



*Supplement of*

## **Earthworm-invaded boreal forest soils harbour distinct microbial communities**

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## 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 [°C]	MAP [mm]	Coordinates		Textural class		Forest floor thickness [cm]		CaCl <sub>2</sub> pH		TN [%]		TC [%]	
						Control	Invaded	Control	Invaded	Control	Invaded	Control	Invaded	Control	Invaded
Luvisol (EMEND)	Glacial till	1.4	413	56°46'N 118°22'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	46°55'N 71°36'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	47°40'N 70°50'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 ( $\pm 1$  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
<b>Fungi</b>				
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
<b>Bacteria</b>				
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
<b>Fungal guilds</b>								
<b>Ectomycorrhizae</b>								
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		
<b>Pathogens</b>								
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		
<b>Saprotrophs</b>								
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		
<b>Ectomycorrhizal:Saprotrophic</b>								
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		
<b>Fungal phyla</b>								
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		
<b>Mucoromycota</b>								
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		
<b>Species richness</b>								
<b>All fungi</b>								
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		
<b>Ectomycorrhizae</b>								
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			
<b>Pathogens</b>								
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		
<b>Saprotrophs</b>								
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		
<b>Species diversity</b>								
<b>All fungi</b>								
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		
<b>Ectomycorrhizae</b>								
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		
<b>Pathogens</b>								
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		
<b>Saprotrophs</b>								
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
<b>Bacterial phyla</b>								
<b>Actinobacteriota</b>								
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		
<b>Acidobacteriota</b>								
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		
<b>Bacteroidota</b>								
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		
<b>Chloroflexi</b>								
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		
<b>Firmicutes</b>								
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		
<b>Gemmatimonadota</b>								
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		
<b>Planctomycetota</b>								
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		
<b>Proteobacteria</b>								
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		
<b>Alphaproteobacteria</b>								
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		
<b>Gammaproteobacteria</b>								
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		
<b>Verrucomicrobiota</b>								
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		
<b>Proteobacteria:Acidobacteriota</b>								
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		
<b>Bacterial families</b>								
<b>Acidothermaceae</b>								
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		
<b>Chitinophagaceae</b>								
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		
<b>Chthoniobacteraceae</b>								
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		
<b>Gemmatimonadaceae</b>								
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		
<b>Nitrosomonadaceae</b>								
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		
<b>Pirellulaceae</b>								
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		
<b>Reyranellaceae</b>								
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		
<b>Solibacteraceae</b>								
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		
<b>Solirubrobacteraceae</b>								
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		
<b>Thermoanaerobaculaceae</b>								
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		
<b>Xiphinematobacteraceae</b>								
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		
<b>Species richness</b>								
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		
<b>Species diversity</b>								
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 cy19:0 $\omega$ 9 and cy19:0 $\omega$ 7 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
<b>Total PLFA biomass</b>								
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		
<b>PLFA 15:0</b>								
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		
<b>Gram(+) bacteria</b>								
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		
<b>PLFA i14:0</b>								
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		
<b>PLFA i15:0</b>								
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		
<b>PLFA a15:0</b>								
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		
<b>PLFA i16:0</b>								
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		

<b>PLFA a16:0</b>								
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		
<b>PLFA i17:0</b>								
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		
<b>PLFA a17:0</b>								
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		
<b>Gram(-) bacteria</b>								
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		
<b>PLFA 16:1<math>\omega</math>7</b>								
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		
<b>PLFA 18:1<math>\omega</math>7</b>								
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		
<b>PLFA cy17:0</b>								
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		
<b>PLFA cy19:0</b>								
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		
<b>PLFA 18:2<math>\omega</math>6</b>								
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		
<b>Eukaryotes</b>								
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		
<b>PLFA 20:4ω6</b>								
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		
<b>PLFA 20:5ω3</b>								
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		
<b>PLFA 20:1ω9</b>								
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		
<b>Ratios</b>								
<b>Gram(+):Gram(-)</b>								
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		
<b>Fungi:Bacteria</b>								
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		
<b>10Me ratio</b>								
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		
<b>Cyclo ratio</b>								
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

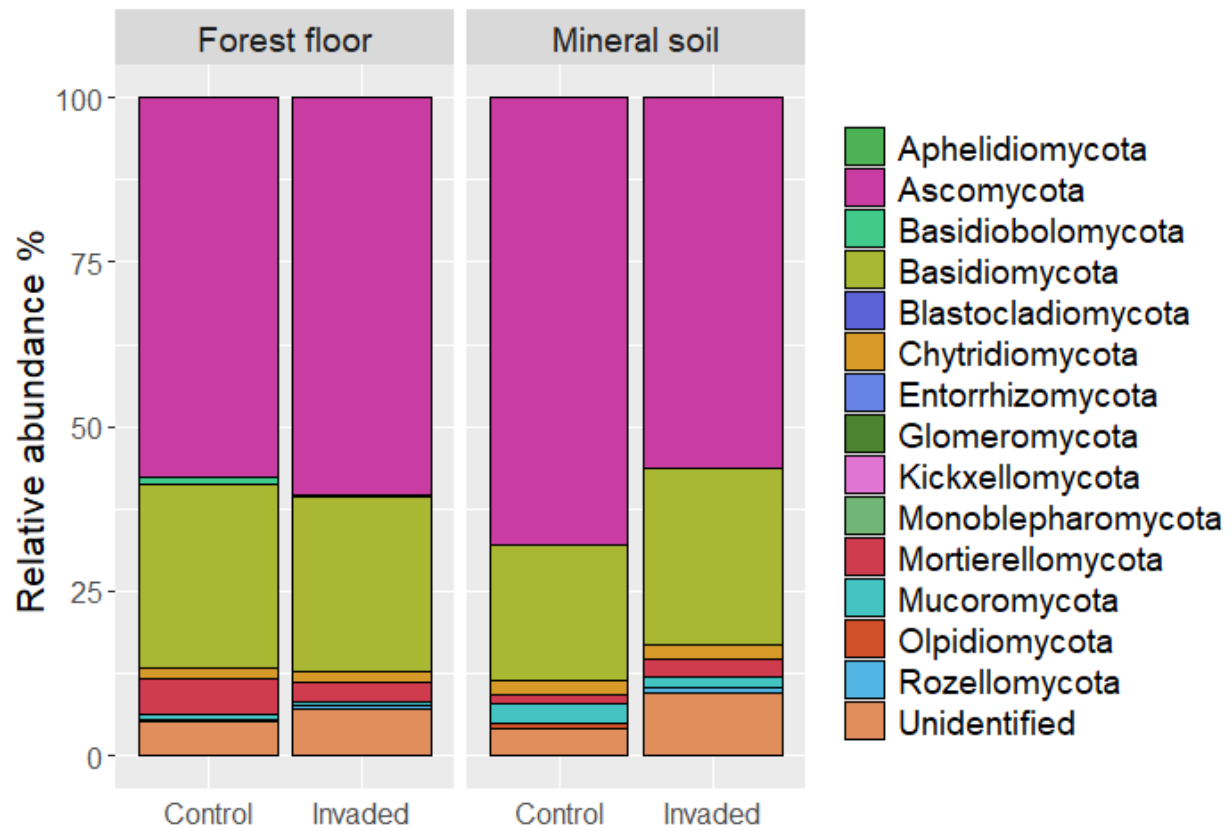


Figure S1. Average relative abundances (as number of reads) of fungal phyla in control and earthworm-invaded forest floors and mineral soils.

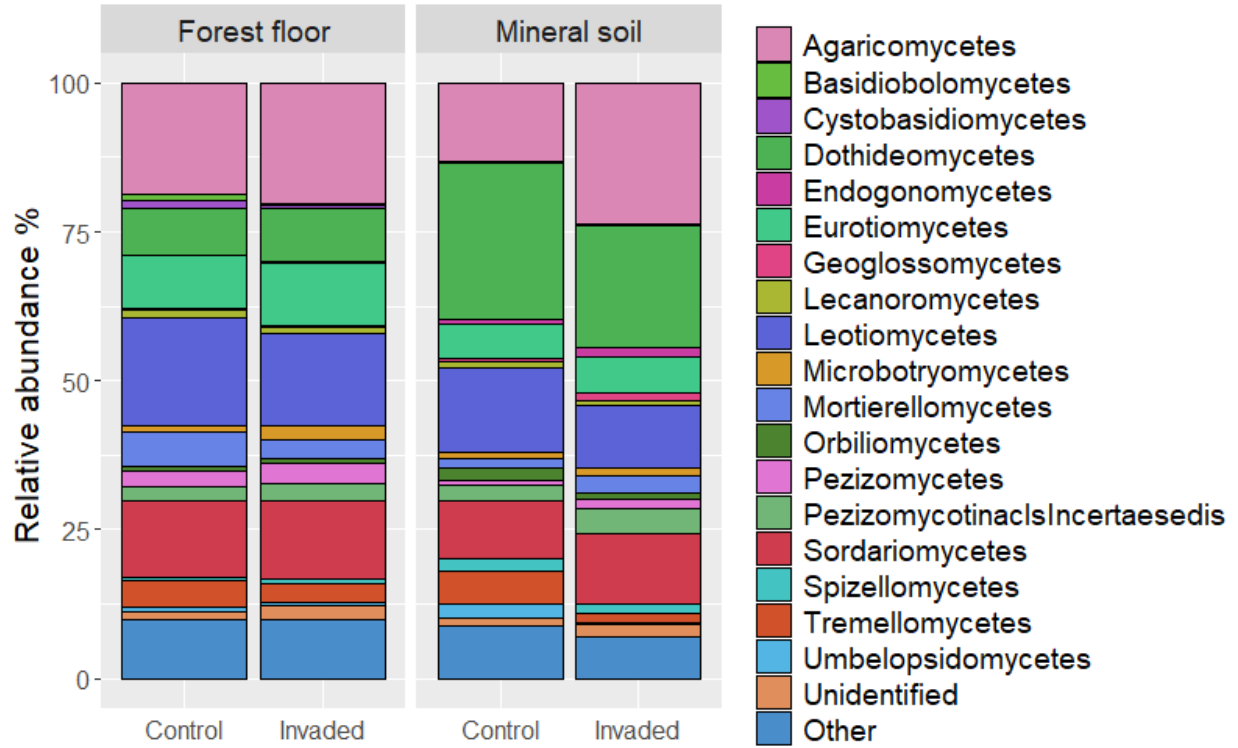


Figure S2. Average relative abundances (as number of reads) of fungal classes representing > 1% of the number of reads in control and earthworm-invaded forest floors and mineral soils.

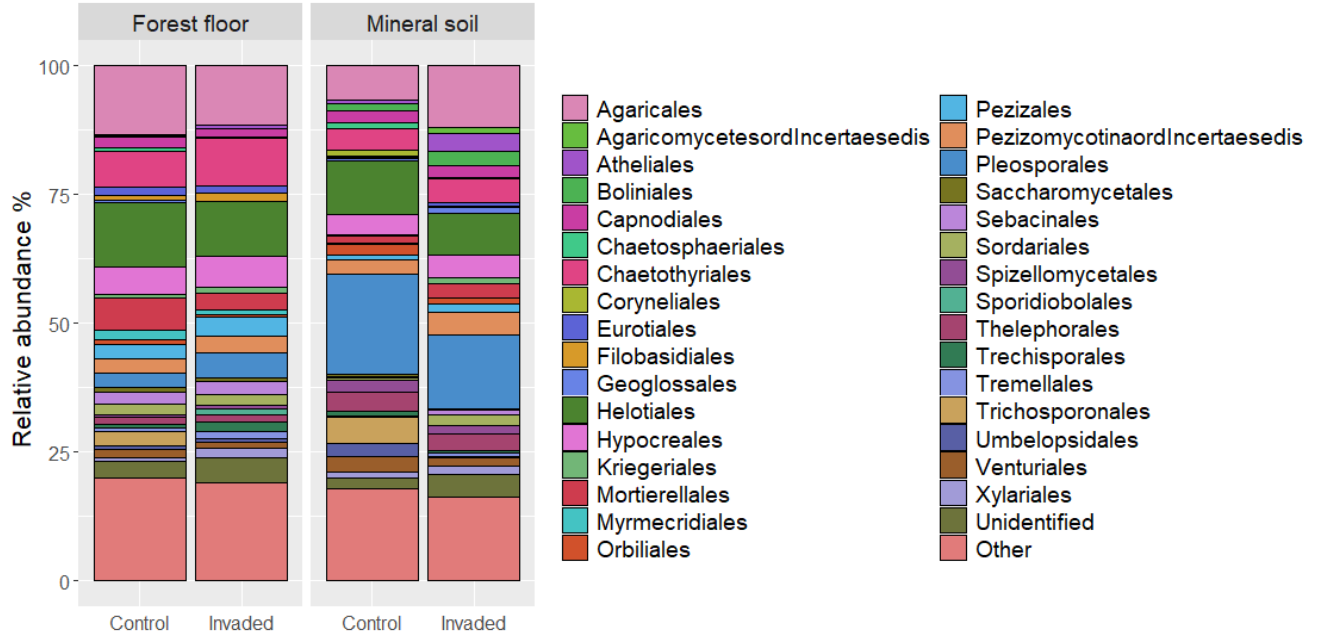


Figure S3. Average relative abundances (as number of reads) of fungal orders representing > 1% of the number of reads in control and earthworm-invaded forest floors and mineral soils.

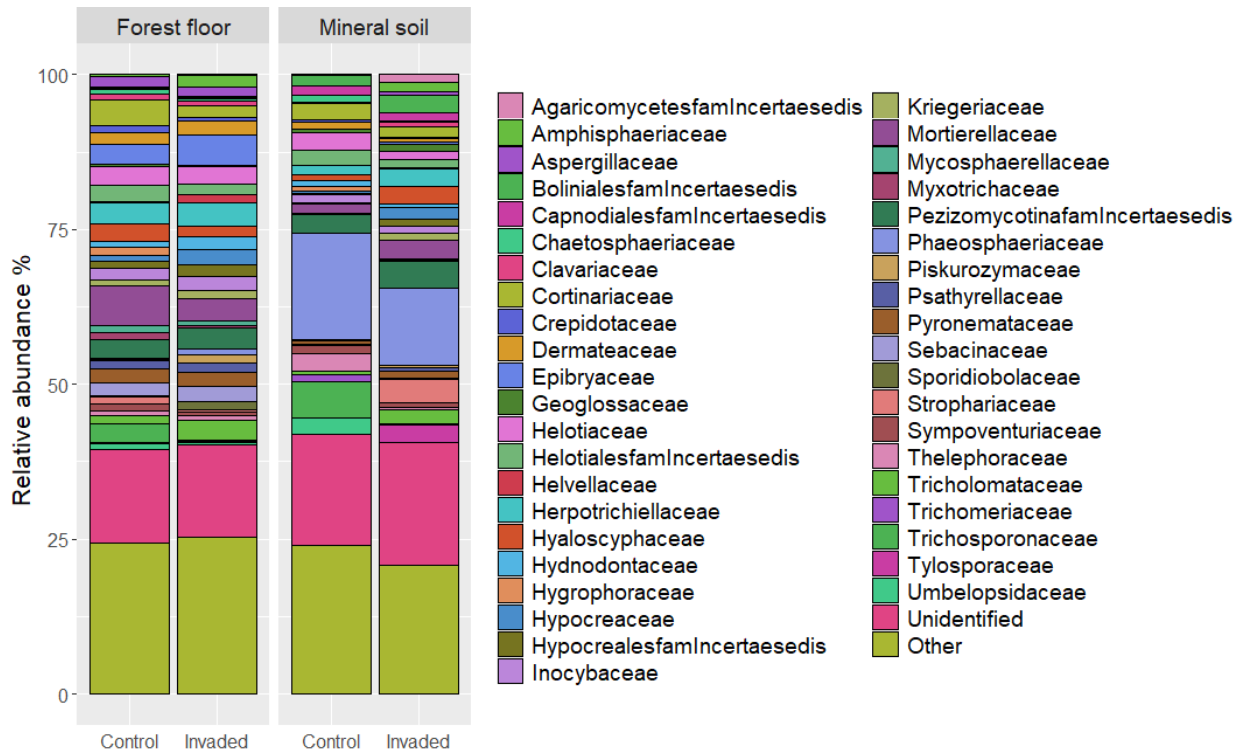


Figure S4. Average relative abundances (as number of reads) of fungal families representing > 1% of the number of reads in control and earthworm-invaded forest floors and mineral soils.

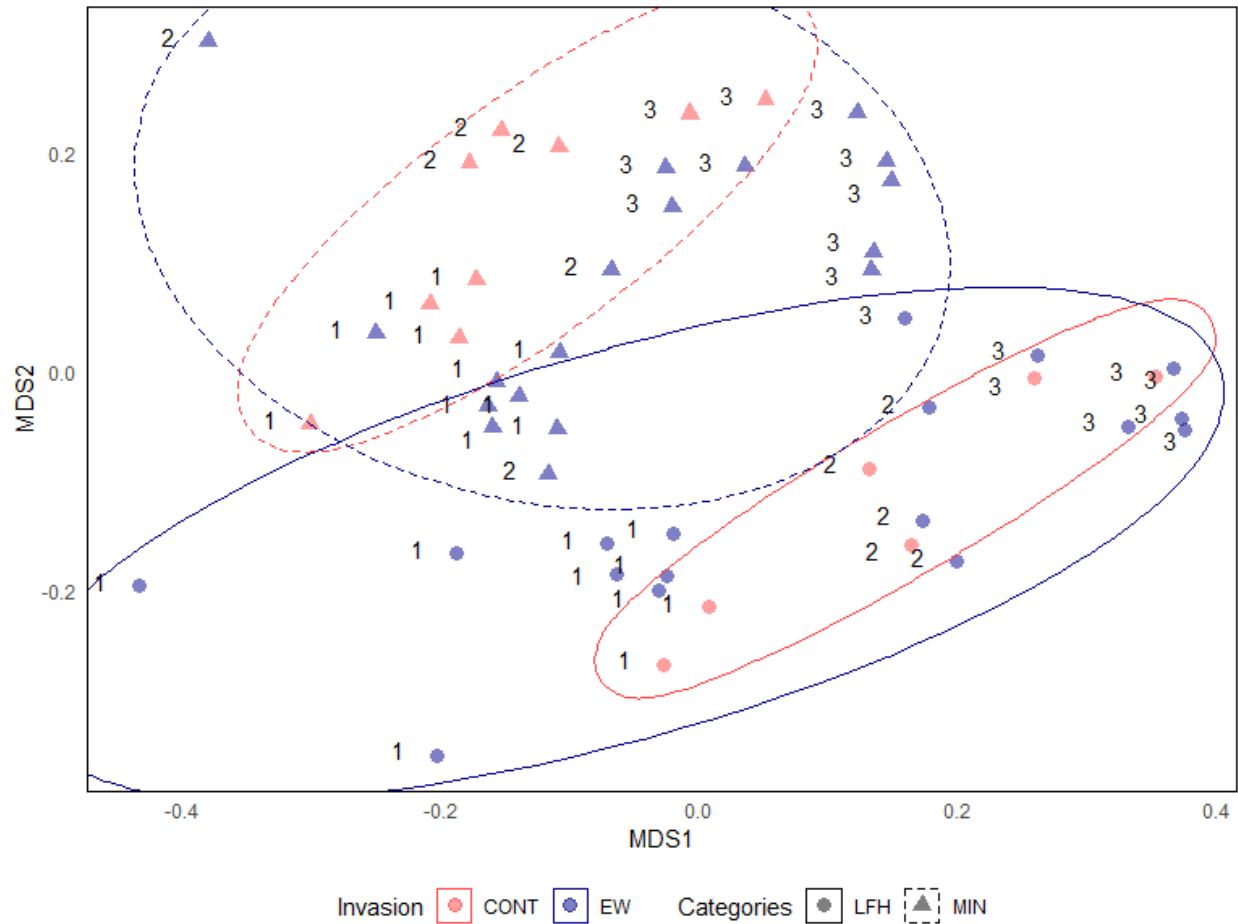


Figure S5. Non-metric multidimensional scaling of fungal amplicon sequence variants (ASVs) using metaMDS function from the vegan package on Bray-Curtis distance matrices after Hellinger transformation of individual ASV abundance (Anderson and Willis, 2003; Legendre and Gallagher, 2001; Oksanen et al., 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.

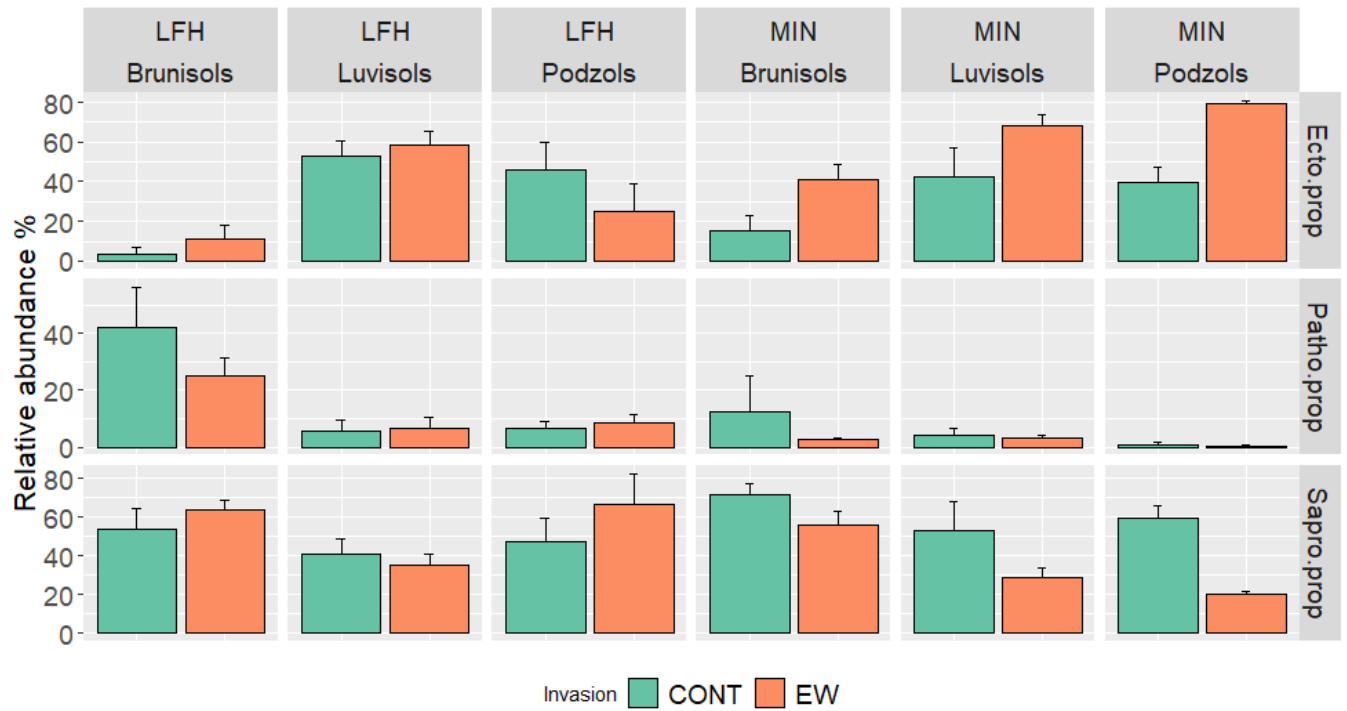


Figure S6. Average ( $\pm 1$  SE) relative abundances (as number of reads) of fungal guilds for each individual site.



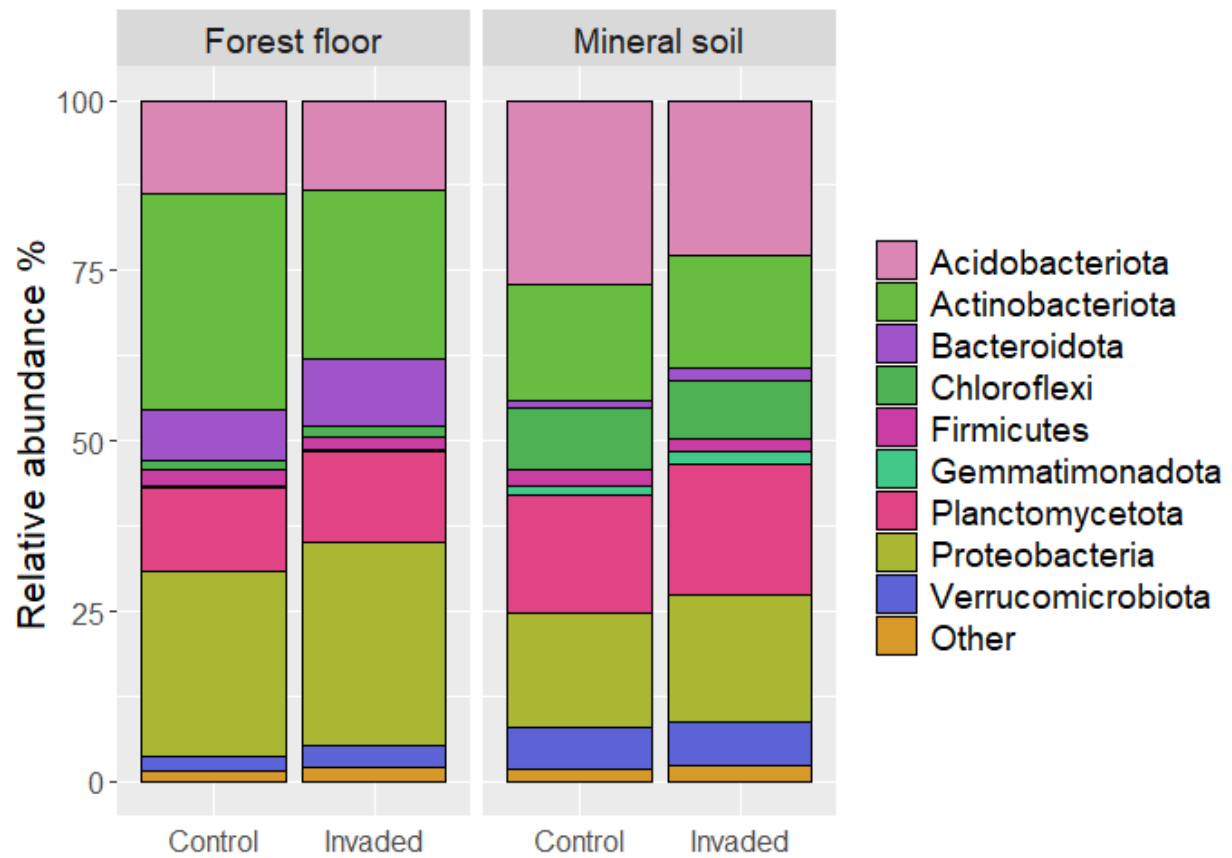


Figure S7. Average relative abundances (as number of reads) of bacterial phyla representing > 1% of the number of reads in control and earthworm-invaded forest floors and mineral soils.

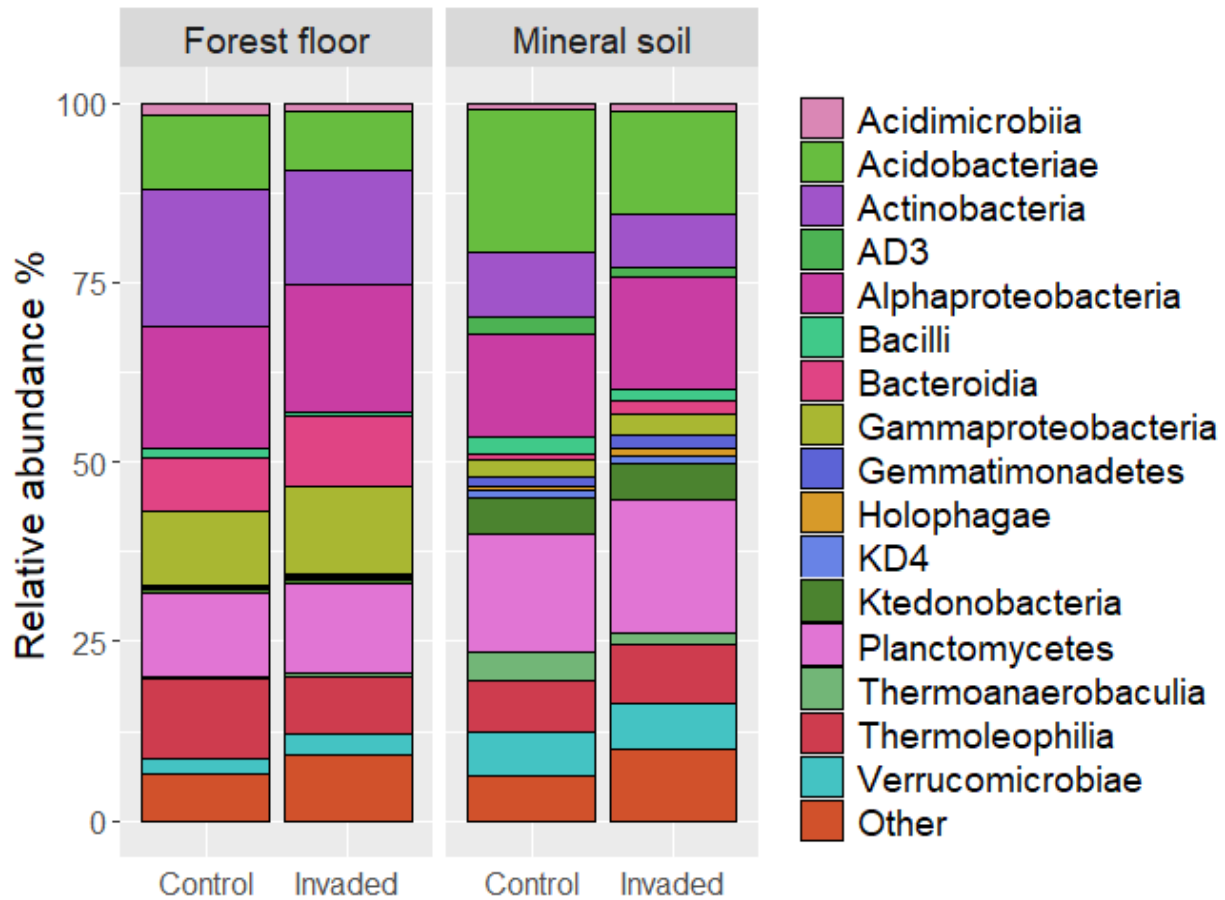


Figure S8. Average relative abundances (as number of reads) of bacterial classes representing > 1% of the number of reads in control and earthworm-invaded forest floors and mineral soils.

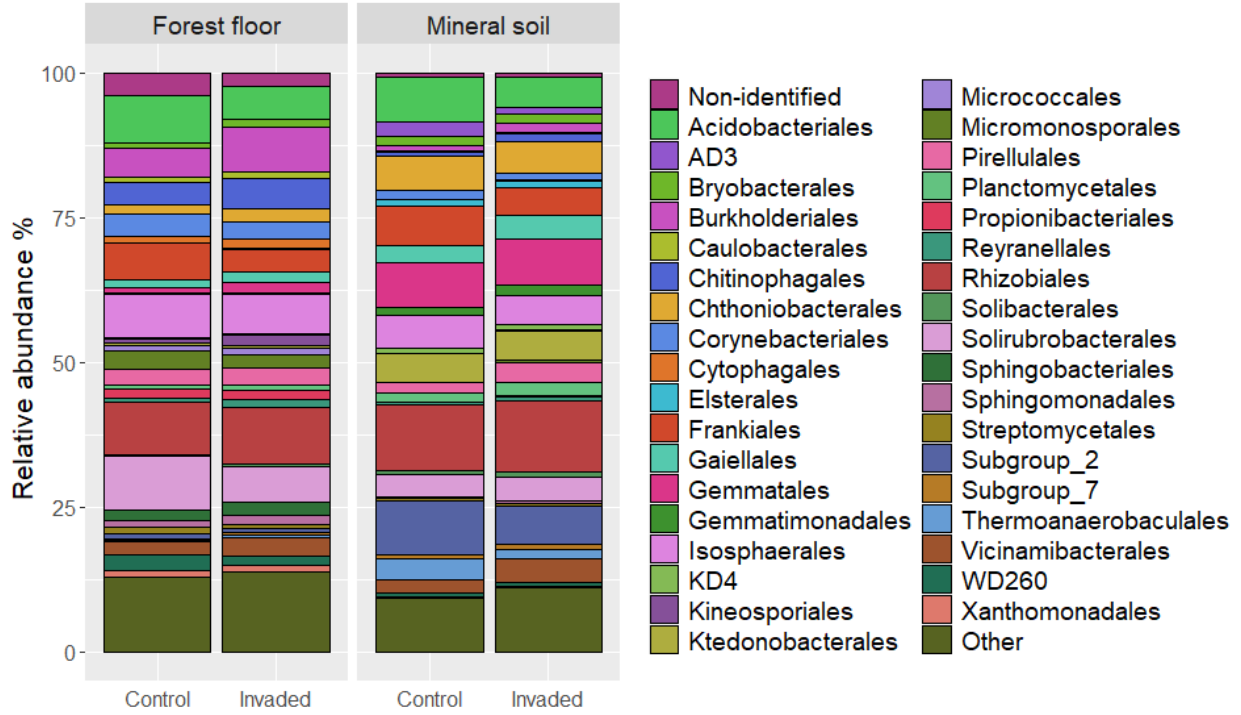


Figure S9. Average relative abundances (as number of reads) of bacterial orders representing > 1% of the number of reads in control and earthworm-invaded forest floors and mineral soils.

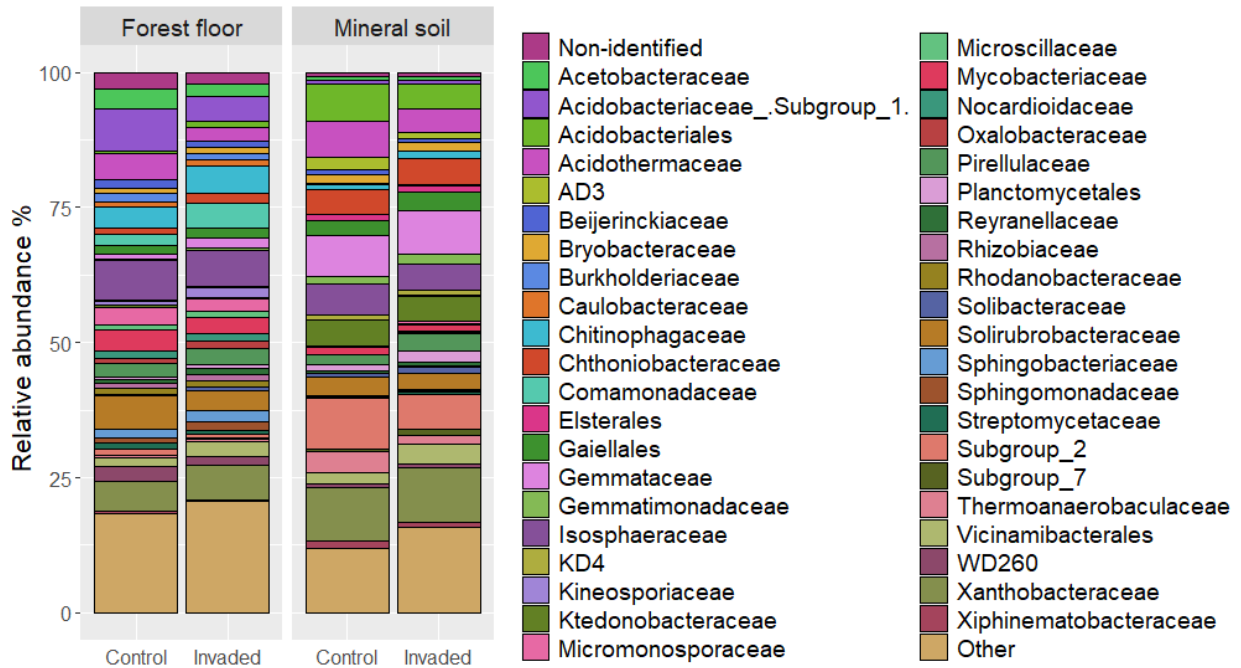


Figure S10. Average relative abundances (as number of reads) of bacterial families representing > 1% of the number of reads in control and earthworm-invaded forest floors and mineral soils.

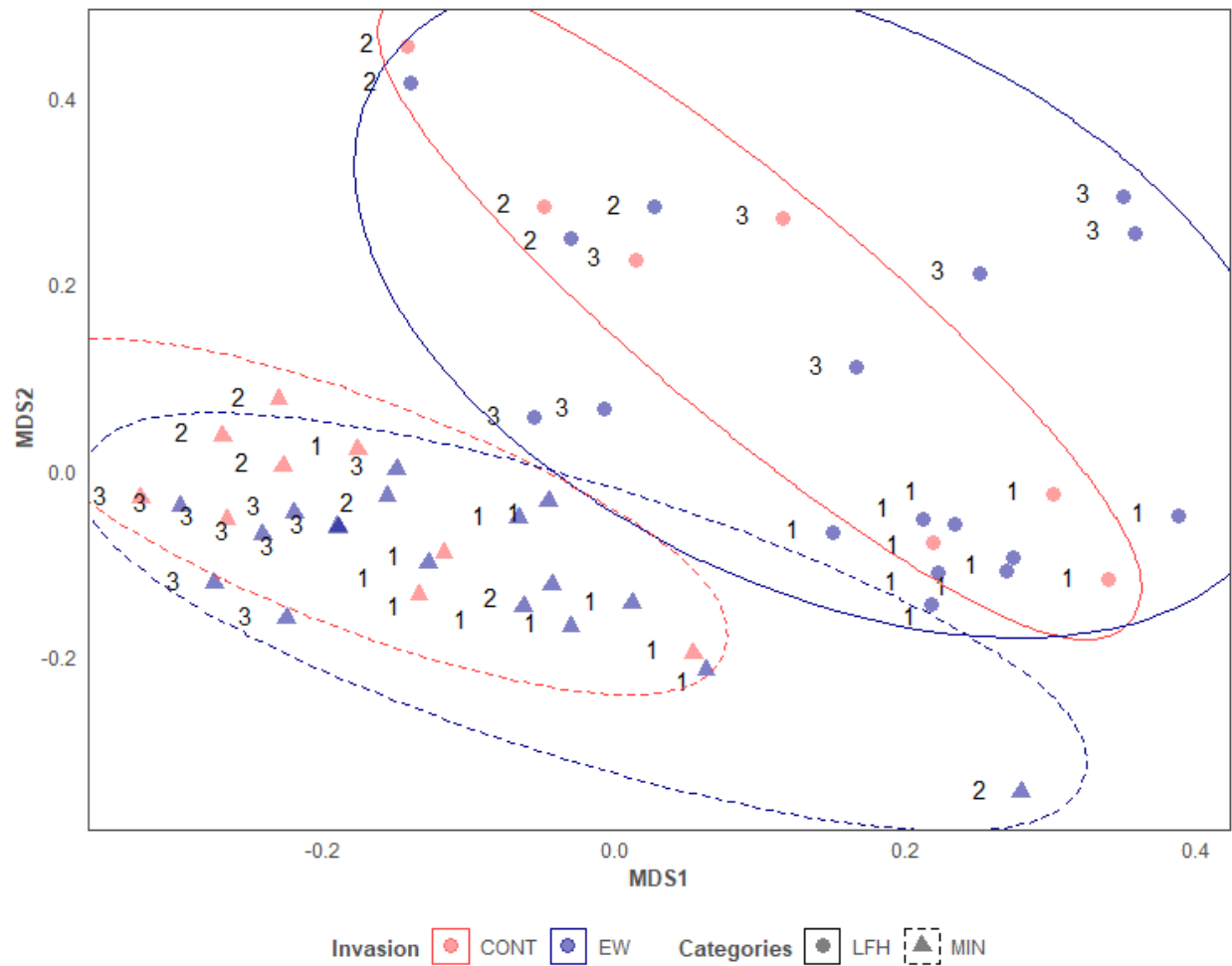


Figure S11. Non-metric multidimensional scaling of bacterial amplicon sequence variants (ASVs) using metaMDS function from the vegan package on Bray-Curtis distance matrices after Hellinger transformation of individual ASV abundance (Anderson and Willis, 2003; Legendre and Gallagher, 2001; Oksanen et 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.

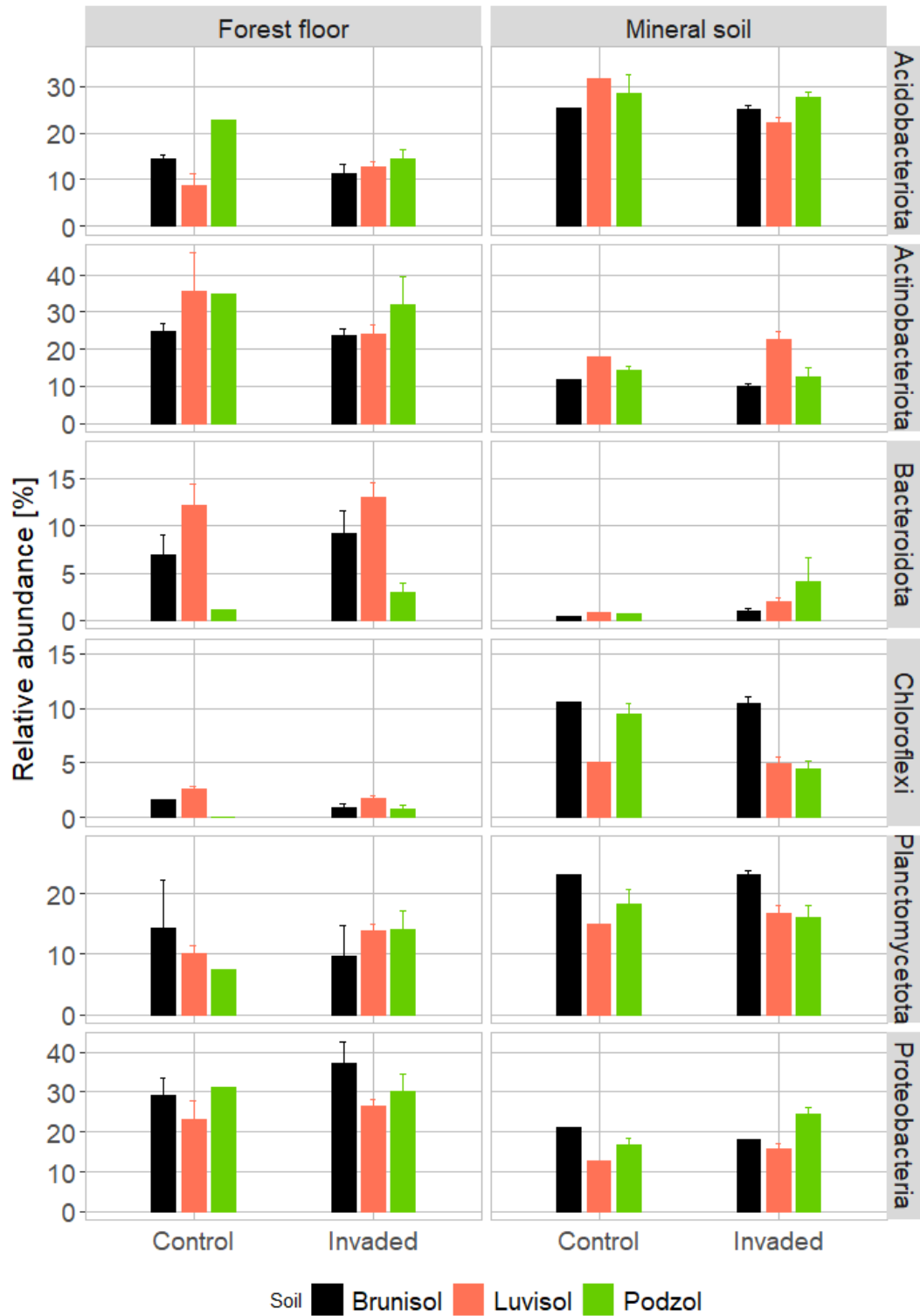


Figure S12. Average ( $\pm 1$  SE) relative abundances (as number of reads) of bacterial phyla for each individual site.

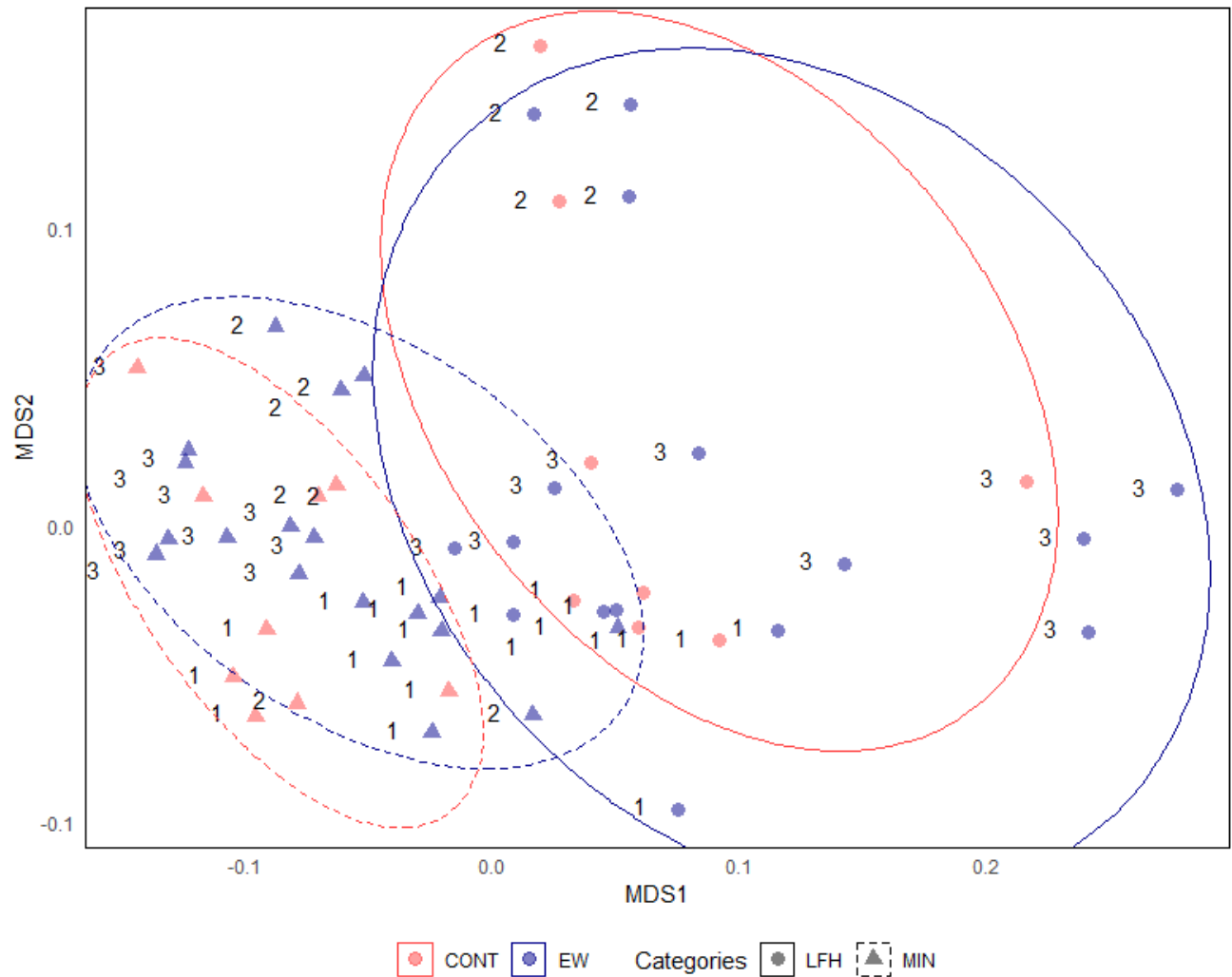


Figure S13. Non-metric multidimensional scaling of phospholipid fatty acids (PLFAs) using *metaMDS* function from the *vegan* package on Bray-Curtis distance matrices after Hellinger transformation of individual PLFA abundance (Anderson and Willis, 2003; Legendre and Gallagher, 2001; Oksanen et al., 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.

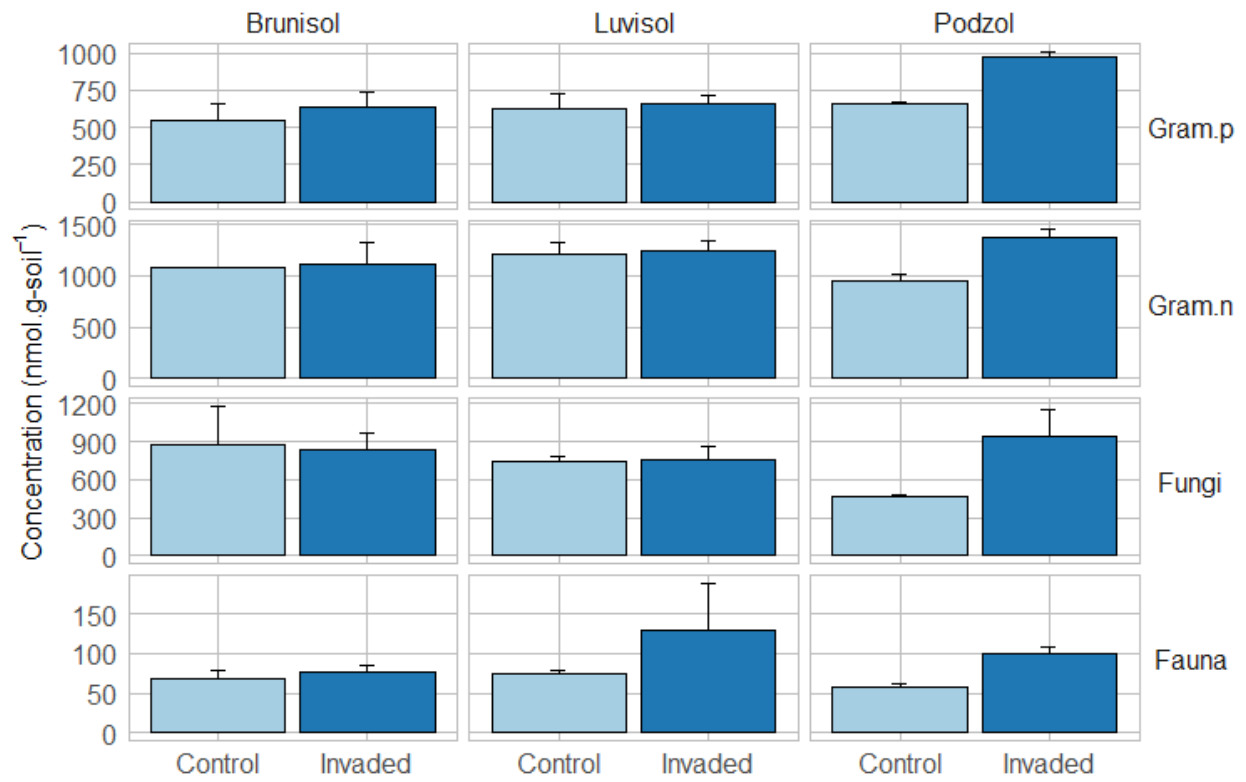


Figure S14. Average ( $\pm 1$  SE) concentrations of PLFA groups in forest floors for each individual site.

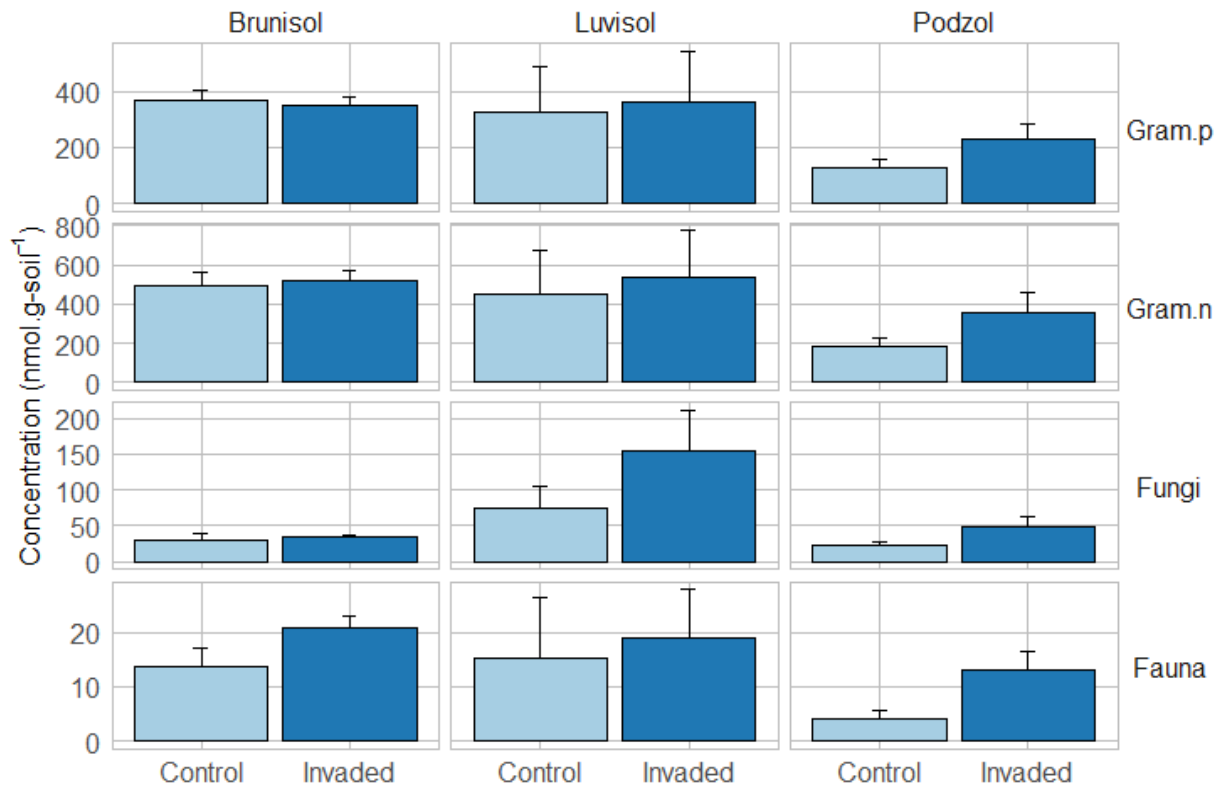


Figure S15. Average ( $\pm 1$  SE) concentrations of PLFA groups in mineral soils for each individual site.