

**Supporting information:**

Table 1S. Bacterial community composition at the phylum level for samples from 9 different types of mushroom (n=17) as determined from pyrosequencing of 16S rRNA genes.

taxon	Percent of total sequences recovered	Range across samples (%)	Number of positive samples
Proteobacteria	83.90	11.73-99.89	17
Gammaproteobacteria	76.39	8.34-99.39	17
Betaproteobacteria	5.70	0.3-46.30	17
Alphaproteobacteria	1.52	0-12.68	14
unclassified Proteobacteria	0.276	0-2.37	10
Deltaproteobacteria	0.013	0-0.391	3
Bacteroidetes	13.26	0-72.06	16
Firmicutes	2.19	0-58.28	9
Actinobacteria	0.442	0-3.39	12
Acidobacteria	0.05	0-0.958	3
Chlamydiae	0.008	0-0.113	2
Deinococcus-Thermus	0.005	0-0.160	1
unclassified bacteria	0.153	0-0.782	13

Table 2S. The most abundant bacterial genera identified in samples from 9 different types of mushroom (n=17) as determined by pyrosequencing of 16S rRNA genes. Only genera that accounted for over 1% of the sequences recovered from at least one sample are shown.

Taxon	Percent of total sequences	Range across samples (%)	Number positive samples
<i>Pseudomonas</i>	66.97	1.90-99.26	17
<i>Flavobacterium</i>	7.40	0-56.20	12
unclassified Enteric Bacteria cluster	4.88	0-72.48	10
unclassified Oxalobacteraceae	2.54	0-40.84	12
<i>Pedobacter</i>	2.43	0-24.66	15
<i>Serratia</i>	2.14	0-41.75	8
<i>Mucilaginibacter</i>	1.61	0-28.23	7
unclassified Gammaproteobacteria	1.43	0.02-9.43	17
<i>Duganella</i>	1.30	0-25.10	8
<i>Chryseobacterium</i>	0.90	0-17.11	6
<i>Janthinobacterium</i>	0.54	0-4.39	6
<i>Lactococcus</i>	0.52	0-7.70	3
<i>Planococcus</i>	0.43	0-18.25	2
unclassified Carnobacteriaceae	0.40	0-14.86	4
<i>Herbaspirillum</i>	0.36	0-5.07	6
unclassified Enterobacteriaceae	0.35	0-7.22	8
<i>Staphylococcus</i>	0.29	0-13.95	4
<i>Burkholderia</i>	0.27	0-2.63	5
unclassified Rhizobiales	0.27	0-1.53	12
<i>Sphingobacterium</i>	0.22	0-3.68	7
Microbacteriaceae	0.22	0-2.25	10
uncultured Phyllobacteriaceae	0.19	0-4.60	1
unclassified Flavobacteriaceae	0.16	0-1.42	9
unclassified Burkholderiales	0.12	0-1.35	9
<i>Buttiauxella</i>	0.09	0-2.15	3
<i>Brevundimonas</i>	0.08	0-1.20	7
<i>Rhodanobacter</i>	0.07	0-1.18	3
<i>Carnobacterium</i>	0.07	0-3.00	2
unclassified Planococcaceae	0.06	0-1.60	2
<i>Leuconostoc</i>	0.05	0-1.32	2
<i>Chitinophaga</i>	0.05	0-1.07	1
unclassified Kurthia	0.04	0-1.96	1

Table 3S. Mean percentages and range of bacterial phyla and genera in portobello (n=16) and white button (n=12) mushroom samples as determined from pyrosequencing of 16S rRNA genes.

Taxon	Portobello		White button	
	%	Range	%	Range
Proteobacteria	97.12	81.63-100	97.26	77.64 -99.9
<i>Pseudomonas</i>	95.88	74.78-99.94	95.90	70.56-99.86
unclassified Gammaproteobacteria	0.332	0-2.08	0.284	0.016-0.547
<i>Serratia</i>	0.228	0-1.71	0.017	0-0.234
unclassified Oxalobacteraceae	0.122	0-3.15	0.021	0-0.127
<i>Duganella</i>	0.036	0-0.464	0.011	0-0.079
<i>Herbaspirillum</i>	0.027	0-0.695	0.002	0-0.033
unclassified Enteric Bacteria cluster	0.003	0-0.027	0.038	0-0.549
<i>Janthinobacterium</i>	0.142	0-1.80	0.00	0
unclassified Enterobacteriaceae	0.012	0-0.065	0.00	0
unclassified Rhizobiales	0.027	0-0.384	0.083	0-0.434
unclassified Burkholderiales	0.002	0-0.020	0.028	0-0.218
<i>Dechloromonas</i>	0.00	0	0.061	0-1.20
Bacteroidetes	2.71	0-17.94	0.87	0.036-3.83
<i>Flavobacterium</i>	1.44	0-11.68	0.072	0-0.663
<i>Pedobacter</i>	0.476	0-5.66	0.653	0-2.89
<i>Sphingobacterium</i>	0.509	0-6.78	0.038	0-0.523
<i>Chryseobacterium</i>	0.108	0-1.27	0.004	0-0.033
<i>Mucilaginibacter</i>	0.062	0-0.613	0.009	0-0.167
unclassified Flavobacteriaceae	0.017	0-0.110	0.040	0-0.449
Actinobacteria	0.122	0-0.439	0.32	0-3.24
unclassified Microbacteriaceae	0.026	0-0.439	0.019	0-0.121
<i>Propionibacterium</i>	0.00	0	0.168	0-2.23
<i>Corynebacterium</i>	0.00	0	0.087	0-1.05
Firmicutes	0.015	0-0.105	1.41	0-16.67
<i>Staphylococcus</i>	0.00	0	0.051	0-0.665
unclassified Bacilli	0.002	0-0.027	0.170	0-2.470
unclassified Firmicutes	0.012	0-0.105	0.923	0-10.78
<i>Streptococcus</i>	0.00	0	0.159	0-2.38
unclassified Bacteria	0.041	0-0.265	0.14	0-2.35