Supplemental Information Table of Contents

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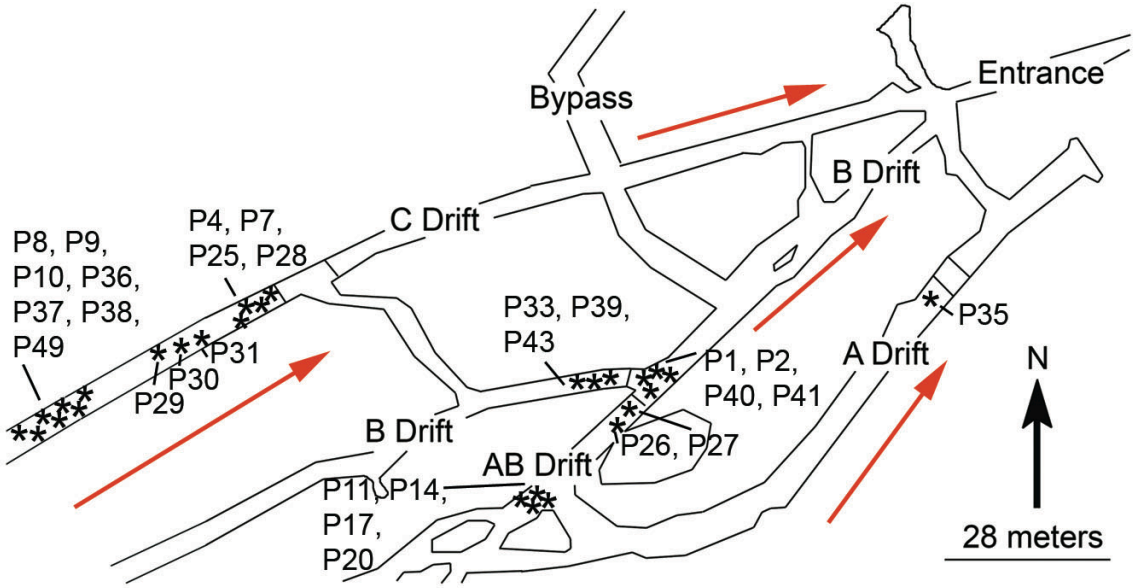
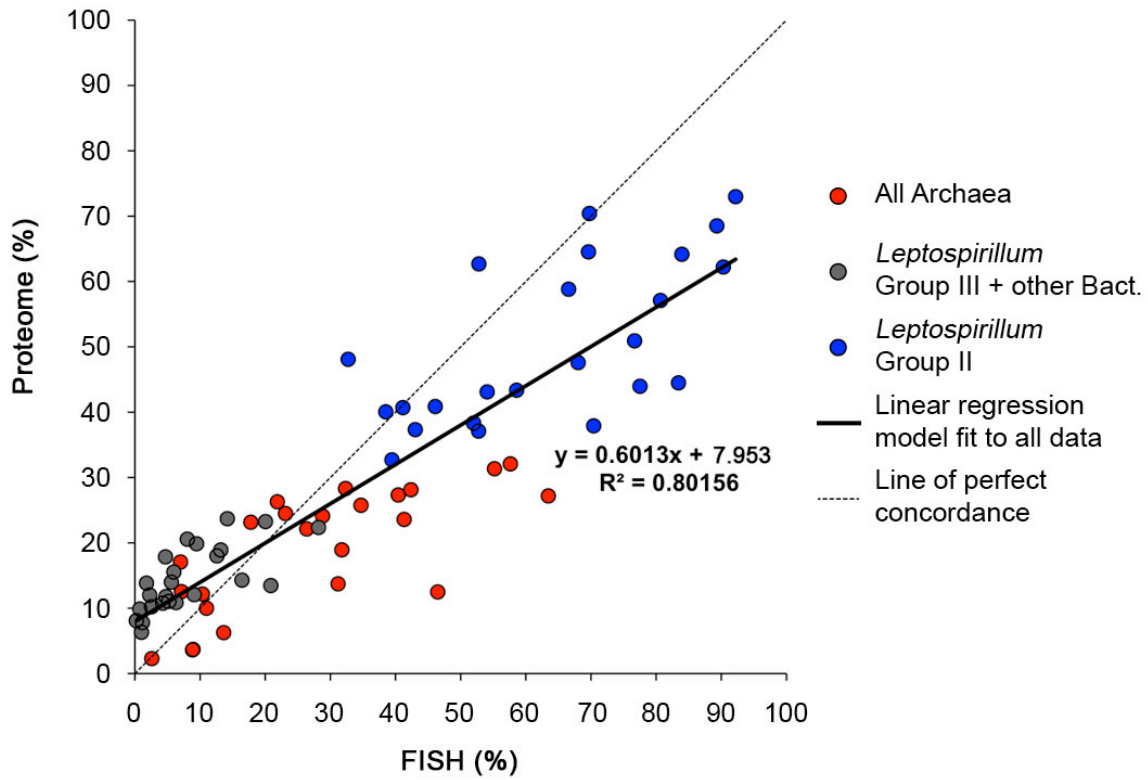
Figure S1



Map of Richmond Mine. Asterisks note collection sites for each sample and red arrows represent the direction of flow through the mine.

Figure S2



Pair-wise Scatter Plot of FISH Relative Abundance Data Versus Proteomic Relative Abundance Data Proteomic relative abundance data is based on the percentage of total proteins identified in a given sample summed for an organism (e.g summed NSAF values for *Leptospirillum* Group II) or across an organismal group (e.g. summed NSAF values for all Archaea). Dashed line of perfect concordance represents a 1:1 fit of the two data sets to each other.

Figure S3A

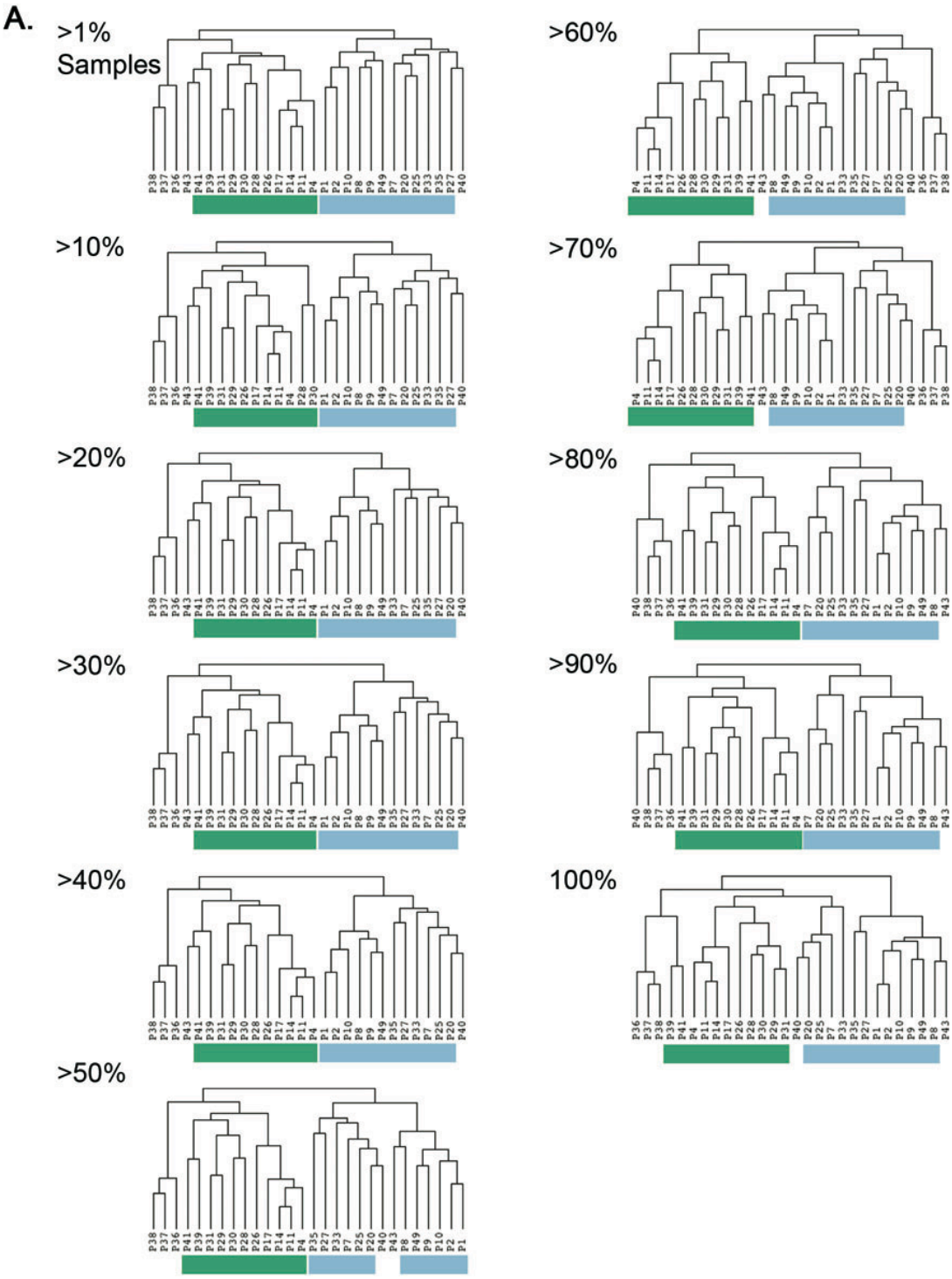
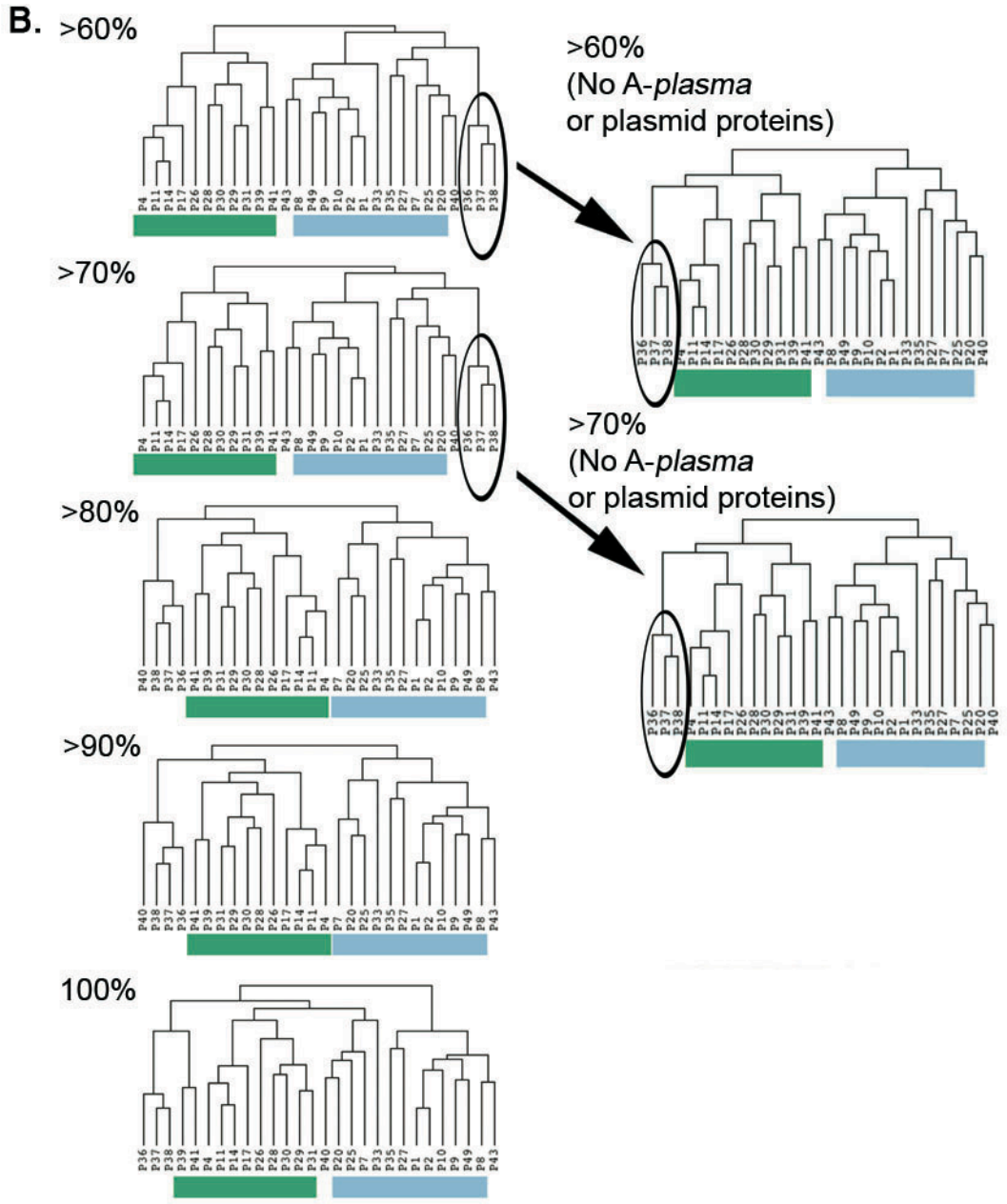
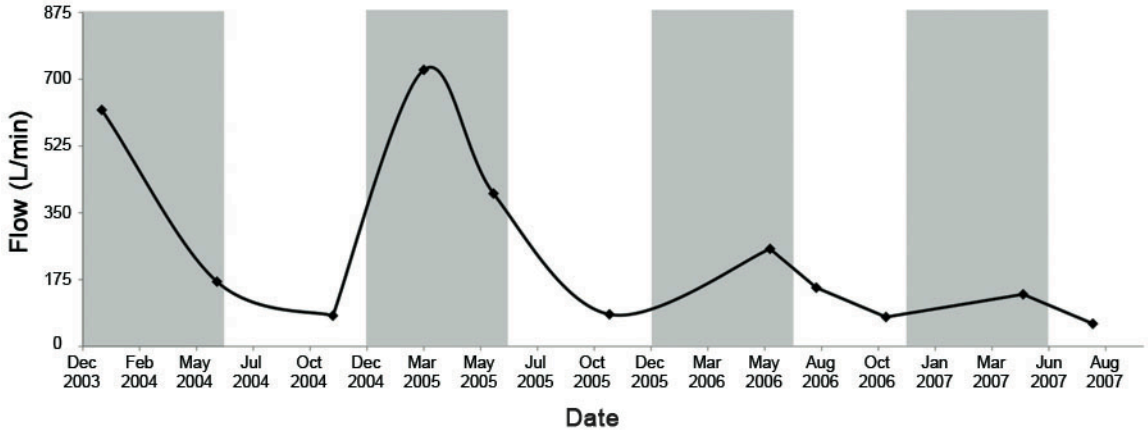


Figure S3B



Hierarchical Clustering of Samples Using Defined Subsets of Proteins From Whole-community Proteomes A. Un-centered, average linkage clustering of proteome samples based on Pearson correlation metric using subsets of protein abundance data. ***B.*** Un-centered, average linkage clustering of proteome samples based on Pearson correlation metric using subsets of protein abundance data that do not include proteins from the plasmid or A-*plasma* category. When A-*plasma* and plasmid proteins are removed from the analysis the inconsistent samples (P36, P37 and P38) group back with the green expression group.

Figure S4



Values of Flow Across all Sampling Dates Values represent total outflow of the AMD solution on the day of sampling and are consistently highest during the rainy months of the year (Dec. – Jun. represented by shaded rectangles), reflecting seasonal precipitation rates.