

## Supplementary Information

### Supplementary Methods

*Sample sites and benthic cover.* Field studies were conducted across four islands in the Southern Line Island archipelago (southern portion) spanning 4°01'S to 11°26'S from October 18 to November 6, 2013. Mean daily PAR at 10m depth on the forereef measured of  $312 \pm 214 \mu\text{mol photons m}^{-1} \text{ s}^{-1}$  (LI-COR, Inc., [www.licor.com](http://www.licor.com)) and water temperature ranged from  $28.1 \pm 0.5^\circ\text{C}$ . The percent cover of benthic corals and algae was estimated in each tent mesocosm using photoquads and the program photogrid as described in Smith et al., (1).

*In situ reef collections.* Collapsible benthic isolation tents (cBITs), referred to in text as benthic chambers, were used to assess effects of specific benthic communities *in situ*. The triangular pyramids, which were developed and built at the Smith and Rohwer laboratories, primarily consist of three transparent polycarbonate side panels joined by flexible polyvinyl chloride strips connected by stainless steel cables (as described in Haas et al., (2)). Benthic chambers were deployed at 10 m on the fore reef habitat on all four southern Line Islands described in this study. All benthic chambers were equipped with autonomous multiprobe (MANTA2 Eureka Water Probes, [www.waterprobes.com](http://www.waterprobes.com)) that monitored temperature (precision  $0.01^\circ\text{C}$ ), DO (precision  $0.01 \text{ mg l}^{-1}$ , accuracy  $\pm 1\%$ , automatic temperature and pressure compensated and salinity corrected), pH and conductivity (accuracy  $\pm 1\%$ , automatic temperature compensated) at 15 min intervals.

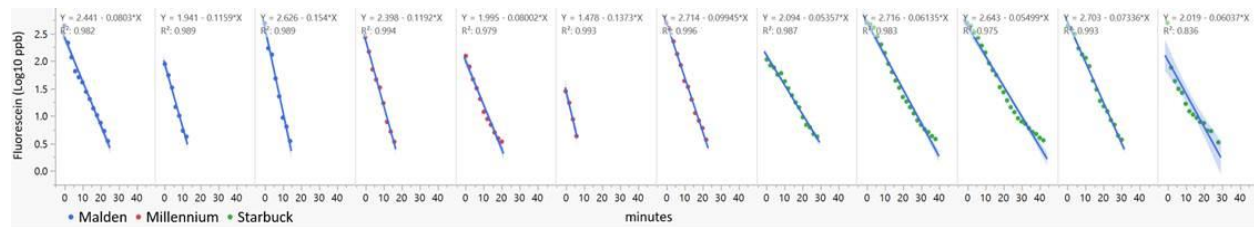
The rate of water exchange in the benthic chambers was calculated using dilution rates of Fluorescein dye. Fluorescein dye was injected into control chambers on Malden, Millennium, and Starbuck and the concentrations measured using a multiprobe sensor with a fluorometer (precision  $0.01\text{ppb}$ ; Manta2, Eureka Water Probes, TX, USA). Chamber flushing rates,  $F$  ( $\text{liters min}^{-1}$ ) were calculated from the dilution rate,  $D$  (slope,  $\log_{10}\text{ppb min}^{-1}$  divided by the initial concentration,  $\log_{10}\text{ppb}$ ) multiplied by chamber volume (100 liters). Mean flushing rates were  $5.04$ ,  $5.48$ , and  $2.52 \text{ liters min}^{-1}$  for Malden ( $n=3$ ), Millennium ( $n=4$ ), and Starbuck ( $n=5$ ), respectively (Supplementary Figure 1).

*Sequence library preparation and bioinformatics.* Nucleic acids were extracted from microbial communities collected on Sterivex filters using a modified protocol of the Nucleospin Tissue Kit (Machery-Nagel, Santa Clara, USA) as described previously by Kelly et al., (3). DNA for each sample was normalized to  $0.2\text{ng}/\mu\text{l}$  and libraries were built using Nextera XT (Illumina, San Diego, USA). Metagenomic libraries were sequenced on the MiSeq2 using the 600 cycle PE sequencing reagent kit (Illumina, San Diego, USA). The shotgun sequence libraries were post-processed using Prinseq (4) to remove low quality reads (ambiguous bases, low complexity, short read length, replicates). Sequence reads were compared to the SEED database for metabolic and taxonomic assignments using SUPERFOCUS (5), which aligns sequence similarities using RAPSearch2 (6) and performs a 98% clustering of the proteins in the database to reduce computational taxation. Metagenomic reads aligned against the SEED database to get the functional annotation were subsequently extracted to identify the taxa that are encoding the respective protein coding genes from NCBI using Taxonkit (<http://bioinf.shenwei.me/taxonkit/>). For putative 16S rRNA gene sequences, alignment, classification, sequence distance calculation, OTU clustering, phylogenetic tree construction and calculation of among-sample phylogenetic distances were done using the software package mothur (7) following previously published bioinformatics pipelines (8). Additional phylogenetics were conducted using the SINA multiple

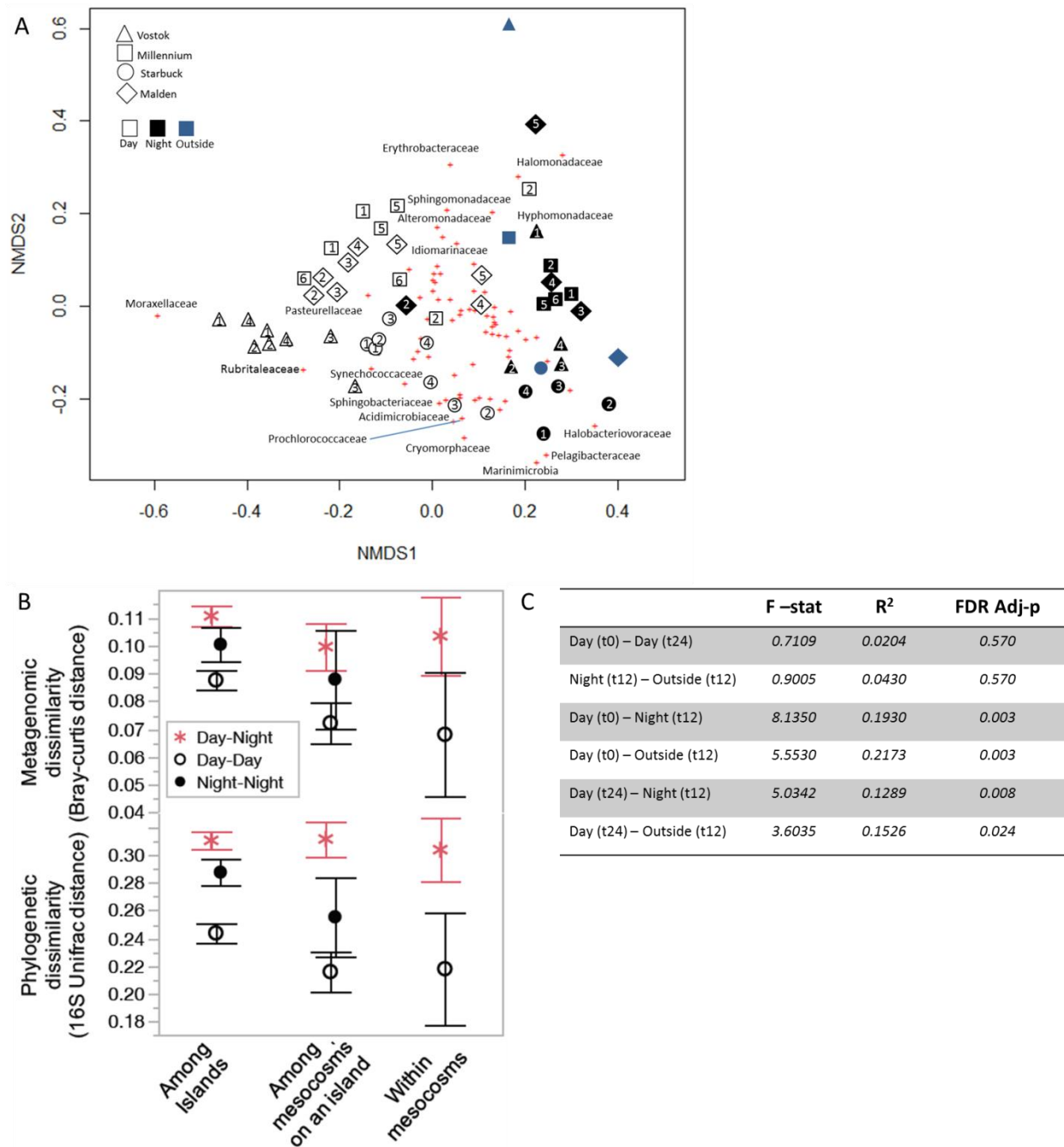
sequence alignment algorithm (9) and the RaxML maximum likelihood phylogeny reconstruction algorithm (10).

### Supplementary References

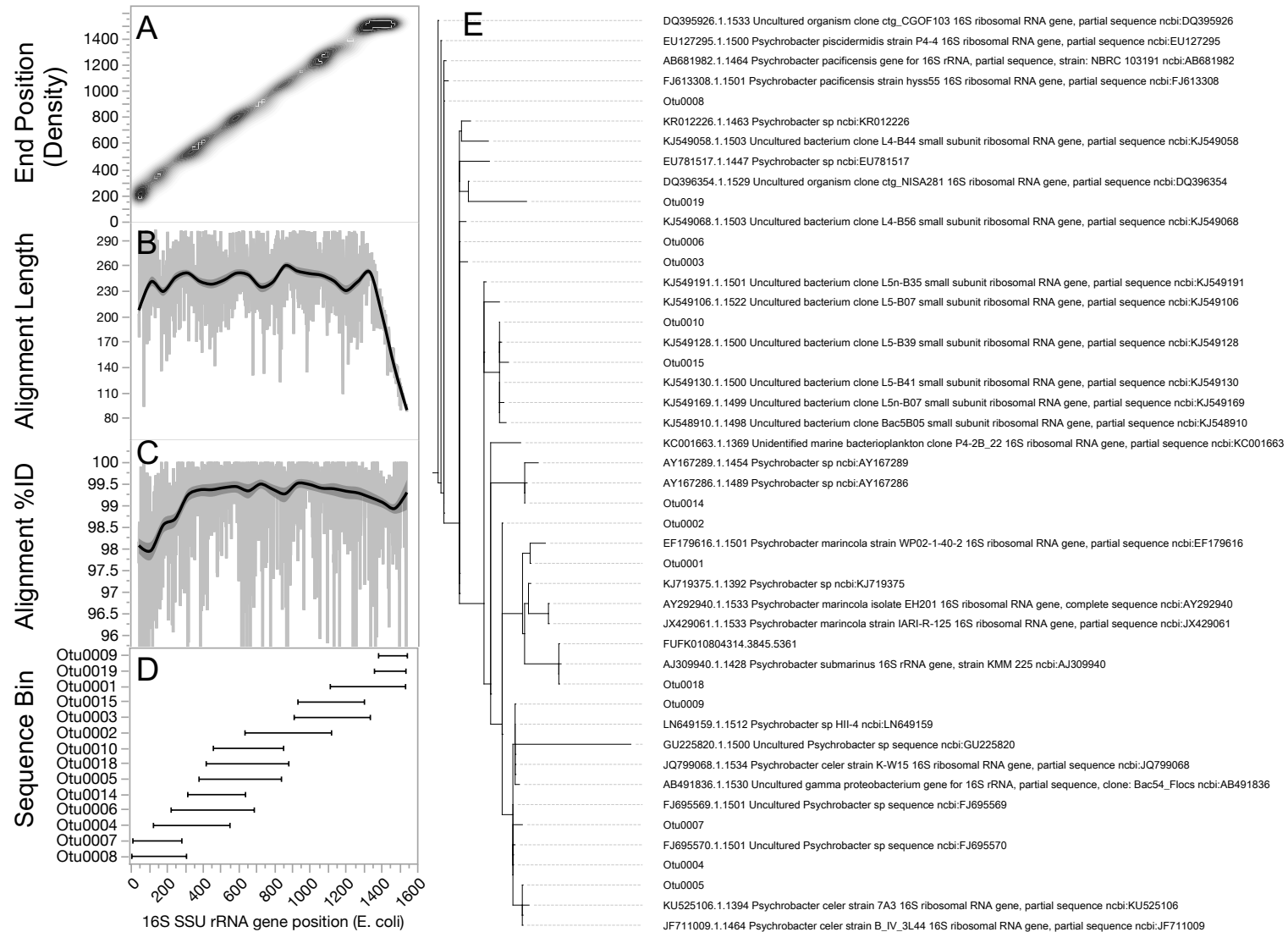
1. Smith JE, *et al.* Re-evaluating the health of coral reef communities: baselines and evidence for human impacts across the central Pacific. *Proceedings of the Royal Society B* 283: rspb20151985 (2016).
2. Haas AF, *et al.* Influence of coral and algal exudates on microbially mediated reef metabolism. *PeerJ* 1:e106 (2013).
3. Kelly LW, *et al.* Local genomic adaptation of coral reef-associated microbiomes to gradients of natural variability and anthropogenic stressors. *P Natl Acad Sci USA* 111(28):10227-10232 (2014).
4. Schmieder R & Edwards R. Quality control and preprocessing of metagenomic datasets. *Bioinformatics* 27(6):863-864 (2011).
5. Silva GGZ, Green KT, Dutilh BE, & Edwards RA. SUPER-FOCUS: a tool for agile functional analysis of shotgun metagenomic data. *Bioinformatics* 32(3):354-361 (2016).
6. Zhao Y, Tang H, & Ye Y. RAPSearch2: a fast and memory-efficient protein similarity search tool for next-generation sequencing data. *Bioinformatics* 28(1):125-126 (2012).
7. Schloss PD, *et al.* Introducing mothur: Open-Source, Platform-Independent, Community-Supported Software for Describing and Comparing Microbial Communities. *Appl Environ Microb* 75(23):7537-7541 (2009).
8. Nelson CE & Carlson CA. Tracking differential incorporation of dissolved organic carbon types among diverse lineages of Sargasso Sea bacterioplankton. *Environ Microbiol* 14(6):1500-1516 (2012).
9. Pruesse E1, Peplies J, Glöckner FO. SINA: accurate high-throughput multiple sequence alignment of ribosomal RNA genes. *Bioinformatics* 28(14):1823-1829 (2012).
10. Stamatakis A. RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics*. 30(9):1312-1313 (2014).
11. Benjamini Y & Hochberg Y. Controlling the False Discovery Rate - a Practical and Powerful Approach to Multiple Testing. *J Roy Stat Soc B Met* 57(1):289-300 (1995).



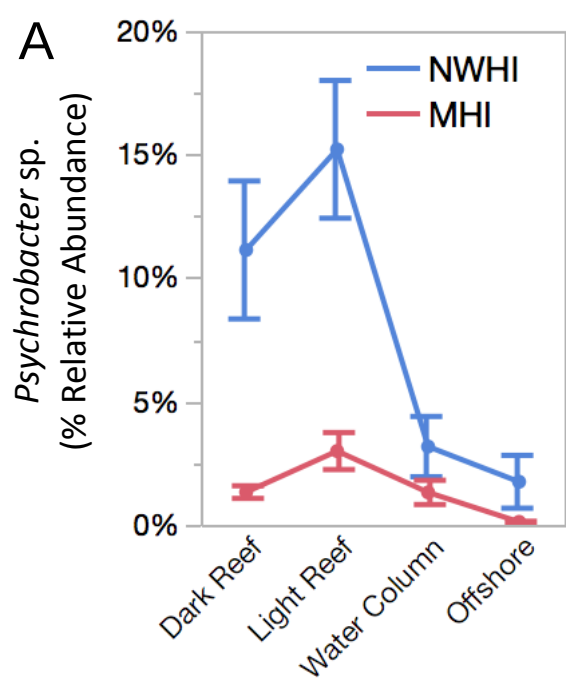
**Supplementary Figure 1. Measurement of benthic chamber flushing rates.** Estimates of water exchange in the benthic chambers were calculated using Fluorescein dye dilution rates. Dilution of Fluorescein dye was measured in control chambers on Malden, Millennium, and Starbuck using a multiprobe sensor with a fluorometer (Manta2, Eureka Water Probes, TX, USA). Chamber flushing rates,  $F$  (liters  $\text{min}^{-1}$ ) were calculated from the dilution rate,  $D$  (slope,  $\log_{10}\text{ppb min}^{-1}$  divided by the initial concentration,  $\log_{10}\text{ppb}$ ) multiplied by chamber volume (100 liters). Mean flushing rates were 5.04, 5.48, and 2.52 liters  $\text{min}^{-1}$  for Malden, Millennium, and Starbuck, respectively. Therefore, the turnover rate or *residence time* of seawater within the benthic chambers is estimated to be between 20 and 40 minutes.



**Supplementary Figure 2: Day-night community dissimilarity of reef microbes.** (A) Nonmetric Multidimensional scaling (NMDS, stress = 0.13) of the metagenomic taxonomic composition of the reef microbial communities (Family level). Pairwise comparisons are grouped according to time of day (symbols) and location (categories across the x-axis); “Outside” refers to nighttime samples collected from the ambient reef, while T0 samples are considered daytime samples collected from the ambient reef. (B) Comparison of pairwise microbial community distances of protein coding genes (metagenomic dissimilarity) and species composition (phylogenetic dissimilarity) among sample sets; error bars depict the 95% confidence interval of the mean. (C) PERMANOVA tests (package *adonis* in R) of pairwise community dissimilarity showing that daytime ambient (T0) and tent (T24) communities do not differ ( $p = 0.57$ ), nighttime ambient (outside) and tent (T12) communities do not differ ( $p = 0.57$ ), but all other pairwise comparisons are significant ( $p < 0.05$ ). Including Island in the full model or either daytime or nighttime data subsets always yields a significant Island effect and a nonsignificant interaction term, clarifying that diel patterning does not differ among islands. The false discovery rate was controlled by adjusting p-values according to Benjamini and Hochberg 1995 (11).



Supplementary Figure 3. Alignment of shotgun metagenomic 16S rRNA coding sequences assigned to OTUs classified as *Psychrobacter* by SINA alignment to the SILVA database. Distribution density (A), alignment length (B) and alignment identity (C) of reads clustered into positional OTUs (D) and consensus sequences visualized in a maximum likelihood phylogeny (E) with nearest neighbors from SILVA v132 RefNR and built by RaxML using the GTR model.



**B**

| Island     | Year Collected | % RA Moraxellaceae |   |       |
|------------|----------------|--------------------|---|-------|
|            |                | Min                | - | Max   |
| Flint      | 2009           | 1.22               |   | 33.89 |
| Vostok     | 2009           | 4.22               |   | 4.22  |
| Millennium | 2009           | 1.99               |   | 3.54  |
| Starbuck   | 2009           | 1.31               |   | 1.76  |
| Malden     | 2009           | 7.11               |   | 7.36  |
| Jarvis     | 2010           | 0.32               |   | 17.28 |
| Kiritimati | 2010           | 0.62               |   | 0.67  |
| Tabuaeran  | 2010           | 5.11               |   | 11.00 |
| Teraina    | 2010           | 3.68               |   | 39.93 |
| Palmyra    | 2010           | 0.55               |   | 0.55  |
| Kingman    | 2010           | 0.79               |   | 0.79  |

**Supplementary Figure 4: Prevalence of *Psychrobacter* spp. on 22 Pacific islands.** (A) *Psychrobacter* sp. abundance (based on 16S rRNA gene amplicon libraries) in the Main and North-west Hawaiian Islands collected in 2016. (B) Moraxellaceae Family abundance from metagenomic libraries on 11 Line Island collected in 2009 and 2010 published in Kelly et al., 2014 (3). RA, relative abundance.

**Supplementary Table 1** | Metagenomic library details and benthic cover for reef sites

| Location                            | Metagenomic sequences |            |                 |                  |                         |                  | Benthic coverage |             |                 |                  |             |
|-------------------------------------|-----------------------|------------|-----------------|------------------|-------------------------|------------------|------------------|-------------|-----------------|------------------|-------------|
|                                     | Tent                  | Time Point | Total QC Reads  | Mean Length (bp) | Signif. Protein assign. | SSU rDNA aligns. | Stony coral      | CCA         | Calc macr algae | Flesh macr algae | Turf algae  |
| Vostok<br>-10.0609,<br>-152.309     | 1                     | 0          | 112419          | 226              | 43387                   | 261              | 78.4             | 16.2        | 2.7             | 0.0              | 2.7         |
|                                     | 1                     | 12         | 160942          | 236              | 68245                   | 361              |                  |             |                 |                  |             |
|                                     | 1                     | 24         | 289495          | 223              | 109807                  | 567              |                  |             |                 |                  |             |
|                                     | 2                     | 0          | 551521          | 255              | 212725                  | 1023             | 89.4             | 6.4         | 2.1             | 0.0              | 2.1         |
|                                     | 2                     | 12         | 261171          | 205              | 95229                   | 470              |                  |             |                 |                  |             |
|                                     | 2                     | 24         | 216358          | 215              | 74548                   | 462              |                  |             |                 |                  |             |
|                                     | 3                     | 0          | 145292          | 235              | 48379                   | 263              | 80.9             | 14.9        | 2.1             | 2.1              | 0.0         |
|                                     | 3                     | 12         | 507301          | 235              | 197283                  | 923              |                  |             |                 |                  |             |
|                                     | 3                     | 24         | 91486           | 220              | 34418                   | 225              |                  |             |                 |                  |             |
|                                     | 4                     | 0          | 267200          | 236              | 105523                  | 470              | 59.1             | 38.6        | 2.3             | 0.0              | 0.0         |
|                                     | 4                     | 12         | 601378          | 232              | 239285                  | 894              |                  |             |                 |                  |             |
|                                     | 4                     | 24         | 1059949         | 245              | 424904                  | 1795             |                  |             |                 |                  |             |
| Millennium<br>-9.95080,<br>-150.215 | 1                     | 0          | 216679          | 218              | 86649                   | 396              | 45.7             | 0.0         | 37.0            | 0.0              | 17.4        |
|                                     | 1                     | 12         | 328081          | 229              | 117653                  | 384              |                  |             |                 |                  |             |
|                                     | 1                     | 24         | 376630          | 162              | 100241                  | 449              |                  |             |                 |                  |             |
|                                     | 2                     | 0          | 50094           | 237              | 21617                   | 103              | 55.3             | 8.5         | 36.2            | 0.0              | 0.0         |
|                                     | 2                     | 12         | 238917          | 237              | 91397                   | 303              |                  |             |                 |                  |             |
|                                     | 2                     | 24         | 227765          | 208              | 67977                   | 295              |                  |             |                 |                  |             |
|                                     | 5                     | 0          | 434091          | 224              | 173168                  | 658              | 25.5             | 6.4         | 40.4            | 4.3              | 21.3        |
|                                     | 5                     | 12         | 339092          | 207              | 109184                  | 292              |                  |             |                 |                  |             |
|                                     | 5                     | 24         | 377883          | 175              | 123651                  | 496              |                  |             |                 |                  |             |
|                                     | 6                     | 0          | 553261          | 238              | 212044                  | 888              | 84.4             | 13.3        | 2.2             | 0.0              | 0.0         |
|                                     | 6                     | 12         | 437404          | 195              | 140268                  | 487              |                  |             |                 |                  |             |
|                                     | 6                     | 24         | 170765          | 212              | 65008                   | 318              |                  |             |                 |                  |             |
| Starbuck<br>-5.62891,<br>-155.925   | 1                     | 0          | 562775          | 231              | 218129                  | 872              | 15.9             | 27.3        | 50.0            | 0.0              | 6.8         |
|                                     | 1                     | 12         | 397508          | 194              | 117393                  | 467              |                  |             |                 |                  |             |
|                                     | 1                     | 24         | 374457          | 231              | 141614                  | 635              |                  |             |                 |                  |             |
|                                     | 2                     | 0          | 582724          | 231              | 206118                  | 914              | 0.0              | 15.2        | 82.6            | 0.0              | 2.2         |
|                                     | 2                     | 12         | 575240          | 219              | 169406                  | 635              |                  |             |                 |                  |             |
|                                     | 2                     | 24         | 381406          | 229              | 119125                  | 500              |                  |             |                 |                  |             |
|                                     | 3                     | 0          | 524438          | 229              | 166269                  | 644              | 68.1             | 25.5        | 2.1             | 0.0              | 4.3         |
|                                     | 3                     | 12         | 588108          | 230              | 197717                  | 643              |                  |             |                 |                  |             |
|                                     | 3                     | 24         | 389186          | 232              | 132111                  | 546              |                  |             |                 |                  |             |
|                                     | 4                     | 0          | 418233          | 194              | 300986                  | 1254             | 0.0              | 22.0        | 78.0            | 0.0              | 0.0         |
|                                     | 4                     | 12         | 326790          | 222              | 147150                  | 496              |                  |             |                 |                  |             |
|                                     | 4                     | 24         | 959770          | 218              | 111198                  | 534              |                  |             |                 |                  |             |
| Malden<br>-4.01407,<br>-154.973     | 2                     | 0          | 81666           | 257              | 34687                   | 151              | 50.0             | 28.3        | 2.2             | 2.2              | 17.4        |
|                                     | 2                     | 12         | 246420          | 213              | 90704                   | 405              |                  |             |                 |                  |             |
|                                     | 2                     | 24         | 207829          | 248              | 83601                   | 415              |                  |             |                 |                  |             |
|                                     | 3                     | 0          | 215998          | 249              | 81969                   | 430              | 91.8             | 8.2         | 0.0             | 0.0              | 0.0         |
|                                     | 3                     | 12         | 210712          | 204              | 81026                   | 307              |                  |             |                 |                  |             |
|                                     | 3                     | 24         | 295866          | 210              | 116751                  | 525              |                  |             |                 |                  |             |
|                                     | 4                     | 0          | 175898          | 274              | 64945                   | 226              | 35.7             | 28.6        | 0.0             | 14.3             | 21.4        |
|                                     | 4                     | 12         | 229756          | 246              | 92219                   | 345              |                  |             |                 |                  |             |
|                                     | 4                     | 24         | 198693          | 188              | 70448                   | 338              |                  |             |                 |                  |             |
|                                     | 5                     | 0          | 280773          | 255              | 92874                   | 296              | 41.7             | 20.8        | 0.0             | 2.1              | 35.4        |
|                                     | 5                     | 12         | 191105          | 263              | 90746                   | 407              |                  |             |                 |                  |             |
|                                     | 5                     | 24         | 364154          | 219              | 141204                  | 562              |                  |             |                 |                  |             |
| <b>Total</b>                        | <b>16</b>             | <b>3</b>   | <b>16.8 mil</b> | <b>225</b>       | <b>6.03 mil</b>         | <b>25330</b>     | <b>51.4</b>      | <b>17.5</b> | <b>21.2</b>     | <b>1.56</b>      | <b>8.19</b> |

QC, quality control; bp, base pairs; signif., significant; assign, assignments; align., alignment; CCA, crustose coralline algae; Flesh macr, fleshy macro-, Calc macr, calcified macro-; mil, million. Total represents sum or mean, where appropriate.

**Supplementary Table 2 | Microbial taxa enriched during the day and night.** Diel enrichment of Family level taxons (metagenomic sequence similarities to the SEED database) are shown for “Common”, “Semi-common”, and “Rare” taxa (maximum abundance >5%, 0.5% - 5%, and <0.5%, respectively). Significant enrichment (t-test, two-tailed,  $p < 0.05$ ) and false discovery rate corrected p-values (FDR Adj-p) are shown. RA, Relative abundance.

| Phylum              | Family                               | Max RA | Prevalence | t    | P-value  | FDR Adj-P |
|---------------------|--------------------------------------|--------|------------|------|----------|-----------|
| Day Enriched        |                                      |        |            |      |          |           |
| Cyanobacteria       | Chroococcales Unclassified           | 22.396 | Common     | 2.4  | 1.87E-02 | 5.18E-02  |
| Gammaproteobacteria | Moraxellaceae                        | 80.626 |            | 8.3  | 1.12E-10 | 3.50E-08  |
| Cyanobacteria       | Pleurocapsales Unclassified          | 0.262  | Rare       | 2.0  | 4.72E-02 | 1.02E-01  |
|                     | Prochlorotrichaceae                  | 0.055  |            | 2.6  | 1.35E-02 | 4.10E-02  |
| Firmicutes          | Planococcaceae                       | 0.138  |            | 2.5  | 1.48E-02 | 4.39E-02  |
|                     | Streptococcaceae                     | 0.065  |            | 2.6  | 1.29E-02 | 3.97E-02  |
| Betaproteobacteria  | Neisseriaceae                        | 0.191  |            | 4.4  | 5.78E-05 | 3.56E-04  |
| Gammaproteobacteria | Pasteurellaceae                      | 0.331  |            | 2.6  | 1.22E-02 | 3.84E-02  |
| Verrucomicrobia     | Rubritaleaceae                       | 0.251  |            | 4.5  | 5.30E-05 | 3.33E-04  |
|                     | Verrucomicrobiaceae                  | 0.158  |            | 2.4  | 2.20E-02 | 5.86E-02  |
|                     | Akkermansiaceae                      | 0.127  |            | 3.8  | 4.87E-04 | 2.25E-03  |
| Night Enriched      |                                      |        |            |      |          |           |
| Alphaproteobacteria | Rhodobacteraceae                     | 63.086 | Common     | -4.1 | 1.60E-04 | 9.11E-04  |
|                     | Pelagibacteraceae                    | 15.997 |            | -3.7 | 6.61E-04 | 3.01E-03  |
| Gammaproteobacteria | Alteromonadaceae                     | 45.653 |            | -4.5 | 4.09E-05 | 2.73E-04  |
|                     | Halomonadaceae                       | 42.258 |            | -3.8 | 4.61E-04 | 2.16E-03  |
| Bacteroidetes       | Flavobacteriia Unclassified          | 2.625  | Semi-      | -2.8 | 8.48E-03 | 2.92E-02  |
| Cyanobacteria       | Prochlorococcaceae                   | 3.662  | common     | -3.8 | 4.21E-04 | 2.03E-03  |
| Alphaproteobacteria | Alphaproteobacteria                  | 2.878  |            | -6.8 | 2.05E-08 | 9.15E-07  |
|                     | Unclassified                         |        |            |      |          |           |
|                     | Bradyrhizobiaceae                    | 0.772  |            | -6.1 | 2.31E-07 | 4.83E-06  |
|                     | Phyllobacteriaceae                   | 0.618  |            | -5.6 | 1.31E-06 | 1.79E-05  |
|                     | Rhizobiaceae                         | 1.106  |            | -5.8 | 5.36E-07 | 8.87E-06  |
|                     | Rhodobacterales Unclassified         | 1.552  |            | -6.7 | 2.88E-08 | 1.00E-06  |
|                     | Rhodospirillaceae                    | 2.112  |            | -6.8 | 1.54E-08 | 8.08E-07  |
| Betaproteobacteria  | Burkholderiaceae                     | 0.645  |            | -4.5 | 5.15E-05 | 3.30E-04  |
| Deltaproteobacteria | Halobacteriovoraceae                 | 2.986  |            | -3.3 | 1.70E-03 | 7.36E-03  |
| Gammaproteobacteria | Cellvibrionaceae                     | 0.771  |            | -5.3 | 3.23E-06 | 3.62E-05  |
|                     | Ectothiorhodospiraceae               | 0.551  |            | -6.7 | 2.33E-08 | 9.15E-07  |
|                     | Enterobacteriaceae                   | 1.342  |            | -2.4 | 2.29E-02 | 6.05E-02  |
|                     | Halieaceae                           | 0.623  |            | -6.9 | 1.31E-08 | 8.08E-07  |
|                     | Idiomarinaceae                       | 0.908  |            | -2.0 | 4.91E-02 | 1.06E-01  |
|                     | Marinimicrobia - SAR186 (Candidatus) | 0.627  |            | -3.3 | 1.76E-03 | 7.36E-03  |
|                     | Oceanospirillaceae                   | 4.345  |            | -4.8 | 1.87E-05 | 1.47E-04  |
|                     | Pseudoalteromonadaceae               | 1.249  |            | -4.8 | 1.80E-05 | 1.45E-04  |

|                     |                             |       |      |      |          |          |
|---------------------|-----------------------------|-------|------|------|----------|----------|
|                     | Shewanellaceae              | 0.665 |      | -3.9 | 2.75E-04 | 1.44E-03 |
|                     | Vibrionaceae                | 1.703 |      | -3.8 | 3.67E-04 | 1.83E-03 |
|                     | Xanthomonadaceae            | 0.762 |      | -2.7 | 8.76E-03 | 2.94E-02 |
| Acidithiobacillia   | Acidithiobacillaceae        | 0.036 | Rare | -5.3 | 3.65E-06 | 3.82E-05 |
| Acidobacteria       | Blastocatellia Unclassified | 0.004 |      | -2.4 | 1.99E-02 | 5.42E-02 |
| Actinobacteria      | Cellulomonadaceae           | 0.026 |      | -2.6 | 1.27E-02 | 3.95E-02 |
|                     | Corynebacteriaceae          | 0.131 |      | -2.1 | 4.53E-02 | 1.01E-01 |
|                     | Frankiaceae                 | 0.181 |      | -2.2 | 3.18E-02 | 7.67E-02 |
|                     | Gordoniaceae                | 0.067 |      | -2.6 | 1.17E-02 | 3.75E-02 |
|                     | Intrasporangiaceae          | 0.055 |      | -2.7 | 9.20E-03 | 3.04E-02 |
|                     | Kineosporiaceae             | 0.029 |      | -3.1 | 3.27E-03 | 1.27E-02 |
|                     | Micrococcaceae              | 0.095 |      | -2.1 | 4.29E-02 | 9.83E-02 |
|                     | Micromonosporaceae          | 0.183 |      | -2.3 | 2.66E-02 | 6.91E-02 |
|                     | Nocardiodaceae              | 0.138 |      | -2.3 | 2.73E-02 | 7.03E-02 |
|                     | Nocardiopsaceae             | 0.143 |      | -2.1 | 4.36E-02 | 9.86E-02 |
|                     | Pseudonocardaceae           | 0.168 |      | -2.7 | 8.81E-03 | 2.94E-02 |
|                     | Sporichthyaceae             | 0.043 |      | -2.4 | 1.84E-02 | 5.17E-02 |
|                     | Streptomycetaceae           | 0.438 |      | -2.6 | 1.20E-02 | 3.81E-02 |
|                     | Streptosporangiaceae        | 0.064 |      | -2.9 | 5.64E-03 | 2.03E-02 |
|                     | Thermomonosporaceae         | 0.050 |      | -2.8 | 7.67E-03 | 2.70E-02 |
|                     | Tsukamurellaceae            | 0.016 |      | -2.1 | 4.56E-02 | 1.01E-01 |
| Aquificae           | Aquificaceae                | 0.046 |      | -2.2 | 3.32E-02 | 7.89E-02 |
|                     | Desulfurobacteriaceae       | 0.012 |      | -2.3 | 2.42E-02 | 6.34E-02 |
|                     | Hydrogenothermaceae         | 0.048 |      | -2.2 | 2.97E-02 | 7.34E-02 |
| Bacteroidetes       | Bacteroidetes Unclassified  | 0.358 |      | -2.4 | 2.20E-02 | 5.86E-02 |
|                     | Cyclobacteriaceae           | 0.301 |      | -2.1 | 3.97E-02 | 9.23E-02 |
| Chloroflexi         | Chloroflexi Unclassified    | 0.002 |      | -2.0 | 4.71E-02 | 1.02E-01 |
| Chrysiogenetes      | Chrysiogenaceae             | 0.022 |      | -3.6 | 7.66E-04 | 3.44E-03 |
| Deferribacteres     | Deferribacteraceae          | 0.059 |      | -2.9 | 5.15E-03 | 1.88E-02 |
| Deinococcus-Thermus | Deinococcaceae              | 0.046 |      | -4.1 | 1.62E-04 | 9.11E-04 |
| Firmicutes          | Alicyclobacillaceae         | 0.042 |      | -2.4 | 2.01E-02 | 5.44E-02 |
|                     | Leuconostocaceae            | 0.012 |      | -2.2 | 2.95E-02 | 7.34E-02 |
|                     | Natranaerobiaceae           | 0.019 |      | -2.8 | 7.43E-03 | 2.65E-02 |
|                     | Paenibacillaceae            | 0.141 |      | -2.5 | 1.47E-02 | 4.39E-02 |
|                     | Peptococcaceae              | 0.131 |      | -2.9 | 4.99E-03 | 1.86E-02 |
|                     | Symbiobacteriaceae          | 0.018 |      | -4.5 | 4.45E-05 | 2.91E-04 |
|                     | Syntrophomonadaceae         | 0.026 |      | -2.5 | 1.55E-02 | 4.44E-02 |
|                     | Tissierellia Unclassified   | 0.019 |      | -2.5 | 1.59E-02 | 4.51E-02 |
|                     | Veillonellaceae             | 0.075 |      | -2.2 | 3.21E-02 | 7.69E-02 |
| Fusobacteria        | Fusobacteriaceae            | 0.060 |      | -2.4 | 1.93E-02 | 5.33E-02 |
|                     | Leptotrichiaceae            | 0.031 |      | -2.1 | 4.36E-02 | 9.86E-02 |
| Lentisphaeria       | Victivallaceae              | 0.006 |      | -2.1 | 4.43E-02 | 9.93E-02 |
| Nitrospinae         | Nitrospinaceae              | 0.037 |      | -2.9 | 5.07E-03 | 1.87E-02 |

|                       |                               |       |      |          |          |
|-----------------------|-------------------------------|-------|------|----------|----------|
| Alphaproteobacteria   | Acetobacteraceae              | 0.483 | -6.3 | 1.03E-07 | 2.70E-06 |
|                       | Anaplasmataceae               | 0.156 | -4.7 | 2.80E-05 | 2.00E-04 |
|                       | Aurantimonadaceae             | 0.272 | -5.2 | 4.60E-06 | 4.66E-05 |
|                       | Bartonellaceae                | 0.164 | -5.1 | 5.53E-06 | 5.12E-05 |
|                       | Beijerinckiaceae              | 0.120 | -7.6 | 1.24E-09 | 1.30E-07 |
|                       | Brucellaceae                  | 0.350 | -6.1 | 1.82E-07 | 4.09E-06 |
|                       | Hyphomicrobiaceae             | 0.268 | -5.9 | 4.04E-07 | 7.05E-06 |
|                       | Kiloniellaceae                | 0.262 | -7.6 | 1.22E-09 | 1.30E-07 |
|                       | Kordiimonadaceae              | 0.157 | -4.9 | 1.40E-05 | 1.19E-04 |
|                       | Magnetococcaceae              | 0.056 | -3.8 | 3.73E-04 | 1.83E-03 |
|                       | Methylobacteriaceae           | 0.350 | -5.8 | 5.94E-07 | 8.88E-06 |
|                       | Methylocystaceae              | 0.141 | -5.4 | 2.26E-06 | 2.83E-05 |
|                       | Midichloriaceae Candidatus    | 0.004 | -2.5 | 1.56E-02 | 4.44E-02 |
|                       | Paracaedibacteraceae          | 0.027 | -4.6 | 3.32E-05 | 2.27E-04 |
|                       | Candidatus                    |       |      |          |          |
|                       | Rhodobiaceae                  | 0.300 | -4.8 | 1.67E-05 | 1.38E-04 |
|                       | Rhodospirillales Unclassified | 0.020 | -4.3 | 9.75E-05 | 5.89E-04 |
|                       | Rickettsiaceae                | 0.114 | -2.6 | 1.14E-02 | 3.69E-02 |
|                       | Xanthobacteraceae             | 0.242 | -5.8 | 5.68E-07 | 8.88E-06 |
| Betaproteobacteria    | Chromobacteriaceae            | 0.145 | -4.1 | 1.82E-04 | 9.92E-04 |
|                       | Hydrogenophilaceae            | 0.044 | -4.2 | 1.25E-04 | 7.40E-04 |
|                       | Methylophilales Unclassified  | 0.054 | -4.6 | 3.30E-05 | 2.27E-04 |
|                       | Nitrosomonadaceae             | 0.086 | -3.3 | 2.12E-03 | 8.65E-03 |
|                       | Oxalobacteraceae              | 0.152 | -3.1 | 3.00E-03 | 1.18E-02 |
|                       | Rhodocyclaceae                | 0.193 | -6.5 | 4.42E-08 | 1.39E-06 |
|                       | Sulfuricellaceae              | 0.003 | -5.4 | 2.54E-06 | 3.06E-05 |
| Deltaproteobacteria   | Sutterellaceae                | 0.008 | -2.1 | 4.09E-02 | 9.44E-02 |
|                       | Bdellovibrionaceae            | 0.179 | -4.7 | 2.26E-05 | 1.65E-04 |
|                       | Deltaproteobacteria           | 0.078 | -3.4 | 1.53E-03 | 6.78E-03 |
|                       | Unclassified                  |       |      |          |          |
|                       | Desulfobacteraceae            | 0.108 | -2.1 | 3.97E-02 | 9.23E-02 |
|                       | Desulfobulbaceae              | 0.115 | -4.0 | 2.21E-04 | 1.18E-03 |
|                       | Desulfohalobiaceae            | 0.020 | -2.5 | 1.50E-02 | 4.39E-02 |
|                       | Desulfomicrobiaceae           | 0.020 | -3.0 | 3.80E-03 | 1.45E-02 |
|                       | Desulfovibrionaceae           | 0.134 | -3.9 | 2.92E-04 | 1.48E-03 |
|                       | Desulfuromonadaceae           | 0.113 | -3.9 | 2.89E-04 | 1.48E-03 |
|                       | Geobacteraceae                | 0.193 | -3.2 | 2.74E-03 | 1.09E-02 |
|                       | Myxococcaceae                 | 0.060 | -2.8 | 7.91E-03 | 2.76E-02 |
|                       | Syntrophaceae                 | 0.029 | -3.8 | 4.35E-04 | 2.07E-03 |
|                       | Syntrophobacteraceae          | 0.024 | -2.2 | 3.07E-02 | 7.52E-02 |
| Epsilonproteobacteria | Campylobacteraceae            | 0.097 | -2.5 | 1.43E-02 | 4.31E-02 |
|                       | Campylobacterales             | 0.004 | -2.3 | 2.77E-02 | 7.04E-02 |
|                       | Unclassified                  |       |      |          |          |

|                       |                                 |       |      |          |          |
|-----------------------|---------------------------------|-------|------|----------|----------|
| Gammaproteobacteria   | Epsilonproteobacteria           | 0.021 | -2.3 | 2.78E-02 | 7.04E-02 |
|                       | Unclassified                    |       |      |          |          |
|                       | Nautiliaceae                    | 0.016 | -2.2 | 3.17E-02 | 7.67E-02 |
|                       | Aeromonadaceae                  | 0.268 | -5.5 | 1.49E-06 | 1.95E-05 |
|                       | Alteromonadales Unclassified    | 0.065 | -4.2 | 1.28E-04 | 7.42E-04 |
|                       | Chromatiaceae                   | 0.266 | -5.9 | 3.89E-07 | 7.05E-06 |
|                       | Colwelliaceae                   | 0.172 | -5.3 | 3.37E-06 | 3.65E-05 |
|                       | Francisellaceae                 | 0.098 | -3.0 | 3.84E-03 | 1.45E-02 |
|                       | Gammaproteobacteria             | 0.361 | -6.0 | 3.14E-07 | 6.16E-06 |
|                       | Unclassified                    |       |      |          |          |
|                       | Hahellaceae                     | 0.402 | -5.1 | 5.54E-06 | 5.12E-05 |
|                       | Halothiobacillaceae             | 0.019 | -5.7 | 8.59E-07 | 1.23E-05 |
|                       | Methylococcaceae                | 0.229 | -6.4 | 8.26E-08 | 2.36E-06 |
|                       | Microbulbiferaceae              | 0.123 | -5.3 | 3.12E-06 | 3.62E-05 |
|                       | Moritellaceae                   | 0.052 | -5.1 | 7.22E-06 | 6.48E-05 |
|                       | Piscirickettsiaceae             | 0.267 | -6.2 | 1.39E-07 | 3.37E-06 |
|                       | Porticoccaceae                  | 0.081 | -4.7 | 2.26E-05 | 1.65E-04 |
|                       | Psychromonadaceae               | 0.093 | -4.1 | 1.83E-04 | 9.92E-04 |
|                       | Rhodanobacteraceae              | 0.061 | -4.7 | 2.11E-05 | 1.61E-04 |
|                       | Saccharospirillaceae            | 0.139 | -7.1 | 6.38E-09 | 5.01E-07 |
|                       | Salinisphaeraceae               | 0.010 | -3.3 | 1.74E-03 | 7.36E-03 |
|                       | Sinobacteraceae                 | 0.028 | -3.2 | 2.74E-03 | 1.09E-02 |
|                       | Spongiibacteraceae              | 0.175 | -5.0 | 7.71E-06 | 6.73E-05 |
|                       | Succinivibrionaceae             | 0.011 | -2.0 | 4.73E-02 | 1.02E-01 |
|                       | Thiotrichaceae                  | 0.088 | -3.3 | 1.80E-03 | 7.43E-03 |
| Zetaproteobacteria    | Mariprofundaceae                | 0.028 | -5.2 | 5.15E-06 | 5.06E-05 |
|                       | Zetaproteobacteria Unclassified | 0.039 | -2.3 | 2.84E-02 | 7.14E-02 |
| Synergistia           | Synergistaceae                  | 0.037 | -2.7 | 8.65E-03 | 2.94E-02 |
| Thermodesulfobacteria | Thermodesulfobacteriaceae       | 0.005 | -2.5 | 1.51E-02 | 4.39E-02 |
| Thermotogae           | Fervidobacteriaceae             | 0.044 | -2.7 | 1.06E-02 | 3.47E-02 |
|                       | Kosmotogaceae                   | 0.012 | -2.2 | 3.56E-02 | 8.41E-02 |
|                       | Thermotogaceae                  | 0.035 | -3.3 | 1.74E-03 | 7.36E-03 |

---

**Supplementary Table 3 | Metabolic pathways enriched during the day and night.** Diel enrichment (Cohen's d, the difference in day mean and night mean divided by the standard deviation (Std Dev);  $|d| > 0.5$  is considered moderately enriched) of protein-coding gene families (SEED Level 3 Subsystems). Significant enrichment ( $p < 0.05$ ) were corrected for false discovery rate (FDR Adj-p).

| Subsystem Level 1          | Subsystem Level 2                                                 | Subsystem Level 3                                                                | Cohen's d | FDR Adj-p | Mean Day | Mean Night | Std Dev |
|----------------------------|-------------------------------------------------------------------|----------------------------------------------------------------------------------|-----------|-----------|----------|------------|---------|
| <b>Day Enriched</b>        |                                                                   |                                                                                  |           |           |          |            |         |
| Amino Acids                | Amino acid racemase                                               | Amino acid racemase                                                              | 1.61      | 4.33E-04  | 0.0306   | 0.0328     | 0.0021  |
|                            | Arginine; urea cycle, polyamines                                  | Arginine Biosynthesis extended                                                   | 1.09      | 1.23E-02  | 0.0169   | 0.0211     | 0.0046  |
|                            |                                                                   | Polyamine Metabolism                                                             | 0.02      | 2.97E-03  | 0.0349   | 0.0397     | 0.0043  |
|                            |                                                                   | Urea decomposition                                                               | 0.99      | 1.64E-02  | 0.0188   | 0.0314     | 0.0096  |
|                            | Aromatic amino acids & derivatives                                | Chorismate Synthesis                                                             | 0.21      | 3.44E-02  | 0.0208   | 0.0329     | 0.0089  |
|                            |                                                                   | Common Pathway For Synthesis of Aromatic Compounds (DAHP synthase to chorismate) | 0.20      | 4.34E-02  | 0.0269   | 0.0324     | 0.0042  |
|                            |                                                                   | Tryptophan synthesis                                                             | 1.21      | 4.62E-04  | 0.0252   | 0.0139     | 0.0070  |
|                            | Branched-chain amino acids                                        | HMG CoA Synthesis                                                                | 1.23      | 1.15E-02  | 0.0598   | 0.0566     | 0.0029  |
|                            | Glutamine, glutamate, aspartate, asparagine; ammonia assimilation | Glutamate dehydrogenases                                                         | 1.32      | 3.12E-03  | 0.0083   | 0.0121     | 0.0034  |
|                            |                                                                   | Histidine Metabolism                                                             | 1.00      | 4.27E-03  | 0.0661   | 0.0660     | 0.0049  |
| Carbohydrates              | Central carbohydrate metabolism                                   | Cysteine Biosynthesis, MCB 432                                                   | 1.54      | 2.75E-04  | 0.0632   | 0.0548     | 0.0085  |
|                            |                                                                   | Lysine fermentation                                                              | 0.84      | 2.76E-04  | 0.0271   | 0.0365     | 0.0109  |
|                            |                                                                   |                                                                                  |           |           |          |            |         |
|                            | TCA Cycle - Acinetobacter                                         |                                                                                  | 0.40      | 7.14E-03  | 0.0495   | 0.0486     | 0.0041  |
|                            |                                                                   |                                                                                  | 1.29      | 3.04E-03  | 0.0450   | 0.0441     | 0.0046  |
|                            |                                                                   |                                                                                  | 0.83      | 1.34E-02  | 0.0721   | 0.0671     | 0.0042  |
|                            | Fermentation                                                      | Fermentations: Mixed acid                                                        | 0.91      | 1.40E-02  | 0.0402   | 0.0319     | 0.0067  |
|                            | Monosaccharides                                                   | Mannose Metabolism                                                               | 1.01      | 5.82E-03  | 0.0303   | 0.0319     | 0.0040  |
|                            | One-carbon Metabolism                                             | Formaldehyde assimilation: Ribulose monophosphate pathway                        | 1.31      | 1.00E-02  | 0.0404   | 0.0468     | 0.0068  |
|                            | Organic acids                                                     | Methylcitrate cycle                                                              | 1.17      | 1.23E-02  | 0.0146   | 0.0193     | 0.0039  |
| Cell Division & Cell Cycle | Bacterial Cytoskeleton                                            | Bacterial Cytoskeleton                                                           | 1.29      | 2.28E-03  | 0.0381   | 0.0470     | 0.0071  |
|                            | Two cell division clusters relating to chromosome partitioning    | Two cell division clusters relating to chromosome partitioning                   | 0.87      | 1.12E-03  | 0.0401   | 0.0561     | 0.0122  |
| Cell Wall & Capsule        | Capsular & extracellular polysaccharides                          | Capsular Polysaccharide (CPS) of Campylobacter                                   | 1.01      | 2.74E-02  | 0.0350   | 0.0265     | 0.0064  |
|                            | Capsular & extracellular polysaccharides                          | Capsular Polysaccharides Biosynthesis & Assembly                                 | 1.29      | 2.76E-04  | 0.0230   | 0.0299     | 0.0056  |
|                            | Capsular & extracellular polysaccharides                          | Streptococcal Hyaluronic Acid Capsule                                            | 1.15      | 3.08E-02  | 0.0537   | 0.0462     | 0.0075  |

|                                 |                                         |                                         |      |          |        |        |        |
|---------------------------------|-----------------------------------------|-----------------------------------------|------|----------|--------|--------|--------|
|                                 | Gram-Negative cell wall components      | KDO2-Lipid A biosynthesis               | 1.25 | 7.81E-05 | 0.0548 | 0.0574 | 0.0052 |
|                                 | Gram-Negative cell wall components      | Lipopolysaccharide assembly             | 0.83 | 1.79E-02 | 0.0564 | 0.0439 | 0.0081 |
|                                 | Gram-Negative cell wall components      | Major Outer Membrane Proteins           | 1.58 | 1.57E-04 | 0.0535 | 0.0497 | 0.0044 |
|                                 | Gram-Negative cell wall components      | Outer membrane                          | 0.53 | 2.78E-02 | 0.0055 | 0.0081 | 0.0025 |
|                                 | Murein Hydrolases                       | Murein Hydrolases                       | 1.25 | 9.49E-03 | 0.0429 | 0.0480 | 0.0057 |
|                                 | Peptidoglycan biosynthesis--gjo         | Peptidoglycan biosynthesis--gjo         | 0.98 | 3.70E-02 | 0.0273 | 0.0293 | 0.0019 |
|                                 | Raj MurE                                | Raj MurE                                | 1.44 | 7.68E-04 | 0.0622 | 0.0656 | 0.0069 |
|                                 | Recycling of Peptidoglycan Amino Sugars | Recycling of Peptidoglycan Amino Sugars | 1.42 | 4.02E-03 | 0.0253 | 0.0331 | 0.0096 |
| Cofactors, Vitamins, & Pigments | CLO thiaminPP biosynthesis              | CLO thiaminPP biosynthesis              | 1.62 | 5.61E-04 | 0.0595 | 0.0578 | 0.0043 |
|                                 | Coenzyme A                              | coA-FolK                                | 1.49 | 2.76E-04 | 0.0135 | 0.0203 | 0.0051 |
|                                 |                                         | dcernst CoA Salvage                     | 1.49 | 1.52E-03 | 0.0489 | 0.0644 | 0.0131 |
|                                 |                                         |                                         |      |          |        |        |        |
|                                 | Folate & pterines                       | 5-FCL-like protein                      | 1.46 | 1.97E-03 | 0.0244 | 0.0350 | 0.0102 |
|                                 |                                         | Folate Biosynthesis                     | 0.15 | 6.31E-03 | 0.0234 | 0.0326 | 0.0099 |
|                                 |                                         | Pterin carbinolamine dehydratase        | 1.32 | 1.56E-03 | 0.0408 | 0.0462 | 0.0046 |
|                                 |                                         | Pterin metabolism 3                     | 1.49 | 1.79E-04 | 0.0692 | 0.0614 | 0.0060 |
|                                 |                                         | YgfZ                                    | 1.57 | 2.76E-04 | 0.0448 | 0.0387 | 0.0072 |
|                                 | Lipoic acid                             | BEY LIP                                 | 0.24 | 8.02E-03 | 0.0611 | 0.0679 | 0.0047 |
|                                 | Molybdopterin cytosine dinucleotide     | Molybdopterin cytosine dinucleotide     | 1.59 | 1.07E-03 | 0.0817 | 0.0875 | 0.0058 |
|                                 | NAD & NADP                              | NAD regulation                          | 1.57 | 3.46E-04 | 0.0828 | 0.0833 | 0.0057 |
|                                 | Quinone cofactors                       | Pyrroloquinoline Quinone biosynthesis   | 0.82 | 3.74E-02 | 0.0320 | 0.0421 | 0.0084 |
|                                 |                                         | Ubiquinone Biosynthesis                 | 1.26 | 4.17E-03 | 0.0200 | 0.0276 | 0.0065 |
|                                 |                                         | Ubiquinone biosynthesis -- gjo          | 1.18 | 3.05E-03 | 0.0148 | 0.0205 | 0.0049 |
|                                 | Riboflavin, FMN, FAD                    | Test - Riboflavin                       | 1.38 | 3.97E-04 | 0.0266 | 0.0273 | 0.0026 |
|                                 | Test - DHFR                             | Test - DHFR                             | 1.20 | 1.99E-03 | 0.0108 | 0.0158 | 0.0044 |
|                                 | Test - Thiamin                          | Test - Thiamin                          | 0.37 | 4.71E-02 | 0.0405 | 0.0547 | 0.0110 |
|                                 | Thiamin Copy RZ                         | Thiamin Copy RZ                         | 1.20 | 2.75E-03 | 0.0043 | 0.0080 | 0.0035 |
| DNA Metabolism                  | CRISPs                                  | CRISPRs                                 | 1.29 | 1.21E-02 | 0.0148 | 0.0227 | 0.0066 |
|                                 | DNA repair                              | 2-phosphoglycolate salvage              | 0.88 | 1.77E-02 | 0.0050 | 0.0087 | 0.0037 |
|                                 |                                         | DNA repair, RecBCD pathway              | 0.94 | 2.40E-02 | 0.0136 | 0.0147 | 0.0029 |
|                                 |                                         | DNA repair, RecFOR pathway              | 0.50 | 2.59E-02 | 0.0294 | 0.0352 | 0.0054 |
|                                 |                                         | RecA & RecX                             | 1.33 | 6.52E-03 | 0.0173 | 0.0238 | 0.0051 |

|                                    |                                                          |                                                                                  |      |          |        |        |        |
|------------------------------------|----------------------------------------------------------|----------------------------------------------------------------------------------|------|----------|--------|--------|--------|
|                                    |                                                          | Uracil-DNA glycosylase                                                           | 1.15 | 3.19E-02 | 0.0365 | 0.0311 | 0.0060 |
|                                    | DNA replication                                          | DNA-replication                                                                  | 1.50 | 5.61E-04 | 0.0294 | 0.0440 | 0.0102 |
|                                    | Restriction-Modification System                          | Restriction-Modification System                                                  | 1.23 | 4.17E-03 | 0.0113 | 0.0209 | 0.0076 |
|                                    | Type I Restriction-Modification                          | Type I Restriction-Modification                                                  | 1.20 | 5.40E-03 | 0.0306 | 0.0389 | 0.0094 |
|                                    | YcfH                                                     | YcfH                                                                             | 1.32 | 1.10E-02 | 0.0282 | 0.0387 | 0.0089 |
| Dormancy & Sporulation             | Persister Cells                                          | Persister Cells                                                                  | 1.01 | 6.28E-03 | 0.0038 | 0.0075 | 0.0035 |
| Fatty Acids, Lipids, & Isoprenoids | Betaine lipids in bacteria                               | Betaine lipids in bacteria                                                       | 0.40 | 1.21E-02 | 0.0335 | 0.0464 | 0.0090 |
|                                    | Fatty acids                                              | Fatty acid degradation regulons                                                  | 1.24 | 1.21E-02 | 0.0174 | 0.0254 | 0.0082 |
|                                    |                                                          | Mycobacterial gene cluster associated with resistance against FAS-II antibiotics | 1.59 | 6.76E-04 | 0.0083 | 0.0149 | 0.0049 |
|                                    | Isoprenoids                                              | Isoprenoinds for Quinones                                                        | 0.94 | 1.49E-02 | 0.0181 | 0.0194 | 0.0038 |
|                                    |                                                          | Nonmevalonate Branch of Isoprenoid Biosynthesis                                  | 0.17 | 4.22E-03 | 0.0429 | 0.0399 | 0.0029 |
|                                    | Phospholipids                                            | Glycerolipid & Glycerophospholipid Metabolism in Bacteria                        | 1.22 | 9.57E-03 | 0.0149 | 0.0192 | 0.0043 |
|                                    | Triacylglycerols                                         | Triacylglycerol metabolism                                                       | 1.29 | 9.19E-03 | 0.0283 | 0.0393 | 0.0092 |
| Membrane Transport                 | Protein & nucleoprotein secretion system, Type IV        | Type IV pilus                                                                    | 1.57 | 2.76E-04 | 0.0454 | 0.0408 | 0.0036 |
|                                    |                                                          | Twin-arginine translocation system                                               | 1.38 | 3.92E-03 | 0.0272 | 0.0284 | 0.0021 |
|                                    | Transport of Molybdenum                                  | Transport of Molybdenum                                                          | 1.59 | 2.75E-04 | 0.0074 | 0.0114 | 0.0043 |
|                                    | Transport of Zinc                                        | Transport of Zinc                                                                | 1.44 | 1.97E-03 | 0.0296 | 0.0352 | 0.0042 |
|                                    | TRAP transporters                                        | A TRAP transporter & a hypothetical                                              | 1.58 | 8.71E-04 | 0.0466 | 0.0365 | 0.0086 |
|                                    | Uni- Sym- & Antiporters                                  | Proton-dependent Peptide Transporters                                            | 1.49 | 2.52E-03 | 0.0195 | 0.0284 | 0.0073 |
| Metabolism of Aromatic Compounds   | Anaerobic degradation of aromatic compounds              | Anaerobic benzoate metabolism                                                    | 0.27 | 5.41E-03 | 0.0051 | 0.0082 | 0.0050 |
|                                    | Peripheral pathways for catabolism of aromatic compounds | Chloroaromatic degradation pathway                                               | 1.41 | 1.61E-03 | 0.0057 | 0.0166 | 0.0068 |
| Motility & Chemotaxis              | Social motility & nonflagellar swimming in bacteria      | Bacterial motility:Gliding                                                       | 1.46 | 4.08E-05 | 0.0077 | 0.0158 | 0.0067 |
| Macronutrients                     | Sulfur Metabolism                                        | Sulfur - Dimethylsulfoniopropionate (DMSP) mineralization, gjo                   | 1.21 | 5.16E-03 | 0.0502 | 0.0657 | 0.0104 |
|                                    |                                                          | Sulfur - Dimethylsulfoniopropionate (DMSP) mineralization, WBW                   | 1.21 | 5.16E-03 | 0.0375 | 0.0632 | 0.0176 |
|                                    |                                                          | Sulfur Inorganic Sulfur Assimilation                                             | 1.45 | 1.48E-03 | 0.0133 | 0.0219 | 0.0059 |
|                                    |                                                          | L-Cystine Uptake & Metabolism                                                    | 1.47 | 7.68E-04 | 0.0077 | 0.0108 | 0.0030 |
|                                    | Nitrogen Metabolism                                      | Nitrosative stress                                                               | 1.46 | 4.53E-04 | 0.0171 | 0.0256 | 0.0060 |
|                                    | Phosphorus Metabolism                                    | Phosphate metabolism                                                             | 0.31 | 4.17E-02 | 0.0627 | 0.0557 | 0.0054 |
|                                    | Potassium Metabolism                                     | Potassium homeostasis                                                            | 1.28 | 9.19E-03 | 0.0621 | 0.0582 | 0.0044 |

|                                                    |                                                              |                                                                                                 |      |          |        |        |        |
|----------------------------------------------------|--------------------------------------------------------------|-------------------------------------------------------------------------------------------------|------|----------|--------|--------|--------|
|                                                    | Iron acquisition & metabolism                                | RCJ pfr                                                                                         | 0.37 | 1.63E-03 | 0.0192 | 0.0291 | 0.0063 |
| Phages, Prophages, Transposable elements, Plasmids | Phages, Prophages                                            | Phage tail fiber proteins                                                                       | 0.97 | 4.56E-02 | 0.0132 | 0.0081 | 0.0051 |
| Protein Metabolism                                 | Protein biosynthesis                                         | Ribosome biogenesis bacterial                                                                   | 0.64 | 2.81E-03 | 0.0382 | 0.0259 | 0.0095 |
|                                                    |                                                              | Single-copy ribosomal proteins                                                                  | 1.22 | 9.57E-03 | 0.0141 | 0.0179 | 0.0040 |
|                                                    |                                                              | tRNA aminoacylation, Asp & Asn                                                                  | 1.02 | 1.85E-02 | 0.0339 | 0.0393 | 0.0052 |
|                                                    | Protein degradation                                          | EC 3.4.11.- Aminopeptidases                                                                     | 0.88 | 7.07E-03 | 0.0265 | 0.0329 | 0.0058 |
|                                                    |                                                              | Proteolysis in bacteria, ATP-dependent                                                          | 1.13 | 1.56E-03 | 0.0469 | 0.0555 | 0.0078 |
|                                                    | Protein folding                                              | Peptidyl-prolyl cis-trans isomerase                                                             | 1.21 | 3.42E-03 | 0.0413 | 0.0511 | 0.0074 |
|                                                    |                                                              | Periplasmic disulfide interchange                                                               | 1.13 | 1.47E-02 | 0.0405 | 0.0351 | 0.0047 |
|                                                    |                                                              | Protein chaperones                                                                              | 1.37 | 8.19E-03 | 0.0010 | 0.0049 | 0.0029 |
|                                                    | Protein processing & modification                            | Lipoprotein Biosynthesis                                                                        | 1.16 | 1.27E-02 | 0.0817 | 0.0744 | 0.0058 |
|                                                    |                                                              | N-linked Glycosylation in Bacteria                                                              | 1.42 | 2.17E-03 | 0.0100 | 0.0125 | 0.0032 |
|                                                    |                                                              | Peptide methionine sulfoxide reductase                                                          | 1.43 | 1.25E-03 | 0.0286 | 0.0300 | 0.0042 |
|                                                    |                                                              | Ribosomal protein S12p Asp methylthiotransferase                                                | 1.16 | 1.89E-02 | 0.0614 | 0.0506 | 0.0130 |
|                                                    |                                                              | Signal peptidase                                                                                | 1.43 | 7.55E-04 | 0.0342 | 0.0416 | 0.0082 |
| Regulation & Cell signaling                        | cAMP signaling in bacteria                                   | cAMP signaling in bacteria                                                                      | 0.29 | 4.30E-03 | 0.0202 | 0.0340 | 0.0090 |
|                                                    | DNA-binding regulatory proteins, strays                      | DNA-binding regulatory proteins, strays                                                         | 0.91 | 2.15E-02 | 0.0393 | 0.0221 | 0.0109 |
|                                                    | Ioja                                                         | Ioja                                                                                            | 1.47 | 1.58E-03 | 0.0230 | 0.0215 | 0.0027 |
|                                                    | Programmed Cell Death & Toxin-antitoxin Systems              | Murein hydrolase regulation & cell death                                                        | 1.31 | 2.91E-03 | 0.0541 | 0.0488 | 0.0043 |
|                                                    |                                                              | Toxin-antitoxin replicon stabilization systems                                                  | 1.38 | 2.16E-03 | 0.0391 | 0.0364 | 0.0028 |
|                                                    | Pseudomonas quinolone signal PQS                             | Pseudomonas quinolone signal PQS                                                                | 0.89 | 3.16E-02 | 0.0366 | 0.0303 | 0.0044 |
|                                                    | Two-component regulatory systems in Campylobacter            | Two-component regulatory systems in Campylobacter                                               | 0.77 | 1.12E-02 | 0.0309 | 0.0259 | 0.0035 |
| Respiration                                        | Biogenesis of cbb3-type cytochrome c oxidases                | Biogenesis of cbb3-type cytochrome c oxidases                                                   | 1.20 | 4.30E-02 | 0.0847 | 0.0855 | 0.0059 |
|                                                    |                                                              | Biogenesis of c-type cytochromes                                                                | 1.48 | 1.92E-03 | 0.0216 | 0.0157 | 0.0036 |
|                                                    | Electron accepting reactions                                 | Ubiquinone Menaquinone-cytochrome c reductase complexes                                         | 0.07 | 7.78E-03 | 0.0469 | 0.0405 | 0.0043 |
|                                                    | Electron donating reactions                                  | Na(+)-translocating NADH-quinone oxidoreductase & mf-like group of electron transport complexes | 1.16 | 7.68E-04 | 0.0373 | 0.0382 | 0.0024 |
|                                                    | Quinone oxidoreductase family                                | Quinone oxidoreductase family                                                                   | 1.24 | 1.31E-03 | 0.0390 | 0.0306 | 0.0057 |
|                                                    | Soluble cytochromes & functionally related electron carriers | Soluble cytochromes & functionally related electron carriers                                    | 0.04 | 1.63E-03 | 0.0525 | 0.0409 | 0.0080 |

|                              |                                                              |                                                                              |                    |           |           |          |            |         |
|------------------------------|--------------------------------------------------------------|------------------------------------------------------------------------------|--------------------|-----------|-----------|----------|------------|---------|
| RNA Metabolism               | RNA processing & modification                                | methyl t6A                                                                   | 1.41               | 3.14E-03  | 0.0648    | 0.0643   | 0.0032     |         |
|                              |                                                              | RNA processing & degradation, bacterial                                      | 0.95               | 1.02E-02  | 0.0178    | 0.0138   | 0.0030     |         |
|                              |                                                              | RNA pseudouridine syntheses                                                  | 1.45               | 3.15E-04  | 0.0355    | 0.0284   | 0.0048     |         |
|                              |                                                              | t(6)A synthesis in bacteria                                                  | 1.27               | 9.19E-03  | 0.0807    | 0.0613   | 0.0124     |         |
|                              |                                                              | Threonylcarbamoyladenine                                                     | 1.32               | 2.14E-02  | 0.0636    | 0.0625   | 0.0045     |         |
|                              |                                                              | tRNA processing                                                              | 0.92               | 2.38E-02  | 0.0260    | 0.0264   | 0.0022     |         |
|                              |                                                              | YrdC-YciO                                                                    | 1.11               | 2.95E-03  | 0.0268    | 0.0276   | 0.0022     |         |
|                              |                                                              | YrdC-YciO-Sua5 & associated protein families                                 | 1.58               | 2.02E-04  | 0.0380    | 0.0197   | 0.0115     |         |
|                              |                                                              | Transcription                                                                | RNA polymerase III | 1.39      | 4.90E-02  | 0.0345   | 0.0187     | 0.0101  |
| Stress Response              | Carbon Starvation                                            | Carbon Starvation                                                            | 1.17               | 4.74E-02  | 0.0427    | 0.0429   | 0.0024     |         |
|                              | Detoxification                                               | Nudix KE                                                                     | 1.18               | 8.09E-03  | 0.0430    | 0.0434   | 0.0023     |         |
|                              | Flavo-haemoglobin                                            | Flavo-haemoglobin                                                            | 1.27               | 1.21E-02  | 0.0220    | 0.0237   | 0.0044     |         |
|                              | Osmotic stress                                               | Osmoregulation                                                               | 1.48               | 5.00E-04  | 0.0255    | 0.0207   | 0.0058     |         |
|                              |                                                              | Glutaredoxins                                                                | 1.23               | 1.58E-02  | 0.0688    | 0.0582   | 0.0084     |         |
|                              |                                                              | Redox-dependent regulation of nucleus processes                              | 1.10               | 3.12E-03  | 0.0417    | 0.0369   | 0.0041     |         |
| Virulence, Disease & Defense | Mycobacterium virulence operon involved in DNA transcription | Mycobacterium virulence operon involved in DNA transcription                 | 0.51               | 2.52E-03  | 0.0447    | 0.0377   | 0.0050     |         |
|                              |                                                              | Mycobacterium virulence operon possibly involved in quinolinate biosynthesis | 0.33               | 3.45E-02  | 0.0609    | 0.0543   | 0.0054     |         |
|                              | Resistance to antibiotics & toxic compounds                  | Arsenic resistance                                                           | 1.19               | 8.45E-03  | 0.0317    | 0.0307   | 0.0028     |         |
|                              |                                                              | BlaR1 Family Regulatory Sensor-transducer Disambiguation                     | 1.46               | 2.16E-03  | 0.0307    | 0.0409   | 0.0075     |         |
|                              |                                                              | Cobalt-zinc-cadmium resistance                                               | 1.18               | 1.83E-02  | 0.0465    | 0.0531   | 0.0111     |         |
|                              |                                                              | Copper homeostasis                                                           | 1.27               | 2.10E-02  | 0.0295    | 0.0266   | 0.0024     |         |
|                              |                                                              | Copper homeostasis: copper tolerance                                         | 1.54               | 1.62E-03  | 0.0254    | 0.0142   | 0.0087     |         |
|                              |                                                              | Methicillin resistance in Staphylococci                                      | 1.30               | 2.47E-04  | 0.0045    | 0.0067   | 0.0029     |         |
|                              |                                                              | Monika MRSA                                                                  | 1.58               | 2.34E-04  | 0.0248    | 0.0222   | 0.0030     |         |
|                              |                                                              | The mdtABCD multidrug resistance cluster                                     | 1.08               | 7.38E-03  | 0.0701    | 0.0739   | 0.0036     |         |
|                              | Bacteriocins, ribosomally synthesized antibacterial peptides | Tolerance to colicin E2                                                      | 1.48               | 1.32E-03  | 0.0136    | 0.0215   | 0.0075     |         |
|                              |                                                              | Detection                                                                    | MLST               | 1.68      | 1.09E-04  | 0.0466   | 0.0387     | 0.0084  |
|                              | Subsystem Level 1                                            | Subsystem Level 2                                                            | Subsystem Level 3  | Cohen's d | FDR Adj-p | Mean Day | Mean Night | Std Dev |
|                              | Night enriched                                               |                                                                              |                    |           |           |          |            |         |

|                           |                                                                   |                                                      |       |          |        |        |        |
|---------------------------|-------------------------------------------------------------------|------------------------------------------------------|-------|----------|--------|--------|--------|
| Amino Acids & Derivatives | Alanine, serine, & glycine                                        | Alanine biosynthesis                                 | -1.03 | 1.64E-02 | 0.0483 | 0.0463 | 0.0038 |
|                           |                                                                   | Glycine Biosynthesis                                 | -0.91 | 3.76E-03 | 0.0174 | 0.0109 | 0.0049 |
|                           |                                                                   | Glycine cleavage system                              | -1.10 | 3.96E-04 | 0.0287 | 0.0250 | 0.0033 |
|                           |                                                                   | Sarcosine oxidases, monomeric & heterotetrameric     | -1.32 | 2.70E-04 | 0.1188 | 0.1069 | 0.0079 |
|                           |                                                                   | Sarcosine temp                                       | -1.35 | 1.86E-04 | 0.0323 | 0.0402 | 0.0115 |
|                           |                                                                   | Serine Biosynthesis                                  | -1.33 | 6.76E-04 | 0.0552 | 0.0402 | 0.0122 |
|                           | Arginine; urea cycle, polyamines                                  | Arginine Deiminase Pathway                           | -1.11 | 6.37E-03 | 0.0465 | 0.0349 | 0.0097 |
|                           | Aromatic amino acids & derivatives                                | Aromatic amino acid interconversions with aryl acids | -0.86 | 1.79E-04 | 0.0271 | 0.0230 | 0.0032 |
|                           | Branched-chain amino acids                                        | HMG-CoA                                              | -0.40 | 6.31E-03 | 0.0231 | 0.0198 | 0.0033 |
|                           |                                                                   | Isoleucine degradation                               | -0.95 | 7.14E-03 | 0.0046 | 0.0089 | 0.0042 |
|                           |                                                                   | Ketoisovalerate oxidoreductase                       | -1.22 | 7.03E-03 | 0.0088 | 0.0167 | 0.0056 |
|                           |                                                                   | Leucine Degradation & HMG-CoA Metabolism             | -1.26 | 2.39E-02 | 0.0055 | 0.0044 | 0.0029 |
|                           | Creatine & Creatinine Degradation                                 | Creatine & Creatinine Degradation                    | -1.31 | 7.95E-05 | 0.0556 | 0.0428 | 0.0103 |
|                           | Glutamine, glutamate, aspartate, asparagine; ammonia assimilation | Glutamine synthetases                                | -1.24 | 2.76E-04 | 0.0134 | 0.0023 | 0.0070 |
|                           | Lysine, threonine, methionine, & cysteine                         | Cysteine Biosynthesis                                | -0.50 | 1.61E-04 | 0.0092 | 0.0129 | 0.0066 |
|                           |                                                                   | Threonine anaerobic catabolism gene cluster          | -1.00 | 1.82E-02 | 0.0063 | 0.0117 | 0.0043 |
|                           |                                                                   | Threonine degradation                                | -0.90 | 2.34E-03 | 0.0414 | 0.0434 | 0.0025 |
|                           | Proline & 4-hydroxyproline                                        | Proline Synthesis                                    | -1.05 | 2.14E-02 | 0.0114 | 0.0131 | 0.0018 |
|                           |                                                                   | Proline, 4-hydroxyproline uptake & utilization       | -0.48 | 1.59E-03 | 0.0329 | 0.0296 | 0.0035 |
| Carbohydrates             | Aminosugars                                                       | Chitin & N-acetylglucosamine utilization             | -0.81 | 2.00E-02 | 0.0348 | 0.0345 | 0.0020 |
|                           | Central carbohydrate metabolism                                   | Dihydroxyacetone kinases                             | -1.33 | 2.69E-02 | 0.0852 | 0.0804 | 0.0039 |
|                           |                                                                   | Entner-Doudoroff Pathway                             | -1.18 | 2.76E-04 | 0.0478 | 0.0540 | 0.0062 |
|                           |                                                                   | Ethylmalonyl-CoA pathway of C2 assimilation          | -1.05 | 7.95E-05 | 0.0340 | 0.0226 | 0.0088 |
|                           |                                                                   | Ethylmalonyl-CoA pathway of C2 assimilation, GJO     | -0.94 | 1.78E-04 | 0.0300 | 0.0287 | 0.0033 |

|                        |                                                                |       |          |        |        |        |
|------------------------|----------------------------------------------------------------|-------|----------|--------|--------|--------|
|                        | Glycolate, glyoxylate interconversions                         | -1.19 | 2.45E-02 | 0.0143 | 0.0181 | 0.0076 |
|                        | Pyruvate metabolism I: anaplerotic reactions, PEP              | -1.44 | 7.32E-04 | 0.0119 | 0.0189 | 0.0063 |
|                        | Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate | -1.01 | 2.14E-02 | 0.0083 | 0.0133 | 0.0046 |
|                        | TCA Cycle                                                      | -0.09 | 3.77E-02 | 0.0160 | 0.0086 | 0.0051 |
| CO2 fixation           | Calvin-Benson cycle                                            | -1.19 | 4.36E-03 | 0.0277 | 0.0383 | 0.0102 |
| Di- & oligosaccharides | Beta-Glucoside Metabolism                                      | -1.17 | 2.76E-04 | 0.1074 | 0.1063 | 0.0036 |
|                        | Fructooligosaccharides(FOS) & Raffinose Utilization            | -1.18 | 9.19E-03 | 0.0031 | 0.0076 | 0.0036 |
|                        | Lactose & Galactose Uptake & Utilization                       | -0.29 | 4.77E-02 | 0.0499 | 0.0578 | 0.0080 |
|                        | Lactose utilization                                            | -1.14 | 1.54E-03 | 0.0169 | 0.0253 | 0.0097 |
|                        | Maltose & Maltodextrin Utilization                             | -1.29 | 4.97E-03 | 0.0871 | 0.0784 | 0.0068 |
|                        | Melibiose Utilization                                          | -1.06 | 7.64E-03 | 0.0262 | 0.0333 | 0.0047 |
|                        | Sucrose utilization                                            | -1.20 | 2.52E-06 | 0.0185 | 0.0316 | 0.0099 |
|                        | Sucrose utilization Shewanella                                 | -1.00 | 4.70E-03 | 0.0060 | 0.0090 | 0.0025 |
|                        | Trehalose Uptake & Utilization                                 | -0.39 | 4.97E-02 | 0.0468 | 0.0402 | 0.0054 |
| Fermentation           | Acetoin, butanediol metabolism                                 | -1.09 | 4.24E-02 | 0.0468 | 0.0402 | 0.0054 |
|                        | Fermentations: Lactate                                         | -1.27 | 9.30E-04 | 0.0481 | 0.0416 | 0.0045 |
| Monosaccharides        | Deoxyribose & Deoxynucleoside Catabolism                       | -1.43 | 2.76E-04 | 0.0494 | 0.0538 | 0.0042 |
|                        | D-galactonate catabolism                                       | -1.27 | 7.95E-05 | 0.0157 | 0.0063 | 0.0064 |
|                        | D-Galacturonate & D-Glucuronate Utilization                    | -0.89 | 9.43E-03 | 0.0166 | 0.0295 | 0.0092 |
|                        | D-ribose utilization                                           | -1.17 | 6.87E-03 | 0.0290 | 0.0416 | 0.0101 |
|                        | D-Sorbitol(D-Glucitol) & L-Sorbose Utilization                 | -1.03 | 1.77E-02 | 0.0441 | 0.0665 | 0.0172 |
|                        | Fructose utilization                                           | -1.43 | 2.76E-04 | 0.0555 | 0.0620 | 0.0097 |
|                        | L-Arabinose utilization                                        | -0.98 | 4.17E-02 | 0.0504 | 0.0554 | 0.0088 |
|                        | L-fucose utilization temp                                      | -1.34 | 5.12E-03 | 0.0154 | 0.0222 | 0.0066 |
|                        | L-rhamnose utilization                                         | -0.34 | 3.31E-02 | 0.0041 | 0.0063 | 0.0036 |

|                     |                                                  |                                                           |       |          |        |        |        |
|---------------------|--------------------------------------------------|-----------------------------------------------------------|-------|----------|--------|--------|--------|
|                     |                                                  | Unspecified monosaccharide transport cluster              | -0.98 | 1.08E-02 | 0.0209 | 0.0324 | 0.0107 |
|                     |                                                  | Xylose utilization                                        | -1.20 | 5.00E-04 | 0.0075 | 0.0136 | 0.0052 |
|                     | One-carbon Metabolism                            | One-carbon metabolism by tetrahydropterines               | -0.57 | 1.32E-02 | 0.0109 | 0.0241 | 0.0101 |
|                     | Organic acids                                    | 2-methylcitrate to 2-methylaconitate metabolism cluster   | -0.94 | 2.13E-02 | 0.0180 | 0.0266 | 0.0070 |
|                     |                                                  | Glycerate metabolism                                      | -1.33 | 7.53E-04 | 0.0648 | 0.0278 | 0.0236 |
|                     |                                                  | Propionyl-CoA to Succinyl-CoA Module                      | -1.21 | 7.95E-05 | 0.0233 | 0.0316 | 0.0082 |
|                     |                                                  | Tricarballoylate Utilization                              | -0.63 | 2.76E-04 | 0.0385 | 0.0499 | 0.0163 |
|                     | Sugar alcohols                                   | Erythritol utilization                                    | -1.61 | 5.81E-04 | 0.0081 | 0.0140 | 0.0055 |
|                     |                                                  | Ethanolamine utilization                                  | -1.21 | 2.21E-02 | 0.0272 | 0.0225 | 0.0034 |
|                     |                                                  | Glycerol & Glycerol-3-phosphate Uptake & Utilization      | -1.50 | 8.02E-03 | 0.1098 | 0.1295 | 0.0208 |
|                     |                                                  | Inositol catabolism                                       | -1.46 | 5.61E-04 | 0.0231 | 0.0300 | 0.0075 |
|                     |                                                  | Mannitol Utilization                                      | -1.46 | 7.06E-04 | 0.0134 | 0.0056 | 0.0049 |
|                     | Unknown carbohydrate utilization ( cluster Ydj ) | Unknown carbohydrate utilization ( cluster Ydj )          | -1.44 | 2.10E-03 | 0.0075 | 0.0125 | 0.0038 |
| Cell Wall & Capsule | Capsular & extracellular polysacchrides          | Capsular heptose biosynthesis                             | -1.55 | 3.15E-04 | 0.0280 | 0.0109 | 0.0109 |
|                     |                                                  | Colanic acid biosynthesis                                 | -0.97 | 2.76E-04 | 0.0264 | 0.0398 | 0.0093 |
|                     |                                                  | dTDP-rhamnose synthesis                                   | -1.06 | 2.88E-02 | 0.0285 | 0.0216 | 0.0047 |
|                     |                                                  | Exopolysaccharide Biosynthesis                            | -1.11 | 2.16E-03 | 0.0232 | 0.0225 | 0.0028 |
|                     |                                                  | Rhamnose containing glycans                               | -1.10 | 7.68E-04 | 0.0169 | 0.0213 | 0.0051 |
|                     |                                                  | Sialic Acid Metabolism                                    | -1.32 | 2.25E-03 | 0.0143 | 0.0229 | 0.0063 |
|                     |                                                  | YjbEFGH Locus Involved in Exopolysaccharide Production    | -1.34 | 3.54E-03 | 0.0072 | 0.0115 | 0.0046 |
|                     | Gram-Negative cell wall components               | Lipid A modifications                                     | -0.77 | 9.93E-03 | 0.0243 | 0.0291 | 0.0047 |
|                     |                                                  | Lipid A-Ara4N pathway ( Polymyxin resistance )            | -0.33 | 2.80E-02 | 0.0151 | 0.0242 | 0.0074 |
|                     |                                                  | Lipopolysaccharide-related cluster in Alphaproteobacteria | -0.90 | 1.32E-03 | 0.0352 | 0.0385 | 0.0055 |
|                     |                                                  | LOS core oligosaccharide biosynthesis                     | -1.53 | 4.62E-04 | 0.0158 | 0.0232 | 0.0068 |
| Cofactors,          | Biotin                                           | Biotin synthesis & utilization                            | -0.14 | 1.94E-02 | 0.0233 | 0.0307 | 0.0061 |

|                                    |                                                |                                                                         |       |          |        |        |        |
|------------------------------------|------------------------------------------------|-------------------------------------------------------------------------|-------|----------|--------|--------|--------|
| Vitamins, & Pigments               | Coenzyme A                                     | Coenzyme A Biosynthesis                                                 | -0.37 | 9.76E-03 | 0.0280 | 0.0318 | 0.0043 |
|                                    | Lipoic acid                                    | Lipoate transport                                                       | -0.18 | 2.49E-03 | 0.0068 | 0.0129 | 0.0058 |
|                                    |                                                | Lipoic acid metabolism                                                  | -0.38 | 4.56E-02 | 0.0162 | 0.0108 | 0.0038 |
|                                    | Pyridoxine                                     | Pyridoxin (Vitamin B6) Biosynthesis                                     | -0.06 | 1.89E-02 | 0.0047 | 0.0075 | 0.0030 |
|                                    |                                                | Test Pyridoxin B6                                                       | -0.15 | 9.57E-03 | 0.0092 | 0.0144 | 0.0040 |
|                                    | Quinone cofactors                              | Menaquinone biosynthesis from chorismate via 1,4-dihydroxy-2-naphthoate | -0.37 | 9.25E-03 | 0.0075 | 0.0107 | 0.0032 |
|                                    | Tetrapyrroles                                  | Cobalamin synthesis                                                     | -1.37 | 6.04E-04 | 0.0056 | 0.0082 | 0.0038 |
|                                    |                                                | Coenzyme B12 biosynthesis                                               | -0.60 | 3.84E-02 | 0.0128 | 0.0170 | 0.0055 |
| DNA Metabolism                     | DNA phosphorothioation                         | DNA phosphorothioation                                                  | -0.78 | 3.16E-02 | 0.0444 | 0.0614 | 0.0124 |
|                                    | DNA repair                                     | DNA Repair Base Excision                                                | -1.04 | 2.74E-02 | 0.0552 | 0.0889 | 0.0218 |
|                                    |                                                | DNA repair, bacterial DinG & relatives                                  | -1.05 | 1.18E-02 | 0.0161 | 0.0239 | 0.0063 |
|                                    | DNA replication                                | Plasmid replication                                                     | -0.69 | 3.56E-04 | 0.0642 | 0.0456 | 0.0127 |
| Dormancy & Sporulation             | Spore Core Dehydration                         | Spore Core Dehydration                                                  | -1.04 | 9.43E-04 | 0.0068 | 0.0087 | 0.0021 |
|                                    | Sporulation gene orphans                       | Sporulation gene orphans                                                | -1.41 | 5.00E-04 | 0.0387 | 0.0480 | 0.0068 |
| Fatty Acids, Lipids, & Isoprenoids | Head-to-head olefinic hydrocarbon biosynthesis | Head-to-head olefinic hydrocarbon biosynthesis                          | -0.56 | 3.34E-03 | 0.0075 | 0.0107 | 0.0034 |
|                                    | Isoprenoids                                    | Acyclic terpenes utilization                                            | -1.28 | 2.41E-02 | 0.0839 | 0.0884 | 0.0048 |
|                                    |                                                | Isoprenoid Biosynthesis                                                 | -0.81 | 3.20E-02 | 0.0531 | 0.0587 | 0.0069 |
|                                    |                                                | Isoprenoid Biosynthesis: Interconversions                               | -0.96 | 4.55E-03 | 0.0565 | 0.0602 | 0.0033 |
|                                    | Polyhydroxybutyrate metabolism                 | Polyhydroxybutyrate metabolism                                          | -1.00 | 1.89E-02 | 0.0356 | 0.0404 | 0.0061 |
|                                    |                                                |                                                                         |       |          |        |        |        |
| Membrane Transport                 | ABC transporters                               | ABC transporter alkylphosphonate                                        | -1.25 | 1.44E-03 | 0.0063 | 0.0106 | 0.0035 |
|                                    |                                                | ABC transporter branched-chain amino acid                               | -1.31 | 4.62E-04 | 0.0157 | 0.0203 | 0.0039 |
|                                    |                                                | ABC transporter dipeptide                                               | -0.67 | 3.15E-03 | 0.0137 | 0.0193 | 0.0055 |
|                                    |                                                | ABC transporter oligopeptide                                            | -0.57 | 1.21E-02 | 0.0147 | 0.0195 | 0.0040 |
|                                    |                                                | ABC transporter tungstate                                               | -1.03 | 6.19E-04 | 0.0098 | 0.0065 | 0.0033 |
|                                    |                                                | ATP-dependent efflux pump transporter Ybh                               | -0.63 | 4.17E-02 | 0.0150 | 0.0206 | 0.0055 |

|                                  |                                                                                           |                                                                       |       |          |        |        |        |
|----------------------------------|-------------------------------------------------------------------------------------------|-----------------------------------------------------------------------|-------|----------|--------|--------|--------|
|                                  |                                                                                           | Periplasmic-Binding-Protein-Dependent Transport System for Glucosides | -1.07 | 2.76E-04 | 0.0020 | 0.0048 | 0.0035 |
|                                  | ECF class transporters                                                                    | ECF class transporters                                                | -1.17 | 4.83E-05 | 0.0033 | 0.0077 | 0.0039 |
|                                  | Protein & nucleoprotein secretion system, Type IV                                         | Mannose-sensitive hemagglutinin type 4 pilus                          | -1.31 | 1.79E-04 | 0.0592 | 0.0571 | 0.0033 |
|                                  |                                                                                           | pVir Plasmid of Campylobacter                                         | -1.22 | 4.48E-03 | 0.0766 | 0.0708 | 0.0047 |
|                                  | Protein secretion system, Type II                                                         | General Secretion Pathway                                             | -1.01 | 4.97E-03 | 0.0234 | 0.0262 | 0.0031 |
|                                  |                                                                                           | Widespread colonization island                                        | -0.70 | 1.63E-03 | 0.0397 | 0.0356 | 0.0040 |
|                                  | Protein secretion system, Type VIII (Extracellular nucleation/precipitation pathway, ENP) | Curli production                                                      | -1.07 | 4.17E-03 | 0.0060 | 0.0103 | 0.0041 |
|                                  | Ton & Tol transport systems                                                               | Ton & Tol transport systems                                           | -0.94 | 9.86E-04 | 0.0562 | 0.0534 | 0.0032 |
|                                  | Transport of Manganese                                                                    | Transport of Manganese                                                | -0.92 | 3.56E-03 | 0.0118 | 0.0164 | 0.0050 |
|                                  | Transport of Nickel & Cobalt                                                              | Transport of Nickel & Cobalt                                          | -1.30 | 7.64E-03 | 0.0163 | 0.0209 | 0.0054 |
|                                  | TRAP transporters                                                                         | Tricarboxylate transport system                                       | -1.44 | 1.24E-02 | 0.0306 | 0.0462 | 0.0104 |
| Metabolism of Aromatic Compounds | Aromatic Amin Catabolism                                                                  | Aromatic Amin Catabolism                                              | -0.87 | 1.73E-02 | 0.0832 | 0.0769 | 0.0056 |
|                                  | Benzoate transport & degradation cluster                                                  | Benzoate transport & degradation cluster                              | -1.37 | 1.38E-03 | 0.0204 | 0.0277 | 0.0057 |
|                                  | Metabolism of central aromatic intermediates                                              | 4-Hydroxyphenylacetic acid catabolic pathway                          | -0.93 | 7.83E-03 | 0.0387 | 0.0307 | 0.0066 |
|                                  |                                                                                           | Catechol branch of beta-ketoadipate pathway                           | -1.01 | 1.35E-03 | 0.0402 | 0.0334 | 0.0060 |
|                                  |                                                                                           | Central meta-cleavage pathway of aromatic compound degradation        | -1.23 | 7.87E-03 | 0.0572 | 0.0504 | 0.0050 |
|                                  |                                                                                           | Homogentisate pathway of aromatic compound degradation                | -0.59 | 1.89E-02 | 0.0322 | 0.0283 | 0.0034 |
|                                  |                                                                                           | N-heterocyclic aromatic compound degradation                          | -1.08 | 3.96E-04 | 0.0426 | 0.0314 | 0.0079 |
|                                  |                                                                                           | Protocatechuate branch of beta-ketoadipate pathway                    | -1.22 | 9.53E-03 | 0.0400 | 0.0347 | 0.0037 |
|                                  |                                                                                           | Salicylate & gentisate catabolism                                     | -0.88 | 2.91E-03 | 0.0288 | 0.0261 | 0.0023 |
|                                  | Peripheral pathways for catabolism of aromatic compounds                                  | Biphenyl Degradation                                                  | -1.05 | 2.71E-03 | 0.0131 | 0.0148 | 0.0018 |
|                                  |                                                                                           | Naphtalene & antracene degradation                                    | -0.95 | 1.21E-02 | 0.0287 | 0.0243 | 0.0031 |
|                                  |                                                                                           | p-Hydroxybenzoate degradation                                         | -1.30 | 1.03E-02 | 0.0048 | 0.0090 | 0.0038 |

|                           |                                           |                                                                         |       |          |        |        |        |
|---------------------------|-------------------------------------------|-------------------------------------------------------------------------|-------|----------|--------|--------|--------|
|                           |                                           | Salicylate ester degradation                                            | -1.00 | 5.12E-03 | 0.0158 | 0.0212 | 0.0047 |
|                           |                                           | Toluene degradation                                                     | -0.69 | 4.39E-04 | 0.0654 | 0.0636 | 0.0062 |
|                           | Phenylacetyl-CoA catabolic pathway (core) | Phenylacetyl-CoA catabolic pathway (core)                               | -0.76 | 3.56E-02 | 0.0270 | 0.0218 | 0.0058 |
| Motility & Chemotaxis     | Flagellar motility in Prokaryota          | Flagellar motility                                                      | -1.37 | 9.78E-04 | 0.0132 | 0.0210 | 0.0055 |
|                           |                                           | Flagellum                                                               | -1.55 | 5.81E-04 | 0.0326 | 0.0230 | 0.0065 |
|                           |                                           | Flagellum in Campylobacter                                              | -1.25 | 5.46E-03 | 0.0376 | 0.0256 | 0.0092 |
| Macronutrients            | Nitrogen Metabolism                       | Cyanate hydrolysis                                                      | -1.10 | 2.62E-03 | 0.0087 | 0.0150 | 0.0042 |
|                           |                                           | Dissimilatory nitrite reductase                                         | -1.11 | 4.16E-02 | 0.0121 | 0.0139 | 0.0041 |
|                           | Sulfur Metabolism                         | Bacterial pathways for dimethylsulfoniopropionate & acrylate catabolism | -1.52 | 1.84E-04 | 0.0111 | 0.0050 | 0.0044 |
|                           |                                           | CFE Sulfur Oxidation                                                    | -1.32 | 1.24E-04 | 0.0135 | 0.0097 | 0.0043 |
|                           |                                           | Dimethylsulfoniopropionate (DMSP) mineralization                        | -1.18 | 7.80E-04 | 0.0042 | 0.0098 | 0.0051 |
|                           |                                           | Organic sulfur assimilation - CsdL protein family                       | -1.06 | 1.58E-03 | 0.0233 | 0.0208 | 0.0032 |
|                           |                                           | Sulfur oxidation                                                        | -1.41 | 7.95E-05 | 0.0290 | 0.0400 | 0.0084 |
|                           | Phosphorus Metabolism                     | Phosphonate metabolism                                                  | -1.24 | 1.38E-03 | 0.0454 | 0.0369 | 0.0070 |
|                           |                                           | Alkylphosphonate utilization                                            | -1.04 | 1.83E-02 | 0.0061 | 0.0121 | 0.0050 |
|                           | Potassium Metabolism                      | pH adaptation potassium efflux system                                   | -0.87 | 2.76E-04 | 0.0027 | 0.0044 | 0.0034 |
|                           |                                           | Glutathione-regulated potassium-efflux system & associated functions    | -1.00 | 2.16E-03 | 0.0219 | 0.0313 | 0.0090 |
|                           | Iron acquisition & Metabolism             | Siderophore Aerobactin                                                  | -0.49 | 3.34E-02 | 0.0794 | 0.0676 | 0.0080 |
| Nucleosides & Nucleotides | Adenosyl nucleosidases                    | Adenosyl nucleosidases                                                  | -0.90 | 3.96E-02 | 0.0113 | 0.0177 | 0.0055 |
|                           | Hydantoin metabolism                      | Hydantoin metabolism                                                    | -1.36 | 1.05E-02 | 0.0501 | 0.0571 | 0.0059 |
|                           | Pseudouridine Metabolism                  | Pseudouridine Metabolism                                                | -0.96 | 2.76E-04 | 0.0727 | 0.0737 | 0.0034 |
|                           | Purines                                   | Purine conversions                                                      | -0.94 | 3.01E-02 | 0.0077 | 0.0115 | 0.0044 |
|                           |                                           | Purine Utilization                                                      | -0.81 | 3.00E-02 | 0.0421 | 0.0419 | 0.0031 |
|                           | Pyrimidines                               | pyrimidine conversions                                                  | -1.12 | 2.95E-02 | 0.0216 | 0.0333 | 0.0095 |
|                           |                                           | Pyrimidine utilization                                                  | -0.78 | 2.16E-03 | 0.0116 | 0.0218 | 0.0105 |
| Phages,                   | Integrans                                 | Integrans                                                               | -1.22 | 6.49E-03 | 0.0643 | 0.0522 | 0.0104 |

|                                          |                                                            |                                                                    |       |          |        |        |        |
|------------------------------------------|------------------------------------------------------------|--------------------------------------------------------------------|-------|----------|--------|--------|--------|
| Prophages,<br>Transposons, &<br>Plasmids | Pathogenicity islands                                      | Staphylococcal pathogenicity islands SaPI                          | -1.19 | 4.06E-03 | 0.0499 | 0.0573 | 0.0058 |
|                                          | Phages, Prophages                                          | Phage head & packaging                                             | -1.02 | 1.89E-02 | 0.0305 | 0.0250 | 0.0045 |
|                                          |                                                            | Phage packaging machinery                                          | -1.21 | 1.30E-02 | 0.0050 | 0.0093 | 0.0030 |
|                                          |                                                            | Staphylococcal phi-Mu50B-like prophages                            | -1.03 | 3.85E-03 | 0.0406 | 0.0404 | 0.0042 |
|                                          | Plasmid related functions                                  | Plasmid-encoded T-DNA transfer                                     | -0.79 | 9.15E-03 | 0.0119 | 0.0061 | 0.0041 |
| Photosynthesis                           | Electron transport & photophosphorylation                  | Photosystem II-type photosynthetic reaction center                 | -1.12 | 2.94E-03 | 0.0564 | 0.0523 | 0.0043 |
| Protein<br>Metabolism                    | Protein biosynthesis                                       | Translation elongation factor G family                             | -0.91 | 1.73E-03 | 0.0417 | 0.0298 | 0.0082 |
|                                          |                                                            | tRNA aminoacylation, His                                           | -1.05 | 5.41E-03 | 0.0122 | 0.0101 | 0.0016 |
|                                          | Protein degradation                                        | EC 3.4.19.- Omega peptidases                                       | -0.91 | 7.64E-03 | 0.0128 | 0.0103 | 0.0019 |
|                                          |                                                            | EC 3.4.21.- Serine endopeptidase                                   | -0.86 | 1.24E-02 | 0.0542 | 0.0492 | 0.0055 |
|                                          |                                                            | Proteasome bacterial                                               | -1.50 | 4.80E-04 | 0.0332 | 0.0270 | 0.0056 |
|                                          |                                                            | Putative TldE-TldD proteolytic complex                             | -1.27 | 5.61E-04 | 0.0471 | 0.0361 | 0.0070 |
|                                          | Protein processing & modification                          | Ribosomal protein S5p acylation                                    | -0.98 | 2.41E-02 | 0.0060 | 0.0006 | 0.0039 |
|                                          | Secretion                                                  | Protein secretion by ABC-type exporters                            | -1.12 | 3.02E-03 | 0.0050 | 0.0076 | 0.0025 |
|                                          | Selenoproteins                                             | Selenocysteine metabolism                                          | -1.14 | 5.41E-03 | 0.0026 | 0.0048 | 0.0029 |
|                                          |                                                            |                                                                    |       |          |        |        |        |
| Regulation &<br>Cell signaling           | Global Two-component Regulator PrrBA in Proteobacteria     | Global Two-component Regulator PrrBA in Proteobacteria             | -1.41 | 3.08E-03 | 0.0026 | 0.0047 | 0.0028 |
|                                          | Programmed Cell Death & Toxin-antitoxin Systems            | Phd-Doc, YdcE-YdcD toxin-antitoxin (programmed cell death) systems | -1.20 | 6.71E-03 | 0.0293 | 0.0494 | 0.0150 |
|                                          | Rcs phosphorelay signal transduction pathway               | Rcs phosphorelay signal transduction pathway                       | -1.49 | 7.09E-04 | 0.0322 | 0.0219 | 0.0088 |
|                                          | Regulation of virulence                                    | A conserved operon linked to TyrR & possibly involved in virulence | -1.10 | 1.97E-02 | 0.0181 | 0.0238 | 0.0039 |
|                                          | Sex pheromones in Enterococcus faecalis & other Firmicutes | Sex pheromones in Enterococcus faecalis & other Firmicutes         | -0.44 | 3.55E-02 | 0.0282 | 0.0238 | 0.0037 |
|                                          | The Chv regulatory system of Alphaproteobacteria           | The Chv regulatory system of Alphaproteobacteria                   | -1.04 | 7.68E-04 | 0.0227 | 0.0345 | 0.0076 |

|                      |                                                              |                                                                                 |       |          |        |        |        |
|----------------------|--------------------------------------------------------------|---------------------------------------------------------------------------------|-------|----------|--------|--------|--------|
| Respiration          | ATP synthases                                                | V-Type ATP synthase                                                             | -0.49 | 7.07E-03 | 0.0092 | 0.0134 | 0.0041 |
|                      | Biogenesis of cytochrome c oxidases                          | Biogenesis of cytochrome c oxidases                                             | -1.32 | 2.47E-04 | 0.0466 | 0.0400 | 0.0051 |
|                      | Carbon monoxide dehydrogenase maturation factors             | Carbon monoxide dehydrogenase maturation factors                                | -1.14 | 1.81E-04 | 0.0320 | 0.0406 | 0.0056 |
|                      | Electron accepting reactions                                 | Anaerobic respiratory reductases                                                | -1.19 | 7.72E-05 | 0.0164 | 0.0228 | 0.0080 |
|                      |                                                              | Terminal cytochrome C oxidases                                                  | -0.31 | 1.03E-02 | 0.0295 | 0.0188 | 0.0073 |
|                      |                                                              | Terminal cytochrome O ubiquinol oxidase                                         | -0.88 | 1.94E-02 | 0.0184 | 0.0286 | 0.0081 |
|                      | Electron donating reactions                                  | CO Dehydrogenase                                                                | -1.23 | 1.84E-04 | 0.0482 | 0.0432 | 0.0041 |
|                      |                                                              | Hydrogenases                                                                    | -0.98 | 2.15E-02 | 0.0516 | 0.0537 | 0.0036 |
|                      | Formate hydrogenase                                          | Formate hydrogenase                                                             | -1.29 | 1.77E-02 | 0.0443 | 0.0476 | 0.0039 |
|                      | Sodium Ion-Coupled Energetics                                | Na <sup>+</sup> translocating decarboxylases & related biotin-dependent enzymes | -1.45 | 1.58E-03 | 0.0053 | 0.0097 | 0.0042 |
| Secondary Metabolism | Bacterial cytostatics, differentiation factors & antibiotics | Phenazine biosynthesis                                                          | -1.04 | 2.18E-02 | 0.0216 | 0.0171 | 0.0041 |
|                      | Biosynthesis of phenylpropanoids                             | Biflavonoid biosynthesis                                                        | -0.75 | 9.15E-03 | 0.0167 | 0.0186 | 0.0022 |
|                      |                                                              | Tannin biosynthesis                                                             | -0.73 | 1.07E-02 | 0.0366 | 0.0398 | 0.0028 |
| Stress Response      | Bacterial hemoglobins                                        | Bacterial hemoglobins                                                           | -1.34 | 1.81E-03 | 0.0138 | 0.0172 | 0.0053 |
|                      | Detoxification                                               | Housecleaning nucleoside triphosphate pyrophosphatases                          | -1.45 | 1.24E-04 | 0.0210 | 0.0293 | 0.0070 |
|                      |                                                              | Uptake of selenate & selenite                                                   | -1.57 | 7.95E-05 | 0.0507 | 0.0483 | 0.0049 |
|                      | Dimethylarginine metabolism                                  | Dimethylarginine metabolism                                                     | -1.01 | 1.32E-02 | 0.0186 | 0.0175 | 0.0031 |
|                      | Hfl operon                                                   | Hfl operon                                                                      | -1.54 | 6.37E-03 | 0.0367 | 0.0307 | 0.0050 |
|                      | Osmotic stress                                               | Ectoine biosynthesis & regulation                                               | -0.80 | 6.31E-03 | 0.0387 | 0.0290 | 0.0067 |
|                      |                                                              | Synthesis of osmoregulated periplasmic glucans                                  | -1.27 | 2.70E-04 | 0.1230 | 0.1035 | 0.0165 |
|                      |                                                              | Glutathione: Biosynthesis & gamma-glutamyl cycle                                | -0.60 | 1.48E-03 | 0.1097 | 0.0899 | 0.0156 |
|                      |                                                              | Glutathione: Non-redox reactions                                                | -0.86 | 2.41E-02 | 0.0349 | 0.0191 | 0.0102 |
|                      |                                                              | Glutathionylspermidine & Trypanothione                                          | -1.07 | 2.82E-02 | 0.0201 | 0.0161 | 0.0030 |
|                      |                                                              | Rubryerythrin                                                                   | -0.92 | 2.74E-02 | 0.0175 | 0.0102 | 0.0046 |

|                              |                                                    |                                         |       |          |        |        |        |
|------------------------------|----------------------------------------------------|-----------------------------------------|-------|----------|--------|--------|--------|
|                              | Periplasmic Stress                                 | Periplasmic Stress Response             | -1.13 | 2.55E-02 | 0.0096 | 0.0057 | 0.0036 |
|                              | Phage shock protein (psp) operon                   | Phage shock protein (psp) operon        | -0.63 | 2.16E-03 | 0.0120 | 0.0178 | 0.0044 |
|                              | SigmaB stress response regulation                  | SigmaB stress response regulation       | -1.19 | 1.86E-04 | 0.0529 | 0.0590 | 0.0242 |
| Virulence, Disease & Defense | Resistance to antibiotics & toxic compounds        | Zinc resistance                         | -1.33 | 3.38E-02 | 0.0193 | 0.0078 | 0.0078 |
|                              | Type III, Type IV, Type VI, ESAT secretion systems | Type 4 secretion & conjugative transfer | -0.25 | 4.91E-02 | 0.0272 | 0.0093 | 0.0107 |
|                              | Invasion & intracellular resistance                | Cytolysin & Lipase operon in Vibrio     | -0.89 | 3.01E-02 | 0.0013 | 0.0035 | 0.0024 |