Table S1. Biocrust samples collected in the surroundings of German potash tailings and their description.

Sample	Site	Type	pH	C/N	Amplicon Sequencing *			
					Bacteria	Cyanobactertia	Eukaryotes	Fungi
SY-2	Shreyahn	young	8.3	21.3			+	
OD-1	Oedesse	mature	8.3	35.9			+	
NN-4	Not named	mature	7.2	6.9	+	+	+	+
WT-1	Wietze	mature	8.1	12.9			+	
WT-2		mature	7.9	25.4	+	+	+	+
WT-3		mature	8.1	15.7	+	+	+	
WT-4		young	8.4	33.9	+	+	+	+
TT-1	Teutschenthal	mature	8.5	3.3	+	+		+
TT-3		mature	8.8	7.7	+	+		
TT-6		mature	8.7	7.6	+	+	+	+
TTF-2		young	6.1	13.1	+	+	+	+

*Samples which produced sufficient results by amplicon sequencing marked as "+".

Table S2. List of primers used in this study and their description.

Gene	Organism	Primers	Sequence	Primer Reference
16S	Bacteria	341F	CCTACGGGRSGCAGCAG	
		802R	TACNVGGGTATCTAATCC	
	Cyanobacteria	CYA_F	GGGGAATYTTCCGCAATGGG	[1]
		CYA_R	GACTACWGGGGTATCTAATCCCWTT	
ITS	Fungi	Fungi_F	CAHCGATGAAGAACGYRG	[2]
		Fungi_R	TCCTSCGCTTATTGATATGC	
18S	Eukaryotes	tarEuk_F	CCAGCASCYGCGGTAATTCC	[3]
		tarEUk_R	ACTTTCGTTCTTGATYRA	

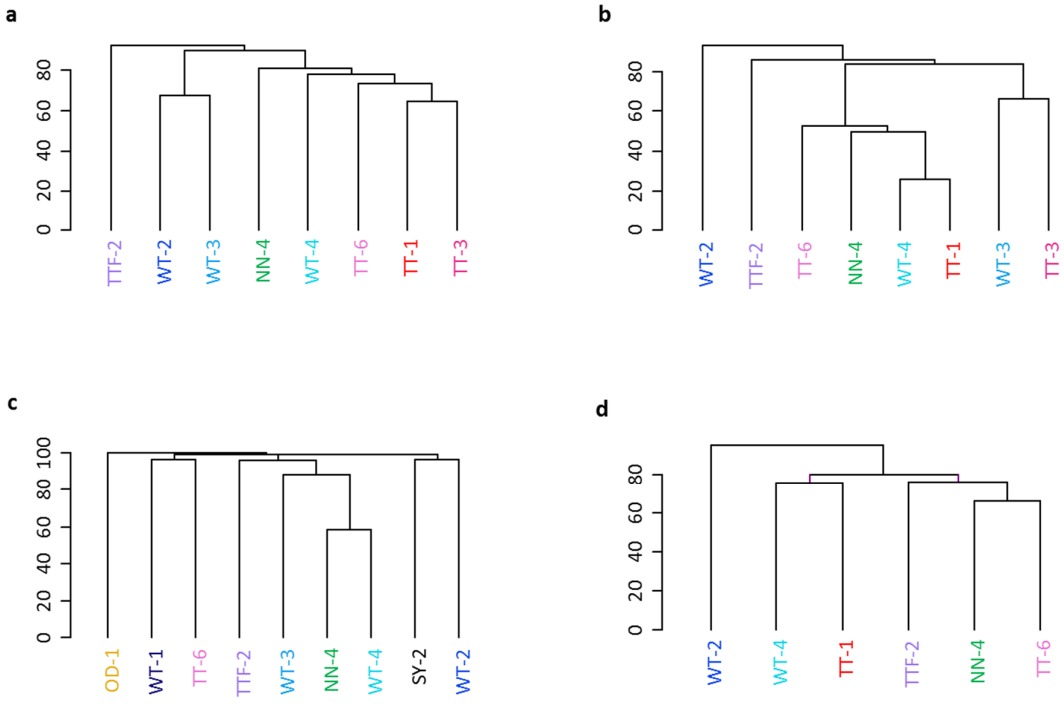

Figure S1. – Microbial community dissimilarities between the studied biocrust samples using SIMPROF analysis: a – bacteria, b – cyanobacteria, c – eukaryotes, d – fungi. SY, OD, WT, TT and NN correspond to Shreyahn, Oedesse, Wietze, Teutschenthal and not named site, respectively.

References

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