Table S1. Primer used for qPCR.

Group	Primer	Sequence (5′→3′)	Size (bp)	Reference
Bacteria	338F	ACTCCTACGGGAGGCAGCAG		
	518R	ATTACCGCGGCTGCTGG	196	Fierer et al. [1]
Archaea	Arch346aF	CGGGGYGCASCAGGCGCGAA		
	Arch934b	GTGCTCCCCCGCCAATTCCT	570	Hoshino et al. [2]
AOB	amoA-1F	GGGGTTTCTACTGGTGGT		
	amoA-2R	CCCCTCKGSAAAGCCTTCTTC	491	Rotthauwe et al. [3]
AOA	amoA19F	ATGGTCTGGCTWAGACG		Leininger et al. [4]
	CrenamoA616r48x	GCCATCCABCKRTANGTCCA	624	Schauss et al. [5]
nirK	nirK876	ATYGGCGG VAYGGCGA		
	nirK1040	GCCTCGAT CAGRTTRTGGT	160	Henry et al. [6]
nirS	nirSCd3aF	AACGYSAAGGARACSGG		
	nirSR3cd	GASTTCGGRTGSGTCTTSAYGAA	425	Kandeler et al. [7]

Table S2. Equations and efficiency of qPCR standard curves for samples processed in 2018 and 2019. The results for ammonia-oxidizing bacteria (AOB), ammonia-oxidizing archaea (AOA), nitrite reductase genes (*nirS* and *nirK*), *Bacteria*, and *Archaea* are indicated.

Gen	Group	Year	Equation	R^2	Efficiency (%)
16S rRNA	*Bacteria*	2018	$Ct = 40.12 - 3.66 \log_{10}$ (copy number)	0.999	87.00
		2019	$Ct = 39.76 - 3.67 \log_{10}$ (copy number)	0.999	87.29
16S rRNA	*Archaea*	2018	$Ct = 37.9 - 3.74 \log_{10}$ (copy number)	1	85.20
		2019	$Ct = 37.25 - 3.7 \log_{10}$ (copy number)	0.984	86.34
amoA	AOA	2018	$Ct = 35.04 - 3.86 \log_{10}$ (copy number)	0.999	81.69
		2019	$Ct = 36.82 - 3.78 \log_{10}$ (copy number)	1	84.05
amoA	AOB	2018	$Ct = 43.17 - 3.87 \log_{10}$ (copy number)	0.999	81.45
		2019	$Ct = 36.99 - 4.03 \log_{10}$ (copy number)	1	77.04
nirK	*nirK*	2018	$Ct = 35.8 - 3.56 \log_{10}$ (copy number)	0.999	90.88
		2019	$Ct = 39.68 - 3.67 \log_{10}$ (copy number)	1	86.68
nirS	*nirS*	2018	$Ct = 36.9 - 3.56 \log_{10}$ (copy number)	0.999	90.86
		2019	$Ct = 42.51 - 3.72 \log_{10}$ (copy number)	0.996	85.67

Table S3. Principal component analysis of bacteria genera showing the eigenvector, the eigenvalue, and the cumulative proportion the of the dataset variability explained by each of the seven principal components (PCs) extracted. Genera with loadings >|0.45| are bolded.

	PC1	**PC2**	**PC3**	**PC4**	**PC5**	**PC6**	**PC7**
Eigenvalue	5.93	3.70	2.57	2.10	1.73	1.56	1.47
Proportion	0.22	0.14	0.10	0.08	0.06	0.06	0.05
Cum. proportion	0.22	0.36	0.45	0.53	0.59	0.65	0.71
Eigenvector	Component correlation scores						
Abditibacterium	-0.07	**0.68**	0.19	0.30	-0.05	-0.22	-0.24
Azoarcus	0.30	**-0.46**	0.24	**0.51**	-0.22	-0.24	0.29
Brevifollis	**-0.58**	0.12	0.18	**-0.52**	0.19	-0.20	0.02
Brevundimonas	0.44	0.13	0.06	0.03	0.21	**0.46**	-0.30
Chitinispirillum	**-0.53**	-0.13	-0.27	-0.15	0.25	0.21	0.28
Curvibacter	**0.65**	0.40	0.05	-0.09	0.24	0.27	-0.17
Duganella	**0.70**	0.35	-0.18	-0.06	-0.02	-0.17	0.27
Erythrobacter	**0.70**	-0.35	-0.12	-0.19	0.06	-0.39	0.19
Flaviaesturariibacter	0.05	0.39	-0.44	0.36	0.17	-0.11	-0.36
Flavilitoribacter	**0.61**	0.07	-0.01	-0.39	-0.35	0.05	-0.11
Geminisphaera	-0.14	-0.18	**0.63**	-0.17	0.29	-0.36	-0.11
Gemmata	0.43	-0.16	**0.47**	0.38	0.15	0.07	-0.14
Gp17	0.05	**-0.69**	-0.26	-0.29	0.00	0.13	-0.44
Kineosporia	0.30	0.11	0.27	-0.35	**-0.59**	0.17	0.11
Lacunisphaera	**-0.49**	0.22	-0.25	0.13	0.19	0.34	0.35
Litorilinea	-0.34	**-0.60**	0.28	0,26	0.19	0.24	-0.04
Longimicrobium	**0.49**	-0.24	-0.18	-0,32	**0.54**	-0.15	0.11
Marmoricola	0.08	0.21	-0.17	-0,39	-0.04	0.34	0.36
Massilia	**0.77**	**0.53**	-0.05	0,10	0.13	0.11	-0.02
Methylobacterium	0.01	0.37	**0.67**	0,17	0.07	0.19	0.37
Nocardioides	**-0.57**	0.22	-0.44	0,30	-0.05	0.13	0.16
Novosphingobium	**0.78**	0.15	-0.05	-0,14	0.05	0.05	0.04
Parviterribacter	**0.48**	**-0.58**	0.21	0,13	-0.13	0.26	0.28
Phenylobacterium	**0.53**	-0.14	-0.07	0,37	-0.08	0.23	-0.06
Sediminibacterium	-0.40	**0.54**	0.18	-0,08	-0.45	-0.17	-0.05
Stella	0.39	-0.07	**-0.58**	0,31	-0.03	-0.39	0.27
Thermanaerothrix	-0.13	**-0.46**	-0.33	0,03	**-0.50**	0.12	-0.21

Table S4. Principal component analysis of fungal genera showing the eigenvector, the eigenvalue, and the cumulative proportion the of the dataset variability explained by each of the eight principal components (PCs) extracted. Genera with loadings >|0.45| are bolded.

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
Eigenvalue	4.10	3.37	2.76	2.33	2.27	1.86	1.56	1.38
Proportion	0.15	0.12	0.10	0.09	0.08	0.07	0.06	0.05
Cum. proportion	0.15	0.28	0.38	0.47	0.55	0.62	0.68	0.73
Eigenvector	Component correlation scores							
Alternaria	**0.74**	0.33	0.08	0.05	0.20	-0.20	-0.06	0.16
Atradidymella	0.20	0.10	-0.13	0.42	-0.37	-0.07	0.28	0.38
Auricularia	-0.26	**0.58**	-0.27	-0.05	0.24	-0.32	-0.15	0.12
Corynascus	-0.31	**0.47**	**-0.48**	-0.01	0.00	-0.17	-0.13	-0.09
Davidiella	**0.75**	-0.10	0.30	0.17	0.32	-0.08	0.13	0.03
Dokmaia	**-0.54**	0.29	**0.53**	0.10	0.09	0.00	-0.01	0.26
Edenia	0.32	**-0.51**	-0.14	-0.27	**-0.47**	0.04	-0.01	-0.10
Elaphocordyceps	-0.18	**-0.54**	0.10	0.14	0.07	0.34	0.27	-0.26
Exophiala	0.22	**0.50**	-0.21	0.15	0.20	**0.59**	-0.09	-0.23
Haematonectria	**-0.51**	0.01	0.43	-0.04	-0.04	-0.12	0.34	0.24
Lecythophora	0.40	-0.05	**0.50**	-0.39	-0.19	0.04	-0.27	0.19
Microdochium	0.40	0.14	-0.18	**0.46**	-0.16	-0.24	-0.26	0.00
Mycena	-0.21	-0.40	**-0.57**	-0.05	0.12	-0.36	0.36	-0.03
Myrmecridium	0.00	**-0.52**	-0.18	0.26	0.19	0.23	**-0.60**	0.12
Periconia	0.31	-0.18	-0.22	-0.20	-0.04	-0.19	0.24	**-0.56**
Phaeosphaeria	-0.18	0.28	-0.23	**-0.72**	-0.02	-0.14	-0.01	0.20
Phialocephala	0.03	**0.49**	-0.02	0.15	**0.58**	0.19	-0.08	-0.37
Phialophora	**-0.48**	-0.16	0.25	0.45	0.35	-0.38	0.18	-0.13
Phoma	0.43	**-0.49**	-0.07	-0.07	0.30	-0.08	0.19	0.14
Podospora	**0.85**	0.24	-0.02	0.13	0.12	-0.02	0.21	0.26
Powellomyces	-0.09	-0.25	-0.05	**-0.63**	0.25	0.19	-0.20	0.08
Preussia	-0.19	-0.42	-0.41	-0.01	0.35	0.32	-0.05	0.39
Pseudallescheria	0.16	**0.59**	0.22	-0.43	-0.22	0.25	0.36	-0.15
Rhizopycnis	0.26	-0.25	**0.76**	-0.07	0.19	-0.11	-0.13	-0.18
Sclerostagonospora	0.19	-0.01	-0.15	0.13	**-0.65**	-0.28	-0.31	-0.16
Spizellomyces	**-0.48**	-0.03	0.42	0.16	-0.31	-0.07	-0.28	-0.16
Tricladium	-0.10	0.10	-0.09	0.35	-0.45	**0.64**	0.25	0.12

Table S5. Matrix of Pearson's correlation coefficients among microbial indicator groups for each taxon responsive to treatments (Bacteria PC1 and PC3, Fungi PC1) and soil properties of nitrate (NO_3^-), ammonium (NH_4^+), and available P (Pa).

	BPC1	BPC3	FPC1	NH_4^+	NO_3^-	Pa
BPC1†	1					
BPC3	0	1				
FPC1	**0,53**	−0,35	1			
NH_4^+	−0,24	0,07	**−0,41**	1		
NO_3^-	**−0,41**	0,24	**−0,51**	**0,68**	1	
Pa	0,03	−0,14	−0,07	−0,13	−0,15	1

†BPC1, BPC3, Bacteria PC1 and PC3, respectively; FPC1, Fungi PC1. Bolded correlation coefficients indicate statistical significance at $\alpha = 0.05$.

Table S6. Matrix of Pearson's correlation coefficients among the abundance of nitrogen cycle genes (AOA, AOB, *nirS,* and *nirK*) and soil properties of nitrate (NO_3^-), ammonium (NH_4^+), and available P (Pa).

	AOB	AOA	nirS	nirK	NH_4^+	NO_3^-	Pa
AOB	1,00						
AOA	0,31	1,00					
nirS	**−0,75**	−0,29	1,00				
nirK	**0,91**	0,40	**−0,84**	1,00			
NH_4^+	**0,86**	0,39	**−0,78**	**0,90**	1,00		
NO_3^-	**0,41**	**0,50**	**−0,51**	**0,53**	**0,68**	1,00	
Pa	−0,07	−0,10	0,39	−0,13	−0,13	−0,15	1,00

Bolded correlation coefficients indicate statistical significance at $\alpha = 0.05$.

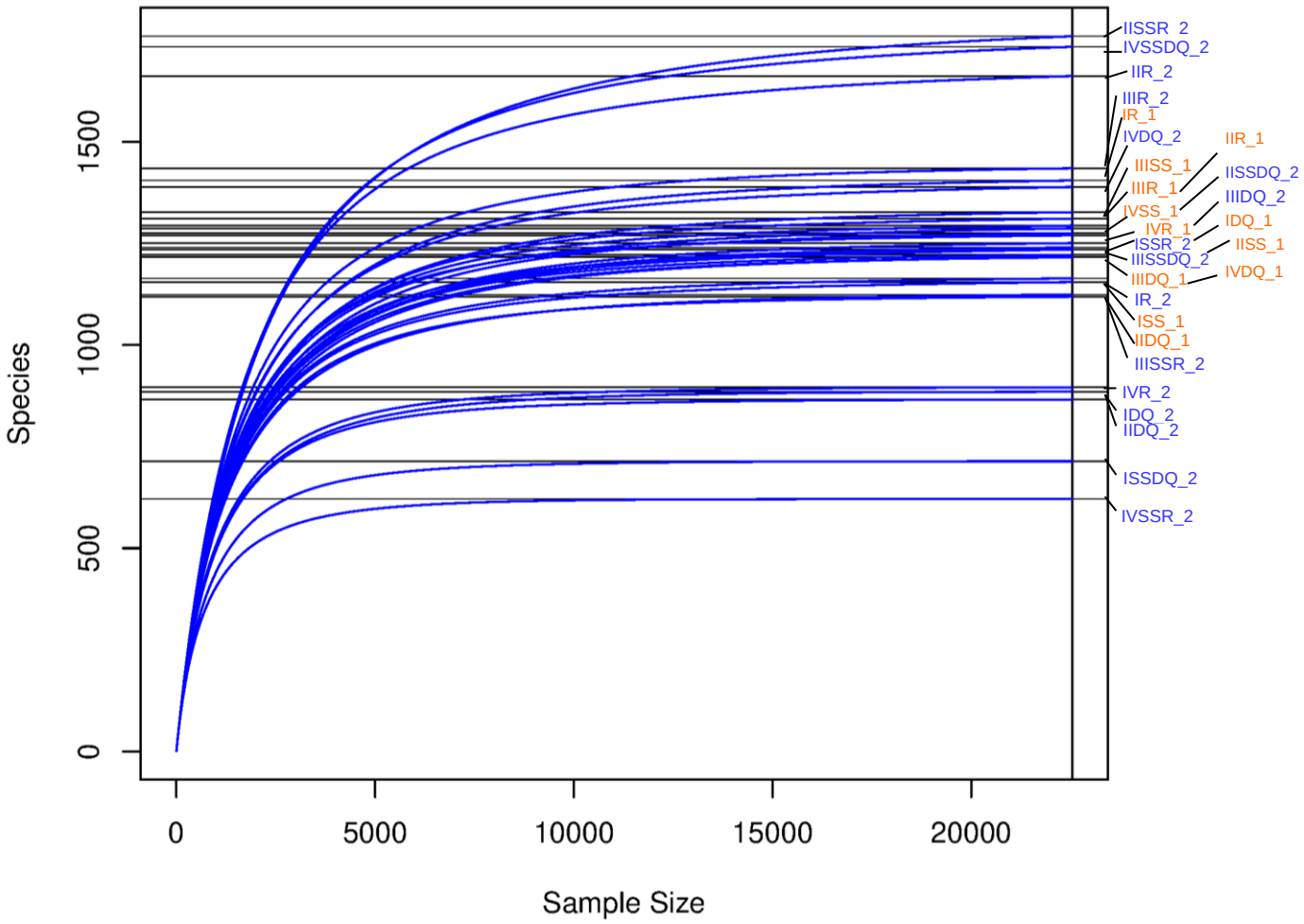

Figure S1. Rarefaction curves of the different samples analyzed through barcoded amplicon-sequencing. The number of amplicon sequence variants ("species") of Bacteria is indicated for an increasing sampling effort ("sample size"). The letters DQ indicate chemical suppression, letters R rolling, and letters SS no suppression. The Roman numerals (I to IV) identify the replicates of each treatment and the 2018 samples are indicated in orange and the 2019 samples in blue.

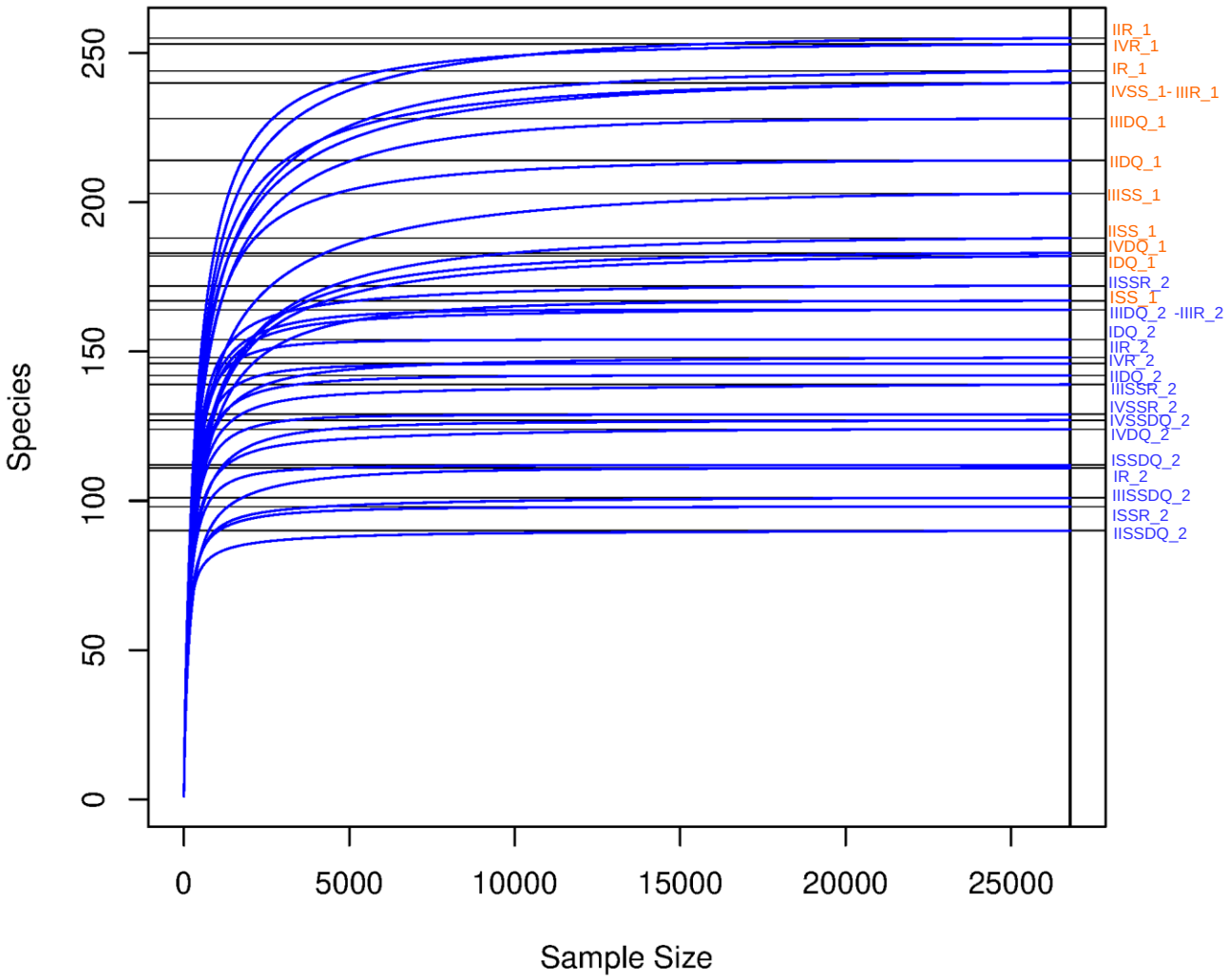

Figure S2. Rarefaction curves of the different samples analyzed through barcoded amplicon-sequencing. The number of amplicon sequence variants ("species") of Fungi is indicated for an increasing sampling effort ("sample size"). The letters DQ indicate chemical suppression, letters R rolling, and letters SS no suppression. The Roman numerals (I to IV) identify the replicates of each treatment and the 2018 samples are indicated in orange and the 2019 samples in blue.

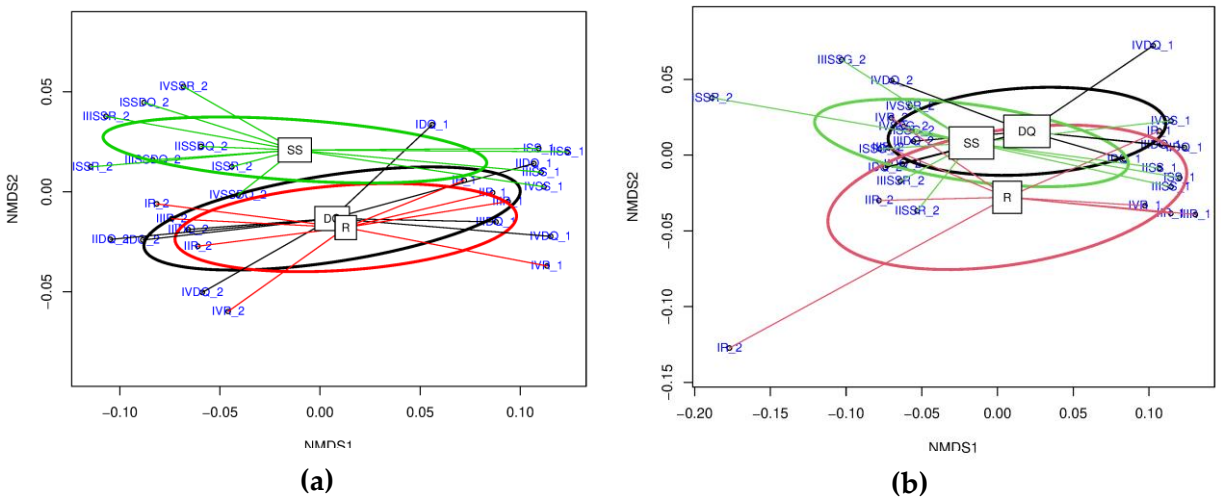

Figure S3. Non-metric multidimensional scaling of Bacteria (Stress = 0.08) (**a**) and Fungi (Stress = 0.105) (**b**) using generalized UniFrac distance. The letters DQ indicate chemical suppression, letters R rolling, and letters SS no suppression, Roman numerals (I to IV) identify the replicates and the number 1 indicating the 2018 samples and the number 2 indicating the 2019 samples. Centroids are indicated by boxes. The standard error of DQ, R and SS are indicated by black, red, and green ellipses, respectively.

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