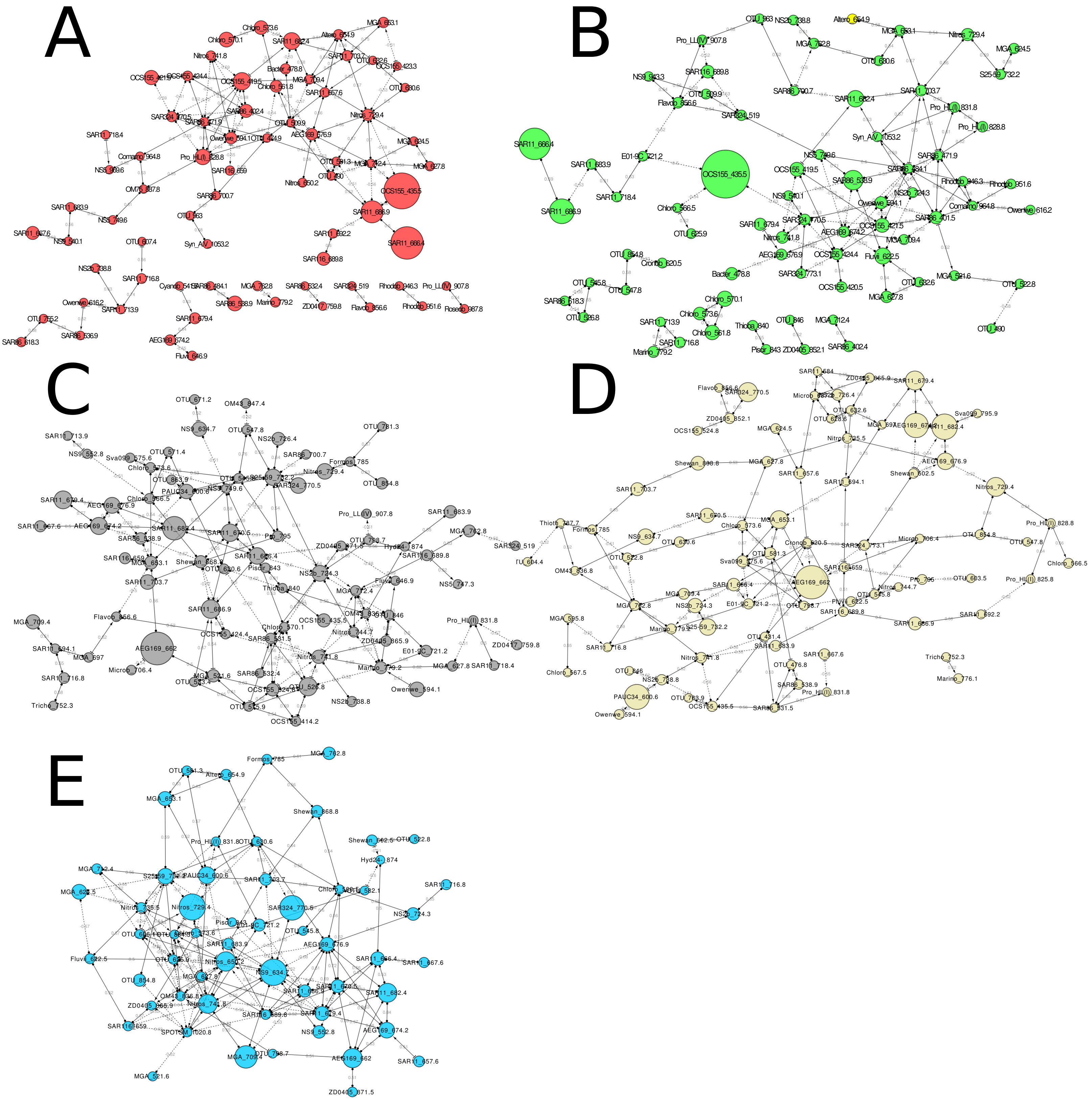

Figure S1. Association network showing statistically significant, positive and negative time lagged and non time-lagged correlations between bacterial nodes within each depth (A, 5m; B, DCM; C, 150m; D, 500m; E, 890m). Nodes represent bacterial OTUs (circles) at each depth. Edges (lines) represent correlations, sometimes time lagged, between the bacterial OTUs. Shown are bacteria that occur at least 25 times and edges that have lagged Spearman correlations such that |R|>0.55, P<0.01, Q<0.05. Solid edges represent positive correlations, dashed edges represent negative correlations. Arrows indicate time lagged associations. Node identities are indicated in Table 3 and there is a legend in Figure 3.

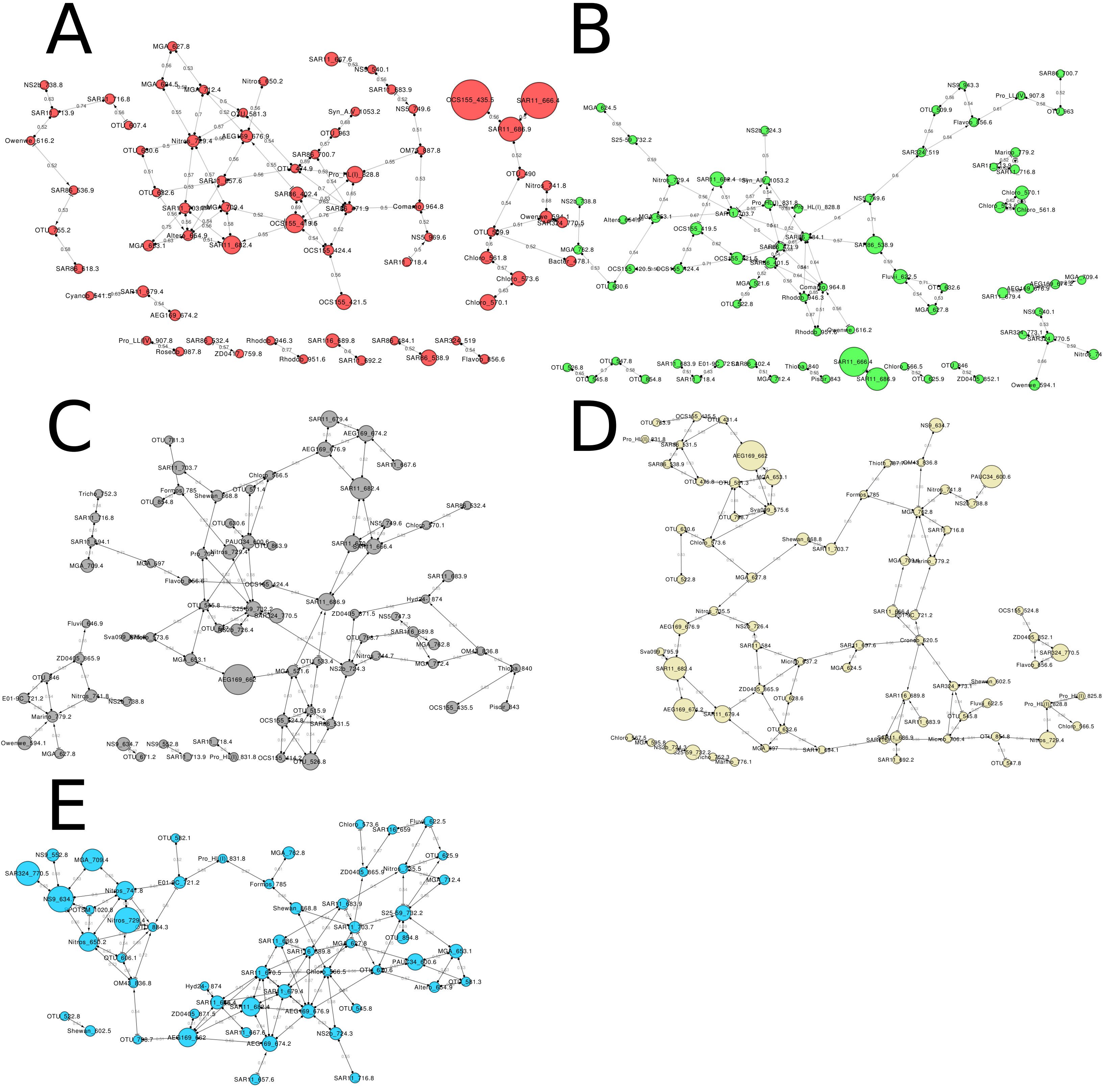

Figure S2. Association network showing statistically significant, positive time lagged and non time-lagged correlations between bacterial nodes within each depth (A, 5m; B, DCM; C, 150m; D, 500m; E, 890m). Nodes and edges are as in Figure S1, though only positive associations also present.

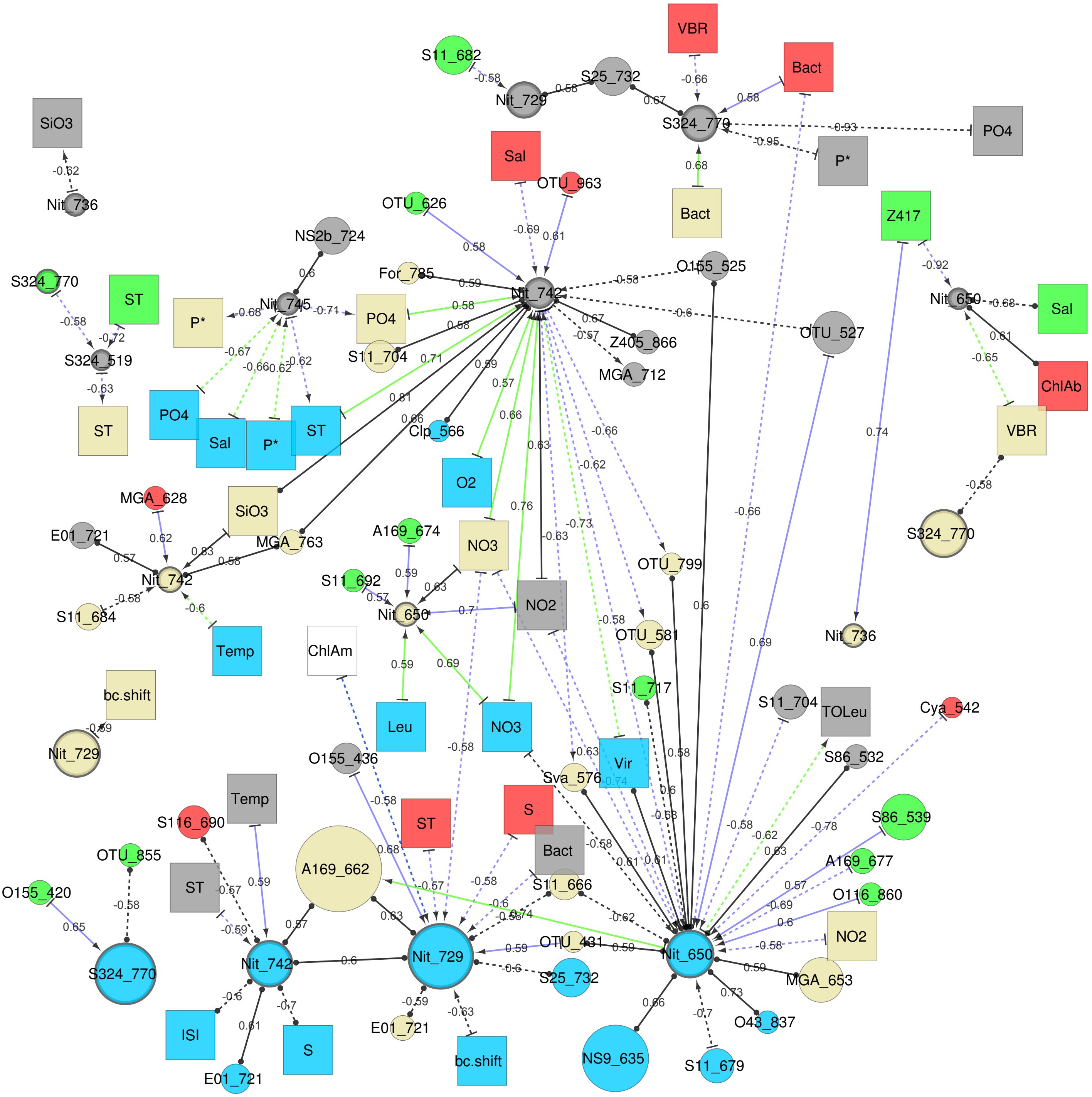

Figure S3. Association network of correlations between Deltaproteobacteria OTUs at 150, 500 and 890m and other bacteria and environmental parameters found at every depth throughout the water column. All bacteria shown have a mean abundance of greater than 1% and are found with a relative abundance of greater than 0.01% in more than 36 samples. Lines represent statistically significant, potentially time lagged correlations (Spearman |R| > 0.57, P<0.01, Q < 0.05). Nodes represent individual measurements of bacterial abundances (circles) or environmental parameters (squares). Abbreviated names are followed by OTU fragment size. Node Sizes of bacterial nodes represent the average abundance of OTUs. Solid lines show a positive correlation, dashed lines show a negative correlation, arrows indicate a 1-month shift in the correlation. Abbreviations for the nodes are translated in Table S1. Edge labels represent Spearman R values. Edge colors are the same as in Figure 2. Legends are present in Figures 2 and 3.

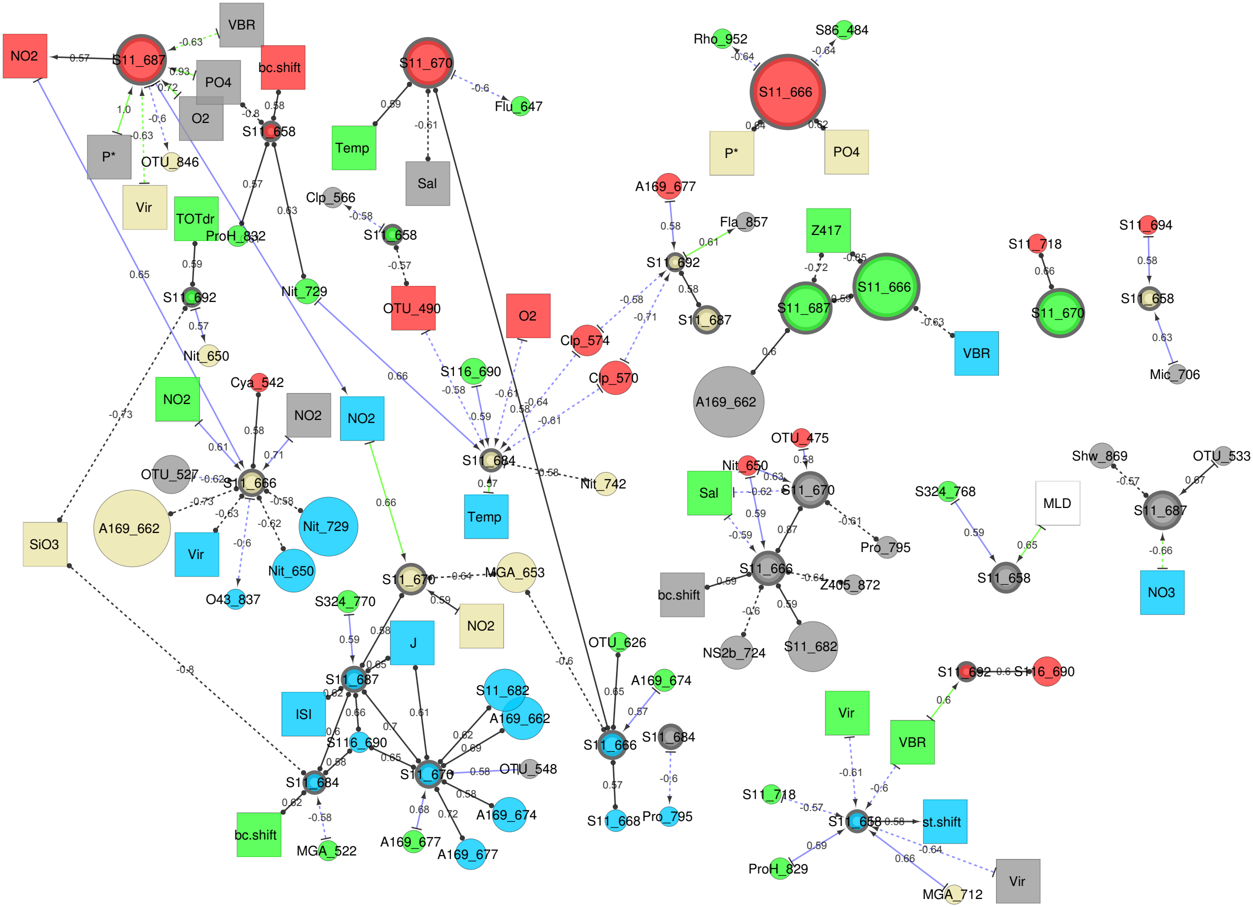

Figure S4. Association network of correlations between bacteria from the SAR11 Surface-1 clade and other bacteria and environmental parameters found at every depth throughout the water column. Nodes and edges have the same thresholds (P, Q, and R values for Edges, mean abundance and occurrence thresholds for bacterial nodes) as in Figure S3.

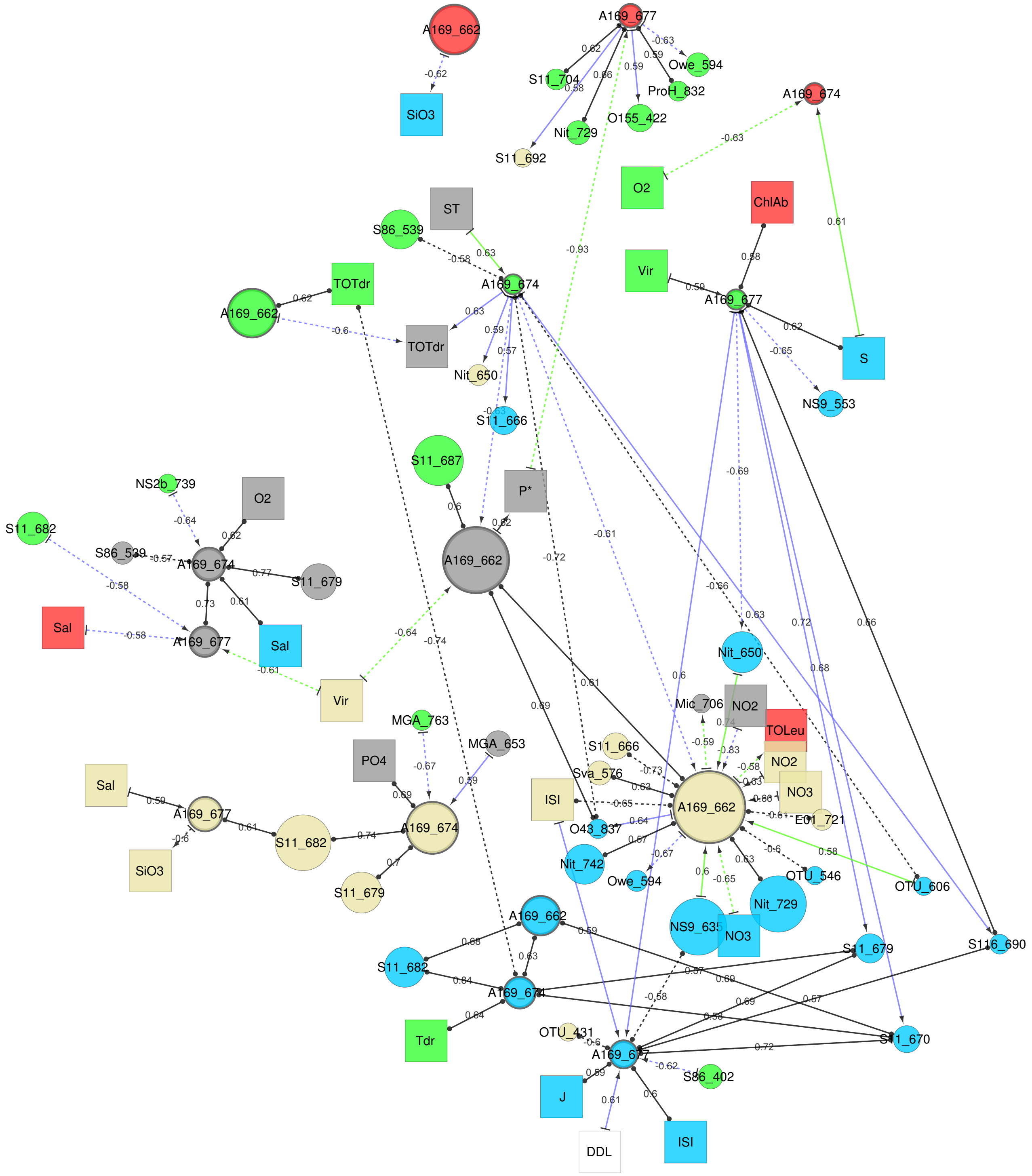

Figure S5. Association network of correlations between bacteria from the AEGEAN-169 clade and other bacteria and environmental parameters found at every depth throughout the water column. Nodes and edges have the same thresholds (P, Q, and R values for Edges, mean abundance and occurrence thresholds for bacterial nodes) as in Figure S3.

Code	*Type*	*Parameter*	*Taxonomy Note*
A169	ARISA	AEGEAN-169	Alphaproteobacteria
Bav	ARISA	Bacteriovoraceae	Deltaproteobacteria
Clp	ARISA	Chloroplast	Chloroplast
Clp	ARISA	Chloroplast	Chloroplast
Com	ARISA	Comamonadaceae	Betaproteobacteria
Cro	ARISA	Cronobacter	Gammaproteobacteria
Cya	ARISA	Cyanobacteria	Cyanobacteria
E01	ARISA	E01-9C-26	Gammaprotobacteria
Fla	ARISA	Flavobacteriaceae	Flavobacteria
Flu	ARISA	Fluviicola	Flavobacteria
For	ARISA	Formosa	Flavobacteria
Hyd	ARISA	Hyd24-01	Gammaprotobacteria
Mar	ARISA	Marinoscillum	Sphinobacteria
Mic	ARISA	Microbacteriaceae	Actinobacteria
Nit	ARISA	Nitrospina	Deltaproteobacteria
NS2b	ARISA	NS2b	Flavobacteria
NS5	ARISA	NS5	Flavobacteria
NS9	ARISA	NS9	Flavobacteria
O116	ARISA	OCS116	Alphaproteobacteria
O155	ARISA	OCS155	Actinobacteria
O43	ARISA	OM43	Betaproteobacteria
O75	ARISA	OM75	Alphaproteobacteria
OTU	ARISA	Unidentified Operational Taxonomic Unit	
Owe	ARISA	Owenweeksia	Flavobacteria
P34	ARISA	PAUC34f or Marine Group A	
Pis	ARISA	Piscirickettsiaceae	Gammaproteobacteria
Pro	ARISA	Prochlorococcus	Cyanobacteria
SynAV	ARISA	Synecococcus A.V	Cyanobacteria
ProH	ARISA	Prochlorococcus Low Light I	Cyanobacteria
ProL	ARISA	Prochlorococcus Low Light IV	Cyanobacteria
Rho	ARISA	Rhodobacteraceae	Alphaproteobacteria
Ros	ARISA	Roseobacter	Alphaproteobacteria
S25	ARISA	S25-593	Alphaproteobacteria
S11	ARISA	SAR11	Alphaproteobacteria
S116	ARISA	SAR116	Alphaproteobacteria
S324	ARISA	SAR324	Gammaprotobacteria
MGA	ARISA	Marine Goup A	
S86	ARISA	SAR86	Gammaproteobacteria
Sed	ARISA	Sediminibacterium	Sphingobacteria
Shw	ARISA	Shewanella	Gammaproteobacteria
SPM	ARISA	SPOTSMAY03-890m3	Gammaproteobacteria

Code	*Type*	*Parameter*	*Taxonomy Note*
Sva	ARISA	Sva0996	Actinobacteria
Thb	ARISA	Thiobacillus	Betaproteobacteria
Tht	ARISA	Thiothrix	Gammaproteobacteria
Tri	ARISA	Trichodesmium	Cyanobacteria
Z405	ARISA	ZD0405	Gammaprotobacteria
Z417	ARISA	ZD0417	Gammaprotobacteria
AmoA	Env	ammonia monooxigenase gene	
AWP	Env	Average Wave Period	
AW	Env	Average Wind Speed	
Bact	Env	Bacterial Abundance	
bc.shift	Env	Bray Curtis Rate of Community Change	
BeamA	Env	Beam Attenuation	
BeamT	Env	Beam Transmission	
CDOM	Env	Colored Dissolved Organic Matter	
ChlAb	Env	Chlorophyll A (Bottle)	
ChlAm	Env	Chlorophyll A (Monthly Satellite Estimate)	
ChlA8	Env	Chlorophyll A (8 Day Satellite Estimate)	
Curl	Env	Wind Stress Curl	
DL	Env	Day Length	
DDL	Env	Day Length Change Per Month	
DosEck	Env	Direction of Offshore Component of Eckman Transport	
eO2	Env	Estimated Oxygen Concentration	
eO2p	Env	Estimated Oxygen Percent	
Fluor	Env	Fluorescence	
ISI	Env	Inverse Simpson biodiversity ndex	
Leu	Env	Bacterial Productivity (Leucine)	
MEI	Env	Multivariate El-Niño Southern Oscillation Index	
MLD	Env	Mixed Layer Depth	
NO2	Env	Nitrite Concentration	
NO3	Env	Nitrate Concentration	
Nwind	Env	Northward Wind Vector	
O2	Env	Oxygen Concentration (Bottle + CTD)	
PAR	Env	Photo synthetically active radiation	
J	Env	Pielou's Evenness Index	
PO4	Env	Phosphate Concentration	
POC	Env	Particulate Organic Carbon (Satellite)	
PRCP	Env	Precipitation	
PRCPcat	Env	Precipitation Category	
ProdM	Env	Primary Productivity Satellite Estimate (Monthly)	
Prod8	Env	Primary Productivity Satellite Estimate (8 Day)	
P*	Env	Excess phosphate	
S	Env	Richness (OTUs with > 0.1% Abundance)	

Code	*Type*	*Parameter*	*Taxonomy Note*
Sal	Env	Salinity	
SalCTD	Env	Salinity (CTD)	
ST	Env	Seawater density	
SiO3	Env	Silicate Concentration	
SSHD	Env	Sea Surface Height Differential	
st.shift	Env	Change in Salinity or Temperature (Euclidean Distance)	
Svd	Env	Sverdrup Transport	
Temp	Env	Temperature	
TempMin	Env	Minimum Daily Air Temperature	
Tdr	Env	Bacterial Productivity (Thymidine)	
TOLeu	Env	Bacterial Turnover Time (Leucine)	
TOTdr	Env	Bacterial Turnover Time (Thymidine)	
Upw	Env	Upwelling	
VBR	Env	Virus to Bacteria Ratio	
Vir	Env	Viral Abundance	
WavH	Env	Mean Wave Height (day of sampling)	
WinG	Env	Maximum 2 minute wind speed gust	

Table S1. Description of nodes seen in networks. Node type indicates whether nodes are bacterial OTUs (ARISA) or environmental or biotic parameters (Env). Code is the abriviation seen in the networks themselves. ARISA OTU codes are always followed in the networks by ITS length. Parameters describe taxonomy of OTUs and environmental parameters. Taxonomy note provides phylum information to OTUs that are defined at a finer than phylum taxonomic resolution.

	Variable/Formula	AllvAll	5m-DCM	5m-150m	5m-500m	5m-890m	DCM-150m	DCM-500m	DCM-890m	150m-500m	150m-890m	500m-890m
Nodes	N	446	165	164	157	141	163	168	153	160	144	148
Edges	E	1339	292	259	225	246	239	253	314	261	274	311
Within Depth Nodes	Ni	342	139	143	142	122	146	145	125	149	129	128
Within Depth Edges	Ei	445	161	176	172	179	175	171	178	186	193	189
Cross Depth Edges	Eo	894	131	83	53	67	64	82	136	75	81	122
Within Depth Density	Ei/Ei_Max	4.6%	5.7%	5.9%	5.9%	6.3%	3.9%	3.8%	4.0%	4.0%	4.2%	4.0%
Cross Depth Density	Eo/Eo_max	1.1%	2.1%	1.2%	0.8%	1.0%	0.7%	0.9%	1.6%	0.8%	0.9%	1.4%
Density Ratio	(Ei/EiM)/(Eo/EoM)	3.38	1.58	2.84	4.36	4.62	4.53	3.47	2.77	4.31	5.16	3.38
Upward	U	50 (5.6%)	3 (2.3%)	5 (6.0%)	6 (11.3%)	7 (10.4%)	3 (4.7%)	3 (3.7%)	7 (5.1%)	2 (2.7%)	2 (2.5%)	12 (9.8%)
Unlagged	F	280 (31.3%)	75 (57.3%)	15 18.1%)	17 (32.1%)	11 (16.4%)	20 (31.3%)	17 (20.7%)	24 (17.6%)	24 (32.0%)	36 (44.4%)	41 (33.6%)
Downward	D	564 (63.1%)	53 (40.5%)	63 (75.9%)	30 (56.6%)	49 (73.1%)	41 (64.1%)	62 (75.6%)	105 (77.2%)	49 (65.3%)	43 (53.1%)	69 (56.6%)

Table S2. Summary Statistics for networks that examine cross correlations between bacteria at different depths. This table complements Table 1 and treats *only positive interactions* between variabiles, rather than both positive and negative interactions. Note that 58% of the edges in the AllvAll network represent positive correlations, which are addressed here. The AllvAll column reflects the network shown in Figure 2. The other columns reflect the nodes within and connecting pairs of depths. Nodes (N) are the number of bacterial OTUs at a specific depth that occur at least 25 times in the data set connected by at least one edge (correlation) in the specified network. Edges (E) are the total number of Spearman correlations with R > 0.55 in that network. Within Depth Nodes (Ni) are the nodes in these networks that are connected by at least one edge to another node at that same depth. Within depth edges (Ei) are those edges that connect pairs of nodes from the same depth. Cross Depth Edges (Eo) are those edges that connect two nodes from different depths. Within Depth Density, reflects the probability that a pair of nodes from the same depth are connected by an edge; it is the quotient of the number of edges found connecting nodes that are from the same depth, divided by the maximum number of edges that could possibly connect nodes of the same depth in that network. Cross Depth Density (Eo/Eo_max) reflects the probability that two nodes from different depths are connected by an edge; it is the total number of edges connecting nodes from different depths, compared to the number of possible edges that could connect nodes from those depths. The density ratio (ei/eim)/(eo/eom), reflects how much likelier two nodes are to be connected if they are from the same depth, than if they are from different depths; it is the quotient of the Within Depth Density and the Cross Depth Density of a network. Uphill (U) is the number of time lagged edges that connect pairs of nodes from different depths such that changes in the node at the deeper depth precede changes in the done at the shallower depth. Unlagged (F) is the number of non time lagged edges that connect pairs of nodes from different depths. Downhill is the number of time lagged edges that connect pairs of odes from different depths such that the changes in the shallower node precede correlated changes in the deeper node.

	5m	DCM	150m	500m	890m	AllvAll
Nodes (N)	68	71	75	74	54	446
Edges (E)	81	80	95	91	98	1339
Cl	0.28	0.33	0.26	0.21	0.38	0.18
L	2.07	1.85	2.08	1.63	1.75	3.82
Cl_r	0.03	0.03	0.03	0.03	0.07	0.01
L_r	4.37	4.60	4.29	4.38	3.11	3.60
Cl/Cl_R	8.79	10.20	9.02	7.12	5.79	13.67
L/L_R	0.47	0.40	0.48	0.37	0.56	1.06
Density	3.6%	3.2%	3.4%	3.4%	6.8%	1.3%
Outgoing Density	1.6%	1.1%	0.9%	1.2%	1.0%	NA
Density Ratio	2.19	2.98	3.85	2.84	7.09	NA

Table S3. Topological statistics for networks of bacteria at each depth (Figure 1), and for a network of OTUs at all depths (Figure 2) in which *only positive correlations* were considered. This complements Table 2 which shows statistics for networks connected by both positive and negative nodes and Figure S2 which visually depicts the described networks. These networks include only nodes for bacteria that are present at >0.01% abundance greater than 25 times and edges that have a possibly time lagged, global, absolute Spearman R value of greater than 0.5. Parameters are as described in Table 1. Permutation tests suggest that clustering and path length coefficients are statistically significantly different than those for random networks (P<0.001) Similar patterns can be seen as in Table 1, though the density ratio is much higher at 890m when only positive edges are considered, than it is in Table 1 where negative edges are also considered.