Figure 4. Taxonomic composition of functional categories by time and lake. We next investigated the taxonomy of functional categories and how phylogenetic groups change expression over time. The x-axis indicates the number of genes from each category assigned to each phylum, summed across both days of the time series. Proteobacteria were split by class due to the high diversity of this phylum. RNA polymerase, used as an indicator of growth, was phylogenetically diverse in all lakes, although less well-classified in Sparkling Lake, likely due to the lack of reference genomes from this site. Cyanobacteria contributed to photosynthesis in all lakes, particularly in Lake Mendota. General sugar transport was encoded primarily by Cyanobacteria and Actinobacteria in Lake Mendota, Actinobacteria and Betaproteobacteria in Trout Bog, and Actinobacteria and Armatimonadetes in Sparkling Lake.