

Table S1 Results of mantel test showing the correlations of associated (AB) and whole water (WWB) bacterial communities with each environmental factor. The variations in bacterial communities were expressed using phylogenetic (β MNTD) and non-phylogenetic (bray-cutis) distances. Only the significant values are exhibited in the table ($p < 0.05$).

	AB		WWB	
	bray-cutis	β MNTD	bray-cutis	β MNTD
TN			$r = 0.1122, p = 0.013$	$r = 0.1483, p = 0.007$
NO ₃ -N			$r = 0.2452, p = 0.001$	$r = 0.2333, p = 0.001$
NH ₄ -N			$r = 0.0990, p = 0.032$	
TP				
PO ₄ -N				
T	$r = 0.4779, p = 0.001$	$r = 0.5022, p = 0.001$	$r = 0.5323, p = 0.001$	$r = 0.6099, p = 0.001$
WL	$r = 0.2551, p = 0.001$	$r = 0.2110, p = 0.001$	$r = 0.3740, p = 0.001$	$r = 0.4534, p = 0.001$
SD				$r = 0.2165, p = 0.001$
COD				
pH	$r = 0.1715, p = 0.008$	$r = 0.1693, p = 0.022$	$r = 0.1860, p = 0.001$	$r = 0.1821, p = 0.003$
DO	$r = 0.2503, p = 0.001$	$r = 0.2055, p = 0.002$	$r = 0.1648, p = 0.001$	$r = 0.1929, p = 0.002$
ORP				
EC	$r = 0.1738, p = 0.018$		$r = 0.3105, p = 0.001$	$r = 0.1776, p = 0.002$
NTU				
Chl a	$r = 0.2056, p = 0.016$		$r = 0.3502, p = 0.001$	$r = 0.4041, p = 0.001$

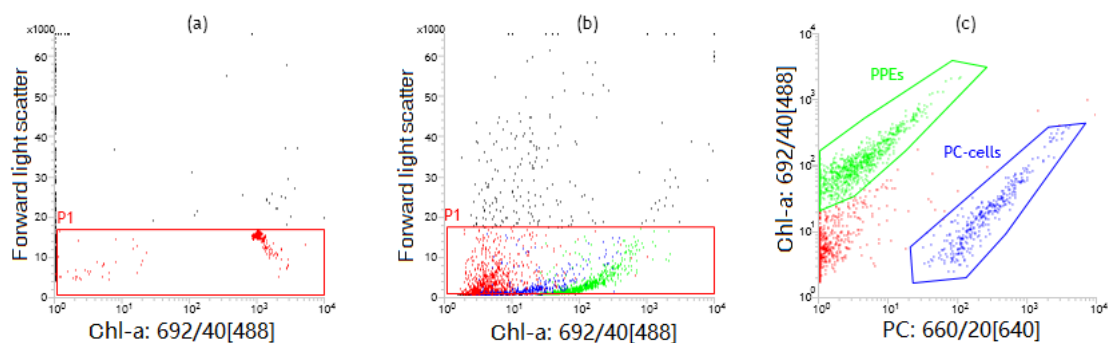


Figure S1 Picophytoplankton groups identified by flow cytometry. (a) Cytogram showing the 3 μ m SPHERO Standard beads for size control. (b) Cytogram of Chl a fluorescence vs. forward scatter (FSC). (b) Cytogram of PC fluorescence vs Chl a fluorescence. The PPEs group was sorted for subsequent molecular analyses.

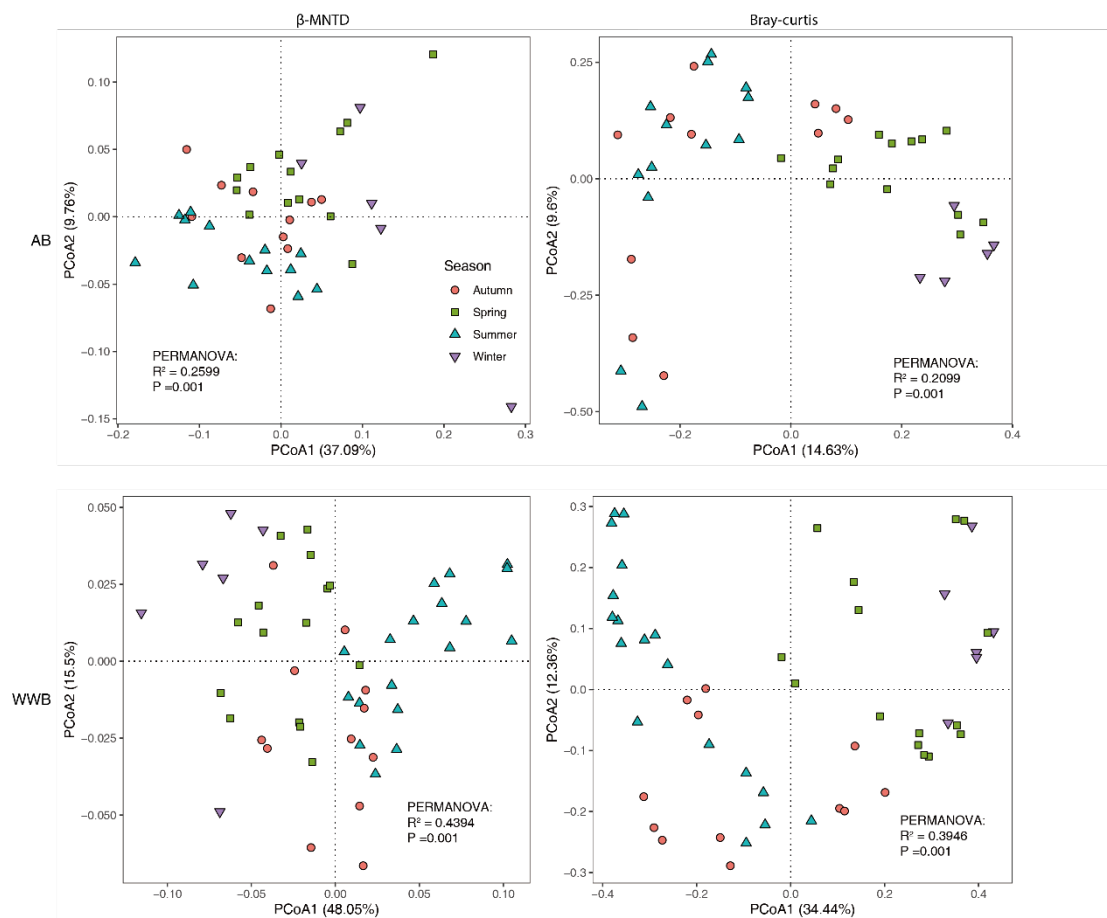


Figure S2 Principal co-ordinate analysis (PCoA) plots showing the seasonal community variations of associated bacteria (AB, upper panel) and whole water bacteria (WWB, lower panel) based on phylogenetic (left panel) and taxonomic (right panel) distances.

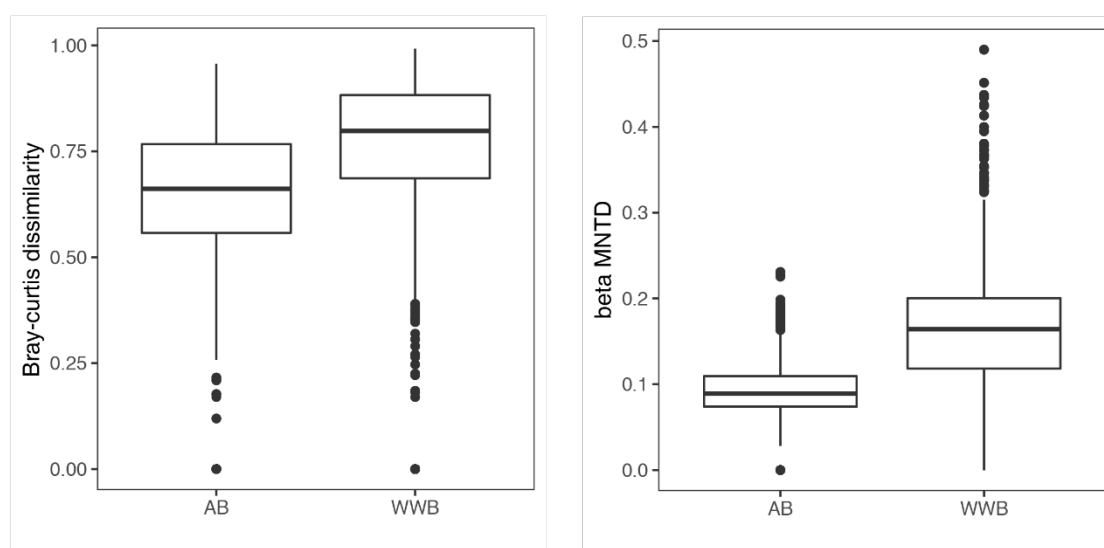


Figure S3 The phylogenetic (left) and taxonomic (right) dissimilarities within the associated bacteria (AB) and whole water bacteria (WWB) communities ($P < 0.01$, t-test).

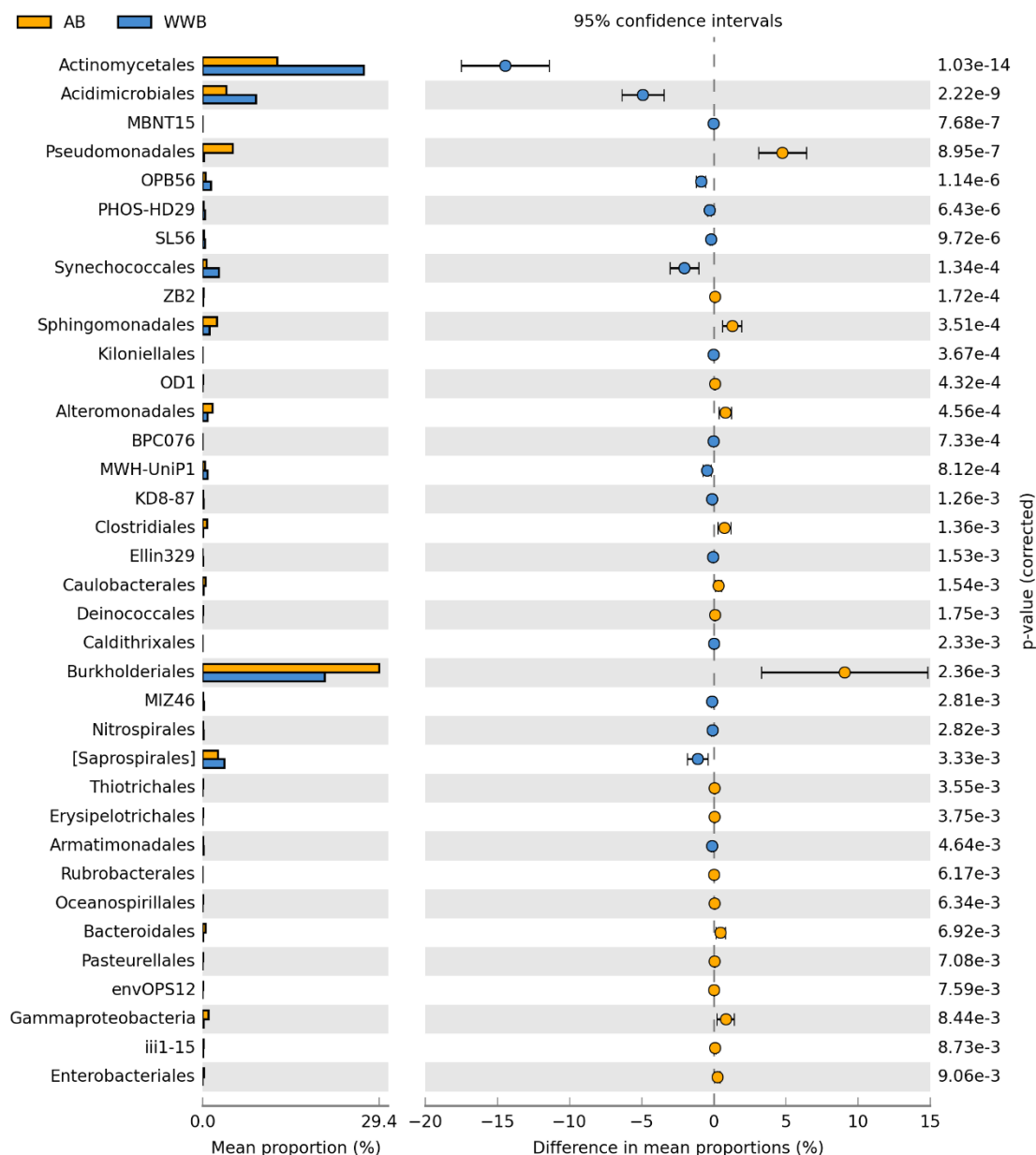


Figure S4 The bacterial orders significantly changed between the communities of associated bacteria and whole water bacteria (Welch’s t-test, $P < 0.01$)

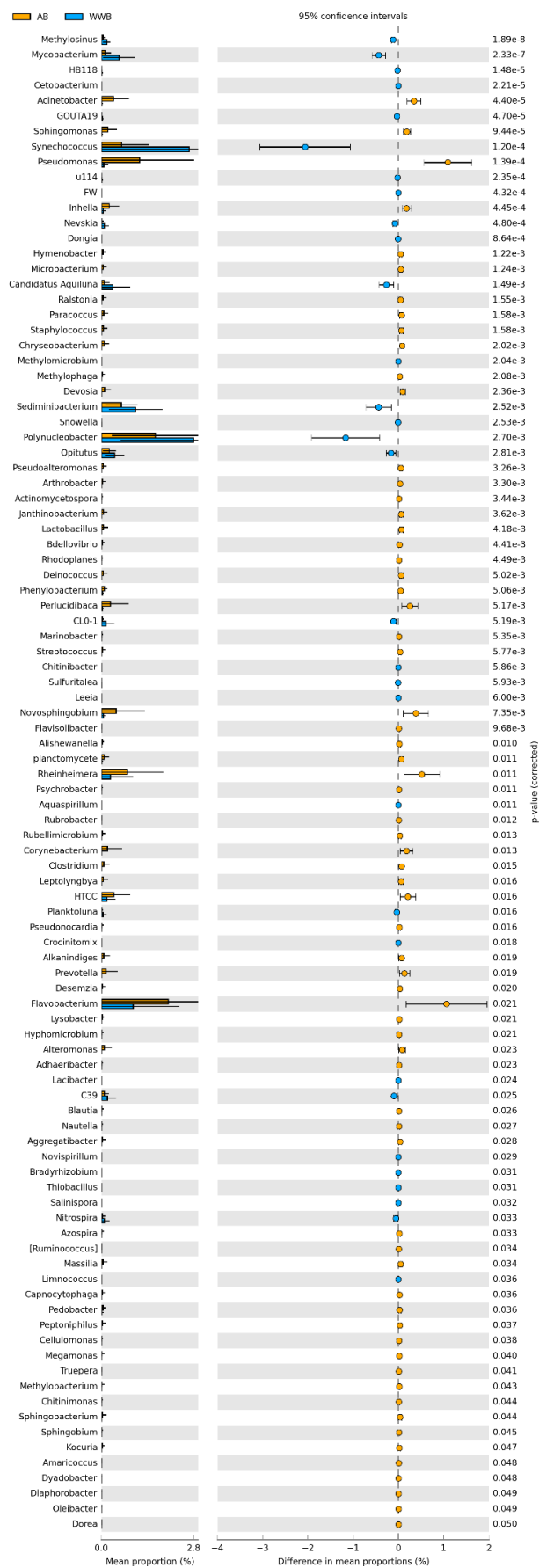


Figure S5 The bacterial genera significantly changed between the communities of associated bacteria and

whole water bacteria (Welch’s t-test, $P < 0.05$)

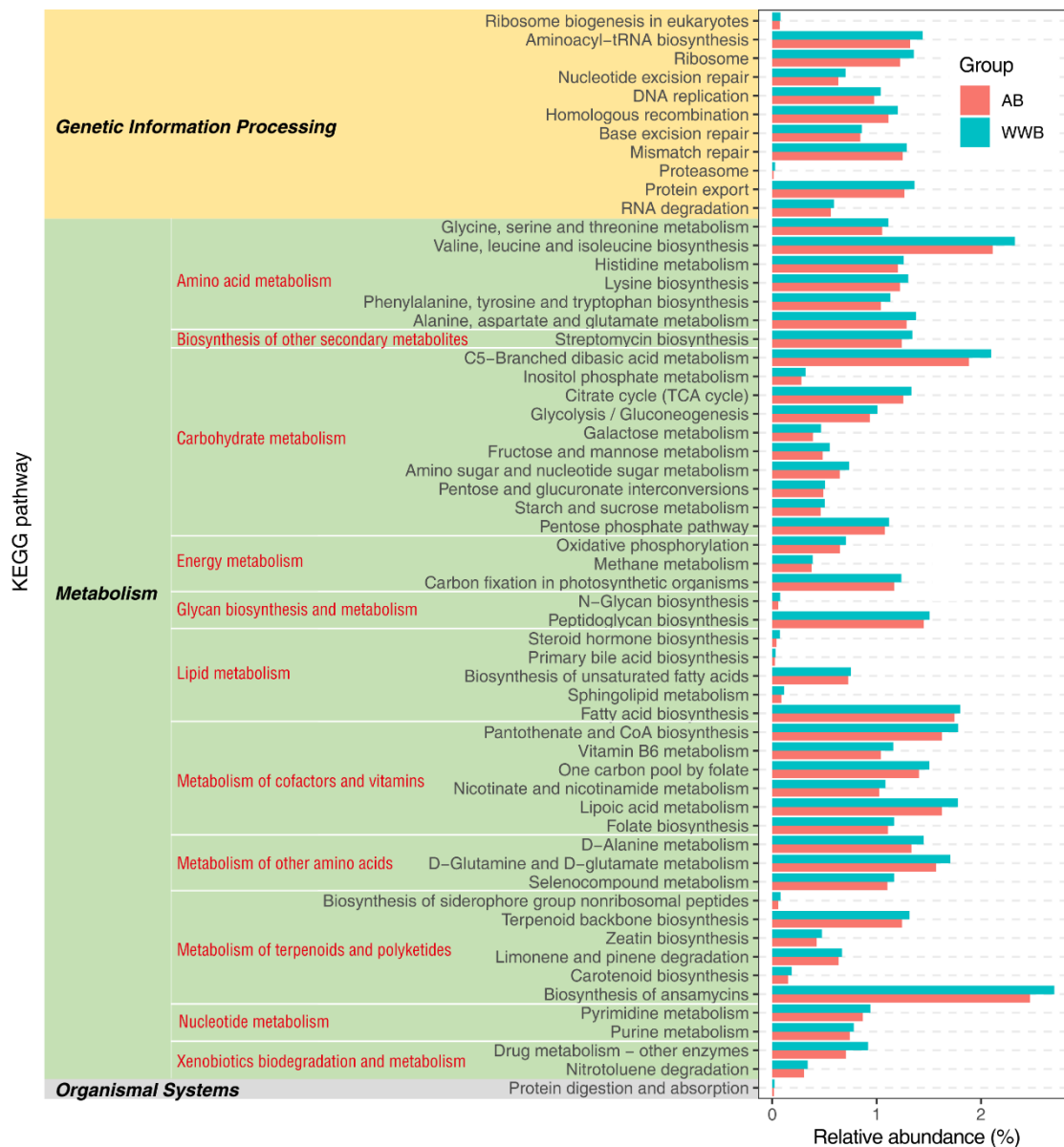


Figure S6 The KEGG pathway significantly depleted in the associated bacterial communities of photo-synthetic picoeukaryotes (Welch’s t-test, $P < 0.05$).