***New Phytologist* Supporting Information**

Article title: Extreme rainfall affects assembly of the root associated fungal community

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The following Supporting Information is available for this article:

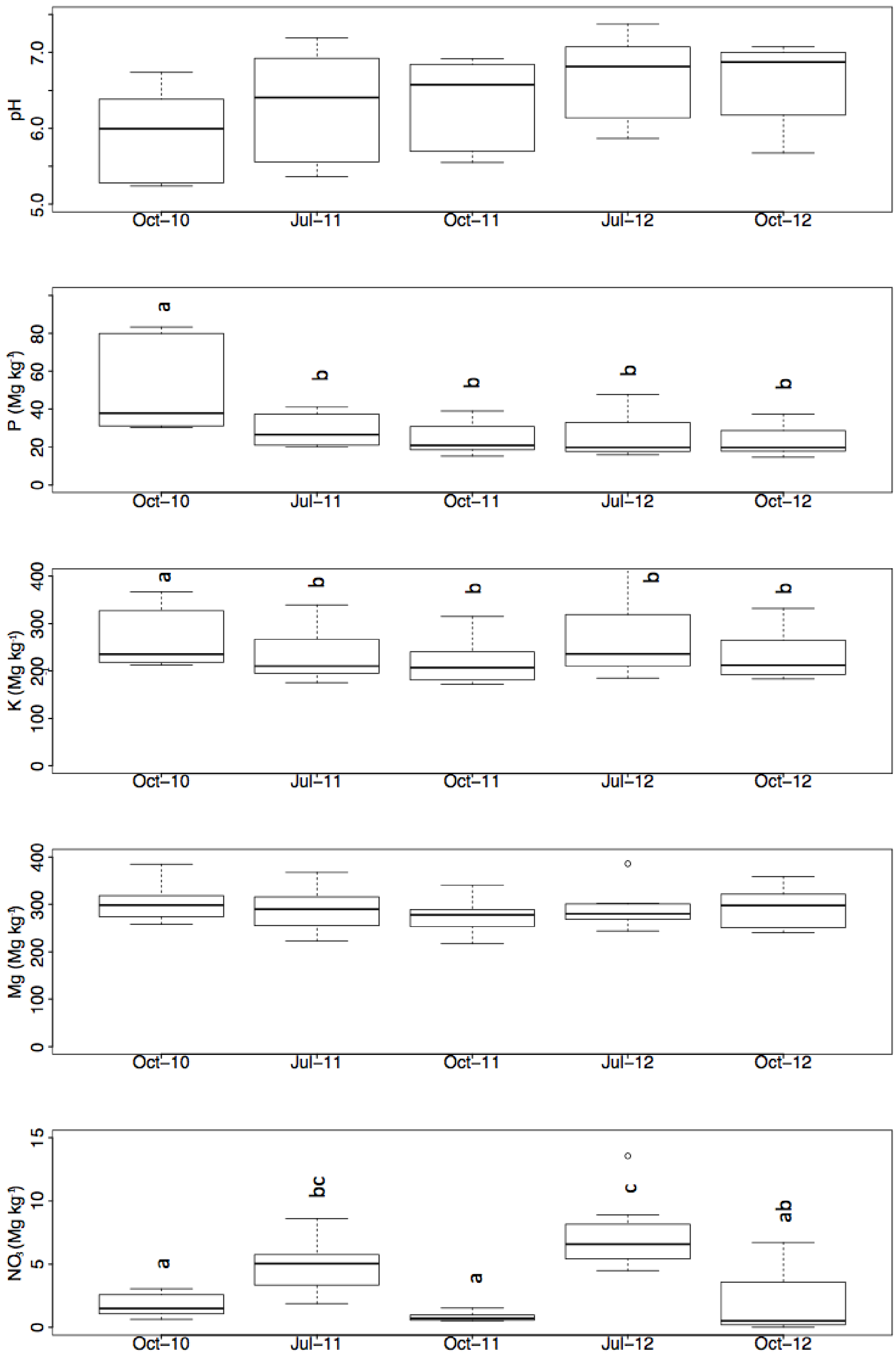

Fig. S1 Boxplots of nutrient content for each sampling time points (a) pH, (b) P (mg kg^{-1}), (c) K (mg kg^{-1}), (d) Mg (mg kg^{-1}) and (e) NO$_3$ kg^{-1} (mg kg^{-1}). Different lower-case letters indicate differences within temporal replicates using Tukey's HSD at α = 0.05.

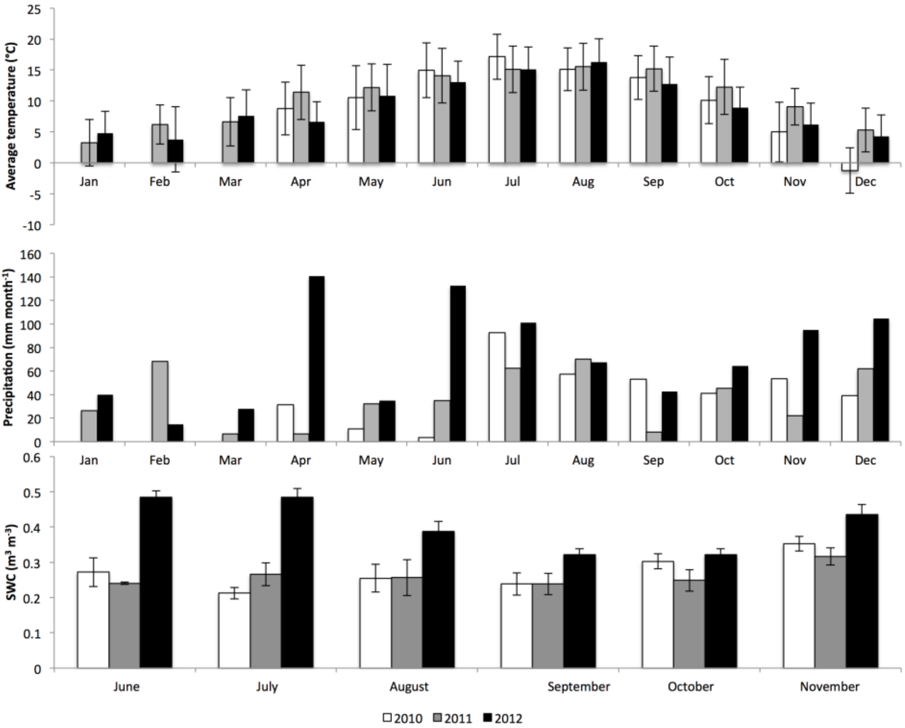

Fig. S2 Weather data from the willow site over the 3-year sampling period. a.) Monthly average temperature (˚C) b.) Monthly average rainfall (mm of precipitation month^{-1}) c.) soil water content (m^3 m^{-3}) that was only monitored between the June to November period of each year. Error bars represent ±1 standard deviation of the mean.

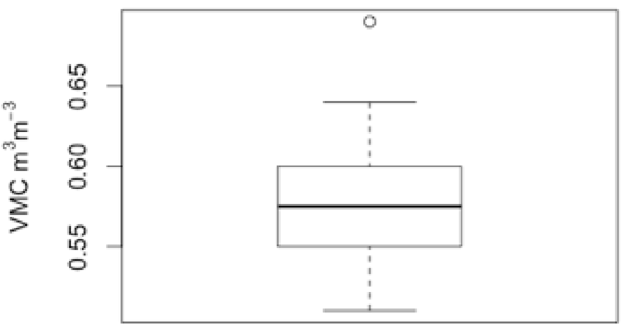

Fig. S3 Boxplot showing distribution of soil VMC which corresponded with full saturation.

Fig. S4 Evidence of surface water found within July 2012 that was not present in any other the other sampling events.

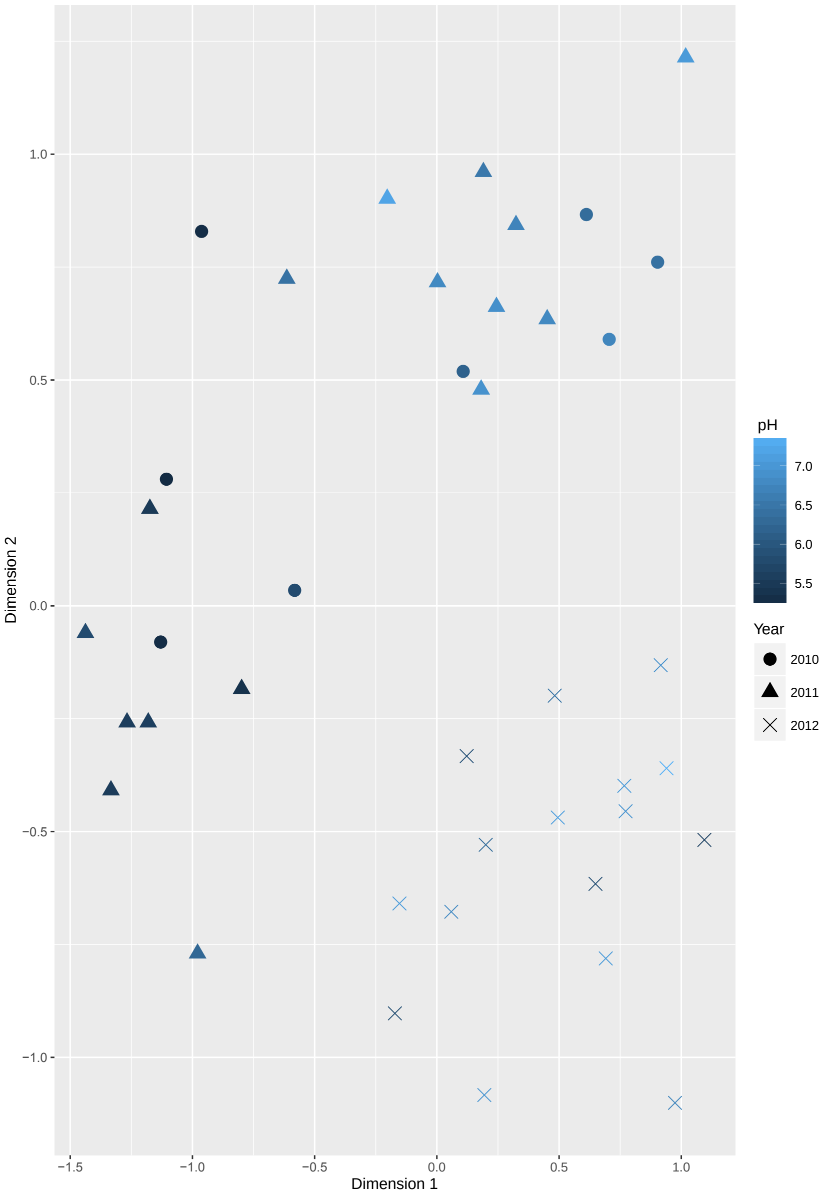

Fig. S5 Non-metric dimensional scaling showing clustering based on similarity of the root-associated fungal communities and pH shown by colour.

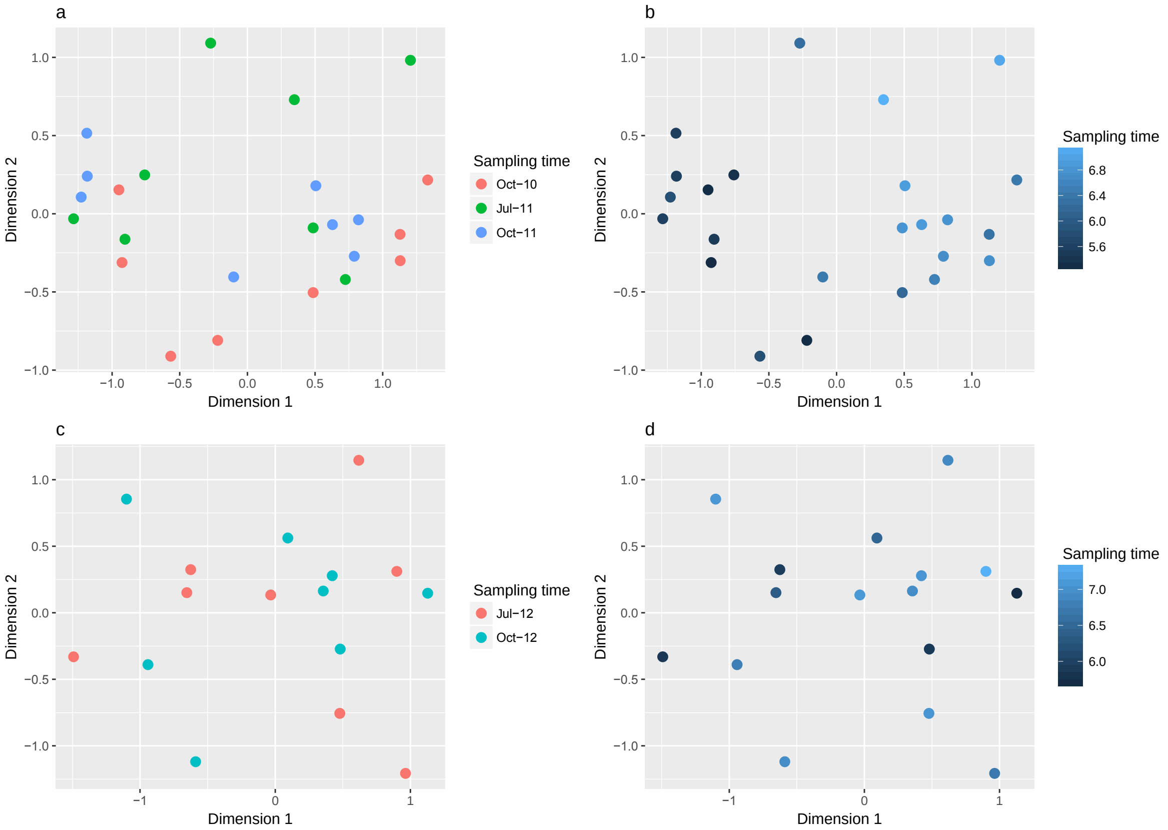

Fig. S6 Non-metric dimensional scaling showing clustering based on similarity of the root-associated fungal communities. (a) and (b) are the fungal communities of 2010 and, with colour representing sampling time (a) and pH (b). (c) and (d) are the fungal communities of 2012, with colour representing sampling time (a) and pH (b).

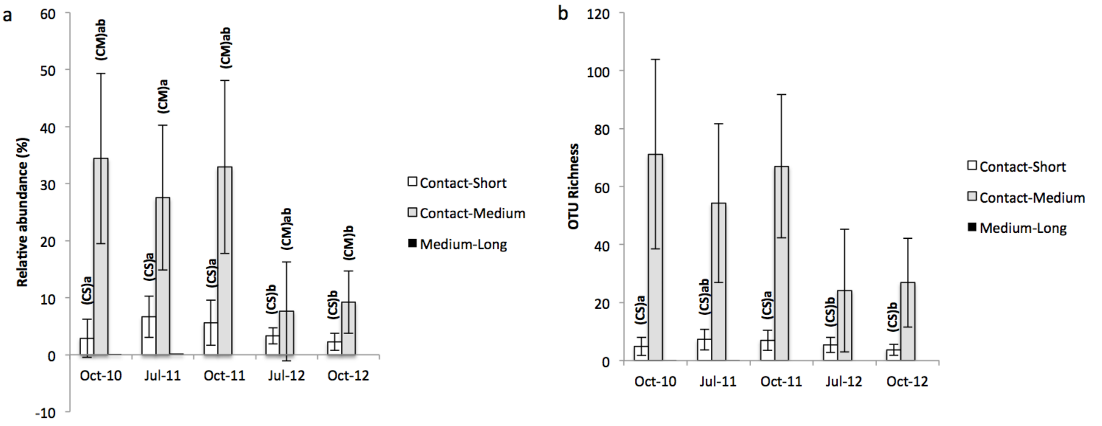

Fig. S7 Average (a) relative abundances and (b) OTU richness of the ECM fungi divided by exploration type. ECM were extracted from willow roots over the three year sampling period. Error bars represent ±1 standard deviation of the mean. Different letters in parentheses represent the exploration type and lower-case letters indicate differences within temporal replicates using Tukey's HSD at $\alpha = 0.05$.

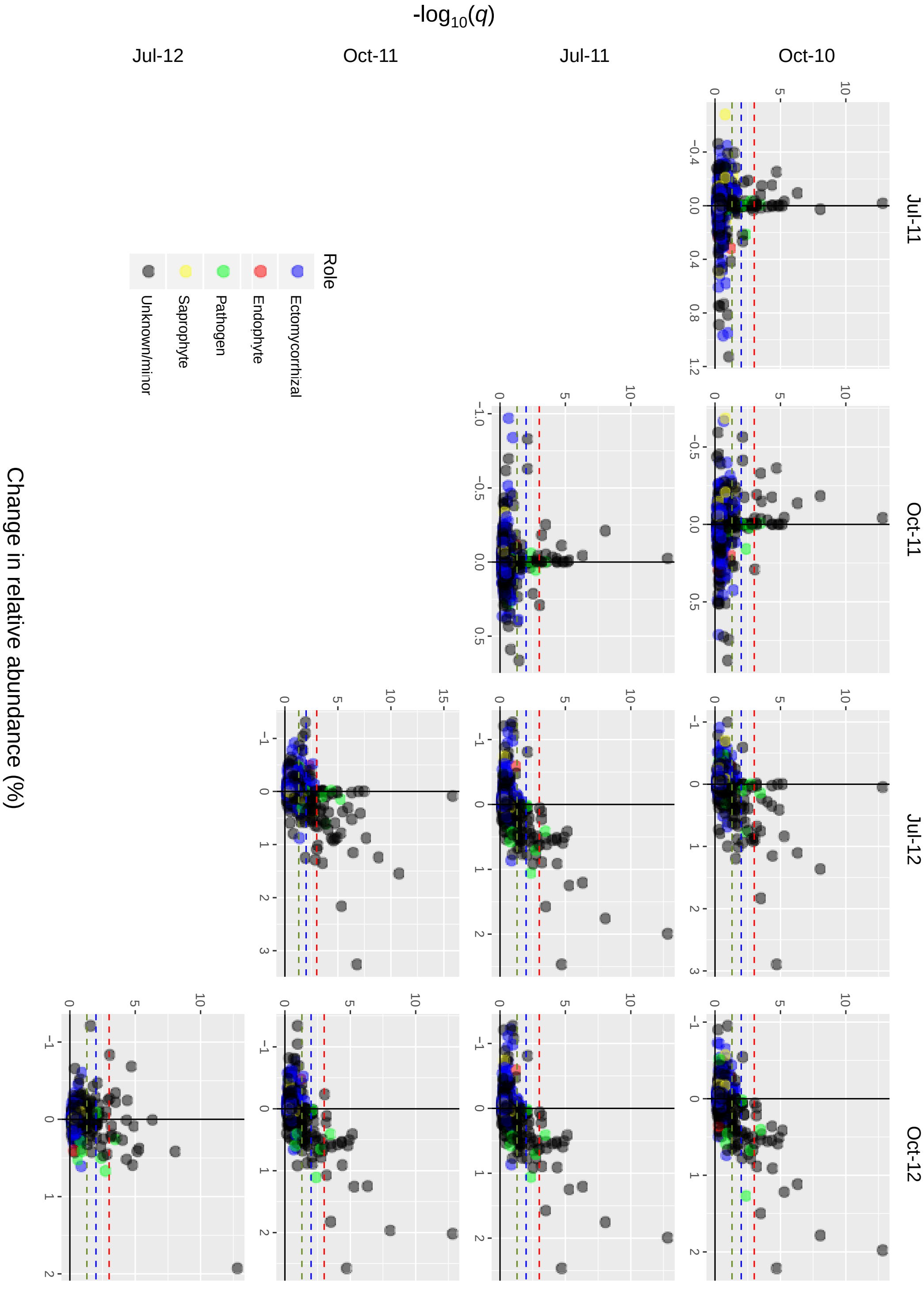

Fig. S8 Volcano plots of change in relative abundance of each OTU between seasons plotted against -log$_{10}$(q) values generated from repeated measure ANOVAs (using data from all sampling times) (Newbold *et al.*, 2017). Negative changes in abundance were considered positive during transformations, before reversion back to negative after the transformation. The dashed red, blue and dark green lines indicates significance at q>0.001, q>0.01 and q>0.05 respectively. For clarity, minor life strategies including soil yeasts and lichenized fungi were included within the unknown fungal group.

Table S2 Relative importance of season, geographical distance (between samples) and soil properties on the root-associated fungal communities of willow as revealed by PERMANOVA. Given the large shift in composition between the 2011 and 2012 communities, the pre-shift communities (October 2010, July 2011 and October 2012) and post-shift communities (July 2012 and October 2012) were analysed in separate analyses.

2010 and 2011 samples

Parameter	Degrees of freedom	*F*-value	R^2	*P*-value
pH	1	6.260	0.216	0.001
Season	1	1.342	0.046	0.174
Distance	1	1.283	0.044	0.203
NO_3	1	0.992	0.034	0.391
Mg	1	0.994	0.034	0.375
K	1	1.076	0.037	0.304
P	1	1.064	0.037	0.313
Residuals	16	0.552		
Total	23			

2012 samples

Parameter	Degrees of freedom	*F*-value	R^2	*P*-value
pH	1	0.862	0.060	0.674
Season	1	1.300	0.090	0.116
Distance	1	0.867	0.060	0.688
NO_3	1	0.933	0.065	0.547
Mg	1	0.782	0.054	0.820
K	1	0.791	0.055	0.800
P	1	0.910	0.063	0.574
Residuals	8	0.554		
Total	15			

Table S3 Average relative abundance and OTU richness of ECM families within SRC willow root-associated fungal communities sampled over the three year period.

Family	Family	Oct-10		Jul-11		Oct-11		Jul-12		Oct-12	
		Rel. Ab. (%)	OTU Rich.	Rel. Ab. (%)	OTU Rich.	Rel. Ab. (%)	OTU Rich.	Rel. Ab. (%)	OTU Rich.	Rel. Ab. (%)	OTU Rich.
Ascomycota	Helvellaceae	0.28	0.50	0.23	0.38	0.18	0.50	0.25	0.50	0.21	0.75
	Pyronemataceae	0.15	0.38	1.14	0.75	0.35	0.63	0.01	0.13	0.11	0.38
	Tuberaceae	1.21	3.13	2.12	2.25	1.45	2.50	0.06	0.50	0.10	0.50
Basidiomycota	Bolbitiaceae	1.34	3.50	2.58	3.50	3.12	4.75	0.86	1.88	0.59	1.75
	Cortinariaceae	34.82	72.50	28.49	55.38	33.78	68.75	9.27	26.50	10.25	28.50
	Hymenogasteraceae	0.00	0.00	0.08	0.25	0.13	0.13	0.00	0.00	0.02	0.25
	Paxillaceae	0.16	0.13	0.24	0.13	0.00	0.00	0.00	0.00	0.00	0.00
	Russulaceae	1.80	2.00	4.15	4.75	3.59	3.88	1.02	1.88	0.82	1.38
	Sebacinales	4.37	4.13	5.13	3.50	3.85	3.13	3.80	3.00	3.88	3.25
	Thelephoraceae	0.08	0.38	0.02	0.13	0.14	0.63	0.00	0.00	0.00	0.00

References

Newbold LK, Burthe SJ, Oliver AE, Gweon HS, Barnes CJ, Daunt F, van der Gast. (2017). Helminth burden and ecological factors associated with alterations in wild host gastrointestinal microbiota. *ISME J* **11**: 663–675.