

Supplementary Table 2. Averages of square root-transformed abundances (Av. Abund) in the two sample groups of Fig. 1 (groups from unconstrained divisive tree method: 400 μ atm CO₂ (F1-4, F9-12, F17-F20) and 1200 μ atm CO₂ (F5-F8, F13-F16, F21-F24)), and breakdown of average similarity (Av. Sim) within each group (**A** and **B**) and average dissimilarity (Av. Diss) between the two groups (**C**), into contributions from each OTU (bold). OTUs were ordered in decreasing contribution, until at least 70% of average similarity within each group or dissimilarity between the two groups was attained (see last column). Ratios Sim/SD and Diss./SD (also bold) identify consistent discriminators by dividing average similarity or average dissimilarity by its SD. The SIMPER (similarity percentages – OTUs contributions) One-Way analysis was based on the Bray-Curtis similarity.

A- Contributions from each OTU to similarity between samples from group 400 μ atm CO₂ (average similarity: **65.24)**

OTU	Av.Abund	Av.Sim	Sim/SD	Contrib%	Cum.%
<i>Propionibacteriaceae</i>	2.14	14.22	9.42	21.80	21.80
<i>Flavobacteriaceae</i>	1.97	13.32	7.32	20.41	42.21
<i>Streptococcaceae</i>	1.61	10.64	15.84	16.31	58.52
<i>Rhodobacteraceae</i>	1.75	10.20	2.01	15.64	74.16

B- Contributions from each OUTU to similarity between samples from group 1200 μ atm CO₂ (average similarity: **60.93)**

OTU	Av.Abund	Av.Sim	Sim/SD	Contrib%	Cum.%
Vibrionaceae	2.90	18.17	6.15	29.83	29.83
Alteromonadaceae	1.63	11.05	4.16	18.13	47.96
Rhodobacteraceae	1.75	9.52	2.45	15.62	63.58
SAR11	1.38	8.32	3.01	13.66	77.24

C- Contributions from each OUT to dissimilarity between samples from groups 400 μ atm CO₂ and 1200 μ atm CO₂ (average dissimilarity **60.97)**

OTU	Av.Abund	Av.Abund	Av.Diss	Diss/SD	Contrib%	Cum.%
Vibrionaceae	0.00	2.90	10.88	3.58	17.84	17.84
Propionibacteriaceae	2.14	0.33	6.62	3.03	10.86	28.70
Alteromonadaceae	0.00	1.63	6.06	5.21	9.94	38.64
Streptococcaceae	1.61	0.00	5.91	6.16	9.69	48.33
SAR11	1.08	1.38	3.29	1.57	5.40	53.73
Verrucomicrobiaceae	0.00	0.91	3.26	1.15	5.35	59.08
Oxalobacteraceae	1.00	0.33	3.20	1.17	5.25	64.33
Burkholderiaceae	0.88	0.30	2.86	1.24	4.68	69.02
Flavobacteriaceae	1.97	1.43	2.55	1.48	4.17	73.19