Table S1. The description of age characteristics and soil properties of the study sites[a]

Age	Plot	Soil textural classification	Tree species composition (%)	Age of the trees[b]	Year of last fire	Trees/ha	Soil pH (humus layer)	Soil temperature (growing season) (°C)	Soil gravimetric water content (%)	SoilN (g m^{-2})	Ergosterol μg g^{-1} SOM	SoilC (C g m^{-2})	TRootBiom (kg m^{-2})
2y	1	Loamy sand	92 Pi, 8 Bi	35/**40**/258	2009	1550	4.0 (± 0.08)	11.3	34 (± 3.2)	47,73 ± 13,78	217,77 ± 10,63	1474,33 ± 309,02	0,34 ± 0,00
	2	Loamy sand	95 Pi, 5 Bi	21/**52**/143	2009	900	4.1 (± 0.1)	11.6	37 (± 2.2)	42,68 ± 9,73	224,86 ± 4,66	1519,54 ± 76,39	0,22 ± 0,00
42y	1	Loamy sand	100 Pi	24/**39**/343	1969	820	3.6 (± 0.06)	11.7	45 (± 4.1)	51,72 ± 14,94	235,26 ± 17,19	1420,74 ± 139,98	0,16 ± 0,00
	2	Loamy sand	99 Pi, 1 Bi	20/**39**/249	1969	1300	3.6 (± 0.11)	11.1	41 (± 6.1)	66,58 ± 13,41	236,67 ± 23,71	1622,53 ± 202,05	0,16 ± 0,00
60y-A	1	Loamy sand	98Pi, 2 Bi	39/**61**/123	1951	1250	3.8 (± 0.21)	10.4	54 (± 5.1)	71,68 ± 19,83	281,74 ± 23,85	2366,40 ± 278,60	0,24 ± 0,00
	2	Loamy sand	98Pi, 2 Bi	34/**61**/153	1951	900	3.7 (± 0.16)	10.5	51 (± 5.1)	71,68 ± 19,83	255,65 ± 11,22	2084,37 ± 317,27	0,31 ± 0,00
60y-B	1	Loamy sand	95 Pi, 5 Bi	43/**61**/155	1951	625	3.8 (± 0.21)	10.8	49 (± 4.9)	72,40 ± 10,73	235,42 ± 46,01	2372,49 ± 463,03	0,22 ± 0,00
	2	Loamy sand	99 Pi, 1 Bi	43/**61**/169	1951	1150	3.8 (± 0.13)	10.6	50 (± 6.4)	81,55 ± 11,38	258,01 ± 56,86	2304,06 ± 223,32	0,23 ± 0,00
152y	1	Loamy sand	96 Pi, 4 Bi	104/**150**/272	1859	200	3.7 (± 0.17)	10.4	57 (± 4.2)	55,76 ± 5,78	274,76 ± 16,15	2411,06 ± 222,92	0,29 ± 0,00
	2	Loamy sand	98Pi, 2 Bi	84/**150**/341	1859	225	3.8 (± 0.11)	10.5	56 (± 4.9)	63,65 ± 5,20	302,33 ± 31,17	2430,15 ± 429,59	0,37 ± 0,00

[a] All the data were derived from Köster et al.(Köster K, Berninger F, Lindén A, Köster E, Pumpanen J. Geoderma, 235: 74-82, 2014) , except data from 60y-B site.

[b] representing the age of youngest living tree/average age of the stand/oldest living tree on the study site. Pi — Scots pine, Bi — Birch.

Standard errors of the means are in parentheses (n=5).

Table S2. Commands used in Mothur to analyse pyrosequencing data and scripts code used in R to analyze GeoChip data

Name	Command / Code
Mothur command used in pyrosequencing data analysis	
1	mothur > sffinfo
2	mothur > summary.seqs
3	mothur > trim.seqs
4	mothur > summary.seqs
5	mothur > unique.seqs
6	mothur > summary.seqs
7	mothur > chimera.uchime
8	mothur > remove.seqs
9	mothur > summary.seqs
10	mothur > pre.cluster
11	mothur > count.groups
12	mothur > pairwise.seqs
13	mothur > cluster
14	Mothur >make.shared
15	mothur > count.groups
16	mothur > split.abund
17	mothur > classify.seqs
18	mothur > remove.lineage
19	mothur > sub.sample
20	mothur > collect.single
21	mothur > summary.single
22	mothur > rarefaction.single
23	mothur > mothur > classify.otu
24	mothur > parsimony

R code used in GeoChip data analysis

```
#NMDS    fungi_metaMDS<-metaMDS(t(GEO_data_Only_Fungi_reduced))
         fungi_metaMDS
         fungi_env_fit<-envfit(fungi_metaMDS, New_EnvFactors_GEOdata, permu=999, na.rm=TRUE)
         fungi_env_fit
         site_codes<-c(15,15,15,2,2,2,18,18,18)
         data_NMDS<-data.matrix(fungi_metaMDS$points)
         pdf(file="New_NMDS_GEO.pdf", height=10, width=10)
         plot(fungi_metaMDS, display=c("sites", "species"), type="n",
            ylim=c(-0.15,0.15), main="NMDS (GEO data)")
         points(fungi_metaMDS, display=c("sites", "species"),
             pch=site_codes, cex=2)
         text(fungi_metaMDS, pos=c(2,3,4), cex=.8)
         plot(fungi_env_fit, cex=.8, col="blue", font=1, p.max=0.05)
         abline(h=0, v=0, lty=3)
         dev.off()

#CCA      GEO_CCA_analysis<-cca(t(GEO_data_Only_Fungi_reduced))
         env_factor_CCA<-envfit(GEO_CCA_analysis, Species_Lifestyle_merged)
         GEO_CCA_analysis
```

```
          env_factor_CCA
          pdf(file="New_CCA_analysis_GEO.pdf", width=10, height=10)
          plot(GEO_CCA_analysis, display="sites", type="n",
            xlab="CCA1 (29.4%)", ylab="CCA2 (25.9%)", main="CCA (GEO data)")
          plot(env_factor_CCA, p.max=0.05, font=1, cex=.5)
          points(GEO_CCA_analysis, pch=c(15,15,15,2,2,2,18,18,18), cex=2)
          dev.off()
          Distance_GEO_fungi<-vegdist(GEO_data_fungi_ANOSIM[c(1:6),1:3042])

#ANOSIM   ANOSIM_analysis_fungi<-anosim(Distance_GEO_fungi,
                       grouping=as.factor(GEO_data_fungi_ANOSIM$Group[c(1:6)]),
                       permutations=999, distance="bray")
          summary(ANOSIM_analysis_fungi)
          pdf(file="ANOSIM.pdf", width=10, height=7)
          plot(ANOSIM_analysis_fungi, main="ANOSIM, analysis of similarity of the GEO data (Fungi)",
           name.arg=c("2y-152y", "60y", "test")
          dev.off()
```

Table S3. The abundance (%) and function of the top 50 genera detected in each site

Genus	2y	42y	60y-A	60y-B	152y	Average	Function[*]
Cortinarius	4,69	17,21	19,35	8,81	42,48	18,5	ECM
Piloderma	13,83	22,49	21,60	11,09	2,17	14,2	ECM
Rhizoscyphus	5,57	5,80	6,02	6,66	3,98	5,6	ERM
Suillus	0,28	5,64	1,71	1,79	1,62	2,2	ECM
Lactarius	1,43	5,74	3,06	0,57	0,02	2,2	ECM
Russula	0,00	0,00	0,00	9,56	0,00	1,9	ECM
Mortierella	1,89	0,78	0,66	1,00	0,97	1,1	SAP
Meliniomyces	0,91	0,93	1,06	0,78	1,11	1,0	ERM
Oidiodendron	1,02	0,65	0,57	1,06	0,76	0,8	ERM
Trechispora	2,69	0,83	0,40	0,26	0,08	0,9	ECM
Archaeorhizomyces	0,17	0,58	0,00	0,07	0,10	0,2	ECM
Mycena	0,17	0,18	0,75	0,04	0,02	0,2	SAP
Phialocephala	0,94	0,25	0,20	0,34	0,08	0,4	ERM
Penicillium	0,34	0,18	0,13	0,26	0,09	0,2	SAP
Cladophialophora	1,17	0,03	0,03	0,03	0,04	0,3	SAP
Umbelopsis	0,70	0,08	0,05	0,04	0,03	0,2	SAP
Lecythophora	0,76	0,07	0,02	0,02	0,00	0,2	SAP
Xenopolyscytalum	0,04	0,08	0,13	0,23	0,08	0,1	SAP
Coltricia	0,87	0,00	0,00	0,00	0,00	0,2	ECM
Mollisia	0,57	0,05	0,03	0,01	0,03	0,1	SAP
Coltricia	0,87	0,00	0,00	0,00	0,00	0,2	ECM
Mollisia	0,57	0,05	0,03	0,01	0,03	0,1	SAP
Galerina	0,17	0,03	0,01	0,04	0,17	0,1	SAP
Hygrophorus	0,07	0,01	0,03	0,30	0,00	0,1	SAP
Gymnopus	0,00	0,00	0,11	0,00	0,24	0,1	SAP
Beauveria	0,00	0,36	0,00	0,00	0,01	0,1	SAP
Tricholoma	0,00	0,00	0,39	0,00	0,09	0,1	ECM
Thelephora	0,38	0,00	0,00	0,01	0,00	0,1	ECM
Placynthiella	0,01	0,39	0,00	0,00	0,00	0,1	SAP
Xenasmatella	0,00	0,05	0,17	0,03	0,03	0,1	SAP
Cystoderma	0,00	0,01	0,04	0,10	0,10	0,1	SAP
Colpoma	0,01	0,07	0,08	0,01	0,00	0,0	SAP
Tylospora	0,30	0,00	0,00	0,00	0,02	0,1	ECM
Verticillium	0,06	0,02	0,04	0,03	0,02	0,0	SAP
Sistotrema	0,00	0,12	0,00	0,00	0,00	0,0	ECM
Capronia	0,02	0,10	0,01	0,01	0,00	0,0	SAP
Tomentella	0,05	0,01	0,08	0,00	0,00	0,0	ECM
Hyaloscypha	0,00	0,01	0,04	0,06	0,00	0,0	SAP
Exobasidium	0,18	0,01	0,01	0,00	0,00	0,0	SAP
Hyphodontia	0,01	0,00	0,00	0,10	0,00	0,0	SAP
Sydowia	0,12	0,01	0,01	0,00	0,00	0,0	SAP
Syzygospora	0,00	0,03	0,01	0,01	0,02	0,0	SAP
Pochonia	0,02	0,05	0,00	0,01	0,01	0,0	SAP
Leccinum	0,00	0,00	0,05	0,07	0,00	0,0	ECM
Parmeliopsis	0,02	0,02	0,00	0,04	0,00	0,0	SAP
Cadophora	0,00	0,00	0,00	0,07	0,00	0,0	SAP
Nematoctonus	0,05	0,00	0,00	0,01	0,01	0,0	SAP
Hyphodontiella	0,00	0,00	0,06	0,00	0,00	0,0	SAP
Sporormiella	0,00	0,01	0,05	0,00	0,00	0,0	SAP
Chroogomphus	0,00	0,00	0,01	0,05	0,00	0,0	ECM

[*] ECM: Ectomycorrhizae; SAP: Saprotroph; ERM: Ericoid mycorrhizae

Table S4. Fungal richness and diversity index for ITS2 region libraries in the soil from each site differing in fire histories

Years after fire	No. of Sequences[a]	OTUs[b]		OTUs coverage (%)	Invsimpson[b]	Normalization 1[c]			Normalization 2[d]
		Observed	Estimated			Observed OTUs	Estimated OTUs	Invsimpson	Invsimpson
2	4292 ± 1700	226 ± 42	334 ± 60	0.98	17.6 ± 8.4	182 ± 25	298 ± 46	17.6 ± 8.4	17.5 ± 8.3
42	8156 ± 4215	240 ± 42	369 ± 51	0.99	9.2 ± 3.3	145 ± 24	258 ± 48	9.1 ± 3.2	9.2 ± 3.3
60-A	6152 ± 2114	196 ± 48	302 ± 89	0.99	8.6 ± 3.0	129 ± 11	227 ± 41	8.5 ± 2.9	8.6 ± 3.0
60-B	5964 ± 2004	199 ± 45	322 ± 59	0.98	9.0 ± 5.8	132 ± 18	228 ± 47	9.1 ± 6.0	9.0 ± 5.8
152	6788 ± 1649	186 ± 57	281 ± 91	0.99	8.6 ± 5.1	122 ± 28	212 ± 28	8.6 ± 5.3	8.6 ± 5.1

[a] Average number of sequence obtained from the ten replicates in each site with standard deviation.

[b] Data were calculated at 3% genetic distance level with standard deviation in Mothur and OTUs containing singleton sequence was discarded.

[c] Data were calculated at 3% genetic distance level with standard deviation based on the same number of sequences from each replicate (2400/sample) in Mothur .

[d] Data were calculated at 3% genetic distance level with standard deviation based on cumulative-sum scaling (CSS) method without sub-sampling.

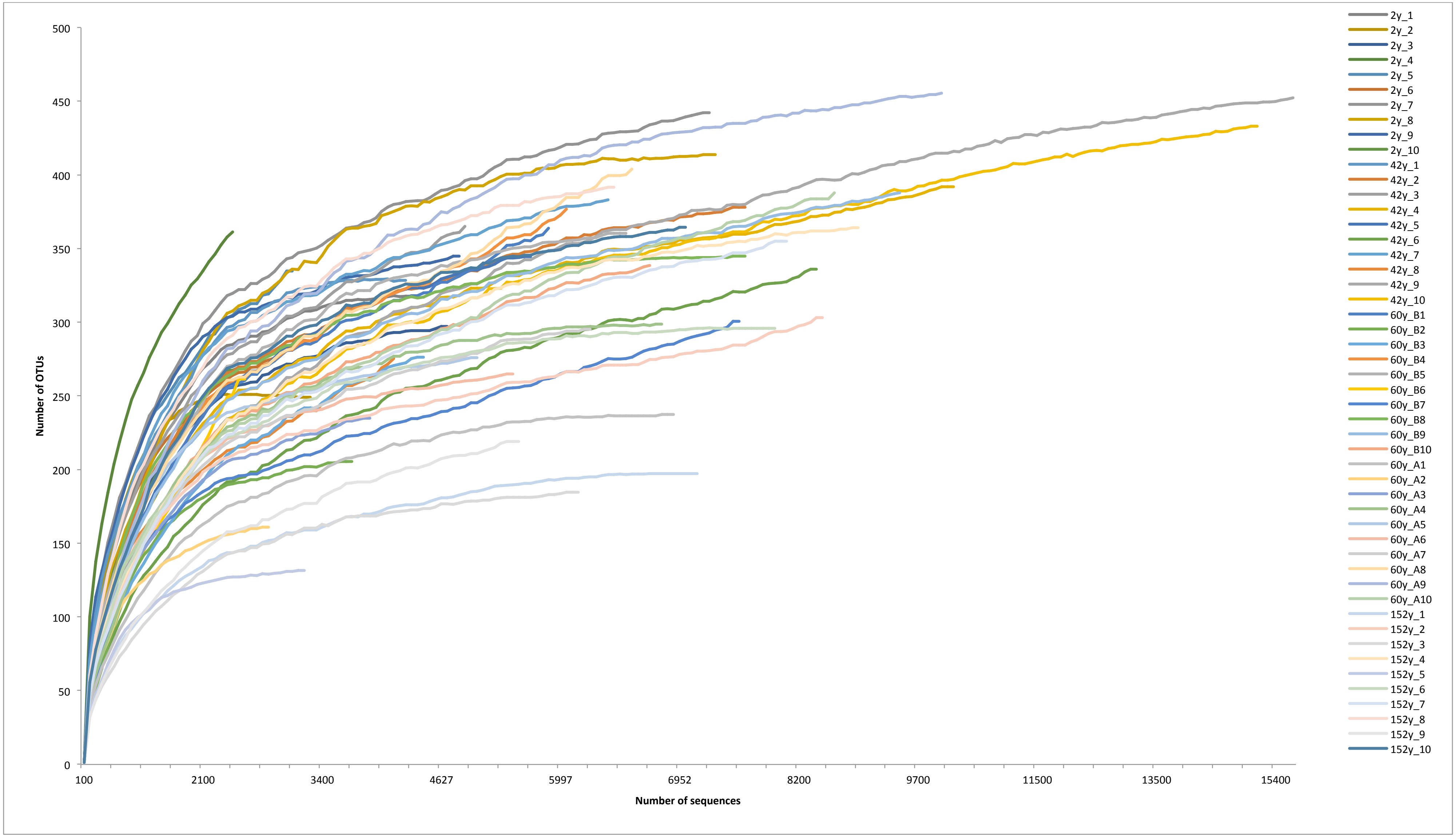

Figure S1. Rarefaction curve showing the observed number of operational taxonomic units (OTUs) at genetic distance of 3% in each sampling site. The number 1-10 in the legend indicates the 10 replicates in each site.

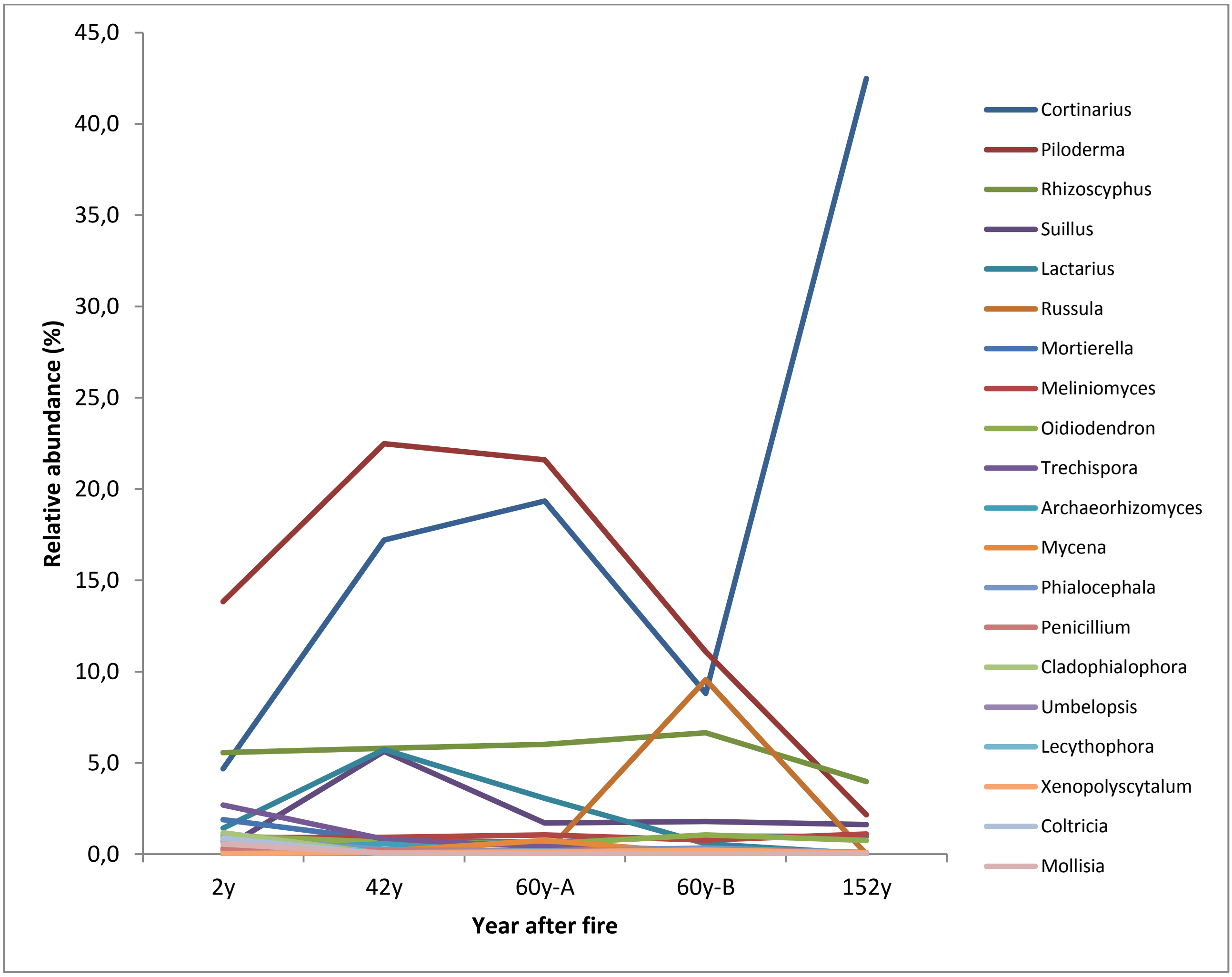

Figure S2. Distribution of phylogenetic groups at genus level across the four ages after fire

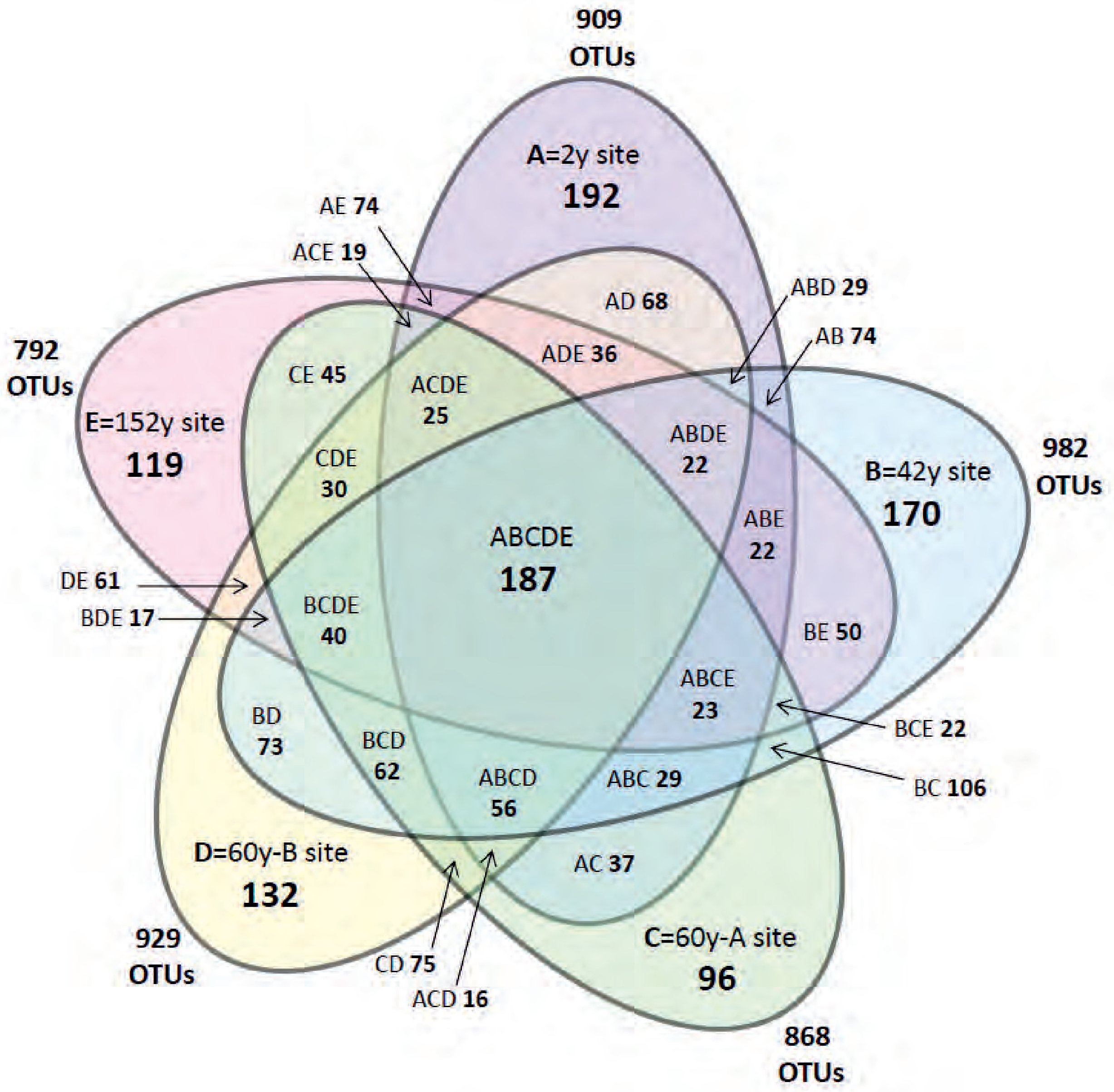

Figure S3.Unique and shared OTUs between the sites after fire. The number of OTUs in each site after fire: 909 in 2y site; 982 in 42y site; 868 in 60y-A site; 929 in 60y-B site and 792 in 152y site.

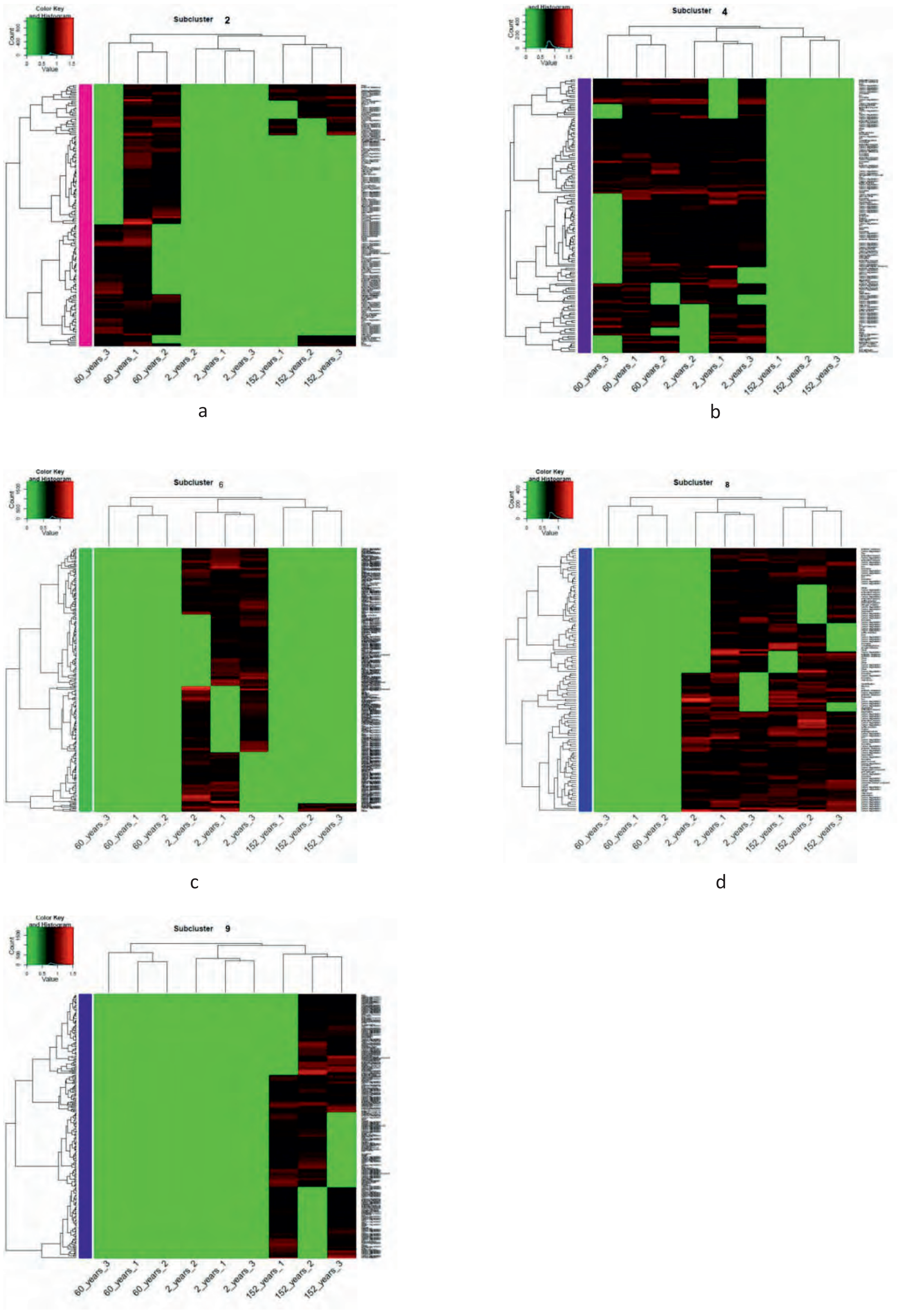

Figure S4. Hierarchical sub-clustered genes with different functions in each burned sites. Subcluster 2 (3a), subcluster 4 (3b), subcluster 6 (3c), subcluster 8 (3e) and subcluster 9 (3f). The number after site represents the replicates from each site.

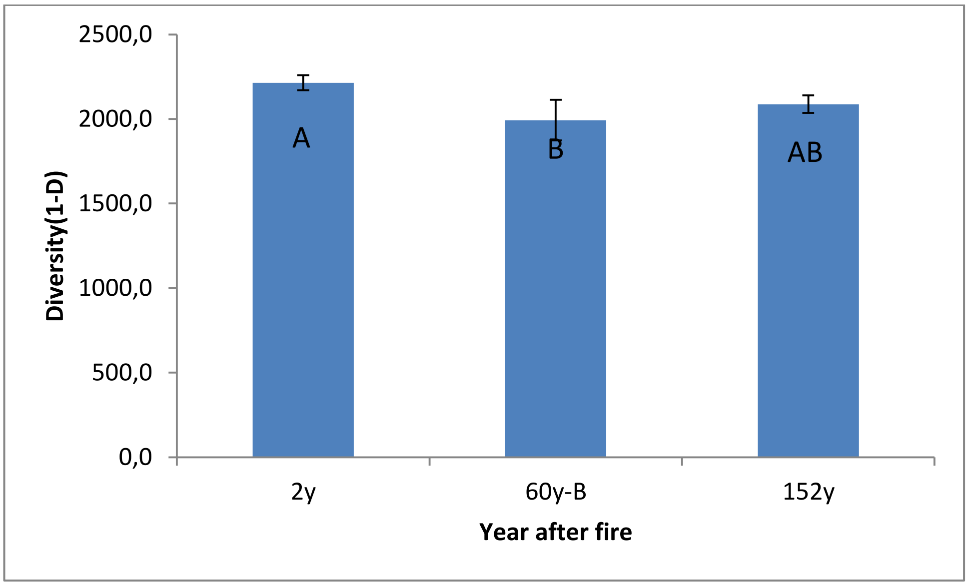

Figure S5. Diversity of fungal functional genes detected in the three sites differing in fire histories. The bar represents standard deviation and letters represent Tukey's significance at $P = 0.05$.