Supplementary data

Table S1. Chemical composition of sorghum stover.

Table S2. ^{13}C chemical shift assignments in solid state CP-MAS analysis.

Figure S1. Released reducing sugar of untreated wild-type (WT), *bmr6* mutant (b6), *bmr12* mutant (b12) and *bmr6*/*bmr12* double mutant (b6b12) sorghum stover after 48h hydrolysis with different cellulase loadings (3.0, 4.5 and 6.0 FPU/g sorghum) at 28 ℃.

Figure S2. Reducing sugar concentration of the cultivation supernatant during the conversion of wild type (solid square), *bmr6* mutant (solid triangle), *bmr12* mutant (open square) and *bmr6*/*bmr12* double mutant (open triangle) sorghum biomass by *C. echinulata* FR3.

Figure S3. Solid state ^{13}C CPMAS NMR analysis of control and fungus-treated sorghum biomass. (A) wild-type sorghum without fungal conversion; (B) sample 1 of wild-type sorghum after 6 days of fungal conversion by *C. echinulata* FR3; (C) sample 2 of wild-type sorghum after 6 days of fungal conversion by *C. echinulata* FR3; (D) sample 3 of wild-type sorghum after 6 days of fungal conversion by *C. echinulata* FR3; (E) *bmr6*/*bmr12*double mutant sorghum without fungal conversion; (F) sample 1 of *bmr6*/*bmr12*double mutant sorghum after 6 days of fungal conversion by *C. echinulata* FR3; (G) sample 2 of *bmr6*/*bmr12*double mutant sorghum after 6 days of fungal conversion by *C. echinulata* FR3; and (H) sample 3 of *bmr6*/*bmr12* double mutant sorghum after 6 days of fungal conversion by *C. echinulata* FR3.

Figure S4. Comparison of the expanded ^{13}C CPMAS NMR region of fungus-conversed sorghum by *C. echinulata* FR3 and their corresponding controls. (A) aromatic resonances, (B) carbohydrate carbon resonances. (black) wild-type sorghum without fungal conversion; (red) sample 1 of wild-type sorghum after 6 days of fungal conversion by *C. echinulata* FR3; (blue) sample 2 of wild-type sorghum after 6 days of fungal conversion by *C. echinulata* FR3; (green) sample 3 of wild-type sorghum after 6 days of fungal conversion by *C. echinulata* FR3; (magenta) *bmr6*/*bmr12* double mutant sorghum without fungal conversion; (lite blue) sample 1 of *bmr6*/*bmr12* double mutant sorghum after 6 days of fungal conversion by *C. echinulata* FR3; (orange) sample 2 of*bmr6*/*bmr12* double mutant sorghum after 6 days of fungal conversion by *C. echinulata* FR3; and (olive) sample 3 of *bmr6*/*bmr12* double mutant sorghum after 6 days of fungal conversion by *C. echinulata* FR3.

Figure S5. GC/MS analysis of lipid profile of *C. echinulata* FR3 after growing 6 days on dilute acid pretreated wild-type sorghum and un-pretreated *bmr6*/*bmr12* double mutant sorghum biomass.

Figure S6. Functional analysis of lignocellulose degradation gene categories based on CAZy database. (A). Distribution of glycoside hydrolases (GH), glycosyl transferases (GT), polysaccharide lyases (PL), carbohydrate esterases (CE) and auxiliary activities (AA) among the CAZy orthologous genes. (B). Distribution of each GH family among the putative glycoside hydrolases genes.

Figure S7. Phylogenetic analysis of CeFR1943 laccase-like multiple copper oxidase with the other 35 published laccases from 30 different species including fungus (ascomycetes and basidiomycetes) and plants.

Genotype	Cellulose (%)	Hemicellulose (%)	Lignin (%)	Ash (%)
Wild type	24.71	19.00	17.28	4.42
bmr6 mutant	25.31	19.85	16.49	5.20
bmr12 mutant	24.60	19.30	16.72	5.52
bmr6/bmr12 double mutant	24.10	18.45	15.50	6.23

Table S1

δ_C (ppm)	**Assignment**
198	Aromatic carbonyl (-CO-) resonances
185-175	Aliphatic carbonyl/carboxyl (-COOR, -COO-) resonances
160-200	Carbonyl and carboxyl carbon resonances
175-165	Aromatic carboxyl (-COO-) resonances
155-160	C4 resonances in *p*-coumarate ester/*p*-hydroxyphenyl unit
100-162	Aromatic ring resonances (H,G,S)
149-152	C3,C5 in etherified S- and C3 in etherified G-unit
147-149	C3, C5 in non-etherified S- and C3 in non-etherified G-unit.
136-140	C1 resonances in etherified H,G and S-unit
132-134	C1 resonances in non-etherified H,G and S-unit
103-130	C2, C6 in S- /C3,C5 in H- /C5 in G-unit
60-100	Carbohydrate carbon resonances
52-55	Methoxyl in S- and G-unit
40-20	Aliphatic carbon resonances of fatty acids & triglycerides

Table S2

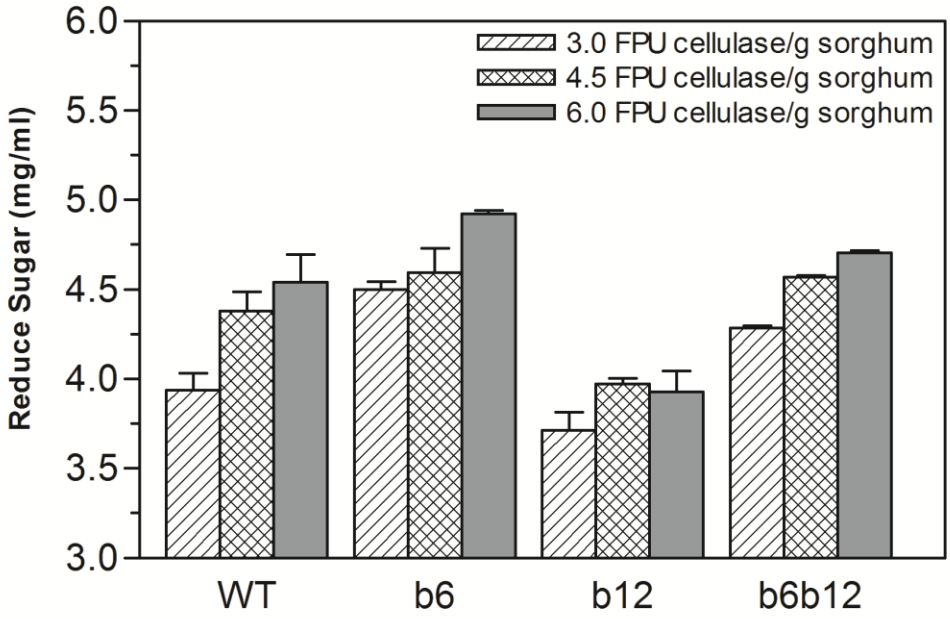
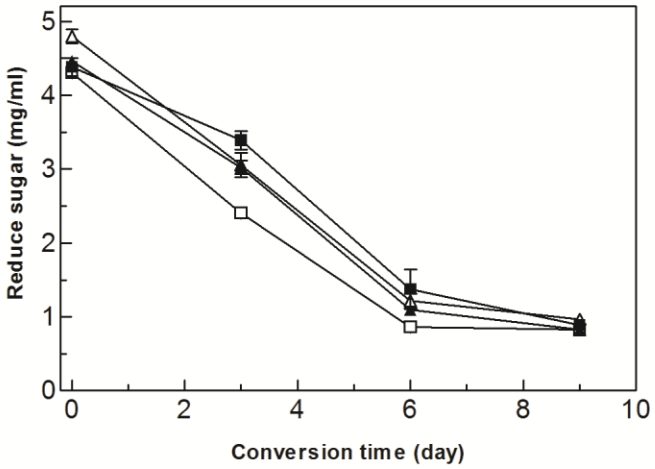

6.0
5.5
5.0
4.5
4.0
3.5
3.0
Reduce Sugar (mg/ml)
3.0 FPU cellulase/g sorghum
4.5 FPU cellulase/g sorghum
6.0 FPU cellulase/g sorghum
WT
b6
b12
b6b12

Figure S1



52

53 Figure S2

54

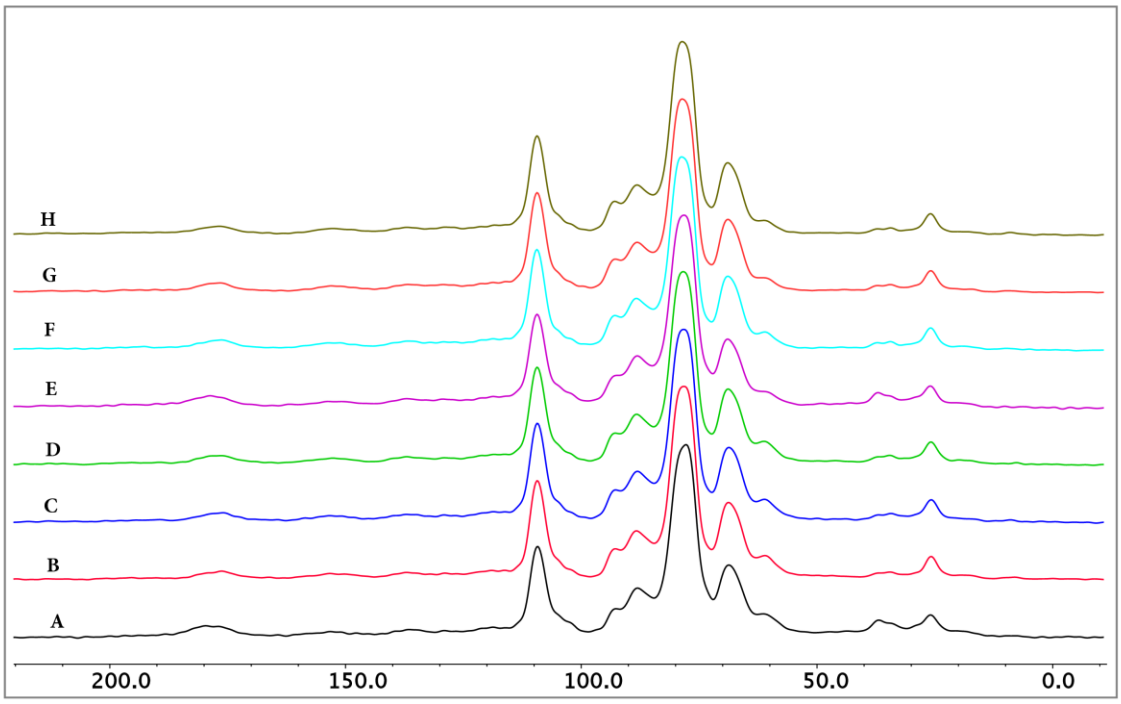
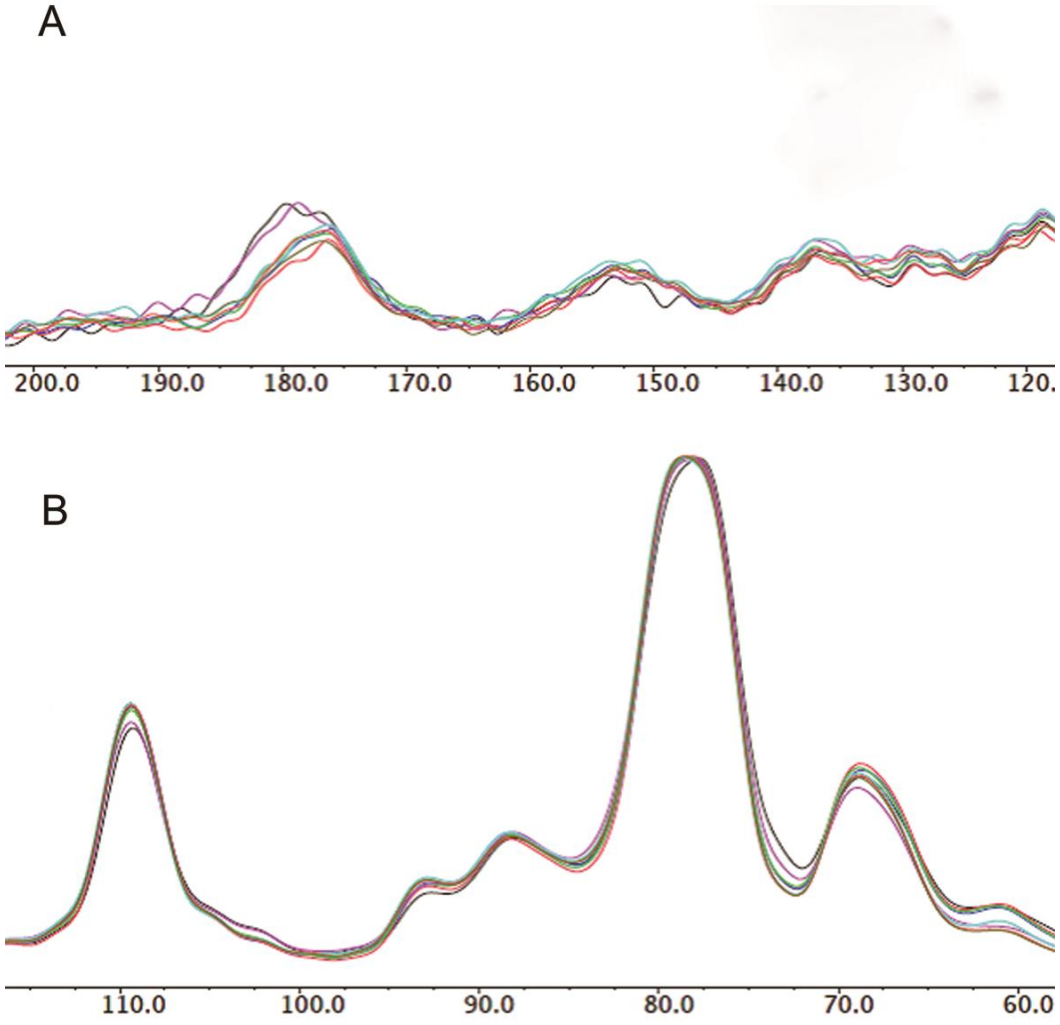


Figure S3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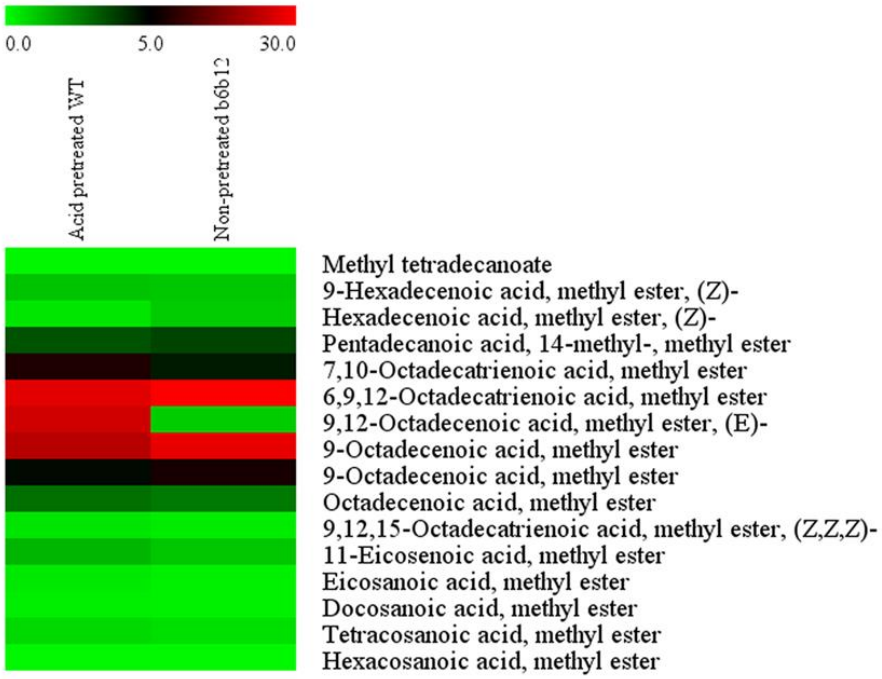
180.0
170.0
160.0
150.0
140.0
130.0
120.
B
110.0
100.0
90.0
80.0
70.0
60.0

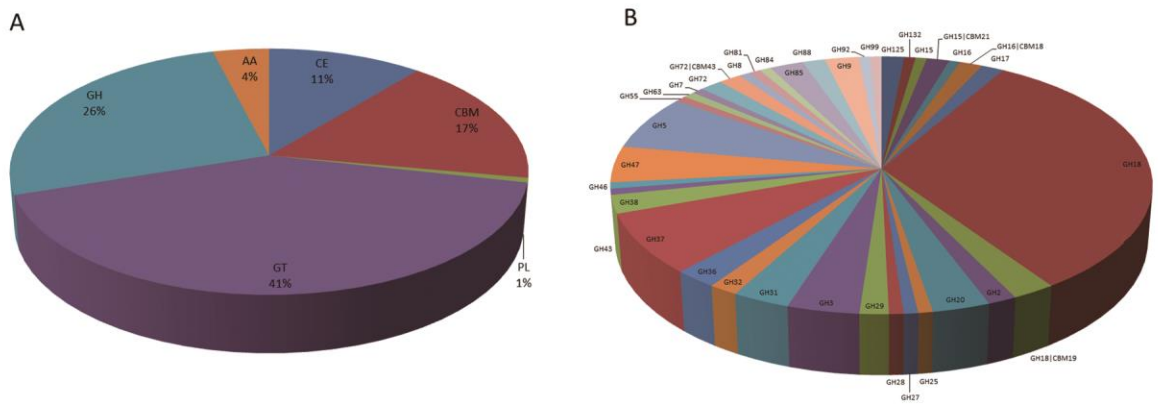
Figure S4



61

62 Figure S5

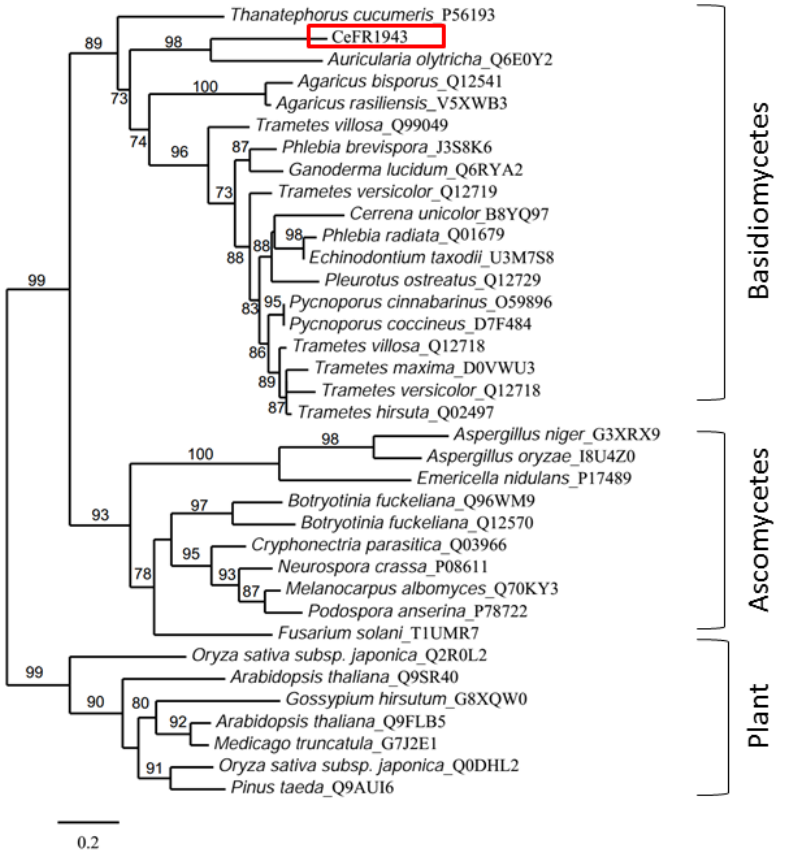
63



64

65 Figure S6

66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CeFR1943
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Phlebia brevispora_J3S8K6
Ganoderma lucidum_Q6RYA2
Trametes versicolor_Q12719
Cerrena unicolor_B8YQ97
Phlebia radiata_Q01679
Echinodontium taxodii_U3M7S8
Pleurotus ostreatus_Q12729
Pycnoporus cinnabarinus_O59896
Pycnoporus coccineus_D7F484
Trametes villosa_Q12718
Trametes maxima_D0VWU3
Trametes versicolor_Q12718
Trametes hirsuta_Q02497
Aspergillus niger_G3XRX9
Aspergillus oryzae_I8U4Z0
Emericella nidulans_P17489
Botryotinia fuckeliana_Q96WM9
Botryotinia fuckeliana_Q12570
Cryphonectria parasitica_Q03966
Neurospora crassa_P08611
Melanocarpus albomyces_Q70KY3
Podospora anserina_P78722
Fusarium solani_T1UMR7
Oryza sativa subsp. japonica_Q2R0L2
Arabidopsis thaliana_Q9SR40
Gossypium hirsutum_G8XQW0
Arabidopsis thaliana_Q9FLB5
Medicago truncatula_G7J2E1
Oryza sativa subsp. japonica_Q0DHL2
Pinus taeda_Q9AUI6
Basidiomycetes
Ascomycetes
Plant
0.2

Figure S7