TABLE S1A. Relative average abundances of phyla classified with RDPII taxonomy across all 88 soils and soils grouped into various pH categories. Values represent % of total non-redundant sequences (*n*=132,090) classified with the RDPII taxonomy for all soils combined or the specific sub-set of soils. The number of soils included in each pH category is described in Fig. 2. Asterisks indicate sequences classified to the domain Bacteria, but not classified to a specific phylum.

Phylum	Total	<4.0	4to5	5to6	6to7	7to8	>8.0
Acidobacteria	30.9	63.2	50.2	29.7	19.1	20.3	15.8
Alphaproteobacteria	18.2	16.1	18.8	20.1	17.6	16.9	16.9
Actinobacteria	13.0	5.35	5.12	8.82	16.7	19.9	24.3
Bacteroidetes	11.2	1.69	3.62	10.7	14.5	17.1	17.3
Beta/Gammaproteobacteria	9.14	4.41	8.72	11.9	10.9	8.21	5.14
*Proteobacteria**	6.84	5.79	7.06	8.36	6.76	5.75	5.37
Firmicutes	2.90	0.82	1.36	2.50	4.92	2.31	5.05
Deltaproteobacteria	2.28	0.54	2.28	2.52	2.83	2.32	1.91
Gemmatimonadetes	1.53	0.54	1.00	1.80	2.24	1.53	1.26
TM7	0.96	0.53	0.39	1.18	1.46	1.00	0.75
Verrucomicrobia	0.90	0.67	0.74	1.22	1.05	0.77	0.51
Cyanobacteria	0.74	0.04	0.05	0.14	0.31	1.65	3.14
Chloroflexi	0.42	0.00	0.16	0.12	0.53	0.90	0.92
Nitrospira	0.36	0.15	0.10	0.42	0.56	0.39	0.40
OD1	0.17	0.05	0.15	0.19	0.22	0.12	0.18
Deinococcus-Thermus	0.12	0.00	0.00	0.00	0.00	0.01	0.98
Planctomycetes	0.09	0.07	0.11	0.09	0.05	0.14	0.08
*Bacteria**	0.08	0.00	0.00	0.00	0.00	0.52	0.00
WS3	0.07	0.00	0.02	0.16	0.09	0.05	0.01
OP10	0.04	0.04	0.03	0.04	0.07	0.02	0.02
BRC1	0.02	0.00	0.00	0.01	0.02	0.04	0.02
Spirochaetes	0.01	0.00	0.01	0.03	0.01	0.00	0.00
OP11	0.01	0.01	0.01	0.01	0.00	0.00	0.01
SR1	0.00	0.00	0.00	0.00	0.02	0.00	0.01
Epsilonproteobacteria	0.00	0.00	0.00	0.00	0.00	0.00	0.01

TABLE S1B. Relative abundances of sub-phyla determined in the same manner as for Table S1A. Numbers in bold represent the sum of sequences within each of the phylum (identical to those shown in Table S1A). Asterisks indicate sequences classified to the phylum level only.

Group	Total	<4.0	4to5	5to6	6to7	7to8	>8.0
Acidobacteria	**30.9**	**63.2**	**50.2**	**29.7**	**19.1**	**20.3**	**15.8**
Gp1	9.27	26.2	21.3	10.7	2.18	0.18	0.02
Gp2	6.22	25.4	14.6	5.48	0.37	0.12	0.01
Gp4	5.82	0.01	0.37	3.62	8.51	12.4	9.64
Gp3	4.78	8.77	10.0	5.06	2.69	1.32	1.46
Gp6	2.41	0.76	1.21	2.37	2.95	3.89	2.56
Other	2.42	2.01	2.75	2.50	2.40	2.38	2.06
Actinobacteria	**13.0**	**5.35**	**5.12**	**8.82**	**16.7**	**19.9**	**24.3**
Actinobacteridae	8.71	4.71	4.22	6.92	11.9	12.7	11.7
Rubrobacteridae	3.54	0.20	0.52	1.19	3.98	6.12	11.6
*Actinobacteria**	0.70	0.44	0.37	0.69	0.80	0.94	0.94
Acidimicrobidae	0.04	0.00	0.00	0.02	0.02	0.14	0.07
Bacteroidetes	**11.2**	**1.69**	**3.62**	**10.7**	**14.5**	**17.1**	**17.3**
Sphingobacteria	9.19	1.44	2.75	8.33	12.0	14.9	14.0
*Bacteroidetes**	1.40	0.23	0.74	1.39	1.50	1.60	2.79
Flavobacteria	0.59	0.01	0.07	0.93	0.98	0.58	0.39
Bacteroidetes	0.05	0.01	0.06	0.01	0.11	0.03	0.08
Alphaproteobacteria	**18.2**	**16.1**	**18.8**	**20.1**	**17.6**	**16.9**	**16.9**
Rhizobiales	11.2	9.36	12.3	12.4	11.0	9.86	9.84
*Alphaproteobacteria**	3.21	4.52	3.81	4.05	2.66	2.09	1.91
Rhodospirillales	1.59	1.60	1.66	1.52	1.16	2.10	1.62
Sphingomonadales	1.39	0.03	0.30	1.13	2.01	2.12	2.53
Caulobacterales	0.65	0.59	0.71	0.95	0.58	0.47	0.26
Other	0.20	0.02	0.02	0.11	0.19	0.29	0.71
Beta/Gammaproteobacteria	**9.14**	**4.41**	**8.72**	**11.9**	**10.9**	**8.21**	**5.14**
Burkholderiales	4.95	2.44	4.52	6.44	6.29	4.01	3.02
*Betaproteobacteria**	1.56	0.60	1.72	2.18	1.83	1.22	0.57
*Other Betaproteobacteria**	0.34	0.01	1.10	0.13	0.31	0.10	0.20
*Gammaproteobacteria**	1.02	0.78	0.80	0.96	1.04	1.53	0.91
Xanthomonadales	0.62	0.22	0.22	1.23	0.74	0.47	0.12
Other Gammaproteobacteria	0.65	0.36	0.36	0.92	0.72	0.87	0.32

FIG. S1. Scatter plots of soil pH versus Faith's index of phylogenetic diversity for those phyla with significant regression coefficients (Table 2). Faith's index of phylogenetic diversity was calculated for individual phyla holding the number of sequences per sample constant (see Methods).

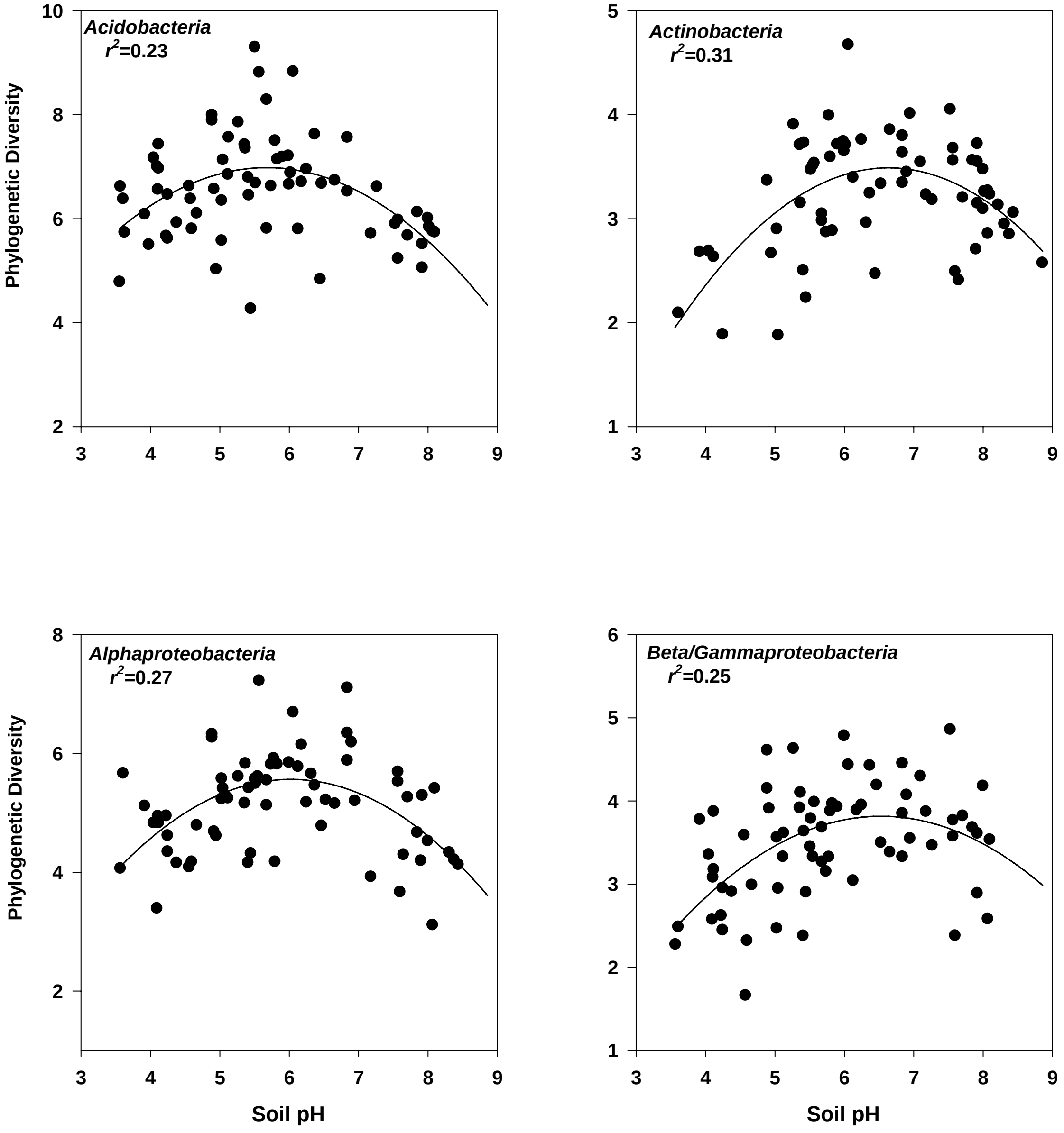

TABLE S2: Comparison of bacterial phyla with respect to the average number of phylotypes per soil and the average phylogenetic diversity (Faith's PD) per soil. The values were calculated from 100 randomly selected sequences per soil. Standard deviations of the mean are shown in parentheses.

Phylum	**No. of phylotypes per soil**	**Average phylogenetic diversity per soil**
Acidobacteria	74.5 (7.2)	3.7 (0.5)
Actinobacteria	73.2 (7.3)	3.2 (0.5)
Alphaproteobacteria	71.4 (6.7)	3.3 (0.5)
Beta/Gammaproteobacteria	66.7 (9.7)	3.5 (0.7)
Bacteroidetes	68.8 (10.0)	3.6 (0.6)