

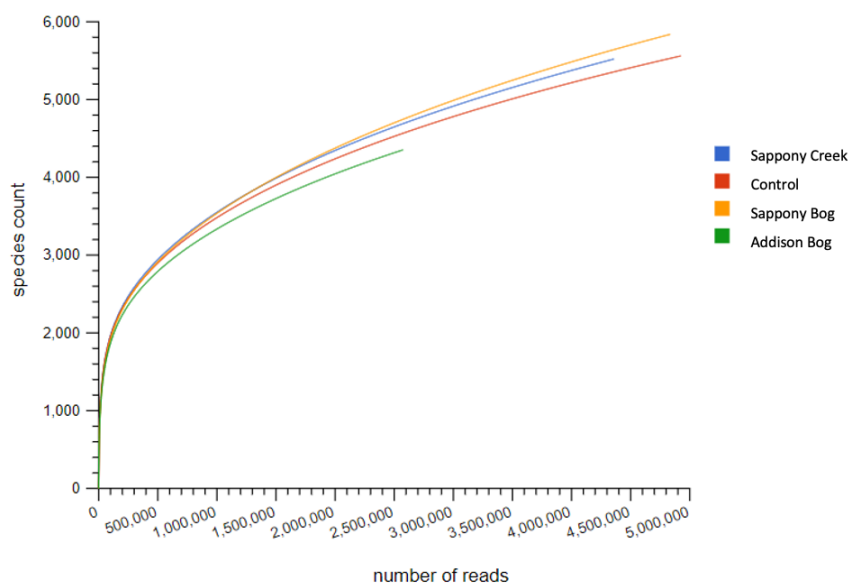
Suppl. Table S1. Common features of sample collection sites.

MG-RAST Project ID	mgp15161
biome	temperate woodland biome
collection_date	2015-07-26
country	USA
env_package	soil
feature	headwater
material	loam
collection_timezone	UTC-5
continent	North America
location	Waverly, VA

Suppl. Table S2. Shotgun metagenome sequenced soil microbiome data form other studies

Sample No	MG-RAST ID	Name	bp count	seq count	biome	feature	material	location
5	mgm4664919.3	HARV.016.50	975,817,348	6,119,472	temperate woodland	woody wetland	surface soil	MA
6	mgm4664903.3	HARV.016.xx	1,117,683,890	7,058,306	temperate woodland	woody wetland	surface soil	MA
7	mgm4637852.3	JERC.006	1,101,149,827	6,615,248	terrestrial	mixed forest	surface soil	GA
8	mgm4664908.3	OSBS.001	1,631,646,794	9,688,330	terrestrial	woody wetland	surface soil	FL
9	mgm4664913.3	OSBS.087	1,776,935,210	10,752,514	terrestrial	mixed forest	surface soil	FL
10	mgm4664896.3	SCBI.002	1,901,198,569	11,102,264	terrestrial	mixed forest	surface soil	VA
11	mgm4664851.3	SCBI.003	1,714,299,175	10,125,449	terrestrial	mixed forest	surface soil	VA
12	mgm4664929.3	TALL.002	1,721,708,257	10,519,094	terrestrial	mixed forest	surface soil	AL
13	mgm4524591.3	Barley_	2,776,145,032	17,537,694	terrestrial	Plant-associated habitat	rhizosphere	Germany
14	mgm4508940.3	Nocton_Soy	3,081,990,561	17,442,824	Temperate broadleaf and mixed forest	farm	Agricultural soil	IN
15	mgm4508941.3	Sedgewick	1,997,174,632	11,066,959	Temperate broadleaf and mixed forest	Canopy	Leaf wood soil	IN
16	mgm4552600.3	2012_13_Corn	2,918,474,743	28,877,883	Temperate broadleaf and mixed forest	Farm	Agricultural soil	IN
17	mgm4552608.3	2012_20_Soy	1,286,824,690	12,735,016	Temperate broadleaf and mixed forest	Farm	Agricultural soil	IN
18	mgm4552617.3	2013_11_Soy	1,144,230,699	11,311,337	Temperate broadleaf and mixed forest	Farm	Agricultural soil	IN

Suppl. Fig. S1. Rarefaction curves of the numbers of species from four sampling sites.



Suppl. Table S3. Sequence statistics of taxonomic and function annotation

Sample ID	Taxonomic Hits		Functional hits				
	Number of reads	(%)	ribosomal RNA	annotated protein	unknown function	total	(%)
Addison Bog	1,063,619	53.3	69,619 (3.78%)	729,386 (39.60%)	1,043,092 (56.63%)	1,842,097	92.3
Sappony Bog	1,724,580	43.7	173,776 (4.75%)	1,107,029 (30.25%)	2,379,205 (65.01%)	3,660,010	92.7
Sappony Creek	1,701,184	50.0	138,566 (4.36%)	1,171,302 (36.86%)	1,867,508 (58.78%)	3,177,376	93.5
Control	1,785,394	45.1	186,400 (62.74%)	1,218,311 (32.32%)	2,364,972 (62.74%)	3,769,683	95.2

Suppl. Table S4. Metagenome composition among four different Virginia habitats.

(a) Domain

Domain	Addison Bog		Sappony Bog		Sappony Creek		Control	
	No. of reads	(%)	No. of reads	(%)	No. of reads	(%)	No. of reads	(%)
Archaea	8,071	(0.76)	13,277	(0.77)	18,148	(1.07)	26,511	(1.48)
Bacteria	1,043,567	(98.11)	1,683,192	(97.60)	1,665,226	(97.89)	1,742,562	(97.60)
Eukaryota	11,610	(1.09)	27,676	(1.60)	17,198	(1.01)	15,907	(0.89)
Viruses	328	(0.03)	398	(0.02)	566	(0.03)	369	(0.02)
other	43	(0.00)	37	(0.00)	46	(0.00)	45	(0.00)

(b) Phyla in three main domains

Domain	Phylum	Addison Bog (%)		Sappony Bog (%)		Sappony Creek (%)		Control (%)	
Archaea	Euryarchaeota	6870	(0.65)	10932	(0.63)	14570	(0.86)	20851	(1.17)
	Crenarchaeota	991	(0.09)	1975	(0.11)	2529	(0.15)	3419	(0.19)
	Thaumarchaeota	129	(0.01)	235	(0.01)	887	(0.05)	1973	(0.11)
Bacteria	Proteobacteria	561644	(52.80)	960891	(55.72)	888435	(52.22)	930902	(52.14)
	Acidobacteria	175055	(16.46)	235031	(13.63)	235616	(13.85)	181903	(10.19)
	Actinobacteria	97801	(9.20)	165184	(9.58)	157245	(9.24)	173958	(9.74)
	Firmicutes	35427	(3.33)	67206	(3.90)	83146	(4.89)	104271	(5.84)
	Verrucomicrobia	45197	(4.25)	49344	(2.86)	69868	(4.11)	62165	(3.48)
	Planctomycetes	38207	(3.59)	47500	(2.75)	52526	(3.09)	64561	(3.62)
	Bacteroidetes	25372	(2.39)	40308	(2.34)	44126	(2.59)	56827	(3.18)
	Cyanobacteria	22996	(2.16)	39601	(2.30)	43786	(2.57)	45150	(2.53)
	Chloroflexi	15807	(1.49)	30545	(1.77)	34040	(2.00)	46783	(2.62)
	Chlorobi	4661	(0.44)	8300	(0.48)	10471	(0.62)	12124	(0.68)
	Deinococcus-Thermus	4811	(0.45)	8704	(0.50)	9363	(0.55)	11526	(0.65)
	Nitrospirae	2536	(0.24)	4202	(0.24)	6133	(0.36)	11503	(0.64)
	Spirochaetes	2268	(0.21)	3760	(0.22)	4675	(0.27)	6118	(0.34)
	Aquificae	1689	(0.16)	3071	(0.18)	3765	(0.22)	4756	(0.27)
	Thermotogae	1435	(0.13)	2695	(0.16)	3350	(0.20)	4580	(0.26)
	Gemmatimonadetes	1792	(0.17)	3140	(0.18)	3327	(0.20)	5985	(0.34)
	unclassified (derived from Bacteria)	1459	(0.14)	2606	(0.15)	2810	(0.17)	4067	(0.23)
	Chlamydiae	1270	(0.12)	3386	(0.20)	2749	(0.16)	2778	(0.16)
	Synergistetes	834	(0.08)	1496	(0.09)	1828	(0.11)	2456	(0.14)
	Deferribacteres	684	(0.06)	1285	(0.07)	1710	(0.10)	2190	(0.12)
Eukaryota	Ascomycota	5562	(0.52)	14570	(0.84)	5464	(0.32)	3939	(0.22)
	Streptophyta	1813	(0.17)	3617	(0.21)	3529	(0.21)	3604	(0.20)
	Chordata	1085	(0.10)	2640	(0.15)	2493	(0.15)	2563	(0.14)

Suppl. Table S5. Metagenome composition of Eukaryotes (those observed with >100 reads) in four rhizospheres associated with *S. flava* in Virginia.

Phylum	Class	Order	Family	Genus	Addison Bog	Sappony Bog	Sappony Creek	Control
Apicomplexa	Aconoidasida	Haemosporida	unclassified	Plasmodium	33	110	110	71
Arthropoda	Arachnida	Ixodida	Ixodidae	Ixodes	44	92	83	104
	Insecta	Diptera	Culicidae	Aedes	67	112	135	141
				Anopheles	60	163	146	144
Ascomycota	Dothideomycetes	Pleosporales	Drosophilidae	Drosophila	187	492	420	464
			Phaeosphaeriaceae	Phaeosphaeria	244	452	221	142
			Pleosporaceae	Pyrenophora	144	250	124	81
	Eurotiomycetes	Eurotiales	Trichocomaceae	Aspergillus	462	1180	656	489
				Emericella	159	389	181	144
				Neosartorya	629	1634	642	481
				Penicillium	216	584	195	142
				Talaromyces	149	383	159	76
		Onygenales	Ajellomycetaceae	Ajellomyces	107	329	94	95
				Arthroderma	92	256	97	84
				Coccidioides	147	488	114	84
	Leotiomycetes	Helotiales	Sclerotiniaceae	Botryotinia	296	968	150	69
				Sclerotinia	314	1105	177	101
	Pezizomycetes	Pezizales	Tuberaceae	Tuber	66	218	55	44
	Saccharomycetes	Saccharomycetales	Debaryomycetaceae	Scheffersomyces	43	118	58	71
			Dipodasceae	Yarrowia	54	194	71	79
			Saccharomycetaceae	Saccharomyces	64	181	122	118
			unclassified	Candida	32	104	61	46
	Schizosaccharomycetes	Schizosaccharomycetales	Schizosaccharomycetaceae	Schizosaccharomyces	137	429	160	186
	Sordariomycetes	Hypocreales	Nectriaceae	Gibberella	624	1339	457	336
				Nectria	218	393	167	105
		Magnaporthales	Magnaporthaceae	Magnaportha	229	652	268	149
		Phyllachorales	unclassified	Verticillium	65	226	80	59
		Sordariales	Chaetomiaceae	Chaetomium	160	374	152	78
			Lasiosphaeriaceae	Podospira	172	372	190	98
Bacillariophyta	Bacillariophyceae	Naviculales	Phaeodactylaceae	Phaeodactylum	65	84	94	124
	Coscinodiscophyceae	unclassified	Thalassiosiraceae	Thalassiosira	80	110	91	101
	Agaricomycetes	Agaricales	Psathyrellaceae	Coprinopsis	59	123	64	80
			Schizophyllaceae	Schizophyllum	58	153	101	88
			Tricholomataceae	Laccaria	123	184	80	75
Basidiomycota	Tremellomycetes	Tremellales	Tremellaceae	Filobasidiella	123	340	213	179
	Ustilaginomycetes	Ustilaginales	Ustilaginaceae	Ustilago	102	234	129	129
Chlorophyta	Chlorophyceae	Chlamydomonadales	Chlamydomonadaceae	Chlamydomonas	108	202	208	215
			Volvocaceae	Volvox	90	180	214	244
	Prasinophyceae	Mamiellales	unclassified	Micromonas	86	148	146	150
			unclassified	Ostreococcus	101	169	162	192
Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Danio	113	261	252	226
	Amphibia	Anura	Pipidae	Xenopus	186	362	327	361
	Ascidacea	Enterogona	Cionidae	Ciona	45	124	100	105
	Aves	Galliformes	Phasianidae	Gallus	41	101	91	97
	Mammalia	Primates	Hominidae	Homo	89	224	241	289
		Rodentia	Muridae	Mus	104	275	288	246
		Rodentia	Muridae	Rattus	83	214	203	205
		unclassified	unclassified	Bos	85	192	223	211
	unclassified	unclassified	Branchiostomidae	Branchiostoma	122	298	240	270
Chytridiomycota	Chytridiomycetes	Cladochytriales	Cladochytriaceae	Cladochytrium	0	104	0	0
Cnidaria	Anthozoa	Actiniaria	Edwardsiidae	Nematostella	120	259	236	281
	Hydrozoa	Hydroida	Hydridae	Hydra	82	190	153	164
Echinodermata	Echinoidea	Echinoida	Strongylocentrotidae	Strongylocentrotus	70	172	179	114
Hemichordata	Enteropneusta	unclassified	Harrimaniidae	Saccoglossus	28	103	73	70
Nematoda	Chromadorea	Rhabditida	Rhabditidae	Caenorhabditis	186	374	323	303
Placozoa	unclassified	unclassified	unclassified	Trichoplax	66	135	136	125
Streptophyta	Bryopsida	Funariales	Funariaceae	Physcomitrella	156	335	344	389
	Isoetopsida	Selaginellales	Selaginellaceae	Selaginella	81	176	179	220
	Liliopsida	Poales	Poaceae	Oryza	134	264	301	254
				Sorghum	76	186	245	178
	unclassified	Brassicales	Brassicaceae	Arabidopsis	494	948	1033	1096
		Malpighiales	Euphorbiaceae	Ricinus	638	1156	1001	1022
			Salicaceae	Populus	90	207	206	213

		Vitales	Vitaceae	Vitis	100	240	142	159
unclassified (derived from Eukaryota)	Heterolobosea	Schizopyrenida	Vahlkampfiidae	Naegleria	75	152	152	146
	unclassified	Choanoflagellida	Codonosigidae	Monosiga	72	121	113	126
		Dictyosteliida	unclassified	Dictyostelium	238	464	391	414
		Kinetoplastida	Trypanosomatidae	Leishmania	57	114	116	117
		Peronosporales	unclassified	Phytophthora	95	162	111	168
		Trichomonadida	Trichomonadidae	Trichomonas	52	58	108	98
unclassified (derived from Fungi)		Entomophthorales	Basidiobolaceae	Basidiobolus	0	131	1	0

Suppl. Table S6. Normalized metagenome composition of Proteobacteria in study sites.

Class	Order	Family	Genus	Addison Bog	Sappony Bog	Sappony Creek	Control
Alpha	Caulobacterales	Caulobacteraceae	Asticcacaulis	0.0013	0.0014	0.0014	0.0011
			Brevundimonas	0.0026	0.0028	0.0022	0.0019
			Caulobacter	0.0196	0.0168	0.0142	0.0114
			Phenylobacterium	0.0061	0.0051	0.0043	0.0037
	Parvularculales	Parvularculaceae	Parvularcula	0.0007	0.0008	0.0007	0.0006
	Rhizobiales	Aurantimonadaceae	Aurantimonas	0.0021	0.0022	0.0020	0.0019
			Fulvimarina	0.0005	0.0008	0.0006	0.0006
		Bartonellaceae	Bartonella	0.0009	0.0012	0.0010	0.0010
		Beijerinckiaceae	Beijerinckia	0.0056	0.0050	0.0048	0.0036
			Methylocella	0.0103	0.0082	0.0072	0.0052
		Bradyrhizobiaceae	Afipia	0.0043	0.0052	0.0053	0.0054
			Bradyrhizobium	0.0768	0.0810	0.0775	0.0678
			Nitrobacter	0.0231	0.0267	0.0265	0.0231
			Oligotropha	0.0048	0.0057	0.0056	0.0058
			Rhodopseudomonas	0.0449	0.0563	0.0560	0.0559
		Brucellaceae	Brucella	0.0032	0.0047	0.0048	0.0044
			Ochrobactrum	0.0028	0.0029	0.0031	0.0024
		Hyphomicrobiaceae	Hyphomicrobium	0.0026	0.0028	0.0028	0.0045
			Rhodomicrobium	0.0030	0.0032	0.0040	0.0031
		Methylobacteriaceae	Methylobacterium	0.0317	0.0335	0.0339	0.0264
			Methylosinus	0.0046	0.0038	0.0038	0.0032
		Phyllobacteriaceae	Chelativorans	0.0046	0.0047	0.0044	0.0042
			Hoeflea	0.0009	0.0010	0.0010	0.0010
			Mesorhizobium	0.0148	0.0144	0.0137	0.0108
			Parvibaculum	0.0074	0.0076	0.0057	0.0061
		Rhizobiaceae	Agrobacterium	0.0071	0.0075	0.0071	0.0061
			Candidatus Liberibacter	0.0000	0.0001	0.0001	0.0001
			Rhizobium	0.0177	0.0182	0.0185	0.0145
			Sinorhizobium	0.0156	0.0164	0.0169	0.0129
		Xanthobacteraceae	Azorhizobium	0.0063	0.0065	0.0064	0.0058
			Starkeya	0.0057	0.0057	0.0053	0.0051
			Xanthobacter	0.0109	0.0102	0.0090	0.0086
		unclassified	Candidatus Hodgkinia	0.0000	0.0000	0.0000	0.0000
Rhodobacterales	Hyphomonadaceae		Hirschia	0.0005	0.0007	0.0006	0.0006
			Hyphomonas	0.0022	0.0023	0.0018	0.0019
			Maricaulis	0.0019	0.0020	0.0017	0.0017
			Oceanicaulis	0.0009	0.0011	0.0010	0.0009

Phylum	Class	Order	Genus					
			Genus	Genus	Genus	Genus		
Proteobacteria	Rhodobacteraceae	Ahrensia	0.0005	0.0007	0.0006	0.0006		
		Citreicella	0.0006	0.0007	0.0007	0.0006		
		Dinoroseobacter	0.0013	0.0015	0.0016	0.0014		
		Jannaschia	0.0013	0.0014	0.0014	0.0014		
		Ketogulonicigenium	0.0005	0.0005	0.0005	0.0005		
		Labrenzia	0.0031	0.0035	0.0034	0.0032		
		Loktanella	0.0004	0.0005	0.0004	0.0005		
		Maritimibacter	0.0010	0.0011	0.0011	0.0011		
		Oceanibulbus	0.0002	0.0003	0.0003	0.0003		
		Oceanicola	0.0015	0.0016	0.0016	0.0015		
		Octadecabacter	0.0013	0.0013	0.0014	0.0009		
		Paracoccus	0.0020	0.0021	0.0019	0.0018		
		Pelagibaca	0.0006	0.0007	0.0006	0.0005		
		Phaeobacter	0.0002	0.0003	0.0003	0.0003		
		Pseudovibrio	0.0009	0.0010	0.0010	0.0010		
		Rhodobacter	0.0043	0.0051	0.0052	0.0048		
		Roseibium	0.0009	0.0011	0.0012	0.0011		
		Roseobacter	0.0035	0.0041	0.0038	0.0039		
		Roseovarius	0.0017	0.0021	0.0020	0.0021		
		Ruegeria	0.0035	0.0039	0.0036	0.0035		
		Sagittula	0.0005	0.0006	0.0005	0.0005		
		Sulfitobacter	0.0005	0.0007	0.0007	0.0007		
		Thalassobium	0.0002	0.0002	0.0001	0.0002		
		unclassified	0.0008	0.0011	0.0009	0.0009		
		unclassified	unclassified	0.0005	0.0007	0.0006	0.0006	
		Rhodospirillales	Acetobacteraceae	Acetobacter	0.0015	0.0017	0.0015	0.0011
				Acidiphilium	0.0097	0.0094	0.0080	0.0057
				Gluconacetobacter	0.0052	0.0058	0.0051	0.0034
				Gluconobacter	0.0026	0.0027	0.0022	0.0016
				Granulibacter	0.0065	0.0063	0.0052	0.0037
				Roseomonas	0.0050	0.0050	0.0042	0.0035
			Rhodospirillaceae	Azospirillum	0.0076	0.0078	0.0060	0.0054
Magnetospirillum	0.0128			0.0139	0.0112	0.0112		
Rhodospirillum	0.0139			0.0143	0.0109	0.0100		
Rickettsiales	Anaplasmataceae	Anaplasma	0.0001	0.0001	0.0001	0.0001		
		Ehrlichia	0.0001	0.0002	0.0002	0.0002		
		Neorickettsia	0.0001	0.0001	0.0001	0.0001		
		Wolbachia	0.0003	0.0005	0.0004	0.0004		
	Rickettsiaceae	Orientia	0.0001	0.0001	0.0001	0.0001		
		Rickettsia	0.0007	0.0012	0.0010	0.0011		
	unclassified	Candidatus Pelagibacter	0.0005	0.0006	0.0005	0.0006		
		unclassified	0.0001	0.0002	0.0002	0.0002		
Sphingomonadales	Erythrobacteraceae	Erythrobacter	0.0022	0.0023	0.0022	0.0024		
	Sphingomonadaceae	Citromicrobium	0.0004	0.0004	0.0004	0.0004		

			Novosphingobium	0.0028	0.0026	0.0026	0.0028
			Sphingobium	0.0028	0.0029	0.0029	0.0025
			Sphingomonas	0.0062	0.0063	0.0058	0.0055
			Sphingopyxis	0.0022	0.0023	0.0022	0.0020
			Zymomonas	0.0010	0.0012	0.0012	0.0010
	unclassified	unclassified	Candidatus Puniceispirillum	0.0008	0.0008	0.0007	0.0007
			unclassified	0.0083	0.0086	0.0064	0.0060
Beta	Burkholderiales	Alcaligenaceae	Achromobacter	0.0035	0.0039	0.0039	0.0044
			Bordetella	0.0070	0.0084	0.0084	0.0095
		Burkholderiaceae	Burkholderia	0.0552	0.0614	0.0562	0.0482
			Cupriavidus	0.0151	0.0164	0.0170	0.0178
			Limnobacter	0.0005	0.0006	0.0006	0.0006
			Polynucleobacter	0.0013	0.0014	0.0014	0.0016
			Ralstonia	0.0094	0.0106	0.0113	0.0111
		Comamonadaceae	Acidovorax	0.0049	0.0054	0.0061	0.0081
			Albidiferax	0.0034	0.0034	0.0042	0.0051
			Alicyclophilus	0.0009	0.0011	0.0011	0.0015
			Comamonas	0.0013	0.0016	0.0016	0.0021
			Delftia	0.0020	0.0019	0.0020	0.0025
			Polaromonas	0.0070	0.0070	0.0076	0.0092
			Variovorax	0.0029	0.0030	0.0032	0.0043
			Verminephrobacter	0.0033	0.0034	0.0033	0.0038
		Oxalobacteraceae	Candidatus Zinderia	0.0000	0.0000	0.0000	0.0000
			Collimonas	0.0000	0.0000	0.0000	0.0000
			Herbaspirillum	0.0017	0.0018	0.0019	0.0020
			Herminiimonas	0.0016	0.0019	0.0020	0.0024
			Janthinobacterium	0.0025	0.0028	0.0027	0.0030
			Oxalobacter	0.0005	0.0007	0.0007	0.0008
		unclassified	Leptothrix	0.0023	0.0022	0.0027	0.0039
			Methylibium	0.0032	0.0033	0.0035	0.0050
			Thiomonas	0.0012	0.0012	0.0013	0.0013
			unclassified	0.0002	0.0003	0.0003	0.0002
	Gallionellales	Gallionellaceae	Gallionella	0.0011	0.0011	0.0013	0.0017
			Sideroxydans	0.0018	0.0016	0.0020	0.0027
	Hydrogenophilales	Hydrogenophilaceae	Thiobacillus	0.0020	0.0021	0.0023	0.0037
	Methylophilales	Methylophilaceae	Methylobacillus	0.0013	0.0016	0.0017	0.0023
			Methylothera	0.0012	0.0014	0.0015	0.0021
			Methylovorus	0.0008	0.0010	0.0011	0.0017
		unclassified	unclassified	0.0001	0.0001	0.0001	0.0001
	Neisseriales	Neisseriaceae	Chromobacterium	0.0028	0.0025	0.0026	0.0029
			Eikenella	0.0001	0.0001	0.0001	0.0001
			Kingella	0.0001	0.0001	0.0001	0.0001
			Laribacter	0.0007	0.0008	0.0007	0.0010

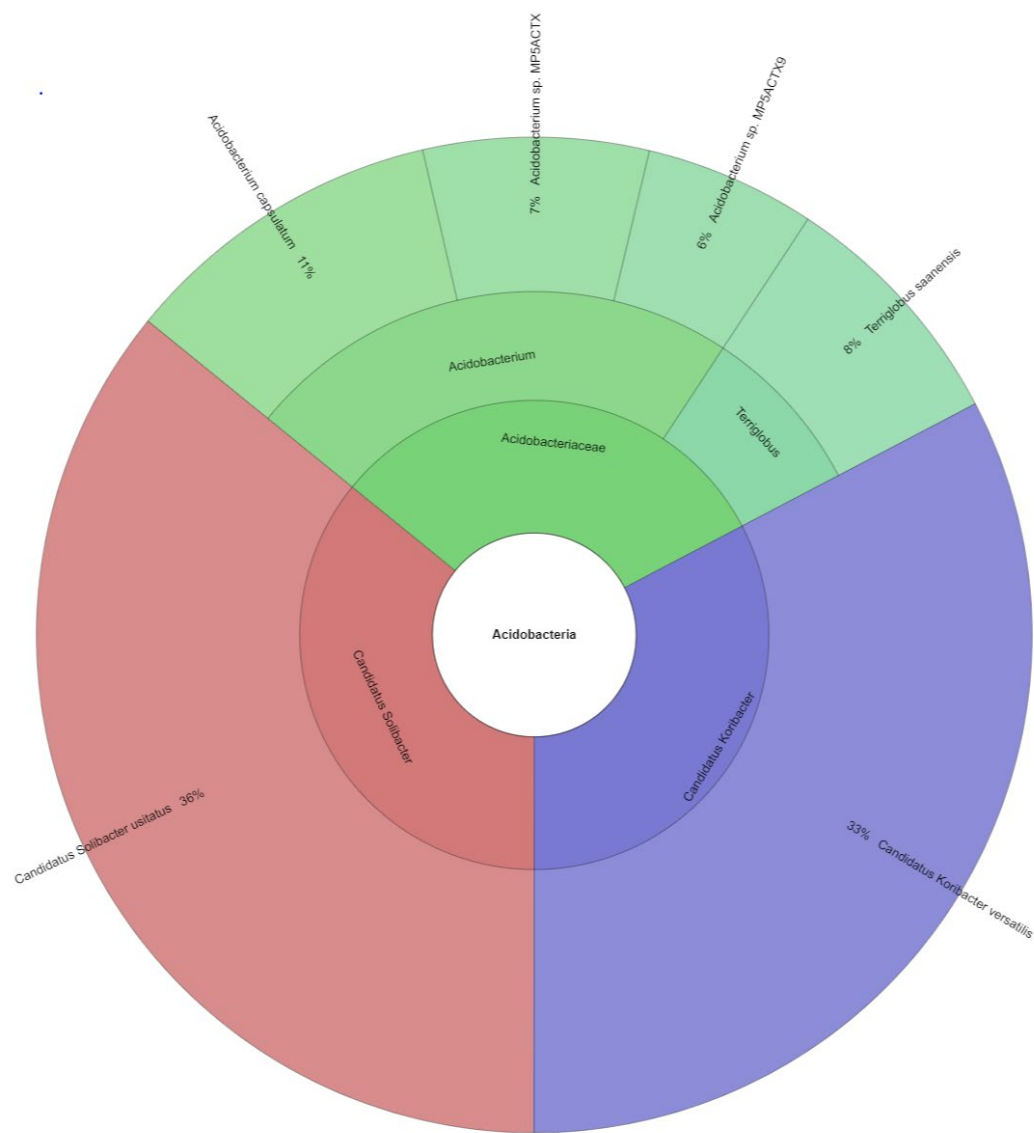
			Lutiella	0.0013	0.0013	0.0014	0.0017
			Neisseria	0.0008	0.0011	0.0013	0.0016
			Simonsiella	0.0001	0.0001	0.0001	0.0001
	Nitrosomonadales	Nitrosomonadaceae	Nitrosomonas	0.0031	0.0034	0.0037	0.0052
			Nitrospira	0.0028	0.0028	0.0029	0.0041
	Rhodocyclales	Rhodocyclaceae	Aromatoleum	0.0041	0.0041	0.0046	0.0051
			Azoarcus	0.0032	0.0033	0.0035	0.0049
			Dechloromonas	0.0038	0.0037	0.0043	0.0055
			Thauera	0.0017	0.0020	0.0022	0.0029
	unclassified	unclassified	Candidatus Accumulibacter	0.0039	0.0034	0.0040	0.0048
		unclassified	unclassified	0.0001	0.0001	0.0001	0.0001
Delta	Bdellovibrionales	Bdellovibrionaceae	Bdellovibrio	0.0017	0.0016	0.0016	0.0017
	Desulfarculales	Desulfarculaceae	Desulfarculus	0.0009	0.0009	0.0013	0.0017
	Desulfobacterales	Desulfobacteraceae	Desulfatibacillum	0.0016	0.0017	0.0024	0.0028
			Desulfobacterium	0.0011	0.0010	0.0015	0.0015
			Desulfococcus	0.0013	0.0013	0.0019	0.0022
		Desulfobulbaceae	Desulfotalea	0.0010	0.0009	0.0014	0.0016
			Desulfurivibrio	0.0007	0.0007	0.0012	0.0015
		Desulfohalobiaceae	Desulfohalobium	0.0006	0.0006	0.0010	0.0009
			Desulfonatronospira	0.0005	0.0005	0.0007	0.0007
		Desulfomicrobiaceae	Desulfomicrobium	0.0009	0.0010	0.0014	0.0017
		Desulfovibrionaceae	Desulfovibrio	0.0082	0.0087	0.0110	0.0123
			Lawsonia	0.0003	0.0004	0.0004	0.0004
	Desulfuromonadales	Desulfuromonadaceae	Desulfuromonas	0.0008	0.0009	0.0012	0.0018
		Geobacteraceae	Geobacter	0.0251	0.0211	0.0323	0.0447
		Pelobacteraceae	Pelobacter	0.0072	0.0057	0.0082	0.0109
	Myxococcales	Cystobacteraceae	Stigmatella	0.0071	0.0069	0.0072	0.0080
		Haliangiaceae	Haliangium	0.0050	0.0044	0.0049	0.0055
		Myxococcaceae	Anaeromyxobacter	0.0166	0.0168	0.0223	0.0341
			Myxococcus	0.0105	0.0096	0.0106	0.0117
		Nannocystaceae	Plesiocystis	0.0021	0.0019	0.0020	0.0023
		Polyangiaceae	Sorangium	0.0149	0.0108	0.0110	0.0096
	Syntrophobacterales	Syntrophaceae	Syntrophus	0.0028	0.0028	0.0044	0.0051
		Syntrophobacteraceae	Syntrophobacter	0.0051	0.0046	0.0069	0.0072
	unclassified	unclassified	unclassified	0.0021	0.0023	0.0035	0.0033
Epsilon	Campylobacterales	Campylobacteraceae	Arcobacter	0.0003	0.0003	0.0003	0.0004
			Campylobacter	0.0007	0.0008	0.0009	0.0011
			Sulfurospirillum	0.0001	0.0001	0.0001	0.0002
		Helicobacteraceae	Helicobacter	0.0005	0.0006	0.0006	0.0008
			Sulfuricurvum	0.0001	0.0001	0.0001	0.0001
			Sulfurimonas	0.0002	0.0002	0.0003	0.0003
			Wolinella	0.0002	0.0003	0.0003	0.0003

		unclassified	unclassified	0.0001	0.0001	0.0001	0.0001
	Nautiliales	Nautiliaceae	Caminibacter	0.0000	0.0001	0.0001	0.0001
			Nautilia	0.0001	0.0001	0.0001	0.0001
	unclassified	unclassified	Nitratiruptor	0.0003	0.0003	0.0003	0.0004
			Sulfurovum	0.0004	0.0003	0.0004	0.0004
Gamma	Acidithiobacillales	Acidithiobacillaceae	Acidithiobacillus	0.0023	0.0022	0.0022	0.0021
	Aeromonadales	Aeromonadaceae	Aeromonas	0.0013	0.0014	0.0017	0.0041
			Tolumonas	0.0005	0.0004	0.0004	0.0005
	Alteromonadales	Alteromonadaceae	Alteromonas	0.0005	0.0006	0.0007	0.0006
			Glaciecola	0.0000	0.0000	0.0000	0.0000
			Marinobacter	0.0022	0.0025	0.0026	0.0029
			Saccharophagus	0.0011	0.0010	0.0012	0.0012
		Colwelliaceae	Colwellia	0.0007	0.0008	0.0008	0.0009
		Ferrimonadaceae	Ferrimonas	0.0003	0.0003	0.0004	0.0005
		Idiomarinaceae	Idiomarina	0.0007	0.0008	0.0007	0.0008
		Moritellaceae	Moritella	0.0002	0.0002	0.0002	0.0002
		Pseudoalteromonadaceae	Pseudoalteromonas	0.0018	0.0020	0.0021	0.0024
		Psychromonadaceae	Psychromonas	0.0006	0.0007	0.0007	0.0009
		Shewanellaceae	Shewanella	0.0048	0.0056	0.0061	0.0067
		unclassified	Teredinibacter	0.0005	0.0006	0.0007	0.0008
			unclassified	0.0002	0.0001	0.0001	0.0002
	Cardiobacteriales	Cardiobacteriaceae	Cardiobacterium	0.0002	0.0002	0.0002	0.0002
			Dichelobacter	0.0002	0.0002	0.0002	0.0003
	Chromatiales	Chromatiaceae	Allochromatium	0.0014	0.0014	0.0015	0.0019
			Nitrosococcus	0.0059	0.0059	0.0065	0.0073
		Ectothiorhodospiraceae	Alkalilimnicola	0.0021	0.0020	0.0019	0.0024
			Halorhodospira	0.0012	0.0013	0.0013	0.0016
			Nitrococcus	0.0021	0.0020	0.0022	0.0022
			Thioalkalivibrio	0.0026	0.0028	0.0025	0.0037
		Halothiobacillaceae	Halothiobacillus	0.0006	0.0006	0.0005	0.0006
	Enterobacteriales	Enterobacteriaceae	Buchnera	0.0001	0.0002	0.0001	0.0001
			Candidatus Blochmannia	0.0000	0.0001	0.0000	0.0000
			Candidatus Hamiltonella	0.0001	0.0001	0.0001	0.0001
			Candidatus Regiella	0.0000	0.0000	0.0000	0.0000
			Candidatus Riesia	0.0000	0.0000	0.0000	0.0000
			Citrobacter	0.0086	0.0044	0.0039	0.0065
			Cronobacter	0.0064	0.0017	0.0017	0.0015
			Dickeya	0.0029	0.0015	0.0016	0.0012
			Edwardsiella	0.0009	0.0008	0.0026	0.0007
			Enterobacter	0.0424	0.0164	0.0108	0.0172
			Erwinia	0.0019	0.0012	0.0013	0.0009
			Escherichia	0.0110	0.0078	0.0071	0.0080
			Klebsiella	0.0119	0.0115	0.0071	0.0048

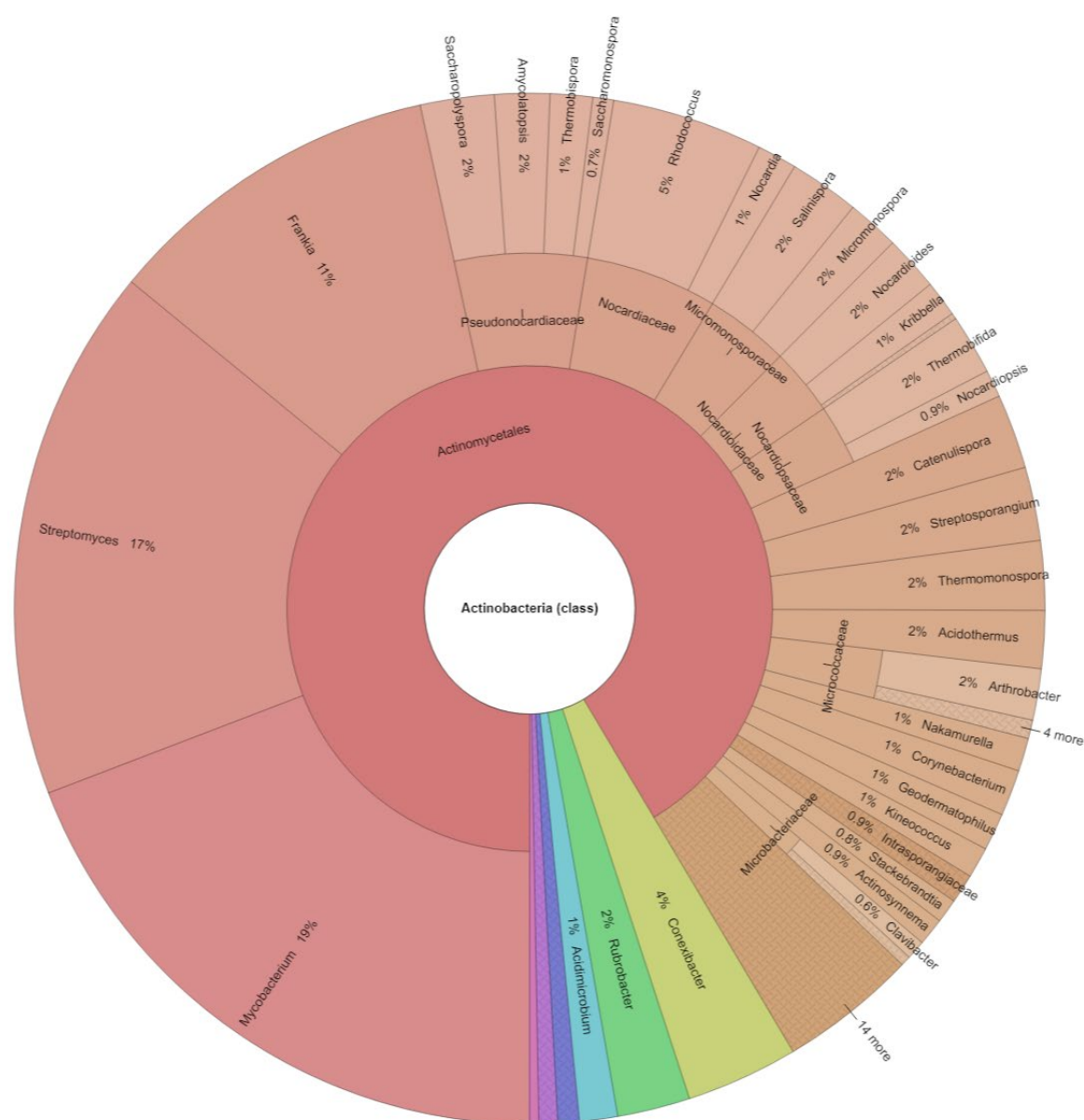
		Pantoea	0.0043	0.0018	0.0020	0.0015
		Pectobacterium	0.0027	0.0020	0.0024	0.0014
		Photorhabdus	0.0011	0.0012	0.0014	0.0010
		Proteus	0.0005	0.0005	0.0006	0.0004
		Providencia	0.0006	0.0006	0.0007	0.0005
		Salmonella	0.0088	0.0054	0.0049	0.0057
		Serratia	0.0049	0.0098	0.0067	0.0022
		Shigella	0.0016	0.0013	0.0012	0.0012
		Sodalis	0.0004	0.0003	0.0003	0.0002
		Wigglesworthia	0.0000	0.0000	0.0000	0.0000
		Xenorhabdus	0.0004	0.0004	0.0005	0.0003
		Yersinia	0.0046	0.0054	0.0077	0.0036
Legionellales	Coxiellaceae	Coxiella	0.0008	0.0014	0.0011	0.0012
		Rickettsiella	0.0002	0.0002	0.0002	0.0002
	Legionellaceae	Fluoribacter	0.0000	0.0000	0.0000	0.0000
		Legionella	0.0031	0.0043	0.0041	0.0035
Methylococcales	Methylococcaceae	Methylobacter	0.0016	0.0016	0.0018	0.0028
		Methylococcus	0.0035	0.0032	0.0038	0.0043
Oceanospirillales	Alcanivoracaceae	Alcanivorax	0.0011	0.0011	0.0011	0.0013
		Kangiella	0.0004	0.0005	0.0005	0.0007
	Hahellaceae	Hahella	0.0018	0.0018	0.0020	0.0023
	Halomonadaceae	Chromohalobacter	0.0011	0.0011	0.0011	0.0012
		Halomonas	0.0005	0.0005	0.0006	0.0006
	Oceanospirillaceae	Bermanella	0.0002	0.0002	0.0002	0.0003
		Marinomonas	0.0013	0.0012	0.0012	0.0013
		Neptuniibacter	0.0003	0.0003	0.0003	0.0003
Pasteurellales	Pasteurellaceae	Actinobacillus	0.0005	0.0005	0.0006	0.0006
		Aggregatibacter	0.0001	0.0002	0.0002	0.0002
		Basfia	0.0002	0.0002	0.0002	0.0002
		Bibersteinia	0.0000	0.0000	0.0000	0.0000
		Haemophilus	0.0005	0.0007	0.0007	0.0008
		Histophilus	0.0001	0.0002	0.0002	0.0002
		Mannheimia	0.0001	0.0001	0.0001	0.0001
		Pasteurella	0.0002	0.0003	0.0003	0.0003
Pseudomonadales	Moraxellaceae	Acinetobacter	0.0019	0.0023	0.0024	0.0024
		Enhydrobacter	0.0001	0.0001	0.0001	0.0001
		Moraxella	0.0001	0.0001	0.0001	0.0001
		Psychrobacter	0.0006	0.0007	0.0006	0.0008
	Pseudomonadaceae	Azotobacter	0.0016	0.0015	0.0016	0.0015
		Cellvibrio	0.0008	0.0009	0.0009	0.0010
		Pseudomonas	0.0407	0.0421	0.0421	0.0359
Thiotrichales	Francisellaceae	Francisella	0.0004	0.0006	0.0006	0.0006
	Piscirickettsiaceae	Methylophaga	0.0003	0.0003	0.0003	0.0005

			Thiomicrospira	0.0005	0.0005	0.0005	0.0006
		Thiotrichaceae	Beggiatoa	0.0009	0.0008	0.0010	0.0012
		unclassified	unclassified	0.0000	0.0000	0.0000	0.0000
Vibrionales	Vibrionaceae	Aliivibrio		0.0005	0.0005	0.0006	0.0006
		Listonella		0.0000	0.0000	0.0000	0.0000
		Photobacterium		0.0010	0.0011	0.0013	0.0014
		Vibrio		0.0029	0.0034	0.0039	0.0041
		unclassified		0.0002	0.0002	0.0002	0.0002
	unclassified	unclassified		0.0000	0.0001	0.0001	0.0001
Xanthomonadales	Xanthomonadaceae	Stenotrophomonas		0.0020	0.0022	0.0022	0.0025
		Xanthomonas		0.0068	0.0083	0.0090	0.0086
		Xylella		0.0010	0.0014	0.0015	0.0013
unclassified	unclassified	Candidatus Carsonella		0.0000	0.0000	0.0000	0.0000
		Congregibacter		0.0010	0.0010	0.0012	0.0013
		Endoriftia		0.0002	0.0003	0.0002	0.0003
		Reinekea		0.0004	0.0005	0.0005	0.0006
		unclassified		0.0043	0.0045	0.0042	0.0051
Zeta	Mariprofundales	Mariprofundaceae	Mariprofundus	0.0005	0.0006	0.0006	0.0007
unclassified	unclassified	unclassified	Magnetococcus	0.0020	0.0020	0.0022	0.0022
			unclassified	0.0000	0.0000	0.0001	0.0000

Suppl. Fig. S2. Metagenome distribution of Acidobacteria in the natural habitat (Sappony Creek).



Suppl. Fig. S3. Metagenome distribution of Actinobacteria in the natural habitat (Sappony Creek).

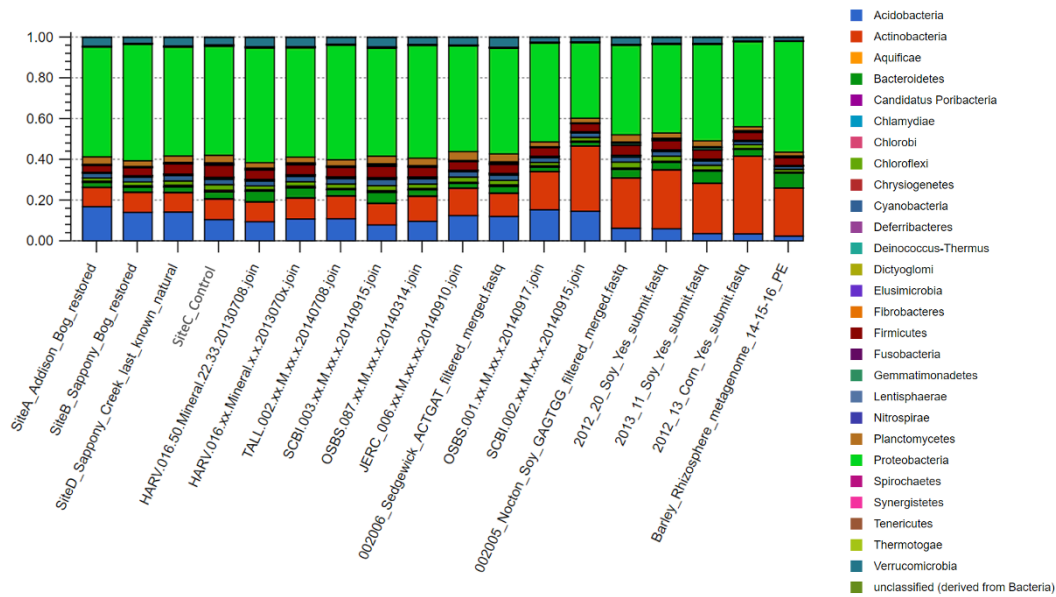


Suppl. Table S7. List of top ranked genera in four *S. flava* habitats with minimum abundance of 1%.

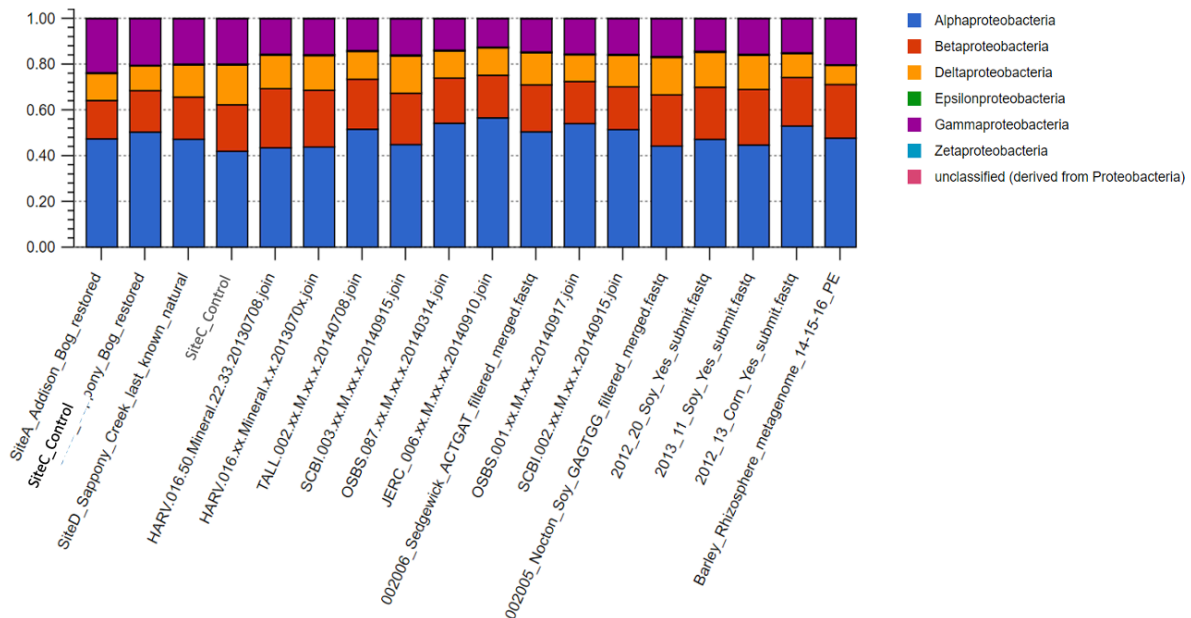
phylum	Class	family	genus	Sappony_Bog	Addison_Bog	Control_Site	Sappony_Creek
Acidobacteria	Acidobacteria (class)	Acidobacteriaceae	<i>Acidobacterium</i>	3.22%	4.01%	2.08%	3.31%
			<i>Terriglobus</i>	1.06%	1.25%	0.75%	1.14%
	Solibacteres	Solibacteraceae	<i>Candidatus Solibacter</i>	5.27%	6.53%	4.41%	5.07%
	unclassified	unclassified	<i>Candidatus Koribacter</i>	4.41%	4.98%	3.19%	4.62%
Actinobacteria	Actinobacteria (class)	Frankiaceae	<i>Frankia</i>	0.99%	1.18%	1.05%	1.01%
		Mycobacteriaceae	<i>Mycobacterium</i>	2.52%	1.67%	1.37%	1.81%
		Streptomycetaceae	<i>Streptomyces</i>	1.49%	1.49%	1.77%	1.58%
Firmicutes	Bacilli	Bacillaceae	<i>Bacillus</i>	0.64%	0.52%	1.05%	0.75%
Planctomycetes	Planctomycetacia	Planctomycetaceae	<i>Planctomyces</i>	0.85%	1.03%	1.15%	0.97%
Proteobacteria	Alphaproteobacteria	Bradyrhizobiaceae	<i>Bradyrhizobium</i>	4.62%	4.13%	3.62%	4.13%
			<i>Nitrobacter</i>	1.52%	1.24%	1.23%	1.41%
			<i>Rhodopseudomonas</i>	3.22%	2.42%	2.99%	2.99%
		Caulobacteraceae	<i>Caulobacter</i>	0.96%	1.06%	0.61%	0.76%
		Methylobacteriaceae	<i>Methylobacterium</i>	1.91%	1.71%	1.41%	1.81%
		Rhizobiaceae	<i>Rhizobium</i>	1.04%	0.95%	0.78%	0.99%
	Betaproteobacteria	Burkholderiaceae	<i>Burkholderia</i>	3.50%	2.97%	2.58%	3.00%
	Deltaproteobacteria	Geobacteraceae	<i>Geobacter</i>	1.20%	1.35%	2.39%	1.72%
		Myxococcaceae	<i>Anaeromyxobacter</i>	0.96%	0.89%	1.82%	1.19%
	Gammaproteobacteria	Enterobacteriaceae	<i>Enterobacter</i>	0.94%	2.28%	0.92%	0.58%
		Pseudomonadaceae	<i>Pseudomonas</i>	2.41%	2.19%	1.92%	2.25%
Verrucomicrobia	Verrucomicrobiae	Verrucomicrobia subdivision 3	unclassified	1.19%	1.88%	1.49%	1.78%

Suppl. Figure S4. Microbiomes across 18 locations.

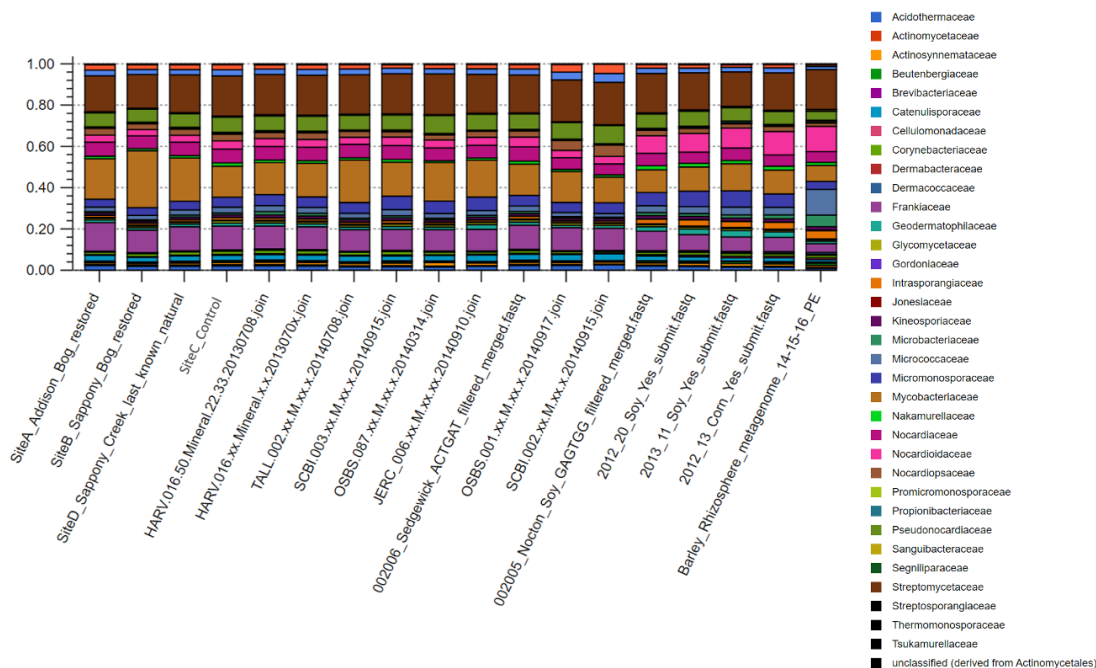
(a) Bacteria



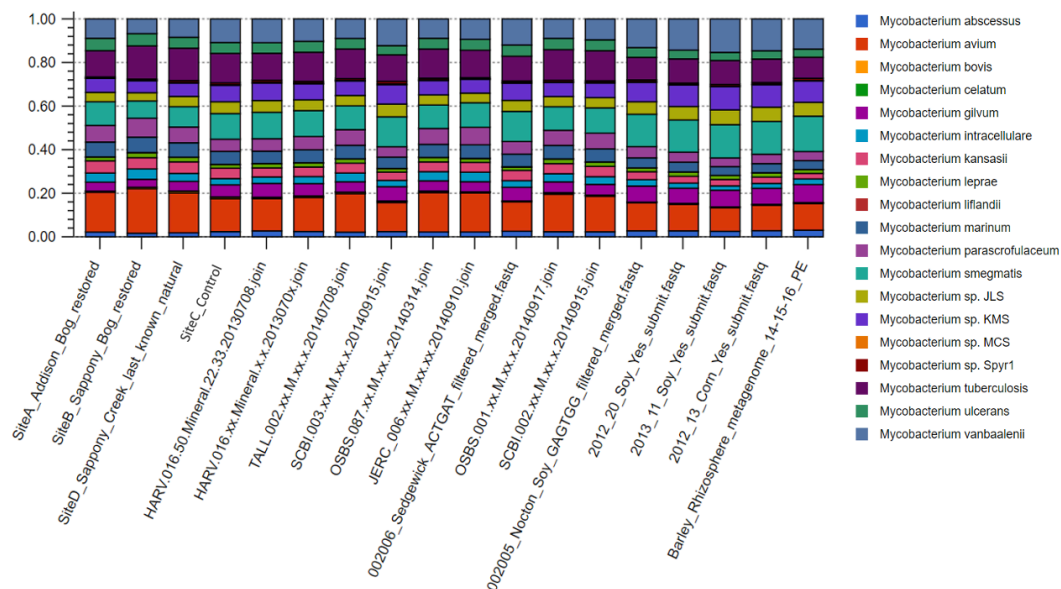
(b) Proteobacteria



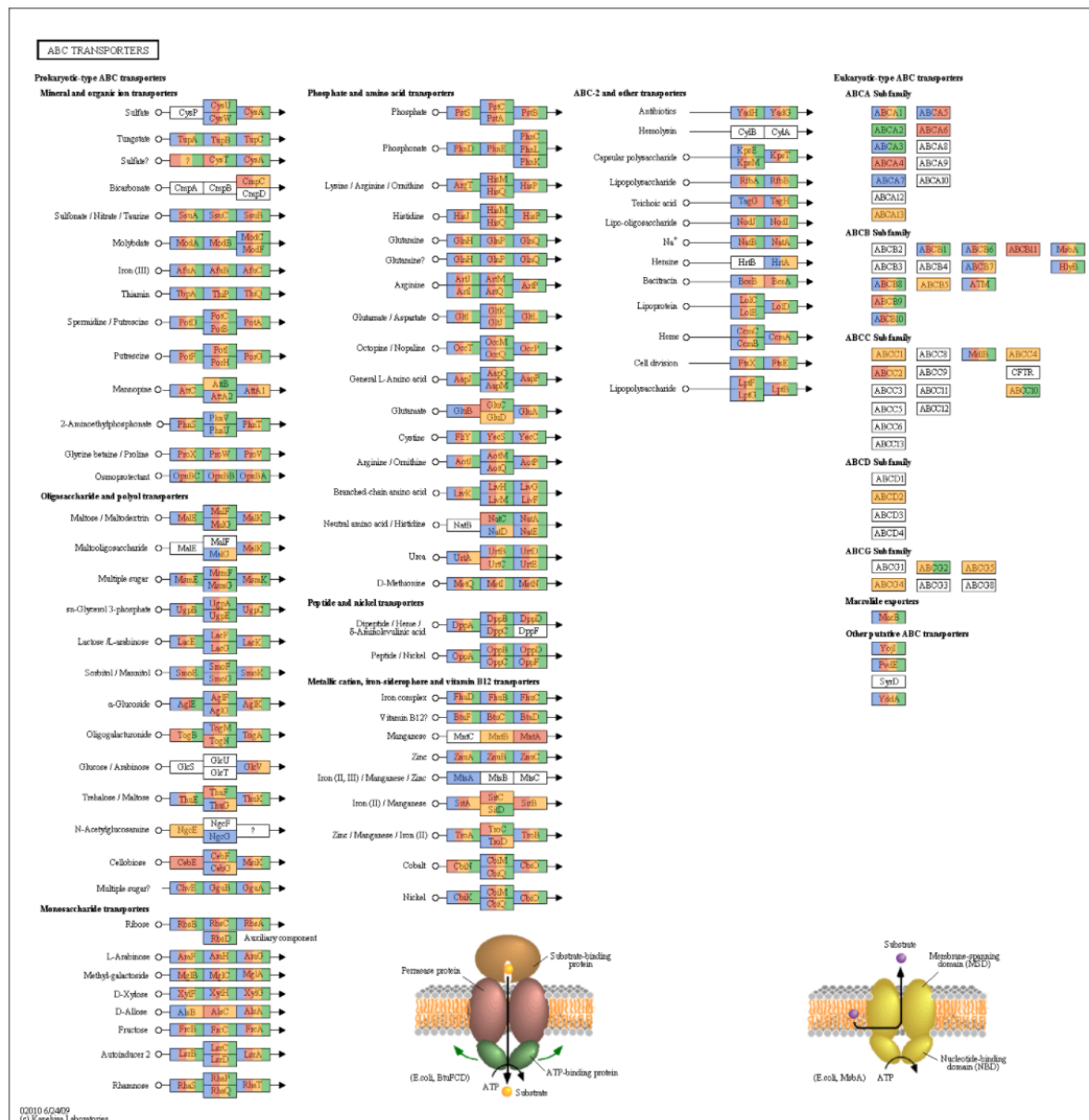
(c) Actinomycetales



(d) Mycobacterium

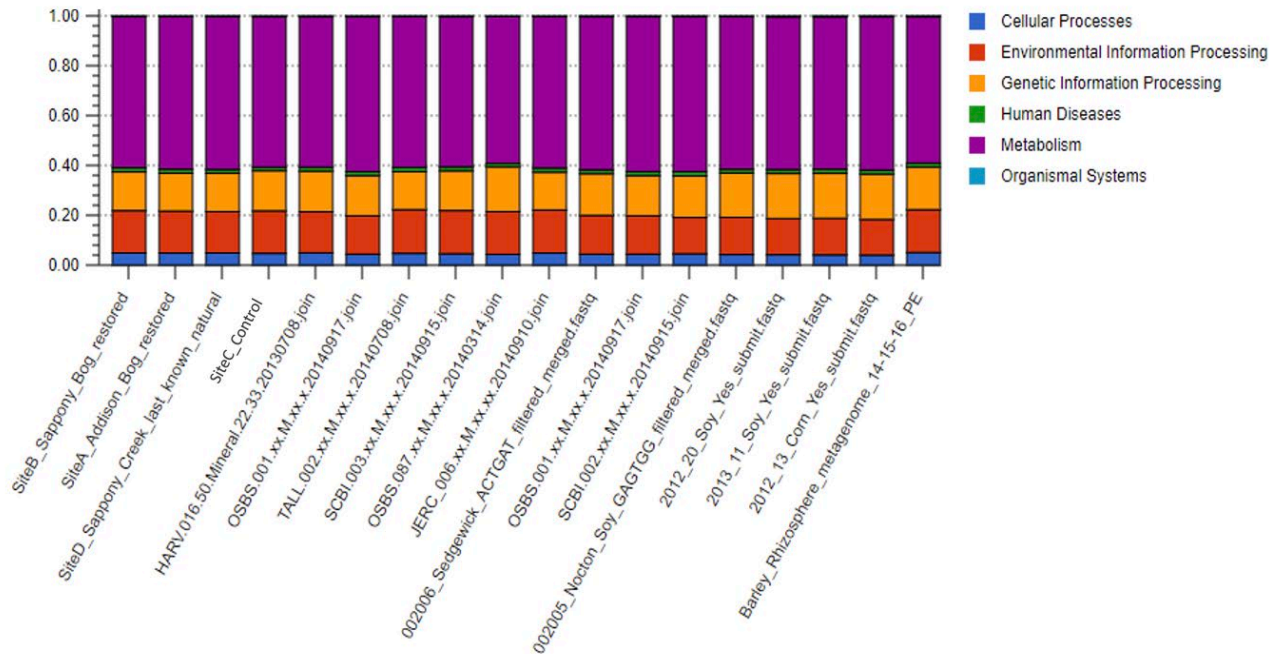


Suppl. Figure S5. KEGG pathway of ABC transporters.

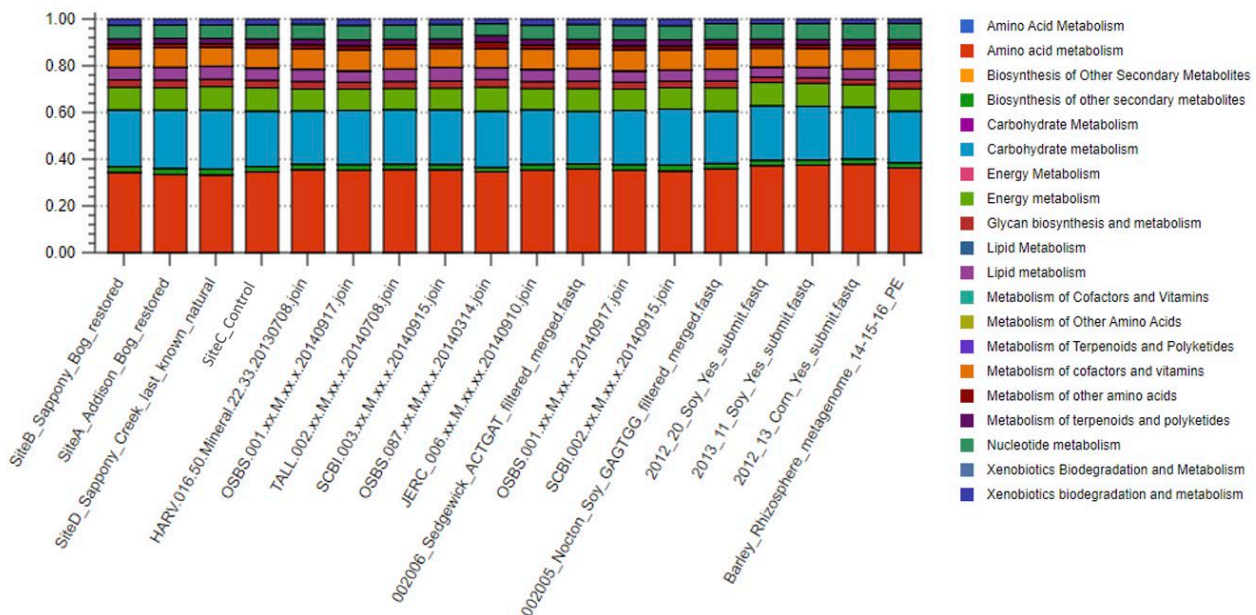


Suppl. Figure S6. Functional annotation of 18 metagenomes based on KEGG orthology database.

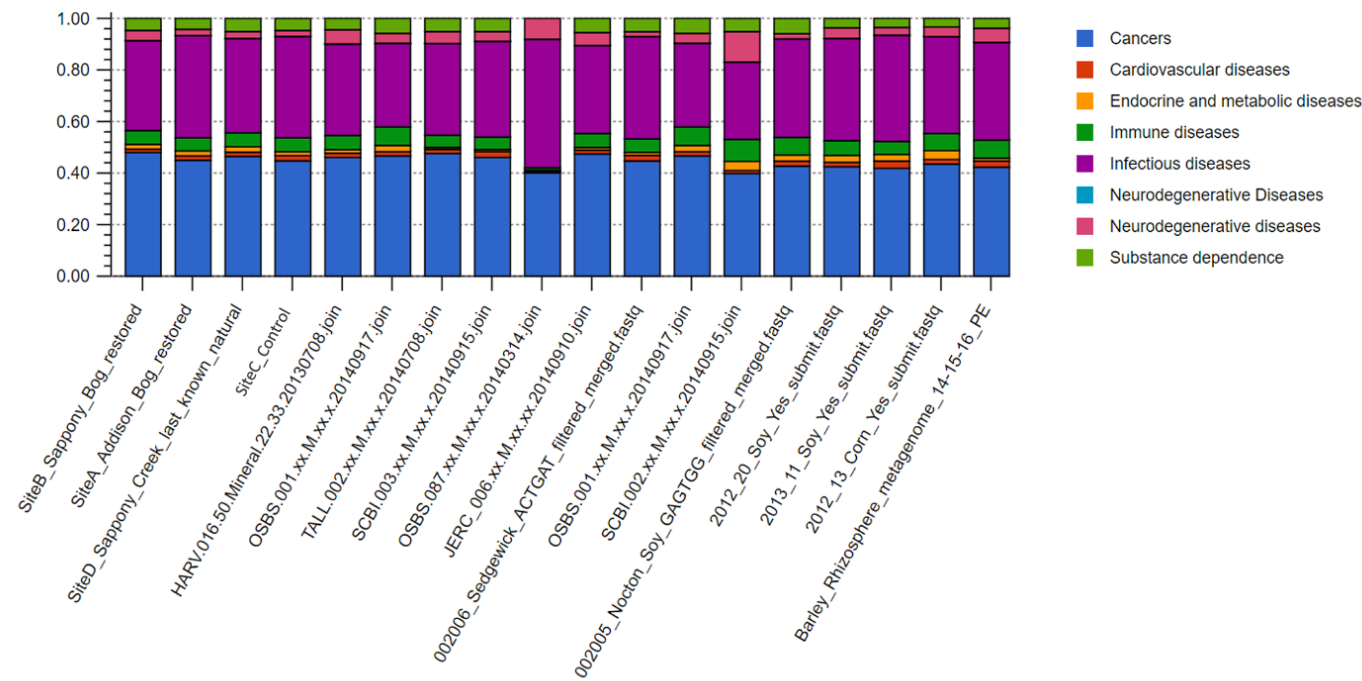
(a) Level 1



(b) Metabolism (Level2)



(C) Human Diseases (Level 2)



(d) Xenobiotics biodegradation and metabolism (Level 3)

