

Figure S1: Trends of genetic diversity (Shannon-Weaver index) of surface bacterial communities at E2 during a 3.5-year monthly time series (A) and as a mean annual cycle (B) when two different OTU similarity cutoff are used: 0.01 (solid line) and 0.03 (dashed line).

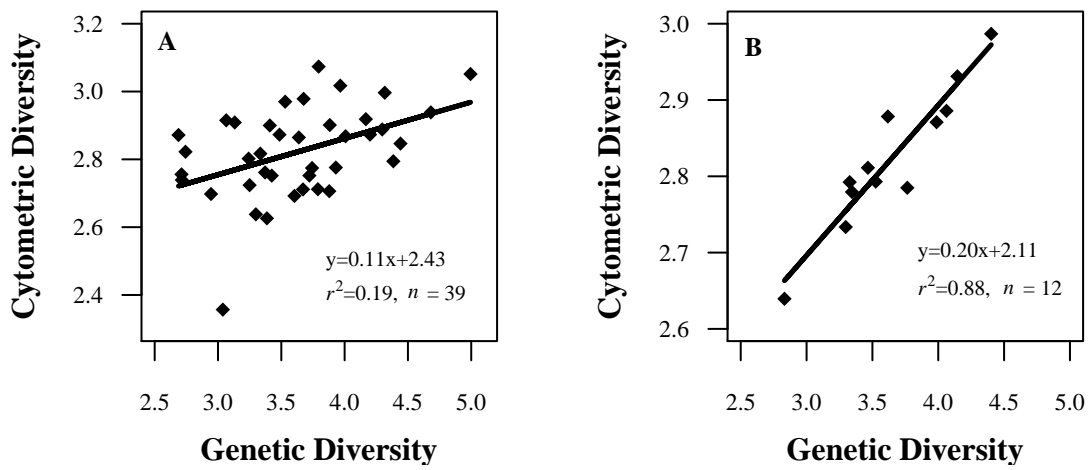


Figure S2: Correlation analysis between genetic (OTU genetic distance cutoff 0.01) and cytometric diversity (Shannon-Weaver index) using the 3.5-year monthly sampled database and mean annual cycle.

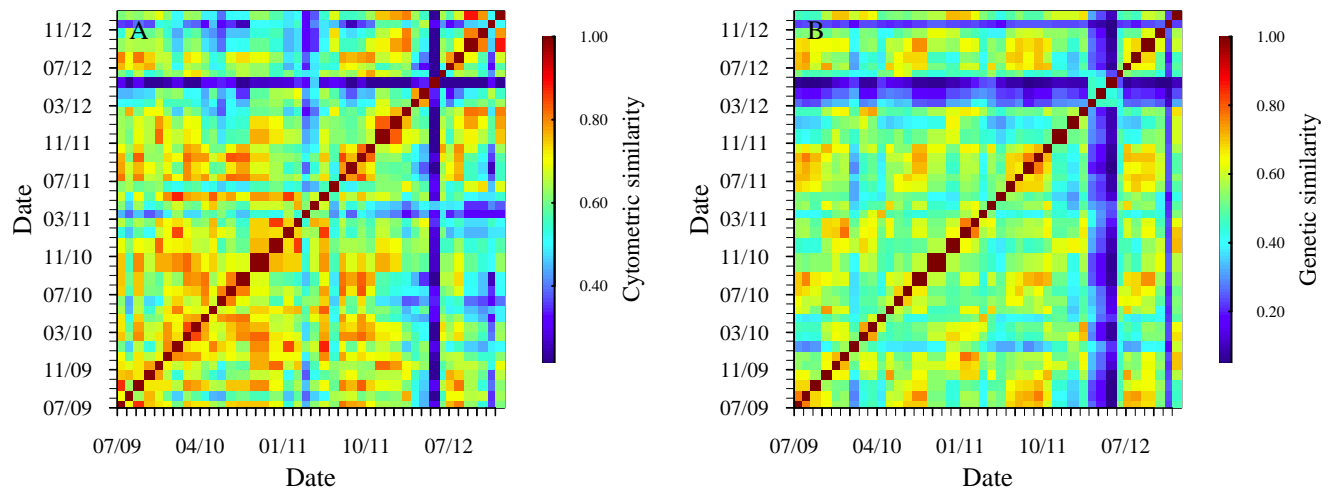


Figure S3: Bacterioplankton similarity matrix estimated using Bray-Curtis algorithm with 3.5-year monthly surface samples analyzed by flow-cytometry (left panel) and by pyrosequencing techniques (right panel).

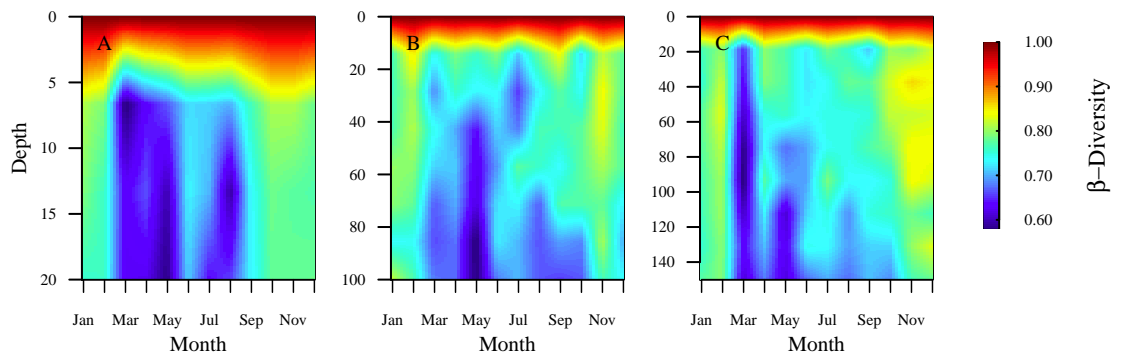


Figure S4: Community similarity data estimated from a 10-year monthly time series database collected in the Cantabrian Sea. Community similarity was estimated as the Jaccard similarity between surface data and the different depths across the water column. Warm colours represent high similarity with the surface sample and cool colours represent low similarity with the surface sample. Surface similarity value is 1 because represent similarity with itself.

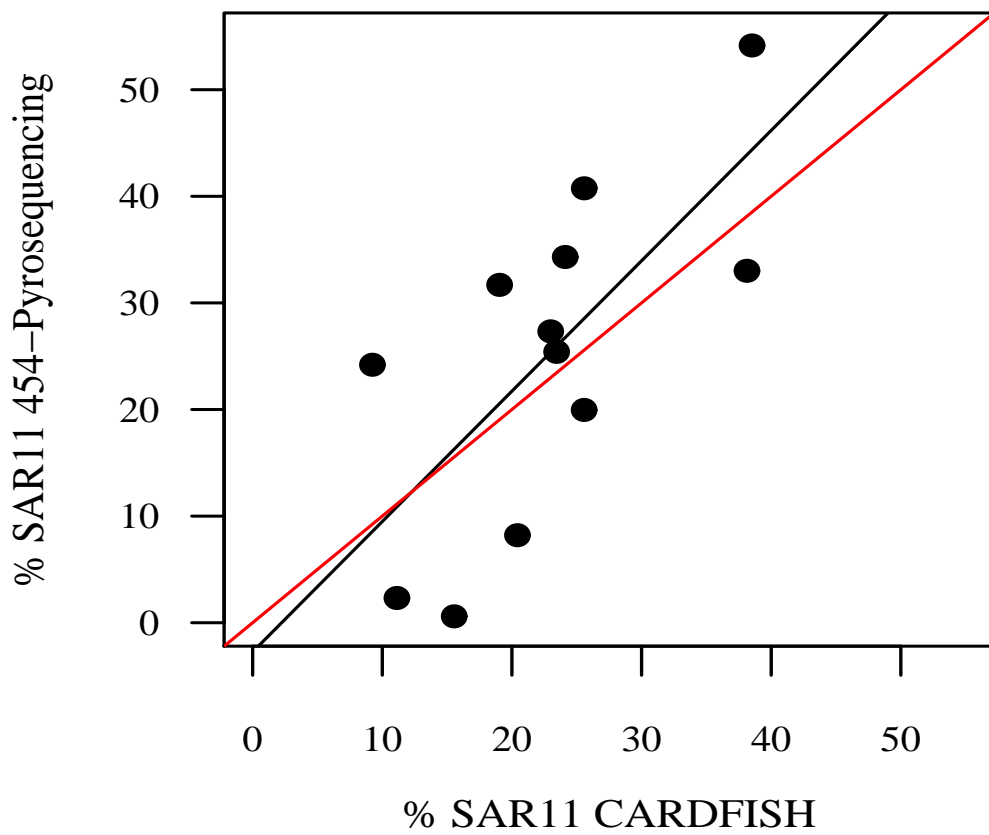


Figure S5: Percentage of SAR11 detected by 454 Pyrosequencing method (y-axis) and CARD-FISH (x-axis). Black line is the model fitting and red line represents the line (0,1).