Bacterial and fungal communities of table olives stored under modified atmosphere packaging (MAP)

16S and 18S rRNA gene metabarcoding (NGS): relative abundance data

1. Dataset description

The microbial communities of table olives stored under modified atmosphere packaging (MAP) were analysed with next-generation sequencing (NGS) of the 16S rRNA gene (bacteria) and the 18S rRNA gene (eukaryotes/fungi). Samples were analysed at four storage times: 0, 6, 12 and 18 months. Sequences were clustered into operational taxonomic units (OTUs) and assigned taxonomically with the SILVA database. Relative abundances are expressed as the percentage of reads assigned to each taxon out of the total reads of each sample.

Matrix	Table olives, modified atmosphere packaging (MAP)
Storage time	0, 6, 12 and 18 months (one sample per time point)
Markers	16S rRNA gene (bacteria); 18S rRNA gene (eukaryotes)
Taxonomy	SILVA reference database
16S rRNA	294,978 reads; 2,715 OTUs
18S rRNA	508,811 reads; 1,778 OTUs (1,636 fungal), after removal of plant (host) and unassigned sequences

2. Sequencing summary and alpha diversity

Table 1. Bacterial community (16S rRNA): sequencing statistics and alpha diversity

Parameter	0 months	6 months	12 months	18 months
Number of reads	44,861	167,255	60,193	22,669
Observed OTUs (non-rarefied)	1,246	1,426	946	540
Observed OTUs*	856	561	603	540
Chao1*	1,912	1,082	1,065	951
Shannon index (H')*	3.43	2.63	2.83	2.75
Simpson index (1 − D)*	0.896	0.737	0.767	0.812
Good's coverage*	0.979	0.988	0.988	0.989

** Calculated after rarefaction to 22,669 reads per sample (mean of 20 iterations).*

Table 2. Fungal community (18S rRNA, fungal OTUs only): sequencing statistics and alpha diversity

Parameter	0 months	6 months	12 months	18 months
Number of reads	213,888	136,671	79,215	74,596
Observed OTUs (non-rarefied)	490	632	991	297
Observed OTUs*	334	493	962	297
Chao1*	488	780	1,744	414
Shannon index (H')*	0.78	1.75	3.02	0.73
Simpson index (1 − D)*	0.254	0.617	0.885	0.236
Good's coverage*	0.998	0.997	0.994	0.999

** Calculated after rarefaction to 74,596 reads per sample (mean of 20 iterations).*

3. Bacterial community (16S rRNA)

Table 3. Relative abundance (%) of bacterial phyla

Phylum	0 mo (%)	6 mo (%)	12 mo (%)	18 mo (%)
Firmicutes	86.24	79.12	71.78	85.26
Proteobacteria	12.84	19.10	25.83	13.79
Actinobacteria	0.12	0.93	1.34	0.53
Bacteroidetes	0.70	0.56	0.67	0.20
Deinococcus-Thermus	0.02	0.24	0.31	0.16
Gemmatimonadetes	<0.01	0.02	0.02	0.03
Chloroflexi	0	<0.01	0.02	0.02
Planctomycetes	<0.01	0.01	<0.01	<0.01
Verrucomicrobia	0.02	<0.01	<0.01	0
Cyanobacteria	0.01	0	0	<0.01
Epsilonbacteraeota	0.01	0	0	0
Others (<0.01% at every time point; n = 10)	0.02	<0.01	<0.01	<0.01

Table 4. Relative abundance (%) of bacterial families (≥ 0.5% in at least one time point)

Family	0 mo (%)	6 mo (%)	12 mo (%)	18 mo (%)
Lactobacillaceae	82.39	79.02	71.72	85.23
Burkholderiaceae	8.60	4.76	5.67	3.45
Sphingomonadaceae	0.46	1.86	3.33	1.72
Caulobacteraceae	0.31	2.05	3.10	1.61
Rhodobacteraceae	0.24	1.42	2.21	1.69
Stappiaceae	0.35	1.97	2.06	1.08
Moraxellaceae	0.60	1.39	2.41	0.86
Rhizobiaceae	0.23	1.10	1.72	0.89
Bacillaceae	3.70	0.01	0.01	<0.01
Pseudomonadaceae	0.22	1.20	1.35	0.67
Alteromonadaceae	0.20	1.13	1.23	0.54
Beijerinckiaceae	0.14	0.98	0.73	0.21
Nocardioidaceae	0.07	0.50	0.81	0.35
Azospirillaceae	0.03	0.28	0.55	0.35
Pleomorphomonadaceae	0.06	0.31	0.51	0.26
Others (<0.5% at every time point; n = 118)	2.41	2.02	2.58	1.08

4. Eukaryotic and fungal community (18S rRNA)

Table 5. Relative abundance (%) of major eukaryotic groups

Group	0 mo (%)	6 mo (%)	12 mo (%)	18 mo (%)
Fungi	99.95	98.43	97.35	99.99
Metazoa	<0.01	1.54	2.31	<0.01
Other eukaryotes	0.04	0.03	0.33	<0.01

Table 6. Relative abundance (%) of fungal families (≥ 0.5% in at least one time point)

Family	0 mo (%)	6 mo (%)	12 mo (%)	18 mo (%)
Pichiaceae	93.06	61.83	36.14	93.43
Saccharomycetaceae	4.72	13.14	16.43	6.55
Cladosporiaceae	0.05	11.79	19.59	<0.01
Aspergillaceae	0.04	1.80	8.36	0
Malasseziaceae	<0.01	3.44	4.72	0
Pleosporaceae	0.04	1.79	5.83	<0.01
Nectriaceae	0.01	1.42	0.61	0
Unclassified *Starmerella-Candida clade*	0.19	0.05	0.82	0
Debaryomycetaceae	0.30	0.57	0.14	0
Unclassified *Emericellopsis*	0	0	0.90	0
Unclassified *Saccharomycetales*	0.76	0	0	0
Unclassified *Acremonium*	0	0.09	0.63	0
Unclassified *Pleosporales*	0	0.56	0.12	0
Trichomonascaceae	0.68	0	0	0
Others (<0.5% at every time point; n = 53)	0.10	1.94	3.06	<0.01

Appendix A. Bacterial genera: complete abundance data (16S rRNA)

Relative abundance (%) and number of reads per genus. "Unclassified" denotes OTUs not assigned at genus level; the lowest assigned rank is given.

Table A1. Bacterial genera

Genus	0 mo (%)	6 mo (%)	12 mo (%)	18 mo (%)	0 mo (reads)	6 mo (reads)	12 mo (reads)	18 mo (reads)
Lactobacillus	45.33	76.84	70.54	81.31	20,337	128,518	42,460	18,432
Pediococcus	37.06	2.18	1.18	3.92	16,625	3,652	710	888
Curvibacter	6.19	0	0	0	2,778	0	0	0
Sphingomonas	0.30	1.51	2.85	1.49	136	2,526	1,713	338
Pannonibacter	0.35	1.97	2.06	1.08	156	3,290	1,242	244
Phenylobacterium	0.22	1.42	2.08	1.13	99	2,368	1,251	257
Acidovorax	0.39	1.64	1.63	0.85	173	2,743	984	193
Bacillus	3.70	0.01	0.01	<0.01	1,658	19	7	2
Pseudomonas	0.22	1.20	1.35	0.67	100	2,009	813	151
Enhydrobacter	0.17	0.92	1.76	0.50	77	1,533	1,057	114
Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium	0.19	0.86	1.35	0.70	85	1,440	810	158
Delftia	0.10	0.83	0.99	1.00	44	1,386	593	227
Paracoccus	0.11	0.74	1.31	0.67	49	1,243	791	151
Alishewanella	0.16	1.04	1.12	0.49	72	1,743	674	112
Rubellimicrobium	0.07	0.67	0.90	1.03	33	1,124	540	233
Brevundimonas	0.08	0.60	0.99	0.46	37	997	593	105
Comamonas	0.08	0.74	0.80	0.49	35	1,238	481	112
Aquabacterium	0.08	0.61	1.01	0.40	38	1,023	609	91
Acinetobacter	0.42	0.43	0.61	0.34	190	715	370	77
Nocardioides	0.07	0.50	0.81	0.35	31	836	489	80
Noviherbaspirillum	0.06	0.54	0.63	0.33	25	901	381	74
Microvirga	0.10	0.73	0.29	0.04	45	1,218	175	9
Chthonobacter	0.06	0.31	0.51	0.26	25	517	308	59
Flavobacterium	0.08	0.45	0.47	0.13	35	755	282	29
Ramlibacter	0.03	0.29	0.39	0.24	15	491	234	55
Variovorax	0.90	0	0	0	403	0	0	0
Azospirillum	0.02	0.20	0.39	0.27	11	331	236	61
Deinococcus	0.02	0.24	0.31	0.16	9	406	188	36
Unclassified *Beijerinckiaceae*	0.03	0.20	0.36	0.14	14	329	215	32
Burkholderia-Caballeronia-Paraburkholderia	0.63	0	0	0	283	0	0	0
Devosia	0.02	0.18	0.29	0.11	9	304	173	25
Blastococcus	0.02	0.17	0.32	0.07	8	287	195	16
Lysobacter	0.02	0.17	0.24	0.11	8	289	146	26
Unclassified *Rhodospirillales*	0.03	0.12	0.20	0.11	13	206	121	26
Unclassified *Rhizobiaceae*	0.02	0.12	0.18	0.07	8	202	107	16
Salinibacter	0.36	0	0	0	163	0	0	0

Genus	0 mo (%)	6 mo (%)	12 mo (%)	18 mo (%)	0 mo (reads)	6 mo (reads)	12 mo (reads)	18 mo (reads)
Blastomonas	0.03	0.09	0.16	0.07	14	158	96	17
Cnuella	0.02	0.08	0.16	0.05	9	131	94	12
Microbacterium	<0.01	0.14	0.12	0.04	2	235	72	8
Rheinheimera	0.04	0.09	0.11	0.05	16	149	65	11
Unclassified *Sphingomonadaceae*	0.02	0.09	0.13	0.05	7	144	76	12
Tianweitania	<0.01	0.07	0.12	0.07	3	122	71	17
Sphingoaurantiacus	<0.01	0.07	0.13	0.06	3	120	77	14
Pseudoalteromonas	0.26	0	0	0	118	0	0	0
Massilia	0.01	0.06	0.11	0.06	6	107	67	14
Vibrio	<0.01	0.05	0.09	0.04	3	81	56	9
Sediminibacterium	0.17	<0.01	<0.01	0	76	1	2	0
Tepidimonas	<0.01	0.02	0.07	0.06	3	37	42	13
Methylobacterium	<0.01	0.04	0.07	0.03	3	72	43	6
Kluyvera	0.15	0	0	0	66	0	0	0
Rhodocista sp. SCSIO 13435	0	0.04	0.06	0.03	0	71	38	6
Roseomonas	0	0.06	0.04	<0.01	0	98	27	2
Unclassified *Methylophilaceae*	0.11	0	0	0	50	0	0	0
Azospirillum sp. MIMtkN9	<0.01	0.02	0.06	0.02	1	34	36	5
Alkanindiges	<0.01	0.04	0.03	0.02	3	71	19	5
Rhodovibrio	0.10	0	0	0	45	0	0	0
Leuconostoc	0.10	0	0	0	44	0	0	0
Skermanella	<0.01	0.02	0.03	0.04	1	40	20	8
Ellin6055	<0.01	0.05	0.02	0.02	2	78	14	4
Pseudorhizobium	<0.01	0.02	0.04	0.02	3	28	23	5
Dongia	0.08	<0.01	0	0	37	1	0	0
Unclassified *Longimicrobiaceae*	<0.01	0.02	0.02	0.03	2	32	14	7
Altererythrobacter	<0.01	0.04	0.02	0.01	3	59	13	3
Enterobacter	0.07	0	<0.01	0	33	0	1	0
Cutibacterium	<0.01	0.02	0.02	0.02	4	41	12	4
Polycyclovorans	0.06	0	0	0	28	0	0	0
Sphingopyxis	0.06	0	<0.01	0	26	0	1	0
Aureimonas	<0.01	0.01	0.03	0.01	1	23	17	3
Caulobacter	<0.01	0.02	0.02	<0.01	1	34	15	2
Citrobacter	0.06	0	0	0	25	0	0	0
Bdellovibrio	<0.01	0.01	0.03	<0.01	1	24	17	2
Marinobacter	0.05	0	0	0	24	0	0	0
Unclassified *Solimonadaceae*	0.05	0	0	0	24	0	0	0
Klebsiella	0.05	0	0	0	23	0	0	0
Muricoccus	<0.01	0.01	<0.01	0.02	1	24	5	5
Halomonas	0.04	0	0	0	20	0	0	0
Streptococcus	0.01	0.01	0.02	0	6	21	11	0
Finegoldia	<0.01	0.03	0	<0.01	4	48	0	1
Leucobacter	<0.01	0.02	0.01	0	3	34	9	0

Genus	0 mo (%)	6 mo (%)	12 mo (%)	18 mo (%)	0 mo (reads)	6 mo (reads)	12 mo (reads)	18 mo (reads)
Stenotrophomonas	0	0.01	0.01	0.01	0	19	8	3
Unclassified *Burkholderiaceae*	0.03	<0.01	<0.01	<0.01	13	1	2	1
Aeromonas	<0.01	<0.01	0.02	<0.01	3	10	11	1
PMMR1	0	0.02	0.01	0	0	35	7	0
Corynebacterium 1	0	<0.01	<0.01	0.02	0	6	4	5
Unclassified *JG30-KF-CM45*	0	<0.01	0.02	<0.01	0	11	10	2
Mesorhizobium	<0.01	<0.01	<0.01	<0.01	3	13	5	2
Hydrogenophaga	0.03	<0.01	<0.01	0	12	2	1	0
Novosphingobium	<0.01	<0.01	<0.01	<0.01	4	16	4	1
Pelagibaca	0.03	0	0	0	13	0	0	0
Sphingobium	0.02	0	<0.01	<0.01	9	0	2	1
Exiguobacterium	0	0.01	0.01	0	0	19	9	0
Porphyrobacter	<0.01	<0.01	0.01	<0.01	2	6	8	1
Rhabdobacter	0	<0.01	0.02	<0.01	0	5	11	1
Rhodoferax	0.02	0	0	0	11	0	0	0
Mucilaginibacter	0.02	0	0	0	11	0	0	0
Tahibacter	0.02	0	0	0	11	0	0	0
Micrococcus	0	0.02	0	0	0	40	0	0
Rhodopirellula	0	0.01	<0.01	<0.01	0	18	5	1
Reyranella	0.02	0	0	0	10	0	0	0
Staphylococcus	<0.01	<0.01	<0.01	<0.01	4	10	1	1
Limnohabitans	0.02	0	0	0	9	0	0	0
Pontibacter	<0.01	<0.01	<0.01	<0.01	1	11	4	1
Unclassified *Microscillaceae*	0.02	0	0	0	8	0	0	0
Terrimicrobium	0.02	0	0	0	8	0	0	0
Rothia	0	<0.01	0	0.01	0	7	0	3
Mycobacterium	<0.01	<0.01	<0.01	<0.01	1	4	2	2
Bosea	<0.01	<0.01	<0.01	0	1	12	4	0
Limimonas	0.02	0	0	0	7	0	0	0
Unclassified *Caulobacteraceae*	<0.01	<0.01	<0.01	<0.01	1	2	2	2
Diaphorobacter	0	<0.01	0.01	0	0	6	7	0
Shewanella	<0.01	<0.01	<0.01	<0.01	3	3	1	1
Anaerococcus	0	<0.01	<0.01	<0.01	0	13	1	1
Dietzia	<0.01	<0.01	<0.01	0	1	8	4	0
Amphiplicatus	0.01	0	0	0	6	0	0	0
Arcobacter	0.01	0	0	0	6	0	0	0
Legionella	0.01	0	0	0	6	0	0	0
Komagataeibacter	0.01	0	0	0	6	0	0	0
Unclassified *Chitinophagaceae*	0	<0.01	<0.01	<0.01	0	7	2	1
Pseudoxanthomonas	0.01	<0.01	0	0	5	1	0	0
Agrococcus	0	<0.01	<0.01	0	0	9	3	0
Schlegelella	0	<0.01	<0.01	<0.01	0	7	1	1
Unclassified *Gaiellales*	0	<0.01	<0.01	0	0	3	5	0

Genus	0 mo (%)	6 mo (%)	12 mo (%)	18 mo (%)	0 mo (reads)	6 mo (reads)	12 mo (reads)	18 mo (reads)
Paraburkholderia tropica	0	<0.01	0	<0.01	0	2	0	2
Haemophilus	0	<0.01	<0.01	<0.01	0	3	2	1
Pelomonas	<0.01	<0.01	0	0	4	1	0	0
Kocuria	0	<0.01	0	<0.01	0	8	0	1
Pseudooceanicola	<0.01	0	0	0	4	0	0	0
Candidatus Nucleicultrix	<0.01	0	0	0	4	0	0	0
Methylotenera	<0.01	0	0	0	4	0	0	0
Lactococcus	<0.01	0	0	0	4	0	0	0
Unclassified *Obscuribacterales*	<0.01	0	0	0	4	0	0	0
Unclassified *uncultured bacterium*	<0.01	<0.01	0	<0.01	1	3	0	1
Lawsonella	<0.01	<0.01	0	<0.01	1	1	0	1
Aliihoeflea	0	<0.01	<0.01	0	0	6	2	0
Cobetia	<0.01	0	0	0	3	0	0	0
Salegentibacter	<0.01	0	0	0	3	0	0	0
Lacunisphaera	<0.01	0	0	0	3	0	0	0
Marinomonas	<0.01	0	0	0	3	0	0	0
OM43 clade	<0.01	0	0	0	3	0	0	0
Luteitalea	0	<0.01	<0.01	0	0	8	1	0
Flaviaesturariibacter	0	<0.01	<0.01	0	0	5	2	0
Escherichia-Shigella	0	<0.01	0	<0.01	0	3	0	1
Undibacterium	<0.01	0	<0.01	0	2	0	1	0
Unclassified *Micavibrionales*	0	<0.01	<0.01	0	0	4	2	0
Psychrobacter	<0.01	0	<0.01	0	1	0	2	0
Unclassified *Saccharimonadaceae*	<0.01	0	<0.01	0	1	0	2	0
SH-PL14	<0.01	<0.01	0	0	1	5	0	0
Erythrobacter	<0.01	<0.01	<0.01	0	1	2	1	0
Veillonella	0	0	<0.01	0	0	0	3	0
Modestobacter	0	0	<0.01	0	0	0	3	0
Limnobacter	0	<0.01	<0.01	0	0	5	1	0
Methylocella	0	<0.01	<0.01	0	0	5	1	0
Amaricoccus	0	<0.01	<0.01	0	0	2	2	0
Rubrobacter	<0.01	<0.01	<0.01	0	1	1	1	0
Unclassified *Frankiales*	<0.01	<0.01	<0.01	0	1	1	1	0
Ferribacterium	<0.01	0	0	0	2	0	0	0
WDS1C4	<0.01	0	0	0	2	0	0	0
Caedibacter	<0.01	0	0	0	2	0	0	0
Sediminimonas	<0.01	0	0	0	2	0	0	0
Dactylococcopsis PCC-8305	<0.01	0	0	0	2	0	0	0
Winogradskyella	<0.01	0	0	0	2	0	0	0
Domibacillus	<0.01	0	0	0	2	0	0	0
Polaromonas	<0.01	0	0	0	2	0	0	0
Halopeptonella	<0.01	0	0	0	2	0	0	0
Methyloversatilis	<0.01	0	0	0	2	0	0	0

Genus	0 mo (%)	6 mo (%)	12 mo (%)	18 mo (%)	0 mo (reads)	6 mo (reads)	12 mo (reads)	18 mo (reads)
Leptothrix	<0.01	0	0	0	2	0	0	0
Unclassified *Magnetospirillaceae*	<0.01	0	0	0	2	0	0	0
Unclassified *Paracaedibacteraceae*	<0.01	0	0	0	2	0	0	0
Unclassified *Lineage IV*	<0.01	0	0	0	2	0	0	0
Pantoea	<0.01	0	0	0	2	0	0	0
Pseudarcicella	<0.01	0	0	0	2	0	0	0
Pseudonocardia	0	0	0	<0.01	0	0	0	1
Peptostreptococcus	0	0	0	<0.01	0	0	0	1
Rudanella	0	0	0	<0.01	0	0	0	1
Erysipelatoclostridium	0	0	0	<0.01	0	0	0	1
Acholeplasma	0	0	0	<0.01	0	0	0	1
Blastocatella	0	0	0	<0.01	0	0	0	1
Brevibacterium	0	<0.01	0	0	0	7	0	0
Vogesella	0	<0.01	0	0	0	7	0	0
Flavihumibacter	0	<0.01	0	0	0	7	0	0
Chryseomicrobium	0	<0.01	<0.01	0	0	1	2	0
Diaminobutyricimonas	0	<0.01	0	0	0	6	0	0
Gemella	0	0	<0.01	0	0	0	2	0
Herbaspirillum	0	0	<0.01	0	0	0	2	0
Rhodococcus	0	0	<0.01	0	0	0	2	0
Rhodocytophaga	0	0	<0.01	0	0	0	2	0
Qipengyuania	0	0	<0.01	0	0	0	2	0
Unclassified *Rhizobiales*	0	0	<0.01	0	0	0	2	0
Unclassified *Rhodocyclaceae*	0	0	<0.01	0	0	0	2	0
Quadrisphaera	0	0	<0.01	0	0	0	2	0
Pedobacter	0	0	<0.01	0	0	0	2	0
Akkermansia	0	0	<0.01	0	0	0	2	0
alphaI cluster	0	<0.01	<0.01	0	0	2	1	0
Curtobacterium	0	<0.01	<0.01	0	0	2	1	0
Planomicrobium	0	<0.01	<0.01	0	0	2	1	0
Geodermatophilus	0	<0.01	0	0	0	4	0	0
Flavisolibacter	0	<0.01	0	0	0	4	0	0
Brachybacterium	0	<0.01	0	0	0	4	0	0
Enterococcus	0	<0.01	0	0	0	4	0	0
Alicycliphilus	0	<0.01	<0.01	0	0	1	1	0
Belnapia	0	<0.01	<0.01	0	0	1	1	0
Ottowia	0	<0.01	<0.01	0	0	1	1	0
Abiotrophia	0	<0.01	<0.01	0	0	1	1	0
Janthinobacterium	0	<0.01	<0.01	0	0	1	1	0
Pseudohongiella	<0.01	0	0	0	1	0	0	0
Unclassified *uncultured*	<0.01	0	0	0	1	0	0	0
Unclassified *Rhodobacteraceae*	<0.01	0	0	0	1	0	0	0
Unclassified *TRA3-20*	<0.01	0	0	0	1	0	0	0

Genus	0 mo (%)	6 mo (%)	12 mo (%)	18 mo (%)	0 mo (reads)	6 mo (reads)	12 mo (reads)	18 mo (reads)
Bifidobacterium	<0.01	0	0	0	1	0	0	0
Unclassified *UBA12409*	<0.01	0	0	0	1	0	0	0
Oceanicaulis	<0.01	0	0	0	1	0	0	0
Phaeobacter sp. DCSW07	<0.01	0	0	0	1	0	0	0
Ornithinimicrobium	<0.01	0	0	0	1	0	0	0
Unclassified *Planococcaceae*	<0.01	0	0	0	1	0	0	0
Terrimonas	<0.01	0	0	0	1	0	0	0
Silanimonas	<0.01	0	0	0	1	0	0	0
Cellulosimicrobium	<0.01	0	0	0	1	0	0	0
Neochlamydia	<0.01	0	0	0	1	0	0	0
Salinicola	<0.01	0	0	0	1	0	0	0
Empedobacter	<0.01	0	0	0	1	0	0	0
Roseivivax	<0.01	0	0	0	1	0	0	0
Crocinitomix	<0.01	0	0	0	1	0	0	0
Dyella	<0.01	0	0	0	1	0	0	0
Croceicoccus	<0.01	0	0	0	1	0	0	0
Schlesneria	<0.01	0	0	0	1	0	0	0
Sediminibacillus	<0.01	0	0	0	1	0	0	0
Halanaerobium	<0.01	0	0	0	1	0	0	0
Unclassified *Micavibrionaceae*	<0.01	0	0	0	1	0	0	0
Unclassified *Desulfobacteraceae*	<0.01	0	0	0	1	0	0	0
Clostridium sensu stricto 12	<0.01	0	0	0	1	0	0	0
Bacteroides	<0.01	0	0	0	1	0	0	0
Asticcacaulis	<0.01	0	0	0	1	0	0	0
Anaeromyxobacter	<0.01	0	0	0	1	0	0	0
Bradyrhizobium	<0.01	0	0	0	1	0	0	0
Caenispirillum	<0.01	0	0	0	1	0	0	0
Unclassified *Bradymonadaceae*	<0.01	0	0	0	1	0	0	0
Sulfuritalea	<0.01	0	0	0	1	0	0	0
Unclassified *Holosporaceae*	<0.01	0	0	0	1	0	0	0
Anaerobacillus	0	<0.01	0	0	0	3	0	0
Porphyromonas	0	<0.01	0	0	0	3	0	0
Afipia	0	<0.01	0	0	0	3	0	0
Ideonella	0	<0.01	0	0	0	3	0	0
Gardnerella	0	<0.01	0	0	0	3	0	0
Cloacibacterium	0	<0.01	0	0	0	3	0	0
Caldimonas	0	<0.01	0	0	0	3	0	0
Sphingobacterium	0	0	<0.01	0	0	0	1	0
CHKCI001	0	0	<0.01	0	0	0	1	0
Prevotella	0	0	<0.01	0	0	0	1	0
Meiothermus	0	0	<0.01	0	0	0	1	0
Aggregatibacter	0	0	<0.01	0	0	0	1	0
Alloprevotella	0	0	<0.01	0	0	0	1	0

Genus	0 mo (%)	6 mo (%)	12 mo (%)	18 mo (%)	0 mo (reads)	6 mo (reads)	12 mo (reads)	18 mo (reads)
C39	0	0	<0.01	0	0	0	1	0
Lautropia	0	0	<0.01	0	0	0	1	0
Atopobium	0	0	<0.01	0	0	0	1	0
Peredibacter	0	0	<0.01	0	0	0	1	0
Naasia	0	0	<0.01	0	0	0	1	0
Streptomyces	0	<0.01	0	0	0	2	0	0
Parasegetibacter	0	<0.01	0	0	0	2	0	0
Arthrobacter	0	<0.01	0	0	0	2	0	0
Atopostipes	0	<0.01	0	0	0	2	0	0
Planococcus	0	<0.01	0	0	0	2	0	0
Cellvibrio	0	<0.01	0	0	0	2	0	0
Blautia	0	<0.01	0	0	0	2	0	0
Caenimonas	0	<0.01	0	0	0	2	0	0
Thermoactinomyces	0	<0.01	0	0	0	2	0	0
Cupriavidus	0	<0.01	0	0	0	2	0	0
Microcella	0	<0.01	0	0	0	2	0	0
Jeotgalicoccus	0	<0.01	0	0	0	2	0	0
Arenimonas	0	<0.01	0	0	0	1	0	0
Unclassified *Peptostreptococcaceae*	0	<0.01	0	0	0	1	0	0
Unclassified *Nocardiopsaceae*	0	<0.01	0	0	0	1	0	0
Unclassified *Microtrichales*	0	<0.01	0	0	0	1	0	0
Unclassified *Solirubrobacteraceae*	0	<0.01	0	0	0	1	0	0
Lysinibacillus	0	<0.01	0	0	0	1	0	0
Peptoniphilus	0	<0.01	0	0	0	1	0	0
Actinomyces	0	<0.01	0	0	0	1	0	0
Neomicrococcus	0	<0.01	0	0	0	1	0	0
Friedmanniella	0	<0.01	0	0	0	1	0	0
OM27 clade	0	<0.01	0	0	0	1	0	0
Nitrospira	0	<0.01	0	0	0	1	0	0
Kroppenstedtia	0	<0.01	0	0	0	1	0	0
Falsirhodobacter	0	<0.01	0	0	0	1	0	0
Leptotrichia	0	<0.01	0	0	0	1	0	0
Sideroxydans	0	<0.01	0	0	0	1	0	0
Corynebacterium	0	<0.01	0	0	0	1	0	0
Leifsonia	0	<0.01	0	0	0	1	0	0
Brevifollis	0	<0.01	0	0	0	1	0	0
Cellulomonas	0	<0.01	0	0	0	1	0	0
Chitinimonas	0	<0.01	0	0	0	1	0	0
Clostridium sensu stricto 1	0	<0.01	0	0	0	1	0	0
Ciceribacter	0	<0.01	0	0	0	1	0	0
Truepera	0	<0.01	0	0	0	1	0	0
Simplicispira	0	<0.01	0	0	0	1	0	0

Genus	0 mo (%)	6 mo (%)	12 mo (%)	18 mo (%)	0 mo (reads)	6 mo (reads)	12 mo (reads)	18 mo (reads)
Unclassified *Clostridiales vadinBB60 group*	0	<0.01	0	0	0	1	0	0
Unclassified *Absconditabacteriales (SR1)*	0	<0.01	0	0	0	1	0	0
Achromobacter	0	<0.01	0	0	0	1	0	0
Yonghaparkia	0	<0.01	0	0	0	1	0	0

Appendix B. Fungal genera: complete abundance data (18S rRNA)

Relative abundance (%) out of all eukaryotic reads and number of reads per genus.

Table B1. Fungal genera

Genus	0 mo (%)	6 mo (%)	12 mo (%)	18 mo (%)	0 mo (reads)	6 mo (reads)	12 mo (reads)	18 mo (reads)
Pichia	92.38	61.83	13.83	0.47	197,684	85,860	11,251	351
Brettanomyces	<0.01	0	22.32	92.96	4	0	18,158	69,353
Cladosporium	0.05	11.79	19.50	<0.01	97	16,365	15,870	1
Issatchenkia	4.29	12.66	0.21	6.55	9,180	17,585	173	4,887
Saccharomyces	0.33	0.48	16.22	0	714	663	13,195	0
Aspergillus	<0.01	1.80	7.39	0	20	2,504	6,012	0
Malassezia	<0.01	3.44	4.72	0	20	4,773	3,844	0
Alternaria	0.04	1.79	5.24	<0.01	80	2,482	4,261	2
Fusarium	0.01	1.42	0.61	0	24	1,977	497	0
Starmerella-Candida clade	0.19	0.05	0.82	0	406	67	667	0
Penicillium	0.03	0	0.97	0	70	0	786	0
Emericellopsis	0	0	0.90	0	0	0	731	0
Unclassified *Saccharomycetales*	0.76	0	0	0	1,625	0	0	0
Acremonium	0	0.09	0.63	0	0	131	516	0
Scheffersomyces	<0.01	0.57	0.13	0	1	790	105	0
Unclassified *Pleosporales*	0	0.56	0.12	0	0	784	94	0
Ogataea-Candida clade	0.68	0	0	0	1,454	0	0	0
Zygoascus-Candida clade	0.64	0	0	0	1,364	0	0	0
Curvularia	0	0	0.58	0	0	0	471	0
Talaromyces	<0.01	0.16	0.39	0	1	225	318	0
Unclassified *Aureobasidiaceae*	<0.01	0.06	0.42	0	14	82	340	0
Stachybotrys	0	0.35	0.08	0	0	488	62	0
Chaetomium	<0.01	0	0.32	0	1	0	259	0
Trichaptum	0	0	0.29	0	0	0	238	0
Phoma	<0.01	0.15	0.13	0	17	203	102	0
Buckleyzyma	0	0.27	0	0	0	380	0	0
Singerocybe	0	0.26	0	0	0	359	0	0
Yamadazyma-Candida clade	0.25	0	0	0	525	0	0	0
Phaeodothis	0	0	0.22	0	0	0	178	0
Sarocladium	0	0.13	0.06	0	0	184	50	0
Vishniacozyma	<0.01	0.13	0.05	0	2	183	44	0
Trichoderma	0	0	0.15	0	0	0	125	0
Yarrowia	<0.01	0.05	0.10	0	3	64	83	0
Scopulariopsis	0	0.14	0	0	0	201	0	0
Papiliotrema	0	0	0.14	0	0	0	111	0
Phanerochaete	0	0	0.12	0	0	0	98	0
Schizophyllum	0	0.10	0	0	0	143	0	0

Genus	0 mo (%)	6 mo (%)	12 mo (%)	18 mo (%)	0 mo (reads)	6 mo (reads)	12 mo (reads)	18 mo (reads)
Tausonia	0.01	0	0.09	0	26	0	72	0
Valsa	0	0	0.10	0	0	0	79	0
Kluyveromyces	0.09	0	0	0	203	0	0	0
Toxicocladosporium	0	<0.01	0.08	0	0	1	68	0
Plectosphaerella	0	0	0.07	0	0	0	53	0
Unclassified *Tremellales*	0	0	0.07	0	0	0	53	0
Sporobolomyces	0	0	0.06	0	0	0	49	0
Unclassified *Agaricales*	0	0	0.05	0	0	0	41	0
Symmetrospora	0	0.05	0	0	0	65	0	0
Udeniomyces	0	0.04	0	0	0	61	0	0
Unclassified *Halosphaeriaceae*	0	<0.01	0.04	0	0	7	31	0
Wicherhamiella-Candida clade	0.04	0	0	0	87	0	0	0
Fonsecaea	<0.01	0	0.04	0	1	0	32	0
Oxyporus	0	0	0.03	0	0	0	24	0
Rhodotorula	0.01	0.02	0	0	23	25	0	0
Candida-Lodderomyces clade	0.03	0	0	0	60	0	0	0
Trichosporon	0	0	0.03	0	0	0	22	0
Microascus	0	0	0.03	0	0	0	21	0
Kurtzmaniella-Candida clade	0.01	0	<0.01	0	29	0	5	0
Geotrichum	0.02	0	0	0	39	0	0	0
Bipolaris	0	0	0.01	0	0	0	10	0
Starmera-Candida clade	0.01	0	0	0	22	0	0	0
Debaryomyces	<0.01	0	0	0	21	0	0	0
Sclerotinia	0	<0.01	0	0	0	11	0	0
Filobasidium	<0.01	0	0	0	16	0	0	0
Monascus	0	0	<0.01	0	0	0	5	0
Cystofilobasidium	<0.01	0	0	0	10	0	0	0
Barnettozyma-Candida clade	<0.01	0	0	0	7	0	0	0
Hanseniaspora	<0.01	0	0	0	6	0	0	0
Kockovaella	0	0	<0.01	0	0	0	2	0
Leucogyrophana	0	0	<0.01	0	0	0	2	0
Kazachstania-Candida clade	0	0	<0.01	0	0	0	2	0
Zygotorulaspora	<0.01	0	0	0	5	0	0	0
Leucosporidium	<0.01	0	0	0	4	0	0	0
Unclassified *Dothideomycetes*	0	<0.01	0	0	0	2	0	0
Wickerhamomyces-Candida clade	<0.01	0	0	0	3	0	0	0
Citeromyces	<0.01	0	0	0	3	0	0	0
Torula	0	0	0	<0.01	0	0	0	1
Wallemia	0	0	0	<0.01	0	0	0	1
Byssochlamys	0	0	<0.01	0	0	0	1	0

Genus	0 mo (%)	6 mo (%)	12 mo (%)	18 mo (%)	0 mo (reads)	6 mo (reads)	12 mo (reads)	18 mo (reads)
Fibricium	0	0	<0.01	0	0	0	1	0
Xerochrysium	0	0	<0.01	0	0	0	1	0
Sporisorium	0	0	<0.01	0	0	0	1	0
Richoniella	0	0	<0.01	0	0	0	1	0
Parastagonospora	<0.01	<0.01	0	0	1	1	0	0
Candida	<0.01	0	0	0	2	0	0	0
Dioszegia	<0.01	0	0	0	2	0	0	0
Beauveria	<0.01	0	0	0	2	0	0	0
Xenoacremonium	<0.01	0	0	0	2	0	0	0
Nectria	0	<0.01	0	0	0	1	0	0
Hamigera	0	<0.01	0	0	0	1	0	0
Neophaeosphaeria	0	<0.01	0	0	0	1	0	0
Erythrobasidium	0	<0.01	0	0	0	1	0	0
Infundibulicybe	0	<0.01	0	0	0	1	0	0
Knufia	<0.01	0	0	0	1	0	0	0
Blumeria	<0.01	0	0	0	1	0	0	0
Nakazawaea	<0.01	0	0	0	1	0	0	0
Saccharomycopsis	<0.01	0	0	0	1	0	0	0
Pleurotopsis	<0.01	0	0	0	1	0	0	0
Staurothele	<0.01	0	0	0	1	0	0	0
Unclassified *Mycosphaerellaceae*	<0.01	0	0	0	1	0	0	0
Unclassified *Polyporales*	<0.01	0	0	0	1	0	0	0