Supplementary tables

Table S1. Main site characteristics and key soil properties. Climate data were obtained from Alberta Climate Information Service (2020) for Alberta (AB) and from Environment Canada (2010) for Québec (QC). Total nitrogen (TN) and total organic carbon (TC) were analyzed by the dry combustion method on a ThermoScientific Flash 2000 Organic Elemental Analysis instrument (ThermoFisher Scientific, Waltham, MA, USA).

Site	Parent material	MAT [ºC]	MAP [mm]	Coordinates		Textural class		Forest floor thickness [cm]		$CaCl_2$ pH		TN [%]		TC [%]	
						Control	Invaded	Control	Invaded	Control	Invaded	Control	Invaded	Control	Invaded
Luvisol (EMEND)	Glacial till	1.4	413	56º46’N 118º22’W	Forest floor			10.7	7.7	5.6	5.7	2.29	1.86	43.0	38.7
					Mineral soil	Loam	Loam			5.2	5.4	0.14	0.20	1.7	2.6
Brunisol (Valcartier)	Fluvial deposit	1.6	1460	46º55’N 71º36’W	Forest floor			7.8	3.1	3.2	4.8	1.99	1.48	45.1	35.4
					Mineral soil	Sandy loam	Clay loam			3.1	4.3	0.46	0.49	7.8	7.7
Podzol (Grands Jardins)	Sandy glacial till	3.7	930	47º40’N 70º50’W	Forest floor			10.5	5.3	3.0	3.7	1.40	1.31	48.9	42.3
					Mineral soil	Sandy loam	Sandy clay loam			3.4	4.6	0.15	0.27	4.1	6.1

Table S2. Average (±1 SE) relative abundances (%) of the fungal and bacterial phyla accounting for > 1% of relative abundance (n=7–18). Different letters represent significant differences between control and earthworm invaded soils (p-value < 0.1) and are presented separately for the forest floors and mineral soils.

	Forest floor		Mineral soil	
	Control	Invaded	Control	Invaded
Fungi				
Ascomycota	57.7 (4.8) a	60.3 (2.6) a	67.9 (4.3) a	56.3 (3.3) b
Basidiomycota	28.0 (4.0) a	26.7 (1.9) a	20.5 (4.3) a	26.9 (2.8) a
Chytridiomycota	1.5 (0.6) a	1.6 (0.4) a	2.2 (1.0) a	2.0 (0.6) a
Mortierellomycota	5.4 (2.0) a	2.9 (0.8) a	1.4 (0.6) a	2.6 (0.8) a
Mucoromycota	0.9 (0.3) a	0.7 (0.3) a	3.1 (2.3) a	1.7 (1.0) a
Bacteria				
Acidobacteriota	13.6 (2.0) a	13.3 (1.0) a	26.9 (1.7) a	22.7 (1.2) b
Actinobacteriota	31.7 (3.0) a	24.8 (2.0) b	17.2 (1.9) a	16.6 (1.4) a
Bacteroidota	7.5 (1.8) a	9.8 (1.3) a	1.0 (0.4) b	1.9 (0.5) a
Chloroflexi	1.5 (0.4) a	1.4 (0.3) a	9.1 (1.1) a	8.4 (1.0) b
Firmicutes	2.3 (1.6) a	1.9 (1.0) a	2.5 (0.8) a	1.9 (0.4) a
Gemmatimonadota	0.3 (0.2) a	0.3 (0.1) a	1.4 (0.5) a	1.9 (0.4) a
Planctomycetota	12.3 (2.2) a	13.4 (1.7) a	17.2 (1.2) a	19.2 (1.1) a
Proteobacteria	27.2 (2.1) a	29.9 (1.9) a	16.7 (1.0) b	18.7 (0.8) a
Verrucomicrobiota	2.2 (0.4) b	3.1 (0.4) a	6.2 (1.1) a	6.4 (0.7) a

Table S3. Two-way analyses of variance (factors: earthworm invasion and site) of fungal guild and phylum relative abundances (as number of reads), fungal ratio, and diversity indices, for forest floors and mineral soils separately. Df stands for degrees of freedom and Sum sq for sum of squares.

	FOREST FLOOR				MINERAL SOIL			
	Df	Sum Sq	F value	p-value	Df	Sum Sq	F value	p-value
Fungal guilds								
Ectomycorrhizae								
Invasion	1	0.00	0.00	0.96	1	0.49	13.94	<0.01
Site	2	1.06	15.51	<0.001	2	0.52	7.38	<0.01
Interaction	2	0.06	0.94	0.41	2	0.02	0.31	0.74
Residuals	18	0.62			21	0.74		
Pathogens								
Invasion	1	0.02	0.52	0.48	1	0.01	0.34	0.57
Site	2	0.49	7.57	<0.01	2	0.11	3.24	0.06
Interaction	2	0.02	0.36	0.70	2	0.00	0.00	1.00
Residuals	18	0.58			21	0.36		
Saprotrophs								
Invasion	1	0.01	0.37	0.55	1	0.38	11.86	<0.01
Site	2	0.33	6.38	<0.01	2	0.42	6.49	<0.01
Interaction	2	0.05	0.99	0.39	2	0.04	0.68	0.52
Residuals	18	0.46			21	0.68		
Ectomycorrhizal:Saprotrophic								
Invasion	1	0.00	0.01	0.94	1	0.01	12.84	<0.01
Site	2	2.35	13.72	<0.001	2	0.01	7.58	<0.01
Interaction	2	0.10	0.58	0.57	2	0.00	0.25	0.78
Residuals	18	1.54			21	0.01		
Fungal phyla								
Ascomycota								
Invasion	1	66.02	0.74	0.40	1	891.50	4.60	<0.05
Site	2	923.25	5.20	<0.05	2	96.40	0.25	0.78
Interaction	2	141.09	0.80	0.47	2	339.10	0.88	0.43
Residuals	18	1596.70			21	4067.60		
Basidiomycota								
Invasion	1	28.11	0.44	0.52	1	271.72	1.91	0.18
Site	2	397.68	3.11	0.07	2	235.97	0.83	0.45
Interaction	2	2.06	0.02	0.98	2	310.67	1.09	0.35
Residuals	18	1151.77			21	2987.87		
Chytridiomycota								
Invasion	1	0.10	0.06	0.80	1	0.01	0.04	0.85
Site	2	23.31	7.73	<0.01	2	0.88	2.68	0.09
Interaction	2	0.40	0.13	0.88	2	1.00	3.04	0.07
Residuals	18	27.14			21	3.44		
Mortierellomycota								
Invasion	1	20.03	2.48	0.13	1	0.39	1.18	0.29
Site	2	123.81	7.68	<0.01	2	0.02	0.04	0.96

Interaction	2	33.42	2.07	0.15	2	0.01	0.02	0.98
Residuals	18	145.13			21	6.93		
Mucoromycota								
Invasion	1	0.25	1.46	0.24	1	0.29	1.46	0.24
Site	2	1.36	3.99	<0.05	2	3.91	9.98	<0.001
Interaction	2	0.10	0.30	0.74	2	1.03	2.62	0.10
Residuals	18	3.08			21	4.11		
Species richness								
All fungi								
Invasion	1	648	0.62	0.44	1	<0.01	10.97	<0.01
Site	2	2218	1.06	0.37	2	<0.01	4.17	<0.05
Interaction	2	1990	0.95	0.41	2	<0.01	1.14	0.34
Residuals	15	15653			17	<0.01		
Ectomycorrhizae								
Invasion	1	44.56	2.61	0.13	1	95.09	9.12	<0.01
Site	2	1022.85	29.94	<0.001	2	10.68	0.51	0.61
Interaction	2	39.02	1.14	0.35	2	52.35	2.51	0.11
Residuals	15	256.20			17			
Pathogens								
Invasion	1	2.50	0.39	0.54	1	0.85	3.49	0.08
Site	2	80.84	6.38	<0.01	2	1.66	3.39	0.06
Interaction	2	25.34	2.00	0.17	2	0.45	0.93	0.41
Residuals	15	94.97			17	4.16		
Saprotrophs								
Invasion	1	22.86	0.39	0.54	1	0.01	9.02	<0.01
Site	2	994.86	8.54	<0.01	2	0.01	6.53	<0.01
Interaction	2	66.13	0.57	0.58	2	<0.01	0.95	0.40
Residuals	15	873.87			17	0.01		
Species diversity								
All fungi								
Invasion	1	89	0.74	0.40	1	<0.01	1.44	0.25
Site	2	1515	6.33	<0.05	2	0.01	7.27	<0.01
Interaction	2	103	0.43	0.66	2	<0.01	0.40	0.68
Residuals	15	1796			17	0.02		
Ectomycorrhizae								
Invasion	1	1.59	0.41	0.53	1	5.50	1.08	0.31
Site	2	121.38	15.44	<0.001	2	2.97	0.29	0.75
Interaction	2	0.75	0.10	0.91	2	13.32	1.30	0.30
Residuals	15	58.97			17	86.97		
Pathogens								
Invasion	1	0.36	0.20	0.66	1	0.41	11.89	<0.01
Site	2	32.62	9.11	<0.01	2	0.06	0.92	0.42
Interaction	2	2.54	0.71	0.51	2	0.03	0.49	0.62
Residuals	15	26.86			17	0.58		
Saprotrophs								
Invasion	1	4.86	0.26	0.62	1	93.72	11.22	<0.01
Site	2	456.68	12.24	<0.001	2	81.63	4.88	<0.05
Interaction	2	22.16	0.59	0.56	2	22.56	1.35	0.29
Residuals	15	279.72			17	142.04		

Table S4. Two-way analyses of variance (ANOVA; factors: earthworm invasion and site) of relative abundance (as number of reads) of bacterial phyla and family levels, and global diversity indices, for forest floors and mineral soils separately. At the family-level, taxa present in >60% of the samples and representing >0.5% of average relative abundance were selected for ANOVA and only families significantly affected by earthworm invasion in forest floors and/or mineral soils are displayed. Missing groups for either the forest floor or the mineral soil correspond to those that did not meet the selection criteria. Df stands for degrees of freedom and Sum sq for sum of squares.

	FOREST FLOOR				MINERAL SOIL			
	Df	Sum Sq	F value	p-value	Df	Sum Sq	F value	p-value
Bacterial phyla								
Actinobacteriota								
Invasion	1	0.02	3.19	0.09	1	0.00	0.00	1.00
Site	2	0.03	2.41	0.12	2	0.05	17.57	<0.001
Interaction	2	0.01	0.82	0.46	2	0.00	0.23	0.79
Residuals	18	0.10			21	0.03		
Acidobacteriota								
Invasion	1	0.00	0.00	0.98	1	0.01	3.24	0.09
Site	2	0.01	1.78	0.20	2	0.01	2.10	0.15
Interaction	2	0.01	1.59	0.23	2	0.00	0.35	0.71
Residuals	18	0.03			21	0.05		
Bacteroidota								
Invasion	1	0.00	0.91	0.35	1	1.26	9.37	<0.01
Site	2	0.03	11.68	<0.001	2	2.15	7.99	<0.01
Interaction	2	0.00	0.06	0.94	2	0.34	1.26	0.30
Residuals	18	0.02			21	2.82		
Chloroflexi								
Invasion	1	0.00	0.22	0.64	1	0.00	3.54	0.07
Site	2	0.00	9.70	<0.01	2	0.02	15.42	<0.001
Interaction	2	0.00	1.04	0.37	2	0.00	1.61	0.22
Residuals	18	0.00			21	0.01		
Firmicutes								
Invasion	1	0.07	0.03	0.86	1	0.00	0.81	0.38
Site	2	2.95	0.74	0.49	2	0.00	0.04	0.96
Interaction	2	3.78	0.95	0.41	2	0.00	2.98	0.07
Residuals	18	35.92			21	0.01		
Gemmatimonadota								
Invasion	1	0.00	0.08	0.78	1	0.00	2.66	0.12
Site	2	0.00	66.61	<0.001	2	0.00	15.62	<0.001
Interaction	2	0.00	0.10	0.91	2	0.00	0.52	0.60
Residuals	18	0.00			21	0.00		
Planctomycetota								
Invasion	1	0.00	0.13	0.72	1	0.00	0.38	0.55
Site	2	0.00	0.04	0.96	2	0.02	7.91	<0.01
Interaction	2	0.00	0.09	0.92	2	0.00	0.90	0.42

Residuals	18	0.09			21	0.02		
Proteobacteria								
Invasion	1	0.00	0.81	0.38	1	0.00	6.81	<0.05
Site	2	0.03	3.53	0.05	2	0.01	14.40	<0.001
Interaction	2	0.00	0.36	0.70	2	0.01	7.74	<0.01
Residuals	18	0.08			21	0.01		
Alphaproteobacteria								
Invasion	1	0.02	0.62	0.44	1	0.83	1.49	0.24
Site	2	0.19	3.00	0.07	2	24.21	21.71	<0.001
Interaction	2	0.04	0.59	0.57	2	6.34	5.69	<0.05
Residuals	18	0.57			21	11.71		
Gammaproteobacteria								
Invasion	1	0.01	0.23	0.64	1	0.00	5.28	<0.05
Site	2	0.09	1.76	0.20	2	0.03	15.86	<0.001
Interaction	2	0.01	0.30	0.75	2	0.00	0.18	0.83
Residuals	18	0.44			21	0.02		
Verrucomicrobiota								
Invasion	1	0.00	6.43	<0.05	1	0.00	0.74	0.40
Site	2	0.00	31.96	<0.001	2	0.01	7.48	<0.01
Interaction	2	0.00	0.92	0.42	2	0.00	0.14	0.87
Residuals	18	0.00			21	0.01		
Proteobacteria:Acidobacteriota								
Invasion	1	0.44	0.38	0.55	1	0.18	7.66	<0.05
Site	2	3.30	1.43	0.26	2	0.06	1.25	0.31
Interaction	2	2.32	1.00	0.39	2	0.02	0.40	0.67
Residuals	18	20.76			21	0.49		
Bacterial families								
Acidothermaceae								
Invasion	1	0.04	1.38	0.26	1	1.83	3.45	0.08
Site	2	0.96	18.55	<0.001	2	2.76	2.61	<0.1
Interaction	2	0.05	0.93	0.41	2	1.62	1.53	0.24
Residuals	18	0.47			21	11.11		
Chitinophagaceae								
Invasion	1	12.03	3.17	0.09	1	0.03	5.34	<0.05
Site	2	155.33	20.48	<0.001	2	0.10	8.10	<0.01
Interaction	2	4.30	0.57	0.58	2	0.01	0.60	0.56
Residuals	18	68.28			21	0.13		
Chthoniobacteraceae								
Invasion	1	0.12	11.12	<0.01	1	7.92	2.44	0.13
Site	2	0.96	44.07	<0.001	2	179.94	27.75	<0.001
Interaction	2	0.03	1.21	0.32	2	10.46	1.61	0.22
Residuals	18	0.20			21	68.09		
Gemmatimonadaceae								
Invasion					1	0.12	7.36	<0.05
Site					2	0.75	23.39	<0.001
Interaction					2	0.09	2.85	0.08
Residuals					21	0.34		
Nitrosomonadaceae								
Invasion					1	0.47	5.97	<0.05

Site					2	0.43	2.70	0.09
Interaction					2	0.26	1.67	0.21
Residuals					21	1.66		
Pirellulaceae								
Invasion	1	0.00	0.00	0.96	1	17.28	14.50	<0.01
Site	2	100.22	26.77	<0.001	2	4.80	2.01	0.16
Interaction	2	1.76	0.47	0.63	2	6.47	1.46	0.26
Residuals	18	33.70			21	25.03		
Reyranellaceae								
Invasion	1	0.29	3.10	<0.1	1	0.60	8.26	<0.01
Site	2	2.42	12.84	<0.001	2	0.52	3.64	<0.05
Interaction	2	0.02	0.12	0.89	2	0.18	1.23	0.31
Residuals	18	1.70			21	1.51		
Solibacteraceae								
Invasion					1	0.53	3.30	0.08
Site					2	1.28	3.95	<0.05
Interaction					2	0.27	0.83	0.45
Residuals					21	3.40		
Solirubrobacteraceae								
Invasion	1	0.92	7.23	<0.05	1	0.09	0.10	0.76
Site	2	1.88	7.40	<0.01	2	0.83	0.46	0.64
Interaction	2	0.21	0.84	0.45	2	6.48	3.57	<0.05
Residuals	18	2.28			21	19.07		
Thermoanaerobaculaceae								
Invasion					1	0.71	5.19	<0.05
Site					2	0.43	1.57	0.23
Interaction					2	1.63	5.96	<0.01
Residuals					21	2.87		
Xiphinematobacteraceae								
Invasion					1	0.64	10.91	<0.01
Site					2	1.21	10.38	<0.001
Interaction					2	0.79	6.73	<0.01
Residuals					21	1.23		
Species richness								
Invasion	1	8875	3.37	0.08	1	12004	11.74	<0.01
Site	2	114472	21.70	<0.001	2	6136	3.00	0.07
Interaction	2	187	0.04	0.97	2	966	0.47	0.63
Residuals	18	47472			22	22487		
Species diversity								
Invasion	1	1041	1.65	0.22	1	1758	6.57	<0.05
Site	2	45005	35.67	<0.001	2	219	0.41	0.67
Interaction	2	64	0.05	0.95	2	106	0.20	0.82
Residuals	18	11354			21	5887		

Table S5. Two-way analyses of variance (factors: earthworm invasion and site) for phospholipid fatty acid (PLFA) concentration of individual PLFAs as well as groups (total, Gram(+) and Gram(-) bacteria, and fungi) and microbial ratios, for forest floors and mineral soils separately. The 10Me ratio was obtained by dividing the phospholipid fatty acid (PLFA) 10Me16:0 by 16:0 and the Cyclo ratio by dividing the sum of cy19:0ω9 and cy19:0ω7 divided by 18:0. The Proteobacteria:Acidobacteriota (Proteo:Acido) ratio was calculated from the number of reads corresponding to the two phyla. Df stands for degrees of freedom and Sum sq for sum of squares.

	FOREST FLOOR				MINERAL SOIL			
	Df	Sum Sq	F value	p-value	Df	Sum Sq	F value	p-value
Total PLFA biomass								
Invasion	1	3999847	2.63	0.12	1	0.00	1.64	0.21
Site	2	2415436	0.79	0.47	2	0.00	3.13	<0.1
Interaction	2	5020883	1.65	0.22	2	0.00	1.01	0.38
Residuals	18	27357255			22	0.00		
PLFA 15:0								
Invasion	1	0.00	2.36	0.14	1	0.01	2.60	0.12
Site	2	0.00	13.98	<0.001	2	0.02	2.87	0.08
Interaction	2	0.00	1.76	0.20	2	0.01	1.68	0.21
Residuals	18	0.00			22	0.07		
Gram(+) bacteria								
Invasion	1	0.00	1.13	0.30	1	0.00	0.44	0.51
Site	2	0.01	2.59	0.10	2	0.00	3.74	<0.05
Interaction	2	0.00	0.47	0.63	2	0.00	0.92	0.41
Residuals	18	0.03			22	0.01		
PLFA i14:0								
Invasion	1	8.21	4.54	<0.05	1	0.03	2.34	0.14
Site	2	52.10	14.41	<0.001	2	0.02	0.76	0.48
Interaction	2	3.41	0.94	0.41	2	0.02	0.84	0.44
Residuals	18	32.55			22	0.25		
PLFA i15:0								
Invasion	1	0.00	0.18	0.68	1	0.00	0.21	0.65
Site	2	0.00	5.34	<0.05	2	0.01	4.01	<0.05
Interaction	2	0.00	0.23	0.79	2	0.00	0.64	0.54
Residuals	18	0.01			22	0.04		
PLFA a15:0								
Invasion	1	0.52	2.38	0.14	1	0.00	0.94	0.34
Site	2	0.80	1.83	0.19	2	0.00	2.40	0.11
Interaction	2	0.22	0.51	0.61	2	0.00	1.04	0.37
Residuals	18	3.94			22	0.01		
PLFA i16:0								
Invasion	1	0.65	1.25	0.28	1	0.00	0.01	0.95
Site	2	2.14	2.08	0.15	2	0.05	6.21	<0.01
Interaction	2	1.25	1.21	0.32	2	0.00	0.24	0.79
Residuals	18	9.26			22	0.09		

PLFA a16:0								
Invasion	1	18.22	0.44	0.52	1	1.41	1.74	0.20
Site	2	139.10	1.66	0.22	2	0.13	0.08	0.92
Interaction	2	77.73	0.93	0.41	2	1.54	0.95	0.40
Residuals	18	753.25			22	17.81		
PLFA i17:0								
Invasion	1	1.32	0.42	0.53	1	0.00	0.28	0.60
Site	2	4.65	0.74	0.49	2	0.03	5.07	<0.05
Interaction	2	2.22	0.35	0.71	2	0.00	0.47	0.63
Residuals	18	56.69			22	0.06		
PLFA a17:0								
Invasion	1	0.00	4.61	<0.05	1	0.01	2.36	0.14
Site	2	0.02	10.36	<0.01	2	0.01	1.66	0.21
Interaction	2	0.00	1.43	0.26	2	0.01	1.21	0.32
Residuals	18	0.01			22	0.10		
Gram(-) bacteria								
Invasion	1	14999	0.52	0.48	1	0.00	1.28	0.27
Site	2	24504	0.42	0.66	2	0.00	3.28	0.06
Interaction	2	27389	0.47	0.63	2	0.00	0.81	0.46
Residuals	18	521854			22	0.01		
PLFA 16:1ω7								
Invasion	1	0.00	1.71	0.21	1	0.00	2.82	0.11
Site	2	0.00	2.05	0.16	2	0.00	1.95	0.16
Interaction	2	0.00	0.48	0.63	2	0.00	0.98	0.39
Residuals	18	0.00			22	0.01		
PLFA 18:1ω7								
Invasion	1	63133	0.24	0.63	1	0.00	1.52	0.23
Site	2	1458794	2.76	0.09	2	0.01	3.73	<0.05
Interaction	2	70452	0.13	0.88	2	0.00	0.75	0.49
Residuals	18	4757624			22	0.02		
PLFA cy17:0								
Invasion	1	0.00	0.70	0.41	1	0.01	2.76	0.11
Site	2	0.00	2.15	0.15	2	0.01	1.53	0.24
Interaction	2	0.00	1.32	0.29	2	0.01	2.08	0.15
Residuals	18	0.00			22	0.08		
PLFA cy19:0								
Invasion	1	5893459	0.02	0.88	1	2.59	2.54	0.13
Site	2	353813238	0.69	0.51	2	4.35	2.13	0.14
Interaction	2	166864618	0.33	0.73	2	0.99	0.49	0.62
Residuals	18	4602455820			22	22.42		
PLFA 18:2ω6								
Invasion	1	56373	0.56	0.46	1	0.01	8.27	<0.01
Site	2	20356	0.10	0.90	2	0.02	12.34	<0.001
Interaction	2	218745	1.09	0.36	2	0.00	0.72	0.50
Residuals	18	1798436			22	0.01		
Eukaryotes								
Invasion	1	0.00	2.07	0.17	1	0.20	3.94	0.06
Site	2	0.00	0.84	0.45	2	0.17	1.65	0.21
Interaction	2	0.00	1.12	0.35	2	0.02	0.23	0.79

Residuals	18	0.00			22	1.10		
PLFA 20:4ω6								
Invasion	1	0.00	4.83	<0.05	1	5.49	4.73	<0.05
Site	2	0.00	0.34	0.72	2	3.26	1.41	0.27
Interaction	2	0.00	2.02	0.16	2	1.61	0.69	0.51
Residuals	18	0.00			22	25.55		
PLFA 20:5ω3								
Invasion	1	0.01	2.17	0.16	1	0.78	1.58	0.22
Site	2	0.07	13.66	<0.001	2	0.91	0.92	0.41
Interaction	2	0.00	0.77	0.48	2	1.05	1.07	0.36
Residuals	18	0.05			22	10.81		
PLFA 20:1ω9								
Invasion	1	1293	0.68	0.42	1	1.47	0.43	0.51
Site	2	18289	4.78	<0.05	2	13.66	2.01	0.16
Interaction	2	10737	2.81	0.09	2	3.77	0.56	0.58
Residuals	18	34417			22	74.73		
Ratios								
Gram(+):Gram(-)								
Invasion	1	0.31	1.53	0.23	1	0.06	9.29	<0.01
Site	2	2.20	5.51	<0.05	2	0.02	1.47	0.25
Interaction	2	0.16	0.41	0.67	2	0.00	0.07	0.93
Residuals	18	3.60			22	0.14		
Fungi:Bacteria								
Invasion	1	0.00	0.00	1.00	1	0.10	3.49	0.08
Site	2	0.03	0.47	0.63	2	1.72	29.55	<0.001
Interaction	2	0.01	0.19	0.83	2	0.05	0.78	0.47
Residuals	18	0.55			22	0.64		
10Me ratio								
Invasion	1	0.00	0.09	0.77	1	0.14	9.05	<0.01
Site	2	0.09	2.64	0.10	2	0.26	8.78	<0.01
Interaction	2	0.01	0.38	0.69	2	0.02	0.51	
Residuals	18	0.29			22	0.33		
Cyclo ratio								
Invasion	1	0.79	0.99	0.34	1	0.03	8.49	<0.01
Site	2	29.64	18.49	<0.001	2	0.10	13.61	<0.001
Interaction	2	0.71	0.45	0.65	2	0.00	0.36	0.70
Residuals	18	12.82			22	0.08		

Supplementary figures

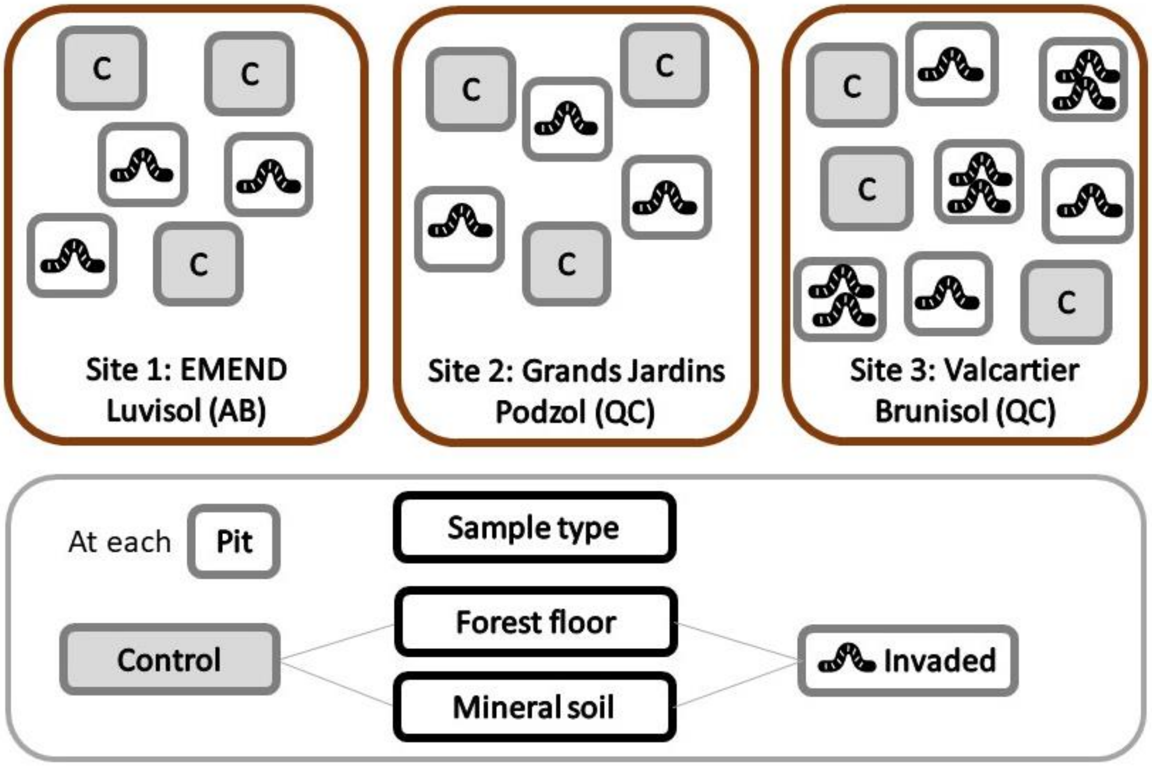

Figure S1. Schematic of the sampling design.

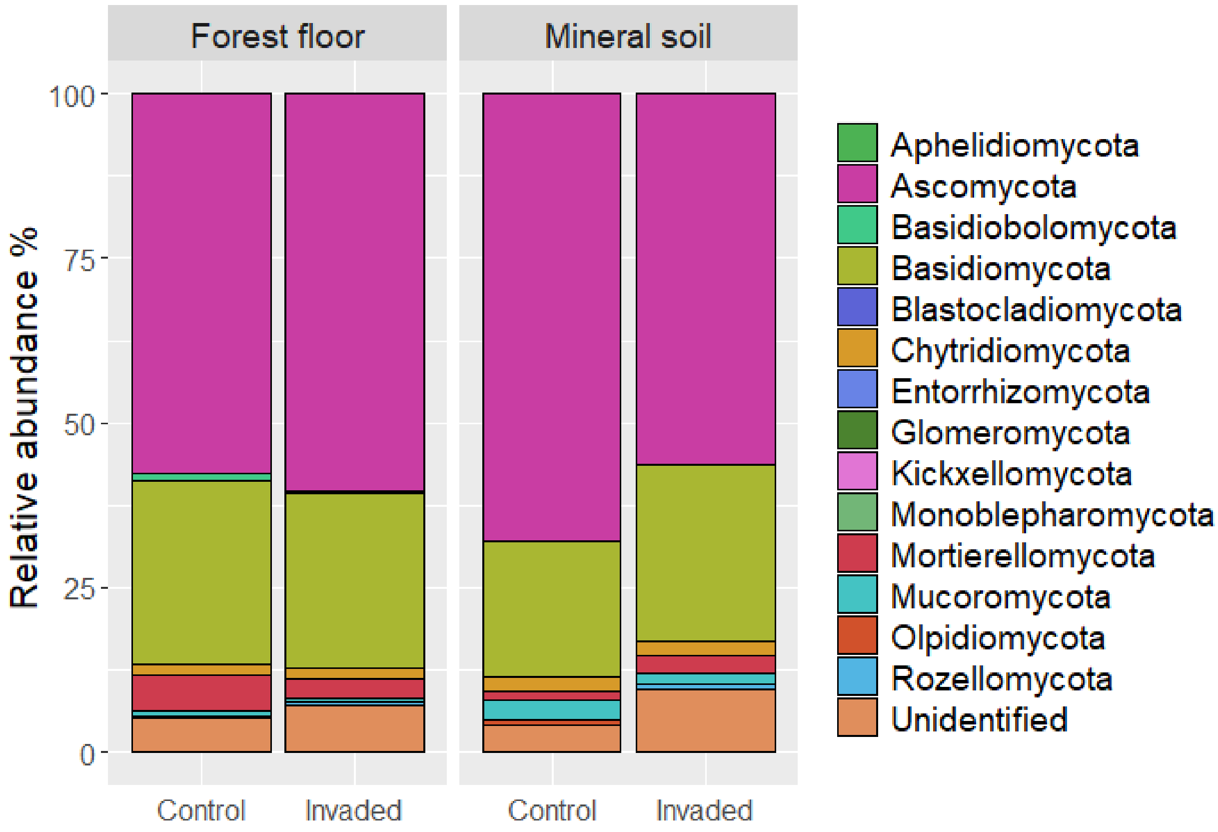

Figure S2. Average relative abundances (as number of reads) of fungal phyla in control and earthworm-invaded forest floors and mineral soils.

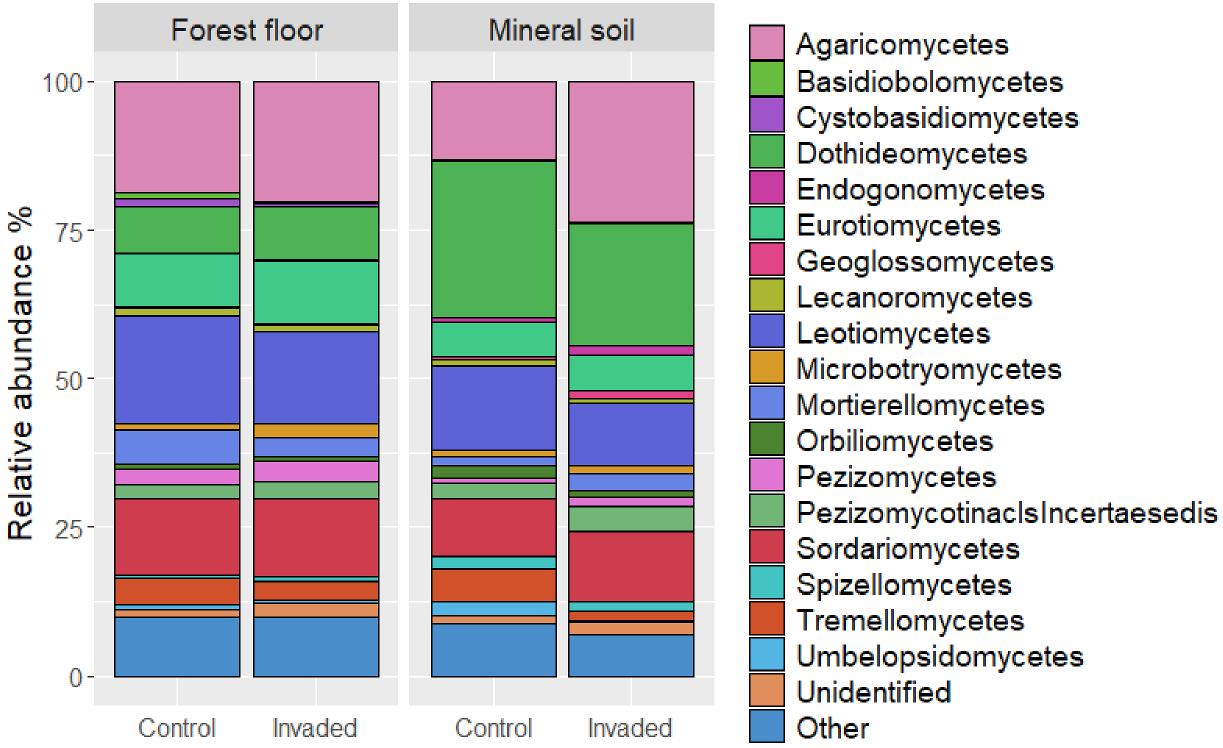

Figure S3. Average relative abundances (as number of reads) of fungal classes representing > 1% of the number of reads in control and earthworm-invaded forest floors and mineral soils.

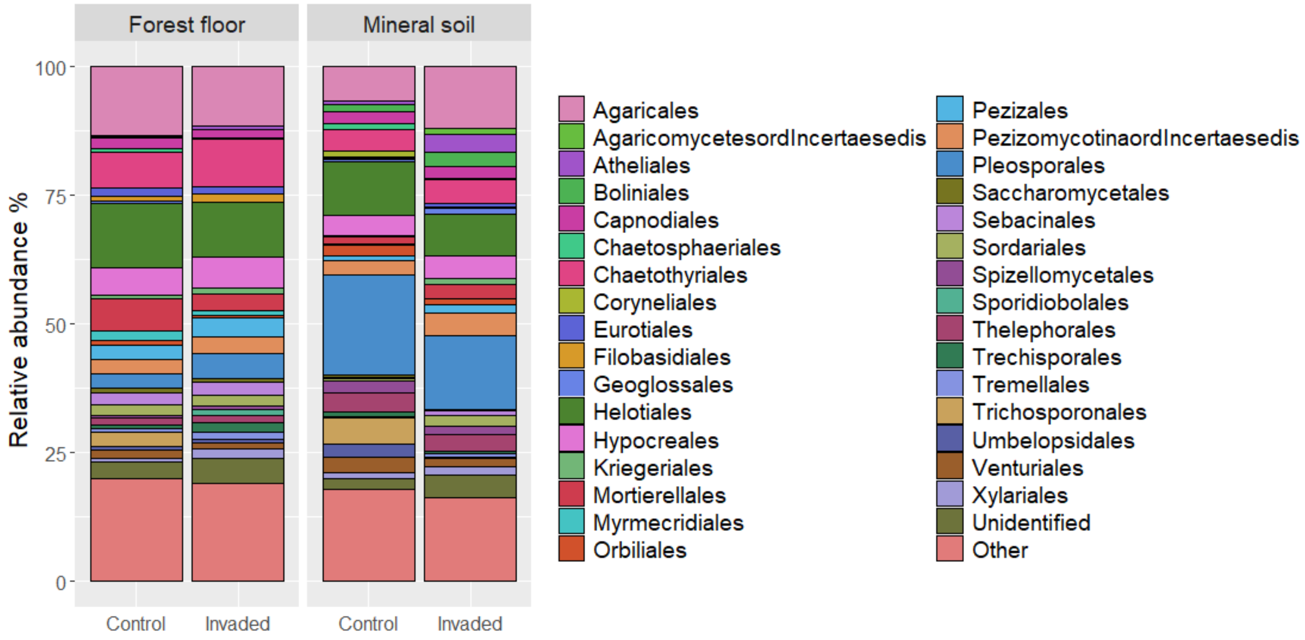

Figure S4. Average relative abundances (as number of reads) of fungal orders representing > 1% of the number of reads in control and earthworm-invaded forest floors and mineral soils.

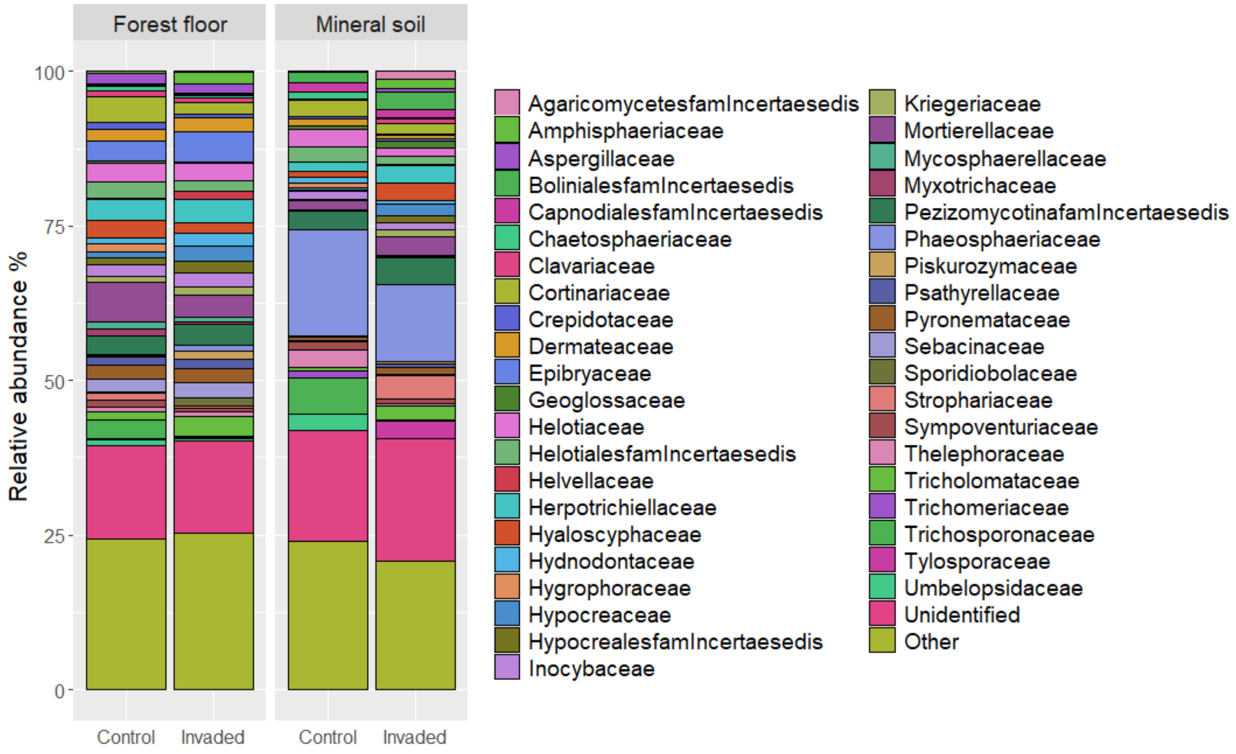

Figure S5. Average relative abundances (as number of reads) of fungal families representing > 1% of the number of reads in control and earthworm-invaded forest floors and mineral soils.

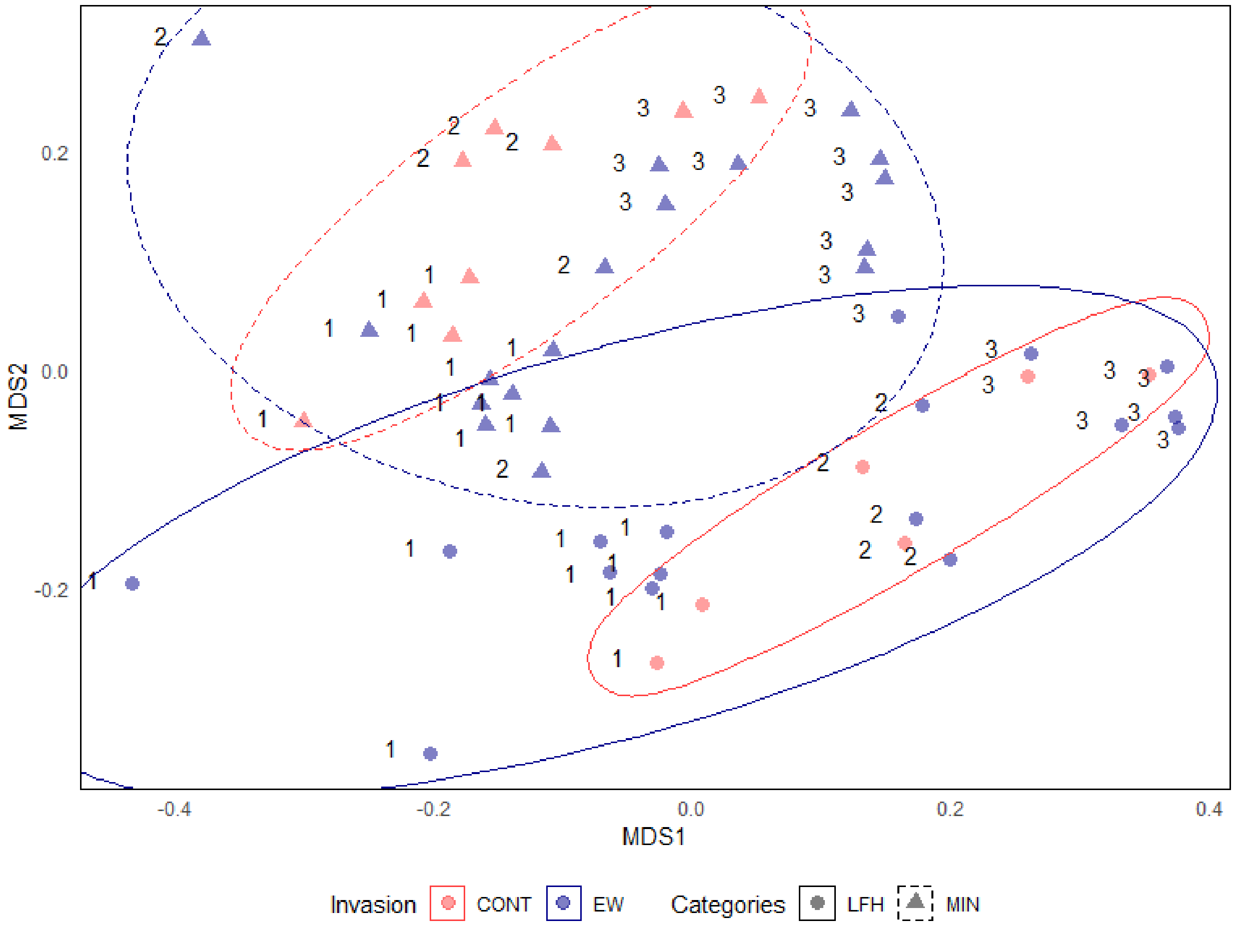

Figure S6. Non-metric multidimensional scaling of fungal amplicon sequence variants (ASVs) using metaMDS function from the vegan package on Bray-Curtis distance matrices after Hellinger transformation of individual ASV abundance (Anderson and Willis, 2003; Legendre and Gallagher, 2001; Oksanen et al., 2019). The final stress was 0.16, non-metric fit R^2=0.97 and linear fit R^2=0.87. Numbers correspond to sites: EMEND (1), Grands Jardins (2) and Valcartier (3). Earthworm invaded sites denoted by purple circles, non-invaded sites by pink circles; forest floors (LFH) represented by circles and mineral soils (MIN) by triangles.

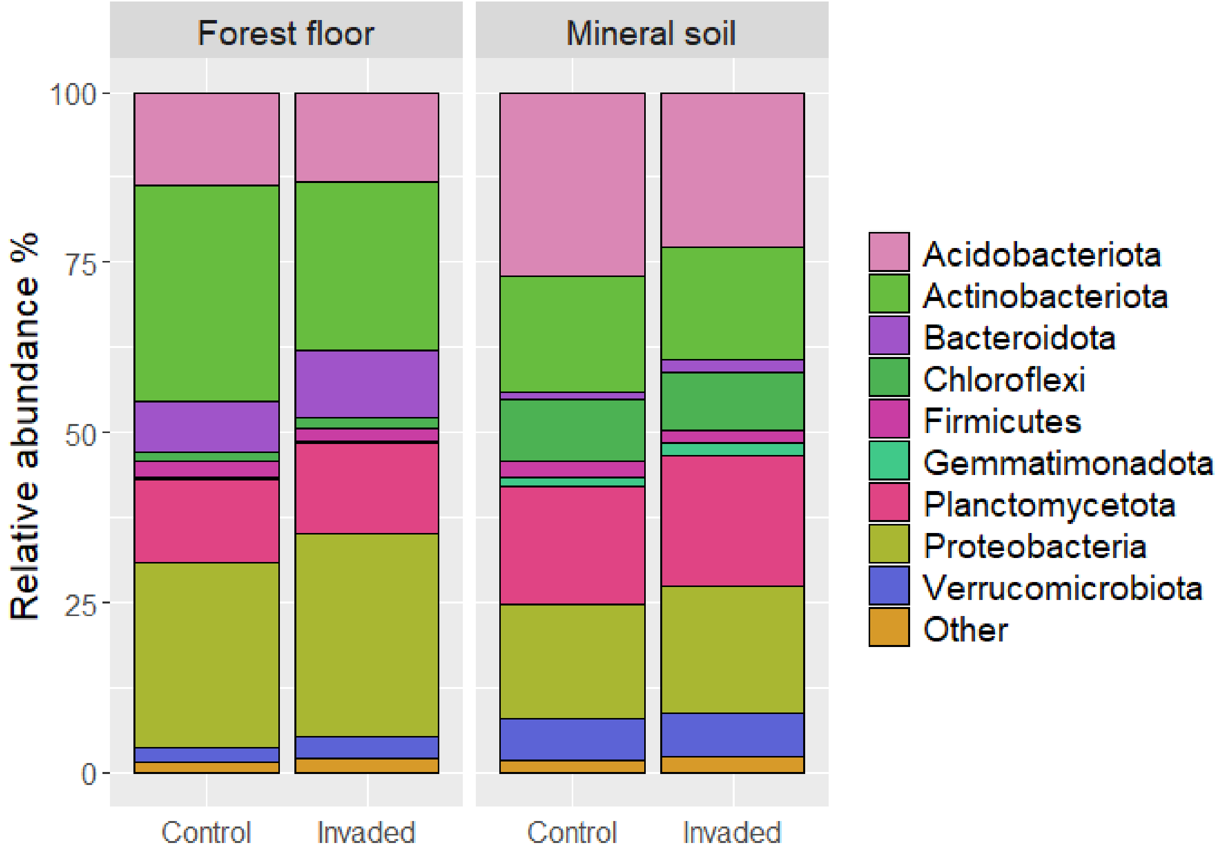

Figure S7. Average relative abundances (as number of reads) of bacterial phyla representing > 1% of the number of reads in control and earthworm-invaded forest floors and mineral soils.

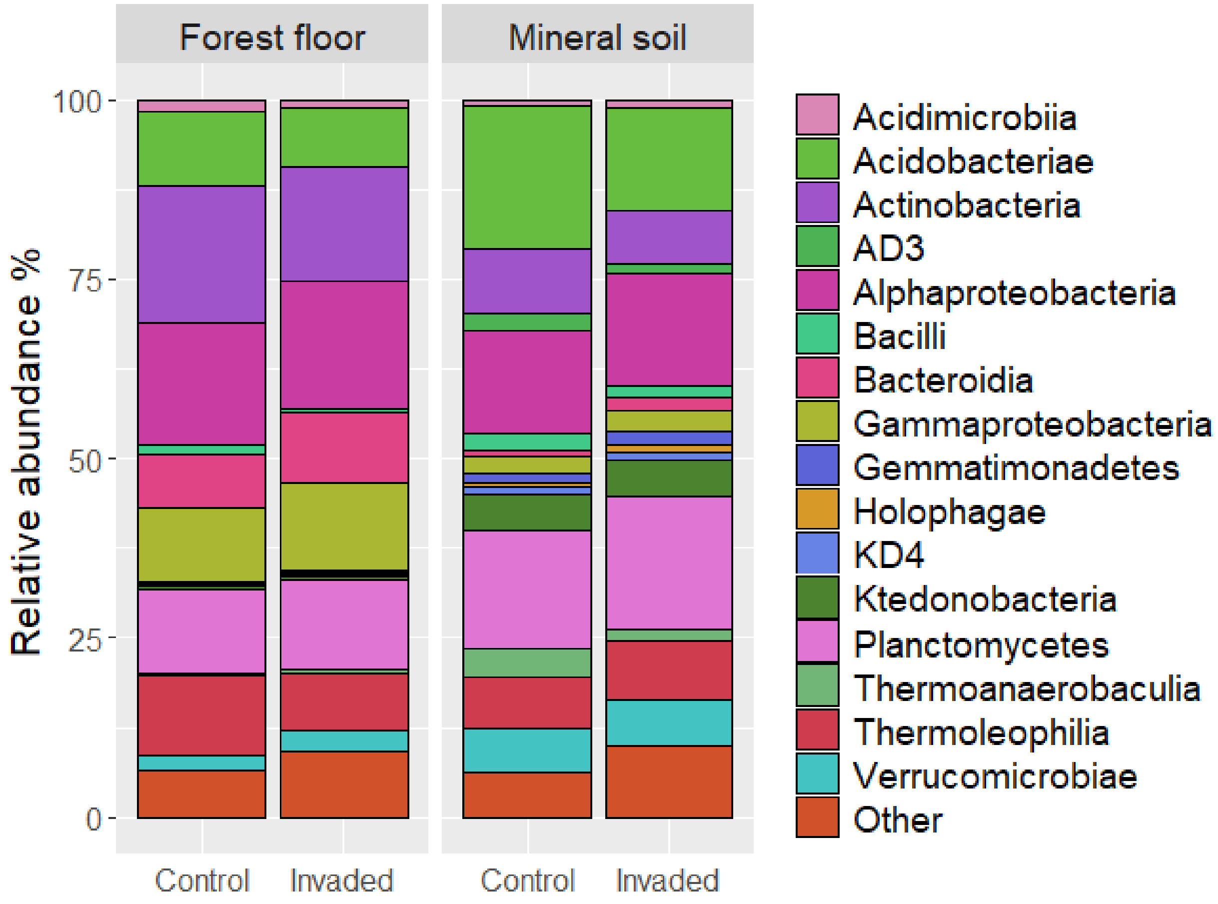

Figure S8. Average relative abundances (as number of reads) of bacterial classes representing > 1% of the number of reads in control and earthworm-invaded forest floors and mineral soils.

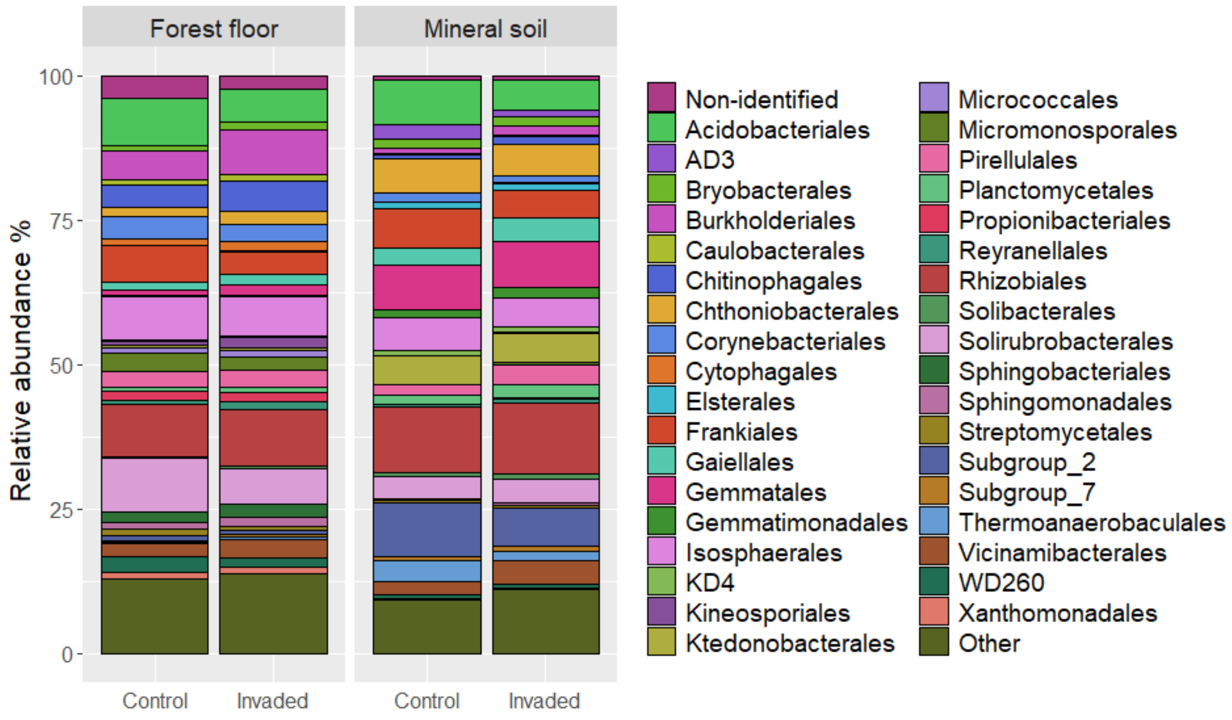

Figure S9. Average relative abundances (as number of reads) of bacterial orders representing > 1% of the number of reads in control and earthworm-invaded forest floors and mineral soils.

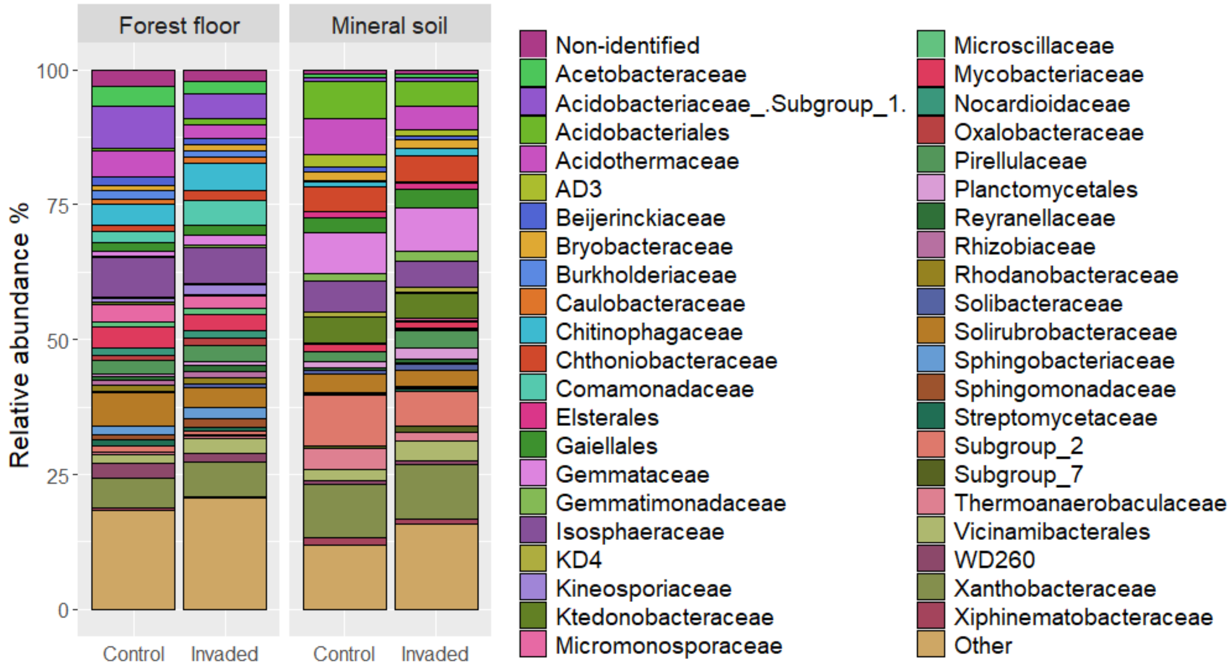

Figure S10. Average relative abundances (as number of reads) of bacterial families representing > 1% of the number of reads in control and earthworm-invaded forest floors and mineral soils.

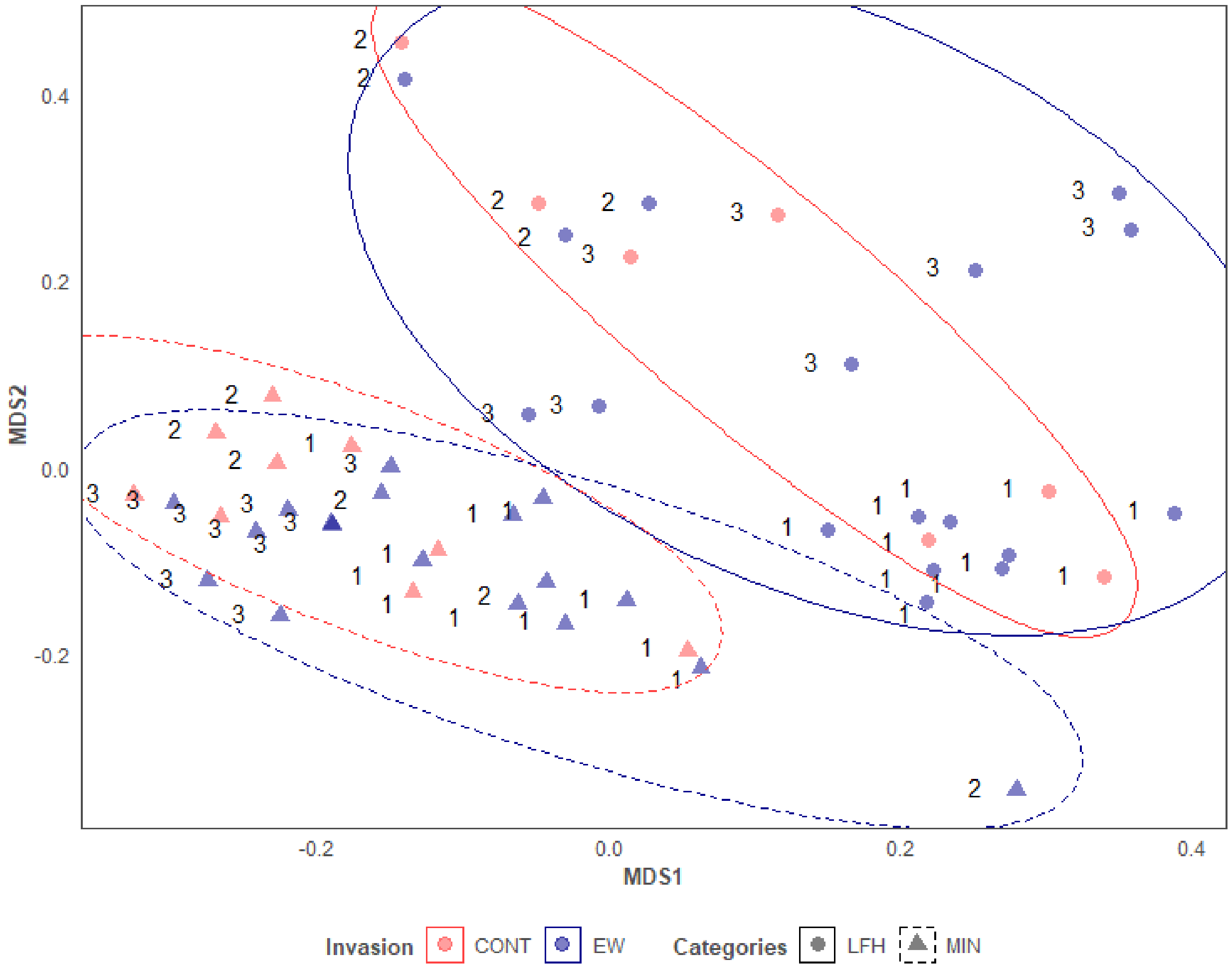

Figure S11. Non-metric multidimensional scaling of bacterial amplicon sequence variants (ASVs) using metaMDS function from the vegan package on Bray-Curtis distance matrices after Hellinger transformation of individual ASV abundance (Anderson and Willis, 2003; Legendre and Gallagher, 2001; Oksanen et al., 2019). The final stress was 0.08, non-metric fit R^2*=0.99 and linear fit* R^2*=0.97. Numbers correspond to sites: EMEND (1), Grands Jardins (2) and Valcartier (3). Earthworm invaded sites denoted by purple circles, non-invaded sites by pink circles; forest floors (LFH) represented by circles and mineral soils (MIN) by triangles.*

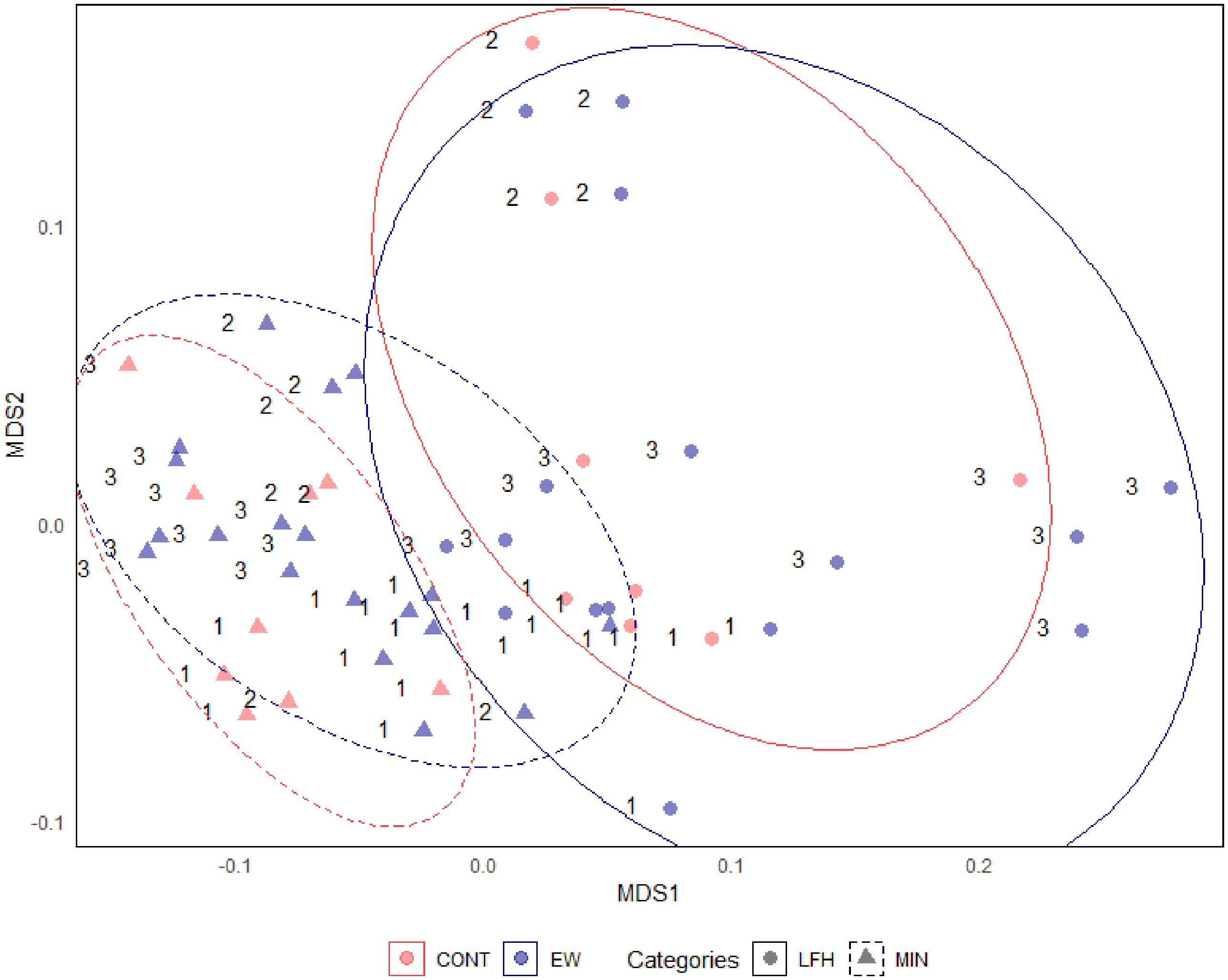

Figure S12. Non-metric multidimensional scaling of phospholipid fatty acids (PLFAs) using metaMDS function from the vegan package on Bray-Curtis distance matrices after Hellinger transformation of individual PLFA abundance (Anderson and Willis, 2003; Legendre and Gallagher, 2001; Oksanen et al., 2019). The final stress was 0.09, non-metric fit R^2=0.99 and linear fit R^2=0.97. Numbers correspond to sites: EMEND (1), Grands Jardins (2) and Valcartier (3). Earthworm invaded sites denoted by purple circles, non-invaded sites by pink circles; forest floors (LFH) represented by circles and mineral soils (MIN) by triangles.