

# Supplementary Material to: Dynamics of the bacterial community associated with *Phaeodactylum tricornutum* cultures

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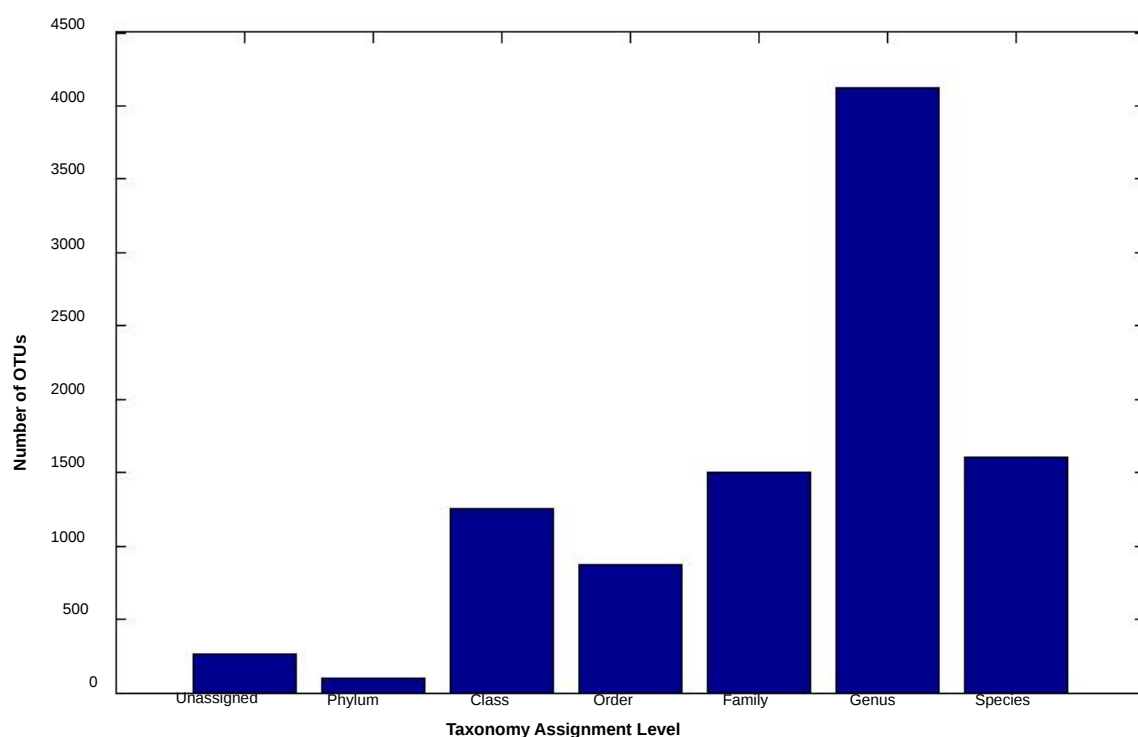
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## 1 Experimental setup and data analysis



Figure S1: **Non-axenic *Phaeodactylum tricornutum* culture set up.** 5L polyethylene bags with a “V” shaped bottom were created using the heat sealer machine. The bags were then rinsed and filled with 5L of filtered seawater. Afterwards each bag was sealed and hung approximately 30 cm from the light source. A small incision was made to insert the aeration tubing. This consists of a 10ml pipette attached to silicon tubing which is attached to an sterile air filter connecting it to the main air supply. A modified access port was created to take samples and measure the environmental parameters (Photographs courtesy of Maria Rubio Bernal)



**Figure S2: Operational Taxonomic Unit (OTU) Taxonomy Assignment Level.** The 16S rRNA gene sequences were clustered to defined Operational Taxonomic Units (OTUs) at  $\geq 97\%$  sequence identity. Most OTUs could be assigned to the genera level, using the SILVA database (v.118) [1]

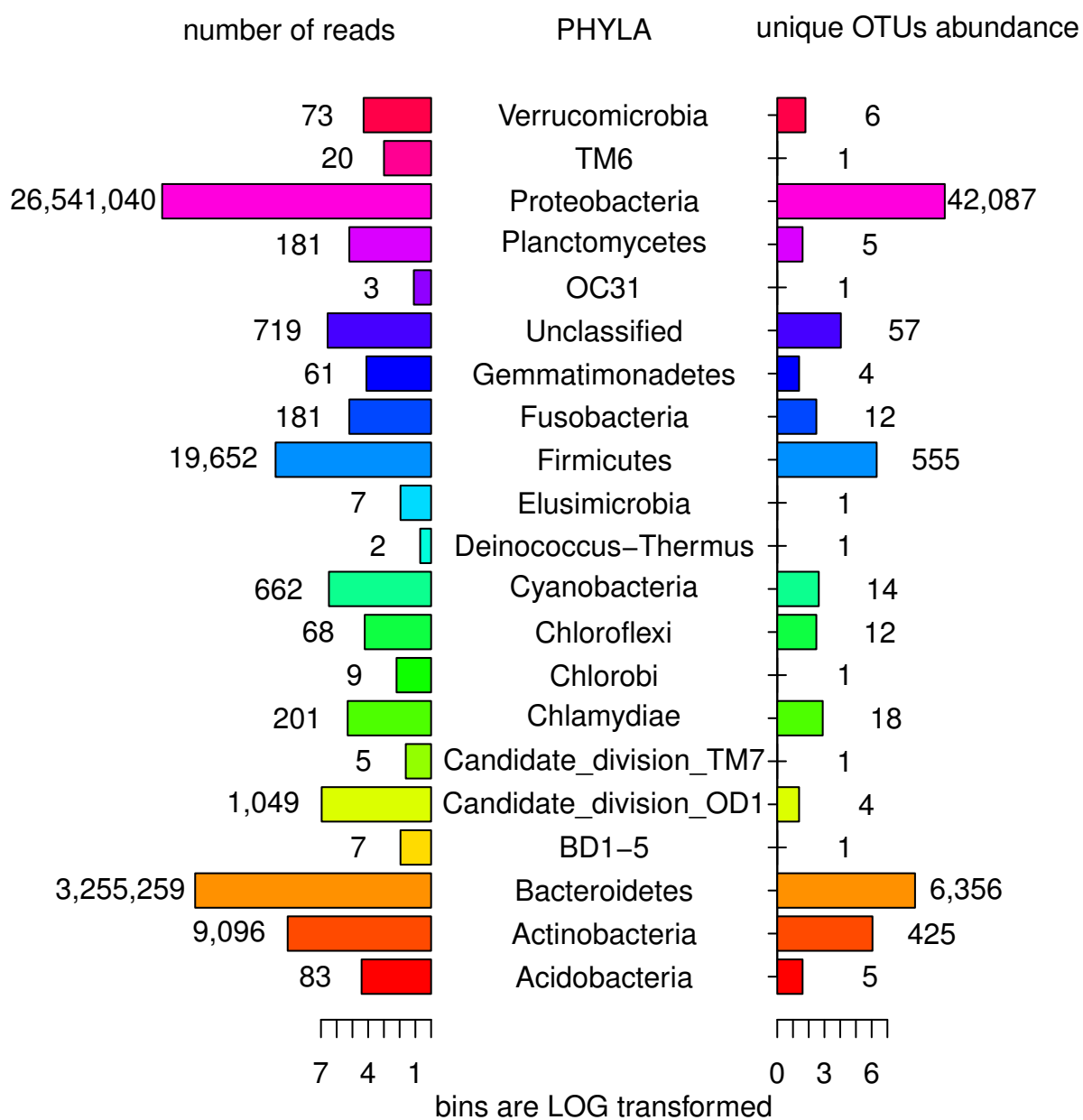


Figure S3: **Number of reads per unique OTU abundance (at the phylum level).** A comparison of the number of individual reads to the number of unique OTUs shows that phyla with high number of reads do not result in single OTUs

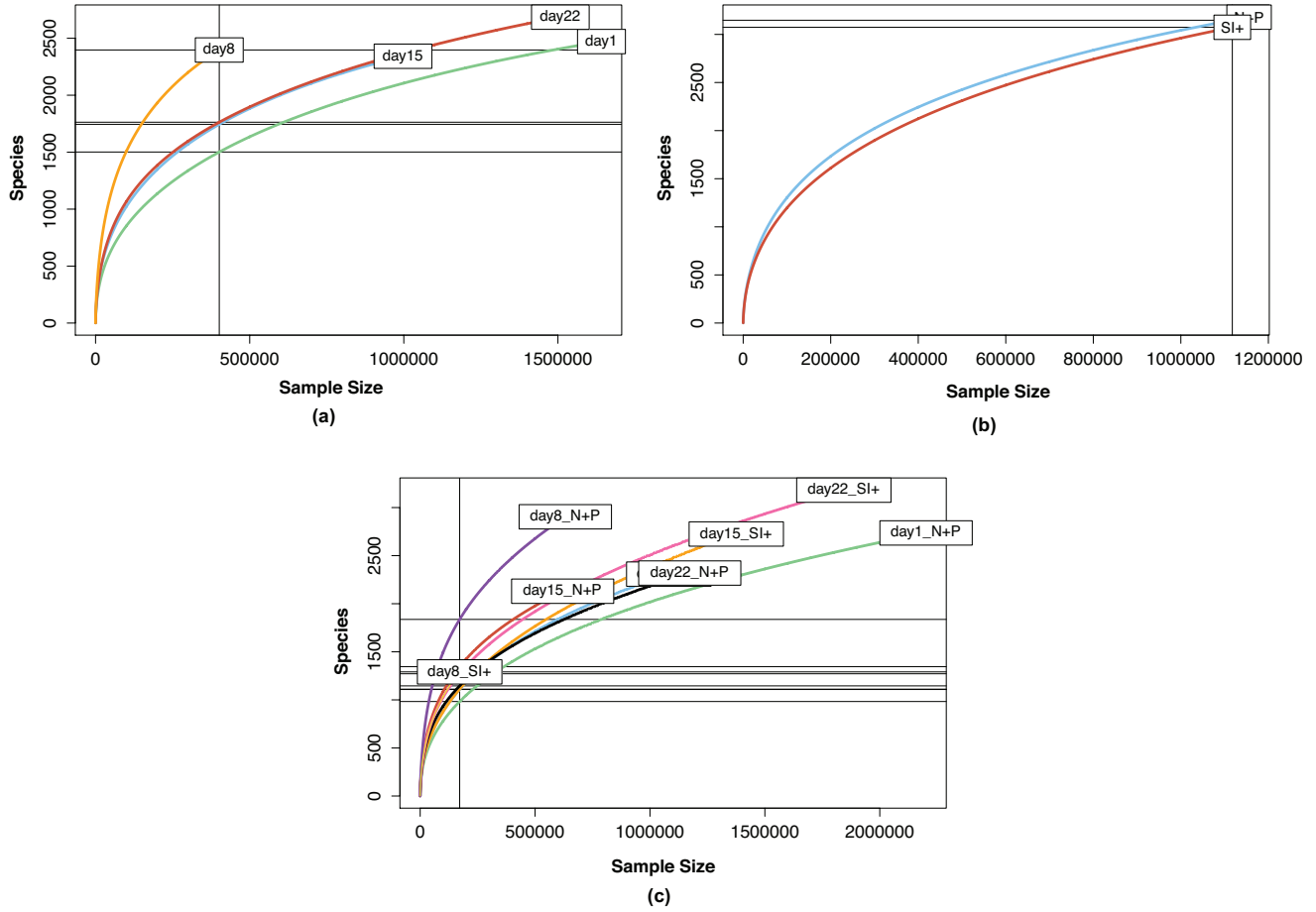
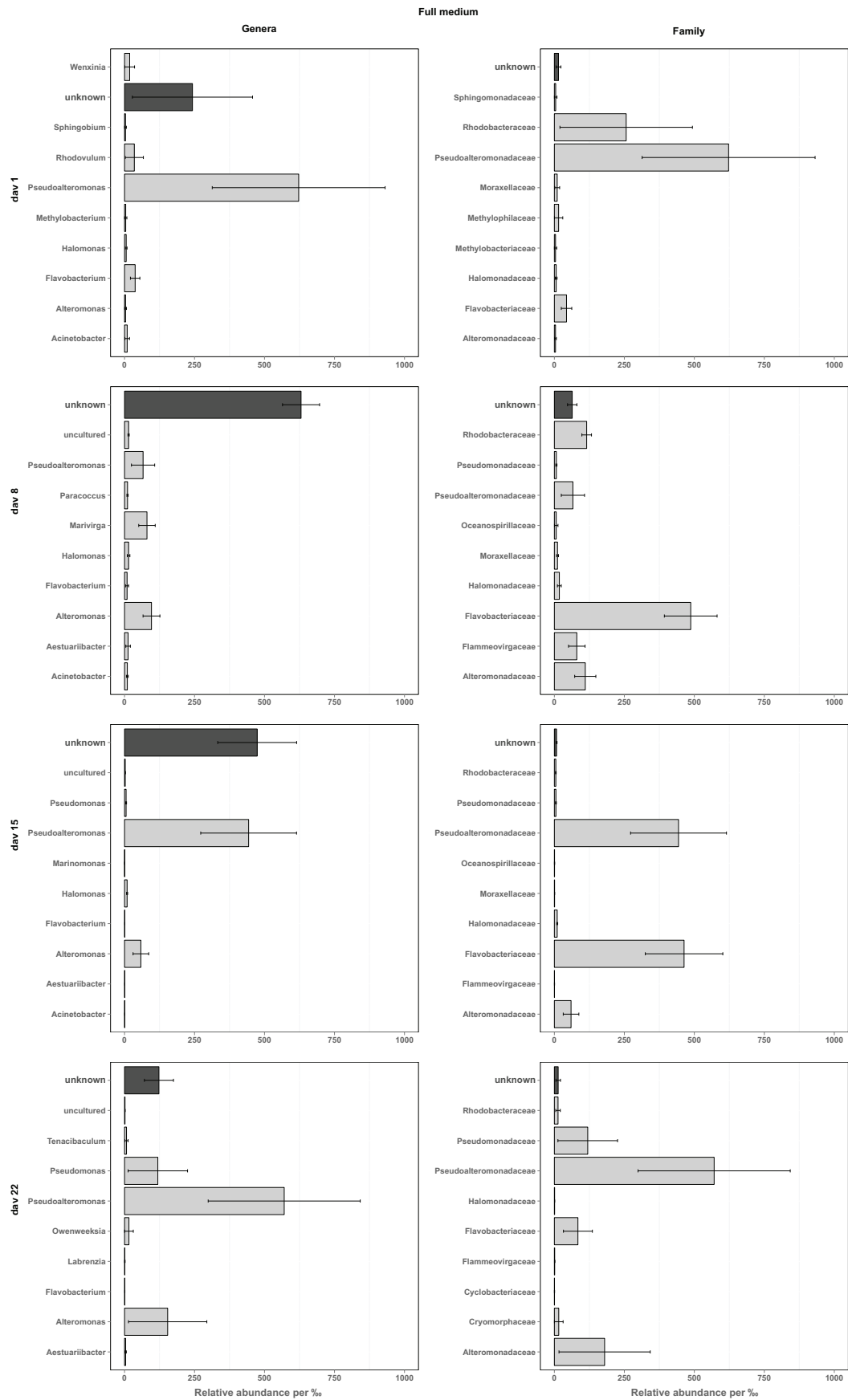


Figure S4: **Alpha diversity**. Rarefaction curves were used to evaluate the Alpha diversity in the different media conditions as well as at the different time points. Species richness in both minimal and complete media was  $\sim 3\,000$ . Species richness over time remained between  $\sim 2\,400$  and  $2\,600$ , with reduced species richness ( $\sim 1\,300$ ) on Day 8 (both minimal and complete media) possibly due to elevated levels of 16S *P. tricornutum* chloroplast reads which had to be omitted. Greatest species richness ( $\sim 3\,000$ ) was shown on Day 22



**Figure S5: Comparison between bacterial community at genera level and family level (complete media).** We show no dynamical difference within the genera that cannot be observed at the family level. Encircled in red, there are a greater number of OTUs that could not be assigned a taxonomy ('unknowns') at the genera level than at the family level. By investigating the bacterial community dynamics at the family level, we also include taxonomical information that is unavailable at the genus level

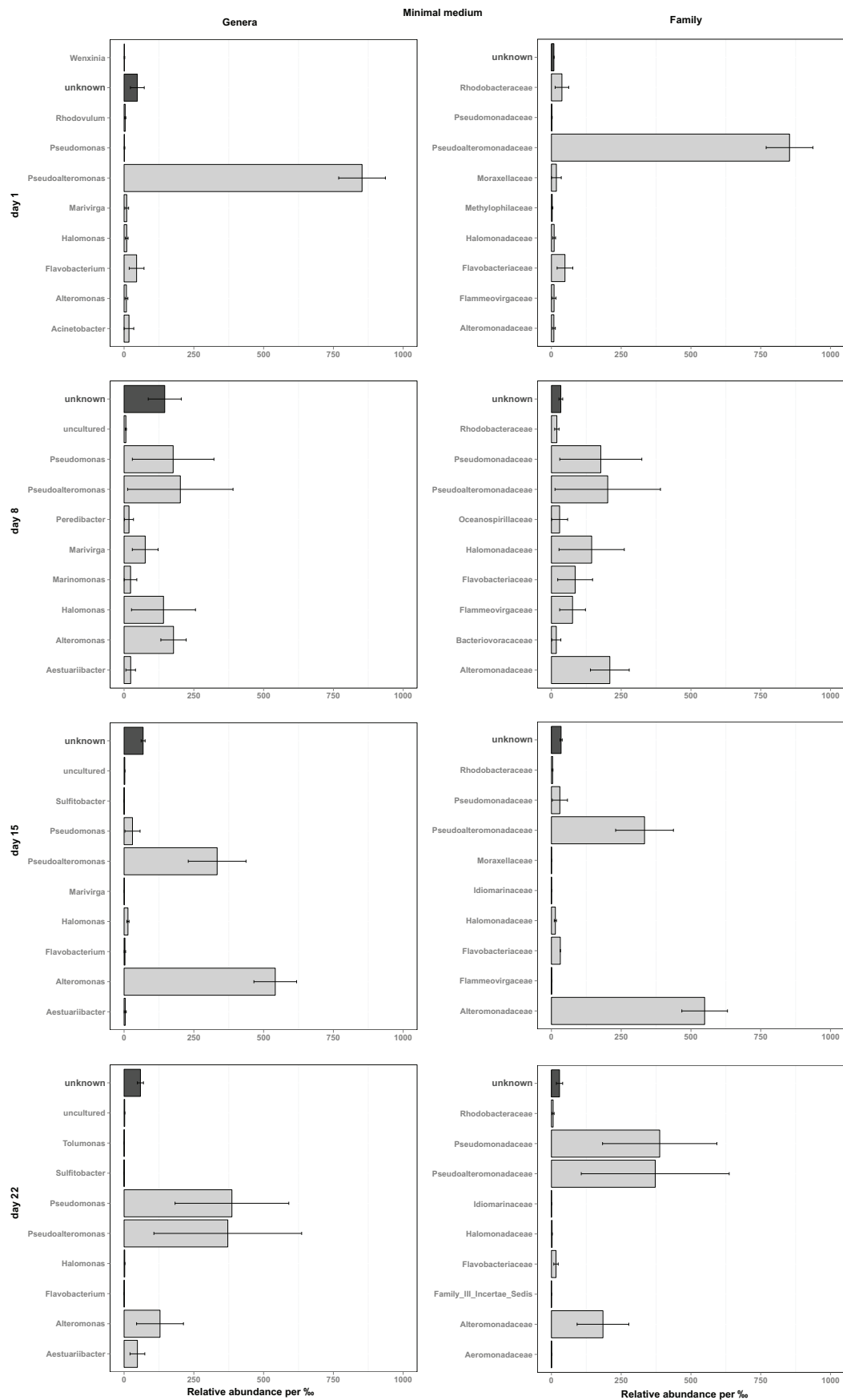


Figure S6: **Comparison between bacterial community at genera level and family level (minimal media).** We show no dynamical difference within the genera that cannot be observed at the family level. Encircled in red, there are a greater number of OTUs that could not be assigned a taxonomy ('unknowns') at the genera level than at the family level. By investigating the bacterial community dynamics at the family level, we also include taxonomical information that is unavailable at the genus level

Table S1: **16S V6 rRNA primer sequences.** ‘Max’ is the complete media. ‘Min’ is the minimal media. ‘A’, ‘B’, and ‘C’ are the three replicates

Description	Barcode Name	Adaptor A Sequence	Barcode Sequence	Forward V6 Primer Sequence	Reverse V6 Primer Sequence
Day 1_Max_A	IonXpress.071	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TGAGGCTCCGAC	MWACGCGARGAACCTTACC	CGACARCCATGCANCACCT
Day 1_Max_B	IonXpress.072	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CGAAGGCCACAC	MWACGCGARGAACCTTACC	CGACARCCATGCANCACCT
Day 1_Max_C	IonXpress.073	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TCTGCCTGTC	MWACGCGARGAACCTTACC	CGACARCCATGCANCACCT
Day 1_Min_A	IonXpress.074	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CGATCGGTTC	MWACGCGARGAACCTTACC	CGACARCCATGCANCACCT
Day 1_Min_B	IonXpress.075	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TCAGGAATAC	MWACGCGARGAACCTTACC	CGACARCCATGCANCACCT
Day 1_Min_C	IonXpress.076	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CGGAAGAACCTC	MWACGCGARGAACCTTACC	CGACARCCATGCANCACCT
Day 8_Max_A	IonXpress.077	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CGAAGCGATTTC	MWACGCGARGAACCTTACC	CGACARCCATGCANCACCT
Day 8_Max_B	IonXpress.078	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CAGCCAATTCTC	MWACGCGARGAACCTTACC	CGACARCCATGCANCACCT
Day 8_Max_C	IonXpress.079	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CCTGGTTGTC	MWACGCGARGAACCTTACC	CGACARCCATGCANCACCT
Day 8_Min_A	IonXpress.080	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TCGAAGGCAGGC	MWACGCGARGAACCTTACC	CGACARCCATGCANCACCT
Day 8_Min_B	IonXpress.081	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CCTGCCATTTCG	MWACGCGARGAACCTTACC	CGACARCCATGCANCACCT
Day 8_Min_C	IonXpress.082	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TTGGCATCTC	MWACGCGARGAACCTTACC	CGACARCCATGCANCACCT
Day 15_Max_A	IonXpress.083	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CTAGGACATTTC	MWACGCGARGAACCTTACC	CGACARCCATGCANCACCT
Day 15_Max_B	IonXpress.084	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CTTCCATAAC	MWACGCGARGAACCTTACC	CGACARCCATGCANCACCT
Day 15_Max_C	IonXpress.085	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CCAGCCTCAAC	MWACGCGARGAACCTTACC	CGACARCCATGCANCACCT
Day 15_Min_A	IonXpress.086	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CTTGGTTATTC	MWACGCGARGAACCTTACC	CGACARCCATGCANCACCT
Day 15_Min_B	IonXpress.087	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TTGGCTGGAC	MWACGCGARGAACCTTACC	CGACARCCATGCANCACCT
Day 15_Min_C	IonXpress.088	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CCGAACACTTC	MWACGCGARGAACCTTACC	CGACARCCATGCANCACCT
Day 22_Max_A	IonXpress.090	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CTAACCACGGC	MWACGCGARGAACCTTACC	CGACARCCATGCANCACCT
Day 22_Max_B	IonXpress.091	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CGGAAGGATGC	MWACGCGARGAACCTTACC	CGACARCCATGCANCACCT
Day 22_Max_C	IonXpress.092	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CTAGGAACCGC	MWACGCGARGAACCTTACC	CGACARCCATGCANCACCT
Day 22_Min_A	IonXpress.093	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CTTGTCCAATC	MWACGCGARGAACCTTACC	CGACARCCATGCANCACCT
Day 22_Min_B	IonXpress.094	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TCCGACAAGC	MWACGCGARGAACCTTACC	CGACARCCATGCANCACCT
Day 22_Min_C	IonXpress.095	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CGGACAGATC	MWACGCGARGAACCTTACC	CGACARCCATGCANCACCT

Table S2: **Generalized UniFrac distances of bacterial communities in complete and minimal media over time.** Generalized UniFrac distance contains an extra parameter  $\alpha$  controlling the weight on abundant lineages so the distance is not dominated by highly abundant lineages.  $\alpha = 0.5$  has overall the best power

		DAY 1		DAY 8		DAY 15		DAY 22	
		Minimal	Complete	Minimal	Complete	Minimal	Complete	Minimal	Complete
DAY 1	Minimal	0	0.5158104	0.7195151	0.8637909	0.6668939	0.7504169	0.6655156	0.6608732
	Complete	0.5158104	0	0.7020723	0.7203046	0.7176411	0.7125498	0.7019796	0.6733559
DAY 8	Minimal	0.7195151	0.7020723	0	0.6641379	0.5844515	0.6637369	0.5905962	0.497263
	Complete	0.8637909	0.7203046	0.6641379	0	0.8558383	0.5896856	0.8340209	0.7723285
DAY 15	Minimal	0.6668939	0.7176411	0.5844515	0.8558383	0	0.6605545	0.4569922	0.5042935
	Complete	0.7504169	0.7125498	0.6637369	0.5896856	0.6605545	0	0.630498	0.5720828
DAY 22	Minimal	0.6655156	0.7019796	0.5905962	0.8340209	0.4569922	0.630498	0	0.4597439
	Complete	0.6608732	0.6733559	0.497263	0.7723285	0.5042935	0.5720828	0.4597439	0

## References

- [1] C. Quast, E. Pruesse, P. Yilmaz, J. Gerken, T. Schweer, P. Yarza, J. Peplies, and F. O. Glockner. The SILVA ribosomal RNA gene database project: improved data processing and web-based tools. *Nucleic Acids Research*, 41(D1):D590–D596, 2013.