

	Pine-30D-4	Pine-30D-5	Pine-30D-6	Spruce-30D-4	Spruce-30D-5	Spruce-30D-6	Aspen-5D-1	Aspen-5D-2	Aspen-5D-3	Pine-5D-1	Pine-5D-2	Pine-5D-3	Spruce-5D-2	Spruce-5D-3	Spruce-5D-1
Pine-30D-4	1.00	0.84	0.92	0.72	0.71	0.79	0.24	0.23	0.19	0.32	0.20	0.24	0.24	0.20	0.18
Pine-30D-5	0.84	1.00	0.87	0.96	0.94	0.96	0.20	0.19	0.24	0.30	0.17	0.21	0.31	0.22	0.23
Pine-30D-6	0.92	0.87	1.00	0.82	0.83	0.88	0.19	0.19	0.20	0.28	0.17	0.21	0.25	0.19	0.19
Spruce-30D-4	0.72	0.96	0.82	1.00	0.98	0.97	0.17	0.15	0.24	0.27	0.14	0.19	0.31	0.22	0.24
Spruce-30D-5	0.71	0.94	0.83	0.98	1.00	0.98	0.18	0.17	0.24	0.27	0.15	0.20	0.32	0.22	0.24
Spruce-30D-6	0.79	0.96	0.88	0.97	0.98	1.00	0.21	0.19	0.24	0.29	0.17	0.22	0.33	0.23	0.24
Aspen-5D-1	0.24	0.20	0.19	0.17	0.18	0.21	1.00	0.96	0.44	0.93	0.96	0.89	0.80	0.85	0.62
Aspen-5D-2	0.23	0.19	0.19	0.15	0.17	0.19	0.96	1.00	0.34	0.94	0.92	0.81	0.73	0.76	0.53
Aspen-5D-3	0.19	0.24	0.20	0.24	0.24	0.24	0.44	0.34	1.00	0.54	0.57	0.67	0.64	0.70	0.83
Pine-5D-1	0.32	0.30	0.28	0.27	0.27	0.29	0.93	0.94	0.54	1.00	0.93	0.88	0.79	0.83	0.66
Pine-5D-2	0.20	0.17	0.17	0.14	0.15	0.17	0.96	0.92	0.57	0.93	1.00	0.95	0.86	0.92	0.74
Pine-5D-3	0.24	0.21	0.21	0.19	0.20	0.22	0.89	0.81	0.67	0.88	0.95	1.00	0.91	0.96	0.86
Spruce-5D-2	0.24	0.31	0.25	0.31	0.32	0.33	0.80	0.73	0.64	0.79	0.86	0.91	1.00	0.96	0.88
Spruce-5D-3	0.20	0.22	0.19	0.22	0.22	0.23	0.85	0.76	0.70	0.83	0.92	0.96	0.96	1.00	0.92
Spruce-5D-1	0.18	0.23	0.19	0.24	0.24	0.24	0.62	0.53	0.83	0.66	0.74	0.86	0.88	0.92	1.00

**Supplementary Figure S1. Pearson's correlation between samples.** Raw read counts were used as input for the calculation.

**Supplementary Table S1.** Reads alignments.

Library	Filtered reads	Mapped reads	Mapping rate
Pine-30D-4	10,907,540	9,914,794	90.90%
Pine-30D-5	12,340,565	11,330,711	91.82%
Pine-30D-6	12,073,619	10,942,616	90.63%
Spruce-30D-6	16,813,935	15,302,579	91.01%
Spruce-30D-5	16,628,360	15,147,650	91.10%
Spruce-30D-5	12,821,901	11,548,856	90.07%
Aspen-5D-1	17,252,636	13,652,388	79.13%
Aspen-5D-2	19,275,033	17,453,461	90.55%
Aspen-5D-3	18,703,720	14,026,912	75.00%
Pine-5D-1	17,455,078	13,796,245	79.04%
Pine-5D-2	16,634,692	14,257,903	85.71%
Pine-5D-3	19,833,307	16,220,407	81.78%
Spruce-5D-2	15,978,872	13,239,527	82.86%
Spruce-5D-3	16,299,746	13,490,015	82.76%
Spruce-5D-1	14,994,961	10,939,960	72.96%

**Supplementary Table S2.** Annotation of genes involved in Fenton reaction. We define orthologs as members of Markov clustering and homologs as BLASTp hits (E value cutoff 1E-5). The CAZy, Enzyme Commission (EC), and Pfam annotations are available in the MycoCosm (<https://mycocosm.jgi.doe.gov/>).

Pathway	Name	Annotation
Quinone redox cycling and hydroquinone biosynthesis	Quinone reductase	CAZy:AA6
	Phenol monooxygenase	EC:1.14.13.7
	Aromatic ring monooxygenase	Orthologs of Posp11 54109, Posp11 23052, and Posp11 129128
	Phenylalanine ammonia-lyase	Pfam:PF00221
	O-methyltransferase	EC:2.1.1.64
Fe <sup>3+</sup> reduction to Fe <sup>2+</sup>	Glycopeptides	Homologs of Phchr2 3023986 (glp1) and Phchr2 3023982 (glp2)
H <sub>2</sub> O <sub>2</sub> generation	Aryl-alcohol oxidase	CAZy:AA3_2*
	Alcohol oxidase	CAZy:AA3_3
	Glyoxal oxidase	CAZy:AA5_1
	Copper radical oxidases	CAZy:AA5_2
	Amino acid Amine oxidases	Orthologs of Posp11 47008 and Posp11 110689
Iron reduction and homeostasis genes	Ferric iron reductase	Pfam:PF08030,PF01794
	Iron permease	Pfam:PF03239
	Fe <sup>2+</sup> transporter	Orthologs of Posp11 52765 and Posp11 43266
	Ferroxidase	CAZy:AA1_2
Oxalate metabolism	Glyoxylate dehydrogenase	Orthologs of Posp11 121561 and Posp11 115965
	Oxaloacetate acetylhydrolase	Orthologs of Posp11 112832
	Oxalate decarboxylase	Orthologs of Posp11 46778

\*AA3\_2 family has eight subgroups of which one subgroup has aryl-alcohol oxidase activity. See the methods in the main text.

**Supplementary Table S3.** Brown rot fungal genomes for comparative analysis. Each genome portal can be accessible via [https://mycocosm.jgi.doe.gov/\[PORTAL\\_ID\]](https://mycocosm.jgi.doe.gov/[PORTAL_ID]).

Strain	Portal ID in MycoCosm	Genome paper (Pubmed ID)
<i>Daedalea quercina</i>	Daequ1	26659563
<i>Fomitopsis pinicola</i> FP-58527 SS1	Fompi3	22745431
<i>Laetiporus sulphureus</i> var. <i>sulphureus</i>	Laesu1	26659563
<i>Postia placenta</i> MAD-698-R-SB12	PosplRSB12_1	28831381
<i>Wolfiporia cocos</i> MD-104 SS10	Wolco1	22745431

**Supplementary Table S4.** The genes involved in Fenton reaction up-regulated during early decay reported in *Postia placenta*, and their orthologs also up-regulated in submerged ground wood in *Fibroporia radiculosa*. The genes with a false discovery rate <0.05 and fold change >4 are assigned as differentially expressed (same as performed in the *P. placenta* study).

Gene family	<i>P. placenta</i> in early decay (reported by Zhang et al.)	<i>F. radiculosa</i> in ground wood (observed in this study)
Glucose oxidase	44331	657
Alcohol oxidase	128830	3364
	55972	6239
	129158/126217	
Glyoxal oxidase	46390	5062**
Amino acid/amine oxidase	47008	2469*
Amino acid/amine oxidase	110689	1927
Iron reductase	130025	2484*
Iron reductase	130030/130043	-
Fe <sup>2+</sup> transporters	52765/43266	-
Benzoquinone reductase	124517/64069	8914
Phenylalanine ammonia-lyase	111514	6596
Aromatic ring monooxygenases	54109/46071	1441
	23052/62058	4445
	129128	

\*They are differentially expressed (false discovery rate <0.05), but have fold change values from two to four.

\*\*The genes are not in the same gene family, but they are annotated having the same function and are reciprocal best hit in the BLAST alignment.

**Supplementary Table S5.** The genes encoding plant cell wall-degrading enzymes up-regulated in late decay reported in *Postia placenta*, and their orthologs also up-regulated in wood wafers in *Fibroporia radiculosa*. The genes with a false discovery rate <0.05 and fold change >4 are assigned as differentially expressed (same as performed in the *P. placenta* study).

Gene family	<i>P. placenta</i> in late decay (reported by Zhang et al.)	<i>F. radiculosa</i> in 30 days (observed in this study)
Endoglucanases Cel5A	115648/108962	3096
Endoglucanases Cel5B	103675/117690	3097
		4239
Endoglucanases Cel12A	121191/112658	9027
		3175
Xylanase Xyn10A-1	113670/90657	1548
		1546*
		1549*
Mannanase Man5A	57321/121831	1048
		2871

\*They are differentially expressed (false discovery rate <0.05), but have lower fold change values from two to four.