q | STM14_0694 | STM0596 | *entE* | enterobactin synthase subunit E | -2.02 | 4.06E-02 |
| *Translation, ribosomal structure & biogenesis (J)* | | | | | | |
| COG0268J | STM14_0052 | STM0043 | *rpsT* | 30S ribosomal protein S20 | -2.54 | 6.69E-03 |
| COG0809J | STM14_0478 | STM0404 | *queA* | S-adenosylmethionine--tRNA ribosyltransferase-isomerase | -2.31 | 1.95E-02 |
| *COG0513LKJ | STM14_0951 | STM0820 | *rhlE* | ATP-dependent RNA helicase RhlE | -3.54 | 2.75E-04 |
| COG0621J | STM14_0996 | STM0852 | *yliG* | putative FeS oxidoreductase | -3.90 | 4.19E-05 |
| COG0361J | STM14_1075 | STM0953 | *infA* | translation initiation factor IF-1 | -3.55 | 9.21E-05 |
| COG0539J | STM14_1110 | STM0981 | *rpsA* | 30S ribosomal protein S1 | -2.15 | 2.45E-02 |
| COG0482J | STM14_1412 | STM1234.S | *trmU* | tRNA (5-methyl aminomethyl-2-thiouridylate)-methyltransferase | -1.96 | 4.63E-02 |
| *COG0252EJ | STM14_1571 | STM1294 | *ansA* | asparaginase | -2.15 | 3.14E-02 |
| COG0016J | STM14_1624 | STM1337 | *pheS* | phenylalanyl-tRNA synthetase subunit alpha | -2.73 | 3.93E-03 |
| *COG0513LKJ | STM14_2001 | STM1655 | *dbpA* | ATP-dependent RNA helicase DbpA | -2.11 | 4.28E-02 |
| COG0023J | STM14_2063 | STM1706 | *yciH* | translation initiation factor Sui1 | -3.04 | 2.40E-03 |
| COG1187J | STM14_2082 | STM1719 | *yciL* | 23S rRNA pseudouridylate synthase B | -2.80 | 4.25E-03 |
| COG0144J | STM14_2237 | STM1850 | *yebU* | rRNA (cytosine-C(5)-)-methyltransferase RsmF | -2.66 | 9.13E-03 |
| COG0018J | STM14_2322 | STM1909 | *argS* | arginyl-tRNA synthetase | -2.27 | 1.78E-02 |
| COG0231J | STM14_2733 | STM2211.S | *yeiP* | elongation factor P | -2.36 | 1.31E-02 |
| COG2890J | STM14_2934 | STM2385 | *yfcB* | N5-glutamine S-adenosyl-L-methionine-dependent methyltransferase | -2.21 | 2.21E-02 |

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|---|---|---|---|---|---|---|
| COG0336J | STM14_3277 | STM2674 | *trmD* | tRNA (guanine-N(1)-)-methyltransferase | -2.35 | 1.25E-02 |
| COG0806J | STM14_3278 | STM2675 | *rimM* | 16S rRNA-processing protein | -2.52 | 7.25E-03 |
| COG0828J | STM14_3886 | STM3209 | *rpsU* | 30S ribosomal protein S21 | -4.78 | 1.11E-07 |
| COG2813J | STM14_3899 | STM3220 | *ygjO* | putative methyltransferase | -2.24 | 2.03E-02 |
| *COG0513LKJ | STM14_3962 | STM3280.S | *deaD* | ATP-dependent RNA helicase DeaD | -2.49 | 9.58E-03 |
| COG0184J | STM14_3966 | STM3283 | *rpsO* | 30S ribosomal protein S15 | -2.60 | 5.31E-03 |
| COG0211J | STM14_3990 | STM3303 | *rpmA* | 50S ribosomal protein L27 | -2.16 | 2.32E-02 |
| COG0261J | STM14_3991 | STM3304 | *rplU* | 50S ribosomal protein L21 | -2.64 | 4.56E-03 |
| COG0102J | STM14_4037 | STM3345 | *rplM* | 50S ribosomal protein L13 | -2.43 | 9.46E-03 |
| COG0042J | STM14_4082 | STM3384 | *yhdG* | tRNA-dihydrouridine synthase B | -3.18 | 4.68E-04 |
| COG0203J | STM14_4117 | STM3414 | *rplQ* | 50S ribosomal protein L17 | -2.14 | 2.51E-02 |
| COG0522J | STM14_4119 | STM3416 | *rpsD* | 30S ribosomal protein S4 | -2.33 | 1.31E-02 |
| COG0100J | STM14_4120 | STM3417 | *rpsK* | 30S ribosomal protein S11 | -2.06 | 3.24E-02 |
| COG1841J | STM14_4125 | STM3422 | *rpmD* | 50S ribosomal protein L30 | -1.97 | 4.07E-02 |
| COG0098J | STM14_4126 | STM3423 | *rpsE* | 30S ribosomal protein S5 | -2.27 | 1.67E-02 |
| COG0256J | STM14_4127 | STM3424 | *rplR* | 50S ribosomal protein L18 | -2.32 | 1.36E-02 |
| COG0097J | STM14_4128 | STM3425 | *rplF* | 50S ribosomal protein L6 | -2.55 | 6.41E-03 |
| COG0096J | STM14_4129 | STM3426 | *rpsH* | 30S ribosomal protein S8 | -3.32 | 2.75E-04 |
| COG0199J | STM14_4130 | STM3427.S | *rpsN* | 30S ribosomal protein S14 | -3.19 | 4.43E-04 |
| COG0094J | STM14_4131 | STM3428 | *rplE* | 50S ribosomal protein L5 | -2.66 | 4.25E-03 |
| COG0198J | STM14_4132 | STM3429 | *rplX* | 50S ribosomal protein L24 | -2.46 | 9.13E-03 |
| COG0185J | STM14_4139 | STM3436 | *rpsS* | 30S ribosomal protein S19 | -2.35 | 1.26E-02 |
| COG0090J | STM14_4140 | STM3437 | *rplB* | 50S ribosomal protein L2 | -2.01 | 3.66E-02 |
| COG0089J | STM14_4141 | STM3438 | *rplW* | 50S ribosomal protein L23 | -2.45 | 9.13E-03 |
| COG0088J | STM14_4142 | STM3439 | *rplD* | 50S ribosomal protein L4 | -2.35 | 1.25E-02 |
| COG0087J | STM14_4143 | STM3440 | *rplC* | 50S ribosomal protein L3 | -2.41 | 1.01E-02 |
| COG0051J | STM14_4144 | STM3441 | *rpsJ* | 30S ribosomal protein S10 | -3.08 | 6.95E-04 |
| COG0049J | STM14_4151 | STM3447 | *rpsG* | 30S ribosomal protein S7 | -2.49 | 8.23E-03 |
| COG0267J | STM14_4489 | STM3727 | *rpmG* | 50S ribosomal protein L33 | -3.09 | 6.80E-04 |
| COG0227J | STM14_4490 | STM3728 | *rpmB* | 50S ribosomal protein L28 | -2.38 | 1.13E-02 |
| COG0689J | STM14_4496 | STM3734 | *rph* | ribonuclease PH | -2.86 | 2.40E-03 |
| COG0230J | STM14_4634 | STM3839 | *rpmH* | 50S ribosomal protein L34 | -2.33 | 1.31E-02 |
| COG0594J | STM14_4635 | STM3840 | *rnpA* | ribonuclease P | -3.52 | 1.08E-04 |
| COG0080J | STM14_4986 | STM4149 | *rplK* | 50S ribosomal protein L11 | -2.15 | 2.45E-02 |
| COG0360J | STM14_5275 | STM4391 | *rpsF* | 30S ribosomal protein S6 | -3.38 | 2.16E-04 |
| COG0238J | STM14_5277 | STM4393 | *rpsR* | 30S ribosomal protein S18 | -3.66 | 5.61E-05 |
| COG2813J | STM14_5473 | STM4556 | *rsmC* | 16S ribosomal RNA m2G1207 methyltransferase | -2.50 | 9.74E-03 |
| COG4108J | STM14_5478 | STM4560 | *prfC* | peptide chain release factor 3 | -2.43 | 1.06E-02 |
| *Transcription (K)* | | | | | | |

| | | | | | | |
|---|---|---|---|---|---|---|
| *COG0553KL | STM14_0116 | STM0096 | *hepA* | ATP-dependent helicase HepA | -2.09 | 3.46E-02 |
| COG1278K | STM14_0732 | STM0629 | *cspE* | cold shock protein CspE | -3.42 | 1.65E-04 |
| *COG0513LKJ | STM14_0951 | STM0820 | *rhlE* | ATP-dependent RNA helicase RhlE | -3.54 | 2.75E-04 |
| COG1609K | STM14_1727 | STM1430 | *purR* | DNA-binding transcriptional repressor PurR | -2.33 | 1.69E-02 |
| *COG0513LKJ | STM14_2001 | STM1655 | *dbpA* | ATP-dependent RNA helicase DbpA | -2.11 | 4.28E-02 |
| COG4776K | STM14_2056 | STM1702 | *rnb* | exoribonuclease II | -2.25 | 1.89E-02 |
| COG1414K | STM14_3742 | STM3098 | - | putative transcriptional regulator | -2.07 | 4.85E-02 |
| *COG0513LKJ | STM14_3962 | STM3280.S | *deaD* | ATP-dependent RNA helicase DeaD | -2.49 | 9.58E-03 |
| *COG2901KL | STM14_4083 | STM3385 | *fis* | DNA-binding protein Fis | -3.85 | 2.71E-05 |
| COG0202K | STM14_4118 | STM3415 | *rpoA* | DNA-directed RNA polymerase subunit alpha | -1.98 | 4.03E-02 |
| *Replication, recombination & repair (L)* | | | | | | |
| *COG0553KL | STM14_0116 | STM0096 | *hepA* | ATP-dependent helicase HepA | -2.09 | 3.46E-02 |
| *COG0513LKJ | STM14_0951 | STM0820 | *rhlE* | ATP-dependent RNA helicase RhlE | -3.54 | 2.75E-04 |
| COG0116L | STM14_1204 | STM1061 | *ycbY* | 23S rRNA m(2)G2445 methyltransferase | -2.48 | 1.01E-02 |
| COG0188L | STM14_2804 | STM2272 | *gyrA* | DNA gyrase subunit A | -2.04 | 3.46E-02 |
| *COG2901KL | STM14_4083 | STM3385 | *fis* | DNA-binding protein Fis | -3.85 | 2.71E-05 |
| COG3344L | STM14_4641 | STM3846.s | - | putative reverse transcriptase | -2.47 | 9.13E-03 |
| COG2965L | STM14_5276 | STM4392 | *priB* | primosomal replication protein N | -2.88 | 1.83E-03 |
| *COG0513LKJ | STM14_2001 | STM1655 | *dbpA* | ATP-dependent RNA helicase DbpA | -2.11 | 4.28E-02 |
| *COG0513LKJ | STM14_3962 | STM3280.S | *deaD* | ATP-dependent RNA helicase DeaD | -2.49 | 9.58E-03 |
| *Signal transduction mechanisms (T)* | | | | | | |
| COG3109T | STM14_2233 | STM1846 | *proQ* | putative solute/DNA competence effector | -2.47 | 9.13E-03 |
| *Cell wall/membrane/envelope biogenesis (M)* | | | | | | |
| COG0768M | STM14_0148 | STM0122 | *ftsI* | division specific transpeptidase | -2.22 | 1.95E-02 |
| COG0463M | STM14_0651 | STM0558 | *yfdH* | putative glycosyltransferase | -4.37 | 3.91E-05 |
| COG3137M | STM14_1611 | STM1327 | *ydiY* | putative outer membrane protein | -3.74 | 4.75E-05 |
| COG0768M | STM14_2324 | STM1910 | - | putative penicillin-binding protein | -2.53 | 1.06E-02 |
| COG4623M | STM14_3147 | STM2567 | *yfhD* | putative transglycosylase | -2.34 | 1.38E-02 |
| COG0463M | STM14_5055 | STM4205 | - | putative phage glycosyltransferase | -3.24 | 4.46E-04 |
| COG1346M | STM14_5138 | STM4272 | - | putative inner membrane protein | -2.38 | 1.57E-02 |
| *Cell motility (N)* | | | | | | |
| *COG1261NO | STM14_1343 | STM1173 | *flgA* | flagellar basal body P-ring biosynthesis protein FlgA | -2.77 | 5.12E-03 |
| COG1815N | STM14_1345 | STM1174 | *flgB* | flagellar basal body rod protein FlgB | -2.02 | 3.72E-02 |
| COG2063N | STM14_1351 | STM1180 | *flgH* | flagellar basal body L-ring protein | -2.78 | 4.56E-03 |
| *COG1298NU | STM14_2327 | STM1913 | *flhA* | flagellar biosynthesis protein FlhA | -2.13 | 3.08E-02 |
| *COG1377NU | STM14_2328 | STM1914 | *flhB* | flagellar biosynthesis protein FlhB | -2.60 | 9.13E-03 |

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|---|---|---|---|---|---|---|
| *COG1677NU | STM14_2388 | STM1968 | *fliE* | flagellar hook-basal body protein FliE | -2.89 | 5.93E-03 |
| *COG1766NU | STM14_2390 | STM1969 | *fliF* | flagellar MS-ring protein | -2.36 | 1.26E-02 |
| COG1536N | STM14_2391 | STM1970 | *fliG* | flagellar motor switch protein G | -2.02 | 3.72E-02 |
| *Intracellular trafficking, secretion, & vesicular transport (U)* | | | | | | |
| COG0848U | STM14_0868 | STM0746 | *tolR* | colicin uptake protein TolR | -2.03 | 3.66E-02 |
| *COG1298NU | STM14_2327 | STM1913 | *flhA* | flagellar biosynthesis protein FlhA | -2.13 | 3.08E-02 |
| *COG1377NU | STM14_2328 | STM1914 | *flhB* | flagellar biosynthesis protein FlhB | -2.60 | 9.13E-03 |
| *COG1677NU | STM14_2388 | STM1968 | *fliE* | flagellar hook-basal body protein FliE | -2.89 | 5.93E-03 |
| *COG1766NU | STM14_2390 | STM1969 | *fliF* | flagellar MS-ring protein | -2.36 | 1.26E-02 |
| COG1314U | STM14_3976 | STM3293 | *secG* | preprotein translocase subunit SecG | -1.98 | 4.03E-02 |
| COG0706U | STM14_4637 | STM3842 | *yidC* | putative inner membrane protein translocase component YidC | -2.78 | 2.75E-03 |
| COG0805U | STM14_4781 | STM3975 | *tatC* | TatABCE protein translocation system subunit | -2.05 | 3.46E-02 |
| COG0690U | STM14_4984 | STM4147 | *secE* | preprotein translocase subunit SecE | -2.14 | 2.77E-02 |
| *Posttranslational modification, protein turnover, chaperones (O)* | | | | | | |
| COG1067O | STM14_1212 | STM1068 | *lonH* | putative protease | -2.26 | 1.89E-02 |
| *COG1261NO | STM14_1343 | STM1173 | *flgA* | flagellar basal body P-ring biosynthesis protein FlgA | -2.77 | 5.12E-03 |
| COG1214O | STM14_2202 | STM1820 | *yeaZ* | putative molecular chaperone | -2.43 | 1.87E-02 |
| COG0826O | STM14_2634 | STM2136 | *yegQ* | putative protease | -3.38 | 5.08E-04 |
| *General function prediction only (R)* | | | | | | |
| COG1054R | STM14_1324 | STM1156 | *yceA* | hypothetical protein | -2.65 | 4.93E-03 |
| COG2915R | STM14_1411 | STM1233 | *ycfC* | hypothetical protein | -2.54 | 8.96E-03 |
| COG4106R | STM14_2317 | STM1905 | *yecO* | putative SAM-dependent methyltransferase | -2.45 | 1.08E-02 |
| COG1160R | STM14_3089 | STM2519 | *engA* | GTP-binding protein EngA | -2.38 | 1.23E-02 |
| COG0820R | STM14_3097 | STM2525 | *yfgB* | hypothetical protein | -2.62 | 5.19E-03 |
| COG1159R | STM14_3160 | STM2580 | *era* | GTP-binding protein Era | -2.33 | 1.38E-02 |
| COG0536R | STM14_3988 | STM3301 | *obgE* | GTPase ObgE | -2.47 | 9.46E-03 |
| COG2252R | STM14_4646 | STM3851.S | *yieG* | putative xanthine/uracil permease family protein | -2.07 | 4.03E-02 |
| COG2252R | STM14_5133 | STM4268 | *yjcD* | hypothetical protein | -2.15 | 4.39E-02 |
| COG1380R | STM14_5137 | STM4271 | - | LrgA family protein | -2.14 | 3.44E-02 |
| *Function unknown (S)* | | | | | | |
| COG1576S | STM14_0749 | STM0641 | *ybeA* | SPOUT methyltransferase superfamily protein | -2.15 | 3.74E-02 |
| COG0799S | STM14_0750 | STM0642 | *ybeB* | hypothetical protein | -2.64 | 9.73E-03 |
| COG1376S | STM14_977 | STM0837 | *ybiS* | hypothetical protein | -2.82 | 2.64E-03 |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
| COG1944S | STM14_1101 | STM0975 | *ycaO* | putative cytoplasmic protein | -3.12 | 7.68E-04 |
| COG3781S | STM14_1845 | STM1527 | - | putative inner membrane protein | -2.64 | 6.09E-03 |
| COG2983S | STM14_2190 | STM1811 | *ycgN* | hypothetical protein | -2.18 | 3.15E-02 |
| COG3101S | STM14_2930 | STM2381 | *yfcM* | putative cytoplasmic protein | -1.92 | 4.97E-02 |
| COG2990S | STM14_3352 | STM2781 | *virK* | virulence protein | -3.38 | 2.76E-04 |
| COG2862S | STM14_3818 | STM3153 | *yqhA* | hypothetical protein | -2.21 | 2.52E-02 |
| COG3036S | STM14_4114 | STM3411 | - | putative cytoplasmic protein | -1.96 | 4.85E-02 |
| COG2860S | STM14_4502 | STM3738 | - | putative inner membrane protein | -2.61 | 7.47E-03 |
| COG0759S | STM14_4636 | STM3841 | - | hypothetical protein | -3.31 | 4.43E-04 |
| COG3085S | STM14_4694 | STM3898 | *yifE* | hypothetical protein | -1.92 | 4.77E-02 |
| COG2246S | STM14_5056 | STM4206 | - | putative phage glucose translocase | -2.33 | 2.32E-02 |
| COG3242S | STM14_5246 | STM4365 | *yjeT* | putative inner membrane protein | -2.07 | 4.04E-02 |
| *Not assigned* |  |  |  |  |  |  |
|  | STM14_0296 | - | - | hypothetical protein | -5.68 | 2.21E-09 |
|  | STM14_0731 | STM0628 | *pagP* | palmitoyl transferase for Lipid A | -2.90 | 3.53E-03 |
|  | STM14_1076 | STM0954 | - | putative inner membrane protein | -3.21 | 4.40E-04 |
|  | STM14_1493 | STM1242 | *envE* | putative envelope protein | -3.49 | 8.10E-04 |
|  | STM14_1760 | STM1461.S | *ydgT* | oriC-binding nucleoid-associated protein | -2.14 | 2.89E-02 |
|  | STM14_1982 | STM1638 | - | putative SAM-dependent methyltransferase | -2.25 | 2.72E-02 |
|  | STM14_2366 | - | - | putative inner membrane protein | -2.57 | 6.92E-03 |
|  | STM14_2367 | STM1949 | *yecF* | hypothetical protein | -1.97 | 4.05E-02 |
|  | STM14_2489 | STM2005 | - | putative endoprotease | -4.86 | 5.54E-06 |
|  | STM14_2562 | - | - | hypothetical protein | -4.22 | 5.54E-06 |
|  | STM14_2881 | - | - | hypothetical protein | -2.14 | 2.78E-02 |
|  | STM14_3146 | STM2566 | - | hypothetical protein | -2.55 | 1.83E-02 |
|  | STM14_3353 | - | - | hypothetical protein | -2.65 | 5.55E-03 |
| COG5653 | STM14_3354 | STM2782 | *mig-14* | putative transcriptional activator | -2.25 | 1.85E-02 |
|  | STM14_3467 | STM2868 | *orgC* | putative cytoplasmic protein | -2.30 | 2.03E-02 |
|  | STM14_3468 | STM2869 | *orgB* | needle complex export protein | -2.70 | 4.25E-03 |
|  | STM14_3732 | STM3089 | *yqgD* | putative inner membrane protein | -2.22 | 2.10E-02 |
|  | STM14_4633 | - | - | hypothetical protein | -2.39 | 2.11E-02 |
|  | STM14_4640 | STM3845 | - | putative inner membrane protein | -2.10 | 2.95E-02 |
|  | STM14_4797 | - | - | hypothetical protein | -5.59 | 2.69E-09 |
|  | STM14_4898 | - | - | hypothetical protein | -2.25 | 3.06E-02 |
|  | STM14_4970 | - | - | hypothetical protein | -5.49 | 3.97E-09 |
|  | STM14_5054 | STM4204 | - | putative inner membrane protein | -2.85 | 2.50E-03 |
|  | STM14_5196 | - | - | hypothetical protein | -3.02 | 1.66E-03 |

*****Genes assigned to more than one COG

## Table S4: Up-regulated genes under acidified $NaNO_2$ adaptation in *S*. Typhimurium 14028 WT

| COG | 14028 identifier | LT2 identifier | Gene name | Product | $\log_2$ FC | p-value (BH-adjusted) |
|---|---|---|---|---|---|---|
| *Energy production & conversion (C)* | | | | | | |
| COG1151C | STM14_1052 | STM0937 | *hcp* | hydroxylamine reductase | 3.38 | 2.74E-04 |
| COG1018C | STM14_3135 | STM2556 | *hmpA* | nitric oxide dioxygenase | 4.53 | 1.62E-06 |
| *Carbohydrate transport & metabolism (G)* | | | | | | |
| COG1129G | STM14_4899 | STM4074 | *ego* | putative ABC-type aldose transport system ATPase component | 2.89 | 2.88E-03 |
| COG1172G | STM14_4900 | STM4075 | *ydeY* | putative sugar transport protein | 2.74 | 5.86E-03 |
| COG1172G | STM14_4901 | STM4076 | *ydeZ* | putative sugar transport protein | 2.92 | 2.61E-03 |
| COG1879G | STM14_4902 | STM4077 | *yneA* | putative sugar transport protein | 2.34 | 2.42E-02 |
| COG1830G | STM14_4903 | STM4078 | *yneB* | aldolase | 2.15 | 4.66E-02 |
| *Amino acid transport & metabolism (E)* | | | | | | |
| COG0531E | STM14_0817 | STM0700 | *potE* | putrescine transporter | 3.40 | 2.60E-04 |
| COG1982E | STM14_0818 | STM0701 | *speF* | ornithine decarboxylase | 3.23 | 5.40E-04 |
| COG2502E | STM14_4674 | STM3877 | *asnA* | asparagine synthetase AsnA | 2.15 | 4.66E-02 |
| COG0531E | STM14_5166 | STM4294 | *yjdE* | arginine:agmatin antiporter | 3.59 | 1.97E-04 |
| COG1982E | STM14_5169 | STM4296 | *adi* | catabolic arginine decarboxylase | 2.81 | 4.01E-03 |
| COG0078E | STM14_5358 | STM4465 | - | ornithine carbamoyltransferase | 3.56 | 1.97E-04 |
| COG0549E | STM14_5360 | STM4466 | - | carbamate kinase | 2.89 | 4.80E-03 |
| COG2235E | STM14_5361 | STM4467 | - | arginine deiminase | 2.72 | 5.86E-03 |
| *Coenzyme transport & metabolism (H)* | | | | | | |
| *COG1120PH | STM14_0688 | STM0590 | *fepC* | iron-enterobactin transporter ATP-binding protein | 4.50 | 7.64E-06 |
| *COG1169HQ | STM14_0693 | STM0595 | *entC* | isochorismate synthase | 3.42 | 4.84E-04 |
| *Lipid transport & metabolism (I)* | | | | | | |
| *COG1028IQR | STM14_0696 | STM0598 | *entA* | 2,3-dihydroxybenzoate-2,3-dehydrogenase | 4.57 | 7.64E-06 |
| *Inorganic ion transport & metabolism (P)* | | | | | | |
| COG1629P | STM14_0228 | STM0191 | *fhuA* | ferrichrome outer membrane transporter | 4.05 | 1.04E-05 |
| COG0614P | STM14_0230 | STM0193 | *fhuD* | iron-hydroxamate transporter substrate-binding subunit | 4.18 | 1.53E-05 |
| COG0609P | STM14_0231 | STM0194 | *fhuB* | iron-hydroxamate transporter permease subunit | 4.46 | 5.57E-06 |
| COG4771P | STM14_0682 | STM0585 | *fepA* | outer membrane receptor FepA | 2.40 | 1.97E-02 |
| *COG1120PH | STM14_0688 | STM0590 | *fepC* | iron-enterobactin transporter ATP-binding protein | 4.50 | 7.64E-06 |

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|---|---|---|---|---|---|---|
| COG4592P | STM14_0692 | STM0594 | *fepB* | iron-enterobactin transporter periplasmic binding protein | 2.24 | 4.27E-02 |
| COG3615P | STM14_1534 | STM1271 | *yeaR* | putative cytoplasmic protein | 3.37 | 2.87E-04 |
| COG3615P | STM14_2185 | STM1808 | - | putative cytoplasmic protein | 4.41 | 5.57E-06 |
| COG4771P | STM14_2713 | STM2199 | *cirA* | colicin I receptor | 2.37 | 2.74E-02 |
| COG0803P | STM14_3458 | STM2861 | *sitA* | putative periplasmic binding protein | 2.67 | 7.65E-03 |
| COG2906P | STM14_4147 | STM3444 | *bfd* | bacterioferritin-associated ferredoxin | 4.72 | 7.45E-07 |
| COG1918P | STM14_4221 | STM3505 | *feoA* | ferrous iron transport protein A | 2.87 | 3.61E-03 |
| COG0370P | STM14_4222 | STM3506 | *feoB* | ferrous iron transport protein B | 2.64 | 7.57E-03 |
| *Secondary metabolites biosynthesis, transport & catabolism (Q)* |  |  |  |  |  |  |
| COG1020Q | STM14_0686 | STM0588 | *entF* | enterobactin synthase subunit F | 3.03 | 1.75E-03 |
| *COG1169HQ | STM14_0693 | STM0595 | *entC* | isochorismate synthase | 3.42 | 4.84E-04 |
| COG1021Q | STM14_0694 | STM0596 | *entE* | enterobactin synthase subunit E | 3.52 | 2.74E-04 |
| COG1535Q | STM14_0695 | STM0597 | *entB* | 2,3-dihydro-2,3-dihydroxybenzoate synthetase | 5.58 | 1.23E-07 |
| *COG1028IQR | STM14_0696 | STM0598 | *entA* | 2,3-dihydroxybenzoate-2,3-dehydrogenase | 4.57 | 7.64E-06 |
| COG0179Q | STM14_2684 | STM2177 | - | putative flutathione S-transferase | 2.62 | 1.21E-02 |
| *Transcription (K)* |  |  |  |  |  |  |
| *COG2197TK | STM14_3463 | STM2866 | *sprB* | transcriptional regulator | 2.46 | 1.48E-02 |
| COG2207K | STM14_3465 | STM2867 | *hilC* | invasion regulatory protein | 2.21 | 3.85E-02 |
| *Defense mechanisms (V)* |  |  |  |  |  |  |
| COG0841V | STM14_2626 | STM2128 | *yegO* | multidrug efflux system subunit MdtC | 2.34 | 2.83E-02 |
| *Signal transduction mechanisms (T)* |  |  |  |  |  |  |
| *COG2197TK | STM14_3463 | STM2866 | *sprB* | transcriptional regulator | 2.46 | 1.48E-02 |
| *Cell wall/membrane/envelope biogenesis (M)* |  |  |  |  |  |  |
| COG0810M | STM14_2100 | STM1737 | *tonB* | transporter | 2.67 | 8.01E-03 |
| COG2222M | STM14_4331 | STM3601 | - | putative phosphosugar isomerase | 2.27 | 3.47E-02 |
| *Intracellular trafficking, secretion, & vesicular transport (U)* |  |  |  |  |  |  |
| COG0848U | STM14_3824 | STM3158 | *exbD* | biopolymer transport protein ExbD | 2.19 | 4.24E-02 |
| *General function prediction only (R)* |  |  |  |  |  |  |
| *COG1028IQR | STM14_0696 | STM0598 | *entA* | 2,3-dihydroxybenzoate-2,3-dehydrogenase | 4.57 | 7.64E-06 |
| COG3467R | STM14_0816 | STM0699 | - | putative cytoplasmic protein | 3.44 | 2.60E-04 |
| COG4114R | STM14_5466 | STM4550 | *fhuF* | ferric hydroximate transport ferric iron reductase | 2.62 | 1.04E-02 |
| *Function unknown (S)* |  |  |  |  |  |  |
| COG3391S | STM14_1918 | STM1586 | - | hypothetical protein | 2.28 | 2.89E-02 |
| COG2128S | STM14_3385 | STM2804 | - | putative cytoplasmic protein | 3.32 | 6.83E-04 |

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|---|---|---|---|---|---|---|
| COG1917S | STM14_4895 | STM4071 | - | putative mannose-6-phosphate isomerase | 2.31 | 2.89E-02 |
| *Not assigned* | | | | | | |
| | STM14_0227 | - | - | hypothetical protein | 3.75 | 4.88E-05 |
| | STM14_0819 | - | - | hypothetical protein | 2.21 | 3.85E-02 |
| | STM14_1535 | STM1272 | *yoaG* | putative cytoplasmic protein | 3.03 | 1.38E-03 |
| | STM14_1885 | STM1562 | *hdeB* | acid-resistance protein | 7.12 | 1.78E-13 |
| | STM14_2227 | STM1841 | - | hypothetical protein | 2.55 | 1.12E-02 |
| | STM14_2269 | STM1868A | - | lytic enzyme | 3.17 | 7.45E-04 |
| | STM14_2270 | - | - | hypothetical protein | 3.29 | 4.18E-04 |
| | STM14_2271 | - | - | hypothetical protein | 4.24 | 7.82E-06 |
| | STM14_3456 | STM2860 | *ygbA* | hypothetical protein | 4.20 | 7.64E-06 |
| | STM14_4223 | STM3507 | *yhgG* | putative cytoplasmic protein | 2.82 | 5.37E-03 |

*Genes assigned to more than one COG

## Table S5: Down-regulated genes under acidified $NaNO_2$ adaptation in *S.* Typhimurium 14028 WT

| COG | 14028 identifier | LT2 identifier | Gene name | Product | $log_2$ FC | p-value (BH-adjusted) |
|---|---|---|---|---|---|---|
| *Energy production & conversion (C)* | | | | | | |
| COG0243C | STM14_1089 | STM0964 | *dmsA* | anaerobic dimethyl sulfoxide reductase subunit A | -2.75 | 4.94E-03 |
| COG0437C | STM14_1090 | STM0965 | *dmsB* | anaerobic dimethyl sulfoxide reductase subunit B | -4.56 | 1.04E-05 |
| COG0243C | STM14_1677 | STM1383 | *ttrA* | tetrathionate reductase complex subunit A | -3.88 | 2.38E-05 |
| COG0437C | STM14_1679 | STM1385 | *ttrB* | tetrathionate reductase complex subunit B | -2.19 | 4.10E-02 |
| COG0437C | STM14_1893 | STM1569 | *fdnH* | formate dehydrogenase-N beta subunit | -2.84 | 3.75E-03 |
| COG2181C | STM14_2129 | STM1761 | *narI* | nitrate reductase 1 subunit gamma | -2.54 | 1.12E-02 |
| COG2180C | STM14_2130 | STM1762 | *narJ* | nitrate reductase 1 subunit delta | -2.51 | 1.21E-02 |
| COG1140C | STM14_2131 | STM1763 | *narH* | nitrate reductase 1 subunit beta | -2.61 | 7.95E-03 |
| COG3005C | STM14_2784 | STM2255 | *napC* | cytochrome c-type protein NapC | -3.97 | 1.53E-05 |
| COG3043C | STM14_2785 | STM2256 | *napB* | diheme cytochrome c550 | -4.31 | 5.57E-06 |
| COG0348C | STM14_2786 | STM2257 | *napH* | quinol dehydrogenase membrane component | -3.73 | 5.57E-05 |
| COG0437C | STM14_2787 | STM2258 | *napG* | quinol dehydrogenase periplasmic component | -4.34 | 1.04E-05 |
| COG0243C | STM14_2788 | STM2259 | *napA* | nitrate reductase | -3.26 | 4.84E-04 |

| | | | | | | |
|---|---|---|---|---|---|---|
| COG4231C | STM14_2790 | STM2261 | *napF* | ferredoxin-type protein | -2.51 | 1.21E-02 |
| COG0243C | STM14_3103 | STM2530 | - | putative anaerobic dimethylsulfoxide reductase | -2.71 | 8.23E-03 |
| COG0243C | STM14_5178 | STM4305.S | - | putative anaerobic dimethylsulfoxide reductase subunit A | -2.51 | 1.26E-02 |
| COG0437C | STM14_5179 | STM4306 | - | putative anaerobic dimethylsulfoxide reductase subunit B | -3.23 | 8.77E-04 |
| *Carbohydrate transport & metabolism (G)* | | | | | | |
| COG3414G | STM14_2888 | STM2343 | - | putative cytoplasmic protein | -2.32 | 3.85E-02 |
| *Amino acid transport & metabolism (E)* | | | | | | |
| COG0747E | STM14_1515 | STM1255 | - | putative ABC transporter periplasmic binding protein | -2.28 | 2.89E-02 |
| *COG0601EP | STM14_1516 | STM1256 | - | putative ABC transporter protein | -2.34 | 2.53E-02 |
| *COG1173EP | STM14_1517 | STM1257 | - | putative ABC transporter protein | -2.45 | 1.75E-02 |
| *COG1124EP | STM14_1519 | STM1259 | - | ABC transporter ATP-binding protein | -2.71 | 6.49E-03 |
| *Inorganic ion transport & metabolism (P)* | | | | | | |
| *COG0601EP | STM14_1516 | STM1256 | - | putative ABC transporter protein | -2.34 | 2.53E-02 |
| *COG1173EP | STM14_1517 | STM1257 | - | putative ABC transporter protein | -2.45 | 1.75E-02 |
| *COG1124EP | STM14_1519 | STM1259 | - | ABC transporter ATP-binding protein | -2.71 | 6.49E-03 |
| COG3301P | STM14_1678 | STM1384 | *ttrC* | tetrathionate reductase complex subunit C | -2.63 | 7.70E-03 |
| COG1528P | STM14_2353 | STM1935 | *ftn* | ferritin | -2.81 | 3.75E-03 |
| COG3062P | STM14_2789 | STM2260 | *napD* | assembly protein for periplasmic nitrate reductase | -2.94 | 2.51E-03 |
| COG1118P | STM14_3716 | STM3075 | - | putative ABC-type cobalt transport system ATP-binding component | -2.52 | 1.93E-02 |
| COG1858P | STM14_4612 | STM3820 | - | putative cytochrome c peroxidase | -2.61 | 8.01E-03 |
| COG0376P | STM14_4936 | STM4106 | *katG* | hydroperoxidase | -2.38 | 1.97E-02 |
| COG3303P | STM14_5143 | STM4277 | *nrfA* | cytochrome c nitrite reductase | -3.44 | 2.60E-04 |
| *Transcription (K)* | | | | | | |
| *COG0378OK | STM14_3451 | STM2855 | *hypB* | hydrogenase nickel incorporation protein HypB | -2.50 | 1.33E-02 |
| *COG3604KT | STM14_3455 | STM2859 | *fhlA* | formate hydrogen-lyase transcriptional activator | -2.20 | 4.28E-02 |
| *Signal transduction mechanisms (T)* | | | | | | |
| *COG3604KT | STM14_3455 | STM2859 | *fhlA* | formate hydrogen-lyase transcriptional activator | -2.20 | 4.28E-02 |

| | | | | | | |
|---|---|---|---|---|---|---|
| *Cell wall/membrane/envelope biogenesis (M)* | | | | | | |
| COG3047M | STM14_2095 | STM1732 | *ompW* | outer membrane protein W | -2.30 | 2.78E-02 |
| *Cell motility (N)* | | | | | | |
| *COG3188NU | STM14_2653 | STM2150 | *stcC* | putative outer membrane protein | -2.55 | 1.26E-02 |
| *COG3539NU | STM14_2655 | STM2152 | *stcA* | putative fimbrial-like protein | -3.72 | 5.44E-05 |
| *Intracellular trafficking, secretion & vesicular transport (U)* | | | | | | |
| *COG3188NU | STM14_2653 | STM2150 | *stcC* | putative outer membrane protein | -2.55 | 1.26E-02 |
| *COG3539NU | STM14_2655 | STM2152 | *stcA* | putative fimbrial-like protein | -3.72 | 5.44E-05 |
| *Posttranslational modification, protein turnover, chaperones (O)* | | | | | | |
| COG4133O | STM14_2783 | STM2254 | *ccmA_1* | cytochrome c biogenesis protein CcmA | -3.11 | 2.52E-03 |
| *COG0378OK | STM14_3451 | STM2855 | *hypB* | hydrogenase nickel incorporation protein HypB | -2.50 | 1.33E-02 |
| COG0409O | STM14_3453 | STM2857 | *hypD* | putative hydrogenase formation protein | -2.18 | 4.66E-02 |
| COG0309O | STM14_3454 | STM2858 | *hypE* | putative hydrogenase formation protein | -2.97 | 3.19E-03 |
| COG0826O | STM14_3956 | STM3274 | *yhbU* | putative protease | -2.78 | 4.70E-03 |
| COG0826O | STM14_3957 | STM3275.S | *yhbV* | putative protease | -3.51 | 2.12E-04 |
| COG1138O | STM14_5147 | STM4281 | *nrfE* | formate-dependent nitrite reductase | -2.94 | 4.57E-03 |
| COG1180O | STM14_5484 | STM4565 | *yjjW* | pyruvate formate lyase-activating enzyme | -2.31 | 3.81E-02 |
| *General function prediction only (R)* | | | | | | |
| COG1123R | STM14_1518 | STM1258 | - | ABC transporter ATP-binding protein | -3.18 | 8.66E-04 |
| COG2962R | STM14_3601 | STM2986.Sc | - | putative integral membrane protein | -2.64 | 7.65E-03 |
| COG1661R | STM14_3712 | STM3071 | - | putative DNA-binding protein | -2.82 | 4.57E-03 |
| COG0375R | STM14_3808 | STM3144 | *hypA_2* | hydrogenase nickel incorporation protein HybF | -2.25 | 4.48E-02 |
| COG3381R | STM14_5181 | STM4308 | - | putative anaerobic dehydrogenase component | -3.24 | 8.34E-04 |
| *Function unknown (S)* | | | | | | |
| COG1584S | STM14_0009 | STM0009 | *yaaH* | hypothetical protein | -2.62 | 1.22E-02 |
| *Not assigned* | | | | | | |
| | STM14_1092 | - | - | hypothetical protein | -2.48 | 2.17E-02 |
| | STM14_2354 | STM1936 | *yecH* | putative cytoplasmic protein | -2.32 | 2.89E-02 |
| | STM14_2652 | STM2149 | *stcD* | putative outer membrane lipoprotein | -2.46 | 1.82E-02 |
| | STM14_3211 | - | - | hypothetical protein | -2.59 | 8.23E-03 |
| | STM14_3713 | STM3072 | - | putative inner membrane protein | -2.77 | 4.84E-03 |
| | STM14_5485 | STM4566 | *yjjI* | hypothetical protein | -2.22 | 3.85E-02 |

*Genes assigned to more than one COG