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. The expression of clustered, nonredundant genes was aggregated by phylum and compared to the coverage of those phyla in metagenomes (A-C). Genes that could not be classified in a phylum were not included in this analysis. No positive relationship was observed between expression and abundance. One phylum, Chloroflexi, was removed from the plot of Lake Mendota due to orders of magnitude higher expression and abundance; this phylum was likely misclassfield. We repeated this analysis on selected freshwater clades (D-F). Note that some clades, including LD12, are not plotted because of low read counts in the metagenomes.