



Figure 4. Taxonomic assignments of functional categories with significant differential expression in day vs. night. Categories found to have significant differential expression were further assessed for differences in the taxonomic assignments of genes expressed in day vs. night. The total number of expressed reads noted on each profile. With some exceptions, taxonomy profiles were remarkably similar in day vs. night, indicating that microbes expressing these functions act in concert rather than partitioning by time. The best available phylum-level taxonomic assignment for each gene was used in this analysis; this was calculated for genomes when available, at the contig level when contigs were unbinned, and at the gene level when contigs were too short to classify. Proteobacteria were split into classes due to the high diversity of this phylum.