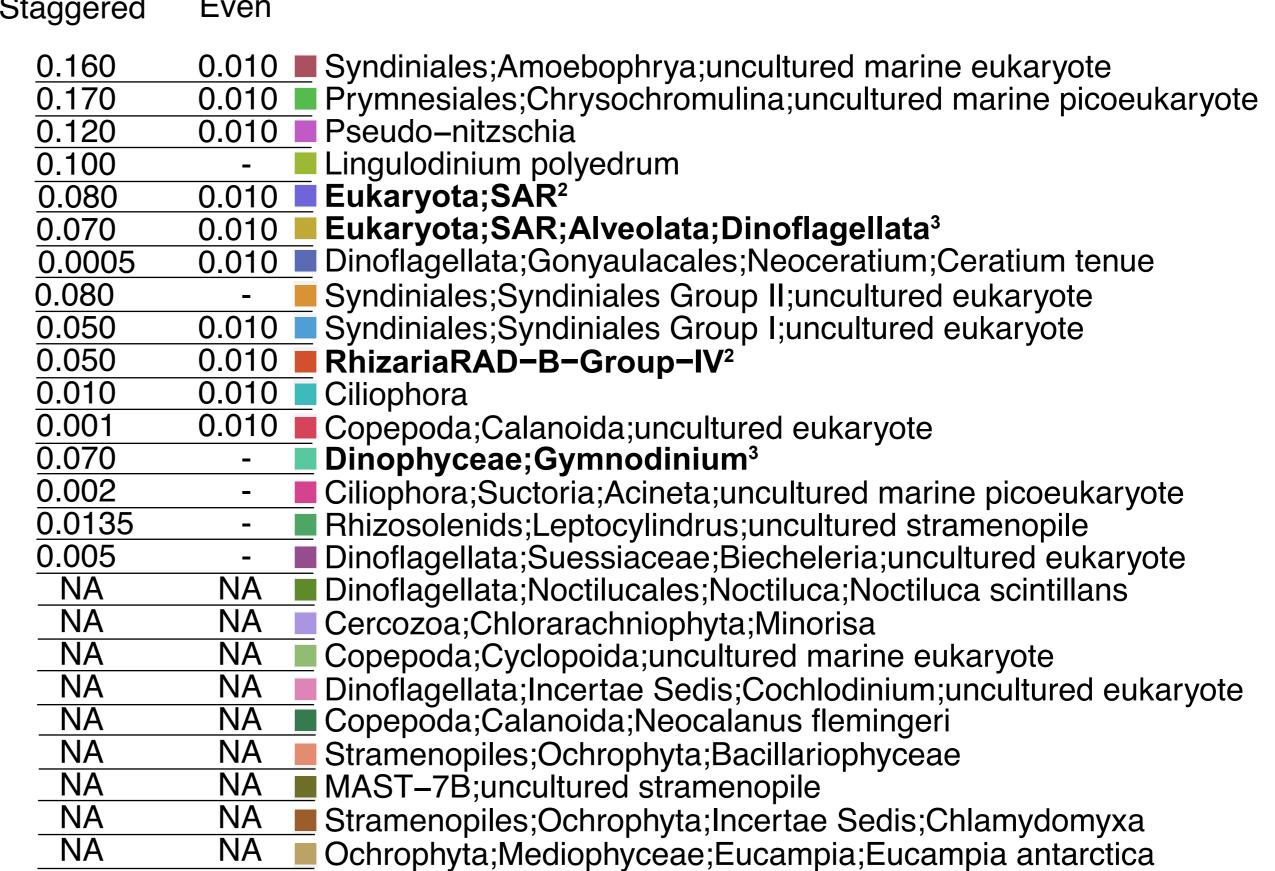


Expected 16S V4-V5 Mock Community

Expected 18SV9 Mock Community

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Staggered	Even	Staggered	Even
0.090	0.091 Nitrosopumilaceae;Candidatus Nitrosopumilus	0.160	0.010 ■ Syndiniales; Amoebo
0.315	0.091 ■ SAR11 clade;Clade I;Clade Ia	0.170	0.010 Prymnesiales; Chrys
0.018	0.091 Marine Group II;marine metagenome	0.120	0.010 Pseudo-nitzschia
0.158	0.091 Actinomarinaceae; Candidatus Actinomarina; uncultured marine bacterium	0.100	 Lingulodinium polye
0.068	0.091 Prochlorococcus MIT9313	0.080	0.010 Eukaryota;SAR ²
0.018	0.091 ■ Pirellulaceae;Blastopirellula;uncultured Pirellula sp.	0.070	0.010 ■ Eukaryota;SAR;Alv
0.090	- Actinomarinaceae;Candidatus Actinomarina	<u>0.0005</u>	0.010 ■ Dinoflagellata;Gonya
0.018	0.091 ■ NS2b marine group;uncultured marine bacterium	0.080	Syndiniales;Syndinia
0.018	0.091 SAR202 clade;uncultured Chloroflexi bacterium	0.050	0.010 Syndiniales; Syndinia
0.014	0.091 Bacteria; Marinimicrobia (SAR406 clade); unidentified marine bacterioplankton		0.010 ■ RhizariaRAD-B-G ı
0.023	<u>0.091</u> SAR116 clade	0.010	0.010 Ciliophora
0.045	0.091 SAR86 clade;Rhodobacteraceae bacterium REDSEA-S29_B10	0.001	0.010 Copepoda;Calanoida
<u>0.018</u>	- SAR116 clade;Candidatus Puniceispirillum;uncultured bacterium	0.070	Dinophyceae;Gymı
0.009	 Nitrosopumilaceae;uncultured marine archaeon 	0.002	Ciliophora;Suctoria;
0.023	Rhodospirillales;AEGEAN-169 marine group	0.0135	- Rhizosolenids;Lepto
0.009	Flavobacteriaceae;Formosa	0.005	Dinoflagellata;Suess
0.009	Oceanospirillales;Pseudohongiellaceae;Pseudohongiella	NA	NA Dinoflagellata;Noctile
0.009	- NS9 marine group;marine metagenome	NA	NA Cercozoa;Chlorarac
0.009	SAR92 clade	NA	NA Copepoda;Cyclopoid
0.009	MB11C04 marine group	NA	NA Dinoflagellata;Incert
0.007	Rhodobacteraceae;uncultured;marine metagenome	NA	NA Copepoda;Calanoida
0.009	- SAR86 clade;marine metagenome	NA	NA Stramenopiles;Ochro
0.005	- Flavobacteriaceae;NS5 marine group	NA	NA MAST-7B;unculture
0.007	SAR86 clade;metagenome	NA	NA Stramenopiles;Ochro
0.001	- SAR116 clade;uncultured Oceanibaculum sp.	_NA	NA Ochrophyta;Medioph
0.001	SAR202_b¹		
0.002	SAR86 clade;uncultured bacterium		



18sv9 Mock Communities

NA

NA Propionibacteriaceae;Cutibacterium

