

SUPPLEMENTAL INFORMATION

Dysbiosis in the urban tree microbiome

SECTION S1: METHODS

Sample biogeochemical and physiochemical measurements

Physicochemical and biogeochemistry measurements were made on soil samples collected for DNA extraction and microbial community analysis. Soils from the same sampling depths per tree and leaves from the same tree were pooled together (91 trees x 2 depths = 182 soil samples, 91 trees x 1 sample = 91 leaf samples). Gravimetric soil moisture content was measured by drying the soil at 65 °C for more than 48 hours. Soil pH was measured on a 1:2 soil/water suspension using a pH meter (Seven Compact S220 pH/ion meter, Mettler Toledo, Columbus, OH, USA). Soil organic matter content was measured by combusting dried soil at 450 °C for 4 hours in a muffle furnace. Soil soluble N was extracted with 2 mol/L KCl at a 1:10 fresh soil/extractant ratio to measure soil available nitrate and ammonium¹. Soil temperature was measured in field soil at each sampling point using a Hanna Instruments Thermistor Thermometer (± 0.4 °C for one year excluding probe error; Waterproof Thermistor Thermometer: HI93510N, 2021) at 7 cm depth for the 0-15 cm soil layer and 22 cm depth for the 15-30 cm soil layer.

Root biomass and density

Root biomass was measured in each soil sample using the “roots on sieve” method²⁻⁴. Roots were first washed on top of a 2 mm sieve with DI water. Using forceps, each root was picked from the sieve and placed in a coin envelope. The roots were dried for 72 hours at 60 °C in an oven and weighed to calculate total root biomass as g root per g soil.

24 ***DNA extractions***

25 Soil DNA extractions. To extract DNA from the upper soil (0-15 cm), we used the DNeasy
26 PowerSoil Pro Kit (QIAGEN, Hilden, Germany), and for lower soil samples (15-30 cm), we
27 used the DNeasy PowerLyzer PowerSoil Kit (QIAGEN, Hilden, Germany). Both kits were
28 modified similarly: after adding approximately 0.25 g of soil to each PowerBead Pro Tube, we
29 added 750 µL of Solution CD1 and 50 µL of Buffer ATL (QIAGEN, Hilden, Germany)⁵ for the
30 PowerSoil Pro kit or 750 µL of PowerBead Solution and 60 µL of Solution C1 for the
31 PowerLyzer PowerSoil kit, vortexed the tubes briefly, and then incubated the samples for 15
32 minutes at 60 °C in a water bath. Instead of vortexing the samples to homogenize them, we
33 performed 4 cycles for the PowerSoil Pro kit or 5 cycles for the PowerLyzer PowerSoil kit of
34 freezing the tubes in liquid N, thawing them in a 60 °C water bath for 5 minutes, and grinding the
35 samples in a Mini-Beadbeater-96 (Biospec Products, Bartlesville, OK) for 1 minute. Finally,
36 during the elution step, we used 50 µL of PCR-grade water instead of the kits' provided elution
37 buffer to elute the DNA. We allowed the water to sit on the filter for 1 minute before
38 centrifuging the tubes, and then after centrifuging, we put the flow-through back onto the filter
39 and repeated the elution step.

40 Leaf DNA extractions. To extract DNA from leaves, we used the DNeasy Plant Pro Kit
41 (QIAGEN, Hilden, Germany) with the following modifications: we removed the provided 2.38
42 mm stainless steel beads from the PowerBead Tubes and replaced them with 10 2 mm Zirconia
43 beads. After adding approximately 0.03 g of leaf tissue to each PowerBead Tube, we added 450
44 µL of Solution CD1 and 50 µL of the Phenolic Separation Solution, vortexed the tubes briefly,
45 and then incubated the samples for 10 minutes at 60 °C in a water bath. Instead of vortexing the
46 samples to homogenize them, we performed 5-12 cycles of freezing the tubes in liquid N,

thawing them in a 60 °C water bath for 5 minutes, and grinding the samples in a Mini-Beadbeater-96 (Biospec Products, Bartlesville, OK) for 1 minute. Finally, during the elution step, we used 50 µL of PCR-grade water instead of the kits' provided elution buffer to elute the DNA. We allowed the water to sit on the filter for 1 minute before centrifuging the tubes, and then after centrifuging, we put the flow-through back onto the filter and repeated the elution step.

Root DNA extractions. To extract DNA from roots, we applied a cetyltrimethylammonium bromide (CTAB)/chloroform extraction and LiCl precipitation method⁶ to 10-15 fine roots (approximately 0.2 g) per sample. We cleaned the extracted root DNA with AMPure XP Bead-Based Reagent (Beckman-Coulter Life Sciences, Indianapolis, IN) with the modifications following Chen et al. (2021)⁷. Samples were stored at -80 °C until further analysis.

PCR and amplicon sequencing

PCR amplification of both 16S and ITS amplicons from every sample type was carried out in 25 µL reactions following Tatsumi et al. (2023)⁸ with the following modifications: amplification of root DNA used 1 µL of undiluted genomic DNA, 1.0 µL of each 10 µM primer, 5 µL of 10 × OneTaq Standard Reaction Buffer, 0.5 µL of 10 mM dNTPs, 1.3 µL of BSA, and 0.13 µL of hot start Taq polymerase; and amplification of DNA extracts from lower soil and leaf samples used 2 µL of 20-fold diluted genomic DNA, 1.25 µL of each 10 µM primer, 5 µL of Q5 Reaction Buffer (New England BioLabs, Ipswich MA), 0.5 µL of 10 mM dNTPs, 5 µL of Q5 GC Enhancer (New England BioLabs, Ipswich MA), 1.3 µL BSA, and 0.250 µL of Q5 Taq polymerase (New England BioLabs, Ipswich MA). The PCR conditions for 16S using the Q5 Taq polymerase were: denaturation at 98 °C for 30 sec; 30 cycles of 10 sec at 98 °C, 30 sec at 54 °C and 30 sec at 72 °C; followed by a 2 min final extension at 72 °C. The PCR conditions for ITS using the Q5

Taq polymerase were: denaturation at 98 °C for 30 sec; 35 cycles of 10 sec at 98 °C, 30 sec at 60 °C and 30 sec at 72 °C; followed by a 2 min final extension at 72 °C. The amplification was confirmed by electrophoresis. Amplicons were cleaned using Just-a-Plate 96 PCR Purification and Normalization Kit (Charm Biotech, MO, USA) and quantified using Qubit HS-dsDNA kit (Invitrogen, Carlsbad, California, USA) on a Tecan Infinite F200 Pro plate reader, reading at 485 nm excitation and 530 nm emission.

Bioinformatics

The 16S and ITS sequencing data were processed using BU16S (<https://github.com/Boston-University-Microbiome-Initiative/BU16s>), a customized QIIME2⁹ pipeline designed to operate on Boston University's Shared Computing Cluster. In summary, BU16S performed quality filtration with DADA2¹⁰. The filtered reads were then de-replicated and denoised, and the 16S paired ends were merged, removing the quality score truncation threshold. For ITS, only the forward reads were used, as reverse reads did not pair well with the forward reads. Then, chimeric sequences were removed. The pipeline calculates amplicon sequence variants (ASVs) that are 99% similar in rDNA sequence then classifies ASVs with 95% or greater sequence identity to a database using VSEARCH. SILVA99 (v138.1)¹¹ was used as the database for bacterial taxonomy and UNITE dynamic database (v9.0)¹² was used for fungal taxonomy. An Aitchison distance matrix was calculated separately for fungal and bacterial data from each sample type with the aDist function of the robCompositions package in R (version 2.4.1)¹³ and an NMDS was performed with the metaMDS function of the vegan package in R (version 2.6-4)¹⁴. Outlier samples identified in these NMDS plots were removed from the dataset, along with samples with low read counts after the BU16S pipeline (for fungal samples, leaf samples with

fewer than 10,000 reads, root samples with fewer than 5,000 reads, upper soil samples with fewer than 5,000 reads, and lower soil samples with fewer than 8,000 reads were removed from the dataset, and for bacterial samples, leaf samples with fewer than 10,000 reads, root samples with fewer than 10,000 reads, upper soil samples with fewer than 8,000 reads, and lower soil samples with fewer than 8,000 reads were removed from the dataset; see Table S2). Contaminants were identified in the sequencing data using the negative control prevalence method in the isContaminant function of the decontam R package (version 1.20.0)¹⁵ and then removed with the prune_taxa function of the phyloseq R package (version 1.44.0)¹⁶. Non-fungal ASVs were removed from the fungal ASV table and non-bacterial or archaeal ASVs were removed from the bacterial ASV table. The final, cleaned dataset consisted of a total of 49,980,377 16S sequences across 833 samples and 33,193,586 ITS sequences across 823 samples, with an average of $57,714.06 \pm 19,911.21$ 16S sequences and $38,913.93 \pm 34,478.45$ ITS sequences per sample (Table S2).

To assign fungal and bacterial taxa to functional groups, fungal genera were searched against the FungalTrait database¹⁷, and bacterial genera were searched against an in-house functional database generated based on the presence of genes coding for enzymes in specific biochemical pathways^{18,19}, following Tatsumi et al. (2023)⁸.

Supplemental Methods Tables

Table S1. Site characteristics. The two most common tree species in each forest/neighborhood are shown in order of abundance. UNE Harvard Forest sites are numbered according to the Tatsumi et al. (2023)⁸ and Caron et al. (2023)¹ numbering scheme and the urbanization categories follow the Garvey et al (2022)²⁰ classifications. Distance from Boston, impervious

surface area, and edge aspect data for urban forest sites and UNE-1 and UNE-2 sites came from Garvey et al. (2022)²⁰. Impervious surface area data for Harvard Forest Biomass plots and Boston neighborhoods were calculated from data from MassGIS Impervious Surface 2005 (2007)²¹; boundaries for Boston neighborhoods for impervious surface area calculations came from Boston Maps, Boston Neighborhood Boundaries (2024)²². Dominant tree species and tree basal area data for urban forest sites and UNE-1 and UNE-2 sites came from Tatsumi et al. (2023)⁸, for Harvard Forest Biomass Plots came from Matthes et al. (2024)²³, and for Boston neighborhoods came from Boston Maps, Treekeeper Street Trees (2024)²⁴. Soil type data came from Natural Resource Conservation Service-U.S. Department of Agriculture²⁵.
See below.

Table S2. Amplicon DNA sequence data statistics. Data cleaning included quality control with the BU16S pipeline²⁶, removing outliers and low-read samples (for fungal samples, leaf samples with fewer than 10,000 reads, root samples with fewer than 5,000 reads, upper soil samples with fewer than 5,000 reads, and lower soil samples with fewer than 8,000 reads were removed from the dataset, and for bacterial samples, leaf samples with fewer than 10,000 reads, root samples with fewer than 10,000 reads, upper soil samples with fewer than 8,000 reads, and lower soil samples with fewer than 8,000 reads were removed from the dataset), and removing contamination ASVs with the decontam R package (version 1.20.0)¹⁵ and non-fungal and non-bacterial or archaeal reads from the fungal and bacterial datasets, respectively.

See below.

Table S3. Fungal pathogens detected in leaf samples across the urbanization gradient.

Numbers are sums of species counts normalized by rarefaction in leaf samples of each tree type.

% identity refers to the % match of ITS sequence from the tree microbiome dataset to the ITS sequence match in the UNITE database, which corresponded to a genus-level name match in the FungalTraits database.

See below.

Table S4. Fungal pathogens detected in upper soil samples across the urbanization

gradient. Numbers are sums of species counts normalized by rarefaction in upper soil (0-15 cm depth) samples of each tree type. % identity refers to the % match of ITS sequence from the tree microbiome dataset to the ITS sequence match in the UNITE database, which corresponded to a genus-level name match in the FungalTraits database.

See below.

Table S5. Fungal pathogens detected in lower soil samples across the urbanization

gradient. Numbers are sums of species counts normalized by rarefaction in lower soil (15-30 cm depth) samples of each tree type. % identity refers to the % match of ITS sequence from the tree microbiome dataset to the ITS sequence match in the UNITE database, which corresponded to a genus-level name match in the FungalTraits database.

See below.

Table S6. Fungal pathogens detected in root samples across the urbanization gradient.

Numbers are sums of species counts normalized by rarefaction in root samples of each tree type.

% identity refers to the % match of ITS sequence from the tree microbiome dataset to the ITS

sequence match in the UNITE database, which corresponded to a genus-level name match in the FungalTraits database.

See below.

Table S7. Bacterial pathogens detected in leaf samples across the urbanization gradient.

Numbers are sums of species counts normalized by rarefaction in leaf samples of each tree type.

% identity refers to the % match of 16S sequence from the tree microbiome dataset to the 16S sequence in the Multiple Bacterial Pathogen Detection database.

See below.

Table S8. Bacterial pathogens detected in upper soil samples across the urbanization

gradient. Numbers are sums of species counts normalized by rarefaction in upper soil (0-15 cm depth) samples of each tree type. % identity refers to the % match of 16S sequence from the tree microbiome dataset to the 16S sequence in the Multiple Bacterial Pathogen Detection database.

See below.

Table S9. Bacterial pathogens detected in lower soil samples across the urbanization

gradient. Numbers are sums of species counts normalized by rarefaction in lower soil (15-30 cm depth) samples of each tree type. % identity refers to the % match of 16S sequence from the tree microbiome dataset to the 16S sequence in the Multiple Bacterial Pathogen Detection database.

See below.

184 **Table S10. Bacterial pathogens detected in root samples across the urbanization gradient.**

185 Numbers are sums of species counts normalized by rarefaction in root samples of each tree type.

186 % identity refers to the % match of 16S sequence from the tree microbiome dataset to the 16S

187 sequence in the Multiple Bacterial Pathogen Detection database.

188 *See below.*

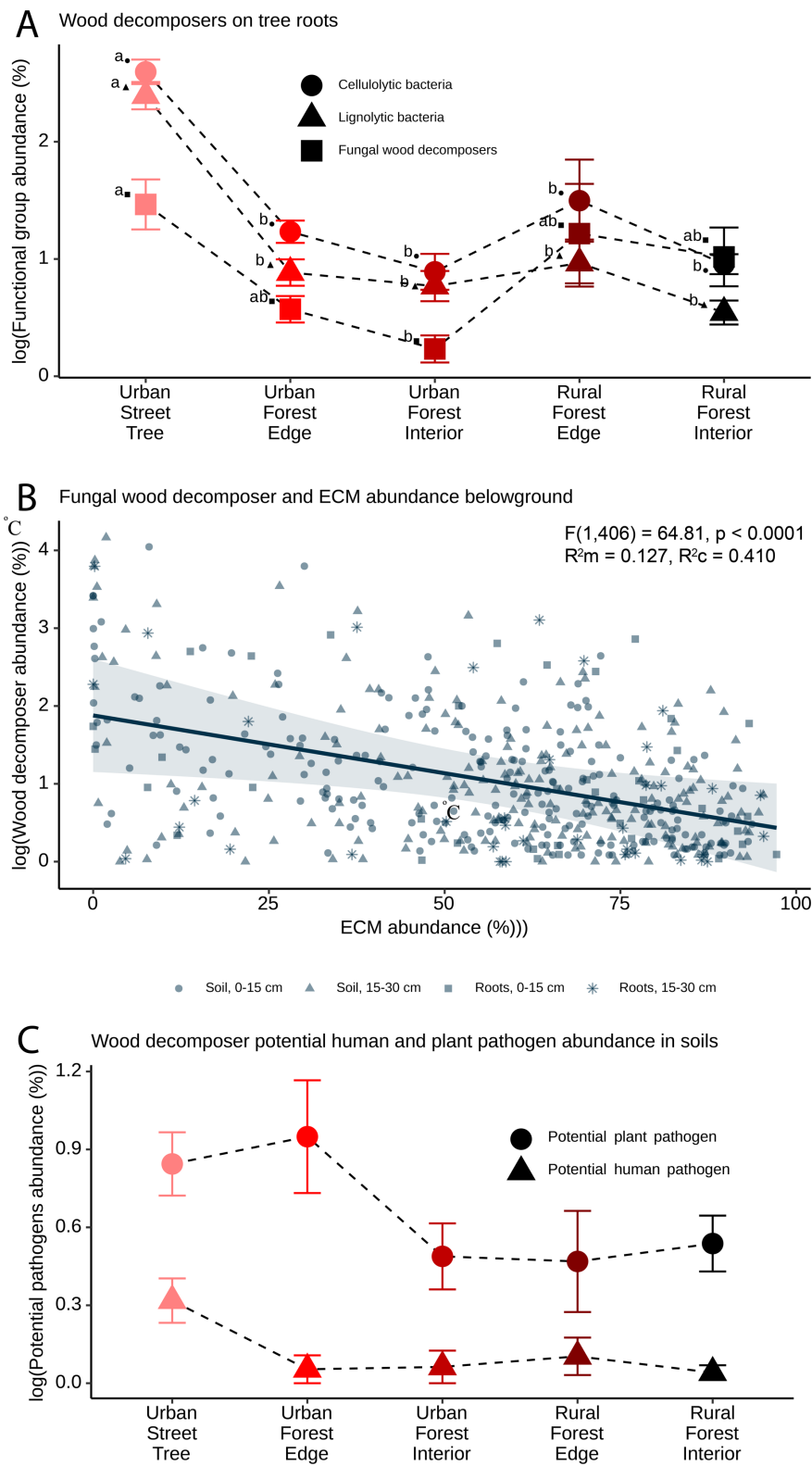


Fig. S1. Wood decomposers across site types in root samples (a), the relationship between ECM fungal and wood decomposer abundances in belowground samples (b), and wood decomposers that may act as human and plant pathogens across site types in soil samples (c). Error bars in (a), and (c) represent standard error around the mean (n = 52 trees in the fungal wood decomposers on tree root analysis, n = 56 trees in the bacterial wood decomposers on tree root analysis, n = 90 trees in the wood decomposer and ECM abundance belowground analysis, n = 87 trees in the wood decomposer potential plant pathogen in soils analysis). Letters in (a) denote Tukey groups (p < 0.05) based on linear mixed-model regression analyses. Shapes in (b) represent belowground sample types.

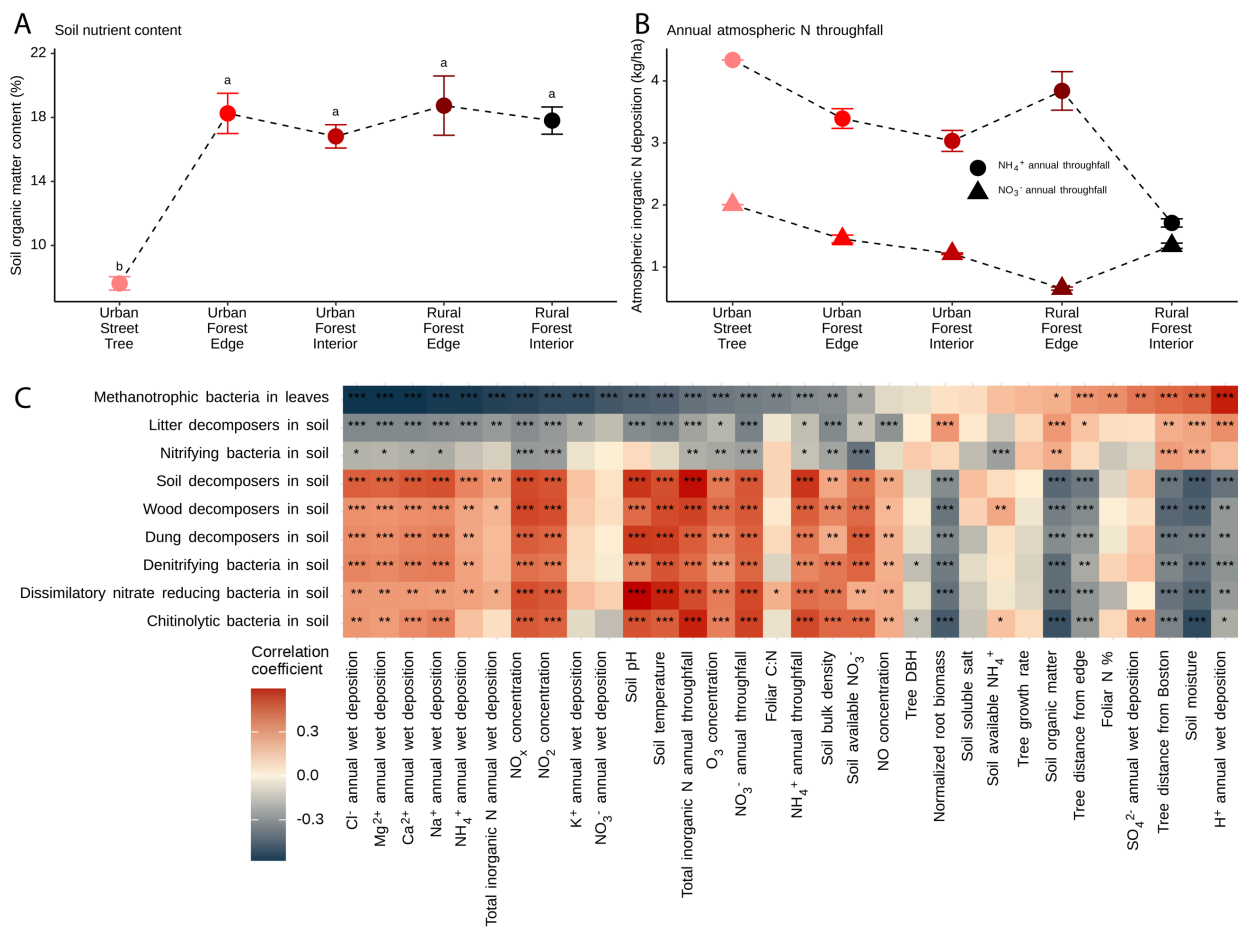


Fig. S2. Soil organic matter (a) and annual atmospheric inorganic N throughfall (b) across site types and relationships between nutrient-cycling microbial functional groups and environmental factors are shown in (c). Error bars in (a), and (b) represent standard error around the mean (n = 88 trees). Letters in (a) denote Tukey groups (p < 0.05) based on linear mixed-model regression analyses and asterisks in (c) denote p values (* p < 0.05, ** p < 0.01, *** p < 0.001).

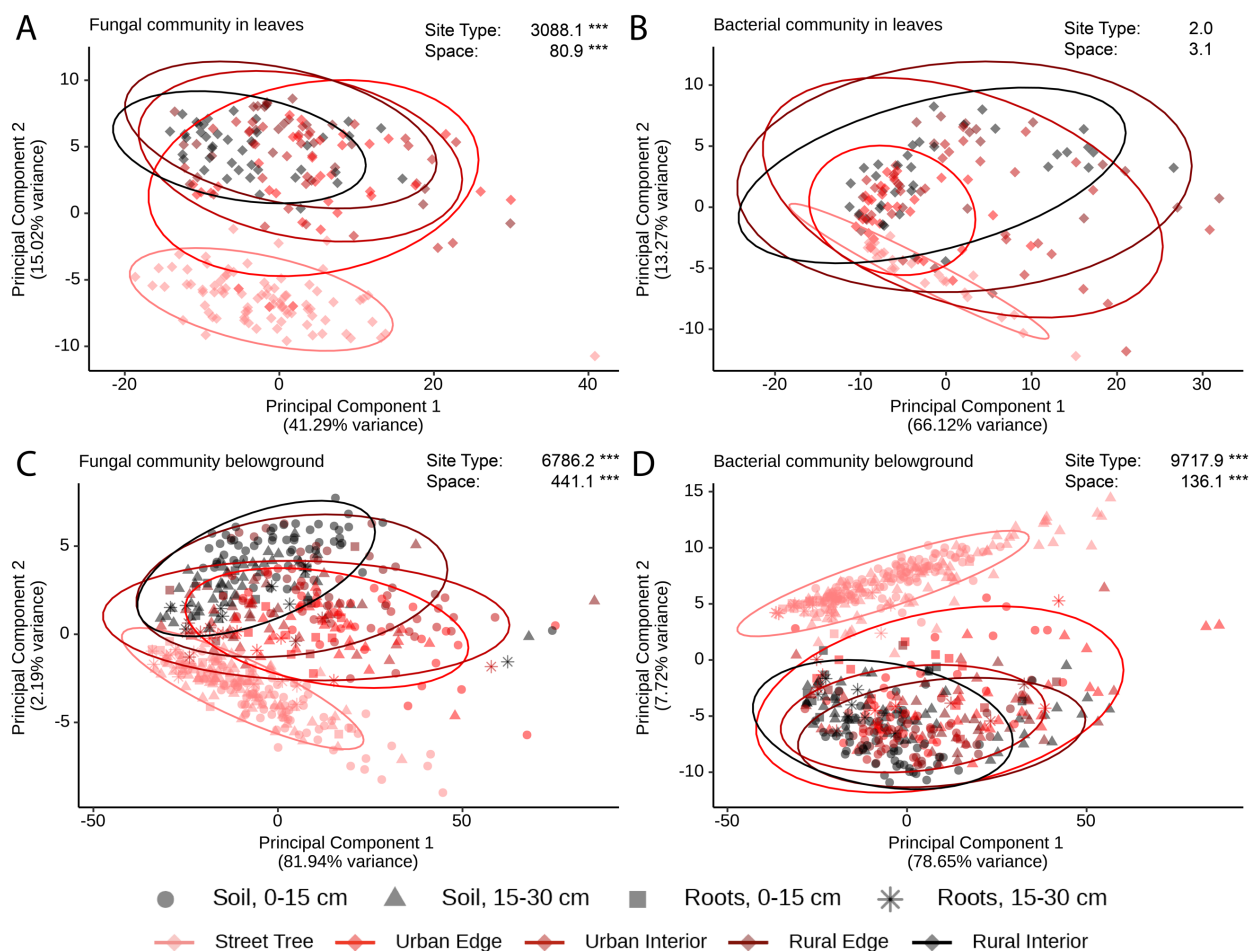


Fig. S3. Community composition of fungal (a, c) and bacterial (b, d) communities in leaves (a, b) and belowground (c, d). Point color represents site type and point shape represents sample type. Points represent each of three replicate samples collected from an individual tree (n = 85 trees with fungal data in leaves, n = 62 trees with bacterial data in leaves, n = 90 trees with

belowground fungal data, n = 91 trees with belowground bacterial data). The F values of Multiple Regression on distance Matrices (MRM) to test the effect of site type and physical spatial distance between trees in km on community composition are shown on each plot, where asterisks represent p values (***) $p < 0.001$.

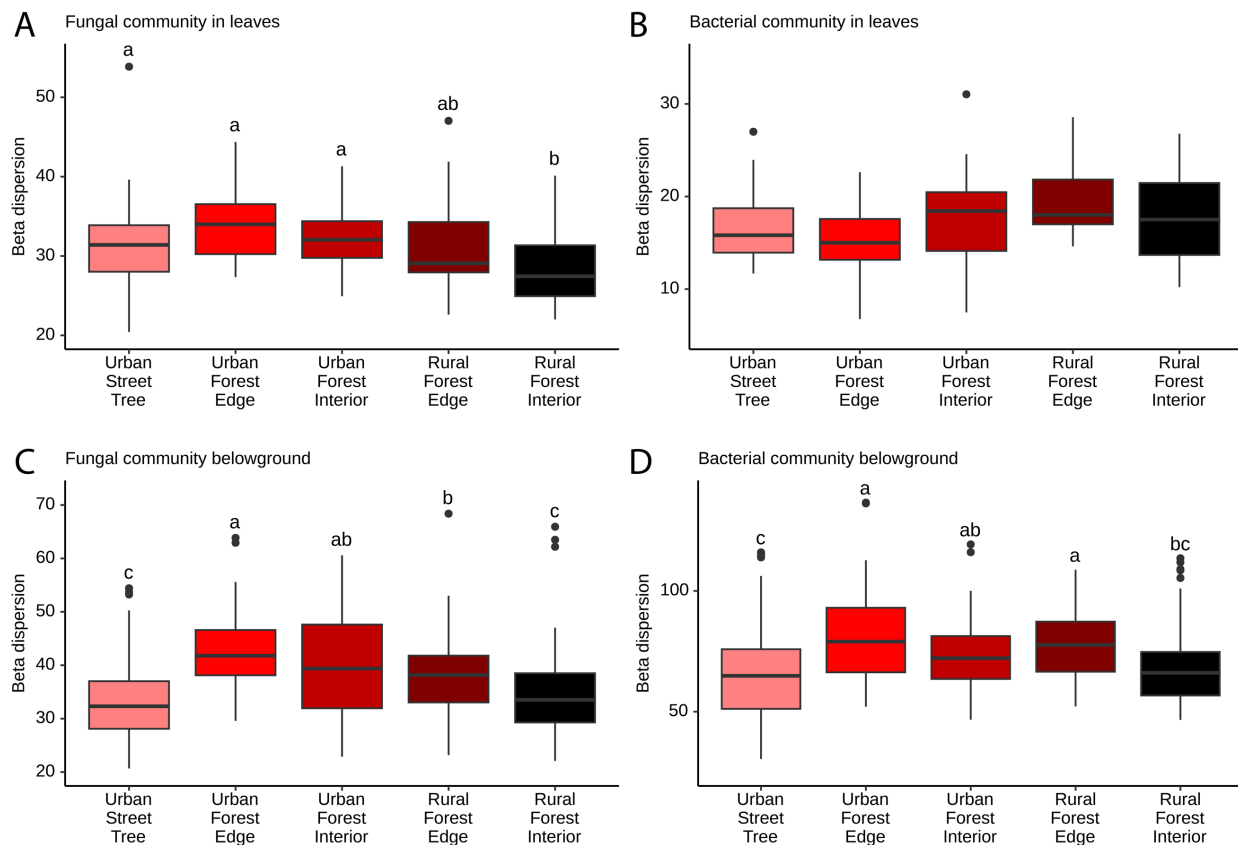


Fig. S4. Beta dispersion, a measure of heterogeneity, of fungal (a, c) and bacterial (b, d) communities in leaves (a, b) and belowground (c, d) (n = 85 trees with fungal data in leaves, n = 62 trees with bacterial data in leaves, n = 90 trees with belowground fungal data, n = 91 trees with belowground bacterial data). Letters denote Tukey groups ($p < 0.05$).

SECTION S3: REFERENCES

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Site	City or township (MA)	Distance from Boston (km)	Impervious surface area (%)	Urbanization category	Dominant tree species	Edge type	Edge aspect	Tree basal area (m ² /ha)	Soil Type
Arnold Arboretum	Boston	8.01	26.17	Urban Forest	Quercus spp., Pinus strobus	Road	NW	32.4 ± 6.4	Hollis
Hammond Woods	Newton	9.63	13.59	Urban Forest	Acer rubrum, Quercus rubra	Road	E	35.0 ± 17.4	Hollis
Sutherland Woods	Lexington	13.2	27.46	Urban Forest	Quercus rubra, Carya glabra	Parking lot	SW	29.0 ± 11.6	Charlton
Blue Hills Observatory	Milton	16.34	6.43	Rural Forest	Quercus rubra, Acer rubrum	Clearing, ski	NE	19.9 ± 3.7	Rock Outcrop/ Hollis
Broad Meadow	Worcester	60.41	25.99	Urban Forest	Quercus rubra, Betula lenta	Clearing, pov	SW	25.4 ± 4.5	Chatfield
Harvard Forest (UNE-1)	Petersham	92.63	4.04	Rural Forest	Quercus rubra, Tsuga canadensis	Road	SW	43.6 ± 13.1	Woodbridge
Harvard Forest (UNE-2)	Petersham	95.16	0.64	Rural Forest	Acer rubrum, Acer saccharum	Open field	E	51.8 ± 18.1	Paxton/ Woodbridge
Harvard Forest Biomass Plots	Petersham	93.31	0	Rural Forest	Acer rubrum, Quercus rubra	N/A	N/A	35.73 ± 0.53	Becket
Allston-Brighton	Boston	8.36	49.79	Urban Street Tree	Gleditsia triacanthos, Tilia cordata	Road	N/A	0.0031 ± 1.55e-6	Newport
Back Bay	Boston	1.52	63.34	Urban Street Tree	Gleditsia triacanthos, Pyrus calleryana	Road	N/A	0.0099 ± 7.34e-6	Urban land
Dorchester	Boston	7.67	46.26	Urban Street Tree	Gleditsia triacanthos, Fraxinus pennsylvanica	Road	N/A	0.0026 ± 7.09e-7	Newport
Jamaica Plain	Boston	6.74	25.62	Urban Street Tree	Tilia cordata, Gleditsia triacanthos	Road	N/A	0.0021 ± 1.40e-6	Merrimac/ Udorthents
Roxbury	Boston	2.79	43.2	Urban Street Tree	Gleditsia triacanthos, Fraxinus pennsylvanica	Road	N/A	0.0033 ± 1.55e-6	Udorthents
Mattapan	Boston	7.98	34.86	Urban Street Tree	Acer platanoides, Gleditsia triacanthos	Road	N/A	0.0032 ± 3.05e-6	Urban Land/ Udorthents/ Woodbridge
South Boston	Boston	3.66	44.53	Urban Street Tree	Gleditsia triacanthos, Acer platanoides	Road	N/A	0.0024 ± 1.40e-6	Merrimac/ Newport

South End	Boston	2.25	61.68	Urban Street Tree	Gleditsia triacanthos, Tilia cordata	Road	N/A	0.0142 ± 6.70e-6	Urban Land/ Udorthents
West Roxbury	Boston	11.12	24.41	Urban Street Tree	Acer platanoides, Tilia cordata	Road	N/A	0.0047 ± 1.55e-6	Newport

Table S2. Amplicon DNA sequence data statistics. Data cleaning included quality control with the BU16S pipeline, removing outliers and low-read samples (for fungal samples, leaf samples with fewer than 10,000 reads, root samples with fewer than 5,000 reads, upper soil samples with fewer than 5,000 reads, and lower soil samples with fewer than 8,000 reads were removed from the dataset, and for bacterial samples, leaf samples with fewer than 10,000 reads, root samples with fewer than 10,000 reads, upper soil samples with fewer than 8,000 reads, and lower soil samples with fewer than 8,000 reads were removed from the dataset), and removing contamination ASVs with the decontam R package (version 1.20.0) and non-fungal and non-bacterial or archaeal reads from the fungal and bacterial datasets, respectively.

	Sample type	Number of samples sequenced	Raw read count per sample	Read count per sample after BU16S & quality control	Read count per sample after removing outliers and low-read samples	Read count per sample after negative control decontamination	Samples remaining after data cleaning	Samples removed
Fungi	Leaf	251	45,464.43 $\pm$ 20,230.99	35,596.22 $\pm$ 15,810.01	36,458.98 $\pm$ 14,947.61	25,285.23 $\pm$ 11,415.65	241	10
	Upper Soil	248	35,840.33 $\pm$ 14,524.71	28,189.64 $\pm$ 13,155.42	28,708.65 $\pm$ 12,773.80	25,307.76 $\pm$ 11,768.65	243	5
	Lower Soil	229	37,649.9 $\pm$ 19,486.25	27,225.1 $\pm$ 15,895.17	27,549.06 $\pm$ 15,026.11	23,956.17 $\pm$ 13,416.48	215	14
	Root	95	41,932.71 $\pm$ 23,667.01	29,296.32 $\pm$ 16,390.1	29,787.82 $\pm$ 15,550.85	23,309.72 $\pm$ 12,836.61	88	7
Bacteria	Leaf	256	45,875.31 $\pm$ 16,927.02	37,305.32 $\pm$ 16,835.49	43,077.56 $\pm$ 15,885.27	15,75.75 $\pm$ 16,51.75	142	114
	Upper Soil	255	68,055.47 $\pm$ 29,277.41	30,023.06 $\pm$ 12,510.38	30,200.03 $\pm$ 10,421.77	29,197.61 $\pm$ 10,095.82	243	12
	Lower Soil	229	53,331.17 $\pm$ 29,295.8	35,509.65 $\pm$ 21,999.08	37,490.02 $\pm$ 21,231.70	35,491.15 $\pm$ 20,226.55	215	14
	Root	93	72,269.82 $\pm$ 45,988.31	40,980.39 $\pm$ 26,979.53	35,071.03 $\pm$ 19,528.47	14,715.27 $\pm$ 10,227.42	78	15

Table S3. Fungal pathogens detected in leaf samples across the urbanization gradient. Numbers are sums of species counts normalized by rarefaction in leaf samples of each tree type. % identity refers to the % match of ITS sequence from the tree microbiome dataset to the ITS sequence match in the UNITE database, which corresponded to a genus-level name match in the FungalTraits database.

Fungal Species	Pathogen Type	% Identity ($\pm$ standard deviation when >1 ASV sequence match)	Urban Street Tree	Urban Forest Edge	Urban Forest Interior	Rural Forest Edge	Rural Forest Interior
Acephala sp.	root-associated	96.23% $\pm$ 0.47	0	0	3	5	0
Acremonium charticola	leaf/fruit/seed pathogen	97.31%	8	0	0	0	0
Acremonium persicinum	leaf/fruit/seed pathogen	99.56%	0	0	0	4	0
Aequabiliella effusa	leaf/fruit/seed pathogen	98.62% $\pm$ 0	0	0	1	0	10
Akanthomyces lecanii	invertebrate parasite	99.54%	9	0	0	0	0
Akanthomyces muscarius	invertebrate parasite	99.77% $\pm$ 0.33	169	3	2	16	331
Alpinaria rhododendri	wood pathogen	98.84% $\pm$ 1.64	0	3	0	0	9
Alpinaria sp.	wood pathogen	95.41%	0	0	0	0	1
Alternaria angustioidea	leaf/fruit/seed pathogen	97.97% $\pm$ 0.76	18645	2639	474	1046	937
Alternaria armoraciae	leaf/fruit/seed pathogen	100%	0	0	0	2	0
Alternaria eichhorniae	leaf/fruit/seed pathogen	98.6% $\pm$ 0.72	1123	790	40	49	13
Alternaria metachromatica	leaf/fruit/seed pathogen	99.42% $\pm$ 0.45	132	82	1	2	7
Alternaria pobletensis	leaf/fruit/seed pathogen	99.3% $\pm$ 0.33	9	0	0	0	21
Alternaria rosae	leaf/fruit/seed pathogen	99.77% $\pm$ 0.33	23	0	5	13	8
Alternaria subcucurbitae	leaf/fruit/seed pathogen	99.21% $\pm$ 0.99	79	0	0	3	0
Alternaria tropica	leaf/fruit/seed pathogen	100%	6	0	0	0	0
Ampelomyces quisqualis	leaf/fruit/seed pathogen	96.58%	7	0	0	0	0
Ampelomyces sp.	leaf/fruit/seed pathogen	96.77%	1	0	81	0	0
Apenidiella sp.	leaf/fruit/seed pathogen	98.14% $\pm$ 1.06	3	2	3	3	11
Apenidiella strumelloidea	leaf/fruit/seed pathogen	97.58%	0	0	0	0	5
Apiognomonina errabunda	leaf/fruit/seed pathogen	100%	39	12	0	0	0
Apiospora guiyangensis	leaf/fruit/seed pathogen	99.52%	0	0	1	0	0
Arachnomycetes sp.	animal parasite/opportunistic human parasite	95.43% $\pm$ 0	54	0	0	8	14
Armillaria borealis	wood pathogen	99.20%	0	0	1	0	0
Ascochyta medicaginicola var. macrospora	leaf/fruit/seed pathogen	98.68%	13	0	66	1	2
Atractiella sp.	root pathogen	96.22% $\pm$ 0.69	223	3	1	0	8
Aureobasidium iraniamum	leaf/fruit/seed pathogen, animal parasite	96.68%	0	1	0	0	0
Aureobasidium pullulans	leaf/fruit/seed pathogen, animal parasite	98.55% $\pm$ 1.35	66983	4910	13534	5438	4106
Beauveria bassiana	invertebrate parasite	98.26%	0	0	0	0	9
Beauveria pseudobassiana	invertebrate parasite	97.86%	9	0	0	0	0
Biatrispora sp.	opportunistic human parasite	98.55%	0	1	0	0	0
Bipolaris eleusines	leaf/fruit/seed pathogen	98.34%	15	0	0	0	0
Biscogniauxia marginata	wood pathogen	99.53%	3	0	0	0	0
Biscogniauxia mediterranea	wood pathogen	99.06%	11	1	0	0	0
Bjerkandera adusta	wood pathogen	98.35% $\pm$ 0.58	2	0	0	0	2
Botrytis caroliniana	leaf/fruit/seed pathogen	99% $\pm$ 1	40	4	4	4	11
Bryochiton monascus	leaf/fruit/seed pathogen	97.25% $\pm$ 0.35	0	4	21	0	47
Bryochiton sp.	leaf/fruit/seed pathogen	98.19% $\pm$ 1.8	0	1	5	10	0
Caliciopsis beckhausii	leaf/fruit/seed pathogen	99.76% $\pm$ 0.33	318	34	22	46	1730
Caliciopsis moriondi	leaf/fruit/seed pathogen	100%	0	0	0	0	2

<i>Caliciopsis</i> sp.	leaf/fruit/seed pathogen	99.78% ± 0.31	711	584	665	120	151
<i>Caliciopsis valentina</i>	leaf/fruit/seed pathogen	98.59% ± 0.67	0	17	15	0	8
<i>Calyptella capula</i>	leaf/fruit/seed pathogen	100%	1	0	0	0	0
<i>Candida palmioleophila</i>	animal-associated/opportunistic human parasite	100%	0	0	4	0	0
<i>Candida railenensis</i>	animal-associated/opportunistic human parasite	100%	0	0	0	0	6
<i>Capronia</i> sp.	animal parasite/opportunistic human parasite	98.46% ± 1.54	1	12	6	1	5
<i>Catenulostroma hermanusense</i>	leaf/fruit/seed pathogen	97.93% ± 1.65	120	80	107	18	8
<i>Celosporium</i> sp.	leaf/fruit/seed pathogen	97.7% ± 0.37	1795	114	64	35	43
<i>Ceratobasidium</i> sp.	leaf/fruit/seed pathogen	98.33% ± 1.52	6	0	2	33	0
<i>Cercosporidium californicum</i>	leaf/fruit/seed pathogen	97.98% ± 0.54	38	59	7	0	2
<i>Chaetosphaeronema achilleae</i>	leaf/fruit/seed pathogen	100%	0	2	0	0	0
<i>Chaetosphaeronema</i> sp.	leaf/fruit/seed pathogen	100%	15	0	0	0	0
<i>Chalara</i> sp.	wood pathogen, leaf/fruit/seed pathogen	95.98% ± 0	1	12	5	113	4
<i>Chloridium aseptatum</i>	root pathogen, opportunistic human parasite	99.54%	2	0	0	0	0
<i>Chloridium</i> sp.	root pathogen, opportunistic human parasite	96.57%	0	2	2	0	0
<i>Cladophialophora</i> sp.	animal parasite/opportunistic human parasite	98.75% ± 0.78	18	13	16	2	6
<i>Cladosporium aphidis</i>	leaf/fruit/seed pathogen, animal parasite	95.50%	0	0	0	0	1
<i>Cladosporium austrohemisphaericum</i>	leaf/fruit/seed pathogen, animal parasite	97.74%	54	0	0	0	5
<i>Cladosporium domesticum</i>	leaf/fruit/seed pathogen, animal parasite	99.53%	16	1	0	0	1
<i>Cladosporium halotolerans</i>	leaf/fruit/seed pathogen, animal parasite	99.76% ± 0.33	19	6	3	2	5
<i>Cladosporium herbarum</i>	leaf/fruit/seed pathogen, animal parasite	97.63% ± 0.6	9393	1354	1177	2598	3488
<i>Cladosporium</i> sp.	leaf/fruit/seed pathogen, animal parasite	97.79% ± 1.24	12268	3067	2177	5310	7364
<i>Cladosporium sphaerospermum</i>	leaf/fruit/seed pathogen, animal parasite	99.69% ± 0.27	20	3	0	0	4
<i>Clarireedia bennettii</i>	leaf/fruit/seed pathogen	98.53%	0	1	0	0	0
<i>Clavulinopsis helvola</i>	root-associated	98.81%	1	0	0	0	0
<i>Clavulinopsis</i> sp.	root-associated	98.05%	0	3	0	0	0
<i>Clonostachys rosea</i>	leaf/fruit/seed pathogen, nematophagous	98.06% ± 1.27	0	0	1312	1	0
<i>Coccomyces</i> sp.	leaf/fruit/seed pathogen	97.04%	0	0	0	0	2
<i>Colletotrichum gloeosporioides</i>	leaf/fruit/seed pathogen	98.28%	1	0	0	0	0
<i>Colletotrichum kniphofiae</i>	leaf/fruit/seed pathogen	99.28% ± 0.34	1711	121	240	269	270
<i>Colletotrichum laticiphilum</i>	leaf/fruit/seed pathogen	99.53%	72	0	0	0	0
<i>Colletotrichum psidii</i>	leaf/fruit/seed pathogen	97.42%	3	0	0	0	0
<i>Colletotrichum sansevieriae</i>	leaf/fruit/seed pathogen	100%	4	0	0	0	0
<i>Colpoma</i> sp.	leaf/fruit/seed pathogen	99.51%	0	0	0	0	4
<i>Coniochaeta fasciculata</i>	leaf/fruit/seed pathogen, animal parasite	100%	11	0	0	0	0
<i>Corynelia uberata</i>	leaf/fruit/seed pathogen	99.52%	224	141	58	89	1
<i>Coryneum modonium</i>	leaf/fruit/seed pathogen	96.02% ± 0.75	0	3	3	5	7
<i>Cryptocline arctostaphyli</i>	leaf/fruit/seed pathogen	98.89% ± 0.78	1689	3395	3168	790	1505
<i>Cryptococcus aureus</i>	animal-associated/opportunistic human parasite	99.37% ± 0.3	5	0	0	0	1
<i>Cryptococcus festuosus</i>	animal-associated/opportunistic human parasite	100%	6	0	0	0	0
<i>Cryptococcus</i> sp.	animal-associated/opportunistic human parasite	98.04% ± 1.98	7	34	133	13	45
<i>Cryptococcus waticus</i>	animal-associated/opportunistic human parasite	98.81%	0	0	2	0	0
<i>Cryptodiaporthe galericulata</i>	leaf/fruit/seed pathogen	99.55%	0	0	0	0	25
<i>Cunninghamella</i> sp.	opportunistic human parasite	95.62%	0	0	9	0	0
<i>Curvularia americana</i>	leaf/fruit/seed pathogen, opportunistic human parasite	98.18%	1	0	0	0	0
<i>Curvularia austriaca</i>	leaf/fruit/seed pathogen, opportunistic human parasite	99.32% ± 0.32	52	5	21	3	6

<i>Curvularia canadensis</i>	leaf/fruit/seed pathogen, opportunistic human parasite	100%	8	0	0	0	0
<i>Curvularia intermedia</i>	leaf/fruit/seed pathogen, opportunistic human parasite	98.86% ± 0.99	46	3	0	0	0
<i>Curvularia protuberata</i>	leaf/fruit/seed pathogen, opportunistic human parasite	100%	5	0	0	1	0
<i>Curvularia pseudoprotuberata</i>	leaf/fruit/seed pathogen, opportunistic human parasite	99.08%	0	1	0	0	0
<i>Curvularia xishuangbannaensis</i>	leaf/fruit/seed pathogen, opportunistic human parasite	99.54%	3	0	0	0	0
<i>Cyberindnra jadinii</i>	animal parasite/opportunistic human parasite	100%	0	2	0	0	0
<i>Cylindrium desperesense</i>	leaf/fruit/seed pathogen	98.86% ± 1.58	543	68	187	246	2481
<i>Cylindrium magnoliae</i>	leaf/fruit/seed pathogen	97.93% ± 0.59	36	602	363	94	77
<i>Cyphellophora livistonae</i>	animal parasite/opportunistic human parasite	100%	0	0	1	0	0
<i>Cyphellophora sambuci</i>	animal parasite/opportunistic human parasite	97.72%	0	1	6	1	0
<i>Cyphellophora sessilis</i>	animal parasite/opportunistic human parasite	99.38% ± 0.54	3	3	3	167	93
<i>Cyphellophora sp.</i>	animal parasite/opportunistic human parasite	97.68% ± 2.05	1	5	3	10	2
<i>Cyphellophora vermisporea</i>	animal parasite/opportunistic human parasite	100%	10	0	0	0	0
<i>Cytospora ailanthicola</i>	leaf/fruit/seed pathogen	97.01%	0	0	1	0	0
<i>Cytospora galegicola</i>	leaf/fruit/seed pathogen	98.96% ± 0.93	0	24	2	0	20
<i>Cytospora nitschkei</i>	leaf/fruit/seed pathogen	95.72% ± 0.26	38	0	36	0	0
<i>Cytospora sp.</i>	leaf/fruit/seed pathogen	99.55%	12	0	0	0	0
<i>Dendrophoma cytisporoides</i>	leaf/fruit/seed pathogen	100%	19	7	53	5	2
<i>Dendrophoma sp.</i>	leaf/fruit/seed pathogen	99.52%	2	0	0	0	0
<i>Dendrostoma chinense</i>	wood pathogen	96.95% ± 1.55	0	6	3	10	16
<i>Dendrostoma covidicola</i>	wood pathogen	97.45% ± 0.33	0	0	3	1	0
<i>Dendrostoma shandongense</i>	wood pathogen	98.15%	0	0	0	4	7
<i>Devriesia sp.</i>	leaf/fruit/seed pathogen	99.12% ± 0.63	5	266	374	105	245
<i>Diaporthe alleghaniensis</i>	leaf/fruit/seed pathogen	97.47% ± 0.42	2	0	0	0	12
<i>Diaporthe betulae</i>	leaf/fruit/seed pathogen	98.9% ± 0.31	60	3	1	0	0
<i>Diaporthe bicincta</i>	leaf/fruit/seed pathogen	97.68% ± 0.42	204	2	0	0	4
<i>Diaporthe caulivora</i>	leaf/fruit/seed pathogen	97.87%	5	0	0	0	0
<i>Diaporthe cichorii</i>	leaf/fruit/seed pathogen	98.62%	9	1	0	0	0
<i>Diaporthe columnaris</i>	leaf/fruit/seed pathogen	98.21%	0	0	0	1	0
<i>Diaporthe conica</i>	leaf/fruit/seed pathogen	97%	0	0	0	0	2
<i>Diaporthe cuppatea</i>	leaf/fruit/seed pathogen	100%	1	0	0	0	0
<i>Diaporthe kochmanii</i>	leaf/fruit/seed pathogen	98.24%	6	0	0	0	0
<i>Diaporthe melonis</i>	leaf/fruit/seed pathogen	95.60%	2	0	0	0	0
<i>Diaporthe perijuncta</i>	leaf/fruit/seed pathogen	97.68% ± 0.46	2	0	1	9	2
<i>Diaporthe sp.</i>	leaf/fruit/seed pathogen	97.6% ± 2.41	356	1	3	0	0
<i>Diatrype stigma</i>	leaf/fruit/seed pathogen	98.56%	8	0	0	0	0
<i>Diatrypella favacea</i>	leaf/fruit/seed pathogen	96.89%	0	3	0	0	0
<i>Didymella arachidicola</i>	leaf/fruit/seed pathogen, animal parasite	98.46% ± 0.31	436	181	0	44	0
<i>Didymella bellidis</i>	leaf/fruit/seed pathogen, animal parasite	98.88% ± 0.32	565	100	55	101	30
<i>Didymella ellipsoidea</i>	leaf/fruit/seed pathogen, animal parasite	98.02% ± 0.31	279	0	0	0	0
<i>Didymella gardeniae</i>	leaf/fruit/seed pathogen, animal parasite	99.56%	0	0	0	17	0
<i>Didymella sp.</i>	leaf/fruit/seed pathogen, animal parasite	99.52%	3	0	0	0	2
<i>Didymella urticicola</i>	leaf/fruit/seed pathogen, animal parasite	97.40%	7	0	0	0	0
<i>Diplodia corticola</i>	leaf/fruit/seed pathogen	98.53% ± 0.25	117	1087	444	513	150
<i>Diplodia pseudoseriata</i>	leaf/fruit/seed pathogen	98.24%	45	0	5	0	0
<i>Diplodia scrobiculata</i>	leaf/fruit/seed pathogen	99.12%	7	7	1	0	20

<i>Discosia rubi</i>	leaf/fruit/seed pathogen	98.61%	44	22	7	0	0
<i>Discosia</i> sp.	leaf/fruit/seed pathogen	99.53%	0	184	41	0	0
<i>Dissoconium proteae</i>	leaf/fruit/seed pathogen	99.53%	0	0	0	0	22
<i>Distomycovellosiella brachycarpa</i>	leaf/fruit/seed pathogen	98.13%	0	0	1	0	0
<i>Dothidotthia symphoricarpi</i>	leaf/fruit/seed pathogen	97.68%	7	0	0	0	0
<i>Dothiorella sempervirentis</i>	leaf/fruit/seed pathogen	99.09% ± 0.63	33	0	0	0	0
<i>Elsinoe anacardii</i>	leaf/fruit/seed pathogen	97.80%	75	0	0	0	0
<i>Elsinoe salicina</i>	leaf/fruit/seed pathogen	98.09% ± 0.98	6749	741	155	204	335
<i>Elsinoe salignae</i>	leaf/fruit/seed pathogen	96.71%	1	0	0	0	0
<i>Elsinoe</i> sp.	leaf/fruit/seed pathogen	97.97% ± 0.24	48	0	0	0	0
<i>Elsinoe violae</i>	leaf/fruit/seed pathogen	95.33% ± 0.31	5	737	42	36	50
<i>Entoloma sericeum</i>	root-associated	100%	3	0	0	0	0
<i>Entyloma polysporum</i>	leaf/fruit/seed pathogen	98.01%	1	0	1	0	0
<i>Epicleosporium ramularioides</i>	leaf/fruit/seed pathogen	100%	12	9	2	5	6
<i>Eutiarospora dactylidis</i>	leaf/fruit/seed pathogen	100%	11	0	0	0	0
<i>Eutypa</i> sp.	leaf/fruit/seed pathogen	96.54%	6	0	0	0	0
<i>Eutypella zelkovae</i>	leaf/fruit/seed pathogen	95.24%	0	4	0	0	0
<i>Exobasidium japonicum</i>	leaf/fruit/seed pathogen	97.41% ± 3.1	0	0	0	10	6
<i>Exobasidium maculosum</i>	leaf/fruit/seed pathogen	98.66% ± 0.88	40	54	47	214	273
<i>Exobasidium miyabei</i>	leaf/fruit/seed pathogen	99.12% ± 0.33	322	169	104	25	95
<i>Exobasidium</i> sp.	leaf/fruit/seed pathogen	99.35% ± 0.3	951	105	105	1863	2224
<i>Exophiala equina</i>	root-associated, animal parasite/opportunistic human parasite	100%	28	5	7	0	1
<i>Exophiala eucalyptorum</i>	root-associated, animal parasite/opportunistic human parasite	100%	2	0	0	0	0
<i>Exophiala heteromorpha</i>	root-associated, animal parasite/opportunistic human parasite	99.8% ± 0.28	8	0	0	1	0
<i>Exophiala nagquensis</i>	root-associated, animal parasite/opportunistic human parasite	95.42%	0	0	1	0	0
<i>Exophiala opportunistica</i>	root-associated, animal parasite/opportunistic human parasite	98.61% ± 0.28	23	0	0	0	0
<i>Exophiala pisciphila</i>	root-associated, animal parasite/opportunistic human parasite	100%	1	0	0	0	0
<i>Exophiala sideris</i>	root-associated, animal parasite/opportunistic human parasite	98.18% ± 0.29	0	1	3	0	5
<i>Exophiala</i> sp.	root-associated, animal parasite/opportunistic human parasite	97.06% ± 1.17	6	13	39	10	5
<i>Exophiala xenobiotica</i>	root-associated, animal parasite/opportunistic human parasite	99.57%	0	1	0	0	0
<i>Exserohilum rostratum</i>	leaf/fruit/seed pathogen	99.59%	0	0	0	0	1
<i>Farysia acheniorum</i>	leaf/fruit/seed pathogen	100%	0	0	0	5	0
<i>Farysia itapuensis</i>	leaf/fruit/seed pathogen	96.81% ± 0	4	2	1	0	0
<i>Filobasidium chernovii</i>	opportunistic human parasite	99.20%	0	0	2	1	0
<i>Filobasidium magnum</i>	opportunistic human parasite	99.8% ± 0.28	117	0	4	0	21
<i>Filobasidium mucilaginum</i>	opportunistic human parasite	96.83% ± 1.68	6	0	10	1	0
<i>Filobasidium oeirensae</i>	opportunistic human parasite	100%	9	0	2	0	0
<i>Filobasidium</i> sp.	opportunistic human parasite	99.33% ± 0.83	35	13	33	28	0
<i>Filobasidium wieringae</i>	opportunistic human parasite	99.73% ± 0.23	1454	13	14	10	2
<i>Fomitiporia punctata</i>	wood pathogen	98.81%	0	0	1	0	0
<i>Funiliomyces</i> sp.	leaf/fruit/seed pathogen	99.52% ± 0.01	0	0	0	1	1
<i>Fusarium acaciae-mearnsii</i>	leaf/fruit/seed pathogen, opportunistic human parasite	100%	0	0	0	0	1
<i>Fusarium graminearum</i>	leaf/fruit/seed pathogen, opportunistic human parasite	99.76% ± 0.34	6	0	1	0	2
<i>Fusarium lateritium</i>	leaf/fruit/seed pathogen, opportunistic human parasite	99.55% ± 0.64	33	5	3	0	0
<i>Fusarium oxysporum</i>	leaf/fruit/seed pathogen, opportunistic human parasite	100%	2	8	0	2	0
<i>Fusarium</i> sp.	leaf/fruit/seed pathogen, opportunistic human parasite	99.52% ± 0.68	4	0	10	0	0

<i>Fusarium tricinctum</i>	leaf/fruit/seed pathogen, opportunistic human parasite	99.54% ± 0.45	120	24	20	6	8
<i>Galerina lacustris</i>	leaf/fruit/seed pathogen	98.41%	0	5	0	0	0
<i>Ganoderma leucocontextum</i>	wood pathogen	98.41% ± 0.56	40	0	0	0	0
<i>Ganoderma lucidum</i>	wood pathogen	98.61% ± 0.28	6	3	0	0	0
<i>Ganoderma meredithiae</i>	wood pathogen	100%	0	3	0	0	0
<i>Gibellulopsis nigrescens</i>	leaf/fruit/seed pathogen	100%	4	0	0	0	0
<i>Gjaerumia minor</i>	leaf/fruit/seed pathogen	99.6% ± 0	0	10	2	0	0
<i>Gliophorus</i> sp.	root-associated	98.41%	0	2	0	0	0
<i>Gloioxanthomyces nitidus</i>	root-associated	99.21%	0	0	0	1	0
<i>Haradamyces foliicola</i>	leaf/fruit/seed pathogen	96.65%	0	0	1	0	56
<i>Helminthosporium velutinum</i>	leaf/fruit/seed pathogen	100%	2	0	0	0	0
<i>Herpotrichia pinetorum</i>	leaf/fruit/seed pathogen	96.30%	7	0	0	0	0
<i>Heterobasidion irregulare</i>	wood pathogen	99.60%	0	0	0	0	1
<i>Heterosporicola beijingsensis</i>	leaf/fruit/seed pathogen	99.04%	0	0	1	0	0
<i>Heterotruncatella spartii</i>	leaf/fruit/seed pathogen	100% ± 0	6	1	0	0	1
<i>Hirsutella lecaniicola</i>	invertebrate parasite	97.44% ± 0.33	2	0	0	5	0
<i>Hirsutella rhossiliensis</i>	invertebrate parasite	100%	0	0	0	0	5
<i>Hirsutella thompsonii</i>	invertebrate parasite	99.55%	0	1	0	0	0
<i>Hormonema macrosporum</i>	animal-associated/opportunistic human parasite	98.57% ± 0.85	302	172	87	52	1287
<i>Hormonema</i> sp.	animal-associated/opportunistic human parasite	100%	16	1	3	1	0
<i>Hygrocybe acutoconica</i>	root-associated	98.77%	5	0	0	0	0
<i>Hymenochaete curtisii</i>	wood pathogen	99.21%	0	0	1	0	0
<i>Hymenoscyphus imberbis</i>	leaf/fruit/seed pathogen	96.77%	2	4	4	3	1
<i>Insolibasidium deformans</i>	leaf/fruit/seed pathogen	100%	0	0	0	1	0
<i>Itersonilia perplexans</i>	leaf/fruit/seed pathogen	99.8% ± 0.28	3	3	1	1	1
<i>Kabatina thujae</i>	wood pathogen	98.17%	0	2	0	0	0
<i>Knufia cryptophialidica</i>	leaf/fruit/seed pathogen, opportunistic animal parasite	97.28% ± 0.3	0	0	26	0	0
<i>Knufia</i> sp.	leaf/fruit/seed pathogen, opportunistic animal parasite	98% ± 1.98	35	6	0	0	1
<i>Knufia tsuneda</i>	leaf/fruit/seed pathogen, opportunistic animal parasite	97.34%	1	0	0	0	0
<i>Laetiporus</i> sp.	wood pathogen	99.60%	0	0	1	0	0
<i>Laetiporus sulphureus</i>	wood pathogen	100%	1	1	0	0	0
<i>Laetisaria fuciformis</i>	wood pathogen	99.21%	0	0	0	0	4
<i>Lecanicillium flavidum</i>	invertebrate parasite	100%	0	1	0	0	0
<i>Lecanicillium psalliotae</i>	invertebrate parasite	99.54%	0	1	0	0	0
<i>Lentinellus ursinus</i>	wood pathogen	98.01% ± 0.4	6	0	2	2	2
<i>Leptobacillium chinense</i>	invertebrate parasite	98.17% ± 1.67	2201	56	8	0	384
<i>Leptosillia macrospora</i>	unspecified plant pathogen	95.14% ± 0.01	1	0	0	4	0
<i>Leptosphaeria</i> sp.	wood pathogen	98.56%	6	6	0	0	1
<i>Limonomyces</i> sp.	wood pathogen	95.85% ± 0.28	0	0	0	0	4
<i>Lophodermium macci</i>	leaf/fruit/seed pathogen	98.35% ± 0.7	7	2	3	8	8
<i>Malassezia arunalokei</i>	root-associated, animal-associated/opportunistic human parasite	97.73% ± 1.04	2	6	0	0	5
<i>Malassezia globosa</i>	root-associated, animal-associated/opportunistic human parasite	100%	9	0	0	0	0
<i>Malassezia restricta</i>	root-associated, animal-associated/opportunistic human parasite	99.6% ± 0.4	180	2	0	1	17
<i>Malassezia</i> sp.	root-associated, animal-associated/opportunistic human parasite	100%	0	5	0	0	0
<i>Marasmius nigrobrunneus</i>	leaf/fruit/seed pathogen	99.4% ± 0.28	0	0	0	18	0
<i>Melampsora epitea</i>	leaf/fruit/seed pathogen	99% ± 0.85	2	0	0	0	0

Melampsora medusae	leaf/fruit/seed pathogen	98.73% ± 0.25	420	23	0	0	6
Melanchlenus sp.	opportunistic human parasite	98.31%	2	5	0	0	3
Metacordyceps chlamydosporia	animal parasite	97.99%	0	0	0	1	0
Metarhizopsis microspora	animal parasite	100%	0	0	0	0	1
Metarhizium brunneum	animal parasite	97.59%	0	2	0	4	0
Microcera rubra	animal parasite	99.16%	3	0	0	0	0
Microcyclospora malicola	leaf/fruit/seed pathogen	99.15% ± 0.6	714	5351	2443	3506	11161
Microcyclospora sp.	leaf/fruit/seed pathogen	97.58% ± 0.89	2475	5028	3386	12646	20773
Microcyclospora tardicrescens	leaf/fruit/seed pathogen	99.01% ± 1.06	13	0	6	60	854
Microcyclosporella mali	leaf/fruit/seed pathogen	97.5% ± 1.42	675	372	77	778	31
Microdiplodia sp.	leaf/fruit/seed pathogen	100%	4	0	0	0	0
Microdochium neoqueenslandicum	leaf/fruit/seed pathogen	100%	0	0	0	2	0
Microdochium seminicola	leaf/fruit/seed pathogen	95.26%	0	0	0	3	0
Microdochium sp.	leaf/fruit/seed pathogen	99.77% ± 0.32	5	0	0	0	0
Microstroma bacarum	leaf/fruit/seed pathogen	99.08% ± 0.65	1013	598	189	22	19
Miuraea degenerans	leaf/fruit/seed pathogen	99.50%	0	1	0	0	0
Mixia osmundae	leaf/fruit/seed pathogen	98.44% ± 1.08	0	27	8	4	14
Moesziomyces aphidis	leaf/fruit/seed pathogen	99.8% ± 0.28	4	0	0	0	0
Mollisia albogrisea	leaf/fruit/seed pathogen	99.07% ± 1.31	0	0	0	5	0
Mollisia diesbachiana	leaf/fruit/seed pathogen	96.55% ± 0.46	5	4	2	8	2
Mollisia sp.	leaf/fruit/seed pathogen	98.09% ± 2.31	15	0	0	0	0
Monochaetia castaneae	leaf/fruit/seed pathogen	98.47% ± 1.5	67	42	35	4553	5875
Monochaetia dimorphospora	leaf/fruit/seed pathogen	98.54% ± 1.44	731	107	7	63	839
Monochaetia ilicis	leaf/fruit/seed pathogen	98.06% ± 0.54	24	437	198	1703	2034
Monochaetia massachusettsianum	leaf/fruit/seed pathogen	100%	48	1691	1227	814	1198
Monochaetia sinensis	leaf/fruit/seed pathogen	98.66% ± 0.45	3712	949	407	445	239
Mortierella antarctica	root-associated, opportunistic human parasite	97.61%	11	0	0	0	0
Mortierella pulchella	root-associated, opportunistic human parasite	98.41%	9	0	0	0	0
Mortierella sp.	root-associated, opportunistic human parasite	99.01% ± 0.83	1	1	4	0	2
Mucor circinelloides	opportunistic human parasite	99.58%	5	0	0	0	0
Muriphaeosphaeria viburni	leaf/fruit/seed pathogen	99.29% ± 0.34	77	0	174	0	0
Mycena juniperina	leaf/fruit/seed pathogen	99.60%	3	1	0	0	0
Mycena leptcephala	leaf/fruit/seed pathogen	99.60%	0	9	0	0	0
Mycena meliigena	leaf/fruit/seed pathogen	99.15% ± 0.27	71	5	0	0	0
Mycena polygramma	leaf/fruit/seed pathogen	98.41%	0	0	0	1	0
Mycena purpureofusca	leaf/fruit/seed pathogen	98.41%	0	0	0	5	0
Mycena sp.	leaf/fruit/seed pathogen	98% ± 1.14	0	0	0	4	1
Mycosphaerella ribis	leaf/fruit/seed pathogen	97.37% ± 3.04	11	2212	1865	2	1
Mycosphaerella ulmi	leaf/fruit/seed pathogen	99.50%	2	0	0	0	0
Mycosphaerelloides madeirae	leaf/fruit/seed pathogen	100%	2	0	0	0	0
Myriangium sp.	arthropod parasite	97.01% ± 1.64	725	753	1809	50	78
Myriosclerotinia curreyana	leaf/fruit/seed pathogen	96.75% ± 0.69	2	22	30	43	227
Naevala sp.	leaf/fruit/seed pathogen	97.83% ± 0.76	0	1	12	0	2
Neoascochyta desmazieri	leaf/fruit/seed pathogen	99.29% ± 0.34	130	2	7	1	2
Neoascochyta europaea	leaf/fruit/seed pathogen	100%	0	0	0	0	1
Neoascochyta exitialis	leaf/fruit/seed pathogen	100%	0	0	0	2	0

<i>Neosascochyta graminicola</i>	leaf/fruit/seed pathogen	100%	0	0	0	6	2
<i>Neosascochyta rosicola</i>	leaf/fruit/seed pathogen	98.57%	0	8	0	20	0
<i>Neosascochyta tardicrescens</i>	leaf/fruit/seed pathogen	98.57%	5	0	0	0	0
<i>Neocatenulostroma microsporum</i>	leaf/fruit/seed pathogen	99.32% ± 0.32	57	3	0	0	0
<i>Neocoleroa metrosideri</i>	leaf/fruit/seed pathogen	96.38% ± 0.34	2	0	1	0	0
<i>Neodevriesia agapanthi</i>	leaf/fruit/seed pathogen	98.15%	3	0	0	0	0
<i>Neodevriesia capensis</i>	leaf/fruit/seed pathogen	98.53%	0	0	0	1	0
<i>Neodevriesia hilliana</i>	leaf/fruit/seed pathogen	96.14% ± 0.32	0	0	2	3	0
<i>Neodevriesia imbrexigena</i>	leaf/fruit/seed pathogen	100%	6	8	0	0	2
<i>Neodevriesia kalakoutsii</i>	leaf/fruit/seed pathogen	98.05%	36	0	0	0	0
<i>Neodevriesia metrosideri</i>	leaf/fruit/seed pathogen	99.52% ± 0.48	10	0	0	1	0
<i>Neodevriesia poagena</i>	leaf/fruit/seed pathogen	99.64% ± 0.34	11	7	2	6	11
<i>Neodevriesia</i> sp.	leaf/fruit/seed pathogen	100%	2	0	0	0	0
<i>Neofusicoccum parvum</i>	leaf/fruit/seed pathogen	99.33% ± 0.26	96	37	3	41	42
<i>Neophaeococcomyces aloes</i>	leaf/fruit/seed pathogen	98.1% ± 0.89	57	0	0	0	0
<i>Neophaeococcomyces catenatus</i>	leaf/fruit/seed pathogen	100%	30	76	15	0	0
<i>Neophaeococcomyces</i> sp.	leaf/fruit/seed pathogen	99.2% ± 1.13	180	150	173	7	29
<i>Neophaeomoniella eucalypti</i>	leaf/fruit/seed pathogen	99.14%	100	0	0	0	0
<i>Neophaeomoniella ossiformis</i>	leaf/fruit/seed pathogen	99.57% ± 0.43	8	3	35	0	64
<i>Nigrograna cangshanensis</i>	animal parasite	97.7% ± 0.01	9	1	0	0	0
<i>Nigrograna magnoliae</i>	animal parasite	98.53%	0	4	0	0	0
<i>Ochroconis</i> sp.	leaf/fruit/seed pathogen, opportunistic human parasite	96.92%	0	0	0	1	0
<i>Oidiodendron periconioides</i>	root-associated	97.65% ± 2.63	0	0	7	1	0
<i>Ophiocordyceps retorta</i>	animal parasite	99.53%	0	0	0	0	2
<i>Ophiosphaerella agrostidis</i>	leaf/fruit/seed pathogen	99.06%	0	1	0	0	0
<i>Pallidocercospora crystallina</i>	leaf/fruit/seed pathogen	100%	4	0	4	0	0
<i>Pallidocercospora</i> sp.	leaf/fruit/seed pathogen	98.52%	7	0	0	0	0
<i>Paramycosphaerella intermedia</i>	leaf/fruit/seed pathogen	99.67% ± 0.29	311	19	6	11	0
<i>Paramycosphaerella</i> sp.	leaf/fruit/seed pathogen	98.87% ± 0.74	2	1	2	28	91
<i>Parapenidiella pseudotasmaniensis</i>	leaf/fruit/seed pathogen	96.60%	8	0	0	0	0
<i>Paraphaeomoniella capensis</i>	leaf/fruit/seed pathogen	97.31%	0	0	0	0	11
<i>Paraphoma dioscoreae</i>	wood pathogen	99.01% ± 0.01	3	9	0	3	0
<i>Paraphoma ledniceana</i>	wood pathogen	99.67% ± 0.29	0	0	0	5	2
<i>Parastagonospora poae</i>	leaf/fruit/seed pathogen	97.58%	8	0	0	0	0
<i>Parastagonospora poagena</i>	leaf/fruit/seed pathogen	99.03%	0	0	0	1	2
<i>Parastagonospora</i> sp.	leaf/fruit/seed pathogen	97.09%	5	0	0	0	0
<i>Passalora bacilligera</i>	leaf/fruit/seed pathogen	99.28% ± 0.34	402	16	0	0	0
<i>Passalora chaetomium</i>	leaf/fruit/seed pathogen	98.36% ± 0.33	3	14	0	9	5
<i>Peltaster fruticola</i>	unspecified plant pathogen	98.12% ± 1.13	8006	20507	8526	17769	33638
<i>Peltaster gemmifer</i>	unspecified plant pathogen	99.37% ± 0.54	23615	7954	62	88	12
<i>Penicillium</i> sp.	opportunistic human parasite	98.29% ± 1.04	20	3	1	0	4
<i>Penicillium yunnanense</i>	opportunistic human parasite	99.57%	1	0	0	0	0
<i>Peniophora cinerea</i>	wood pathogen	98% ± 0.41	1763	82	50	62	317
<i>Peniophora laxitexta</i>	wood pathogen	98.53% ± 0.23	39	2	0	0	0
<i>Peniophora lilacea</i>	wood pathogen	96.76% ± 0	8	0	0	3	0
<i>Peniophora malaiensis</i>	wood pathogen	95.47% ± 0.23	4	0	8	2	0

<i>Peniophora pseudopini</i>	wood pathogen	98.76% ± 0.39	0	1	3	0	1
<i>Peniophora</i> sp.	wood pathogen	96.57% ± 0.32	3	11	4	7	0
<i>Peniophora tamaricicola</i>	wood pathogen	96.91% ± 0.41	49	3	1	2	1
<i>Periconia byssoides</i>	leaf/fruit/seed pathogen	100%	63	19	24	15	10
<i>Periconia celtidis</i>	leaf/fruit/seed pathogen	99.52% ± 0.39	80	7	14	7	5
<i>Periconia chimonanthi</i>	leaf/fruit/seed pathogen	100%	0	0	1	2	1
<i>Periconia homothallica</i>	leaf/fruit/seed pathogen	100%	0	6	9	0	0
<i>Periconia macrospinos</i>	leaf/fruit/seed pathogen	100%	1	0	0	0	0
<i>Periconia</i> sp.	leaf/fruit/seed pathogen	98.35% ± 0.47	7	0	0	4	8
<i>Periconia verrucosa</i>	leaf/fruit/seed pathogen	100%	19	0	3	0	0
<i>Periconiella</i> sp.	leaf/fruit/seed pathogen	97.13% ± 1.59	16	0	0	0	16
<i>Peroneutypa scoparia</i>	leaf/fruit/seed pathogen	100%	17	4	0	0	4
<i>Pestalotiopsis iberica</i>	leaf/fruit/seed pathogen	99.3% ± 0.24	15	273	98	40	27
<i>Pestalotiopsis jesteri</i>	leaf/fruit/seed pathogen	94.9% ± 0.29	0	0	0	82	99
<i>Pestalotiopsis macadamiae</i>	leaf/fruit/seed pathogen	98.94% ± 0.3	18	5	116	0	24
<i>Pestalotiopsis rhododendri</i>	leaf/fruit/seed pathogen	98.16% ± 1.36	94	11	8	5	0
<i>Pezicula ericae</i>	leaf/fruit/seed pathogen	94.62% ± 0.28	2	0	0	0	3
<i>Pezicula heterochroma</i>	leaf/fruit/seed pathogen	95.62%	0	0	0	5	0
<i>Phaeoacremonium pseudopanacis</i>	unspecified plant pathogen	96.61%	6	0	0	0	0
<i>Phaeoannellomyces</i> sp.	animal parasite/opportunistic human parasite	99.57%	0	0	2	0	0
<i>Phaeobotryon</i> sp.	leaf/fruit/seed pathogen	99.77% ± 0.33	347	0	0	0	0
<i>Phaeomoniella</i> sp.	leaf/fruit/seed pathogen	97.67% ± 1.59	24	9	34	0	0
<i>Phaeothecoidiella illinoisensis</i>	leaf/fruit/seed pathogen	98.64% ± 0.77	5181	3564	28	5	2
<i>Phaeothecoidiella missouriensis</i>	leaf/fruit/seed pathogen	99.52%	596	517	3	59	3
<i>Phellinus viticola</i>	wood pathogen	98.67% ± 0.23	9	0	0	0	0
<i>Phialemonium dimorphosporum</i>	animal parasite	97.63%	0	0	0	1	0
<i>Phialemonium inflatum</i>	animal parasite	99.32% ± 0.32	0	4	1	0	0
<i>Phialemonium</i> sp.	animal parasite	99.15%	1	0	0	0	1
<i>Phialocephala helenae</i>	root-associated	98.36% ± 1.18	43	3	0	2	0
<i>Phialocephala repens</i>	root-associated	99.06%	3	0	0	5	8
<i>Phialophora cyclaminis</i>	leaf/fruit/seed pathogen, animal parasite	99.08%	1	0	0	0	0
<i>Pholiota mixta</i>	wood pathogen	99.60%	0	0	0	10	0
<i>Phoma laundoniae</i>	leaf/fruit/seed pathogen	99.05% ± 1.35	41	0	0	0	0
<i>Phoma</i> sp.	leaf/fruit/seed pathogen	96.25% ± 2.61	0	0	0	0	54
<i>Phyllactinia leveilluloides</i>	leaf/fruit/seed pathogen	96.64%	72	0	0	0	0
<i>Phyllactinia linderiae</i>	leaf/fruit/seed pathogen	100%	5	0	0	0	0
<i>Phyllosticta capitalensis</i>	leaf/fruit/seed pathogen	96.09% ± 0	20	0	0	0	0
<i>Phyllosticta philoprina</i>	leaf/fruit/seed pathogen	99.53%	0	0	1	0	0
<i>Plectosphaerella oratosquillae</i>	leaf/fruit/seed pathogen, nematophagous	98.29%	0	1	0	0	0
<i>Plectosphaerella slobbergiarum</i>	leaf/fruit/seed pathogen, nematophagous	98% ± 0.31	0	0	2	5	1
<i>Plenodomus collinsoniae</i>	leaf/fruit/seed pathogen	100%	0	0	0	0	2
<i>Pleospora leptosphaerulinoides</i>	leaf/fruit/seed pathogen	98.10%	5	0	0	0	0
<i>Pleurophoma</i> sp.	wood pathogen	98.81% ± 0.34	0	13	0	2	0
<i>Polyporus varius</i>	wood pathogen	98.02%	1	0	0	0	0
<i>Polyscytalum</i> sp.	leaf/fruit/seed pathogen	100%	0	0	0	0	1
<i>Propolis farinosa</i>	leaf/fruit/seed pathogen	99.01%	0	1	0	0	0

<i>Pseudomassaria chondrospora</i>	leaf/fruit/seed pathogen	99.50%	4	0	0	0	0
<i>Pseudomicrostroma glucosiphilum</i>	leaf/fruit/seed pathogen	98.48% ± 0.88	3388	338	971	2	0
<i>Pseudomicrostroma phylloplanum</i>	leaf/fruit/seed pathogen	99% ± 0.43	15286	4655	2993	1182	491
<i>Pseudomicrostroma</i> sp.	leaf/fruit/seed pathogen	97.77% ± 0.67	258	2218	677	5	42
<i>Pseudophloeospora jollyi</i>	leaf/fruit/seed pathogen	96.80%	1	0	3	2	0
<i>Pseudopithomyces rosae</i>	leaf/fruit/seed pathogen	100%	121	17	16	4	35
<i>Puccinia coronata</i>	leaf/fruit/seed pathogen	99.87% ± 0.23	32	0	0	0	0
<i>Puccinia graminis</i>	leaf/fruit/seed pathogen	100%	6	0	0	0	0
<i>Puccinia striiformis</i>	leaf/fruit/seed pathogen	99.60%	0	2	0	0	0
<i>Purpureocillium lilacinum</i>	arthropod parasite	99.54%	15	0	0	0	0
<i>Pyrenopeziza revincta</i>	leaf/fruit/seed pathogen	98.61% ± 0.82	8	4	1	4	9
<i>Pyrenopeziza</i> sp.	leaf/fruit/seed pathogen	99.16%	0	0	0	0	1
<i>Pyrenophora biseptata</i>	leaf/fruit/seed pathogen	99.77% ± 0.33	0	0	0	4	0
<i>Pyrenophora bromi</i>	leaf/fruit/seed pathogen	99.53%	0	0	0	0	1
<i>Pyrenophora poae</i>	leaf/fruit/seed pathogen	100%	1	0	0	0	0
<i>Ramularia simplex</i>	leaf/fruit/seed pathogen	98.66% ± 1.39	547	1336	719	347	703
<i>Ramularia unterseheri</i>	leaf/fruit/seed pathogen	98.61%	0	0	0	0	1
<i>Ramulispora sorghiphila</i>	leaf/fruit/seed pathogen	98.47%	0	1	0	0	0
<i>Rhinocladiella</i> sp.	root-associated, animal parasite/opportunistic human parasite	98.6% ± 0.91	5	16	22	11	9
<i>Rhodotorula graminis</i>	opportunistic human parasite	100%	3	0	0	0	0
<i>Rhodotorula mucilaginoso</i>	opportunistic human parasite	99.8% ± 0.28	3	0	0	0	0
<i>Rhodotorula</i> sp.	opportunistic human parasite	99.20%	0	0	0	0	1
<i>Rhytisma acerinum</i>	leaf/fruit/seed pathogen	100%	0	0	2	0	0
<i>Rosellinia subiculata</i>	wood pathogen	99.14% ± 0.61	2	0	5	1	0
<i>Sagenomella diversispora</i>	opportunistic human parasite	99.45% ± 0.42	5	1	0	3	20
<i>Samsoniella hepiali</i>	invertebrate parasite	100%	0	0	1	1	3
<i>Sarcodontia pachyodon</i>	wood pathogen	98.39%	0	1	0	0	0
<i>Sawadaea tulasnei</i>	leaf/fruit/seed pathogen	100%	7	0	0	0	0
<i>Schizophyllum commune</i>	opportunistic human parasite	99.07% ± 0.23	113	2	0	0	0
<i>Schizothyrium</i> sp.	leaf/fruit/seed pathogen	99.03% ± 0.48	981	335	214	1929	2296
<i>Schizothyrium tardicrescens</i>	leaf/fruit/seed pathogen	98.7% ± 0.74	3	945	2392	2996	1382
<i>Schizothyrium wisconsinense</i>	leaf/fruit/seed pathogen	100%	0	3	0	3	3
<i>Scleromitrella calthicola</i>	leaf/fruit/seed pathogen	97.09%	0	6	40	27	0
<i>Scleroramularia abundans</i>	leaf/fruit/seed pathogen	99.06% ± 0.46	0	0	2	4	7
<i>Scleroramularia pomigena</i>	leaf/fruit/seed pathogen	98.93% ± 0.23	0	1	0	3	11
<i>Sclerostagonospora ericae</i>	leaf/fruit/seed pathogen	98.35% ± 0.33	73	21	8	3	0
<i>Sclerostagonospora rosae</i>	leaf/fruit/seed pathogen	99.29% ± 0.33	16	82	0	0	0
<i>Sclerostagonospora</i> sp.	leaf/fruit/seed pathogen	98.09% ± 0	34	0	0	1	0
<i>Sclerostagonospora sulcata</i>	leaf/fruit/seed pathogen	100%	43	0	0	0	0
<i>Seimatosporium discosioides</i>	leaf/fruit/seed pathogen	96.78% ± 0.45	31	9	9	0	1
<i>Seimatosporium lichenicola</i>	leaf/fruit/seed pathogen	97.79% ± 0.36	0	12	2	18	55
<i>Seimatosporium rosigenum</i>	leaf/fruit/seed pathogen	98.67%	137	0	19	2	56
<i>Septobasidium mariani</i>	arthropod parasite	97.88% ± 1.5	0	8	8	0	1
<i>Septobasidium</i> sp.	arthropod parasite	95.62%	0	5	0	0	0
<i>Setomelanomma holmii</i>	wood pathogen	99.19% ± 0.53	334	62	29	1	641
<i>Setophaeosphaeria badalingensis</i>	leaf/fruit/seed pathogen	99.52%	2	0	1	0	0

<i>Setoseptoria englandensis</i>	wood pathogen	96.68% ± 2.52	4	2	0	6	0
<i>Sphaerellopsis filum</i>	leaf/fruit/seed pathogen	99.52% ± 0.48	16	9	0	10	11
<i>Sphaerulina abeliceae</i>	leaf/fruit/seed pathogen	98.68% ± 0.98	624	187	81	521	2639
<i>Sporocadus cornicola</i>	leaf/fruit/seed pathogen	97.88% ± 1.14	37	15	9	0	40
<i>Sporocadus microcylus</i>	leaf/fruit/seed pathogen	98.67%	9	0	0	0	0
<i>Sporothrix inflata</i>	wood pathogen, opportunistic human parasite	100%	2	0	0	0	0
<i>Sporothrix sclerotialis</i>	wood pathogen, opportunistic human parasite	98.26%	5	0	0	0	0
<i>Stachylidium bicolor</i>	animal parasite	100%	0	0	0	0	2
<i>Stagonospora bicolor</i>	leaf/fruit/seed pathogen	96.10%	0	0	0	0	3
<i>Stagonospora heteroderae</i>	leaf/fruit/seed pathogen	100%	0	0	1	0	0
<i>Stagonospora pseudoperfecta</i>	leaf/fruit/seed pathogen	97.6% ± 0.31	0	0	1	1	0
<i>Stagonospora pseudovitensis</i>	leaf/fruit/seed pathogen	97.6% ± 0.93	93	0	1	0	4
<i>Stagonospora sp.</i>	leaf/fruit/seed pathogen	98.23% ± 2.27	10	3	2	2	0
<i>Stagonospora trichophorica</i>	leaf/fruit/seed pathogen	98.69%	0	0	0	1	0
<i>Stagonosporopsis loticola</i>	leaf/fruit/seed pathogen	99.56%	2	0	0	0	0
<i>Stagonosporopsis tanacetii</i>	leaf/fruit/seed pathogen	99.53%	7	3	0	0	0
<i>Stagonosporopsis valerianellae</i>	leaf/fruit/seed pathogen	98.25%	0	0	0	4	0
<i>Stagonosporopsis vannaccii</i>	leaf/fruit/seed pathogen	98.67%	1	0	0	0	0
<i>Stemphylium sp.</i>	leaf/fruit/seed pathogen	98.83% ± 1.65	13	0	1	3	0
<i>Strelitziana africana</i>	leaf/fruit/seed pathogen	97.42%	1	0	0	0	0
<i>Strelitziana albisiae</i>	leaf/fruit/seed pathogen	99.34% ± 0.46	93	23	35	49	169
<i>Synfenestella sorbi</i>	leaf/fruit/seed pathogen	95.28%	0	1	0	0	0
<i>Talaromyces cecidicola</i>	opportunistic human parasite	100%	0	0	2	0	1
<i>Talaromyces coprophilus</i>	opportunistic human parasite	98.63%	0	0	1	0	0
<i>Talaromyces pseudostromaticus</i>	opportunistic human parasite	99.55%	0	0	0	0	1
<i>Talaromyces yunnanensis</i>	opportunistic human parasite	99.76% ± 0.34	0	4	0	10	0
<i>Taphrina americana</i>	leaf/fruit/seed pathogen	97.61%	1	0	0	0	0
<i>Taphrina caerulescens</i>	leaf/fruit/seed pathogen	99.67% ± 0.16	3409	66	39	0	14
<i>Taphrina confusa</i>	leaf/fruit/seed pathogen	100%	42	0	0	0	0
<i>Taphrina inositophila</i>	leaf/fruit/seed pathogen	98.32% ± 1.62	207	24	142	8	2
<i>Taphrina letifera</i>	leaf/fruit/seed pathogen	99.54% ± 0.3	62	2	6	8	39
<i>Taphrina pruni</i>	leaf/fruit/seed pathogen	100%	1	0	0	0	0
<i>Taphrina robinsoniana</i>	leaf/fruit/seed pathogen	100%	13	0	0	0	0
<i>Taphrina sacchari</i>	leaf/fruit/seed pathogen	98.81%	3	0	0	6	0
<i>Taphrina sp.</i>	leaf/fruit/seed pathogen	98.9% ± 0.44	77	30	26	1	39
<i>Taphrina tormentillae</i>	leaf/fruit/seed pathogen	99.60%	13	0	0	0	0
<i>Thoreauomyces humboldtii</i>	algal parasite	99% ± 1.41	5	1	7	0	0
<i>Tilletia setariae-parviflorae</i>	leaf/fruit/seed pathogen	99.4% ± 0.28	65	1	0	0	1
<i>Tilletia sp.</i>	leaf/fruit/seed pathogen	99.60%	3	0	0	0	0
<i>Tilletiopsis lilacina</i>	leaf/fruit/seed pathogen	100%	26	94	0	5	2
<i>Tilletiopsis washingtonensis</i>	leaf/fruit/seed pathogen	99.20%	0	125	0	5	0
<i>Tolypocladium sp.</i>	animal parasite	97.17% ± 1.9	0	0	3	3	6
<i>Tolypocladium tropicale</i>	animal parasite	99.55%	0	0	1	2	0
<i>Toxicocladosporium glendoranum</i>	leaf/fruit/seed pathogen	99.28% ± 1.02	17	6	0	0	0
<i>Toxicocladosporium irritans</i>	leaf/fruit/seed pathogen	99.51% ± 0.69	23	3	0	0	0
<i>Toxicocladosporium sp.</i>	leaf/fruit/seed pathogen	98.28% ± 0.35	31	1	0	0	0

Tremateia chromolaenae	leaf/fruit/seed pathogen	99.04%	13	8	0	0	6
Trichoderma atroviride	leaf/fruit/seed pathogen	100%	0	4	0	0	0
Trichoderma decipiens	leaf/fruit/seed pathogen	100%	0	0	0	5	0
Trichoderma hamatum	leaf/fruit/seed pathogen	97.96%	0	0	0	0	1
Trichoderma harzianum	leaf/fruit/seed pathogen	99.79% ± 0.29	3	0	6	0	0
Trichoderma sp.	leaf/fruit/seed pathogen	98.32% ± 0.51	1	0	0	1	0
Trichosporon asteroides	animal parasite/opportunistic human parasite	100%	0	0	1	0	0
Trichosporon sp.	animal parasite/opportunistic human parasite	100%	1	0	0	0	0
Tubakia dryinoides	leaf/fruit/seed pathogen	99.13% ± 0.43	0	0	8	0	2
Umbelopsis sp.	root-associated	98.41% ± 0.32	6	3	0	0	0
Urocystis tritici	leaf/fruit/seed pathogen	99.58%	0	0	1	0	0
Ustilago nunavutica	leaf/fruit/seed pathogen	97.21%	0	2	0	0	0
Ustilago sp.	leaf/fruit/seed pathogen	98.03% ± 1.08	7	0	0	0	0
Venturia inaequalis	leaf/fruit/seed pathogen	98.64%	93	0	0	0	0
Veronaea japonica	leaf/fruit/seed pathogen, opportunistic animal parasite	97.60%	0	8	0	0	0
Veronaea sp.	leaf/fruit/seed pathogen, opportunistic animal parasite	95.94%	29	0	0	0	0
Virosphaerella irregularis	leaf/fruit/seed pathogen	98.56%	2	0	0	2	0
Xenocylindrosporium sp.	leaf/fruit/seed pathogen	96.71% ± 0.92	5	0	0	2	0
Xenopyrenochaetopsis pratorum	leaf/fruit/seed pathogen	100%	21	0	0	0	0
Xenoramularia neerlandica	leaf/fruit/seed pathogen	99.68% ± 0.27	1	0	0	5	7
Yarrowia lipolytica	opportunistic human parasite	99.20%	2	0	0	0	0
Zasmidium angulare	leaf/fruit/seed pathogen	99.04%	3	0	0	0	0
Zasmidium cerophilum	leaf/fruit/seed pathogen	99.02%	8	7	0	0	0
Zasmidium fructigenum	leaf/fruit/seed pathogen	99.18% ± 0.28	5	0	1	6	0
Zasmidium nocoxi	leaf/fruit/seed pathogen	99.02%	0	0	0	0	2
Zeloasperisporium eucalyptorum	leaf/fruit/seed pathogen	97.99% ± 1.04	289	84	126	0	39
Zeloasperisporium sp.	leaf/fruit/seed pathogen	98.24% ± 0.28	3481	157	86	16	900
Zymoseptoria crescenta	leaf/fruit/seed pathogen	98.54%	6	0	0	0	0
Zymoseptoria sp.	leaf/fruit/seed pathogen	98.63% ± 0.94	4	2	4	16	38
Zymoseptoria verkleyi	leaf/fruit/seed pathogen	99.06% ± 0.94	4	9	1	2	0

Table S4. Fungal pathogens detected in upper soil samples across the urbanization gradient. Numbers are sums of species counts normalized by rarefaction in upper soil (0-15 cm depth) samples of each tree type. % identity refers to the % match of ITS sequence from the tree microbiome dataset to the ITS sequence match in the UNITE database, which corresponded to a genus-level name match in the FungalTraits database.

Fungal Species	Pathogen Type	% Identity ($\pm$ standard deviation when >1 ASV sequence match)	Urban Street Tree	Urban Forest Edge	Urban Forest Interior	Rural Forest Edge	Rural Forest Interior
Acaulium retardatum	animal parasite/opportunistic human parasite	99.59%	28	0	0	0	0
Acephala sp.	root-associated	96.71% $\pm$ 1.51	16	11	21	4	1
Acremonium bisectum	leaf/fruit/seed pathogen	97.20%	0	0	0	0	1
Acremonium persicinum	leaf/fruit/seed pathogen	99.57% $\pm$ 0.61	13	0	0	0	0
Acremonium pinkertoniae	leaf/fruit/seed pathogen	100%	16	0	0	0	0
Acremonium sp.	leaf/fruit/seed pathogen	98.14%	12	0	0	0	0
Akanthomyces muscarius	invertebrate parasite	100%	68	0	0	0	0
Allobostryotrichum blastosporum	leaf/fruit/seed pathogen	98.63%	23	0	0	0	0
Allophoma minor	leaf/fruit/seed pathogen	97.82%	5	0	0	0	0
Alternaria angustioidea	leaf/fruit/seed pathogen	98.48% $\pm$ 0.31	200	10	5	0	0
Alternaria chlamydospora	leaf/fruit/seed pathogen	99.53%	249	0	0	0	0
Alternaria chlamydosporigena	leaf/fruit/seed pathogen	100%	2	0	0	0	0
Alternaria eichhorniae	leaf/fruit/seed pathogen	98.91% $\pm$ 0.31	81	0	0	0	0
Alternaria subcucurbitae	leaf/fruit/seed pathogen	100%	21	0	0	0	0
Alternaria tropica	leaf/fruit/seed pathogen	100%	38	0	0	0	0
Ampelomyces sp.	leaf/fruit/seed pathogen	96.33%	0	0	4	0	0
Angulomyces argentinensis	leaf/fruit/seed pathogen	95.24%	1	0	0	0	0
Aphanoascus keratinophilus	opportunistic human parasite	96.92% $\pm$ 0.34	10	0	0	0	0
Arachnomycetes sp.	animal parasite/opportunistic human parasite	98.03% $\pm$ 2.26	45	1	0	0	0
Archaeorhizomyces sp.	root-associated	98% $\pm$ 0.73	2	12	0	0	0
Armillaria borealis	wood pathogen	99% $\pm$ 0.85	0	0	2	27	7
Arthrocladium sp.	animal parasite/opportunistic human parasite	98.43% $\pm$ 1.58	6	2	0	0	0
Arthroderma insingulare	animal parasite/opportunistic human parasite	99.56% $\pm$ 0.62	2	1	0	0	0
Arthropopsis sp.	animal parasite	99.85% $\pm$ 0.27	22	18	13	7	5
Arxiella terrestris	leaf/fruit/seed pathogen	99.16%	2	0	0	0	0
Ascochyta medicaginicola var. macrospora	leaf/fruit/seed pathogen	98.68%	7	0	0	0	0
Aspergillus brasiliensis	animal parasite/opportunistic human parasite	99.55%	1	0	0	0	0
Aspergillus caninus	animal parasite/opportunistic human parasite	98.64% $\pm$ 0	9	0	0	0	0
Aspergillus chlamydosporus	animal parasite/opportunistic human parasite	98.63% $\pm$ 0.74	143	0	0	0	0
Aspergillus citrisporus	animal parasite/opportunistic human parasite	100%	0	0	0	1	1
Aspergillus fennelliae	animal parasite/opportunistic human parasite	99.11%	1	0	0	0	0
Aspergillus flavus	animal parasite/opportunistic human parasite	100%	6	0	0	0	0
Aspergillus fumigatus	animal parasite/opportunistic human parasite	99.58%	10	0	0	0	0
Aspergillus granulosus	animal parasite/opportunistic human parasite	100%	8	0	0	0	0
Aspergillus iizukae	animal parasite/opportunistic human parasite	98.71%	10	0	0	0	0
Aspergillus inflatus	animal parasite/opportunistic human parasite	100%	1	0	0	0	0
Aspergillus insuetus	animal parasite/opportunistic human parasite	99.17%	2	0	0	0	0
Aspergillus japonicus	animal parasite/opportunistic human parasite	99.52%	4	0	0	0	0
Aspergillus limoniformis	animal parasite/opportunistic human parasite	99.09%	54	0	0	0	0

<i>Aspergillus nutans</i>	animal parasite/opportunistic human parasite	99.55%	39	13	0	0	0
<i>Aspergillus pachycaulis</i>	animal parasite/opportunistic human parasite	99.55%	1	0	0	0	0
<i>Aspergillus puulauensis</i>	animal parasite/opportunistic human parasite	100%	1	0	0	0	0
<i>Aspergillus ruber</i>	animal parasite/opportunistic human parasite	100%	13	0	0	0	0
<i>Aspergillus</i> sp.	animal parasite/opportunistic human parasite	98.98% $\pm$ 1.75	298	21	6	0	0
<i>Aspergillus westerdijkiae</i>	animal parasite/opportunistic human parasite	98.70%	2	0	0	0	0
<i>Athelia bombacina</i>	algal parasite	99.20%	0	0	0	0	5
<i>Atractiella</i> sp.	root pathogen	96.81%	0	2	0	0	0
<i>Aureobasidium pullulans</i>	leaf/fruit/seed pathogen, animal parasite	99.31% $\pm$ 0.48	221	20	24	0	1
<i>Barnettozyma californica</i>	opportunistic human parasite	98.69%	1	0	0	0	0
<i>Basidiobolus magnus</i>	animal parasite/opportunistic human parasite	96.41%	0	0	0	0	1
<i>Basidiobolus</i> sp.	animal parasite/opportunistic human parasite	98.41% $\pm$ 0.56	2	0	0	0	1
<i>Beauveria bassiana</i>	invertebrate parasite	98.26% $\pm$ 0.44	9	4	0	0	20
<i>Beauveria caledonica</i>	invertebrate parasite	98.36% $\pm$ 1.44	0	1	13	48	32
<i>Beauveria pseudobassiana</i>	invertebrate parasite	97.86%	10	11	4	0	0
<i>Beauveria</i> sp.	invertebrate parasite	99.16%	3	0	0	0	0
<i>Berkeleyomyces rouxiae</i>	root pathogen	100%	3	0	0	0	0
<i>Biatrispora</i> sp.	opportunistic human parasite	98.54%	0	0	0	0	2
<i>Bipolaris eleusines</i>	leaf/fruit/seed pathogen	99.57%	52	0	0	0	0
<i>Biscogniauxia mediterranea</i>	wood pathogen	98.91% $\pm$ 0.27	3	1	7	2	0
<i>Bjerkandera</i> sp.	wood pathogen	97.98%	4	0	0	0	0
<i>Boletinus merulioides</i>	root-associated, arthropod-associated	99.60%	0	0	0	5	0
<i>Botrytis caroliniana</i>	leaf/fruit/seed pathogen	99.5% $\pm$ 0.71	117	8	282	66	66
<i>Bradomyces graniticola</i>	fish parasite	99.41% $\pm$ 0.26	67	0	0	0	0
<i>Bryochiton</i> sp.	leaf/fruit/seed pathogen	99.52%	0	0	1	0	0
<i>Cadophora</i> sp.	leaf/fruit/seed pathogen	98.4% $\pm$ 1.29	17	26	1	4	0
<i>Caliciopsis valentina</i>	leaf/fruit/seed pathogen	98.11%	0	0	2	0	0
<i>Calyptrozyma</i> sp.	opportunistic human parasite	98.01%	0	0	0	1	7
<i>Candida albicans</i>	animal-associated/opportunistic human parasite	100%	9	0	0	0	0
<i>Candida palmioleophila</i>	animal-associated/opportunistic human parasite	100%	198	0	0	0	0
<i>Candida railenensis</i>	animal-associated/opportunistic human parasite	99.59% $\pm$ 0.41	2	0	0	74	91
<i>Candida santamariae</i>	animal-associated/opportunistic human parasite	99.60%	2	0	0	0	0
<i>Candida zeylanoides</i>	animal-associated/opportunistic human parasite	98.41%	2	0	0	0	0
<i>Capronia epimyces</i>	animal parasite/opportunistic human parasite	99.19% $\pm$ 0	0	0	1	0	1
<i>Capronia pulcherrima</i>	animal parasite/opportunistic human parasite	99.01% $\pm$ 0.47	6	2	0	4	0
<i>Capronia semiimmersa</i>	animal parasite/opportunistic human parasite	98.77% $\pm$ 1.49	224	4	0	0	2
<i>Capronia</i> sp.	animal parasite/opportunistic human parasite	98.06% $\pm$ 1	36	1172	1508	755	1898
<i>Castanediella</i> sp.	leaf/fruit/seed pathogen	99.03% $\pm$ 0.66	28	6	0	0	23
<i>Ceratobasidium</i> sp.	leaf/fruit/seed pathogen	98.26% $\pm$ 1.1	175	13	0	5	22
<i>Chaetosphaeronema</i> sp.	leaf/fruit/seed pathogen	98.81% $\pm$ 0.34	25	0	0	0	0
<i>Chalara pseudoaffinis</i>	wood pathogen, leaf/fruit/seed pathogen	98.52%	1	0	0	0	0
<i>Chalara</i> sp.	wood pathogen, leaf/fruit/seed pathogen	99.03% $\pm$ 0.79	193	18	5	0	1
<i>Chloridium aseptatum</i>	root pathogen, opportunistic human parasite	98.73% $\pm$ 0.69	193	10	3	0	0
<i>Chloridium</i> sp.	root pathogen, opportunistic human parasite	98.13% $\pm$ 0.94	6	22	32	36	139
<i>Chloridium submersum</i>	root pathogen, opportunistic human parasite	98.76% $\pm$ 0.85	0	11	0	6	3

<i>Cladophialophora arxii</i>	animal parasite/opportunistic human parasite	99.60%	1	0	0	0	0
<i>Cladophialophora bantiana</i>	animal parasite/opportunistic human parasite	100%	2	0	0	0	0
<i>Cladophialophora carrionii</i>	animal parasite/opportunistic human parasite	99.58% ± 0.42	40	0	0	0	0
<i>Cladophialophora chaetospora</i>	animal parasite/opportunistic human parasite	97.08% ± 0.83	44	0	8	3	0
<i>Cladophialophora emmonsii</i>	animal parasite/opportunistic human parasite	99.1% ± 0.68	71	0	0	0	0
<i>Cladophialophora humicola</i>	animal parasite/opportunistic human parasite	98.68%	0	13	0	0	0
<i>Cladophialophora immunda</i>	animal parasite/opportunistic human parasite	99.58%	3	0	0	0	0
<i>Cladophialophora lanosa</i>	animal parasite/opportunistic human parasite	97.01%	1	0	0	0	0
<i>Cladophialophora minutissima</i>	animal parasite/opportunistic human parasite	99.13%	0	10	0	0	0
<i>Cladophialophora nyingchiensis</i>	animal parasite/opportunistic human parasite	99.71% ± 0.25	3	30	0	0	0
<i>Cladophialophora recurvata</i>	animal parasite/opportunistic human parasite	100%	5	0	0	0	0
<i>Cladophialophora sp.</i>	animal parasite/opportunistic human parasite	98.53% ± 0.96	1147	2106	2590	1030	1999
<i>Cladophialophora sylvestris</i>	animal parasite/opportunistic human parasite	100%	0	11	9	1	12
<i>Cladorrhinum flexuosum</i>	leaf/fruit/seed pathogen	100%	6	0	0	0	0
<i>Cladorrhinum foecundissimum</i>	leaf/fruit/seed pathogen	100%	13	0	0	0	0
<i>Cladorrhinum sp.</i>	leaf/fruit/seed pathogen	99.76% ± 0.34	6	0	0	0	0
<i>Cladosporium austrohemisphaericum</i>	leaf/fruit/seed pathogen, animal parasite	97.48% ± 0.9	3	1	0	0	9
<i>Cladosporium herbarum</i>	leaf/fruit/seed pathogen, animal parasite	97.96% ± 0.32	22	0	0	0	0
<i>Cladosporium sp.</i>	leaf/fruit/seed pathogen, animal parasite	97.34% ± 1.06	838	36	12	10	104
<i>Cladosporium sphaerospermum</i>	leaf/fruit/seed pathogen, animal parasite	99.77% ± 0.33	9	0	0	0	0
<i>Cladosporium velox</i>	leaf/fruit/seed pathogen, animal parasite	100%	1	0	0	0	0
<i>Clarireedia bennettii</i>	leaf/fruit/seed pathogen	98.86% ± 0.57	105	0	0	0	0
<i>Clavaria falcata</i>	root-associated	98.12% ± 0.22	0	19	0	1	0
<i>Clavaria flavipes</i>	root-associated	97.82% ± 0.28	0	0	0	444	0
<i>Clavaria sp.</i>	root-associated	98.88% ± 0.85	0	25	40	21	0
<i>Clavaria sphagnicola</i>	root-associated	98.41%	0	0	0	2	0
<i>Clavaria zollingeri</i>	root-associated	99.34% ± 0.41	4	0	0	966	379
<i>Clavulinopsis fusiformis</i>	root-associated	98.9% ± 0.68	0	0	0	0	1941
<i>Clavulinopsis helvola</i>	root-associated	98.81%	0	0	18	0	0
<i>Clavulinopsis sp.</i>	root-associated	98.63% ± 1.01	37	3	0	692	3105
<i>Clonostachys candelabrum</i>	leaf/fruit/seed pathogen, nematophagous	99.21% ± 0.72	0	147	2	45	0
<i>Clonostachys eriocamporesii</i>	leaf/fruit/seed pathogen, nematophagous	96.27%	3	0	0	0	0
<i>Clonostachys rosea</i>	leaf/fruit/seed pathogen, nematophagous	98.48% ± 0.24	369	26	21	6	7
<i>Clonostachys swieteniae</i>	leaf/fruit/seed pathogen, nematophagous	97.10%	28	0	0	0	0
<i>Coleophoma sp.</i>	leaf/fruit/seed pathogen	97.48%	2	0	0	0	0
<i>Colletotrichum atractylodicola</i>	leaf/fruit/seed pathogen	96.98%	4	0	0	0	0
<i>Colletotrichum coccodes</i>	leaf/fruit/seed pathogen	100%	29	0	0	0	0
<i>Colletotrichum hemerocallidis</i>	leaf/fruit/seed pathogen	99.10%	12	0	0	0	0
<i>Colletotrichum kniphofiae</i>	leaf/fruit/seed pathogen	99.2% ± 0.55	22	8	0	0	0
<i>Colletotrichum trichellum</i>	leaf/fruit/seed pathogen	100%	2	0	0	0	0
<i>Colletotrichum zhejiangense</i>	leaf/fruit/seed pathogen	99.09%	5	0	0	0	0
<i>Collophora sp.</i>	wood pathogen	97.51%	0	0	0	1	0
<i>Conidiobolus coronatus</i>	animal parasite/opportunistic human parasite	99.60%	0	3	0	0	0
<i>Coniochaeta acaciae</i>	leaf/fruit/seed pathogen, animal parasite	99.14%	2	0	0	0	0
<i>Coniochaeta fasciculata</i>	leaf/fruit/seed pathogen, animal parasite	99.52% ± 0.31	336	0	0	0	0

<i>Coniochaeta gigantospora</i>	leaf/fruit/seed pathogen, animal parasite	99.52%	10	0	0	0	0
<i>Coniochaeta ligniaria</i>	leaf/fruit/seed pathogen, animal parasite	99.05% ± 0.39	98	0	0	0	0
<i>Coniochaeta</i> sp.	leaf/fruit/seed pathogen, animal parasite	99.1% ± 0.08	24	0	0	0	0
<i>Coniothyrium</i> sp.	leaf/fruit/seed pathogen	99.05%	2	0	0	0	0
<i>Cordana mercadoana</i>	other plant pathogen	99.51%	3	0	0	0	0
<i>Cordyceps cateniannulata</i>	animal parasite	98.68% ± 0.62	0	2	3	0	0
<i>Cordyceps</i> sp.	animal parasite	99.09%	0	3	0	0	1
<i>Corynespora smithii</i>	leaf/fruit/seed pathogen	99.54%	0	2	0	0	0
<i>Cotylidia carpatica</i>	moss-associated	100%	5	0	0	0	0
<i>Cryptocline arctostaphyli</i>	leaf/fruit/seed pathogen	98.93% ± 0.95	4	0	1	0	0
<i>Cryptococcus aureus</i>	animal-associated/opportunistic human parasite	99.58%	9	0	0	0	0
<i>Cryptococcus festuocus</i>	animal-associated/opportunistic human parasite	100%	2	0	0	0	0
<i>Cryptococcus pseudolongus</i>	animal-associated/opportunistic human parasite	100%	0	0	6	1	54
<i>Cryptococcus</i> sp.	animal-associated/opportunistic human parasite	97.55% ± 1.66	0	112	18	5	148
<i>Cryptococcus waticus</i>	animal-associated/opportunistic human parasite	98.61% ± 0.28	389	0	0	0	0
<i>Cunninghamella echinulata</i>	opportunistic human parasite	98.81%	1	0	0	0	0
<i>Cunninghamella elegans</i>	opportunistic human parasite	98.66% ± 0.23	16	6	0	0	0
<i>Cunninghamella</i> sp.	opportunistic human parasite	96.61% ± 1.41	283	0	0	0	0
<i>Cuphophyllus borealis</i>	root-associated	100%	0	0	48	0	0
<i>Cuphophyllus canescens</i>	root-associated	99.60%	0	0	0	0	17
<i>Cuphophyllus pseudopallidus</i>	root-associated	99.20%	0	0	0	1	0
<i>Cuphophyllus subviolaceus</i>	root-associated	99.73% ± 0.23	9	0	0	2	1193
<i>Curvularia austriaca</i>	leaf/fruit/seed pathogen, opportunistic human parasite	99.1% ± 0	293	0	1	0	0
<i>Curvularia canadensis</i>	leaf/fruit/seed pathogen, opportunistic human parasite	100%	199	0	0	0	0
<i>Curvularia inaequalis</i>	leaf/fruit/seed pathogen, opportunistic human parasite	100%	40	0	0	0	0
<i>Curvularia intermedia</i>	leaf/fruit/seed pathogen, opportunistic human parasite	98.28% ± 0	8	2	0	0	0
<i>Curvularia protuberata</i>	leaf/fruit/seed pathogen, opportunistic human parasite	100%	3	0	0	0	0
<i>Curvularia pseudoprotuberata</i>	leaf/fruit/seed pathogen, opportunistic human parasite	100%	35	0	0	0	0
<i>Curvularia xishuangbannaensis</i>	leaf/fruit/seed pathogen, opportunistic human parasite	99.54%	16	0	0	0	0
<i>Cutaneotrichosporon middelhovenii</i>	animal parasite/opportunistic human parasite	100%	1	9	0	0	0
<i>Cutaneotrichosporon moniliiforme</i>	animal parasite/opportunistic human parasite	99.66% ± 0.44	208	3	8	0	1
<i>Cutaneotrichosporon smithiae</i>	animal parasite/opportunistic human parasite	99.54%	7	0	0	0	0
<i>Cutaneotrichosporon terricola</i>	animal parasite/opportunistic human parasite	99.77% ± 0.32	11	0	0	0	0
<i>Cyberlindnera culbertsonii</i>	animal parasite/opportunistic human parasite	100%	3	0	0	0	0
<i>Cyberlindnera saturnus</i>	animal parasite/opportunistic human parasite	100%	6	0	0	0	0
<i>Cyberlindnera veronae</i>	animal parasite/opportunistic human parasite	97.76% ± 0	3	0	0	0	0
<i>Cylindrium magnoliae</i>	leaf/fruit/seed pathogen	97.98% ± 0.71	53	38	14	3	59
<i>Cylindrium</i> sp.	leaf/fruit/seed pathogen	98.07%	3	0	0	0	0
<i>Cyphellophora gamsii</i>	animal parasite/opportunistic human parasite	100%	3	0	0	0	0
<i>Cyphellophora livistonae</i>	animal parasite/opportunistic human parasite	99.1% ± 0.64	4	0	0	0	0
<i>Cyphellophora reptans</i>	animal parasite/opportunistic human parasite	100%	1	0	0	0	0
<i>Cyphellophora sessilis</i>	animal parasite/opportunistic human parasite	99.58%	0	0	0	0	2
<i>Cyphellophora</i> sp.	animal parasite/opportunistic human parasite	99.14%	13	0	0	0	0
<i>Cyphellophora vermisporea</i>	animal parasite/opportunistic human parasite	99.38% ± 0.54	147	0	0	0	0
<i>Cytospora ailanthicola</i>	leaf/fruit/seed pathogen	97.01%	0	0	1	0	0

<i>Cytospora galegicola</i>	leaf/fruit/seed pathogen	100%	1	0	0	0	0
<i>Cytospora nitschkei</i>	leaf/fruit/seed pathogen	95.8% ± 0.31	3	0	1	0	0
<i>Cytospora</i> sp.	leaf/fruit/seed pathogen	99.32% ± 0.32	2	0	0	0	2
<i>Dendrophoma cytisporoides</i>	leaf/fruit/seed pathogen	99.79% ± 0.3	9	0	1	1	0
<i>Dendrophoma</i> sp.	leaf/fruit/seed pathogen	99.22% ± 0.65	68	0	0	0	0
<i>Diaporthe betulae</i>	leaf/fruit/seed pathogen	98.68%	4	0	0	0	0
<i>Diaporthe columnaris</i>	leaf/fruit/seed pathogen	98.65% ± 1.19	73	9	0	0	0
<i>Diaporthe lusitanicae</i>	leaf/fruit/seed pathogen	98.62%	2	0	0	0	0
<i>Diaporthe</i> sp.	leaf/fruit/seed pathogen	95.61%	29	0	0	0	0
<i>Diatrypella favacea</i>	leaf/fruit/seed pathogen	97.32%	0	0	0	0	1
<i>Dictyolus</i> sp.	leaf/fruit/seed pathogen	95.45% ± 0.28	0	0	19	0	21
<i>Didymella arachidicola</i>	leaf/fruit/seed pathogen, animal parasite	98.68%	30	0	0	0	0
<i>Didymella bellidis</i>	leaf/fruit/seed pathogen, animal parasite	99.11%	36	0	0	0	0
<i>Didymella qilianensis</i>	leaf/fruit/seed pathogen, animal parasite	95.22%	10	0	0	0	0
<i>Diplodia corticola</i>	leaf/fruit/seed pathogen	98.68%	3	8	3	1	2
<i>Diplodia pseudoseriata</i>	leaf/fruit/seed pathogen	98.24%	8	0	1	0	0
<i>Discosia pseudoartocreas</i>	leaf/fruit/seed pathogen	98.15%	0	0	0	0	4
<i>Discosia rubi</i>	leaf/fruit/seed pathogen	98.23% ± 0.35	863	110	49	1	12
<i>Dothidea</i> sp.	leaf/fruit/seed pathogen	97.67%	4	0	0	0	0
<i>Endogone</i> sp.	root-associated	98.81%	0	0	0	2	0
<i>Entoloma abortivum</i>	root-associated	99.4% ± 0.28	3	0	0	0	0
<i>Entoloma alboubonatum</i>	root-associated	98.94% ± 0.23	0	0	0	0	3
<i>Entoloma brunneosericum</i>	root-associated	97.99%	3	0	0	0	0
<i>Entoloma fernandae</i>	root-associated	99.60%	0	0	1	0	0
<i>Entoloma foliomarginatum</i>	root-associated	100%	0	0	0	2	0
<i>Entoloma fuscocosquamosum</i>	root-associated	99.60%	0	0	0	2	3
<i>Entoloma neglectum</i>	root-associated	96.05%	1	0	0	0	0
<i>Entoloma paraconferendum</i>	root-associated	98.02% ± 0.23	0	0	0	12	45
<i>Entoloma rhodocylix</i>	root-associated	98.25% ± 0.45	0	3	5	5	1
<i>Entoloma rivulare</i>	root-associated	99.60%	0	2	0	0	0
<i>Entoloma sericeum</i>	root-associated	100%	2	0	0	0	0
<i>Entoloma sinuatum</i>	root-associated	99.6% ± 0.4	0	0	0	0	115
<i>Entoloma</i> sp.	root-associated	98.62% ± 1	36	30	31	80	59
<i>Entoloma vernum</i>	root-associated	100%	0	0	0	1	0
<i>Entoloma zuccherellii</i>	root-associated	97.56%	0	0	1	0	0
<i>Entorrhiza aschersoniana</i>	root pathogen	98.05%	15	0	0	0	0
<i>Entyloma cosmi</i>	leaf/fruit/seed pathogen	100%	7	0	0	0	0
<i>Eocronartium</i> sp.	leaf/fruit/seed pathogen	99.6% ± 0.4	69	0	0	0	0
<i>Epicoccum draconis</i>	leaf/fruit/seed pathogen	98.68%	82	0	0	0	0
<i>Exobasidium kishianum</i>	leaf/fruit/seed pathogen	96.63% ± 0.84	0	1	0	0	1
<i>Exobasidium maculosum</i>	leaf/fruit/seed pathogen	99.21%	0	0	0	0	1
<i>Exobasidium miyabei</i>	leaf/fruit/seed pathogen	98.81%	0	0	1	0	0
<i>Exobasidium</i> sp.	leaf/fruit/seed pathogen	98.79%	0	0	0	2	0
<i>Exophiala alcalophila</i>	root-associated, animal parasite/opportunistic human parasite	100%	3	0	0	0	0
<i>Exophiala attenuata</i>	root-associated, animal parasite/opportunistic human parasite	99.21%	11	0	0	0	0

<i>Exophiala bergeri</i>	root-associated, animal parasite/opportunistic human parasite	98.4% ± 0.49	8	1	0	0	0
<i>Exophiala cinerea</i>	root-associated, animal parasite/opportunistic human parasite	98.21%	0	0	0	0	3
<i>Exophiala clavispora</i>	root-associated, animal parasite/opportunistic human parasite	99.60%	45	0	0	0	0
<i>Exophiala ellipsoidea</i>	root-associated, animal parasite/opportunistic human parasite	99.04%	8	0	0	0	0
<i>Exophiala equina</i>	root-associated, animal parasite/opportunistic human parasite	100%	1859	2	0	2	0
<i>Exophiala heteromorpha</i>	root-associated, animal parasite/opportunistic human parasite	100%	94	0	0	0	0
<i>Exophiala nagquensis</i>	root-associated, animal parasite/opportunistic human parasite	98.39%	13	0	0	0	0
<i>Exophiala opportunistica</i>	root-associated, animal parasite/opportunistic human parasite	98.54% ± 0.23	252	0	0	0	0
<i>Exophiala pisciphila</i>	root-associated, animal parasite/opportunistic human parasite	99.8% ± 0.29	38	0	0	0	0
<i>Exophiala quercina</i>	root-associated, animal parasite/opportunistic human parasite	99.60%	0	1	0	0	0
<i>Exophiala radicans</i>	root-associated, animal parasite/opportunistic human parasite	99.6% ± 0.4	146	4	0	1	1
<i>Exophiala</i> sp.	root-associated, animal parasite/opportunistic human parasite	97.86% ± 1.51	35	3	9	1	4
<i>Exophiala xenobiotica</i>	root-associated, animal parasite/opportunistic human parasite	99.43% ± 0.25	379	0	0	0	0
<i>Farysia magdalenana</i>	leaf/fruit/seed pathogen	100%	3	0	0	0	0
<i>Farysia setubalensis</i>	leaf/fruit/seed pathogen	99.8% ± 0.28	3	0	0	0	0
<i>Filobasidium magnum</i>	opportunistic human parasite	99.6% ± 0.56	1	2	0	0	0
<i>Filobasidium wieringae</i>	opportunistic human parasite	100%	3	0	0	0	0
<i>Fimicolochytrium jonesii</i>	algal parasite	98.61% ± 0.28	7	0	0	0	0
<i>Fimicolochytrium</i> sp.	algal parasite	99.02% ± 1.16	52	1	0	0	0
<i>Fistulina hepatica</i>	wood pathogen	98.02%	0	0	0	1	0
<i>Fonsecaea</i> sp.	animal parasite/opportunistic human parasite	100%	0	0	0	0	1
<i>Fusarium graminearum</i>	leaf/fruit/seed pathogen, opportunistic human parasite	99.52%	53	0	0	0	0
<i>Fusarium langsethiae</i>	leaf/fruit/seed pathogen, opportunistic human parasite	98.05%	6	0	0	0	0
<i>Fusarium lateritium</i>	leaf/fruit/seed pathogen, opportunistic human parasite	98.87% ± 0.32	565	0	2	0	0
<i>Fusarium oxysporum</i>	leaf/fruit/seed pathogen, opportunistic human parasite	100% ± 0	3851	30	2	0	0
<i>Fusarium</i> sp.	leaf/fruit/seed pathogen, opportunistic human parasite	100% ± 0	299	0	1	0	0
<i>Fusarium tricinctum</i>	leaf/fruit/seed pathogen, opportunistic human parasite	99.09% ± 1.24	205	2	0	0	1
<i>Gaertneriomyces spectabilis</i>	algal parasite	100%	3	0	0	0	0
<i>Galerina lacustris</i>	leaf/fruit/seed pathogen	98.25% ± 0.45	0	0	0	2	34
<i>Galerina</i> sp.	leaf/fruit/seed pathogen	99.4% ± 0.28	0	0	0	0	18
<i>Ganoderma leucocontextum</i>	wood pathogen	98.25% ± 0.45	4	0	2	1	2
<i>Ganoderma lobatum</i>	wood pathogen	99.60%	1	0	0	0	0
<i>Ganoderma lucidum</i>	wood pathogen	98.27% ± 0.33	173	1	0	0	0
<i>Ganoderma meredithiae</i>	wood pathogen	99.45% ± 0.63	5	0	0	0	1
<i>Geoglossum simile</i>	root-associated	98.63%	0	10	9	1	0
<i>Geoglossum</i> sp.	root-associated	97.80%	0	0	710	1	0
<i>Gibellulopsis simonii</i>	leaf/fruit/seed pathogen	99.56%	5	0	0	0	0
<i>Gliophorus irrigatus</i>	root-associated	98.92% ± 0.95	0	0	0	7	755
<i>Gliophorus laetus</i>	root-associated	97.46% ± 0.28	0	0	113	0	14
<i>Gliophorus</i> sp.	root-associated	97.81% ± 1.2	14	337	897	440	359
<i>Gloioxanthomyces nitidus</i>	root-associated	98.81% ± 0.32	0	0	0	0	660
<i>Glutinoglossum</i> sp.	root-associated	100%	0	0	0	16	0
<i>Herpotrichia pinetorum</i>	leaf/fruit/seed pathogen	98.7% ± 0.39	787	0	0	0	0
<i>Herpotrichia</i> sp.	leaf/fruit/seed pathogen	98.9% ± 0.92	156	0	0	0	8
<i>Heterophoma sylvatica</i>	leaf/fruit/seed pathogen	98.68%	20	0	0	0	0

<i>Heterosporicola beijingensis</i>	leaf/fruit/seed pathogen	99.04%	1	0	0	0	0
<i>Hirsutella rhossiliensis</i>	invertebrate parasite	100%	0	0	11	0	2
<i>Hirsutella vermicola</i>	invertebrate parasite	100%	6	0	0	0	0
<i>Hormonema macrosporum</i>	animal-associated/opportunistic human parasite	99.55%	0	0	12	0	0
<i>Humidicutis marginata</i>	root-associated	98.73% $\pm$ 0.33	0	0	0	4	132
<i>Humidicutis</i> sp.	root-associated	98.81%	0	0	0	0	1
<i>Hyaloscypha desmidiacea</i>	leaf/fruit/seed pathogen	98.74% $\pm$ 1.78	8	0	0	0	0
<i>Hyaloscypha</i> sp.	leaf/fruit/seed pathogen	98.51%	0	0	0	0	4
<i>Hyaloscypha variabilis</i>	leaf/fruit/seed pathogen	97.66%	0	0	0	0	2
<i>Hygrocybe acutoconica</i>	root-associated	98.24% $\pm$ 1.09	0	4	8	0	60
<i>Hygrocybe cantharellus</i>	root-associated	99.4% $\pm$ 0.28	0	0	0	102	1
<i>Hygrocybe chlorophana</i>	root-associated	97.23%	0	0	0	52	0
<i>Hygrocybe reidii</i>	root-associated	98.53% $\pm$ 1.24	0	0	0	2343	1
<i>Hygrocybe</i> sp.	root-associated	97.85% $\pm$ 1.34	2	0	10	0	5
<i>Hymenochaete curtisii</i>	wood pathogen	99.21%	0	0	0	2	0
<i>Hymenoscyphus imberbis</i>	leaf/fruit/seed pathogen	96.54% $\pm$ 0.27	4551	24	10	3	3
<i>Hymenoscyphus</i> sp.	leaf/fruit/seed pathogen	97.99% $\pm$ 0.73	0	2	0	0	3
<i>Immersidiscosia eucalypti</i>	leaf/fruit/seed pathogen	100%	12	0	0	0	0
<i>Inocutis rheades</i>	wood pathogen	99.20%	0	0	0	0	2
<i>Kluyveromyces marxianus</i>	opportunistic human parasite	100%	7	0	0	0	0
<i>Knufia marmoricola</i>	leaf/fruit/seed pathogen, opportunistic animal parasite	96.67%	6	0	0	0	0
<i>Knufia perforans</i>	leaf/fruit/seed pathogen, opportunistic animal parasite	95.04%	22	0	0	0	0
<i>Knufia</i> sp.	leaf/fruit/seed pathogen, opportunistic animal parasite	98.27% $\pm$ 1.36	240	70	0	0	1
<i>Knufia tsunedae</i>	leaf/fruit/seed pathogen, opportunistic animal parasite	98.51% $\pm$ 1.15	1212	34	12	0	0
<i>Kochiomyces dichotomus</i>	algal parasite	99.4% $\pm$ 0.84	12	0	0	0	0
<i>Kochiomyces</i> sp.	algal parasite	98.41% $\pm$ 0.4	0	4	0	0	0
<i>Kordyana</i> sp.	leaf/fruit/seed pathogen	100%	12	0	0	0	0
<i>Laetiporus</i> sp.	wood pathogen	99.4% $\pm$ 0.28	1	0	1	0	0
<i>Lecanicillium flavidum</i>	invertebrate parasite	100%	0	0	0	0	14
<i>Lecanicillium fungicola</i>	invertebrate parasite	99.77% $\pm$ 0.33	0	7	0	4	0
<i>Lecanicillium fusisporum</i>	invertebrate parasite	100%	0	0	0	1	0
<i>Lecanicillium psalliotae</i>	invertebrate parasite	99.31% $\pm$ 0.33	1	7	1	0	0
<i>Leohumicola minima</i>	root-associated	99.5% $\pm$ 0	0	0	2	1	0
<i>Leohumicola</i> sp.	root-associated	100%	0	0	0	0	4
<i>Leptobacillium leptobactrum</i>	invertebrate parasite	99.21% $\pm$ 0.54	0	10	8	9	50
<i>Leptonia</i> sp.	root-associated	98.80%	0	0	1	0	0
<i>Leucothecium emdenii</i>	invertebrate parasite	96.05%	0	1	0	0	0
<i>Lophodermium</i> sp.	leaf/fruit/seed pathogen	97.65%	1	0	0	0	0
<i>Maasoglossum aseptatum</i>	root-associated	99.77% $\pm$ 0.33	0	0	2	0	1
<i>Macrophomina phaseolina</i>	root pathogen	100%	9	0	0	0	0
<i>Malassezia arunalokei</i>	root-associated, animal-associated/opportunistic human parasite	100%	9	0	0	0	0
<i>Malassezia globosa</i>	root-associated, animal-associated/opportunistic human parasite	99.60%	1	0	1	0	0
<i>Malassezia restricta</i>	root-associated, animal-associated/opportunistic human parasite	99.8% $\pm$ 0.28	2	0	0	7	1
<i>Malassezia</i> sp.	root-associated, animal-associated/opportunistic human parasite	99.2% $\pm$ 0.56	1	0	0	0	1
<i>Melanchlenus</i> sp.	opportunistic human parasite	98.31%	6	0	0	0	0

Metacordyceps chlamydosporia	animal parasite	98.31% ± 0.34	61	0	0	0	0
Metacordyceps sp.	animal parasite	99.58%	1	0	0	0	0
Metarhizium anisopliae	animal parasite	98.39%	0	9	5	0	0
Metarhizium brunneum	animal parasite	97.6% ± 0.39	20	364	736	608	5
Metarhizium gaoligongense	animal parasite	100%	0	0	1	0	0
Metarhizium sp.	animal parasite	99.29% ± 0.93	46	1	56	3	74
Microascus albonigrescens	leaf/fruit/seed pathogen, opportunistic human parasite	98.32%	2	0	0	0	0
Microcyclospora malicola	leaf/fruit/seed pathogen	99.51%	0	0	1	0	0
Microcyclospora sp.	leaf/fruit/seed pathogen	99.02%	0	2	0	0	0
Microdochium colombiense	leaf/fruit/seed pathogen	96.67%	4	0	0	0	0
Microdochium neoqueenlandicum	leaf/fruit/seed pathogen	100%	1	0	0	0	0
Microdochium phragmitis	leaf/fruit/seed pathogen	98.63%	1	0	0	0	0
Microdochium poae	leaf/fruit/seed pathogen	97.08%	2	0	0	0	0
Microdochium sorghi	leaf/fruit/seed pathogen	99.11%	11	0	0	0	0
Moesziomyces antarcticus	leaf/fruit/seed pathogen	98.81%	3	0	0	0	0
Moesziomyces aphidis	leaf/fruit/seed pathogen	99.6% ± 0.56	12	0	0	0	0
Mollisia albogrisea	leaf/fruit/seed pathogen	100%	0	0	0	2	0
Mollisia sp.	leaf/fruit/seed pathogen	96.49% ± 0.23	8	0	0	0	0
Monochaetia castaneae	leaf/fruit/seed pathogen	99.53%	5	0	0	0	2
Monochaetia dimorphospora	leaf/fruit/seed pathogen	99.10%	2	0	0	0	0
Monochaetia ilicis	leaf/fruit/seed pathogen	97.98% ± 0.32	0	0	0	0	2
Monochaetia sinensis	leaf/fruit/seed pathogen	99.10%	1	0	0	0	0
Monographella sp.	leaf/fruit/seed pathogen	99.02% ± 0.7	3	0	0	0	0
Monosporascus sp.	leaf/fruit/seed pathogen	97.33%	2	0	0	0	0
Mortierella alliacea	root-associated, opportunistic human parasite	99.43% ± 0.51	0	12	71	58	307
Mortierella ambigua	root-associated, opportunistic human parasite	99.21%	11	0	0	0	0
Mortierella angusta	root-associated, opportunistic human parasite	99.7% ± 0.2	240	71	53	11	36
Mortierella antarctica	root-associated, opportunistic human parasite	97.61%	3	0	0	0	0
Mortierella bainieri	root-associated, opportunistic human parasite	99.8% ± 0.28	0	3	5	0	1
Mortierella basiparvispora	root-associated, opportunistic human parasite	98.41% ± 0.63	0	24	71	6	5
Mortierella bisporalis	root-associated, opportunistic human parasite	98.81% ± 1.13	0	1	0	1	0
Mortierella calciphila	root-associated, opportunistic human parasite	99.21% ± 0	0	1	0	1	0
Mortierella fatshederae	root-associated, opportunistic human parasite	98.80%	16	0	0	0	0
Mortierella gemmifera	root-associated, opportunistic human parasite	98.57% ± 1.45	0	7	11	32	560
Mortierella hypsichladia	root-associated, opportunistic human parasite	98.41%	0	0	2	0	0
Mortierella indohii	root-associated, opportunistic human parasite	100%	1	0	0	0	0
Mortierella macrocystis	root-associated, opportunistic human parasite	98.71% ± 1.61	1	440	457	302	825
Mortierella pulchella	root-associated, opportunistic human parasite	98.8% ± 1.05	2	9	33	67	808
Mortierella reticulata	root-associated, opportunistic human parasite	100%	2	0	0	0	0
Mortierella sp.	root-associated, opportunistic human parasite	98.85% ± 0.88	1780	2353	2434	2137	3061
Mortierella tsukubaensis	root-associated, opportunistic human parasite	99.47% ± 0.23	0	7	5	0	0
Mucor abundans	opportunistic human parasite	97.59% ± 0.93	0	0	0	1	11
Mucor circinelloides	opportunistic human parasite	98.96% ± 0.86	147	0	0	0	0
Mucor griseocyaneus	opportunistic human parasite	97.90%	4	1	0	0	0
Mucor hiemalis	opportunistic human parasite	98.01% ± 0.63	45	0	0	0	0

<i>Mucor inaequisporus</i>	opportunistic human parasite	98.67%	0	0	0	0	26
<i>Mucor koreanus</i>	opportunistic human parasite	99.60%	10	0	0	0	0
<i>Mucor lusitanicus</i>	opportunistic human parasite	100%	7	0	0	0	0
<i>Mucor minutus</i>	opportunistic human parasite	99.20%	0	2	0	0	0
<i>Mucor moelleri</i>	opportunistic human parasite	99.5% ± 0.32	141	1	2	0	3
<i>Mucor racemosus</i>	opportunistic human parasite	99.09% ± 0.82	15	0	3	0	0
<i>Mucor silvaticus</i>	opportunistic human parasite	99.06% ± 0.23	0	3	0	3	10
<i>Mucor</i> sp.	opportunistic human parasite	99.05% ± 0.99	0	43	2	0	31
<i>Mycena aetites</i>	leaf/fruit/seed pathogen	97.22%	0	1	0	0	0
<i>Mycena albiceps</i>	leaf/fruit/seed pathogen	99.03% ± 0.39	0	43	8	191	13
<i>Mycena alcalina</i>	leaf/fruit/seed pathogen	99.60%	0	0	0	0	16
<i>Mycena alphitophora</i>	leaf/fruit/seed pathogen	98.42%	0	1	0	0	0
<i>Mycena epipterygia</i>	leaf/fruit/seed pathogen	99.60%	0	32	0	0	26
<i>Mycena griseoviridis</i>	leaf/fruit/seed pathogen	98.42% ± 0.32	1	15	3	0	8
<i>Mycena leptoccephala</i>	leaf/fruit/seed pathogen	99.60%	453	281	0	0	0
<i>Mycena meliigena</i>	leaf/fruit/seed pathogen	99.4% ± 0.28	1	0	1	0	0
<i>Mycena metata</i>	leaf/fruit/seed pathogen	99.34% ± 0.61	0	58	682	13	0
<i>Mycena pura</i>	leaf/fruit/seed pathogen	99.6% ± 0.56	0	0	0	12	9
<i>Mycena purpureofusca</i>	leaf/fruit/seed pathogen	98.96% ± 0.22	0	0	45	15	44
<i>Mycena rebaudengoi</i>	leaf/fruit/seed pathogen	99.2% ± 0.56	10	5	0	0	0
<i>Mycena rosea</i>	leaf/fruit/seed pathogen	100%	5	0	0	0	0
<i>Mycena sanguinolenta</i>	leaf/fruit/seed pathogen	98.71% ± 1.16	0	68	948	24	2
<i>Mycena</i> sp.	leaf/fruit/seed pathogen	98.81% ± 0.65	233	343	803	2	796
<i>Mycena stylobates</i>	leaf/fruit/seed pathogen	100%	8	0	0	0	0
<i>Mycena yuezhuoi</i>	leaf/fruit/seed pathogen	98.01%	0	0	0	1	0
<i>Myriangium</i> sp.	arthropod parasite	98.69% ± 1.04	6	2	3	0	2
<i>Myriosclerotinia curreyana</i>	leaf/fruit/seed pathogen	96.38% ± 0.28	158	3	93	5	2
<i>Myxotrichum cancellatum</i>	root-associated	99.51%	0	0	0	4	0
<i>Nannizzia gypsea</i>	opportunistic human parasite	99.8% ± 0.28	5	0	0	0	0
<i>Nannizziopsis mirabilis</i>	animal parasite	99.55%	5	0	0	0	0
<i>Nectria ramulariae</i>	leaf/fruit/seed pathogen	99.77% ± 0.32	24	0	0	0	0
<i>Nectria</i> sp.	leaf/fruit/seed pathogen	99.71% ± 0.25	1	1	0	1	0
<i>Neosascochyta desmazieri</i>	leaf/fruit/seed pathogen	98.57% ± 1.29	750	0	0	1	0
<i>Neosascochyta tardicrescens</i>	leaf/fruit/seed pathogen	98.57%	2	0	0	0	0
<i>Neodevriesia imbrexigena</i>	leaf/fruit/seed pathogen	100%	4	0	0	0	0
<i>Neonectria major</i>	leaf/fruit/seed pathogen	96.86%	2	0	0	0	0
<i>Neopestalotiopsis hispanica</i>	leaf/fruit/seed pathogen	100%	3	0	0	0	0
<i>Neophaeococcomyces aloes</i>	leaf/fruit/seed pathogen	98.40%	3	0	0	0	0
<i>Neophaeococcomyces</i> sp.	leaf/fruit/seed pathogen	100%	0	1	0	0	0
<i>Nigrograna cangshanensis</i>	animal parasite	97.55% ± 0.26	41	0	0	0	0
<i>Nigrograna jinghongensis</i>	animal parasite	97.57%	1	0	0	0	0
<i>Ochroconis</i> sp.	leaf/fruit/seed pathogen, opportunistic human parasite	98.6% ± 1.34	129	236	0	19	9
<i>Oidiodendron periconioides</i>	root-associated	97.2% ± 2.43	6	63	74	14	231
<i>Oidiodendron</i> sp.	root-associated	97.95% ± 1.19	0	29	92	73	75
<i>Olpidiaster brassicae</i>	root pathogen	98.89% ± 0.59	55	0	0	0	0

<i>Olpidium</i> sp.	leaf/fruit/seed pathogen,algal parasite	98.41%	2	0	0	0	0
<i>Ovicillium subglobosum</i>	arthropod parasite	99.77% ± 0.33	0	2	0	0	3
<i>Paecilomyces</i> sp.	invertebrate parasite	99.14%	9	0	0	0	0
<i>Paecilomyces subglobosus</i>	invertebrate parasite	97.48%	8	0	0	0	0
<i>Paecilomyces zollerniae</i>	invertebrate parasite	97.79% ± 1.24	18	0	0	0	0
<i>Paracladophialophora</i> sp.	leaf/fruit/seed pathogen	98.84% ± 0.33	0	0	0	0	3
<i>Paracremonium binnewijzendii</i>	animal parasite/opportunistic human parasite	96.58%	2	0	0	0	0
<i>Paraphoma ledniceana</i>	wood pathogen	99.45% ± 0.49	303	0	0	0	0
<i>Paraphoma variabilis</i>	wood pathogen	99.05%	3	0	0	0	0
<i>Paraphyton cookei</i>	opportunistic human parasite	99.2% ± 0.69	11	0	0	0	0
<i>Parascedosporium putredinis</i>	opportunistic human parasite	98.79% ± 0.75	39	0	0	0	0
<i>Parastagonospora poae</i>	leaf/fruit/seed pathogen	97.58% ± 0	4	1	0	0	0
<i>Parastagonospora poagena</i>	leaf/fruit/seed pathogen	99.03%	1	0	0	0	0
<i>Peltaster fruticola</i>	unspecified plant pathogen	98.53% ± 1.42	0	3	7	0	3
<i>Peltaster gemmifer</i>	unspecified plant pathogen	100%	2	0	3	0	0
<i>Penicillium aethiopicum</i>	opportunistic human parasite	97.83% ± 3.07	11	0	0	0	0
<i>Penicillium arianae</i>	opportunistic human parasite	100% ± 0	0	2	2	3	1
<i>Penicillium bialowiezense</i>	opportunistic human parasite	98.73% ± 0.75	2	1	0	0	0
<i>Penicillium bissettii</i>	opportunistic human parasite	100%	0	1	0	0	0
<i>Penicillium cainii</i>	opportunistic human parasite	99.56%	0	2	0	0	0
<i>Penicillium catalanicum</i>	opportunistic human parasite	97.95% ± 1.38	0	43	60	0	2
<i>Penicillium catenatum</i>	opportunistic human parasite	99.54%	0	1	4	0	0
<i>Penicillium citrinum</i>	opportunistic human parasite	100%	28	0	0	0	0
<i>Penicillium cryptum</i>	opportunistic human parasite	99.2% ± 0.78	131	55	3	0	0
<i>Penicillium granulatum</i>	opportunistic human parasite	99.54%	0	0	56	0	10
<i>Penicillium hermansii</i>	opportunistic human parasite	93.6% ± 0.27	11	0	0	0	0
<i>Penicillium improvisum</i>	opportunistic human parasite	100%	3	17	22	0	0
<i>Penicillium lividum</i>	opportunistic human parasite	100%	0	0	0	0	1
<i>Penicillium miczynskii</i>	opportunistic human parasite	99.31% ± 0.98	0	3	2	6	6
<i>Penicillium neoherquei</i>	opportunistic human parasite	100%	0	1	22	0	0
<i>Penicillium parvulum</i>	opportunistic human parasite	98.25%	10	0	0	0	0
<i>Penicillium penicillioides</i>	opportunistic human parasite	98.86% ± 0.32	0	0	0	5	2
<i>Penicillium roseopurpureum</i>	opportunistic human parasite	98.65% ± 0.01	29	0	0	0	0
<i>Penicillium senticosum</i>	opportunistic human parasite	99.07%	14	1	0	18	4
<i>Penicillium</i> sp.	opportunistic human parasite	98.55% ± 1.71	1482	465	345	707	68
<i>Penicillium sublectaticum</i>	opportunistic human parasite	100%	0	8	0	0	0
<i>Penicillium thomii</i>	opportunistic human parasite	100%	94	5	2	7	22
<i>Penicillium variratense</i>	opportunistic human parasite	100%	6	0	0	0	0
<i>Penicillium verhagenii</i>	opportunistic human parasite	99.32% ± 0.32	0	6	0	0	17
<i>Penicillium zhuangii</i>	opportunistic human parasite	100%	0	0	4	0	0
<i>Peniophora cinerea</i>	wood pathogen	98.12% ± 0.37	4	14	11	1	1
<i>Peniophora</i> sp.	wood pathogen	96.34% ± 0	0	0	2	0	0
<i>Periconia celtidis</i>	leaf/fruit/seed pathogen	100%	0	3	0	0	0
<i>Periconia macrospinoso</i>	leaf/fruit/seed pathogen	98.79% ± 0.68	63	0	1	0	0
<i>Periconia</i> sp.	leaf/fruit/seed pathogen	97.32%	1	0	0	0	0

<i>Peroneutypa scoparia</i>	leaf/fruit/seed pathogen	100%	2	0	0	0	0
<i>Pestalotiopsis chiaroscuro</i>	leaf/fruit/seed pathogen	98.75%	2	0	0	0	0
<i>Pestalotiopsis iberica</i>	leaf/fruit/seed pathogen	99.58%	116	0	3	0	0
<i>Pestalotiopsis jesteri</i>	leaf/fruit/seed pathogen	95.10%	0	0	0	0	1
<i>Pestalotiopsis macadamiae</i>	leaf/fruit/seed pathogen	98.73% ± 0.6	78	3	0	0	0
<i>Pestalotiopsis rhododendri</i>	leaf/fruit/seed pathogen	99.79% ± 0.3	2	0	1	0	0
<i>Petriella guttulata</i>	opportunistic animal parasite	99.58% ± 0.42	14	2	0	0	0
<i>Petriella sordida</i>	opportunistic animal parasite	100%	44	0	0	0	0
<i>Pezicula ericae</i>	leaf/fruit/seed pathogen	95.86% ± 0.45	21	13	2	4	6
<i>Pezicula heterochroma</i>	leaf/fruit/seed pathogen	95.88% ± 0.23	416	23	0	67	0
<i>Pezicula</i> sp.	leaf/fruit/seed pathogen	98.28% ± 0.35	212	3	3	0	0
<i>Pezizella</i> sp.	leaf/fruit/seed pathogen	95.59%	0	0	18	0	0
<i>Pezoloma ericae</i>	leaf/fruit/seed pathogen	97.07%	0	0	7	0	0
<i>Phaeobotryon</i> sp.	leaf/fruit/seed pathogen	99.77% ± 0.33	13	2	0	0	0
<i>Phaeomoniella</i> sp.	leaf/fruit/seed pathogen	100%	0	1	0	0	0
<i>Phaeothecoidiella illinoisensis</i>	leaf/fruit/seed pathogen	100%	0	1	0	0	0
<i>Phialea</i> sp.	leaf/fruit/seed pathogen	100%	0	0	0	0	3
<i>Phialemonium atrogiseum</i>	animal parasite	99.23% ± 0.22	25	0	0	0	0
<i>Phialemonium inflatum</i>	animal parasite	98.54% ± 1.44	1119	0	0	0	0
<i>Phialemonium</i> sp.	animal parasite	96.45% ± 2.38	34	0	0	0	0
<i>Phialocephala glacialis</i>	root-associated	97.38% ± 0.96	0	0	0	0	37
<i>Phialocephala helenae</i>	root-associated	97.37% ± 0.91	215	70	105	36	154
<i>Phialocephala repens</i>	root-associated	98.59% ± 0.67	139	12	4	0	0
<i>Phialophora cyclaminis</i>	leaf/fruit/seed pathogen, animal parasite	99% ± 0.45	1340	0	2	0	0
<i>Phlogicylindrium</i> sp.	leaf/fruit/seed pathogen	99.34% ± 0.31	0	0	0	1	1
<i>Phliota adiposa</i>	wood pathogen	98.41%	0	0	0	0	2
<i>Phliota gummosa</i>	wood pathogen	99.60%	1	0	0	0	0
<i>Phliota highlandensis</i>	wood pathogen	100%	0	0	2	0	0
<i>Phliota lenta</i>	wood pathogen	99.8% ± 0.28	0	0	0	0	2
<i>Phliota mixta</i>	wood pathogen	99.6% ± 0	0	0	0	0	17
<i>Phliota terrestris</i>	wood pathogen	98.4% ± 1.13	2	0	0	0	1
<i>Phoma</i> sp.	leaf/fruit/seed pathogen	98.56%	1	0	0	0	0
<i>Pichia myanmarensis</i>	animal parasite/opportunistic human parasite	100%	3	0	0	0	0
<i>Plectosphaerella cucumerina</i>	leaf/fruit/seed pathogen, nematophagous	99.11%	10	0	0	0	0
<i>Plectosphaerella niemeijerarum</i>	leaf/fruit/seed pathogen, nematophagous	99.33% ± 0.31	43	0	0	0	0
<i>Plectosphaerella oratosquillae</i>	leaf/fruit/seed pathogen, nematophagous	98.29%	2	0	0	0	0
<i>Plectosphaerella slobbergiarum</i>	leaf/fruit/seed pathogen, nematophagous	97.33% ± 0.63	185	0	0	0	0
<i>Pleurophoma</i> sp.	wood pathogen	99.05%	2	0	0	0	0
<i>Polyscytalum neofecundissimum</i>	leaf/fruit/seed pathogen	98.01%	0	6	0	0	0
<i>Polyscytalum pinicola</i>	leaf/fruit/seed pathogen	98.41%	0	0	0	0	14
<i>Polyscytalum</i> sp.	leaf/fruit/seed pathogen	99.78% ± 0.31	0	0	0	0	23
<i>Polyscytalum vaccinii</i>	leaf/fruit/seed pathogen	97.71% ± 0.68	0	0	1	5	10
<i>Powellomyces</i> sp.	algal parasite	98.81% ± 0.8	14	0	0	0	0
<i>Pseudallescheria boydii</i>	opportunistic human parasite	98.92% ± 0.62	81	0	0	0	0
<i>Pseudallescheria fimeti</i>	opportunistic human parasite	98.21%	1	0	0	0	0

<i>Pseudocoleophoma</i> sp.	leaf/fruit/seed pathogen	99.03% ± 0.68	7	0	0	0	0
<i>Pseudogymnoascus alpinus</i>	opportunistic animal parasite <i>G. destructans</i>	99.16%	0	5	0	0	2
<i>Pseudogymnoascus appendiculatus</i>	opportunistic animal parasite <i>G. destructans</i>	98.63% ± 0	338	0	0	0	0
<i>Pseudogymnoascus roseus</i>	opportunistic animal parasite <i>G. destructans</i>	99.08%	0	0	1	0	0
<i>Pseudomicrostroma glucosiphilum</i>	leaf/fruit/seed pathogen	99.6% ± 0.4	7	0	0	0	0
<i>Pseudomicrostroma phylloplanum</i>	leaf/fruit/seed pathogen	99.21% ± 0.4	15	11	5	1	0
<i>Pseudopithomyces rosae</i>	leaf/fruit/seed pathogen	100%	13	0	0	0	0
<i>Puccinia coronata</i>	leaf/fruit/seed pathogen	100%	4	0	0	0	0
<i>Puccinia striiformis</i>	leaf/fruit/seed pathogen	99.8% ± 0.28	6	0	0	0	0
<i>Purpureocillium lilacinum</i>	arthropod parasite	99.38% ± 0.71	103	1	1	1	0
<i>Ramariopsis flavescens</i>	root-associated	99.21%	0	0	1	0	0
<i>Ramariopsis</i> sp.	root-associated	99.16% ± 1	0	8	2	8	30
<i>Ramularia simplex</i>	leaf/fruit/seed pathogen	100%	3	0	0	0	0
<i>Ramulispora sorghiphila</i>	leaf/fruit/seed pathogen	97.73%	8	0	0	0	0
<i>Rasamsonia emersonii</i>	opportunistic human parasite	100% ± 0	11	0	0	0	0
<i>Rasamsonia</i> sp.	opportunistic human parasite	96.46%	0	0	32	0	0
<i>Rhinocladia quercus</i>	root-associated, animal parasite/opportunistic human parasite	99.4% ± 0.84	0	2	8	0	0
<i>Rhinocladia</i> sp.	root-associated, animal parasite/opportunistic human parasite	98.15% ± 1.02	137	23	36	0	17
<i>Rhizidium phycophilum</i>	algal parasite	99.54% ± 0.39	0	4	5	7	16
<i>Rhizidium</i> sp.	algal parasite	99.28% ± 0.7	0	2	5	6	17
<i>Rhizophlyctis rosea</i>	algal parasite	99.09% ± 0.83	74	5	0	0	0
<i>Rhizophlyctis</i> sp.	algal parasite	98.94% ± 1.05	22	4	0	0	0
<i>Rhizophydium</i> sp.	algal parasite	98.95% ± 0.89	106	69	23	10	1
<i>Rhizopus arrhizus</i>	leaf/fruit/seed pathogen, opportunistic human parasite	100%	9	0	0	0	0
<i>Rhodotorula dairenensis</i>	opportunistic human parasite	99.8% ± 0.28	11	0	0	0	0
<i>Rhodotorula graminis</i>	opportunistic human parasite	100%	5	0	0	0	0
<i>Rhodotorula mucilaginoso</i>	opportunistic human parasite	99.6% ± 0.4	7	3	0	0	0
<i>Rhodotorula</i> sp.	opportunistic human parasite	99.12% ± 1.11	60	0	0	5	0
<i>Rhodotorula toruloides</i>	opportunistic human parasite	100%	10	0	0	0	0
<i>Rickenella indica</i>	leaf/fruit/seed pathogen	97.98%	0	3	0	0	0
<i>Rosellinia subiculata</i>	wood pathogen	99.35% ± 0.3	0	0	0	0	6
<i>Sagenomella diversispora</i>	opportunistic human parasite	99.39% ± 0.5	373	277	223	260	179
<i>Sagenomella oligospora</i>	opportunistic human parasite	99.39% ± 0.61	78	0	0	0	0
<i>Sagenomella verticillata</i>	opportunistic human parasite	98.42% ± 1.62	48	40	240	132	265
<i>Saksenaea</i> sp.	opportunistic human parasite	97.27%	3	0	0	0	0
<i>Samsoniella hepiali</i>	invertebrate parasite	100%	1	2	1	0	3
<i>Scedosporium boydii</i>	opportunistic human parasite	99.2% ± 0.56	14	0	0	0	0
<i>Scedosporium dehoogii</i>	opportunistic human parasite	100%	330	0	0	0	0
<i>Scedosporium prolificans</i>	opportunistic human parasite	98.55% ± 0.84	28	0	0	0	0
<i>Schizophyllum commune</i>	opportunistic human parasite	99.20%	0	4	0	0	0
<i>Schwannomyces occidentalis</i>	opportunistic human parasite	100%	31	0	0	0	0
<i>Scleromitrla calthicola</i>	leaf/fruit/seed pathogen	97.7% ± 0.87	18	1	0	0	0
<i>Sclerostagonospora ericae</i>	leaf/fruit/seed pathogen	98.58%	2	0	0	0	0
<i>Sclerostagonospora</i> sp.	leaf/fruit/seed pathogen	98.61% ± 1.18	1724	0	0	1	19
<i>Scolecobasidium bacilliforme</i>	leaf/fruit/seed pathogen, animal parasite	99.79% ± 0.3	4	0	0	0	0

<i>Scolecobasidium constrictum</i>	leaf/fruit/seed pathogen, animal parasite	99.60%	4	0	0	0	0
<i>Scolecobasidium ramosum</i>	leaf/fruit/seed pathogen, animal parasite	100%	2	0	0	0	0
<i>Scolecobasidium</i> sp.	leaf/fruit/seed pathogen, animal parasite	98.66% ± 0.83	0	2	27	0	11
<i>Scytalidium album</i>	opportunistic human parasite	99.02% ± 0	0	0	8	2	2
<i>Scytalidium lignicola</i>	opportunistic human parasite	100%	3	0	0	0	0
<i>Scytalidium</i> sp.	opportunistic human parasite	99.17% ± 0.69	126	0	0	0	0
<i>Seimatosporium rosigenum</i>	leaf/fruit/seed pathogen	97.79%	0	0	1	0	0
<i>Seiridium aquaticum</i>	leaf/fruit/seed pathogen	100%	4	0	0	0	0
<i>Septobasidium</i> sp.	arthropod parasite	96.02% ± 0.56	6	2	0	0	0
<i>Setomelanomma holmii</i>	wood pathogen	99.29% ± 1.01	13	0	0	0	0
<i>Setophaeosphaeria badalingensis</i>	leaf/fruit/seed pathogen	99.76% ± 0.34	18	0	0	0	0
<i>Setophoma</i> sp.	root pathogen	97.82% ± 1.87	4	0	0	0	0
<i>Simplicillium aogashimaense</i>	invertebrate parasite	100%	7	0	0	0	0
<i>Simplicillium</i> sp.	invertebrate parasite	99.59%	0	0	1	0	0
<i>Sphaerellopsis filum</i>	leaf/fruit/seed pathogen	100%	1	0	0	0	0
<i>Spiromastix</i> sp.	opportunistic animal parasite	98.74%	28	0	0	0	0
<i>Sporopachydermia lactativora</i>	other plant pathogen, opportunistic human parasite	99.60%	4	0	0	0	0
<i>Sporothrix sclerotialis</i>	wood pathogen, opportunistic human parasite	98.04% ± 0.31	156	0	0	0	0
<i>Stachylidium bicolor</i>	animal parasite	100%	1	0	0	0	0
<i>Stagonospora heteroderae</i>	leaf/fruit/seed pathogen	99.52% ± 0.39	242	0	0	0	0
<i>Stagonospora</i> sp.	leaf/fruit/seed pathogen	98.72% ± 1.46	1	0	3	0	0
<i>Stagonospora trichophoricola</i>	leaf/fruit/seed pathogen	97.82%	1	0	0	0	0
<i>Stagonosporopsis loticola</i>	leaf/fruit/seed pathogen	99.56% ± 0.62	30	1	0	0	0
<i>Stagonosporopsis valerianellae</i>	leaf/fruit/seed pathogen	98.25%	277	0	0	0	0
<i>Stagonosporopsis weymaniae</i>	leaf/fruit/seed pathogen	99.13%	19	0	0	0	0
<i>Strelitziana albiziae</i>	leaf/fruit/seed pathogen	98.98% ± 0.67	3	0	0	0	0
<i>Stromatinia</i> sp.	other plant pathogen	99.52%	0	0	4	0	0
<i>Talaromyces albisclerotius</i>	opportunistic human parasite	99.52%	0	48	0	0	0
<i>Talaromyces albobiverticillius</i>	opportunistic human parasite	99.52%	3	0	0	0	0
<i>Talaromyces assiutensis</i>	opportunistic human parasite	98.85% ± 0.97	35	0	0	0	0
<i>Talaromyces bannicus</i>	opportunistic human parasite	98.47% ± 0.94	2	3	11	1	1
<i>Talaromyces calidominioluteus</i>	opportunistic human parasite	97.76% ± 0.86	116	6	6	0	7
<i>Talaromyces columbinus</i>	opportunistic human parasite	100%	1	0	0	0	0
<i>Talaromyces coprophilus</i>	opportunistic human parasite	98.17% ± 0.81	844	54	16	4	2
<i>Talaromyces domesticus</i>	opportunistic human parasite	99.52% ± 0.48	174	0	0	0	0
<i>Talaromyces germanicus</i>	opportunistic human parasite	97.94% ± 0.97	0	0	1	0	1
<i>Talaromyces infraolivaceus</i>	opportunistic human parasite	97.50%	7	2	3	0	0
<i>Talaromyces juglandicola</i>	opportunistic human parasite	97.11%	0	5	0	0	0
<i>Talaromyces minioluteus</i>	opportunistic human parasite	99.31% ± 0.32	31	0	15	0	0
<i>Talaromyces neofusisporus</i>	opportunistic human parasite	99.76% ± 0.33	72	0	0	0	0
<i>Talaromyces proteolyticus</i>	opportunistic human parasite	99.34% ± 0.93	0	36	29	15	0
<i>Talaromyces purpureogenus</i>	opportunistic human parasite	100%	5	0	0	0	0
<i>Talaromyces rubicundus</i>	opportunistic human parasite	98.86% ± 0.32	43	0	7	0	0
<i>Talaromyces rubrifaciens</i>	opportunistic human parasite	98.58% ± 1.22	20	71	41	7	8
<i>Talaromyces</i> sp.	opportunistic human parasite	99.31% ± 0.26	74	0	0	0	0

<i>Talaromyces subaurantiacus</i>	opportunistic human parasite	100%	1	0	0	0	0
<i>Talaromyces subtropicalis</i>	opportunistic human parasite	100%	57	0	0	0	0
<i>Talaromyces wortmannii</i>	opportunistic human parasite	99.56%	8	0	0	0	0
<i>Talaromyces xishaensis</i>	opportunistic human parasite	99.05%	4	0	0	0	0
<i>Talaromyces yunnanensis</i>	opportunistic human parasite	99.52% ± 0.68	1187	0	0	10	0
<i>Taphrina caerulescens</i>	leaf/fruit/seed pathogen	99.4% ± 0.28	4	0	0	0	0
<i>Taphrina inositophila</i>	leaf/fruit/seed pathogen	99.4% ± 0.28	3	0	0	0	0
<i>Thanatephorus</i> sp.	leaf/fruit/seed pathogen	98.8% ± 0.56	40	0	0	0	0
<i>Thoreauomyces humboldtii</i>	algal parasite	100%	0	4	0	0	0
<i>Tolypocladium album</i>	animal parasite	100%	0	0	0	1	4
<i>Tolypocladium cylindrosporum</i>	animal parasite	99.07%	0	0	3	0	75
<i>Tolypocladium geodes</i>	animal parasite	99.77% ± 0.33	0	0	37	25	0
<i>Tolypocladium inegoense</i>	animal parasite	98.9% ± 0.72	0	6	3	40	12
<i>Tolypocladium inflatum</i>	animal parasite	99.53%	2	76	0	0	2
<i>Tolypocladium</i> sp.	animal parasite	97.07% ± 1.61	4	150	21	204	24
<i>Tolypocladium tropicale</i>	animal parasite	99.44% ± 0.43	2	552	134	51	0
<i>Toxicocladosporium irritans</i>	leaf/fruit/seed pathogen	99.03%	1	0	0	0	0
<i>Trichoderma achlamyosporum</i>	leaf/fruit/seed pathogen	98.33%	0	0	2	0	0
<i>Trichoderma asperellum</i>	leaf/fruit/seed pathogen	99.8% ± 0.29	0	0	0	16	132
<i>Trichoderma atroviride</i>	leaf/fruit/seed pathogen	100%	7	0	0	0	0
<i>Trichoderma fomicicola</i>	leaf/fruit/seed pathogen	99.55%	6	0	0	2	0
<i>Trichoderma hamatum</i>	leaf/fruit/seed pathogen	97.75% ± 0.29	43	19	45	34	0
<i>Trichoderma harzianum</i>	leaf/fruit/seed pathogen	99.38% ± 0.57	81	13	4	13	22
<i>Trichoderma minutisporum</i>	leaf/fruit/seed pathogen	100%	0	9	0	0	0
<i>Trichoderma neorufum</i>	leaf/fruit/seed pathogen	96.97% ± 0.28	0	0	0	5	3
<i>Trichoderma parapluliferum</i>	leaf/fruit/seed pathogen	100%	0	0	0	0	18
<i>Trichoderma peberdyi</i>	leaf/fruit/seed pathogen	97.45% ± 0.49	0	2	0	9	0
<i>Trichoderma pubescens</i>	leaf/fruit/seed pathogen	98.78% ± 0	0	87	18	31	0
<i>Trichoderma rodmanii</i>	leaf/fruit/seed pathogen	100%	0	0	0	0	2
<i>Trichoderma</i> sp.	leaf/fruit/seed pathogen	98.49% ± 1.13	1002	82	62	5	5
<i>Trichoderma stellatum</i>	leaf/fruit/seed pathogen	99.17% ± 0.18	52	46	1	19	1
<i>Trichoderma strictipile</i>	leaf/fruit/seed pathogen	100%	0	0	1	0	0
<i>Trichoderma strigosum</i>	leaf/fruit/seed pathogen	98.9% ± 0.31	9	0	1	0	0
<i>Trichoderma tsugarense</i>	leaf/fruit/seed pathogen	98.32%	3	0	0	0	0
<i>Trichoderma turrialbense</i>	leaf/fruit/seed pathogen	100%	26	0	0	0	0
<i>Trichoderma viride</i>	leaf/fruit/seed pathogen	98.85% ± 0.5	0	44	23	11	36
<i>Trichoderma yunnanense</i>	leaf/fruit/seed pathogen	99.19%	0	0	0	0	5
<i>Trichoglossum</i> sp.	root-associated	98.99% ± 0.86	0	0	0	17	0
<i>Trichomonascus vanleenenianus</i>	opportunistic human parasite	99.78% ± 0.31	26	0	0	0	0
<i>Trichophyton ajelloi</i>	animal parasite	98.73%	4	0	0	0	0
<i>Trichosporon asteroides</i>	animal parasite/opportunistic human parasite	99.78% ± 0.31	230	0	0	0	0
<i>Trichothecium crotocinigenum</i>	leaf/fruit/seed pathogen	99.14% ± 0	16	0	0	0	0
<i>Truncatella angustata</i>	leaf/fruit/seed pathogen	100%	126	0	0	0	0
<i>Tulasnella</i> sp.	root-associated	98.15% ± 1.08	20	0	3	0	1
<i>Umbelopsis angularis</i>	root-associated	99.3% ± 0.38	0	2	6	0	20

<i>Umbelopsis autotrophica</i>	root-associated	100%	7	0	20	0	0
<i>Umbelopsis changbaiensis</i>	root-associated	99.6% ± 0	0	0	0	101	37
<i>Umbelopsis isabellina</i>	root-associated	98.27% ± 1.06	0	31	57	31	215
<i>Umbelopsis ramanniana</i>	root-associated	99.12% ± 0.65	19	12	0	0	0
<i>Umbelopsis</i> sp.	root-associated	98.29% ± 1.01	2172	1366	984	738	1930
<i>Urocystis tritici</i>	leaf/fruit/seed pathogen	99.38% ± 0.29	8	0	0	0	0
<i>Ustilago nunavutica</i>	leaf/fruit/seed pathogen	96.28% ± 0.83	7	0	0	0	0
<i>Ustilago</i> sp.	leaf/fruit/seed pathogen	98.03% ± 1.08	33	0	0	0	0
<i>Ustilentyloma</i> sp.	leaf/fruit/seed pathogen	96.80%	1	0	0	0	0
<i>Valsa</i> sp.	leaf/fruit/seed pathogen	99.55% ± 0.64	10	0	0	0	0
<i>Venturia catenospora</i>	leaf/fruit/seed pathogen	96.38%	0	0	0	0	9
<i>Veronaea</i> sp.	leaf/fruit/seed pathogen, opportunistic animal parasite	97.35% ± 1.54	7	1	0	1	0
<i>Waitea arvalis</i>	leaf/fruit/seed pathogen	99.32% ± 0.85	146	0	0	0	0
<i>Wickerhamomyces anomalus</i>	opportunistic human parasite	99.18%	1	0	0	0	0
<i>Xanthothecium peruvianum</i>	opportunistic human parasite	99.77% ± 0.33	75	0	0	0	0
<i>Xenocylindrosporium</i> sp.	leaf/fruit/seed pathogen	99.06%	1	0	0	0	0
<i>Xenopyrenochaetopsis pratorum</i>	leaf/fruit/seed pathogen	98.38% ± 1.69	18	0	0	0	2
<i>Zygoascus biomembranicola</i>	opportunistic human parasite	99.33% ± 0.95	0	0	0	0	3

Table S5. Fungal pathogens detected in lower soil samples across the urbanization gradient. Numbers are sums of species counts normalized by rarefaction in lower soil (15-30 cm depth) samples of each tree type. % identity refers to the % match of ITS sequence from the tree microbiome dataset to the ITS sequence match in the UNITE database, which corresponded to a genus-level name match in the FungalTraits database.

Fungal Species	Pathogen Type	% Identity ($\pm$ standard deviation when >1 ASV sequence match)	Urban				
			Street Tree	Forest Edge	Forest Interior	Rural Forest Edge	Rural Forest Interior
Abortiporus biennis	root pathogen	99.8% $\pm$ 0.28	4	0	0	0	0
Acephala sp.	root-associated	97.65% $\pm$ 2.05	21	0	0	0	19
Acremonium persicinum	leaf/fruit/seed pathogen	100%	1	0	0	0	0
Acremonium sp.	leaf/fruit/seed pathogen	98.61%	5	0	0	0	0
Aequabiliella effusa	leaf/fruit/seed pathogen	98.62%	0	0	0	0	26
Akanthomyces muscarius	invertebrate parasite	99.69% $\pm$ 0.27	8	0	3	0	1
Alternaria angustiovoidea	leaf/fruit/seed pathogen	97.61% $\pm$ 1.22	80	5	0	14	2
Alternaria eichhorniae	leaf/fruit/seed pathogen	99.13%	108	7	0	12	27
Alternaria rosae	leaf/fruit/seed pathogen	100%	1	0	0	0	0
Alternaria subcucurbitae	leaf/fruit/seed pathogen	100%	20	0	0	0	0
Alternaria tropica	leaf/fruit/seed pathogen	100%	7	0	0	0	0
Aphanoascus keratinophilus	opportunistic human parasite	97.16% $\pm$ 0.47	30	0	0	0	0
Aphanoascus sp.	opportunistic human parasite	99.52%	0	1	0	0	0
Arachnomyces gracilis	animal parasite/opportunistic human parasite	100%	1	0	0	0	0
Arachnomyces minimus	animal parasite/opportunistic human parasite	100%	2	0	0	0	0
Arachnomyces sp.	animal parasite/opportunistic human parasite	97.15% $\pm$ 2.06	13	0	6	0	0
Armillaria borealis	wood pathogen	99.60%	3	0	0	0	0
Arthroderma insingulare	animal parasite/opportunistic human parasite	100%	3	0	0	0	0
Arthropis sp.	animal parasite	100%	38	5	6	4	0
Ascochyta sp.	leaf/fruit/seed pathogen	96.88%	1	0	0	0	0
Aspergillus fumigatus	animal parasite/opportunistic human parasite	99.58%	2	0	0	0	0
Aspergillus iizukae	animal parasite/opportunistic human parasite	98.71%	2	0	0	0	0
Aspergillus nutans	animal parasite/opportunistic human parasite	99.55%	22	2	0	0	0
Aspergillus piperis	animal parasite/opportunistic human parasite	99.55%	3	0	0	0	0
Aspergillus salwaensis	animal parasite/opportunistic human parasite	97.92%	0	0	2	0	0
Aspergillus sp.	animal parasite/opportunistic human parasite	100% $\pm$ 0	9	0	0	0	0
Aureobasidium pullulans	leaf/fruit/seed pathogen, animal parasite	98.92% $\pm$ 1.36	644	23	474	22	19
Beauveria bassiana	invertebrate parasite	98.48% $\pm$ 0.31	3	3	0	0	2
Beauveria caledonica	invertebrate parasite	100%	0	0	6	288	22
Beauveria pseudobassiana	invertebrate parasite	97.86%	3	31	0	0	0
Beauveria sp.	invertebrate parasite	99.16%	5	0	0	0	0
Biatrispora sp.	opportunistic human parasite	98.55%	0	0	0	0	2
Bipolaris eleusines	leaf/fruit/seed pathogen	99.57%	5	0	0	0	0
Bjerkandera sp.	wood pathogen	99.60%	1	0	0	0	0
Boeremia populi	leaf/fruit/seed pathogen	97.41%	20	0	0	0	0
Boletinellus meruloides	root-associated, arthropod-associated	99.60%	3	0	0	0	0
Botrytis caroliniana	leaf/fruit/seed pathogen	99.5% $\pm$ 0.71	1	0	0	3	67

<i>Bradymyces graniticola</i>	fish parasite	99.41% ± 0.26	50	0	0	0	0
<i>Cadophora</i> sp.	leaf/fruit/seed pathogen	99.01% ± 0.86	23	17	0	3	0
<i>Caliciopsis beckhausii</i>	leaf/fruit/seed pathogen	100%	0	0	0	0	4
<i>Caliciopsis</i> sp.	leaf/fruit/seed pathogen	100%	0	2	0	0	0
<i>Calyptrozyna</i> sp.	opportunistic human parasite	98.01%	0	2	0	0	2
<i>Candida albicans</i>	animal-associated/opportunistic human parasite	100%	2	0	0	0	0
<i>Candida railenensis</i>	animal-associated/opportunistic human parasite	100%	0	0	0	4	19
<i>Capronia epimyces</i>	animal parasite/opportunistic human parasite	99.19%	0	1	0	0	0
<i>Capronia pulcherrima</i>	animal parasite/opportunistic human parasite	99.17% ± 0	1	1	0	0	0
<i>Capronia semiimmersa</i>	animal parasite/opportunistic human parasite	97.97% ± 1.67	1	1	0	0	0
<i>Capronia</i> sp.	animal parasite/opportunistic human parasite	98.04% ± 1.03	18	896	1631	2277	1643
<i>Castanediella</i> sp.	leaf/fruit/seed pathogen	100%	0	0	0	0	1
<i>Catenulostroma hermanusense</i>	leaf/fruit/seed pathogen	97.55% ± 1.41	4	1	0	0	0
<i>Celosporium</i> sp.	leaf/fruit/seed pathogen	98.17%	42	0	0	0	0
<i>Ceratobasidium</i> sp.	leaf/fruit/seed pathogen	97.85% ± 1.13	41	1	0	0	22
<i>Chalara pseudoaffinis</i>	wood pathogen, leaf/fruit/seed pathogen	98.52%	0	3	0	0	0
<i>Chalara</i> sp.	wood pathogen, leaf/fruit/seed pathogen	99.05% ± 1	10	2	0	0	0
<i>Chloridium aseptatum</i>	root pathogen, opportunistic human parasite	98.61% ± 0.8	318	0	0	0	16
<i>Chloridium</i> sp.	root pathogen, opportunistic human parasite	98.62% ± 0.41	47	61	2	115	205
<i>Chloridium submersum</i>	root pathogen, opportunistic human parasite	98.85% ± 1.03	0	3	3	3	200
<i>Cladophialophora chaetospora</i>	animal parasite/opportunistic human parasite	97.98%	2	0	0	0	0
<i>Cladophialophora emmonsii</i>	animal parasite/opportunistic human parasite	99% ± 0.28	4	0	0	0	0
<i>Cladophialophora humicola</i>	animal parasite/opportunistic human parasite	98.68%	0	5	0	0	0
<i>Cladophialophora</i> sp.	animal parasite/opportunistic human parasite	98.36% ± 0.96	78	434	221	1337	1246
<i>Cladophialophora sylvestris</i>	animal parasite/opportunistic human parasite	99.76% ± 0.35	0	7	0	0	6
<i>Cladosporium austrohemisphaericum</i>	leaf/fruit/seed pathogen, animal parasite	96.83% ± 0.91	36	0	122	0	2
<i>Cladosporium domesticum</i>	leaf/fruit/seed pathogen, animal parasite	99.06%	0	0	23	0	0
<i>Cladosporium halotolerans</i>	leaf/fruit/seed pathogen, animal parasite	100% ± 0	1	1	22	1	7
<i>Cladosporium herbarum</i>	leaf/fruit/seed pathogen, animal parasite	97.44% ± 0.69	57	1	0	12	10
<i>Cladosporium</i> sp.	leaf/fruit/seed pathogen, animal parasite	97.89% ± 0.69	697	25	57	8	28
<i>Cladosporium sphaerospermum</i>	leaf/fruit/seed pathogen, animal parasite	99.69% ± 0.27	3	0	17	0	4
<i>Cladosporium velox</i>	leaf/fruit/seed pathogen, animal parasite	100%	2	0	0	0	0
<i>Clarireedia bennettii</i>	leaf/fruit/seed pathogen	98.53%	2	0	0	0	0
<i>Clavaria argillacea</i>	root-associated	100%	0	0	0	8	0
<i>Clavaria falcata</i>	root-associated	98.37%	0	1	0	0	0
<i>Clavaria flavipes</i>	root-associated	98.02% ± 0.4	0	0	0	23	0
<i>Clavaria</i> sp.	root-associated	98.62% ± 0.82	0	6	18	278	3
<i>Clavaria zollingeri</i>	root-associated	99.27% ± 0.16	0	0	0	439	70
<i>Clavulinopsis fusiformis</i>	root-associated	99.2% ± 0.56	0	0	0	0	593
<i>Clavulinopsis helvola</i>	root-associated	98.81%	0	0	61	0	0
<i>Clavulinopsis</i> sp.	root-associated	98.59% ± 1.32	0	11	0	19	20
<i>Clonostachys candelabrum</i>	leaf/fruit/seed pathogen, nematophagous	100%	0	5	2	24	0
<i>Clonostachys rosea</i>	leaf/fruit/seed pathogen, nematophagous	98.62% ± 0.48	237	300	65	1	2
<i>Colletotrichum atractylodiolica</i>	leaf/fruit/seed pathogen	96.98%	13	0	0	0	0

<i>Colletotrichum coccodes</i>	leaf/fruit/seed pathogen	100%	3	0	0	0	0
<i>Colletotrichum destructivum</i>	leaf/fruit/seed pathogen	100%	3	0	0	0	0
<i>Colletotrichum hemerocallidis</i>	leaf/fruit/seed pathogen	99.10%	4	0	0	0	0
<i>Colletotrichum kniphofiae</i>	leaf/fruit/seed pathogen	99.52%	0	1	0	0	0
<i>Colletotrichum trichellum</i>	leaf/fruit/seed pathogen	100%	1	0	0	0	0
<i>Coniella quercicola</i>	leaf/fruit/seed pathogen	100%	18	4	0	0	0
<i>Coniochaeta fasciculata</i>	leaf/fruit/seed pathogen, animal parasite	98.56% $\pm$ 2.03	273	1	8	0	0
<i>Coniochaeta ligniaria</i>	leaf/fruit/seed pathogen, animal parasite	99.29% $\pm$ 0.34	25	0	0	0	0
<i>Coniochaeta lignicola</i>	leaf/fruit/seed pathogen, animal parasite	99.76% $\pm$ 0.34	70	0	0	0	0
<i>Coniochaeta</i> sp.	leaf/fruit/seed pathogen, animal parasite	98.57% $\pm$ 1.38	26	1	0	0	0
<i>Cordyceps cateniannulata</i>	animal parasite	98.68% $\pm$ 0.62	0	24	0	0	0
<i>Cordyceps</i> sp.	animal parasite	99.09%	0	15	0	0	0
<i>Cryptocline arctostaphyli</i>	leaf/fruit/seed pathogen	99.32% $\pm$ 0.97	23	0	0	0	0
<i>Cryptococcus aureus</i>	animal-associated/opportunistic human parasite	99.37% $\pm$ 0.3	22	0	0	0	0
<i>Cryptococcus festuosus</i>	animal-associated/opportunistic human parasite	100%	2	0	0	0	0
<i>Cryptococcus pseudolongus</i>	animal-associated/opportunistic human parasite	100%	0	0	0	1	2408
<i>Cryptococcus</i> sp.	animal-associated/opportunistic human parasite	98.93% $\pm$ 1.5	4	60	1	1	27
<i>Cryptococcus wattiicus</i>	animal-associated/opportunistic human parasite	98.8% $\pm$ 0.4	77	0	0	0	0
<i>Cuphophyllus borealis</i>	root-associated	100%	0	0	43	0	0
<i>Cuphophyllus subviolaceus</i>	root-associated	99.8% $\pm$ 0.28	0	0	0	5	102
<i>Curvularia austriaca</i>	leaf/fruit/seed pathogen, opportunistic human parasite	99.10%	78	1	0	0	0
<i>Curvularia canadensis</i>	leaf/fruit/seed pathogen, opportunistic human parasite	100%	53	0	0	0	0
<i>Curvularia inaequalis</i>	leaf/fruit/seed pathogen, opportunistic human parasite	100%	10	0	0	0	0
<i>Curvularia intermedia</i>	leaf/fruit/seed pathogen, opportunistic human parasite	98.28%	9	0	0	0	0
<i>Curvularia kusanoi</i>	leaf/fruit/seed pathogen, opportunistic human parasite	99.54%	1	0	0	0	0
<i>Curvularia protuberata</i>	leaf/fruit/seed pathogen, opportunistic human parasite	100%	3	0	0	0	0
<i>Curvularia pseudoprotuberata</i>	leaf/fruit/seed pathogen, opportunistic human parasite	99.54% $\pm$ 0.65	22	2	0	0	0
<i>Curvularia xishuangbannaensis</i>	leaf/fruit/seed pathogen, opportunistic human parasite	99.54%	3	0	0	0	0
<i>Cutaneotrichosporon middelhovenii</i>	animal parasite/opportunistic human parasite	100%	0	1	0	0	0
<i>Cutaneotrichosporon moniliiforme</i>	animal parasite/opportunistic human parasite	99.77% $\pm$ 0.32	532	1	0	0	0
<i>Cutaneotrichosporon terricola</i>	animal parasite/opportunistic human parasite	99.77% $\pm$ 0.32	8	0	0	0	0
<i>Cyberlindnera saturnus</i>	animal parasite/opportunistic human parasite	100%	10	0	0	0	0
<i>Cylindrium desperesense</i>	leaf/fruit/seed pathogen	100%	0	0	2	0	0
<i>Cylindrium magnoliae</i>	leaf/fruit/seed pathogen	98.2% $\pm$ 0.24	31	237	4	6	31
<i>Cylindrium</i> sp.	leaf/fruit/seed pathogen	98.06%	0	2	0	0	0
<i>Cyphellophora livistonae</i>	animal parasite/opportunistic human parasite	99.55%	5	0	0	0	0
<i>Cyphellophora sessilis</i>	animal parasite/opportunistic human parasite	98.75%	0	0	0	0	1
<i>Cyphellophora</i> sp.	animal parasite/opportunistic human parasite	99.14%	6	0	0	0	0
<i>Cyphellophora vermisporea</i>	animal parasite/opportunistic human parasite	99.58% $\pm$ 0.59	39	0	0	0	0
<i>Cytospora beilinensis</i>	leaf/fruit/seed pathogen	99.13%	0	8	0	0	0
<i>Cytospora nitschkei</i>	leaf/fruit/seed pathogen	95.58%	3	0	0	0	0
<i>Cytospora populina</i>	leaf/fruit/seed pathogen	99.53%	0	0	0	0	1
<i>Cytospora</i> sp.	leaf/fruit/seed pathogen	99.55%	3	2	0	0	3
<i>Cytospora xinjiangensis</i>	leaf/fruit/seed pathogen	95.34%	11	0	0	0	0

<i>Dactylonectria macrodidyma</i>	leaf/fruit/seed pathogen	100%	4	0	0	0	0
<i>Dendrophoma cytisporoides</i>	leaf/fruit/seed pathogen	100%	4	0	0	0	0
<i>Dendrophoma</i> sp.	leaf/fruit/seed pathogen	99.35% $\pm$ 0.75	351	1	0	0	0
<i>Diaporthe bicincta</i>	leaf/fruit/seed pathogen	97.47%	14	1	0	0	0
<i>Diaporthe columnaris</i>	leaf/fruit/seed pathogen	99.1% $\pm$ 1.27	10	1	0	0	0
<i>Diaporthe goulteri</i>	leaf/fruit/seed pathogen	100%	2	0	0	0	0
<i>Diaporthe</i> sp.	leaf/fruit/seed pathogen	95.61%	119	0	0	0	0
<i>Diatractium</i> sp.	leaf/fruit/seed pathogen	99.56%	1	0	0	0	0
<i>Diatrype</i> sp.	leaf/fruit/seed pathogen	99.52%	3	0	0	0	0
<i>Diatrype stigma</i>	leaf/fruit/seed pathogen	98.8% $\pm$ 0.34	1	0	0	0	1
<i>Dictyolus</i> sp.	leaf/fruit/seed pathogen	95.65%	0	0	1	0	15
<i>Didymella arachidicola</i>	leaf/fruit/seed pathogen, animal parasite	98.68%	5	0	0	0	0
<i>Didymella bellidis</i>	leaf/fruit/seed pathogen, animal parasite	99.11%	0	0	3	0	0
<i>Diplodia corticola</i>	leaf/fruit/seed pathogen	98.68%	5	0	1	0	4
<i>Discosia rubi</i>	leaf/fruit/seed pathogen	98.61%	1652	4	0	0	2
<i>Dothiorella sempervirentis</i>	leaf/fruit/seed pathogen	98.65%	4	0	0	0	0
<i>Elsinoe salicina</i>	leaf/fruit/seed pathogen	98.66% $\pm$ 0	8	0	0	0	1
<i>Entoloma cuspidiferum</i>	root-associated	98.41%	0	0	0	1	0
<i>Entoloma rhodocylix</i>	root-associated	98.41% $\pm$ 0	0	2	0	1	0
<i>Entoloma sinuatum</i>	root-associated	99.6% $\pm$ 0.33	0	0	0	0	58
<i>Entoloma</i> sp.	root-associated	98.97% $\pm$ 0.79	1	0	2	12	9
<i>Entoloma unicolor</i>	root-associated	100%	0	1	0	0	0
<i>Entoloma vernum</i>	root-associated	100%	0	0	0	1	0
<i>Epicoccum draconis</i>	leaf/fruit/seed pathogen	98.9% $\pm$ 0.31	31	4	0	0	0
<i>Eucasphaeria</i> sp.	leaf/fruit/seed pathogen	100%	2	0	0	0	0
<i>Exobasidium</i> sp.	leaf/fruit/seed pathogen	99.19%	0	0	0	1	0
<i>Exophiala alcalophila</i>	root-associated, animal parasite/opportunistic human parasite	100%	1	0	0	0	0
<i>Exophiala attenuata</i>	root-associated, animal parasite/opportunistic human parasite	99.21%	2	0	0	0	0
<i>Exophiala bergeri</i>	root-associated, animal parasite/opportunistic human parasite	97.38% $\pm$ 1.85	8	0	0	0	0
<i>Exophiala clavispora</i>	root-associated, animal parasite/opportunistic human parasite	99.60%	13	0	0	0	0
<i>Exophiala ellipsoidea</i>	root-associated, animal parasite/opportunistic human parasite	99.04%	3	0	0	0	0
<i>Exophiala equina</i>	root-associated, animal parasite/opportunistic human parasite	100%	644	0	0	8	0
<i>Exophiala heteromorpha</i>	root-associated, animal parasite/opportunistic human parasite	100%	18	0	0	0	0
<i>Exophiala mesophila</i>	root-associated, animal parasite/opportunistic human parasite	99.21%	15	0	0	0	0
<i>Exophiala nagquensis</i>	root-associated, animal parasite/opportunistic human parasite	98.39%	3	0	0	0	0
<i>Exophiala nishimurae</i>	root-associated, animal parasite/opportunistic human parasite	99.16%	3	0	0	0	0
<i>Exophiala opportunistica</i>	root-associated, animal parasite/opportunistic human parasite	98.51% $\pm$ 0.68	77	0	0	0	0
<i>Exophiala pisciphila</i>	root-associated, animal parasite/opportunistic human parasite	99.8% $\pm$ 0.29	188	4	0	0	0
<i>Exophiala radicis</i>	root-associated, animal parasite/opportunistic human parasite	99.6% $\pm$ 0.4	125	4	0	2	0
<i>Exophiala</i> sp.	root-associated, animal parasite/opportunistic human parasite	98.46% $\pm$ 1.81	15	8	21	0	3
<i>Exophiala tremulae</i>	root-associated, animal parasite/opportunistic human parasite	99.20%	0	1	0	0	0
<i>Exophiala xenobiotica</i>	root-associated, animal parasite/opportunistic human parasite	99.36% $\pm$ 0.25	272	0	0	0	0
<i>Exserohilum rostratum</i>	leaf/fruit/seed pathogen	99.59%	2	1	0	1	0
<i>Farysia magdalenana</i>	leaf/fruit/seed pathogen	100%	29	0	0	0	0

<i>Filobasidium oerense</i>	opportunistic human parasite	100%	3	0	0	0	0
<i>Filobasidium wieringae</i>	opportunistic human parasite	100%	10	1	0	0	0
<i>Fimicolochytrium</i> sp.	algal parasite	100% ± 0	11	0	0	0	0
<i>Fonsecaea</i> sp.	animal parasite/opportunistic human parasite	100%	4	0	0	0	0
<i>Fusarium graminearum</i>	leaf/fruit/seed pathogen, opportunistic human parasite	100%	0	3	0	0	0
<i>Fusarium langsethiae</i>	leaf/fruit/seed pathogen, opportunistic human parasite	98.05%	0	6	0	0	0
<i>Fusarium lateritium</i>	leaf/fruit/seed pathogen, opportunistic human parasite	99.10%	258	0	0	0	0
<i>Fusarium oxysporum</i>	leaf/fruit/seed pathogen, opportunistic human parasite	100%	1091	8	0	0	0
<i>Fusarium</i> sp.	leaf/fruit/seed pathogen, opportunistic human parasite	99.84% ± 0.27	129	0	0	4	0
<i>Fusarium tricinctum</i>	leaf/fruit/seed pathogen, opportunistic human parasite	99.66% ± 0.44	99	0	0	0	0
<i>Galerina allospora</i>	leaf/fruit/seed pathogen	100%	0	0	0	0	2
<i>Galerina lacustris</i>	leaf/fruit/seed pathogen	98.81%	0	0	0	3	4
<i>Galerina</i> sp.	leaf/fruit/seed pathogen	98.01%	3	0	0	0	0
<i>Ganoderma leucocontextum</i>	wood pathogen	98.21% ± 0.28	1	1	0	0	9
<i>Ganoderma lobatum</i>	wood pathogen	99.60%	2	0	0	0	0
<i>Ganoderma lucidum</i>	wood pathogen	98.49% ± 0.33	269	0	0	0	0
<i>Ganoderma meredithiae</i>	wood pathogen	98.98% ± 1.45	2382	0	0	0	0
<i>Geoglossum glabrum</i>	root-associated	98.16%	0	0	0	0	3
<i>Geoglossum simile</i>	root-associated	98.63%	0	0	0	34	1
<i>Gliophorus irrigatus</i>	root-associated	99.07% ± 0.7	5	0	0	2	387
<i>Gliophorus</i> sp.	root-associated	98.54% ± 0.61	0	11	8	2	6
<i>Gloioxanthomyces nitidus</i>	root-associated	98.81% ± 0.4	0	0	0	0	390
<i>Grifola frondosa</i>	wood pathogen	96.81%	2	0	0	0	1
<i>Herpotrichia pinetorum</i>	leaf/fruit/seed pathogen	98.84% ± 0.33	50	1	1	0	0
<i>Herpotrichia</i> sp.	leaf/fruit/seed pathogen	99.43% ± 0.37	350	0	0	0	0
<i>Heterophoma sylvatica</i>	leaf/fruit/seed pathogen	98.68%	6	0	0	0	0
<i>Hirsutella proturicola</i>	invertebrate parasite	99.60%	3	0	0	0	0
<i>Hirsutella rhossiliensis</i>	invertebrate parasite	100%	7	8	3	4	11
<i>Hirsutella vermicola</i>	invertebrate parasite	99.3% ± 0.99	5	0	0	0	3
<i>Hongkongmyces pedis</i>	animal parasite/opportunistic human parasite	97.61%	1	0	0	0	0
<i>Hongkongmyces thailandicus</i>	animal parasite/opportunistic human parasite	95.04%	7	0	0	0	0
<i>Hormonema macrosporum</i>	animal-associated/opportunistic human parasite	99.11% ± 0.63	0	2	0	0	0
<i>Humidicutis marginata</i>	root-associated	98.41%	0	1	0	0	0
<i>Humidicutis</i> sp.	root-associated	98.81%	0	0	0	0	2
<i>Hygrocybe cantharellus</i>	root-associated	99.60%	0	0	0	17	0
<i>Hygrocybe reidii</i>	root-associated	99.60%	0	0	0	39	0
<i>Hygrocybe</i> sp.	root-associated	97.62% ± 1.68	0	6	130	30	0
<i>Hymenochaete curtisii</i>	wood pathogen	99.21%	0	0	0	9	0
<i>Hymenoscyphus imberbis</i>	leaf/fruit/seed pathogen	96.43% ± 0.23	1330	44	0	26	7
<i>Ilyonectria liriiodendri</i>	leaf/fruit/seed pathogen	100%	4	0	0	0	0
<i>Knufia perforans</i>	leaf/fruit/seed pathogen, opportunistic animal parasite	95.04%	1	0	0	0	0
<i>Knufia</i> sp.	leaf/fruit/seed pathogen, opportunistic animal parasite	98.68% ± 0.54	49	269	0	0	0
<i>Knufia tsunedae</i>	leaf/fruit/seed pathogen, opportunistic animal parasite	98.39% ± 1.18	485	57	0	1	0
<i>Kochiomyces dichotomus</i>	algal parasite	99.4% ± 0.28	10	0	0	0	0

<i>Lecanicillium flavidum</i>	invertebrate parasite	100%	0	0	0	0	8
<i>Lecanicillium fungicola</i>	invertebrate parasite	99.77% ± 0.33	0	1	0	0	1
<i>Lecanicillium fusisporum</i>	invertebrate parasite	99.54%	0	0	0	0	1
<i>Lecanicillium psalliotae</i>	invertebrate parasite	99.54%	0	3	0	1	0
<i>Lecanicillium saksenae</i>	invertebrate parasite	98.68%	4	0	0	0	0
<i>Lecanicillium</i> sp.	invertebrate parasite	99.53%	27	0	0	0	0
<i>Leohumicola minima</i>	root-associated	99.75% ± 0.35	0	0	1	2	0
<i>Leohumicola</i> sp.	root-associated	98.26% ± 2.46	2	0	0	0	15
<i>Leptobacillium leptobactrum</i>	invertebrate parasite	99.18% ± 0.65	0	16	0	14	60
<i>Limonomyces</i> sp.	wood pathogen	96.83% ± 1.66	1	0	1	0	0
<i>Malassezia arunalokei</i>	root-associated, animal-associated/opportunistic human parasite	97.23% ± 0.56	12	0	0	0	4
<i>Malassezia globosa</i>	root-associated, animal-associated/opportunistic human parasite	100%	0	0	1	0	1
<i>Malassezia restricta</i>	root-associated, animal-associated/opportunistic human parasite	99.6% ± 0.4	81	1	43	14	31
<i>Malassezia</i> sp.	root-associated, animal-associated/opportunistic human parasite	99.8% ± 0.28	2	0	0	2	1
<i>Malassezia sympodialis</i>	root-associated, animal-associated/opportunistic human parasite	100%	0	0	1	0	0
<i>Melanchlenus</i> sp.	opportunistic human parasite	98.31%	0	1	0	0	0
<i>Metacordyceps chlamydosporia</i>	animal parasite	98.29% ± 0.38	44	0	0	0	0
<i>Metarhizium anisopliae</i>	animal parasite	98.39%	10	54	0	0	0
<i>Metarhizium brunneum</i>	animal parasite	97.7% ± 0.37	5	953	342	65	0
<i>Metarhizium flavoviride</i>	animal parasite	99.20%	1	0	0	0	0
<i>Metarhizium gaoligongense</i>	animal parasite	100%	0	7	18	0	0
<i>Metarhizium</i> sp.	animal parasite	99.25% ± 1.29	20	3	9	2	13
<i>Microascus gracilis</i>	leaf/fruit/seed pathogen, opportunistic human parasite	100%	1	0	0	0	0
<i>Microdochium poae</i>	leaf/fruit/seed pathogen	97.08%	1	0	0	0	0
<i>Microdochium sorghi</i>	leaf/fruit/seed pathogen	99.11%	0	0	2	0	0
<i>Microstroma bacarum</i>	leaf/fruit/seed pathogen	99.4% ± 0.84	16	0	0	0	0
<i>Miuraea degenerans</i>	leaf/fruit/seed pathogen	100%	5	0	0	0	0
<i>Moesziomyces aphidis</i>	leaf/fruit/seed pathogen	99.8% ± 0.28	12	0	0	0	0
<i>Monochaetia dimorphospora</i>	leaf/fruit/seed pathogen	99.55%	0	0	159	0	0
<i>Monochaetia quercus</i>	leaf/fruit/seed pathogen	99.10%	0	0	0	0	1
<i>Mortierella alliacea</i>	root-associated, opportunistic human parasite	100%	0	3	0	1	20
<i>Mortierella ambigua</i>	root-associated, opportunistic human parasite	99.21%	3	0	0	0	0
<i>Mortierella angusta</i>	root-associated, opportunistic human parasite	100%	40	7	5	5	3
<i>Mortierella antarctica</i>	root-associated, opportunistic human parasite	99.3% ± 0.5	71	0	0	0	0
<i>Mortierella basiparvispora</i>	root-associated, opportunistic human parasite	98.65% ± 0.67	5	5	12	2	0
<i>Mortierella gemmifera</i>	root-associated, opportunistic human parasite	99.4% ± 0.28	0	3	7	2	29
<i>Mortierella macrocystis</i>	root-associated, opportunistic human parasite	99.4% ± 0.84	0	41	144	40	81
<i>Mortierella pulchella</i>	root-associated, opportunistic human parasite	99.2% ± 1.13	2	2	0	4	55
<i>Mortierella</i> sp.	root-associated, opportunistic human parasite	98.99% ± 0.76	675	622	598	211	582
<i>Mortierella tsukubaensis</i>	root-associated, opportunistic human parasite	99.6% ± 0.4	5	3	0	0	0
<i>Mucor circinelloides</i>	opportunistic human parasite	99.79% ± 0.29	3	0	0	0	0
<i>Mucor moelleri</i>	opportunistic human parasite	99.78% ± 0.3	5	0	0	0	0
<i>Mucor racemosus</i>	opportunistic human parasite	98.73%	1	0	0	0	0
<i>Mycena algeriensis</i>	leaf/fruit/seed pathogen	96.83%	0	0	0	5	0

<i>Mycena epipterygia</i>	leaf/fruit/seed pathogen	99.60%	0	0	0	0	4
<i>Mycena griseoviridis</i>	leaf/fruit/seed pathogen	98.51% ± 0.2	114	3	0	0	2
<i>Mycena leptocephala</i>	leaf/fruit/seed pathogen	99.60%	229	4	0	0	0
<i>Mycena metata</i>	leaf/fruit/seed pathogen	99.4% ± 0.84	0	4	479	0	0
<i>Mycena pura</i>	leaf/fruit/seed pathogen	98.78%	0	0	0	10	0
<i>Mycena purpureofusca</i>	leaf/fruit/seed pathogen	98.8% ± 0.4	5	0	0	4	17
<i>Mycena sanguinolenta</i>	leaf/fruit/seed pathogen	97.6% ± 1.68	0	0	0	5	14
<i>Mycena sp.</i>	leaf/fruit/seed pathogen	99.09% ± 0.54	11	1	235	2	415
<i>Mycena stylobates</i>	leaf/fruit/seed pathogen	100%	2	0	0	0	0
<i>Myriangium sp.</i>	arthropod parasite	96.43% ± 0.78	22	0	0	0	0
<i>Myriosclerotinia curreyana</i>	leaf/fruit/seed pathogen	96.38% ± 0.34	6	3	0	1	4
<i>Myxotrichum cancellatum</i>	root-associated	99.51%	14	126	0	9	0
<i>Nannizziopsis mirabilis</i>	animal parasite	100% ± 0	17	0	0	0	0
<i>Nectria ramulariae</i>	leaf/fruit/seed pathogen	100%	7	0	0	0	0
<i>Nectria sp.</i>	leaf/fruit/seed pathogen	99.36% ± 0.3	5	0	0	0	0
<i>Neosascochyta desmazieri</i>	leaf/fruit/seed pathogen	99.52%	78	0	0	5	0
<i>Neosascochyta rosicola</i>	leaf/fruit/seed pathogen	98.57%	0	0	61	0	0
<i>Neosascochyta tardicrescens</i>	leaf/fruit/seed pathogen	98.57%	5	0	0	0	0
<i>Neodevriesia imbrexigena</i>	leaf/fruit/seed pathogen	100%	2	0	0	0	0
<i>Neophaeococcomyces aloes</i>	leaf/fruit/seed pathogen	98.80%	3	0	0	0	0
<i>Neophaeomoniella ossiformis</i>	leaf/fruit/seed pathogen	97.86%	0	0	0	0	1
<i>Nigrograna antibiotica</i>	animal parasite	100%	17	0	0	0	0
<i>Nigrograna cangshanensis</i>	animal parasite	97.55% ± 0.26	103	0	0	0	2
<i>Nigrograna magnoliae</i>	animal parasite	98.53%	5	0	0	0	0
<i>Ochroconis sp.</i>	leaf/fruit/seed pathogen, opportunistic human parasite	98.42% ± 1.31	24	38	0	0	6
<i>Oidiodendron periconioides</i>	root-associated	98.7% ± 1.95	209	1132	60	366	1240
<i>Oidiodendron sp.</i>	root-associated	96.91% ± 1.43	263	585	452	1189	1244
<i>Oidiodendron tenuissimum</i>	root-associated	100%	0	0	0	0	7
<i>Paecilomyces lagunculariae</i>	invertebrate parasite	100%	72	0	0	0	0
<i>Paecilomyces sp.</i>	invertebrate parasite	99.14%	1	0	0	0	0
<i>Paecilomyces subglobosus</i>	invertebrate parasite	98.53% ± 1.49	14	0	0	0	0
<i>Paecilomyces zollerniae</i>	invertebrate parasite	97.21% ± 1.34	366	0	0	0	0
<i>Paracremonium binnewijzendii</i>	animal parasite/opportunistic human parasite	96.37% ± 0.3	113	0	0	0	0
<i>Paraphoma fimeti</i>	wood pathogen	99.52%	1	0	0	0	0
<i>Paraphoma ledniceana</i>	wood pathogen	99.5% ± 0.41	67	0	0	0	0
<i>Paraphoma radicina</i>	wood pathogen	99.04%	1	0	0	0	0
<i>Paraphyton cookei</i>	opportunistic human parasite	100%	3	0	0	0	0
<i>Parascenedosporium putredinis</i>	opportunistic human parasite	99.19%	6	0	0	0	0
<i>Parastagonospora poae</i>	leaf/fruit/seed pathogen	97.58%	7	0	0	0	0
<i>Parastagonospora sp.</i>	leaf/fruit/seed pathogen	97.57%	2	0	0	0	0
<i>Peltaster gemmifer</i>	unspecified plant pathogen	99.41% ± 0.44	50	1	2	3	1
<i>Penicillium bialowiezense</i>	opportunistic human parasite	98.73%	4	0	0	0	0
<i>Penicillium catalanicum</i>	opportunistic human parasite	99.14%	2	0	0	0	0
<i>Penicillium catenatum</i>	opportunistic human parasite	99.54%	0	0	1	0	0

<i>Penicillium citrinum</i>	opportunistic human parasite	100%	2	0	0	0	0
<i>Penicillium cryptum</i>	opportunistic human parasite	98.94% $\pm$ 0.69	42	2	0	0	0
<i>Penicillium daleae</i>	opportunistic human parasite	98.74%	0	3	0	0	0
<i>Penicillium granulatum</i>	opportunistic human parasite	99.09%	1	0	0	0	0
<i>Penicillium lividum</i>	opportunistic human parasite	100%	0	0	1	0	0
<i>Penicillium menonorum</i>	opportunistic human parasite	100%	2	0	0	0	0
<i>Penicillium nepalense</i>	opportunistic human parasite	96.47%	1	0	0	0	0
<i>Penicillium raperi</i>	opportunistic human parasite	99.14%	168	0	0	0	0
<i>Penicillium senticosum</i>	opportunistic human parasite	99.07%	4	0	0	0	0
<i>Penicillium sp.</i>	opportunistic human parasite	98.65% $\pm$ 1.57	72	6	18	34	15
<i>Penicillium thomii</i>	opportunistic human parasite	100%	11	3	0	0	0
<i>Penicillium variatense</i>	opportunistic human parasite	100%	7	0	0	0	0
<i>Penicillium yunnanense</i>	opportunistic human parasite	99.57%	30	0	0	0	0
<i>Penicillium zhuangii</i>	opportunistic human parasite	99.54%	0	0	0	1	0
<i>Peniophora cinerea</i>	wood pathogen	98.14% $\pm$ 0.22	15	6	0	0	0
<i>Peniophora laxitexta</i>	wood pathogen	97.99%	0	1	0	0	0
<i>Peniophora pseudopini</i>	wood pathogen	98.74%	1	0	0	0	0
<i>Peniophora sp.</i>	wood pathogen	97.77% $\pm$ 2.03	1	0	48	0	0
<i>Perennicordyceps prolifica</i>	arthropod parasite	100%	0	0	0	2	0
<i>Periconia celtidis</i>	leaf/fruit/seed pathogen	100%	0	0	0	0	1
<i>Periconia macrospinosa</i>	leaf/fruit/seed pathogen	98.88% $\pm$ 0.93	71	0	0	0	0
<i>Periconia sp.</i>	leaf/fruit/seed pathogen	98.21%	14	0	0	0	0
<i>Periconia verrucosa</i>	leaf/fruit/seed pathogen	100%	0	0	0	0	5
<i>Pestalotiopsis iberica</i>	leaf/fruit/seed pathogen	99.58%	14	5	23	0	0
<i>Pestalotiopsis macadamiae</i>	leaf/fruit/seed pathogen	99.16%	1	0	0	0	0
<i>Pestalotiopsis rhododendri</i>	leaf/fruit/seed pathogen	99.15%	5	0	0	0	0
<i>Pezicula ericae</i>	leaf/fruit/seed pathogen	95.62% $\pm$ 0.63	240	21	30	23	95
<i>Pezicula heterochroma</i>	leaf/fruit/seed pathogen	95.92% $\pm$ 0.38	211	9	0	9	0
<i>Pezicula sp.</i>	leaf/fruit/seed pathogen	98.52%	0	0	10	0	0
<i>Pezoloma ericae</i>	leaf/fruit/seed pathogen	96.81% $\pm$ 0.37	0	0	15	2	0
<i>Phaeobotryon sp.</i>	leaf/fruit/seed pathogen	100%	1	0	0	0	0
<i>Phaeomoniella sp.</i>	leaf/fruit/seed pathogen	97.44%	0	0	0	0	4
<i>Phaeothecoidiella illinoisensis</i>	leaf/fruit/seed pathogen	98.33% $\pm$ 0.34	13	0	0	0	13
<i>Phialemonium inflatum</i>	animal parasite	97.75% $\pm$ 1.42	2991	0	0	0	0
<i>Phialemonium sp.</i>	animal parasite	96.45% $\pm$ 2.38	45	0	0	0	0
<i>Phialocephala glacialis</i>	root-associated	96.30%	0	0	0	0	5
<i>Phialocephala helenae</i>	root-associated	97.35% $\pm$ 0.43	47	28	113	75	155
<i>Phialocephala helvetica</i>	root-associated	99.16%	2	0	0	0	0
<i>Phialocephala repens</i>	root-associated	98.82% $\pm$ 0.33	29	9	0	1	0
<i>Phialocephala sp.</i>	root-associated	100%	6	0	0	0	0
<i>Phialophora cyclaminis</i>	leaf/fruit/seed pathogen, animal parasite	99.23% $\pm$ 0.27	84	0	0	0	0
<i>Phlogicylindrium sp.</i>	leaf/fruit/seed pathogen	99.13%	0	0	0	0	3
<i>Pholiota highlandensis</i>	wood pathogen	100%	0	0	31	0	0
<i>Pholiota mixta</i>	wood pathogen	99.6% $\pm$ 0	3	0	0	0	49

<i>Pholiota terrestris</i>	wood pathogen	99.60%	3	0	0	0	0
<i>Pichia myanmarensis</i>	animal parasite/opportunistic human parasite	100%	1	0	0	0	0
<i>Plectosphaerella niemeijerorum</i>	leaf/fruit/seed pathogen, nematophagous	99.33% ± 0.31	9	0	0	0	0
<i>Plectosphaerella slobbergierum</i>	leaf/fruit/seed pathogen, nematophagous	97.78%	151	0	0	0	0
<i>Polyccephalomyces</i> sp.	invertebrate parasite	95.67%	0	0	0	0	1
<i>Polyscytalum</i> sp.	leaf/fruit/seed pathogen	100%	0	0	0	0	3
<i>Polyscytalum vaccinii</i>	leaf/fruit/seed pathogen	98.41%	0	0	12	0	0
<i>Powellomyces</i> sp.	algal parasite	99.2% ± 1.13	6	0	0	0	0
<i>Pseudallescheria boydii</i>	opportunistic human parasite	99.6% ± 0.56	5	0	0	0	0
<i>Pseudocercospora fijiensis</i>	leaf/fruit/seed pathogen	100%	0	0	0	0	17
<i>Pseudocoleophoma polygonicola</i>	leaf/fruit/seed pathogen	99.53%	4	0	0	0	0
<i>Pseudocoleophoma</i> sp.	leaf/fruit/seed pathogen	98.79% ± 1.02	7	0	0	0	0
<i>Pseudogymnoascus appendiculatus</i>	opportunistic animal parasite <i>G. destructans</i>	97.72% ± 1.21	479	0	0	0	0
<i>Pseudogymnoascus roseus</i>	opportunistic animal parasite <i>G. destructans</i>	99.08%	0	4	0	0	0
<i>Pseudomicrostroma glucosiphilum</i>	leaf/fruit/seed pathogen	100%	13	0	0	0	0
<i>Pseudomicrostroma phylloplanum</i>	leaf/fruit/seed pathogen	99.34% ± 0.23	59	0	59	1	1
<i>Pseudopithomyces rosae</i>	leaf/fruit/seed pathogen	100%	0	0	19	0	0
<i>Puccinia striiformis</i>	leaf/fruit/seed pathogen	100%	1	0	0	0	0
<i>Purpureocillium lilacinum</i>	arthropod parasite	99.26% ± 0.53	850	1	0	0	0
<i>Ramariopsis</i> sp.	root-associated	98.15% ± 2.25	0	1	0	3	1
<i>Ramularia simplex</i>	leaf/fruit/seed pathogen	97.17%	0	0	0	0	1
<i>Ramulispora sorghiphila</i>	leaf/fruit/seed pathogen	97.73%	4	0	0	0	0
<i>Rasamsonia composticola</i>	opportunistic human parasite	100%	1	0	0	0	0
<i>Rasamsonia emersonii</i>	opportunistic human parasite	99.85% ± 0.26	16	0	0	0	0
<i>Rhinocladiella quercus</i>	root-associated, animal parasite/opportunistic human parasite	99.60%	0	0	1	0	0
<i>Rhinocladiella</i> sp.	root-associated, animal parasite/opportunistic human parasite	98.25% ± 0.91	48	9	2	0	0
<i>Rhizophlyctis rosea</i>	algal parasite	99.1% ± 0.38	24	0	0	0	0
<i>Rhizophlyctis</i> sp.	algal parasite	97.22%	2	0	0	0	0
<i>Rhizophydium</i> sp.	algal parasite	98.8% ± 0.01	1	0	2	0	0
<i>Rhizopus arrhizus</i>	leaf/fruit/seed pathogen, opportunistic human parasite	100%	7	0	0	0	0
<i>Rhodotorula mucilaginosa</i>	opportunistic human parasite	99.6% ± 0.4	23	2	0	0	0
<i>Rhodotorula paludigena</i>	opportunistic human parasite	99.60%	1	0	0	0	0
<i>Rhodotorula</i> sp.	opportunistic human parasite	100%	3	0	0	0	0
<i>Rhodotorula toruloides</i>	opportunistic human parasite	99.60%	3	0	0	0	0
<i>Rosellinia subiculata</i>	wood pathogen	98.71%	0	1	0	0	0
<i>Sagenomella diversispora</i>	opportunistic human parasite	98.88% ± 0.78	1357	2006	1203	1666	1565
<i>Sagenomella oligospora</i>	opportunistic human parasite	99.27% ± 0.34	2	0	0	4	0
<i>Sagenomella verticillata</i>	opportunistic human parasite	97.85% ± 1.75	44	104	192	194	1082
<i>Samsoniella hepiali</i>	invertebrate parasite	100%	0	1	11	5	10
<i>Sarcopodium araliae</i>	leaf/fruit/seed pathogen, opportunistic human parasite	99.16%	4	0	0	0	0
<i>Scedosporium aurantiacum</i>	opportunistic human parasite	100%	1	0	0	0	0
<i>Scedosporium boydii</i>	opportunistic human parasite	98.61% ± 1.23	471	0	0	0	0
<i>Scedosporium dehoogii</i>	opportunistic human parasite	99.8% ± 0.28	113	0	0	0	0
<i>Scedosporium prolificans</i>	opportunistic human parasite	98.77% ± 1.14	40	0	0	0	0

<i>Schizothyrium tardicrescens</i>	leaf/fruit/seed pathogen	98.54%	1	0	0	0	0
<i>Scleromitruia calthicola</i>	leaf/fruit/seed pathogen	95.37% ± 0.35	6	0	0	0	0
<i>Sclerostagonospora ericae</i>	leaf/fruit/seed pathogen	98.58%	3	0	0	0	0
<i>Sclerostagonospora</i> sp.	leaf/fruit/seed pathogen	97.94% ± 1.11	58	0	72	2	8
<i>Scolecobasidium bacilliforme</i>	leaf/fruit/seed pathogen, animal parasite	99.58%	2	0	0	0	0
<i>Scolecobasidium constrictum</i>	leaf/fruit/seed pathogen, animal parasite	100% ± 0	10	0	0	0	0
<i>Scolecobasidium icarus</i>	leaf/fruit/seed pathogen, animal parasite	99.53%	6	0	0	0	0
<i>Scolecobasidium ramosum</i>	leaf/fruit/seed pathogen, animal parasite	100%	17	0	0	0	0
<i>Scolecobasidium</i> sp.	leaf/fruit/seed pathogen, animal parasite	99% ± 0.7	0	4	0	0	163
<i>Scytalidium album</i>	opportunistic human parasite	99.02%	3	0	0	0	0
<i>Scytalidium</i> sp.	opportunistic human parasite	99.36% ± 0.69	92	0	0	0	0
<i>Setophaeosphaeria badalingensis</i>	leaf/fruit/seed pathogen	99.52% ± 0.68	7	0	0	0	0
<i>Simplicillium</i> sp.	invertebrate parasite	99.59%	0	1	0	0	0
<i>Sphaerulina abeliceae</i>	leaf/fruit/seed pathogen	99.52%	2	0	0	0	0
<i>Spiromastix</i> sp.	opportunistic animal parasite	98.74%	12	0	0	0	0
<i>Stachylidium bicolor</i>	animal parasite	100% ± 0	10	0	3	0	0
<i>Stagonospora heteroderae</i>	leaf/fruit/seed pathogen	100%	86	0	0	0	0
<i>Stagonosporopsis loticola</i>	leaf/fruit/seed pathogen	99.34% ± 0.31	5	0	0	0	0
<i>Stagonosporopsis valerianellae</i>	leaf/fruit/seed pathogen	98.25%	231	21	0	0	0
<i>Stagonosporopsis weymaniae</i>	leaf/fruit/seed pathogen	99.13%	6	0	0	0	0
<i>Talaromyces aerius</i>	opportunistic human parasite	100%	2	0	0	0	0
<i>Talaromyces albisclerotius</i>	opportunistic human parasite	99.52%	0	16	0	0	0
<i>Talaromyces assiutensis</i>	opportunistic human parasite	98.85% ± 0.97	289	0	0	0	4
<i>Talaromyces bannicus</i>	opportunistic human parasite	98.17%	0	19	0	24	0
<i>Talaromyces barcinensis</i>	opportunistic human parasite	100%	7	0	0	0	0
<i>Talaromyces beijiangensis</i>	opportunistic human parasite	99.05%	4	0	0	0	0
<i>Talaromyces calidominioluteus</i>	opportunistic human parasite	97.85% ± 0.73	141	10	3	0	20
<i>Talaromyces columbinus</i>	opportunistic human parasite	100%	9	0	0	0	0
<i>Talaromyces coprophilus</i>	opportunistic human parasite	98.06% ± 0.44	1226	111	0	19	10
<i>Talaromyces diversus</i>	opportunistic human parasite	100%	6	0	0	0	0
<i>Talaromyces domesticus</i>	opportunistic human parasite	99.52% ± 0.48	582	8	0	0	0
<i>Talaromyces infraolivaceus</i>	opportunistic human parasite	97.78% ± 0.48	176	19	0	0	0
<i>Talaromyces juglandicola</i>	opportunistic human parasite	97.11%	0	3	0	0	0
<i>Talaromyces minioluteus</i>	opportunistic human parasite	99.08%	60	11	1	89	0
<i>Talaromyces neofusisporus</i>	opportunistic human parasite	99.76% ± 0.33	143	0	0	0	0
<i>Talaromyces proteolyticus</i>	opportunistic human parasite	100%	2	85	2	26	0
<i>Talaromyces purpureogenus</i>	opportunistic human parasite	100%	24	0	0	0	0
<i>Talaromyces rademirici</i>	opportunistic human parasite	96.38%	2	0	0	0	0
<i>Talaromyces radicus</i>	opportunistic human parasite	99.56%	1	0	0	0	0
<i>Talaromyces rubicundus</i>	opportunistic human parasite	99.09%	114	0	0	0	0
<i>Talaromyces rubifaciens</i>	opportunistic human parasite	98.74% ± 1.44	20	31	16	5	0
<i>Talaromyces rugulosus</i>	opportunistic human parasite	99.79% ± 0.29	13	0	2	10	0
<i>Talaromyces</i> sp.	opportunistic human parasite	98.49% ± 1.66	168	0	0	0	0
<i>Talaromyces subaurantiacus</i>	opportunistic human parasite	100%	8	0	0	0	0

<i>Talaromyces subinflatus</i>	opportunistic human parasite	98.67%	0	0	0	2	2
<i>Talaromyces subtropicalis</i>	opportunistic human parasite	100%	321	0	0	0	0
<i>Talaromyces ucrainicus</i>	opportunistic human parasite	95.15%	4	0	0	0	0
<i>Talaromyces wortmannii</i>	opportunistic human parasite	99.56% ± 0	12	0	0	0	0
<i>Talaromyces yunnanensis</i>	opportunistic human parasite	99.84% ± 0.39	4081	0	0	0	4
<i>Taphrina caerulescens</i>	leaf/fruit/seed pathogen	100%	17	1	0	0	6
<i>Taphrina inositophila</i>	leaf/fruit/seed pathogen	98.41% ± 1.69	0	0	0	0	2
<i>Taphrina</i> sp.	leaf/fruit/seed pathogen	99.60%	25	0	0	0	0
<i>Thanatephorus</i> sp.	leaf/fruit/seed pathogen	98.41% ± 0	2	0	0	0	0
<i>Thermomyces ibadanensis</i>	leaf/fruit/seed pathogen	99.56%	2	0	0	0	0
<i>Tolypocladium album</i>	animal parasite	100%	0	0	0	0	8
<i>Tolypocladium cylindrosporum</i>	animal parasite	99.23% ± 0.71	0	0	0	17	224
<i>Tolypocladium geodes</i>	animal parasite	99.77% ± 0.33	1	4	1122	85	34
<i>Tolypocladium inegoense</i>	animal parasite	98.5% ± 0.98	8	4	0	46	0
<i>Tolypocladium inflatum</i>	animal parasite	99.53%	10	307	0	35	18
<i>Tolypocladium</i> sp.	animal parasite	97.32% ± 1.56	7	249	63	346	41
<i>Tolypocladium tropicale</i>	animal parasite	99.32% ± 0.58	0	562	125	58	2
<i>Tremateia chromolaenae</i>	leaf/fruit/seed pathogen	99.04%	0	1	0	0	0
<i>Trichoderma achlamyosporum</i>	leaf/fruit/seed pathogen	98.33%	0	0	1	0	5
<i>Trichoderma albolutescens</i>	leaf/fruit/seed pathogen	99.55%	13	0	0	0	0
<i>Trichoderma asperellum</i>	leaf/fruit/seed pathogen	99.8% ± 0.29	0	0	0	17	53
<i>Trichoderma atroviride</i>	leaf/fruit/seed pathogen	98.48% ± 2.14	0	11	0	0	0
<i>Trichoderma caerulescens</i>	leaf/fruit/seed pathogen	98.70%	0	0	0	3	0
<i>Trichoderma chlorosporum</i>	leaf/fruit/seed pathogen	100%	0	5	0	0	0
<i>Trichoderma citrinum</i>	leaf/fruit/seed pathogen	100%	0	0	2	4	0
<i>Trichoderma decipiens</i>	leaf/fruit/seed pathogen	100%	0	0	0	0	8
<i>Trichoderma fomiticola</i>	leaf/fruit/seed pathogen	99.55%	533	0	0	0	0
<i>Trichoderma hamatum</i>	leaf/fruit/seed pathogen	97.96%	6	82	38	14	0
<i>Trichoderma harzianum</i>	leaf/fruit/seed pathogen	99.34% ± 0.63	84	71	47	4	26
<i>Trichoderma minutisporum</i>	leaf/fruit/seed pathogen	100%	0	0	0	0	8
<i>Trichoderma neorufum</i>	leaf/fruit/seed pathogen	97.17%	0	0	0	0	3
<i>Trichoderma nybergianum</i>	leaf/fruit/seed pathogen	97.30%	0	0	6	0	0
<i>Trichoderma parasiluliferum</i>	leaf/fruit/seed pathogen	100% ± 0	0	0	0	1	16
<i>Trichoderma peberdyi</i>	leaf/fruit/seed pathogen	97.11%	0	9	0	6	0
<i>Trichoderma pubescens</i>	leaf/fruit/seed pathogen	98.78%	0	65	2	14	0
<i>Trichoderma rodmanii</i>	leaf/fruit/seed pathogen	100%	0	0	0	1	6
<i>Trichoderma</i> sp.	leaf/fruit/seed pathogen	98.82% ± 0.97	522	139	29	5	9
<i>Trichoderma spirale</i>	leaf/fruit/seed pathogen	100%	7	0	0	0	0
<i>Trichoderma stellatum</i>	leaf/fruit/seed pathogen	99.25% ± 0.26	54	36	0	15	7
<i>Trichoderma strigosum</i>	leaf/fruit/seed pathogen	99.12%	6	11	3	6	39
<i>Trichoderma turrialbense</i>	leaf/fruit/seed pathogen	100%	89	0	0	0	0
<i>Trichoderma viride</i>	leaf/fruit/seed pathogen	99.03% ± 0.22	1	72	9	17	38
<i>Trichoglossum</i> sp.	root-associated	99.60%	0	0	0	5	0
<i>Trichoglossum walteri</i>	root-associated	96.41%	0	0	0	76	0

<i>Trichomonascus vanleenenianus</i>	opportunistic human parasite	100%	15	0	0	0	0
<i>Trichophyton ajelloi</i>	animal parasite	98.73%	5	0	0	0	0
<i>Trichosporon asahii</i>	animal parasite/opportunistic human parasite	100%	8	0	0	0	0
<i>Trichosporon asteroides</i>	animal parasite/opportunistic human parasite	100%	46	0	0	0	0
<i>Trichothecium crocacinigenum</i>	leaf/fruit/seed pathogen	99.15% $\pm$ 0.52	16	0	1	0	0
<i>Truncatella angustata</i>	leaf/fruit/seed pathogen	100%	17	0	0	0	0
<i>Umbelopsis angularis</i>	root-associated	99.20%	0	0	1	0	0
<i>Umbelopsis autotrophica</i>	root-associated	100%	3	0	0	0	0
<i>Umbelopsis changbaiensis</i>	root-associated	99.6% $\pm$ 0	0	0	1	1	3
<i>Umbelopsis isabellina</i>	root-associated	97.71% $\pm$ 0.94	0	9	41	40	13
<i>Umbelopsis ramanniana</i>	root-associated	98.61% $\pm$ 0.28	0	9	0	1	0
<i>Umbelopsis</i> sp.	root-associated	98.6% $\pm$ 0.97	2648	616	533	155	474
<i>Ustilago maydis</i>	leaf/fruit/seed pathogen	99.60%	1	0	0	0	0
<i>Ustilago</i> sp.	leaf/fruit/seed pathogen	98.03% $\pm$ 1.08	2	0	0	0	0
<i>Venturia catenospora</i>	leaf/fruit/seed pathogen	96.15% $\pm$ 0.32	0	0	0	0	12
<i>Venturia fuliginosa</i>	leaf/fruit/seed pathogen	96.83%	0	0	0	0	4
<i>Veronaea japonica</i>	leaf/fruit/seed pathogen, opportunistic animal parasite	98.01%	91	0	0	0	0
<i>Veronaea</i> sp.	leaf/fruit/seed pathogen, opportunistic animal parasite	99.17%	1	0	0	0	0
<i>Verticillium albo-atrum</i>	leaf/fruit/seed pathogen, nematophagous	99.12%	0	0	0	2	0
<i>Waitea arvalis</i>	leaf/fruit/seed pathogen	99.8% $\pm$ 0.29	22	0	0	0	0
<i>Waitea</i> sp.	leaf/fruit/seed pathogen	96.07% $\pm$ 0.29	6	0	0	0	0
<i>Wickerhamomyces anomalus</i>	opportunistic human parasite	98.36%	0	0	89	0	0
<i>Xanthothecium peruvianum</i>	opportunistic human parasite	99.77% $\pm$ 0.33	57	0	0	0	0
<i>Xenoacremonium falcatum</i>	opportunistic human parasite	100%	2	0	0	0	0
<i>Xenopyrenochaetopsis pratorum</i>	leaf/fruit/seed pathogen	99.5% $\pm$ 0.7	26	0	0	11	0

Table S6. Fungal pathogens detected in root samples across the urbanization gradient. Numbers are sums of species counts normalized by rarefaction in root samples of each tree type. % identity refers to the % match of ITS sequence from the tree microbiome dataset to the ITS sequence match in the UNITE database, which corresponded to a genus-level name match in the FungalTraits database.

Fungal Species	Pathogen Type	% Identity ($\pm$ standard deviation when >1 ASV sequence match)	Urban Street Tree	Urban Forest Edge	Urban Forest Interior	Rural Forest Edge	Rural Forest Interior
Acephala sp.	root-associated	96.24% $\pm$ 0.65	7	8	0	14	8
Alternaria angustiovoidea	leaf/fruit/seed pathogen	98.26% $\pm$ 0.36	2	17	4	0	0
Alternaria eichhorniae	leaf/fruit/seed pathogen	99.13%	17	3	0	0	0
Alternaria subcucurbitae	leaf/fruit/seed pathogen	100%	2	0	0	0	0
Armillaria borealis	wood pathogen	99.4% $\pm$ 0.28	0	0	0	0	1796
Arthropis sp.	animal parasite	100%	0	19	0	0	0
Aspergillus citrisporus	animal parasite/opportunistic human parasite	100%	0	0	0	0	1
Aspergillus fumigatus	animal parasite/opportunistic human parasite	99.58%	2	0	0	0	0
Aspergillus japonicus	animal parasite/opportunistic human parasite	99.52%	9	0	0	0	0
Aspergillus sp.	animal parasite/opportunistic human parasite	100% $\pm$ 0	2	5	0	0	0
Athelia bombacina	algal parasite	99.2% $\pm$ 0.56	0	0	0	0	19
Aureobasidium pullulans	leaf/fruit/seed pathogen, animal parasite	99.23% $\pm$ 0.96	15	43	31	0	1
Beauveria caledonica	invertebrate parasite	100%	0	0	1	7	2
Botrytis caroliniana	leaf/fruit/seed pathogen	99%	623	0	0	0	0
Cadophora sp.	leaf/fruit/seed pathogen	99.50%	2	0	0	0	0
Caliciopsis beckhausii	leaf/fruit/seed pathogen	100%	0	2	0	4	0
Candida railenensis	animal-associated/opportunistic human parasite	100%	0	0	0	0	11
Capronia semiimmersa	animal parasite/opportunistic human parasite	100%	3	0	0	0	0
Capronia sp.	animal parasite/opportunistic human parasite	98.23% $\pm$ 0.92	0	1275	199	568	2067
Castanediella sp.	leaf/fruit/seed pathogen	99.55%	5	0	0	0	0
Celosporium sp.	leaf/fruit/seed pathogen	98.17%	0	2	0	0	0
Ceratobasidium sp.	leaf/fruit/seed pathogen	97.79% $\pm$ 0.98	324	0	0	0	20
Chalara angustata	wood pathogen, leaf/fruit/seed pathogen	98.58%	0	1	0	0	0
Chalara sp.	wood pathogen, leaf/fruit/seed pathogen	100%	4	0	0	0	0
Chloridium aseptatum	root pathogen, opportunistic human parasite	98.84% $\pm$ 0.98	9	0	0	0	0
Chloridium sp.	root pathogen, opportunistic human parasite	98.52% $\pm$ 0.49	0	7	0	12	54
Chloridium submersum	root pathogen, opportunistic human parasite	98.27% $\pm$ 0.34	0	0	0	0	8
Cladophialophora chaetospora	animal parasite/opportunistic human parasite	97.98%	27	0	0	0	0
Cladophialophora sp.	animal parasite/opportunistic human parasite	98.4% $\pm$ 0.93	61	1190	130	815	2850
Cladophialophora sylvestris	animal parasite/opportunistic human parasite	100%	0	0	0	2	18
Cladosporium herbarum	leaf/fruit/seed pathogen, animal parasite	98.19%	0	3	0	0	12
Cladosporium sp.	leaf/fruit/seed pathogen, animal parasite	98.42% $\pm$ 0.32	22	64	3	6	4
Clavaria flavipes	root-associated	97.82% $\pm$ 0.28	0	0	0	7	0
Clavaria sp.	root-associated	99% $\pm$ 0.85	0	2	0	8	6
Clavaria zollingeri	root-associated	99.8% $\pm$ 0.28	0	0	0	45	0
Clavulinopsis helvola	root-associated	98.81%	0	0	1	0	0
Clavulinopsis sp.	root-associated	98.82% $\pm$ 1.1	0	0	0	11	112

<i>Clonostachys candelabrum</i>	leaf/fruit/seed pathogen, nematophagous	100%	0	6	0	0	0
<i>Clonostachys rosea</i>	leaf/fruit/seed pathogen, nematophagous	98.34% ± 0	25	0	0	5	0
<i>Coniochaeta fasciculata</i>	leaf/fruit/seed pathogen, animal parasite	100%	25	0	0	0	0
<i>Cryptocline arctostaphyli</i>	leaf/fruit/seed pathogen	100%	0	4	2	0	5
<i>Cryptococcus pseudolongus</i>	animal-associated/opportunistic human parasite	100%	0	0	0	0	10
<i>Cryptococcus sp.</i>	animal-associated/opportunistic human parasite	97.21%	0	14	0	0	57
<i>Cryptococcus waticus</i>	animal-associated/opportunistic human parasite	98.81%	2	0	0	0	0
<i>Cunninghamella elegans</i>	opportunistic human parasite	98.80%	0	8	0	0	0
<i>Cuphophyllus subviolaceus</i>	root-associated	99.8% ± 0.28	0	0	0	0	398
<i>Curvularia austriaca</i>	leaf/fruit/seed pathogen, opportunistic human parasite	98.64% ± 0.64	9	0	0	0	0
<i>Curvularia canadensis</i>	leaf/fruit/seed pathogen, opportunistic human parasite	100%	2	0	0	0	0
<i>Curvularia pseudoprotuberata</i>	leaf/fruit/seed pathogen, opportunistic human parasite	100%	0	0	0	0	2
<i>Curvularia xishuangbannaensis</i>	leaf/fruit/seed pathogen, opportunistic human parasite	99.54%	3	0	0	0	0
<i>Cylindrium algarvense</i>	leaf/fruit/seed pathogen	99.02%	0	0	0	0	1
<i>Cylindrium desperesense</i>	leaf/fruit/seed pathogen	98.53% ± 2.08	1	0	0	1	0
<i>Cyphellophora livistonae</i>	animal parasite/opportunistic human parasite	99.55%	1	0	0	0	0
<i>Cyphellophora vermispora</i>	animal parasite/opportunistic human parasite	100%	1	0	0	0	0
<i>Diaporthe alleghaniensis</i>	leaf/fruit/seed pathogen	97.47%	0	4	0	0	0
<i>Diaporthe columnaris</i>	leaf/fruit/seed pathogen	98.65% ± 1.19	1554	0	0	0	0
<i>Diaporthe sp.</i>	leaf/fruit/seed pathogen	95.61%	297	0	0	0	0
<i>Dictyolus sp.</i>	leaf/fruit/seed pathogen	95.65%	0	0	0	0	22
<i>Didymella bellidis</i>	leaf/fruit/seed pathogen, animal parasite	99.11%	0	1	0	0	0
<i>Discosia rubi</i>	leaf/fruit/seed pathogen	98.61%	2	3	0	0	0
<i>Elsinoe salicina</i>	leaf/fruit/seed pathogen	98.66%	0	1	0	0	0
<i>Entoloma foliomarginatum</i>	root-associated	100%	0	0	0	1	0
<i>Entoloma paraconferendum</i>	root-associated	98.41%	0	0	0	0	16
<i>Entoloma rhodocylix</i>	root-associated	98.41% ± 0	0	79	0	0	0
<i>Entoloma sinuatum</i>	root-associated	99.6% ± 0.56	0	0	0	0	45
<i>Entoloma sp.</i>	root-associated	98.67% ± 0.77	2	1192	0	3	10
<i>Exobasidium sp.</i>	leaf/fruit/seed pathogen	100%	0	1	0	0	0
<i>Exophiala equina</i>	root-associated, animal parasite/opportunistic human parasite	100%	60	0	0	0	2
<i>Exophiala pisciphila</i>	root-associated, animal parasite/opportunistic human parasite	99.8% ± 0.29	74	0	0	0	0
<i>Exophiala radialis</i>	root-associated, animal parasite/opportunistic human parasite	99.39% ± 0.23	108	0	0	1	0
<i>Exophiala sp.</i>	root-associated, animal parasite/opportunistic human parasite	99.19%	0	0	0	0	1
<i>Exophiala xenobiotica</i>	root-associated, animal parasite/opportunistic human parasite	99.57%	16	0	0	0	8
<i>Fimicolochytrium sp.</i>	algal parasite	97.21%	1	0	0	0	0
<i>Fusarium graminearum</i>	leaf/fruit/seed pathogen, opportunistic human parasite	99.52%	2	0	0	0	0
<i>Fusarium lateritium</i>	leaf/fruit/seed pathogen, opportunistic human parasite	99.10%	101	0	0	0	0
<i>Fusarium oxysporum</i>	leaf/fruit/seed pathogen, opportunistic human parasite	100%	726	0	0	0	0
<i>Fusarium sp.</i>	leaf/fruit/seed pathogen, opportunistic human parasite	100%	18	0	0	0	0
<i>Fusarium tricinctum</i>	leaf/fruit/seed pathogen, opportunistic human parasite	99.77% ± 0.32	86	0	0	0	0
<i>Galerina allospora</i>	leaf/fruit/seed pathogen	100%	0	0	0	0	17
<i>Galerina lacustris</i>	leaf/fruit/seed pathogen	98.54% ± 0.23	0	0	0	0	1327
<i>Galerina sp.</i>	leaf/fruit/seed pathogen	98.2% ± 1.42	19	137	0	0	0

<i>Ganoderma lucidum</i>	wood pathogen	98.81%	317	0	0	0	0
<i>Gliophorus irrigatus</i>	root-associated	98.68% ± 1.11	0	0	0	0	1205
<i>Gliophorus</i> sp.	root-associated	98.71% ± 0.6	0	110	156	137	2
<i>Gloioxanthomyces nitidus</i>	root-associated	99.01% ± 0.28	0	0	0	0	56
<i>Glutinoglossum peregrinans</i>	root-associated	97.18%	0	0	0	0	4
<i>Herpotrichia pinetorum</i>	leaf/fruit/seed pathogen	98.5% ± 0.69	95	0	0	0	0
<i>Herpotrichia</i> sp.	leaf/fruit/seed pathogen	98.68% ± 1.12	1012	0	0	44	0
<i>Hyaloscypha desmidiacea</i>	leaf/fruit/seed pathogen	100%	32	0	0	0	0
<i>Hyaloscypha</i> sp.	leaf/fruit/seed pathogen	100%	0	0	0	0	3
<i>Hyaloscypha variabilis</i>	leaf/fruit/seed pathogen	98.29% ± 0.27	0	0	0	0	9
<i>Hygrocybe acutoconica</i>	root-associated	97.98% ± 1.69	0	0	0	0	10
<i>Hygrocybe chlorophana</i>	root-associated	96.18% ± 0.99	0	0	0	257	0
<i>Hygrocybe reidii</i>	root-associated	99.60%	0	0	0	134	0
<i>Hymenoscyphus imberbis</i>	leaf/fruit/seed pathogen	96.47% ± 0.27	1259	0	0	3	2
<i>Hymenoscyphus</i> sp.	leaf/fruit/seed pathogen	99.51%	0	0	0	5	0
<i>Ilyonectria liriiodendri</i>	leaf/fruit/seed pathogen	100%	10	0	0	0	0
<i>Knufia</i> sp.	leaf/fruit/seed pathogen, opportunistic animal parasite	99% ± 0.67	33	0	0	0	0
<i>Knufia tsunetae</i>	leaf/fruit/seed pathogen, opportunistic animal parasite	97.7% ± 1.58	121	0	0	0	1
<i>Lecanicillium flavidum</i>	invertebrate parasite	100%	0	0	0	0	177
<i>Lecanicillium fungicola</i>	invertebrate parasite	100%	0	0	0	1	0
<i>Lecanicillium fusisporum</i>	invertebrate parasite	100%	0	0	0	0	3
<i>Leptobacillium leptobactrum</i>	invertebrate parasite	99.04% ± 0.48	0	0	2	0	19
<i>Lophodermium macii</i>	leaf/fruit/seed pathogen	99.01% ± 0	0	0	0	2	3569
<i>Malassezia</i> sp.	root-associated, animal-associated/opportunistic human parasite	97.21%	1	0	0	0	0
<i>Metacordyceps chlamydosporia</i>	animal parasite	98.19% ± 0.28	8	0	0	0	0
<i>Metarhizium brunneum</i>	animal parasite	97.79% ± 0.28	0	46	9	0	0
<i>Metarhizium gaoligongense</i>	animal parasite	100%	0	0	0	1	0
<i>Metarhizium</i> sp.	animal parasite	97.76%	0	0	0	0	8
<i>Microcyclospora malicola</i>	leaf/fruit/seed pathogen	100%	0	1	0	0	0
<i>Microcyclospora</i> sp.	leaf/fruit/seed pathogen	98.2% ± 0.28	0	25	0	8	13
<i>Monochaetia castaneae</i>	leaf/fruit/seed pathogen	99.53%	0	2	2	0	0
<i>Monochaetia dimorphospora</i>	leaf/fruit/seed pathogen	99.10%	0	0	0	1	0
<i>Monochaetia ilicis</i>	leaf/fruit/seed pathogen	97.76%	0	4	0	0	0
<i>Monochaetia sinensis</i>	leaf/fruit/seed pathogen	98.66%	0	0	0	1	0
<i>Monosporascus</i> sp.	leaf/fruit/seed pathogen	97.78%	2	0	0	0	0
<i>Mortierella alliacea</i>	root-associated, opportunistic human parasite	99.33% ± 0.83	0	2	2	8	12
<i>Mortierella ambigua</i>	root-associated, opportunistic human parasite	99.21%	1	0	0	0	0
<i>Mortierella angusta</i>	root-associated, opportunistic human parasite	100%	0	12	2	0	1
<i>Mortierella basiparvispora</i>	root-associated, opportunistic human parasite	98.81%	3	3	0	0	0
<i>Mortierella gemmifera</i>	root-associated, opportunistic human parasite	99.4% ± 0.28	0	13	0	0	6
<i>Mortierella macrocystis</i>	root-associated, opportunistic human parasite	99.8% ± 0.28	0	22	2	31	14
<i>Mortierella pulchella</i>	root-associated, opportunistic human parasite	99.2% ± 1.13	0	0	0	12	86
<i>Mortierella</i> sp.	root-associated, opportunistic human parasite	99.08% ± 0.86	15	144	49	65	134
<i>Mucor circinelloides</i>	opportunistic human parasite	100%	7	0	0	0	0

<i>Mucor inaequisporus</i>	opportunistic human parasite	98.67%	0	0	0	0	2
<i>Mucor moelleri</i>	opportunistic human parasite	99.57%	2	0	0	0	0
<i>Mucor silvaticus</i>	opportunistic human parasite	99.4% ± 0.28	0	0	0	0	5
<i>Mucor</i> sp.	opportunistic human parasite	99.56%	0	4	0	0	0
<i>Mycena albiceps</i>	leaf/fruit/seed pathogen	99.60%	0	0	0	0	1
<i>Mycena griseoviridis</i>	leaf/fruit/seed pathogen	98.41%	9	0	0	0	0
<i>Mycena leptcephala</i>	leaf/fruit/seed pathogen	99.60%	0	107	0	0	0
<i>Mycena metata</i>	leaf/fruit/seed pathogen	100%	0	0	2	0	0
<i>Mycena purpureofusca</i>	leaf/fruit/seed pathogen	98.8% ± 0.56	0	0	46	25	1745
<i>Mycena rebaudengoi</i>	leaf/fruit/seed pathogen	98.94% ± 0.61	387	0	0	0	0
<i>Mycena sanguinolenta</i>	leaf/fruit/seed pathogen	97.69% ± 1.36	0	28	0	266	198
<i>Mycena</i> sp.	leaf/fruit/seed pathogen	98.4% ± 1.01	260	14	15	34	218
<i>Mycena stylobates</i>	leaf/fruit/seed pathogen	100%	61	0	0	0	0
<i>Mycosphaerella ribis</i>	leaf/fruit/seed pathogen	95.22%	0	0	2	0	0
<i>Myxotrichum cancellatum</i>	root-associated	99.51%	0	21	0	0	1
<i>Neosascochyta desmazieri</i>	leaf/fruit/seed pathogen	99.52%	296	0	0	0	0
<i>Neodevriesia imbrexigena</i>	leaf/fruit/seed pathogen	100%	2	0	0	0	0
<i>Ochroconis</i> sp.	leaf/fruit/seed pathogen, opportunistic human parasite	99.3% ± 0.33	10	3	0	0	0
<i>Oidiodendron periconioides</i>	root-associated	95.79%	5	16	2	0	76
<i>Oidiodendron</i> sp.	root-associated	97.91% ± 1.59	15	1	1	12	60
<i>Olpidiaster brassicae</i>	root pathogen	99.60%	5	0	0	0	0
<i>Paraphoma ledniceana</i>	wood pathogen	99.52%	4	0	0	0	0
<i>Paraphoma radicina</i>	wood pathogen	99.04% ± 0	6	0	0	0	0
<i>Peltaster fruticola</i>	unspecified plant pathogen	99.12%	0	27	0	18	19
<i>Penicillium arianeae</i>	opportunistic human parasite	100%	0	0	2	0	0
<i>Penicillium bissettii</i>	opportunistic human parasite	100%	0	1	0	0	0
<i>Penicillium catalonicum</i>	opportunistic human parasite	98.70%	0	3	0	0	0
<i>Penicillium cryptum</i>	opportunistic human parasite	98.18%	15	0	0	0	0
<i>Penicillium neoherquei</i>	opportunistic human parasite	100%	0	0	4	2	0
<i>Penicillium</i> sp.	opportunistic human parasite	99.09% ± 0.69	24	82	10	9	11
<i>Penicillium sublectaticum</i>	opportunistic human parasite	100%	1	0	0	0	0
<i>Penicillium thomii</i>	opportunistic human parasite	100%	0	0	0	1	2
<i>Penicillium verhagenii</i>	opportunistic human parasite	99.09%	0	0	0	0	3
<i>Pestalotiopsis macadamiae</i>	leaf/fruit/seed pathogen	98.31%	0	0	0	1	0
<i>Pezicula ericae</i>	leaf/fruit/seed pathogen	95.89% ± 0.6	8	122	21	364	97
<i>Pezicula heterochroma</i>	leaf/fruit/seed pathogen	95.75% ± 0.23	741	12	0	0	2
<i>Pezoloma</i> sp.	leaf/fruit/seed pathogen	99.16%	0	6	0	0	0
<i>Phialemonium inflatum</i>	animal parasite	98.87% ± 0.32	62	0	0	0	0
<i>Phialocephala glacialis</i>	root-associated	97.38% ± 0.96	0	0	0	5	240
<i>Phialocephala helenae</i>	root-associated	97.21% ± 0.47	438	530	1521	209	1999
<i>Phialocephala repens</i>	root-associated	98.59% ± 0.47	2	0	1	4	0
<i>Phialocephala</i> sp.	root-associated	100%	11	0	0	0	0
<i>Phialocephala sphaeroides</i>	root-associated	99.32% ± 0.97	0	0	0	0	8
<i>Phialophora cyclaminis</i>	leaf/fruit/seed pathogen, animal parasite	99.54%	3	0	0	0	0

<i>Phlogicylindrium</i> sp.	leaf/fruit/seed pathogen	99.56%	0	0	0	2	0
<i>Phlyctochytrium arcticum</i>	algal parasite, nematophagous	100%	4	0	0	0	0
<i>Pholiota mixta</i>	wood pathogen	99.6% ± 0	0	0	0	0	758
<i>Polyscytalum</i> sp.	leaf/fruit/seed pathogen	100%	0	0	0	0	8
<i>Polyscytalum vaccinii</i>	leaf/fruit/seed pathogen	98.01%	0	0	2	0	0
<i>Protomyces</i> sp.	leaf/fruit/seed pathogen	99.56%	3	0	0	0	0
<i>Pseudogymnoascus alpinus</i>	opportunistic animal parasite <i>G. destructans</i>	99.16%	0	21	0	0	0
<i>Pseudogymnoascus appendiculatus</i>	opportunistic animal parasite <i>G. destructans</i>	98.63%	26	0	0	0	0
<i>Puccinia graminis</i>	leaf/fruit/seed pathogen	99.60%	1	0	0	0	0
<i>Purpureocillium lilacinum</i>	arthropod parasite	100%	5	0	0	0	0
<i>Ramariopsis</i> sp.	root-associated	98.8% ± 1.12	0	0	0	5	0
<i>Rhexocercosporidium panacis</i>	root pathogen	97.16%	9	0	0	0	0
<i>Rhinocladiella</i> sp.	root-associated, animal parasite/opportunistic human parasite	98.26%	0	0	1	2	0
<i>Rhizidium phycophilum</i>	algal parasite	100%	0	0	0	0	1
<i>Rhizophlyctis rosea</i>	algal parasite	99.20%	0	1	0	0	0
<i>Rhizophydium</i> sp.	algal parasite	98.6% ± 0.29	2	0	0	0	0
<i>Sagenomella diversispora</i>	opportunistic human parasite	99.56% ± 0.36	4	31	13	46	32
<i>Sagenomella verticillata</i>	opportunistic human parasite	98.07% ± 2.12	0	13	0	0	16
<i>Samsoniella hepiali</i>	invertebrate parasite	100%	0	0	0	0	1
<i>Scedosporium dehoogii</i>	opportunistic human parasite	100%	3	0	0	0	0
<i>Schizothyrium</i> sp.	leaf/fruit/seed pathogen	98.55%	0	3	0	0	0
<i>Scleromitrua calthicola</i>	leaf/fruit/seed pathogen	96.10%	1	0	0	0	0
<i>Sclerostagonospora</i> sp.	leaf/fruit/seed pathogen	98.02% ± 1.54	25	0	0	0	1
<i>Scolecobasidium</i> sp.	leaf/fruit/seed pathogen, animal parasite	99% ± 0.7	0	0	2	0	99
<i>Scytalidium album</i>	opportunistic human parasite	99.02%	0	0	0	0	2
<i>Scytalidium</i> sp.	opportunistic human parasite	98.54%	2	0	0	0	0
<i>Seimatosporium lichenicola</i>	leaf/fruit/seed pathogen	97.34%	0	1	0	0	0
<i>Setomelanomma holmii</i>	wood pathogen	99.05%	0	11	0	0	0
<i>Setophaeosphaeria badalingensis</i>	leaf/fruit/seed pathogen	100%	2	0	0	0	0
<i>Sphaerulina abeliceae</i>	leaf/fruit/seed pathogen	99.52%	0	1	0	0	0
<i>Sporothrix sclerotialis</i>	wood pathogen, opportunistic human parasite	98.26%	4	0	0	0	0
<i>Stagonospora heteroderae</i>	leaf/fruit/seed pathogen	100%	768	0	0	0	0
<i>Stagonosporopsis valerianellae</i>	leaf/fruit/seed pathogen	98.25%	123	0	0	0	0
<i>Talaromyces albisclerotius</i>	opportunistic human parasite	99.52%	0	1	0	0	0
<i>Talaromyces bannicus</i>	opportunistic human parasite	98.17%	0	0	0	0	1
<i>Talaromyces coprophilus</i>	opportunistic human parasite	98.17% ± 0.65	113	3	0	0	0
<i>Talaromyces domesticus</i>	opportunistic human parasite	99.52%	41	0	0	0	0
<i>Talaromyces infraolivaceus</i>	opportunistic human parasite	97.50%	3	0	0	0	0
<i>Talaromyces proteolyticus</i>	opportunistic human parasite	100%	0	4	0	0	0
<i>Talaromyces</i> sp.	opportunistic human parasite	99.05%	0	0	0	2	0
<i>Talaromyces subtropicalis</i>	opportunistic human parasite	100%	33	0	0	0	4
<i>Talaromyces yunnanensis</i>	opportunistic human parasite	100%	817	0	0	0	0
<i>Thanatephorus</i> sp.	leaf/fruit/seed pathogen	98.41%	10	0	0	0	0
<i>Tolypocladium album</i>	animal parasite	100%	0	0	0	0	1

Tolypocladium cylindrosporum	animal parasite	99.07%	0	0	0	0	9
Tolypocladium geodes	animal parasite	99.54%	0	0	4	0	0
Tolypocladium inflatum	animal parasite	99.53%	0	5	0	0	0
Tolypocladium sp.	animal parasite	98.05% $\pm$ 1.14	0	4	0	0	3
Tolypocladium tropicale	animal parasite	99.32% $\pm$ 0.32	0	21	1	0	28
Trichoderma asperellum	leaf/fruit/seed pathogen	99.8% $\pm$ 0.29	0	0	0	11	23
Trichoderma hamatum	leaf/fruit/seed pathogen	97.96%	0	0	1	0	0
Trichoderma harzianum	leaf/fruit/seed pathogen	100%	15	0	0	0	0
Trichoderma parasiluliferum	leaf/fruit/seed pathogen	100%	0	0	0	0	50
Trichoderma pubescens	leaf/fruit/seed pathogen	98.78%	0	23	0	0	0
Trichoderma sp.	leaf/fruit/seed pathogen	97.21% $\pm$ 1.8	13	14	0	1	7
Trichoderma strigosum	leaf/fruit/seed pathogen	98.25%	0	0	1	0	0
Trichoderma viride	leaf/fruit/seed pathogen	99.13%	0	0	0	0	12
Trichoglossum sp.	root-associated	98.38%	0	0	0	1	0
Trichosporon asteroides	animal parasite/opportunistic human parasite	100%	13	0	0	0	0
Trichothecium crotocinigenum	leaf/fruit/seed pathogen	99.14%	9	0	0	0	0
Umbelopsis changbaiensis	root-associated	99.60%	0	0	0	9	2
Umbelopsis isabellina	root-associated	98.21% $\pm$ 0.23	0	4	2	2	17
Umbelopsis sp.	root-associated	98.43% $\pm$ 0.89	49	138	13	12	34
Venturia catenospora	leaf/fruit/seed pathogen	96.38%	0	0	0	0	2
Xenoacremonium falcatum	opportunistic human parasite	98.62%	25	0	0	0	0
Xenopyrenochaetopsis pratorum	leaf/fruit/seed pathogen	100%	10	0	0	0	0
Zygoascus biomembranicola	opportunistic human parasite	98.44% $\pm$ 0.32	0	0	0	0	3

Table S7. Bacterial pathogens detected in leaf samples across the urbanization gradient. Numbers are sums of species counts normalized by rarefaction in leaf samples of each tree type. % identity refers to the % match of 16S sequence from the tree microbiome dataset to the 16S sequence in the Multiple Bacterial Pathogen Detection database.

Bacterial Species	Pathogen Type	% Identity ($\pm$ standard deviation when >1 ASV matched to a pathogenic sequence)	Urban	Urban	Urban	Rural Forest	Rural Forest
			Street Tree	Forest Edge	Forest Interior	Edge	Interior
Acetobacteraceae bacterium	Animal	96.44%	0	0	0	1	14
Acinetobacter radioresistens	Zoonotic	100%	0	0	1	0	0
Actinomadura sp.	Animal, Zoonotic	96.84%	0	0	1	0	0
Arthrobacter sp.	Zoonotic	99.61%	0	8	0	0	0
Aurantimonadaceae bacterium	Animal	97.63%	0	3	0	0	0
Bacillus anthracis	Zoonotic	99.41% $\pm$ 0.84	0	4	0	0	0
Bacillus sp.	Animal	95.28%	0	1	0	0	0
Bacillus sp.	Zoonotic	100%	22	14	1	1	0
Bordetella hinzii	Animal	99.61%	0	3	0	0	4
Buchnera aphidicola	Animal	98.42% $\pm$ 0	3	1	0	0	0
Burkholderia sp.	Animal	99.21%	0	8	1	3	0
Candidatus Trichorickettsia	Animal, Zoonotic	97.23% $\pm$ 0.4	0	0	1	0	28
Castanea mollissima	Animal	99.41% $\pm$ 0.28	12	0	4	5	3
Cellulomonas denverensis	Animal	97.64%	0	0	9	0	0
Chryseobacterium sp.	Zoonotic	96.06%	0	1	0	0	0
Corticibacterium populi	Plant	95.69%	1	0	0	2	0
Corynebacterium kroppenstedtii	Animal	99.61%	19	9	0	0	4
Cystobacter ferrugineus	Animal	98.42%	0	0	0	1	0
Erwinia sp.	Plant, Animal	99.61%	0	0	27	36	0
Escherichia coli	Zoonotic	100%	0	2	0	0	0
Flavobacterium rivuli	Animal	97.63%	0	0	0	3	0
Frigoribacterium sp.	Plant, Animal, Zoonotic	97.23%	0	11	0	0	0
Kineosporia mesophila	Animal	95.26%	0	4	3	0	0
Klebsiella pneumoniae	Plant, Animal, Zoonotic	100%	2	0	37	0	38
Klebsiella sp.	Plant, Animal	99.61%	0	1	0	0	0
Lactobacillus delbrueckii	Animal	100%	0	0	2	0	0

Massilia lurida	Plant	97.63%	2	3	0	0	0
Massilia sp.	Plant	98.81%	0	0	1	0	0
Mycoplasma wenyonii	Animal	98.81%	0	0	0	0	2
Paenibacillus glucanolyticus	Zoonotic	95.64%	0	0	0	3	0
Paenibacillus sp.	Zoonotic	95.24%	0	2	0	0	0
Pectobacterium carotovorum	Plant, Animal	100%	0	17	22	1	0
Prevotella disiens	Animal	100%	2	0	0	0	0
Pseudokineococcus lusitanus	Animal	95.65%	0	4	1	0	0
Pseudomonas aeruginosa	Zoonotic	100%	0	0	0	18	0
Pseudomonas fluorescens	Zoonotic	100%	16	0	5	0	0
Pseudomonas syringae	Plant, Animal, Zoonotic	100%	13	31	2	0	0
Rhizobium sp.	Plant	98.02%	0	0	4	5	0
Rhizobium sp.	Zoonotic	97.43% $\pm$ 0.84	4	17	0	0	0
Rhodopseudomonas rhenobacensis	Animal	96.44%	1	0	0	0	0
Roseomonas elaeocarpi	Animal	97.64%	10	3	0	0	0
Roseomonas vinacea	Animal	95.65%	0	1	0	0	0
Serratia marcescens	Zoonotic	100%	0	0	0	0	6
Serratia symbiotica	Animal	95.26%	0	0	0	8	0
Sphingomonas glacialis	Animal, Zoonotic	98.02%	0	0	4	0	2
Sphingomonas kwangyangensis	Animal	97.83% $\pm$ 0.28	0	0	4	0	5
Sphingomonas sp.	Animal	97.29% $\pm$ 1.6	7	10	9	3	0
Sphingomonas sp.	Plant, Animal	99.61%	0	13	0	0	0
Stenotrophomonas maltophilia	Zoonotic	98.19% $\pm$ 2.48	10	17	41	2	15
Stenotrophomonas sp.	Animal	100%	0	0	2	0	0
Tardiphaga robiniae	Animal	99.21%	0	0	0	3	0
Variovorax sp.	Animal	98.81%	0	0	1	0	0
Vibrio metschnikovii	Animal	99.61%	0	0	0	0	2

Table S8. Bacterial pathogens detected in upper soil samples across the urbanization gradient. Numbers are sums of species counts normalized by rarefaction in upper soil (0-15 cm depth) samples of each tree type. % identity refers to the % match of 16S sequence from the tree microbiome dataset to the 16S sequence in the Multiple Bacterial Pathogen Detection database.

Bacterial Species	Pathogen Type	% Identity ($\pm$ standard deviation when >1 ASV matched to a pathogenic sequence)	Urban	Urban	Rural Forest	Rural Forest	Urban
			Street Tree	Forest Edge	Edge	Interior	Forest Interior
<i>Acinetobacter baumannii</i>	Zoonotic	100%	13	0	0	0	0
<i>Acinetobacter radioresistens</i>	Zoonotic	100%	50	0	0	6	0
<i>Actinoallomurus coprocola</i>	Animal	95.26%	2	0	0	0	0
<i>Actinoallomurus oryzae</i>	Animal, Zoonotic	95.31%	73	0	0	0	0
<i>Actinoallomurus</i> sp.	Animal, Zoonotic	95.29% $\pm$ 0.02	167	0	0	0	0
<i>Actinomadura keratinilytica</i>	Zoonotic	95.28%	11	0	0	0	0
<i>Actinomadura oligospora</i>	Animal, Zoonotic	96.44%	2	0	0	0	0
<i>Actinomadura rubrobrunea</i>	Zoonotic	95.65%	5	0	0	0	0
<i>Actinomadura scrupuli</i>	Animal, Zoonotic	97.04% $\pm$ 0.28	0	42	0	5	22
<i>Actinomadura</i> sp.	Animal, Zoonotic	97.23%	0	9	0	33	6
<i>Actinosynnema</i> sp.	Animal	98.42%	0	34	0	0	0
<i>Afipia felis</i>	Animal	100%	95	0	0	0	0
<i>Afipia</i> sp.	Animal	97.23%	3	0	0	0	0
<i>Agrococcus</i> sp.	Plant	99.21%	69	0	0	0	0
<i>Aldersonia kunmingensis</i>	Animal, Zoonotic	99.21%	22	0	0	0	0
<i>Amycolatopsis</i> sp.	Plant	98.02%	86	0	6	0	0
<i>Arthrobacter crystallopoietes</i>	Animal	98.42%	31	0	0	0	0
<i>Arthrobacter</i> sp.	Plant	98.81%	289	8	0	0	16
<i>Arthrobacter</i> sp.	Plant, Zoonotic	97.23%	63	0	0	0	0
<i>Arthrobacter</i> sp.	Zoonotic	98.5% $\pm$ 0.9	3357	0	9	0	0
<i>Bacillus acidicola</i>	Animal, Zoonotic	98.42%	0	0	2	26	0
<i>Bacillus azotoformans</i>	Animal, Zoonotic	98.42%	22	0	0	0	0
<i>Bacillus clausii</i>	Animal	97.26%	55	0	0	0	0
<i>Bacillus coagulans</i>	Animal	100%	16	0	0	0	0
<i>Bacillus hackensackii</i>	Zoonotic	98.02%	1139	0	0	0	0
<i>Bacillus horikoshii</i>	Animal, Zoonotic	99.21%	0	0	42	23	34
<i>Bacillus lentus</i>	Animal	97.23%	519	0	0	0	0

Bacillus lentus	Animal, Zoonotic	98.81%	876	12	0	0	16
Bacillus lycopersici	Zoonotic	96.44%	0	0	0	16	0
Bacillus salitolerans	Zoonotic	97.63%	0	0	3	0	0
Bacillus smithii	Zoonotic	98.02%	464	0	0	0	0
Bacillus sp.	Animal	98.42% $\pm$ 1.68	189	0	8	0	0
Bacillus sp.	Animal, Zoonotic	98.42% $\pm$ 1.05	324	0	24	0	0
Bacillus sp.	Zoonotic	98.91% $\pm$ 1.27	360	0	6	0	2
Bacillus sporothermodurans	Animal	98.02%	52	7	3	25	0
Bacillus thermolactis	Zoonotic	97.23%	28	0	0	0	0
Bradyrhizobium sp.	Animal	99.21% $\pm$ 0.56	1376	111	20	0	13
Brevibacillus borstelensis	Animal	99.60%	25	0	0	0	0
Brevibacillus laterosporus	Animal	100%	169	0	0	0	0
Brevibacillus sp.	Animal	99.21%	71	0	0	0	0
Burkholderia sp.	Animal	98.48% $\pm$ 0.88	805	641	437	1022	308
Burkholderia sp.	Animal, Zoonotic	98.95% $\pm$ 0.91	43	0	0	28	0
Burkholderia sp.	Plant, Animal, Zoonotic	98.02%	0	0	0	17	0
Caballeronia concitans	Animal	99.21%	53	0	0	0	0
Caballeronia pterochthonis	Animal	99.61%	11	0	0	0	0
Candidatus Metachlamydia	Animal	95.44% $\pm$ 0.29	32	20	21	50	22
Candidatus Mycoplasma	Animal	95.24%	2	0	0	0	0
Candidatus Paracaedibacter	Animal	97.65%	1	0	0	0	0
Candidatus Protochlamydia	Animal	95.89% $\pm$ 0.72	9	1	3	6	9
Candidatus Trichorickettsia	Animal, Zoonotic	97.63%	5	0	0	0	0
Cellulomonas sp.	Animal	99.41% $\pm$ 0.28	167	0	0	0	0
Cereibacter changlensis	Animal	96.05%	1	0	0	0	0
Chromobacterium sp.	Animal	99.21%	0	0	0	4	0
Chryseobacterium sp.	Zoonotic	96.06%	11	0	0	0	0
Clostridium argentinense	Animal	99.61%	5	0	0	0	0
Clostridium beijerinckii	Plant, Animal	99.8% $\pm$ 0.28	93	0	0	0	0
Clostridium botulinum	Animal	100% $\pm$ 0	12	0	8	0	13
Clostridium frigidicarnis	Animal	96.84%	14	2	0	0	0
Clostridium gasigenes	Animal	96.05%	2	0	0	0	0
Clostridium magnum	Animal	97.63%	6	0	0	0	0
Clostridium perfringens	Zoonotic	100%	107	0	0	0	0

<i>Collimonas fungivorans</i>	Animal	97.23%	0	0	0	16	4
<i>Corallococcus coralloides</i>	Animal	96.84% $\pm$ 0.56	77	0	0	2	0
<i>Coxiella endosymbiont</i>	Animal	96.44%	0	1	0	0	0
<i>Croceobacterium</i> sp.	Plant	97.23%	154	0	0	0	0
<i>Cryocola antiquus</i>	Plant	99.21%	0	0	3	0	0
<i>Cupriavidus campinensis</i>	Animal	99.61%	11	0	0	0	0
<i>Cystobacter ferrugineus</i>	Animal	98.81%	0	0	2	0	0
<i>Cystobacter gracilis</i>	Animal	97.63%	36	0	0	0	0
<i>Derxia</i> sp.	Animal	97.23%	8	0	0	0	0
<i>Diaminobutyricibacter tongyongensis</i>	Plant	99.21%	25	0	0	0	0
<i>Dictyostelium polycephalum</i>	Animal	95.65%	1	0	0	0	0
<i>Domibacillus tundrae</i>	Plant, Animal	98.42%	0	5	2	0	0
<i>Duganella</i> sp.	Plant	97.04% $\pm$ 0.84	16	2	0	0	0
<i>Flavobacterium</i> sp.	Animal	95.85% $\pm$ 0.28	0	1	1	0	0
<i>Flexivirga alba</i>	Animal	96.44%	16	0	0	0	0
<i>Frankia</i> sp.	Animal	95.39% $\pm$ 0.23	77	0	1	0	0
<i>Geobacillus thermodenitrificans</i>	Animal, Zoonotic	97.23%	193	0	0	0	0
<i>Geobacter</i> sp.	Animal	97.23% $\pm$ 0.56	0	0	43	1	0
<i>Goodfellowiella coeruleoviolacea</i>	Animal	98.42%	0	0	0	0	9
<i>Gryllotalpicola ginsengisoli</i>	Plant, Animal	96.05%	47	0	0	0	0
<i>Herbaspirillum</i> sp.	Plant	99.61%	22	0	0	0	0
<i>Homoserinibacter</i> sp.	Plant, Animal	99.61%	23	0	0	0	0
<i>Humibacter ginsengiterrae</i>	Plant, Animal	98.02%	98	0	0	0	0
<i>Janthinobacterium</i> sp.	Plant	97.23%	3	0	0	0	0
<i>Jatrophihabitans</i> sp.	Animal	96.05%	6	0	0	0	0
<i>Klebsiella pneumoniae</i>	Plant, Animal, Zoonotic	100%	0	0	6	9	0
<i>Lactococcus lactis</i>	Zoonotic	100%	9	52	0	0	0
<i>Legionella adelaidensis</i>	Animal	96.84%	0	1	0	0	0
<i>Legionella donaldsonii</i>	Animal	99.21%	0	0	5	0	0
<i>Legionella drancourtii</i>	Animal	98.42%	7	0	0	0	0
<i>Legionella dresdenensis</i>	Animal	97.63%	1	0	0	0	0
<i>Legionella londiniensis</i>	Animal	96.84%	4	0	0	0	0
<i>Legionella maceachernii</i>	Animal	97.05% $\pm$ 0.84	0	0	0	0	3
<i>Legionella norrlandica</i>	Animal	95.26%	0	0	0	1	0

Legionella sp.	Animal	97.08% $\pm$ 1.03	10	0	7	11	7
Legionella steigerwaltii	Animal	99.21%	7	0	0	0	0
Leucobacter populi	Plant	96.44%	4	0	0	0	0
Luteimonas vadosa	Plant	97.23%	15	0	0	0	0
Lysobacter sp.	Plant	96.64% $\pm$ 1.4	14	0	0	0	0
Massilia sp.	Plant	98.42% $\pm$ 0.56	0	8	7	0	0
Mesorhizobium sp.	Animal	95.65%	19	0	0	0	0
Mesorhizobium sp.	Plant	96.46%	19	0	0	0	0
Mesorhizobium sp.	Zoonotic	98.02%	9	0	0	0	0
Methylocella palustris	Animal	95.26%	0	6	9	9	0
Methylosinus trichosporium	Animal	96.46%	21	0	0	0	0
Mycobacterium conspicuum	Animal	99.61%	0	0	131	375	0
Mycobacterium sp.	Animal	98.81%	0	0	0	53	31
Mycobacterium sp.	Animal, Zoonotic	98.62% $\pm$ 0.51	92	19	0	4	14
Mycoplasma wenyonii	Animal	99.5% $\pm$ 0.38	12	2	0	2	0
Nakamurella endophytica	Animal	95.45% $\pm$ 0.28	111	0	0	0	15
Nocardia nova	Animal	99.21% $\pm$ 0.97	81	0	2	0	0
Nocardia pseudobrasiliensis	Animal	100%	4	16	0	0	6
Nocardia sp.	Animal	98.62% $\pm$ 1.19	6	0	0	2	2
Nocardia vermiculata	Animal	98.03% $\pm$ 0.55	2	0	0	0	1
Novosphingobium piscinae	Animal	96.05%	38	0	0	0	0
Oceanobacillus sp.	Zoonotic	95.26%	0	0	0	8	0
Ornithinibacillus contaminans	Animal	97.83% $\pm$ 0.28	156	0	0	0	0
Oryzihumus leptocrescens	Animal	97.63%	3	0	0	0	0
Oryzihumus terrae	Animal	96.98% $\pm$ 0.6	192	0	0	0	0
Paenibacillus anaericanus	Zoonotic	97.22%	0	27	19	56	12
Paenibacillus barengoltzii	Zoonotic	97.22%	13	0	0	0	0
Paenibacillus donghaensis	Zoonotic	96.83%	0	17	0	3	9
Paenibacillus ehimensis	Zoonotic	95.26%	0	0	2	0	0
Paenibacillus koleovorans	Animal	96.83%	0	0	8	0	0
Paenibacillus larvae	Animal	97.23%	0	0	0	10	0
Paenibacillus polymyxa	Zoonotic	98.02%	54	0	10	23	7
Paenibacillus quercus	Animal	95.24%	0	0	4	0	0
Paenibacillus rigui	Zoonotic	95.24%	0	3	0	0	0

Paenibacillus sp.	Animal	96.19% ± 0.66	208	4	29	32	42
Paenibacillus sp.	Zoonotic	96.83% ± 0.63	0	24	27	8	35
Paeniclostridium sordellii	Animal	100%	162	1	0	0	0
Paraburkholderia jirisanensis	Animal	97.23%	0	0	0	6	0
Paraburkholderia sartisoli	Zoonotic	99.61%	110	0	0	0	0
Paraburkholderia sp.	Animal, Zoonotic	98.81%	0	24	0	10	69
Parachlamydia sp.	Animal	96.05% ± 0	34	0	0	0	0
Parachlamydiaceae bacterium	Animal	95.53% ± 0.45	9	4	0	35	0
Paracoccus sp.	Animal	98.42%	5	0	0	0	0
Paralcaligenes ureilyticus	Animal	97.23%	24	0	0	0	0
Pelistega europaea	Animal	96.44%	7	0	0	0	0
Prauserella sp.	Animal	97.64%	0	0	0	7	12
Pseudaminobacter salicylatoxidans	Zoonotic	96.47%	0	0	25	0	0
Pseudoclavibacter caeni	Animal	95.28%	2	0	0	0	0
Pseudomonas fluorescens	Zoonotic	100%	7	0	0	0	0
Pseudomonas sp.	Animal, Zoonotic	100%	3	0	0	0	0
Pseudomonas syringae	Plant, Animal, Zoonotic	100%	3	0	0	0	0
Pseudonocardia spinosipora	Animal	96.46%	0	9	0	0	0
Pseudoxanthomonas spadix	Plant	96.84%	0	8	0	0	0
Pseudoxanthomonas yeongjuensis	Animal	96.84%	24	0	0	0	0
Psychrobacillus sp.	Animal	98.81%	0	0	58	3	0
Pullulanibacillus uraniitolerans	Zoonotic	97.23%	0	9	0	0	0
Pusillimonas sp.	Animal	96.84%	84	0	0	0	0
Ralstonia pickettii	Animal	100%	4	0	0	0	0
Ramlibacter sp.	Animal	98.81%	140	0	0	0	0
Raoultella planticola	Animal	98.81%	0	0	0	1	0
Rhizobium sp.	Plant	98.42% ± 0.56	23	5	0	0	1
Rhizobium sp.	Zoonotic	96.84%	13	0	0	0	0
Rhodococcus hoagii	Animal, Zoonotic	100%	74	5	0	0	0
Rhodopseudomonas sp.	Animal	97.23%	52	0	0	0	0
Romboutsia hominis	Animal	98.02%	6	0	0	4	0
Roseateles depolymerans	Plant, Animal	99.21%	60	0	0	0	0
Rudaibacter terrae	Plant	98.81%	22	0	0	0	0
Rummeliibacillus stabekisii	Animal	97.64%	23	0	0	0	0

Sanguibacter suarezii	Animal	98.42%	25	0	0	0	0
Serratia marcescens	Zoonotic	100%	0	0	0	6	0
Solimicrobium silvestre	Plant	97.63%	0	0	0	16	0
Sphingomonas glacialis	Animal, Zoonotic	98.02%	14	0	5	0	0
Sphingomonas sediminicola	Animal	98.42%	256	0	0	0	0
Sphingomonas sp.	Animal	99.14% $\pm$ 0.63	171	8	0	0	0
Sporosarcina pasteurii	Animal	99.61%	1188	0	0	0	0
Sporosarcina siberiensis	Zoonotic	98.81%	137	0	0	0	0
Sporosarcina sp.	Animal	98.81%	79	0	0	0	0
Sporosarcina thermotolerans	Zoonotic	98.42%	788	0	0	0	4
Stenotrophomonas maltophilia	Plant, Zoonotic	100%	12	2	0	0	0
Stenotrophomonas maltophilia	Zoonotic	100% $\pm$ 0	10	0	0	15	0
Streptacidiphilus anmyonensis	Plant	99.61%	0	49	0	0	0
Streptoalloteichus tenebrarius	Animal	95.65%	0	16	0	11	12
Streptomyces abietis	Plant	99.21%	55	0	0	0	0
Streptomyces cattleya	Animal	100%	26	0	0	0	0
Streptomyces lannensis	Animal	99.01% $\pm$ 0.28	149	0	0	0	0
Streptomyces sp.	Animal	98.75% $\pm$ 1.08	1647	122	39	19	67
Streptomyces sp.	Animal, Zoonotic	99.21%	38	0	0	0	0
Streptomyces sp.	Plant	99.6% $\pm$ 0.43	321	0	5	26	0
Streptomyces sp.	Plant, Animal	98.42% $\pm$ 0.56	107	0	0	0	0
Streptomyces sulfonofaciens	Plant, Animal	98.42%	47	0	0	0	0
Streptomyces tyrosinilyticus	Animal	99.21%	0	4	0	0	0
Streptomyces yeochonensis	Animal	99.21%	0	0	0	5	0
Streptomycetaceae bacterium	Animal	99.61%	25	0	0	0	0
Tardiphaga robiniae	Animal	99.21%	22	0	0	0	0
Tetrasphaera sp.	Animal	98.81%	44	0	0	0	0
Thermomonosporaceae bacterium	Animal, Zoonotic	96.64% $\pm$ 0.68	306	3	0	0	7
Tsukamurella sp.	Animal	95.67%	12	0	0	0	0
Ureibacillus thermosphaericus	Animal	96.44%	26	0	0	0	0
Vibrio metschnikovii	Animal	99.41% $\pm$ 0.84	8	2	0	0	0
Weissella ceti	Animal	98.42%	17	0	0	0	0
Williamsia sp.	Animal	97.23%	23	4	0	0	0
Xanthomonadaceae bacterium	Plant	96.05%	0	0	0	0	7

Table S9. Bacterial pathogens detected in lower soil samples across the urbanization gradient. Numbers are sums of species counts normalized by rarefaction in lower soil (15-30 cm depth) samples of each tree type. % identity refers to the % match of 16S sequence from the tree microbiome dataset to the 16S sequence in the Multiple Bacterial Pathogen Detection database.

Bacterial Species	Pathogen Type	% Identity ($\pm$ standard deviation when >1 ASV matched to a pathogenic sequence)	Urban Street Tree	Urban Forest Edge	Urban Forest Interior	Rural Forest Edge	Rural Forest Interior
Acetobacteraceae bacterium	Animal	96.05%	0	0	0	0	1
Acinetobacter baumannii	Zoonotic	100%	1	0	3	0	0
Actinoallomurus coprocola	Animal	95.26%	9	0	0	0	0
Actinoallomurus oryzae	Animal, Zoonotic	95.31%	16	0	0	0	0
Actinoallomurus sp.	Animal, Zoonotic	95.29% $\pm$ 0.02	450	4	0	0	0
Actinocorallia lasiicapitis	Animal, Zoonotic	96.44%	0	0	0	0	3
Actinomadura keratinilytica	Zoonotic	95.28%	4	0	0	0	0
Actinomadura rubrobrunea	Zoonotic	95.65%	25	0	0	0	0
Actinomadura scrupuli	Animal, Zoonotic	96.84% $\pm$ 0.5	0	18	31	2	7
Actinomadura sp.	Animal, Zoonotic	96.44% $\pm$ 1.12	16	27	4	16	0
Actinomycetospora sp.	Animal	95.67%	4	0	0	0	0
Actinophytocola sediminis	Animal	95.69%	13	0	0	0	0
Actinosynnema sp.	Animal	98.1% $\pm$ 0.65	49	22	17	9	0
Afipia felis	Animal	100%	6	0	0	0	0
Afipia sp.	Animal	97.23%	3	2	0	0	0
Agrococcus sp.	Plant	99.21%	15	0	0	0	0
Agromyces aureus	Plant, Animal	97.23%	3	0	0	0	0
Agromyces ramosus	Plant, Animal	98.42%	6	0	0	0	0
Allokutzneria albata	Animal	97.64%	6	0	0	0	0
Amycolatopsis nigrescens	Animal	96.47%	1	0	0	0	0
Amycolatopsis samaneae	Animal	95.65%	1	0	0	0	0
Amycolatopsis sp.	Animal	95.28%	5	0	0	0	0
Amycolatopsis sp.	Plant	98.42% $\pm$ 0.56	196	28	0	0	5
Aneurinibacillus thermoaerophilus	Zoonotic	98.02%	4	0	0	0	0
Aquamicrobium soli	Animal	95.65%	4	0	0	0	0
Aquitalea sp.	Animal	96.44%	1	0	0	0	0

Arthrobacter crystallopoietes	Animal	98.42%	6	0	0	0	0
Arthrobacter ginkgonis	Zoonotic	98.81%	2	0	0	0	0
Arthrobacter sp.	Plant	98.81%	650	396	372	46	34
Arthrobacter sp.	Plant, Zoonotic	97.23%	16	0	0	0	0
Arthrobacter sp.	Zoonotic	98.81% $\pm$ 0.65	699	3	26	0	0
Azotobacter chroococcum	Animal, Zoonotic	97.64%	1	0	0	0	0
Bacillus acidicola	Animal, Zoonotic	98.42%	0	0	0	0	3
Bacillus azotoformans	Animal, Zoonotic	98.42%	1	0	0	0	0
Bacillus clausii	Animal	97.26%	10	2	0	0	0
Bacillus coagulans	Animal	100%	48	0	0	0	0
Bacillus firmus	Animal	98.42%	0	3	0	0	0
Bacillus funiculus	Animal	98.81%	9	0	0	0	0
Bacillus hackensackii	Zoonotic	97.83% $\pm$ 0.28	86	0	3	0	0
Bacillus halodurans	Zoonotic	98.81%	0	0	4	0	0
Bacillus horikoshii	Animal, Zoonotic	99.21%	0	12	7	0	5
Bacillus lentus	Animal	97.23%	22	1	5	0	0
Bacillus lentus	Animal, Zoonotic	98.81%	39	0	3	6	0
Bacillus licheniformis	Animal, Zoonotic	100%	69	0	0	0	0
Bacillus lycopersici	Zoonotic	96.44%	0	0	0	4	2
Bacillus plakortidis	Animal	98.02%	0	0	5	0	0
Bacillus salitolerans	Animal, Zoonotic	96.44%	5	0	0	0	0
Bacillus salitolerans	Zoonotic	97.63%	0	0	0	12	0
Bacillus smithii	Zoonotic	98.02%	89	0	0	0	0
Bacillus sp.	Animal	98.35% $\pm$ 1.1	21	3	3	11	2
Bacillus sp.	Animal, Zoonotic	98.58% $\pm$ 0.77	56	0	17	2	0
Bacillus sp.	Zoonotic	98.74% $\pm$ 1.17	122	2	11	5	0
Bacillus sporothermodurans	Animal	98.02%	20	0	0	11	0
Bacillus thermolactis	Zoonotic	97.23%	38	0	0	0	0
Bauldia consociata	Animal	95.26%	0	2	0	0	0
beta proteobacterium	Animal	98.42%	26	0	0	0	0
Beutenbergia cavernae	Plant	96.84%	38	0	0	0	0
Bradyrhizobium sp.	Animal	99.21% $\pm$ 0.4	220	41	31	5	1
Brevibacillus borstelensis	Animal	99.60%	231	0	0	0	0
Brevibacillus ginsengisoli	Animal	98.61% $\pm$ 0.28	13	1	0	0	0

Brevibacillus laterosporus	Animal	100%	14	0	0	2	1
Brevibacillus sp.	Animal	97.22%	0	0	0	1	0
Brevibacillus thermoruber	Animal	95.24%	1	0	0	0	0
Brevibacterium sp.	Animal	98.02%	1	0	0	0	0
Brevundimonas diminuta	Animal	100%	1	0	0	2	0
Burkholderia sp.	Animal	98.21% $\pm$ 1.01	297	240	105	261	397
Burkholderia sp.	Animal, Zoonotic	98.95% $\pm$ 0.91	48	3	0	0	0
Burkholderia sp.	Plant, Animal, Zoonotic	98.02%	0	0	0	0	10
Caballeronia concitans	Animal	99.21%	6	0	0	0	0
Caballeronia pterochthonis	Animal	99.61%	11	0	0	0	0
Caenimonas sp.	Plant	98.81%	0	0	2	0	0
Candidatus Mesochlamydia	Animal	95.26%	0	1	0	0	0
Candidatus Metachlamydia	Animal	95.5% $\pm$ 0.27	53	15	14	1	21
Candidatus Mycoplasma	Animal	95.24%	0	0	3	0	0
Candidatus Protochlamydia	Animal	96.16% $\pm$ 0.67	41	5	1	4	15
Candidatus Trichorickettsia	Animal, Zoonotic	98.02% $\pm$ 1.68	0	1	0	0	1
Cellulomonas sp.	Animal	99.41% $\pm$ 0.28	11	3	0	0	0
Cereibacter changlensis	Animal	96.05%	9	0	0	0	0
Chromobacterium sp.	Animal	99.21%	0	0	0	0	3
Chryseobacterium hominis	Animal	96.05%	7	0	19	1	0
Chryseobacterium sp.	Zoonotic	96.06%	2	0	0	0	0
Clostridium akagii	Animal	97.63%	6	0	0	0	0
Clostridium arbusti	Animal	98.81%	10	0	0	0	0
Clostridium argentinense	Animal	99.8% $\pm$ 0.28	34	0	0	0	0
Clostridium autoethanogenum	Animal	100%	1	0	0	0	0
Clostridium baratii	Animal	100%	1	0	0	0	0
Clostridium beijerinckii	Plant, Animal	100%	23	0	0	0	0
Clostridium botulinum	Animal	100% $\pm$ 0	7	2	0	2	0
Clostridium frigidicarnis	Animal	96.84% $\pm$ 0	9	1	1	1	0
Clostridium hydrogeniformans	Animal	95.26%	4	0	0	0	0
Clostridium kluyveri	Animal	100%	2	0	0	0	0
Clostridium magnum	Animal	97.63%	3	0	0	0	0
Clostridium perfringens	Zoonotic	100%	7	0	0	0	0
Clostridium saccharolyticum	Animal	95.28%	2	0	0	0	0

<i>Clostridium sardiniense</i>	Animal	98.42%	2	0	0	0	0
<i>Clostridium</i> sp.	Animal	97.37% $\pm$ 0.6	4	0	0	0	0
<i>Collimonas fungivorans</i>	Animal	97.23%	0	1	7	0	0
<i>Collimonas fungivorans</i>	Plant, Animal	97.63%	12	0	0	0	0
<i>Corallococcus coralloides</i>	Animal	97.23%	3	0	0	0	1
<i>Corynebacterium glucuronolyticum</i>	Animal	100%	0	0	4	0	0
<i>Corynebacterium kroppenstedtii</i>	Animal	99.61%	0	0	18	0	0
<i>Coxiella burnetii</i>	Animal, Zoonotic	95.65%	5	0	0	0	0
<i>Coxiella burnetii</i>	Zoonotic	95.45% $\pm$ 0.28	1	1	0	0	0
<i>Coxiella endosymbiont</i>	Animal	96.93% $\pm$ 0.38	4	0	5	4	3
<i>Croceobacterium</i> sp.	Plant	97.23%	25	0	0	0	0
<i>Cryocolla antiquus</i>	Plant	99.21%	33	0	0	7	6
<i>Cupriavidus taiwanensis</i>	Zoonotic	98.42%	10	0	0	0	0
<i>Cystobacter armeniaca</i>	Animal	98.42%	6	0	0	0	0
<i>Cystobacter gracilis</i>	Animal	97.43% $\pm$ 0.28	2	0	0	0	0
<i>Derxia</i> sp.	Animal	97.23%	2	0	0	0	0
<i>Diaminobutyricibacter tongyongensis</i>	Plant	99.21%	4	0	0	0	0
<i>Domibacillus tundrae</i>	Plant, Animal	98.42%	0	1	0	0	0
<i>Duganella</i> sp.	Plant	97.04% $\pm$ 0.84	10	0	0	0	0
<i>Enterobacteriaceae</i> bacterium	Animal	100%	0	0	0	0	14
<i>Escherichia coli</i>	Zoonotic	100%	0	0	3	3	2
<i>Flavobacterium</i> sp.	Animal	96.06% $\pm$ 0.55	1	0	2	0	0
<i>Flexivirga alba</i>	Animal	96.44%	8	0	0	0	0
<i>Frankia</i> sp.	Animal	95.39% $\pm$ 0.2	67	2	0	1	2
<i>Geobacillus stearothermophilus</i>	Animal, Zoonotic	95.26%	0	0	4	0	0
<i>Geobacillus subterraneus</i>	Animal, Zoonotic	96.44%	2	0	0	0	0
<i>Geobacillus thermodenitrificans</i>	Animal, Zoonotic	97.23%	120	0	0	0	0
<i>Geobacter</i> sp.	Animal	96.68% $\pm$ 0.91	26	0	0	14	32
<i>Goodfellowiella coeruleoviolacea</i>	Animal	98.62% $\pm$ 0.28	11	16	15	7	4
<i>Gracilibacillus dipsosauri</i>	Animal	96.44%	7	0	0	0	0
<i>Herbaspirillum</i> sp.	Plant	99.61%	2	0	0	0	0
<i>Herbihabitans rhizosphaerae</i>	Animal	97.63%	8	0	0	0	0
<i>Humibacter antri</i>	Plant	98.02%	55	0	0	0	2
<i>Humibacter ginsengiterrae</i>	Plant, Animal	98.02%	112	0	0	0	0

Janibacter corallicola	Animal	98.42%	7	0	0	0	0
Janthinobacterium sp.	Plant	97.23%	2	0	0	0	0
Kineothrix alysoides	Animal	96.06%	3	0	0	0	0
Klebsiella pneumoniae	Plant, Animal, Zoonotic	100%	22	0	0	2	0
Labedaea rhizosphaerae	Animal	98.81%	3	0	0	0	0
Lactobacillus delbrueckii	Animal	100%	0	0	2	0	0
Lactococcus garvieae	Animal, Zoonotic	100%	0	0	0	0	1
Lactococcus lactis	Zoonotic	100%	0	0	2	0	0
Legionella adelaidensis	Animal	97.23% $\pm$ 0	4	0	0	0	0
Legionella dresdenensis	Animal	97.63%	0	0	0	2	0
Legionella nagasakiensis	Animal	95.68% $\pm$ 0.54	2	2	0	0	0
Legionella nautarum	Animal	99.21%	2	0	0	0	0
Legionella norrlandica	Animal	95.26%	0	0	0	1	1
Legionella pittsburghensis	Animal	95.28%	6	0	0	0	0
Legionella pneumophila	Animal	98.16% $\pm$ 0.54	15	0	1	3	4
Legionella quinlivanii	Animal	96.25% $\pm$ 0.84	2	0	2	0	0
Legionella sp.	Animal	97.42% $\pm$ 0.92	35	4	10	2	10
Leifsonia sp.	Plant, Animal	99.61%	0	0	3	0	0
Lysinimonas kribbensis	Plant, Animal, Zoonotic	97.23%	0	0	3	0	0
Lysobacter sp.	Plant	96.64% $\pm$ 1.4	28	0	0	0	0
Massilia sp.	Plant	97.23%	11	0	0	0	0
Mesorhizobium albiziae	Plant	95.26%	5	0	0	0	0
Mesorhizobium sp.	Animal	95.65%	5	1	1	0	0
Mesorhizobium sp.	Plant	97.23%	0	2	0	0	0
Mesorhizobium sp.	Plant, Animal	97.23%	3	0	0	0	0
Mesorhizobium sp.	Zoonotic	98.02%	41	0	0	0	0
Methylocapsa acidiphila	Animal	95.65%	0	0	0	0	2
Methylocella palustris	Animal	95.26%	0	7	3	13	26
Methylocella silvestris	Animal	95.26%	0	0	0	8	1
Methylocystis bryophila	Animal	95.65%	35	0	0	0	0
Methylocystis sp.	Animal	95.65%	27	0	0	0	0
Methylosinus sp.	Animal	96.44%	0	0	0	6	0
Methylosinus trichosporium	Animal	96.46%	13	0	0	0	0
Micrococcineae bacterium	Plant	98.02%	11	0	0	0	0

mine drainage	Animal	98.82%	7	0	0	0	0
Mobiluncus curtisii	Animal	100%	0	0	0	0	3
Mycobacterium conspicuum	Animal	99.61%	4	10	0	20	141
Mycobacterium leprae	Zoonotic	96.44%	0	3	0	0	0
Mycobacterium sp.	Animal	99.11% $\pm$ 0.88	7	10	13	22	35
Mycobacterium sp.	Animal, Zoonotic	98.62% $\pm$ 0.51	142	10	18	5	31
Mycoplasma wenyonii	Animal	99.8% $\pm$ 0.28	0	0	6	0	0
Myroides marinus	Animal	99.61%	0	1	0	0	0
Nakamurella endophytica	Animal	95.52% $\pm$ 0.23	34	1	8	0	0
Nocardia brasiliensis	Animal	100%	6	0	0	0	0
Nocardia concava	Animal	100%	23	0	0	0	0
Nocardia jejuensis	Animal	100%	0	0	0	1	0
Nocardia nova	Animal	99.29% $\pm$ 0.86	200	7	9	0	0
Nocardia pseudobrasiliensis	Animal	100% $\pm$ 0	47	41	0	32	0
Nocardia sp.	Animal	98.43% $\pm$ 1.59	29	4	9	1	1
Nocardia takedensis	Animal	99.8% $\pm$ 0.28	15	0	0	0	0
Nocardia vermiculata	Animal	98.33% $\pm$ 1.22	138	28	28	3	19
Oceanobacillus sp.	Zoonotic	95.45% $\pm$ 0.28	2	0	2	0	3
Ochrobactrum sp.	Zoonotic	97.23% $\pm$ 1.68	3	0	0	0	2
Ornithinibacillus composti	Zoonotic	98.81%	0	0	0	1	0
Ornithinibacillus contaminans	Animal	97.83% $\pm$ 0.28	10	0	0	0	0
Oryzihumus leptocrescens	Animal	97.63%	10	0	0	0	0
Oryzihumus terrae	Animal	96.98% $\pm$ 0.6	111	0	0	0	0
Paenalcaligenes suwonensis	Animal	98.81%	0	0	0	0	5
Paenibacillus anaericanus	Zoonotic	97.22%	0	1	2	1	9
Paenibacillus barengoltzii	Zoonotic	97.22%	16	0	0	0	0
Paenibacillus cathormii	Zoonotic	95.64%	3	0	0	0	0
Paenibacillus cavernae	Animal	95.67%	2	0	0	0	0
Paenibacillus doosanensis	Animal	96.43%	0	0	0	1	0
Paenibacillus edaphicus	Animal	96.03%	8	0	0	0	0
Paenibacillus ehimensis	Zoonotic	95.26%	0	0	0	2	0
Paenibacillus glucanolyticus	Zoonotic	95.64%	0	0	0	0	3
Paenibacillus koleovorans	Animal	96.83% $\pm$ 0	2	1	3	1	1
Paenibacillus macerans	Zoonotic	96.43%	7	0	0	0	0

Paenibacillus mucilaginosus	Animal	96.83%	0	0	0	1	0
Paenibacillus phoenicis	Zoonotic	97.62%	1	0	0	0	0
Paenibacillus physcomitrellae	Zoonotic	96.43% $\pm$ 1.12	10	0	0	0	0
Paenibacillus polymyxa	Zoonotic	98.02%	28	5	4	8	1
Paenibacillus profundus	Zoonotic	98.02%	0	3	0	0	0
Paenibacillus rigui	Zoonotic	95.24%	0	0	1	0	0
Paenibacillus sp.	Animal	96.16% $\pm$ 0.62	86	14	40	15	7
Paenibacillus sp.	Zoonotic	97.07% $\pm$ 0.97	26	24	3	10	4
Paeniclostridium sordellii	Animal	100%	7	0	0	0	0
Pandoraea pulmonicola	Animal	100%	0	0	0	0	4
Paraburkholderia sartisoli	Zoonotic	99.61%	264	0	0	0	0
Paraburkholderia sp.	Animal, Zoonotic	98.81%	0	15	0	4	0
Parachlamydia acanthamoebae	Animal	95.78% $\pm$ 0.23	14	0	0	0	2
Parachlamydia sp.	Animal	96.24% $\pm$ 0.99	11	2	0	1	1
Parachlamydiaceae bacterium	Animal	95.66% $\pm$ 0.28	6	2	0	3	10
Paracaligenes ginsengisoli	Animal	98.42%	5	0	0	0	0
Paracaligenes ureilyticus	Animal	97.23%	1	0	0	0	0
Phenylobacterium sp.	Animal	95.26%	9	0	0	0	0
Phreatobacter cathodiphilus	Zoonotic	95.65%	0	0	2	0	0
Polaromonas sp.	Animal	99.61%	18	0	0	0	0
Prauserella sp.	Animal	97.64%	0	36	23	15	45
Pseudochrobactrum sp.	Zoonotic	97.63%	0	0	0	0	2
Pseudomonas sp.	Animal, Zoonotic	99.34% $\pm$ 0.6	16	0	4	0	0
Pseudomonas sp.	Plant	99.61%	0	0	1	0	0
Pseudonocardia sp.	Animal	97.24% $\pm$ 0.39	15	0	0	0	0
Pseudonocardia spinospora	Animal	96.06% $\pm$ 0.56	0	23	0	0	1
Pseudoxanthomonas daejeonensis	Plant, Animal, Zoonotic	95.65%	3	0	0	0	0
Pseudoxanthomonas putridarboris	Zoonotic	97.64%	1	0	0	0	0
Pseudoxanthomonas sp.	Plant, Animal, Zoonotic	95.26%	3	0	0	0	0
Pseudoxanthomonas yeongjuensis	Animal	96.84%	4	0	0	0	0
Psychrobacillus sp.	Animal	98.81%	8	13	3	0	0
Pusillimonas sp.	Animal	96.84%	21	0	0	0	0
Ralstonia pickettii	Animal	100%	13	0	0	0	0
Ramlibacter sp.	Animal	98.81%	44	0	0	0	0

Raoultella planticola	Animal	100%	0	0	3	0	0
Rhizobium sp.	Plant	97.23%	5	0	0	0	0
Rhizobium sp.	Zoonotic	97.63% $\pm$ 1.12	8	0	0	0	0
Rhodobacter sphaeroides	Animal	96.84%	5	0	0	0	0
Rhodococcus hoagii	Animal, Zoonotic	99.6% $\pm$ 0.32	28	2	17	0	0
Rhodococcus koreensis	Animal	98.81%	2	0	0	0	0
Rhodopseudomonas palustris	Animal	99.21%	0	0	3	0	0
Rhodopseudomonas sp.	Animal	97.23%	18	0	0	0	0
Romboutsia hominis	Animal	98.02%	4	0	0	0	0
Roseateles depolymerans	Plant, Animal	99.21%	4	0	0	0	0
Rudaibacter terrae	Plant	98.81%	49	0	0	0	0
Rummeliibacillus stabekisii	Animal	97.64%	3	0	0	0	0
Salmonella enterica	Zoonotic	100%	4	0	0	0	0
Sanguibacter suarezii	Animal	98.42%	1	0	0	0	0
Serratia marcescens	Zoonotic	100%	1	0	0	0	0
Smaragdicoccus niigatensis	Animal, Zoonotic	95.26%	1	0	0	0	0
Soonwooa purpurea	Animal, Zoonotic	96.05%	0	0	0	0	1
Sphingomonas crusticola	Animal	97.23%	20	0	0	0	0
Sphingomonas fennica	Animal	96.84%	1	0	0	0	0
Sphingomonas glacialis	Animal, Zoonotic	98.02%	6	0	6	0	0
Sphingomonas sediminicola	Animal	98.42%	63	0	0	0	0
Sphingomonas soli	Animal, Zoonotic	98.02%	2	0	0	0	0
Sphingomonas sp.	Animal	98.45% $\pm$ 1.04	66	0	3	2	0
Sphingomonas zeicaulis	Animal	99.21%	3	0	0	0	0
Sporolactobacillus dextrus	Animal	97.04% $\pm$ 0.28	9	1	0	0	0
Sporosarcina pasteurii	Animal	99.61%	60	0	0	0	0
Sporosarcina siberiensis	Zoonotic	98.81%	7	0	0	0	0
Sporosarcina thermotolerans	Zoonotic	98.42%	66	0	3	0	0
Stenotrophomonas maltophilia	Plant, Zoonotic	100%	0	1	0	0	0
Stenotrophomonas maltophilia	Zoonotic	100% $\pm$ 0	15	0	1	0	1
Streptacidiphilus anmyonensis	Plant	99.61%	28	42	6	8	0
Streptacidiphilus jeojiense	Plant	98.81%	26	0	0	0	0
Streptoalloteichus sp.	Animal	96.67% $\pm$ 0.83	72	0	3	0	0
Streptoalloteichus tenebrarius	Animal	95.85% $\pm$ 0.28	0	44	47	45	44

<i>Streptomyces abietis</i>	Plant	99.21%	30	0	0	0	0
<i>Streptomyces cattleya</i>	Animal	100%	30	0	0	0	0
<i>Streptomyces cinnamoneus</i>	Plant, Animal	99.61%	0	0	5	0	0
<i>Streptomyces hoynatensis</i>	Animal	97.23%	11	0	0	0	0
<i>Streptomyces lannensis</i>	Animal	99.01% $\pm$ 0.28	271	0	0	0	0
<i>Streptomyces polygonati</i>	Plant	99.21%	104	0	0	0	0
<i>Streptomyces pulveraceus</i>	Animal	99.21%	9	0	0	0	0
<i>Streptomyces</i> sp.	Animal	98.9% $\pm$ 0.96	1641	115	83	36	19
<i>Streptomyces</i> sp.	Animal, Zoonotic	99.21%	9	0	0	0	0
<i>Streptomyces</i> sp.	Plant	99.37% $\pm$ 0.53	453	52	19	13	36
<i>Streptomyces</i> sp.	Plant, Animal	98.56% $\pm$ 0.67	226	0	0	0	0
<i>Streptomyces sulfonofaciens</i>	Plant, Animal	98.42% $\pm$ 0	66	0	0	0	0
<i>Streptomyces tremellae</i>	Plant, Animal	98.81%	3	0	0	0	0
<i>Streptomyces uncialis</i>	Plant, Animal	99.21%	0	0	1	0	0
<i>Streptomyces yeochonensis</i>	Animal	99.01% $\pm$ 0.28	3	0	0	0	3
<i>Tardiphaga robiniae</i>	Animal	99.21%	23	0	0	0	0
<i>Telmatobacter bradus</i>	Animal	96.06%	0	2	0	0	0
<i>Terribacillus goriensis</i>	Animal, Zoonotic	96.84%	3	0	0	0	0
<i>Tetrasphaera</i> sp.	Animal	98.81%	1	0	1	0	0
<i>Thermomonosporaceae</i> bacterium	Animal, Zoonotic	96.64% $\pm$ 0.68	150	1	11	0	4
<i>Tsukamurella</i> sp.	Animal	96.85%	0	0	2	0	0
<i>Uliginosibacterium</i> sp.	Animal	97.23%	14	0	0	0	0
<i>Ureibacillus thermosphaericus</i>	Animal	96.44%	50	0	0	0	0
<i>Vagococcus entomophilus</i>	Animal, Zoonotic	99.21%	0	0	0	0	6
<i>Variovorax paradoxus</i>	Plant	98.81%	9	0	0	0	0
<i>Variovorax</i> sp.	Animal	98.81%	3	0	0	0	0
<i>Williamsia</i> sp.	Animal	97.23%	24	0	0	0	0
<i>Xanthomonadaceae</i> bacterium	Plant	96.05%	0	0	6	0	0
<i>Xenorhabdus nematophila</i>	Animal	100%	0	0	0	0	5

Table S10. Bacterial pathogens detected in root samples across the urbanization gradient. Numbers are sums of species counts normalized by rarefaction in root samples of each tree type. % identity refers to the % match of 16S sequence from the tree microbiome dataset to the 16S sequence in the Multiple Bacterial Pathogen Detection database.

Bacterial Species	Pathogen Type	% Identity ($\pm$ standard deviation when >1 ASV matched to a pathogenic sequence)	Urban Street Tree	Urban Forest Edge	Urban Forest Interior	Rural Forest Edge	Rural Forest Interior
Acinetobacter radioresistens	Zoonotic	100%	1	0	0	0	0
Actinoallomurus sp.	Animal, Zoonotic	95.28%	10	0	0	0	0
Actinocorallia lasiicapitis	Animal, Zoonotic	96.44%	12	0	0	0	0
Actinomadura formosensis	Animal, Zoonotic	97.63%	17	0	0	0	0
Actinomadura scrupuli	Animal, Zoonotic	96.44%	0	0	0	0	3
Actinomadura sp.	Animal, Zoonotic	97.83% $\pm$ 0.84	33	0	0	0	3
Actinosynnema sp.	Animal	97.63% $\pm$ 1.4	16	34	1	0	2
Amycolatopsis sp.	Plant	98.02%	47	1	0	0	0
Arthrobacter crystallopoietes	Animal	98.42%	7	0	0	0	0
Arthrobacter sp.	Plant	97.04% $\pm$ 2.52	14	2	0	3	1
Arthrobacter sp.	Zoonotic	99.61%	13	0	0	0	0
Azospirillum sp.	Animal	96.84%	6	0	0	0	0
Bacillus hackensackii	Zoonotic	98.02%	48	0	0	0	0
Bacillus lentus	Animal, Zoonotic	98.81%	13	0	0	0	0
Bacillus smithii	Zoonotic	98.02%	21	0	0	0	0
Bacillus sp.	Animal, Zoonotic	97.23%	12	0	0	0	0
Bacillus sp.	Zoonotic	100%	0	0	1	0	0
Bradyrhizobium sp.	Animal	98.81%	290	38	10	18	0
Burkholderia sp.	Animal	98.88% $\pm$ 0.84	99	206	30	155	373
Burkholderia sp.	Animal, Zoonotic	98.42%	0	9	0	0	0
Candidatus Metachlamydia	Animal	95.39% $\pm$ 0.23	7	2	0	3	0
Candidatus Phytoplasma	Plant	100%	6	0	0	0	0
Caulobacter ginsengisoli	Animal	95.26%	4	0	0	0	0

Cereibacter changlensis	Animal	96.05%	1	0	0	0	0
Clostridium baratii	Animal	100%	2	0	0	0	0
Clostridium beijerinckii	Plant, Animal	100%	3	0	0	0	0
Clostridium frigidicarnis	Animal	96.84%	0	0	1	0	0
Clostridium perfringens	Zoonotic	100%	0	1	0	0	0
Collimonas fungivorans	Animal	97.23%	0	3	29	8	0
Coxiella burnetii	Zoonotic	95.65%	0	0	0	0	3
Coxiella endosymbiont	Animal	96.44% $\pm$ 0.4	3	0	0	1	2
Cryocola antiquus	Plant	99.21%	0	3	0	0	0
Derxia sp.	Animal	96.84%	16	0	0	0	0
Enterobacteriaceae bacterium	Animal	100%	0	0	0	0	2
Flavobacterium sp.	Animal	96.44%	6	0	0	0	0
Frankia sp.	Animal	95.26%	16	9	0	0	0
Goodfellowiella coeruleoviolacea	Animal	98.42%	17	27	28	0	0
Homoserinibacter sp.	Plant, Animal	99.61%	8	0	0	0	0
Humibacter ginsengiterrae	Plant, Animal	98.02%	11	0	0	0	0
Janthinobacterium sp.	Plant	97.23%	2	0	0	0	0
Legionella birminghamensis	Animal	96.84%	0	0	1	0	0
Legionella pneumophila	Animal	98.02%	3	0	0	0	0
Legionella quinlivanii	Animal	96.84%	0	0	0	0	2
Legionella sp.	Animal	96.58% $\pm$ 0.83	1	1	2	0	0
Massilia sp.	Plant	98.81%	0	11	0	0	0
Mesorhizobium sp.	Animal	95.65%	21	0	0	0	0
Mycobacterium conspicuum	Animal	99.61%	0	0	0	9	6
Mycobacterium leprae	Zoonotic	96.05%	0	0	1	0	0
Mycobacterium sp.	Animal	98.81%	0	0	17	0	0
Mycobacterium sp.	Animal, Zoonotic	98.69% $\pm$ 0.6	10	0	1	4	0
Nocardia concava	Animal	100%	0	0	1	0	0
Nocardia jejuensis	Animal	99.21%	0	0	1	0	0
Nocardia nova	Animal	99.34% $\pm$ 1.14	86	0	0	0	0
Nocardia pseudobrasiliensis	Animal	100%	0	6	0	0	0
Nocardia sp.	Animal	98.81% $\pm$ 0.56	0	4	0	4	0

Nocardia vermiculata	Animal	98.03% ± 0.45	177	4	5	0	0
Ochrobactrum sp.	Zoonotic	96.05%	6	0	0	0	0
Paenibacillus quercus	Animal	95.24%	0	0	0	2	0
Paraburkholderia sartisoli	Zoonotic	99.61%	319	0	0	0	0
Parachlamydiaceae bacterium	Animal	95.26%	0	0	0	0	5
Paralcaligenes ginsengisoli	Animal	98.42%	12	0	0	0	0
Paralcaligenes ureilyticus	Animal	96.84%	5	0	0	0	0
Prauserella sp.	Animal	97.64%	0	27	15	0	0
Promicromonospora sp.	Animal	96.84%	55	0	0	0	0
Ramlibacter sp.	Animal	98.81%	9	0	0	0	0
Rhizobium alvei	Plant, Zoonotic	99.61%	9	0	0	0	0
Rhodopseudomonas palustris	Animal	99.21%	0	0	0	2	0
Sphingomonas naphthae	Animal	95.65%	0	2	0	0	0
Sporosarcina thermotolerans	Zoonotic	98.42%	6	0	0	0	0
Stenotrophomonas maltophilia	Zoonotic	100% ± 0	0	30	5	0	0
Streptacidiphilus anmyonensis	Plant	99.61%	0	3	0	0	0
Streptoalloteichus sp.	Animal	97.26%	90	14	0	0	0
Streptoalloteichus tenebrarius	Animal	95.65%	0	0	0	1	8
Streptomyces ipomoeae	Plant	100%	96	0	0	0	0
Streptomyces panayensis	Animal, Zoonotic	95.65%	9	0	0	0	0
Streptomyces polygonati	Plant	99.01% ± 0.28	125	0	0	0	0
Streptomyces rhizosphaerihabitans	Animal, Zoonotic	98.03%	10	0	0	0	0
Streptomyces sp.	Animal	99.47% ± 0.23	388	1	0	0	0
Streptomyces sp.	Animal, Zoonotic	99.21%	45	0	0	0	0
Streptomyces sp.	Plant	99.53% ± 0.43	447	0	0	0	3
Streptomyces sp.	Plant, Animal	98.42% ± 0	20	0	0	0	0
Thermomonosporaceae bacterium	Animal, Zoonotic	96.57% ± 0.82	62	9	9	0	3
Tsukamurella sp.	Animal	95.67%	13	0	0	0	0
Undibacterium danionis	Plant, Animal	97.63%	0	0	0	0	1
Vagococcus entomophilus	Animal, Zoonotic	99.21%	0	0	0	0	2
Vibrio metschnikovii	Animal	99.21%	0	3	0	0	0