Method Notes: The programs dada21 & phyloseq2 were used to analyze the data. A total of approximately 27 million reads were generated. On average, 41.7±7.6% of those were retained per sample. Of those discarded, roughly half contained ambiguous base pairs, and the remaining fraction were chimeric or contained sequencing errors. The Silva v128 database was used to assign taxonomy to sequences. Approximately 60,901 unique sequence variants (operational taxonomic units) were observed in the data. All the sequencing data figures were generated using a rarefied sequencing table, where all samples were subsampled down to an even size of 4,199.

1. Callahan, B. J., McMurdie, P. J., Rosen, M. J., Han, A. W., Johnson, A. J. A., & Holmes, S. P. (2016). DADA2: high-resolution sample inference from Illumina amplicon data. Nature methods, 13(7), 581-583.
2. McMurdie, P. J., & Holmes, S. (2013). phyloseq: an R package for reproducible interactive analysis and graphics of microbiome census data. PloS one, 8(4), e61217.

Figure 1: The Shannon diversity in each sample. The different monitoring stations are listed on the horizontal axis. Higher number stations are located farther south. Samples taken at different months are colored. Lower values of Shannon Diversity represent less diverse communities, but not necessarily a lower concentration of microbes.

Figure 2: A projection of all of the samples from 2016 onto the two axes that explain the most variation in the Bray-Curtis distance matrix, as calculated by Principal Component Analysis. Each point is colored by monitoring station.

Figure 3: A bar plot containing the relative abundances of the 30 most common unique sequence variants throughout the water column between years. The two panels are labelled by year and contain fractions of relative abundance on the vertical axis and depths on the horizontal axis. Fractions of the bar graph are colored by Family. The full taxonomic designation is contained in Table 1. Note that although only 6 types are depicted, a total of 30 unique variants are contained within each designation

Table 1: The full taxonomic designations depicted in Figure 3