

Supplemental tables

Table S1. *P. carnosus* sequencing summary.

Library	Library_Type	Raw_Reads	Raw_Bases	Trimmed_Bases	Assem_Reads	Assem_Bases	Coverage	Insert	Insert_StdDev
GCXT	454	3,250,968	1,314,960,768	1,313,748,704	3,127,914	1,260,244,475	29.05x	NA	
GUPU	454	1,000,756	405,503,493	404,997,892	974,429	396,177,643	9.13x	NA	
GHOC	454PE	1,312,895	327,864,098	295,946,764	1,234,416	287,653,280	6.63x	3560	889
GCNX	454PE	572,197	177,323,735	162,914,495	543,132	158,464,822	3.65x	14475	3618
GFYP	454PE	199,868	66,367,587	60,638,155	191,898	59,079,037	1.36x	6149	1537
GFYS	454PE	110,638	47,728,082	43,425,668	106,417	42,060,278	0.97x	5218	1729
GATS	SANGER	190,290	167,187,218	147,358,060	182,501	140,250,273	3.23x	2918	729
GUPW	SANGER	13,332	11,769,040	9,601,641	12,434	8,723,897	0.20x	39372	9843
NODE	SOLEXA	192,038	171,143,486	171,141,890	188,005	168,072,328	3.87x	NA	
TOTAL		6,842,982	2,689,847,507	2,609,773,269	6,561,146	2,520,726,033	58.10x		

Table S2. *P. carnosa* assembly summary.

Genome Assembly size	46.29Mb
Sequencing read coverage depth	58.10
# of contigs	2272
# of scaffolds	1137
Scaffold N50/ L50	6/3.53Mb

Table S3. Gene model support by different lines of evidence.

	<i>P. carnosa</i>	<i>P. chrysosporium</i>
# of models	13,937	10,048
% complete (start + stop)	12,449 (89%)	8352 (83%)
% supported by nr homolog	10,619 (76%)	ND
% supported by Swissprot homolog	7736 (56%)	6621 (66%)
% with Pfam domain	6449 (46%)	4769 (47%)
% with EST support (>25%)	12062(87%)	ND
% with full-length EST support	8823(63%)	ND
Gene length (nt)	1448	1363
Transcript length (nt)	1190	1116
Protein length (aa)	313	372
Exon length (nt)	159	138
Intron length (nt)	57	55
# exons / gene	4	5
# single exon genes	2695	1202

Table S4. Summary of *P.carnosus* annotations.

KEGG pathway		
Amino Acid Metabolism	594	4%
Biosynthesis of Polyketides and Nonribosomal Peptides	118	1%
Biosynthesis of Secondary Metabolites	375	3%
Carbohydrate Metabolism	588	4%
Energy Metabolism	134	1%
Glycan Biosynthesis and Metabolism	195	1%
Lipid Metabolism	568	4%
Metabolism of Cofactors and Vitamins	466	3%
Metabolism of Other Amino Acids	145	1%
Nucleotide Metabolism	268	2%
Biosynthetic pathways	402	3%
Xenobiotics Biodegradation and Metabolism	456	3%
Total KEGG annotated genes	4309	31%
KOG Classification		
Cell wall/membrane/envelope biogenesis	95	1%
Cell motility	5	0%
Posttranslational modification	700	5%
Signal transduction mechanisms	652	5%
Intracellular trafficking, secretion, & vesicular transport	319	2%
Defense mechanisms	132	1%
Extracellular structures	69	0%
Nuclear structure	93	1%
Cytoskeleton	219	2%
RNA processing and modification	382	3%
Chromatin structure and dynamics	184	1%
Translation, ribosomal structure and biogenesis	346	2%
Transcription	396	3%
Replication, recombination and repair	231	2%
Energy production and conversion	393	3%
Cell cycle control, cell division, chromosome partitioning	219	2%
Amino acid transport and metabolism	252	2%
Nucleotide transport and metabolism	84	1%
Carbohydrate transport and metabolism	343	2%
Coenzyme transport and metabolism	101	1%
Lipid transport and metabolism	362	3%
Inorganic ion transport and metabolism	157	1%
Secondary metabolism	490	4%
Total KOG annotated genes	6224	45%
GO Term		
Biological process	3731	27%
Cellular component	1972	14%
Molecular function	5748	41%
Total GO annotated genes	6100*	44%*

*In GO, the same gene can be assigned to multiple categories.

Table S5. Top 50 PFAM domains in *Phanerochaete* genomes.

PfamId	Phchr	Phaca	Other 31 Basidiomycetes*			Pfam Description
			Avg	Max	Min	
PF00067	113	207	91	204	4	p450
PF07690	141	172	148	427	22	MFS_1
PF00400	109	202	113	197	49	WD40
PF00069	106	114	104	152	56	Pkinase
PF00106	84	77	82	189	14	adh_short
PF00646	70	86	74	199	7	F-box
PF00271	59	82	80	158	32	Helicase C
PF00248	53	69	36	72	9	Aldo_ket_red
PF00026	52	68	24	51	2	Asp
PF01370	50	59	37	79	11	Epimerase
PF00076	50	55	56	79	19	RRM_1
PF00107	52	50	40	97	11	ADH_zinc_N
PF00005	50	48	38	64	17	ABC_tran
PF00501	30	64	25	76	8	AMP-binding
PF00172	35	56	68	244	5	Zn_clus
PF04082	36	52	45	198	2	Fungal_trans
PF05199	32	54	20	53	1	GMC_oxred_C
PF08240	47	38	40	112	12	ADH_N
PF00096	35	48	51	112	15	zf-C2H2
PF00004	39	44	37	49	17	AAA
PF02985	42	41	38	49	14	HEAT
PF00732	31	50	19	51	2	GMC_oxred_N
PF00098	57	23	40	166	1	zf-CCHC
PF01494	31	47	28	72	3	FAD_binding_3
PF00270	33	43	46	67	14	DEAD
PF01266	35	41	30	70	8	DAO
PF00385	69	6	6	24	1	Chromo
PF00083	39	36	42	123	9	Sugar_tr
PF00097	28	47	42	102	15	zf-C3HC4
PF00692	67	3	2	15	0	dUTPase
PF07993	29	39	27	68	7	NAD_binding_4
PF00561	27	39	26	56	8	Abhydrolase_1
PF00153	34	31	33	40	8	Mito_carr
PF08477	32	29	31	54	4	Miro
PF08242	29	31	28	68	9	Methyltransf_12
PF01753	23	37	27	129	1	zf-MYND
PF08241	29	30	31	60	11	Methyltransf_11
PF00071	30	28	30	53	6	Ras
PF07719	27	30	28	40	15	TPR_2
PF00734	28	28	8	44	0	CBM_1
PF00583	24	31	23	40	6	Acetyltransf_1
PF02798	16	37	16	56	2	GST_N
PF00023	20	32	29	92	12	Ank
PF08659	27	23	32	95	8	KR
PF00515	23	27	27	36	14	TPR_1
PF00226	22	27	29	50	13	DnaJ
PF00018	22	25	25	36	14	SH3_1
PF00702	25	22	25	38	8	Hydrolase
PF00149	19	27	22	31	13	Metallophos

*Gene counts include predicted gene models.

Table S8. Comparison of the number of CAZymes in wood-decaying basidiomycotina.

	GH	GT	PL	CE	Total no.	CBM
<i>Phanerochaete_carnosa</i> _HHB-10118-sp	193	74	8	17	292	43
<i>Phanerochaete_chrysosporium</i> [5, 6]	182	66	4	16	268	48
<i>Postia_placenta</i> _Mad-698-R [12]	143	75	6	10	234	16
<i>Serpula_lacrymans</i> _S7.3 [17]	154	63	6	12	235	29
<i>Schizophyllum_commune</i> _H4-8 [78]	236	75	16	30	357	30
<i>Coprinopsis_cinerea</i> [79]	211	72	13	51	347	89
Average	187	71	9	23	289	43

Table S9. CAZymes that showed <60% identity to Phchr orthologs.

Family	Protein	Identity	E-value	Putative target in wood component	Heatmap ^a				
					Y	F	P	S	M
GH5	183787	55.60%	1.00E-072	Cellulose/Hemicellulose	Light Blue	Light Blue	Light Blue	Light Blue	Light Blue
GH5	168586	55.56%	3.00E-130	Cellulose/Hemicellulose	Dark Blue	Dark Blue	Light Green	Light Blue	Light Blue
GH5	253799	49.14%	3.00E-088	Cellulose/Hemicellulose	Light Blue	Light Blue	Yellow	Light Green	Light Green
GH5	93346	44.07%	1.00E-020	Cellulose/Hemicellulose	Dark Blue	Dark Blue	Black	Dark Blue	Dark Blue
GH5	194761	34.23%	8.00E-017	Cellulose/Hemicellulose					
GH5	194783	30.63%	2.00E-010	Cellulose/Hemicellulose					
GH7	191400	59.40%	1.00E-079	Cellulose					
GH7	205265	55.71%	2.00E-079	Cellulose					
GH7	258037	54.64%	6.00E-143	Cellulose					
GH16	136813	58.68%	0.00E+000	Hemicellulose	Light Green	Light Blue	Light Blue	Light Blue	Light Blue
GH16	127529	54.17%	2.00E-110	Hemicellulose	Light Blue	Dark Blue	Dark Blue	Dark Blue	Light Blue
GH16	153747	33.51%	8.00E-019	Hemicellulose					
GH23	258390	42.01%	0.38						
GH28	82797	28.32%	2.00E-013	Pectin					
GH45	258456	37.66%	3.00E-010	Cellulose					
GH61	251219	53.41%	1.00E-068	Cellulose	Dark Blue	Light Blue	Orange	Light Green	Light Green
GH79	266539	57.41%	4.00E-032	Hemicellulose					
GH79	266550	55.70%	2.00E-020	Hemicellulose					
GH79	266185	53.01%	7.00E-020	Hemicellulose					
GH79	189750	51.26%	4.00E-026	Hemicellulose	Light Blue	Light Blue	Light Blue	Light Blue	Light Blue
GH79	266219	50.00%	7.00E-023	Hemicellulose					
GH79	257835	28.61%	4.00E-021	Hemicellulose					
GH79	252537	24.53%	2.00E-018	Hemicellulose					
GT1	210347	53.35%	3.00E-131		Dark Blue	Light Green	Dark Blue	Light Blue	Dark Blue
GT1	205009	50.57%	2.00E-124		Dark Blue	Light Blue	Dark Blue	Dark Blue	Dark Blue
GT1	205674	49.77%	1.00E-118						
GT1	205698	48.05%	2.00E-112						
GT22	180449	26.07%	1.00E-005						
GT22	214615	25.42%	3.00E-005						
GT22	160814	25.00%	0.38						
GT49	187889	50.00%	4.00E-022						
PL14	260328	37.50%	4.00E-044		Light Blue	Light Blue	Light Blue	Light Blue	Light Blue
PL14	146440	37.16%	8.00E-032		Light Blue	Light Blue	Light Blue	Light Blue	Light Blue
PL14	260353	30.89%	6.00E-006						
PL14	265869	29.91%	2.00E-006						
CE16	258413	50.00%	6.10E-001	Hemicellulose					
CE16	255713	37.59%	8.00E-045	Hemicellulose	Light Blue	Light Blue	Light Green	Light Green	Light Blue
CE16	195373	28.43%	1.00E-023	Hemicellulose	Light Blue	Light Blue	Light Blue	Light Blue	Dark Blue
CE16	185435	25.93%	1.90E-001	Hemicellulose					
CE16	255913	25.28%	5.00E-017	Hemicellulose	Light Blue	Light Blue	Light Blue	Light Blue	Light Blue

^aData obtained from MacDonald et al. [10]. Heat map represents the level of gene transcripts as described in Fig. S2

Table S11. Comparison of the number of FOlymes of *P. carnosae* and selected Agaricomycotina.

Species	FOlyme														
	LO1	LO2	LO3	LDA1	LDA2	LDA3	LDA4	LDA5	LDA6	LDA7	LDA8				
<i>Phanerochaete carnosae</i> ^a	0	11	1	4	0	1	0	0	1	3					
<i>Phanerochaete chrysosporium</i> ^{a,b}	16	1	3	0	0	1	1	0	1	4	0				
<i>Coprinopsis cinerea</i> ^b	17	1	1	18	0	0	0	0	1	2	0				
<i>Schizophyllum commune</i> ^b	2	0	1	1	0	2	1	0	4	4	1				
<i>Postia placenta</i> ^b	2	0	0	3	0	0	0	0	0	1	2				
Reference^c	LAC2	LIG8	P	CDH_PAAC7274	VAOX_P	AAA337	P2OX_PHXP_95915XP_00291	AAD2102	AAB5784						
	PLEOS	HACH	HACH	7	ENSI	47	LGI	3	0108	5	9				

Data from ^athis study; ^bOhm et al. [78];

^cReference genes are Genbank Accessions of genes that have been characterized. *P. carnosae* sequences were annotated to the putative function of the reference protein when the best hits to NCBI represented sequences of interest and the alignment showed at least 30% amino acid identity to the reference protein.

Table S12. Summary of oxidoreductases potentially involved in lignocellulose degradation by *P. carnosus* (Phaca) and *P. chrysosporium* (Phchr).

Putative Function	EC Class	Phaca (no.)	Phaca ID	Phchr (no.)	Phchr ID	Ref. Gene
Peroxide generation						
Methanol oxidase ^a	1.1.3.13	4	252324, 121157, 126707, 213078	3	126879, 5574, 6010	ALOX_ PICAN
Aryl alcohol oxidase ^a	1.1.3.7	4	260543, 100299, 132559, 147295	3	37188, 135972, 6199	AAC72 747
Glucose oxidase ^a	1.1.3.4	0 / 1	- / 179599	0 / 1	- / 6270	GOX_A SPNG / XP_002 910108
Pyranose-2-oxidase	1.1.3.10	0	-	1	137275	
Glyoxal oxidase	-	1	258261	1	11088	
Copper radical oxidase	-	5	123913, 259359, 143144, 263533, 263528	6	259359, 123913, 258261, 8882, 121730, 121818	
Iron reduction and homeostasis						
Quinone reductase ^a	1.6.5.5	3	254412, 114036, 141788	4	121028, 129887, 10307, 139901	AF4654 06
Glycoprotein iron reductase	-	3	249086, 169427, 258034	2	AB236889 AB236890	
Cellobiose dehydrogenase	1.1.99.18	1	259608	1	11098	
Iron ferroxidase	1.16.3.1	1	141262	1	26890	
Lignin modification						
Lignin peroxidase	1.11.1.13	4	263501, 213241, 212237, 152156	10	10957, 121822, 131738, 6811, 11110, 122202, 8895, 121806, 131707, 131709	

Mn peroxidase	1.11.1.16	7	262882, 256980, 94399, 256984, 256997, 256991, 144982	5	140708, 3589, 878, 8191, 4636
Low redox peroxidase	1.11.1.7				
Chloroperoxidase ^b	1.11.1.10	3	263009, 249438, 254678	1	1710
Laccase	1.10.3.2	0	-	0	-

^abest hit and $\geq 30\%$ amino acid identity with reference gene; ^bcontains chloroperoxidase Interpro domain.

Reference genes are Genbank Accessions of genes that have been characterized. *P. carnosus* sequences were annotated to the putative function of the reference protein when the best hits to NCBI represented sequences of interest and the alignment showed at least 30% amino acid identity to the reference protein.

Table S13. Tandem duplication of P450 genes in basidiomycete genomes.

Genome origin	P450 genes	Tandemly duplicated genes	Tandem duplication sites	Duplicated genes (%)
<i>Phanerochaete carnosae</i> HHB-10118-sp	244	80	38	33
<i>Phanerochaete chrysosporium</i> RP-78 [5, 6]	131 ^a	23	15	18
<i>Postia placenta</i> MAD-698 [12]	263	59	24	22
<i>Serpula lacrymans</i> S 7.3 [17]	136	37	16	27
<i>Schizophyllum commune</i> H4-8 [78]	106	31	14	29
<i>Coprinopsis cinerea</i> Okayama 7 [79]	122	45	16	37
<i>Laccaria bicolor</i> S238N-H70 [80]	69	23	15	33

^aNumber of genes which has unique protein ID in *P. chrysosporium* v2.0 database.

Table S14: P450ome classification in *P. carnosus* and its membership comparison with *P. chrysosporium*.

Clan	Family	Sub-family	<i>P. chrysosporium</i>		<i>P. carnosus</i>		
			No. of P450s		No. of P450s		
			Family	Clan	Family	Clan	
CYP51	CYP51	F	1	4	2	5	
	CYP5025	NS			1		
	CYP5156	A	2		1		
	CYP5157	A	1		1		
CYP52	CYP63	A	4	24	7	32	
		B	1		1		
		C	2		1		
		CYP5137	A		2		4
	CYP5141	A	4		6		
		B	1				
		C	1		1		
		D	1		1		
	CYP5142	NS					1
			A		3		1
			B		1		2
			C		1		4
			D		1		
	CYP5151	E	1		1		
			A		1		1
			B				1
CYP53	CYP53	C	1	4	6	10	
		NS			1		
	CYP5140	A	1		1		
	CYP5143	A	2		2		
CYP54	CYP512	B	5	14	2	27	
		C	2		9		
		D	1				
		E	1		1		
		F	1		2		
		G	2		7		
		H	1		5		
		J	1				
		NS			1		
		CYP61	CYP61		A		1
CYP64	CYP502	B	1	61	1	124	
		NS			1		
	CYP5037	A	1		1		
		B	3		5		
		C	1		1		
	CYP5144	NS					1
			A		15		19
			B		1		7
			C		8		16
			D		5		3
			E		1		1
			F		1		5
			G		1		7
			H		1		12
J			1	1			
CYP5145	A	3	2				
CYP5146	A	4	5				

		B	1		1	
		C	1		9	
	CYP5147	A	4		6	
		B	1		1	
		C	1			
	CYP5148	A	2		3	
		B			4	
	CYP5149	A	1		3	
	CYP5152	A	2		4	
	CYP5158	A	1		5	
CYP67	CYP5035	A	7	18	6	22
		B	3		3	
		C	1		5	
		D	1			
		E	1			
	CYP5036	A	3		3	
		B	1			
		C	1		5	
CYP505	CYP505	D	7	7	4	4
CYP534	CYP5138	A	1	11	2	29
	CYP5139	A	1		11	
	CYP5150	A	5		6	
		B	1		4	
		C	1			
	CYP5153	A			1	
	CYP5154	A	1		3	
		NS			1	
	CYP5155	A	1		1	
CYP547	CYP5136	A	5	5	6	8
		NS (2)			2	
UA	CYP6001	C			1	4
		NS (3)			3	
Authentic P450s			149			266
Tentative P450s			-			5
Pseudo/doubtful P450s			10			13
Non P450			-			1
Total Hits			159			285

An initial search in the machine annotated *P. carnosus* genome revealed 285 P450 hits. These sequences were subjected to manual annotation based on the presence of the conserved P450 characteristic domains, including the oxygen-binding motif and the heme-binding domain. Initially, 239 gene models that contained both the conserved domains were considered as “Authentic P450s”. One sequence showed no convincing homology to P450 proteins and was therefore grouped as “Non-P450”. Further analysis of the remaining 45 P450 sequences revealed the characteristic P450 signature motifs in 27 gene models which were then grouped under the list of authentic P450s. Taken together, the total authentic P450 count for *P. carnosus* came up to 266. Of the remaining 18 of the 45 sequences, 5 sequences were very short and their flanking genomic DNA sequence quality was not as good (due to errors in genome sequencing) and thus it was not possible to predict the P450 signature motifs. However, the available protein sequences of these 5 P450s showed high homology (>75-83%) to the known P450s; hence we grouped them as “tentative P450s”. The remaining 13 sequences showed either one or no P450 characteristic domains in the existing gene models as well as in manually predicted gene models. These 13 P450s were therefore grouped as “Doubtful P450s or Pseudogenes”. Abbreviations: NS, New-subfamily; UA, unassigned clan.

Table S15. P450s upregulated in wood degrading cultures.

Protein ID	Clan	Family	Heatmap				
			Y	F	P	S	M
260638	CYP547	CYP5136	Blue	Yellow	Yellow	Yellow	Yellow
259665	CYP52	CYP5137	Light Blue	Yellow	Yellow	Yellow	Green
183109	CYP53	CYP53	Green	Yellow	Green	Green	Green
256887	CYP64	CYP5152	Green	Yellow	Yellow	Yellow	Green
254221	CYP64	CYP5148	Green	Yellow	Green	Yellow	Yellow
206285	CYP54	CYP512	Light Blue	Yellow	Green	Green	Green
265475	CYP64	CYP5152	Light Blue	Green	Green	Green	Green
164255	CYP64	CYP5158	Light Blue	Light Blue	Green	Green	Green
246674	CYP54	CYP512	Light Blue	Green	Green	Green	Green
194437	CYP64	CYP5148	Light Blue	Green	Light Blue	Green	Green
109856	CYP52	CYP63	Light Blue	Green	Green	Green	Green
262256	CYP547	CYP5136	Blue	Green	Green	Yellow	Light Blue
265429	CYP534	CYP5150	Blue	Light Blue	Green	Light Blue	Green
253633	CYP534	CYP5150	Light Blue	Light Blue	Green	Green	Green
249950	CYP534	CYP5150	Light Blue	Green	Green	Green	Light Blue
212559	CYP53	CYP53	Light Blue	Green	Green	Green	Light Blue
211048	CYP52	CYP5137	Light Blue	Green	Green	Green	Light Blue
263271	CYP52	CYP5141	Light Blue	Green	Green	Green	Light Blue
211944	CYP52	CYP5141	Light Blue	Green	Green	Green	Light Blue
257741	CYP67	CYP5036	Light Blue	Green	Green	Green	Green
261326	CYP52	CYP5141	Light Blue	Green	Light Blue	Light Blue	Light Blue
208499	CYP64	CYP5144	Light Blue	Green	Light Blue	Light Blue	Light Blue
250554	CYP534	CYP5139	Light Blue	Light Blue	Light Blue	Light Blue	Green
265238	CYP64	CYP5144	Light Blue	Light Blue	Green	Light Blue	Light Blue
209385	CYP64	CYP5144	Light Blue	Green	Blue	Light Blue	Light Blue
256807	CYP64	CYP5144	Blue	Light Blue	Light Blue	Green	Light Blue
253615	CYP64	CYP5037	Light Blue	Light Blue	Light Blue	Green	Light Blue
207382	CYP64	CYP5144	Light Blue	Light Blue	Green	Light Blue	Light Blue

Gene expression data were obtained from MacDonald et al. [10]. Y: YMPG culture, F: balsam fir, P: lodgepole pine, S: white spruce, M: sugar maple. Heat map represents the level of gene transcripts as described in Fig. S2.

Table S16. UPLC peaks corresponding to wood-derived phenolic compounds that were transformed by *P. carnosus* or *P. chrysosporium*.

Retention time	Component	S. maple		Y. birch		T. aspen		R. spruce		W. spruce		B. fir		R. pine	
		Pca	Pch	Pca	Pch	Pca	Pch	Pca	Pch	Pca	Pch	Pca	Pch	Pca	Pch
Heartwood, 350nm															
1.81	ρ -Coumaric acid									+					
2.49	(-) – Epicatechin gallate									++	++		+		
2.88	Benzoic acid	++	++			++	++	++	++			+	+		+
3.35	Kaempferol 3-O- β -D-glucoside							++	++	++	++				
3.84	Naringin									++	++				
4.89	Kaempferol 3-O- β -L-rhamnoside														
5.31	Unidentified														
6.77	Unidentified														
6.93	Unidentified														
8.32	Unidentified														
9.24	Unidentified														
Heartwood, 280nm															
7.91	Unidentified														
Sapwood, 350nm															
2.89	Benzoic acid														
3.5	Quercetin 3-O- β -L-rhamnoside														
7.29	Luteolin														
9.08	Unidentified														
9.11	Kaempferol														
9.27	Unidentified														
9.38	Unidentified														
9.53	Unidentified														
9.67	Unidentified														
Sapwood, 280nm															
1.62	Unidentified														

++: Significantly decreased, +: Detectable decrease, Blank: Not significantly affected or peaks not observed.

Table S17. Assignment of FT-IR peaks decomposed by *P. carnosus* and *P. chrysosporium*.

Wave number (cm-1)	Peak description	PCA loading			
		Aspen H	Aspen S	Pine H	Pine S
<i>Peaks decreased by P. carnosus</i>					
1700-1550	Conjugated carbonyl stretches, conjugated and nonconjugated C=C stretches; characteristic of both lignin and carbohydrates [81]				1622*
1515-1505	C1/4C stretching of the aromatic ring (G units)		1522 1508		1518
1470-1455	C-H asymmetric deformation in -OCH ₃ , CH ₂ in pyran ring symmetric scissoring		1465		
1375-1365	CH bending in cellulose I and cellulose II and hemicellulose			1384	1384*
1268-1273	Guaiacyl ring breathing with carbonyl stretching [82]		1261		
1235-1230	Syringyl ring breathing and C-O stretching in lignin and xylan		1229		
1162-1125	C-O-C asymmetric stretching in cellulose I and cellulose II		1127		
1128-1110	Aromatic C-H in-plane deformation (typical for S units), C1/4O stretch	1124*	1127		
1128-1110	Aromatic C-H in-plane deformation (typical for S units), C1/4O stretch			1105	
1086-1075	C-O deformation in secondary alcohols and aliphatic ethers			1091	
1060-1015	C-O valence vibration mainly from C(3)-O(3)H			1062 1035	1056 1030
1047-1004	C-O stretching in cellulose I and cellulose II			1035	1030
996-985	C-O valence vibration	990*			
<i>Additional peaks decreased only by P. chrysosporium</i>					
1650-1640	Water associated with lignin or cellulose	1644			
1470-1455	C-H asymmetric deformation in -OCH ₃ , CH ₂ in pyran ring symmetric scissoring				1477
1162-1125	C-O-C asymmetric stretching in cellulose I and cellulose II			1168	1183
1128-1110	Aromatic C-H in-plane deformation (typical for S units), C1/4O stretch			1125 1114	
1060-1015	C-O valence vibration mainly from C(3)-O(3)H		1060 1037		
1047-1004	C-O stretching in cellulose I and cellulose II			1003	
996-985	C-O valence vibration			985	
					981

*Peaks representing components decomposed only by *P. carnosus* as shown in Fig. S7(C).
Peak description not referenced in the table are from Popescu et al. [83]

Table S18. Gradient method of UPLC elution.

Time	Flow Rate (mL/min)	% A	% B	Curve
Initial	0.50	95.0	5.0	0
1.00	0.50	85.0	15.0	6
8.00	0.50	80.0	20.0	6
10.00	0.60	50.0	50.0	6
12.00	0.60	20.0	80.0	6
13.00	0.60	95.0	5.0	6

Solvent A: 0.1% Formic Acid

Solvent B: Acetonitrile