Inhalable microorganisms in Beijing's PM2.5 and PM10 pollutants during a severe smog event

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Supporting Information

Contents

Detailed Methods

PM and meteorological data

To address the increasing public health concerns, China revised its Ambient Air Quality Standard in 2012, including $PM_{2.5}$ as an air quality index in addition to PM_{10}[1]. The 24 h average concentrations (9:00 AM- 9:00 AM the next day) of $PM_{2.5}$ and PM_{10} from the 3 nearest official monitoring sites in Haidian District and the averaged $PM_{2.5}$ concentration of Beijing from 35 monitoring sites, operated by the Beijing Municipal Environmental Monitoring Center, were recorded from the official website (http://zx.bjmemc.com.cn/) as a comparison (Figure 1A and Supporting Information, Figure S7, Table S4). Air Quality Index (AQI) data (Supporting Information, Table S4) of the same 3 monitoring sites were provided by Beijing Municipal Environmental Protection Bureau website (http://www.bjepb.gov.cn/). Meteorological data of Haidian District, including temperature (°C), relative humidity (%), atmospheric pressure (Hpa), and wind velocity (m/s) were downloaded from the China Meteorological Data Sharing Service System (http://cdc.bjmb.gov.cn/) hourly (Supporting Information, Table S4 and Figure S8). The meteorological data of Beijing were recorded from the National Meteorological Center of China Meteorological Administration (http://www.nmc.gov.cn/). Daily $PM_{2.5}$ concentrations of the 74 key cities in the national $PM_{2.5}$ monitoring network were provided by China National Environmental Monitoring Center (http://113.108.142.147:20035/emcpublish/).

Scanning Electron Microscopy

Scanning Electron Microscopy (SEM) was performed using a QUANTA 200 SEM (FEI, Chech). Small pieces (0.5 cm×0.5 cm) of Tissuquartz filter samples were mounted on aluminum SEM stubs using double-sided adhesive carbon tapes, and gold-coated using an Ion Sputtering Instrument E-1010 (Hitachi, Japan) prior to imaging. The beam voltage was set to 15.0 kV.

OC and EC analysis

We analyzed the organic carbon (OC) and elemental carbon (EC) concentrations of the collected filter samples using a DRI 2001A thermal optical reflectance (TOR) carbon analyzer (Atmoslytic Inc Corp., CA, US). Its detection limits for OC and EC were 0.82 and 0.20 μg C/cm^2, respectively. The IMPROVE_A temperature program was used in our analysis[2,3]. For OC, a small sample (0.522 cm^2) from the quartz filter was heated under four temperatures sequentially (140, 280, 480, and 580 °C) under a helium environment. In this procedure, carbon compounds in the PM samples were transformed to carbon dioxide, which was then reduced to methane over a manganese dioxide catalyst. A flame ionization detector (FID) was used to detect the peak area of methane for estimating the concentration of organic carbon. For EC, the filter was heated at the temperatures of 580, 740, and 840 °C, respectively, and the carrier gas used was a mixture of oxygen (2%) and helium (98%). Elemental carbon was oxidized to carbon dioxide first, followed by reduction to methane and detection using FID. The reflectance of the filter was monitored with a laser to determine the cut-point of OC and EC. Both helium and oxygen were purchased from Beijing AP BAIF Gases Industry Co., Ltd (Beijing, China).

Elemental analysis

Energy dispersive X-ray fluorescence (PANalytical B. V., the Netherlands Corp., NED) was used to measure the concentrations of elements in the PM samples[4]. Nine elements (Ti, Mn, Ni, Cr, Zn, As, Pb, Fe, and Br) were analyzed. Filter papers from the

MicroMatter company film (Micromatter Corp., Vancouver, Canada) and the NIST SRM 2783 standard substance were used to calibrate the instrument. In addition, for every ten samples, we randomly selected one of them to check for repeatability. A blank filter was analyzed as a negative control. The margin of error was <5% for Fe and Zn, <10% for Mn and Br, and 15% for Ti, Cr, and Pb, respectively. Since Ni and As were low in abundance in samples, the error was ~20%.

Water soluble ions

Ion chromatography (IC) was used to measure the water soluble ions in the PM samples[4], including five anions (SO_4^{2-}, NO^{3-}, Cl^-, F^-, and PO_4^{3-}) and five cations (Na^+, K^+, Mg^{2+}, Ca^{2+}, and NH^{4+}). Dionex ICS-2000 with CS12 columns (Dionex Corp., CA, US) were used for the cation analysis, and Dionex ICS-90A with AS11-HC columns (Dionex Corp., CA, US) were used for the anion analysis. A blank filter was analyzed as a negative control. The method detection limits were 0.01 mg/L for K^+, Na^+, and Mg^{2+}, 0.02 mg/L for F^-, Cl^-, NH_4^+, and Ca^{2+}, and 0.05 mg/L for SO_4^{2-}, PO_4^{3-} , and NO_3^-.

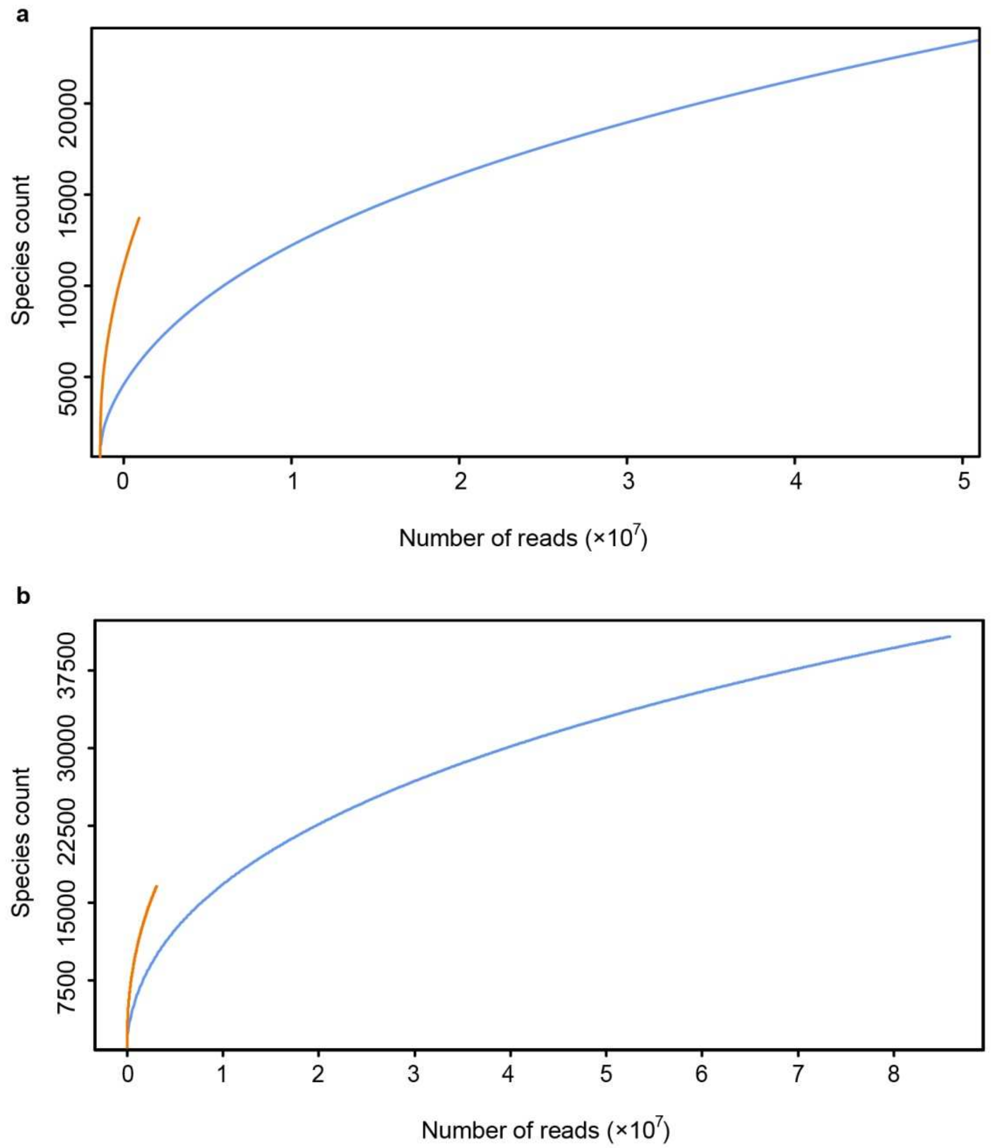
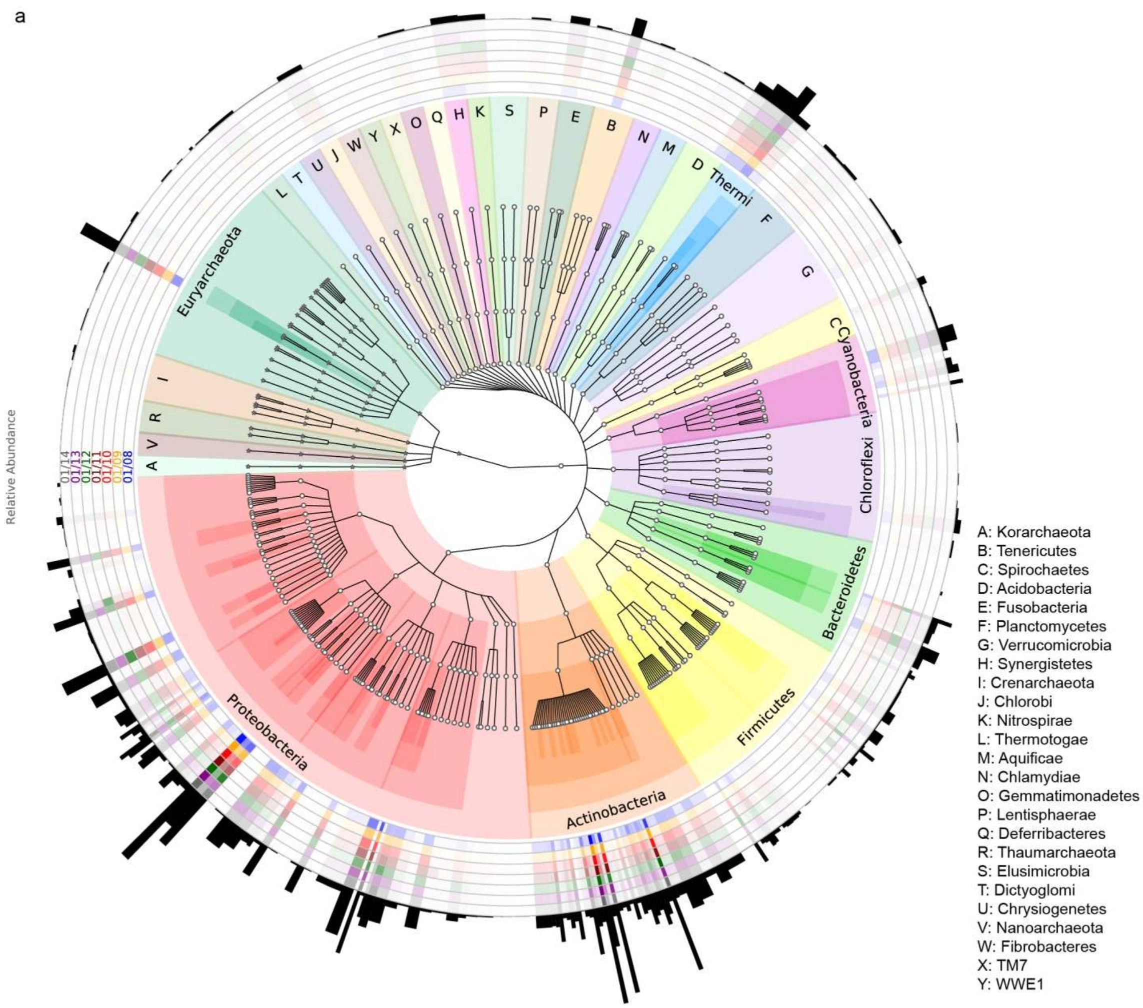


Figure S1. Rarefaction curves of $PM_{2.5}$ and PM_{10} samples sequenced by MiSeq and HiSeq platforms.

Rarefaction curves of **a**) $PM_{2.5}$ and **b**) PM_{10} samples collected on January 14, 2013, analyzed by MG-RAST. Orange lines correspond to the MiSeq data, while the blue lines correspond to the HiSeq data of the same day.


a
Relative Abundance
01/14
01/13
01/12
01/11
01/10
01/09
01/08
Euryarchaeota
A
V
R
I
L
T
U
J
W
Y
X
O
Q
H
K
S
P
E
B
N
M
D
Thermi
F
G
C
Cyanobacteria
Chloroflexi
Bacteroidetes
Firmicutes
Actinobacteria
Proteobacteria
A: Korarchaeota
B: Tenericutes
C: Spirochaetes
D: Acidobacteria
E: Fusobacteria
F: Planctomycetes
G: Verrucomicrobia
H: Synergistetes
I: Crenarchaeota
J: Chlorobi
K: Nitrospirae
L: Thermotogae
M: Aquificae
N: Chlamydiae
O: Gemmatimonadetes
P: Lentisphaerae
Q: Deferribacteres
R: Thaumarchaeota
S: Elusimicrobia
T: Dictyoglomi
U: Chrysiogenetes
V: Nanoarchaeota
W: Fibrobacteres
X: TM7
Y: WWE1

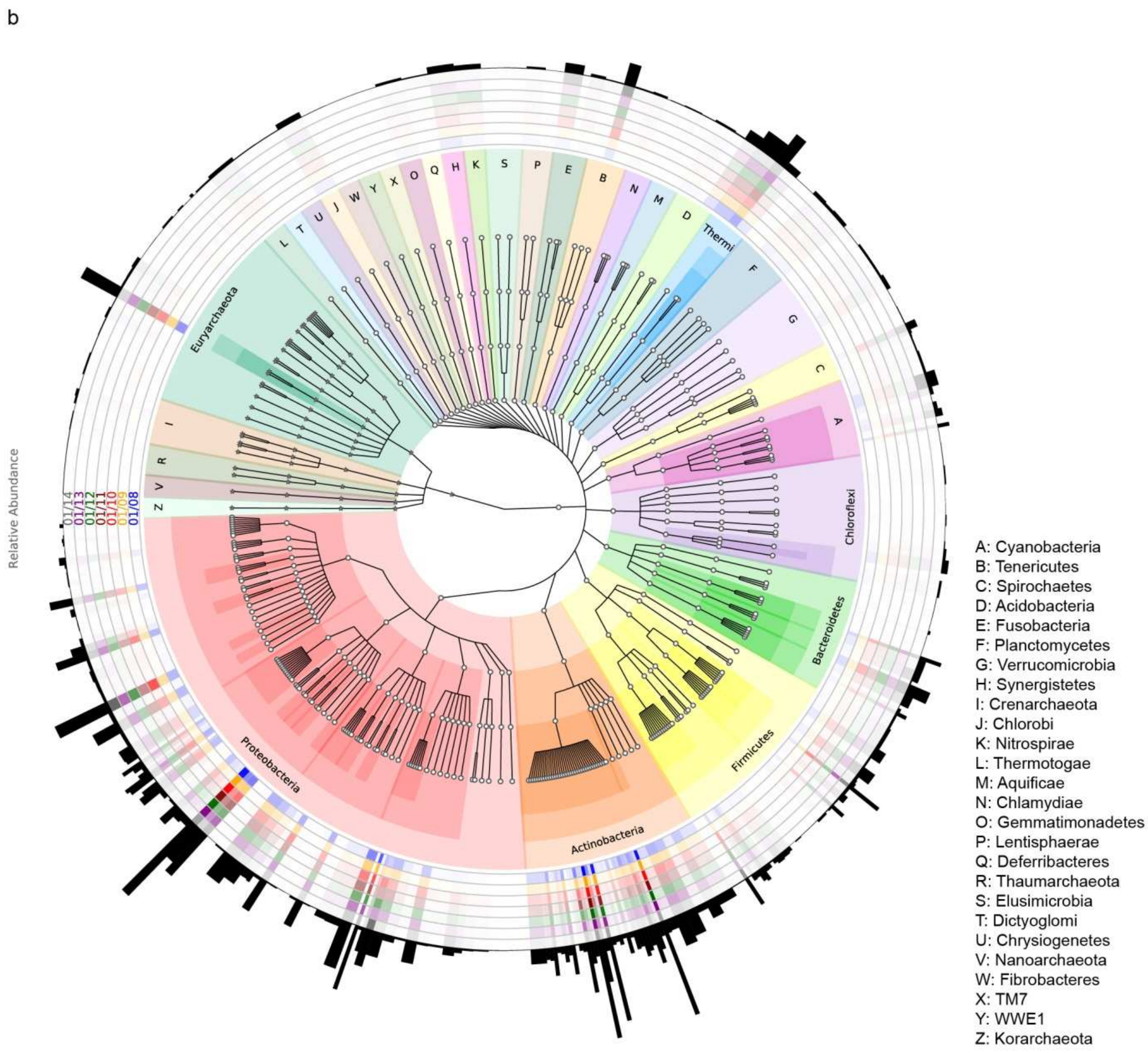
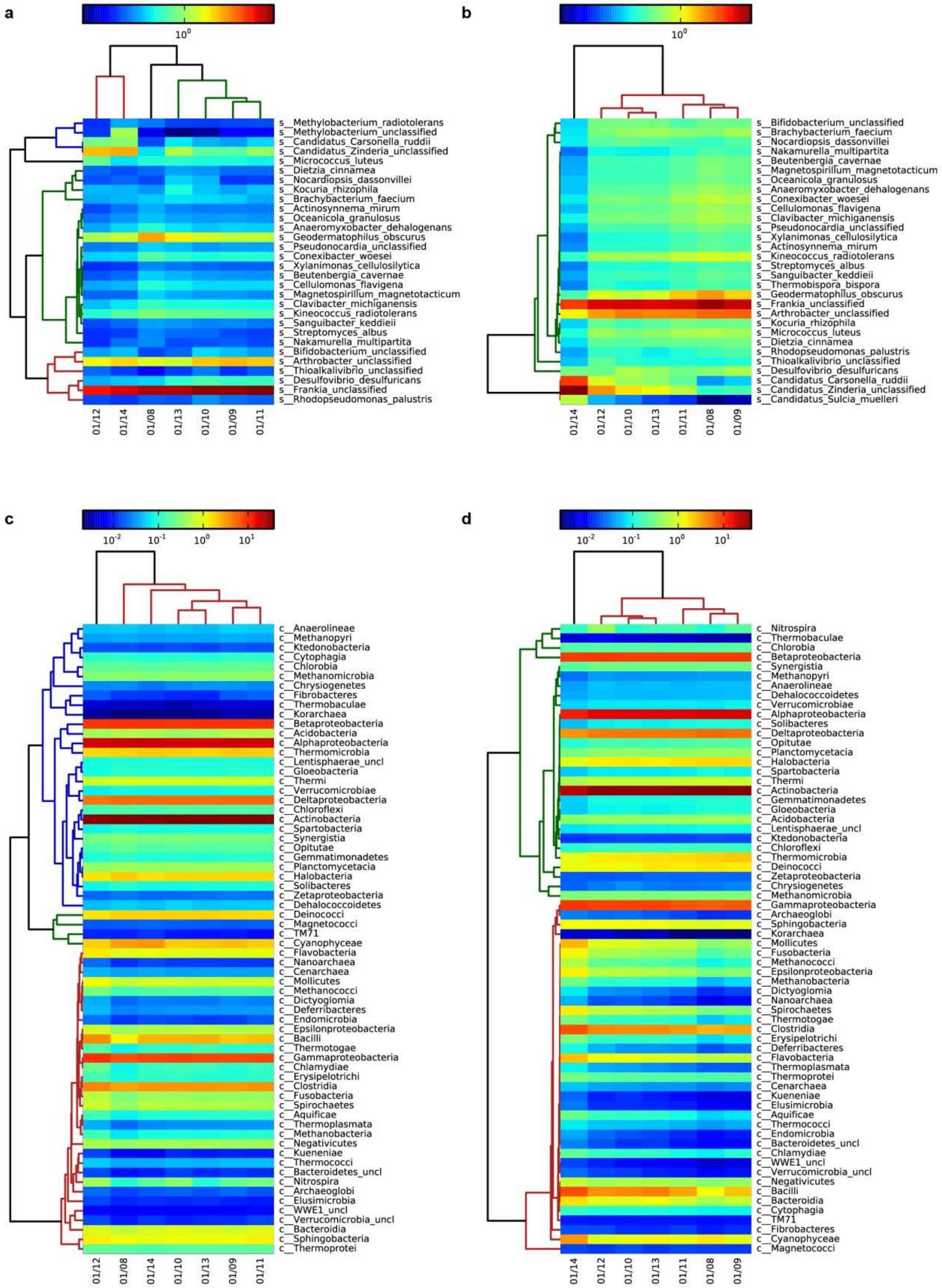


Figure S2. Phylogenetic tree of bacteria and archaea identified from $PM_{2.5}$ and PM_{10} samples.

Each phylum and species with >1% relative abundance were labeled by different colors at the class, order, and family levels. Black bars in the outmost ring represent the overall relative abundance of each family by height. The 7 transparent rings show the relative abundance of each family during the 7 sampling days, represented by the shade of the color blocks. **a**) $PM_{2.5}$ samples. **b**) PM_{10} samples.


a
10^0
s__Methylobacterium_radiotolerans
s__Methylobacterium_unclassified
s__Candidatus_Carsonella_ruddii
s__Candidatus_Zinderia_unclassified
s__Micrococcus_luteus
s__Dietzia_cinnamea
s__Nocardiopsis_dassonvillei
s__Kocuria_rhizophila
s__Brachybacterium_faecium
s__Actinosynnema_mirum
s__Oceanicola_granulosus
s__Anaeromyxobacter_dehalogenans
s__Geodermatophilus_obscurus
s__Pseudonocardia_unclassified
s__Conexibacter_woesei
s__Xylanimonas_cellulosilytica
s__Beutenbergia_cavernae
s__Cellulomonas_flavigena
s__Magnetospirillum_magnetotacticum
s__Clavibacter_michiganensis
s__Kineococcus_radiotolerans
s__Sanguibacter_keddieii
s__Streptomyces_albus
s__Nakamurella_multipartita
s__Bifidobacterium_unclassified
s__Arthrobacter_unclassified
s__Thioalkalivibrio_unclassified
s__Desulfovibrio_desulfuricans
s__Frankia_unclassified
s__Rhodopseudomonas_palustris
01/12
01/14
01/08
01/13
01/10
01/09
01/11
b
10^0
s__Bifidobacterium_unclassified
s__Brachybacterium_faecium
s__Nocardiopsis_dassonvillei
s__Nakamurella_multipartita
s__Beutenbergia_cavernae
s__Magnetospirillum_magnetotacticum
s__Oceanicola_granulosus
s__Anaeromyxobacter_dehalogenans
s__Conexibacter_woesei
s__Cellulomonas_flavigena
s__Clavibacter_michiganensis
s__Pseudonocardia_unclassified
s__Xylanimonas_cellulosilytica
s__Actinosynnema_mirum
s__Kineococcus_radiotolerans
s__Streptomyces_albus
s__Sanguibacter_keddieii
s__Thermobispora_bispora
s__Geodermatophilus_obscurus
s__Frankia_unclassified
s__Arthrobacter_unclassified
s__Kocuria_rhizophila
s__Micrococcus_luteus
s__Dietzia_cinnamea
s__Rhodopseudomonas_palustris
s__Thioalkalivibrio_unclassified
s__Desulfovibrio_desulfuricans
s__Candidatus_Carsonella_ruddii
s__Candidatus_Zinderia_unclassified
s__Candidatus_Sulcia_muelleri
01/14
01/12
01/10
01/13
01/11
01/08
01/09
c
10^-2
10^-1
10^0
10^1
c__Anaerolineae
c__Methanopyri
c__Ktedonobacteria
c__Cytophagia
c__Chlorobia
c__Methanomicrobia
c__Chrysiogenetes
c__Fibrobacteres
c__Thermobaculae
c__Korarchaea
c__Betaproteobacteria
c__Acidobacteria
c__Alphaproteobacteria
c__Thermomicrobia
c__Lentisphaerae_uncl
c__Gloeobacteria
c__Thermi
c__Verrucomicrobiae
c__Deltaproteobacteria
c__Chloroflexi
c__Actinobacteria
c__Spartobacteria
c__Synergistia
c__Opitutae
c__Gemmatimonadetes
c__Planctomycetacia
c__Halobacteria
c__Solibacteres
c__Zetaproteobacteria
c__Dehalococcoidetes
c__Deinococci
c__Magnetococci
c__TM71
c__Cyanophyceae
c__Flavobacteria
c__Nanoarchaea
c__Cenarchaea
c__Mollicutes
c__Methanococci
c__Dictyoglomia
c__Deferribacteres
c__Endomicrobia
c__Epsilonproteobacteria
c__Bacilli
c__Thermotogae
c__Gammaproteobacteria
c__Chlamydiae
c__Erysipelotrichi
c__Clostridia
c__Fusobacteria
c__Spirochaetes
c__Aquificae
c__Thermoplasmata
c__Methanobacteria
c__Negativicutes
c__Kueneniae
c__Thermococci
c__Bacteroidetes_uncl
c__Nitrospira
c__Archaeoglobi
c__Elusimicrobia
c__WWE1_uncl
c__Verrucomicrobia_uncl
c__Bacteroidia
c__Sphingobacteria
c__Thermoprotei
01/12
01/08
01/14
01/10
01/13
01/09
01/11
d
10^-2
10^-1
10^0
10^1
c__Nitrospira
c__Thermobaculae
c__Chlorobia
c__Betaproteobacteria
c__Synergistia
c__Methanopyri
c__Anaerolineae
c__Dehalococcoidetes
c__Verrucomicrobiae
c__Alphaproteobacteria
c__Solibacteres
c__Deltaproteobacteria
c__Opitutae
c__Planctomycetacia
c__Halobacteria
c__Spartobacteria
c__Thermi
c__Actinobacteria
c__Gemmatimonadetes
c__Gloeobacteria
c__Acidobacteria
c__Lentisphaerae_uncl
c__Ktedonobacteria
c__Chloroflexi
c__Thermomicrobia
c__Deinococci
c__Zetaproteobacteria
c__Chrysiogenetes
c__Methanomicrobia
c__Gammaproteobacteria
c__Archaeoglobi
c__Sphingobacteria
c__Korarchaea
c__Mollicutes
c__Fusobacteria
c__Methanococci
c__Epsilonproteobacteria
c__Methanobacteria
c__Dictyoglomia
c__Nanoarchaea
c__Spirochaetes
c__Thermotogae
c__Clostridia
c__Erysipelotrichi
c__Deferribacteres
c__Flavobacteria
c__Thermoplasmata
c__Thermoprotei
c__Cenarchaea
c__Kueneniae
c__Elusimicrobia
c__Aquificae
c__Thermococci
c__Endomicrobia
c__Bacteroidetes_uncl
c__Chlamydiae
c__WWE1_uncl
c__Verrucomicrobia_uncl
c__Negativicutes
c__Bacilli
c__Bacteroidia
c__Cytophagia
c__TM71
c__Fibrobacteres
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01/11
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01/09

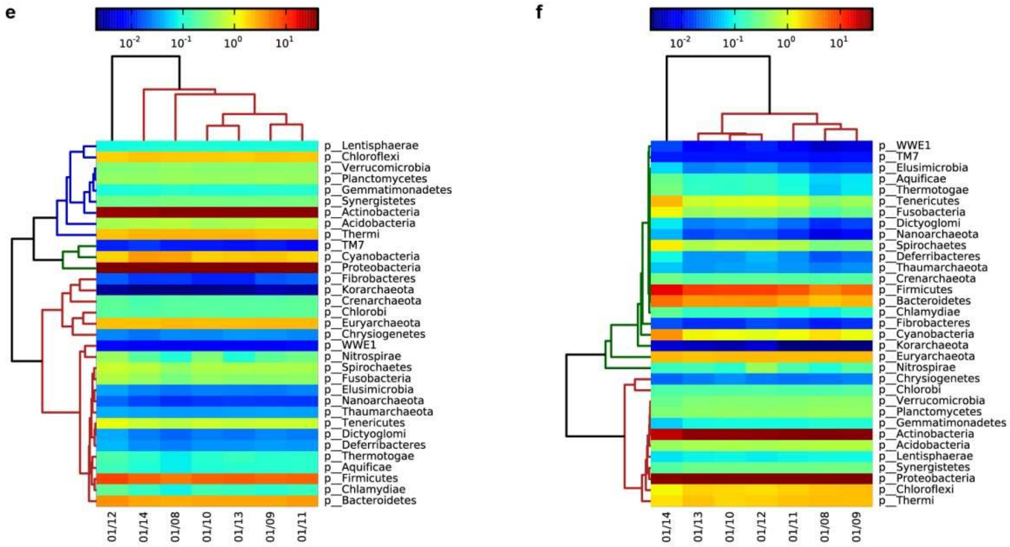
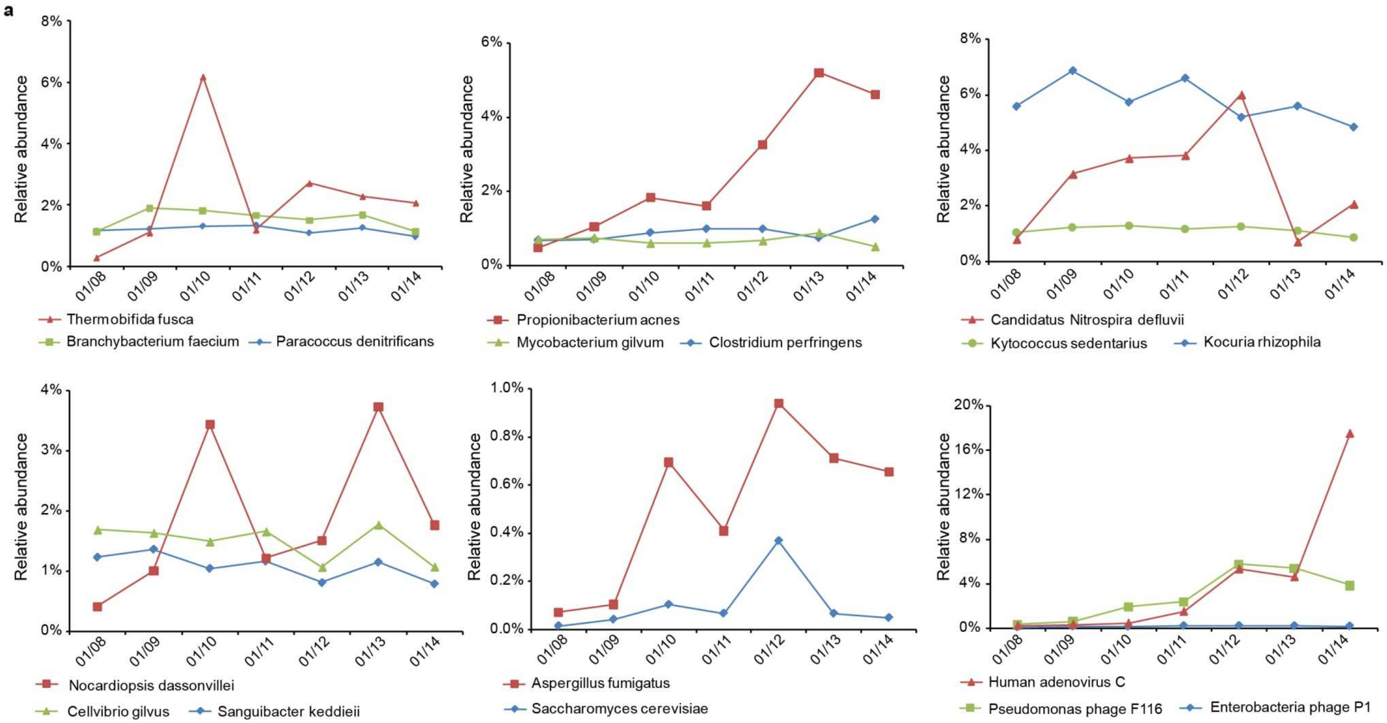


Figure S3. Heatmaps of the relative abundance of bacteria and archaea identified by MetaPhlAn.

The relative abundance ($\log_{10}$ scale) of bacteria and archaea identified by MetaPhlAn at the species (**a**, **b**), class (**c**, **d**) and phylum (**e**, **f**) levels from $PM_{2.5}$ (**a**, **c**, **e**) and PM_{10} (**b**, **d**, **f**) samples during the 7 sampling days (at species level, only the most abundant 30 species were plotted).


a
Relative abundance
8%
6%
4%
2%
0%
01/08
01/09
01/10
01/11
01/12
01/13
01/14
Thermobifida fusca
Branchybacterium faecium
Paracoccus denitrificans
6%
4%
2%
0%
Propionibacterium acnes
Mycobacterium gilvum
Clostridium perfringens
8%
6%
4%
2%
0%
Candidatus Nitrospira defluvii
Kytococcus sedentarius
Kocuria rhizophila
4%
3%
2%
1%
0%
Nocardiopsis dassonvillei
Cellvibrio gilvus
Sanguibacter keddieii
1.0%
0.8%
0.6%
0.4%
0.2%
0.0%
Aspergillus fumigatus
Saccharomyces cerevisiae
20%
16%
12%
8%
4%
0%
Human adenovirus C
Pseudomonas phage F116
Enterobacteria phage P1

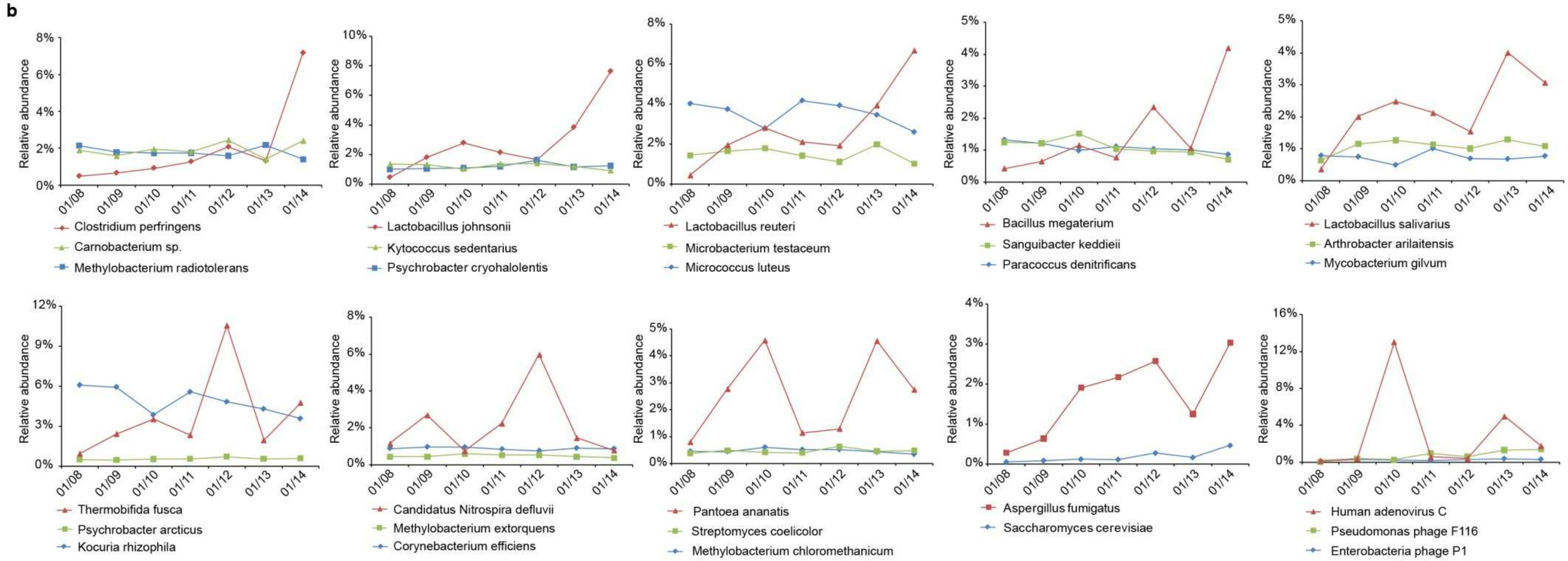


Figure S4. Variations of the genome-size-normalized relative abundance of the most common bacterial, fungal, and viral species. **a**) $PM_{2.5}$ samples. **b**) PM_{10} samples. Species with S.D. value of their relative abundance ($\log_{10}$ scale) in seven days greater than 0.3 were selected as high variation species (plotted in red), and plotted with one or two other species in the same kingdom for comparison.

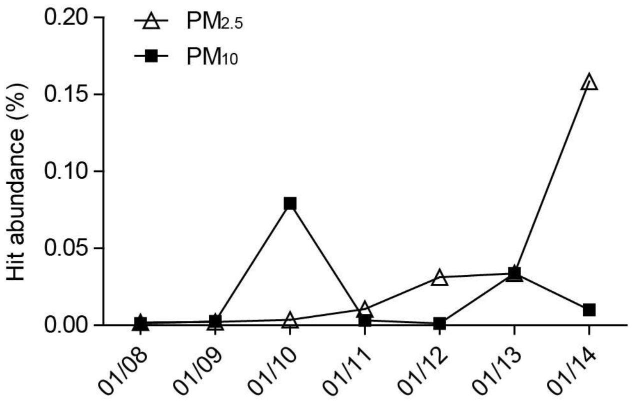


Figure S5. Daily variations of the normalized hit abundance of human adenovirus C in the collected $PM_{2.5}$ and PM_{10} samples.

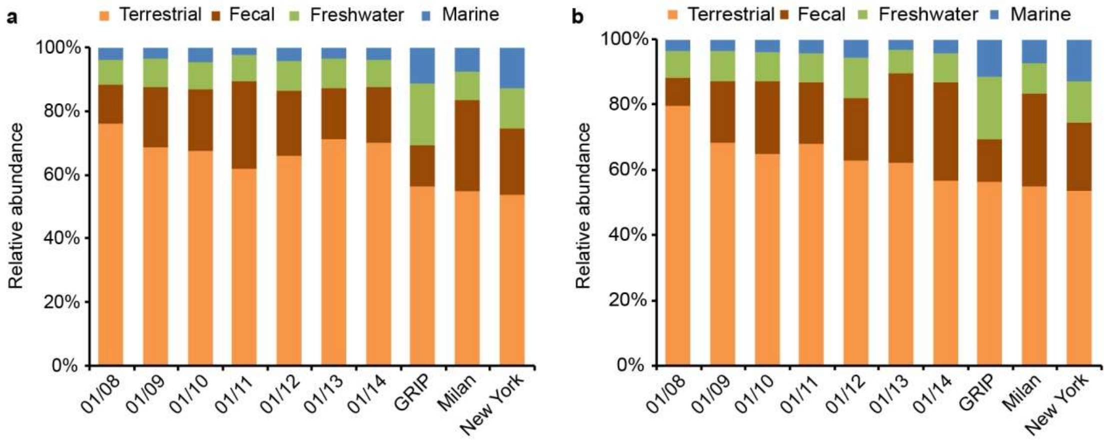


Figure S6. Original habitats of the bacteria identified from the Tsinghua $PM_{2.5}$ and PM_{10} samples compared with three previous studies.

Original habitats of the bacteria identified from the Tsinghua **a**) $PM_{2.5}$ and **b**) PM_{10} samples compared with those from the GRIP high-altitude, Milan urban, and New York subway studies

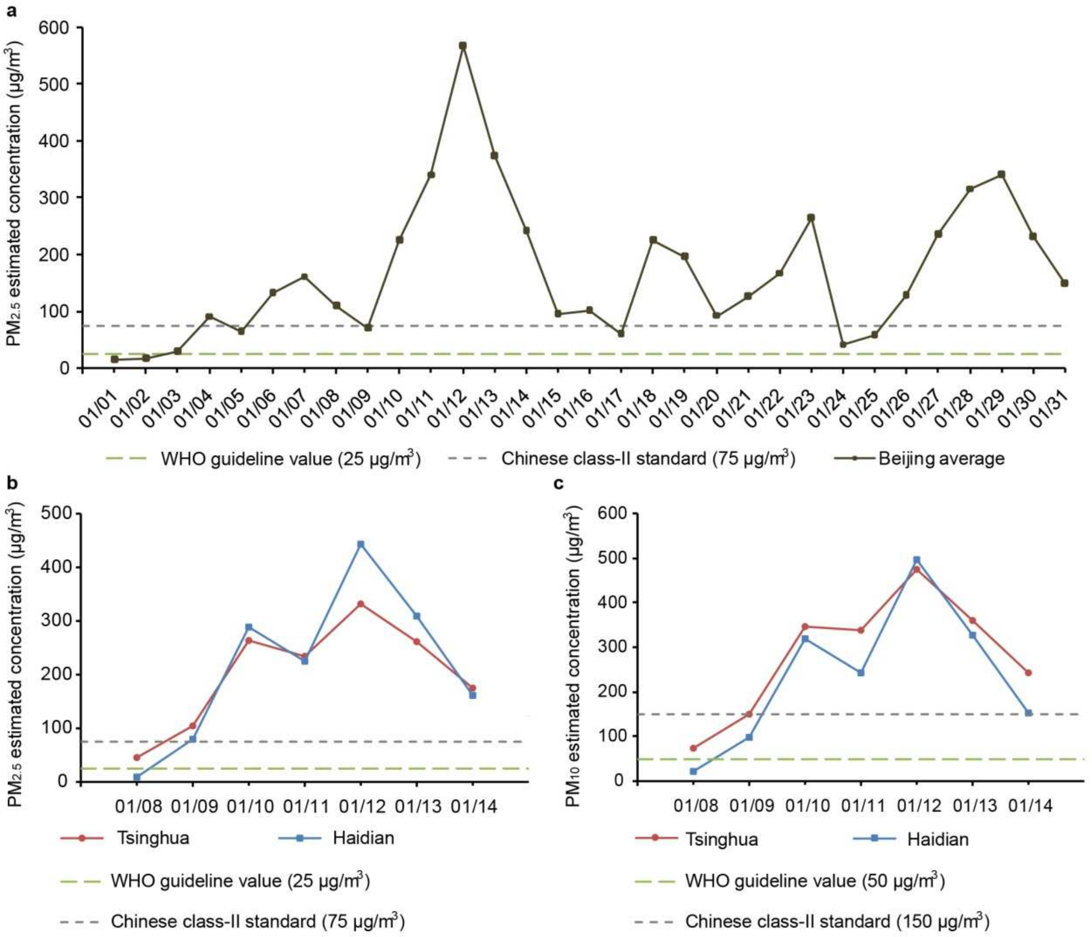


Figure S7. $PM_{2.5}$ and PM_{10} concentration of Beijing, Haidian district and Tsinghua monitoring site.

a) Average $PM_{2.5}$ concentration in Beijing in January 2013. **b**) $PM_{2.5}$ and **c**) PM_{10} concentrations of Tsinghua monitoring site and Haidian district during January 8-14, 2013.

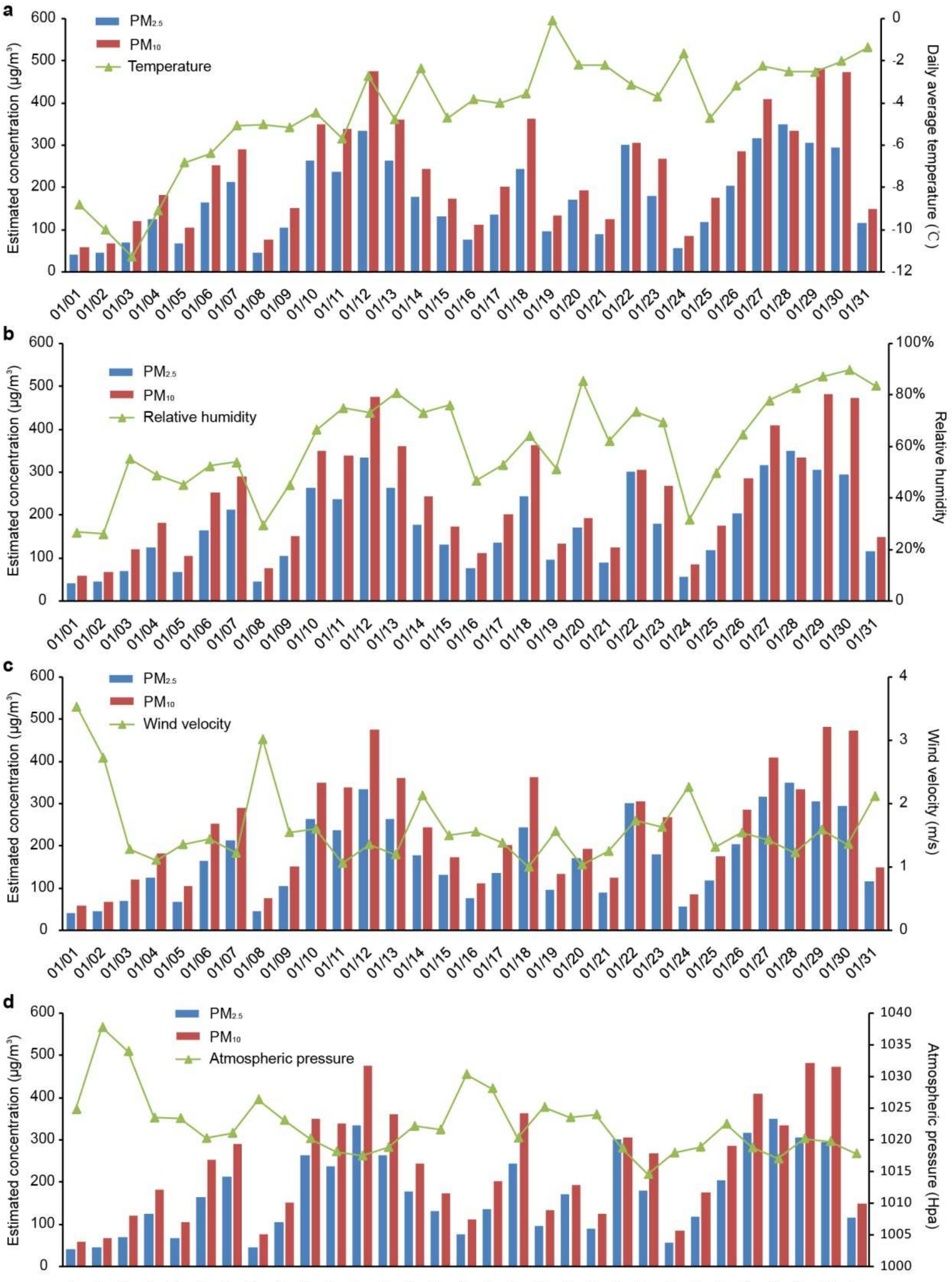


Figure S8. Meteorological data plotted with $PM_{2.5}$ and PM_{10} concentration in January 2013.

a) Daily average temperature, **b**) Relative humidity, **c**) Wind velocity and **d**) Atmospheric pressure were plotted in green lines, $PM_{2.5}$ concentration was plotted in blue bars and PM_{10} concentration was plotted in red bars.

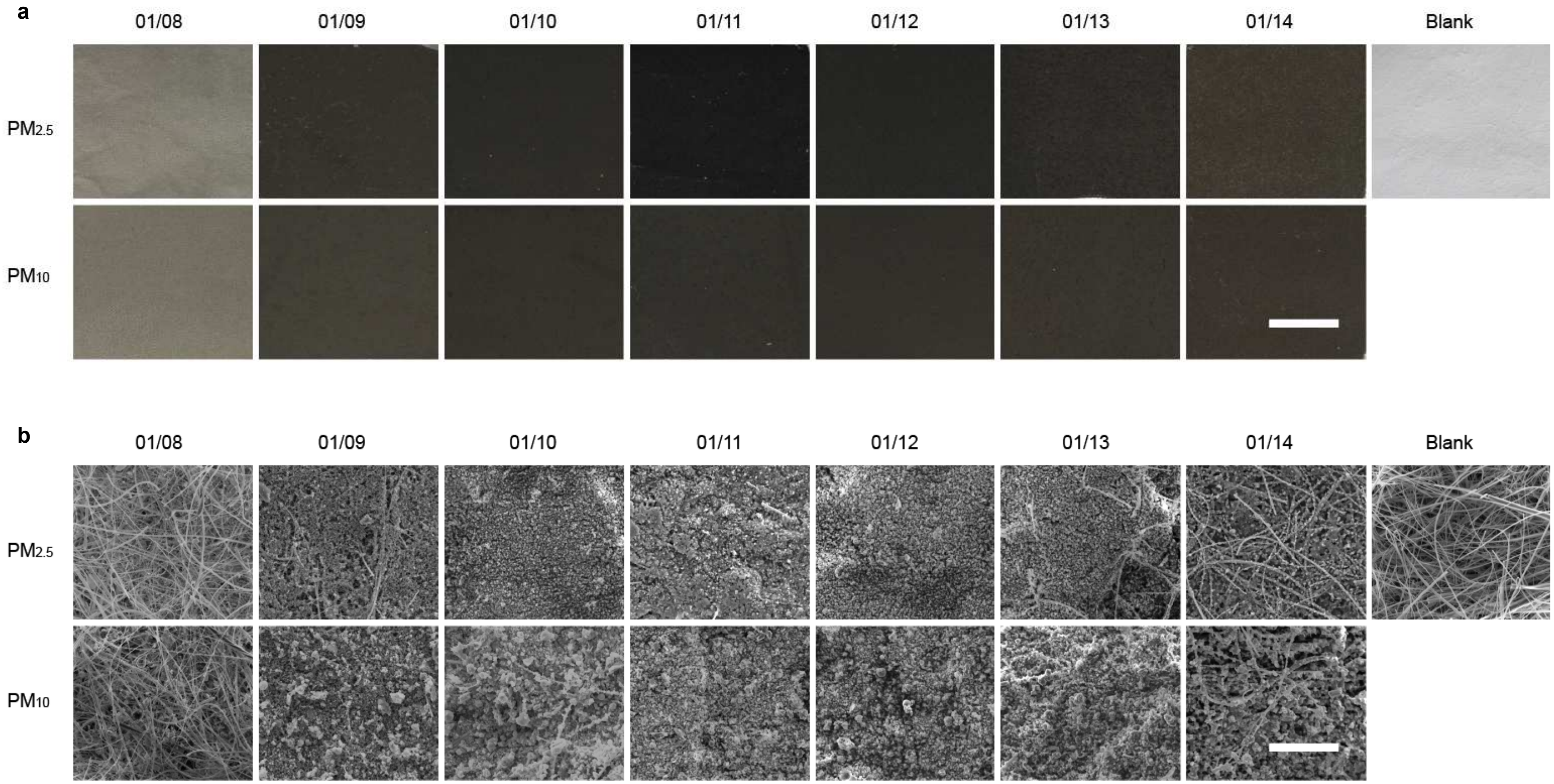


Figure S9. Filter coloration and SEM images of $PM_{2.5}$ and PM_{10} samples.
a) Filter coloration (Scale bar, 2 cm) and **b**) SEM images (Scale bar, 50 µm) of $PM_{2.5}$ and PM_{10} samples collected on the Tissuquartz filters during January 8-14, 2013.

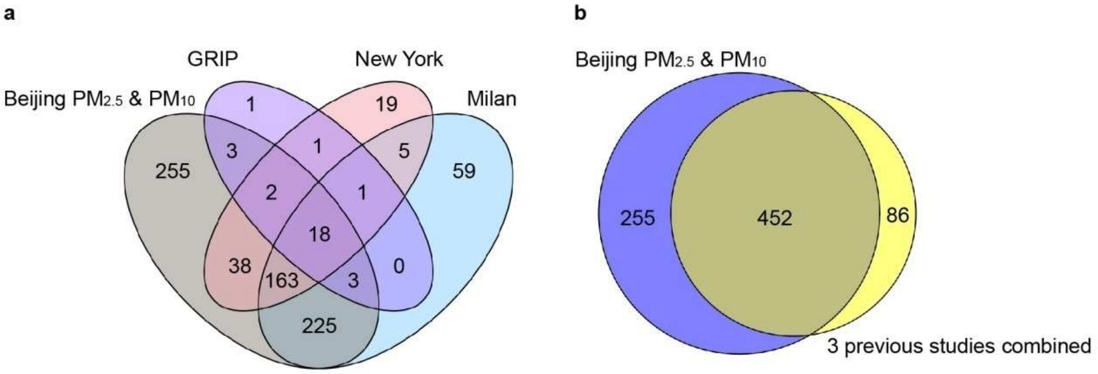


Figure S10. Number of overlapping airborne microbes at the genus level between Tsinghua PM study and three previous studies.

a) Venn diagram of overlapping airborne microbes at the genus level between 4 studies. **b**) Venn diagram of overlapping airborne microbes at the genus level between Tsinghua PM study and three previous studies[5-7].

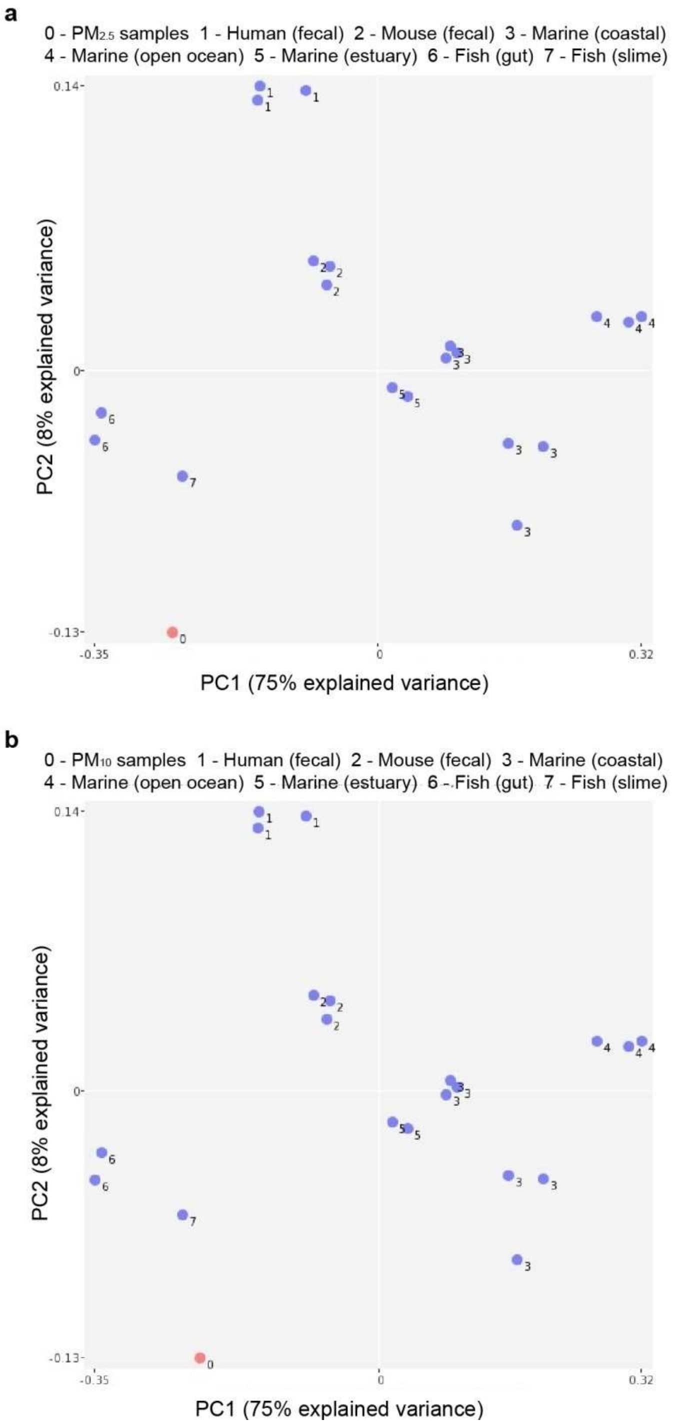


Figure S11. Principle component analysis of dinucleotide frequency of pooled $PM_{2.5}$ samples and PM_{10} samples.

Principle component analysis of dinucleotide frequency of **a**) $PM_{2.5}$ samples and **b**) PM_{10} samples (represented by a red dot, respectively) compared with other metagenomic studies (calculated by PRINSEQ[8]).

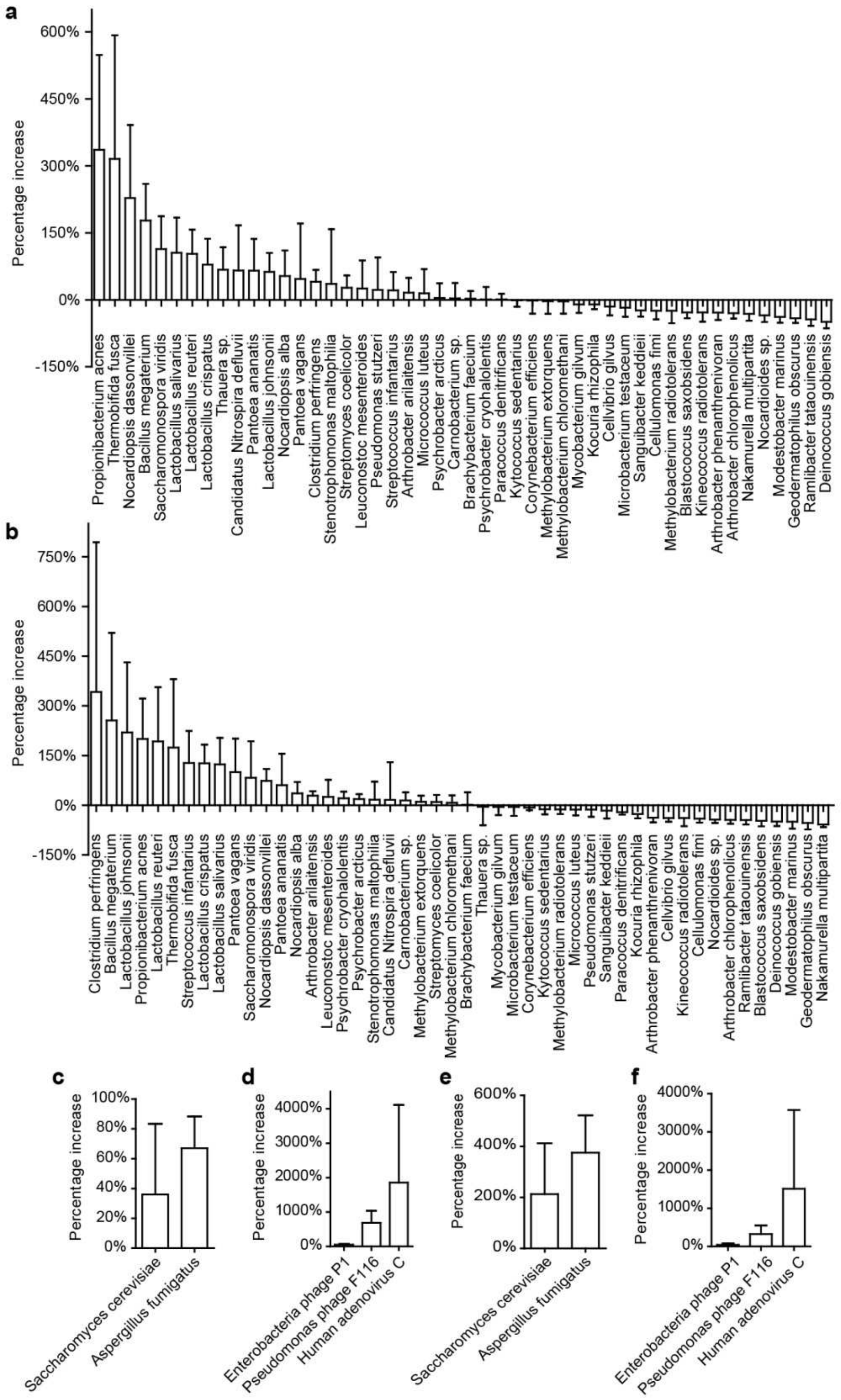


Figure S12. Percentage increase of 53 common species identified from PM samples. Percentage increase of 48 most common bacterial, 2 fungal and 3 viral species from $PM_{2.5}$ (**a**, **c**, **d**) and PM_{10} (**b**, **e**, **f**) samples during the last 5 sampling days compared to the first 2 days. Error bars represent S.D. (n=5).

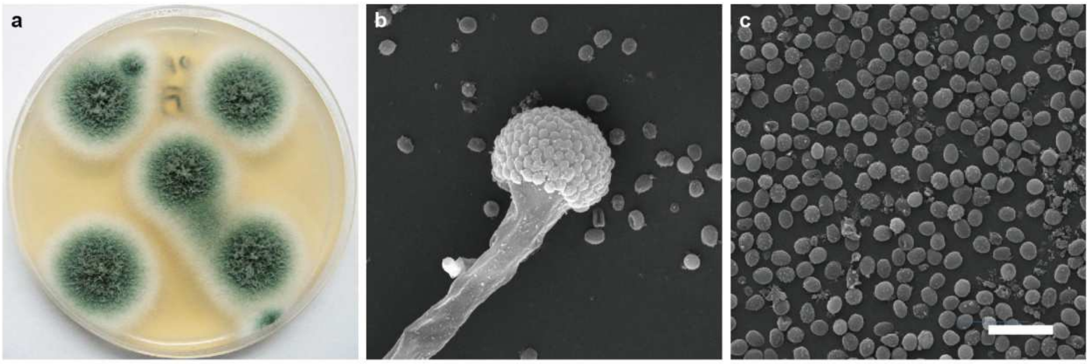


Figure S13. Images of cultured *Aspergillus fumigatus* from PM samples. *Aspergillus fumigatus* colonies on **a**) Potato-Sugar-Agar plate and SEM pictures of the **b**) sporangium and **c**, spores. Scale bar, 10 µm.

Table S1. Summary of sequencing data.

	Sampling date	**DNA quantities for library preparation (ng)**	**Hiseq data**				**Miseq data**		
			Index sequence	Number of reads	Number of bases (bp)	Read length (bp)	Number of reads	Number of bases (bp)	Read length (bp)
$PM_{2.5}$	01/08	5	CGTGAT	89,678,529	8,071,067,610	90	NA*	NA*	NA*
	01/09	5	GCCTAA	71,393,580	6,425,422,200	90	2,530,054	635,043,554	250
	01/10	5	CACTGT	62,009,579	5,580,862,110	90	3,446,228	865,003,228	250
	01/11	5	GATCTG	77,104,586	6,939,412,740	90	3,256,656	817,420,656	250
	01/12	5	CGTGAT	71,059,996	6,395,399,640	90	3,959,272	993,777,272	250
	01/13	3.84	GTAGCC	79,351,275	7,141,614,750	90	2,718,562	682,359,062	250
	01/14	4.70	CTGATC	49,053,564	4,414,820,760	90	2,885,166	724,176,666	250
PM_{10}	01/08	5	GATCTG	101,941,930	9,174,773,700	90	NA*	NA*	NA*
	01/09	5	TGGTCA	72,683,317	6,541,498,530	90	2,899,646	727,811,146	250
	01/10	5	ATTGGC	85,462,603	7,691,634,270	90	3,205,264	804,521,264	250
	01/11	5	TCAAGT	78,209,164	7,038,824,760	90	2,115,626	531,022,126	250
	01/12	4.96	TACAAG	78,721,109	7,084,899,810	90	3,198,546	802,835,046	250
	01/13	5	ACATCG	87,108,549	7,839,769,410	90	3,969,610	996,372,110	250
	01/14	5	AAGCTA	85,878,005	7,729,020,450	90	3,499,914	878,478,414	250
		Total clean data		1,089,655,786	98,069,020,740		32,646,774	8,194,340,274	
		Total raw data		1,192,904,738	107,361,426,420		37,684,544	9,458,820,544	

*Sequencing not performed.

Table S2. Genome coverage of the 48 most common bacterial, 2 fungal, and 3 viral species.

Organism	Species	Genome size (Mb)	Coverage													
			PM$_{2.5}$							PM$_{10}$						
			01/08	01/09	01/10	01/11	01/12	01/13	01/14	01/08	01/09	01/10	01/11	01/12	01/13	01/14
Bacteria	Geodermatophilus obscurus	5.3	54.0%	41.0%	41.0%	43.0%	40.0%	45.0%	35.0%	58.0%	43.0%	34.0%	49.0%	39.0%	39.0%	25.0%
	Modestobacter marinus	5.6	46.0%	39.0%	33.0%	36.0%	28.0%	41.0%	28.0%	42.0%	30.0%	22.0%	38.0%	24.0%	29.0%	17.0%
	Blastococcus saxobsidens	4.9	32.0%	27.0%	28.0%	27.0%	25.0%	33.0%	25.0%	33.0%	29.0%	23.0%	29.0%	24.0%	27.0%	17.0%
	Kocuria rhizophila	2.7	14.0%	17.0%	16.0%	17.0%	17.0%	22.0%	12.0%	17.0%	18.0%	15.0%	17.0%	16.0%	18.0%	14.0%
	Micrococcus luteus	2.5	13.0%	26.0%	18.0%	20.0%	53.0%	25.0%	14.0%	24.0%	19.0%	20.0%	25.0%	26.0%	27.0%	17.0%
	Candidatus Nitrospira defluvii	4.3	11.0%	34.0%	39.0%	40.0%	60.0%	12.0%	23.0%	19.0%	34.0%	12.0%	29.0%	58.0%	26.0%	10.0%
	Methylobacterium radiotolerans	6.1	29.0%	26.0%	20.0%	26.0%	23.0%	22.0%	28.0%	25.0%	21.0%	23.0%	21.0%	19.0%	29.0%	16.0%
	Propionibacterium acnes	2.6	7.1%	13.0%	23.0%	20.0%	42.0%	61.0%	44.0%	10.0%	14.0%	17.0%	27.0%	28.0%	45.0%	37.0%
	Thermobifida fusca	3.6	3.7%	13.0%	57.0%	15.0%	35.0%	35.0%	23.0%	16.0%	31.0%	47.0%	31.0%	80.0%	35.0%	47.0%
	Nocardioides sp.	5.0	12.0%	11.0%	10.0%	10.0%	9.4%	11.0%	7.5%	15.0%	13.0%	12.0%	12.0%	11.0%	12.0%	7.9%
	Nocardiopsis dassonvillei	6.5	4.4%	10.9%	36.0%	13.7%	20.6%	45.7%	18.2%	14.6%	28.4%	46.1%	28.1%	33.6%	39.4%	30.8%
	Brachybacterium faecium	3.6	9.3%	14.0%	16.0%	13.0%	15.0%	18.0%	9.5%	15.0%	31.0%	28.0%	23.0%	19.0%	42.0%	12.0%
	Arthrobacter phenanthrenivorans	4.3	18.0%	15.0%	15.0%	15.0%	12.0%	14.0%	8.1%	26.0%	21.0%	20.0%	20.0%	16.0%	21.0%	11.0%
	Cellvibrio gilvus	3.5	8.6%	7.8%	8.2%	7.9%	6.6%	15.0%	5.8%	9.2%	8.4%	7.5%	7.4%	6.6%	7.4%	4.9%
	Carnobacterium sp.	2.6	18.0%	16.0%	19.0%	16.0%	25.0%	19.0%	8.6%	25.0%	20.0%	26.0%	22.0%	27.0%	23.0%	25.0%
	Microbacterium testaceum	4.0	8.0%	12.0%	10.0%	11.0%	8.9%	11.0%	6.2%	10.0%	12.0%	15.0%	11.0%	8.8%	18.0%	8.6%
	Paracoccus denitrificans	4.6	8.1%	8.0%	8.3%	8.3%	8.3%	9.5%	6.7%	9.7%	8.6%	8.7%	8.4%	8.1%	9.2%	6.7%
	Kytococcus sedentarius	2.8	6.5%	7.8%	9.2%	7.3%	10.0%	9.6%	5.9%	10.0%	10.0%	10.0%	12.0%	12.0%	14.0%	7.7%
	Pantoea vagans	4.0	10.0%	12.0%	32.0%	16.0%	14.0%	9.0%	5.0%	8.8%	20.0%	46.0%	23.0%	17.0%	27.0%	20.0%
	Pseudomonas stutzeri	4.7	12.0%	13.0%	15.0%	9.4%	12.0%	12.0%	25.0%	17.0%	18.0%	19.0%	15.0%	15.0%	21.0%	7.4%
	Kineococcus radiotolerans	4.8	10.0%	8.8%	8.4%	9.9%	6.1%	6.4%	7.9%	11.0%	8.2%	6.1%	11.0%	5.1%	7.2%	3.6%
	Sanguibacter keddieii	4.3	9.5%	10.0%	8.1%	8.1%	7.7%	12.0%	5.9%	9.4%	11.0%	19.0%	8.9%	9.4%	11.0%	6.7%
	Thauera sp.	4.5	6.3%	11.0%	12.0%	17.0%	23.0%	13.0%	11.0%	8.9%	18.0%	10.0%	16.0%	23.0%	13.0%	5.4%
	Pantoea ananatis	4.7	4.2%	15.0%	16.0%	13.0%	26.0%	16.0%	6.6%	13.0%	35.0%	57.0%	16.0%	18.0%	62.0%	31.0%
	Cellulomonas fimi	4.3	8.6%	6.9%	7.1%	7.5%	5.6%	7.5%	5.1%	8.7%	7.7%	6.2%	6.9%	6.0%	6.9%	4.4%
	Lactobacillus johnsonii	2.0	5.2%	13.0%	13.0%	12.0%	22.0%	21.0%	10.0%	8.5%	23.0%	37.0%	28.0%	23.0%	49.0%	58.0%
	Deinococcus gobiensis	3.1	20.0%	14.0%	11.0%	12.0%	9.9%	8.2%	7.3%	19.0%	8.1%	7.6%	9.6%	6.0%	10.0%	4.2%
	Lactobacillus crispatus	2.0	5.2%	12.0%	14.0%	12.0%	23.0%	18.0%	8.1%	8.6%	25.0%	37.0%	30.0%	24.0%	50.0%	32.0%
	Lactobacillus salivarius	1.8	5.0%	9.1%	13.0%	10.0%	22.0%	21.0%	7.0%	6.7%	25.0%	35.0%	28.0%	21.0%	51.0%	33.0%

	Lactobacillus reuteri	2.3	3.2%	11.0%	12.0%	11.0%	20.0%	19.0%	10.0%	8.0%	25.0%	37.0%	28.0%	25.0%	50.0%	51.0%
	Clostridium perfringens	3.3	9.3%	9.1%	12.0%	12.0%	15.0%	12.0%	14.0%	9.1%	9.9%	15.0%	18.0%	26.0%	24.0%	57.0%
	Bacillus megaterium	5.1	3.5%	6.3%	8.5%	9.9%	16.0%	18.0%	16.0%	7.8%	9.7%	19.0%	12.0%	30.0%	20.0%	42.0%
	Psychrobacter cryohalolentis	3.1	9.2%	7.8%	9.1%	9.4%	12.0%	9.6%	5.2%	12.0%	12.0%	14.0%	14.0%	17.0%	17.0%	12.0%
	Arthrobacter arilaitensis	3.9	5.2%	11.0%	9.1%	8.4%	9.7%	12.0%	4.7%	9.2%	15.0%	19.0%	14.0%	13.0%	21.0%	12.0%
	Ramlibacter tataouinensis	4.1	12.0%	9.8%	6.8%	7.8%	5.3%	8.1%	7.5%	11.0%	8.7%	6.8%	7.8%	6.2%	8.1%	3.7%
	Nakamurella multipartita	6.1	12.0%	8.1%	6.0%	6.5%	9.9%	6.0%	8.6%	12.0%	11.0%	5.6%	5.7%	5.3%	5.0%	3.6%
	Streptococcus infantarius	2.0	6.0%	9.8%	8.0%	8.2%	13.0%	17.0%	6.2%	7.9%	12.0%	18.0%	15.0%	13.0%	21.0%	22.0%
	Stenotrophomonas maltophilia	4.9	6.5%	7.2%	23.0%	5.7%	5.4%	6.9%	6.6%	6.0%	8.6%	15.0%	9.9%	6.1%	8.2%	4.2%
	Arthrobacter chlorophenolicus	4.4	8.3%	7.7%	6.4%	7.0%	5.5%	6.5%	6.6%	14.0%	14.0%	11.0%	8.9%	8.7%	10.0%	5.1%
	Mycobacterium gilvum	5.6	8.8%	8.9%	7.4%	6.9%	9.9%	12.0%	5.7%	12.0%	10.0%	8.2%	11.0%	9.6%	11.0%	9.5%
	Methylobacterium extorquens	6.0	9.1%	8.1%	7.3%	9.4%	6.5%	8.7%	9.8%	7.5%	6.6%	9.8%	8.1%	7.9%	8.5%	5.0%
	Methylobacterium chloromethanicum	5.8	8.7%	7.9%	7.7%	9.3%	6.3%	8.4%	9.0%	7.6%	6.6%	9.9%	8.0%	7.8%	8.1%	4.5%
	Corynebacterium efficiens	3.1	6.1%	8.8%	9.8%	9.3%	8.5%	9.2%	3.9%	14.0%	13.0%	15.0%	12.0%	11.0%	16.0%	11.0%
	Saccharomonospora viridis	4.3	2.1%	4.7%	11.0%	5.0%	9.2%	13.0%	5.2%	8.3%	13.0%	16.0%	8.8%	26.0%	13.0%	26.0%
	Nocardiopsis alba	5.8	2.0%	5.8%	9.5%	8.1%	5.3%	8.9%	3.4%	5.3%	11.0%	16.0%	12.0%	10.0%	16.0%	5.9%
	Psychrobacter arcticus	2.7	5.0%	3.9%	4.6%	5.2%	6.1%	5.0%	2.4%	6.6%	5.7%	7.2%	6.2%	7.5%	8.0%	6.1%
	Leuconostoc mesenteroides	2.0	5.5%	3.5%	4.6%	4.5%	11.0%	5.2%	3.6%	7.1%	5.9%	6.1%	6.5%	8.2%	7.1%	11.0%
	Streptomyces coelicolor	8.7	2.3%	3.9%	5.5%	3.6%	4.9%	7.1%	3.3%	5.1%	6.2%	6.4%	5.3%	8.1%	8.0%	5.8%
Fungus	Aspergillus fumigatus Af293	29.4	0.7%	1.0%	8.9%	5.0%	13.4%	11.2%	7.6%	4.7%	9.0%	27.9%	27.8%	31.7%	22.6%	31.7%
	Saccharomyces cerevisiae S288c	12.1	0.2%	0.5%	1.4%	0.9%	5.9%	1.2%	0.6%	1.1%	1.4%	2.2%	1.8%	4.2%	3.5%	6.2%
Virus	Human adenovirus C,	0.036	2.4%	3.6%	4.5%	7.7%	9.8%	9.3%	12.0%	2.9%	3.7%	9.6%	4.8%	4.0%	8.8%	8.0%
	Pseudomonas phage F116	0.065	5.4%	8.0%	18.0%	22.0%	34.0%	35.0%	27.0%	0.7%	5.9%	4.7%	13.0%	8.1%	20.0%	16.0%
	Enterobacteria phage P1	0.095	1.1%	1.5%	1.9%	1.9%	2.5%	2.1%	1.9%	1.3%	2.2%	2.8%	2.2%	2.0%	3.2%	2.6%

Table S3. Genome-size-normalized relative abundance of the 48 most common bacterial, 2 fungal, and 3 viral species.

Organism	Species	Genome size (Mb)	Relative abundance													
			PM$_{2.5}$							PM$_{10}$						
			01/08	01/09	01/10	01/11	01/12	01/13	01/14	01/08	01/09	01/10	01/11	01/12	01/13	01/14
Bacteria	Geodermatophilus obscurus	5.3	24.99%	16.34%	12.57%	15.08%	9.49%	12.66%	10.73%	21.81%	12.64%	6.12%	13.51%	8.20%	7.78%	4.47%
	Modestobacter marinus	5.6	16.79%	14.07%	9.64%	12.11%	6.60%	10.40%	8.90%	13.83%	9.45%	4.51%	9.70%	5.46%	5.97%	3.51%
	Blastococcus saxobsidens	4.9	11.05%	9.25%	7.49%	8.37%	5.37%	8.50%	6.65%	10.21%	8.15%	4.10%	7.21%	4.97%	5.18%	3.02%
	Kocuria rhizophila	2.7	5.59%	6.87%	5.74%	6.60%	5.20%	5.61%	4.85%	6.09%	5.93%	3.85%	5.57%	4.84%	4.30%	3.58%
	Micrococcus luteus	2.5	2.94%	4.71%	3.48%	4.17%	7.98%	3.44%	2.80%	4.03%	3.75%	2.79%	4.18%	3.94%	3.47%	2.61%
	Candidatus Nitrospira defluvii	4.3	0.80%	3.15%	3.72%	3.83%	6.02%	0.71%	2.07%	1.15%	2.69%	0.75%	2.24%	5.98%	1.46%	0.79%
	Methylobacterium radiotolerans	6.1	3.56%	3.08%	1.94%	2.97%	2.05%	1.66%	3.92%	2.14%	1.79%	1.74%	1.74%	1.60%	2.17%	1.40%
	Propionibacterium acnes	2.6	0.48%	1.04%	1.84%	1.61%	3.27%	5.21%	4.62%	0.61%	0.92%	1.02%	1.92%	2.23%	2.76%	3.50%
	Thermobifida fusca	3.6	0.29%	1.10%	6.18%	1.19%	2.71%	2.29%	2.08%	0.95%	2.43%	3.53%	2.35%	10.56%	1.95%	4.76%
	Nocardioides sp.	5.0	2.78%	2.55%	1.99%	2.22%	1.47%	1.79%	1.23%	3.62%	2.77%	1.93%	2.17%	1.92%	1.81%	1.29%
	Nocardiopsis dassonvillei	6.5	0.41%	1.01%	3.43%	1.21%	1.51%	3.72%	1.76%	1.02%	2.43%	3.97%	2.31%	2.86%	2.74%	3.13%
	Brachybacterium faecium	3.6	1.14%	1.90%	1.81%	1.67%	1.51%	1.68%	1.13%	1.60%	3.33%	2.83%	2.47%	2.01%	3.85%	1.37%
	Arthrobacter phenanthrenivorans	4.3	1.98%	1.79%	1.60%	1.68%	1.24%	1.28%	0.91%	2.99%	2.24%	1.85%	2.09%	1.51%	1.66%	1.12%
	Cellvibrio gilvus	3.5	1.69%	1.64%	1.50%	1.66%	1.07%	1.78%	1.08%	1.78%	1.53%	1.01%	1.31%	1.04%	1.00%	0.77%
	Carnobacterium sp.	2.6	1.40%	1.43%	1.71%	1.43%	2.07%	1.35%	0.77%	1.90%	1.59%	1.95%	1.81%	2.43%	1.41%	2.40%
	Microbacterium testaceum	4.0	1.23%	1.82%	1.39%	1.64%	1.09%	1.33%	0.83%	1.44%	1.65%	1.79%	1.42%	1.11%	1.99%	1.02%
	Paracoccus denitrificans	4.6	1.16%	1.22%	1.31%	1.34%	1.10%	1.26%	0.98%	1.32%	1.21%	0.99%	1.11%	1.04%	1.01%	0.86%
	Kytococcus sedentarius	2.8	1.08%	1.26%	1.31%	1.20%	1.28%	1.12%	0.88%	1.36%	1.33%	1.03%	1.37%	1.40%	1.20%	0.92%
	Pantoea vagans	4.0	0.76%	0.94%	3.04%	1.32%	0.95%	0.54%	0.41%	0.52%	1.44%	3.71%	1.60%	1.20%	1.67%	1.63%
	Pseudomonas stutzeri	4.7	0.85%	1.10%	1.23%	0.77%	0.80%	0.76%	2.42%	0.99%	1.30%	1.13%	1.05%	1.10%	1.16%	0.56%
	Kineococcus radiotolerans	4.8	1.41%	1.31%	1.13%	1.36%	0.68%	0.75%	0.94%	1.37%	1.09%	0.67%	1.27%	0.67%	0.72%	0.45%
	Sanguibacter keddieii	4.3	1.23%	1.36%	1.05%	1.17%	0.81%	1.15%	0.79%	1.26%	1.22%	1.52%	1.05%	0.97%	0.94%	0.71%
	Thauera sp.	4.5	0.51%	0.92%	0.98%	1.46%	1.68%	0.85%	0.99%	0.57%	1.40%	0.62%	1.14%	1.79%	0.75%	0.41%
	Pantoea ananatis	4.7	0.28%	1.13%	1.34%	1.07%	1.91%	0.99%	0.54%	0.79%	2.77%	4.59%	1.14%	1.29%	4.57%	2.75%
	Cellulomonas fimi	4.3	1.32%	1.16%	1.05%	1.28%	0.71%	0.94%	0.72%	1.39%	1.16%	0.75%	0.98%	0.76%	0.75%	0.55%
	Lactobacillus johnsonii	2.0	0.35%	1.06%	1.06%	0.97%	1.56%	1.35%	0.82%	0.46%	1.80%	2.79%	2.15%	1.66%	3.85%	7.65%
	Deinococcus gobiensis	3.1	1.84%	1.28%	1.00%	1.06%	0.66%	0.54%	0.71%	1.39%	0.59%	0.46%	0.68%	0.43%	0.59%	0.34%
	Lactobacillus crispatus	2.0	0.35%	0.90%	1.17%	1.02%	1.67%	1.07%	0.67%	0.47%	1.93%	2.79%	2.27%	1.91%	3.68%	2.97%
	Lactobacillus salivarius	1.8	0.34%	0.70%	0.98%	0.83%	1.59%	1.36%	0.57%	0.36%	2.00%	2.49%	2.13%	1.55%	4.01%	3.07%

	Lactobacillus reuteri	2.3	0.22%	0.82%	0.86%	0.89%	1.44%	1.27%	0.82%	0.44%	1.95%	2.82%	2.10%	1.92%	3.93%	6.68%
	Clostridium perfringens	3.3	0.68%	0.70%	0.89%	0.99%	0.99%	0.75%	1.26%	0.49%	0.66%	0.93%	1.28%	2.08%	1.33%	7.17%
	Bacillus megaterium	5.1	0.24%	0.49%	0.63%	0.81%	1.05%	1.11%	1.40%	0.43%	0.65%	1.16%	0.77%	2.35%	1.07%	4.20%
	Psychrobacter cryohalolentis	3.1	0.84%	0.77%	0.86%	0.96%	1.04%	0.73%	0.46%	1.02%	1.06%	1.09%	1.20%	1.62%	1.16%	1.23%
	Arthrobacter arilaitensis	3.9	0.48%	0.96%	0.80%	0.80%	1.19%	0.88%	0.53%	0.64%	1.15%	1.27%	1.13%	1.01%	1.29%	1.08%
	Ramlibacter tataouinensis	4.1	1.23%	1.10%	0.64%	0.85%	0.41%	0.62%	0.78%	1.02%	0.79%	0.52%	0.64%	0.52%	0.52%	0.30%
	Nakamurella multipartita	6.1	1.17%	0.85%	0.60%	0.71%	0.77%	0.49%	0.90%	1.04%	0.94%	0.42%	0.53%	0.45%	0.35%	0.34%
	Streptococcus infantarius	2.0	0.44%	0.83%	0.59%	0.67%	0.93%	1.14%	0.50%	0.43%	0.87%	1.25%	1.13%	1.05%	1.43%	2.59%
	Stenotrophomonas maltophilia	4.9	0.52%	0.61%	2.00%	0.47%	0.36%	0.42%	0.59%	0.36%	0.62%	0.98%	0.70%	0.44%	0.43%	0.32%
	Arthrobacter chlorophenolicus	4.4	0.87%	0.87%	0.65%	0.76%	0.49%	0.52%	0.64%	1.33%	1.29%	0.86%	0.84%	0.78%	0.71%	0.48%
	Mycobacterium gilvum	5.6	0.71%	0.75%	0.60%	0.61%	0.66%	0.88%	0.51%	0.79%	0.75%	0.50%	1.01%	0.70%	0.68%	0.77%
	Methylobacterium extorquens	6.0	0.67%	0.62%	0.54%	0.77%	0.43%	0.53%	0.87%	0.45%	0.44%	0.59%	0.52%	0.52%	0.44%	0.38%
	Methylobacterium chloromethanicum	5.8	0.64%	0.61%	0.57%	0.76%	0.39%	0.51%	0.80%	0.45%	0.44%	0.60%	0.51%	0.52%	0.42%	0.34%
	Corynebacterium efficiens	3.1	0.49%	0.74%	0.79%	0.76%	0.57%	0.56%	0.35%	0.89%	0.97%	0.96%	0.85%	0.77%	0.90%	0.88%
	Saccharomonospora viridis	4.3	0.19%	0.40%	0.90%	0.41%	0.62%	0.80%	0.42%	0.53%	0.92%	0.97%	0.62%	2.06%	0.68%	2.33%
	Nocardiopsis alba	5.8	0.19%	0.49%	0.77%	0.66%	0.36%	0.54%	0.31%	0.37%	0.77%	0.97%	0.83%	0.76%	0.85%	0.44%
	Psychrobacter arcticus	2.7	0.43%	0.36%	0.43%	0.54%	0.50%	0.35%	0.21%	0.53%	0.48%	0.54%	0.55%	0.72%	0.56%	0.61%
	Leuconostoc mesenteroides	2.0	0.37%	0.27%	0.34%	0.34%	0.76%	0.29%	0.30%	0.39%	0.39%	0.34%	0.42%	0.54%	0.34%	0.82%
	Streptomyces coelicolor	8.7	0.23%	0.38%	0.49%	0.34%	0.35%	0.47%	0.29%	0.38%	0.49%	0.42%	0.40%	0.63%	0.45%	0.48%
Fungus	Aspergillus fumigatus Af293	29.4	0.07%	0.11%	0.70%	0.41%	0.94%	0.71%	0.66%	0.29%	0.64%	1.91%	2.18%	2.58%	1.25%	3.04%
	Saccharomyces cerevisiae S288c	12.1	0.02%	0.04%	0.10%	0.07%	0.37%	0.07%	0.05%	0.06%	0.09%	0.12%	0.12%	0.28%	0.17%	0.47%
Virus	Human adenovirus C	0.036	0.25%	0.36%	0.46%	1.52%	5.33%	4.63%	17.55%	0.16%	0.36%	13.03%	0.56%	0.39%	4.97%	1.75%
	Pseudomonas phage F116	0.065	0.37%	0.62%	1.96%	2.42%	5.78%	5.43%	3.87%	0.03%	0.39%	0.26%	0.98%	0.59%	1.31%	1.38%
	Enterobacteria phage P1	0.095	0.09%	0.16%	0.14%	0.22%	0.22%	0.21%	0.18%	0.09%	0.29%	0.22%	0.18%	0.29%	0.36%	0.29%

Table S4. Summary of PM and meteorological data. The daily temperature, relative humidity, atmospheric pressure, and wind velocity data were 23-hour averages.

Sampling date	Cut-point diameter (μm)	Weather	Temperature (℃)	Relative humidity (%)	Atmospheric pressure (Hpa)	Wind velocity (m/s)	Net weight of filters (g)	PM concentration of Tsinghua District (μg/m^3)	PM concentration of Haidian monitoring site (μg/m^3)	AQI of Haidian District		
										BJZWY*	BBXQ*	WL*
01/08	2.5	Clear	-5.03	29.46	1026.36	3.02	0.071	45.21	9.67	83	113	109
	10						0.117	75.03	22.00			
01/09	2.5	Clear	-5.18	44.96	1023.11	1.55	0.163	104.53	80.00	58	NA	77
	10						0.235	150.70	98.33			
01/10	2.5	Overcast	-4.48	66.54	1020.21	1.60	0.411	263.56	288.67	241	242	258
	10						0.543	348.21	321.00			
01/11	2.5	Clear	-5.71	74.88	1018.14	1.06	0.368	235.67	226.67	304	264	413
	10						0.528	338.59	242.67			
01/12	2.5	Misty	-2.75	73.08	1017.49	1.35	0.519	332.82	444.67	360	291	498
	10						0.741	475.18	498.33			
01/13	2.5	Overcast	-4.80	80.75	1018.82	1.20	0.409	261.96	310.33	391	457	401
	10						0.561	359.75	327.67			
01/14	2.5	Clear	-2.38	72.96	1022.15	2.13	0.274	175.39	162.33	280	328	337
	10						0.380	243.68	152.67			

"NA" indicates no available data from the official website of Beijing Municiple Environmental Monitoring Center.

*"BJZWY", "BBXQ", "WL" are the abbreviated names of the three monitoring sites in Haidian District.

Table S5. Airborne bacteria and archaea identified at the genus level from Tsinghua PM study and three previous studies combined$^{5-7}$.

Tsinghua PM study	GRIP, Milan, and New York studies	Overlap
Roseomonas, Chroococcidiopsis, Geodermatophilus, Serinicoccus, Porphyromonas, Streptomyces, Skermanella, Phormidium, Rubellimicrobium, Saccharopolyspora, Friedmanniella, Paracoccus, Alicyclobacillus, Propionicimonas, Aestuariimicrobium, Marmoricola, Deinococcus, Thermoactinomyces, Blastococcus, Nocardioides, Flavisolibacter, Microlunatus, Kaistobacter, Micromonospora, Cellvibrio, Modestobacter, Paenibacillus, Mesorhizobium, Luteococcus, Archangium, Kocuria, Rhodoplanes, Massilia, Candidatus Microthrix, Actinotalea, UA01, Bacteroides, Pontibacter, Sporosarcina, Arthrobacter, Candidatus Nitrososphaera, Pseudonocardia, Propionibacterium, Planomicrobium, Hymenobacter, Iamia, Gillisia, Arsenicicoccus, Tessaracoccus, Sphingomonas, Actinomadura, Bacillus, Rathayibacter, Adhaeribacter, Alkanindiges, Prevotella, Azospirillum, Plesiocystis, Chondromyces, Novosphingobium, Devosia, Mycobacterium, Fusobacterium, Carnobacterium, Actinomycetospora, Turicibacter, Phycicoccus, Amaricoccus, Laceyella, Corynebacterium, Planctomyces, Nitrosomonas, Brevundimonas, Psychrobacter, Thioclava, Myroides, Actinoplanes, Janibacter, Brevibacterium, Alistipes, Clostridium, Desulfovibrio, Epulopiscium, Methylotenera, Nannocystis, Herbaspirillum, Azohydromonas, Leptolyngbya, LE30, Cytophaga, Algoriphagus, Oxalobacter, Aeromicrobium, Euzebia, Planococcus, Lysobacter, Methylobacterium, Coprococcus, Anabaena, Myxococcus, Calothrix, Salinicoccus, Ruminococcus, Agrococcus, Promicromonospora, Segetibacter, Lentibacillus, Georgenia, Ramlibacter, Rhodoferax, Knoellia, Patulibacter, Arcobacter, Allobaculum, Rubrobacter, Treponema, Planifilum, Bifidobacterium, Fibrobacter, Prauserella, Leucobacter, Actinomyces, Microbacterium, Couchioplanes, Flavobacterium, Staphylococcus, Thermobifida, Paludibacter, Bulleidia, Brachybacterium, Candidatus Solibacter, Jeotgalicoccus, Amycolatopsis, Actinoalloteichus, Methanobrevibacter, Brevibacillus, Hahella, Pedobacter, Nitrosovibrio, Virgibacillus, Oerskovia, Gemmata, Oscillatoria, Lactobacillus, Micrococcus, Wautersiella, Microcoleus, Leptospira, Methylibium, Sejongia, Oceanobacillus, Exiguobacterium, Chthoniobacter, Marinilactibacillus, Yaniella, Dietzia, Luteolibacter, Rhodococcus, Asticcacaulis, Megamonas, Dyadobacter, Aerococcus, Rothia, Williamsia, Spirosoma, Enterobacter, Kineococcus, Moraxella, Balneimonas, Weissella, Alkalibacterium, J2-29, Pantoea, Cellulomonas, Caldilinea, Phenylobacterium, Adlercreutzia, Akkermansia, Dehalobacterium, Sphingobium, Parabacteroides, Okibacterium, Pseudomonas, Methylophilus, Shinella, Phascolarctobacterium, Trichococcus, Curtobacterium, Thermomonas, Candidatus Entotheonella, Gemmatimonas, Veillonella, Halomonas, Virgisporangium, Haliangium,	Clostridium, Alkalibacterium, Nocardioides, Azohydromonas, Georgenia, Ureibacillus, Diaphorobacter, Staphylococcus, Propionibacterium, Ralstonia, Microbacterium, Saccharopolyspora, Rhodococcus, Salinicoccus, Pimelobacter, Stenotrophomonas, Coprococcus, Sphingomonas, Streptococcus, Corynebacterium, Acinetobacter, Pseudomonas, Flavobacterium, Pedobacter, Streptomyces, Mycobacterium, Pantoea, Dyadobacter, Ornithinicoccus, Dietzia, Psychrobacter, Prevotella, Jeotgalicoccus, Acidovorax, Modestobacter, Aquabacterium, Kaistobacter, Friedmanniella, Lactobacillus, Rubellimicrobium, Roseateles, Janthinobacterium, Roseomonas, Deinococcus, Salmonella, Methylibium, Cellulomonas, Aerococcus, Alkanindiges, Bacteroides, Hymenobacter, Geodermatophilus, Bdellovibrio, Curvibacter, Nesterenkonia, Blastococcus, Pontibacter, Kocuria, Planococcus, Aeromonas, Bosea, Massilia, Spirosoma, Fusobacterium, Pseudonocardia, Faecalibacterium, Ruminococcus, Propionicimonas, Chryseobacterium, Bacillus, Lactococcus, Novosphingobium, Microcystis, HTCC2207, Microcoleus, Iamia, Pandoraea, Rhodoferax, Anaerococcus, Aurantimonas, Skermanella, Rothia, Catenibacterium, Frankia, Treponema, Paracoccus, Salegentibacter, Janibacter, Terracoccus, Agrococcus, Prauserella, Escherichia, Planomicrobium, Dermacoccus, Saccharomonospora, Chroococcidiopsis, Marmoricola, Gordonia, Blautia, Flavisolibacter, Olivibacter, Sphingobacterium, Methylobacterium, Gemella, Amaricoccus, Enterococcus, Chthoniobacter, Paenibacillus, Brevibacterium, Wautersiella, Parabacteroides, Eubacterium, Actinomycetospora, Afipia, Hydrogenophilus, Brachybacterium, Enhydrobacter, Sphingobium, Cenarchaeum, Burkholderia, Dialister, Micrococcus, Brevundimonas, Bifidobacterium, Roseburia, Oxalobacter, Sejongia, Arthrobacter, Phenylobacterium, Desulfovibrio, Rhizobium, Phormidium, Dokdonella, Alcaligenes, Devosia, Carnobacterium, Glycomyces, Candidatus Xiphinematobacter, Ramlibacter, Cellvibrio, Segetibacter, Pigmentiphaga, Spiroplasma, Micromonospora, Cystobacter, Luteibacter, Marinobacter, Ignatzschineria, Neisseria, Thermobispora, Nocardia, Actinotalea, Halobacterium, Citricoccus, Salinimicrobium, Limnobacter, Alcanivorax, Arsenicicoccus, Rubrobacter, Porphyrobacter, Aestuariimicrobium, Mycoplasma, Knoellia, Variovorax, Arcobacter, Tessaracoccus, Helicobacter, Porphyromonas, Yonghaparkia, Peptostreptococcus, Selenomonas, Shinella, Leuconostoc, Gillisia, Finegoldia, Actinomyces, Lampropedia, Paucibacter, Sodalis, Adhaeribacter, Halomonas, Erythrobacter, Novispirillum, Erwinia, Polaromonas, Lysobacter, PSB-M-3, Nocardiopsis, Mesorhizobium, Candidatus Phytoplasma, Planctomyces, Candidatus Rhabdochlamydia, Rhodopirellula, MC18, Candidatus Endobugula, Algoriphagus, Tatlockia, Achromobacter, Balneimonas, Planifilum, Syntrophus,	Roseomonas, Chroococcidiopsis, Geodermatophilus, Serinicoccus, Porphyromonas, Streptomyces, Skermanella, Phormidium, Rubellimicrobium, Saccharopolyspora, Friedmanniella, Paracoccus, Alicyclobacillus, Propionicimonas, Aestuariimicrobium, Marmoricola, Deinococcus, Thermoactinomyces, Blastococcus, Nocardioides, Flavisolibacter, Microlunatus, Kaistobacter, Micromonospora, Cellvibrio, Modestobacter, Paenibacillus, Mesorhizobium, Luteococcus, Archangium, Kocuria, Rhodoplanes, Massilia, Actinotalea, Bacteroides, Pontibacter, Sporosarcina, Arthrobacter, Candidatus Nitrososphaera, Pseudonocardia, Propionibacterium, Planomicrobium, Hymenobacter, Iamia, Gillisia, Arsenicicoccus, Tessaracoccus, Sphingomonas, Actinomadura, Bacillus, Rathayibacter, Adhaeribacter, Alkanindiges, Prevotella, Novosphingobium, Devosia, Mycobacterium, Fusobacterium, Carnobacterium, Actinomycetospora, Turicibacter, Amaricoccus, Corynebacterium, Planctomyces, Nitrosomonas, Brevundimonas, Psychrobacter, Thioclava, Myroides, Actinoplanes, Janibacter, Brevibacterium, Alistipes, Clostridium, Desulfovibrio, Epulopiscium, Methylotenera, Azohydromonas, Leptolyngbya, LE30, Cytophaga, Algoriphagus, Oxalobacter, Aeromicrobium, Euzebia, Planococcus, Lysobacter, Methylobacterium, Coprococcus, Myxococcus, Salinicoccus, Ruminococcus, Agrococcus, Segetibacter, Georgenia, Ramlibacter, Rhodoferax, Knoellia, Patulibacter, Arcobacter, Allobaculum, Rubrobacter, Treponema, Planifilum, Bifidobacterium, Fibrobacter, Prauserella, Leucobacter, Actinomyces, Microbacterium, Flavobacterium, Staphylococcus, Paludibacter, Bulleidia, Brachybacterium, Candidatus Solibacter, Jeotgalicoccus, Amycolatopsis, Actinoalloteichus, Methanobrevibacter, Brevibacillus, Pedobacter, Gemmata, Lactobacillus, Micrococcus, Wautersiella, Microcoleus, Methylibium, Sejongia, Oceanobacillus, Exiguobacterium, Chthoniobacter, Marinilactibacillus, Yaniella, Dietzia, Luteolibacter, Rhodococcus, Asticcacaulis, Megamonas, Dyadobacter, Aerococcus, Rothia, Williamsia, Spirosoma, Enterobacter, Kineococcus, Moraxella, Balneimonas, Weissella, Alkalibacterium, J2-29, Pantoea, Cellulomonas, Caldilinea, Phenylobacterium, Adlercreutzia, Akkermansia, Dehalobacterium, Sphingobium, Parabacteroides, Pseudomonas, Shinella, Trichococcus, Curtobacterium, Thermomonas, Candidatus Entotheonella, Gemmatimonas, Veillonella, Halomonas, Haliangium, Glycomyces, Salinimicrobium, Nostoc, Aurantimonas, Rhizobium, Sphingobacterium, Pirellula, Sutterella, Ammoniphilus, Dechloromonas, Eubacterium, Frigoribacterium, Blautia, Terracoccus, Thermobispora, Dokdonella, Aquabacterium, Acinetobacter, Streptacidiphilus, Scytonema, Faecalibacterium, Solirubrobacter, Sharpea, Dermacoccus, Nocardiopsis, Caulobacter,

Glycomyces, Salinimicrobium, Nostoc, Aurantimonas, Rhizobium, Sphingobacterium, Pirellula, Sutterella, Ammoniphilus, Dechloromonas, Aeropyrum, Eubacterium, Frigoribacterium, Blautia, Lentzea, Terracoccus, Thermobispora, Dokdonella, Aquabacterium, Jiangella, Acinetobacter, Streptacidiphilus, Gloeobacter, Dermatophilus, Scytonema, Faecalibacterium, Solirubrobacter, Sharpea, Dermacoccus, Shimazuella, Nocardiopsis, Caulobacter, Abiotrophia, Mechercharimyces, Actinopolymorpha, Sorangium, Legionella, Caloramator, Roseburia, p-75-a5, Hydrocarboniphaga, Chryseobacterium, Parachlamydia, Rhodocyclus, Pseudoxanthomonas, Simidua, Pimelobacter, Tissierella, Agromyces, Kouleothrix, Waddlia, Thermaerobacter, Cohnella, Candidatus Cloacamonas, Stenotrophomonas, Azonexus, Methanofollis, Methylocaldum, Helcococcus, Frankia, Cellulosimicrobium, Desulfitobacter, ZD0117, Sodalis, Paenisporosarcina, Isoptericola, Shewanella, Hyphomicrobium, Plantibacter, Ectothiorhodospira, Polaromonas, Comamonas, Marinobacter, Achromobacter, Geobacillus, Tsukamurella, Candidatus Rhabdochlamydia, Rhodopirellula, Planktothricoides, Simplicispira, Oceanospirillum, Nocardia, Methylomonas, Clavibacter, Cryobacterium, Marinibacillus, Candidatus Azobacteroides, Jonesia, Azospira, Aquicella, Streptococcus, Bdellovibrio, Saccharomonospora, Acidovorax, Paucibacter, Janthinobacterium, Spirulina, Chloroflexus, Rarobacter, Nitrosospira, Lachnospira, Pseudobutyrivibrio, Trabulsiella, Arthrospira, Desulfosporosinus, Capnocytophaga, Oribacterium, Xanthobacter, Thauera, Anaerolinea, Natronorubrum, Hylemonella, Candidatus Odyssella, Kaistia, Methylosinus, Solibacillus, Crossiella, Erythromicrobium, Anaeromyxobacter, Rhodopseudomonas, Delftia, Macrococcus, Loktanella, Anaerobiospirillum, Alkaliphilus, Microcella, Pigmentiphaga, MC18, Enterococcus, Oleibacter, Anoxybacillus, u114, Vagococcus, Lactococcus, Candidatus Xiphinematobacter, Lutibacterium, Candidatus Protochlamydia, Chitinophaga, Rubrivivax, Salegentibacter, Methanosarcina, Erythrobacter, Rhodobacter, Acidisoma, Desulfitobacterium, Z4MB24, Aquamonas, Geobacter, Anaerobacillus, Xenococcus, Rheinheimera, Lysinibacillus, Nitrospira, Microbulbifer, Steroidobacter, Niabella, Acetobacter, Gordonia, Edaphobacter, LCP-6, Oscillospira, Verrucomicrobium, Opitutus, Zymomonas, Sporanaerobacter, Pelotomaculum, Facklamia, Sanguibacter, Planktothrix, WCHB1-05, Bosea, Aeromonas, Erwinia, Kribbella, Bradyrhizobium, Methanosphaerula, Thiobacillus, Cryocola, Methyloversatilis, SHD-231, Roseococcus, Rummeliibacillus, Pseudoruegeria, Aminiphilus, Ureibacillus, Thermobacillus, Cryptosporangium, Raoultella, Bartonella, Parapedobacter, Oscillochloris, Desulfobulbus, Inquilinus, Campylobacter, Variovorax, Desulfosporomusa, Labrys, Salinibacterium, Serratia, Luteimonas, Candidatus Koribacter, Mycoplana, Spiroplasma, Actinokineospora,	Rhodoplanes, Hydrocoleum, Solirubrobacter, Megasphaera, Chloroflexus, Nitrosococcus, Acetobacterium, Oribacterium, Nitrosomonas, Microtetraspora, Fructobacillus, Geobacillus, Cytophaga, Blastochloris, Kineococcus, Desulfosporosinus, Sphingopyxis, Photobacterium, Colwellia, Agrobacterium, Sutterella, Vogesella, LE30, Rubrivivax, Ensifer, SGUS388, Chitinophaga, Proteus, Myroides, Pseudanabaena, Candidatus Solibacter, Demequina, Gemmata, Rhodobacter, Parachlamydia, Isoptericola, Alishewanella, Hyphomicrobium, Butyrivibrio, Rhodocyclus, Rickettsiella, Zymomonas, Fluviicola, Vibrio, Alistipes, Candidatus Liberibacter, Dechloromonas, Thalassobacillus, Candidatus Entotheonella, Methyloversatilis, Aquamonas, Thermomonas, Bulleidia, Sanguibacter, A17, Pseudobutyrivibrio, Agromyces, Methanolinea, Thiobacillus, Williamsia, Thioclava, Cronobacter, SJA-88, Candidatus Odyssella, Halobacillus, Shewanella, Parapedobacter, Candidatus Protochlamydia, Caulobacter, Aneurinibacillus, Ideonella, Paludibacter, 4-29, Erythromicrobium, Candidatus Portiera, Exiguobacterium, BHB21, Roseococcus, Methanobrevibacter, Desulfurispirillum, Euzebia, Amycolatopsis, Parvibaculum, Helcococcus, Actinoalloteichus, Pedomicrobium, Singulisphaera, Aeromicrobium, Steroidobacter, Kribbella, Yaniella, Tissierella, A55_D21, Aquicella, Anaeroplasma, Succinivibrio, RFN20, Facklamia, Azotobacter, Aromatoleum, Cupriavidus, Peptoniphilus, Desemzia, Procabacter, Thermonema, Brucella, Luteococcus, Veillonella, Opitutus, Campylobacter, Asticcacaulis, Megamonas, Trichococcus, Candidatus Glomeribacter, Klebsiella, Sharpea, Bradyrhizobium, Luteolibacter, Caldilinea, Runella, Rheinheimera, Lachnobacterium, Zoogloea, Simonsiella, Abiotrophia, Renibacterium, Scytonema, Granulicatella, Leclercia, Mechercharimyces, Xanthomonas, Nitratireductor, Actinopolymorpha, Haemophilus, Hydrogenophaga, Turicibacter, Methylopila, Weissella, Thauera, Coprobacillus, Collinsella, Slackia, Peptococcus, Eggerthella, Gallionella, Thermoactinomyces, Pseudoclavibacter, Buchnera, Elizabethkingia, Sphaerochaeta, Thiomonas, Leptolyngbya, Alicyclobacillus, Methylotenera, Thalassospira, Candidatus Pelagibacter, Adlercreutzia, Epulopiscium, Mycoplana, Delftia, Maribacter, Rhodobaca, Oceanobacillus, Cyclobacterium, Arenimonas, Pirellula, Oscillospira, Caloramator, Marinimicrobium, Thiothrix, BD2-13, Thermicanus, Legionella, Rhodocista, Hylemonella, Cetobacterium, Sarcina, Akkermansia, Solibacillus, L7A_E11, Actinomadura, Desulfonatronovibrio, Comamonas, Magnetospirillum, Methanocorpusculum, Shigella, Aquiflexum, Simplicispira, Actinokineospora, Limnohabitans, WCHB1-05, Yersinia, Bartonella, Salinibacter, Allobaculum, Verrucomicrobium, Candidatus Koribacter, p-75-a5, Cohnella, Leptotrichia, J2-29, Mucispirillum, Prosthecobacter, Bordetella, Fusibacter, Bacteriovorax, Curtobacterium, Nitrospira, Archangium,	Abiotrophia, Mechercharimyces, Actinopolymorpha, Legionella, Caloramator, Roseburia, p-75-a5, Hydrocarboniphaga, Chryseobacterium, Parachlamydia, Rhodocyclus, Pimelobacter, Tissierella, Agromyces, Kouleothrix, Waddlia, Cohnella, Stenotrophomonas, Helcococcus, Frankia, Cellulosimicrobium, Sodalis, Paenisporosarcina, Isoptericola, Shewanella, Hyphomicrobium, Polaromonas, Comamonas, Marinobacter, Achromobacter, Geobacillus, Candidatus Rhabdochlamydia, Rhodopirellula, Simplicispira, Nocardia, Methylomonas, Marinibacillus, Aquicella, Streptococcus, Bdellovibrio, Saccharomonospora, Acidovorax, Paucibacter, Janthinobacterium, Chloroflexus, Lachnospira, Pseudobutyrivibrio, Desulfosporosinus, Capnocytophaga, Oribacterium, Thauera, Hylemonella, Candidatus Odyssella, Solibacillus, Erythromicrobium, Rhodopseudomonas, Delftia, Macrococcus, Pigmentiphaga, MC18, Enterococcus, Lactococcus, Candidatus Xiphinematobacter, Lutibacterium, Candidatus Protochlamydia, Chitinophaga, Rubrivivax, Salegentibacter, Erythrobacter, Rhodobacter, Acidisoma, Aquamonas, Geobacter, Rheinheimera, Nitrospira, Steroidobacter, Acetobacter, Gordonia, Oscillospira, Verrucomicrobium, Opitutus, Zymomonas, Facklamia, Sanguibacter, WCHB1-05, Bosea, Aeromonas, Erwinia, Kribbella, Bradyrhizobium, Thiobacillus, Methyloversatilis, Roseococcus, Ureibacillus, Raoultella, Bartonella, Parapedobacter, Campylobacter, Variovorax, Serratia, Luteimonas, Candidatus Koribacter, Mycoplana, Spiroplasma, Actinokineospora, Nitratireductor, Rhodobaca, Candidatus Amoebophilus, Catellatospora, Pseudoclavibacter, Burkholderia, Pedomicrobium, Mycoplasma, Anaeroplasma, A55_D21, Citricoccus, Anaerofustis, Succinivibrio, Aromatoleum, Salmonella, Frateuria, Butyrivibrio, A17, Zoogloea, Singulisphaera, Pseudaminobacter, Phyllobacterium, Diaphorobacter, Hydrocoleum, Blastochloris, Halobacillus, Granulicatella, Leuconostoc, Runella, Gemella, Agrobacterium, Haererehalobacter, Methylopila, Anaerococcus, Saccharothrix, Afipia, Gallionella, Pseudidiomarina, Ideonella, RFN20, Neisseria, Ralstonia, SJA-88, Halobacterium, Xanthomonas, Coprobacillus, Azotobacter, Zhihengliuella, BD2-13, L7A_E11, Kineosporia, Arcanobacterium, Leptotrichia, Cyclobacterium, Peptococcus, Megasphaera, Demequina, Sphaerochaeta, Alcanivorax, Methanolinea, Aquiflexum, Dolichospermum, Arenimonas, Muricauda, Kushneria, Solimonas, Nesterenkonia, Mitsuokella, Curvibacter, Yonghaparkia, Citrobacter, Dysgonomonas, Ignatzschineria, Dyella, Ochrobactrum, Streptobacillus, Symbiobacterium, Actinoallomurus, Pseudanabaena, Meiothermus, Collinsella, Mucispirillum, Lachnobacterium, Prochlorococcus, Procabacter, Emticicia, Klebsiella, Pseudoalteromonas, Sphingopyxis, Conchiformibius, Syntrophomonas, Teredinibacter, Nitrosococcus, Cupriavidus, Olivibacter, Cystobacter, Alcaligenes, Tatlockia, Sarcina, Haloanella, Caedibacter, Desemzia, Peptoniphilus, Acholeplasma,

Candidatus Methanoregula, Synechococcus, Nitratireductor, Nonomuraea, Rhodobaca, Candidatus Amoebophilus, Catellatospora, Pseudoclavibacter, Burkholderia, Pilimelia, Pedomicrobium, Mycoplasma, Atopobium, Anaeroplasma, Myceligenerans, Salinisphaera, A55_D21, Sedimentibacter, Citricoccus, Anaerofustis, Succinivibrio, Aromatoleum, Crenothrix, Salmonella, Frateuria, Butyrivibrio, Collimonas, A17, Sinorhizobium, Rhodanobacter, Averyella, Zoogloea, Singulisphaera, Pseudaminobacter, Phyllobacterium, Lautropia, Diaphorobacter, Methylophaga, Hydrocoleum, Blastochloris, Schlegelella, Halobacillus, Granulicatella, Leuconostoc, Runella, Gemella, Agrobacterium, Haererehalobacter, Catonella, Mannheimia, Alysiella, Methylopila, Xenophilus, Desulfobacca, Anaerococcus, Saccharothrix, Dorea, Methylobacillus, Sporocytophaga, Afipia, Gallionella, Rhodovibrio, HB2-32-21, Pseudidiomarina, Ideonella, RFN20, Neisseria, Ralstonia, SJA-88, Nordella, Halobacterium, Halorubrum, Xanthomonas, Sphaerospermopsis, Coprobacillus, Kibdelosporangium, Azotobacter, Zhihengliuella, BD2-13, L7A_E11, Dethiobacter, Kineosporia, Arcanobacterium, Candidatus Scalindua, Leptotrichia, Cyclobacterium, Belliella, Peptococcus, Megasphaera, Demequina, Sphaerochaeta, Alcanivorax, Methanolinea, Aequorivita, Fulvivirga, Aquiflexum, Dolichospermum, Arenimonas, Muricauda, Streptomonospora, Kushneria, Solimonas, Methylococcus, Thermomonospora, Chelativorans, Olsenella, Nesterenkonia, Thermacetogenium, Mitsuokella, Thermus, Wolinella, Curvibacter, Yonghaparkia, Leucothrix, Citrobacter, Terribacillus, Chthonomonas, Dysgonomonas, Ignatzschineria, Dyella, Ochrobactrum, Halomicronema, Streptosporangium, Streptobacillus, Symbiobacterium, Actinoallomurus, Pseudanabaena, Meiothermus, Collinsella, Tenacibaculum, Mucispirillum, Lachnobacterium, Polynucleobacter, Prochlorococcus, Procabacter, Emticicia, Acidiphilium, Marinomonas, Klebsiella, Erysipelothrix, Pseudoalteromonas, Ruegeria, Sphingopyxis, Conchiformibius, Actinocorallia, Syntrophomonas, Aminobacter, Teredinibacter, Sinomonas, Hydrogenobaculum, Nitrosococcus, Rivularia, Cupriavidus, Azomonas, Olivibacter, Ancylobacter, Sulfuricurvum, Methanosphaera, Cystobacter, Terriglobus, Azorhizophilus, Alcaligenes, Tatlockia, Sarcina, Haloanella, Caldimonas, Asteroleplasma, Caedibacter, Desemzia, Kitasatospora, Peptoniphilus, Acholeplasma, Heliorestis, Aneurinibacillus, Niastella, Acetivibrio, Pelomonas, Balneola, Luteibacter, Methanocella, Luedemannella, Oceanisphaera, Desulfotomaculum, Trichodesmium, Xylanimicrobium, Moorella, Skermania, Anaerofilum, Providencia, Dactylosporangium, Gardnerella, Catenulispora, Actinobaculum, Renibacterium, Gluconacetobacter, Candidatus Aquirestis, Sporichthya, Coriobacterium, Sulfurospirillum, Candidatus Contubernalis, Marinimicrobium,	Streptobacillus, Wolbachia, Symbiobacterium, Desulfonatronum, Actinoallomurus, Rhodopseudomonas, Pseudoalteromonas, Meiothermus, Dehalobacterium, Alteromonas, Waddlia, Nitrosopumilus, Congregibacter, Oceanithermus, Prochlorococcus, Pelagicoccus, Dysgonomonas, Actinoplanes, Phyllobacterium, Acidobacterium, Acidisoma, nsmpVI18, Lewinella, Conchiformibius, Dolichospermum, Saccharothrix, Candidatus Sulcia, Teredinibacter, Cellulosimicrobium, Mitsuokella, Aquitalea, Serinicoccus, Polaribacter, Dyella, Pelomonas, Oleispira, Plesiomonas, Lutibacterium, Emticicia, Spirochaeta, Acholeplasma, Haloplanus, Caedibacter, Ammoniphilus, Anaerofustis, Verminephrobacter, Methylomonas, Brevibacillus, Catellatospora, Pseudidiomarina, Acetivibrio, Citrobacter, Luedemannella, Caldicellulosiruptor, Desulfotomaculum, Dehalobacter, Sporosarcina, Flectobacillus, Frigoribacterium, Kouleothrix, Actinobaculum, Arcanobacterium, Leucobacter, Streptacidiphilus, Frateuria, Gemmatimonas, Acidimicrobium, Kineosporia, Syntrophomonas, Sphaerotilus, Serratia, Desulfobacterium, Gelidibacter, Nostoc, Luteimonas, Candidatus Amoebophilus, Geobacter, Haliangium, Myxococcus, Desulfomicrobium, Beijerinckia, Cardiobacterium, Fibrobacter, Blastomonas, Nevskia, Methylocystis, Halostagnicola, Enterobacter, Cycloclasticus, Halococcus, Macrococcus, Phaeospirillum, Pseudaminobacter, Solimonas, Salimicrobium, Marinococcus, Lachnospira, Halalkalicoccus, Candidatus Nitrososphaera, Rathayibacter, Natronococcus, Blattabacterium, Idiomarina, Marinibacillus, Tetrathiobacter, Marinilactibacillus, Balneola, Marivita, Zhihengliuella, Microlunatus, Azorhizobium, Haererehalobacter, Verrucosispora, Moraxella, Acetobacter, Raoultella, Hydrocarboniphaga, Haloanella, Xylanimicrobium, Desulfocapsa, Muricauda, Ochrobactrum, Capnocytophaga, Paenisporosarcina, Kurthia, Insolitispirillum, Kushneria, Patulibacter,	Aneurinibacillus, Acetivibrio, Pelomonas, Balneola, Luteibacter, Luedemannella, Desulfotomaculum, Xylanimicrobium, Actinobaculum, Renibacterium, Marinimicrobium, Syntrophus, Gelidibacter, Vibrio, Ensifer, Thalassobacillus, Desulfobacterium, Eggerthella, Phaeospirillum, Magnetospirillum, Fluviicola, Candidatus Liberibacter, 4-29, SGUS388, Ornithinicoccus, Fusibacter, Microcystis, Slackia, Thermicanus, Thiothrix, Spirochaeta, Verrucosispora, Selenomonas, Leclercia, Porphyrobacter, Cetobacterium, Congregibacter, Prosthecobacter, Pandoraea, Rickettsiella, Kurthia, Thiomonas, Flectobacillus, Candidatus Phytoplasma, PSB-M-3, Desulfomicrobium, Candidatus Portiera,

Syntrophus, Gluconobacter, Gelidibacter, Thermosynechococcus, Vibrio, Stigmatella, Ensifer, Oceanimonas, Thalassobacillus, Martelella, Buttiauxella, Segniliparus, Methylarcula, Aphanothece, Desulfobacterium, Eggerthella, Aphanizomenon, Phaeospirillum, Marinospirillum, Octadecabacter, Tropheryma, JG37-AG-70, Fischerella, Azoarcus, Sphaerisporangium, Magnetospirillum, Fluviicola, Candidatus Liberibacter, Chroococcus, Actinocatenispora, Mariprofundus, Avibacterium, 4-29, SGUS388, Candidatus Aquiluna, Candidatus Cardinium, Ornithinicoccus, Rhodovulum, Fusibacter, Telmatospirillum, Microcystis, Slackia, Symploca, Thermicanus, Dermabacter, Thiothrix, Spirochaeta, Ferrimicrobium, Brachyspira, Salinispora, Acrocarpospora, Psychroserpens, Verrucosispora, Selenomonas, Leclercia, Leptospirillum, Thioalkalivibrio, Thermosinus, Porphyrobacter, Natronincola, Cetobacterium, Sneathia, Ignavibacterium, Corallococcus, T78, YNPFFP6, Microbispora, Candidatus Tammella, Rhodothermus, Thiohalospira, Arthronema, Brachymonas, Congregibacter, Haloferula, Prosthecobacter, Rhodobium, Halochromatium, Prochloron, Jannaschia, Methanobacterium, Pandoraea, Saccharospirillum, Halanaerobium, Magnetococcus, Umboniibacter, Rickettsiella, Psychromonas, Kurthia, Dichelobacter, Tetrasphaera, Thiomonas, Thermodesulfovibrio, Thermovenabulum, Thermincola, Flectobacillus, Actinosynnema, Actinopolyspora, Pediococcus, Phaeobacter, Gloeothece, Candidatus Phytoplasma, PSB-M-3, Rickettsia, Pelobacter, Piscirickettsia, Desulfomicrobium, Candidatus Portiera	

Table S6. Public data of metagenomic studies used in PCA analysis (relative abundance as the input variables).

Habitat	Project Name	Project link	Sample ID
Bloom lake	Freshwater Microcystis Bloom Metagenomes	http://metagenomics.anl.gov/linkin.cgi?project=1207	4467058.3, 4467059.3
Agricultural soil	EarlhamMetagenomes2012	http://metagenomics.anl.gov/linkin.cgi?project=2850	4508937.3, 4508938.3, 4508939.3, 4508940.3, 4508941.3, 4508942.3
Open ocean	Global Ocean Sampling Expedition	http://metagenomics.anl.gov/linkin.cgi?project=27	4441126.3, 4441129.3, 4441139.4, 4441615.3, 4441576.3,4441578.3, 4441592.3, 4441661.3, 4441588.3, 4441594.3
Coastal ocean	Global Ocean Sampling Expedition	http://metagenomics.anl.gov/linkin.cgi?project=27	4441580.3, 4441583.3, 4441148.3, 4441613.3, 4441596.4, 4441601.3, 4441586.3, 4441660.3, 4441591.3, 4441605.3
Anarobic sludges	Beer-to-Caproate	http://metagenomics.anl.gov/linkin.cgi?project=397	4480719.3, 4480764.3, 4480776.3, 4480815.3, 4480859.3, 4480861.3, 4480863.3, 4480864.3, 4480865.3, 4480867.3

Table S7. Annotations of the 48 most common bacterial, 2 fungal, and 3 viral species.

Organism	Species	Aerobic /anaerobic	Descriptions	References
Bacteria	Geodermatophilus obscurus	aerobic	soil and rock varnish, lytic capability of yeast cell walls, UV-C resistance, strong production of extracellular functional amyloid and manganese oxidation	9
	Modestobacter marinus	aerobic	predominant in the first two millimeters ofcalcarenite stone surfaces,access tovarious trace carbon sources, availability highly resistant to desiccation and to gamma- and high-energy UV radiations	10
	Blastococcus saxobsidens	aerobic	thriving in inhospitable and bleak biotopes as the interior of stones, thermophilicesterases, resistance to several metals higher than those of its phylogenetic relatives, low resistance toseveraloxidizing stresses	11
	Kocuria rhizophila	aerobic	halotolerant, tolerant to a wide variety of organic solvents, ability to grow rapidly and at high cell density, robust at various growth conditions	12
	Micrococcus luteus	aerobic	diverse chemotaxonomic features dormancy, able to concentrate heavy metals from low-grade ores, Fleming strain	13
	Candidatus Nitrospira defluvii	aerobic	uncultivated nitrite-oxidizing bacteria, resistance to ampicillin	14
	Methylobacterium radiotolerans	aerobic	multilayered cell wall structure, facultative methylotroph, high resistance to gamma radiation	15
	Thermbifida fusca	aerobic	moderately thermophilic, filamentous, a major degrader of plant cell walls in heated organic materials, spores can be allergenic, associated with farmers lung	16
	Nocardioides sp.	aerobic	ability to metabolize unusual substrates, including butane, jet fuel, phenanthrene, p-nitrophenol, trinitrophenol, atrazine, ethene, and vinyl chloride	17
	Propionibacterium acnes	anaerobic	a commensal organism on human skin, implicated invarious infections including acne vulgaris, endocarditis, osteomyelitis, and prostate cancer; the only microorganismthat has been isolated from sarcoid lesions by bacterial culture	18
	Brachybacterium faecium	aerobic	capable of degrading uric acid and fermenting cellobiose, glucose, maltose, and man-nose, but not cellulose, chitin, or gelatin	19
	Cellvibrio gilvus	aerobic	isolated from bovine feces, cellulolytic, disaccharide preference	20
	Arthrobacter phenanthrenivorans	aerobic	phenanthrene andanthracene as sole carbon sources, isolated from a creosote-contaminated site	21
	Nocardiopsis dassonvillei	aerobic	isolated from a large variety of natural habitats such as soil and marine sediments, from different plant and animal materials as well as from human patients, participating actively in biopolymer degradation, associated with actinomycetoma, conjunctivitis, cholangitis	22
	Carnobacterium sp.	facultative	ubiquitous lactic acid bacteria, tolerant to freezing/thawing and high pressure, able to grow at lowtemperatures	23
	Microbacterium testaceum	aerobic	endophytic within plant hosts, N-acylhomoserine lactone-degrading activity	24
	Paracoccus denitrificans	facultative	capable of thriving in soil, ability to single-handedly convert nitrate to dinitrogen via denitrification	25
	Kytococcus sedentarius	aerobic	production of oligoketide antibiotics, opportunistic pathogen causing valve endocarditis, hemorrhagic pneumonia, and pitted keratolysis	26
	Sanguibacter keddieii	facultatively anaerobic	blood isolate, short, irregular rods, mesophilic	27
	Kineococcus radiotolerans	aerobic	isolated from high-level radioactive waste, radiation and desiccation resistance	28

Pantoeaananatis	aerobic	epiphyte or endophyte, an emerging phytopathogen infecting a wide range of important crop andforest plants, an occasional clinical isolateand a presumptive opportunistic human pathogen, associated with septicemia following penetrating trauma with plant material, nosocomial infections due to exposure to contaminated hospital materials, and secondary complications of preexisting illnesses	29
Lactobacillus johnsonii	facultatively anaerobic	acidophilus, attachment to epithelial cells, immunomodulation, competitive exclusion of pathogens	30
Cellulomonas fimi	facultatively anaerobic	cellulolytic, secreting multi-domain glycoside hydrolases	31
Lactobacillus crispatus	aerobic	beneficial microbiota present in the vertebrate gastrointestinal and human genitourinary tracts	32
Deinococcus gobiensis	facultatively anaerobic	higher tolerance to gamma radiation and UV light than all other known microorganisms, isolated from desert	33
Thauera sp.	facultative	isolated from activated sludge samples from industrial wastewater, ability to produce abundant exopolysaccharide and degrade various aromatic compounds with nitrate	34
Pantoea vagans	facultatively anaerobic	enterobacterial plant epiphyte of a broad range of plants, providing effective disease control of fire blight	35
Clostridium perfringens	anaerobic	a common inhabitant of the avian and mammalian gastrointestinal tracts, commensal or pathogenical	36
Lactobacillus reuteri	facultatively anaerobic	heterofermentative lactic acid bacterium that naturally inhabits the gut of humans and other animals, production of the broad-spectrum antimicrobial compound reuterin during anaerobic metabolism of glycerol	37
Pseudomonas stutzeri	facultative	ability to use maltose andstarch as sole carbon and energy sources, degradation of environmental pollutantsand high-molecular-weight polyethylene glycols, production ofdinitrogen gas from nitrate, associated with human infections	38
Psychrobacter cryohalolentis	aerobic	capable of growth at temperatures from -10□ to 30□, isolated from permafrost	39
Lactobacillus salivarius	anaerobic	part of the indigenous microbiotaof the gastrointestinal tract and oral cavity of humans and hamsters, isolated from human breast milk and from the intestinal tracts of swine and chickens	40
Bacillus megaterium	aerobic	with a cell length of up to 4 µm and a diameter of 1.5 µm, nonpathogenic host for the biotechnological production of several substances, including vitamin B12, penicillin acylase, and amylases	41
Arthrobacter arilaitensis	aerobic	one of the main bacterial species found at the surface of cheeses, especially in smear-ripened cheeses, where it contributes to the typical colour, flavour and texture properties of the final product	42
Ramlibacter tataouinensis	aerobic	chemo-organotrophic, cyst-producing, first isolated from meteorite fragments buried in the sands of a desert	43
Nakamurella multipartita	aerobic	polysaccharide-accumulating, septa-forming, isolated from activated sludge acclimated with sugar-containing synthetic waste water	44
Streptococcus infantarius	facultatively anaerobic	ability to grow in the presence of bile, production of β-glucosidase leading to hydrolysis of aesculin	45
Mycobacterium gilvum	aerobic	pleomorphic, acid-fast, resistant to isoniazid, sodium aminosalicylate and rifampicin	46
Arthrobacter chlorophenolicus	aerobic	growth on and degradation of high concentrations of 4-chlorophenol as the sole carbon and	47

			energy source, isolated from soil	
	Methylobacterium extorquens	aerobic	ability to grow on one or several reduced one carbon (C1) compounds other than methane, associated withplants	48
	Methylobacterium chloromethanicum	aerobic	isolated from soil at a petrochemical factory in Tatarstan, Russia, able to grow using chloromethane as the sole carbon and energy source	49
	Corynebacterium efficiens	facultatively anaerobic	thermostability, glutamic-acid-producing, isolated from soil andvegetables	50
	Stenotrophomonas maltophilia	aerobic	commonly found in water and soi land in association with plants, beneficial effects on plants including protection from pathogens, promotionof growth, and biodegradation of pollutants; an emerging opportunistic human pathogen involved in infections at hospitals and in patients with cystic fibrosis	51
	Nocardiopsis alba	aerobic	inhibitory bioactivity against several *Bacillus* isolates, some Gram-positive human pathogens, or honeybee pathogens	52
	Psychrobacter arcticus	facultative	capable of growthat temperatures from -10□ to 28□, isolated from permafrost	39
	Saccharomonospora viridis	aerobic	thermophile, spores can cause farmer’s lung disease, bagassosisand humidifier fever, pentachlorophenol metabolism	53
	Streptomyces coelicolor	aerobic	broad range of metabolic processesand biotransformations, soil-dwelling, production of most natural antibiotics used in human and veterinary medicine	54
	Leuconostoc mesenteroides	facultative	lactic acid bacteria, key players responsiblefor kimchi fermentation	55
Fungus	Aspergillus fumigatus	aerobic	prolificconidia production, isolated from human habitatsand vegetable compost heaps, a primary and opportunistic pathogen, a major allergen, linked to severeasthma and sinusitis	56
	Saccharomyces cerevisiae	facultative	domesticated organism that occasionally establishes synanthropic naturalpopulations, capable of malolactic fermentation, able to form biofilms	57
Virus	Pseudomonas phage F116		temperate, pilus-specific, generalized transducing phage, linear dsDNA	58
	Human adenovirus C		non-enveloped, icosahedral, linear dsDNA, causing a self-limited febrile illness	59
	Enterobacteria phage P1		lysogenizing enteric bacteria as a circular, low-copy-number plasmid	60

Table S8. Primers and Sanger sequencing results.

Primers	Sequence
fungal18sF	5’GATACCGTYGTAGTCTTA3’
fungal18sR	5’TGTCTGGACCTGGTGAGT3’
gliIRTF	5’TCGTTGCTGGAGAATCTGCTGTATGA3’
gliIRTR	5’ACAAAGGGAATCTGGTGGAAGGCGA3’
18s RNA gene PCR product	GATACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGCGGTGTTTCTATGATGACCCGCTCGGCACCTTACGAGAAATCAAAGTTTTTGGGTTCTGGGGGGAGTATGGTCGCAAGGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACAAGGCGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGGAAACTCACCAGGTCCAGACA
gliI gene PCR product	TCGTTGCTGGAGAATCTGCTGTATGACATCTGCGAGCCGGGCAATTGCGACGGGGAGGCGTGTTGATCGAGACGCCGTTCTGGGGTGCGTACCATCGGGGGTTTCGTTGGCACCGCATGCATGGTCTTAGCTGATGTATACGAATAGGGGGCTTCGAGACGAGCTTCGTCCTGCGCTCCAACGTCACCGCTGTTCATGTGAGGCCTCCGTGTCATGGCAATGGATCCGCAGATCTGGATCGTCTCGTGTCGGCGTATATTGAAGCGTACGAACGGGTTCTGCGTCAGGCCCCCTGCCGCATCAAGGCCATCCTCGTGTGTAACCCGCACAATCCATGCGGGCACATCTACCCACCGAGAGTAATCCAGGCCTTGCTTCAATTCGCCCAACGGCATGATCTATTCTACATCTCCGATGAGATCTACGCCCTCTCCACGCTGGATGAGCAAACCGCCTTCACCTCGGTCCTGAGCATCGATGTAGCCGCCCTGGGTGTAGACCTGGCGCGCGTATTCACCCTGTACAGTATCAGCAAAGACCTCGGCAGTAGCGGATTGCGACTGGTATACTGTCTTATCTCCTCCGACTCTCAAGGCCTCCGCAGAACTGACACTGTGCAGGGCTTCGGCATCACCCAAGCACATCCCGACCTGCGTCTCTCCCTCGCCATCTCGAACCATTCCCGCGTCTCGACATTCACCTCGCTGGTCATCACCGCTCTCCTGCACGACCCGGAAGCCGCCACGGCAATCCTGCACCAGAATCGAGCCGCTCTGCAGCGCAGCGCCAGCTCATCAGAAAACTTTCTCGCCTCACGACCGTTGGGAGAGAGTGAGAGAGAAATCGCCTTCCACCAGATTCCCTTTGT

Table S9. Estimated concentrations of organic carbon and elemental carbon measured in $PM_{2.5}$ and PM_{10} samples.

	$PM_{2.5}$		**PM_{10}**	
Sampling date	OC (μg/m^3)	EC (μg/m^3)	OC (μg/m^3)	EC (μg/m^3)
01/08	6.753	2.151	9.93	3.283
01/09	28.537	6.351	36.421	6.904
01/10	71.036	13.514	59.588	8.186
01/11	45.022	12.42	53.829	8.12
01/12	68.733	13.667	68.814	8.774
01/13	49.18	9.452	53.9	7.588
01/14	25.429	6.005	32.816	6.068

Table S10. Estimated concentrations of anions and cations measured in $PM_{2.5}$ and PM_{10} samples.

Sampling date	**01/08**		**01/09**		**01/10**		**01/11**		**01/12**		**01/13**		**01/14**	
	$PM_{2.5}$	PM_{10}	$PM_{2.5}$	PM_{10}	$PM_{2.5}$	PM_{10}	$PM_{2.5}$	PM_{10}	$PM_{2.5}$	PM_{10}	$PM_{2.5}$	PM_{10}	$PM_{2.5}$	PM_{10}
SO_4^{2-} (μg/m^3)	3.208	4.256	13.193	16.832	90.795	58.364	57.511	81.258	105.016	111.108	70.914	92.471	43.381	57.847
NH_4^+ (μg/m^3)	5.202	5.698	18.982	21.078	62.365	45.588	44.328	54.280	62.925	63.475	48.271	55.871	36.012	39.618
NO_3^- (μg/m^3)	1.219	1.526	11.616	14.084	52.437	37.954	32.293	49.089	48.984	52.278	36.509	50.547	25.074	33.535
K^+ (μg/m^3)	0.681	0.928	3.553	4.451	14.174	9.214	9.331	12.663	17.149	16.621	19.077	22.134	8.691	11.241
Cl^- (μg/m^3)	0.960	2.285	4.022	6.930	15.694	12.604	8.489	16.881	14.320	18.409	10.072	16.228	5.571	9.740
Na^+ (μg/m3)	1.318	4.213	2.857	8.326	6.924	10.426	5.275	17.956	8.265	16.884	5.963	13.238	3.945	12.261
Ca^{2+} (μg/m^3)	2.566	10.394	2.276	14.256	2.913	15.906	1.758	21.257	3.067	16.324	1.613	17.054	1.376	11.268
Mg^{2+} (μg/m^3)	0.519	0.854	0.524	1.570	0.968	2.471	0.491	3.149	0.828	2.851	0.737	3.444	0.504	2.758
F^- (μg/m^3)	0.060	0.124	0.181	0.442	0.505	0.906	0.270	0.943	0.417	0.741	0.352	1.043	0.148	0.400
PO_4^{3-} (μg/m^3)	0.021	0.031	0.035	0.047	0.070	0.068	0.050	0.080	0.070	0.090	0.051	0.076	0.042	0.061

Table S11. Estimated concentrations of elements measured in $PM_{2.5}$ and PM_{10} samples.

Sampling date	01/08		01/09		01/10		01/11		01/12		01/13		01/14	
	$PM_{2.5}$	PM_{10}	$PM_{2.5}$	PM_{10}	$PM_{2.5}$	PM_{10}	$PM_{2.5}$	PM_{10}	$PM_{2.5}$	PM_{10}	$PM_{2.5}$	PM_{10}	$PM_{2.5}$	PM_{10}
Fe (μg/m^3)	0.249	1.844	0.482	2.479	1.302	3.389	0.824	3.496	2.191	4.543	2.042	8.048	1.016	4.564
Zn (μg/m^3)	0.046	0.068	0.285	0.428	1.227	1.022	0.586	0.842	1.695	1.585	1.104	1.686	0.561	0.870
Pb (μg/m^3)	0.032	0.040	0.164	0.221	0.636	0.452	0.352	0.437	1.114	0.890	1.033	1.271	0.449	0.576
As (ug/m^3)	0.000	0.002	0.031	0.051	0.178	0.168	0.077	0.095	0.237	0.221	0.115	0.139	0.067	0.092
Mn (μg/m^3)	0.000	0.064	0.056	0.110	0.147	0.136	0.085	0.057	0.141	0.181	0.002	0.289	0.080	0.157
Br (μg/m^3)	0.004	0.003	0.025	0.032	0.107	0.067	0.061	0.065	0.139	0.110	0.087	0.115	0.041	0.057
Ti (μg/m^3)	0.020	0.145	0.028	0.190	0.063	0.233	0.029	0.218	0.076	0.240	0.042	0.253	0.025	0.170
Cr (μg/m^3)	0.001	0.006	0.006	0.015	0.018	0.021	0.010	0.020	0.020	0.028	0.020	0.039	0.006	0.020
Ni (μg/m^3)	0.001	0.008	0.003	0.008	0.008	0.005	0.005	0.010	0.007	0.012	0.012	0.021	0.003	0.007

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