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Supplement of

Microbial functional signature in the atmospheric boundary layer

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1 **Microbial functional signature in the atmospheric boundary layer**

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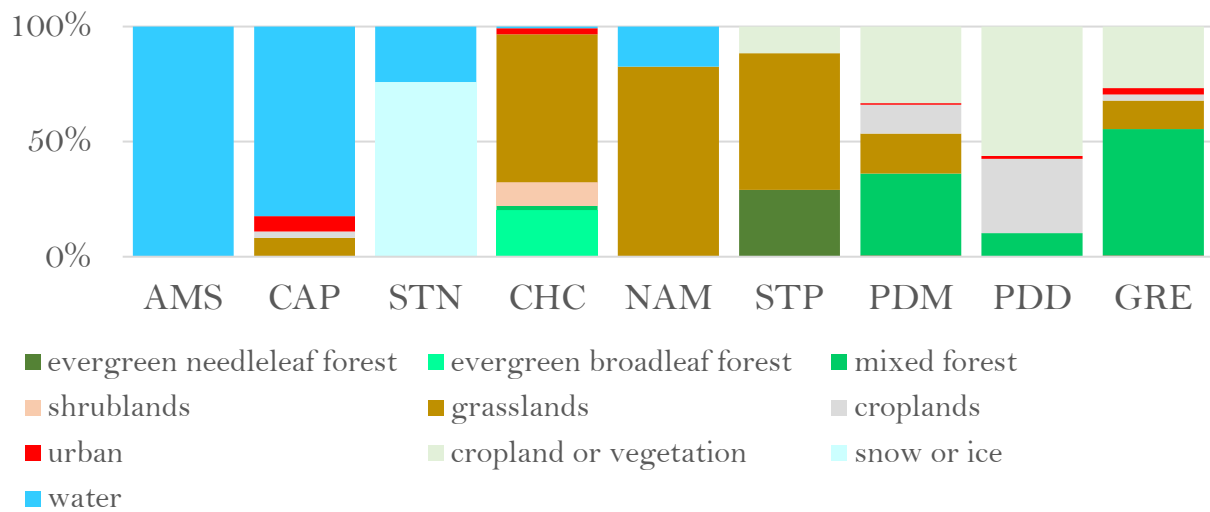
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31 **Fig S1. Surrounding landscapes of the air sampling sites.** The proportions of different landscapes
32 within a perimeter of 50 km have been calculated based on the land cover MODIS approach. AMS:
33 Amsterdam-Island, CAP: Cape-Point, STN: Station Nord, CHC: Chacaltaya, NAM: Namco, STP:
34 Storm Peak, PDM: Pic-du-Midi, PDD: puy de Dôme, GRE: Grenoble.

2 Supplementary Figures

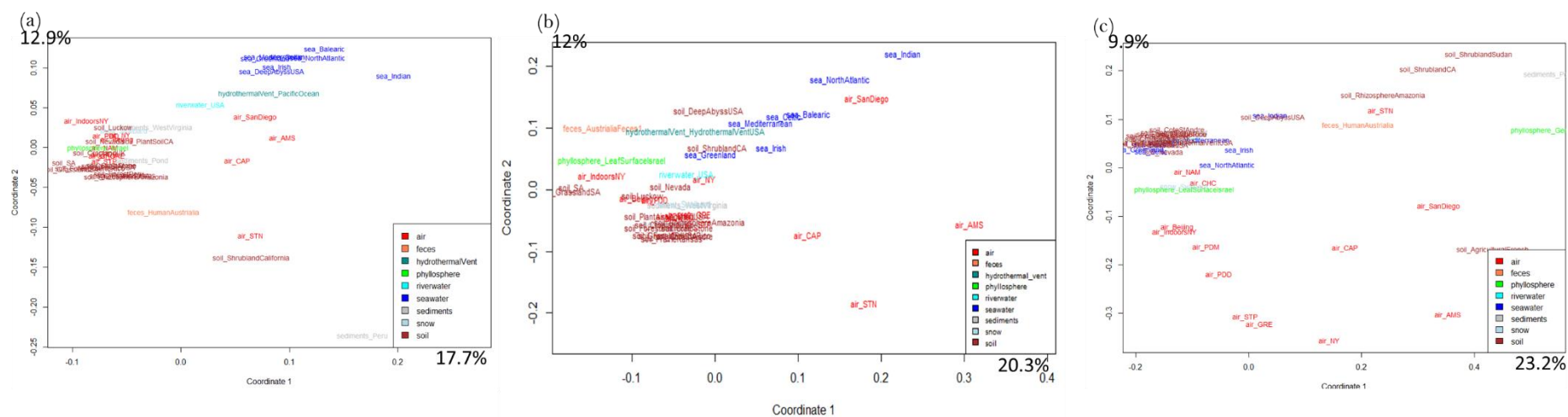


Fig S2. Distribution of the samples based on the microbial functional profile when considering all, bacterial or fungal sequences. PCoA analysis of the Bray-Curtis dissimilarity matrix based on the functional potential structure of each site. All sequences (a), bacterial sequences (b) and fungal sequences (c) have been used for functional annotation. For the site including several metagenomes, the average profile was calculated. Colors indicate the ecosystems in which the sites belong to.

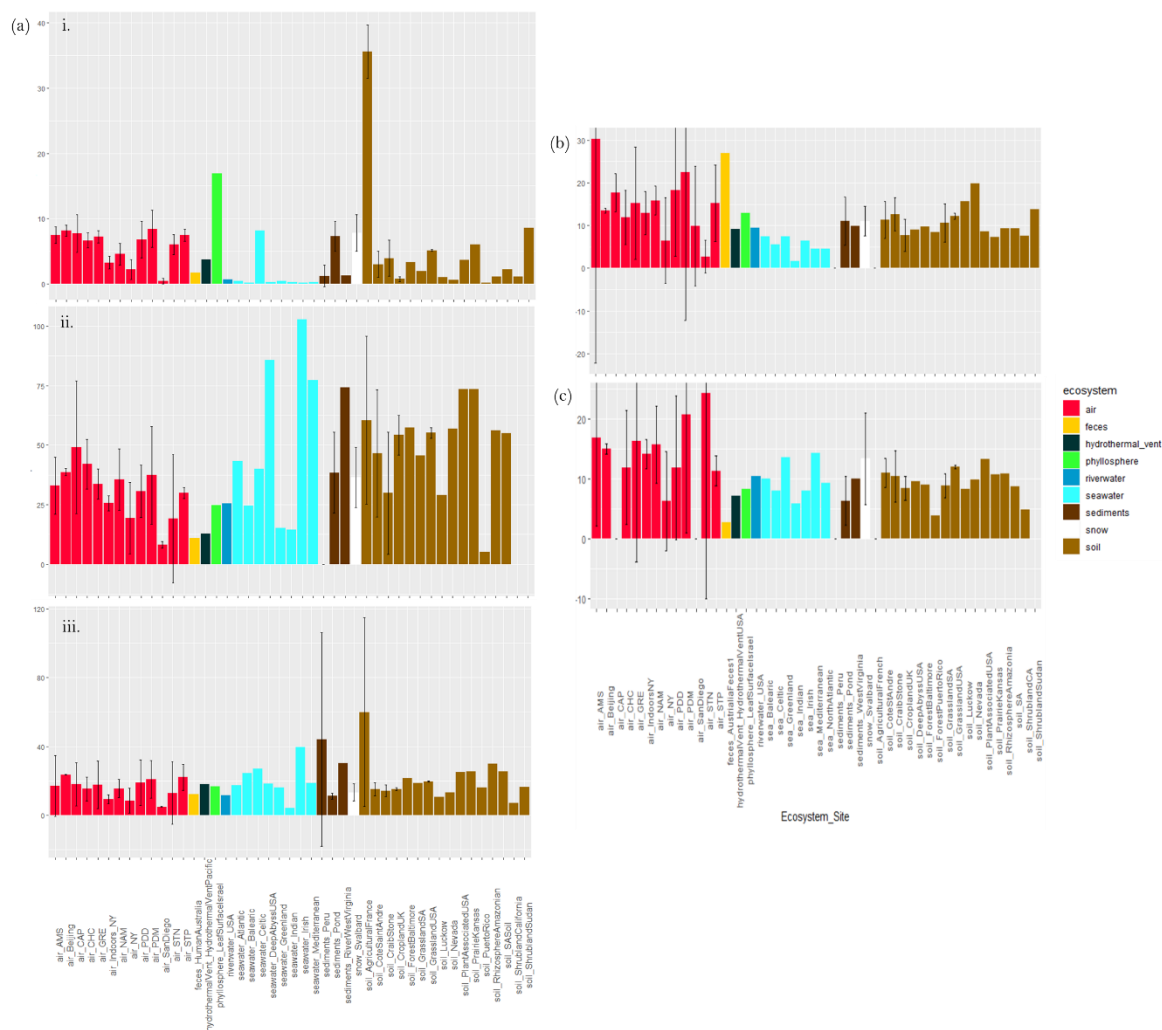


Fig S3. Proportion of sequences annotated as hydrogen peroxide catabolic process related functional proteins as well as proteins potentially implicated in stress resistance in the metagenomes. Average number of sequences annotated as proteins implicated in the hydrogen peroxide catabolic process **(a, left)** per 10000 annotated sequences from **(i)** all sequences, **(ii)** fungal sequences and **(iii)** bacterial sequences per site, and average number of hits of lipoate synthase **(b)** and chromosome plasmid partitioning protein ParA **(c)** per 10000 annotated sequences from all sequences per site. Colors indicate the ecosystems in which the sites belong to. For the sites including several metagenomes, the standard deviation was added.

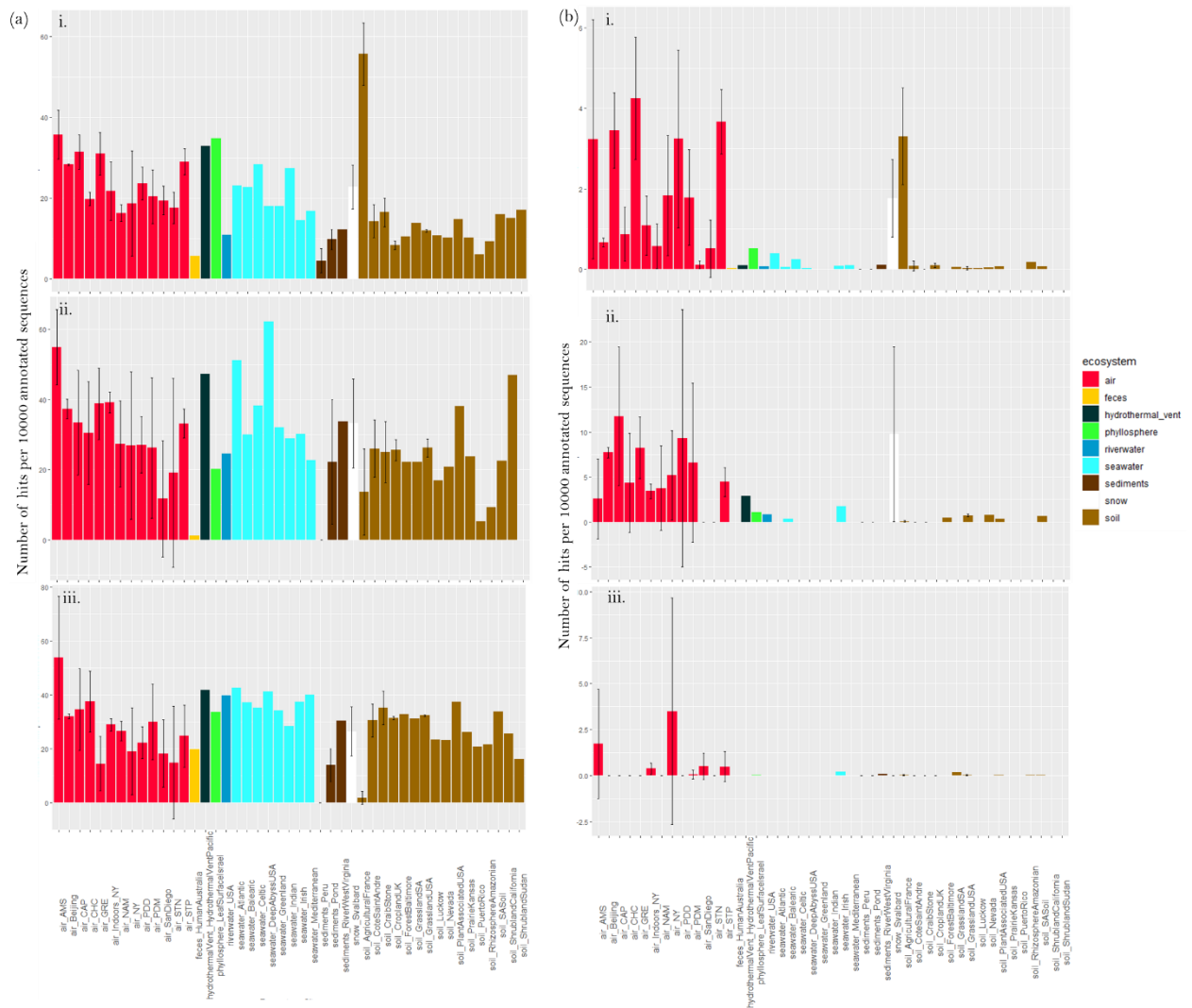


Fig S4. Proportion of sequences annotated as UV protection and desiccation response related functional proteins in the metagenomes. Average number of sequences annotated as proteins implicated in the UV protection and desiccation response (b, right) per 10000 annotated sequences from (i) all sequences, (ii) fungal sequences and (iii) bacterial sequences per site. Colors indicate the ecosystems in which the sites belong to. For the sites including several metagenomes, the standard deviation was added.

3 Supplementary tables

Table S1. Air sample collection characteristics. Standardized collected air volume and sampling starting date of each air sample that we collected for this study. AMS: Amsterdam Island, CAP: Cape Point, CHC: Chacaltaya, GRE: Grenoble, NAM: Namco, PDD: Puy de Dôme, PDM: Pic du Midi, STN: Station Nord, STP: Storm Peak

Site	Sample name	Standardized		Sampling starting date (ending date: exactly 7 days after) (month/day/year)
		collected air volume (m ³)	High volume air sampler	
AMS	AMS_10/09/2016	5232	Digitel PM10 head + pump	10/09/16
AMS	AMS_08/10/2016	4449	Digitel PM10 head + pump	08/10/16
AMS	AMS_21/10/2016	5059	Digitel PM10 head + pump	10/21/16
CAP	CAP_21/10/2016	4679	Digitel DA77 sampler	10/21/16
CAP	CAP_28/10/2016	545	Digitel DA77 sampler	10/28/16
CHC	CHC_23/09/2016	1148	Digitel PM10 head + pump	09/23/16
CHC	CHC_21/10/2016	1154	Digitel PM10 head + pump	10/21/16
CHC	CHC_28/10/2016	1220	Digitel PM10 head + pump	10/28/16
CHC	CHC_01/07/2016	1284	Digitel PM10 head + pump	01/07/16
CHC	CHC_08/07/2016	1284	Digitel PM10 head + pump	08/07/16
CHC	CHC_15/07/2016	1289	Digitel PM10 head + pump	07/15/16
CHC	CHC_12/08/2016	1160	Digitel PM10 head + pump	12/08/16
CHC	CHC_19/08/2016	1158	Digitel PM10 head + pump	08/19/16
CHC	CHC_02/09/2016	1156	Digitel PM10 head + pump	02/09/16
GRE	GRE_03/07/2017	4688	Digitel PM10 head + pump	03/07/17
GRE	GRE_10/07/2017	4717	Digitel PM10 head + pump	10/07/17
GRE	GRE_17/07/2017	4677	Digitel PM10 head + pump	07/17/17
GRE	GRE_24/07/2017	4718	Digitel PM10 head + pump	07/24/17
GRE	GRE_31/07/2017	4665	Digitel PM10 head + pump	07/31/17
GRE	GRE_07/08/2017	4762	Digitel PM10 head + pump	07/08/17
GRE	GRE_14/08/2017	4729	Digitel PM10 head + pump	08/14/17
GRE	GRE_21/08/2017	4707	Digitel PM10 head + pump	08/21/17
GRE	GRE_04/09/2017	4742	Digitel PM10 head + pump	04/09/17
NAM	NAM_17/05/2017	5511	2131 Laowin chinese sampler	05/17/17
NAM	NAM_25/05/2017	5503	2131 Laowin chinese sampler	05/25/17
NAM	NAM_02/06/2017	5513	2131 Laowin chinese sampler	02/06/17
NAM	NAM_13/06/2017	4218	2131 Laowin chinese sampler	06/13/17
NAM	NAM_20/06/2017	5418	2131 Laowin chinese sampler	06/20/17

NAM	NAM_29/06/2017	5415	2131 Laowin chinese sampler	06/29/17
NAM	NAM_07/07/2017	5483	2131 Laowin chinese sampler	07/07/17
NAM	NAM_14/07/2017	5413	2131 Laowin chinese sampler	07/14/17
NAM	NAM_21/07/2017	5465	2131 Laowin chinese sampler	07/21/17
PDD	PDD_07/06/2017	8761	Digitel PM10 head + pump	06/07/17
PDD	PDD_14/06/2017	8360	Digitel PM10 head + pump	06/14/17
PDD	PDD_21/06/2017	8672	Digitel PM10 head + pump	06/21/17
PDD	PDD_28/06/2017	9012	Digitel PM10 head + pump	06/28/17
PDD	PDD_02/08/2017	7399	Digitel PM10 head + pump	08/02/17
PDD	PDD_09/08/2017	9926	Digitel PM10 head + pump	08/09/17
PDD	PDD_30/05/2017	10232	Digitel PM10 head + pump	05/30/17
PDD	PDD_12/07/2017	8713	Digitel PM10 head + pump	07/12/17
PDD	PDD_19/07/2017	8620	Digitel PM10 head + pump	07/19/17
PDD	PDD_26/07/2017	8664	Digitel PM10 head + pump	07/26/17
PDM	PDM_20/06/2016	9664	TISCH TE-5170V sampler	06/20/16
PDM	PDM_29/06/2016	6803	TISCH TE-5170V sampler	06/29/16
PDM	PDM_12/07/2016	7550	TISCH TE-5170V sampler	12/07/16
PDM	PDM_19/07/2016	8040	TISCH TE-5170V sampler	07/19/16
PDM	PDM_26/07/2016	7794	TISCH TE-5170V sampler	07/26/16
PDM	PDM_02/08/2016	8103	TISCH TE-5170V sampler	02/08/16
PDM	PDM_09/08/2016	7747	TISCH TE-5170V sampler	08/09/16
PDM	PDM_16/08/2016	8100	TISCH TE-5170V sampler	08/16/16
PDM	PDM_23/08/2016	7956	TISCH TE-5170V sampler	08/23/16
PDM	PDM_13/09/2016	7931	TISCH TE-5170V sampler	09/13/16
PDM	PDM_20/09/2016	7853	TISCH TE-5170V sampler	09/20/16
PDM	PDM_06/09/2016	7867	TISCH TE-5170V sampler	06/09/16
PDM	PDM_16/08/2016	8100	TISCH TE-5170V sampler	08/16/16
STN	STN_27/03/2017	5153	Digitel DA80 sampler	03/27/17
STN	STN_15/05/2017	5246	Digitel DA80 sampler	05/15/17
STP	STP_14/07/2017	11213	TISCH PM10 sampler	07/14/17
STP	STP_21/07/2017	9333	TISCH PM10 sampler	07/21/17
STP	STP_28/07/2017	5702	TISCH PM10 sampler	07/28/17
STP	STP_11/08/2017	5702	TISCH PM10 sampler	08/11/17
STP	STP_18/08/2017	5702	TISCH PM10 sampler	08/18/17
STP	STP_25/08/2017	5702	TISCH PM10 sampler	08/25/17

Table S2. Characteristics of the metagenomes. Number of samples, ecosystem, sequencing technology, database and accession number, number of sequences per sample (mean + standard deviation), percentage of fungal and bacterial sequences per site and percentage of annotated sequences (mean + standard deviation) per site.

Site	Country/ Ocean	Information on the site	Number of samples	Ecosystem	Sequencing technology	Database and reference numbers or study	Total sequence number	Annotated sequence number by eggNOG- Mapper	Fungi- associated sequences	Percentage of fungi- associated sequences over total read number	Percentage of fungi- associated sequences over fungi- and bacteria- associated sequence number	Percentage of fungi- associated sequences annotated by eggNOG- Mapper	Bacteria- associated sequence number	Percentage of bacteria- associated sequences over total sequence number	Percentage of bacteria-associated sequences over fungi- and bacteria- associated sequence number	Percentage of bacteria-associated sequences annotated by eggNOG- Mapper
Air Amsterdam-Island (AMS)	Sub- Antarctica	marine, remote	3	air	MiSeq	present study	97881 +- 93551	17676 +- 15935	4152 +- 4089	4.1 +- 0.2	71 +- 4	60 +- 2	1670 +- 1549	1.7 +- 0.4	29 +- 4	57 +- 2
Air Beijing	China	urban	2	air	HiSeq	mgm4516366.3, mgm4516459.3	2248590 +- 177298	141849 +- 9576	250843 +- 9161911 +- 3.2	5.2 +- 10	17 +- 1	226290 +- 8208	10.1 +- 1.2	48 +- 10	39 +- 1	
Air Cape-Point (CAP)	South-Africa	coastal	2	air	MiSeq	present study	90043 +- 6341	20479 +- 1447	7227 +- 5972	7.8 +- 6.1	56 +- 29	50 +- 12	4530 +- 1286	5.1 +- 1.8	44 +- 29	61 +- 1
Air Chacaltaya (CHC)	Bolivia	high-altitude mountain peak	9	air	MiSeq	present study	103239 +- 54187	32699 +- 18131	3479 +- 2580	3.5 +- 1.2	27 +- 24	61 +- 7	11113 +- 6411	10.2 +- 2	73 +- 24	67 +- 2
Air Grenoble (GRE)	France	urban	9	air	MiSeq	present study	248064 +- 158109	42853 +- 30690	24234 +- 15561	9.7 +- 0.5	79 +- 10	48 +- 3	7082 +- 8061	2.7 +- 1.6	21 +- 10	59 +- 5
Air New York indoors (indoors_NY)	USA	indoors	4	air	454	SRR1000232, SRR1000254, SRR999213, SRR999215	400997 +- 49680	126245 +- 1274236858 +- 16604	9.2 +- 4.1	52 +- 17	47 +- 8	32035 +- 10923	8.3 +- 3.7	48 +- 17	70 +- 9	
Air Namco (NAM)	China	high-altitude plateau, semi-arid	9	air	MiSeq	present study	149952 +- 92976	48012 +- 36340	2958 +- 1910	2.1 +- 1.1	19 +- 12	68 +- 9	15901 +- 13188	10 +- 2.6	81 +- 12	69 +- 2
Air New York (NY)	USA	urban, coastal	6	air	454	SRR1000260, SRR1000269, SRR999217, SRR999218, SRR999219, SRR999220	521791 +- 277049	99566 +- 51023	85350 +- 41529	20 +- 11.6	56 +- 8	46 +- 41	69161 +- 38301	18.1 +- 14.5	44 +- 8	37 +- 47
Air Puy-de-Dôme (PDD)	France	continental, mountain peak	10	air	MiSeq	present study	396666 +- 364681	65304 +- 68592	25029 +- 32432	5.8 +- 2.5	62 +- 16	50 +- 6	13112 +- 12079	3.9 +- 3	38 +- 16	56 +- 4

Air Pic-du-Midi (PDM)	France	high-altitude mountain peak	13	air	MiSeq	present study	186766 +- 197396	33016 +- 31653	8676 +- 8233	5 +- 2.1	50 +- 10	54 +- 4	8115 +- 7687	5.5 +- 2.6	50 +- 10	63 +- 5
Air San-Diego	USA	urban coastal	2	air	454	SRR999211, SRR999212	781206 +- 65608	229544 +- 3651	5960 +- 4678	0.8 +- 0.7	36 +- 1	44 +- 3	10318 +- 7888	1.4 +- 1.1	64 +- 1	54 +- 13
Air Station-Nord (STN)	Greenland	polar	2	air	MiSeq	present study	23463 +- 24385	5935 +- 5528	1276 +- 1702	3.6 +- 3.5	24 +- 18	59 +- 38	2460 +- 2606	10.2 +- 0.5	76 +- 18	65 +- 3
Air Storm-Peak (STP)	USA	high-altitude mountain peak	6	air	MiSeq	present study	469168 +- 242715	111530 +- 58582	99110 +- 56113	20.7 +- 2.6	88 +- 4	53 +- 2	12559 +- 7185	2.8 +- 1.1	12 +- 4	59 +- 5
Human feces Sydney	Australia	human feces	1	feces	HiSeq	mgm4675774.3	2111825 +- NA	503328 +- NA	28357 +- NA	1.3 +- NA	3 +- NA	29 +- NA	929682 +- NA	44 +- NA	97 +- NA	35 +- NA
Hydrothermal vent Pacific	Pacific Ocean	deep sea water	1	hydrothermal vent	454	mgm4481541.3	758485 +- NA	409294 +- NA	12501 +- NA	1.6 +- NA	9 +- NA	56 +- NA	128294 +- NA	16.9 +- NA	91 +- NA	84 +- NA
Leaf surface Israel	Israel	leaf surface	1	phyllosphere	HiSeq	mgm4534773.3	12272440 +- NA	3274840 +- NA	460612 +- NA	3.8 +- NA	37 +- NA	23 +- NA	784441 +- NA	6.4 +- NA	63 +- NA	70 +- NA
Seawater Atlantic sea	North Atlantic Ocean	surface sea water	1	seawater	MiSeq	mgm4719942.3	1198007 +- NA	301519 +- NA	54904 +- NA	4.6 +- NA	36 +- NA	11 +- NA	99510 +- NA	8.3 +- NA	64 +- NA	51 +- NA
Seawater Balearic sea	Balearic Sea	surface sea water	1	seawater	MiSeq	mgm4719938.3	878884 +- NA	531765 +- NA	50995 +- NA	5.8 +- NA	36 +- NA	60 +- NA	89238 +- NA	10.2 +- NA	64 +- NA	88 +- NA
Seawater Celtic sea	Celtic Sea	surface sea water	1	seawater	MiSeq	mgm4719941.3	1702779 +- NA	283691 +- NA	510855 +- NA	11.4 +- NA	53 +- NA	18 +- NA	112212 +- NA	6.6 +- NA	47 +- NA	55 +- NA
Deep abyss USA	USA	deep sea water	1	seawater	454	mgm4668304.3	2016153 +- NA	330380 +- NA	1895 +- NA	0.1 +- NA	2 +- NA	68 +- NA	90930 +- NA	4.5 +- NA	98 +- NA	75 +- NA
Seawater Greenland sea	Greenland Sea	surface sea water	1	seawater	MiSeq	mgm4719947.3	1358477 +- NA	687315 +- NA	79494 +- NA	5.9 +- NA	28 +- NA	51 +- NA	200245 +- NA	14.7 +- NA	72 +- NA	77 +- NA
Seawater Indian sea	Indian Sea	surface sea water	1	seawater	MiSeq	mgm4719994.3	126564 +- NA	56086 +- NA	2527 +- NA	2 +- NA	11 +- NA	55 +- NA	21431 +- NA	16.9 +- NA	89 +- NA	89 +- NA
Seawater Irish sea	Irish Sea	surface sea water	1	seawater	MiSeq	mgm4719940.3	1362228 +- NA	538286 +- NA	27051 +- NA	2 +- NA	28 +- NA	21 +- NA	69952 +- NA	5.1 +- NA	72 +- NA	70 +- NA
Seawater Mediterranean sea	Eastern Mediterranean Sea	surface sea water	1	seawater	MiSeq	mgm4719936.3	1241549 +- NA	686395 +- NA	17384 +- NA	1.4 +- NA	11 +- NA	43 +- NA	133889 +- NA	10.8 +- NA	89 +- NA	87 +- NA
River water Colorado	USA	river water	1	riverwater	HiSeq	mgm4628878.3	1392059 +- NA	575616 +- NA	39553 +- NA	2.8 +- NA	19 +- NA	31 +- NA	169972 +- NA	12.2 +- NA	81 +- NA	76 +- NA
River sediments West Virginia	USA	river sediments	1	sediments	HiSeq	mgm4589537.3	2072338 +- NA	569631 +- NA	58672 +- NA	2.8 +- NA	26 +- NA	28 +- NA	166079 +- NA	8 +- NA	74 +- NA	71 +- NA
Sediments Peru	Peru	seafloor sediments	2	sediments	454	mgm4440960.3, mgm4459940.3	126239 +- 35030	3606 +- 829	1780 +- 2323	1.2 +- 1.5	53 +- 47	13 +- 16	539 +- 18	0.4 +- 0.1	47 +- 47	33 +- 11
Sediments Pond	France	shallow pond sediments	4	sediments	MiSeq	our lab; Sanchez-Cid <i>et al.</i> , under review	44236 +- 17409	15568 +- 7046	1450 +- 991	3.2 +- 1.2	9 +- 3	80 +- 5	16704 +- 12966	36.7 +- 18.1	91 +- 3	56 +- 8
Snow Svalbard	Norway	fresh snow, artic	7	snow	MiSeq	our lab; Bergk-Pinto <i>et al.</i> , under review	226368 +- 70313	49428 +- 23023	3788 +- 1542	1.7 +- 0.6	18 +- 6	61 +- 12	18469 +- 8699	8.5 +- 3.2	82 +- 6	54 +- 5
Agricultural soil France	France	agricultural soil	3	soil	MiSeq	mgm4705012.3, mgm4697958.3, mgm4697957.3	8209393 +- 2836681	5913635 +- 1326693	194398 +- 108165	2.3 +- 0.5	61 +- 3	60 +- 13	129460 +- 84783	1.5 +- 0.5	39 +- 3	65 +- 11

Soil Cote Saint Andre	France	agricultural soil	6	soil	MiSeq	our lab; Sanchez-Cid <i>et al.</i> , under review	174898 +- 80968	54841 +- 22225	1638 +- 640	1 +- 0.1	9 +- 1	82 +- 2	16806 +- 6846	9.8 +- 0.6	91 +- 1	67 +- 1
Soil CraibStone	Scotland	agricultural soil	5	soil	MiSeq	our lab; Sanchez-Cid <i>et al.</i> , under review	128815 +- 82837	41175 +- 22413	1452 +- 953	1.1 +- 0.1	9 +- 1	78 +- 4	15472 +- 11906	11.5 +- 1.2	91 +- 1	65 +- 1
Cropland UK	United Kingdom	cropland	2	soil	MiSeq	mgm4781436.3, mgm4781437.3	485163 +- 163475	304642 +- 104503	9970 +- 3861	2 +- 0.1	13 +- 0	88 +- NA	66040 +- 25119	13.5 +- 0.6	87 +- 0	95 +- 0
Forest soil Baltimore	USA	temperate deciduous broadleaf forest soil	1	soil	MiSeq	mgm4819073.3	4600481 +- NA	959764 +- NA	34207 +- NA	0.7 +- NA	12 +- NA	62 +- NA	260826 +- NA	5.7 +- NA	88 +- NA	79 +- NA
Grassland USA	South-Africa	tropical grassland	1	soil	MiSeq	mgm4819072.3	2519738 +- NA	638149 +- NA	22974 +- NA	0.9 +- NA	8 +- NA	63 +- NA	279551 +- NA	11.1 +- NA	92 +- NA	79 +- NA
Grassland USA	USA	temperate grassland	2	soil	MiSeq	mgm4623641.3, mgm4623640.3	12195227 +- 1436683	697967 +- 122932	1753640 +- 1903	14.5 +- 1.7	42 +- 1	2 +- 0	2381163 +- 99911	19.6 +- 1.5	58 +- 1	13 +- 2
Soil Lucknow India	India	soil	1	soil	454	mgm4461840.3	1187505 +- NA	658023 +- NA	53911 +- NA	4.5 +- NA	14 +- NA	91 +- NA	322160 +- NA	27.1 +- NA	86 +- NA	91 +- NA
Soil Nevada	USA	soil	1	soil	454	mgm4451106.3	1248623 +- NA	725892 +- NA	29880 +- NA	2.4 +- NA	8 +- NA	84 +- NA	326929 +- NA	26.2 +- NA	92 +- NA	91 +- NA
Plant soil USA	USA	soil	1	soil	HiSeq	mgm4767414.3	17632266 +- NA	1425603 +- NA	253827 +- NA	1.4 +- NA	15 +- NA	33 +- NA	1473019 +- NA	8.4 +- NA	85 +- NA	52 +- NA
Prairie Kansas	USA	prairie soil	1	soil	MiSeq	mgm4477804.3	5348832 +- NA	343702 +- NA	27412 +- NA	0.5 +- NA	9 +- NA	51 +- NA	270464 +- NA	5.1 +- NA	91 +- NA	56 +- NA
Soil PuertoRico	Puerto Rico	subtropical forest	1	soil	454	mgm4446153.3	725275 +- NA	452063 +- NA	10926 +- NA	1.5 +- NA	11 +- NA	88 +- NA	85868 +- NA	11.8 +- NA	89 +- NA	95 +- NA
Rhizosphere Amazonia	Brazil	tropical broadleaf forest	1	soil	HiSeq	mgm4723911.3	8884491 +- NA	1415017 +- NA	2075 +- NA	0 +- NA	0 +- NA	52 +- NA	1027815 +- NA	11.6 +- NA	100 +- NA	60 +- NA
Soil South-Africa	South-Africa	tropical grassland	1	soil	MiSeq	mgm4819068.3	2757834 +- NA	759329 +- NA	25123 +- NA	0.9 +- NA	6 +- NA	64 +- NA	414056 +- NA	15 +- NA	94 +- NA	79 +- NA
Shrubland California	USA	shrubland	1	soil	MiSeq	mgm4806895.3	2213724 +- NA	47591 +- NA	3742 +- NA	0.2 +- NA	1 +- NA	11 +- NA	243528 +- NA	11 +- NA	98 +- NA	7 +- NA
Shrubland Sudan	Sudan	shrubland	1	soil	MiSeq	mgm4806896.3	185966 +- NA	1169 +- NA	1181 +- NA	0.6 +- NA	18 +- NA	7 +- NA	5381 +- NA	2.9 +- NA	82 +- NA	11 +- NA

Table S3. Functional richness and evenness averaged per site. Functional richness and evenness after rarefaction per site, based on the SEED functional classes. For site including several samples, the mean and standard deviation have been calculated.

Site	Ecosystem	All sequences			Fungal sequences				Bacterial sequences				
		Number of annotated sequences using Diamond and MEGAN6	Rarefaction	Functional richness after rarefaction	Functional evenness after rarefaction	Number of annotated sequences using Diamond and MEGAN6	Rarefaction	Functional richness after rarefaction	Functional evenness after rarefaction	Number of annotated sequences using Diamond and MEGAN6	Rarefaction	Functional richness after rarefaction	Functional evenness after rarefaction
air Amsterdam-Island (AMS)	air	3927 +- 3321	1737 +- 456	1087 +- 554	0.94 +- 0.02	81 +- 80	81 +- 80	66 +- 58	0.99 +- 0.01	554 +- 480	360 +- 193	270 +- 197	0.96 +- 0.01
air Beijing	air	180196 +- 11408	2000 +- 0	4060 +- 112	0.86 +- 0	5960 +- 214	500 +- 0	1129 +- 92	0.89 +- 0	82004 +- 5643	500 +- 0	2835 +- 58	0.87 +- 0
air Cape-Point (CAP)	air	8176 +- 4856	2000 +- 0	1634 +- 337	0.93 +- 0.02	211 +- 15	211 +- 15	162 +- 6	0.97 +- 0	1890 +- 726	500 +- 0	739 +- 192	0.95 +- 0.01
air Chacaltaya (CHC)	air	15853 +- 8907	1848 +- 456	2062 +- 714	0.92 +- 0.02	380 +- 219	346 +- 175	223 +- 109	0.96 +- 0.02	5268 +- 3052	467 +- 99	1142 +- 461	0.93 +- 0.02
air Grenoble (GRE)	air	5765 +- 6870	1802 +- 297	1256 +- 700	0.94 +- 0.02	412 +- 382	308 +- 156	235 +- 153	0.97 +- 0.01	2193 +- 2949	445 +- 86	658 +- 528	0.96 +- 0.02
air indoors New York (indoors_NY)	air	32135 +- 11235	2000 +- 0	3302 +- 299	0.91 +- 0.01	1546 +- 802	500 +- 0	697 +- 206	0.95 +- 0.01	10067 +- 4782	500 +- 0	2183 +- 387	0.93 +- 0.01
air Namco (NAM)	air	23081 +- 19276	2000 +- 0	2280 +- 478	0.91 +- 0.01	596 +- 495	381 +- 114	287 +- 136	0.95 +- 0.02	7600 +- 6515	500 +- 0	1300 +- 372	0.92 +- 0.02
air New York (NY)	air	5481 +- 4324	1639 +- 561	1384 +- 849	0.89 +- 0.04	286 +- 231	275 +- 217	150 +- 109	0.91 +- 0.07	769 +- 622	362 +- 205	446 +- 335	0.94 +- 0.02
air Puy-de-Dôme (PDD)	air	11053 +- 9757	1976 +- 75	1700 +- 775	0.93 +- 0.02	656 +- 748	300 +- 198	297 +- 239	0.96 +- 0.03	4277 +- 4138	500 +- 0	989 +- 617	0.94 +- 0.03
air Pic-du-Midi (PDM)	air	9422 +- 8988	1769 +- 490	1575 +- 778	0.94 +- 0.02	363 +- 354	267 +- 185	218 +- 163	0.98 +- 0.02	3252 +- 3366	460 +- 101	832 +- 511	0.95 +- 0.02
air San Diego	air	14573 +- 8176	2000 +- 0	2021 +- 81	0.9 +- 0	184 +- 191	184 +- 191	91 +- 66	0.96 +- 0.04	1737 +- 1841	468 +- 46	628 +- 429	0.95 +- 0.01
air Station-Nord (STN)	air	2863 +- 2408	1580 +- 594	956 +- 547	0.95 +- 0.02	111 +- 111	111 +- 111	88 +- 81	0.98 +- 0.01	1089 +- 1085	411 +- 127	486 +- 400	0.96 +- 0.01
air Storm-Peak (STP)	air	11763 +- 7684	2000 +- 0	1865 +- 519	0.92 +- 0.01	973 +- 537	476 +- 58	392 +- 131	0.94 +- 0.02	3757 +- 3006	500 +- 0	971 +- 409	0.94 +- 0.02
human feces Sydney	feces	560641 +- NA	2000 +- NA	2802 +- NA	0.82 +- NA	3591 +- NA	500 +- NA	317 +- NA	0.61 +- NA	304338 +- NA	500 +- NA	2557 +- NA	0.87 +- NA
leaf surface Israel	phyllosphere	1042866 +- NA	2000 +- NA	4292 +- NA	0.87 +- NA	10644 +- NA	500 +- NA	1336 +- NA	0.85 +- NA	247373 +- NA	500 +- NA	3165 +- NA	0.88 +- NA
river water USA	river water	295902 +- NA	2000 +- NA	3550 +- NA	0.87 +- NA	6142 +- NA	500 +- NA	1001 +- NA	0.89 +- NA	76857 +- NA	500 +- NA	2497 +- NA	0.87 +- NA
seawater Balearic sea	seawater	340618 +- NA	2000 +- NA	2957 +- NA	0.87 +- NA	17554 +- NA	500 +- NA	1825 +- NA	0.9 +- NA	55185 +- NA	500 +- NA	1823 +- NA	0.86 +- NA
seawater Celtic sea	seawater	335790 +- NA	2000 +- NA	3325 +- NA	0.87 +- NA	11736 +- NA	500 +- NA	1831 +- NA	0.91 +- NA	41271 +- NA	500 +- NA	1964 +- NA	0.87 +- NA
deep abyss USA	seawater	333284 +- NA	2000 +- NA	3649 +- NA	0.87 +- NA	1006 +- NA	500 +- NA	390 +- NA	0.92 +- NA	43055 +- NA	500 +- NA	2590 +- NA	0.9 +- NA
seawater Greenland sea	seawater	417826 +- NA	2000 +- NA	3223 +- NA	0.88 +- NA	21407 +- NA	500 +- NA	2164 +- NA	0.91 +- NA	97826 +- NA	500 +- NA	2376 +- NA	0.87 +- NA
hydrothermal Vent Pacific Ocean	hydrothermal vent	217796 +- NA	2000 +- NA	3621 +- NA	0.87 +- NA	3855 +- NA	500 +- NA	950 +- NA	0.9 +- NA	62974 +- NA	500 +- NA	2533 +- NA	0.89 +- NA
seawater Indian sea	seawater	40507 +- NA	2000 +- NA	2178 +- NA	0.9 +- NA	799 +- NA	500 +- NA	476 +- NA	0.96 +- NA	12001 +- NA	500 +- NA	1183 +- NA	0.93 +- NA
seawater Irish sea	seawater	287629 +- NA	2000 +- NA	3283 +- NA	0.88 +- NA	2394 +- NA	500 +- NA	662 +- NA	0.89 +- NA	32848 +- NA	500 +- NA	1843 +- NA	0.86 +- NA

seawater Mediterranean sea	seawater	381180 +- NA	2000 +- NA	3375 +- NA	0.87 +- NA	3999 +- NA	500 +- NA	898 +- NA	0.87 +- NA	74727 +- NA	500 +- NA	2112 +- NA	0.88 +- NA
seawater North Atlantic Ocean	seawater	206085 +- NA	2000 +- NA	3143 +- NA	0.87 +- NA	2956 +- NA	500 +- NA	771 +- NA	0.9 +- NA	35702 +- NA	500 +- NA	1663 +- NA	0.89 +- NA
sediments Peru	sediments	6348 +- 1251	2000 +- 0	1138 +- 7	0.92 +- 0	13 +- 4	13 +- 4	13 +- 4	1 +- 0	133 +- 66	133 +- 66	90 +- 33	0.97 +- 0.02
sediments Pond	sediments	10569 +- 5084	2000 +- 0	1791 +- 252	0.92 +- 0.01	647 +- 422	441 +- 106	367 +- 149	0.97 +- 0.01	7038 +- 5091	500 +- 0	1364 +- 392	0.93 +- 0.01
river sediments West Virginia	sediments	315551 +- NA	2000 +- NA	3869 +- NA	0.87 +- NA	10660 +- NA	500 +- NA	1223 +- NA	0.88 +- NA	74774 +- NA	500 +- NA	2381 +- NA	0.88 +- NA
snow Svalbard	snow	26069 +- 15249	2000 +- 0	2243 +- 498	0.91 +- 0.01	648 +- 360	418 +- 152	329 +- 143	0.96 +- 0.02	8702 +- 4544	500 +- 0	1317 +- 356	0.92 +- 0.02
agricultural soil France	soil	907295 +- 258019	2000 +- 0	764 +- 47	0.72 +- 0.02	8707 +- 6045	442 +- 116	129 +- 74	0.68 +- 0.1	7044 +- 2095	500 +- 0	118 +- 55	0.49 +- 0.05
soil Cote Saint Andre	soil	34947 +- 16517	2000 +- 0	2552 +- 263	0.9 +- 0.01	783 +- 355	491 +- 14	350 +- 92	0.94 +- 0.01	8680 +- 3716	500 +- 0	1418 +- 191	0.91 +- 0.01
soil CraibStone	soil	27629 +- 18784	2000 +- 0	2406 +- 327	0.91 +- 0.01	668 +- 473	465 +- 46	336 +- 127	0.95 +- 0.02	7980 +- 6183	500 +- 0	1346 +- 289	0.92 +- 0.01
cropland UK	soil	122625 +- 44684	2000 +- 0	3490 +- 132	0.87 +- 0	5106 +- 1863	500 +- 0	1001 +- 112	0.89 +- 0.02	34986 +- 13329	500 +- 0	2254 +- 103	0.89 +- 0.01
forest soil Baltimore	soil	606468 +- NA	2000 +- NA	3998 +- NA	0.86 +- NA	33130 +- 27346	500 +- 0	1438 +- 259	0.84 +- 0.02	288964	500 +- 0	2518 +- 4	0.86 +- 0
soil Puerto Rico	soil	170277 +- NA	2000 +- NA	3607 +- NA	0.86 +- NA	6380 +- NA	500 +- NA	971 +- NA	0.88 +- NA	45321 +- NA	500 +- NA	2229 +- NA	0.87 +- NA
grassland SA	soil	191711 +- 271120	1000 +- 1414	2093 +- 2959	0.43 +- 0.61	14252 +- 9262	500 +- 0	1216 +- 199	0.85 +- 0.01	260034	500 +- 0	3147 +- 93	0.9 +- 0.02
grassland USA	soil	926515 +- 144620	2000 +- 0	3496 +- 45	0.86 +- 0	23892 +- 4105	500 +- 0	1539 +- 35	0.84 +- 0	44860	500 +- 0	2332 +- 42	0.86 +- 0
soil lucknow India	soil	303263 +- NA	2000 +- NA	3971 +- NA	0.88 +- NA	19077 +- NA	500 +- NA	1357 +- NA	0.87 +- NA	145062 +- NA	500 +- NA	2707 +- NA	0.89 +- NA
soil Nevada	soil	305066 +- NA	2000 +- NA	3528 +- NA	0.87 +- NA	12931 +- NA	500 +- NA	1324 +- NA	0.85 +- NA	147232 +- NA	500 +- NA	2465 +- NA	0.89 +- NA
plant soil USA	soil	1839508 +- NA	2000 +- NA	3610 +- NA	0.87 +- NA	65330 +- NA	500 +- NA	1663 +- NA	0.84 +- NA	612710 +- NA	500 +- NA	2491 +- NA	0.87 +- NA
prairie Kansas	soil	475235 +- NA	2000 +- NA	3393 +- NA	0.86 +- NA	11087 +- NA	500 +- NA	1155 +- NA	0.85 +- NA	119659 +- NA	500 +- NA	2282 +- NA	0.87 +- NA
rhizosphere Amazonia	soil	1061420 +- NA	2000 +- NA	3330 +- NA	0.81 +- NA	337 +- NA	337 +- NA	157 +- NA	0.91 +- NA	412216 +- NA	500 +- NA	1912 +- NA	0.79 +- NA
soil South-Africa	soil	464748 +- NA	2000 +- NA	4239 +- NA	0.88 +- NA	8883 +- NA	500 +- NA	1092 +- NA	0.85 +- NA	187173 +- NA	500 +- NA	3252 +- NA	0.91 +- NA
shrubland California	soil	65837 +- NA	2000 +- NA	2693 +- NA	0.87 +- NA	298 +- NA	298 +- NA	126 +- NA	0.92 +- NA	14541 +- NA	500 +- NA	1757 +- NA	0.89 +- NA
shrubland Sudan	soil	1751 +- NA	1751 +- NA	864 +- NA	0.96 +- NA	77 +- NA	77 +- NA	68 +- NA	0.99 +- NA	727 +- NA	500 +- NA	437 +- NA	0.97 +- NA

Table S4. Ratio between 16S and 18S rRNA gene copy numbers in air and soil. qPCR on the 16s rRNA gene and on the 18S rRNA gene on air and soil samples, and ratio between these qPCRs. Means and standard deviations were calculated on three (Cote Saint André), nine (Amsterdam-Island and Namco) and ten (Grenoble) samples. qPCR results for the air samples have already been presented in Tignat-Perrier et al., 2019.

	qPCR 18S rRNA gene number	qPCR 16S rRNA gene number	Ratio qPCR16S/qPCR18S
AIR SAMPLES			
NAM (Namco)	$4.97 \times 10^3 \pm 3.44 \times 10^3$	$3.56 \times 10^6 \pm 3.01 \times 10^6$	716
GRE (Grenoble)	$5.28 \times 10^4 \pm 3.61 \times 10^4$	$1.20 \times 10^6 \pm 9.38 \times 10^5$	23
AMS (Amsterdam- Island)	$7.51 \times 10^3 \pm 6.96 \times 10^3$	$1.49 \times 10^5 \pm 9.17 \times 10^4$	20
SOIL SAMPLES			
Côte Saint André	$1.13 \times 10^3 \pm 2.9 \times 10^2$	$3.70 \times 10^6 \pm 1.9 \times 10^6$	3265

Table S5. Dominant SEED functions in the metagenomes. Top 50 of the SEED functions observed in the air samples (mean +/- standard deviation) considering all the sequences (*i.e.* bacterial and fungal sequences).

Function	air_AMS	air_Beijing	air_CAP	air_CHC	air_GRE	air_IndoorsNY	air_NAM	air_NY	air_PDD	air_PDM	air_SanDiego	air_STN	air_STP
\5-FCL-like protein\''''	2.01 +/- 0.66	2.04 +/- 0.12	1.6 +/- 0.13	1.9 +/- 0.13	1.84 +/- 0.33	1.62 +/- 0.08	1.97 +/- 0.15	1.53 +/- 0.54	1.68 +/- 0.32	1.78 +/- 0.37	1.41 +/- 0.12	1.47 +/- 0.24	1.81 +/- 0.31
\Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3)\''''	2.3 +/- 0.09	1.35 +/- 0.3	1.29 +/- 0.47	1.46 +/- 0.25	1.62 +/- 0.27	1.17 +/- 0.2	1.51 +/- 0.12	1.12 +/- 0.53	1.79 +/- 1.2	1.58 +/- 0.22	0.91 +/- 0.02	2.01 +/- 0.45	1.86 +/- 0.42
\TonB-dependent receptor\''''	1.3 +/- 0.44	0.36 +/- 0.03	1.02 +/- 0.4	0.94 +/- 0.14	1.07 +/- 0.46	0.91 +/- 0.15	0.98 +/- 0.12	0.72 +/- 0.12	0.99 +/- 0.51	1.03 +/- 0.28	0.45 +/- 0.04	1.06 +/- 0.52	0.83 +/- 0.27
\3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)\''''	0.65 +/- 0.28	0.55 +/- 0.02	0.75 +/- 0.01	0.9 +/- 0.11	0.8 +/- 0.26	0.62 +/- 0.06	1.04 +/- 0.11	0.56 +/- 0.17	0.75 +/- 0.25	0.79 +/- 0.24	0.45 +/- 0.05	0.84 +/- 0.09	0.91 +/- 0.21
\COG2363\''''	0.53 +/- 0.3	0.5 +/- 0.02	0.58 +/- 0.14	0.51 +/- 0.08	0.58 +/- 0.16	0.56 +/- 0.07	0.49 +/- 0.11	0.26 +/- 0.2	0.54 +/- 0.13	0.55 +/- 0.13	0.56 +/- 0.26	0.48 +/- 0.07	0.45 +/- 0.05
\Aldehyde dehydrogenase (EC 1.2.1.3)\''''	0.43 +/- 0.21	0.4 +/- 0.03	0.44 +/- 0.1	0.31 +/- 0.04	0.58 +/- 0.13	0.29 +/- 0.07	0.39 +/- 0.06	0.68 +/- 1.11	0.42 +/- 0.2	0.35 +/- 0.17	0.29 +/- 0.04	0.25 +/- 0.23	0.47 +/- 0.09
\Adenylate cyclase (EC 4.6.1.1)\''''	0.26 +/- 0.18	0.17 +/- 0.02	0.18 +/- 0.11	0.36 +/- 0.15	0.27 +/- 0.18	0.29 +/- 0.06	0.79 +/- 0.07	0.25 +/- 0.24	0.41 +/- 0.23	0.46 +/- 0.14	0.23 +/- 0.06	0.53 +/- 0.02	0.32 +/- 0.1
\Beta-galactosidase (EC 3.2.1.23)\''''	0.15 +/- 0.06	0.23 +/- 0.05	0.34 +/- 0.03	0.34 +/- 0.15	0.25 +/- 0.14	0.22 +/- 0.05	0.3 +/- 0.06	1.41 +/- 2.13	0.28 +/- 0.16	0.3 +/- 0.21	0.22 +/- 0.08	0.18 +/- 0.25	0.35 +/- 0.07
\DNA-directed RNA polymerase beta' subunit (EC 2.7.7.6)\''''	0.58 +/- 0.13	0.53 +/- 0.03	0.39 +/- 0.07	0.38 +/- 0.07	0.3 +/- 0.13	0.15 +/- 0.04	0.38 +/- 0.04	0.09 +/- 0.08	0.51 +/- 0.42	0.39 +/- 0.11	0.32 +/- 0.11	0.29 +/- 0.17	0.39 +/- 0.07
\Aspartate aminotransferase (EC 2.6.1.1)\''''	0.53 +/- 0.08	0.39 +/- 0.02	0.35 +/- 0.08	0.38 +/- 0.07	0.35 +/- 0.13	0.43 +/- 0.07	0.33 +/- 0.05	0.4 +/- 0.32	0.35 +/- 0.14	0.34 +/- 0.09	0.29 +/- 0.01	0.37 +/- 0.28	0.33 +/- 0.03
\Cobalt-zinc-cadmium resistance protein CzcA\''''	0.17 +/- 0.1	0.3 +/- 0.08	0.2 +/- 0.01	0.36 +/- 0.06	0.26 +/- 0.13	0.49 +/- 0.14	0.26 +/- 0.04	0.72 +/- 0.24	0.4 +/- 0.18	0.38 +/- 0.15	0.24 +/- 0.01	0.63 +/- 0.41	0.22 +/- 0.04
\DNA topoisomerase I (EC 5.99.1.2)\''''	0.07 +/- 0.07	0.17 +/- 0.01	0.08 +/- 0.05	0.12 +/- 0.05	0.08 +/- 0.03	0.12 +/- 0.02	0.16 +/- 0.04	3.08 +/- 4.05	0.14 +/- 0.11	0.1 +/- 0.06	0.16 +/- 0.01	0.27 +/- 0.1	0.1 +/- 0.03
\High-affinity carbon uptake protein Hat/HatR\''''	0.29 +/- 0.04	0.16 +/- 0.09	0.09 +/- 0.05	0.19 +/- 0.09	1.27 +/- 0.94	0.17 +/- 0.06	0.35 +/- 0.18	0.31 +/- 0.18	0.23 +/- 0.15	0.14 +/- 0.09	0.08 +/- 0.04	0.12 +/- 0.17	0.32 +/- 0.19
\Beta-lactamase\''''	0.47 +/- 0.18	0.15 +/- 0.01	0.28 +/- 0.04	0.29 +/- 0.12	0.23 +/- 0.12	0.26 +/- 0.06	0.41 +/- 0.09	0.62 +/- 0.64	0.24 +/- 0.1	0.41 +/- 0.11	0.26 +/- 0	0.2 +/- 0.16	0.3 +/- 0.05
\DNA-directed RNA polymerase beta subunit (EC 2.7.7.6)\''''	0.39 +/- 0.19	0.49 +/- 0.03	0.35 +/- 0.1	0.35 +/- 0.07	0.24 +/- 0.11	0.15 +/- 0.06	0.34 +/- 0.09	0.04 +/- 0.04	0.44 +/- 0.48	0.3 +/- 0.09	0.31 +/- 0.12	0.51 +/- 0.26	0.3 +/- 0.04
\Butyryl-CoA dehydrogenase (EC 1.3.99.2)\''''	0.34 +/- 0.22	0.29 +/- 0.04	0.31 +/- 0.15	0.3 +/- 0.13	0.36 +/- 0.16	0.19 +/- 0.05	0.33 +/- 0.04	0.21 +/- 0.1	0.3 +/- 0.17	0.3 +/- 0.09	0.19 +/- 0.02	0.36 +/- 0.23	0.35 +/- 0.09
\Aspartyl-tRNA(Asn) amidotransferase subunit A (EC 6.3.5.6)\''''	0.16 +/- 0.15	0.08 +/- 0	0.04 +/- 0.06	0.1 +/- 0.14	0.04 +/- 0.05	0.04 +/- 0.03	0.06 +/- 0.03	3.02 +/- 4.05	0.04 +/- 0.03	0.06 +/- 0.05	0.11 +/- 0.02	0.11 +/- 0.09	0.07 +/- 0.03
\FIG039061: hypothetical protein related to heme utilization\''''	0.28 +/- 0.19	0.34 +/- 0.02	0.36 +/- 0.12	0.29 +/- 0.12	0.32 +/- 0.09	0.33 +/- 0.06	0.26 +/- 0.05	0.17 +/- 0.14	0.31 +/- 0.13	0.3 +/- 0.11	0.37 +/- 0.04	0.2 +/- 0.09	0.34 +/- 0.07
\DNA polymerase III alpha subunit (EC 2.7.7.7)\''''	0.32 +/- 0.11	0.39 +/- 0	0.47 +/- 0.15	0.34 +/- 0.06	0.27 +/- 0.13	0.24 +/- 0.02	0.36 +/- 0.03	0.11 +/- 0.09	0.27 +/- 0.09	0.32 +/- 0.2	0.29 +/- 0.06	0.17 +/- 0.12	0.24 +/- 0.09
\D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)\''''	0.48 +/- 0.09	0.26 +/- 0	0.27 +/- 0.06	0.29 +/- 0.08	0.3 +/- 0.13	0.29 +/- 0.02	0.3 +/- 0.06	0.1 +/- 0.08	0.29 +/- 0.12	0.3 +/- 0.12	0.27 +/- 0.14	0.49 +/- 0.41	0.25 +/- 0.08
\3-ketoacyl-CoA thiolase (EC 2.3.1.16)\''''	0.43 +/- 0.06	0.41 +/- 0.03	0.24 +/- 0.1	0.28 +/- 0.04	0.31 +/- 0.17	0.19 +/- 0.02	0.3 +/- 0.04	0.16 +/- 0.1	0.25 +/- 0.11	0.29 +/- 0.14	0.23 +/- 0.12	0.37 +/- 0.16	0.34 +/- 0.1
\Arylsulfatase (EC 3.1.6.1)\''''	0.61 +/- 0.09	0.11 +/- 0.03	1.17 +/- 0.93	0.17 +/- 0.03	0.16 +/- 0.09	0.08 +/- 0.02	0.28 +/- 0.09	0.09 +/- 0.05	0.15 +/- 0.11	0.19 +/- 0.11	2.98 +/- 0.08	0.2 +/- 0.09	0.12 +/- 0.05
\Enoyl-CoA hydratase (EC 4.2.1.17)\''''	0.31 +/- 0.1	0.24 +/- 0	0.24 +/- 0.05	0.31 +/- 0.12	0.27 +/- 0.11	0.26 +/- 0.07	0.34 +/- 0.07	0.16 +/- 0.06	0.24 +/- 0.06	0.3 +/- 0.11	0.21 +/- 0.04	0.46 +/- 0.04	0.27 +/- 0.04
\Acetyl-coenzyme A synthetase (EC 6.2.1.1)\''''	0.15 +/- 0.07	0.38 +/- 0.01	0.36 +/- 0.21	0.35 +/- 0.09	0.29 +/- 0.09	0.21 +/- 0.04	0.27 +/- 0.04	0.27 +/- 0.16	0.24 +/- 0.11	0.28 +/- 0.07	0.2 +/- 0.12	0.23 +/- 0.04	0.31 +/- 0.03
\Copper-translocating P-type ATPase (EC 3.6.3.4)\''''	0.12 +/- 0.05	0.35 +/- 0.05	0.18 +/- 0.04	0.2 +/- 0.09	0.24 +/- 0.17	0.62 +/- 0.21	0.15 +/- 0.04	0.7 +/- 0.23	0.28 +/- 0.18	0.23 +/- 0.14	0.19 +/- 0.14	0.29 +/- 0.17	0.17 +/- 0.08
\diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s)\''''	0.11 +/- 0.14	0.14 +/- 0.01	0.12 +/- 0.07	0.25 +/- 0.08	0.24 +/- 0.14	0.26 +/- 0.02	0.38 +/- 0.06	0.13 +/- 0.08	0.3 +/- 0.18	0.33 +/- 0.14	0.16 +/- 0.08	0.5 +/- 0.1	0.28 +/- 0.08
\Chaperone protein DnaK\''''	0.29 +/- 0.2	0.34 +/- 0.05	0.26 +/- 0.06	0.24 +/- 0.06	0.3 +/- 0.17	0.17 +/- 0.03	0.28 +/- 0.03	0.16 +/- 0.1	0.3 +/- 0.14	0.29 +/- 0.12	0.29 +/- 0.09	0.37 +/- 0.21	0.23 +/- 0.03

\UDP-glucose 4-epimerase (EC 5.1.3.2)\\"	0.27 +/- 0.12	0.22 +/- 0.01	0.22 +/- 0.08	0.35 +/- 0.09	0.24 +/- 0.06	0.19 +/- 0.04	0.4 +/- 0.06	0.09 +/- 0.08	0.22 +/- 0.1	0.29 +/- 0.09	0.17 +/- 0.05	0.41 +/- 0.15	0.23 +/- 0.12
\Excinuclease ABC subunit A\"	0.11 +/- 0.11	0.35 +/- 0.02	0.4 +/- 0.14	0.33 +/- 0.12	0.21 +/- 0.07	0.22 +/- 0.04	0.28 +/- 0.07	0.2 +/- 0.12	0.18 +/- 0.11	0.37 +/- 0.27	0.34 +/- 0.03	0.2 +/- 0.03	0.2 +/- 0.05
\Aconitate hydratase (EC 4.2.1.3)\\"	0.27 +/- 0.16	0.39 +/- 0.03	0.34 +/- 0.27	0.26 +/- 0.06	0.32 +/- 0.17	0.17 +/- 0.04	0.27 +/- 0.07	0.19 +/- 0.1	0.28 +/- 0.13	0.27 +/- 0.1	0.19 +/- 0.04	0.09 +/- 0.12	0.26 +/- 0.09
\Transcription-repair coupling factor\"	0.11 +/- 0.14	0.33 +/- 0.01	0.29 +/- 0.12	0.27 +/- 0.05	0.13 +/- 0.11	0.22 +/- 0.08	0.22 +/- 0.05	0.64 +/- 0.94	0.26 +/- 0.09	0.25 +/- 0.08	0.18 +/- 0.12	0.23 +/- 0.17	0.25 +/- 0.06
\Acriflavin resistance protein\"	0.32 +/- 0.17	0.16 +/- 0	0.41 +/- 0.01	0.26 +/- 0.1	0.16 +/- 0.09	0.32 +/- 0.12	0.23 +/- 0.06	0.23 +/- 0.12	0.2 +/- 0.11	0.31 +/- 0.08	0.5 +/- 0.05	0.33 +/- 0.15	0.2 +/- 0.1
\Alcohol dehydrogenase (EC 1.1.1.1)\\"	0.24 +/- 0.24	0.26 +/- 0.01	0.16 +/- 0.08	0.25 +/- 0.05	0.25 +/- 0.09	0.27 +/- 0.04	0.27 +/- 0.07	0.22 +/- 0.16	0.24 +/- 0.09	0.26 +/- 0.1	0.11 +/- 0.02	0.16 +/- 0.11	0.31 +/- 0.05
\Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39)\\"	0.53 +/- 0.11	0.16 +/- 0.01	0.28 +/- 0.14	0.22 +/- 0.11	0.36 +/- 0.17	0.15 +/- 0.05	0.25 +/- 0.06	0.19 +/- 0.12	0.2 +/- 0.08	0.21 +/- 0.11	0.22 +/- 0.04	0.2 +/- 0.03	0.3 +/- 0.07
\Glutamate synthase [NADPH] large chain (EC 1.4.1.13)\\"	0.45 +/- 0.29	0.38 +/- 0.02	0.34 +/- 0.15	0.26 +/- 0.06	0.2 +/- 0.11	0.17 +/- 0.05	0.27 +/- 0.03	0.1 +/- 0.07	0.19 +/- 0.14	0.26 +/- 0.09	0.2 +/- 0.03	0.28 +/- 0.16	0.24 +/- 0.05
\Carbamoyl-phosphate synthase large chain (EC 6.3.5.5)\\"	0.14 +/- 0.06	0.38 +/- 0	0.24 +/- 0.09	0.25 +/- 0.07	0.2 +/- 0.05	0.16 +/- 0.03	0.24 +/- 0.04	0.12 +/- 0.07	0.27 +/- 0.28	0.31 +/- 0.17	0.26 +/- 0.08	0.28 +/- 0.16	0.17 +/- 0.1
\Heat shock protein 60 family chaperone GroEL\"	0.2 +/- 0.06	0.34 +/- 0	0.48 +/- 0.5	0.28 +/- 0.08	0.2 +/- 0.13	0.14 +/- 0.01	0.28 +/- 0.04	0.08 +/- 0.07	0.26 +/- 0.09	0.23 +/- 0.11	0.48 +/- 0.04	0.15 +/- 0.22	0.2 +/- 0.08
\Thioredoxin reductase (EC 1.8.1.9)\\"	0.2 +/- 0.19	0.24 +/- 0.01	0.22 +/- 0.11	0.3 +/- 0.08	0.18 +/- 0.11	0.2 +/- 0.02	0.29 +/- 0.09	0.16 +/- 0.08	0.26 +/- 0.07	0.24 +/- 0.1	0.11 +/- 0.03	0.18 +/- 0.02	0.24 +/- 0.03
\ClpB protein\"	0.24 +/- 0.12	0.34 +/- 0.02	0.31 +/- 0.1	0.28 +/- 0.08	0.22 +/- 0.08	0.2 +/- 0.03	0.26 +/- 0.05	0.13 +/- 0.08	0.21 +/- 0.09	0.27 +/- 0.11	0.21 +/- 0.04	0.13 +/- 0.19	0.17 +/- 0.09
\DNA gyrase subunit A (EC 5.99.1.3)\\"	0.33 +/- 0.11	0.3 +/- 0.02	0.32 +/- 0.12	0.25 +/- 0.05	0.21 +/- 0.09	0.16 +/- 0.02	0.19 +/- 0.04	0.16 +/- 0.17	0.22 +/- 0.1	0.22 +/- 0.12	0.37 +/- 0.04	0.3 +/- 0.06	0.2 +/- 0.04
\Multimodular transpeptidase-transglycosylase (EC 2.4.1.129) (EC 3.4.-.-)\\"	0.14 +/- 0.05	0.2 +/- 0	0.2 +/- 0.02	0.26 +/- 0.12	0.23 +/- 0.17	0.24 +/- 0.04	0.25 +/- 0.05	0.17 +/- 0.09	0.23 +/- 0.09	0.24 +/- 0.15	0.09 +/- 0.01	0.18 +/- 0.02	0.23 +/- 0.08
\Alkaline phosphatase (EC 3.1.3.1)\\"	0.21 +/- 0.04	0.07 +/- 0.01	0.19 +/- 0.03	0.18 +/- 0.06	0.16 +/- 0.09	0.24 +/- 0.04	0.35 +/- 0.05	0.19 +/- 0.08	0.2 +/- 0.12	0.24 +/- 0.14	0.4 +/- 0.12	0.29 +/- 0.2	0.18 +/- 0.08
\Asparagine synthetase [glutamine-hydrolyzing] (EC 6.3.5.4)\\"	0.12 +/- 0.14	0.12 +/- 0	0.13 +/- 0.02	0.15 +/- 0.08	0.31 +/- 0.21	0.13 +/- 0.03	0.17 +/- 0.06	0.16 +/- 0.11	0.25 +/- 0.12	0.29 +/- 0.2	0.07 +/- 0	0.29 +/- 0.07	0.31 +/- 0.17
\Translation elongation factor G\"	0.24 +/- 0.17	0.35 +/- 0.03	0.24 +/- 0.11	0.25 +/- 0.11	0.22 +/- 0.05	0.11 +/- 0.04	0.22 +/- 0.04	0.08 +/- 0.06	0.25 +/- 0.21	0.24 +/- 0.16	0.23 +/- 0.08	0.21 +/- 0.29	0.2 +/- 0.05
\5-methyltetrahydrofolate--homocysteine methyltransferase (EC 2.1.1.13)\\"	0.14 +/- 0.12	0.3 +/- 0.01	0.27 +/- 0.06	0.24 +/- 0.1	0.19 +/- 0.07	0.13 +/- 0.01	0.29 +/- 0.05	0.11 +/- 0.08	0.19 +/- 0.08	0.25 +/- 0.11	0.16 +/- 0.09	0.27 +/- 0.02	0.2 +/- 0.12
\Threonine dehydrogenase and related Zn-dependent dehydrogenases\"	0.13 +/- 0.05	0.37 +/- 0.1	0.16 +/- 0.02	0.27 +/- 0.11	0.15 +/- 0.1	0.1 +/- 0.04	0.3 +/- 0.06	0.21 +/- 0.26	0.17 +/- 0.1	0.25 +/- 0.15	0.01 +/- 0.02	0.07 +/- 0.09	0.29 +/- 0.09
\Succinate dehydrogenase flavoprotein subunit (EC 1.3.99.1)\\"	0.25 +/- 0.02	0.29 +/- 0.01	0.21 +/- 0.02	0.18 +/- 0.08	0.19 +/- 0.1	0.14 +/- 0.07	0.25 +/- 0.04	0.15 +/- 0.1	0.18 +/- 0.07	0.23 +/- 0.12	0.24 +/- 0.04	0.23 +/- 0.04	0.22 +/- 0.08
\DNA polymerase I (EC 2.7.7.7)\\"	0.14 +/- 0.03	0.2 +/- 0.01	0.4 +/- 0.03	0.22 +/- 0.05	0.18 +/- 0.13	0.21 +/- 0.02	0.24 +/- 0.06	0.13 +/- 0.11	0.19 +/- 0.04	0.22 +/- 0.15	0.19 +/- 0.01	0.2 +/- 0.03	0.17 +/- 0.09
\Catalase (EC 1.11.1.6)\\"	0.08 +/- 0.09	0.28 +/- 0.03	0.15 +/- 0.11	0.22 +/- 0.05	0.22 +/- 0.14	0.15 +/- 0.05	0.17 +/- 0.05	0.13 +/- 0.09	0.28 +/- 0.18	0.22 +/- 0.12	0.05 +/- 0	0.05 +/- 0.08	0.21 +/- 0.06
\Type I restriction-modification system, restriction subunit R (EC 3.1.21.3)\\"	0.26 +/- 0.14	0.25 +/- 0.01	0.25 +/- 0.03	0.23 +/- 0.04	0.17 +/- 0.04	0.31 +/- 0.09	0.21 +/- 0.03	0.23 +/- 0.1	0.15 +/- 0.14	0.14 +/- 0.07	0.06 +/- 0.03	0.35 +/- 0.13	0.19 +/- 0.08

1 References

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