SUPPLEMENTARY MATERIAL FOR THE MANUSCRIPT

ITS1 metabarcoding reveals low specificity of lichen mycobiomes at a local scale

by

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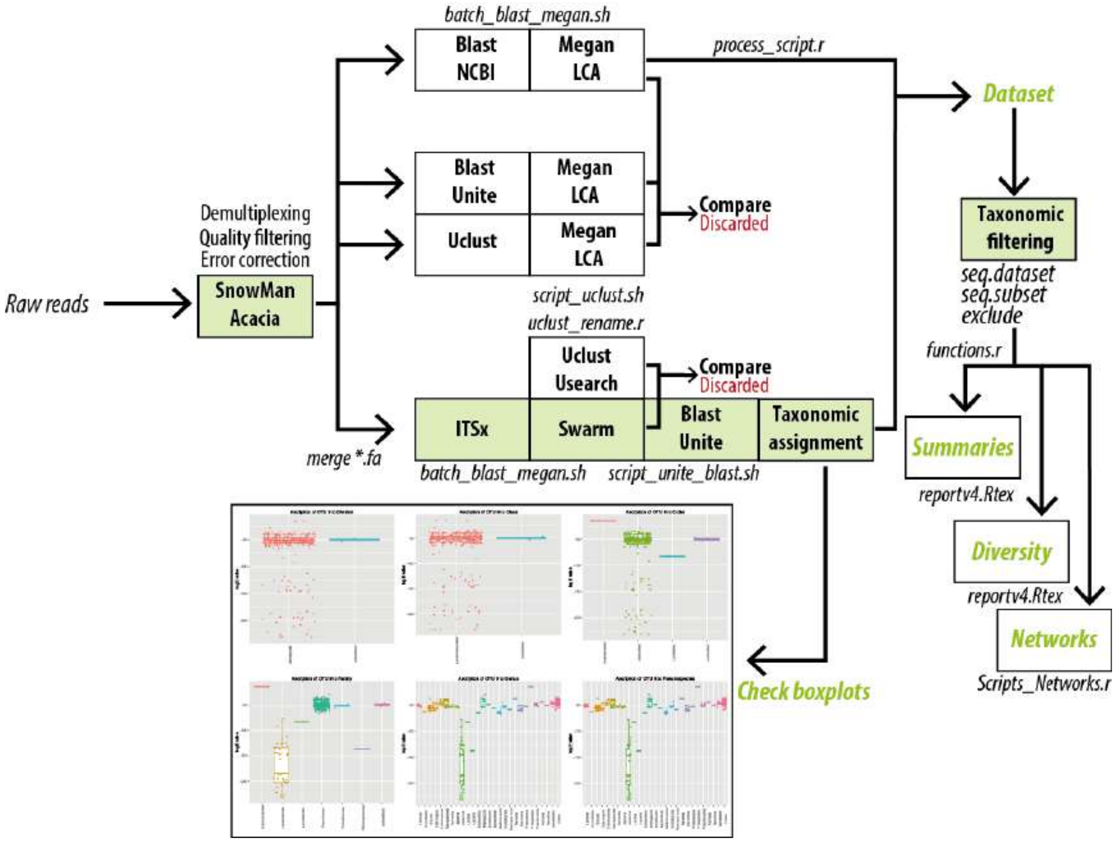
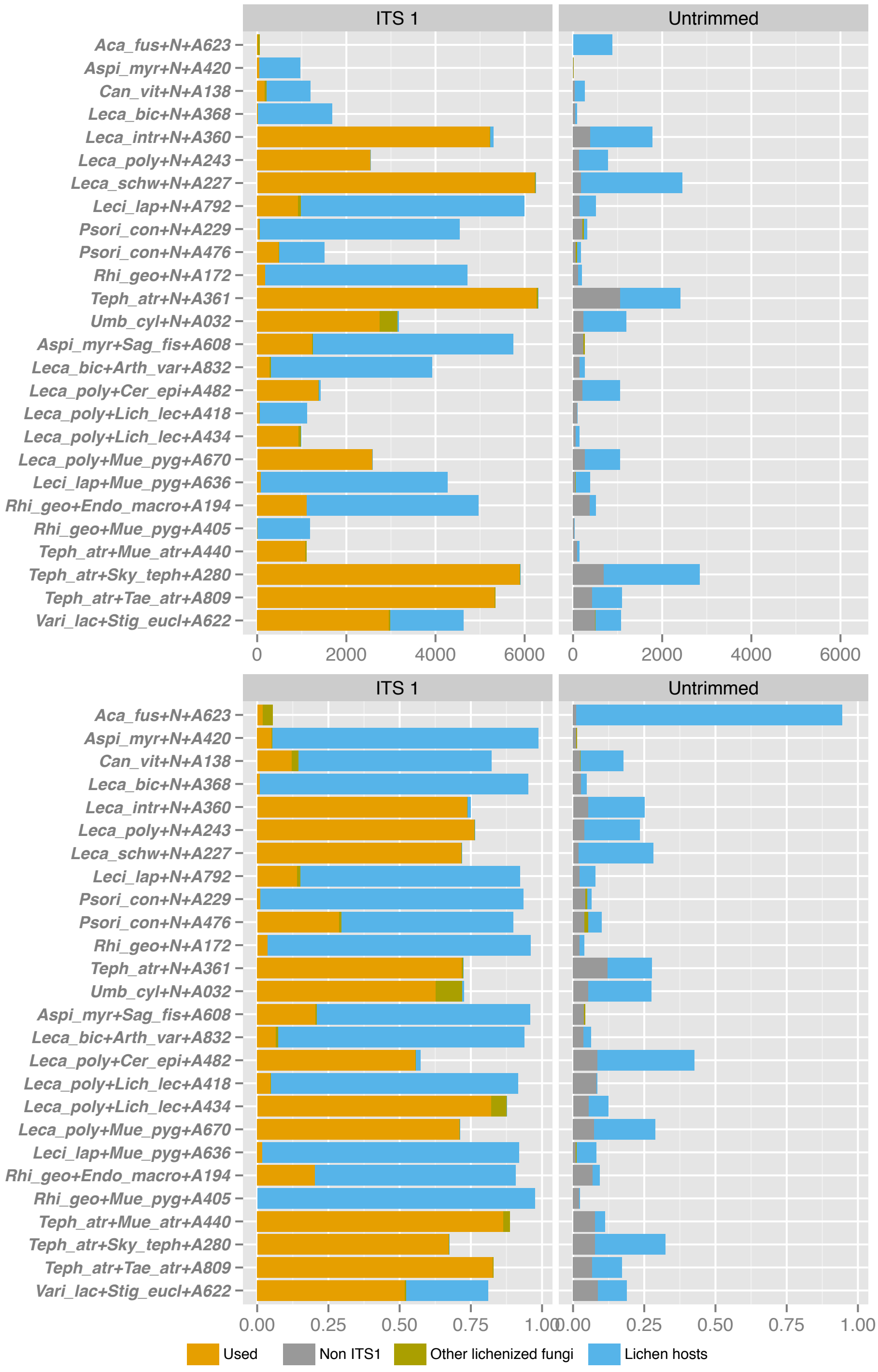
INDEX OF TABLES

INDEX OF FIGURES



Supplementary Figure 1. Schematic representation of the analytical pipeline. Files referred by filename can be found on the gitHub repository. Main pipeline is highlighted green and green names in italics highlight the main resulting data structures. Taxonomic filtering was done manually and included multiple manual and semiautomated validation steps.



Supplementary Figure 2. Summary of reads included and excluded in the analyses per sample. Upper plots show read counts per sample, lower plots the same figures but normalized per sample. The left subplot includes reads that passed the filtering for fungal ITS1; the right subplot those that did not pass the filter. Colours highlight the reads excluded as they do not contain ITS1 fragments (grey), they belong to the host lichen fungus of the sample (blue), or to those of other lichen species found in the neighbouring community (green). Yellow reads are those included in further analyses.

	Mycobiome			Spurious			Mycobiont		
	ITS1	Non	All	ITS1	Non	All	ITS1	Non	All
Aca_fus+N+A623	2	1.1	3.1	3.4	0	3.4	0.1	93.4	93.5
Aspi_myr+N+A420	5.1	1.1	6.2	0.2	0.2	0.4	93.4	0	93.4
Can_vit+N+A138	12.2	2.5	14.7	2.3	0.2	2.5	67.7	15.1	82.8
Leca_bic+N+A368	0.9	2.9	3.8	0	0	0	94.2	2	96.2
Leca_intr+N+A360	73.7	5.4	79.1	0.1	0	0.1	1	19.7	20.7
Leca_poly+N+A243	76.3	4.1	80.4	0.2	0	0.2	0.1	19.4	19.5
Leca_schw+N+A227	71.6	2	73.6	0.2	0	0.2	0	26.1	26.1
Leci_lap+N+A792	14.1	2.3	16.4	1.1	0	1.1	77.1	5.5	82.6
Psori_con+N+A229	1.1	4.5	5.6	0.1	0.5	0.6	92.3	1.5	93.8
Psori_con+N+A476	28.8	3.9	32.7	0.8	1.5	2.3	60.3	4.7	65
Rhi_geo+N+A172	3.6	2.3	5.9	0.2	0	0.2	92.3	1.7	94
Teph_atr+N+A361	71.9	12.1	84	0.4	0	0.4	0	15.5	15.5
Umb_cyl+N+A032	62.8	5.4	68.2	9.2	0	9.2	0.6	22	22.6
Aspi_myr+Sag_fis+A608	20.5	3.8	24.3	0.5	0.4	0.9	74.8	0	74.8
Leca_bic+Arth_var+A832	6.5	3.6	10.1	0.8	0	0.8	86.4	2.7	89.1
Leca_poly+Cer_epi+A482	55.6	8.6	64.2	0.2	0	0.2	1.6	34.1	35.7
Leca_poly+Lich_lec+A418	4.8	8.1	12.9	0.1	0	0.1	86.7	0.3	87
Leca_poly+Lich_lec+A434	82.2	5.6	87.8	5.3	0	5.3	0.1	6.8	6.9
Leca_poly+Mue_pyg+A670	71	7.3	78.3	0.1	0	0.1	0	21.5	21.5
Leci_lap+Mue_pyg+A636	1.8	1	2.8	0	0.2	0.2	90.1	6.9	97
Rhi_geo+Endo_macro+A194	20.3	6.9	27.2	0.1	0	0.1	70.4	2.4	72.8
Rhi_geo+Mue_pyg+A405	0.2	2.2	2.4	0	0	0	97.4	0.2	97.6
Teph_atr+Mue_atr+A440	86.4	7.8	94.2	2.2	0	2.2	0	3.5	3.5
Teph_atr+Sky_teph+A280	67.3	7.8	75.1	0.2	0	0.2	0.1	24.6	24.7
Teph_atr+Tae_atr+A809	82.7	6.7	89.4	0.3	0	0.3	0	10.3	10.3
Vari_lac+Stig_eucl+A622	51.8	8.7	60.5	0.6	0.1	0.7	28.8	10	38.8
Average	**37.51**	**4.91**	**42.42**	**1.10**	**0.12**	**1.22**	**42.90**	**13.46**	**56.36**

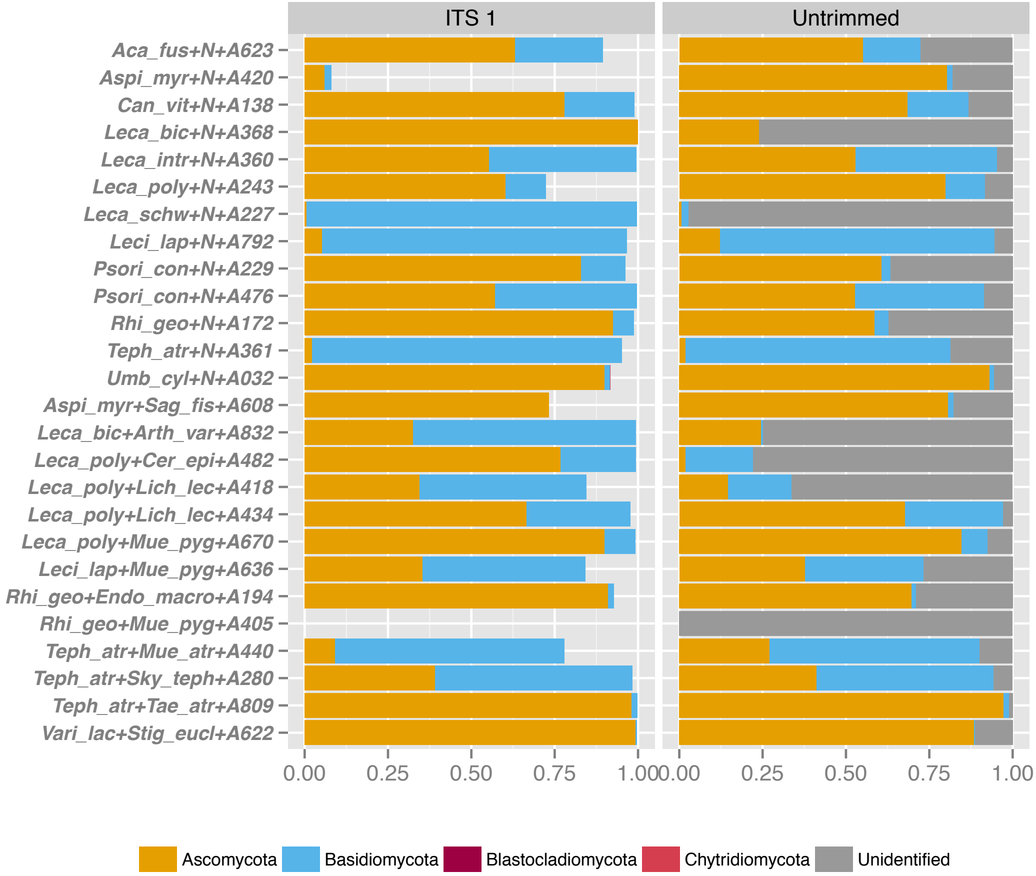
Supplementary table 1. Structure of the dataset accounting for the percentage of reads assignable to the mycobiome, the mycobiont and considered as spurious reads for the ITS1 and non-ITS sample fractions.

	A623	A420	A138IN	A368	A360	A243	A227	A792	A229	A476	A172	A361	A032	A608	A832	A482	A418	A434	A670	A636	A194	A405	A440	A280	A809	A622
Ascomycota	8	3	60	6	588	223	18	28	15	42	32	53	359	155	28	228	4	126	353	14	178	.	44	463	862	409
Dothideomycetes	.	1	20	.	436	68	9	10	.	12	20	51	299	1	8	222	2	49	70	6	12	.	36	209	860	398
Botryosphaeriales	.	**1**	**3**	.	**44**	**2**	**2**	.	.	**3**	**7**	**4**	**204**	.	.	**218**	.	.	**4**	.	**8**	.	**4**	**4**	.	**7**
Capnodiales	.	.	**16**	.	**389**	**42**	**4**	**6**	.	**7**	**13**	**45**	**53**	**1**	**8**	**4**	**2**	**48**	**63**	**5**	**4**	.	**26**	**179**	**859**	**391**
Myriangiales	.	.	1	.	1	2	2	1	.	1	.	.	.	.	.	.	.	.	3	.	.	.	.	23	.	.
Pleosporales	.	.	.	.	2	17	1	3	.	1	.	2	42	.	.	.	.	1	.	1	.	.	.	3	1	.
unidentified	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	6	.	.	.
Eurotiomycetes	5	2	39	.	30	132	3	7	2	29	12	1	22	153	13	1	.	1	159	7	166	.	4	158	1	6
Chaetothyriales	**5**	**2**	**39**	.	**29**	**132**	**3**	**7**	**1**	**29**	**12**	**1**	**22**	**153**	**13**	**1**	.	**1**	**159**	**7**	**1**	.	**4**	**156**	**1**	**6**
Eurotiales	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	2	.	.
Verrucariales	.	.	.	.	1	.	.	.	1	.	.	.	.	.	.	.	.	.	.	.	165	.	.	.	.	.
Lecanoromycetes	3	.	1	6	1	17	3	10	13	.	.	.	24	1	.	5	.	5	124	1	.	.	1	93	.	5
Candelariales	.	.	.	.	.	3	.	1	.	.	.	.	.	.	.	1	.	.	.	.	.	.	.	.	.	.
Lecanorales	3	.	.	.	1	11	2	9	13	.	.	.	11	1	.	3	.	.	122	1	.	.	.	.	.	.
Lecideales	.	.	.	.	.	1	.	.	.	.	.	.	5	.	.	.	.	.	.	.	.	.	.	.	.	3
Ostropales	.	.	.	.	.	.	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	92	.	.
Peltigerales	.	.	.	6	.	.	.	.	.	.	.	.	.	.	.	.	.	5	.	.	.	.	.	.	.	2
Pertusariales	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	1	.	.	.	.	.	.	.	.	.	.
Rhizocarpales	.	.	1	.	.	.	.	.	.	.	.	.	7	.	.	.	.	.	1	.	.	.	.	1	.	.
Umbilicariales	.	.	.	.	.	.	.	.	.	.	.	.	1	.	.	.	.	.	1	.	.	.	1	.	.	.
unidentified	.	.	.	.	.	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
Leotiomycetes	.	.	.	.	.	4	1	.	.	.	.	.	5	.	.	.	.	2	.	.	.	.	3	.	.	.
Helotiales	.	.	.	.	.	4	1	.	.	.	.	.	5	.	.	.	.	2	.	.	.	.	3	.	.	.
Saccharomycetes	.	.	.	.	.	.	.	.	.	.	.	.	1	.	.	.	.	.	.	.	.	.	.	.	.	.
Saccharomycetales	.	.	.	.	.	.	.	.	.	.	.	.	1	.	.	.	.	.	.	.	.	.	.	.	.	.
Sordariomycetes	.	.	.	.	.	2	.	.	.	.	.	.	8	.	.	.	.	2	.	.	.	.	.	.	.	.
Diaporthales	.	.	.	.	.	.	.	.	.	.	.	.	5	.	.	.	.	.	.	.	.	.	.	.	.	.
Hypocreales	.	.	.	.	.	7	.	.	.	.	.	.	3	.	.	.	.	2	.	.	.	.	.	.	.	.
Taphrinales	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	3	.	.
Unidentified Ascomycete	.	.	.	.	121	.	2	1	.	1	.	1	.	.	7	.	2	67	.	.	.	.	.	.	1	.

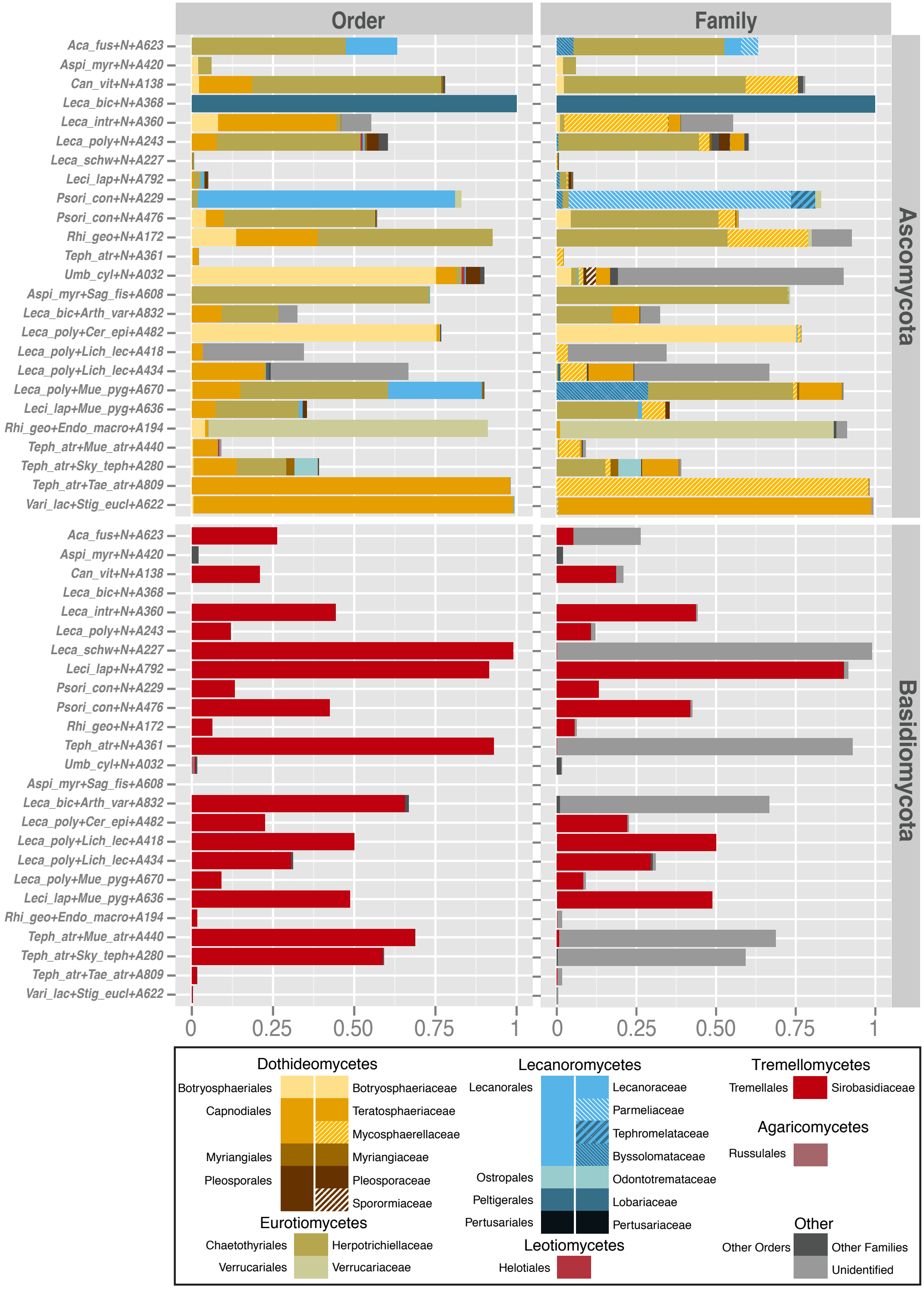
Supplementary table 2. Taxonomic composition of the dataset at order level, Ascomycota. Numbers reflect the raw number of reads.

	A623	A420	A138	A368	A360	A243	A227	A792	A229	A476	A172	A361	A032	A608	A832	A482	A418	A434	A670	A636	A194	A405	A440	A280	A809	A622
Basidiomycota	4	1	13	.	276	51	434	176	4	40	3	506	19	.	31	52	7	62	48	7	9	.	98	319	17	6
Agaricomycetes	.	1	.	.	1	1	.	1	.	.	.	.	17	.	3	.	.	6	.	.	.	.	1	14	1	1
Agaricales	.	.	.	.	.	.	.	.	.	.	.	.	5	.	2	.	.	.	.	.	.	.	.	6	.	1
Auriculariales	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	1	.	.
Cantharellales	.	.	.	.	.	.	.	.	.	.	.	.	1	.	.	.	.	.	.	.	.	.	1	.	.	.
Corticiales	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	1	.	.
Hymenochaetales	.	.	.	.	.	.	.	.	.	.	.	.	.	.	1	.	.	.	.	.	.	.	.	1	1	.
Polyporales	.	.	.	.	1	.	.	.	.	.	.	.	6	.	.	.	.	4	.	.	.	.	.	3	.	.
Russulales	.	.	.	.	.	1	.	1	.	.	.	.	5	.	.	.	.	2	.	.	.	.	.	2	.	.
Sebacinales	.	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
Microbotryomycetes	.	.	.	.	.	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
Sporidiobolales	.	.	.	.	.	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
Tremellomycetes	4	.	13	.	275	49	434	175	4	40	3	506	2	.	28	52	7	56	48	7	9	.	97	304	16	5
Cystofilobasidiales	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	2	.	.
Tremellales	**4**	**.**	**13**	**.**	**275**	**49**	**434**	**175**	**4**	**40**	**3**	**506**	**2**	**.**	**28**	**52**	**7**	**56**	**48**	**7**	**9**	**.**	**97**	**302**	**16**	**5**
unidentified	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	1	.	.
Chytridiomycota	.	.	.	.	.	.	.	.	.	.	.	.	1	.	.	.	.	.	.	.	.	.	.	.	.	.
Blastocladiomycetes	.	.	.	.	.	.	.	.	.	.	.	.	1	.	.	.	.	.	.	.	.	.	.	.	.	.
Blastocladiales	.	.	.	.	.	.	.	.	.	.	.	.	1	.	.	.	.	.	.	.	.	.	.	.	.	.
Unidentified	2	18	2	.	21	59	21	26	2	2	2	273	60	170	2	9	9	18	19	7	37	2	102	85	7	9

Supplementary table 3. Taxonomic composition of the dataset at order level, Basidiomycota. Numbers reflect the raw number of reads.

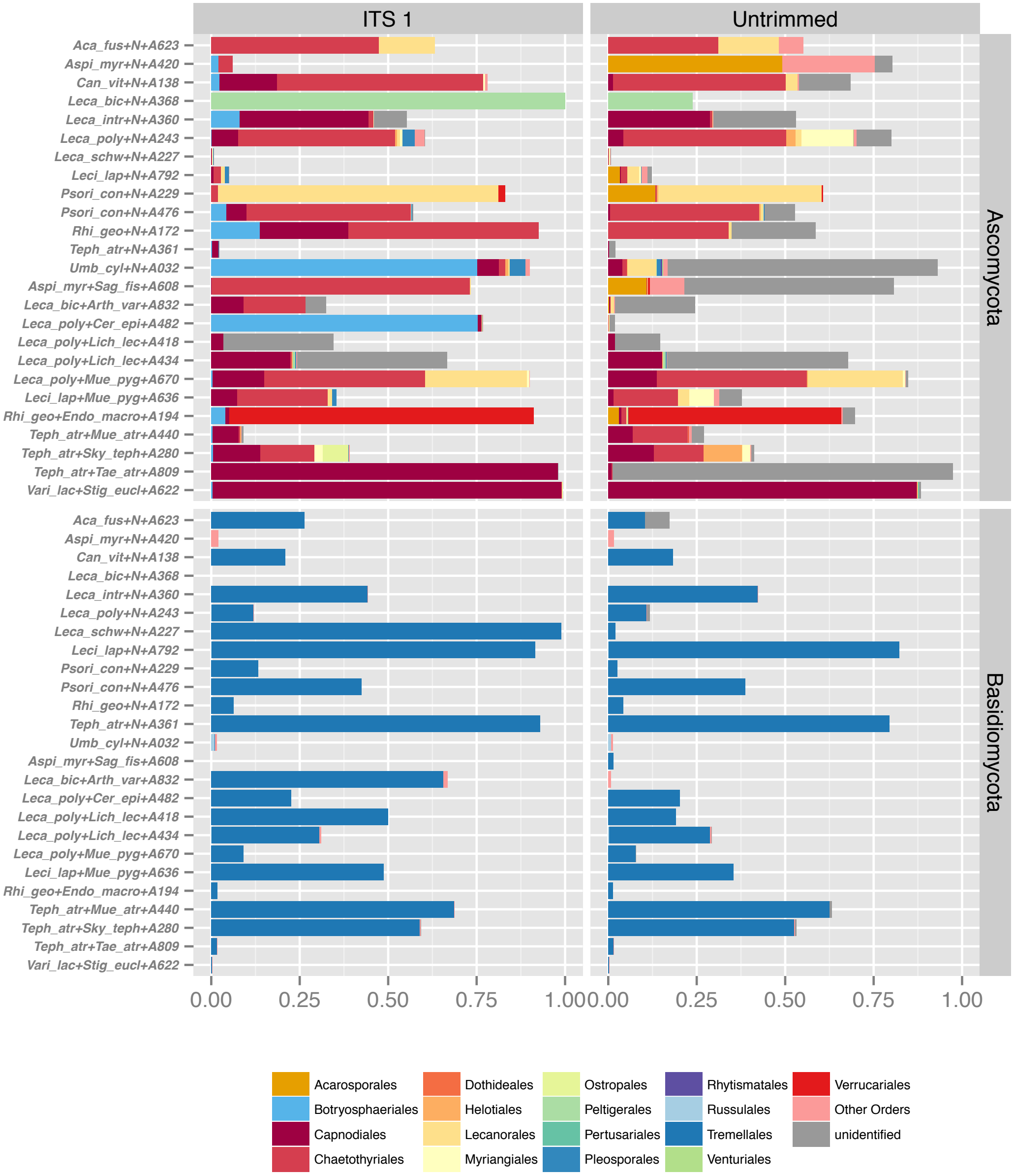


Supplementary Figure 3. Proportion of reads from the ITS1 and from the untrimmed dataset assigned to fungal Divisions. Sequences were identified by blasting to the UNITE database (ITS1) and to NCBI database (complete).



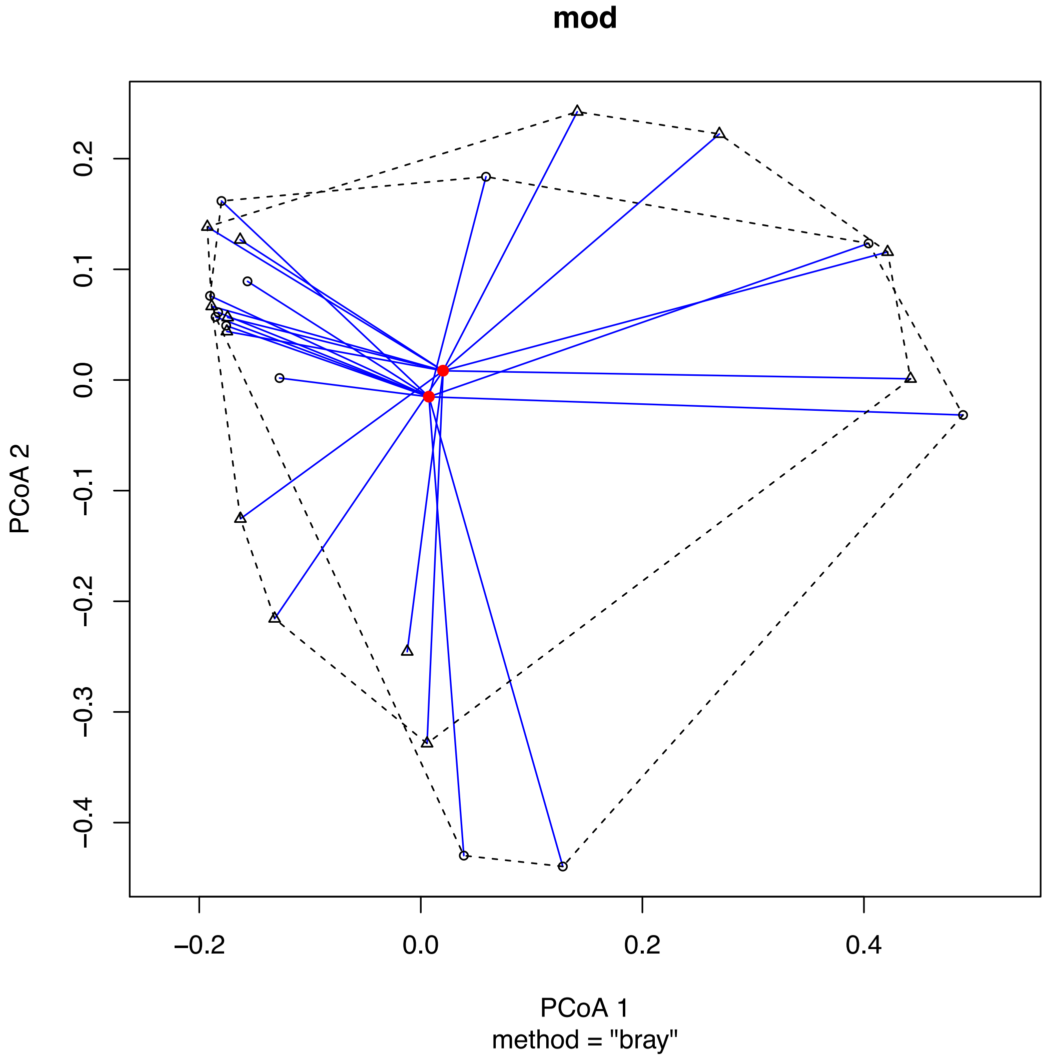
Supplementary Figure 4. Summary of the taxonomic assignment of the dataset to the main fungal classes, orders and families. Bars reflect the proportion of reads from the ITS1 dataset per sample.

Supplementary Figure 5. Taxonomic assignment of the dataset to fungal classes, in the ITS1 and untrimmed datasets.

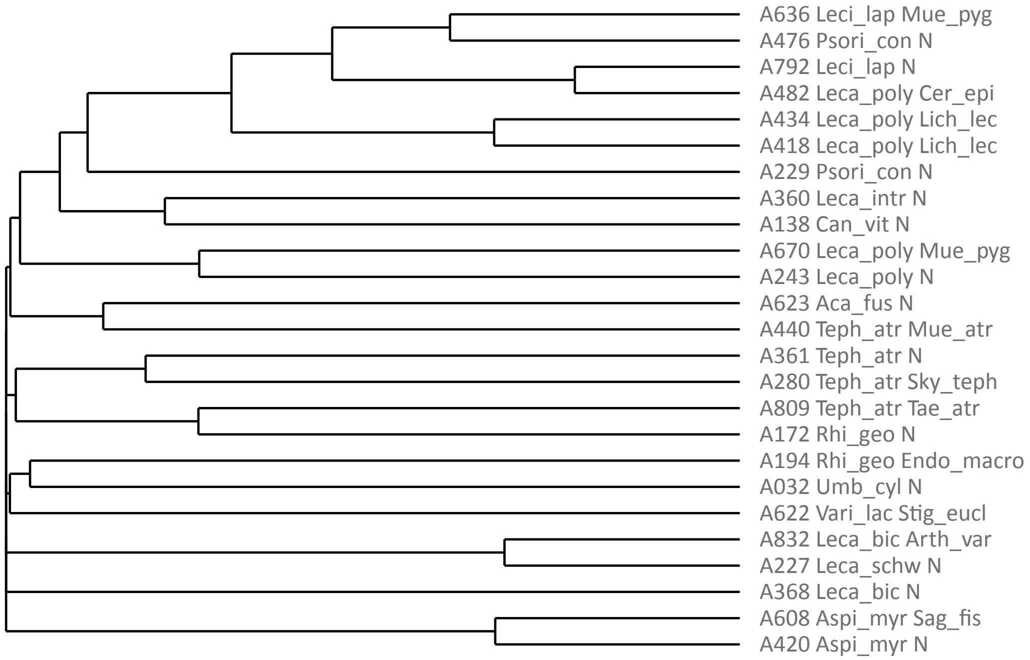


Supplementary Figure 6. Taxonomic assignment of the dataset to fungal orders, in the ITS1 and untrimmed datasets.

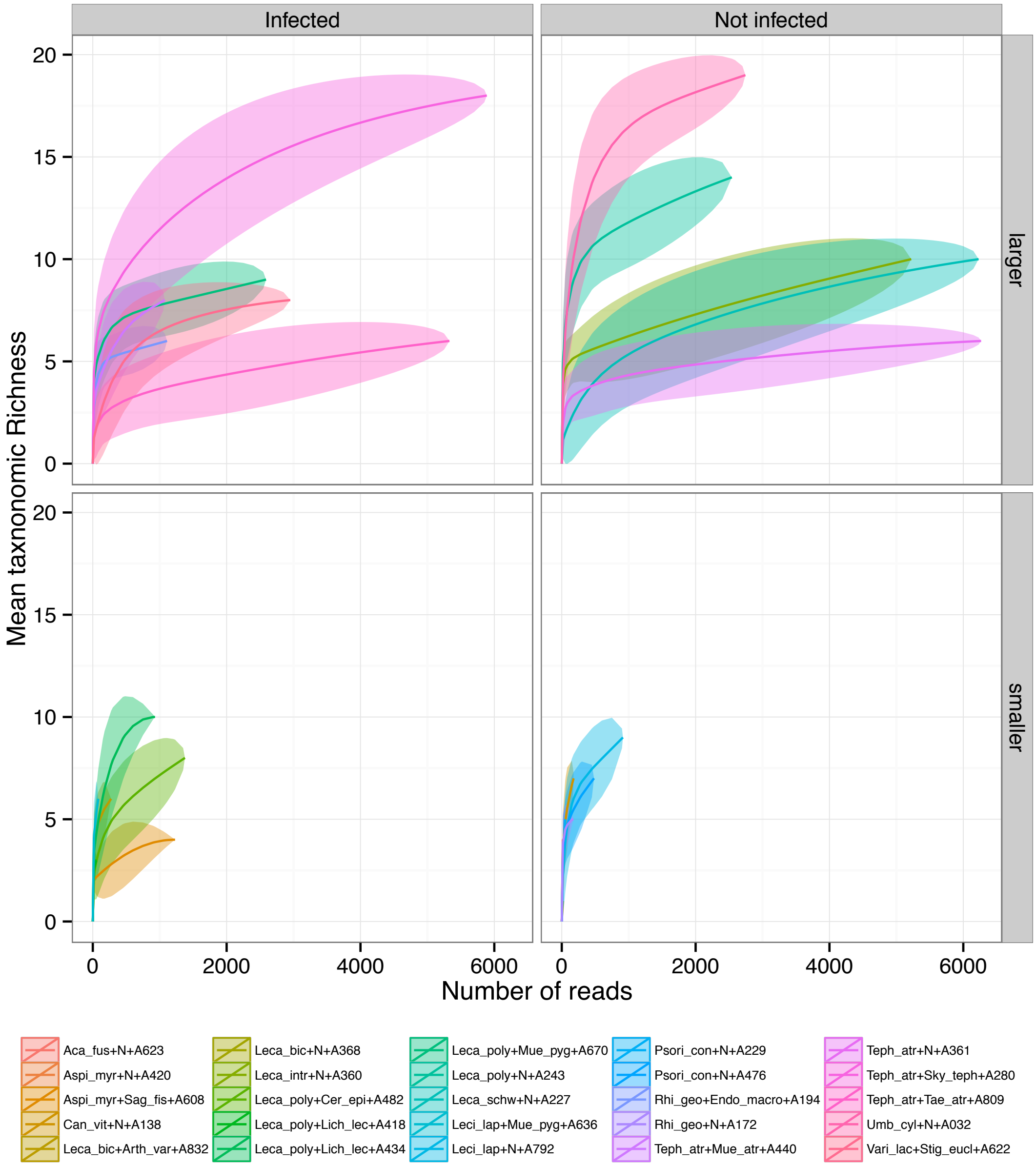
Supplementary Figure 7. Taxonomic assignment of the dataset to fungal families, in the ITS1 and untrimmed datasets.



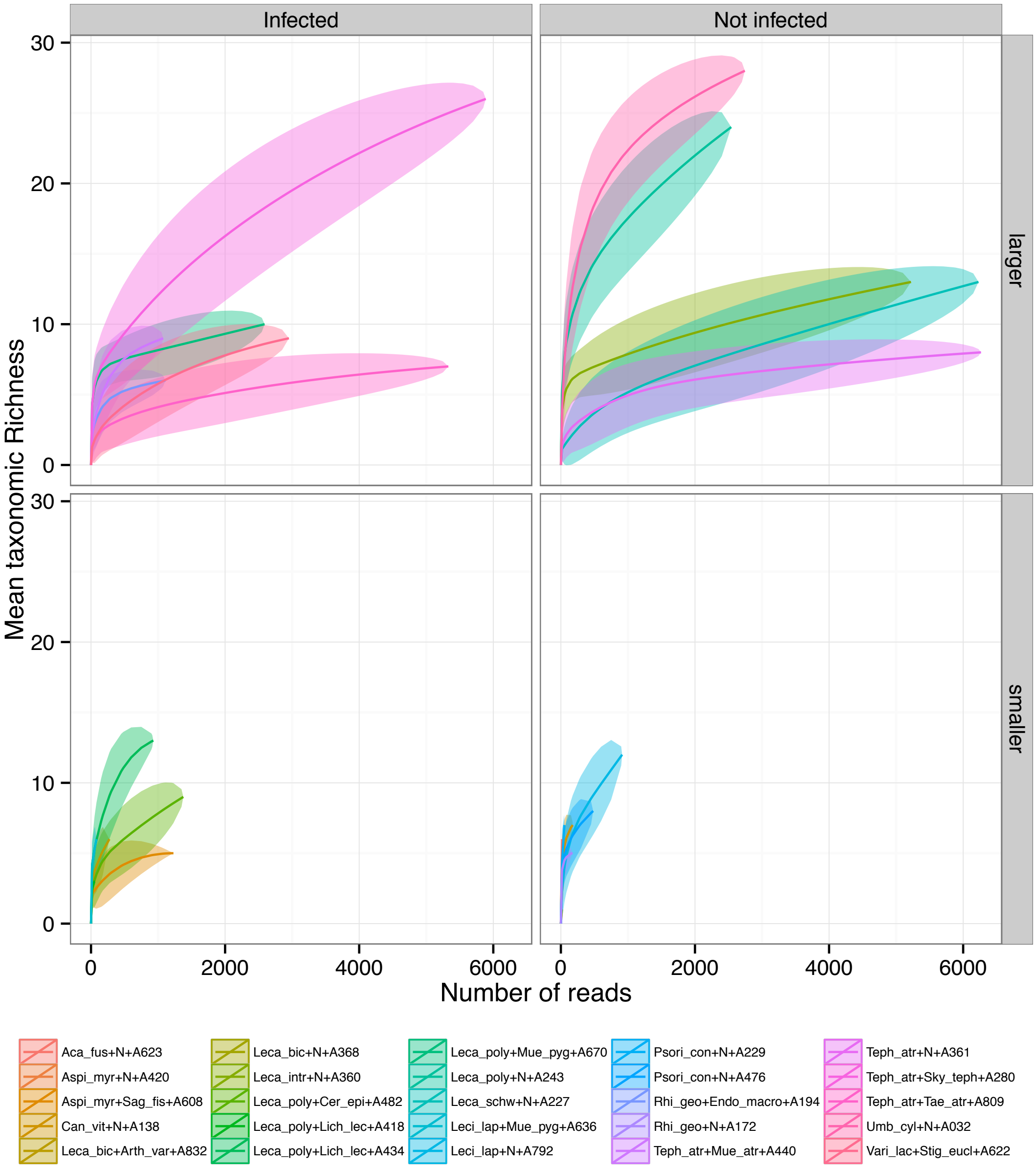
Supplementary Figure 8. Graphic representation of the multidimensional scaling axes based on β-diversity estimates between samples. Samples are sorted by whether they are symptomatically infected by lichenicolous fungi. The position of the two centroids (red dots) of the two sets of samples as well as the overlap between the two groups reinforces the idea that all samples form a single group.



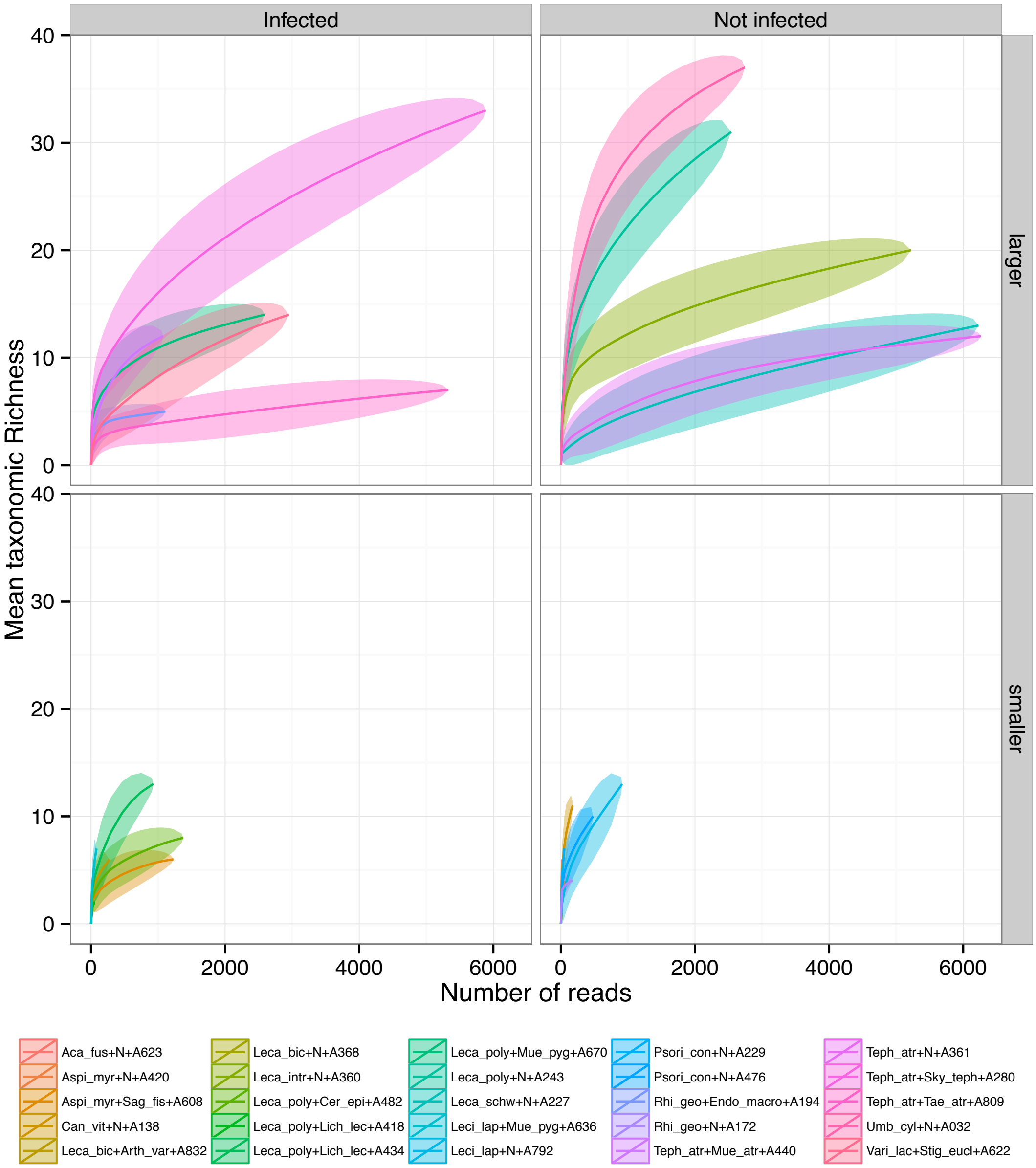
Supplementary Figure 9. Hierarchical clustergram (dendrogram) showing similarity in OTU composition between samples. Hierarchical clustering was carried out on a pairwise Bray-Curtis distance matrix between samples. The long branch lengths of the cladogram reinforce the lack of structure of the dataset. Bray-Curtis distances tend to overestimate the differences due to minoritary species.



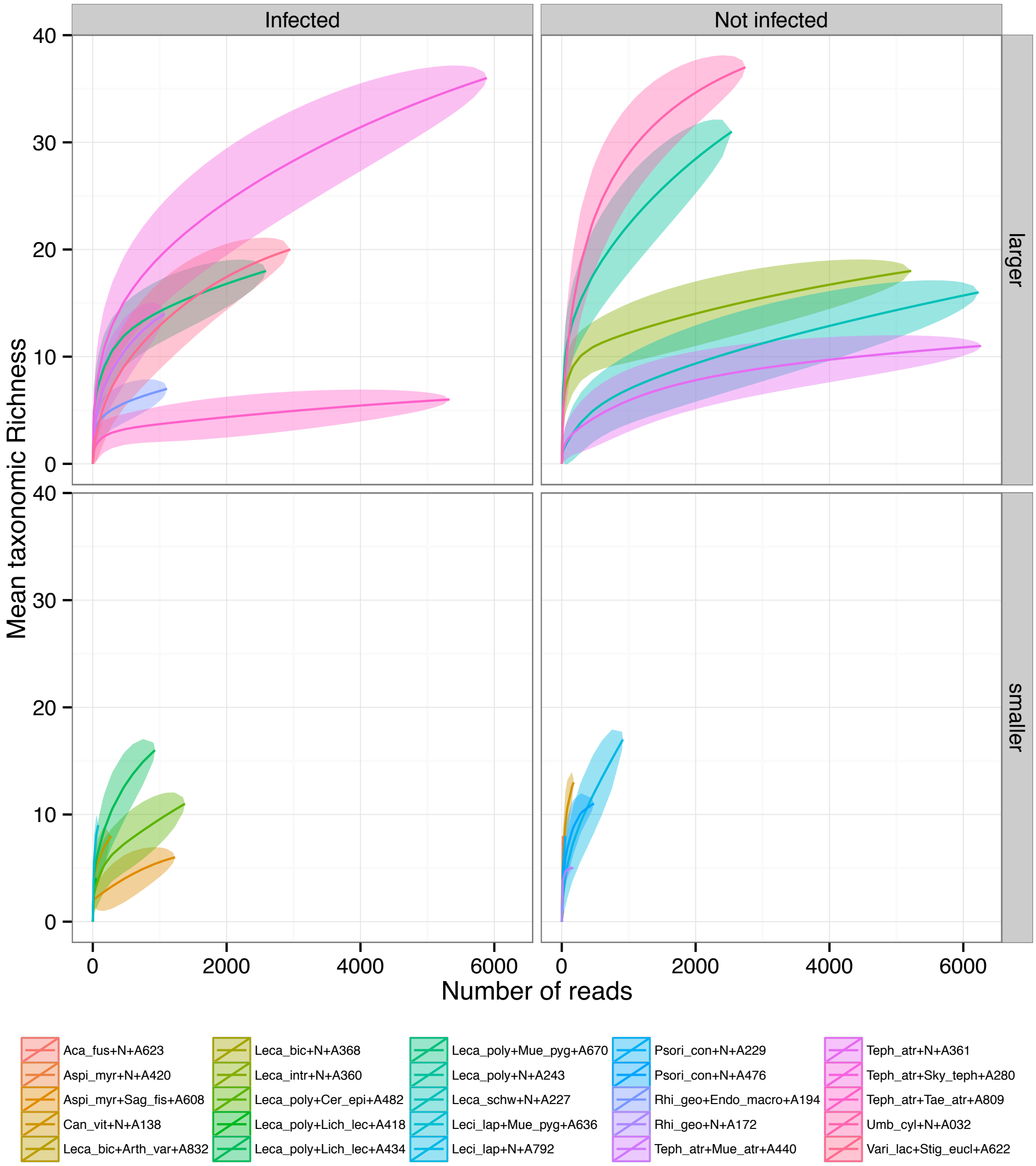
Supplementary Figure 10. Rarefaction curves at order level. Banana plots of rarefied species richness estimates and (bold line) confidence intervals based on standard error estimates. Symptomatic and non infected samples are presented in separate subplots, as well as are samples with higher and lower number of reads.



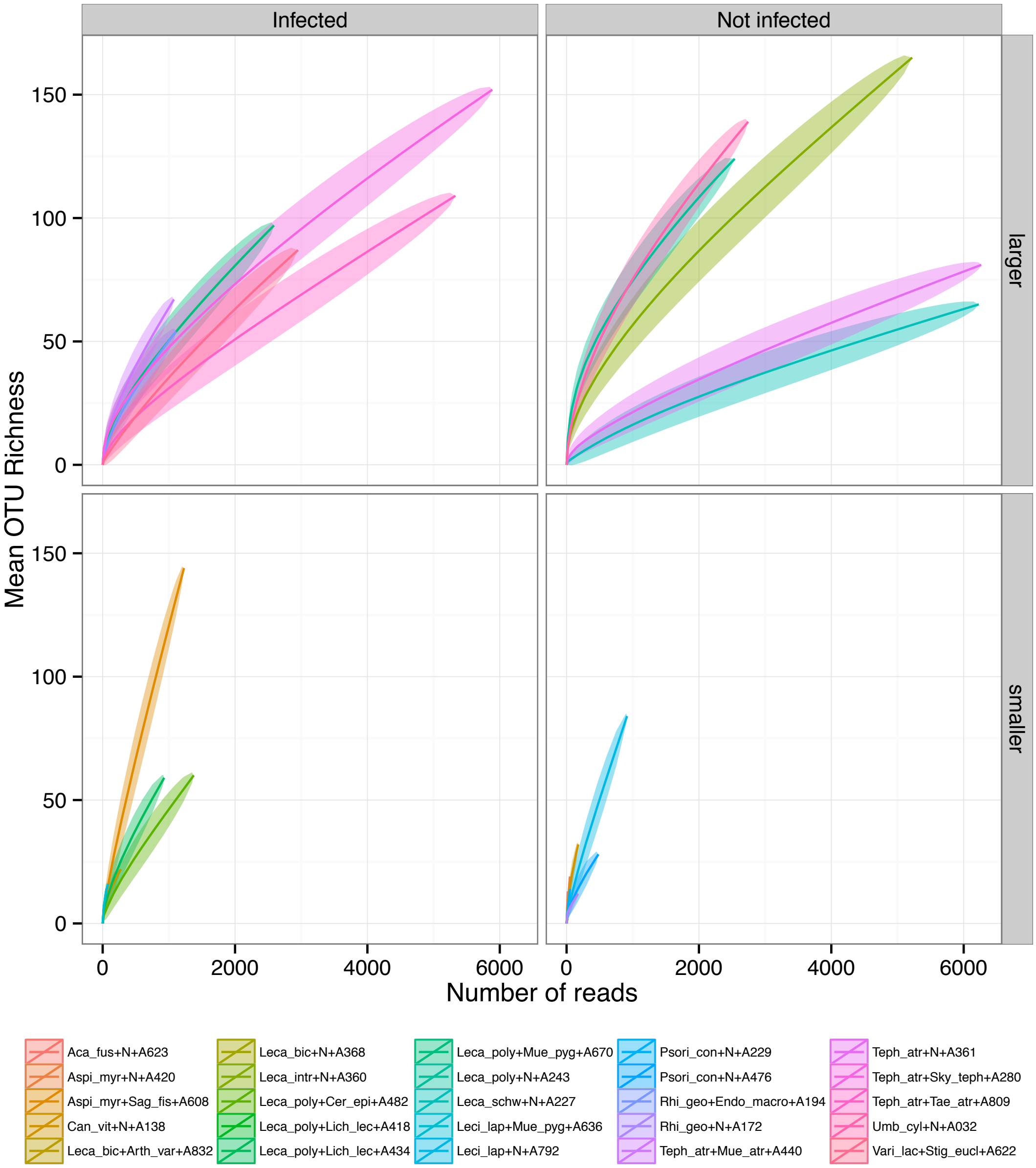
Supplementary Figure 11. Rarefaction curves at family level. Banana plots of rarefied species richness estimates and (bold line) confidence intervals based on standard error estimates. Symptomatic and non infected samples are presented in separate subplots, as well as are samples with higher and lower number of reads.



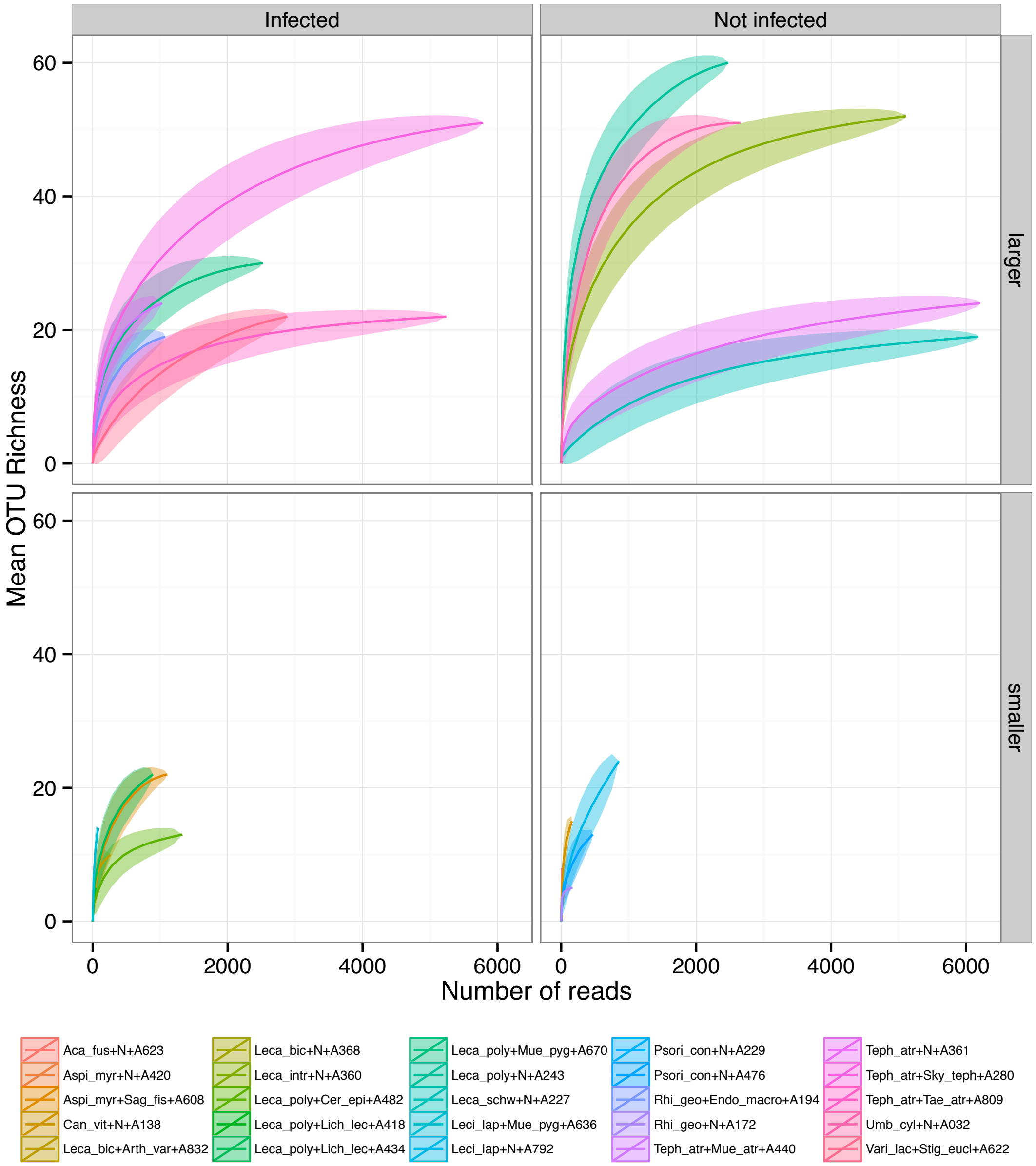
Supplementary Figure 12. Rarefaction curves at genus level. Banana plots of rarefied species richness estimates and (bold line) confidence intervals based on standard error estimates. Symptomatic and non infected samples are presented in separate subplots, as well as are samples with higher and lower number of reads.



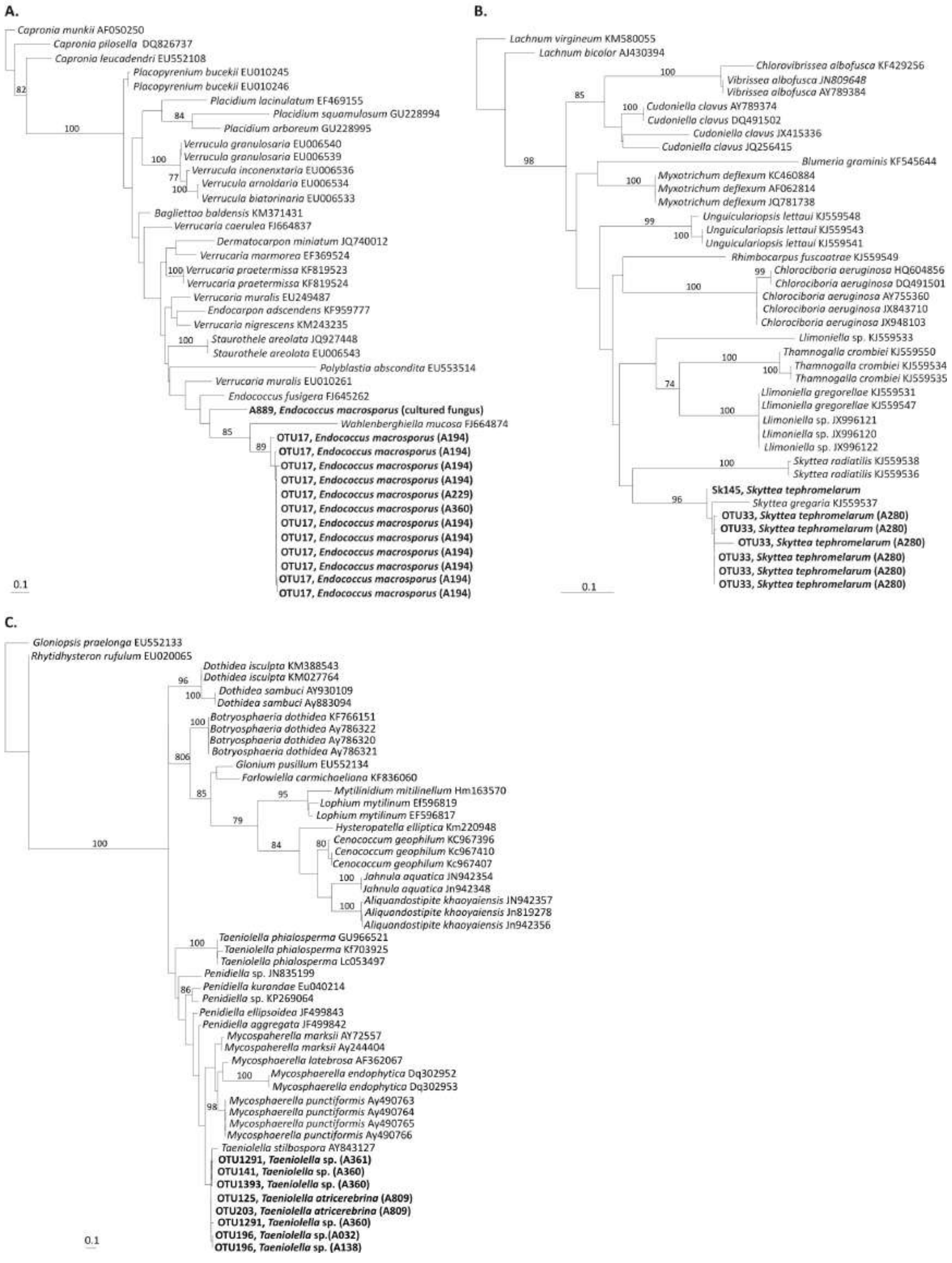
Supplementary Figure 13. Rarefaction curves at species (pseudospecies) level. Banana plots of rarefied species richness estimates and (bold line) confidence intervals based on standard error estimates. Symptomatic and non infected samples are presented in separate subplots, as well as are samples with higher and lower number of reads.



Supplementary Figure 14. Rarefaction curves at OTU level, including singletons. Banana plots of rarefied species richness estimates and (bold line) confidence intervals based on standard error estimates. Symptomatic and non infected samples are presented in separate subplots, as well as are samples with higher and lower number of reads.



Supplementary Figure 15. Rarefaction curves at OTU level, excluding singletons. Banana plots of rarefied species richness estimates and (bold line) confidence intervals based on standard error estimates. Symptomatic and non infected samples are presented in separate subplots, as well as are samples with higher and lower number of reads.



Supplementary Figure 16. Phylogenetic placement of OTUs identified as A) *Endococcus macrosporus*. B) *Skyttea tephromelarum* and C) *Taeniolella sp*. The presented topologies are maximum likelihood topologies calculated in RaxML, numbers above the branches reflect bootstrap support.

SAMPLES	**All**		**Tremellales**		**Botryosphaeriales**		**Capnodiales**		**Chaetothyriales**	
Unipartite networks	**R**	**T**	**R**	**T**	**R**	**T**	**R**	**T**	**R**	**T**
Connectance	0.80	0.47	0.64	0.29	0.14	0.06	0.48	0.33	0.42	0.12
Loss of connectance	.	0.34	.	0.36	.	0.08	.	0.15	.	0.30
Number of links per sample	9.64	5.60	7.72	3.44	1.72	0.76	5.76	4.00	5.00	1.40
Mean number of common links	15.87	7.40	12.26	3.56	1.67	0.77	8.98	5.66	6.33	1.64
Bipartite networks										
Number of MOTUs	**1225**	**130**	**219**	**21**	**63**	**6**	**292**	**26**	**153**	**29**
Number of Samples	**25**	**24**	**23**	**20**	**15**	**10**	**21**	**20**	**23**	**14**
Mean Shared MOTUs per pair of samples	2.95	1.13	1.32	0.54	0.58	0.56	1.07	0.60	0.66	0.47
Mean common samples per pair of MOTUs	0.10	0.22	0.14	0.39	0.57	0.87	0.21	0.24	0.19	0.36
Connectance	0.05	0.08	0.06	0.13	0.09	0.30	0.06	0.10	0.06	0.12
Number of compartments	1	2	1	1	2	2	2	4	3	3
Nestedness	**7.16**	**9.13**	**5.81**	**11.37**	**5.77**	**27.24**	**3.81**	**8.26**	**4.06**	**9.19**
Weighted nestedness	**0.46**	**0.37**	**0.59**	**0.54**	**0.79**	**0.26**	**0.74**	**0.52**	**0.62**	**0.53**
Weighted NODF	**2.32**	**7.80**	**3.89**	**15.64**	**10.67**	**22.22**	**2.87**	**12.22**	**5.71**	**13.02**
cluster coefficient	0.04	0.04	0.04	0.10	0.07	0.35	0.05	0.05	0.04	0.07
cluster coefficient MOTUs	0.31	0.22	0.51	0.35	0.31	0.34	0.43	0.38	0.30	0.28
cluster coefficient Sample	0.05	0.08	0.09	0.15	0.43	0.55	0.17	0.15	0.09	0.15
weighted cluster coefficient MOTUs	0.89	0.65	0.51	0.08	0.34	0.18	0.42	0.20	0.29	0.07
weighted cluster coefficient SAMPLE	0.04	0.22	0.04	0.11	0.04	0.42	0.01	0.12	0.02	0.03
C score MOTU	0.91	0.83	0.86	0.73	0.44	0.58	0.79	0.81	0.82	0.68
C score SAMPLE	0.86	0.77	0.66	0.62	0.70	0.57	0.58	0.54	0.73	0.67

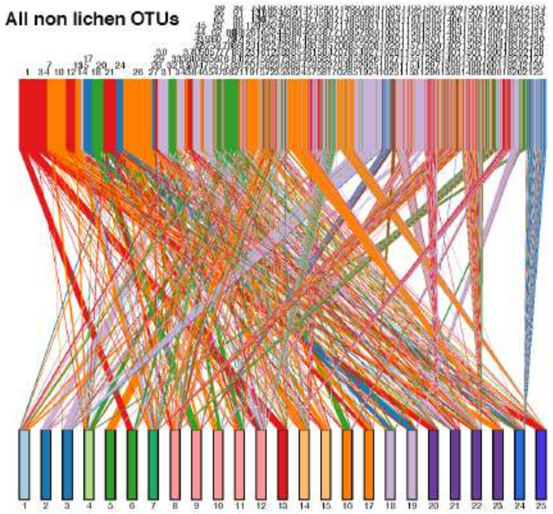
SPECIES	**All**		**Tremellales**		**Botryosphaeriales**		**Capnodiales**		**Chaetothyriales**	
Bipartite networks	**R**	**T**	**R**	**T**	**R**	**T**	**R**	**T**	**R**	**T**
Number of MOTUs	**1225**	**176**	**219**	**41**	**63**	**6**	**292**	**35**	**153**	**25**
Number of Species	**13**	**12**	**13**	**10**	**10**	**6**	**12**	**8**	**13**	**9**
Connectance	**0.09**	**0.11**	**0.09**	**0.14**	**0.13**	**0.44**	**0.10**	**0.17**	**0.10**	**0.17**
Weighted connectance	**0.00**	**0.02**	**0.01**	**0.04**	**0.03**	**0.17**	**0.01**	**0.05**	**0.01**	**0.05**
Number of compartments	**1**	**1**	**1**	**1**	**2**	**1**	**2**	**2**	**1**	**1**
nestedness	**11.95**	**8.44**	**10.24**	**10.86**	**11.55**	**21.94**	**8.99**	**16.53**	**9.84**	**12.53**
weighted nestedness	**0.53**	**0.77**	**0.63**	**0.85**	**0.78**	**0.27**	**0.75**	**0.68**	**0.57**	**0.72**
weighted NODF	**4.19**	**20.06**	**5.06**	**21.20**	**11.02**	**31.11**	**5.07**	**17.01**	**9.40**	**27.61**
Web asymmetry	0.98	0.87	0.89	0.61	0.73	0.00	0.92	0.63	0.84	0.47
Links per species	1.14	1.26	1.12	1.12	1.16	1.33	1.10	1.12	1.14	1.15
cluster coefficient	0.08	0.08	0.08	0.10	0.10	0.50	0.08	0.13	0.08	0.11
cluster coefficient HL	0.38	0.28	0.49	0.45	0.45	0.50	0.48	0.45	0.39	0.37
cluster coefficient LL	0.13	0.24	0.19	0.29	0.44	0.60	0.25	0.26	0.14	0.25
weighted cluster coefficient HL	0.96	0.74	0.66	0.23	0.68	0.48	0.68	0.35	0.46	0.03
weighted cluster coefficient LL	0.03	0.07	0.02	0.03	0.06	0.44	0.02	0.06	0.03	0.02
C score HL	0.81	0.37	0.78	0.28	0.42	0.50	0.67	0.53	0.68	0.09
C score LL	0.86	0.70	0.73	0.49	0.60	0.38	0.59	0.48	0.73	0.51

interaction strength asymmetry	1.45	-0.16	-10.58	1.27	-1.56	-0.37	-6.53	0.80	-4.21	-4.73
specialisation asymmetry	-0.24	-0.07	-0.01	0.06	0.07	0.04	-0.13	-0.01	-0.05	0.14
linkage density	5.31	4.25	2.47	2.27	2.21	2.07	2.69	2.33	2.25	1.84
Shannon diversity	4.36	3.85	2.77	2.50	2.28	1.81	2.75	2.37	2.79	2.18
interaction evenness	0.45	0.50	0.35	0.42	0.35	0.50	0.34	0.42	0.37	0.40
Alatalo interaction evenness	0.49	0.63	0.61	0.71	0.58	0.64	0.43	0.54	0.47	0.60
H2	0.76	0.76	0.71	0.73	0.79	0.71	0.69	0.71	0.83	0.86
mean number of shared partners HL	0.20	0.66	0.23	0.74	0.59	1.13	0.33	0.49	0.33	0.97
mean number of shared partners LL	5.41	1.65	1.38	0.78	1.11	1.20	1.48	0.96	1.26	0.72
niche overlap HL	0.16	0.48	0.18	0.53	0.53	0.33	0.29	0.38	0.27	0.62
niche overlap LL	0.07	0.07	0.20	0.25	0.16	0.22	0.30	0.33	0.20	0.26
togetherness HL	0.05	0.18	0.06	0.25	0.19	0.21	0.10	0.17	0.09	0.33
togetherness LL	0.02	0.03	0.02	0.05	0.06	0.28	0.01	0.06	0.02	0.08
V ratio HL	0.54	1.13	0.80	1.84	1.50	1.22	0.63	1.21	1.10	2.12
V ratio LL	116.38	79.53	26.46	21.45	25.15	1.00	65.56	9.87	32.12	15.58
discrepancy HL	988	97	195	14	34	3	173	20	105	9
discrepancy LL	927	71	167	13	22	4	173	20	93	7
extinction slope HL	1.04	1.20	1.07	1.19	1.11	2.46	1.08	1.25	1.05	1.55
extinction slope LL	1.00	1.00	1.00	1.00	1.00	3.09	1.00	1.00	1.00	1.00
robustness HL	0.51	0.55	0.52	0.54	0.53	0.70	0.52	0.55	0.52	0.60
robustness LL	0.98	0.80	0.85	0.62	0.75	0.76	0.84	0.70	0.87	0.65
functional complementarity HL	18.12	16.94	8.18	7.95	1.32	1.00	3.67	3.60	5.28	4.81
functional complementarity LL	15.55	15.18	7.15	6.99	1.45	1.15	3.83	3.73	5.35	4.95
partner diversity HL	0.57	0.54	0.81	0.76	0.39	0.33	0.75	0.70	0.53	0.50
partner diversity LL	1.96	1.56	0.78	0.63	0.92	0.92	0.91	0.68	0.76	0.42
generality HL	2.05	1.98	2.52	2.41	1.65	1.55	2.50	2.33	1.93	1.85
vulnerability LL	8.58	6.52	2.42	2.13	2.76	2.59	2.88	2.34	2.56	1.82

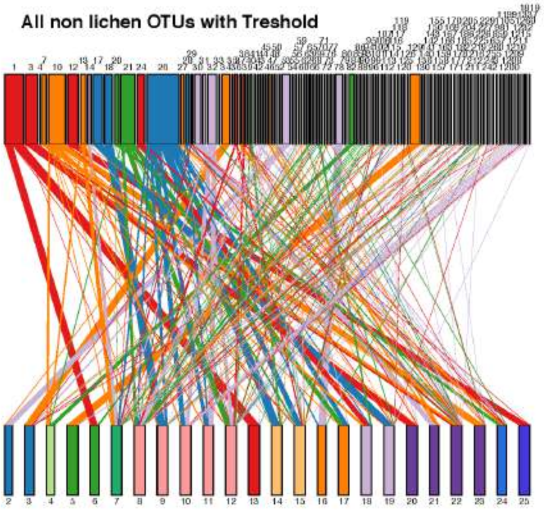
Supplementary table 4. Expanded representation of network statistics for unipartite and bipartite sample networks, as well as for bipartite host species vs. OTUs.

A	All OTUs								Main LIchenicole MOTUs only							
	Complete				Threshold filtered				Complete				Threshold filtered			
	d'	d	dmin	dmax	d'	d	dmin	dmax	d'	d	dmin	dmax	d'	d	dmin	dmax
Acarospora fuscata	**0.39**	2.54	2.12	3.22	**.**	.	.	3..	**.**	.	.	.	**.**	.	.	.
Aspilidea myrinii	**0.97**	2.50	1.73	2.53	**0.99**	2.68	2.02	2.69	**0.97**	2.26	1.52	2.28	**0.99**	2.27	1.52	2.27
Candelariella vitellina	**0.00**	2.08	2.08	3.22	**0.33**	2.48	2.03	3.40	**0.00**	0.83	0.83	3.52	**0.00**	1.00	1.00	3.59
Lecanora bicincta	**0.60**	2.20	1.73	2.53	**0.29**	2.17	2.03	2.51	**.**	.	.	.	**.**	.	.	.
Lecanora intricata	**0.00**	2.03	2.03	3.22	**0.00**	1.94	1.94	3.13	**0.00**	1.32	1.32	4.15	**0.00**	1.33	1.33	4.14
Lecanora polytropa	**0.00**	1.02	1.02	1.61	**0.00**	0.96	0.96	1.50	**0.00**	0.79	0.79	1.19	**0.00**	0.79	0.79	1.19
Lecanora swartzii	**0.51**	2.68	2.12	3.22	**0.52**	2.59	2.03	3.11	**0.00**	1.09	1.09	8.23	**.**	.	.	.
Lecidea lapicida	**0.00**	1.50	1.50	2.53	**0.00**	1.44	1.44	2.44	**0.00**	1.06	1.06	3.56	**0.00**	1.08	1.08	3.56
Psorinia conglomerata	**0.00**	1.66	1.66	2.53	**0.00**	1.64	1.64	2.53	**0.00**	1.23	1.23	2.60	**0.00**	1.37	1.37	2.64
Rhizocarpon geographicum	**0.33**	1.99	1.73	2.53	**0.00**	2.00	2.00	2.47	**0.00**	1.41	1.41	1.88	**0.00**	1.46	1.46	1.88
Tephromela atra	**0.48**	1.53	1.25	1.83	**0.46**	1.52	1.32	1.75	**0.00**	1.36	1.36	1.83	**0.00**	1.36	1.36	1.82
Umbilicaria cylindrica	**0.78**	2.97	2.12	3.22	**0.85**	3.08	2.03	3.26	**0.02**	1.71	1.52	9.20	**.**	.	.	.
Varicellaria lactea	**0.94**	3.15	2.12	3.22	**0.99**	3.12	2.03	3.13	**0.95**	1.99	1.52	2.02	**1.00**	2.01	1.52	2.01
B																
Muellerella pygmaea 21									**0.00**	0.93	0.93	1.71	**0.00**	0.94	0.94	1.70
Sagediopsis fissurisedens 34									**0.96**	2.23	1.19	2.27	**0.96**	2.23	1.19	2.27
Cercidospora epipolytropa 18									**0.00**	1.13	1.13	2.28	**0.00**	1.19	1.19	2.30
Lichenoconium lecanorae 32									**0.00**	1.14	1.14	2.21	**0.00**	1.15	1.15	2.20
Endococcus macrosporus 17									**0.64**	1.79	1.19	2.13	**0.73**	1.88	1.19	2.14
Muellerella atricola 46									**0.24**	1.81	1.19	3.75	**0.25**	1.82	1.19	3.75
Skyttea tephromelarum 33									**0.17**	1.77	1.19	4.63	**0.18**	1.82	1.19	4.63
Taeniolella atricerebrina 10									**0.00**	0.74	0.74	1.52	**0.00**	0.75	0.75	1.52
Stigmidium eucline 12									**0.93**	1.96	1.19	2.01	**1.00**	2.01	1.19	2.01

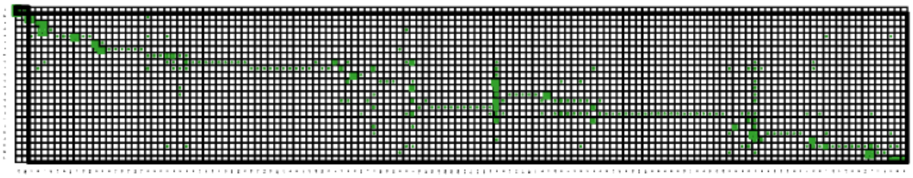
Supplementary table 5. Standarized and raw specialization indices calcultaed for each lichen host species (A) in the networks, as well as for those lichenicolous fungi identifiable as the main MOTUs at sample level (B). The values of d’ range between 0, mening no specialization and 1 meaning perfect specialization.



Supplementary Figure 17. Bipartite network at sample level including all non-lichen OTUs.

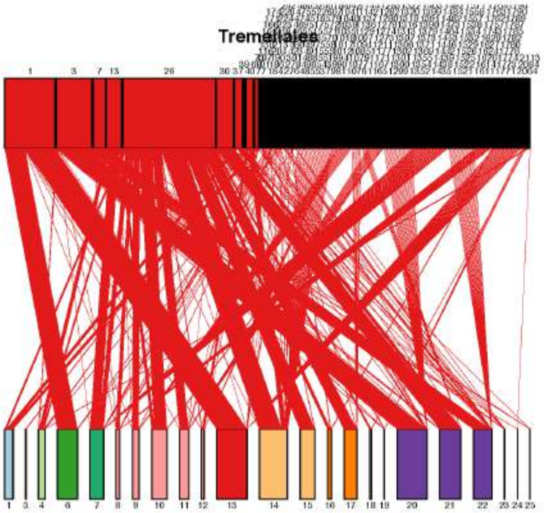


Supplementary Figure 18. Bipartite network at sample level of non-lichen OTUs above a sample specific threshold.

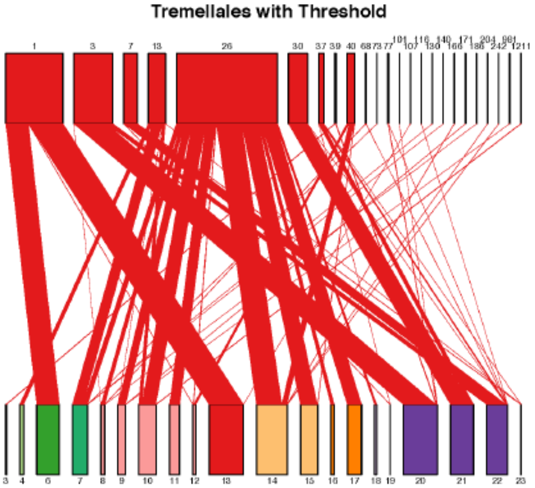


All non lichen OTUs with Treshold

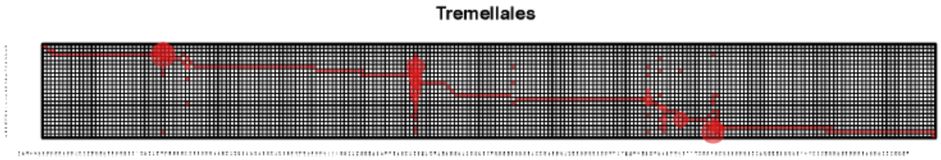
Supplementary Figure 19. Matrix representation showing nestedness and compartmentalization of the bipartite network at species level of non-lichen OTUs above a sample specific threshold.



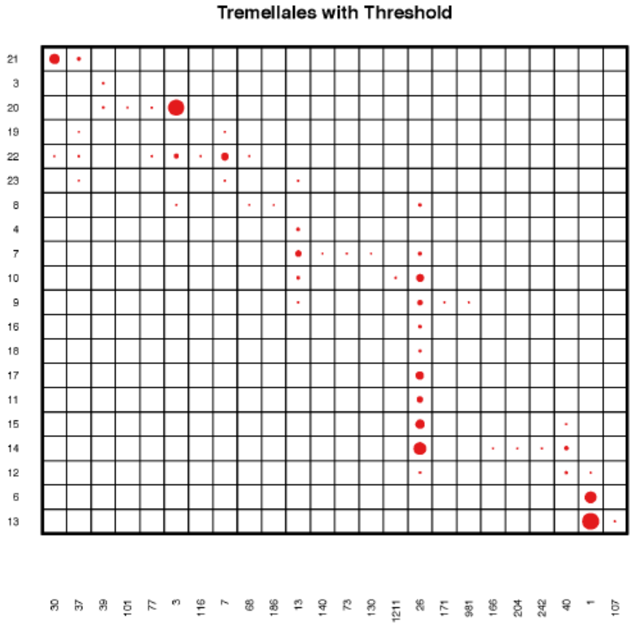
Supplementary Figure 20. Bipartite network at sample level using only OTUs identified as Tremellales.



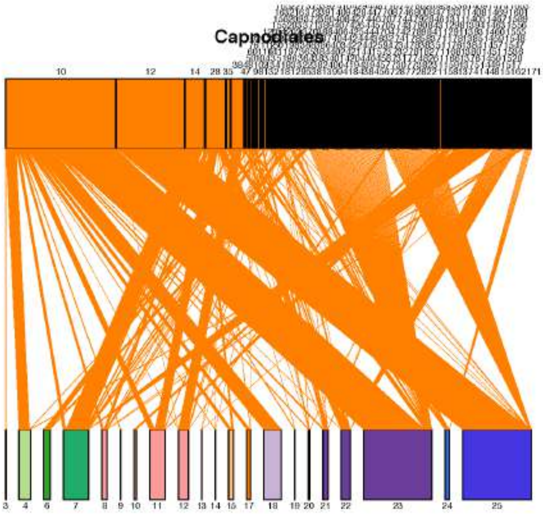
Supplementary Figure 21. Bipartite network at species level using only those OTUs identified as Tremellales found above a sample specific threshold.



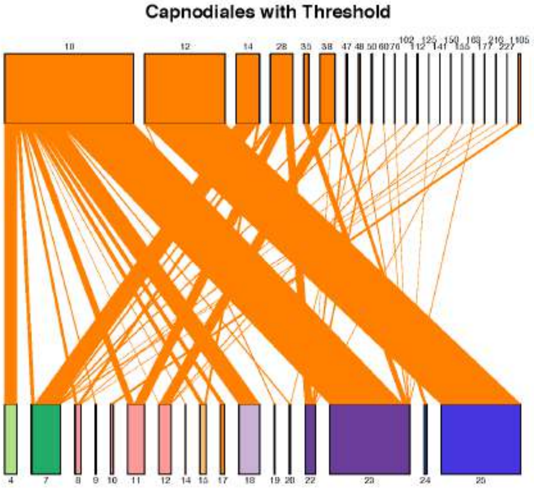
Supplementary Figure 22. Matrix representation showing nestedness and compartmentalization of the bipartite network at species level using all OTUs identified as Tremellales.



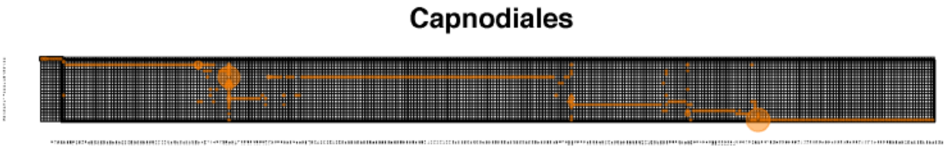
Supplementary Figure 23. Matrix representation showing nestedness and compartmentalization of the bipartite network at species level using only those OTUs identified as Tremellales sequence above a sample specific threshold.



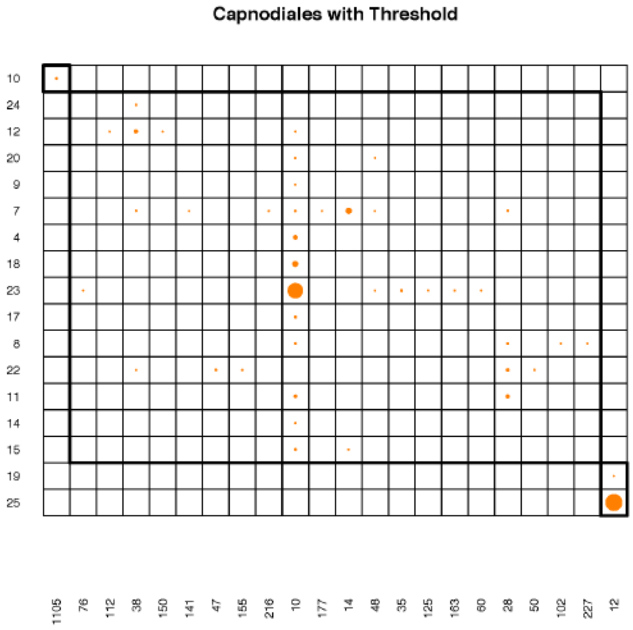
Supplementary Figure 24. Bipartite network at sample level using only OTUs identified as Capnodiales.



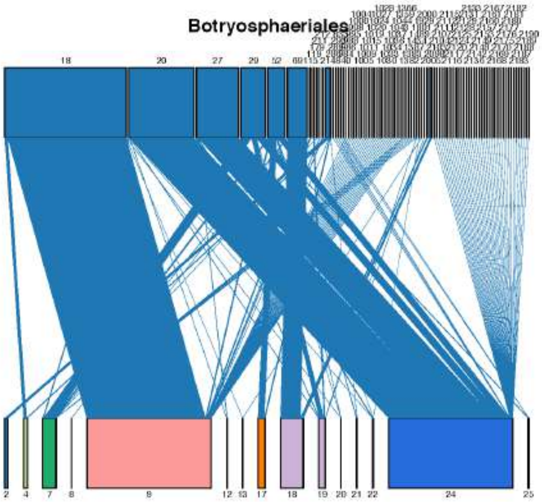
Supplementary Figure 25. Bipartite network at sample level using only those OTUs identified as Capnodiales above a sample specific threshold.



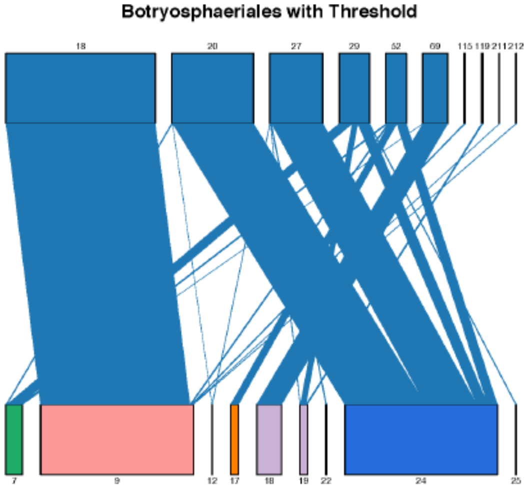
Supplementary Figure 26. Matrix representation showing nestedness and compartmentalization of the bipartite network at species level using all OTUs identified as Capnodiales.



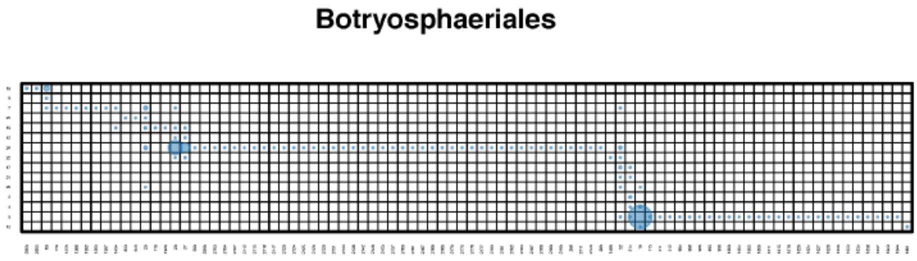
Supplementary Figure 27. Matrix representation showing nestedness and compartmentalization of the bipartite network at species level using only those OTUs identified as Capnodiales sequence above a sample specific threshold.



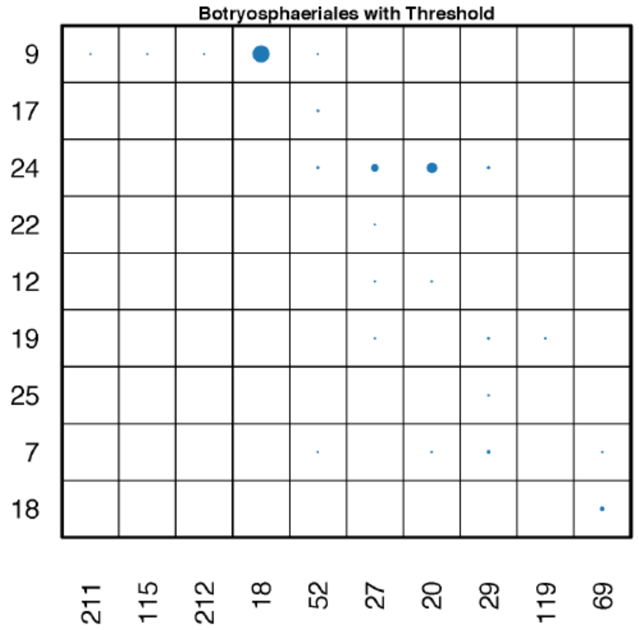
Supplementary Figure 28. Bipartite network at sample level using only OTUs identified as Botryosphaeriales.



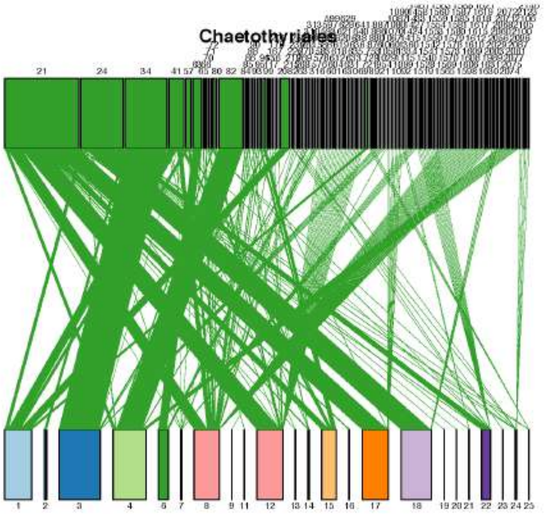
Supplementary Figure 29. Bipartite network at sample level using only those OTUs identified as Botryosphaeriales above a sample specific threshold.



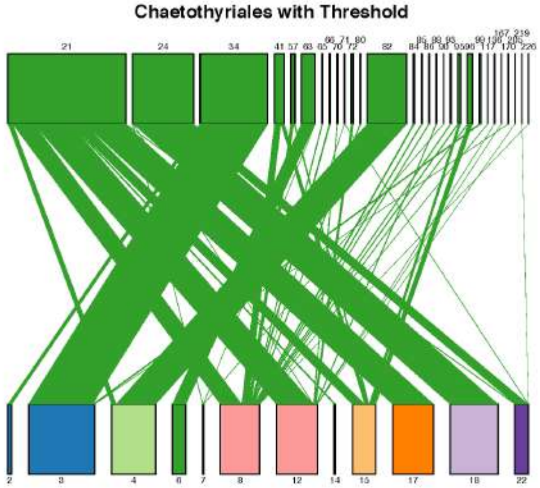
Supplementary Figure 30. Matrix representation showing nestedness and compartmentalization of the bipartite network at species level using all OTUs identified as Botryosphaeriales.



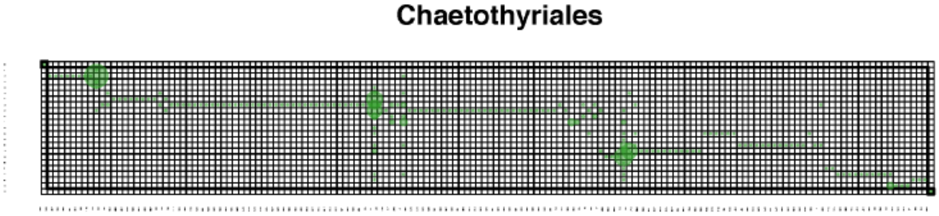
Supplementary Figure 31. Matrix representation showing nestedness and compartmentalization of the bipartite network at species level using only those OTUs identified as Botryosphaeriales sequence above a sample specific threshold.



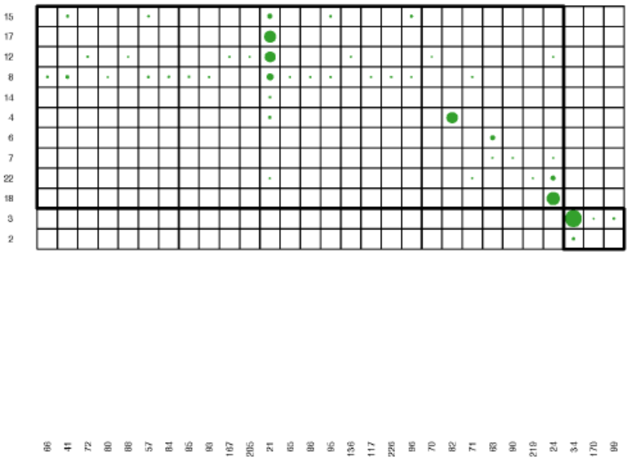
Supplementary Figure 32. Bipartite network at sample level using only OTUs identified as Chaetothyriales.



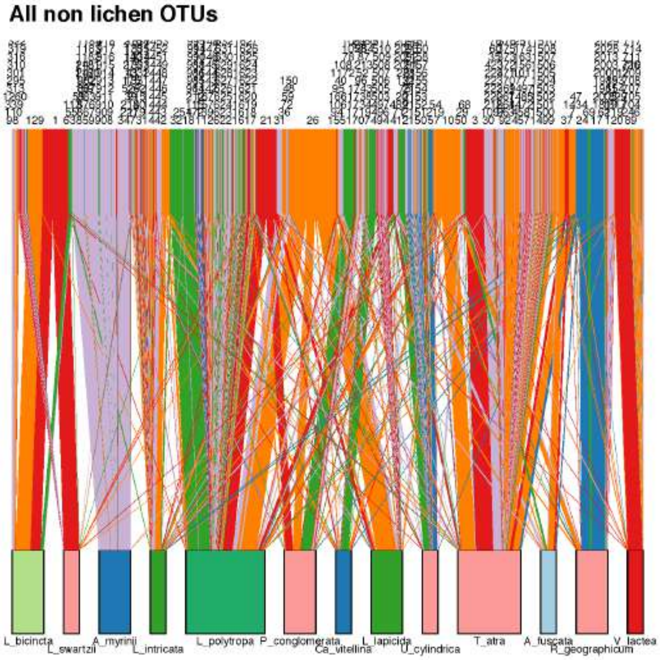
Supplementary Figure 33. Bipartite network at sample level using only those OTUs identified as Chaetothyriales found above a sample specific threshold.



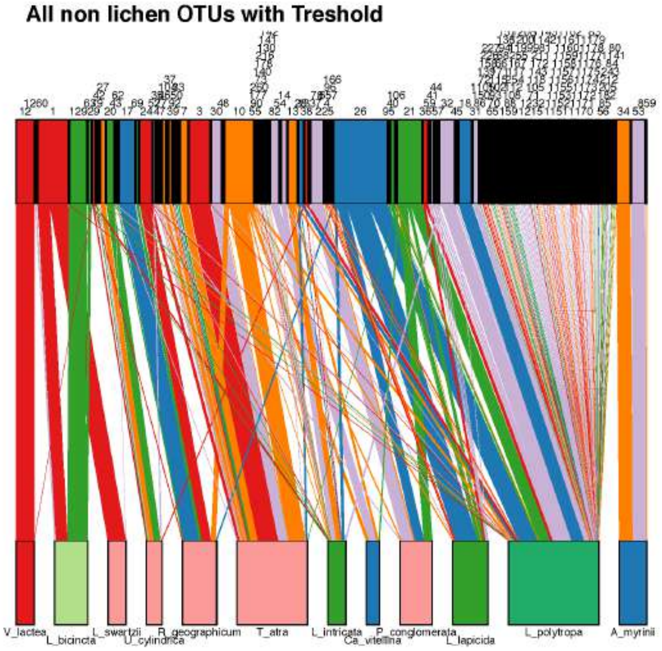
Supplementary Figure 34. Matrix representation showing nestedness and compartmentalization of the bipartite network at sample level using all OTUs identified as Chaetothyriales.



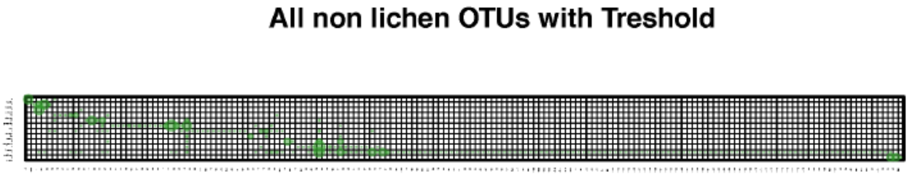
Supplementary Figure 35. Matrix representation showing nestedness and compartmentalization of the bipartite network at species level using only those OTUs identified as Chaetothyriales sequence above a sample specific threshold.



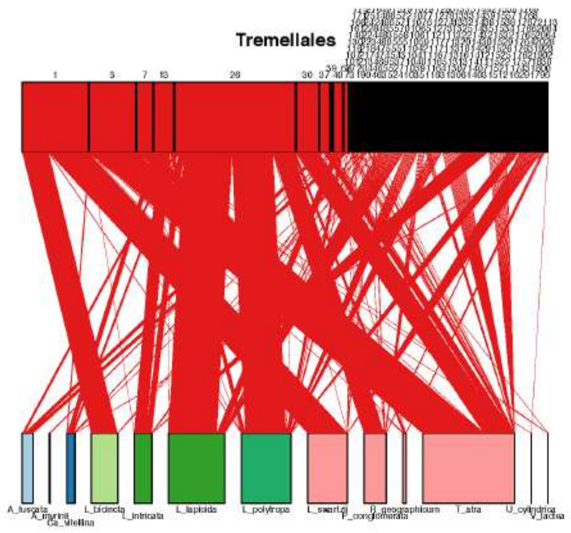
Supplementary Figure 36. Bipartite network at species level including all non-lichen OTUs.



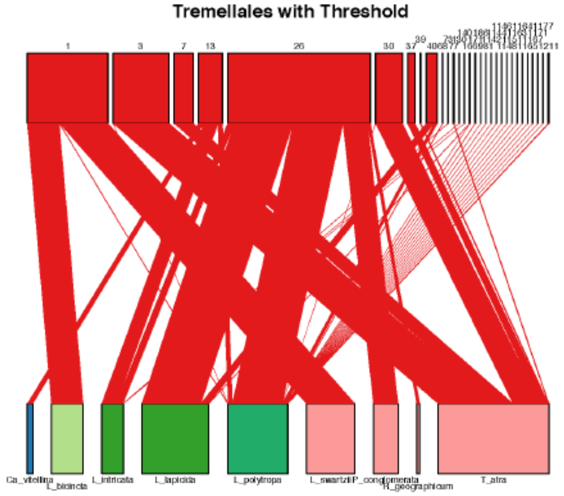
Supplementary Figure 37. Bipartite network at species level of non-lichen OTUs above a sample specific threshold.



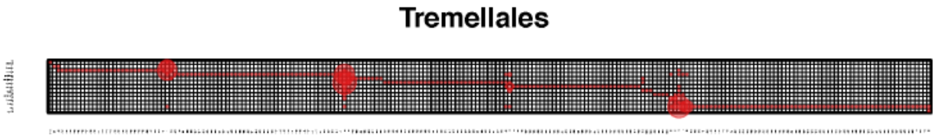
Supplementary Figure 38. Matrix representation showing nestedness and compartmentalization of the bipartite network at species level of non-lichen OTUs above a sample specific threshold.



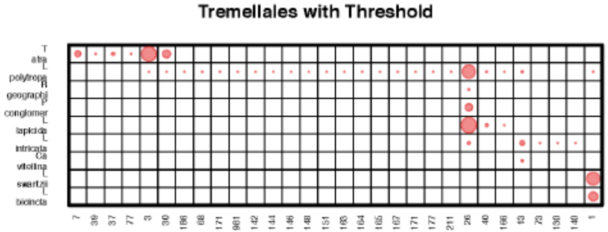
Supplementary Figure 39. Bipartite network at species level using only OTUs identified as Tremellales.



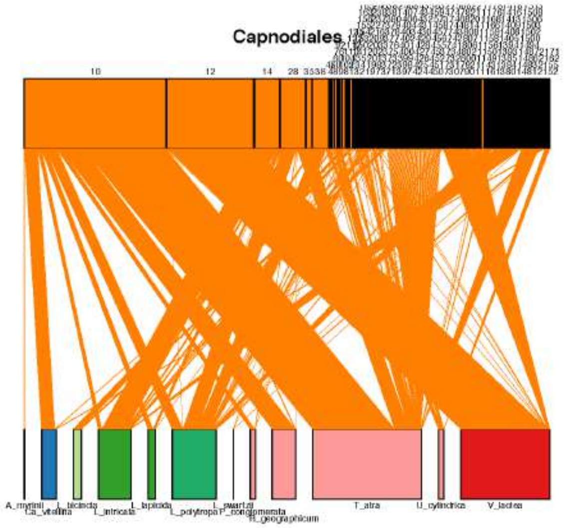
Supplementary Figure 40. Bipartite network at species level using only those OTUs identified as Tremellales found above a sample specific threshold.



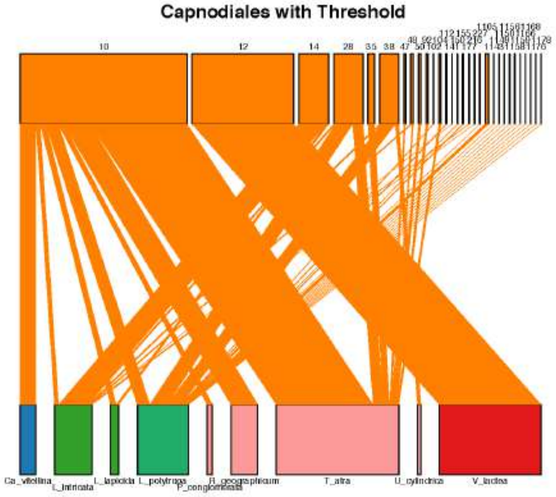
Supplementary Figure 41. Matrix representation showing nestedness and compartmentalization of the bipartite network at species level using all OTUs identified as Tremellales.



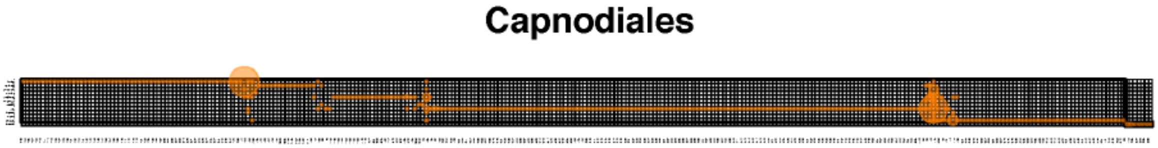
Supplementary Figure 42. Matrix representation showing nestedness and compartmentalization of the bipartite network at species level using only those OTUs identified as Tremellales sequence above a sample specific threshold.



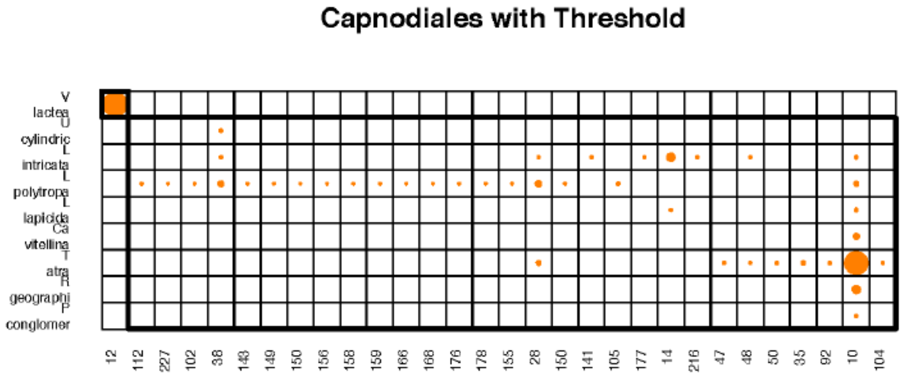
Supplementary Figure 43. Bipartite network at species level using only OTUs identified as Capnodiales.



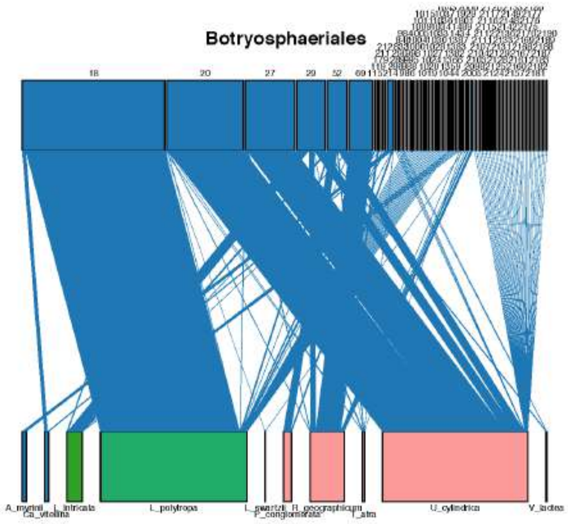
Supplementary Figure 44. Bipartite network at species level using only those OTUs identified as Capnodiales found above a sample specific threshold.



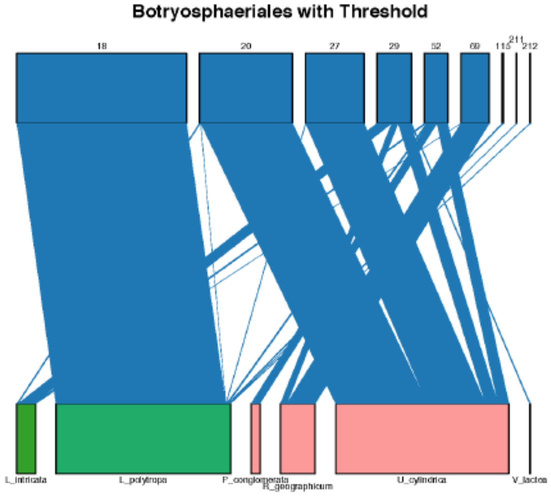
Supplementary Figure 45. Matrix representation showing nestedness and compartmentalization of the bipartite network at species level using all OTUs identified as Capnodiales.



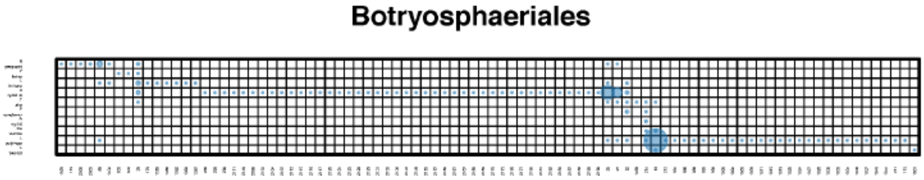
Supplementary Figure 46. Matrix representation showing nestedness and compartmentalization of the bipartite network at species level using only those OTUs identified as Capnodiales sequence above a sample specific threshold.



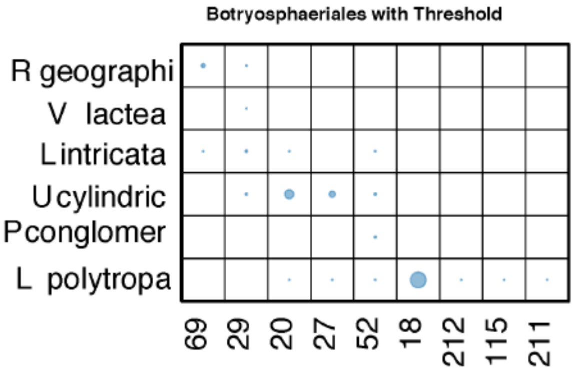
Supplementary Figure 47. Bipartite network at species level using only OTUs identified as Botryosphaeriales.



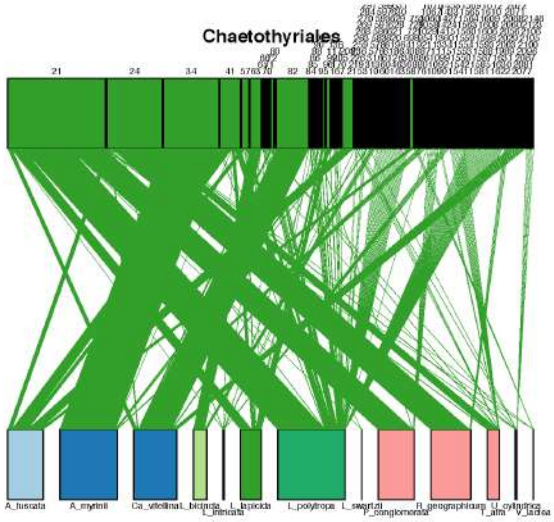
Supplementary Figure 48. Bipartite network at species level using only those OTUs identified as Botryosphaeriales found above a sample specific threshold.



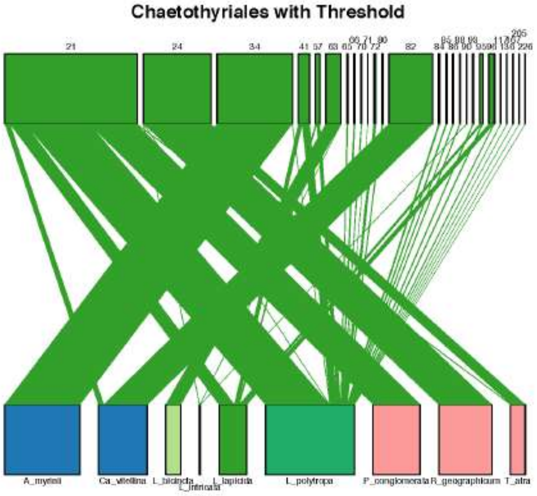
Supplementary Figure 49. Matrix representation showing nestedness and compartmentalization of the bipartite network at species level using all OTUs identified as Botryosphaeriales.



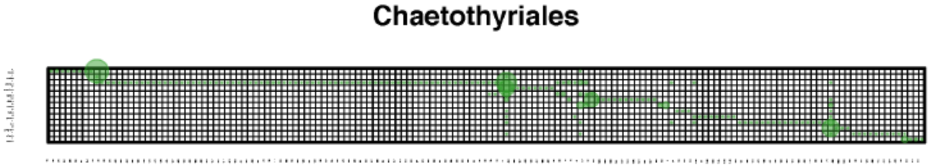
Supplementary Figure 50. Matrix representation showing nestedness and compartmentalization of the bipartite network at species level using only those OTUs identified as Botryosphaeriales sequence above a sample specific threshold.



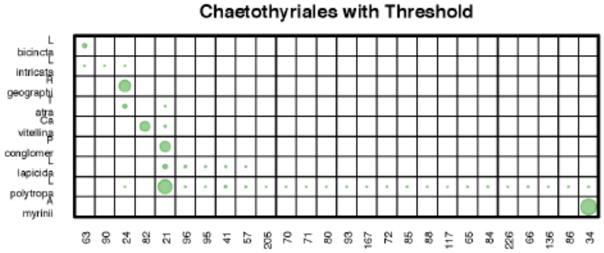
Supplementary Figure 51. Bipartite network at species level using only OTUs identified as Chaetothyriales.



Supplementary Figure 52. Bipartite network at species level using only those OTUs identified as Chaetothyriales found above a sample specific threshold.



Supplementary Figure 53. Matrix representation showing nestedness and compartmentalization of the bipartite network at species level using all OTUs identified as Chaetothyriales.



Supplementary Figure 54. Matrix representation showing nestedness and compartmentalization of the bipartite network at species level using only those OTUs identified as Chaetothyriales sequence above a sample specific threshold.

Supplementary Figure 55. The following pages contain the output of the quality assessment of the raw data obtained using FastQC.

FastQC Report

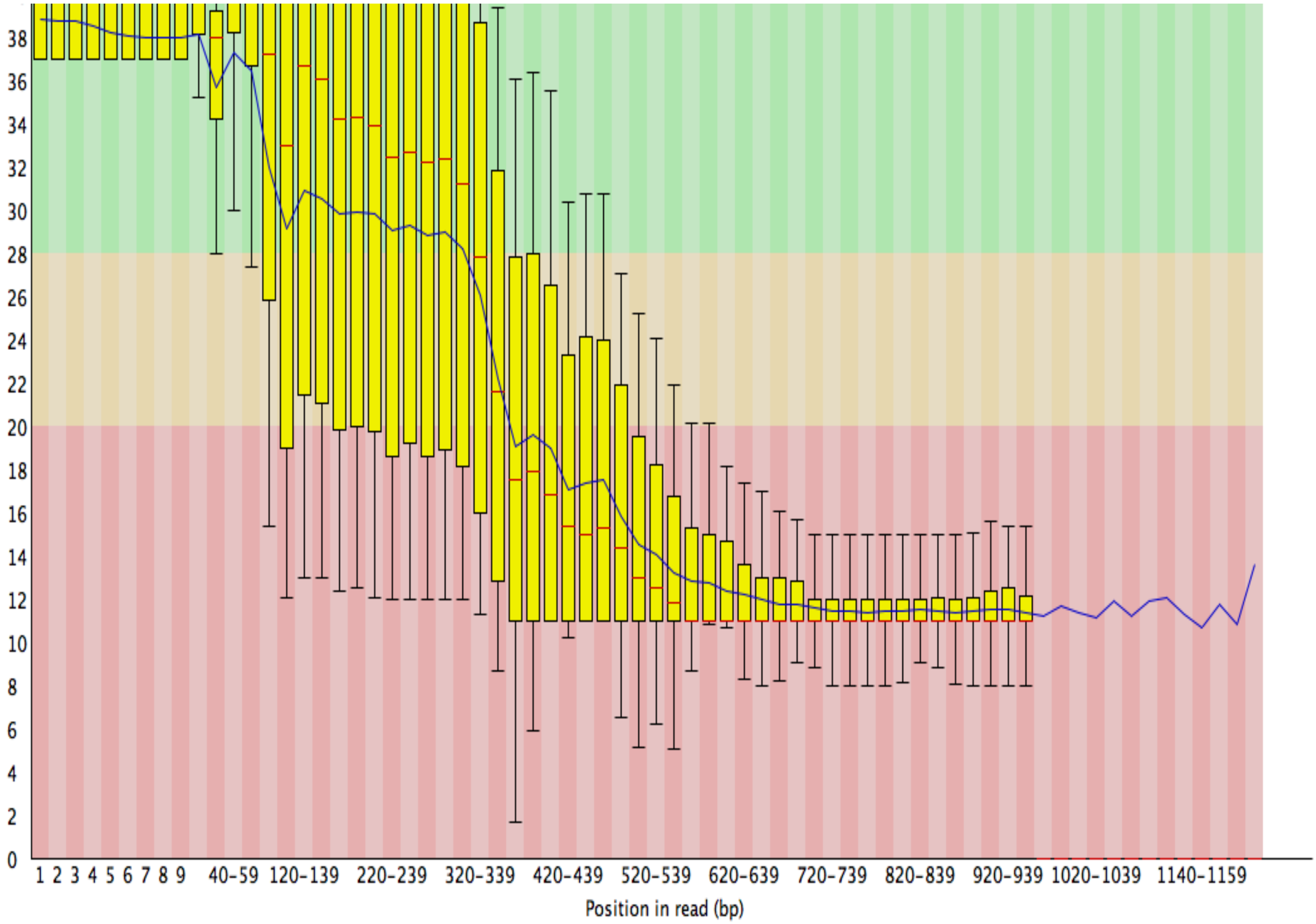
Summary

- ✓ Basic Statistics
- ✗ Per base sequence quality
- ✓ Per sequence quality scores
- ✗ Per base sequence content
- ⚠ Per sequence GC content
- ⚠ Per base N content
- ⚠ Sequence Length Distribution
- ✗ Sequence Duplication Levels
- ✗ Overrepresented sequences
- ✓ Adapter Content
- ⚠ Kmer Content

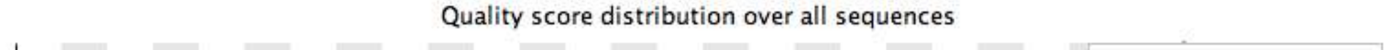
✓ Basic Statistics

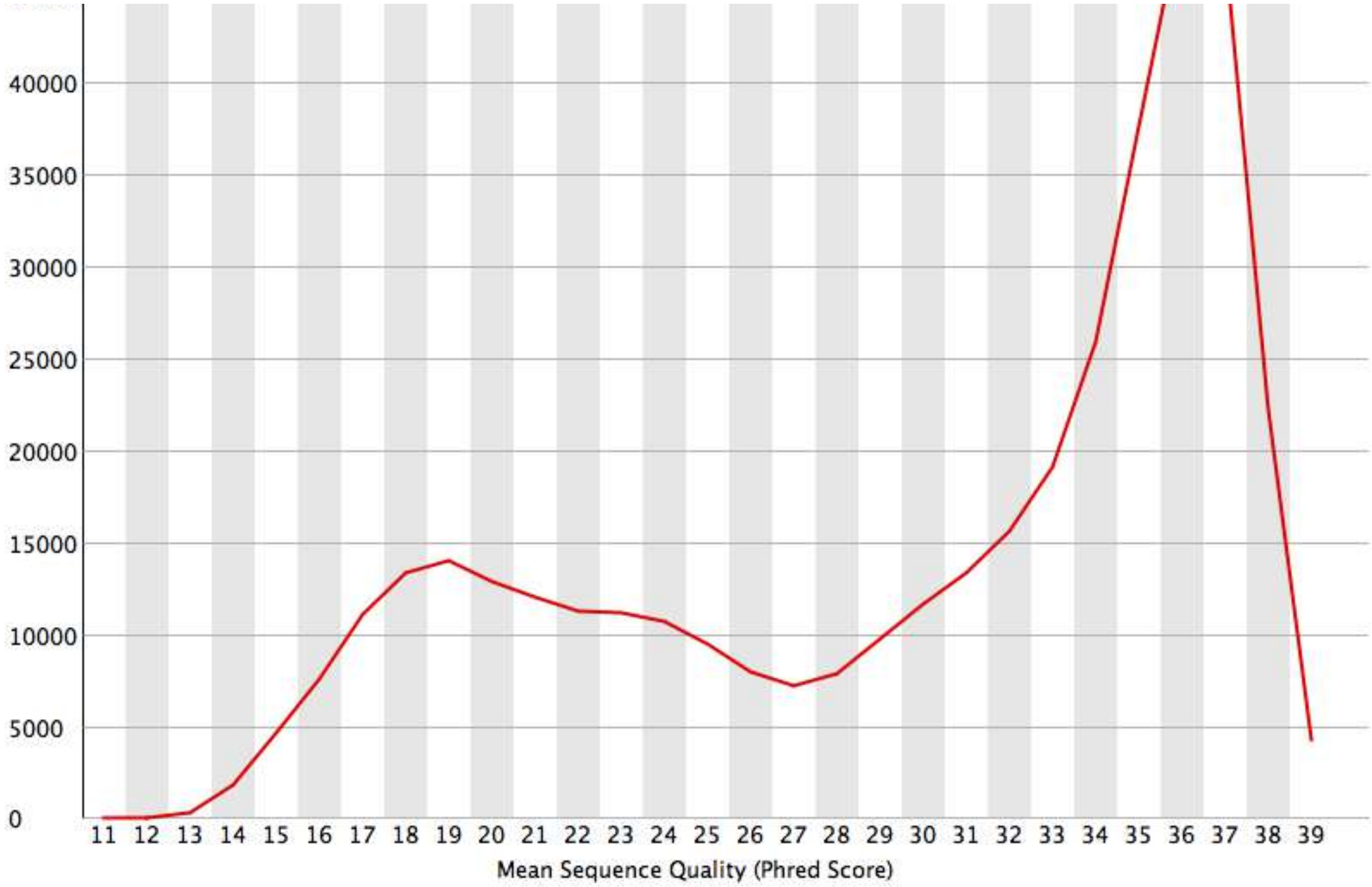
Measure	Value
Filename	merged.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	399593
Sequences flagged as poor quality	0
Sequence length	60-1200
%GC	52

✗ Per base sequence quality

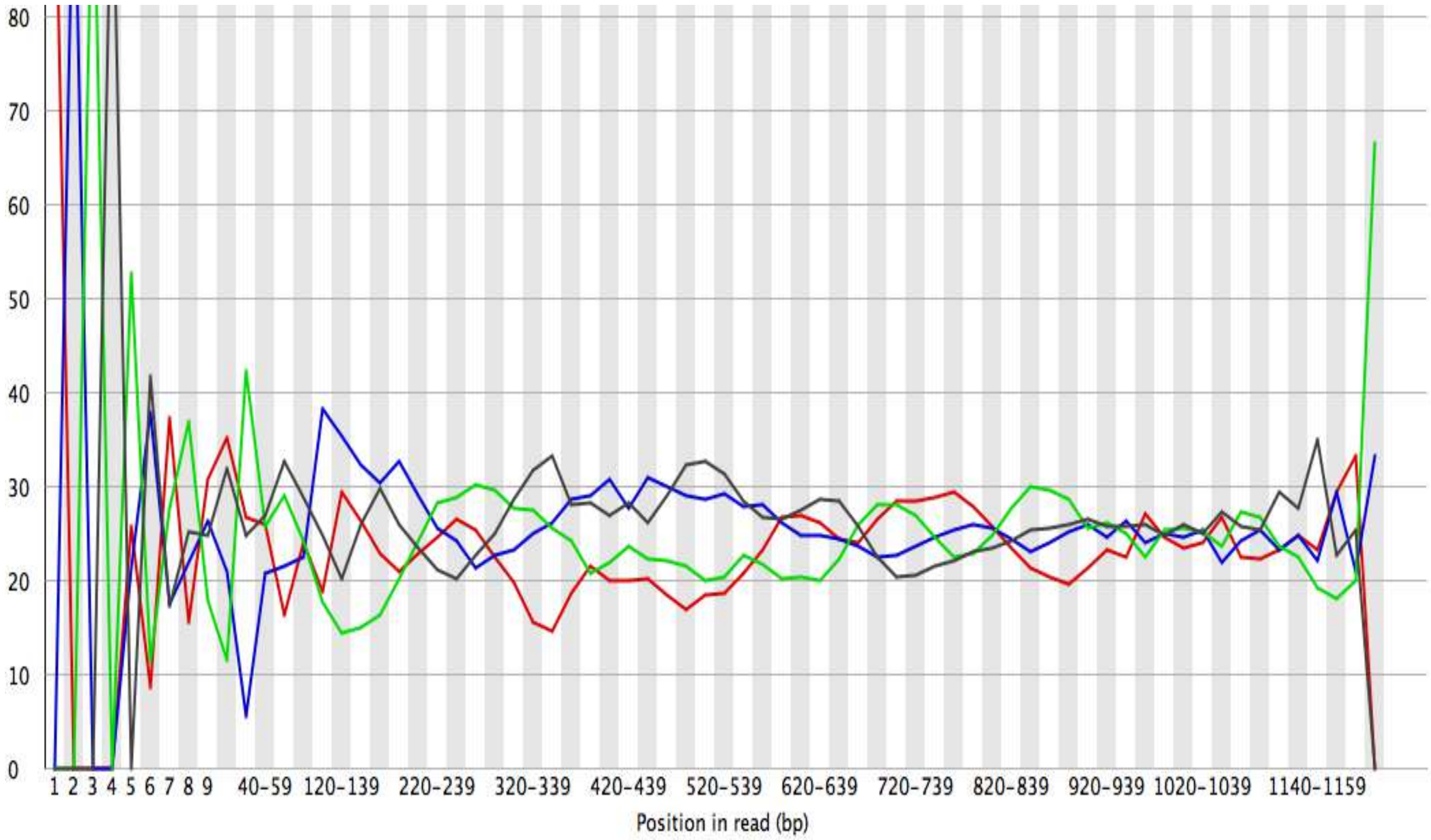


✓ Per sequence quality scores

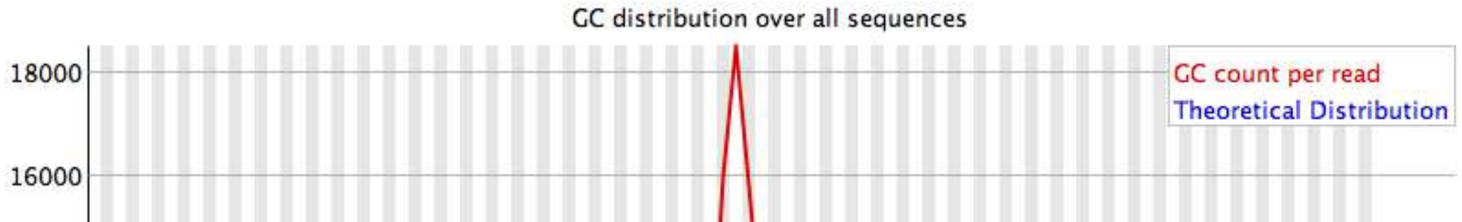


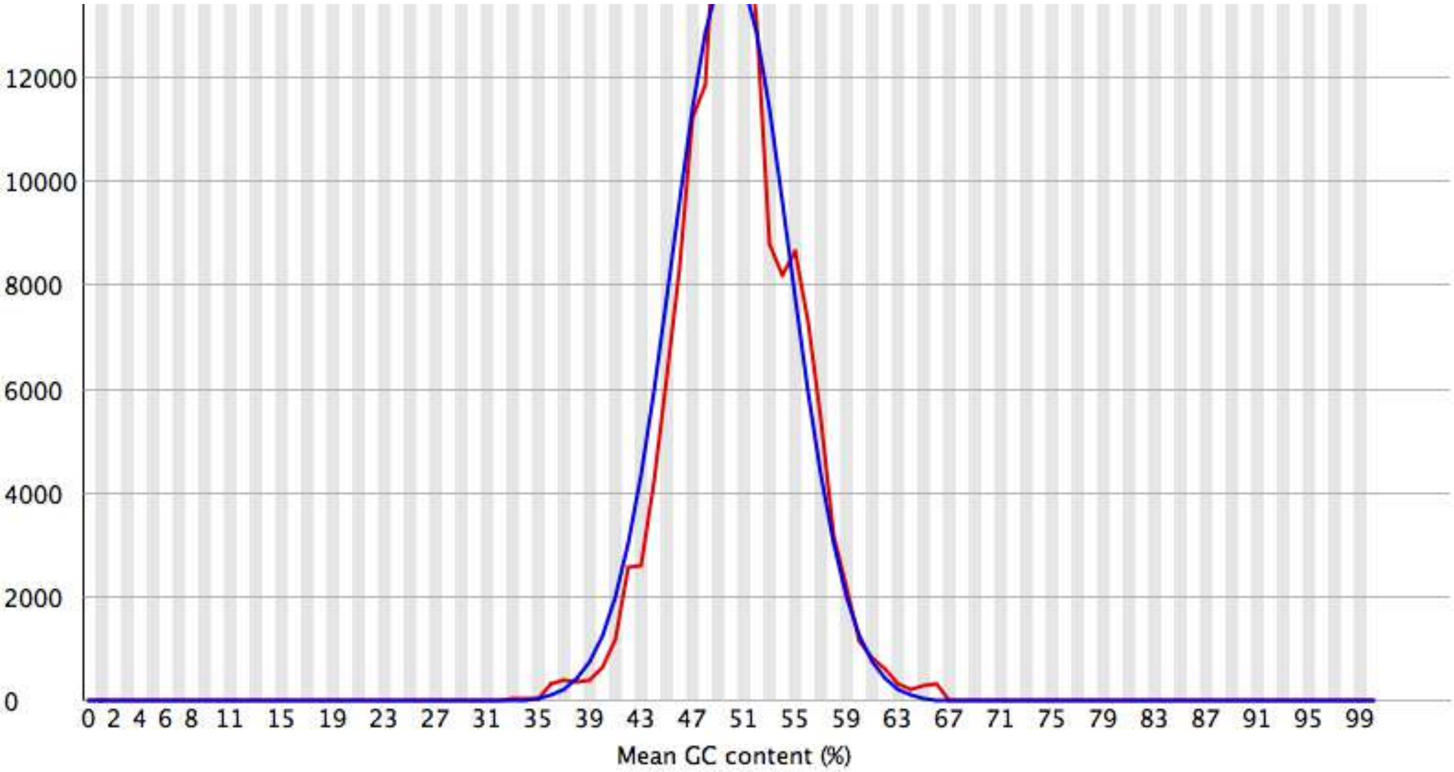


✖ Per base sequence content

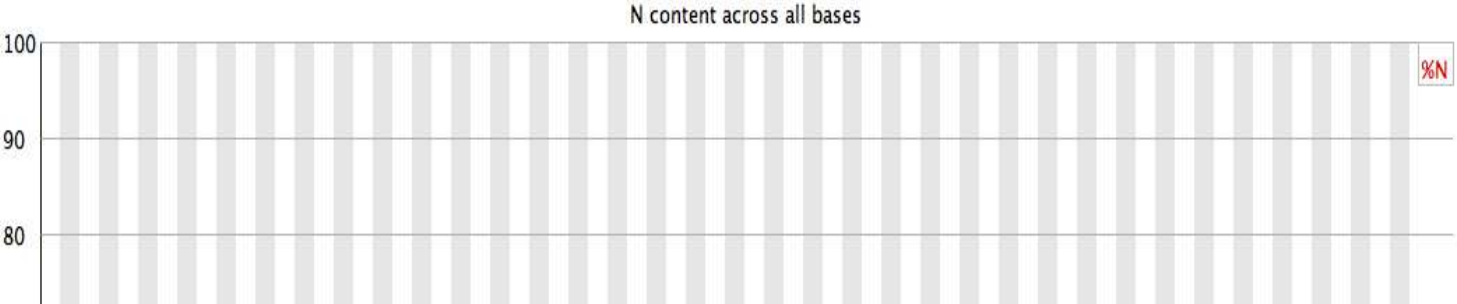


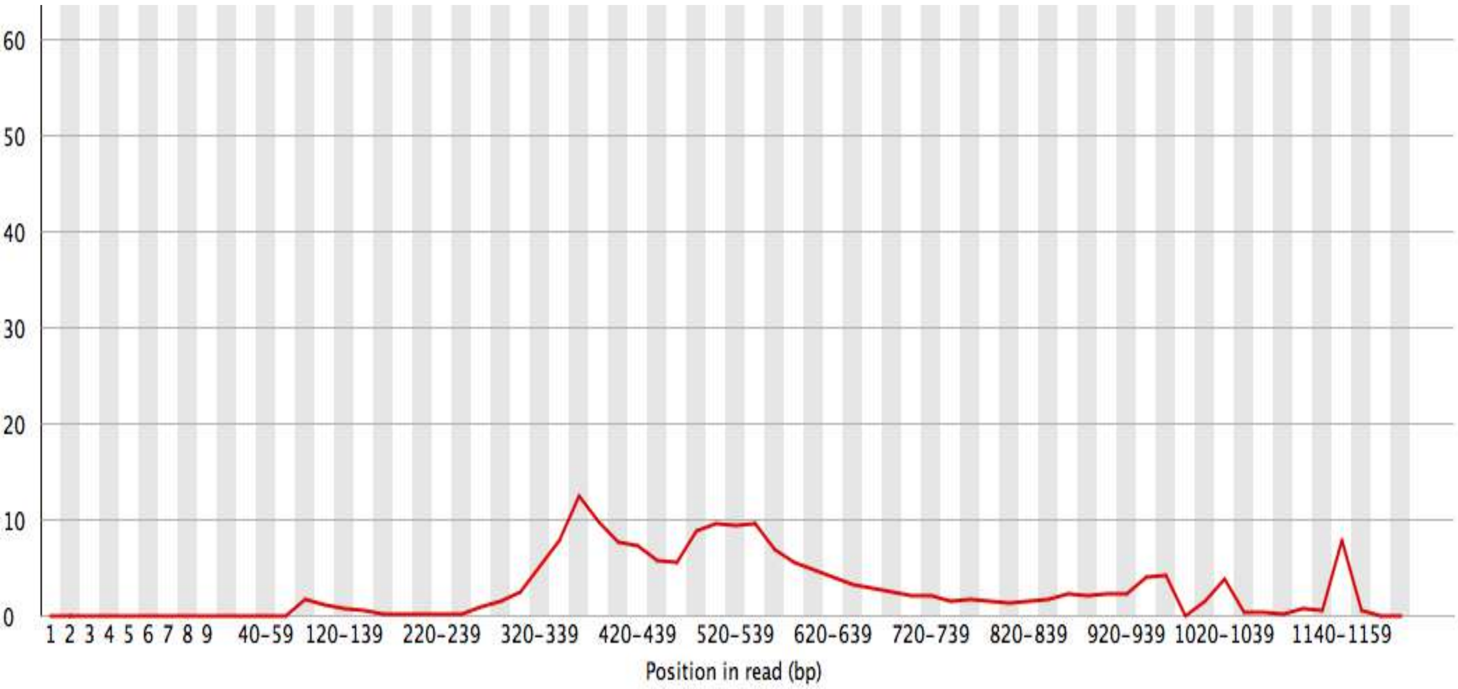
Per sequence GC content



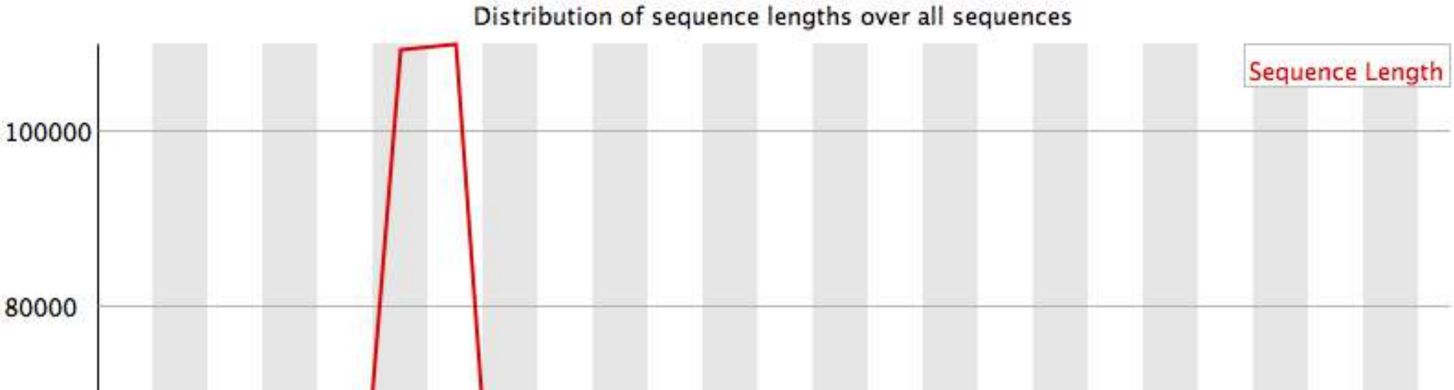


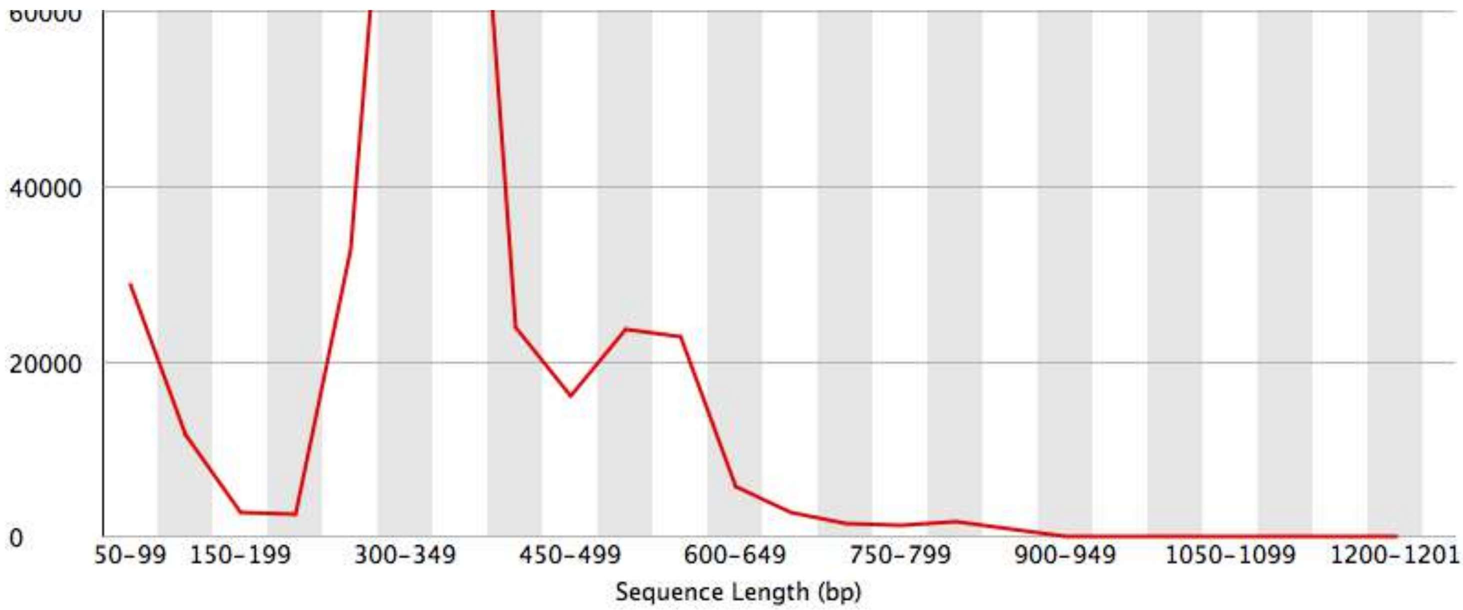
Per base N content



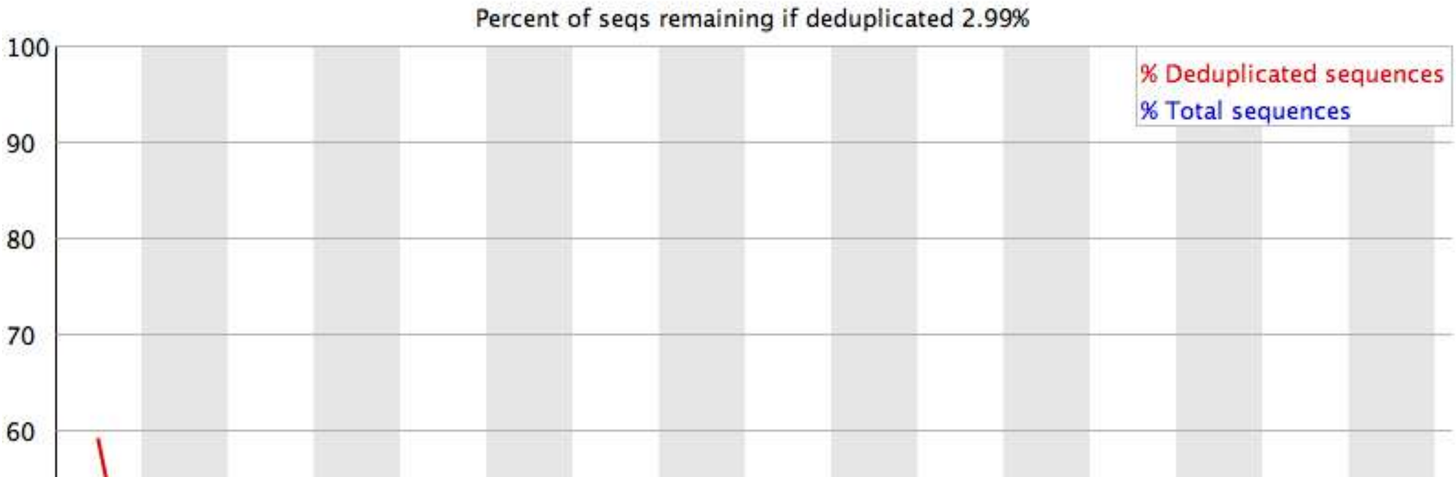


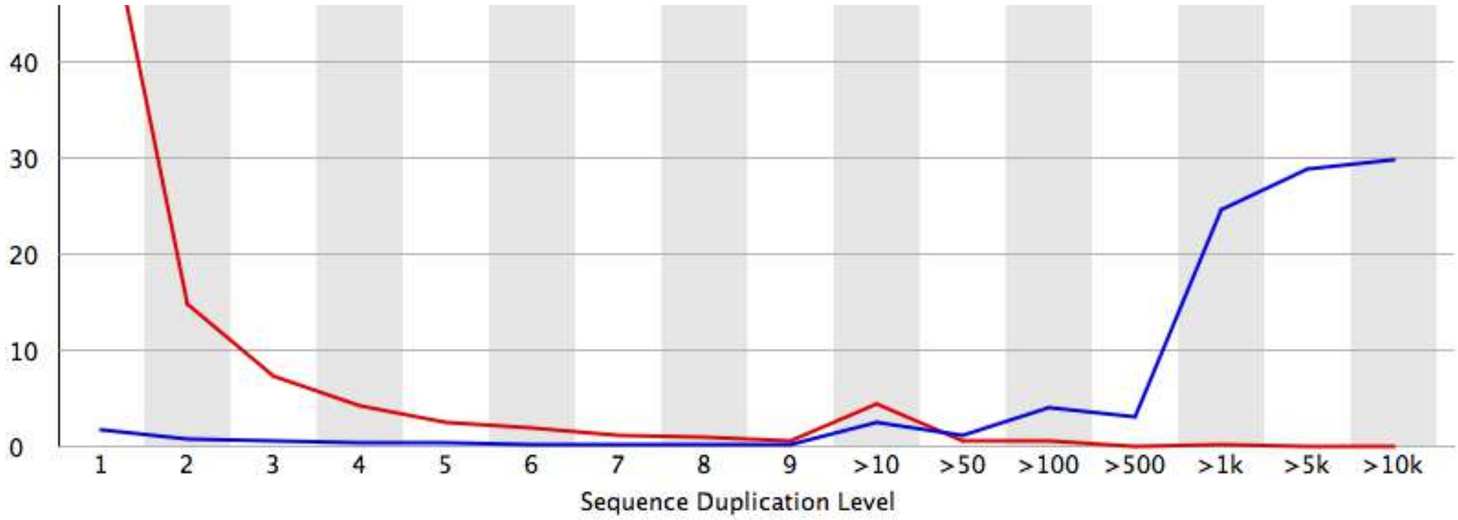
Sequence Length Distribution





Sequence Duplication Levels





Overrepresented sequences

Sequence	Count	Percentage	Possible Source
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TCAGAGACTATACTCTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGG	17043	4.265089728799053	No Hit
TCAGTGATACGTCTCTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGG	16360	4.094165813715456	No Hit
TCAGACTGTACAGTCTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGG	15458	3.8684361337661075	No Hit
TCAGACGAGTGCGTCTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGG	11356	2.8418916247281607	No Hit
TCAGAGCGTCGTCTCTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGG	10826	2.709256668660362	No Hit
TCAGCGTAGACTAGCTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGG	10479	2.6224183106310672	No Hit
TCAGTCTCTATGCGCTTGGTCATTTAGAGGAAGTAAAGTCGTAACAAGGT	10473	2.620916782826526	No Hit
TCAGCGAGAGATACCTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGG	10331	2.5853806247857194	No Hit
TCAGCATAGTAGTGCTTGGTCATTTAGAGGAAGTAAAGTCGTAACAAGGT	9202	2.3028431428978986	No Hit
TCAGATATCGCGAGCTTGGTCATTTAGAGGAAGTAAAGTCGTAACAAGGT	8945	2.2385277019367207	No Hit
TCAGACATACGCGTCTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGG	7974	1.9955304522351491	No Hit
TCAGCGTAGACTAGCTTGGTCATTTAGAGGAAGTAAGCATCGATGAAGAA	7653	1.9151987146921994	No Hit
TCAGACTGTACAGTCTTGGTCATTTAGAGGAAGTAAAGTCGTAACAAGGT	7425	1.8581406581196367	No Hit
TCAGCTCGCGTGTCCTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGG	7234	1.810342023008411	No Hit
TCAGAGACTATACTCTTGGTCATTTAGAGGAAGTAAAGTCGTAACAAGGT	7224	1.8078394766675092	No Hit
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TCAGCGTGTCTCTACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGG	5599	1.4011756962709556	No Hit
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TCAGAGCACTGTAGCTTGGTCATTTAGAGGAAGTAAAGTCGTAACAAGGT	5285	1.3225957411666371	No Hit

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TCAGCGTCTAGTACCTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGG	4515	1.1298996729171933	No Hit
TCAGTACTCTCGTGCTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGG	4325	1.0823512924400578	No Hit
TCAGAGTACGCTATCTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGG	4275	1.0698385607355485	No Hit
TCAGTCTCTATGCGCTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGG	4273	1.069338051467368	No Hit
TCAGTAGAGACGAGCTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGG	4213	1.0543227734219567	No Hit
TCAGATACGACGTACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGG	4179	1.0458141158628904	No Hit
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TCAGTGTACTACTCCTTGGTCATTTAGAGGAAGTAAGCATCGATGAAGAA	1917	0.479738133550888	No Hit
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TCAGTACGAGTATGCTTGGTCATTTAGAGGAAGTAAAGTCGTAACAAGGT	1530	0.38288959015798574	No Hit
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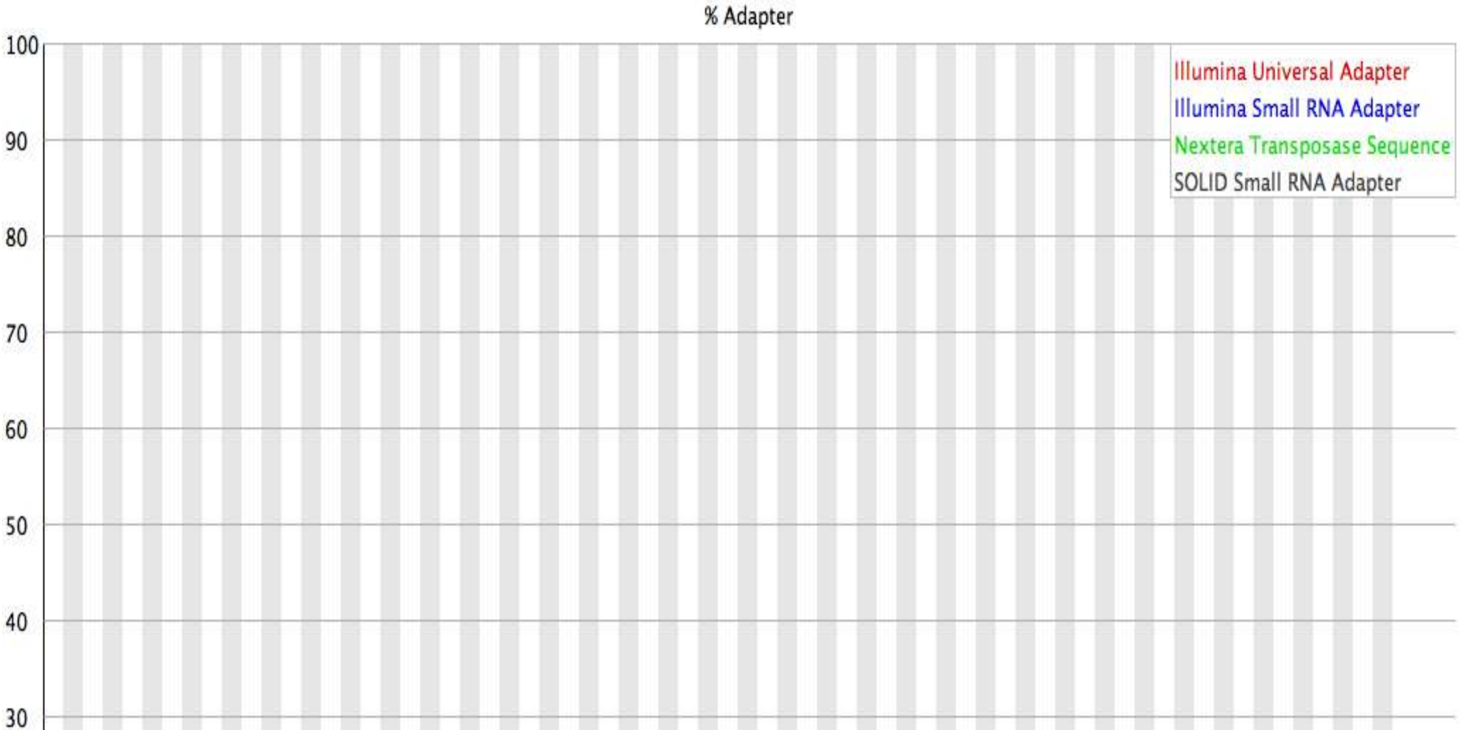
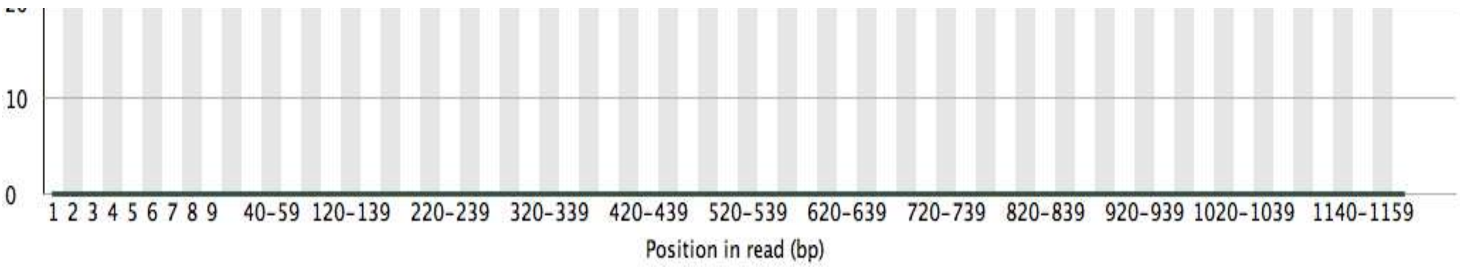
✓ Adapter Content





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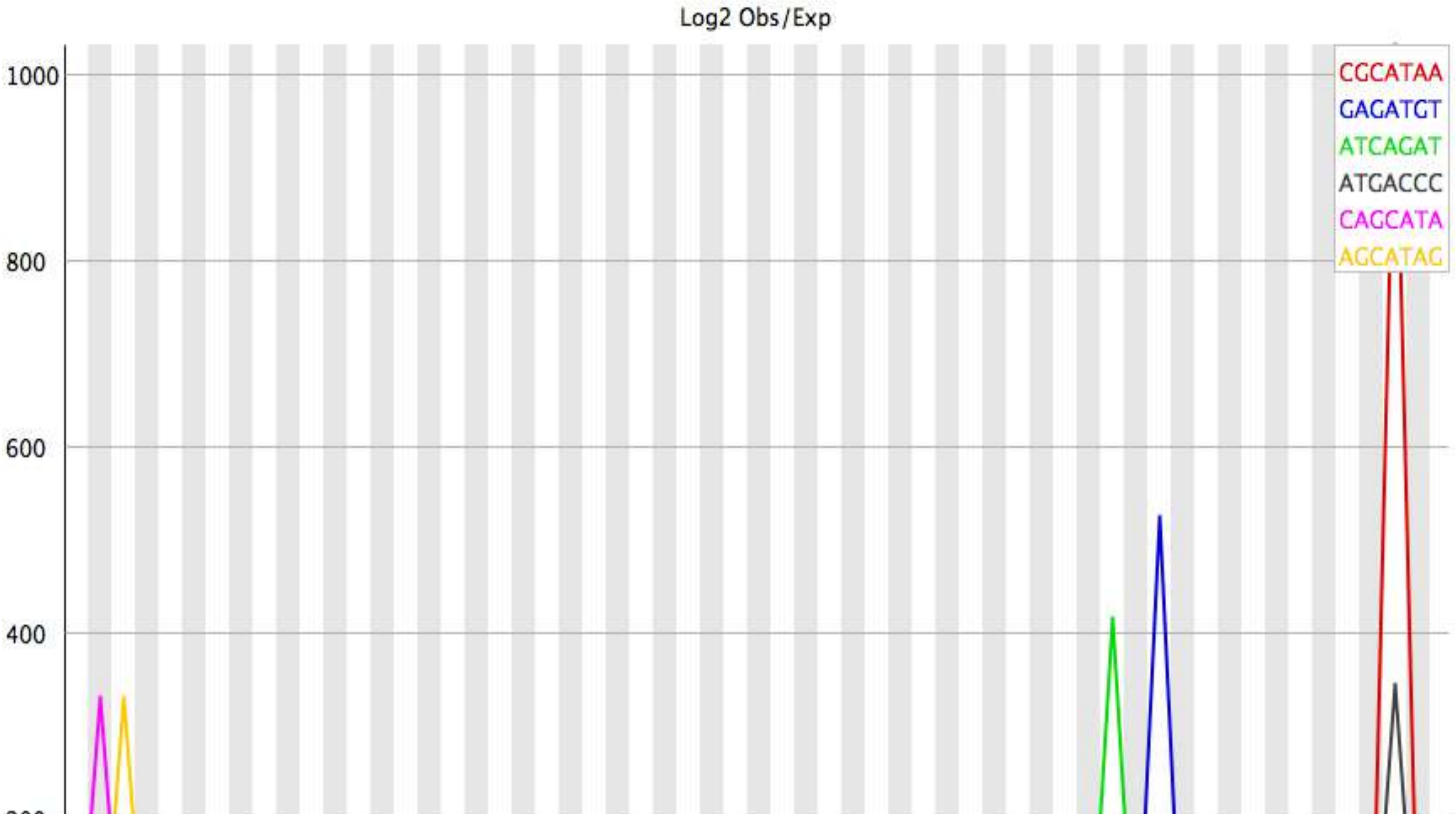

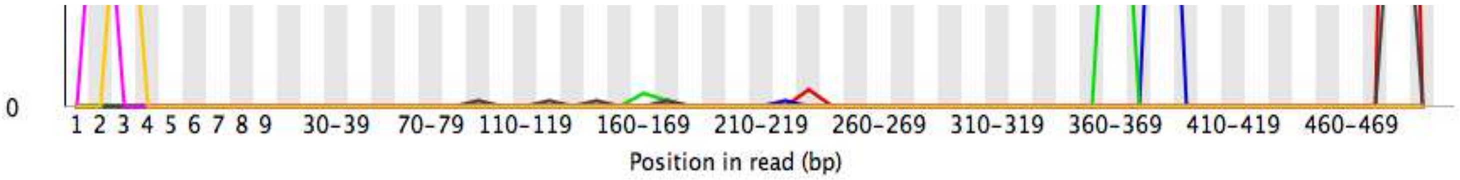

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
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GAGATGT	25	3.5106495E-9	523.90875	380-389
ATCAGAT	25	3.0247826E-4	415.7794	360-369
ATGACCC	30	5.334286E-4	344.05515	480-489
CAGCATA	1235	0.0	330.6081	2
AGCATAG	1235	0.0	330.6081	3
TATGCGC	1720	0.0	328.42105	9
GCGTAGA	2690	0.0	328.25	4
CAGCGTA	2720	0.0	327.68063	2
GATATCG	1105	0.0	327.44592	4
CAGATAC	700	0.0	327.20987	2
AGTATGC	1275	0.0	327.0725	9
AGATACC	1855	0.0	326.91098	9
GCATAGT	1250	0.0	326.6408	4
AGACTAT	2785	0.0	326.62924	5
CAGACGC	2315	0.0	326.2164	2
GAGTATG	1280	0.0	325.7949	8
TGATACG	2520	0.0	325.40643	5
AGACATA	1245	0.0	325.28635	3
CAGACAT	1245	0.0	325.28635	2

Produced by FastQC (version 0.11.4)