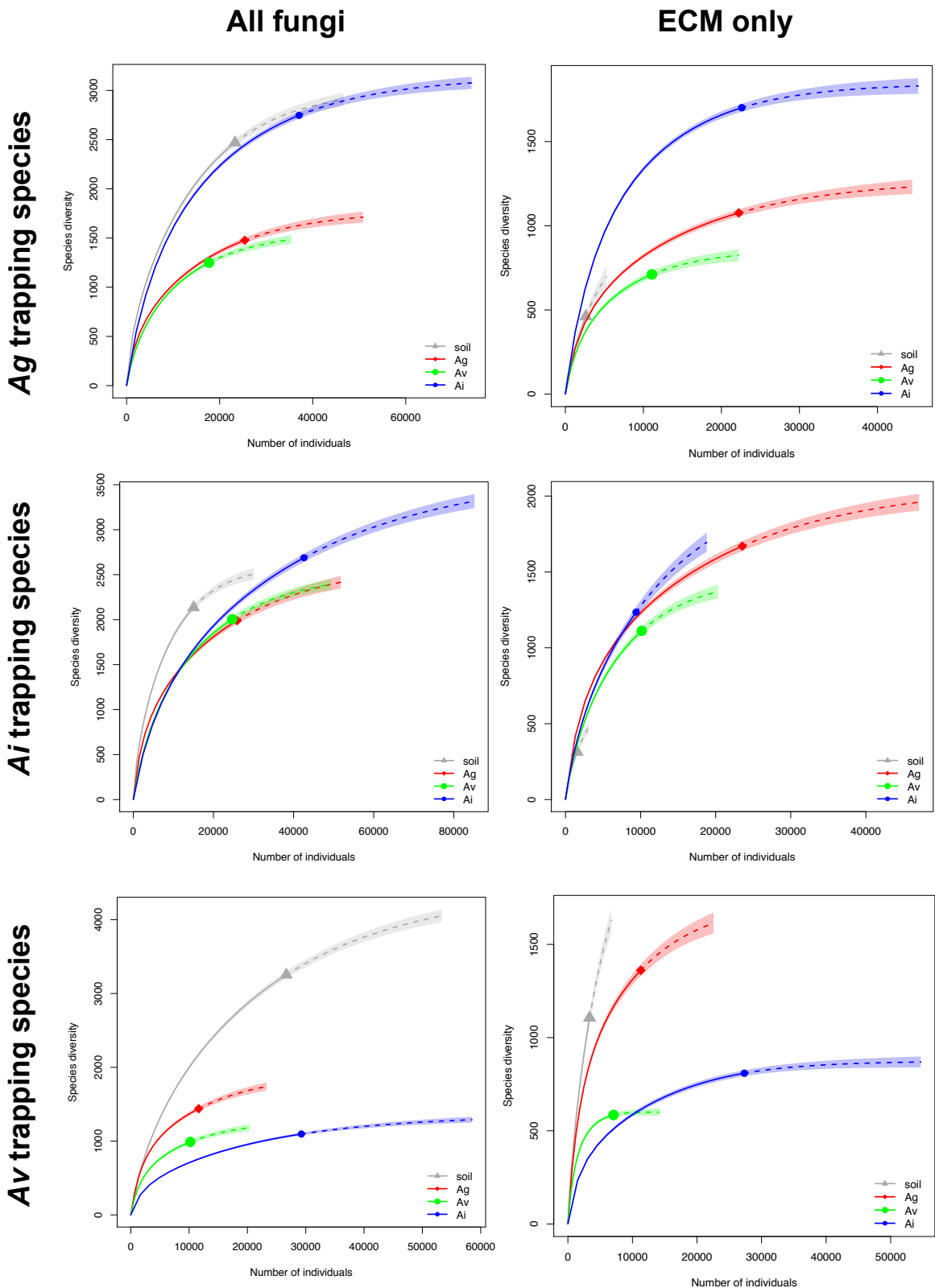


Supplementary data S1. *Frankia* OTUs composition of soils based on *nifH* metabarcoding approach. In red : most represented OTU of *Frankia* in plant trapped nodules



Supplementary data S3. Accumulation curves of fungal (left) and ECM (right) species richness measured on trapping plantlets (colored curves) on soils of *Ag* (red), *Ai* (blue) and *Av* (green) hosts, and compared to soil community (in grey), with extrapolation calculated from Hill numbers of richness ($q=0$). Each graph illustrates for a trapping host-species, the difference between the accumulation curves on its own soil or on other soils.

Supplementary data S2. ITS1 sequences assignment to ECM families.

Family	number of OTUs	Ag soil	Ai soil	Av soil	Ag root	Ai root	Av root	Specificity toward <i>Alnus</i> sub.
Not_assigned_to_ecm	2003	20552	13260	23194	76489	89780	49194	Not investigated
<i>Alnicola badia/umbrina</i>	1	490	285	590	5864	1390	17	Cannot assess host specificity
<i>Thelephoraceae</i> sp.	65	1013	590	1526	2081	1945	1176	Not specific
<i>Alnicola luteolofibrillosa</i>	1	362	150	75	5480	1549	27	Cannot assess host specificity
AMF	102	276	586	212	374	289	61	Not specific
<i>Russula</i> sp.	4	0	0	467	88	111	69	Not specific
<i>Alnicola subconspersa</i>	1	154	0	0	151	307	1	<i>Alnus</i> subgenus
<i>Boletales</i>	7	243	128	110	52	52	26	Not specific
<i>Cortinarius</i> sp.	20	1	160	80	195	97	70	Not specific
<i>Sebacinaceae</i>	19	8	63	307	19	22	16	Not specific
<i>Tarzetta</i> sp.	2	1	0	0	91	136	78	Not specific
<i>Alnicola</i> sp.	1	250	0	0	1	2	3	Not specific
<i>Lactarius lepidotus</i>	1	0	0	180	0	0	0	<i>Alnobetula</i> subgenus
<i>Ceratobasidiaceae</i>	8	14	51	72	3	3	7	Not specific
<i>Paxillus filamentosus</i>	1	0	80	0	1	0	0	specific in experiment
<i>Atheliaceae</i>	3	8	4	32	3	3	4	not specific
<i>Lactarius obscuratus</i>	1	30	0	0	0	0	0	<i>Alnus</i> subgenus
<i>Laccaria</i> sp.	1	5	0	0	3	1	2	Not specific
<i>Lactarius torminosus</i>	1	0	0	7	0	0	0	Not specific
<i>Alnicola longicystis</i>	1	0	4	0	1	0	0	<i>Alnus</i> subgenus
<i>Amanita</i> sp.	1	2	0	0	1	1	0	Not specific
<i>Tricholoma</i> sp.	1	0	0	4	0	0	0	Not specific
<i>Lactarius</i> sp.	1	0	4	0	0	0	0	Not specific
<i>Alnicola citrinella/pallidifolia</i>	1	0	0	2	0	0	0	Cannot assess host specificity
<i>Alnicola xanthophylla</i>	1	0	0	0	0	2	0	<i>Alnus</i> subgenus
<i>Lactarius brunneohepaticus</i>	1	0	0	2	0	0	0	<i>Alnobetula</i> subgenus

Supplementary data S4. Outputs of Anova and Permanova tests on all fungal and ectomycorrhizal diversity and community structures.

Species diversity		Soil					Seedlings							
		Df	Sum of Sq	Mean of Sq	F	Pr(>F)	Df	Sum of Sq	Mean of Sq	F	Pr(>F)			
All fungi	trapping host						2	149491	74746	2.937	0.0679			
	sporulation	1	845867	845867	18.692	0.00099	1	2052	2052	0.081	0.7784			
	indigenous host	2	321809	160905	3.556	0.06128	2	818351	409176	16.075	1.62e-05			
	sporulation observed						3	34181	11394	0.351	0.789			
	IH*SP (ecoregion) residuals	2	459166	229583	5.073	0.02531	31	789063	25454					
ECM fungi	trapping host						2	259541	129771	5.159	0.01164			
	sporulation	1	612	612	0.328	0.5771	1	3181	3181	0.126	0.72453			
	indigenous host	2	108926	54463	29.207	2.45e-05	2	514178	257089	10.220	0.00039			
	sporulation observed						3	81475	27158	0.897	0.45315			
	IH*SP (ecoregion) residuals	2	20289	10145	5.440	0.0208	2	241508	120754	4.800	0.01527			
Community structure		Df	SumsOfSqs	MeanSqs	F. model	R2	Pr(>F)	Df	SumsOfSqs	MeanSqs	F. model	R2	Pr(>F)	
	All fungi	trapping host						2	1.4424	0.72120	2.5192	0.07203	0.001	
		sporulation	1	0.9061	0.90609	3.8235	0.11970	0.001	1	1.3287	1.32869	4.6412	0.06635	0.001
		indigenous host	2	2.0702	1.03510	4.3679	0.27350	0.001	2	2.7458	1.37289	4.7956	0.13711	0.001
		sporulation observed						3	1.7634	0.58781	1.7755	0.08806	0.001	
IH*SP (ecoregion) residuals		2	1.7494	0.87469	3.6910	0.23111	0.001	2	2.4521	1.22605	4.2826	0.12245	0.001	
ECM fungi	trapping host						2	1.3518	0.67592	2.6271	0.06755	0.001		
	sporulation	1	0.8636	0.86358	3.3566	0.11781	0.001	1	1.6266	1.62661	6.3222	0.08128	0.001	
	indigenous host	2	1.9201	0.96005	3.7316	0.26195	0.001	2	3.0146	1.50728	5.8584	0.15064	0.001	
	sporulation observed						3	1.9227	0.64089	2.1284	0.09608	0.001		
	IH*SP (ecoregion) residuals	2	1.4591	0.72956	2.8357	0.19906	0.001	2	2.8584	1.42918	5.5549	0.14284	0.001	
	residuals	12	3.0873	0.25728		0.42118		31	7.9758	0.25728		0.39857		