

# **Variation of Bacterial and Fungal Community Structures in PM<sub>2.5</sub> Collected during the 2014 APEC summit periods**

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## Supporting Information

**Table S1**

Relative abundance of the top 100 OTUs in bacterial communities

	GD	GN	MD	MN	HD	HN	AD	AN
OTU-001	6.55%	4.69%	8.12%	5.59%	5.59%	4.73%	7.16%	4.49%
OTU-002	6.84%	4.67%	7.01%	7.19%	5.41%	3.23%	6.57%	3.63%
OTU-003	4.98%	3.91%	3.47%	4.04%	4.22%	8.30%	2.78%	3.90%
OTU-004	3.20%	2.30%	3.88%	3.97%	2.53%	1.17%	3.59%	2.74%
OTU-005	2.63%	2.14%	3.22%	1.83%	1.63%	5.43%	3.40%	2.34%
OTU-006	3.97%	3.48%	0.70%	0.82%	1.99%	1.73%	3.14%	3.56%
OTU-007	2.06%	1.52%	1.74%	2.05%	3.38%	2.09%	1.80%	1.27%
OTU-008	0.92%	2.14%	1.56%	3.24%	2.98%	2.06%	0.13%	0.60%
OTU-009	1.82%	1.47%	1.25%	1.37%	1.41%	1.16%	1.69%	1.42%
OTU-010	1.29%	0.67%	1.68%	1.26%	1.29%	1.00%	1.46%	1.85%
OTU-011	1.16%	1.75%	1.13%	0.67%	0.26%	0.41%	2.52%	1.95%
OTU-012	0.71%	1.09%	2.10%	1.01%	0.47%	1.23%	0.86%	0.93%
OTU-013	1.52%	0.83%	0.82%	1.47%	1.48%	0.75%	0.01%	1.56%
OTU-014	0.79%	0.69%	0.54%	0.98%	1.68%	2.67%	0.36%	0.85%
OTU-015	0.74%	0.58%	1.38%	0.80%	1.31%	1.55%	0.48%	0.80%
OTU-016	1.25%	1.03%	1.08%	0.97%	0.45%	0.80%	1.13%	0.72%
OTU-017	0.32%	0.64%	1.02%	1.68%	1.45%	1.48%	0.18%	0.54%
OTU-018	0.95%	1.01%	0.72%	0.85%	0.69%	0.64%	1.00%	1.29%
OTU-019	1.00%	0.55%	1.47%	0.78%	0.95%	0.78%	0.90%	0.63%
OTU-020	0.89%	0.71%	1.01%	0.63%	0.42%	0.64%	1.30%	1.27%
OTU-021	0.64%	0.86%	0.91%	1.26%	0.92%	1.26%	0.58%	0.37%
OTU-022	0.84%	0.98%	0.79%	0.98%	0.81%	0.74%	0.90%	0.62%
OTU-023	0.83%	0.78%	0.93%	0.48%	0.40%	0.53%	1.22%	0.96%
OTU-024	0.72%	0.82%	0.99%	0.93%	0.62%	0.53%	0.62%	0.54%
OTU-025	0.54%	0.81%	0.50%	0.99%	0.47%	1.15%	0.71%	0.33%
OTU-026	0.85%	0.69%	1.12%	0.54%	0.65%	0.59%	0.53%	0.37%
OTU-027	0.78%	0.33%	0.39%	0.42%	0.70%	1.16%	0.65%	0.68%
OTU-028	0.54%	0.70%	0.92%	0.59%	0.21%	0.63%	0.55%	0.37%
OTU-029	0.45%	0.61%	0.47%	0.43%	0.60%	0.48%	0.72%	0.60%
OTU-030	0.47%	0.45%	0.47%	0.70%	0.45%	0.52%	0.67%	0.55%
OTU-031	0.25%	0.54%	0.61%	0.93%	0.84%	0.42%	0.33%	0.24%
OTU-032	0.46%	0.48%	0.31%	0.54%	0.89%	0.71%	0.41%	0.43%
OTU-033	0.38%	0.41%	0.44%	0.44%	0.33%	0.23%	0.62%	1.06%
OTU-034	0.12%	0.16%	0.00%	0.08%	3.83%	0.13%	0.01%	0.03%
OTU-035	0.49%	0.36%	0.53%	0.44%	0.40%	0.70%	0.29%	0.50%
OTU-036	0.26%	0.84%	0.27%	0.76%	0.19%	0.34%	0.54%	0.38%
OTU-037	0.56%	0.34%	0.50%	0.29%	0.43%	0.21%	0.75%	0.56%
OTU-038	0.57%	0.36%	0.39%	0.39%	0.54%	0.43%	0.61%	0.35%
OTU-039	0.65%	0.36%	0.24%	0.16%	0.42%	0.93%	0.30%	0.40%

OTU-040	0.20%	0.92%	0.23%	0.40%	0.20%	0.58%	0.37%	0.31%
OTU-041	0.07%	0.00%	0.12%	0.21%	2.77%	0.39%	0.00%	0.00%
OTU-042	0.33%	0.37%	0.43%	0.33%	0.15%	0.21%	0.50%	0.64%
OTU-043	0.28%	0.15%	0.39%	0.21%	0.16%	0.17%	0.41%	1.14%
OTU-044	0.73%	0.64%	0.27%	0.27%	0.24%	0.19%	0.40%	0.33%
OTU-045	0.14%	0.41%	0.76%	0.72%	0.07%	0.36%	0.16%	0.08%
OTU-046	0.52%	0.47%	0.37%	0.30%	0.15%	0.09%	0.41%	0.28%
OTU-047	0.33%	0.18%	0.39%	0.23%	0.14%	0.11%	0.56%	0.51%
OTU-048	0.41%	0.25%	0.24%	0.27%	0.39%	0.59%	0.15%	0.28%
OTU-049	0.37%	0.36%	0.33%	0.15%	0.27%	0.10%	0.49%	0.39%
OTU-050	0.24%	0.21%	0.30%	0.33%	0.38%	0.39%	0.20%	0.41%
OTU-051	0.31%	0.39%	0.24%	0.07%	0.31%	0.59%	0.28%	0.29%
OTU-052	0.28%	0.47%	0.33%	0.20%	0.40%	0.23%	0.29%	0.16%
OTU-053	0.29%	0.55%	0.26%	0.28%	0.22%	0.19%	0.31%	0.21%
OTU-054	0.17%	0.51%	0.08%	0.30%	0.03%	0.27%	0.40%	0.46%
OTU-055	0.49%	0.16%	0.26%	0.16%	0.34%	0.55%	0.21%	0.14%
OTU-056	0.25%	0.27%	0.36%	0.17%	0.42%	0.43%	0.18%	0.17%
OTU-057	0.34%	0.20%	0.41%	0.31%	0.20%	0.27%	0.13%	0.24%
OTU-058	0.24%	0.20%	0.11%	0.59%	0.00%	0.02%	0.06%	0.74%
OTU-059	0.13%	0.29%	0.38%	0.22%	0.28%	0.54%	0.10%	0.14%
OTU-060	0.12%	0.09%	0.33%	0.18%	0.15%	0.39%	0.32%	0.41%
OTU-061	0.43%	0.36%	0.22%	0.28%	0.14%	0.04%	0.28%	0.28%
OTU-062	0.16%	0.39%	0.23%	0.28%	0.35%	0.18%	0.23%	0.18%
OTU-063	0.35%	0.56%	0.17%	0.27%	0.21%	0.32%	0.09%	0.08%
OTU-064	0.20%	0.20%	0.29%	0.42%	0.25%	0.16%	0.25%	0.18%
OTU-065	0.19%	0.32%	0.26%	0.25%	0.49%	0.18%	0.14%	0.18%
OTU-066	0.23%	0.23%	0.31%	0.22%	0.27%	0.46%	0.11%	0.11%
OTU-067	0.28%	0.34%	0.16%	0.20%	0.28%	0.44%	0.15%	0.09%
OTU-068	0.37%	0.77%	0.18%	0.21%	0.11%	0.15%	0.03%	0.09%
OTU-069	0.03%	0.07%	0.19%	0.58%	0.63%	0.18%	0.12%	0.03%
OTU-070	0.23%	0.34%	0.07%	0.18%	0.08%	0.21%	0.43%	0.22%
OTU-071	0.24%	0.16%	0.16%	0.20%	0.15%	0.13%	0.22%	0.50%
OTU-072	0.30%	0.17%	0.21%	0.04%	0.25%	0.48%	0.09%	0.24%
OTU-073	0.30%	0.19%	0.10%	0.16%	0.65%	0.10%	0.14%	0.15%
OTU-074	0.12%	0.13%	0.18%	0.06%	0.03%	0.09%	0.28%	0.68%
OTU-075	0.23%	0.18%	0.16%	0.16%	0.33%	0.21%	0.23%	0.15%
OTU-076	0.13%	0.21%	0.21%	0.23%	0.17%	0.26%	0.12%	0.24%
OTU-077	0.28%	0.10%	0.30%	0.45%	0.20%	0.04%	0.10%	0.07%
OTU-078	0.19%	0.37%	0.25%	0.06%	0.05%	0.33%	0.12%	0.20%
OTU-079	0.14%	0.21%	0.22%	0.36%	0.26%	0.17%	0.09%	0.07%
OTU-080	0.17%	0.25%	0.16%	0.15%	0.10%	0.13%	0.25%	0.29%
OTU-081	0.20%	0.11%	0.20%	0.17%	0.28%	0.19%	0.22%	0.09%
OTU-082	0.14%	0.13%	0.18%	0.15%	0.14%	0.14%	0.22%	0.25%
OTU-083	0.20%	0.16%	0.09%	0.16%	0.12%	0.13%	0.16%	0.34%

OTU-084	0.22%	0.10%	0.16%	0.21%	0.21%	0.21%	0.13%	0.12%
OTU-085	0.13%	0.10%	0.09%	0.20%	0.41%	0.45%	0.03%	0.02%
OTU-086	0.16%	0.25%	0.15%	0.17%	0.17%	0.15%	0.18%	0.12%
OTU-087	0.05%	0.08%	0.27%	0.12%	0.25%	0.35%	0.09%	0.12%
OTU-088	0.13%	0.18%	0.24%	0.16%	0.05%	0.20%	0.10%	0.24%
OTU-089	0.13%	0.32%	0.09%	0.11%	0.00%	0.18%	0.16%	0.28%
OTU-090	0.12%	0.20%	0.11%	0.23%	0.32%	0.22%	0.03%	0.08%
OTU-091	0.12%	0.36%	0.36%	0.08%	0.03%	0.05%	0.12%	0.13%
OTU-092	0.33%	0.17%	0.22%	0.11%	0.13%	0.05%	0.18%	0.07%
OTU-093	0.10%	0.16%	0.03%	0.04%	0.01%	0.02%	0.36%	0.46%
OTU-094	0.10%	0.08%	0.07%	0.30%	0.25%	0.16%	0.20%	0.07%
OTU-095	0.12%	0.25%	0.16%	0.14%	0.05%	0.04%	0.19%	0.25%
OTU-096	0.09%	0.06%	0.35%	0.18%	0.31%	0.11%	0.03%	0.09%
OTU-097	0.11%	0.26%	0.11%	0.18%	0.11%	0.06%	0.28%	0.05%
OTU-098	0.11%	0.13%	0.35%	0.27%	0.14%	0.03%	0.05%	0.04%
OTU-099	0.02%	0.01%	0.08%	0.09%	0.95%	0.13%	0.01%	0.01%
OTU-100	0.12%	0.06%	0.10%	0.21%	0.33%	0.10%	0.09%	0.15%

**Table S2**

Relative abundance of the top 20 OTUs in fungal communities

	GD	GN	MD	MN	HD	HN	AD	AN
OTU-001	4.37%	36.68%	36.03%	43.50%	47.04%	42.78%	40.40%	41.34%
OTU-002	3.93%	39.44%	40.18%	28.26%	21.53%	27.48%	24.27%	20.82%
OTU-003	23.73%	5.59%	5.92%	10.27%	12.08%	21.71%	7.51%	8.16%
OTU-004	18.72%	3.41%	1.68%	1.43%	1.79%	0.71%	5.73%	6.86%
OTU-005	15.98%	1.85%	1.02%	0.97%	1.84%	0.43%	6.57%	6.25%
OTU-006	0.19%	2.07%	1.56%	0.90%	1.37%	0.35%	2.00%	2.10%
OTU-007	2.36%	0.57%	0.48%	0.90%	3.11%	2.00%	0.60%	0.70%
OTU-008	0.13%	2.01%	2.59%	1.21%	0.99%	0.43%	0.68%	0.52%
OTU-009	2.44%	0.50%	0.79%	0.47%	0.41%	0.19%	0.55%	0.67%
OTU-010	2.04%	0.50%	0.82%	0.81%	0.41%	0.23%	0.55%	0.47%
OTU-011	1.50%	0.55%	0.52%	0.37%	0.15%	0.17%	0.02%	0.16%
OTU-012	0.94%	0.18%	0.14%	0.60%	0.60%	0.30%	0.30%	0.15%
OTU-013	1.11%	0.61%	0.37%	0.51%	0.10%	0.27%	0.02%	0.07%
OTU-014	0.30%	0.42%	0.47%	0.87%	0.27%	0.08%	0.16%	0.35%
OTU-015	0.61%	0.20%	0.54%	0.44%	0.33%	0.06%	0.30%	0.18%
OTU-016	0.15%	0.18%	0.74%	0.59%	0.20%	0.03%	0.08%	0.20%
OTU-017	0.45%	0.15%	0.17%	0.39%	0.31%	0.01%	0.05%	0.22%
OTU-018	0.39%	0.04%	0.12%	0.12%	0.31%	0.05%	0.23%	0.34%
OTU-019	0.59%	0.18%	0.30%	0.23%	0.13%	0.10%	0.00%	0.08%
OTU-020	0.34%	0.08%	0.04%	0.01%	0.02%	0.46%	0.05%	0.31%

**Table S3**Relative abundance of all classes of bacteria in total sequences and in each PM<sub>2.5</sub> sample group.

Taxon	Total <sup>a</sup>	HD	HN	MD	MN	GD	GN	AD	AN
Actinobacteria	28.5586%	21.2892%	30.0475%	36.8170%	25.7284%	28.2437%	23.8666%	31.7789%	28.7727%
Alphaproteobacteria	27.8970%	28.6853%	29.3819%	27.8301%	32.1557%	29.5776%	24.5396%	25.8515%	25.4132%
Bacilli	9.6800%	8.0492%	7.6149%	9.1503%	9.4104%	8.5371%	14.0004%	10.9510%	9.1845%
Sphingobacteria	7.9171%	5.4198%	6.4342%	5.8431%	4.9548%	9.1596%	8.4165%	11.7501%	11.1352%
Betaproteobacteria	5.9376%	12.3325%	5.8796%	4.7974%	5.7574%	5.6292%	4.7630%	5.0039%	4.5313%
Clostridia	5.2306%	6.7939%	6.8146%	4.2614%	9.1639%	2.5967%	6.4049%	2.1417%	3.5424%
Gammaproteobacteria	4.0061%	8.2782%	4.2076%	2.8431%	3.5012%	3.9040%	5.4730%	2.3579%	2.6077%
Chloroplast	3.0907%	2.7566%	2.6228%	1.2745%	0.9543%	4.8911%	4.4375%	3.9887%	4.3958%
Deltaproteobacteria	1.3876%	0.7294%	0.9746%	0.8824%	2.0477%	1.7786%	1.4496%	1.0086%	2.1200%
No_Rank <sup>b</sup>	1.2435%	0.8906%	0.9509%	1.0327%	1.1060%	1.2895%	1.3461%	1.4082%	1.8423%
Deinococci	0.8175%	0.8482%	0.3645%	1.3987%	1.4157%	0.7737%	0.7470%	0.2882%	0.5825%
Erysipelotrichia	0.6879%	0.9669%	0.6894%	0.7974%	1.1376%	0.3468%	0.7322%	0.4388%	0.3454%
Bacteroidia	0.5311%	0.2799%	0.7924%	0.4706%	0.4234%	0.3201%	0.6952%	0.5371%	0.6909%
Cyanobacteria	0.4795%	0.6531%	0.4358%	0.8758%	0.1833%	0.3379%	0.1479%	0.1637%	1.0228%
Flavobacteria	0.4459%	0.4241%	0.3962%	0.4183%	0.3476%	0.4535%	0.4216%	0.3799%	0.7247%
Acidobacteria_Gp4	0.3317%	0.1866%	0.2456%	0.1569%	0.0695%	0.4535%	0.4733%	0.4650%	0.6231%
Gemmatimonadetes	0.3045%	0.2205%	0.2456%	0.2026%	0.3918%	0.3201%	0.3106%	0.3209%	0.3996%
Acidobacteria_Gp3	0.2366%	0.0424%	0.1109%	0.1634%	0.2149%	0.3379%	0.3106%	0.2882%	0.3996%
Thermomicrobia	0.2302%	0.3902%	0.2773%	0.0588%	0.1517%	0.0889%	0.1331%	0.1703%	0.5825%
Spartobacteria	0.0825%	0.1527%	0.1506%	0.0392%	0.0316%	0.0800%	0.1035%	0.0720%	0.0610%
Planctomycetacia	0.0761%	0.0933%	0.1585%	0.0850%	0.0569%	0.0534%	0.0370%	0.0393%	0.0948%

Acidobacteria_Gp16	0.0716%	0.0679%	0.1268%	0.0980%	0.0379%	0.0267%	0.1257%	0.0393%	0.0542%
Subdivision3	0.0671%	0.0339%	0.0634%	0.0196%	0.0569%	0.1512%	0.1035%	0.0720%	0.0542%
Acidobacteria_Gp10	0.0662%	0.0085%	0.0475%	0.0784%	0.0758%	0.0978%	0.0518%	0.0720%	0.0881%
Negativicutes	0.0653%	0.0085%	0.2219%	0.0458%	0.0442%	0.0356%	0.1553%	0.0065%	0.0203%
Acidobacteria_Gp7	0.0607%	0.0000%	0.0951%	0.0131%	0.1074%	0.0534%	0.0444%	0.0851%	0.0745%
Fusobacteria	0.0607%	0.0000%	0.0475%	0.0654%	0.0569%	0.0534%	0.1479%	0.0393%	0.0677%
Acidobacteria_Gp6	0.0508%	0.0170%	0.0872%	0.0588%	0.0442%	0.0800%	0.0888%	0.0131%	0.0271%
Epsilonproteobacteria	0.0453%	0.0000%	0.0792%	0.0131%	0.0885%	0.0267%	0.0666%	0.0458%	0.0339%
Anaerolineae	0.0435%	0.0000%	0.0951%	0.0131%	0.0632%	0.0267%	0.0888%	0.0131%	0.0474%
Acidobacteria_Gp1	0.0390%	0.1612%	0.0713%	0.0261%	0.0000%	0.0267%	0.0148%	0.0262%	0.0135%
Armatimonadia	0.0372%	0.0509%	0.0317%	0.0196%	0.0063%	0.0267%	0.0148%	0.0000%	0.1490%
Chlamydiae	0.0363%	0.0424%	0.0317%	0.0261%	0.0253%	0.0622%	0.0666%	0.0196%	0.0271%
Verrucomicrobiae	0.0326%	0.0424%	0.0634%	0.0392%	0.0126%	0.0356%	0.0444%	0.0196%	0.0135%
Spirochaetes	0.0245%	0.0085%	0.0079%	0.0065%	0.0316%	0.0178%	0.0222%	0.0458%	0.0474%
Acidobacteria_Gp2	0.0218%	0.0594%	0.0396%	0.0065%	0.0569%	0.0178%	0.0000%	0.0000%	0.0000%
Caldilineae	0.0199%	0.0000%	0.0158%	0.0327%	0.0000%	0.0178%	0.0222%	0.0196%	0.0474%
Nitrospira	0.0154%	0.0000%	0.0238%	0.0196%	0.0063%	0.0089%	0.0000%	0.0262%	0.0339%
Chloroflexi	0.0109%	0.0085%	0.0000%	0.0000%	0.0000%	0.0000%	0.0370%	0.0065%	0.0339%
Opitutae	0.0100%	0.0000%	0.0000%	0.0065%	0.0063%	0.0178%	0.0000%	0.0065%	0.0406%
Mollicutes	0.0091%	0.0000%	0.0000%	0.0000%	0.0316%	0.0089%	0.0148%	0.0000%	0.0135%
Phycisphaerae	0.0091%	0.0000%	0.0079%	0.0065%	0.0126%	0.0000%	0.0222%	0.0065%	0.0135%
Fibrobacteria	0.0082%	0.0000%	0.0000%	0.0000%	0.0000%	0.0089%	0.0370%	0.0131%	0.0068%
Subdivision5	0.0073%	0.0000%	0.0000%	0.0000%	0.0253%	0.0000%	0.0000%	0.0065%	0.0203%
Ktedonobacteria	0.0054%	0.0000%	0.0396%	0.0000%	0.0000%	0.0089%	0.0000%	0.0000%	0.0000%
Acidobacteria_Gp25	0.0036%	0.0085%	0.0079%	0.0000%	0.0000%	0.0000%	0.0074%	0.0065%	0.0000%

Ignavibacteria	0.0027%	0.0000%	0.0000%	0.0065%	0.0063%	0.0089%	0.0000%	0.0000%	0.0000%
Lentisphaeria	0.0018%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0074%	0.0065%	0.0000%
Acidobacteria_Gp17	0.0009%	0.0000%	0.0000%	0.0000%	0.0000%	0.0089%	0.0000%	0.0000%	0.0000%
Synergistia	0.0009%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0074%	0.0000%	0.0000%

<sup>a</sup> Abundance of one bacterial class in all the sequences

<sup>b</sup> Sequences that cannot be classified under any known phylotypes are marked No\_rank.

**Table S4**Relative abundance of classes of fungi in each PM<sub>2.5</sub> sample group.

	HD	HN	MD	MN	GD	GN	AD	AN
Dothideomycetes	66.5727%	67.1034%	49.9568%	60.6096%	52.4779%	51.4886%	61.0904%	63.3610%
No_rank <sup>a</sup>	24.4893%	28.1055%	41.7916%	30.2951%	22.3832%	41.8710%	31.9994%	28.4283%
Sordariomycetes	6.2378%	4.2063%	4.9150%	5.0151%	17.0025%	4.5680%	3.6596%	4.2423%
Eurotiomycetes	1.8549%	0.2980%	2.9475%	3.0383%	2.4398%	1.4011%	1.3389%	1.4011%
Tremellomycetes	0.1409%	0.0450%	0.0937%	0.2435%	1.4922%	0.2408%	0.7141%	1.0802%
Leotiomycetes	0.5557%	0.1293%	0.2234%	0.2532%	0.7516%	0.0511%	0.4017%	0.5714%
Microbotryomycetes	0.0000%	0.0450%	0.0072%	0.2240%	1.7209%	0.1022%	0.2901%	0.4931%
Cystobasidiomycetes	0.0000%	0.0056%	0.0000%	0.0779%	0.6862%	0.0219%	0.1860%	0.2270%
Exobasidiomycetes	0.0000%	0.0056%	0.0360%	0.0390%	0.6426%	0.1168%	0.0669%	0.0313%
Agaricomycetes	0.0313%	0.0337%	0.0144%	0.1558%	0.1198%	0.0730%	0.1488%	0.0704%
Agaricostilbomycetes	0.0078%	0.0000%	0.0000%	0.0000%	0.1525%	0.0073%	0.0298%	0.0313%
Saccharomycetes	0.0157%	0.0112%	0.0000%	0.0097%	0.0327%	0.0438%	0.0149%	0.0157%
Lecanoromycetes	0.0000%	0.0056%	0.0072%	0.0000%	0.0436%	0.0000%	0.0521%	0.0078%
Pezizomycetes	0.0861%	0.0000%	0.0000%	0.0000%	0.0109%	0.0073%	0.0000%	0.0078%
Chytridiomycetes	0.0000%	0.0000%	0.0000%	0.0292%	0.0218%	0.0000%	0.0074%	0.0000%
Taphrinomycetes	0.0078%	0.0056%	0.0072%	0.0000%	0.0109%	0.0000%	0.0000%	0.0157%
Orbiliomycetes	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0157%
Monoblepharidomycetes	0.0000%	0.0000%	0.0000%	0.0000%	0.0109%	0.0000%	0.0000%	0.0000%
Pucciniomycetes	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0073%	0.0000%	0.0000%
Ustilaginomycetes	0.0000%	0.0000%	0.0000%	0.0097%	0.0000%	0.0000%	0.0000%	0.0000%

<sup>a</sup> Sequences that cannot be classified under any known phylotypes are marked No\_rank.



**Table S5**Similarities of bacterial and fungal communities in some PM<sub>2.5</sub> sample groups

	Pair-wise comparison	Bray-Curtis <sup>a</sup>	Yue & Clayton <sup>a</sup>	Bray-Curtis <sup>b</sup>	Yue & Clayton <sup>b</sup>	Bray-Curtis <sup>c</sup>	Yue & Clayton <sup>c</sup>
Bacterial communities	AD-MD	0.958065	0.992628	0.898028	0.945688	0.835861	0.908084
	AN-MN	0.878726	0.925454	0.813032	0.819015	0.758793	0.75725
	AD-HD	0.855749	0.912223	0.872639	0.914976	0.746948	0.794142
	AN-HN	0.773702	0.813131	0.759599	0.751102	0.712501	0.714213
Fungal communities	AD-MD	0.834058	0.900881	0.820198	0.892638	0.799669	0.882689
	AN-MN	0.943259	0.986837	0.911464	0.969014	0.85812	0.952143
	AD-HD	0.926733	0.978926	0.893611	0.970561	0.853231	0.957532
	AN-HN	0.836879	0.8794	0.813336	0.881508	0.782737	0.880741

<sup>a</sup> Similarity calculation based on the dominant OTUs (relevant abundance > 1% in every sample)<sup>b</sup> Similarity calculation based on the major OTUs (relevant abundance > 0.5% in every sample)<sup>c</sup> Similarity calculation based on the common OTUs (relevant abundance > 0.1% in every sample)

**Table S6**

KEGG pathways predicted based on 16S rRNA gene sequences using the PICRUST algorithm in every sample group.

Pathways	GD	GN	MD	MN	HD	HN	AD	AN	Definition
ko05100	0.003%	0.004%	0.002%	0.002%	0.004%	0.006%	0.005%	0.005%	Bacterial invasion of epithelial cells
ko05110	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	Vibrio cholerae infection
ko05120	0.042%	0.056%	0.043%	0.051%	0.042%	0.045%	0.044%	0.047%	Epithelial cell signaling in Helicobacter pylori infection
ko05130	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	Pathogenic Escherichia coli infection
ko05131	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	Shigellosis
ko05133	0.035%	0.046%	0.029%	0.033%	0.035%	0.035%	0.038%	0.038%	Pertussis
ko05150	0.017%	0.014%	0.012%	0.019%	0.016%	0.016%	0.015%	0.024%	Staphylococcus aureus infection
ko05152	0.259%	0.264%	0.252%	0.254%	0.265%	0.273%	0.275%	0.276%	Tuberculosis

Figure S1

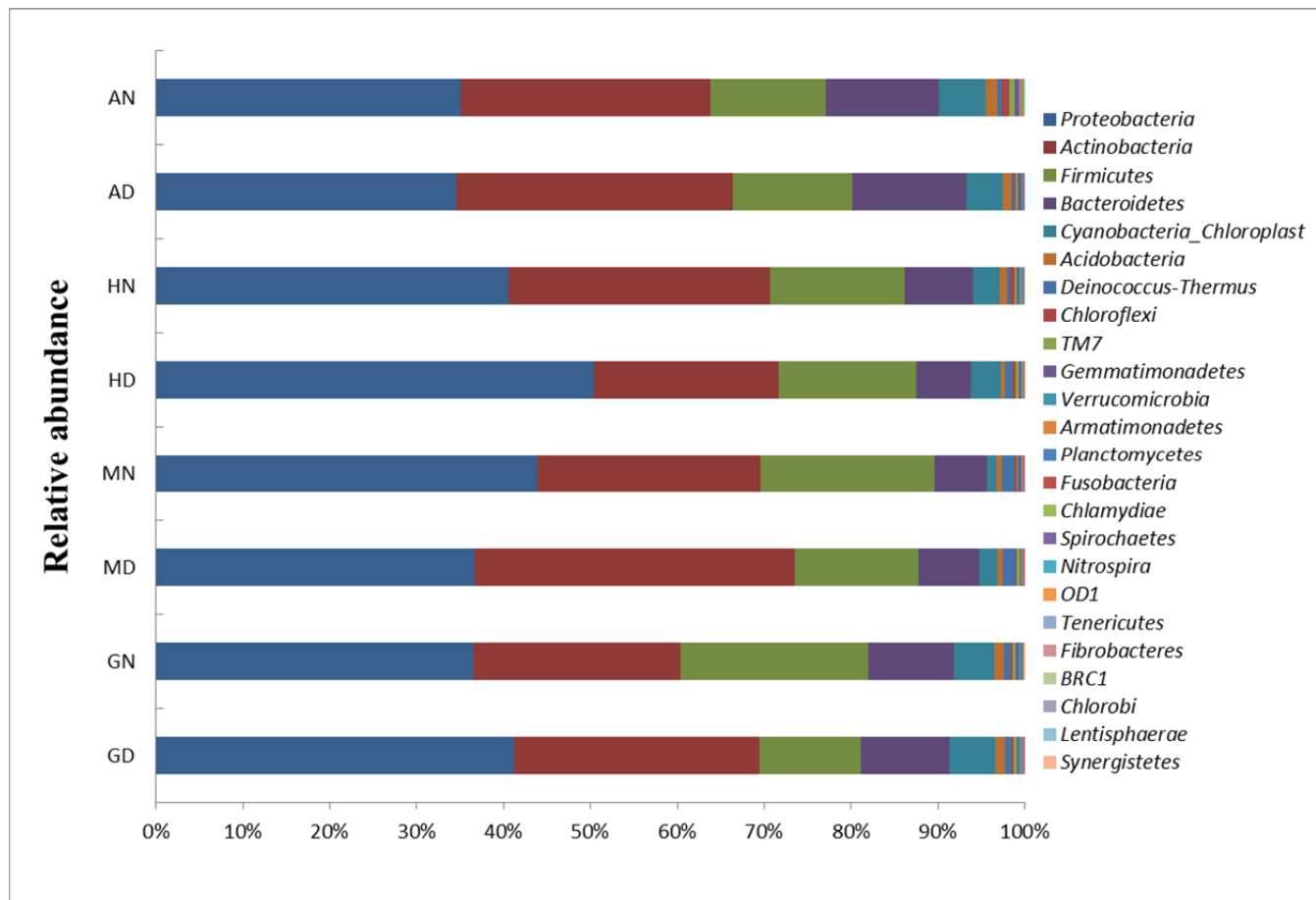


Figure S1 Composition of bacteria in PM2.5 at the phylum level

Figure S2

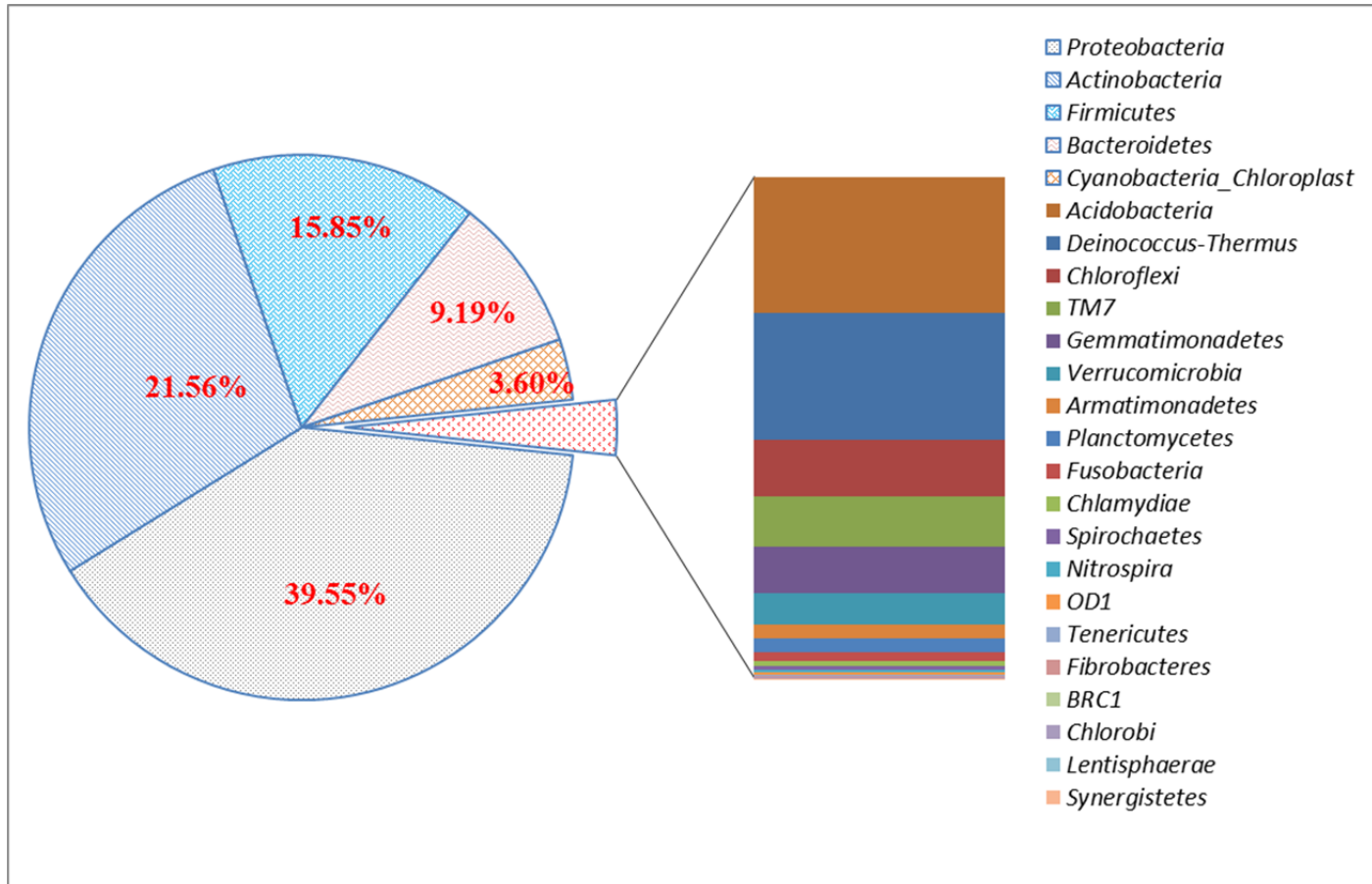


Figure S2. Distribution of bacteria in the PM2.5 at the phylum level. The sector shows top five phyla and the column shows other phyla

Figure S3

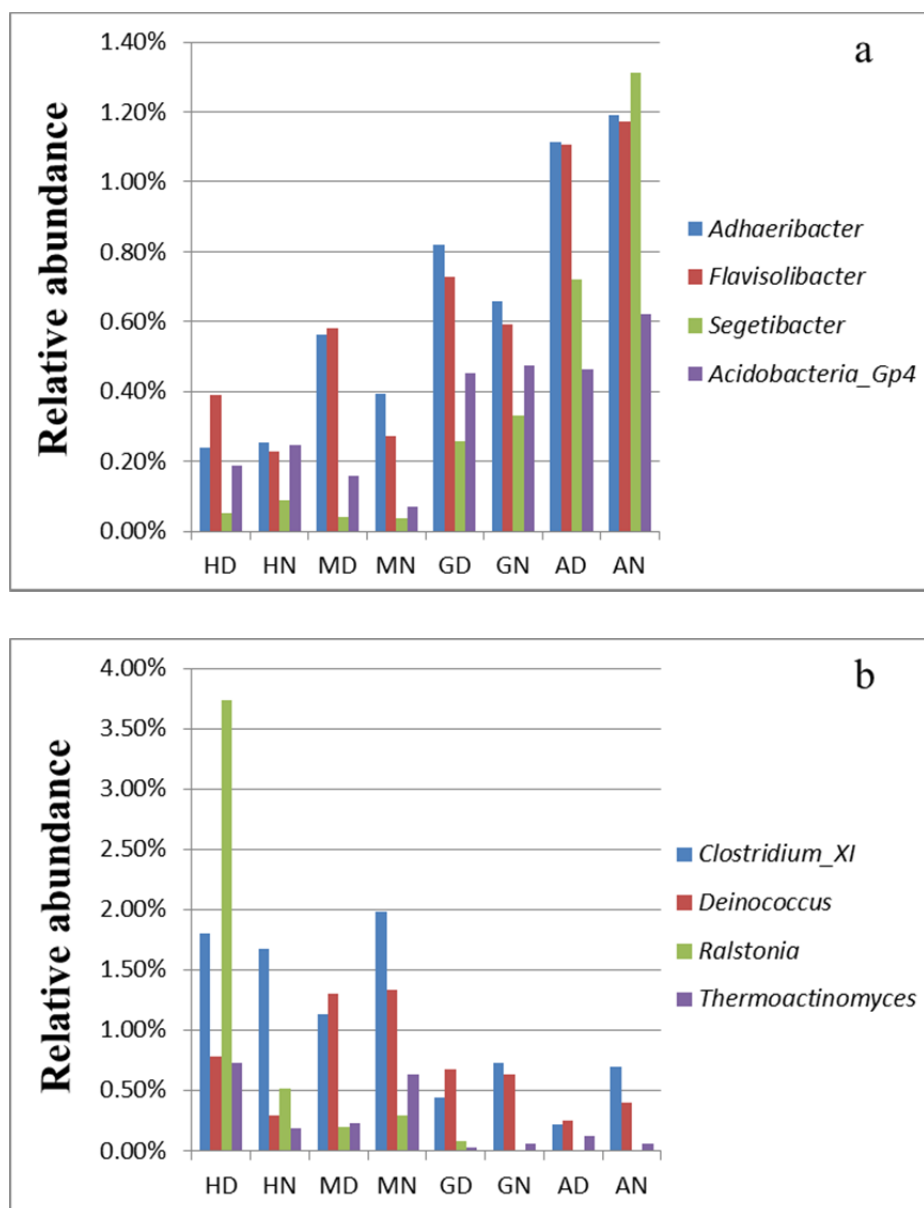


Figure S3. Genera of bacteria that are obviously different between pollution days (AQI > 100) and non-pollution days (AQI ≤ 100). (a) four genera bacteria were more abundant in non-pollution days than in pollution days, (b) four genera bacteria were more abundant in pollution days than in non-pollution days.

Figure S4

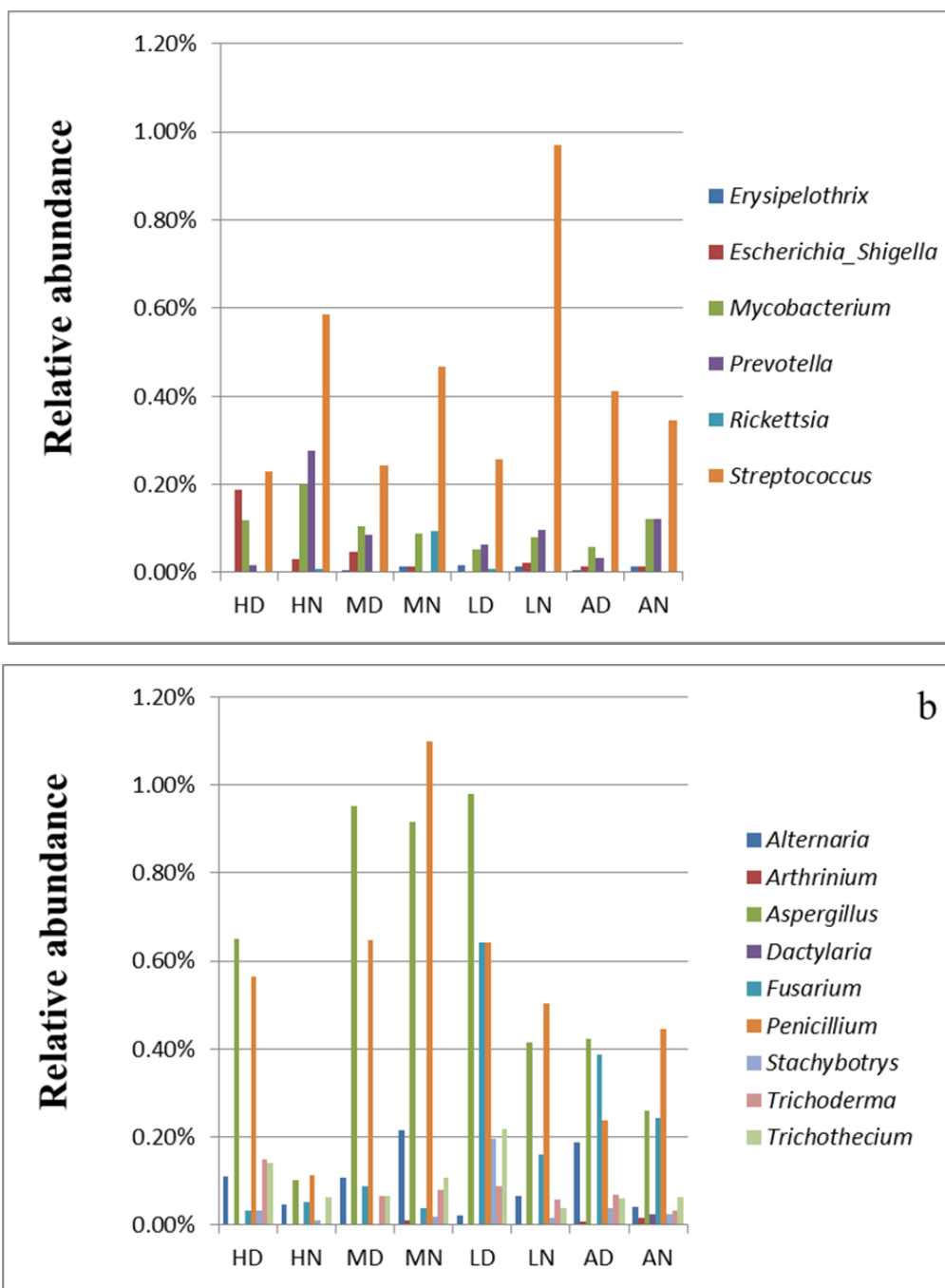


Figure S4. Relative abundance of (a) pathogenic bacteria and (b) fungi in the eight PM2.5 sample groups

**Formulas:**

$$Chao1 = S_{obs} + \frac{n_1(n_1 - 1)}{2(n_2 + 1)}$$

$$Shannon = - \sum_{i=1}^{S_{obs}} \frac{n_i}{N} \ln \frac{n_i}{N}$$

$S_{obs}$  = the number of observed OTUs

$n_i$  = the number of sequences in OTU  $i$

$N$  = the total number of sequences in the community