Supplementary Table S1.
Coverage and richness estimators (Chao and ACE) for each individual water column clone library calculated in Mothur with an OTU cutoff of 0.03, 0.04, or 0.05

| Sample	OTU cutoff	Number of clones	Coverage (%)	Chao	ACE
AnirKa-M1-10m	0.04	13	85	4	0
AnirKa-M1-40m	0.05	19	79	9	16
AnirKa-M1-100m	0.05	29	83	16	1
AnirKa-M1-200m	0.05	17	94	5	7
AnirKa-M2-10m	0.05	23	91	5	7
AnirKa-M2-40m	0.05	14	100	2	2
AnirKa-M2-100m	0.05	15	87	5	7
AnirKa-M2-200m	0.05	15	93	6	6
AnirKb-M1-10m	0.05	17	65	14	17
AnirKb-M1-40m	0.05	18	67	14	17
AnirKb-M1-100m	0.04	17	71	18	22
AnirKb-M1-200m	0.05	17	65	24	20
AnirKb-M2-10m	0.05	20	75	14	15
AnirKb-M2-40m	0.05	16	88	6	8
AnirKb-M2-100m	0.05	15	87	7	7
AnirKb-M2-200m	0.05	15	100	5	5
amoA-M1-10m	0.05	15	80	7	1
amoA-M1-40m	0.04	8	50	11	35
amoA-M1-200m	0.04	13	75	8	9
amoA-M2-40m	0.05	14	79	7	1
amoA-M2-100m	0.05	16	88	6	7
amoA-M2-200m	0.05	14	83	6	7
cDNA-AnirKa-M1-10m	0.04	26	96	3	4
cDNA-AnirKa-M1-40m	0.05	19	95	5	6
cDNA-AnirKa-M1-200m	0.04	13	71	10	13
cDNA-AnirKb-M1-10m	0.05	14	57	17	18
cDNA-AnirKb-M1-40m	0.04	16	56	16	20
cDNA-AnirKb-M1-200m	0.05	19	84	10	11
cDNA-amoA-M1-10m	0.05	17	100	3	3
cDNA-amoA-M1-40m	0.05	23	90	6	9
cDNA-amoA-M1-200m	0.05	21	96	4	6
AnirKa-Cal.Curr.-30m	0.05	16	89	5	8
AnirKa-Cal.Curr.-3000m	0.03	16	94	4	5
AnirKb-Cal.Curr.-30m	0.03	13	92	3	4
AnirKb-Cal.Curr.-3000m	0.03	15	93	5	6
amoA-Cal.Curr.-30m	0.03	7	100	1	1
amoA-Cal.Curr.-3000m	0.05	13	67	10	11

Supplementary Table S2. Monterey Bay CTD and water chemistry data for all samples used in quantitative PCR, '+' indicates if additional molecular analyses were performed in the sample

Station	Date (yy/mm/dd)	Lat	Long	Depth (m)	Temp. (°C)	Salinity ‰	Sigma-T	Chl (mg/m^3)	NO$_2$ (µM)	NO$_3$ (µM)	clone library	mRNA qPCR
C1	10/5/18	36.797	-121.847	30	9.1	33.96	26.28	0.74	0.19	28.35		+
C1	10/5/18	36.797	-121.847	100	8.8	34.01	26.37	0.56	0.21	29.48		+
C1	10/5/18	36.797	-121.847	200	8.6	34.04	26.44	0.81	0.32	30.37		+
M1	10/5/18	36.747	-122.041	10	10.7	33.72	25.82	0.77	0.31	21.23	+	+
M1	10/5/18	36.747	-122.041	30	10.1	33.75	25.95	1.18	0.36	23.37		
M1	10/5/18	36.747	-122.041	40	9.8	33.79	26.04	0.90	0.28	25.05	+	+
M1	10/5/18	36.747	-122.041	100	8.8	34.03	26.38	0.55	0.15	28.65	+	+
M1	10/5/18	36.747	-122.041	150	8.7	34.06	26.44	0.47	0.20	29.66		
M1	10/5/18	36.747	-122.041	200	8.3	34.11	26.54	0.43	0.09	-	+	+
M2	10/5/18	36.687	-122.382	10	11.1	33.43	25.53	2.99	0.25	11.41		+
M2	10/5/18	36.687	-122.382	40	9.6	33.84	26.12	0.82	0.57	25.91		+
M2	10/5/18	36.687	-122.382	100	8.8	34.00	26.36	0.52	0.16	30.59		+
M2	10/5/18	36.687	-122.382	150	8.4	34.09	26.51	0.43	0.08	31.37		+
M2	10/5/18	36.687	-122.382	200	8.1	34.14	26.59	0.42	0.07	32.51		
C1	10/8/02	36.797	-121.846	10	14.0	33.66	25.15	2.08	0.26	6.58		
C1	10/8/02	36.797	-121.846	30	10.6	33.68	25.82	1.10	0.48	22.58		
C1	10/8/02	36.797	-121.846	40	10.0	33.76	25.98	0.63	0.31	25.91		
C1	10/8/02	36.797	-121.846	100	9.3	33.92	26.22	0.40	0.12	25.04		
C1	10/8/02	36.797	-121.846	150	8.8	33.99	26.36	0.38	0.18	31.54		
C1	10/8/02	36.797	-121.846	200	8.1	34.07	26.52	0.36	0.12	30.39		
M1	10/8/02	36.742	-122.024	30	10.5	33.64	25.80	0.92	0.15	22.01		
M1	10/8/02	36.742	-122.024	40	10.2	33.73	25.92	0.70	0.17	24.67		
M1	10/8/02	36.742	-122.024	100	9.5	33.89	26.16	0.45	0.16	24.88		
M1	10/8/02	36.742	-122.024	150	9.1	34.01	26.32	0.37	0.05	30.17		
M1	10/8/02	36.742	-122.024	200	8.9	34.07	26.41	0.38	0.02	31.18		
M2	10/8/02	36.702	-122.4	10	14.5	33.50	24.93	1.36	0.19	3.80		
M2	10/8/02	36.702	-122.4	40	10.6	33.69	25.82	0.73	0.38	21.82		
M2	10/8/02	36.702	-122.4	100	9.0	33.93	26.28	0.36	0.06	28.87		
M2	10/8/02	36.702	-122.4	150	8.5	34.03	26.44	0.37	0.12	29.31		
M2	10/8/02	36.702	-122.4	200	8.3	34.07	26.50	0.38	0.03	30.94		
C1	10/12/02	36.797	-121.847	10	11.5	33.52	25.54	8.98	0.22	6.62		
C1	10/12/02	36.797	-121.847	40	10.5	33.72	25.88	0.45	0.17	23.02		
C1	10/12/02	36.797	-121.847	100	9.6	33.89	26.16	0.41	0.29	27.37		
C1	10/12/02	36.797	-121.847	150	9.3	33.91	26.22	0.45	0.20	26.45		
C1	10/12/02	36.797	-121.847	200	8.9	33.97	26.34	0.42	0.18	29.71		
M1	10/12/02	36.758	-122.034	10	11.3	33.53	25.58	7.47	0.29	8.78		
M1	10/12/02	36.758	-122.034	30	11.3	33.54	25.59	5.52	0.34	10.76		
M1	10/12/02	36.758	-122.034	40	10.7	33.66	25.78	0.57	0.36	23.00		
M1	10/12/02	36.758	-122.034	100	9.4	33.87	26.17	0.35	0.10	28.06		
M1	10/12/02	36.758	-122.034	150	9.2	34.01	26.32	0.35	0.14	29.64		
M1	10/12/02	36.758	-122.034	200	8.7	34.06	26.43	0.34	0.17	31.68		
M2	10/12/02	36.691	-122.385	10	11.5	33.18	25.27	2.25	0.21	7.15		
M2	10/12/02	36.691	-122.385	40	11.5	33.48	25.49	1.85	0.32	12.21		
M2	10/12/02	36.691	-122.385	100	9.8	33.82	26.07	0.38	0.04	25.99		
M2	10/12/02	36.691	-122.385	150	8.9	33.94	26.30	0.33	0.00	28.46		
M2	10/12/02	36.691	-122.385	200	8.5	34.07	26.47	0.34	0.23	31.11		

Supplementary table S3. Spearman rank-order correlation (rho) of environmental parameters compared with the gene copy abundance of AnirKa, AnirKb, AOAamoA, and MGI 16S rRNA gene sequences

| | Environmental parameters | | | | | Gene copy abundance | | | |
	[2]	[3]	[4]	[5]	[6]	AnirKa	AnirKb	amoA	MGI
NO_2 [1]	-0.54 ***	-0.55 ***	0.56 ***	0.69 ***	-0.57 ***	0.00	-0.45 *	-0.41 *	-0.39
NO_3 [2]		0.92 ***	-0.94 ***	-0.81 ***	0.95 ***	0.09	0.76 ***	0.64 ***	0.64 ***
Depth [3]			-0.89 ***	-0.83 ***	0.91 ***	0.01	0.60 ***	0.48 *	0.52 *
Temp. [4]				0.77 ***	-0.97 ***	0.01	-0.68 ***	-0.55 **	-0.64 ***
Chl [5]					-0.79 ***	-0.03	-0.61 ***	-0.47 *	-0.48 *
Sal. [6]						-0.04	0.68 ***	0.53 **	0.63 ***

Significance level: *p<0.05, **p<0.01, ***p<0.001
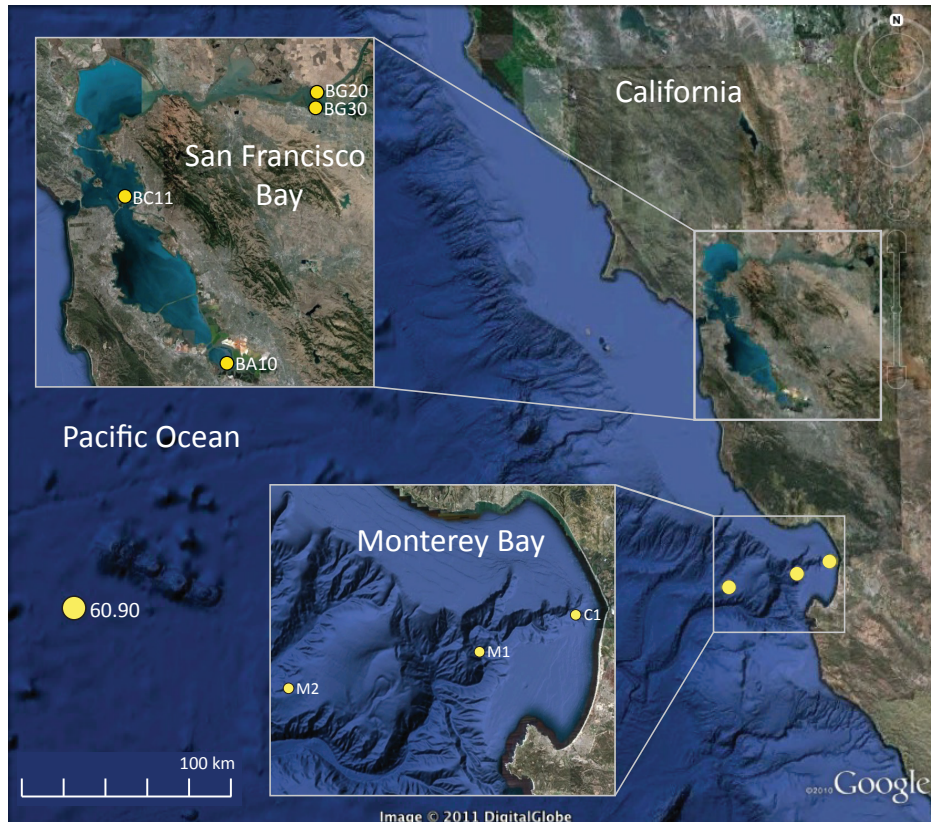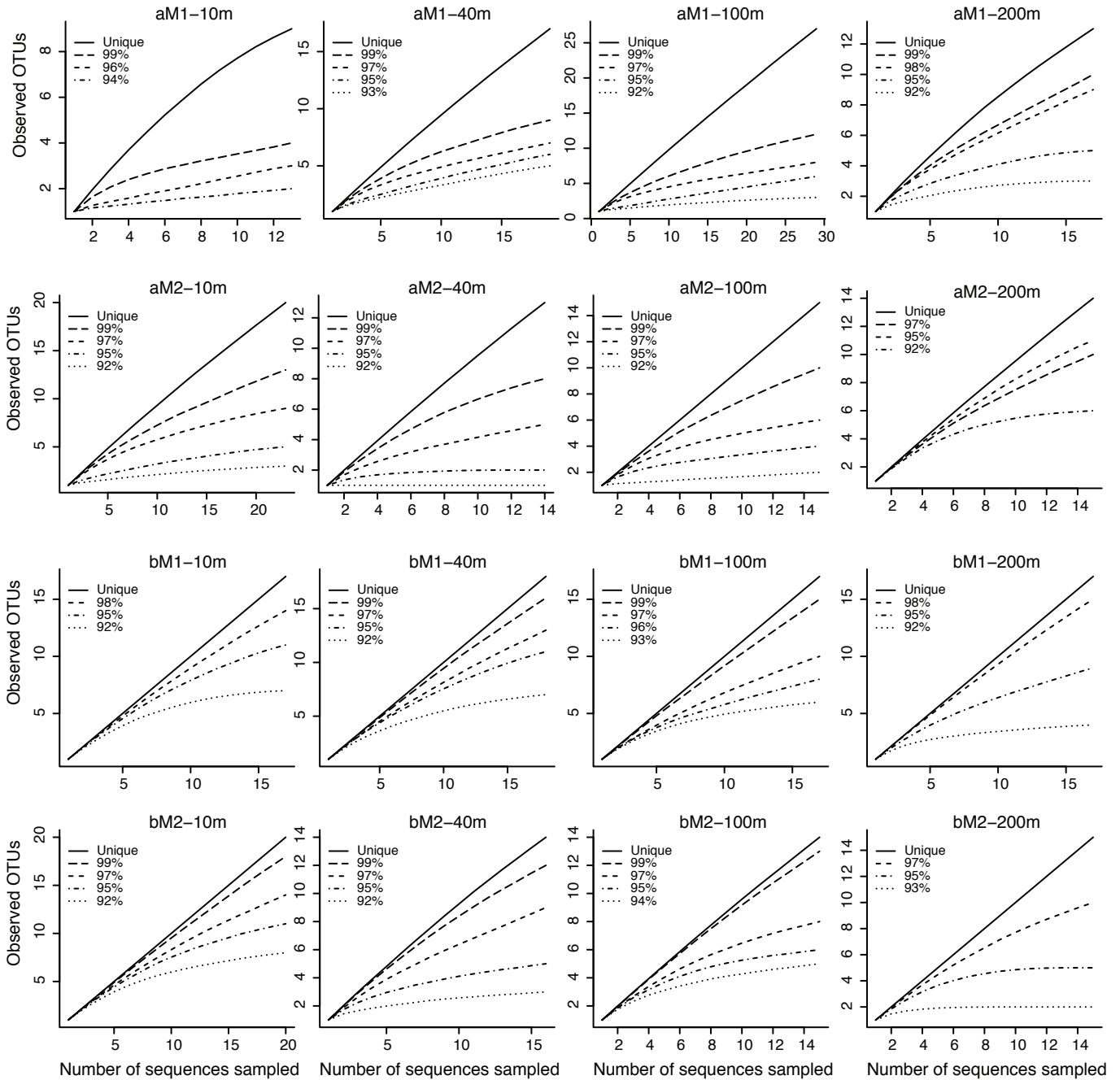
Supplementary Figure S1.
Map of sampling stations in Monterey Bay, California Current (60.90), and San Francisco Bay.
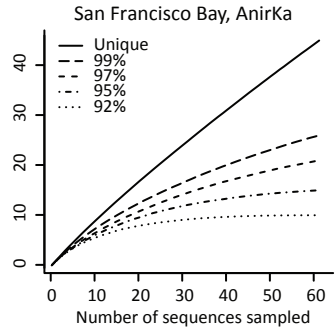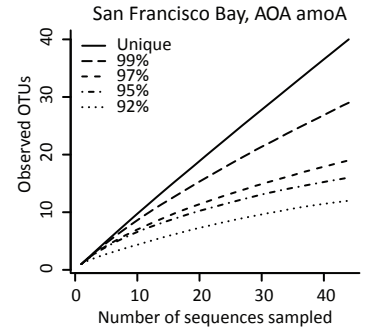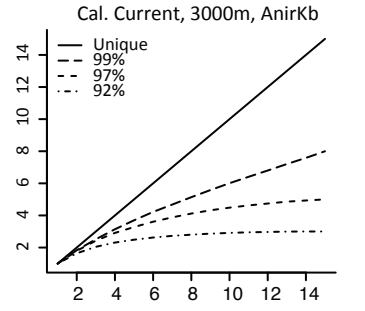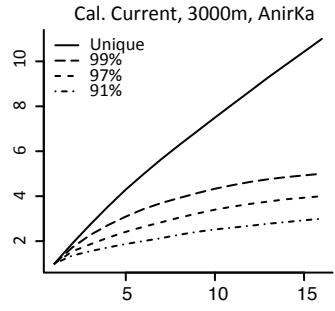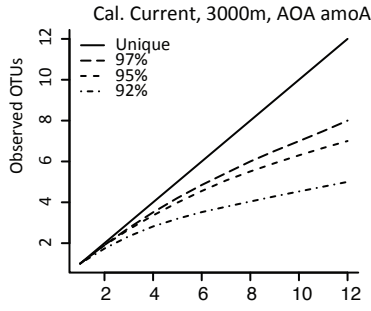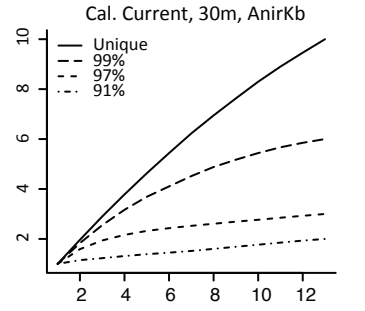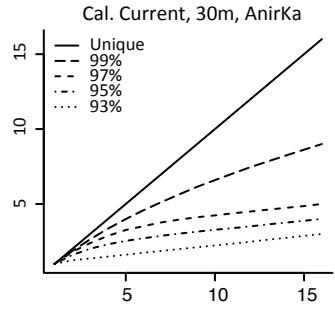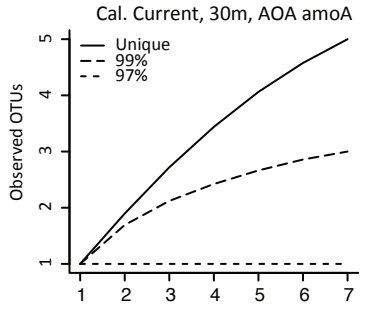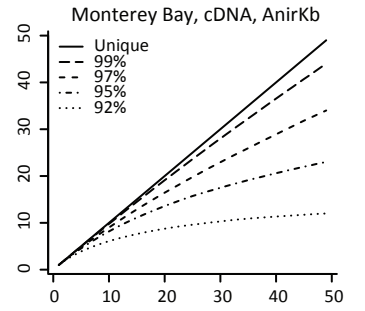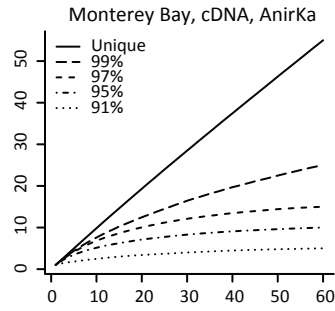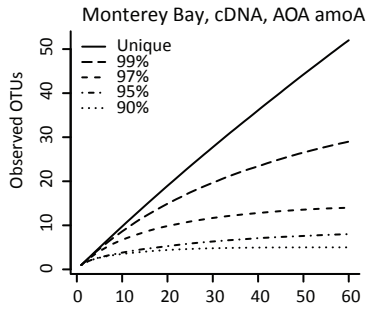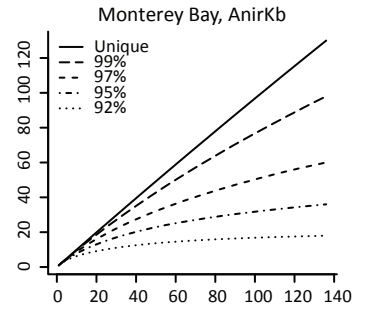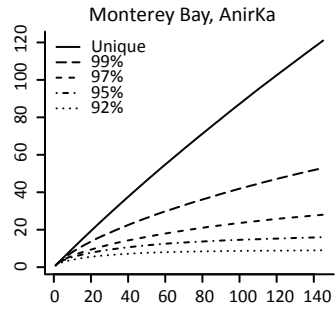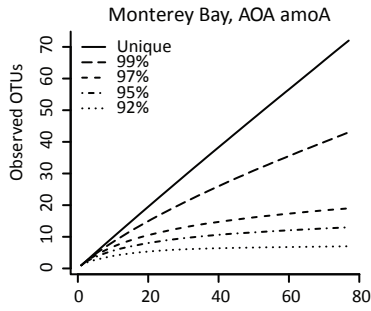
Supplementary Figure S2. page 1/3. Rarefaction curves for AnirKa (477 bp), AnirKb (450 bp), and AOA amoA (594 bp) clone libraries from Monterey Bay, California Current station 60.90 from 30 and 3000m, and San Francisco Bay. Calculated in Mothur.
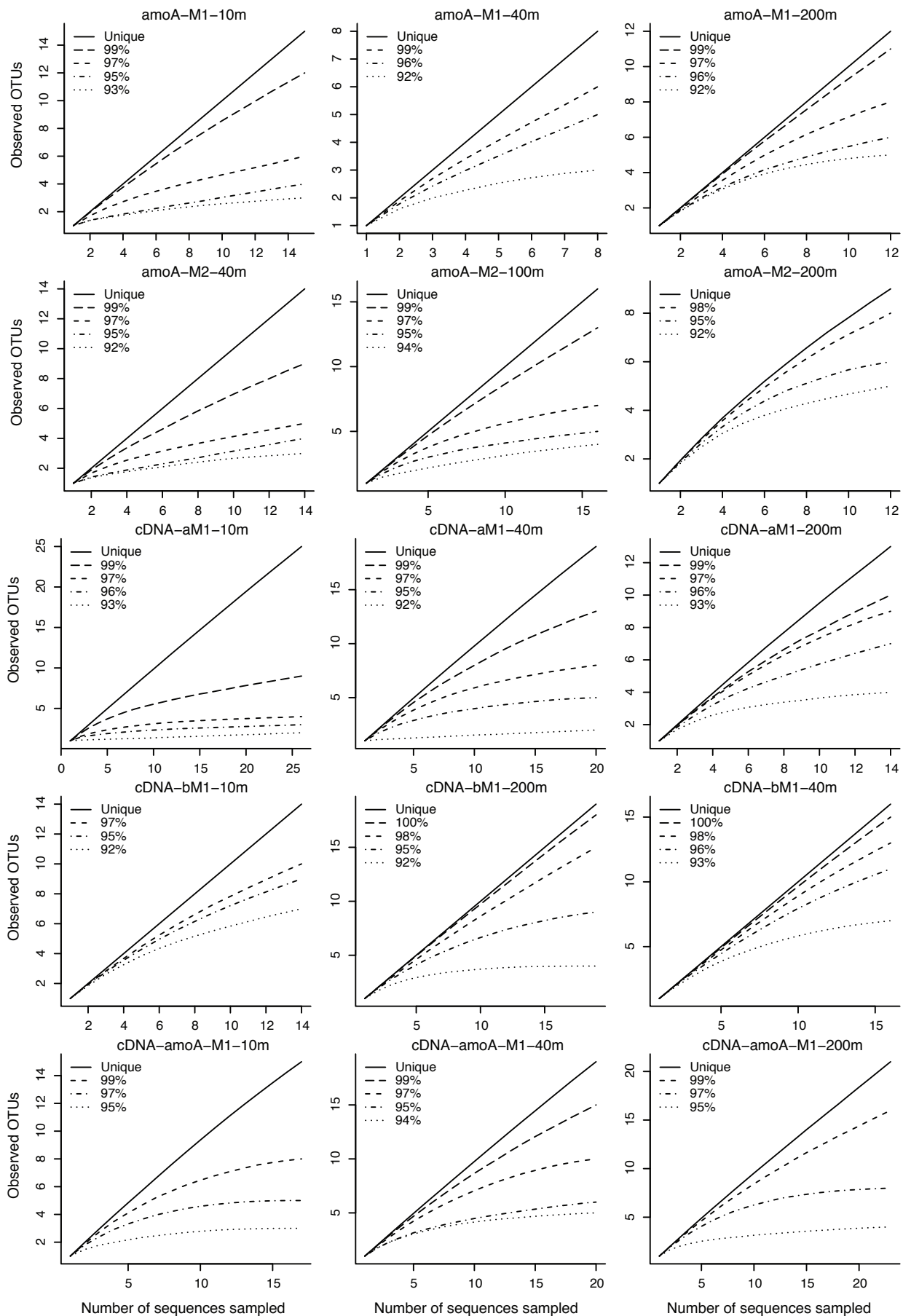
Supplementary Figure S2 continued, page 2/3

Supplementary Figure S2 continued, page 3/3
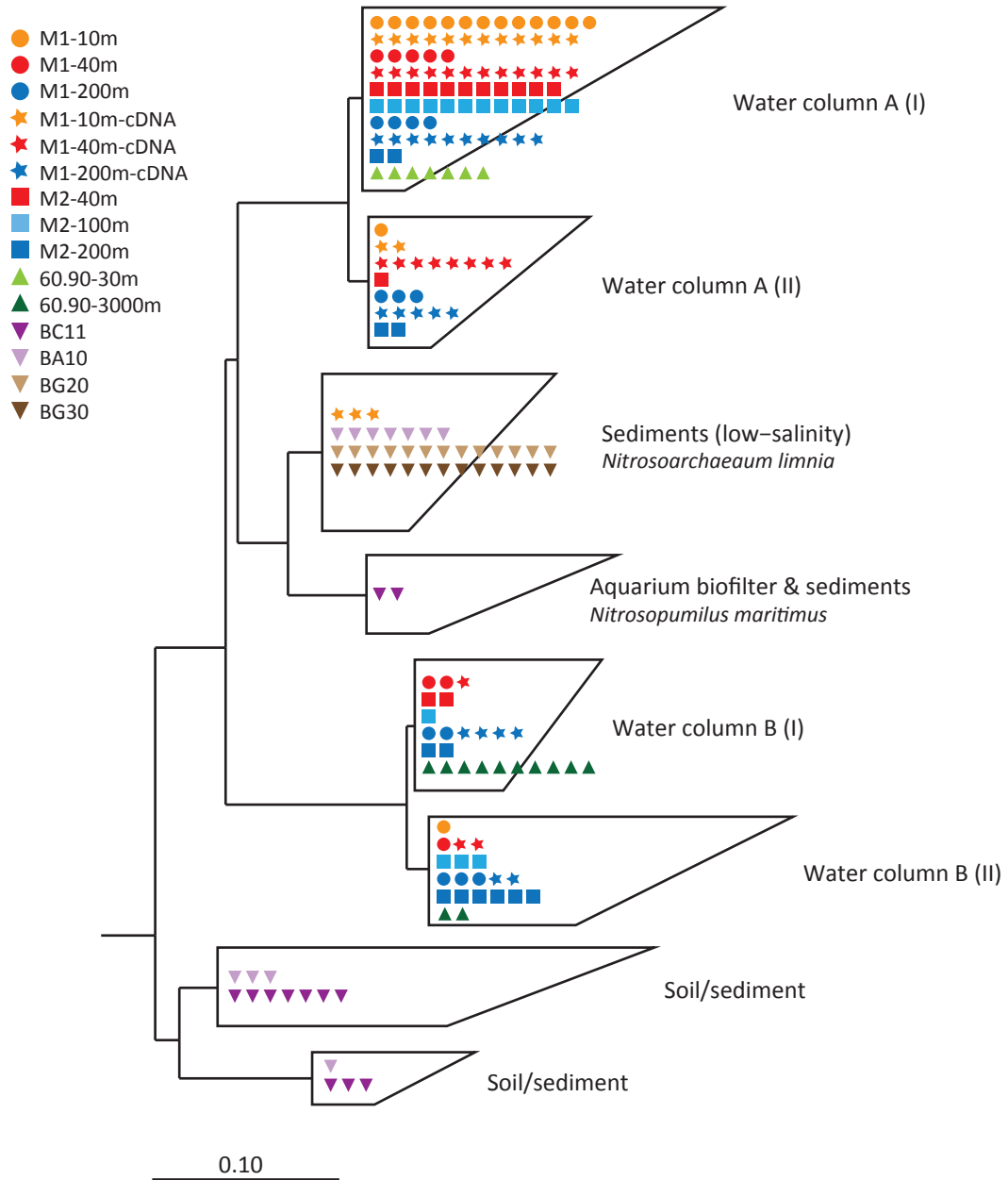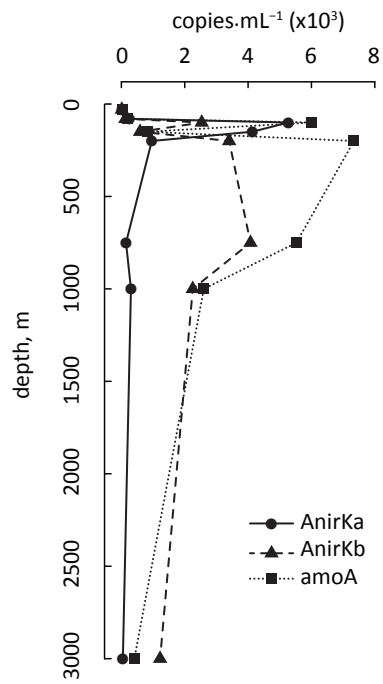
Supplementary Figure S3.
Phylogenetic tree of AOA amoA. Clone library sequences were aligned with GenBank sequences in an excisting ARB database. Nucleotide tree was constructed by Neighbor Joining with Jukes-Cantor correction in ARB from 594 bp. Colored symbols represent total number of clones belonging to each cluster in the tree (see legend).
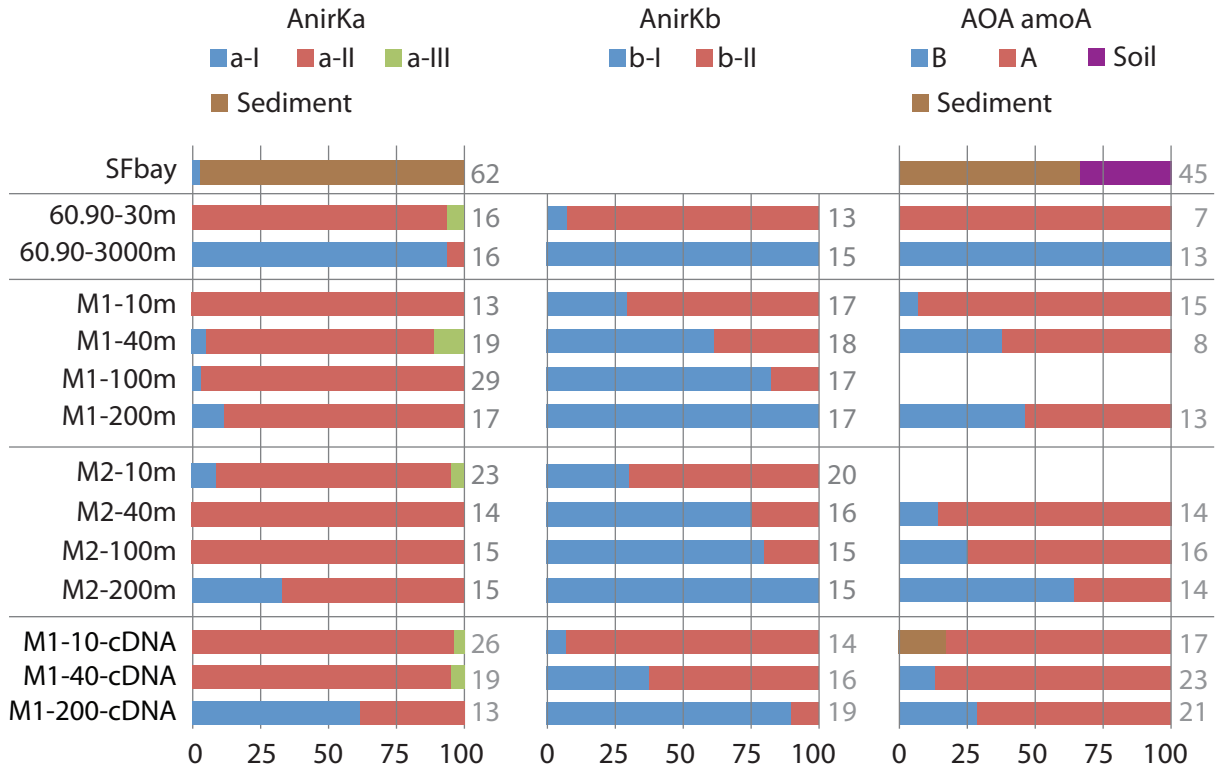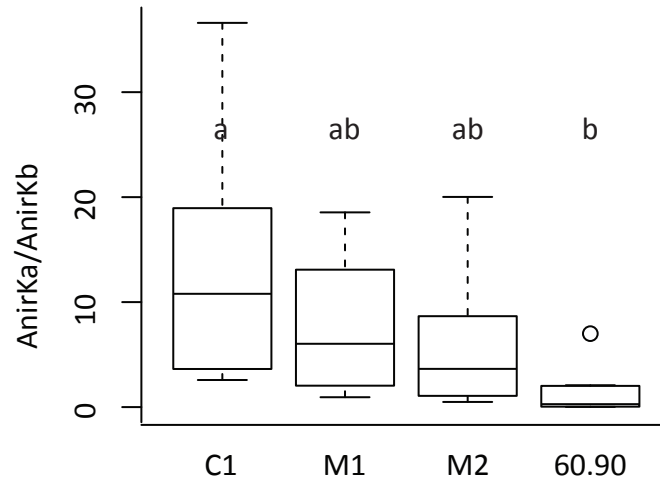
Supplementary Figure S4.
Percent of sequences from each clone library belonging to a major phylogenetic cluster. Number of clones in each library is shown in grey.

Supplementary Figure S6.
Water column profile of AnirKa, AnirKb, and
AOA amoA gene copy abundances in
California Current station 60.90

Supplementary Figure S7.
Boxplot of the gene copy ratio of AnrKa to AnirKb throughout the water column from the three stations in Monterey Bay and station 60.90 in California Current. Letters above plots indicates significantly different average values between stations (one-way ANOVA, p<0.01).