Supplementary Table 1. General information on sequencing results and reads.

Sample Names	Raw Reads from paired-end sequencing (fastq replicates)	Interlaced reads after trimming and rRNA removal	Percent of prokaryotic reads from BLAST (%)	Number of prokaryotic reads from total reads
R_1	25 795 611 25 795 611	31 872 360	8.9	2 860 032
R_2	24 750 021 24 750 021	31 519 356	10.5	3 308 037
A3_2_1*	23 871 679 23 871 679	29 824 202	15.3	5 514 089
A3_2_2*	21 853 684 21 853 684	34 620 685	13.8	4 438 123
FL_1*	20 460 960 20 460 960	36 070 585	18.0	5 373 036
FL_2*	23 556 644 23 556 644	32 099 894	21.7	7 504 148

* The higher number of prokaryotic reads and their higher relative contributions to total reads at A3-2 and F-L as compared to R-2 can be explained by the elevated prokaryotic cell abundances at these sites (Table 1) and differences in the phytoplankton community composition. While larger diatom cells, abundant at the 2 bloom sites, were retained by the 5 µm filter used for the pre-filtration step, phytoplankton biomass at station R-2 was dominated by picoeukaryotes (Lasbleiz et al. 2016) that pass this pore size resulting in a higher number of eukaryote-assigned reads.