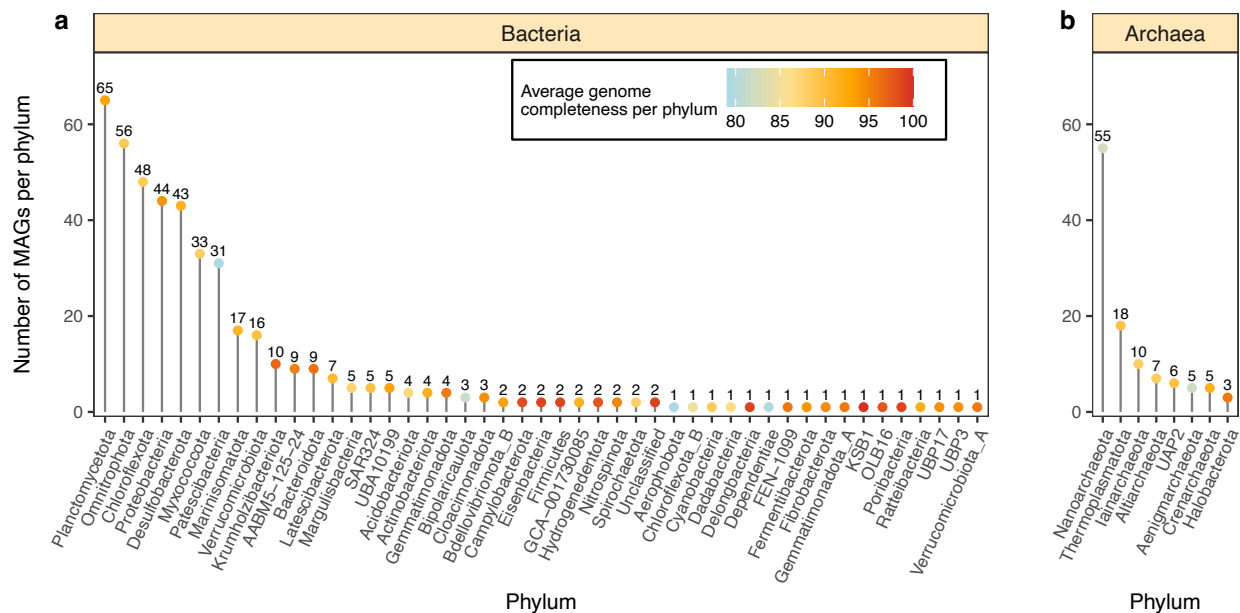
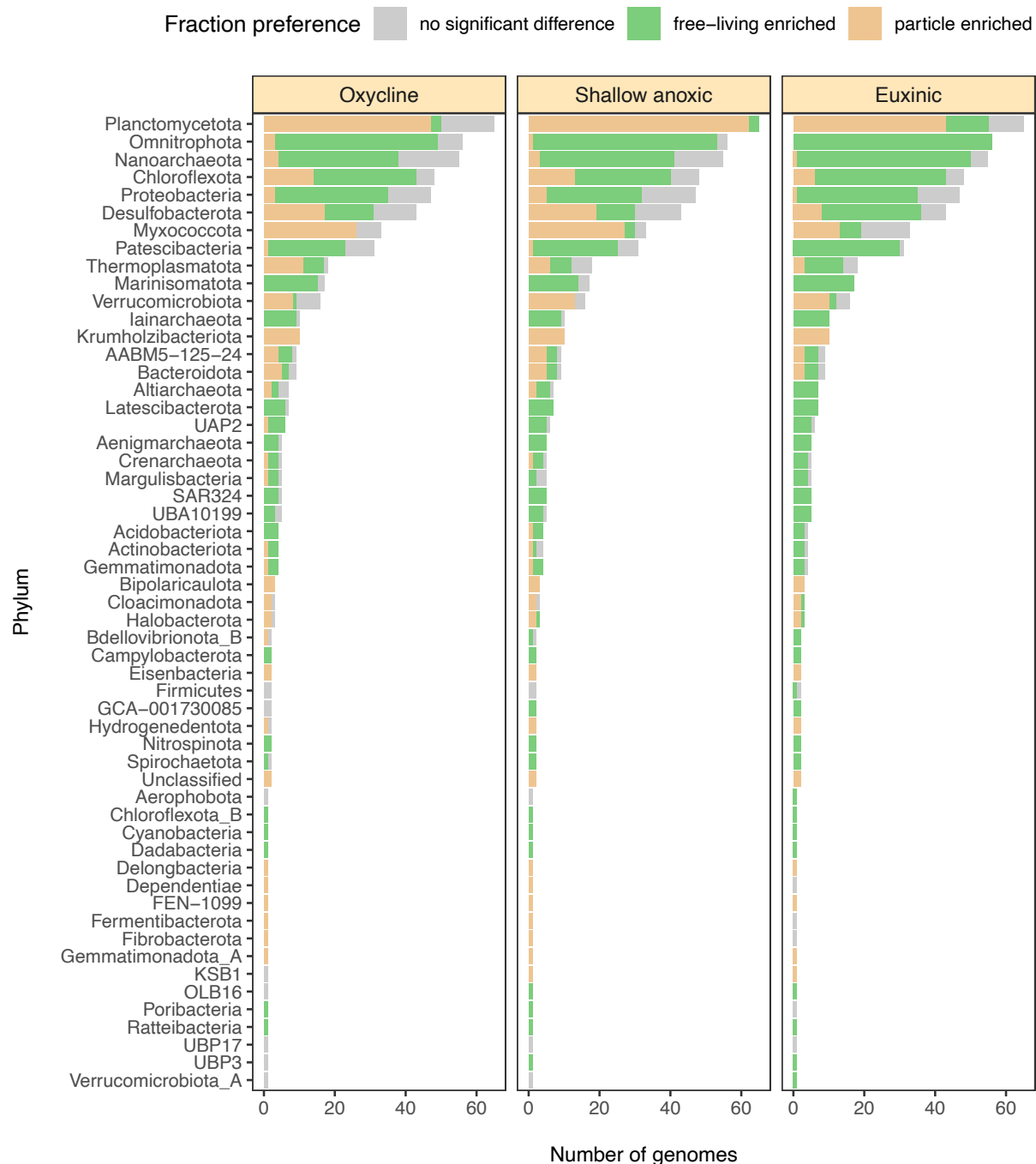




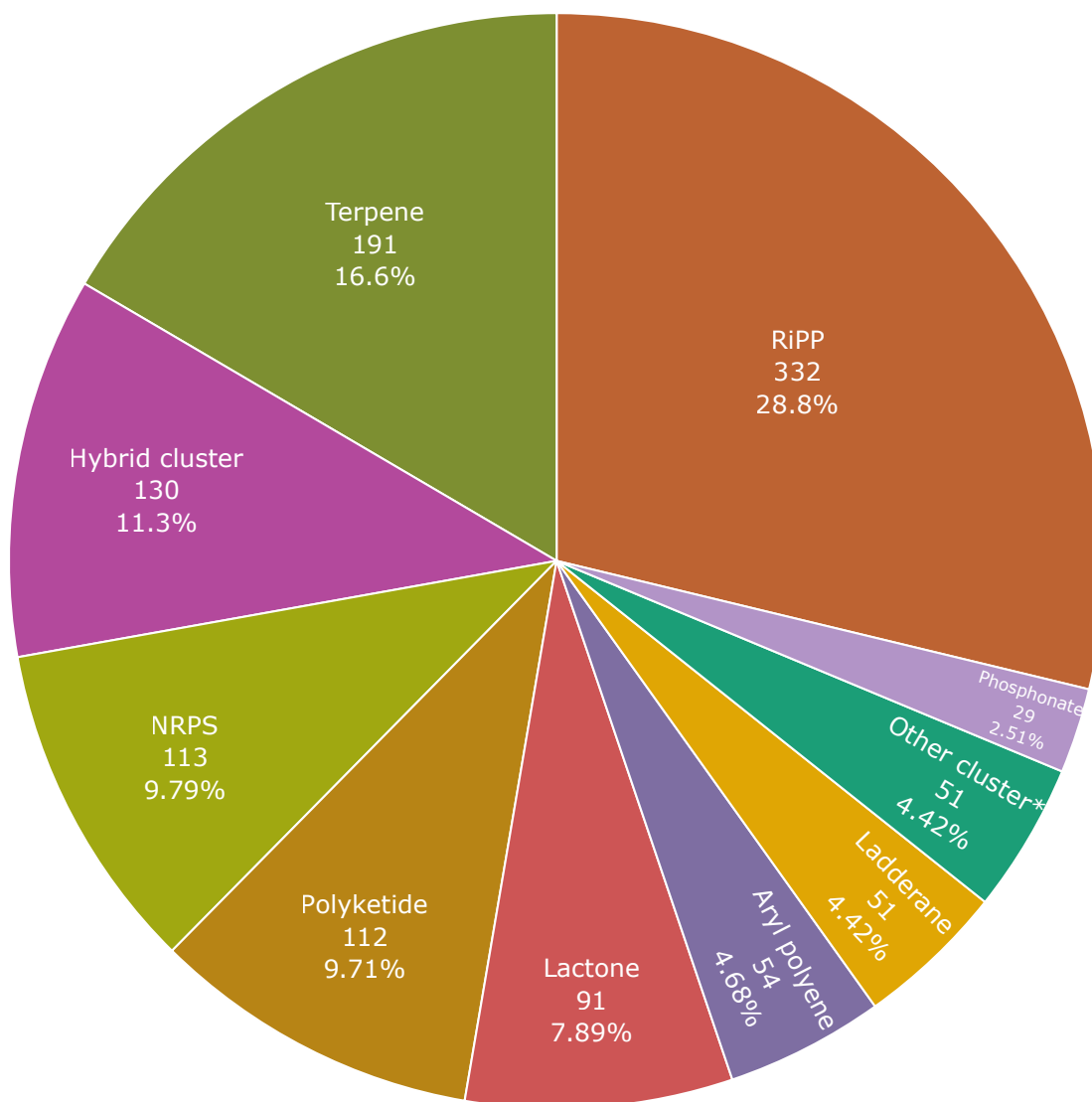
Supplementary Figure 1: Frequency of Cariaco prokaryotic MAGs ($\geq 75\%$ completeness, $\leq 5\%$ contamination) by bacterial (a) and archaeal phylum (b). Colored dots at the end of each line segment correspond to the mean genome completeness of the phylum; the number above the dot quantifies the number of genomes recovered from the phylum. Source data are provided as a Source Data file.



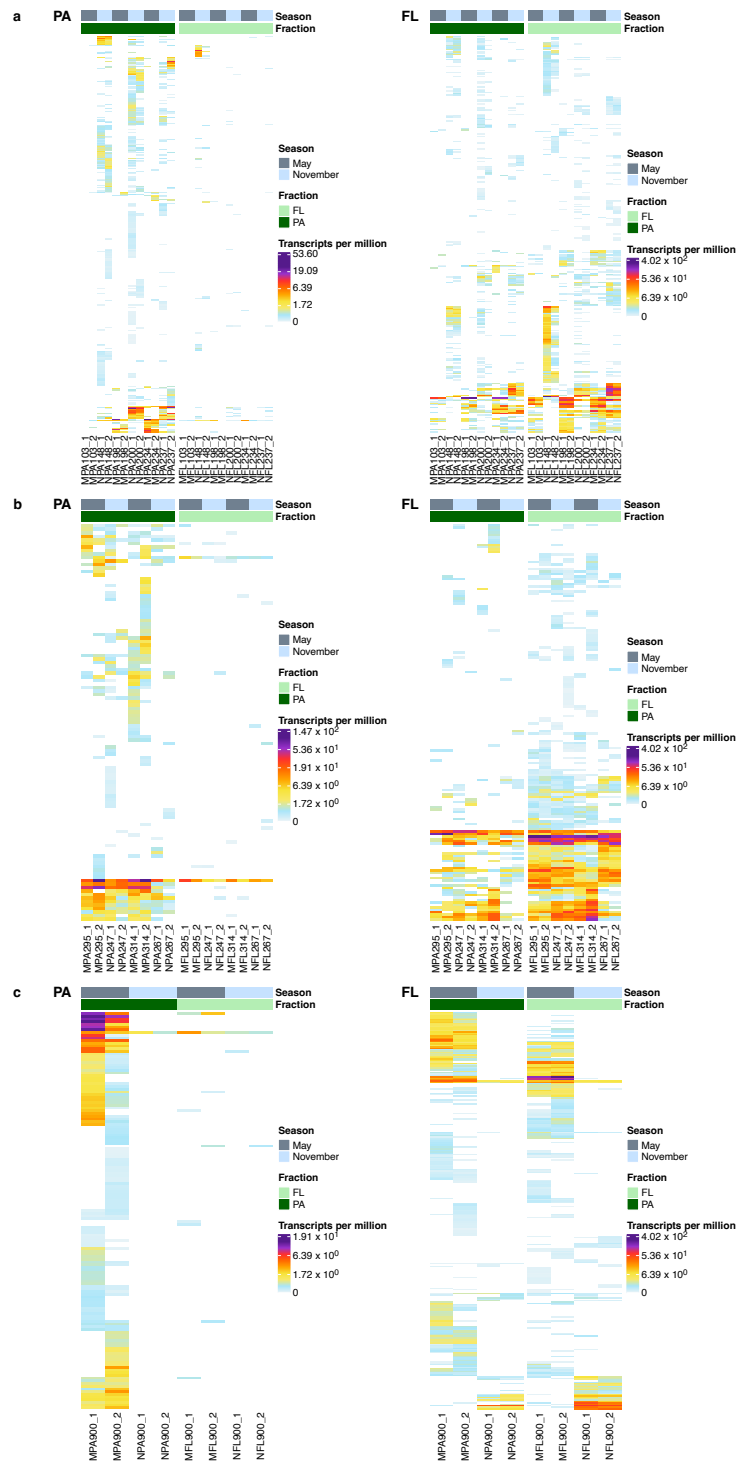
Supplementary Figure 2: MAG relative abundances. The heatmap shows for each column the percentage of total pre-processed reads from a metagenomic sample that mapped to the 100 most abundant MAGs (across all samples) using a log_{1p} scale ranging from 0-32.12% relative abundance. Each row represents an individual MAG (additional information about the MAGs can be found in Supplementary Tables 1-2, 4 and 5). Source data are provided as a Source Data file.



Supplementary Figure 3: MAG differential abundance (fraction preference). Bar charts of the differential abundances of MAGs, grouped by phylum (DESeq2; $P < 0.05$; False Discovery Rate (FDR) = 5%) for each layer of the water column (oxycline, shallow anoxic, euxinic). The light brown color indicates MAGs that were more abundant in the PA metagenomes, the green color represents MAGs that were more abundant in the FL metagenomes, and the grey color indicates there was not statistically significant difference between the FL and PA fractions. Phyla represented in all three panels are from groups for which at least 5 genomes were recovered. Source data are provided as a Source Data file.



Supplementary Figure 4: Distribution of the biosynthetic gene clusters identified using antiSMASH 6.0. Each label corresponds to the total amount of biosynthetic gene clusters ≥ 10 kb recovered from a given class, with the total number listed below the class followed by the percentage (%) out of the total BGC count (1,154). Other cluster* includes resorcinol, nucleoside, linear azol(in)e-containing peptide, acyl amino acid, cyclodipeptide, ectoine, redox-cofactor, non-alpha poly-amino group acid, siderophore, polybrominated diphenyl ether, and indole biosynthetic gene clusters. Source data are provided as a Source Data file.



Supplementary Figure 5: Biosynthetic transcript expression of MAGs with strict PA and FL fraction preferences. Heatmaps of the expression (transcripts per million) of biosynthetic gene cluster transcripts from MAGs with an apparent PA fraction preference (DESeq2; $P < 0.05$; False Discovery Rate (FDR) = 5%) in left-hand panels labelled “PA”, and from MAGs more abundant in the FL fraction layers in the right-hand panels labelled “FL” from **a** oxycline, **b** shallow anoxic and **c** euxinic water layers. Source data are provided as a Source Data file.

