

Figure S1. General and detailed images of the soils sampled at (a, b) site 1, (c, d) site 2, (e, f) site 3 and (g, h) site 4 on Clearwater Mesa, James Ross Island, Antarctic Peninsula. Photos taken by Juan Lirio.

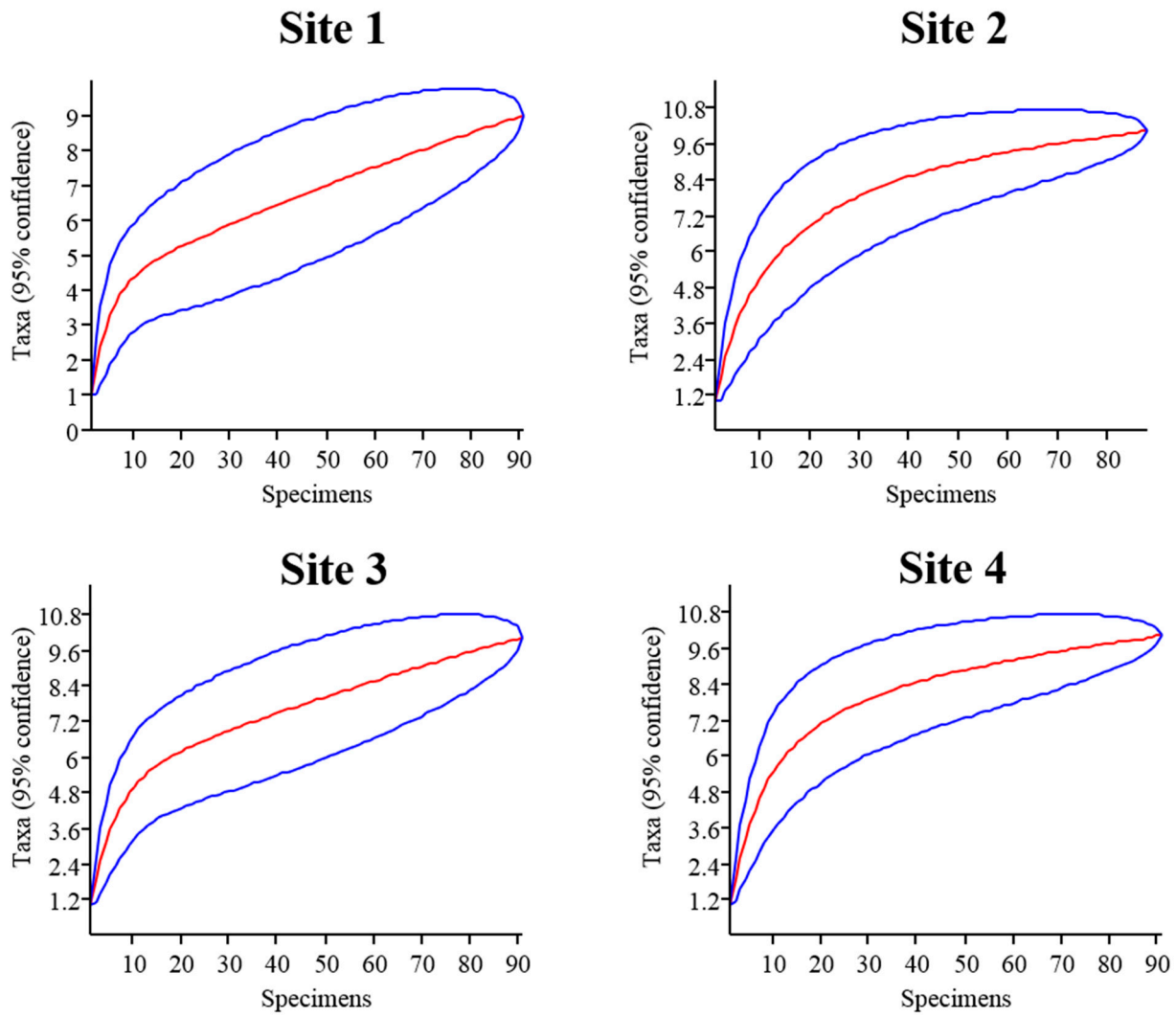
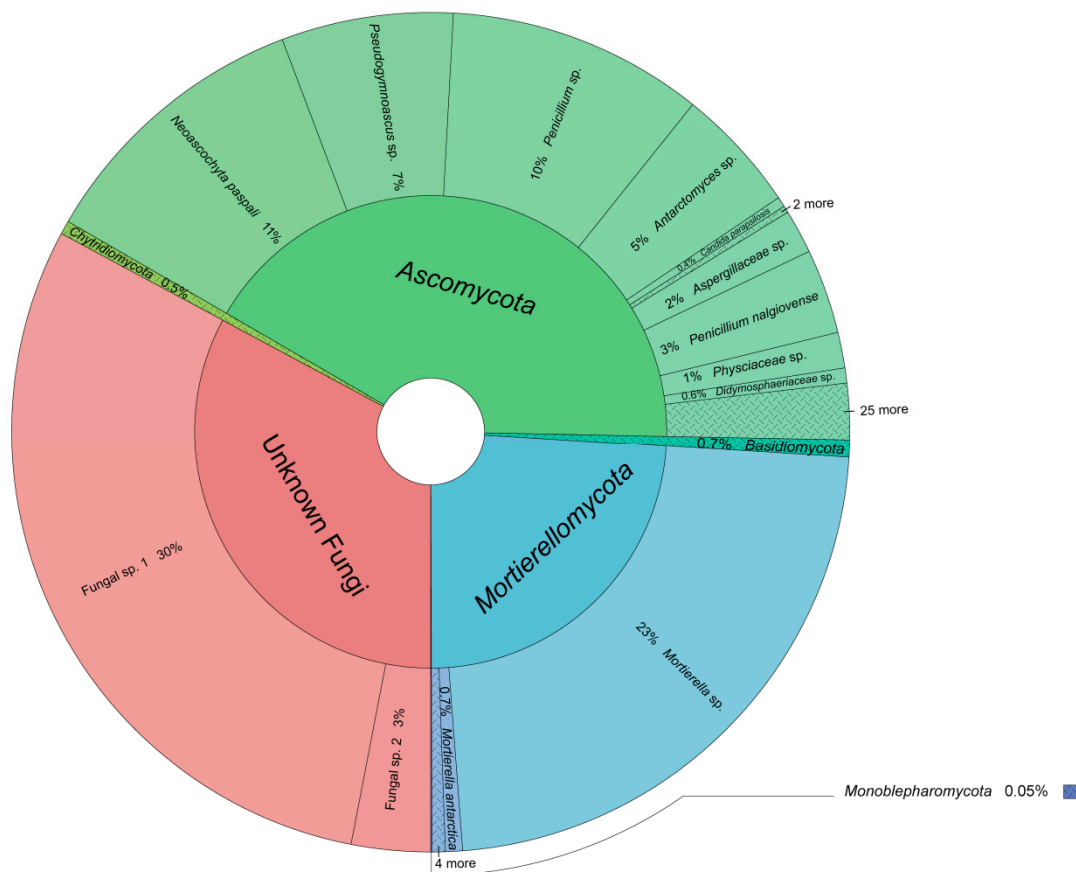


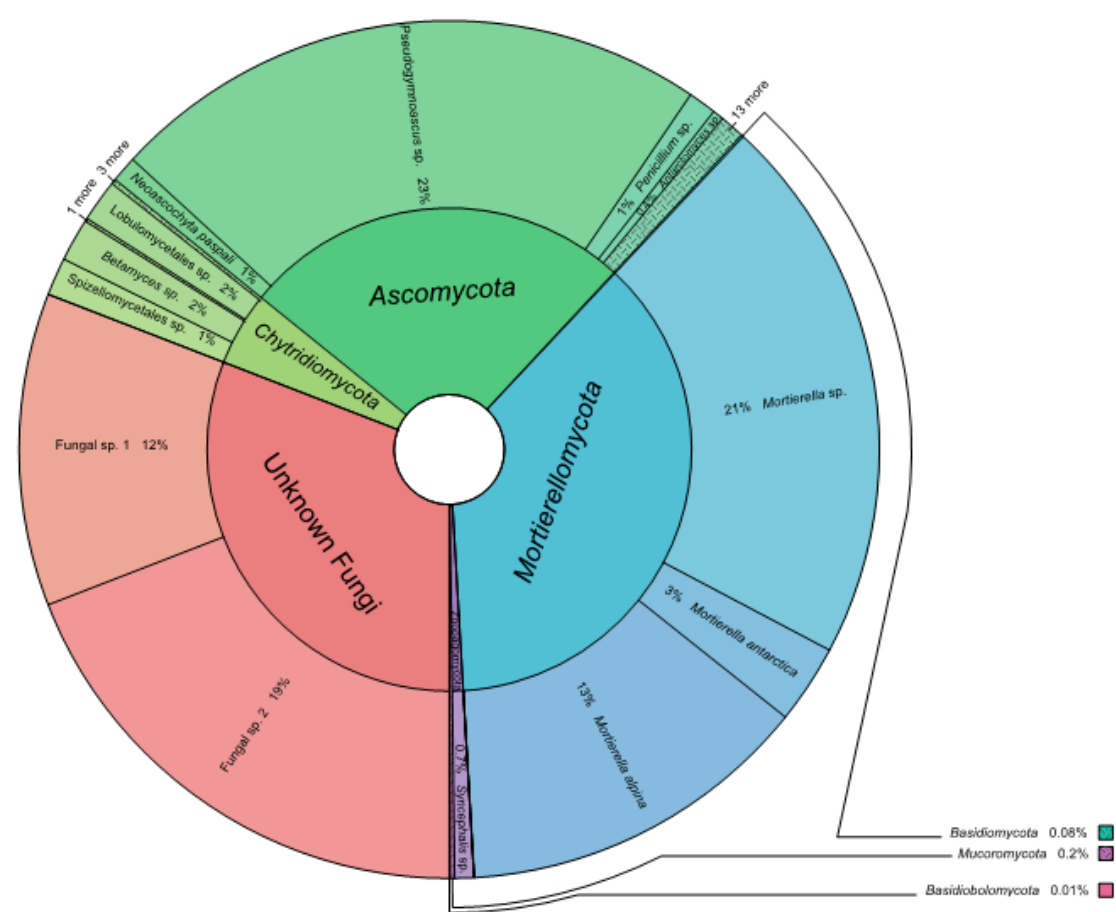
Figure S2. Rarefaction curves, with 95% confidence limits, of fungal amplicon sequence variants (ASVs) obtained from the four soils sampled at Clearwater Mesa, James Ross Island, Antarctic Peninsula.



(a)



(b)



(c)

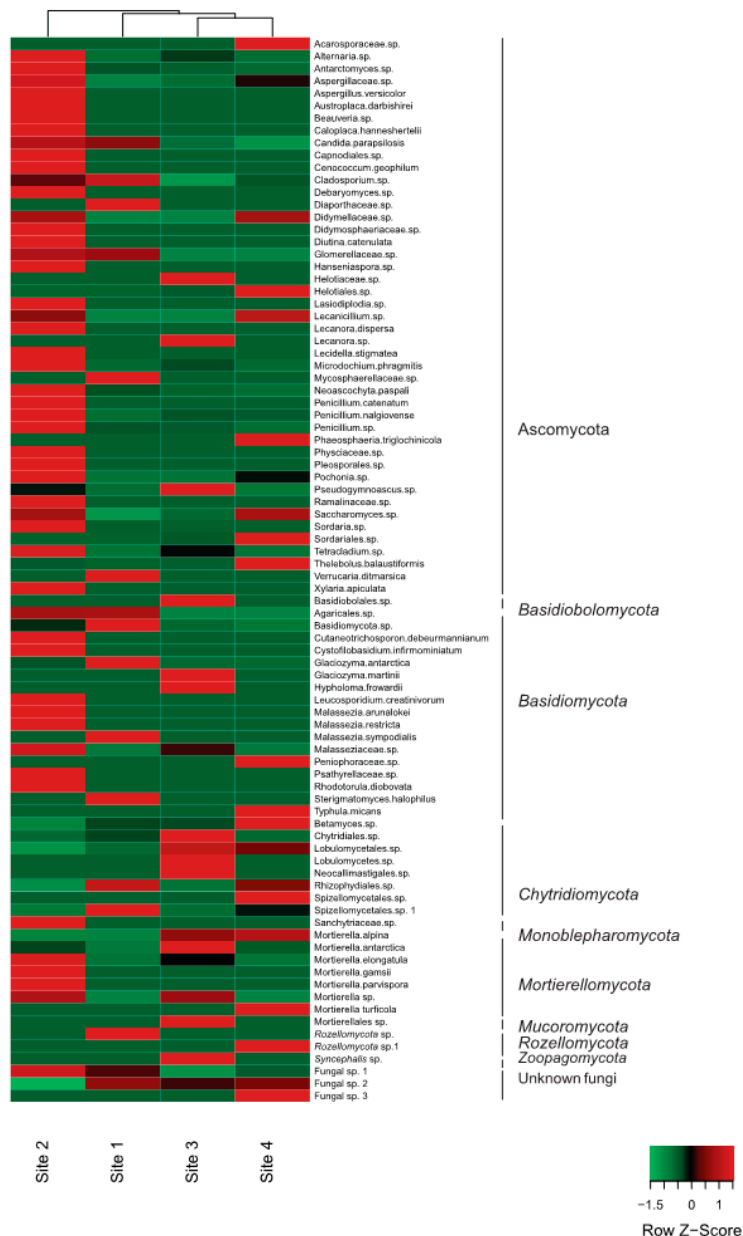


Figure S4. Heat map of fungal assemblage relative abundances detected in the four soils sampled. The color intensities range from red (highest relative abundance) to green (lowest relative abundance). These values represent percentages of DNA fungal reads from sites 1, 2, 3 and 4 at Clearwater Mesa, James Ross Island, Antarctic Peninsula. The heatmap of ASV abundance was created using the following parameters: Average Linkage, Spearman Rank Correlation, and Z-score among samples for each ASV.

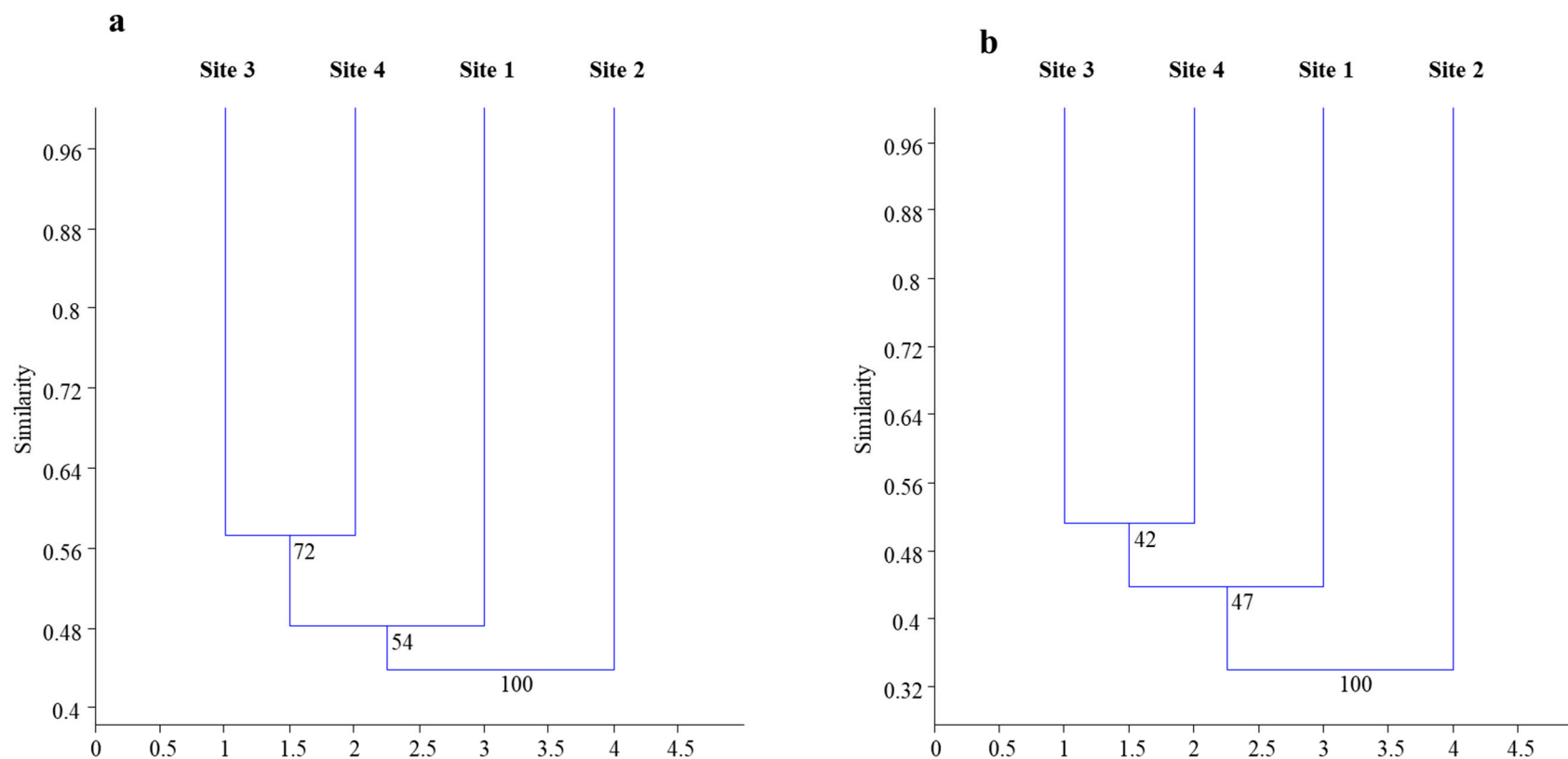
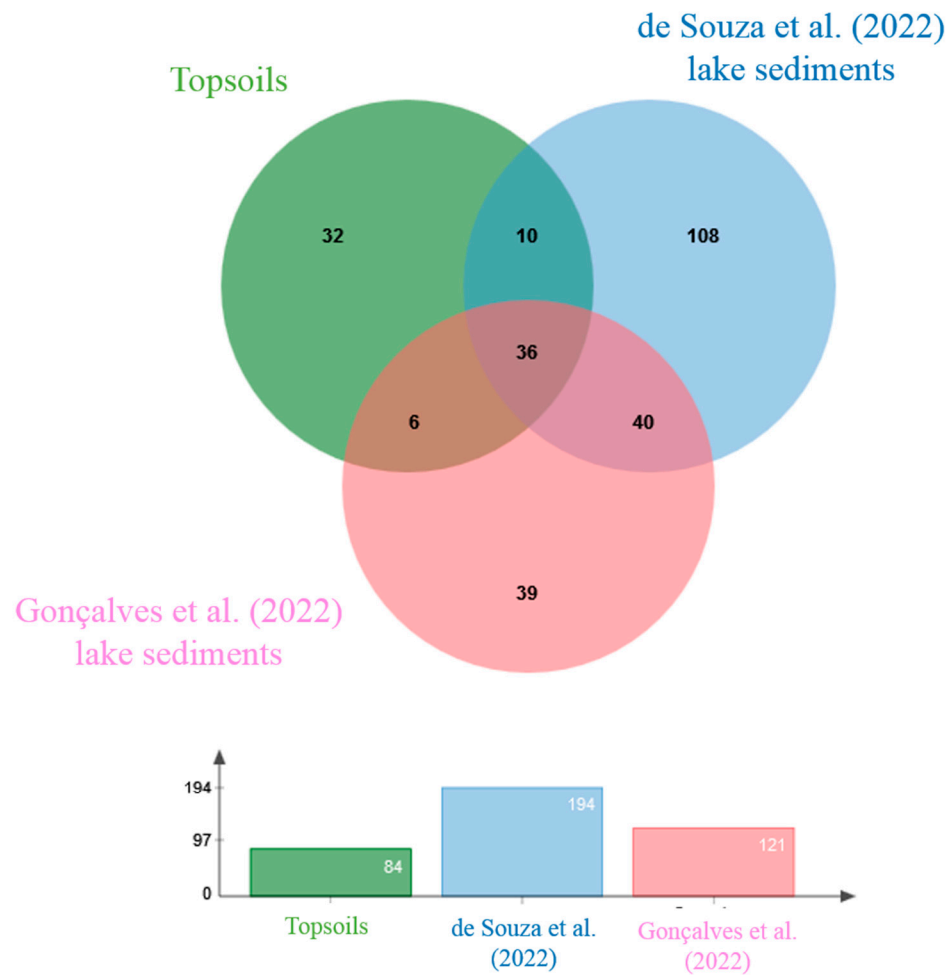


Figure S5. Dendrograms showing the Sorensen (**a**) and (**b**) Bray-Curtis similarity measures for the fungal assemblages detected in soils sampled from the four sites on Clearwater Mesa, James Ross Island, Antarctic Peninsula. The results were obtained with 95% confidence and bootstrap values calculated from 1,000 iterations.



Common fungi in topsoils and lake sediments (de Souza et al. 2022 and Gonçalves et al. 2022):

<i>Pseudogymnoascus</i> sp.	<i>Cutaneotrichosporon debeurmannianum</i>
<i>Neoascochyta paspali</i>	<i>Malassezia arunalokei</i>
<i>Penicillium</i> sp.	<i>Leucosporidium creatinivorum</i>
<i>Thelebolus balaustiformis</i>	<i>Mortierella alpina</i>
<i>Antarctomyces</i> sp.	<i>Mortierella antarctica</i>
<i>Penicillium nalgiovense</i>	<i>Betamyces</i> sp.
<i>Aspergillaceae</i> sp.	<i>Lobulomycetales</i> sp.
<i>Ciliophora</i> sp.	<i>Spizellomycetales</i> sp.
<i>Helotiales</i> sp.	<i>Rhizophydiales</i> sp.
<i>Candida parapsilosis</i>	<i>Chytridiales</i> sp.
<i>Didymosphaeriaceae</i> sp.	<i>Lobulomycetes</i> sp.
<i>Cladosporium</i> sp.	<i>Basidiobolales</i> sp.
<i>Didymellaceae</i> sp.	<i>Agaricales</i> sp.
<i>Microdochium phragmitis</i>	<i>Basidiomycota</i> sp.
<i>Saccharomyces</i> sp.	<i>Sordariales</i> sp.
<i>Tetracladium</i> sp.	<i>Mortierellales</i> sp.
<i>Glaciozyma antarctica</i>	<i>Fungal</i> sp.
<i>Malassezia restricta</i>	

Figure S6. Venn diagram showing the overlap in distribution of fungal amplicon sequence variants (ASVs) among the soils and lake sediments analyzed in the current study and by de Souza et al. (2022) and Gonçalves et al. (2022) at Clearwater Mesa, James Ross Island, Antarctic Pensinsula.

Table S1. Relative abundances of the fungal amplicon sequence variants (ASVs) detected in four soils sampled from Clearwater Mesa, James Ross Island, Antarctic Peninsula.

Database	Kingdom	Phylum	Fungal amplicon variant sequence (ASV)	Relative abundance (%) of fungal ASVs			
				Site 1	Site 2	Site 3	Site 4
UNITE	Fungi	Ascomycota	<i>Pseudogymnoascus</i> sp.	1.529	6.627	22.650	0.252
			<i>Neosascochyta paspali</i>	1.663	10.873	0.991	0.535
			<i>Penicillium</i> sp.	1.334	9.887	1.059	0.462
			<i>Thelebolus balaustiformis</i>	0.000	0.136	0.064	5.843
			<i>Antarctomyces</i> sp.	0.579	4.828	0.415	0.214
			<i>Penicillium nalgiovense</i>	0.000	3.261	0.310	0.237
			<i>Aspergillaceae</i> sp.	0.074	1.696	0.251	0.764
			<i>Ciliophora</i> sp.	2.334	0.000	0.007	0.000
			<i>Helotiales</i> sp.	0.000	0.000	0.029	1.837
			<i>Physciaceae</i> sp.	0.000	1.375	0.000	0.000
			<i>Candida parapsilosis</i>	0.320	0.387	0.133	0.073
			<i>Lecanicillium</i> sp.	0.000	0.369	0.000	0.471
			<i>Didymosphaeriaceae</i> sp.	0.000	0.579	0.000	0.000
			<i>Cladosporium</i> sp.	0.265	0.174	0.020	0.097
			<i>Diaporthaceae</i> sp.	0.333	0.000	0.000	0.000
			<i>Ramalinaceae</i> sp.	0.000	0.294	0.000	0.000
			<i>Didymellaceae</i> sp.	0.000	0.117	0.000	0.114
			<i>Pochonia</i> sp.	0.000	0.148	0.000	0.041
			<i>Aspergillus versicolor</i>	0.000	0.187	0.000	0.000
			<i>Microdochium phragmitis</i>	0.000	0.158	0.017	0.000
			<i>Glomerellaceae</i> sp.	0.080	0.089	0.000	0.000
			<i>Beauveria</i> sp.	0.000	0.127	0.000	0.000
			<i>Saccharomyces</i> sp.	0.000	0.048	0.013	0.050
			<i>Cenococcum geophilum</i>	0.000	0.102	0.000	0.000
			<i>Tetracladium</i> sp.	0.000	0.063	0.019	0.000
			<i>Alternaria</i> sp.	0.000	0.064	0.011	0.000

	<i>Acarosporaceae</i> sp.	0.000	0.000	0.000	0.067
	<i>Penicillium catenatum</i>	0.000	0.058	0.000	0.000
	<i>Caloplaca hanneshtertelii</i>	0.000	0.055	0.000	0.000
	<i>Pleosporales</i> sp.	0.000	0.054	0.000	0.000
	<i>Sordaria</i> sp.	0.000	0.049	0.000	0.000
	<i>Lecanora</i> sp.	0.000	0.000	0.047	0.000
	<i>Verrucaria ditmarsica</i>	0.042	0.000	0.000	0.000
	<i>Mycosphaerellaceae</i> sp.	0.035	0.000	0.000	0.000
	<i>Diutina catenulata</i>	0.000	0.030	0.000	0.000
	<i>Phaeosphaeria triglochinicola</i>	0.000	0.000	0.000	0.029
	<i>Capnodiales</i> sp.	0.000	0.025	0.000	0.000
	<i>Helotiaceae</i> sp.	0.000	0.000	0.016	0.000
	<i>Austroplaca darbishirei</i>	0.000	0.016	0.000	0.000
	<i>Debaryomyces</i> sp.	0.000	0.014	0.000	0.000
	<i>Lecidella stigmatea</i>	0.000	0.012	0.000	0.000
	<i>Lasioidiplodia</i> sp.	0.000	0.012	0.000	0.000
	<i>Xylaria apiculata</i>	0.000	0.012	0.000	0.000
	<i>Lecanora dispersa</i>	0.000	0.009	0.000	0.000
	<i>Hanseniaspora</i> sp.	0.000	0.008	0.000	0.000
<i>Basidiomycota</i>	<i>Glaciozyma antarctica</i>	0.799	0.060	0.000	0.000
	<i>Malassezia restricta</i>	0.000	0.134	0.000	0.000
	<i>Cutaneotrichosporon debeurmannianum</i>	0.000	0.125	0.000	0.000
	<i>Typhula micans</i>	0.000	0.000	0.000	0.105
	<i>Sterigmatomyces halophilus</i>	0.090	0.000	0.000	0.000
	<i>Peniophoraceae</i> sp.	0.000	0.000	0.000	0.082
	<i>Malassezia arunalokei</i>	0.000	0.072	0.000	0.000
	<i>Malassezia sympodialis</i>	0.070	0.000	0.000	0.000
	<i>Leucosporidium creatinivorum</i>	0.000	0.066	0.000	0.000
	<i>Malasseziaceae</i> sp.	0.000	0.043	0.020	0.000
	<i>Cystofilobasidium infirmominiatum</i>	0.000	0.058	0.000	0.000
	<i>Psathyrellaceae</i> sp.	0.000	0.021	0.000	0.000

BLASTn Fungi		<i>Hypholoma frowardii</i>	0.000	0.000	0.020	0.000
		<i>Glaciozyma martinii</i>	0.000	0.000	0.016	0.000
		<i>Rhodotorula diobovata</i>	0.000	0.015	0.000	0.000
	<i>Mortierellomycota</i>	<i>Mortierella</i> sp.	0.000	22.792	20.763	0.000
		<i>Mortierella alpina</i>	0.000	0.328	13.347	16.475
		<i>Mortierella turficola</i>	0.000	0.000	0.000	16.171
		<i>Mortierella antarctica</i>	0.000	0.660	2.979	0.453
		<i>Mortierella parvispora</i>	0.000	0.104	0.000	0.000
		<i>Mortierella elongatula</i>	0.000	0.038	0.012	0.000
		<i>Mortierella gamsii</i>	0.000	0.041	0.000	0.000
	<i>Chytridiomycota</i>	<i>Betamyces</i> sp.	1.778	0.156	1.615	7.057
		<i>Lobulomycetales</i> sp.	0.413	0.068	1.589	1.109
		<i>Spizellomycetales</i> sp. 1	0.000	0.000	0.000	2.311
		<i>Rhizophydiales</i> sp.	0.905	0.000	0.123	0.670
		<i>Chytridiales</i> sp.	0.022	0.000	0.158	0.000
		<i>Lobulomycetes</i> sp.	0.000	0.000	0.022	0.000
	<i>Rozellomycota</i>	<i>Rozellomycota</i> sp. 1	23.846	0.000	0.000	0.000
	<i>Zoopagomycota</i>	<i>Syncephalis</i> sp.	0.000	0.000	0.716	0.000
	<i>Basidiobolomycota</i>	<i>Basidiobolales</i> sp.	0.000	0.000	0.012	0.000
	<i>Monoblepharomycota</i>	<i>Sanchytriaceae</i> sp.	0.000	0.046	0.000	0.000
	<i>Chytridiomycota</i>	<i>Spizellomycetales</i> sp. 2	18.420	0.301	1.428	5.784
		<i>Neocallimastigales</i> sp.	0.000	0.000	0.010	0.000
	<i>Basidiomycota</i>	<i>Agaricales</i> sp.	0.019	0.019	0.000	0.000
		<i>Basidiomycota</i> sp.	0.285	0.070	0.023	0.000
	<i>Ascomycota</i>	<i>Sordariales</i> sp.	0.000	0.000	0.013	0.252
	<i>Rozellomycota</i>	<i>Rozellomycota</i> sp. 2	0.000	0.000	0.000	0.032
	<i>Mucoromycota</i>	<i>Mortierellales</i> sp.	0.000	0.000	0.175	0.000
	Unknown	Fungal sp. 1	21.563	29.792	11.791	16.329
		Fungal sp. 2	23.204	3.046	19.103	22.008
		Fungal sp. 3	0.000	0.000	0.000	0.076

ASV = fungal sequence variant. Green indicates dominant, blue intermediate and orange minor relative abundance (see Methods).

Table S2. Shared fungal amplicon sequence variants (ASVs) detected in soil samples collected in Clearwater Mesa, James Ross Island, Antarctica

[illegible]

Table S3. Ecological profiles obtained from the FUNGuild database and specific citations at generic level of the fungi detected in soil samples obtained from Clearwater Mesa, James Ross Island, Antarctic Peninsula.

Genus	Relative abundance (%) of soil fungal ASVs				Trophic mode	Guild*
	Site 1	Site 2	Site 3	Site 4		
<i>Alternaria</i>	0.000	0.064	0.011	0.000	Pathogenic-Saprotrophic-Symbiotic	Animal Pathogen-Endophyte-Plant Pathogen-Wood Saprotrophic
<i>Antarctomyces</i>	0.579	4.828	0.415	0.214	Saprotrophic	Undefined Saprotrophic
<i>Aspergillus</i>	0.000	0.187	0.000	0.000	Pathogenic-Saprotrophic	Animal Pathogen-Undefined Saprotrophic
<i>Austroplaca</i>	0.000	0.016	0.000	0.000	Symbiotic	Lichenized
<i>Beauveria</i>	0.000	0.127	0.000	0.000	Pathogenic	Animal Pathogen
<i>Betamyces</i>	1.778	0.156	1.615	7.057	Saprotrophic	Freshwater and Soil Saprotrophic (Lepelletier et al. 2014)
<i>Caloplaca</i>	0.000	0.055	0.000	0.000	Symbiotic	Lichenized
<i>Candida</i>	0.320	0.387	0.133	0.073	Pathogenic	Animal Pathogen
<i>Cenococcum</i>	0.000	0.102	0.000	0.000	Symbiotic	Ectomycorrhizal
<i>Ciliophora</i>	2.334	0.000	0.007	0.000	Symbiotic	Endophyte (Sun and Guo 2007)
<i>Cladosporium</i>	0.265	0.174	0.020	0.097	Symbiotic	Endophyte
<i>Cutaneotrichosporon</i>	0.000	0.125	0.000	0.000	Saprotrophic	Undefined Saprotrophic (Li et al. 2020)
<i>Cystofilobasidium</i>	0.000	0.058	0.000	0.000	Pathogenic	Fungal Parasite
<i>Debaryomyces</i>	0.000	0.014	0.000	0.000	Saprotrophic	Undefined Saprotrophic
<i>Diutina</i>	0.000	0.030	0.000	0.000	Pathogenic	Animal Pathogen (Ming et al. 2019)
<i>Glaciozyma</i>	0.799	0.060	0.016	0.000	Saprotrophic	Undefined Saprotrophic (Sampaio 2011)
<i>Hanseniaspora</i>	0.000	0.008	0.000	0.000	Pathogenic-Saprotrophic	Animal Pathogen-Fruits (Fleet et al. 2002; Saubin et al. 2020)
<i>Hypholoma</i>	0.000	0.000	0.020	0.000	Saprotrophic	Undefined Saprotroph
<i>Lasiodiplodia</i>	0.000	0.012	0.000	0.000	Pathogenic	Plant Pathogen
<i>Lecanicillium</i>	0.000	0.369	0.000	0.471	Pathogenic	Animal Pathogen
<i>Lecanora</i>	0.000	0.009	0.047	0.000	Symbiotic	Lichenized
<i>Lecidella</i>	0.000	0.012	0.000	0.000	Symbiotic	Lichenized

<i>Leucosporidium</i>	0.000	0.066	0.000	0.000	Saprotrophic	Soil Saprotrophic-Undefined Saprotrophic
<i>Malassezia</i>	0.070	0.206	0.000	0.000	Pathogenic	Animal Pathogen
<i>Microdochium</i>	0.000	0.158	0.017	0.000	Pathogenic-Symbiotic	Endophyte-Plant Pathogen
<i>Mortierella</i>	0.000	23.963	37.101	33.099	Saprotrophic-Symbiotic	Endophyte-Litter Saprotrophic-Soil Saprotrophic-Undefined Saprotrophic
<i>Neosascochyta</i>	1.663	10.873	0.991	0.535	Pathogenic	Plant Pathogen (Golzar et al. 2019)
<i>Penicillium</i>	1.334	13.206	1.369	0.699	Saprotrophic	Dung Saprotrophic-Undefined Saprotrophic-Wood Saprotrophic
<i>Phaeosphaeria</i>	0.000	0.000	0.000	0.029	Saprotrophic	Undefined Saprotrophic
<i>Pochonia</i>	0.000	0.148	0.000	0.041	Pathogenic	Animal Pathogen
<i>Pseudogymnoascus</i>	1.529	6.627	22.650	0.252	Pathogenic-Saprotrophic-Symbiotic	Animal pathogen-Soil Saprotrophic
<i>Rhodotorula</i>	0.000	0.015	0.000	0.000	Pathogenic-Saprotrophic	Animal Endosymbiont-Animal Pathogen-Endophyte-Plant Pathogen-Undefined Saprotrophic
<i>Saccharomyces</i>	0.000	0.048	0.013	0.050	Saprotrophic	Undefined Saprotrophic
<i>Sordaria</i>	0.000	0.049	0.000	0.000	Saprotrophic	Dung Saprotrophic -Wood Saprotrophic
<i>Sterigmatomyces</i>	0.090	0.000	0.000	0.000	Saprotrophic	Saprotrophic and halotolerant (Al-Tohamy et al. 2020)
<i>Syncephalis</i>	0.000	0.000	0.716	0.000	Pathogenic	Fungal Parasite
<i>Tetracladium</i>	0.000	0.063	0.019	0.000	Saprotrophic	Undefined Saprotrophic
<i>Thelebolus</i>	0.000	0.136	0.064	5.843	Saprotrophic-Symbiotic	Dung Saprotrophic-Endophyte-Undefined Saprotrophic
<i>Typhula</i>	0.000	0.000	0.000	0.105	Pathogenic	Plant Pathogen
<i>Verrucaria</i>	0.042	0.000	0.000	0.000	Symbiotic	Lichenized (Pykälä et al. 2020)
<i>Xylaria</i>	0.000	0.012	0.000	0.000	Saprotrophic-Symbiotic	Endophyte-Undefined Saprotrophic -Wood Saprotrophic

ASV = amplicon sequence variant.

References of Supplementary Table S3

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Table S4. Comparison of fungal sequence diversity present in soils and lake sediments on Clearwater Mesa, James Ross Island.

Type and local	Diversity indices					Citation
	Number of fungal ASVs	Number of DNA reads	Fisher's- α (diversity)	Margalef's (richness)	Simpson's (dominance)	
Soils						
Site 1	25	15,636	10.7	5.21	0.81	Current study
Site 2	59	56,473	60.43	12.6	0.83	
Site 3	39	38,575	23.51	8.25	0.84	
Site 4	31	17,090	15.39	6.51	0.86	
Lake sediments						
Lilia	84	32,428	247.7	18.02	0.77	Gonçalves et al. (2022)
Cecilia	64	27,730	76.66	13.68	0.81	
Soledad	58	28,571	57.66	12.38	0.87	
Adriana	43	22,012	28.61	9.12	0.68	
Katerina	51	54,939	22.1	9.44	0.79	de Souza et al. (2022)
Florencia	171	46,813	559.7	32.09	0.92	

ASV = amplicon sequence variant.