

Supplementary material

Table S1. The concentration of different petroleum hydrocarbon pollutants recorded in the three sampled basins compared with the reference values set by Quebec Government.

Petroleum hydrocarbon	Concentration recorded in the different basins $\mu\text{g}/\text{kg}$			Threshold values set by the Quebec Government (ccme.ca)		
	LC ₁	MC	HC	Residential	Commercial	Industrial
Phenanthrene	1	2700	4300	0.1	5	50
Acenaphrene	0.2	760	620	0.1	10	100
Anthracene	6.7	340	570	0.1	10	100
Fluorene	0.3	710	630	0.1	10	100
1-methylnaphtalene	0.1	320	300	0.1	1	10
1,3-Dimethylnaphtalene	0.1	390	580	0.1	1	10
Total petroleum hydrocarbons (C10-C50)	3000	41000	91000	300	700	3500

¹ Low concentration (LC), moderate concentration (MC) and high concentration (HC).

Table S2. Identification of OTUs. BLAST results (using NCBI and MAARJAM database) of the 36 OTUs are given below. OTUs represented by two or less than two sequences (marked as red color) were not used for future analysis.

OTUs	Identification	Orders	Families	Genera	Accessing code	Similarity
OTU01	<i>Rhizopagus irregulare</i> VTX00114	Glomerale	Glomeraceae	<i>Rhizopagus</i>	FN600536.1	100%
OTU02	<i>Claroideoglomus</i> sp. VTX00193	Glomerale	Claroideoglomeraceae	<i>Claroideoglomus</i>	KJ809525.1	100%
OTU03	<i>Acaulospora</i> sp. VTX00028	Diversisporale	Acaulosporaceae	<i>Acaulospora</i>	EU332727.1	99%
OTU04	<i>Rhizopagus</i> sp. VTX00113	Glomerale	Glomeraceae	<i>Rhizopagus</i>	JX144124.1	99%
OTU05	<i>Diversispora eburnea</i> VTX00060	Diversisporale	Diversisporaceae	<i>Diversispora</i>	AM713429.1	100%
OTU06	<i>Claroideoglomus</i> sp. VTX00276	Glomerale	Claroideoglomeraceae	<i>Claroideoglomus</i>	AB749515.1	99%
OTU07	<i>Paraglomus</i> sp. VTX00350	Paraglomerale	Paraglomeraceae	<i>Paraglomus</i>	HE576915.1	91%
OTU08	<i>Funnelformis mosseae</i> VTX00067	Glomerale	Glomeraceae	<i>Funnelformis</i>	JX461236.1	98%
OTU09	<i>Diversispora celata</i> VTX00060	Diversisporale	Diversisporaceae	<i>Diversispora</i>	AM713423.1	96%
OTU10	<i>Rhizopagus</i> sp. VTX00114	Glomerale	Glomeraceae	<i>Rhizopagus</i>	KC708370	98%
OTU11	Glomeraceae sp. VTX00327	Glomerale	Glomeraceae	-	JF414193	94%
OTU12	<i>Claroideoglomus</i> sp. VTX00193	Glomerale	Claroideoglomeraceae	<i>Claroideoglomus</i>	KJ809525.1	95%
OTU13	Glomeraceae sp. VTX00069	Glomerale	Glomeraceae	-	GU353706.1	96%
OTU14	Glomeraceae sp. VTX00130	Glomerale	Glomeraceae	-	AB698566.1	99%
OTU15	<i>Claroideoglomus</i> sp. VTX00193	Glomerale	Claroideoglomeraceae	<i>Claroideoglomus</i>	KJ809525.1	97%
OTU16	<i>Rhizopagus irregulare</i> VTX00114	Glomerale	Glomeraceae	<i>Rhizopagus</i>	FN600538.1	97%
OTU17	<i>Claroideoglomus</i> sp. VTX00193	Glomerale	Claroideoglomeraceae	<i>Claroideoglomus</i>	KJ809525.1	97%
OTU18	<i>Claroideoglomus</i> sp. VTX00193	Glomerale	Claroideoglomeraceae	<i>Claroideoglomus</i>	KJ809525.1	95%
OTU19	<i>Rhizopagus</i> sp. VTX00113	Glomerale	Glomeraceae	<i>Rhizopagus</i>	HG004504.1	96%
OTU20	<i>Rhizopagus</i> sp. VTX00113	Glomerale	Glomeraceae	<i>Rhizopagus</i>	HG004476.1	97%
OTU21	<i>Rhizopagus irregulare</i> VTX00114	Glomerale	Glomeraceae	<i>Rhizopagus</i>	JX144120.1	97%
OTU22	<i>Claroideoglomus</i> sp. VTX00193	Glomerale	Claroideoglomeraceae	<i>Claroideoglomus</i>	HQ258987.1	96%
OTU23	<i>Claroideoglomus</i> sp. VTX00193	Glomerale	Claroideoglomeraceae	<i>Claroideoglomus</i>	KJ809525.1	98%
OTU24	<i>Rhizopagus</i> sp. VTX00113	Glomerale	Glomeraceae	<i>Rhizopagus</i>	HG004521.1	99%
OTU25	<i>Claroideoglomus</i> sp. VTX00057	Glomerale	Claroideoglomeraceae	<i>Claroideoglomus</i>	KC708358.1	97%
OTU26	<i>Rhizopagus</i> sp. VTX00113	Glomerale	Glomeraceae	<i>Rhizopagus</i>	EU332711.1	96%
OTU27	<i>Claroideoglomus</i> sp. VTX00193	Glomerale	Claroideoglomeraceae	<i>Claroideoglomus</i>	KJ809525.1	98%
OTU28	<i>Claroideoglomus</i> sp. VTX00193	Glomerale	Claroideoglomeraceae	<i>Claroideoglomus</i>	HE615035.1	95%
OTU29	Glomeraceae <i>Glomus</i> sp. VTX00114	Glomerale	Glomeraceae	<i>Rhizopagus</i>	KC708370.1	99%
OTU30	<i>Claroideoglomus</i> sp. VTX00193	Glomerale	Claroideoglomeraceae	<i>Claroideoglomus</i>	HE614983.1	97%
OTU31	<i>Paraglomus</i> sp. VTX00001	Paraglomerale	Paraglomeraceae	<i>Paraglomus</i>	KF386326.1	89%
OTU32	<i>Rhizopagus irregulare</i> VTX00114	Glomerale	Glomeraceae	<i>Rhizopagus</i>	KC708370.1	99%
OTU33	Glomeraceae sp. VTX00166	Glomerale	Glomeraceae	-	FR693470.1	98%
OTU34	<i>Rhizopagus irregulare</i> VTX00114	Glomerale	Glomeraceae	<i>Rhizopagus</i>	KC708370.1	97%
OTU35	<i>Rhizopagus</i> sp. VTX00113	Glomerale	Glomeraceae	<i>Rhizopagus</i>	JX144125.1	96%
OTU36	<i>Acaulospora</i> sp. VTX00028	Diversisporale	Acaulosporaceae	<i>Acaulospora</i>	EU332732.1	97%

Figure S1

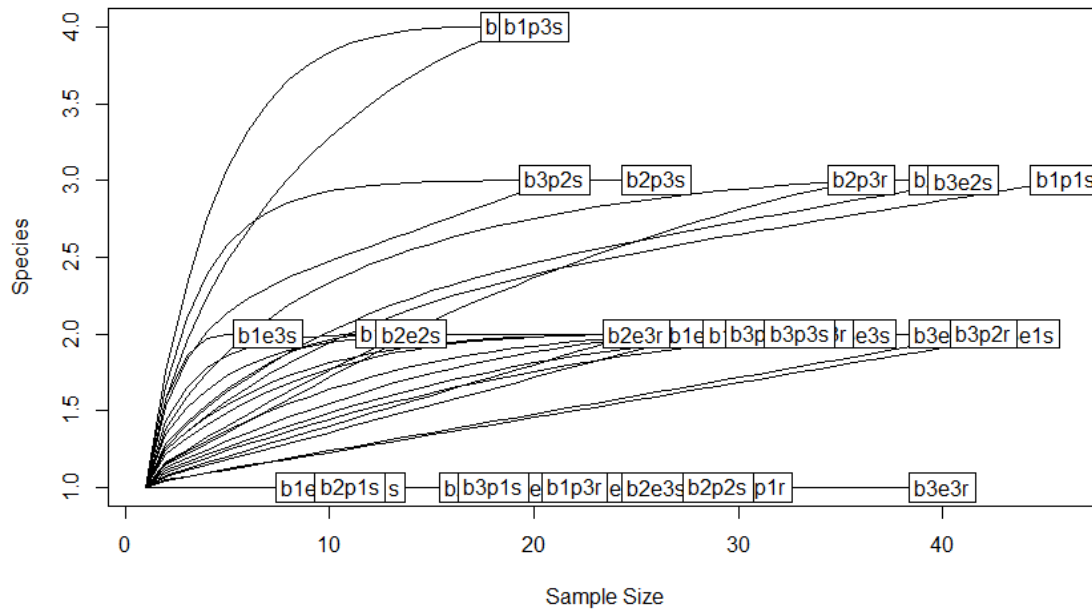
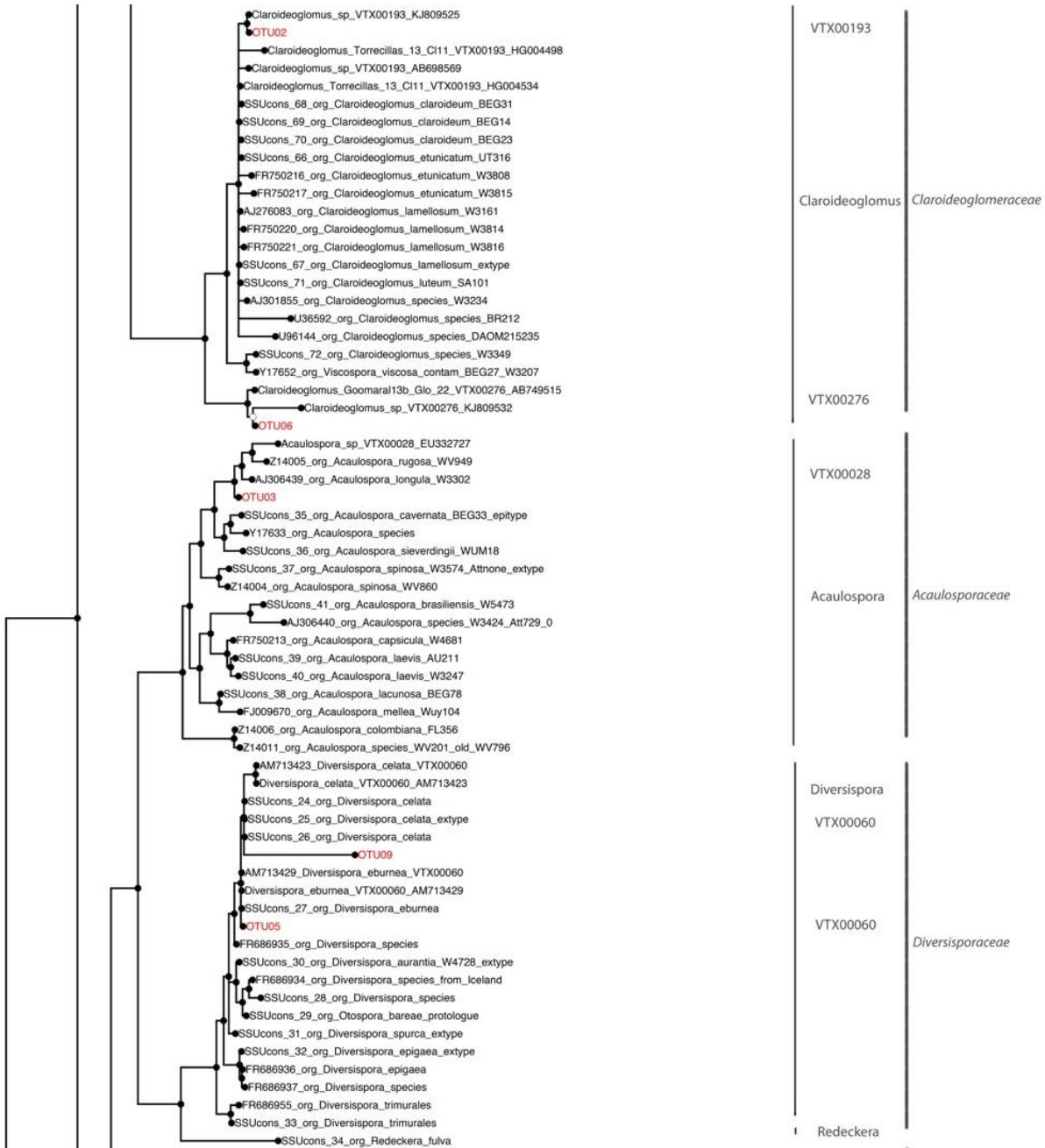


Figure S1. Rarefaction curves of each sample showing the saturation of OTUs richness of *Glomeromycota* associated with *P. tremuloides* and *E. elliptica* from low, moderate and high contamination basins. Rarefaction analysis was based on taxonomic assignment at 97% of sequence similarity.

Figure S2





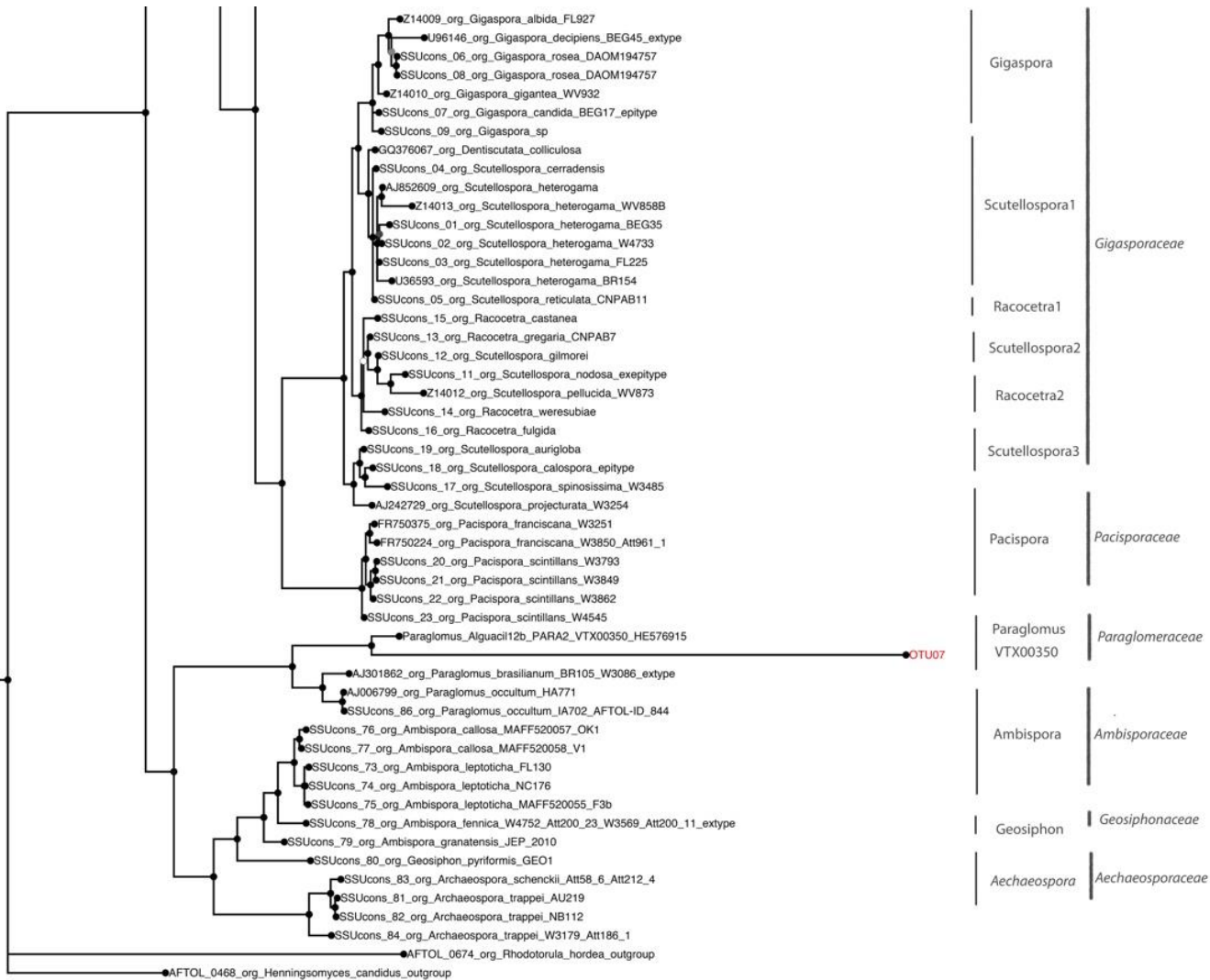


Figure S2. Bayesian phylogenetic tree based on nuclear small subunit (SSU) rDNA consensus sequences showing the distribution of the 9 OTUs recorded in contaminated sites (red labels) among the Glomeromycota phylogenetic tree. Sequence dataset was analyzed with the SSU sequences of the 9 OTUs (red labels) from Krüger et al. (2012) and the closest match recovered from MaarjAM database. Circles on nodes indicate Bayesian posterior probabilities ranging from 0.9 (white) to 1 (black). The scale represents the branch length corresponding to expected substitutions per site.