Exploiting the potential of bioreactors for creating spatial organisation in the soil microbiome: A strategy for increasing sustainable agricultural practices

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Total number of reads
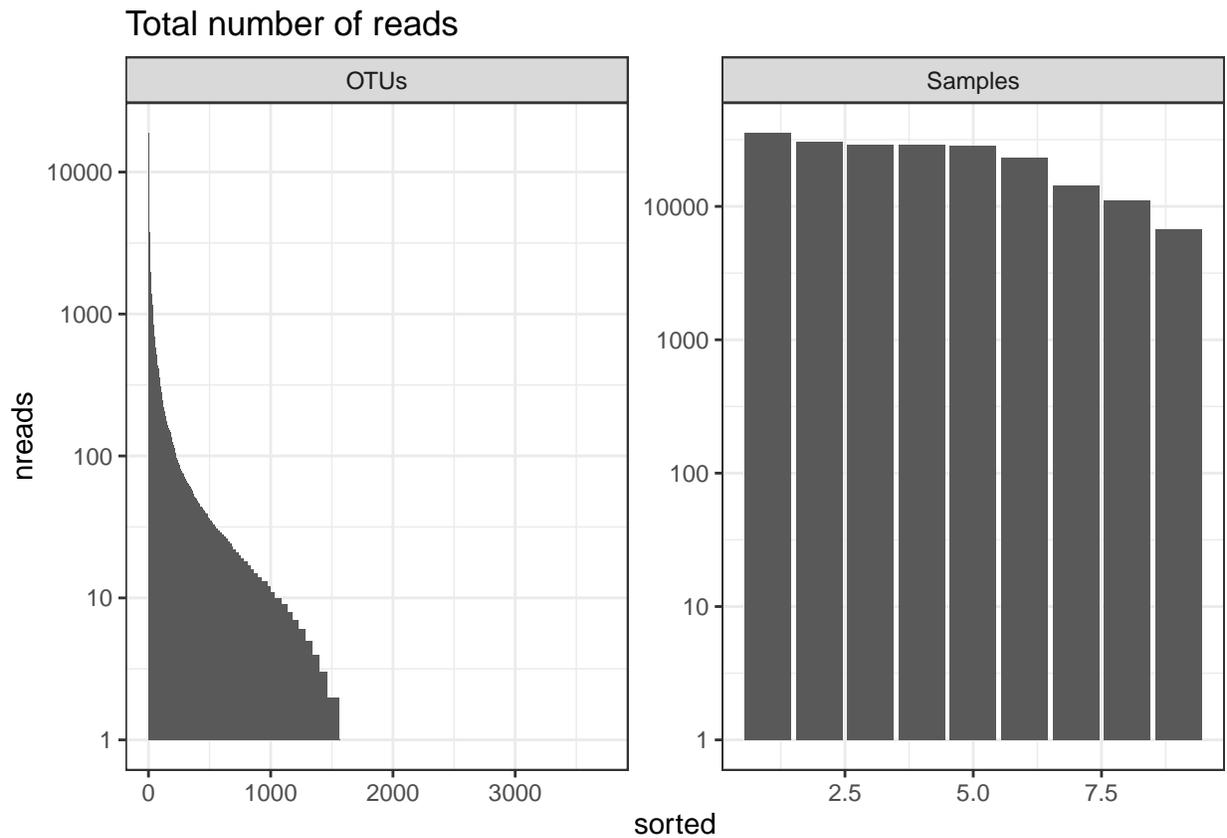
Figure S1: Number of reads obtained after bioinformatic processing shown as (a) number of reads per OTU (or amplicon sequence variants - ASVs) and (b) number of reads per sample.
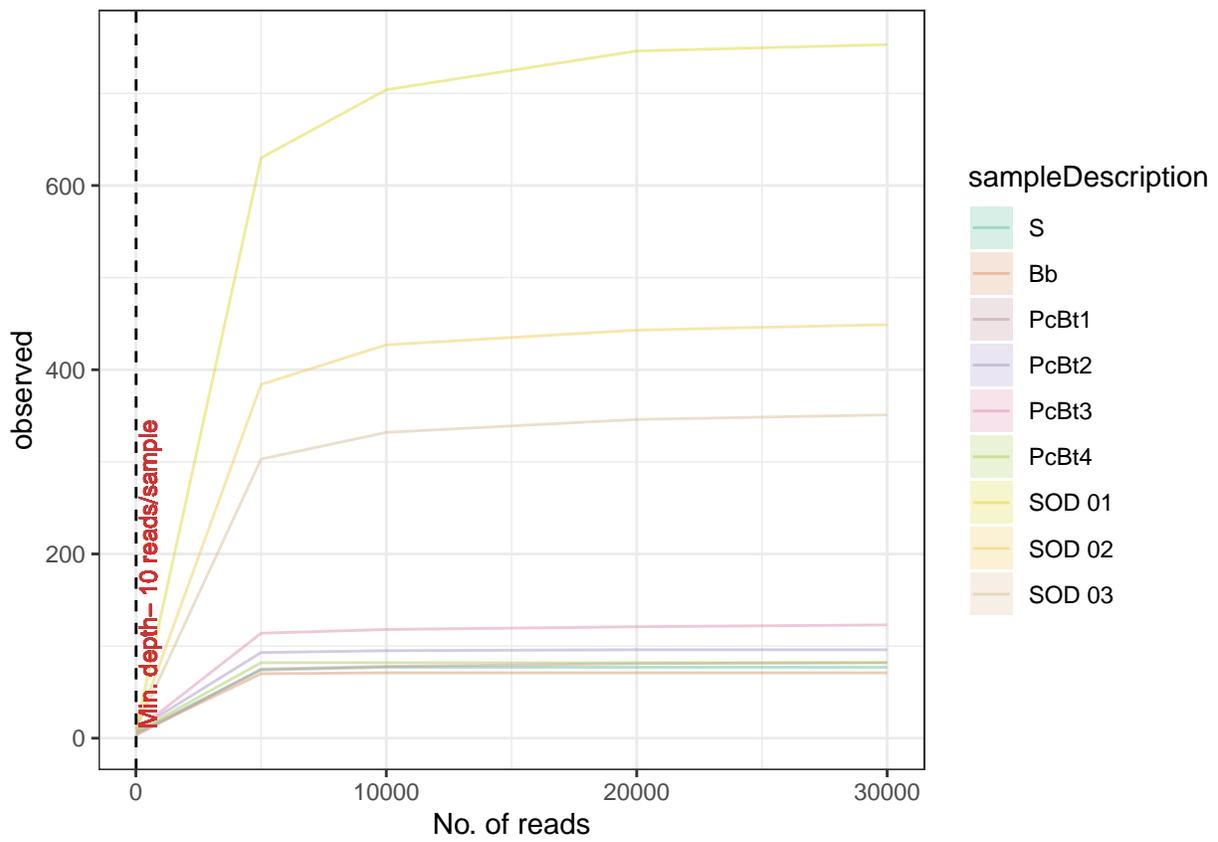
Figure S2: Rarefaction of final taxonomic data from microbiome analysis
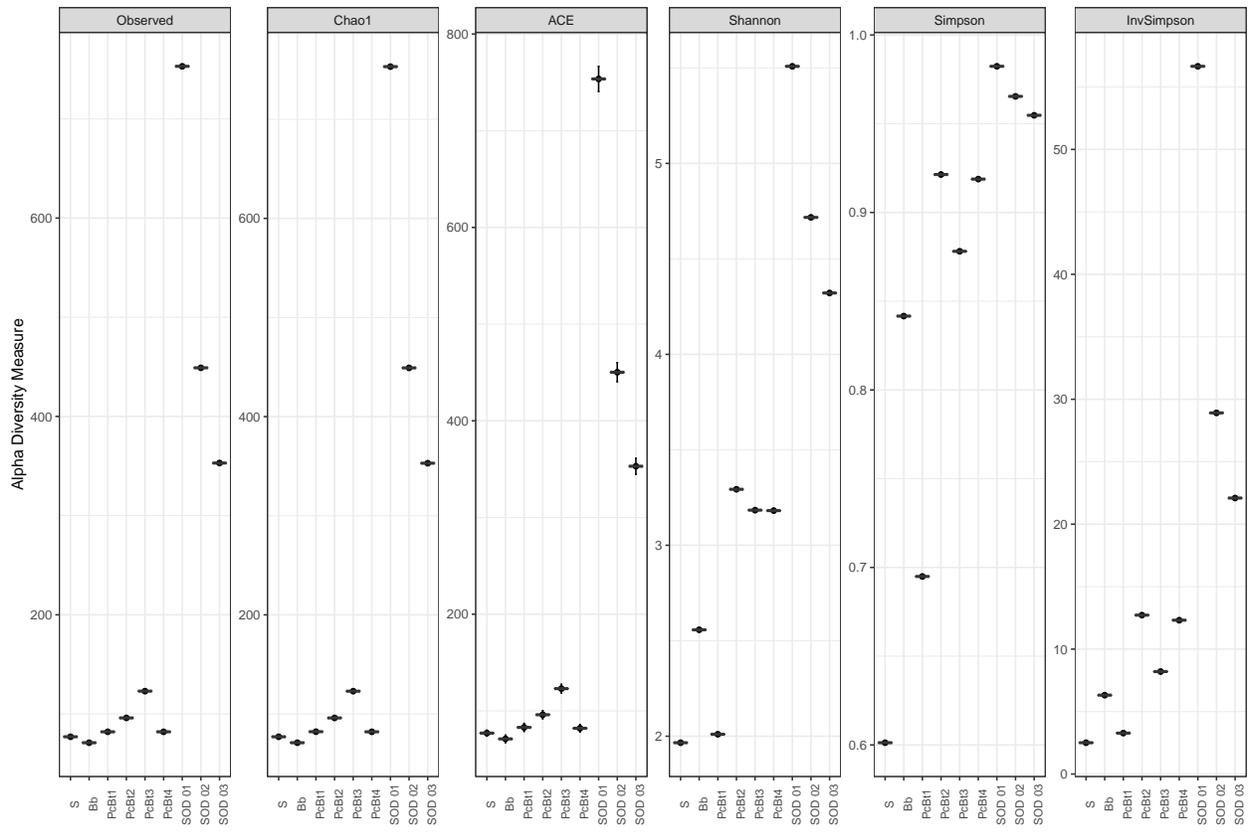
Figure S3: Alpha diveristy analysis using Observed, Chao1, ACE, Shannon, Simpson and Inverse Simpson metrics
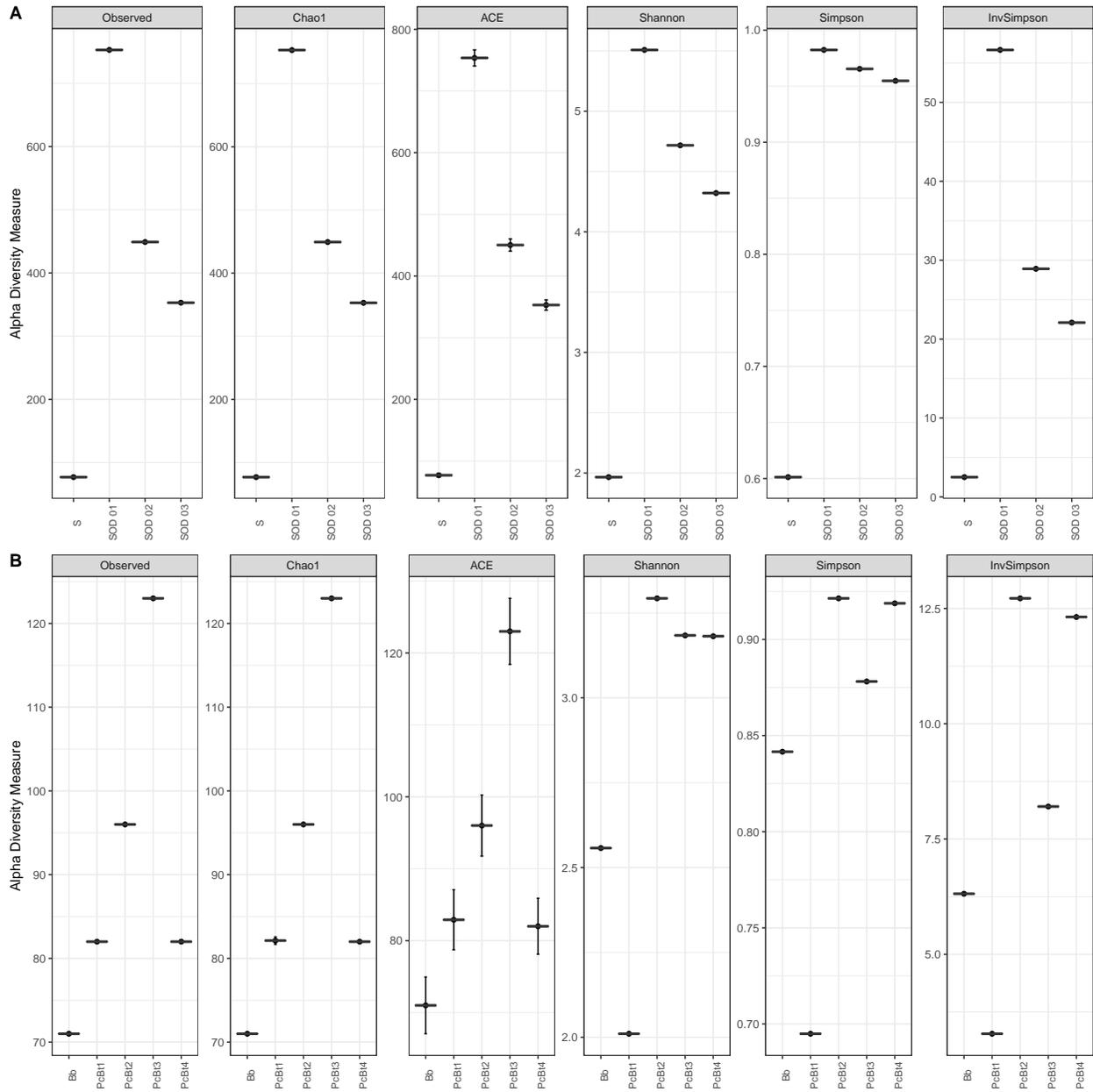
Figure S4: Alpha diveristy analysis using Observed, Chao1, ACE, Shannon, Simpson and Inverse Simpson metrics for subset data

Phylum	Group A				Group B				
	S	SOD 01	SOD 02	SOD 03	Bb	PcBt1	PcBt2	PcBt3	PcBt4
Proteobacteria	9.8	8.2	36.4	38.5	84.9	42.5	81.4	74.9	79.7
Firmicutes	89.8	58.8	0.7	0.8	0.1	0	0	0.2	0.2
Verrucomicrobiota	0	0.5	20.2	26.1	2.1	0.3	2.7	10.3	10.4
Cyanobacteria	0	0.1	0.3	6	4.5	54.5	1.2	4.9	1
Bacteroidota	0.1	0.5	12.8	8	7.8	2.6	13.6	8.1	7.1
Actinobacteriota	0.3	25	6.7	4.5	0.3	0	0.2	0.1	0
Acidobacteriota	0	1.3	10.1	5.6	0	0	0.3	1	0.7
Gemmatimonadota	0	0.4	3.4	5.2	0	0	0	0	0
Planctomycetota	0	0.4	2.7	2.6	0.2	0	0.5	0.6	0.7
Myxococcota	0	1.3	1.6	0.6	0	0	0	0	0
Chloroflexi	0	1.9	0.9	0.4	0	0	0	0	0
Armatimonadota	0	0	2.3	0.6	0	0	0	0	0
Bdellovibrionota	0	0.1	1	0.6	0.2	0	0	0	0
Nitrospirota	0	0.4	0.5	0	0	0	0	0	0
Patescibacteria	0	0.1	0.2	0.2	0	0	0	0	0
Entotheonellaeota	0	0.4	0	0	0	0	0	0	0
Sumerlaeota	0	0	0.1	0.1	0	0	0	0	0
Latescibacterota	0	0.2	0	0	0	0	0	0	0
k__Bacteria_a6d466ebbab3964d45151bface4eaf2b	0	0	0	0	0	0	0	0	0.1
k__Bacteria_954fade30d8b5a53d971b3eaa7b30918	0	0.1	0	0	0	0	0	0	0
Remaining taxa (22)	0.1	0.2	0.1	0.1	0	0	0	0	0

Figure S5: Heatmap showing relative abundance of top 20 phylum taxa identified from samples

	Group A				Group B				
	S	SOD 01	SOD 02	SOD 03	Bb	PcBt1	PcBt2	PcBt3	PcBt4
Alphaproteobacteria	0.9	7	23.9	25.7	52	14.6	52.6	55.7	60.9
Gammaproteobacteria	8.9	1.2	12.5	12.8	32.9	28	28.8	19.2	18.8
Clostridia	74.1	9.8	0	0	0.1	0	0	0	0
Verrucomicrobiae	0	0.5	20.2	26	2	0.3	2.3	10.1	10.1
Vampirivibrionia	0	0.1	0.1	5.5	4.4	54.5	0.8	0.2	0.4
Bacilli	14.1	46	0.7	0.8	0.1	0	0	0	0
Bacteroidia	0.1	0.5	12.2	7.9	7.8	2.6	13.6	8.1	7.1
Actinobacteria	0.3	14.4	6.1	4.4	0.3	0	0.2	0.1	0
Acidobacteriae	0	0.2	7.3	4.1	0	0	0.3	1	0.7
Cyanobacteriia	0	0	0.1	0.6	0.1	0	0.4	4.7	0.6
Planctomycetes	0	0.2	2.2	2.1	0.2	0	0.5	0.6	0.7
Thermoleophilia	0	5.8	0.2	0.1	0	0	0	0	0
Longimicrobia	0	0	0.9	4.1	0	0	0	0	0
Gemmatimonadetes	0	0.4	2.5	1.1	0	0	0	0	0
Acidimicrobiia	0	2.9	0.4	0	0	0	0	0	0
Fimbriimonadia	0	0	2.3	0.6	0	0	0	0	0
Polyangia	0	1.1	1.3	0.4	0	0	0	0	0
Vicinamibacteria	0	0.6	1.4	0.9	0	0	0	0	0
Blastocatellia	0	0.2	1.4	0.7	0	0	0	0	0
Bdellovibrionia	0	0	0.7	0.4	0.2	0	0	0	0
MB−A2−108	0	1.3	0	0	0	0	0	0	0
Chlamydiae	0	0	0	0.1	0.1	0	0.4	0.2	0.3
Desulfitobacteriia	0	1.2	0	0	0	0	0	0	0
Phycisphaerae	0	0.1	0.4	0.5	0	0	0	0	0
TK10	0	0.3	0.5	0.2	0	0	0	0	0
Limnochordia	0	1	0	0	0	0	0	0	0
Nitrospiria	0	0.4	0.5	0	0	0	0	0	0
p__Firmicutes_fa1ddfd395fb61f0bbc60e2858221cc6	0.8	0	0	0	0	0	0	0	0
KD4−96	0	0.7	0	0	0	0	0	0	0
p__Firmicutes_d0a314da17929fe570aff8a6f0d85ebc	0.8	0	0	0	0	0	0	0	0
Remaining taxa (64)	0.1	3.9	2	1	0	0	0	0.1	0.3

Figure S6: Heatmap showing relative abundance of top 30 class identified from samples

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	Group A				Group B				
	S	SOD 01	SOD 02	SOD 03	Bb	PcBt1	PcBt2	PcBt3	PcBt4
Rhizobiales	0.1	4.5	12.4	11	37.8	4.8	10	11.2	25.1
Sphingomonadales	0.3	0.7	4.5	3.6	8.7	2.9	31.2	35.3	20.4
Clostridiales	74.1	5.5	0	0	0.1	0	0	0	0
Burkholderiales	0.2	0.3	7.2	5.9	31	23.6	4.5	4	2.3
Obscuribacterales	0	0.1	0	5.5	4.4	54.5	0.8	0.2	0.4
Opitutales	0	0	17.7	18.6	0	0	0	0	0
Xanthomonadales	0.2	0.1	1.8	2.3	1.6	1.7	3.7	10.3	12.7
Bacillales	12.7	14.1	0.2	0.1	0.1	0	0	0	0
Reyranellales	0	0.3	1.5	1.5	1	1.1	4.4	3.7	10.8
Verrucomicrobiales	0	0	1.6	6.5	0	0	0.1	6.5	7.9
Brevibacillales	0	19.5	0.1	0.1	0	0	0	0	0
c__Bacteroidia_783535a03c2e41866d160d349546fd1b	0	0.1	0.1	0.1	4.6	0.2	6.6	4.4	3.6
Chitinophagales	0	0.3	4.4	4.5	1.8	1.6	4.4	1.3	1.4
Enterobacterales	6.5	0.3	0	0	0.1	0	8.3	2.5	0.8
Salinisphaerales	0	0	0	0.8	0	2.7	11.9	1.4	0.7
Caulobacterales	0	0.2	0.8	1.5	3.6	0.6	2.7	2.4	1.9
Cytophagales	0	0.1	6.7	2.4	1	0.8	0.3	0.2	0.4
Chthoniobacterales	0	0.3	0.2	0.4	2	0.3	2.2	3.6	2.2
Pseudomonadales	2	0.2	2.2	2.7	0	0	0.2	0.9	2.3
Micromonosporales	0	10.3	0	0	0	0	0	0	0
Paenibacillales	1.4	7.2	0.4	0.5	0	0	0	0	0
Ferrovibrionales	0	0	0.1	1.1	0	3.6	2.6	0.8	0.5
Micrococcales	0.3	0.3	4.2	2.8	0.3	0	0.2	0.1	0
Bryobacterales	0	0.1	4.4	2.3	0	0	0	0	0
Chloroplast	0	0	0.1	0.6	0.1	0	0.4	4.7	0.6
Rhodospirillales	0	0	2.1	2.9	0	0	0	0	0
Longimicrobiales	0	0	0.9	4.1	0	0	0	0	0
Flavobacteriales	0	0.1	0.1	0.1	0.1	0	1.7	1.6	1.3
Gaiellales	0	4.6	0	0	0	0	0	0	0
Isosphaerales	0	0	1.3	1.7	0.1	0	0.5	0.5	0.5
Gemmatimonadales	0	0.4	2.5	1.1	0	0	0	0	0
Propionibacteriales	0	1.9	0.9	1.1	0	0	0	0	0
Paracaedibacterales	0	0	0.2	0.6	0.3	1.1	0.4	0.9	0.3
Azospirillales	0	0	0.3	0.5	0	0	0.8	0.9	1.3
Solibacterales	0	0.1	1.9	1.2	0	0	0.2	0	0
Sphingobacteriales	0	0.1	1	0.8	0.3	0	0.4	0.7	0.2
Lachnospirales	0	3.1	0	0	0	0	0	0	0
Acidobacteriae	0	0	0.6	0.6	0	0	0.2	1	0.6
Fimbriimonadales	0	0	2.3	0.6	0	0	0	0	0
Vicinamibacterales	0	0.5	1.4	0.9	0	0	0	0	0
Remaining taxa (190)	2.2	24.9	14.1	8.9	1.2	0.6	1.2	1	1.9

Figure S7: Heatmap showing relative abundance of top 40 order taxa identified from samples

	Group A				Group B				
	S	SOD 01	SOD 02	SOD 03	Bb	PcBt1	PcBt2	PcBt3	PcBt4
Sphingomonadaceae	0.3	0.7	4.5	3.6	8.7	2.9	31.2	35.3	20.4
Clostridiaceae	74.1	4.5	0	0	0.1	0	0	0	0
Obscuribacteraceae	0	0.1	0	5.5	4.4	54.5	0.8	0.2	0.4
Rhodocyclaceae	0	0	0.6	2.5	18.7	22.8	2.3	1.9	1.2
Beijerinckiaceae	0	0.5	2.4	1.8	34.2	2.5	2.2	1.4	0.8
Xanthobacteraceae	0	2.9	3.7	4	1	0.7	4.9	5.9	17.9
Opitutaceae	0	0	17.7	18.6	0	0	0	0	0
Xanthomonadaceae	0.2	0.1	1.7	2.2	1.6	1.7	3.7	10.3	12.7
Reyranellaceae	0	0.3	1.5	1.5	1	1.1	4.4	3.7	10.8
Comamonadaceae	0	0.1	4.7	1.8	11.1	0.7	2.1	2	1.1
Verrucomicrobiaceae	0	0	1.5	6.5	0	0	0.1	6.5	7.9
Brevibacillaceae	0	19.5	0.1	0.1	0	0	0	0	0
c__Bacteroidia_783535a03c2e41866d160d349546fd1b	0	0.1	0.1	0.1	4.6	0.2	6.6	4.4	3.6
Chitinophagaceae	0	0.2	4.3	4.5	1.8	1.6	4.4	1.3	1.4
Enterobacteriaceae	6.3	0.3	0	0	0.1	0	8.3	2.5	0.8
Solimonadaceae	0	0	0	0.8	0	2.7	11.9	1.4	0.7
Bacillaceae	0.8	13.2	0.2	0.1	0	0	0	0	0
Rhizobiaceae	0.1	0.4	2.7	2.2	1.3	0.2	1.3	2.7	3.4
Sporolactobacillaceae	11.6	0.9	0	0	0.1	0	0	0	0
Terrimicrobiaceae	0	0	0.1	0.4	2	0.3	2.2	3.6	2.2
Pseudomonadaceae	2	0.2	2.2	2.7	0	0	0.2	0.9	2.3
Caulobacteraceae	0	0.1	0.5	0.5	3.5	0.6	2.5	1.7	0.9
Micromonosporaceae	0	10.3	0	0	0	0	0	0	0
Paenibacillaceae	1.4	7.2	0.4	0.5	0	0	0	0	0
Ferrovibrionaceae	0	0	0.1	1.1	0	3.6	2.6	0.8	0.5
Microscillaceae	0	0.1	6.4	1.9	0	0	0	0	0
Bryobacteraceae	0	0.1	4.4	2.3	0	0	0	0	0
Chloroplast	0	0	0.1	0.6	0.1	0	0.4	4.7	0.6
Intrasporangiaceae	0	0.1	2.8	2.5	0	0	0	0	0
Rhizobiales_Incertae_Sedis	0	0.1	1.2	0.7	0.3	1.1	0.3	0.2	1.3
Longimicrobiaceae	0	0	0.9	4.1	0	0	0	0	0
Hyphomicrobiaceae	0	0.3	1.2	1.5	0.2	0.1	0.5	0.4	0.5
Isosphaeraceae	0	0	1.3	1.7	0.1	0	0.5	0.5	0.5
Weeksellaceae	0	0	0	0	0.1	0	1.4	1.5	1.3
o__Rhodospirillales_e40fa32b862876e8d638ff2c4d3ed663	0	0	1.7	2.6	0	0	0	0	0
Gemmatimonadaceae	0	0.4	2.5	1.1	0	0	0	0	0
Paracaedibacteraceae	0	0	0.2	0.6	0.3	1.1	0.4	0.9	0.3
Azospirillaceae	0	0	0.2	0.5	0	0	0.8	0.9	1.3
Nocardioidaceae	0	1.5	0.9	1.1	0	0	0	0	0
Solibacteraceae	0	0.1	1.9	1.2	0	0	0.2	0	0
Methylopilaceae	0	0	0	0.1	0.7	0.3	0.8	0.7	0.8
Hyphomonadaceae	0	0	0.3	1	0.1	0	0.2	0.7	1
Lachnospiraceae	0	3.1	0	0	0	0	0	0	0
Spirosomaceae	0	0	0.1	0.4	1	0.8	0.3	0.2	0.4
Acidobacteriae	0	0	0.6	0.6	0	0	0.2	1	0.6
Fimbriimonadaceae	0	0	2.3	0.6	0	0	0	0	0
Thermoactinomycetaceae	0	2.6	0	0	0	0	0	0	0
Caedibacteraceae	0	0	0.1	0.4	0.4	0.4	0.2	0.3	0.5
Burkholderiaceae	0.2	0	0.9	1.2	0	0	0	0	0
Acetobacteraceae	0.5	0.1	0.4	0.7	0.1	0	0.1	0.1	0.2
Devosiaceae	0	0	0.9	0.6	0.2	0	0	0	0.4
Blastocatellaceae	0	0	1.4	0.7	0	0	0	0	0
Vicinamibacteraceae	0	0.4	1	0.6	0	0	0	0	0
Sphingobacteriaceae	0	0	0.4	0.1	0.3	0	0.4	0.7	0.2
Micrococcaceae	0	0.1	1.2	0.3	0	0	0	0	0
Streptomycetaceae	0	0.9	0.6	0	0	0	0	0	0
Pedosphaeraceae	0	0.2	0.8	0.4	0	0	0	0	0
Rhodobacteraceae	0	0	0.4	1	0	0	0	0	0
Methylophilaceae	0	0	0	0	1.2	0.1	0	0.1	0
MB−A2−108	0	1.3	0	0	0	0	0	0	0
Remaining taxa (345)	2.5	27.1	13.7	7.7	1	0.2	1.4	0.9	1.3

Figure S8: Heatmap showing relative abundance of top 60 family taxa identified from samples

Genus	Group A				Group B				
	S	SOD 01	SOD 02	SOD 03	Bb	PcBt1	PcBt2	PcBt3	PcBt4
Sphingobium	0.1	0.1	0.2	0.2	0.7	0.8	21.7	32.6	17.5
Clostridium_sensu_stricto_12	68.2	3	0	0	0.1	0	0	0	0
Candidatus_Obscuribacter	0	0.1	0	5.5	4.4	54.3	0.7	0.1	0.1
Zoogloea	0	0	0.6	2.5	18.1	22.8	0	0	0
Beijerinckia	0	0.2	0.1	0.9	33.4	2.5	2	1.3	0.8
Opitutus	0	0	17.2	18.3	0	0	0	0	0
Pseudoxanthomonas	0	0	1.3	2	1.5	1.7	3.7	10.1	12.2
Xanthobacter	0	0	1.3	2.4	0.5	0.3	4.2	5.2	17.9
Reyranella	0	0.3	1.4	1.4	1	1.1	4.4	3.7	10.8
Brevibacillus	0	19.5	0.1	0.1	0	0	0	0	0
c__Bacteroidia_783535a03c2e41866d160d349546fd1b	0	0.1	0.1	0.1	4.6	0.2	6.6	4.4	3.6
Hydrocarboniphaga	0	0	0	0.7	0	2.7	11.9	1.4	0.7
Novosphingobium	0.1	0.1	0	0.3	7.4	1.1	6.7	0.7	0.4
Prosthecobacter	0	0	0.2	0.1	0	0	0.1	6.5	7.9
Bacillus	0.8	12.3	0.2	0.1	0	0	0	0	0
Sporolactobacillus	11.5	0.9	0	0	0.1	0	0	0	0
Sphingomonas	0	0.3	3.3	2.1	0	0.5	2.4	1.5	1.5
Terrimicrobium	0	0	0.1	0.4	2	0.3	2.2	3.6	2.2
Pelomonas	0	0	0	0	10.1	0.1	0	0	0
Ferrovibrio	0	0	0.1	1.1	0	3.6	2.6	0.8	0.5
f__Chitinophagaceae_9d9e4ad8ee3d7e910f6237bb14bcc4da	0	0	0.5	1	0	0.3	3.9	1	1.4
Pseudomonas	0	0	2.2	2.4	0	0	0.2	0.9	2.3
Roseimicrobium	0	0	1.3	6.2	0	0	0	0	0
Bryobacter	0	0.1	4.4	2.3	0	0	0	0	0
Clostridium_sensu_stricto_1	5.5	1.2	0	0	0	0	0	0	0
Chloroplast	0	0	0.1	0.6	0.1	0	0.4	4.7	0.6
f__Microscillaceae_d4802ec1ee4dc6981e399d101ce8a8d5	0	0	5.3	1.2	0	0	0	0	0
f__Enterobacteriaceae_527a09644f077fbcef30effba12056ff	0	0	0	0	0	0	3.4	1.1	0.8
Paenibacillus	1.4	2.8	0.3	0.5	0	0	0	0	0
Longimicrobium	0	0	0.9	4.1	0	0	0	0	0
Nordella	0	0.1	1	0.6	0.3	1.1	0.3	0.2	1.3
Terrimonas	0	0	0.8	0.9	1.8	1	0	0.1	0
Cloacibacterium	0	0	0	0	0.1	0	1.4	1.5	1.3
o__Rhodospirillales_e40fa32b862876e8d638ff2c4d3ed663	0	0	1.7	2.6	0	0	0	0	0
Phenylobacterium	0	0.1	0.2	0.3	3	0.1	0.1	0.1	0.2
Azonexus	0	0	0	0	0.4	0	1.8	1.1	0.6
f__Isosphaeraceae_136d9eb41806e28a7dfc193424250524	0	0	1.1	1.5	0.1	0	0.5	0.4	0.3
Gemmatimonas	0	0.2	2.3	1.1	0	0	0	0	0
Brevundimonas	0	0	0.2	0	0.3	0	1.1	1.1	0.8
f__Intrasporangiaceae_0cf152dc807b570c5f5ab1a7aea69901	0	0	1.3	2.2	0	0	0	0	0
Candidatus_Finniella	0	0	0	0.4	0.3	1.1	0.4	0.9	0.3
Sphingopyxis	0	0	0.2	0.3	0.6	0.5	0.4	0.5	1
Candidatus_Solibacter	0	0.1	1.9	1.2	0	0	0.2	0	0
Methylopila	0	0	0	0.1	0.7	0.3	0.8	0.7	0.8
Aminobacter	0	0	0.2	0.1	0.6	0.1	0.4	0.8	1
f__Enterobacteriaceae_e8b77cf2f7dd1f17a7c7626f2904d7b3	2.9	0.3	0	0	0	0	0	0	0
Hyphomonas	0	0	0.3	0.9	0	0	0.2	0.7	1
f__Rhizobiaceae_90a634fef584638a5861ac4f26074d88	0	0	0.2	0.2	0	0	0.6	0.9	1.1
Paludibaculum	0	0	0.6	0.6	0	0	0.2	1	0.6
Fimbriimonadaceae	0	0	2.3	0.6	0	0	0	0	0
Micromonospora	0	2.9	0	0	0	0	0	0	0
Fibrisoma	0	0	0	0.2	1	0.8	0.3	0.2	0.4
Anaerocolumna	0	2.7	0	0	0	0	0	0	0
f__Enterobacteriaceae_97822797c63078d0e598100e24f71b7d	0	0	0	0	0	0	1.7	1.1	0
Caulobacter	0	0	0.1	0.2	0.2	0.5	1.2	0.4	0
Pedomicrobium	0	0.3	1.1	1.2	0	0	0	0	0
Klebsiella	2.4	0	0	0	0	0	0	0	0
Pseudacidovorax	0	0	0	0	0	0	1	0.9	0.6
Hyphomicrobium	0	0	0.2	0.3	0.2	0.1	0.5	0.4	0.5
f__Comamonadaceae_61f7050e1641b84a11835f862bb20726	0	0	0	0.3	0.9	0.5	0.3	0.1	0.2
Candidatus_Nucleicultrix	0	0	0.1	0.4	0.4	0.4	0.2	0.3	0.5
Azospirillum	0	0	0.2	0.4	0	0	0	0.5	1
Flavitalea	0	0	1.3	0.9	0	0	0	0	0
f__Enterobacteriaceae_15318ef23ab68840e3368e4d318f95ad	0	0	0	0	0.1	0	1.7	0.3	0
f__Xanthobacteraceae_919ef4fa379e506a07d1d74ac3b7faba	0	0	0	0.2	0.3	0.3	0.6	0.6	0
Azospira	0	0	0	0	0.1	0	0.4	0.8	0.6
Cupriavidus	0	0	0.9	1.1	0	0	0	0	0
Comamonas	0	0	0	0	0	0	0.8	0.9	0.2
Flavihumibacter	0	0	0.6	1.3	0	0	0	0	0
f__Comamonadaceae_15157002701d572334bc12450e742d75	0	0	1.8	0	0	0	0	0	0
Shinella	0	0.1	0.6	0.2	0	0	0	0.4	0.5
Devosia	0	0	0.6	0.6	0.2	0	0	0	0.4
Vicinamibacteraceae	0	0.4	0.8	0.5	0	0	0	0	0
Hydrogenophaga	0	0	0.6	1.1	0	0	0	0	0
f__Pseudomonadaceae_5953c5b70f425e1d94a03e92aebcb6c7	1.5	0.2	0	0	0	0	0	0	0
Nocardioides	0	0.5	0.4	0.8	0	0	0	0	0
Microvirga	0	0.2	1.2	0.2	0	0	0	0	0
Nubsella	0	0	0.1	0.1	0.3	0	0.4	0.6	0.2
Roseomonas	0	0	0.4	0.7	0.1	0	0.1	0.1	0.2
f__Rhizobiaceae_83e49f4390f396afb34415853f5470db	0	0	0	0	0	0	0.1	0.2	0.2
Remaining taxa (743)	5.3	50.7	33	18.6	4.2	0.9	4.8	2.6	3.3

Figure S9: Heatmap showing relative abundance of top 80 genera identified from samples

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## MDS/PCoA on weighted−UniFrac distance
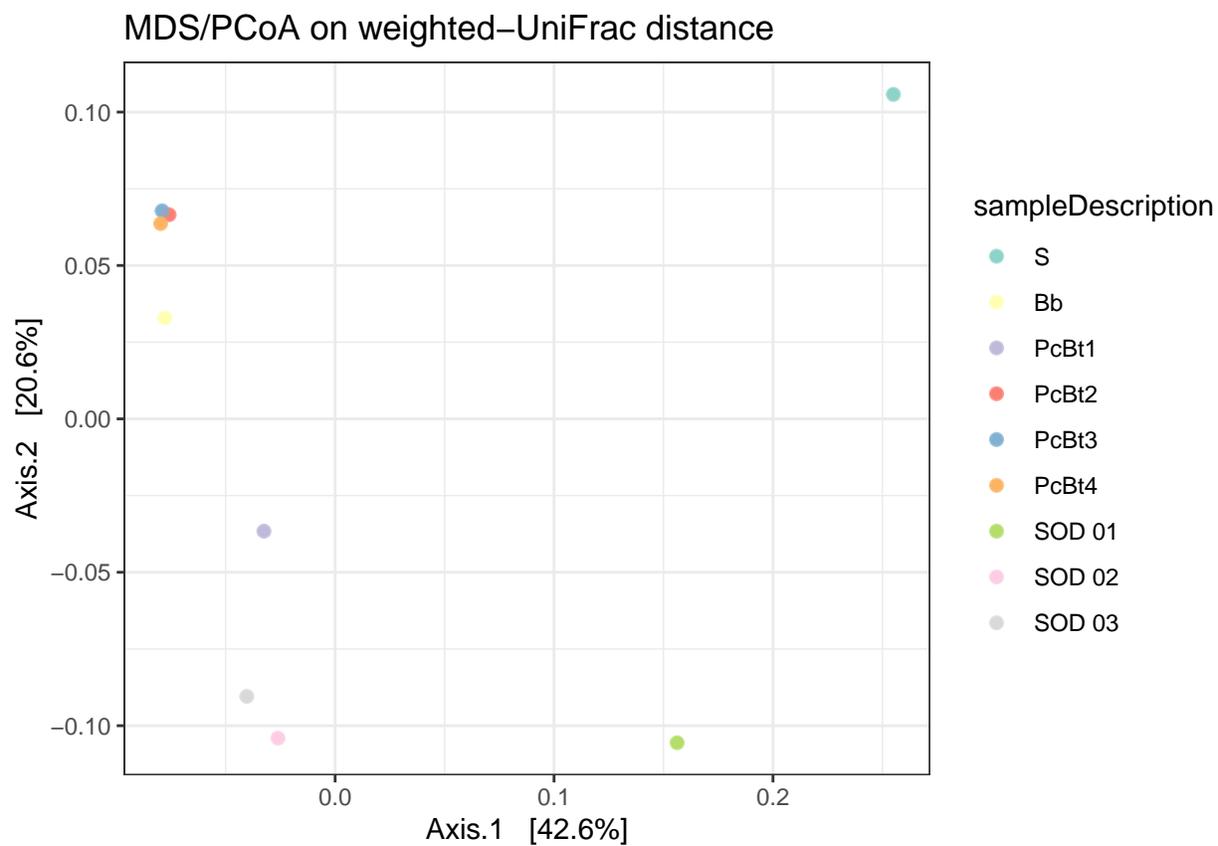
Figure S10: Principal coordinate analysis (multidimensional scaling) of distance matrix using weighted UniFrac metrics. Coordinates for axis 1 and 2 are showin in plot.

Cluster Dendrogram

GPUF
hclust (*, "average")
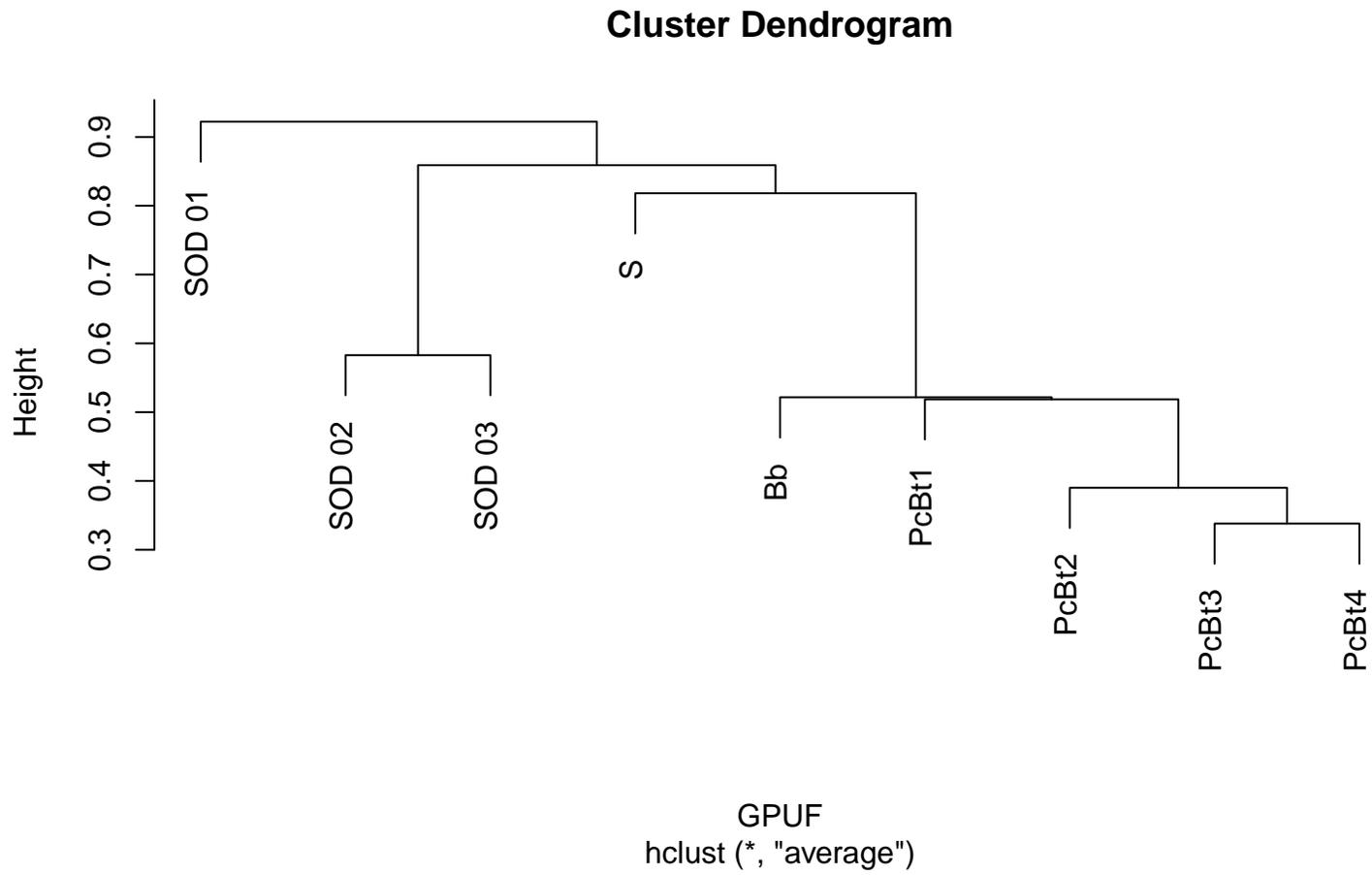
Figure S11: Hierarchical Clustering using UniFrac dissimilarity and UPGMA method.

Cluster Dendrogram

GPUF
hclust (*, "average")
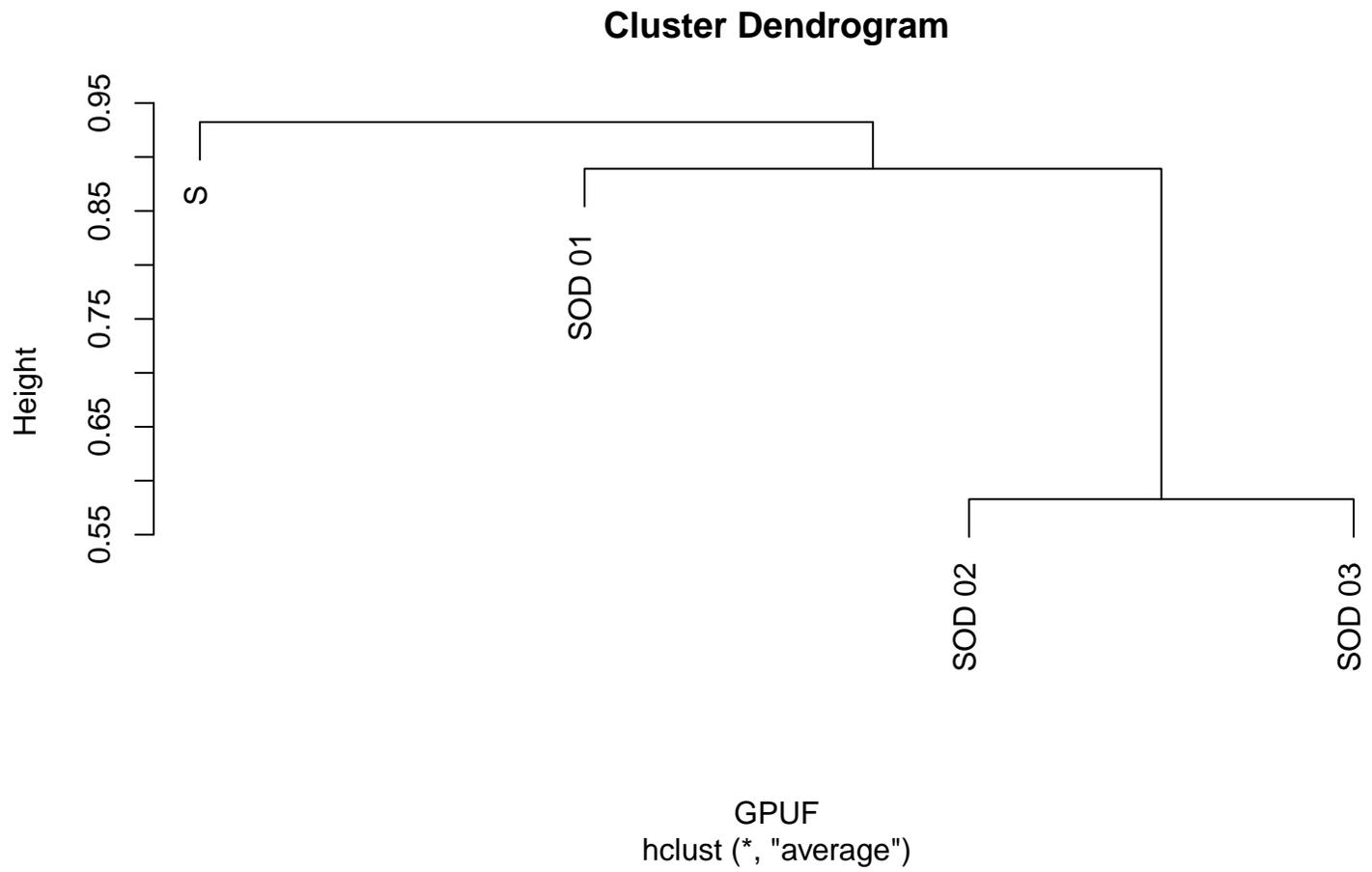
Figure S12: Hierarchical Clustering using UniFrac dissimilarity and UPGMA method of Group A sample group in the present study

Cluster Dendrogram

Height

GPUF
hclust (*, "average")
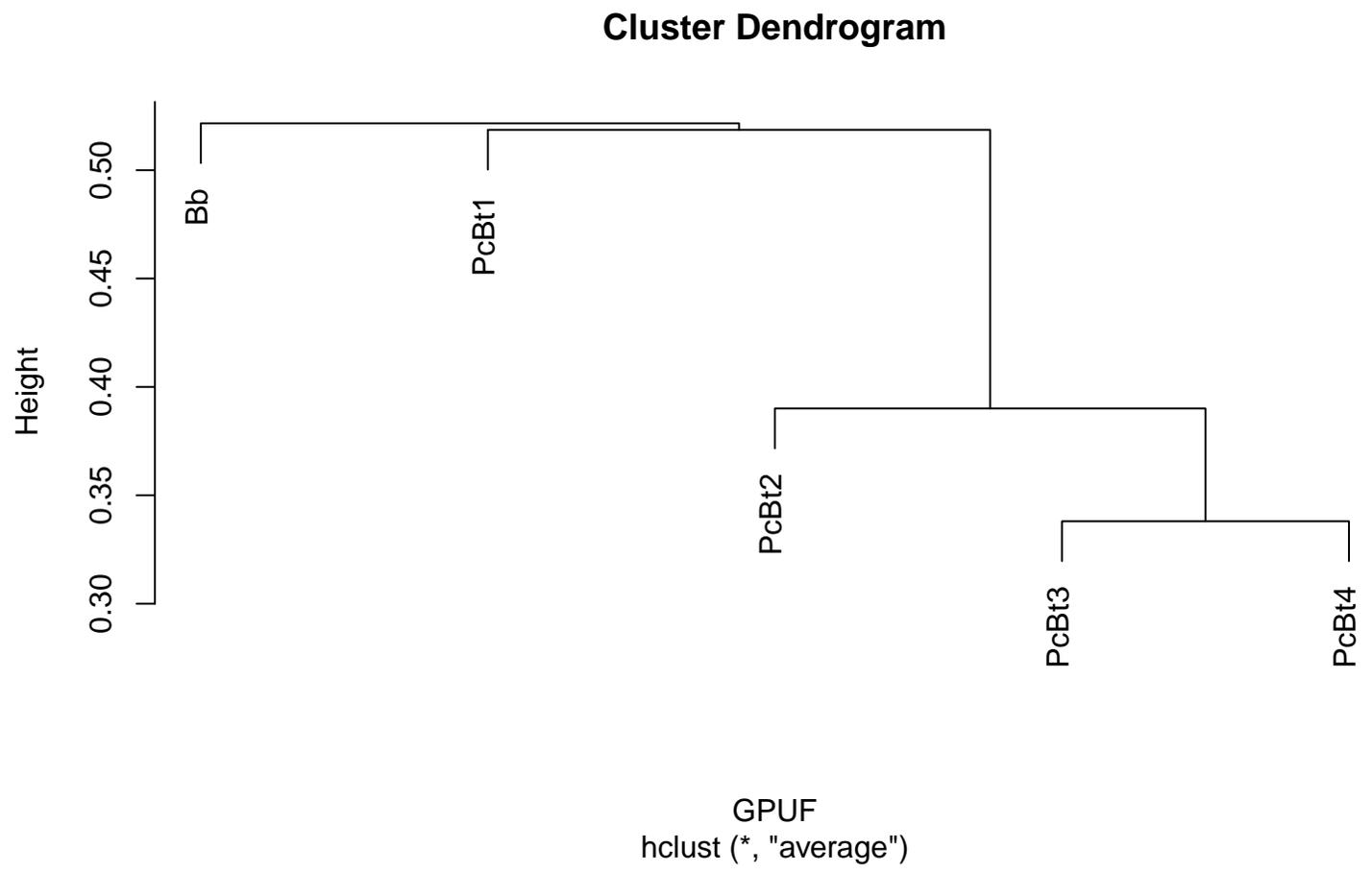
Figure S13: Hierarchical Clustering using UniFrac dissimilarity and UPGMA method of Group B sample group in the present study
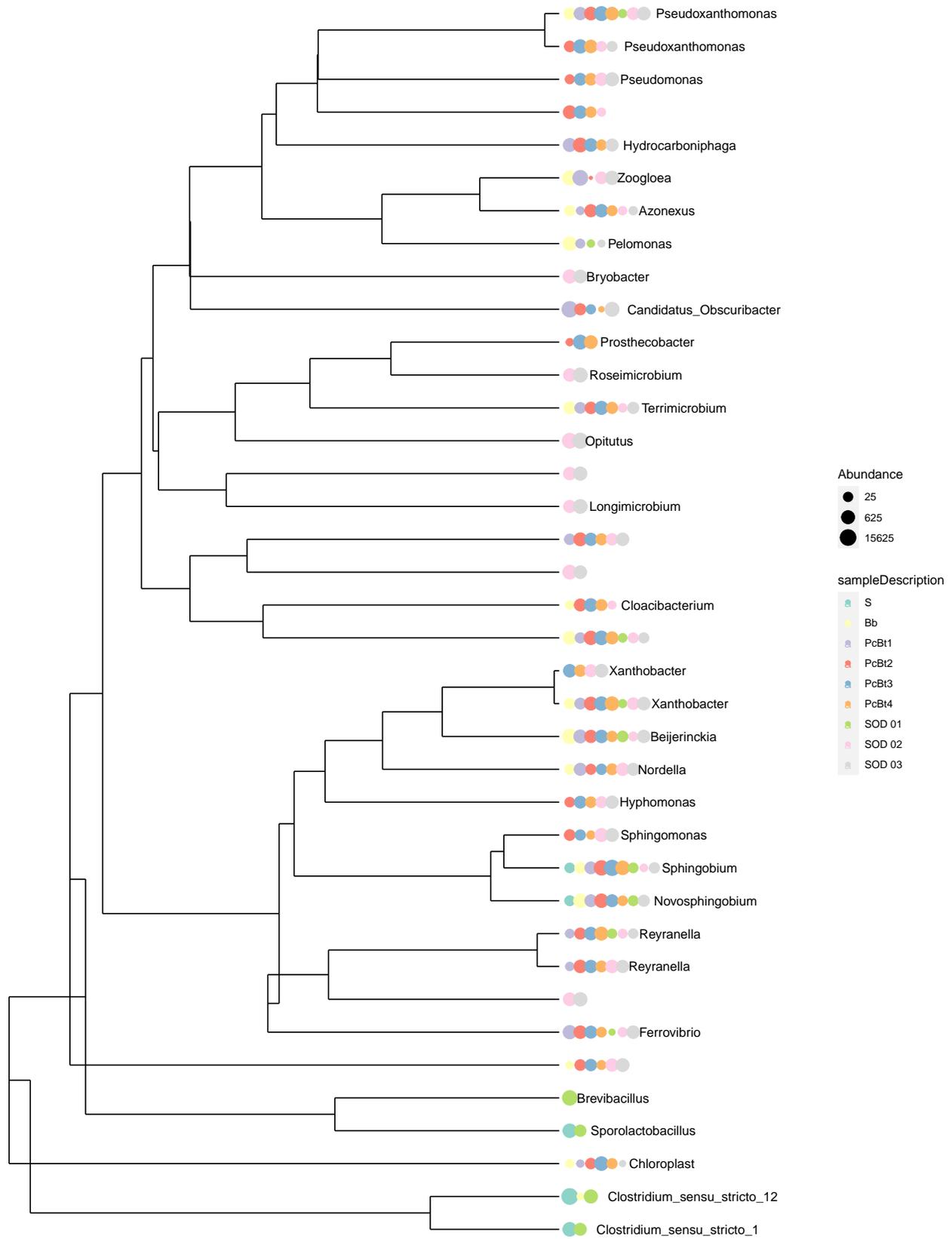
Figure S14: Phylogenetic tree using alignment and UPGMA method done in muscle64.
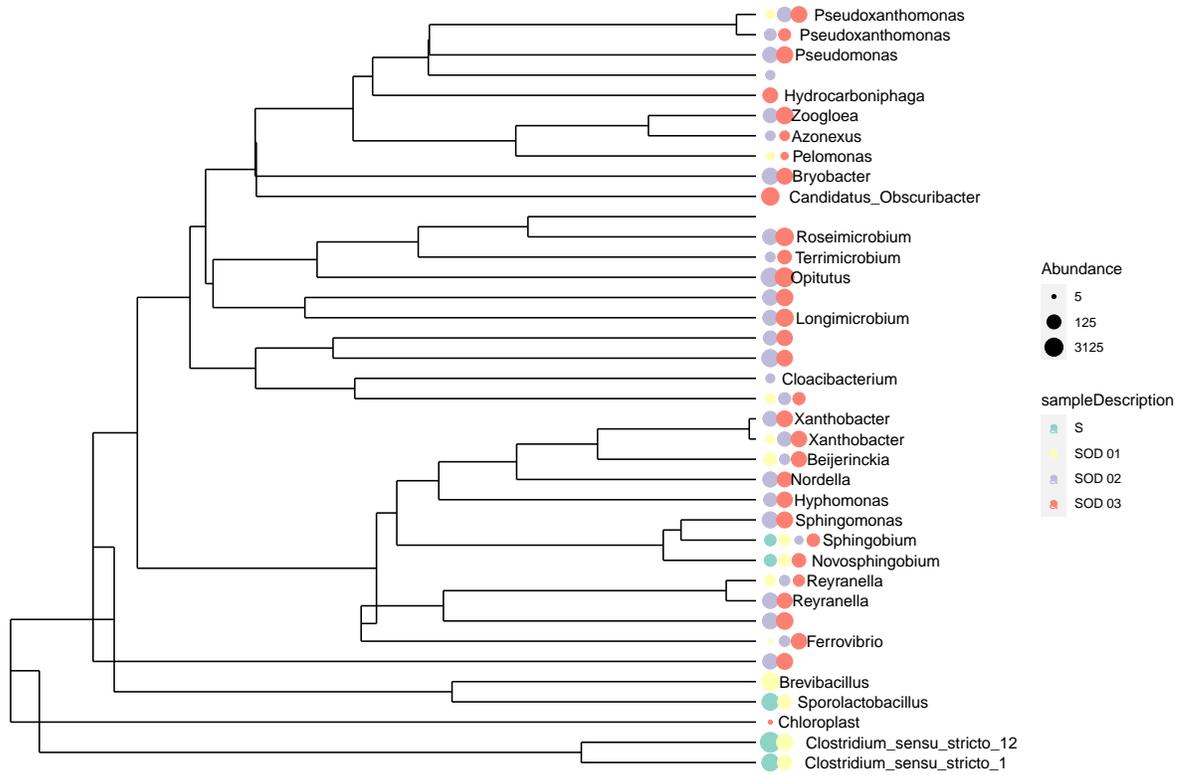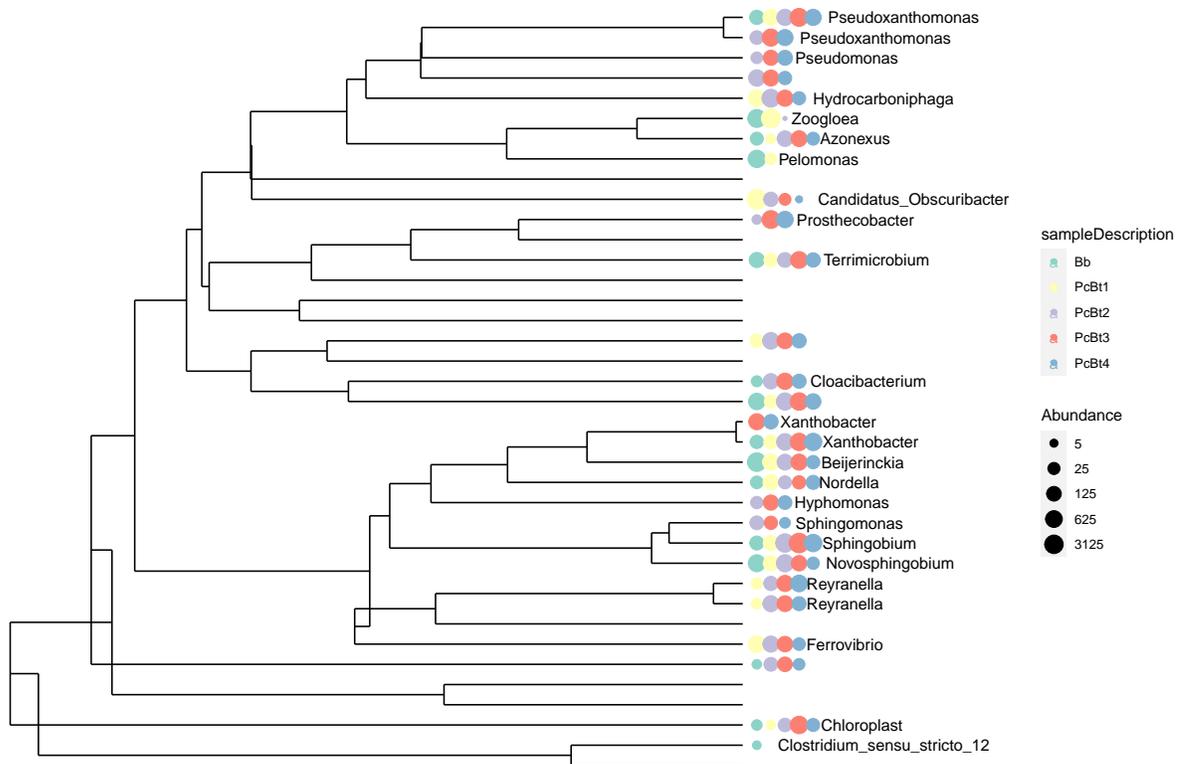
Figure S15: Phylogenetic tree using alignment and UPGMA method done in muscle64 of two sample groups in the present study
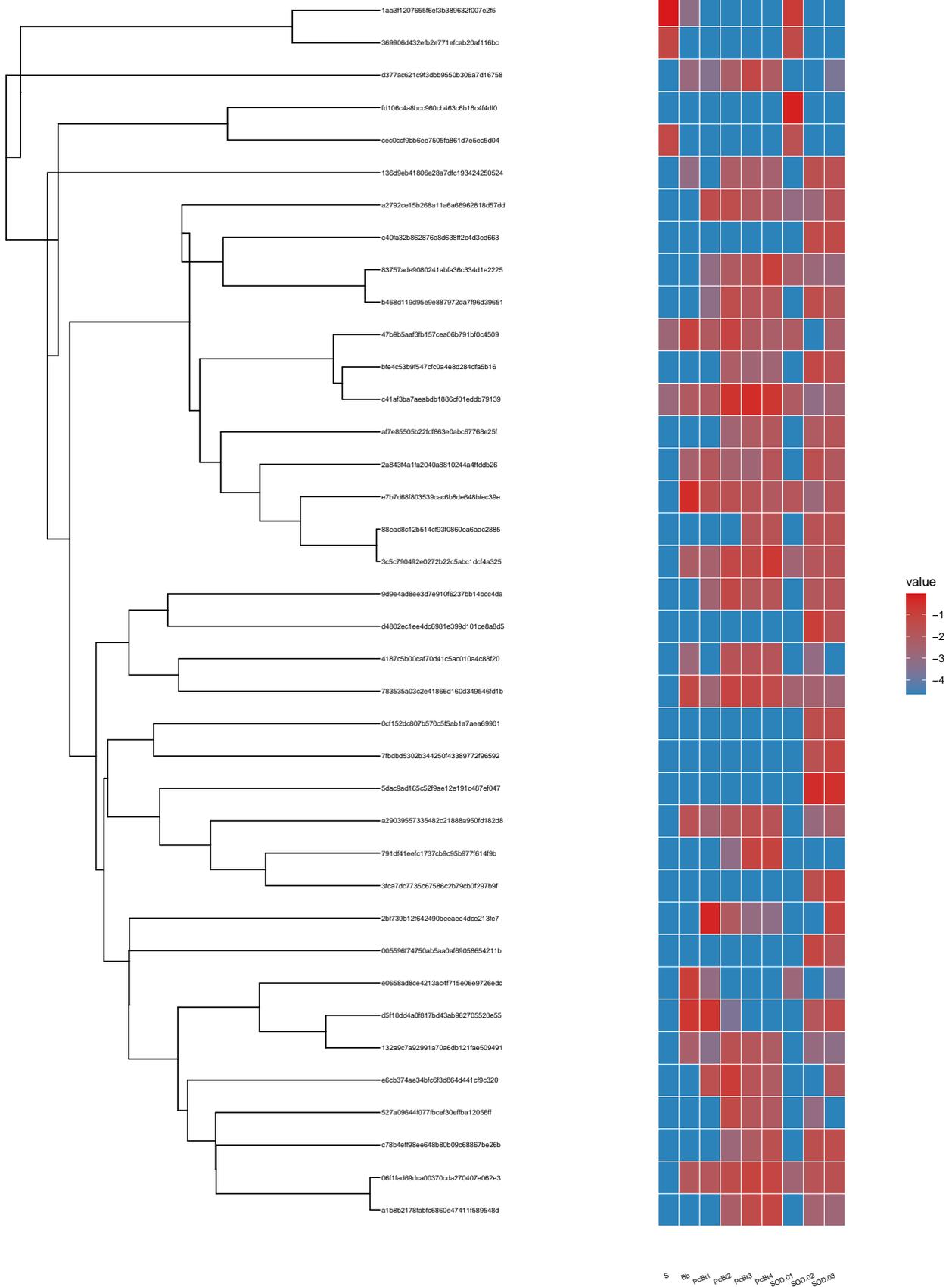
Figure S16: Combined heat map and phylogenetic tree of ASVs with => 1000 total reads (n = 38) from samples.
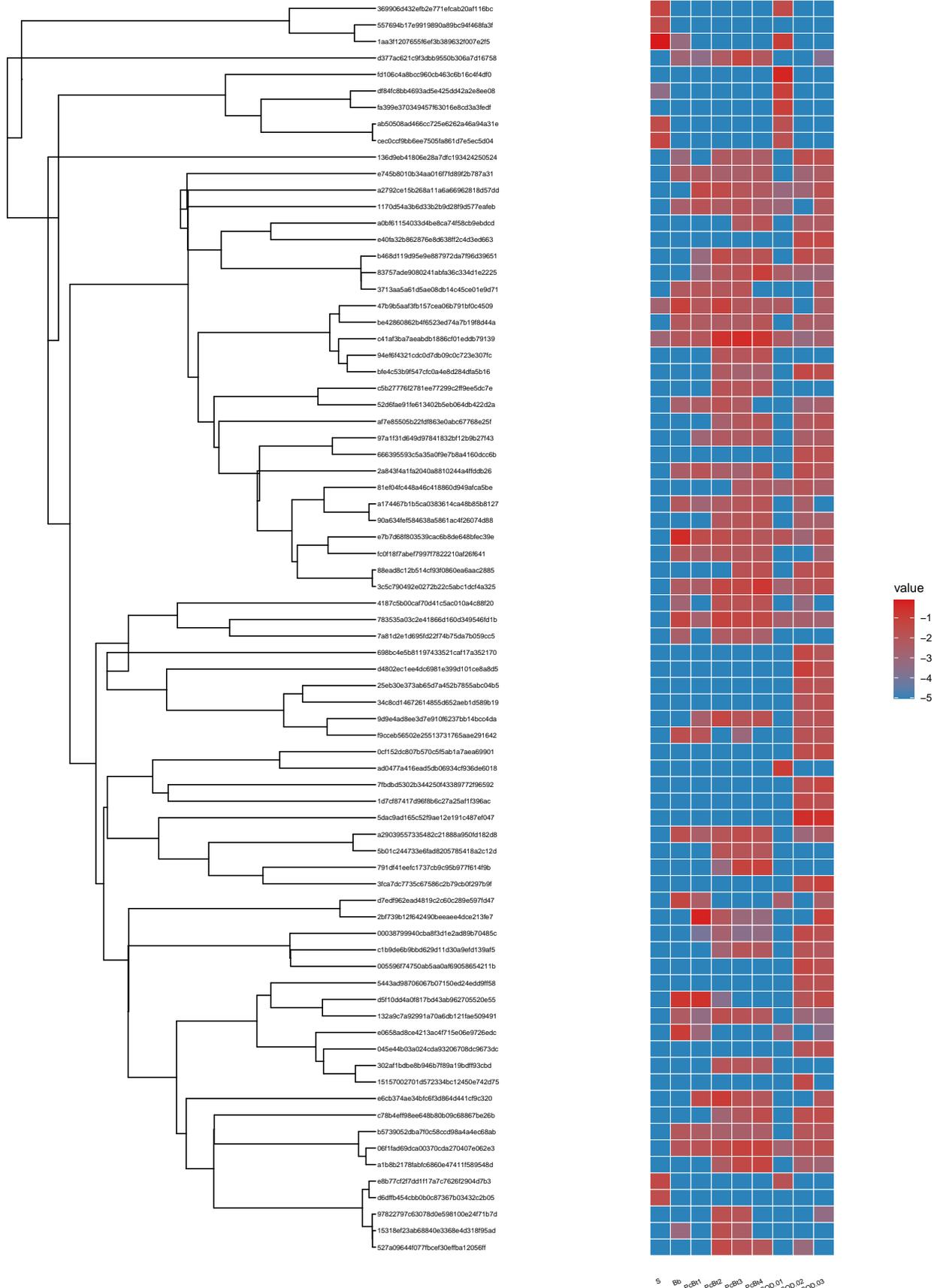
Figure S17: Combined heat map and phylogenetic tree of ASVs with => 500 total reads(n = 76) from samples.