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Supplement of

Diversity and seasonal dynamics of airborne *Archaea*

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Supplementary Text

Quantitative analysis of airborne *Archaea*

In contrast to other airborne microorganisms (e.g., *Fungi*, Fröhlich-Nowoisky et al., 2009 and *Bacteria* (data not shown)), which were studied from the identical air filter samples, the amplification of airborne *Archaea* 16S rRNA gene sequences was more challenging and PCR products were often only produced in a nested PCR or not at all. This was also true for air filter samples from China, the United Kingdom, and North America which were analyzed successfully for *Fungi* (Fröhlich-Nowoisky et al., 2012; Huffman et al., 2013) while *Archaea* could only be amplified for some of the samples (this study).

One explanation might concern the primer choice. Primers that are supposed to cover *Archaea* or subgroups might not have 100% identity across all *Archaea* lineages (Klindworth et al., 2013; Nicol and Prosser, 2011). In addition, *Archaea* taxonomy is continuously increasing due to the discovery of new species. However, the primers used for amplification in this study have been used successfully for soil samples (Angel et al., 2012; Grosskopf et al., 1998). To increase amplification success we also used a combination of 3 primer pairs as well as nested PCR as described in section 2.2. The primer pairs used amplify *Archaea* sequences from several taxonomic lineages, thus it can be assumed that they would equally amplify at least these lineages in air filter samples. Therefore, it is more likely that the *Archaea* lineages were either not present in the air or only in very limited amounts. To judge and compare *Archaea* to *Bacteria* abundance on the air filter samples we quantified *Archaea* and *Bacteria* by performing qPCR assays including a standard with a correlation coefficient of 0.98 in *Bacteria* and 0.99 in *Archaea* and PCR efficiencies of 102.6% in *Bacteria* and 91.5% in *Archaea*.

We compared the abundance of airborne *Archaea* and *Bacteria* with those in environments that are potential bioaerosol sources (see material and methods, Table S4). Although only very rough estimates can be made as concentrations vary between regions, depth, temperatures, seasons etc., in general *Archaea* represent about ~10% of the total prokaryotes quantities in ocean surface water as well as in normal soil (Bates et al., 2011, Cao et al., 2012; DeLong, 1992; Karner et al., 2001; Kemnitz et al., 2007; Yin et al., 2013.).

In one kg of soil the copy numbers of *Archaea* 16S rRNA genes range, very roughly, between $\sim 10^9$ to 10^{11} while *Bacteria* have between $\sim 10^{11}$ to 10^{12} copies (Table S4). *Thaumarchaeota* AOA often even prevail over AOB (Leininger et al., 2006, Pereira e Silva et al., 2012). For air, our results show that *Bacteria* were easily quantifiable and varied between 10^5

and 10^6 16S rRNA gene copies per m^3 of air, which is close to abundances measured for ocean surface water and in agreement with other studies (Bauer et al., 2002, Burrows et al., 2009, Harrison et al., 2005, DeLeon-Rodriguez et al., 2013). In contrast, *Archaea* 16S rRNA gene copies were often below the detection limit, and varied approximately between 1 and 10 copies per m^3 air. Although the quantification is based on six filter samples only, *Archaea* are likely orders of magnitude lower than the *Bacteria* in the same air masses.

Supposing that soil is the primary source of airborne *Archaea* and *Bacteria*, the questions remains why *Archaea* are so difficult to amplify in air, or are not present in amplifiable quantities, while *Bacteria* are. It might be that *Bacteria* have important sources other than soils (e.g., plant surfaces), which *Archaea* might not have. Another possibility might be that *Archaea* are more susceptible to UV damage or other damaging compounds associated with fine particulate matter than *Bacteria*, or decompose faster after sampling. Thirdly, in contrast to *Bacteria*, *Archaea* might occur in larger particles and thus deposit faster from the air. However, the explanations can currently only be speculative and future studies are needed. The observation that airborne *Archaea* are low in number has also been made by Woo and colleagues (2013), and our observation that airborne *Archaea* are difficult to amplify in general is also consistent with the experience other researchers have made (Bowers et al., 2009; Fierer et al., 2008; Woo et al., 2013; Woo, 2012).

The difficulty to obtain DNA extracts that yielded enough archaeal DNA to be amplified, also limited the number of samples that could successfully be analyzed. We calculated rarefaction curves for the air filter samples from Mainz and Cape Verde which agree with our assumptions that although we exhausted laboratory possibilities the gained data can currently only serve as a first rough estimate of the actual species richness of *Archaea* in air.

Statistical analysis of airborne *Archaea* diversity with meteorological parameters

Meteorological conditions are also known to influence airborne communities and bio-aerosol composition (Despres et al., 2012 and references therein), e.g., temperature and relative humidity have been found to correlate with airborne fungal composition (Fröhlich-Nowoisky et al., 2009). We thus compared the diversity of airborne *Archaea* (the normalized (S_n) and relative species richness ($S_{R,i}$, see material and methods)) with meteorological parameters, such as averaged wind speed, temperature, relative humidity and the sum of precipitation for the individual sampling periods. To discriminate between short and long term influ-

ences, we performed linear correlation analyses on a sample to sample basis and also on a monthly basis.

In an initial step, the influence of single meteorological factors was assessed. The Pearson coefficients were calculated between the diversity parameters, $S_{R,j}$, S_n and $S_{R,k}$, and the meteorological factors to preselect possible dependencies for further testing. The results of the averaged meteorological parameters can be seen in Table S6. Due to the nature of environmental samples and the limitations of the applied methods a high variance was expected within the diversity parameters. To account for this, relatively low Pearson coefficient boundaries, of +/- 0.3 for the sample to sample diversity parameter ($S_{R,i}$) and +/- 0.5 for the a monthly diversity parameters (S_n and $S_{R,k}$), were set as a threshold for further testing. The higher boundary for the monthly parameters was chosen as these are based on more data, thus reducing the expected intrinsic error.

Detailed single factor linear regression analyses were then performed on promising candidates. The results can be seen in Table S7 and Figures S2a, S3.

In a second step to assess the dependency of the diversity parameters on combined meteorological factors, multiple factor linear regression analyses were performed. To preselect the best combinations of factors, the best factor subsets were selected using the AIC method. Detailed linear regression analyses were then performed, the results of which can be seen in Table S7 and Figures S2b and 4 of the main text.

On a sample to sample basis, $S_{R,i}$ showed a significant negative correlation to average wind speed (p-value=0.012; Figure S2a). The incorporation of additional variables also revealed a negative correlation to wind speed with a positive correlation to relative humidity (p-value=0.015; Figure S2b).

While on the short term the influence of wind speed seems to play an important role for the observed diversity, on a monthly basis the Pearson's coefficients showed that relative humidity correlated best with diversity. The best single factor for both, S_n and $S_{R,k}$, was found to be relative humidity which in both cases was positively correlated (p-values=0.05 and 0.005; see Figure S3a and b). A negative correlation to temperature was also shown by $S_{R,k}$ (p-value=0.049; See Figure S3c). The multiple linear correlation analysis revealed that S_n negatively correlated with both average temperature and wind speed, while $S_{R,k}$ showed a significant positive correlation with average relative humidity and wind speed, though wind

speed in both variable sets played a secondary role (p-value (S_n)=0.02, p-value ($S_{R,k}$)=0.01; Figure 4, main text).

The sampling site is situated in an area which has a seasonal cycle with lower temperatures and high relative humidity in the fall/winter period. Also, on average the wind speed increases due to the Westerlies prevailing at this time of the year. Thus, the observed positive correlation with relative humidity, as well as the negative correlation with temperature on a long term basis, coincides with our finding that the *Archaea* diversity increases in the fall/winter period. However, it is not possible at this point to determine whether the meteorological parameters influence the diversity of *Archaea* directly. For the soil environment it has been found that *Archaea* diversity reacts to changes in soil temperature and soil moisture (Rasche et al., 2011) thus meteorological parameters could indirectly due to their effect on soil conditions, influence the *Archaea* diversity. On the other hand the diversity could just be influenced by the changing accessibility of aerosolization sources, e.g., availability of bare, harvested fields. In this case the meteorological parameters would not cause changes in diversity, but only be characteristic for the season when the number of bare fields increases.

Supplementary Figures S1-S3

Figure S1a

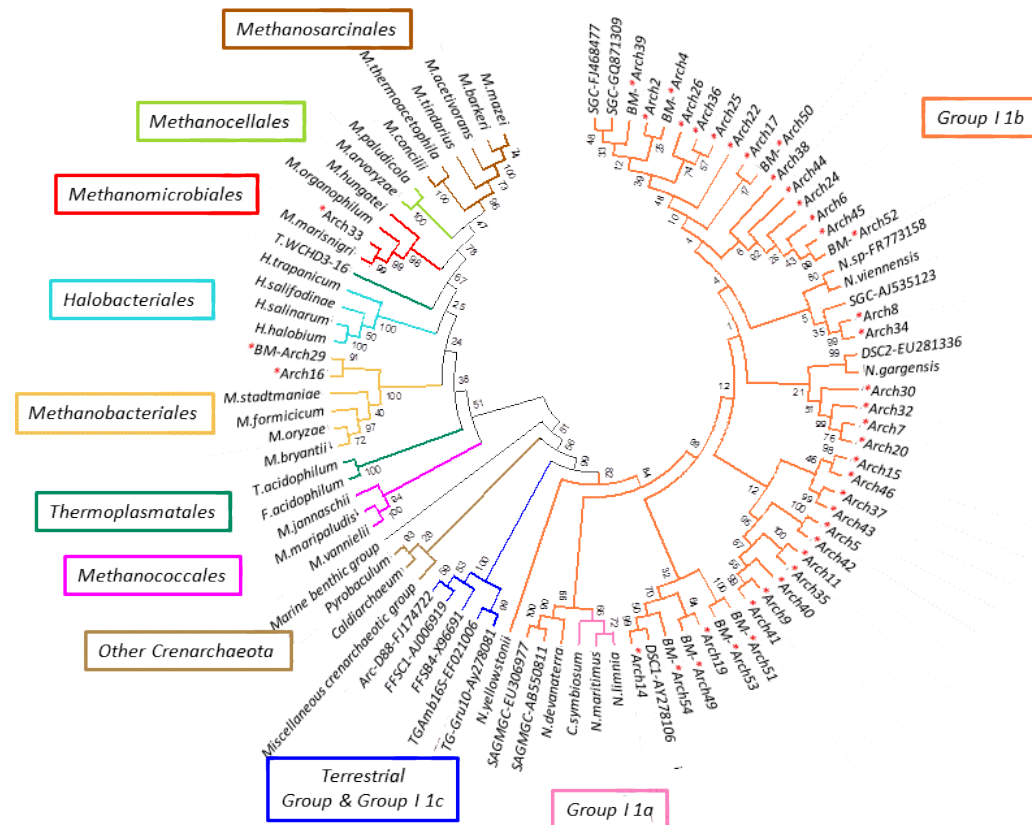


Figure S1b

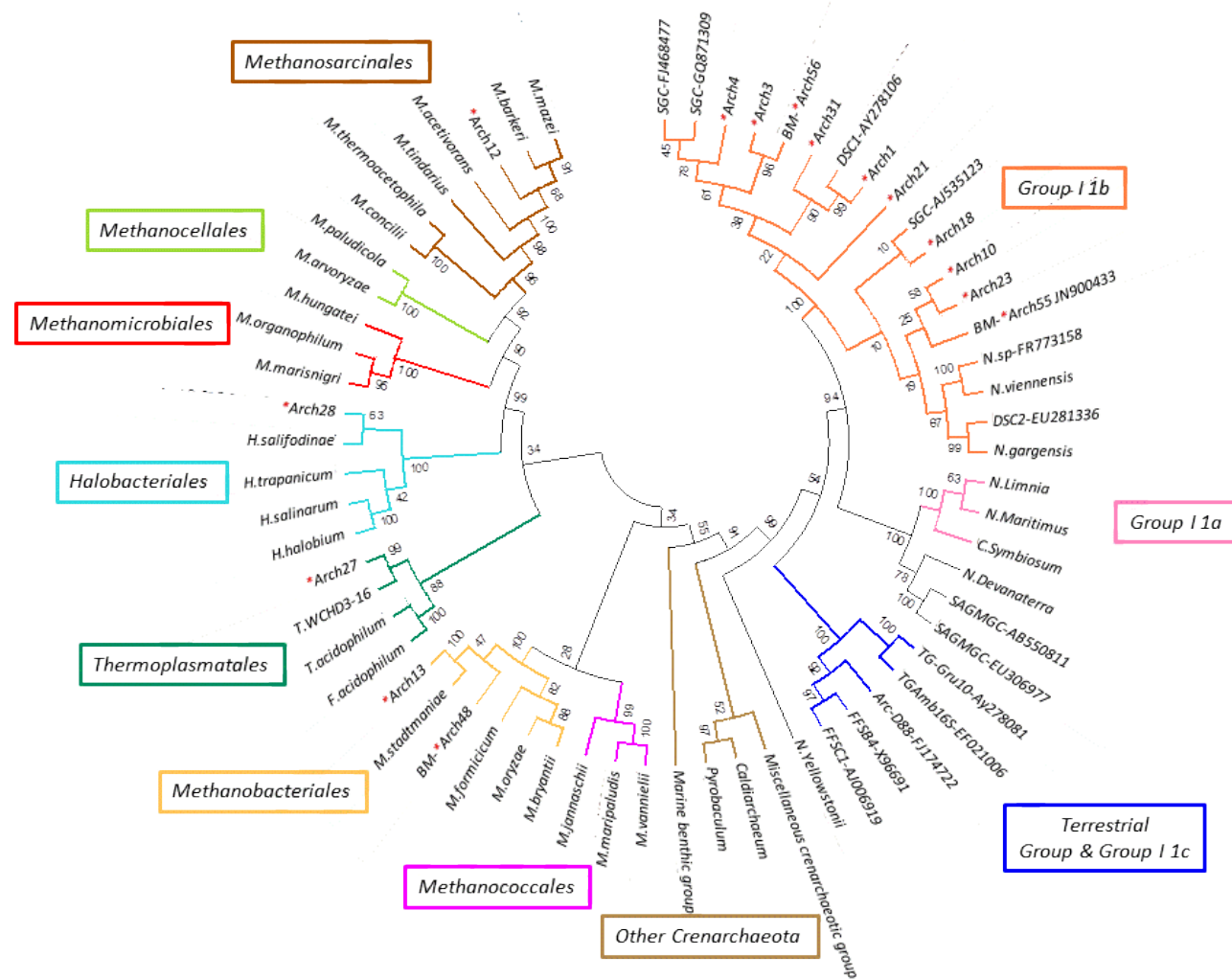


Figure S1: Phylogenetic Tree of airborne *Archaea* in Germany. A Maximum Likelihood Tree was calculated for the published and obtained sequences of this study representing known phylogenetic lineages (given here species names). They are also summarized in Table S2. Two different sequence parts of the 16S region were used, depending on the coverage by the OTUs of the airborne *Archaea* (a, b). Different orders are given in different colors. Red stars mark the presence of airborne *Archaea* of Mainz.

Figure S2a

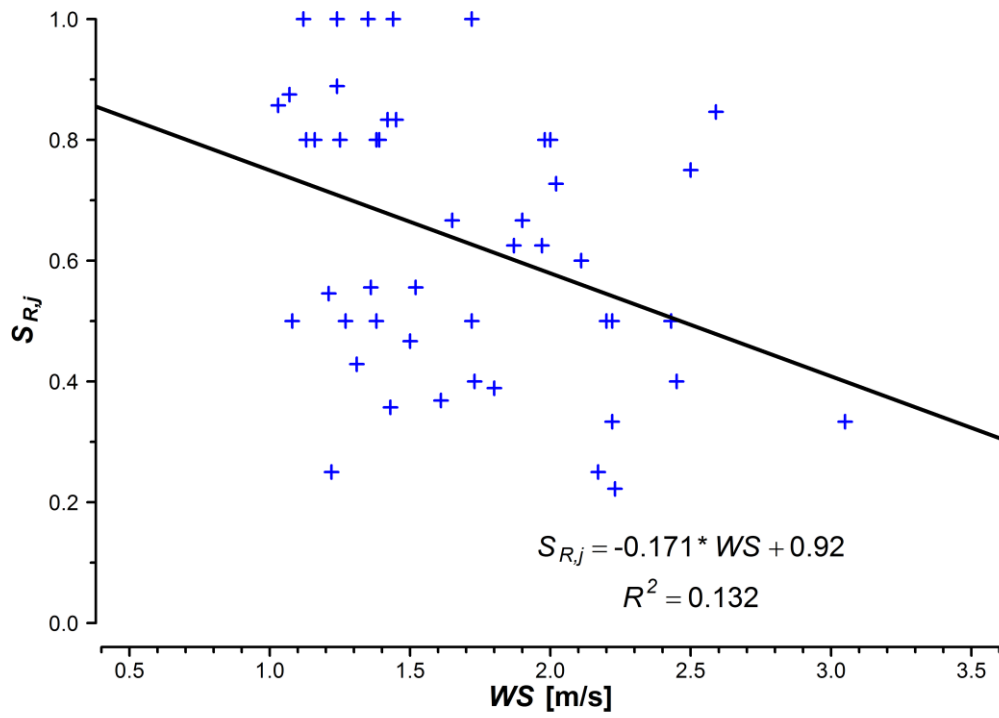


Figure S2b

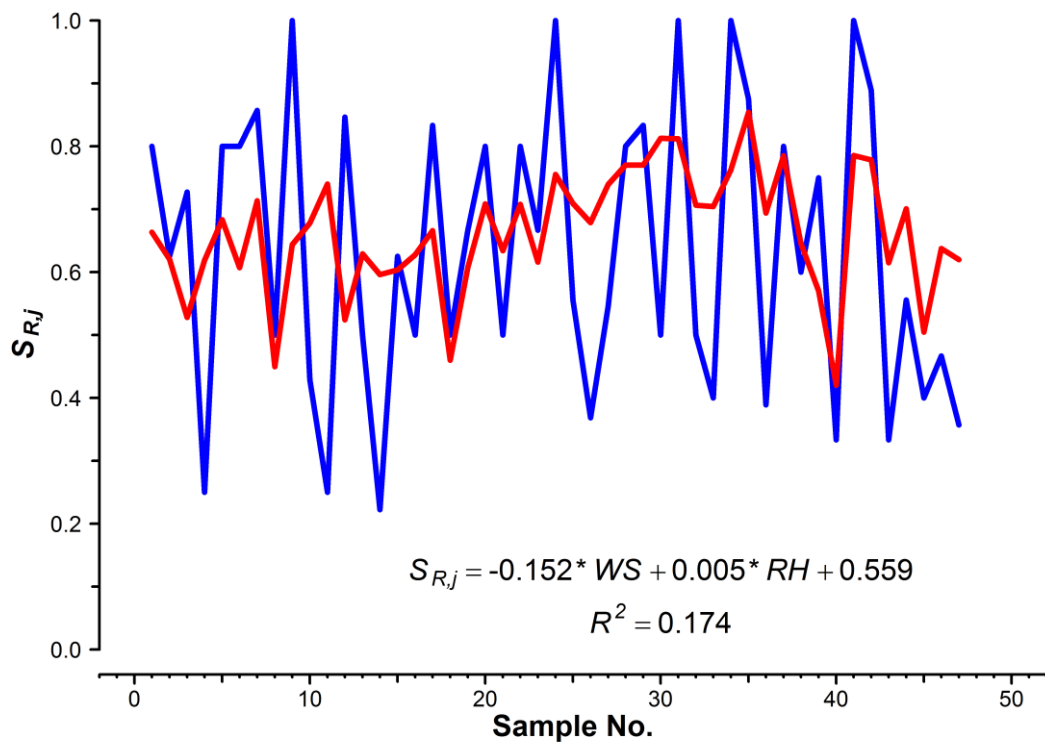


Figure S2: The most significant results of the linear regression analysis between the relative species diversity per sample ($S_{R,j}$) and meteorological factors. (a) Best single factor: $S_{R,j}$ as a function of wind speed (p-value = 0.012). (b) Best variable subset (WS and RH): The sample IDs given on the x-axis correspond to the sampling time given in Table S1. The values for the observed $S_{R,j}$ curve (blue) were calculated using the equation given in Table S3. The modeled $S_{R,j}$ curve (red) was estimated using the depicted equation that was obtained by regression analysis (p-value = 0.015) including the RH and WS values measured during each individual sampling period. WS : average wind Speed [m/s]; RH : average relative humidity [%].

Figure S3a

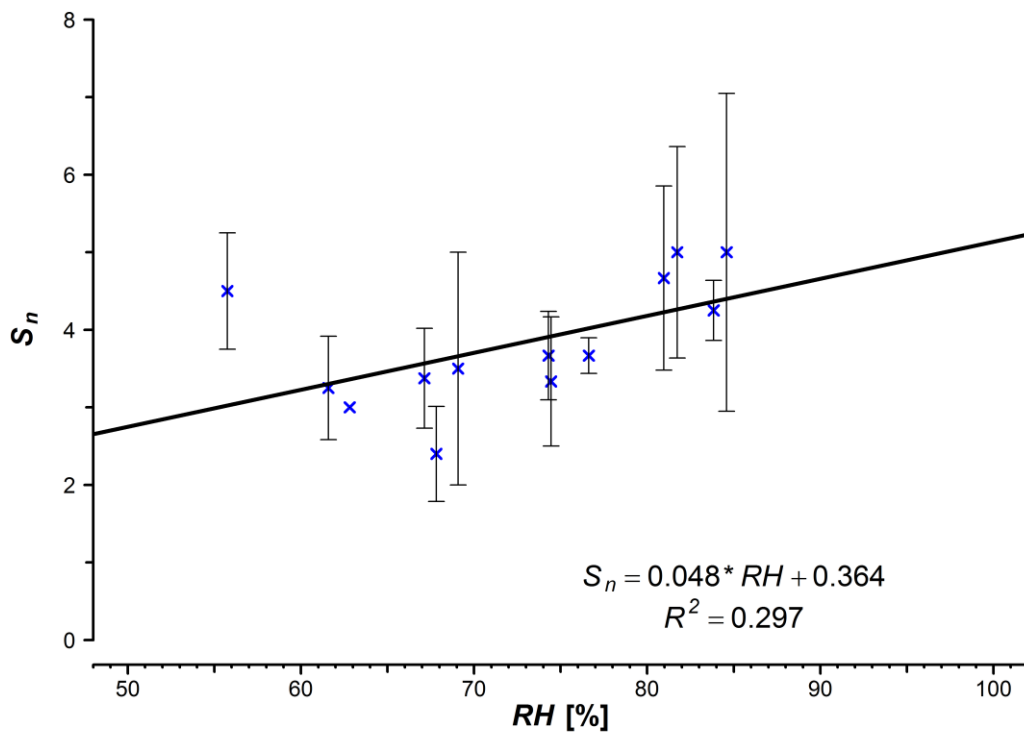
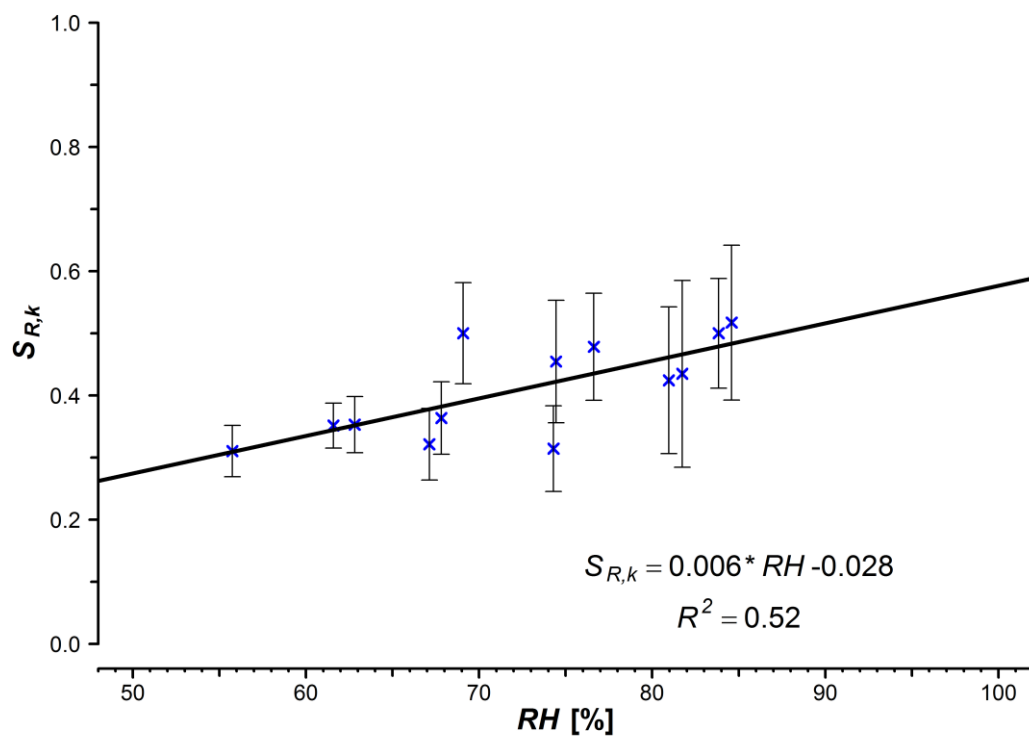


Figure S3b



FigureS3c

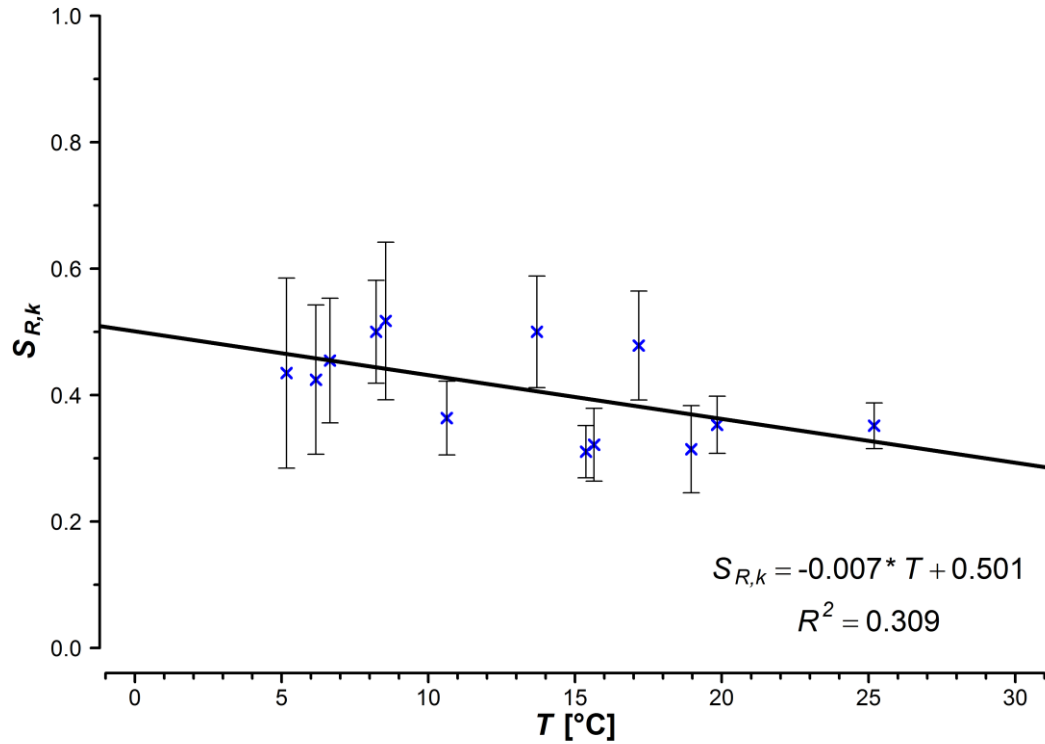


Figure S3: The most significant results of a single variable linear regression analysis between the two dependent variables, normalized species richness per month (S_n) and relative species diversity per month ($S_{R,k}$), and meteorological factors. The values for S_n and $S_{R,k}$ were calculated with the equations given in Table S3 (a) S_n as a function of RH (p-value = 0.055). Error bars: $SE_n(S_n)$ (b) The relative species diversity per month ($S_{R,k}$) as a function of RH (p-value = 0.005). Error bars: $SE_n(S_{R,k})$ (c) The relative Species per month ($S_{R,k}$) as a function of T (p-value = 0.048). Error bars: $SE_n(S_{R,k})$. RH : average relative humidity [%], T : average temperature [$^{\circ}\text{C}$].

Supplementary Tables S1-S7

Table S1. Overview of air samples (aerosol filters) positive for DNA analysis. Sample ID (location and running number), sampling period, sequence region (16S rRNA gene, *amoA*), number of sequences obtained. Abbreviation of sampling location: Cape Verde (CV), China (CH), Germany (MZ), North America (NA), United Kingdom (UK).

Sample ID	Sampling period	Sequence region	Number of sequences (16S, <i>amoA</i>)
MZ 1	24.03.2006 - 31.03.2006	16S	5
MZ 2	31.03.2006 - 07.04.2006	16S	8
MZ 4	07.04.2006 - 12.04.2006	16S, <i>amoA</i>	11, 12
MZ 6	15.04.2006 - 18.04.2006	16S	4
MZ 9	20.04.2006 - 27.04.2006	16S	5
MZ 10	27.04.2006 - 02.05.2006	16S	5
MZ 11	02.05.2006 - 03.05.2006	16S	7
MZ 15	04.05.2006 - 09.05.2006	16S, <i>amoA</i>	16, 12
MZ 18	12.05.2006 - 15.05.2006	16S	7
MZ 19	15.05.2006 - 16.05.2006	16S	7
MZ 21	17.05.2006 - 18.05.2006	16S	4
MZ 24	18.05.2006 - 22.05.2006	16S	13
MZ 25	22.05.2006 - 23.05.2006	16S	12
MZ 26	23.05.2006 - 30.05.2006	16S, <i>amoA</i>	18, 12
MZ 31	01.06.2006 - 06.06.2006	16S	8
MZ 33	08.06.2006 - 13.06.2006	16S	10
MZ 35	14.06.2006 - 21.06.2006	16S	6
MZ 36	21.06.2006 - 22.06.2006	16S, <i>amoA</i>	10, 4
MZ 40	27.06.2006 - 04.07.2006	16S, <i>amoA</i>	9, 12
MZ 41	04.07.2006 - 11.07.2006	16S	5
MZ 45	19.07.2006 - 21.07.2006	16S	18
MZ 47	26.07.2006 - 02.08.2006	16S	5
MZ 50	02.08.2006 - 09.08.2006	16S, <i>amoA</i>	9, 12
MZ 51	09.08.2006 - 16.08.2006	16S	5
MZ 52	16.08.2006 - 23.08.2006	16S, <i>amoA</i>	9, 3
MZ 54	30.08.2006 - 06.09.2006	16S, <i>amoA</i>	19, 12
MZ 59	11.09.2006 - 18.09.2006	16S	11

MZ 60	18.09.2006 - 25.09.2006	16S, <i>amoA</i>	5, 12
MZ 62	02.10.2006 - 09.10.2006	16S, <i>amoA</i>	6, 9
MZ 63	09.10.2006 - 16.10.2006	16S, <i>amoA</i>	12, 9
MZ 66	16.10.2006 - 23.10.2006	16S	4
MZ 67	23.10.2006 - 30.10.2006	16S, <i>amoA</i>	12, 12
MZ 69	02.11.2006 - 09.11.2006	16S	20
MZ 71	16.11.2006 - 23.11.2006	16S	1
MZ 74	23.11.2006 - 30.11.2006	16S	8
MZ 75	30.11.2006 - 07.12.2006	16S	18
MZ 77	14.12.2006 - 21.12.2006	16S	5
MZ 81	28.12.2006 - 04.01.2007	16S	5
MZ 82	04.01.2007 - 11.01.2007	16S	8
MZ 84	18.01.2007 - 25.01.2007	16S	9
MZ 88	01.02.2007 - 08.02.2007	16S, <i>amoA</i>	3, 7
MZ 90	15.02.2007 - 22.02.2007	16S, <i>amoA</i>	9, 9
MZ 93	22.02.2007 - 01.03.2007	16S, <i>amoA</i>	21, 11
MZ 95	08.03.2007 - 15.03.2007	16S, <i>amoA</i>	9, 4
MZ 97	22.03.2007 - 29.03.2007	16S	5
MZ 101	05.04.2007 - 12.04.2007	16S, <i>amoA</i>	15, 12
MZ 103	19.04.2007 - 26.04.2007	16S, <i>amoA</i>	14, 12
CV 1*	03.02.2011 - 04.02.2011	16S	10
CV 2	04.02.2011 - 05.02.2011	16S	9
CV 4	05.02.2011 - 06.02.2011	16S	10
CV 5	06.02.2011 - 07.02.2011	16S	11
CV 6	07.02.2011 - 08.02.2011	16S	4
CV 17	17.02.2011 - 19.02.2011	16S	6
CV 19	21.02.2011 - 23.02.2011	16S	5
CV 20	23.02.2011 - 24.02.2011	16S	9
CV 21	24.02.2011 - 27.02.2011	16S	4
CV 27	08.03.2011 - 11.03.2011	16S	4
NA 1*	24.07.2011 - 25.07.2011	16S	20
CH 4*	10.07.2006 - 11.07.2006	16S	7
UK 1*	06.05.2004 - 13.05.2004	16S	11

*For CV 26, NA 20, CH 14 and UK 12 air filter samples were tested in total (Table 1)

Table S2. Information on the sequences (16S rRNA gene) used for constructing phylogenetic trees. Accession numbers are given as well as the name of the species if available. Phylogenetic trees where these sequences have been used can be found in Figures 2 and S1.

	Acc Nr	Taxonomy
<i>Euryarchaeota</i>	Methanosarcinales	
	M59144	<i>Methanosarcina barkeri</i>
	AF028691	<i>Methanosarcina mazei</i>
	M59137	<i>Methanosarcina acetivorans</i>
	M59135	<i>Methanolobus concilii</i>
	M59141	<i>Methanosaeta thermoacetophila</i>
	Methanomicrobiales	
	M60880	<i>Methanospirillum hungatei</i>
	M59134	<i>Methanoculleus marisnigri</i>
	M59131	<i>Methanogenium organophilum</i>
	Methanobacteriales	
	M59124	<i>Methanobacterium bryantii</i>
	AF028690	<i>Methanobacterium oryzae</i>
	M36508	<i>Methanobacterium formicicum</i>
	AY196684	<i>Methanosphaera stadtmaniae</i>
	NR074235	<i>Methanobrevibacter smithii</i>
	NR044801	<i>Methanobrevibacter filiformis</i>
	Methanocellales	
	AB196288	<i>Methanocella paludicola</i>
	AM114193	<i>Methanocella arvoryzae</i>
	Thermoplasmatales	
	M38637	<i>Thermoplasma acidophilum</i>
	AJ224936	<i>Ferroplasma acidophilum</i>
AF050618	<i>WCHD3-16, Thermoplasmatales</i>	
Methanococcales		
M36507	<i>Methanococcus vannielii</i>	
M59126	<i>Methanocaldococcus jannaschii</i>	
U38484	<i>Methanococcus maripaludis</i>	
Halobacteriales		
DQ256409	<i>Haladaptatus jilantaiense</i>	
EU887285	<i>Haladaptatus litoreus</i>	
DQ344973	<i>Haladaptatus paucihalophilus</i>	
DQ344974	<i>Haladaptatus paucihalophilus</i>	
GQ282623	<i>Halgranum amylolyticum</i>	
GQ282624	<i>Halgranum gelatinilyticum</i>	
EF645681	<i>Haloarcula argentinensis</i>	
EF645693	<i>Haloarcula marismortui</i>	
EF645688	<i>Haloarcula vallismortis</i>	
GQ282625	<i>Halobacteriaceae archaeon</i>	
AJ002949	<i>Halobacterium halobium</i>	
M38280	<i>Halobacterium halobium</i>	
U17364	<i>Halobacterium saccharovororum</i>	
AJ002947	<i>Halobacterium salinarium</i>	
AJ496185	<i>Halobacterium salinarum</i>	
U68538	<i>Halobacterium salinarum</i>	
AJ548827	<i>Halobacterium sp</i>	
D11106	<i>Halococcus morrhuae</i>	
AB004877	<i>Halococcus salifodinae</i>	
<i>Euryarchaeota</i>		

Euryarchaeota	Z28387	<i>Halococcus salifodinae</i>
	AB037474	<i>Haloferax alexandrines</i>
	D14128	<i>Haloferax denitrificans</i>
	AJ420376	<i>Haloferax dombrowskii</i>
	AY458601	<i>Haloferax sulfurifontis</i>
	AY425724	<i>Haloferax volcanii</i>
	AF002984	<i>Halogeometricum borinquenss</i>
	EU887286	<i>Halogeometricum rufum</i>
	EU887283	<i>Halogranum rubrum</i>
	DQ417339	<i>Haloplanus natans</i>
	EU931578	<i>Haloplanus sp.</i>
	DQ987877	<i>Halorubrum luteum</i>
	AY149598	<i>Halorubrum tibetense</i>
	D14125	<i>Halorubrum trapanicum</i>
Thaumarchaeota	EU931577	<i>Halosarcina limi</i>
	AB454051	<i>Salarchaeum japonicum</i>
	JN196516	<i>Salarchaeum sp.</i>
	Group I.1a	
	U51469	<i>Cenarchaeum symbiosum</i>
	DQ085097	<i>Nitrosopumilus maritimus</i>
	AEGP01000029	<i>Cnitrosoarchaeum limnia</i>
	Group I.1b	
	EU281334	<i>Nitrososphaera gargensis</i>
	FR773157	<i>Nitrososphaera viennensis</i>
	FR773158	<i>Nitrososphaera sp.</i>
	Group I.1c	
	AJ006919	<i>FFSC1, Thaumarchaeota, I.1c</i>
	X96691	<i>FFSB4, Thaumarchaeota, I.1c</i>
Thaumarchaeota	Group III	
	EU239960	<i>Nitrosocaldus yellowstonii</i>
	Soil Crenarchaeotic Group (SGC)	
	GQ871309	<i>W5P1-DO1, Thaumarchaeota, SGC</i>
	FJ468477	<i>F5, Thaumarchaeota, SCG</i>
	AJ535123	<i>Gitt-GR, Thaumarchaeota, SCG</i>
	Terrestrial Group (TG)	
	EF021006	<i>Amb_16S, Thaumarchaeota, TG</i>
	AY278081	<i>GRU10, Thaumarchaeota, TG</i>
	FJ174722	<i>Arc-D88, Thaumarchaeota, TG</i>
	South African Gold Mine Group (SAGMGC)	
	AB550811	<i>NG-W-081028-3-5. Thaumarchaeota, SAGMGC</i>
	EU306977	<i>ArcB-cD06, Thaumarchaeota, SAGMGC</i>
	Dominant Soil Crenarchaeotic Group (DSC)	
AY278106	<i>Thaumarchaeota, DSC1</i>	
EU281336	<i>Thaumarchaeota, DSSC2</i>	
Crenarchaeota	Crenarchaeota	
	JN881579	<i>Caldiarchaeum</i>
	HQ214608	<i>Miscellaneous Crenarchaeotic Group</i>
	GQ267189	<i>Marine Benthic Group</i>
	JN227488	<i>Nitrosotalea devanaterria</i>
	Thermoproteales	
	NR040935	<i>Pyrobaculum</i>
	HF546082	<i>Sulfobales</i>
	KC139249	<i>Desulfurococcales</i>
	NR041774	<i>Acidilobales</i>
EF552404	<i>Fervivoccales</i>	

Table S3. Definitions.

Symbol	Quantity/ Definition
D	Simpson's index (Hill et al., 2003), $D = \sum_{i=1}^S \frac{n_i(n_i-1)}{N(N-1)}$
E	Shannon evenness, $E=H'/\ln S$
H'	Shannon index, $H' = -\sum_{i=1}^S (P_i \ln P_i)$
m_j	Number of sequences analyzed for air sample j
m_k	Number of sequences analyzed for air samples in a month k
n_i	Frequency of occurrence of an individual species i (number of samples in which species i was detected)
N	Cumulative frequency of occurrence of investigated sample, $N = \sum_{i=1}^S n_i$
n	Number of investigated air samples
P_i	Relative proportion of an individual species i , $P_i = n_i / N$
S	Species richness measured (number of detected individual species)
S_j	Number of detected individual species in air sample j
S_k	Number of detected individual species in air samples of a month k
S^*	Species richness estimated with the Chao-1 approach (Chao, 1984; Hill et al., 2003), $S^*=S + a^2 / (2 b)$, a = number of species detected only once (singletons) b = number of species detected twice (doubletons)
S_n	Normalized species richness, $S_n = S/n$
$S_{R,j}$	Relative species diversity per sample, $S_{R,j} = S_j/m_j$
$S_{R,k}$	Relative species diversity per month, $S_{R,k} = S_k/m_k$
$SE_n(S_n)$	Normalized standard error of S_n : $= \frac{SE_{\bar{S}}}{\bar{S}} S_n$ \bar{S} = average number of species per sample $SE_{\bar{S}}$ = standard error of \bar{S}
$SE_n(S_{R,k})$	Normalized standard error of $S_{R,k}$: $= \frac{SE_{\overline{S_{R,j}}}}{\overline{S_{R,j}}} S_{R,k}$ $\overline{S_{R,j}}$ = average relative species diversity per sample $SE_{\overline{S_{R,j}}}$ = standard error of $\overline{S_{R,j}}$

Table S4: Estimates of the abundance of *Bacteria* and *Archaea* in different environments. The number of copies (cp) of the 16S rRNA gene was quantified using qPCR.

Source	<i>Archaea</i>	<i>Bacteria</i>	Ratio A/B	Reference
Soil [cp kg ⁻¹]	~10 ⁹ – 10 ¹¹	~10 ¹¹ – 10 ¹²	~10 ⁻² – 10 ⁻¹	Cao et al., 2012; Kemnitz et al., 2007
Ocean surface water [cp L ⁻¹]	~10 ⁶ – 10 ⁷	~10 ⁸ – 10 ⁹	~10 ⁻²	Yin et al. 2013
Air [cp m ⁻³]	~1 – ~10 ¹	~10 ⁴ – 10 ⁶	~10 ⁻⁴ – 10 ⁻⁶	This study

Table S5. Operational taxonomic units (OTUs) attributed to *Archaea* 16S rRNA genes.

Operational ID; frequency of occurrence (number of air samples and coarse or fine particle filters in which the OTU was detected (n.a.= not available); taxonomic family and genus name according to phylogenetic analysis based on the Maximum likelihood approach. Information is given for Germany, Cape Verde, United Kingdom, China, and North America.

OTU	Frequency of occurrence			Family, genus	
	Germany	total	coarse		fine
Arch1		33	32	2	<i>Thaumarchaeota, former Group I 1b</i>
Arch2		26	26	0	<i>Thaumarchaeota, former Group I 1b</i>
Arch3		20	20	4	<i>Thaumarchaeota, former Group I 1b</i>
Arch4		17	16	2	<i>Thaumarchaeota, former Group I 1b</i>
Arch5		15	15	0	<i>Thaumarchaeota, former Group I 1b</i>
Arch6		13	13	1	<i>Thaumarchaeota, former Group I 1b</i>
Arch7		11	11	0	<i>Thaumarchaeota, former Group I 1b</i>
Arch8		9	9	0	<i>Thaumarchaeota, former Group I 1b</i>
Arch9		8	7	1	<i>Thaumarchaeota, former Group I 1b</i>
Arch10		8	7	1	<i>Thaumarchaeota, former Group I 1b</i>
Arch11		7	7	0	<i>Thaumarchaeota, former Group I 1b</i>
Arch12		5	4	1	<i>Methanosarcinaceae, Methanosarcina</i>
Arch13		5	4	1	<i>Methanobacteriaceae; Methanosphaera</i>
Arch14		5	5	0	<i>Thaumarchaeota, former Group I 1b</i>
Arch15		4	4	0	<i>Thaumarchaeota, former Group I 1b</i>
Arch16		3	2	1	<i>Methanobacteriaceae</i>
Arch17		3	3	0	<i>Thaumarchaeota, former Group I 1b</i>

Arch18	3	3	0	<i>Thaumarchaeota, former Group I 1b</i>
Arch19	3	3	0	<i>Thaumarchaeota, former Group I 1b</i>
Arch20	3	3	0	<i>Thaumarchaeota, former Group I 1b</i>
Arch21	2	2	0	<i>Thaumarchaeota, former Group I 1b</i>
Arch22	2	2	0	<i>Thaumarchaeota, former Group I 1b</i>
Arch23	2	2	0	<i>Thaumarchaeota, former Group I 1b</i>
Arch24	2	2	0	<i>Thaumarchaeota, former Group I 1b</i>
Arch25	2	2	0	<i>Thaumarchaeota, former Group I 1b</i>
Arch26	2	2	0	<i>Thaumarchaeota, former Group I 1b</i>
Arch27	1	1	0	<i>Thermoplasmatales</i>
Arch28	1	0	1	<i>Halobacteriaceae, Halococcus</i>
Arch29	1	1	0	<i>Methanobacteriaceae, Methanobrevibacter</i>
Arch30	1	1	0	<i>Thaumarchaeota, former Group I 1b</i>
Arch31	1	1	0	<i>Thaumarchaeota, former Group I 1b</i>
Arch32	1	1	0	<i>Thaumarchaeota, former Group I 1b</i>
Arch33	1	1	0	<i>Methanomicrobiaceae; Methanoculleus</i>
Arch34	1	1	0	<i>Thaumarchaeota, former Group I 1b</i>
Arch35	1	1	0	<i>Thaumarchaeota, former Group I 1b</i>
Arch36	1	1	0	<i>Thaumarchaeota, former Group I 1b</i>
Arch37	1	1	0	<i>Thaumarchaeota, former Group I 1b</i>
Arch38	1	1	0	<i>Thaumarchaeota, former Group I 1b</i>
Arch39	1	0	1	<i>Thaumarchaeota, former Group I 1b</i>

Arch40	1	1	0	<i>Thaumarchaeota, former Group I 1b</i>
Arch41	1	1	0	<i>Thaumarchaeota, former Group I 1b</i>
Arch42	1	1	0	<i>Thaumarchaeota, former Group I 1b</i>
Arch43	1	1	0	<i>Thaumarchaeota, former Group I 1b</i>
Arch44	1	1	0	<i>Thaumarchaeota, former Group I 1b</i>
Arch45	1	1	0	<i>Thaumarchaeota, former Group I 1b</i>
Arch46	1	1	0	<i>Thaumarchaeota, former Group I 1b</i>
Arch47	1	0	1	<i>Thaumarchaeota, former Group I 1b</i>
Arch48	1	1	0	<i>Methanobacteriaceae, Methanobrevibacter</i>
Arch49	1	1	0	<i>Thaumarchaeota, former Group I 1b</i>
Arch50	1	1	0	<i>Thaumarchaeota, former Group I 1b</i>
Arch51	1	1	0	<i>Thaumarchaeota, former Group I 1b</i>
Arch52	1	1	0	<i>Thaumarchaeota, former Group I 1b</i>
Arch53	1	1	0	<i>Thaumarchaeota, former Group I 1b</i>
Arch54	1	1	0	<i>Thaumarchaeota, former Group I 1b</i>
Arch55	1	1	0	<i>Thaumarchaeota, former Group I 1b</i>
Arch56	1	1	0	<i>Thaumarchaeota, former Group I 1b</i>
Arch57	1	1	0	<i>Thaumarchaeota, former Group I 1b</i>

OTU	Frequency of occurrence			Family, genus
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Cape Verde

total	coarse	fine
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CV1	1	n.a.	n.a.	<i>Halobacteriaceae</i>
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CV2	1	n.a.	n.a.	<i>Thaumarchaeota, former Group I 1b</i>
CV3	1	n.a.	n.a.	<i>Halobacteriaceae, Halococcus</i>
CV4	1	n.a.	n.a.	<i>Thaumarchaeota, former Group I 1b</i>
CV5	1	n.a.	n.a.	<i>Thaumarchaeota, former Group I 1b</i>
CV6	1	n.a.	n.a.	<i>Thaumarchaeota, former Group I 1b</i>
CV7	1	n.a.	n.a.	<i>Thermoplasmatales</i>
CV8	1	n.a.	n.a.	<i>Thaumarchaeota, former Group I 1b</i>
CV9	1	n.a.	n.a.	<i>Halobacteriaceae</i>
CV10	1	n.a.	n.a.	<i>Thaumarchaeota, former Group I 1b</i>
CV11	1	n.a.	n.a.	<i>Thaumarchaeota, former Group I 1b</i>
CV12	1	n.a.	n.a.	<i>Thermoplasmatales</i>
CV13	1	n.a.	n.a.	<i>Thermoplasmatales</i>
CV14	1	n.a.	n.a.	<i>Thaumarchaeota, former Group I 1b</i>
CV15	1	n.a.	n.a.	<i>Halobacteriaceae</i>
CV16	1	n.a.	n.a.	<i>Halobacteriaceae</i>
CV17	1	n.a.	n.a.	<i>Halobacteriaceae</i>
CV18	1	n.a.	n.a.	<i>Thaumarchaeota, former Group I 1b</i>
CV19	1	n.a.	n.a.	<i>Thaumarchaeota, former Group I 1b</i>
CV20	1	n.a.	n.a.	<i>Thaumarchaeota, former Group I 1b</i>
CV21	1	n.a.	n.a.	<i>Thaumarchaeota, former Group I 1b</i>
CV22	1	n.a.	n.a.	<i>Thermoplasmatales</i>
CV23	1	n.a.	n.a.	<i>Thaumarchaeota, former Group I 1b</i>

CV24	1	n.a.	n.a.	<i>Thaumarchaeota, former Group I 1b</i>
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CV25	1	n.a.	n.a.	<i>Thaumarchaeota, former Group I 1b</i>
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OTU	Frequency of occurrence			Family, genus
	total	coarse	fine	

UK	total	coarse	fine	
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UK1	1	n.a.	n.a.	<i>Thermoplasmatales</i>
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UK2	1	n.a.	n.a.	<i>Thermoplasmatales</i>
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UK3	1	n.a.	n.a.	<i>Thermoplasmatales</i>
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UK4	1	n.a.	n.a.	<i>Thermoplasmatales</i>
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OTU	Frequency of occurrence			Family, genus
	total	coarse	fine	

China	total	coarse	fine	
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Ch1	1	n.a.	n.a.	<i>Methanobacteriaceae</i>
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OTU	Frequency of occurrence			Family, genus
	total	coarse	fine	

North America	total	coarse	fine	
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Coll	1	n.a.	n.a.	<i>Thaumarchaeota, former Group I 1b</i>
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Table S6: Pearson coefficients results. Pearson coefficients between the diversity indices $S_{R,j}$, S_n and $S_{R,k}$, and the meteorological factors, average temperature (Temp), average relative humidity (RH), average wind speed (WS) and sum of precipitation (Precip). The asterisk mark the cases selected for further testing (See Table S7 and Figures S2a, S3).

	Temp	RH	WS	Precip
$S_{R,j}$	-0.051	0.238	-0.357 *	0.087
S_n	-0.431	0.545 *	-0.302	-0.265
$S_{R,k}$	-0.556*	0.721 *	0.170	0.236

Table S7: Overview the most significant results of the linear regression analysis between the *Archaea* 16S rRNA gene sequence diversity and meteorological parameters. The “+” and “-“ specify whether the diversity parameter has a positive or negative correlation to the meteorological factor (Temp = temperature, RH = relative humidity, WS = wind speed, Precip = precipitation, Sign = significance).

	Temp	RH	WS	Precip	R ²	p-value	Sign.	
per sample	Best single variable							
				-	0.132	0.012	<0.05	
	$S_{R,j}$ (Fig. S2a)							
per month	Best variable subset							
	$S_{R,j}$ (Fig. S2b)	+		-	0.174	0.015	<0.05	
	Best single variable							
	S_n (Fig. S3a)		+			0.297	0.054	~0.05
	$S_{R,k}$ (Fig. S3b)		+			0.520	0.005	<0.01
	$S_{R,k}$ (Fig. S3c)	-				0.309	0.049	<0.05
Best variable subset								
S_n (Fig. 4a)	-			-	0.533	0.022	<0.05	
$S_{R,k}$ (Fig. 4b)		+		+	0.598	0.011	~ 0.01	

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