



**Figure S1.** Comparison of community composition between the two wetlands populations, Cedarburg and Sapa. Bacterial (top) and Eukaryotic (bottom) families identified within pitcher samples, showing data pooled for the 5 samples from each wetland (shown in Fig. 1) for families representing > 0.01% of the total pooled sequences, and sequence numbers are adjusted to the mean of the two populations.