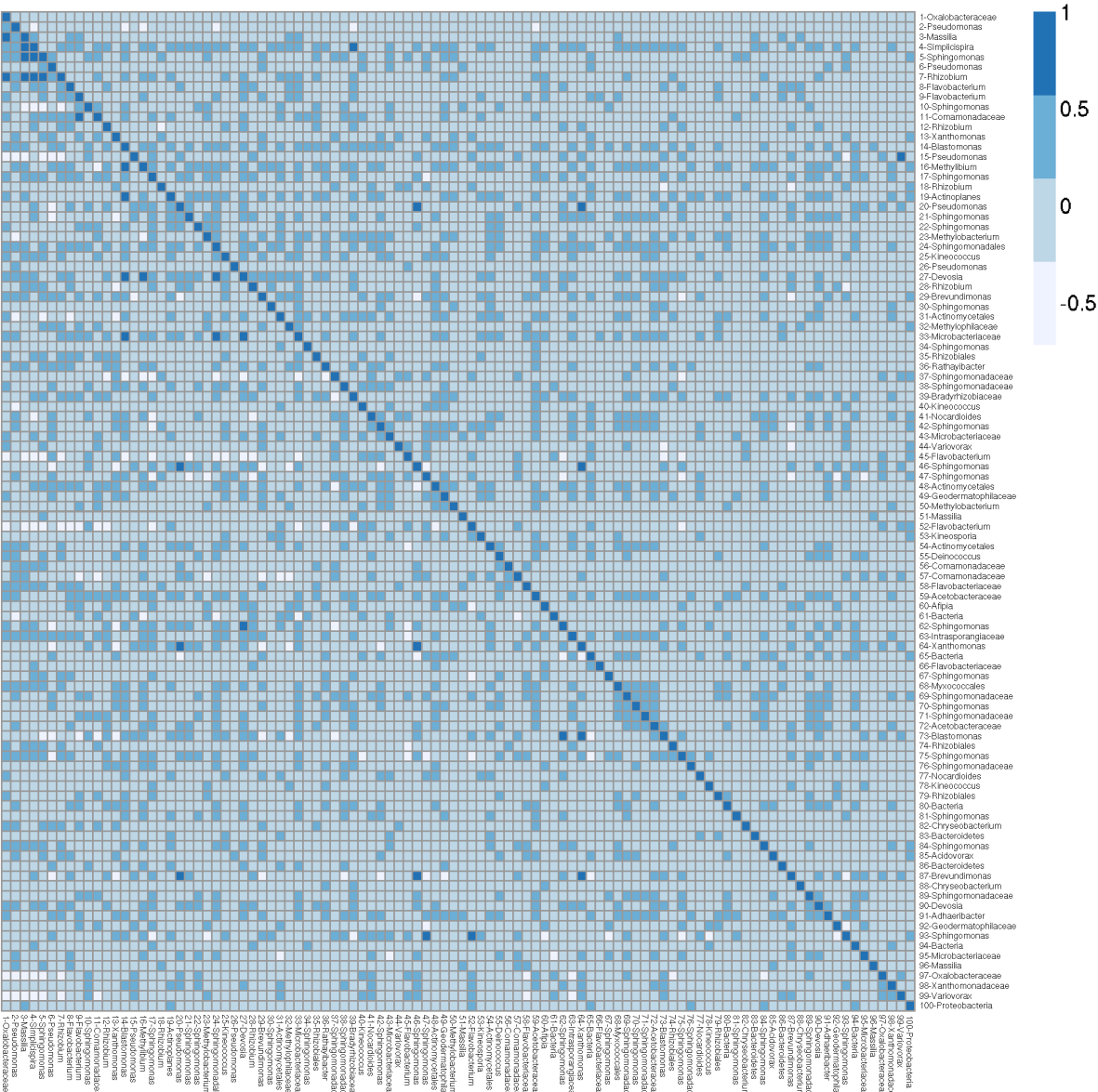


Actinobacteria

Supplementary Figure 1: The leaf microbial community of *A. thaliana*. **a**, Bacterial phyla found in the leaves of a worldwide panel of accessions; the number of OTUs identified in each phylum is indicated in parentheses. The most heavily sequenced phyla include the Proteobacteria (b), Bacteroidetes (c), and Actinobacteria (d). **e**, A large fraction (~35%) of the fungal community has uncertain taxonomic status (*Incertae sedis*) at the phylum level. However, the majority of the fungal community consists of the Ascomycota, including the classes Dothideomycetes (f) and Sordariomycetes (g). The basidiomycete class Tremellomycetes (h) was also observed. Only families described by more than 0.5% of a class's total sequences are shown. The proportion of reads assigned to a family is shown in figures 1b-d, f-h.

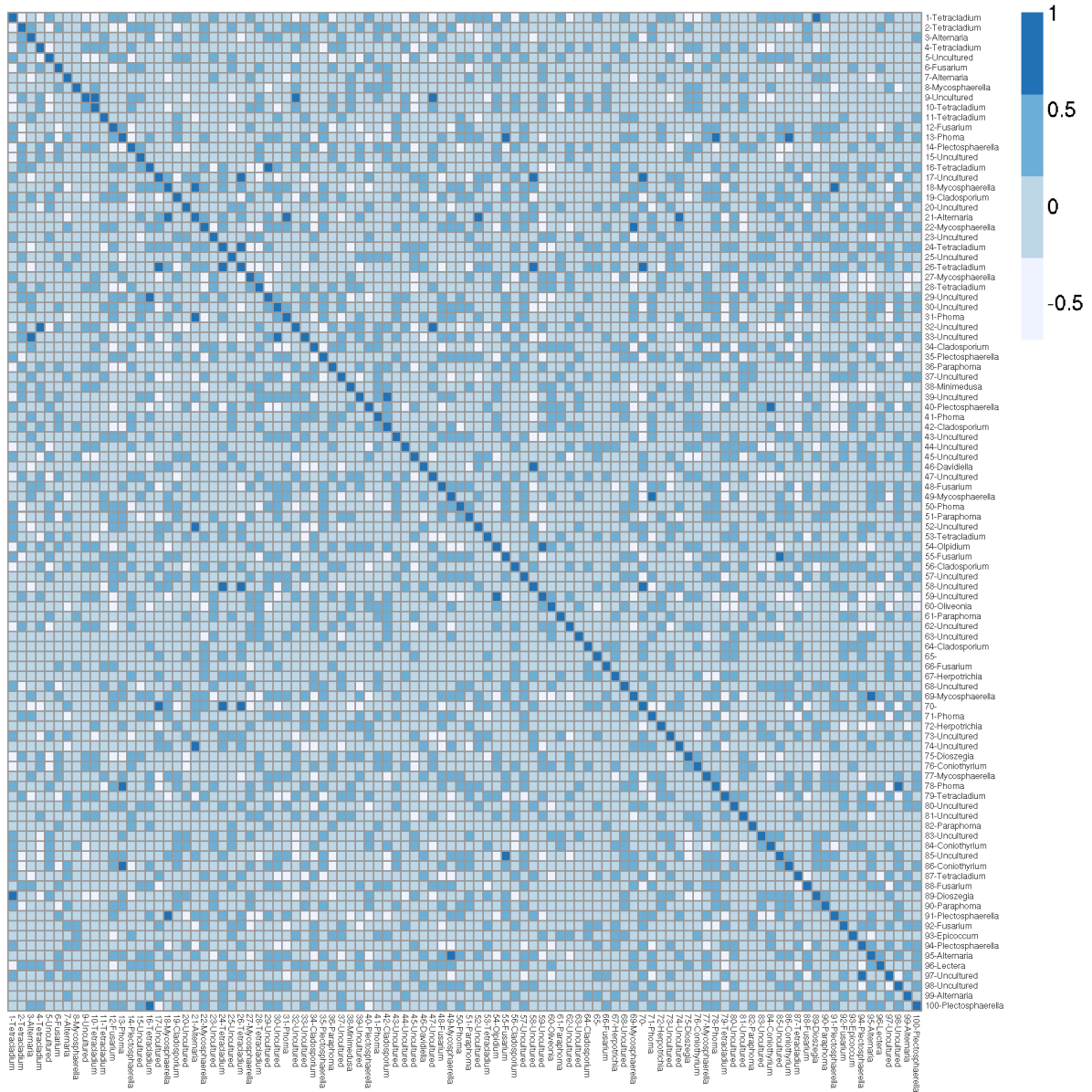


13

14 **Supplementary Figure 2: Spearman correlations within the bacterial community.**

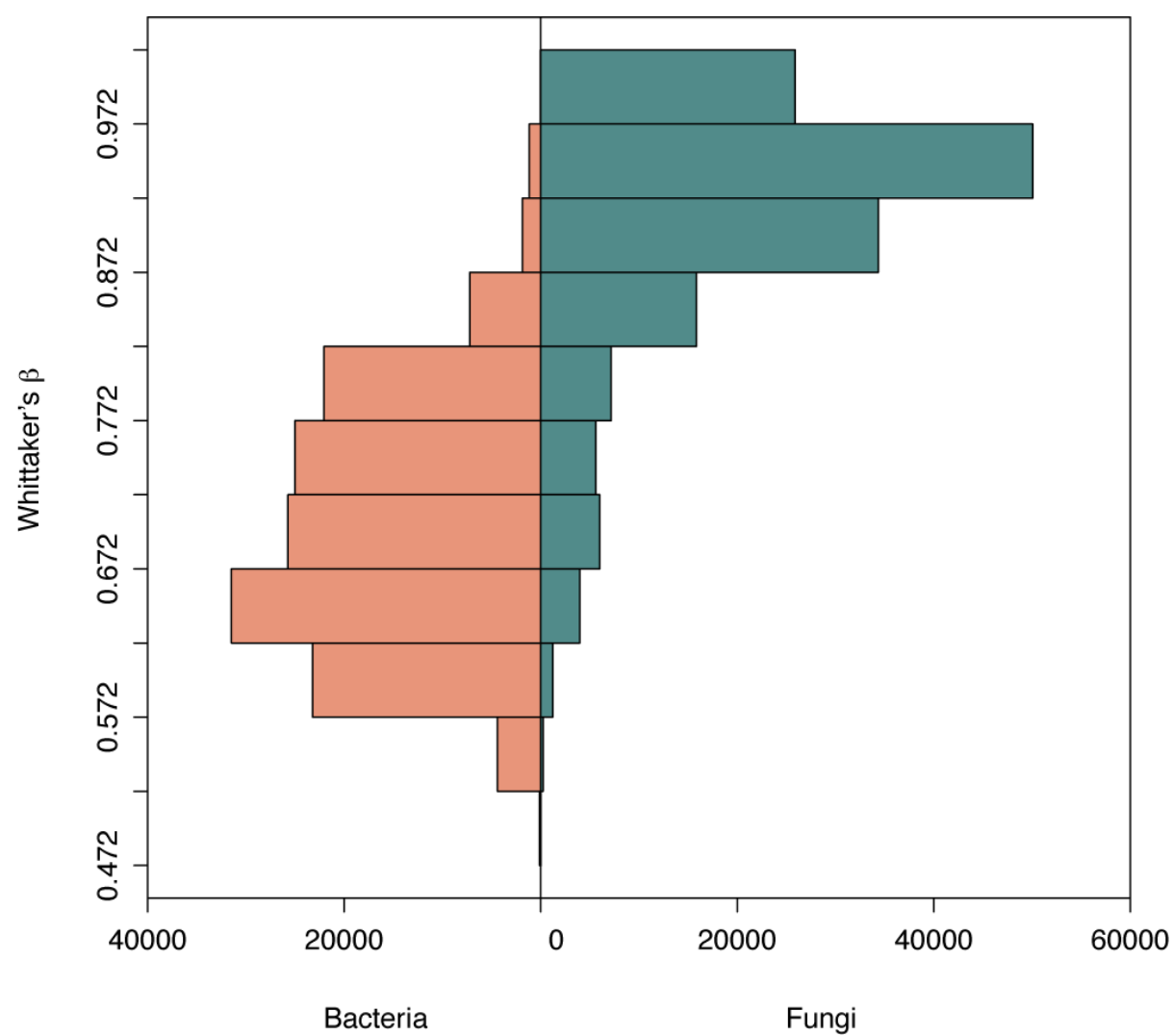
15 Correlations shown are from a model regressing out technical confounders (Methods), while
16 analyzing the presence/absence (i.e. 0/1 matrix, below the diagonal) or abundance of
17 individual bacterial species (above the diagonal). When assigned (Methods), genus names are
18 displayed in the margins. To improve readability, only the 100 most heavily sequenced
19 members of the bacterial community are shown.

20



Supplementary Figure 3: Spearman correlations within the fungal community.

Correlations shown are from a model regressing out technical confounders (Methods), while analyzing the presence/absence (i.e. 0/1 matrix, below the diagonal) or abundance of individual fungal species (above the diagonal). When assigned (Methods), genus names are displayed in the margins. To improve readability, only the 100 most heavily sequenced members of the fungal community are shown.



30

31 **Supplementary Figure 4: Species turnover in the leaf.** On average, species turnover is
32 higher in the fungal community than in the bacterial community (measured using pairwise
33 Whittaker's Beta, β).

34

35 **Supplementary Tables**

Id	Name	Country
8251	Ag-0	France
8252	Alc-0	Spain
8230	Algutsum	Sweden
8253	An-1	Belgium
8254	Ang-0	Belgium
8256	Ba1-2	Sweden
8257	Ba3-3	Sweden
8258	Ba4-1	Sweden
8259	Ba5-1	Sweden
8260	Bay-0	Germany
8261	Bg-2	United States of America
8262	Bil-5	Sweden
8263	Bil-7	Sweden
8264	Bla-1	Spain
8265	Blh-1	Czech Republic
5837	Bor-1	Czech Republic
8268	Bor-4	Czech Republic
8269	Br-0	Czech Republic
8231	Bro1-6	Sweden
8270	Bs-1	Switzerland
8271	Bu-0	Germany
8421	Buckhorn Pass	United States of America
8272	Bur-0	Ireland
8273	C24	Portugal
8274	Can-0	Spain
8275	Cen-0	France
8276	CIBC-17	United Kingdom
8277	CIBC-5	United Kingdom
8278	Co	Portugal
8279	Col-0	United States of America
8280	Ct-1	Italy
8281	Cvi-0	Cape Verde
8233	Dem-4	United States of America
8283	Dra3-1	Sweden
8284	DraII-1	Czech Republic
8285	DraIII-1	Czech Republic
6008	Duk	Czech Rep.

Id	Name	Country
6009	Eden-1	Sweden
8287	Eden-2	Sweden
8288	Edi-0	United Kingdom
6016	Eds-1	Sweden
8289	Ei-2	Germany
8290	En-1	Germany
8291	Est-1	Russia
8292	Fab-2	Sweden
8293	Fab-4	Sweden
8294	Fei-0	Portugal
8422	Fja1-1	Sweden
8295	Ga-0	Germany
8296	Gd-1	Germany
8297	Ge-0	Switzerland
8298	Got-22	Germany
8299	Got-7	Germany
8300	Gr-1	Austria
8301	Gu-0	Germany
8234	Gul1-2	Sweden
8302	Gy-0	France
8303	H55	Czech Republic
8304	Hi-0	Netherlands
8235	Hod	Czech Republic
8423	Hov2-1	Sweden
8306	Hov4-1	Sweden
6039	Hovdala-2	Sweden
8308	HR-10	United Kingdom
8309	HR-5	United Kingdom
8310	Hs-0	Germany
8236	HSm	Czech Republic
8311	In-0	Austria
8312	Is-0	Germany
8313	Jm-0	Czech Republic
8314	Ka-0	Austria
8424	Kas-2	India
8237	Kavlinge-1	Sweden
8420	Kelsterbach-4	Germany
8238	Kent	United Kingdom
8316	Kin-0	United States of America

Id	Name	Country
6040	Kni-1	Sweden
8317	Kno-10	United States of America
8318	Kno-18	United States of America
8239	Koln	Germany
8319	Kondara	Tajikistan
8240	Kulturen-1	Sweden
8320	Kz-1	Kazakhstan
8321	Kz-13	Kazakhstan
8322	Kz-9	Kazakhstan
8323	Lc-0	United Kingdom
8324	Ler-1	Germany
8241	Liarum	Sweden
8242	Lillo-1	Sweden
8325	Lip-0	Poland
8326	Lis-1	Sweden
8222	Lis-2	Sweden
8430	Lisse	Netherlands
8328	LL-0	Spain
8329	Lm-2	France
6042	Lom1-1	Sweden
6043	Lov-1	Sweden
6046	Lov-5	Sweden
8332	Lp2-2	Czech Republic
8333	Lp2-6	Czech Republic
8334	Lu-1	Sweden
8335	Lund	Sweden
8336	Lz-0	France
8337	Mir-0	Italy
8338	Mr-0	Italy
8339	Mrk-0	Germany
8340	Ms-0	Russia
8341	Mt-0	Libya
8342	Mz-0	Germany
8429	N13	Russia
8343	Na-1	France
8246	NC-6	United States of America
8344	Nd-1	Switzerland
8345	NFA-10	United Kingdom
8346	NFA-8	United Kingdom
8347	Nok-3	Netherlands
8348	Nw-0	Germany
6064	Nyl-2	Sweden
8349	Omo2-1	Sweden

Id	Name	Country
8350	Omo2-3	Sweden
6074	Or-1	Sweden
8351	Ost-0	Sweden
8352	Oy-0	Norway
8353	Pa-1	Italy
8354	Per-1	Russia
8355	Petergof	Russia
8243	PHW-2	Italy
8244	PHW-34	France
8356	Pi-0	Austria
8357	Pla-0	Spain
8358	Pna-10	United States of America
8359	Pna-17	United States of America
8360	Pro-0	Spain
8361	Pu2-23	Czech Republic
8362	Pu2-7	Czech Republic
8363	Pu2-8	Czech Republic
8364	Ra-0	France
8365	Rak-2	Czech Republic
8366	Rd-0	Germany
8411	Rd-0	Germany
8367	Ren-1	France
8368	Ren-11	France
8369	Rev-1	Sweden
8370	Rmx-A02	United States of America
8371	Rmx-A180	United States of America
8372	RRS-10	United States of America
8373	RRS-7	United States of America
8374	Rsch-4	Russia
8375	Rubezhnoe-1	Ukraine
8247	San-2	Sweden
8376	Sanna-2	Sweden
8377	Santa Clara	United States of America
8378	Sap-0	Czech Republic
8412	Sav-0	Czech Republic
8379	Se-0	Spain
8245	Seattle-0	United States of America

Id	Name	Country
8380	Sf-1	Spain
8248	Shahdara	Tajikistan
8381	Sorbo	Tajikistan
8382	Spr1-2	Sweden
8383	Spr1-6	Sweden
8384	Sq-1	United Kingdom
8385	Sq-8	United Kingdom
8386	Sr-5	Sweden
8387	St-0	Sweden
8388	Stw-0	Russia
8389	Ta-0	Czech Republic
8390	Tamm-2	Finland
8391	Tamm-27	Finland
6243	Tottarp-2	Sweden
8392	Ts-1	Spain
8393	Ts-5	Spain
8394	Tsu-1	Japan
8395	Tu-0	Italy
8426	Ull1-1	Sweden
8396	Ull2-3	Sweden
8397	Ull2-5	Sweden

Id	Name	Country
8398	Uod-1	Austria
8428	Uod-2	Austria
8399	Uod-7	Austria
8400	Van-0	Canada
8401	Var2-1	Sweden
8402	Var2-6	Sweden
9058	Vastervik	Sweden
8249	Vimmerby	Sweden
9057	Vinslov	Sweden
8403	Wa-1	Poland
8404	Wei-0	Switzerland
8419	Wil-1	Lithuania
100000	Wil-1-Dean-Lab	Lithuania
8405	Ws-0	Russia
8406	Ws-2	Russia
8407	Wt-5	Germany
8408	Yo-0	United States of America
8409	Zdr-1	Czech Republic
8410	Zdr-6	Czech Republic

36

37 **Supplementary Table 1: The list of accessions.**

Kingdom	Technique	Eigenvector	% of variance	Proportion of variance explained by SNPs	Permutation <i>P</i> -value
Fungi	PCA	PC1	16.4%	0.094	0.003*
Fungi	PCA	PC2	10.3%	0.076	0.015*
Fungi	PCA	PC3	9%	0.000	0.993
Fungi	PCA	PC4	8.3%	0.000	0.996
Fungi	PCA	PC5	6%	0.078	0.024*
Bacteria	PCA	PC1	2.3%	0.000	0.993
Bacteria	PCA	PC2	1.7%	0.110	0.001*
Bacteria	PCA	PC3	1.4%	0.000	0.996
Bacteria	PCA	PC4	1%	0.040	0.08
Bacteria	PCA	PC5	0.008%	0.000	0.998
Fungi	CCA	CCA1	NA	0.046	0.09
Fungi	CCA	CCA2	NA	0.090	0.003*
Fungi	CCA	CCA3	NA	0.000	0.996
Fungi	CCA	CCA4	NA	0.005	0.378
Fungi	CCA	CCA5	NA	0.102	0.008*
Bacteria	CCA	CCA1	NA	0.061	0.05*
Bacteria	CCA	CCA2	NA	0.000	0.995
Bacteria	CCA	CCA3	NA	0.000	0.994
Bacteria	CCA	CCA4	NA	0.019	0.257
Bacteria	CCA	CCA5	NA	0.000	0.996
Fungi	DCA	DCA1	NA	0.000	0.999
Fungi	DCA	DCA2	NA	0.034	0.144
Fungi	DCA	DCA3	NA	0.02	0.235
Fungi	DCA	DCA4	NA	0.000	0.992
Bacteria	DCA	DCA1	NA	0.083	0.017*
Bacteria	DCA	DCA2	NA	0.06	0.045*
Bacteria	DCA	DCA3	NA	0.004	0.434
Bacteria	DCA	DCA4	NA	0.065	0.04*

Supplementary Table 2: Proportion of variance explained by genome-wide SNPs (MAF ≥ 0.05) for the structure of the microbial community of *A. thaliana*. *P*-values ≤ 0.05 are denoted by an asterisk (*); the phenotypes (the coordinates along an eigenvector) were permuted 1000 times to estimate each *P*-value (see Methods). The results from the top 5 eigenvectors are displayed for PCA and CCA; the approach used for DCA (Methods) returns 4 axes¹.

Kingdom	Observed sharing	P-value	Chr	Window-start	Window-end	SNP position	OTU	Lineage
Fungi	5	$P = 0.00065$	3	17770001	17780000	17775101	OTU1822	Fungi;;;;;Uncultured
			3	17770001	17780000	17775101	OTU2128	Fungi;Ascomycota;Dothideomycetes;Pleosporales;Didymellaceae;Phoma
			3	17770001	17780000	17775101	OTU3573	Fungi;Ascomycota;Dothideomycetes;Pleosporales;Phaeosphaeriaceae;Phaeosphaeriopsis
			3	17770001	17780000	17775101	OTU3804	Fungi;Ascomycota;Sordariomycetes;Glomerellales;Plectosphaerellaceae;Lectera
			3	17770001	17780000	17775101	OTU910	Fungi;;;;;Uncultured
	5	$P = 0.00065$	3	21840001	21850000	21848321	OTU1084	Fungi;Ascomycota;Dothideomycetes;Pleosporales;;Coniothyrium
			3	21840001	21850000	21848321	OTU1481	Fungi;;;;;Uncultured
			3	21840001	21850000	21848321	OTU2082	Fungi;;;;;Uncultured
			3	21840001	21850000	21848321	OTU2911	Fungi;Ascomycota;Sordariomycetes;Hypocreales;Nectriaceae;Fusarium
			3	21840001	21850000	21848321	OTU776	Fungi;;;;;Uncultured
	5	$P = 0.00065$	4	900001	910000	905505	OTU1822	Fungi;;;;;Uncultured
			4	900001	910000	905505	OTU2877	Fungi;Ascomycota;Dothideomycetes;Capnodiales;Davidiellaceae;Cladosporium
			4	900001	910000	905505	OTU3573	Fungi;Ascomycota;Dothideomycetes;Pleosporales;Phaeosphaeriaceae;Phaeosphaeriopsis
			4	900001	910000	908824	OTU3751	Fungi;Ascomycota;Dothideomycetes;Pleosporales;Melanommataceae;Herpotrichia
			4	900001	910000	905505	OTU910	Fungi;;;;;Uncultured
← Bacteria	9	$P = 1e-05$	3	3850001	3860000	3852573	OTU12	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Micromonosporaceae;Actinoplanes
			3	3850001	3860000	3852573	OTU159	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Blastomonas
			3	3850001	3860000	3852573	OTU190	Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Xanthomonas
			3	3850001	3860000	3852573	OTU197	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas
			3	3850001	3860000	3852573	OTU225	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas
			3	3850001	3860000	3852573	OTU254	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas
			3	3850001	3860000	3852573	OTU37	Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Flavobacterium
			3	3850001	3860000	3852573	OTU52	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomon

								adaceae;Sphingomonas
			3	3850001	3860000	3851036	OTU615	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;
	7	$P = 1e-05$	1	26480001	26490000	26482384	OTU10	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Hyphomicrobiaceae;Devosia
			1	26480001	26490000	26482384	OTU157	Bacteria;Proteobacteria;Betaproteobacteria;Methylophilales;Methylophilaceae;Methylovorus
			1	26480001	26490000	26482384	OTU191	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Simplicispira
			1	26480001	26490000	26482384	OTU32	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;
			1	26480001	26490000	26482384	OTU61	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas
			1	26480001	26490000	26482384	OTU723	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas
			1	26480001	26490000	26482384	OTU93	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas
	7	$P = 1e-05$	4	7650001	7660000	7659493	OTU12	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Micromonosporaceae;Actinoplanes
			4	7650001	7660000	7659456	OTU129	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;
			4	7650001	7660000	7659493	OTU15	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;
			4	7650001	7660000	7659493	OTU28	Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Rhizobiaceae;Rhizobium
			4	7650001	7660000	7659493	OTU37	Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Flavobacterium
			4	7650001	7660000	7659493	OTU452	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;;
			4	7650001	7660000	7659456	OTU648	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;;
	6	$P = 2e-05$	3	18500001	18510000	18508790	OTU200	Bacteria;Proteobacteria;Betaproteobacteria;Methylophilales;Methylophilaceae;
			3	18500001	18510000	18508790	OTU38	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Kineosporiaceae;Kineococcus
			3	18500001	18510000	18508790	OTU40	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;
			3	18500001	18510000	18508790	OTU4	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;
			3	18500001	18510000	18508790	OTU592	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;
			3	18500001	18510000	18508790	OTU59	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;
	5	$P =$	1	25850001	25860000	25858404	OTU1076	Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae

		0.00065						e;Brevundimonas
			1	25850001	25860000	25858404	OTU12	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Micromonosporaceae;Actinoplanes
			1	25850001	25860000	25858404	OTU561	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Geodermatophilaceae;
			1	25850001	25860000	25858404	OTU581	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Kineosporiaceae;Kineococcus
			1	25850001	25860000	25858404	OTU592	Bacteria;Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;

Supplementary Table 3: Genomic regions associated with multiple OTUs in either the bacterial or fungal communities. To evaluate the probability of sharing a genomic region, across association studies, we split the genome into 10-kb windows (in total, there are $n = 11,614$ 10-kb windows). Then, to make results comparable across GWAS, we converted the test statistic for each window (e.g. the minimum P value), into a rank-based score (i.e. an empirical P value). We next used 100,000 permutations to create a null distribution by resampling 11 ($P \leq 0.001$) windows 100 times (i.e. from 100 OTUs); the P values report the number of shared windows in each permutation.

54

Kingdom	Observed sharing	<i>P</i> -value	Chr	Window-start	Window-end	SNP position	OTU	Lineage
Both Bacteria and Fungi	5	<i>P</i> = 0.018	2	14600001	14610000	14603435	OTU507	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas
			2	14600001	14610000	14603435	OTU52	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas
			2	14600001	14610000	14609687	OTU1481	Fungi;;;;Uncultured
			2	14600001	14610000	14603435	OTU3043	Fungi;Ascomycota;Sordariomycetes;Hypocreales;Nectriaceae;Fusarium
			2	14600001	14610000	14609687	OTU883	Fungi;Ascomycota;Dothideomycetes;Pleosporales;Phaeosphaeriaceae;Paraphoma
	5	<i>P</i> = 0.018	1	23410001	23420000	23415964	OTU159	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Blastomonas
			1	23410001	23420000	23415964	OTU225	Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas
			1	23410001	23420000	23414826	OTU1502	Fungi;;;;Uncultured
			1	23410001	23420000	23414826	OTU1549	Fungi;;;;Uncultured
			1	23410001	23420000	23410600	OTU1762	Fungi;;;;Uncultured

55

56 **Supplementary Table 4: Genomic regions associated with multiple OTUs in both the bacterial fungal communities.** To evaluate the
57 probability of sharing a genomic region, across association studies of both communities, we split the genome into 10-kb windows (in total, there
58 are $n = 11,614$ 10-kb windows). Then, to make results comparable across GWAS, we converted the test statistic for each window (e.g. the
59 minimum P value), into a rank-based score (i.e. an empirical P value). We next used 100,000 permutations to create a null distribution by
60 resampling 11 ($P \leq 0.001$) windows 200 times (i.e. 100 OTUs per kingdom); the P values report the number of shared windows in each
61 permutation.

62

Eigenvector technique	Biological process	Eigenvector	Enrichment	Storey's FDR $q < 0.1$
PCA	cortical microtubule cytoskeleton	PC5	20.1	0.023
PCA	microtubule cytoskeleton organization	PC5	5.3	0.052
CCA	microtubule-based process	CCA2	4.4	0.080
CCA	microtubule cytoskeleton	CCA2	7.5	0.080
CCA	microtubule binding	CCA2	2.8	0.082

64

65 **Supplementary Table 5: Microtubule related processes (GO-terms) were enriched in**

66 **the 5% tail from GWAS of eigenvectors from both PCA and CCA of the fungal**

67 **community. Storey's procedure² was used to correct for multiple testing using an FDR of**

68 **10%.**

69

70 **References**

71

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75 *Natl Acad Sci U S A* **100**, 9440-9445 (2003).

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