Supplementary methods

Denaturing Gradient Gel Electrophoresis (DGGE)

Chromosomal DNA of the soil samples was extracted using the PowerSoil DNA Isolation Kit (MoBio) following the protocol of the manufacturer. For DGGE, ~370 bp-long fragments were amplified using primers 31F and 341R (5'-CTGCTGCCTCCCGTAGG-3', with a GC clamp added at its 5' end (1), and analyzed as previously reported (2). DGGE band patterns were compared using the program package GelCompar II (Applied Maths NV, Sint-Martens-Latem, Belgium). For subsequent sequencing, DNA bands were excised and eluted in 25 µl of 10 mM Tris-HCl buffer (pH 8.0) for 1 hour at 37°C, reamplified using the corresponding primers without GC clamp and sequenced. Some DGGE bands contained multiple 16S rRNA gene sequences which were first separated by cloning (see above), then 8 randomly selected clones with different inserts were sequenced.

Reference List

1. **Muyzer G, Dewaal EC, Uitterlinden AG**. 1993. Profiling of Complex Microbial-Populations by Denaturing Gradient Gel-Electrophoresis Analysis of Polymerase Chain Reaction-Amplified Genes-Coding for 16S Ribosomal-Rna. Appl. Environ. Microbiol. **59**:695-700.

2. **Zul D, Denzel S, Kotz A, Overmann J**. 2007. Effects of plant biomass, plant diversity, and water content on bacterial communities in soil lysimeters: Implications for the determinants of bacterial diversity. Appl. Environ. Microbiol. **73**:6916-6929.

Supplementary Table 1. General information on the three regions and mean (± standard deviation) of soil and site parameters for all grassland and forest plots in each region. Naming corresponds to all grassland plots of Schwäbische Alb (AEG), Hainich (HEG), Schorfheide-Chorin (SEG) or all forest plots of Schwäbische Alb (AEW), Hainich (HEW) and Schorfheide-Chorin (SEW).

	Alb		Hainich		Schorfheide	
Latitude	48° 20’ 60.0’’– 48° 32’ 3.7’’ N		50° 56’ 14.5’’ – 51° 22’ 43.4’’ N		52° 47’ 24.8’’ – 53° 13’ 26.0’’ N	
Longitude	9° 12’ 13.0’’ – 9° 34’ 48.9’’ E		10° 10’ 24.0’’ – 10° 46’ 45.0’’ E		13° 23’ 27’’ – 14° 8’ 52.7’’ E	
Altitude [m above sea level]	460 - 860		300 - 400		10 -140	
Mean annual temperature [°C]	6.5 - 8.0		6.0 - 7.5		8.0 - 8.4	
Mean annual precipitation [mm]	940 - 960		750 - 800		520 - 600	
Soil type (predominantly)	Leptosol, Cambisol		Stagnosol, Luvisol		Histosol, Cambisol	
	AEG	AEW	HEG	HEW	SEG	SEW
pH	**6.49** (±0.48)	**4.96** (±0.74)	**7.01** (±0.18)	**5.15** (±1.12)	**6.85** (±0.58)	**3.56** (±0.13)
Corg [g kg^{-1}]	**67** (±15)	**69** (±18)	**50.3** (±22)	**53** (±15)	**150** (±71)	**25** (±6)
Nitrogen [g kg^{-1}]	**6.30** (± 1.40)	**4.87** (±1.11)	**4.73** (±1.83)	**3.76** (±1.27)	**14.02** (±5.39)	**1.42** (±0.32)
Phosphorus [mg kg^{-1}]	**1158** (±391)	**687** (±229)	**1113** (±395)	**553** (±201)	**1046** (±427)	**252** (±93)
Corg/Nitrogen-ratio	**10.59** (±0.67)	**14.12** (±1.30)	**10.36** (±1.01)	**14.35** (±1.29)	**10.48** (±0.95)	**17.72** (±1.47)
Soil moisture [% vol]	**52** (±3)	**47** (±4)	**45** (±5)	**44** (±4)	**44** (±19)	**30** (±3)
Soil temperature [°C]	**6.87** (±0.82)	**4.53** (±0.45)	**9.51** (±2.99)	**6.16** (±1.54)	**14.05** (±0.64)	**7.15** (±0.76)
Soil respiration [µmol CO_2 m^{-2} s^{-1}]	**3.86** (±0.95)	**1.44** (±0.15)	**5.53** (±2.98)	**1.65** (±0.32)	**12.11** (±3.12)	**1.93** (±0.61)
Amoebae [10^4 g^{-1}]	**23** (±22)	**5.53** (±5.07)	**47** (±57)	**0.91** (±0.50)	**10** (±15)	**0.59** (±0.41)

Suppl. Table 1 continued

Flagellates [10^4 g^{-1}]	**2.22** (±2.16)	**5.51** (±2.54)	**3.34** (±1.46)	**1.43** (±0.78)	**2.16** (± 2.33)	**1.62** (±0.50)
Ciliates [10^2 g^{-1}]	**1.97** (±3.01)	**0.23** (±0.29)	**0.54** (±0.75)	**0.40** (±0.41)	**5.12** (± 0.78)	**0.44** (±1.68)
N° of vascular plant species	**32** (±13)	**34** (±18.89)	**20** (±9)	**32** (±15)	**16** (± 3)	**14** (±10)
Land use intensity	**2.64** (±1.96)	**40** (±17)	**3.67** (±1.58)	**42** (±20)	**2.70** (± 2.16)	**42** (±17)
Ammonium [µmol kg^{-1}]	**7.92** (±6.22)	**65** (±39)	**8.88** (±3.91)	**33** (±21)	**9.44** (±7.38)	**154** (±131)
Nitrate [µmol kg^{-1}]	**637** (±549)	**421** (±271)	**595** (±241)	**558** (±344)	**807** (±374)	**276** (±206)

Supplementary Table 2. GenBank a*ccession numbers* of the 2031 acidobacterial 16S rRNA gene sequences of pooled samples of all grassland plots of Schwäbische Alb (AEG), Hainich (HEG), Schorfheide-Chorin (SEG) or all forest plots of Schwäbische Alb (AEW), Hainich (HEW) and Schorfheide-Chorin (SEW) and sequenced DGGE bands.

	accession numbers
AEG	HQ597043 - HQ597396
HEG	HQ597397 - HQ597542
	HQ597544 - HQ597731
SEG	HQ597733 - HQ597739
	HQ597741
	HQ597743 - HQ597754
	HQ597756 - HQ597759
	HQ597761 - HQ597762
	HQ597764 - HQ597768
	HQ597771 - HQ597774
	HQ597776 - HQ597786
	HQ597788 - HQ597893
	HQ597796 - HQ597817
	HQ597819 - HQ597823
	HQ597825 - HQ597826
	HQ597829 - HQ597835
	HQ597837 - HQ597846
	HQ597848 - HQ597850
	HQ597852 - HQ597859
	HQ597864 - HQ597868
	HQ597870 - HQ597871
	HQ597873 - HQ597874
	HQ597876 - HQ597880
	HQ597882
	HQ597884 - HQ597886
	HQ597888 - HQ597889
	HQ597893 - HQ597900
	HQ597902 - HQ597904
	HQ597906 - HQ597917
	HQ597920 - HQ597923
	HQ597925 - HQ597926
	HQ597930
	HQ597932
	HQ597934 - HQ597936
	HQ597939 - HQ597942
	HQ597944 - HQ597950
	HQ597952 - HQ597964
	HQ597967
	HQ597969
	HQ597972
	HQ597974
	HQ597977
	HQ597979 - HQ597980
	HQ597982
	HQ597984
	HQ597986
	HQ597988
	HQ597990 - HQ597991
	HQ597993
	HQ597996 - HQ597997
	HQ729774 - HQ729915
AEW	HQ598095 - HQ598414
HEW	HQ598415 - HQ598744
SEW	HQ598745 - HQ598871
	HQ598873 - HQ599092
DGGE	HQ597998 - HQ598094

Supplementary Table 3. Number of clones (OTUs), coverage and diversity indices of clone libraries at the 3% dissimilarity level. Pooled samples of all grassland plots of Schwäbische Alb (AEG), Hainich (HEG), Schorfheide-Chorin (SEG) or all forest plots of Schwäbische Alb (AEW), Hainich (HEW) and Schorfheide-Chorin (SEW) have been used to generate clone libraries.

	AEG	**HEG**	**SEG**	**AEW**	**HEW**	**SEW**	**all**
Clones	355 (126)	334 (121)	345 (192)	320 (124)	330 (142)	347 (75)	**2031 (414)**
Gp1	6 (4)	4 (3)	16 (10)	83 (34)	106 (34)	295(48)	**510 (66)**
Gp3	13 (7)	8 (5)	49 (35)	36 (17)	24 (14)	35 (16)	**165 (66)**
Gp4	27 (13)	66 (27)	31 (20)	18 (8)	19 (12)	-	**161 (49)**
Gp5	60 (8)	35 (7)	10 (6)	43 (7)	41 (10)	-	**189 (16)**
Gp6	217 (82)	208 (70)	204 (99)	132 (51)	126 (60)	5 (5)	**892 (172)**
Gp9	-	-	2 (1)	-	-	-	**2 (1)**
Gp11	3 (2)	3 (2)	12 (6)	1 (1)	1 (1)	-	**20 (8)**
Gp13	-	-	-	1 (1)	5 (4)	8 (3)	**14 (6)**
Gp15	-	-	1 (1)	-	2 (2)	3 (2)	**6 (4)**
Gp17	25 (9)	9 (6)	20 (14)	6 (5)	6 (5)	1 (1)	**67 (25)**
Gp18	4 (1)	1 (1)	-	-	-	-	**5 (1)**
Coverage (%)	90.1	88.0	67.2	87.2	85.2	94.2	
Shannon	4.3	4.3	4.85	4.2	4.4	3.6	
Faith's PD [1]	2.95	2.85	4.78	3.07	3.48	1.86	
MPD [2]	0.119	0.123	0.122	0.128	0.129	0.086	
MNTD [3]	0.030	0.029	0.033	0.032	0.031	0.028	
NRI [4]	2.53	2.74	4.50	1.59	1.91	5.66	
NTI [4]	3.78	4.99	2.84	3.36	3.91	3.98	
Simpson [5]	0.98	0.98	0.99	0.98	0.98	0.96	
pD [6]	0.059	0.061	0.061	0.064	0.064	0.043	

[1] Faith's index of phylogenetic diversity

[2] Mean pairwise distance between all species in a community

[3] Mean nearest taxon distance – mean distance separating each species in the community from its closest relative

[4] Net Relatedness Index/Nearest Taxon Index – measures of phylogenetic community structure

[5] Simpson's diversity – probability that two individuals from the community belong to different OTUs

[6] Phylogenetic Diversity – expected phylogenetic distance between to randomly selcted individuals from the community

Supplementary Table 4. Number of clones of OTUs with more than 20 sequences. *Acidobacteria* subgroup and dominant *in silico* T-RF of the respective OTU is given. Pooled samples of all grassland plots of Schwäbische Alb (AEG), Hainich (HEG), Schorfheide-Chorin (SEG) or all forest plots of Schwäbische Alb (AEW), Hainich (HEW) and Schorfheide-Chorin (SEW) have been used to generate clone libraries.

	OTU3 Gp5	OTU7 Gp1	OTU31 Gp5	OTU114 Gp1	OTU9 Gp6	OTU115 Gp6	OTU6 Gp6	OTU94 Gp1	OTU32 Gp1	OTU119 Gp1	OTU92 Gp6	OTU2 Gp1	OTU15 Gp5	OTU45 Gp6	OTU99 Gp6
in silico T-RF (bp)	135	88	135	258/260	194	193	167, 194	88	258	258	194	143	137	285	210
AEG	23 (6.5%)		15 (4.2%)		9 (2.5%)	9 (2.5%)	16 (4.5%)				7 (2.0%)		7 (2.0%)	4 (1.1%)	7 (2.0%)
HEG	9 (2.7%)		19 (5.7%)			16 (4.8%)	5 (1.5%)				7 (2.1%)			8 (2.4%)	2 (0.6%)
SEG	1 (0.3%)	6 (1.7%)	4 (1.2%)			9 (2.6%)	1 (0.3%)				7 (2.0%)	2 (0.6%)		7 (2.0%)	10 (2.9%)
AEW	23 (7.2%)	13 (4.1%)	6 (1.9%)	1 (0.3%)	16 (4.1%)	1 (0.3)	6 (1.9%)	2 (0.6%)	3 (0.9%)	1 (0.3%)	3 (0.9%)	6 (1.9%)	9 (2.8%)	3 (0.9%)	1 (0.35)
HEW	16 (4.8%)	19 (5.8%)	6 (1.8%)		12 (3.6%)	1 (0.3%)	4 (1.2%)	4 (1.2%)	5 (1.5%)	7 (2.1%)	2 (0.6%)	4 (1.2%)	7 (2.1%)		2 (0.6%)
SEW		24 (6.9%)		41 (11.8%)	1 (0.3%)			25 (7.2%)	19 (5.5%)	18 (5.2%)		11 (3.2%)			
Total	**72 (3.5%)**	**62 (3.1%)**	**50 (2.5%)**	**42 (2.1%)**	**38 (1.9%)**	**36 (1.8%)**	**32 (1.6%)**	**31 (1.5%)**	**27 (1.3%)**	**26 (1.3%)**	**26 (1.3%)**	**23 (1.1%)**	**23 (1.1%)**	**22 (1.1%)**	**22 (1.1%)**

Supplementary Table 5. Collinearity among soil and site parameters as determined by Spearman's rank correlation coefficient rho. Significantly correlated parameters show Spearman's rank correlation coefficient rho > 0.6 and > -0.6 in bold. Abbreviations: pH – pH, Corg – organic carbon, N – nitrogen, CN – Corg/Nitrogen-ratio, SM – soil moisture, ST – soil temperature, SR – soil respiration, Am – abundance of Amoebae, Fl – abundance of Flagellates, Ci – abundance of Ciliates, VP- number of vascular plant species, LUI – land use intensity, G – grassland, F – forest, NH4 - ammonium, NO3 - nitrate, P – phosphorus.

		pH	Corg	N	CN	SM	ST	SR	Am	Fl	Ci	VP	LUI		NH4	NO3	P
													G	F			
pH		1															
Corg		0.556	1														
N		**0.686**	**0.957**	1													
CN		**-0.840**	-0.467	**-0.667**	1												
SM		0.266	0.371	0.453	-0.447	1											
ST		0.497	0.239	0.367	-0.449	-0.109	1										
SR		**0.669**	0.481	**0.631**	**-0.670**	0.158	**0.801**	1									
Am		0.539	0.438	0.577	**-0.661**	0.517	0.176	0.475	1								
Fl		0.088	0.206	0.166	-0.084	0.252	-0.229	-0.097	0.479	1							
Ci		0.373	0.492	0.560	-0.397	0.198	0.417	0.550	0.260	-0.172	1						
VP		-0.051	0.029	-0.034	0.142	0.179	-0.351	-0.215	0.005	0.145	-0.143	1					
LUI	G	-0.087	0.035	0.088	-0.359	0.013	-0.015	0.109	0.510	0.259	-0.058	-0.316	1				
	F	0.176	0.064	0.112	-0.081	-0.073	0.061	0.020	-0.112	0.026	0.109	-0.196					
NH4		**-0.765**	-0.387	-0.552	**0.745**	-0.389	-0.377	-0.565	-0.397	0.026	-0.507	0.060	-0.024	-0.139	1		
NO3		0.342	0.499	0.557	-0.420	0.296	0.182	0.307	0.352	0.115	0.181	-0.168	0.281	0.231	-0.272	1	
P		**0.760**	0.597	**0.718**	**-0.807**	0.291	0.310	0.562	**0.650**	0.282	0.303	-0.040	0.424	-0.203	**-0.623**	0.339	1

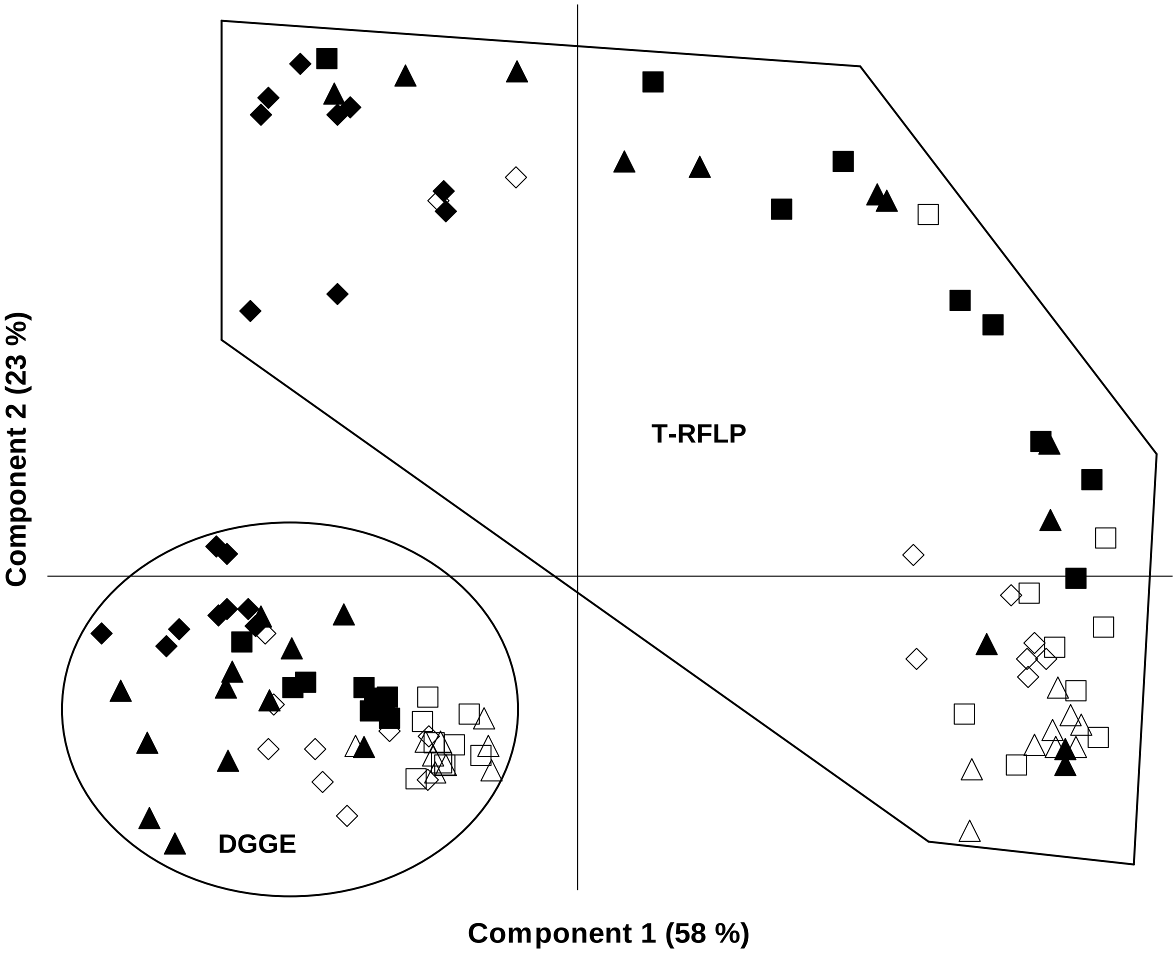
Supplementary Table 6. Results of *in silico* T-RF analysis (T-RF-cut-tool in ARB) of clone sequence data. T-RFs in bold dominated in the respective subgroup. Assignments to *in vivo* T-RFs were calculated from *in silico* T-RFs ± 3 bp.

Acidobacteria subgroup	*in silico* T-RFs	*in vivo* abundant T-RFs
1	**88**, 143, 144, **258**, 260	85, 256
3	135, **141**, **143**, 145, 258	142
4	88, **138**, 139, 276	139
5	**135**, 137	133
6	166, 167, **191**, **193**, **194**, 195, 210, **285**, 287	189, 191, 283, 286
11	462, 464	461
13	90, 166	87, 163
15	74	71
17	**133**, 135, 137, 191, 193	130
18	200, 276	202, 275

Supplementary Figure 1: PCA-Scatterplot of Bray-Curtis similarity measures of 16S rRNA gene T-RFLP and DGGE patterns for the 57 sites. ■ AEW, □ AEG, ▲HEW, Δ HEG, ♦ SEW, ◊ SEG. Naming corresponds to all grassland plots of Schwäbische Alb (AEG), Hainich (HEG), Schorfheide-Chorin (SEG) or all forest plots of Schwäbische Alb (AEW), Hainich (HEW) and Schorfheide-Chorin (SEW).

Supplementary Figure 2. RDA of 16S rRNA gene DGGE patterns of forest soils and 15 environmental variables. N=30, RDA1=11%, RDA2=10%, 59% of total variation in the data can be explained by environmental variables. The longer the arrow and the smaller the angle to a significant axis, the more likely this variable influences the overall community composition. Abbreviations: pH – pH, Corg – organic carbon, N – nitrogen, CN – Corg/N-ratio, SM – soil moisture, ST – soil temperature, SR – soil respiration, Am – abundance of Amoebae, Fl – abundance of Flagellates, Ci – abundance of Ciliates, VP - number of vascular plant species, LUI – land use intensity, G – grassland, F – forest, NH4 - ammonium, NO3 - nitrate, P – phosphorus. RDA for grassland soils was not statistically significant.

Supplementary Figure 1



Supplementary Figure 2