

1 **Shipboard microcosm simulations of eddy-driven water**
2 **mass mixing reveal distinct strategies of prokaryotic and**
3 **eukaryotic microbiomes**

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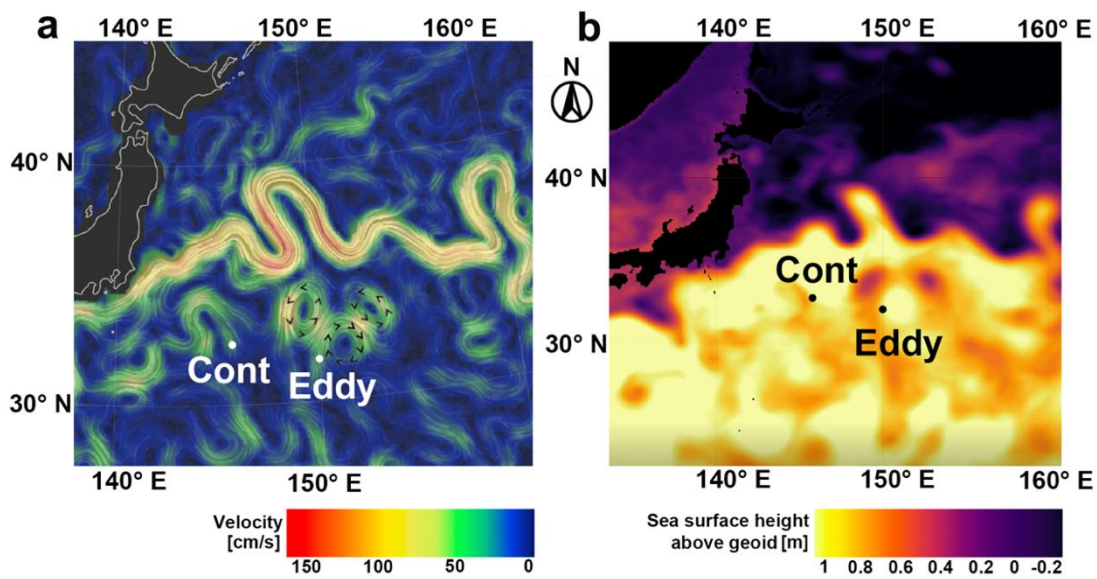


Figure S1. Sampling locations in the *Kuroshio Extension* region. (a) Eddy circulation patterns and (b) sea surface height at sampling sites located within the eddy and non-eddy (Control, abbreviated as “Cont”) regions.

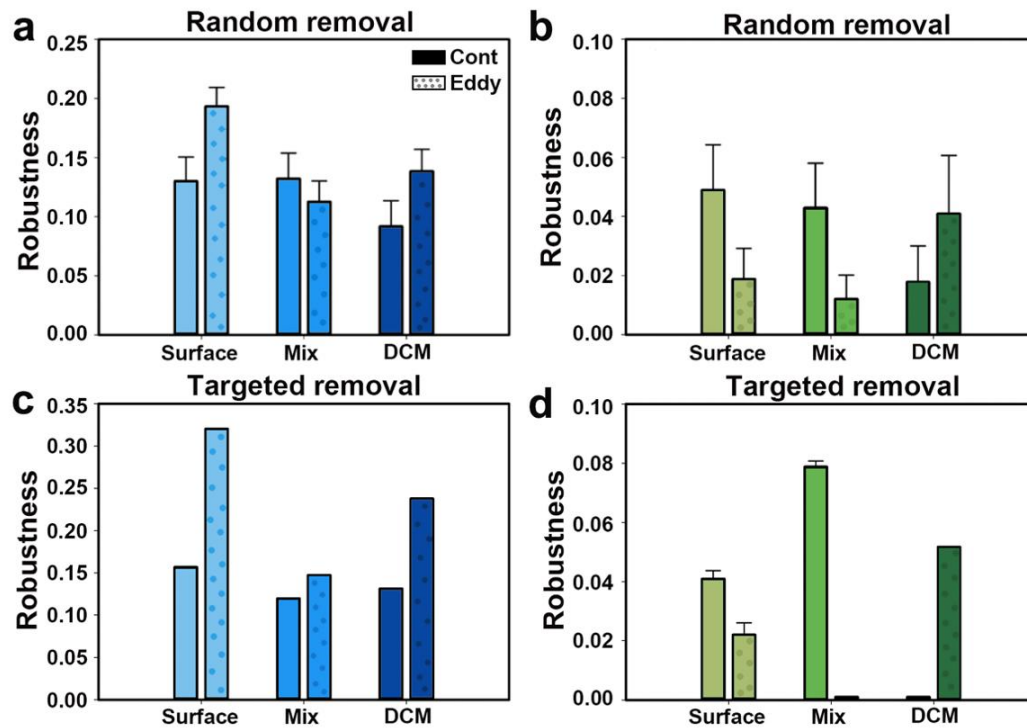


Figure S2. Stability of prokaryotic (a, c) and microeukaryotic (b, d) communities across the Surface, Mix, and DCM layers in eddy and non-eddy (Control, abbreviated as “Cont”) regions.

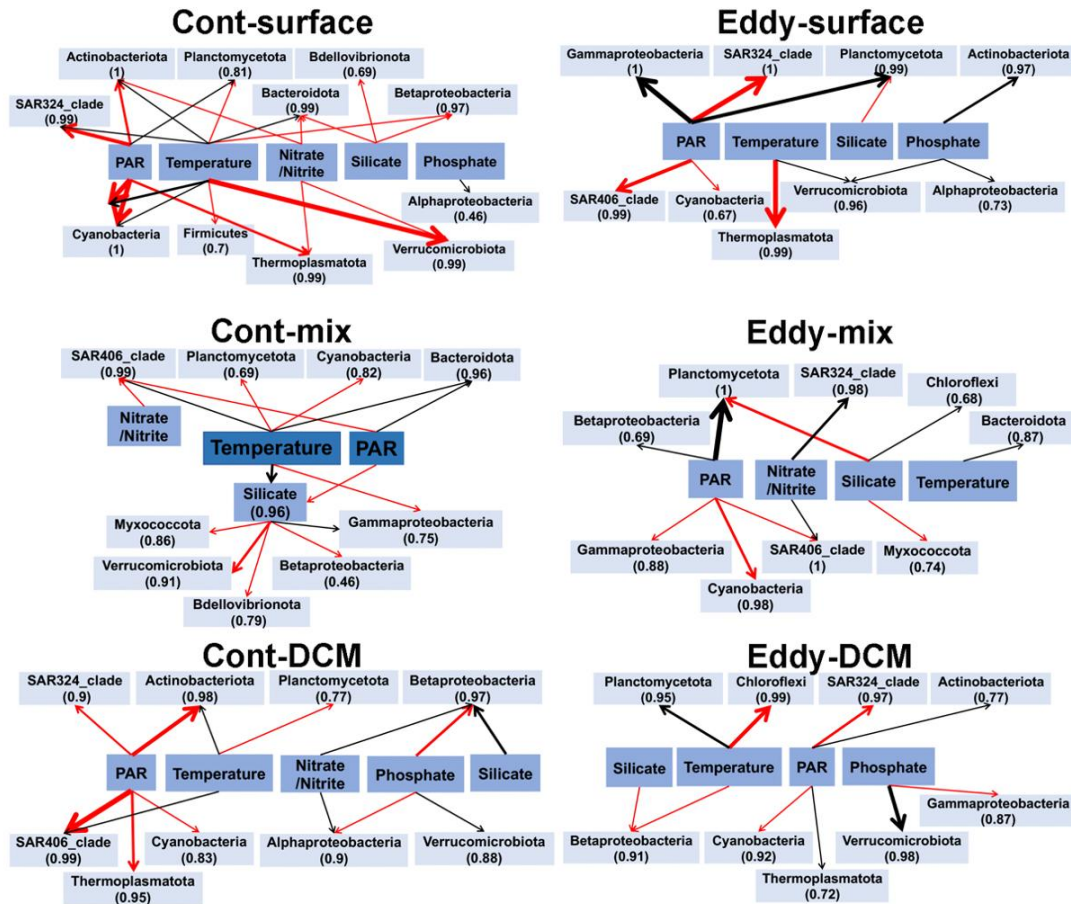


Figure S3. Structural equation model illustrating the relationships between environmental factors and prokaryotic microbiome distributions. Red and black lines, along with the associated numbers, indicate significant negative or positive correlations and the corresponding standardized estimates. The thickness of the arrows and the numbers along each line represent the strength of the correlations. Numbers in parentheses show the proportion of variance explained for each factor.

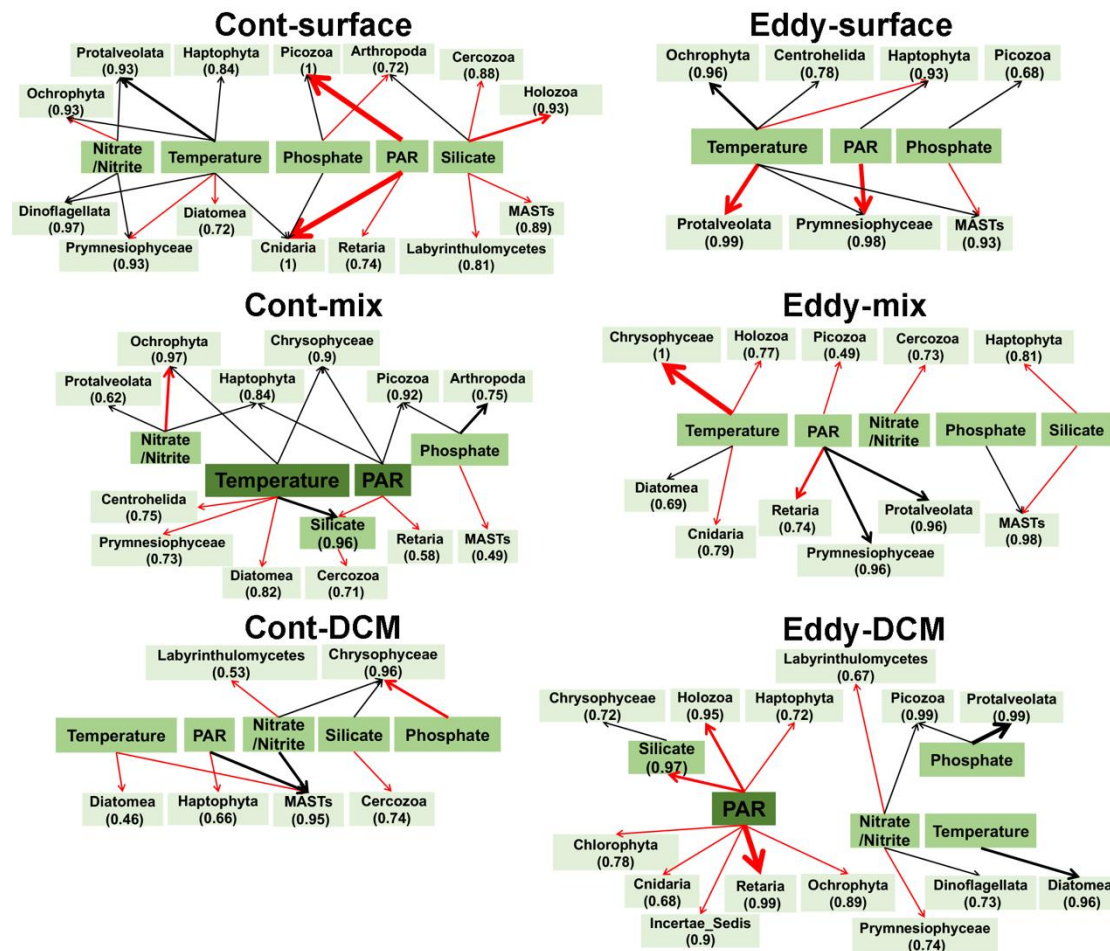


Figure S4. Structural equation model illustrating the relationships between environmental factors and microeukaryotic microbiome distributions. Red and black lines, along with the associated numbers, indicate significant negative or positive correlations and the corresponding standardized estimates. The thickness of the arrows and the numbers along each line represent the strength of the correlations. Numbers in parentheses show the proportion of variance explained for each factor.

42 **Table S1.** Topological properties of co-occurrence networks of microbiomes. “Cont” denotes the control region, and “Eddy” denotes the eddy-
 43 influenced region.

Topological properties	Nodes	Edges	Average degree	Network diameter	Graph density	Modularity	Components	Average Clustering Coefficient	Average path length	Number of Clusters	Number of total samples	Number of samples were included for correlation calculation	Correlation cutoff threshold
Cont-Surface	236	784	6.644	13	0.028	0.526	24	0.36	3.68	32	27	7	0.93
Cont-Mix	392	551	3	15	0.007	0.811	43	0.205	5.064	51	24	4	0.93
Cont-DCM	187	238	2.545	12	0.014	0.853	36	0.421	4.81	40	27	6	0.93
Eddy-Surface	345	820	4.754	16	0.014	0.676	39	0.386	5.079	49	27	6	0.93
Eddy-Mix	439	1826	8.319	13	0.019	0.534	45	0.344	4.391	60	24	4	0.93
Eddy-DCM	286	1166	8.154	10	0.029	0.672	22	0.516	3.863	26	27	7	0.93

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46 **Table S2.** Details of constructing co-occurrence networks of prokaryotic and microeukaryotic communities. “Cont” and “Eddy” denote control
47 and eddy-influenced regions, respectively.

Community type	Networks	Numbers	Numbers of samples	Correlation	Nodes	Edges	Networks	Numbers	Numbers of samples	Correlation	Nodes	Edges
		of total samples	were included for correlation calculation	cutoff threshold				of total samples	were included for correlation calculation	cutoff threshold		
Prokaryotic community	Cont-Surface	24	8	0.88	224	1162	Eddy-Surface	24	8	0.88	325	3085
	Cont-Mix	24	8	0.88	217	528	Eddy-Mix	24	8	0.88	279	855
	Cont-DCM	24	8	0.88	173	329	Eddy-DCM	24	8	0.88	229	1149
Microeukaryotic community	Cont-Surface	24	7	0.88	249	706	Eddy-Surface	24	7	0.88	174	263
	Cont-Mix	24	7	0.88	151	145	Eddy-Mix	24	7	0.88	129	217
	Cont-DCM	24	7	0.88	88	149	Eddy-DCM	24	7	0.88	117	177
Prokaryotic community	Cont-Surface-0-4d	9	4	0.93	355	2961	Eddy-Surface-0-4d	9	4	0.93	511	2551
	Cont-Surface-6-10d	9	4	0.93	248	788	Eddy-Surface-6-10d	9	4	0.93	381	854
	Cont-Surface-12-16d	9	4	0.93	189	295	Eddy-Surface-12-16d	9	4	0.93	294	546
	Cont-Mix-0-4d	8	4	0.93	351	1386	Eddy-Mix-0-4d	8	4	0.93	496	2549
	Cont-Mix-6-10d	9	4	0.93	275	570	Eddy-Mix-6-10d	9	4	0.93	377	579
	Cont-Mix-12-16d	9	4	0.93	281	444	Eddy-Mix-12-16d	9	4	0.93	363	846
	Cont-DCM-0-4d	9	4	0.93	326	1403	Eddy-DCM-0-4d	9	4	0.93	588	3356
	Cont-DCM-6-10d	9	4	0.93	310	622	Eddy-DCM-6-10d	9	4	0.93	180	362
	Cont-DCM-12-16d	9	4	0.93	241	385	Eddy-DCM-12-16d	9	4	0.93	282	842
Microeukaryotic community	Cont-Surface-0-4d	9	4	0.93	457	1794	Eddy-Surface-0-4d	9	4	0.93	597	2845
	Cont-Surface-6-10d	9	4	0.93	240	537	Eddy-Surface-6-10d	9	4	0.93	101	103
	Cont-Surface-12-16d	9	4	0.93	161	180	Eddy-Surface-12-16d	9	4	0.93	73	66
	Cont-Mix-0-4d	8	4	0.93	235	411	Eddy-Mix-0-4d	8	4	0.93	457	1973

Cont-Mix-6-10d	9	4	0.93	185	262	Eddy-Mix-6-10d	9	4	0.93	75	78
Cont-Mix-12-16d	9	4	0.93	115	115	Eddy-Mix-12-16d	9	4	0.93	47	29
Cont-DCM-0-4d	9	4	0.93	302	848	Eddy-DCM-0-4d	9	4	0.93	441	1060
Cont-DCM-6-10d	9	4	0.93	181	281	Eddy-DCM-6-10d	9	4	0.93	111	108
Cont-DCM-12-16d	9	4	0.93	91	76	Eddy-DCM-12-16d	9	4	0.93	53	38

Table S3. Variations in nutrient concentrations in surface (5–10 m) and DCM (70–92 m) waters, including nitrate plus nitrite (NO_x, μM), phosphate (PO₄³⁻, μM), and silicate (Si, μM). Values are presented as mean ± standard error (n = 3) or as ranges (n = 2) for each sampled water mass.

Water	PO ₄ ³⁻	NO ₃ ⁻ +NO ₂ ⁻	SiO ₃ ²⁻
Cont-Surface-0d	0.019	0.109	1.262
Cont-Surface-6d	0.018	0.018	1.219
Cont-Surface-16d	ND	0.057	1.076
Cont-Mix-0d	0.047	0.534	2.222
Cont-Mix-6d	ND	0.105	2.161
Cont-Mix-16d	ND	0.049	1.367
Cont-DCM-0d	0.075	0.877	3.230
Cont-DCM-6d	0.032	0.259	2.837
Cont-DCM-16d	ND	0.027	2.122
Eddy-Surface-0d	0.021	0.062	1.631
Eddy-Surface-8d	ND	0.048	1.671
Eddy-Mix-0d	0.037	0.101	2.086
Eddy-Mix-8d	ND	0.041	2.043
Eddy-DCM-0d	0.054	0.139	2.540
Eddy-DCM-8d	0.014	0.054	2.188

55 **Table S4.** Proportions of different microbial groups in situ in control and eddy-
56 influenced regions. “Cont” and “Eddy” denote control and eddy-influenced regions,
57 respectively.

Community type	Phylums	Cont-Surface	Eddy-Surface	Cont-DCM	Eddy-DCM
Prokaryotic community	Alphaproteobacteria	47.77%	46.80%	39.74%	44.95%
	Bacteroidota	6.85%	10.95%	5.53%	6.75%
	Gammaproteobacteria	19.64%	17.30%	13.33%	12.02%
	Actinobacteriota	3.81%	4.85%	8.38%	12.76%
	Cyanobacteria	19.56%	13.84%	20.18%	8.37%
	Verrucomicrobiota	0.44%	1.33%	0.32%	0.98%
	Planctomycetota	0.04%	0.61%	0.05%	0.59%
	Betaproteobacteria	0.07%	0.24%	0.24%	0.10%
	Firmicutes	0.04%	0.44%	0.05%	0.76%
	other	0.13%	0.89%	0.49%	2.04%
	Bdellovibrionota	0.17%	0.55%	0.15%	0.68%
	Marinimicrobia_(SAR406_clade)	1.00%	0.84%	5.25%	3.66%
	Thermoplasmatota	0.16%	0.34%	3.08%	2.24%
	Patescibacteria	0.00%	0.27%	0.03%	0.60%
	Desulfobacterota	0.08%	0.21%	0.01%	0.24%
	Myxococcota	0.03%	0.07%	0.07%	0.15%
	Crenarchaeota	0.00%	0.08%	0.78%	0.77%
	Dadabacteria	0.05%	0.00%	0.01%	0.05%
	SAR324_clade(Marine_group_B)	0.16%	0.37%	1.70%	1.91%
	WPS-2	0.00%	0.01%	0.19%	0.12%
Microeukaryotic community	Chloroflexi	0.00%	0.03%	0.42%	0.28%
	Dinoflagellata	30.32%	20.73%	20.16%	13.45%
	Diatomea	0.51%	8.35%	0.73%	0.90%
	MASTs	5.22%	5.94%	1.58%	4.41%
	Ochrophyta	5.03%	3.54%	4.93%	11.13%
	Chlorophyta	2.00%	5.37%	8.64%	15.18%
	Protalveolata	17.19%	12.47%	15.01%	26.20%
	Arthropoda	4.62%	3.06%	7.75%	4.53%
	Cerczoa	0.46%	1.22%	0.02%	1.09%
	Bicosoecida	0.15%	0.73%	0.25%	0.09%
	Ciliophora	2.60%	1.21%	1.09%	0.77%
	other	8.58%	13.31%	35.66%	11.66%
	Centrophelida	0.37%	0.90%	0.05%	0.06%
	Prymnesiophyceae	3.76%	1.46%	1.00%	2.73%
	Chrysophyceae	1.82%	1.44%	0.45%	0.26%

Labyrinthulomycetes	0.23%	0.38%	0.34%	1.21%
Incertae_Sedis	1.16%	0.69%	0.72%	1.26%
Cnidaria	13.87%	16.71%	0.54%	3.05%
Cryptophyceae	0.01%	0.03%	0.04%	0.32%
Ascomycota	0.26%	0.31%	0.47%	0.08%
Picozoa	1.33%	1.39%	0.21%	0.97%
Holozoa	0.51%	0.77%	0.39%	0.67%

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Table S5. Results of analysis of similarities (ANOSIM) and Mantel tests for prokaryotic and microeukaryotic communities across different depths and stations.

ANOSIM and Mantel tests	Station		Depth		PAR		Temperature		Time	
Prokaryotes	0.377	***	0.446	***	0.200	***	0.2457	***	0.238	***
Microeukaryotes	0.371	***	0.586	***	0.182	***	0.2962	***	0.318	***

***, $P < 0.001$; **, $P < 0.01$; *, $P < 0.05$.