

Table S3. Summary of ASVs (name grouped by phylum or class name (bold)) within the top 300 ASVs showing enrichment in relative contribution during or shortly following convective mixing in the mesopelagic. Only ASVs with a significant positive correlation to DOC or TDAA C are shown, and the table presents the lagged month of ASV 120-300 m mean relative abundance relative to DOC and/or TDAA C (zero means no lag, negative values mean changes of 120-300 m mean ASV relative abundance lagged the change of 120-300 m mean DOC and/or TDAA C) and max positive CCF correlation coefficient. Only negative lags were considered as those are the cases where DOC or TDAA lead changes in the ASVs.

Name	ASV ID	significantly cross-correlated with DOC		significantly cross-correlated with TDAA C	
		Lag	CCF	Lag	CCF
<i>Alphaproteobacteria</i>					
<i>SAR11_clade_Ia.3</i>	ASV8	-4	0.63	0	0.66
<i>SAR11_clade_Ia.3</i>	ASV74	-4	0.59	-2	0.66
<i>SAR11_clade_Ia.3</i>	ASV14485	-5	0.52	-1	0.65
<i>SAR11_clade_Ia.3</i>	ASV14512	-6	0.32	-1	0.56
<i>SAR11_clade_Ia.3</i>	ASV15			0	0.76
<i>SAR11_clade_Ia.3</i>	ASV42			0	0.68
<i>SAR11_clade_Ia.3</i>	ASV43			0	0.64
<i>SAR11_clade_Ia.3</i>	ASV76			0	0.73
<i>SAR11_clade_Ia.3</i>	ASV14498			-1	0.67
<i>SAR11_clade_Ia.3</i>	ASV14511			-1	0.63
<i>SAR11_clade_Ia.4</i>	ASV143	-2	0.62	0	0.57
<i>SAR11_clade_Ia.4</i>	ASV40			0	0.66
<i>SAR11_clade_Ia.4</i>	ASV14482			-2	0.51
<i>SAR11_clade_Ia.4</i>	ASV14483			-2	0.59
<i>SAR11_clade_Ib.1</i>	ASV7	-4	0.59	0	0.72
<i>SAR11_clade_Ib.2</i>	ASV5	-2	0.56	0	0.66
<i>SAR11_clade_Ib.2</i>	ASV22	-2	0.60		
<i>SAR11_clade_Ib.2</i>	ASV140	-2	0.60		
<i>SAR11_clade_Ib.2</i>	ASV14494	-3	0.54	-1	0.73
<i>SAR11_clade_Ib.2</i>	ASV243			0	0.67
<i>SAR11_clade_Id</i>	ASV190	-2	0.65		
<i>SAR11_clade_Id</i>	ASV14508			-1	0.53
<i>SAR11 clade IIa.A</i>	ASV156	-2	0.54		

Table S3. continued.

Name	ASV ID	significantly cross-correlated with DOC		significantly cross-correlated with TDAA C	
		Lag	CCF	Lag	CCF
<i>SAR11_clade_Ia.A</i>	ASV36			0	0.72
<i>SAR11_clade_Ia.A</i>	ASV164			0	0.66
<i>SAR11_clade_Ia.B</i>	ASV232	-1	0.57		
<i>SAR11_clade_Ia.B</i>	ASV25			0	0.63
<i>SAR11_clade_Ia.B</i>	ASV14502			-1	0.51
<i>SAR11_clade_Ia</i>	ASV104	-2	0.53	0	0.60
<i>SAR11_clade_Ia</i>	ASV69			0	0.71
<i>SAR11_clade_Ia</i>	ASV14487			-3	0.58
<i>SAR11_clade_IIIa</i>	ASV152			0	0.58
<i>SAR11_clade_IV</i>	ASV95	-1	0.66		
<i>SAR11_clade_IV</i>	ASV108	-1	0.56		
<i>SAR11_clade_IV</i>	ASV92	-2	0.66		
<i>SAR11_clade_IV</i>	ASV262			0	0.58
<i>SAR11_clade</i>	ASV161			0	0.84
<i>OCS116_clade</i>	ASV11	-2	0.67	0	0.54
<i>OCS116_clade</i>	ASV126	-2	0.67		
<i>Rhodobacterales_Rhodobacteraceae</i>	ASV167	-3	0.58		
<i>Rhodospirillales_Rhodospirillaceae_OM75_clade</i>	ASV100	-4	0.68	0	0.68
<i>Rhodospirillales_Rhodospirillaceae_Defluviococcus</i>	ASV109	-2	0.52	0	0.56
<i>Rhodospirillales_Rhodospirillaceae_AEGEAN.169_marine_group</i>	ASV146	-2	0.61		
<i>Rhodospirillales_Rhodospirillaceae_AEGEAN.169_marine_group</i>	ASV191	-2	0.63		
<i>Rhodospirillales_Rhodospirillaceae_Magnetospira</i>	ASV130			-3	0.58
<i>Rickettsiales SAR116 clade</i>	ASV123	-4	0.66	0	0.68
<i>Chloroflexi</i>					
<i>SAR202_Clade1</i>	ASV10			0	0.59
<i>SAR202_Clade2</i>	ASV106			-3	0.52
<i>SAR202_Clade2</i>	ASV94			-3	0.56
<i>SAR202_Clade3</i>	ASV119	-6	0.51	-2	0.69
<i>SAR202_Clade</i>	ASV113			0	0.64
<i>Flavobacteriia</i>					
<i>Flavobacteriales_Flavobacteriaceae_NS2b_marine_group</i>	ASV28	-2	0.61		
<i>Flavobacteriales_Flavobacteriaceae_NS2b_marine_group</i>	ASV132	-1	0.52		
<i>Flavobacteriales_Flavobacteriaceae_NS4_marine_group</i>	ASV83	-3	0.54		
<i>Flavobacteriales_Flavobacteriaceae_NS4_marine_group</i>	ASV245	-3	0.56	-1	0.55
<i>Flavobacteriales_Flavobacteriaceae_NS4_marine_group</i>	ASV145	-3	0.52		
<i>Flavobacteriales_Flavobacteriaceae_NS4_marine_group</i>	ASV246	-1	0.62		
<i>Flavobacteriales_Flavobacteriaceae_NS4_marine_group</i>	ASV238	-1	0.59		

Table S3. continued.

Name	ASV ID	significantly cross-correlated with DOC		significantly cross-correlated with TDAA C	
		Lag	CCF	Lag	CCF
Gammaproteobacteria					
<i>Oceanospirillales_SAR86_clade</i>	ASV60	-2	0.60		
<i>Oceanospirillales_SAR86_clade</i>	ASV67	-2	0.55		
<i>Oceanospirillales_SAR86_clade</i>	ASV56	-2	0.66	0	0.59
<i>Oceanospirillales_SAR86_clade</i>	ASV189	-1	0.68		
<i>Oceanospirillales_SAR86_clade</i>	ASV170	-2	0.55		
<i>Oceanospirillales_Oceanospirillaceae_Pseudospirillum</i>	ASV68	-2	0.66		
<i>Oceanospirillales_Oceanospirillaceae_Pseudospirillum</i>	ASV159			-3	0.73
<i>Salinisphaerales_Salinisphaeraceae_ZD0417_marine_group</i>	ASV48	-2	0.62	0	0.68
<i>Salinisphaerales_Salinisphaeraceae_ZD0417_marine_group</i>	ASV111			0	0.73
<i>Alteromonadales_Alteromonadaceae_Alteromonas</i>	ASV11054	-8	0.53	-4	0.52
<i>Alteromonadales_Alteromonadaceae_Alteromonas</i>	ASV2708	-5	0.51	-3	0.67
<i>Cellvibrionales_Haliaceae_OM60.NOR5_clade</i>	ASV198	-3	0.65		
<i>E01.9C.26_marine_group</i>	ASV201			-3	0.59
Verrucomicrobia					
<i>Verrucomicrobiae_Verrucomicrobiales_DEV007</i>	ASV182	-3	0.59		
Acidimicrobiia					
<i>Acidimicrobiales_Sva0996_marine_group</i>	ASV227	-2	0.52		
<i>Acidimicrobiales_Sva0996_marine_group</i>	ASV121			-3	0.65
<i>Acidimicrobiales_Sva0996_marine_group</i>	ASV228			-1	0.60
<i>Acidimicrobiales_OM1_clade_Candidatus_Actinomarina</i>	ASV53	-3	0.57		
<i>Acidimicrobiales_OM1_clade_Candidatus_Actinomarina</i>	ASV18			-1	0.57
<i>Acidimicrobiales_OM1_clade_Candidatus_Actinomarina</i>	ASV58			-1	0.61
<i>Acidimicrobiales_OM1_clade_Candidatus_Actinomarina</i>	ASV230			-1	0.58
Marinimicrobia					
<i>SAR406_clade</i>	ASV79			-3	0.66
<i>SAR406_clade</i>	ASV64			0	0.68
<i>SAR406_clade</i>	ASV97			-3	0.51
<i>SAR406_clade</i>	ASV110			-3	0.51
<i>SAR406_clade</i>	ASV225			-4	0.61
<i>SAR406_clade</i>	ASV147			0	0.64
Deltaproteobacteria					
<i>SAR324_clade_Marine_group_B</i>	ASV45			-3	0.66
<i>Sh765B.TzT.29</i>	ASV148	-2	0.52	0	0.56