



Figure 1. Abundance vs. expression by lake. To determine which phyla were most abundant or most expressed during our time series, we analyzed metagenomic and metatranscriptomic read counts. All read counts are reported in transcripts per liter. The expression of clustered, nonredundant genes was aggregated by phylum and compared to the coverage of those phyla in metagenomes and colored by kingdom (A-C). Axis are reported in proportion of reads assigned to each phylum across the time series. Genes that could not be classified into a phylum were not included in this analysis. Proteobacteria were split into classes due to the high diversity of this phylum. No positive relationship was observed between expression and abundance. We repeated this analysis at a finer resolution by investigating freshwater clades (D-F). Clades are color-coded by phylum to provide taxonomic context.