

Temporal and spatial distributions of marine *Synechococcus* in the Southern California Bight assessed by hybridization to bead-arrays

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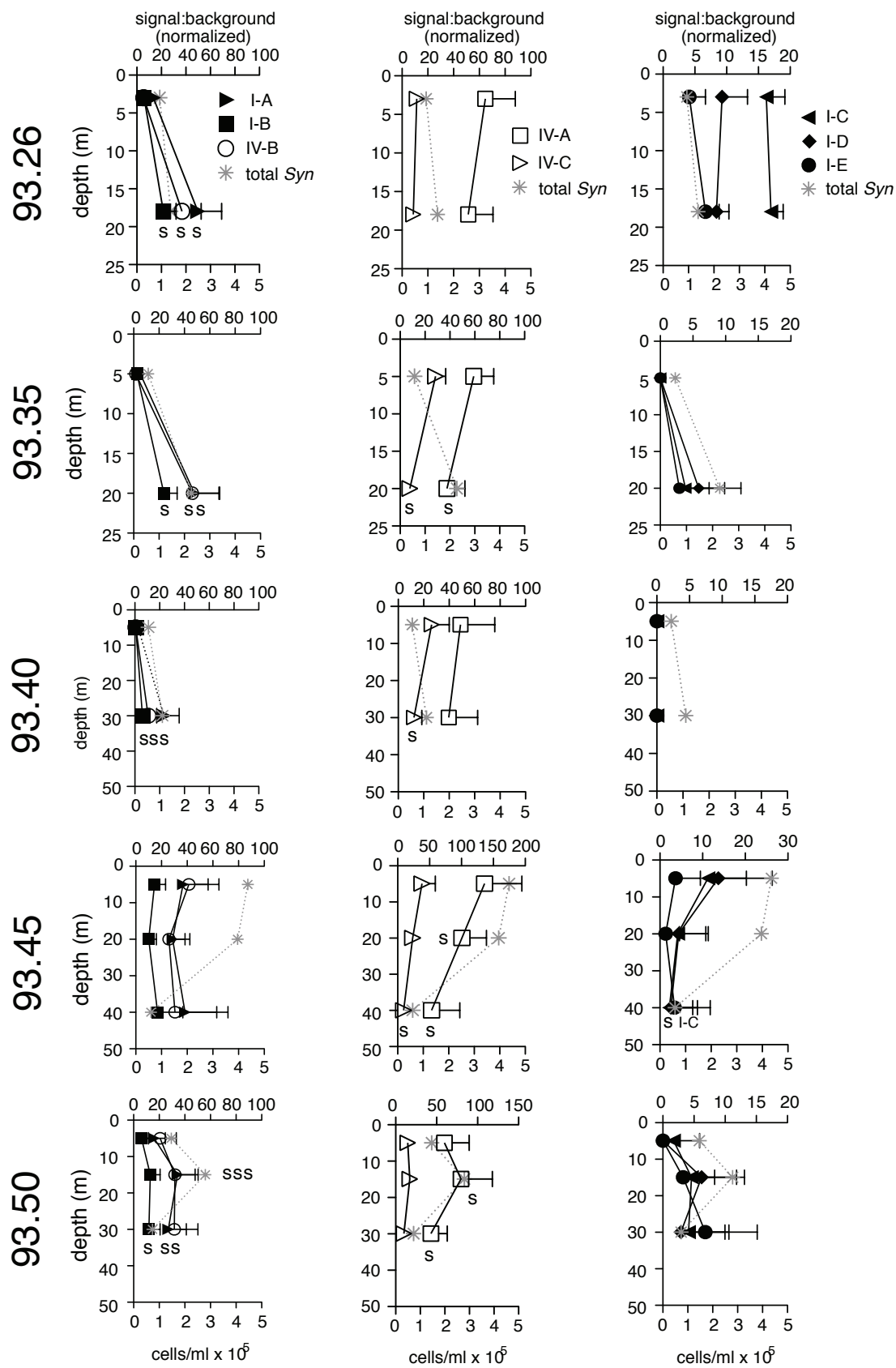
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Fig. S1. Sub-clade Luminex signals with depth for each station sampled along the Line 93 transect. Each row of graphs is from one station. The upper x-axis shows the Luminex signal:background (normalized) while the lower x-axis shows the total *Synechococcus* abundance in cells/ml $\times 10^5$. The left panel of graphs shows the results for sub-clade probes I-A, I-B, and IV-B; the middle, sub-clade probes IV-A and IV-B; the right, sub-clade probes I-C, I-D, and I-E. The mean signal:background from 5 or 6 replicates + the standard deviation is shown. The error bar is shown only above the mean for clarity. s indicates that the Luminex signal for the indicated probe is significantly different ($p < 0.05$) at the sampled depth compared to the surface.

Supplementary Figure 1.



Supplementary Figure 1, continued.

