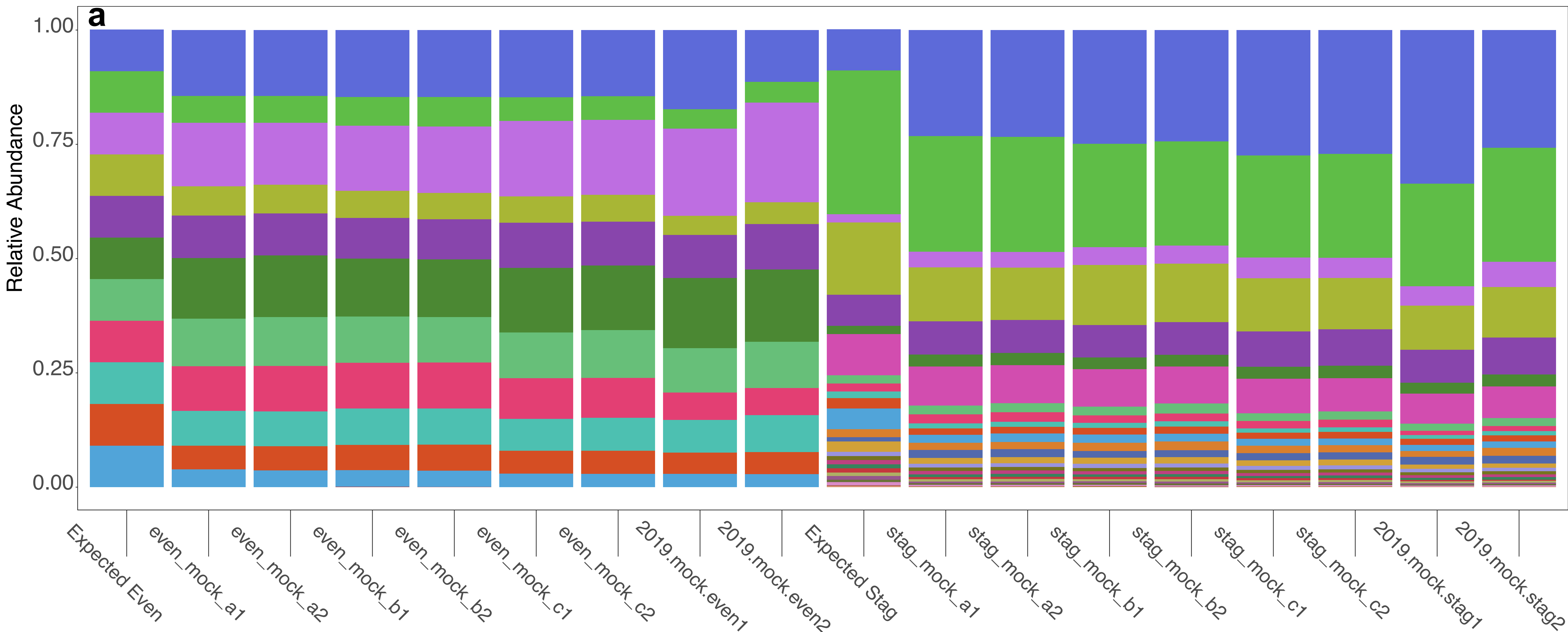






























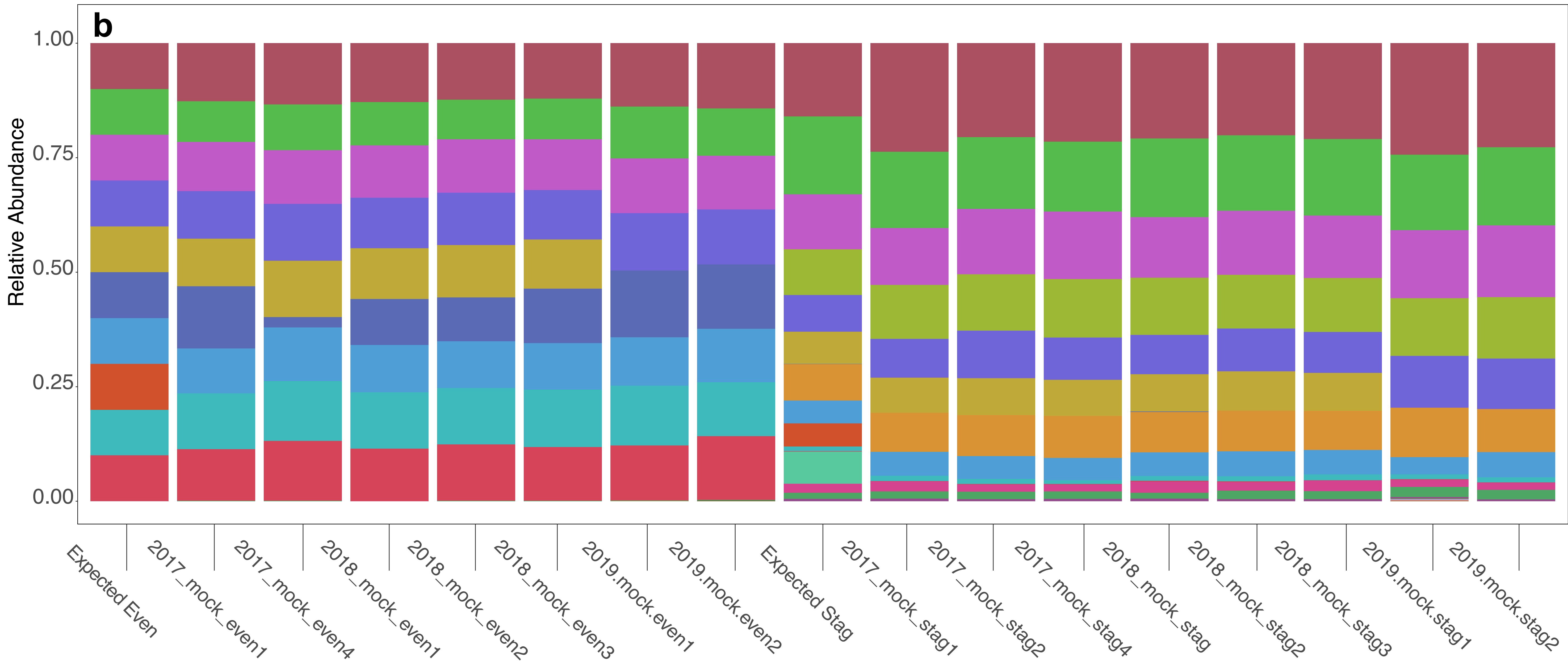
## 16S V4–V5 Mock Communities



Expected		
Staggered	Even	
0.090	0.091	 Nitrosopumilaceae;Candidatus Nitrosopumilus
0.315	0.091	 SAR11 clade;Clade I;Clade Ia
0.018	0.091	 Marine Group II;marine metagenome
0.158	0.091	 Actinomarinaceae;Candidatus Actinomarina;uncultured marine bacterium
0.068	0.091	 Prochlorococcus MIT9313
0.018	0.091	 Pirellulaceae;Blastopirellula;uncultured Pirellula sp.
0.090	-	 Actinomarinaceae;Candidatus Actinomarina
0.018	0.091	 NS2b marine group;uncultured marine bacterium
0.018	0.091	 SAR202 clade;uncultured Chloroflexi bacterium
0.014	0.091	 Bacteria;Marinimicrobia (SAR406 clade);unidentified marine bacterioplankton
0.023	0.091	 SAR116 clade
0.045	0.091	 SAR86 clade;Rhodobacteraceae bacterium REDSEA-S29_B10
0.018	-	 SAR116 clade;Candidatus Puniceispirillum;uncultured bacterium
0.009	-	 Nitrosopumilaceae;uncultured marine archaeon
0.023	-	 Rhodospirillales;AEGEAN-169 marine group
0.009	-	 Flavobacteriaceae;Formosa
0.009	-	 Oceanospirillales;Pseudohongiellaceae;Pseudohongiella
0.009	-	 NS9 marine group;marine metagenome
0.009	-	 SAR92 clade
0.009	-	 MB11C04 marine group
0.007	-	 Rhodobacteraceae;uncultured;marine metagenome
0.009	-	 SAR86 clade;marine metagenome
0.005	-	 Flavobacteriaceae;NS5 marine group
0.007	-	 SAR86 clade;metagenome
0.001	-	 SAR116 clade;uncultured Oceanibaculum sp.
0.001	-	 <b>SAR202_b1</b>
0.002	-	 SAR86 clade;uncultured bacterium
NA	NA	 Propionibacteriaceae;Cutibacterium

**<sup>1</sup>SAR202\_b is expected in our 16S V4-V5 staggered community but is not seen in any samples**

## 18sv9 Mock Communities



Expected		
Staggered	Even	
0.160	0.010	■ Syndiniales;Amoebophrya;uncultured marine eukaryote
0.170	0.010	■ Prymnesiales;Chrysochromulina;uncultured marine picoeukaryote
0.120	0.010	■ Pseudo-nitzschia
0.100	-	■ Lingulodinium polyedrum
0.080	0.010	■ <b>Eukaryota;SAR<sup>2</sup></b>
0.070	0.010	■ <b>Eukaryota;SAR;Alveolata;Dinoflagellata<sup>3</sup></b>
0.0005	0.010	■ Dinoflagellata;Gonyaulacales;Neoceratium;Ceratum tenue
0.080	-	■ Syndiniales;Syndiniales Group II;uncultured eukaryote
0.050	0.010	■ Syndiniales;Syndiniales Group I;uncultured eukaryote
0.050	0.010	■ <b>RhizariaRAD-B-Group-IV<sup>2</sup></b>
0.010	0.010	■ Ciliophora
0.001	0.010	■ Copepoda;Calanoida;uncultured eukaryote
0.070	-	■ <b>Dinophyceae;Gymnodinium<sup>3</sup></b>
0.002	-	■ Ciliophora;Suctorina;Acineta;uncultured marine picoeukaryote
0.0135	-	■ Rhizosolenids;Leptocylindrus;uncultured stramenopile
0.005	-	■ Dinoflagellata;Suessiaceae;Biecheleria;uncultured eukaryote
NA	NA	■ Dinoflagellata;Noctilucales;Noctiluca;Noctiluca scintillans
NA	NA	■ Cercozoa;Chlorarachniophyta;Minoria
NA	NA	■ Copepoda;Cyclopoida;uncultured marine eukaryote
NA	NA	■ Dinoflagellata;Incertae Sedis;Cochlodinium;uncultured eukaryote
NA	NA	■ Copepoda;Calanoida;Neocalanus flemingeri
NA	NA	■ Stramenopiles;Ochrophyta;Bacillariophyceae
NA	NA	■ MAST-7B;uncultured stramenopile
NA	NA	■ Stramenopiles;Ochrophyta;Incertae Sedis;Chlamydomyxa
NA	NA	■ Ochrophyta;Mediophyceae;Eucampia;Eucampia antarctica

<sup>2</sup>Our analyses find an unidentified Eukaryota;SAR, which seems to align with an expected Rhizaria RAD B Group IV

<sup>3</sup>Our analyses find an unidentified Dinoflagellata, which seems to align with an expected Dinophyceae;Gymnodinium