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**Biotransformation of bisphenol F by white-rot fungus *Phanerochaete sordida* YK-624
under non-ligninolytic condition**

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1 **Abstract**

2 Environmental bisphenol F (BPF) has a cyclic endocrine disruption effect, seriously
3 threatening animal and human health. It is frequently detected in environmental samples
4 worldwide. For BPF remediation, biological methods are more environmentally friendly than
5 physicochemical methods. White-rot fungi have been increasingly studied due to their potential
6 capability to degrade environmental pollutants. *Phanerochaete sordida* YK-624 has been
7 shown to degrade BPF by ligninolytic enzymes under ligninolytic conditions. In the present
8 study, degradation of BPF under non-ligninolytic conditions (no production of ligninolytic
9 enzymes) was investigated. Our results showed that BPF could be completely removed after 7
10 d incubation. A metabolite of BPF, 4,4'-dihydroxybenzophenone (DHBP), was identified by
11 mass spectrometry and nuclear magnetic resonance and DHBP was further degraded by this
12 fungus to form 4-hydroxyphenyl 4-hydroxybenzoate (HPHB). DHBP and HPHB were the
13 intermediate metabolites of BPF and would be further degraded by *P. sordida* YK-624. We also
14 found that cytochrome P450s played an important role in BPF degradation. Additionally,
15 transcriptomic analysis further supported the involvement of these enzymes in the action of
16 BPF degradation. Therefore, BPF is transformed to DHBP and then to HPHB likely oxidized
17 by cytochrome P450s in *P. sordida* YK-624. Furthermore, the toxicological studies
18 demonstrated that the order of endocrine-disrupting activity for BPF and its metabolites was
19 HPHB > BPF > DHBP.

20

21 **Key Points:**

22 • White-rot fungus *Phanerochaete sordida* YK-624 could degrade BPF.

23 • Cytochrome P450s were involved in the BPF degradation.

24 • The order of endocrine disrupting activity was: HPHB > BPF > DHBP.

25 **Keywords:** Bisphenol F; White-rot fungi; Degradation metabolism; Cytochrome P450;

26 Transcriptomic analysis

27 **Introduction**

28 Bisphenols are synthetic compounds contain two hydroxyphenyl groups that are used as a
29 necessary raw material in manufacturing (Dhanjai et al. 2018). The most common bisphenol is
30 bisphenol A (BPA; 2,2-bis(4-hydroxyphenyl) propane), which is widely applied in paper
31 products, food packaging, and dental sealants (Thoene et al. 2018). However, BPA was shown
32 to disrupt the synthesis, transport, and metabolism of steroid hormones, and it caused several
33 human diseases (Donato et al. 2017). Considering the association with the health effects of BPA,
34 regulations on its production and usage have been issued around the world (Chen et al. 2016).
35 Therefore, analogues of BPA have been used as replacements in a myriad of industrial
36 production processes. BPF (4,4'-methylenediphenol) is one of the most commonly used
37 replacements for manufacturing epoxy resins and polycarbonates in plastic and food packaging
38 process (Yamazaki et al. 2015).

39 BPF has been found in the environment, consumer products and foodstuffs for its
40 widespread usage, and its good stability and aqueous solubility (Liao and Kannan 2013, 2014;
41 Yamazaki et al. 2015; Yao et al. 2020). Therefore, BPF has been detected in various human
42 organs and even could across the placental barrier (Cabaton et al. 2006). A number of reports
43 have shown that BPF is as toxic as BPA on human and animals. Damage to the respiratory
44 system, reproductive system, and endocrine system is induced by a low-concentration exposure
45 to BPF (Mendy et al. 2020; Reina-Pérez et al. 2021; Ullah et al. 2018). Because of the toxicity
46 of BPF, it is critical to remove it from environmental. Compared with physicochemical
47 remediation methods, biological methods are more environmentally friendly, of lower cost, and
48 result in less secondary pollution (Lacalle et al. 2020). Several bacteria have been shown to can

49 degrade BPF, including *Sphingobium fuliginis* OMI, *Arthrobacter* sp. strain YC-RL1,
50 *Phragmites australis*, *Sphingomonas yanoikuyae* strain FM-2, and *Pseudomonas* sp. HS-2
51 (Inoue et al. 2008; Lu et al. 2016; Ogata et al. 2013; Ren et al. 2016; Toyama et al. 2009; 2013).
52 White-rot fungi are known as the only microorganisms which can mineralize lignin to CO₂ and
53 H₂O, and it had reported that they could degrade a range of organic pollutants (Zhuo and Fan
54 2021). We have previously shown that *Phanerochaete sordida* YK-624 produced ligninolytic
55 enzymes lignin peroxidase (LiP) and manganese peroxidase (MnP) for BPA degradation under
56 ligninolytic conditions, while cytochrome P450s and *O*-methyltransferase might be involved in
57 BPA degradation under non-ligninolytic conditions (Wang et al. 2013a, 2013b, 2014). The
58 results of transcriptomic analysis suggested that LiP and MnP of *P. sordida* YK-624 played
59 important roles in BPF degradation under ligninolytic conditions (Wang et al. 2021). Zdarta et
60 al. reported that BPF dimers and trimers were formed in the ligninolytic degradation process
61 (Zdarta et al. 2018). However, dimers or trimers are unstable, and they might be transformed
62 into the original substance. Thus, BPF degradation by *P. sordida* YK-624 requires mechanisms
63 distinct from the dimerization.

64 The degradation mechanism of BPF by *P. sordida* YK-624 under non-ligninolytic
65 conditions was carried out in the present study. First, the biodegradation of BPF was
66 investigated, and the metabolites of BPF were detected. Then, differentially expressed genes
67 (DEGs) of *P. sordida* YK-624 during BPF degradation were investigated, and the degradation
68 mechanism of BPF was proposed. Furthermore, toxicological experiments of BPF and its
69 metabolites were performed to evaluate the feasibility of BPF degradation by this fungus.

Materials and methods

70 **Chemicals**

71 BPF and piperonyl butoxide (PB) with 99% analytical standards were purchased from
72 Tokyo Chemical Industry Co. (Japan). 4,4'-Dihydroxybenzophenone (DHBP) with a 98%
73 analytical standard was purchased from Shanghai Aladdin Biochemical Technology Co. Ltd.
74 (China). 4-Hydroxyphenyl 4-hydroxybenzoate (HPHB) with 97% analytical standard and
75 bisphenol S (99%) were purchased from Shanghai Macklin Biochemical Co. (China). Methanol
76 (MeOH) used for High-performance liquid chromatography (HPLC) was purchased from
77 Thermo Fisher (HPLC-grade; Thermo Fisher Scientific Inc. Shanghai, China), and other
78 organic solvents (MeOH, ethyl acetate (EtOAc), *n*-hexane) and analytical reagents were
79 purchased from Shanghai Titan Scientific Co. (China).

80 **Degradation experiment and measurement of fungal biomass**

81 The white-rot fungus used in this study was *P. sordida* YK-624 (ATCC 90872) (Hirai et
82 al. 1994). The fungi were maintained at 4 °C with potato dextrose agar (PDA). Fungal inoculum
83 was cultured on PDA plates for 3 days growth at 30 °C prior to use. After incubation, two agar
84 rounds (10 mm in diameter) from PDA plates were inoculated into 10 mL of potato dextrose
85 broth (PDB) medium for 3 days, except for the control flasks without fungi. Then, BPF was
86 added to each flask to start the degrading process at an initial concentration of 0.1 mM and
87 incubated for 0-7 days at 30 °C. Acetone and internal standard material (bisphenol S) were
88 added to the culture, and then homogenized by an IKA T18 ULTRA-TURRAX® homogenizer
89 (Staufen, Germany). The homogenate was evaporated to dryness and then dissolved in MeOH.
90 The residual BPF in each culture was detected by HPLC (Shimadzu, LC-20A). The sampling
91 and analysis methods were reported in detail in our earlier research (Wang et al. 2021).

92 For determination of fungal biomass, mycelia were collected with PDA rounds removed.
93 The collected mycelia were dried at 105 °C for 4 h and weighed at room temperature. Each
94 group of experiments was performed in triplicate.

95 **Cytochrome P450s inhibition experiment**

96 After preincubation for 3 days in PDB medium, the typical cytochrome P450 inhibitor PB
97 was added with three concentration gradients (0.01, 0.1, and 1 mM). Then, the samples were
98 further incubated for another 0-7 days at 30 °C. The qualification of BPF was detected as above.
99 Each group of experiments were performed in triplicate.

100 **RNA-sequencing analysis**

101 RNA-sequencing (RNA-seq) was applied to illustrate the functional genes of *P. sordida*
102 YK-624 in degrading BPF. *P. sordida* YK-624 was incubated in PDB medium at 30 °C with the
103 same concentration (0.1 mM). Each group of experiments were performed in triplicate with no
104 BPF as the control. The mycelia incubated for 7 days, in which BPF was completely degraded,
105 and were then collected for RNA extraction. After extracted RNA was quantified, a cDNA
106 library was constructed and sequenced on an Illumina NovaSeq platform (Novogene
107 Experimental Department) (Parkhomchuk et al. 2009). The sequences were mapped to the
108 reference genome sequences of *P. sordida* YK-624 deposited in the National Center for
109 Biotechnology Information (NCBI; <https://www.ncbi.nlm.nih.gov/nuccore/BPQB00000000.1>).
110 Hisat2 (v2.0.5) was used to align paired-end clean reads to the reference genome for mapping.
111 Then, the mapped reads of each sample were assembled by StringTie (v1.3.3b) in a reference-
112 based approach (Pertea et al. 2015). In addition, featureCounts v1.5.0-p3 was used to calculate
113 the read numbers mapped to each gene. Other detailed analysis methods were reported in our

114 previous study (Wang et al. 2021). The DEGs were defined as having a P value < 0.05 and |
115 $\log_2(\text{fold change})$ | > 1 between BPF-degrading samples and the control. Detailed data of
116 transcriptome was shown in Table S1. DEGs were annotated in the Gene Ontology (GO,
117 <http://geneontology.org/>) and Kyoto Encyclopedia of Genes and Genomes (KEGG,
118 <https://www.genome.jp/kegg/>) databases.

119 **Quantitative real-time PCR (qPCR)**

120 The method of RNA extraction was described as Section above. First-strand cDNA was
121 synthesized by a Hifair® II 1st Strand cDNA Synthesis Kit (Yeasen, Shanghai, China). Then,
122 Hieff® qPCR SYBR Green Master Mix (Low Rox Plus) (Yeasen, Shanghai, China) was adopted
123 for qPCR, and qPCR was performed in an ABI-Vii7 instrument (ABI, America). More detailed
124 methods were described in our previous research (Wang et al. 2021). Actin gene was used as a
125 reference, and the detail of primers used for functional genes verification are listed in Table S2.
126 The levels of relative expression genes were determined by the $\Delta\Delta C_t$ method.

127 **BPF metabolite determination**

128 Fungal inoculum was precultured as described above. Ten agar rounds were inoculated
129 into 150-mm-diameter culture dish conical flasks containing 50 mL of PDB medium for 3 days.
130 A total of 5 L of PDB medium was prepared. Then, 500 μL of 50 mM BPF (final concentration:
131 0.5 mM) was added for biotransformation. According to the results of BPF degradation, the
132 samples were collected after an additional 7 days of incubation. The collected medium was
133 evaporated and extracted three times by EtOAc. The extracting solution was evaporated to
134 dryness and then separated by silica gel flash column chromatography. The gradient elution
135 program was set as follows: *n*-hexane/EtOAc/MeOH (10/0/0, 8/2/0, 7/3/0, 6/4/0, 5/5/0, 4/6/0,

136 3/7/0, 2/8/0, 1/9/0, 0/10/0, 0/9/1, 0/8/2, 0/7/3, 0/6/4, 0/4/6, 0/2/8, and 0/0/10). The obtained
137 fractions were analysed by thin-layer chromatography (TLC) and HPLC (column: InertSustain,
138 C30, 5 μ m, 4.6 \times 250 mm). Subsequently, the metabolite was further purified by HPLC (column:
139 Develosil InertSustain C30, 5 μ m, 20 \times 250 mm), and the pure metabolite was analysed by mass
140 spectrometry (MS; Synapt HDMS G2-Si, Waters, USA) and nuclear magnetic resonance (NMR;
141 Avance III HD 600 MHz, Bruker, Germany).

142 **DHBP degradation and DHBP metabolite determination**

143 To study the further BPF mechanism by *P. sordida* YK-624, degradation experiments of
144 the metabolite DHBP under non-ligninolytic conditions were carried out. After preincubation,
145 100 μ L DHBP was added for its concentration of 0.1 mM and incubated for up to one week.
146 The cytochrome P450 inhibitor experiment was performed as described in Section 2.3. The
147 DHBP was quantified by HPLC. Each group of experiments was performed in triplicate.

148 The incubation of *P. sordida* YK-624 to identify DHBP metabolites and metabolite
149 purification were carried out as Section 2.6. The EtOAc extract was separated by *n*-
150 hexane/EtOAc/MeOH (10/0/0, 8/2/0, 7/3/0, 6/4/0, 5/5/0, 4/6/0, 3/7/0, 2/8/0, 1/9/0, 0/10/0, 0/9/1,
151 0/7/3, 0/5/5, 0/3/7, 0/1/9 and 0/0/10, v/v/v). Meanwhile, the degradation experiment of DHBP
152 metabolite was performed as DHBP degradation method, which 0.1 mM HPHB was added and
153 incubated for up to 6 days.

154 **Exposure experiments of BPF and its metabolites**

155 All the exposure experiments in this study were performed under the Organization for
156 Economic Co-operation and Development (OECD) Test Guidelines 210 and 230 with minor
157 modifications. In brief, wild-type adult zebrafish (*danio rerio*, AB strain) purchased from

158 Nanjing YiShu LiHua Biotechnology Co., Ltd. (Nanjing, China) were maintained in flow
159 aquariums at ~28 °C with a light cycle of 14:10-h light–dark. Zebrafish embryos at 2 h
160 postfertilization (hpf) after washing with embryo rearing medium were randomly selected and
161 exposed to embryo rearing medium (negative control, NC) or 2.5 μM BPF, DHBP or HPHB,
162 with 15 embryos in each example and 6 examples in each treatment group. Two-thirds of the
163 exposure solutions were changed every day with newly prepared solutions until 96 hpf.
164 Zebrafish larvae were then collected, and total RNA was extracted using TRIzol reagent
165 (Ambion, Carlsbad, California, USA). Following RNA quantification on a NanoDrop One
166 spectrophotometer (Thermo Fisher, USA) and reverse transcription using Takara PrimeScript™
167 RT Master Mix (Takara Bio Inc., Shiga, Japan), the transcript abundances of reproductive
168 neuroendocrine-related genes encoding kisspeptin (*kiss1* and *kiss2*), gonadotropin-releasing
169 hormone (*gnrh3*), β-subunit of gonadotropin (*fshβ*) and estrogen receptors (*era*, *erβ1* and *erβ2*)
170 were determined using TB Green™ Premix Ex Taq™ II (Takara Bio Inc., Shiga, Japan) on a
171 LightCycler® 96 Instrument (Roche Molecular Systems, Inc., California, USA).

Results

172 **Efficient degradation of BPF under non-ligninolytic conditions**

173 BPF was rapidly degraded by *P. sordida* YK-624, and the degradation rate reached up to
174 100% within 7 d. *P. sordida* YK-624 showed a lag phase on the first day, followed by a rapid
175 degradation stage (Fig. 1a). The fungal biomass changes during degradation were measured,
176 and there was no significant difference compared with the samples without BPF (Fig. S1).

177 **Effect of cytochrome P450s inhibitor**

178 The degradation of BPF was decreased significantly compared with the complete
179 degradation without PB (Fig. 1b). In the presence of a high concentration (1 mM) of PB, only
180 51.50% BPF was degraded after 7 days of incubation. When PB concentrations of 0.1 and 0.01
181 mM were added, BPF degraded 63.05% and 71.61%, respectively. These degradation rates of
182 BPF were markedly lower than that without PB. This result revealed that cytochrome P450s
183 were involved in the degradation of BPF under non-ligninolytic conditions.

184 **RNA-seq analysis of *P. sordida* YK-624**

185 RNA-seq was used to identify the DEGs of *P. sordida* YK-624, which responded to BPF
186 degradation under non-ligninolytic conditions. DEGs were obtained by comparing the BPF-
187 degrading samples (**BPF_P**) with the samples without BPF (**P_c**). Clean bases of all samples
188 were greater than 6.7 GB, and other more detailed information are shown in Table S3. A total
189 of 365 genes exhibited differential changes between BPF-degrading conditions and conditions
190 without BPF; 189 DEGs were upregulated, and 176 were downregulated (Fig. S2). Seven
191 upregulated DEGs encoded cytochrome P450, and detailed information is listed in Table S4.
192 These cytochrome P450 genes were then quantified with qPCR to verify the reality of RNA-
193 seq, and the trends of the relative expression were consistent with the RNA-seq results (Fig. 2).

194 GO and KEGG pathway analyses were conducted to identify the BPF degradation of
195 DEGs. According to Fig. 3a, GO analysis suggested that upregulated DEGs were mainly
196 enriched in “integral component of membrane” [cellular components, (CC)], “intrinsic
197 component of membrane” (CC), “membrane part” (CC), “carbohydrate metabolic process”
198 [biological process, (BP)], “iron ion binding” [molecular function, (MF)], “oxidoreductase
199 activity” (MF), “heme binding” (MF), and “tetrapyrrole binding” (MF). The top twenty

200 enriched KEGG pathways of upregulated DEGs are shown in Fig. 3b. The top gene was
201 “biosynthesis of secondary metabolites” (eleven genes), followed by five genes: “instarch and
202 sucrose metabolism”, two genes in “glutathione metabolism”, “arginine and proline metabolism”
203 and “biosynthesis of cofactors” (Fig. 3b).

204 **Determination of BPF metabolites and its degradation**

205 Five-litre spread cultivation system of *P. sordida* YK-624 were incubated for the
206 determination of the metabolites of BPF, and a BPF metabolite was purified. The molecular
207 formula of BPF metabolite was calculated to be C₁₃H₉O₃ by Q-TOF-MS, molecular ion was *m/z*
208 213.1200 [M-H]⁻. The molecular formula of the metabolite was increased by 14 compared with
209 BPF, suggesting that methylene (-CH₂) might be transformed to carbonyl groups. Moreover,
210 the metabolite was further characterized by ¹H-NMR analysis, which was the same as the
211 DHBP standard (Fig. S3). The metabolite of BPF was determined to be DHBP (Fig. 4).

212 Further research on DHBP degradation by *P. sordida* YK-624 was performed. *P. sordida*
213 YK-624 could also excellently transform DHBP, and more than 90% of DHBP was degraded
214 after 7 days of incubation (Fig. 1c). The results of the cytochrome P450 inhibition experiment
215 showed a similar tendency to BPF. Only 19.66%, 6.18% and 8.64% degradation of DHBP was
216 detected after 7 days of incubation with three concentration gradients of PB addition 0.01, 0.1
217 and 1 mM, respectively (Fig. 1d). Thus, cytochrome P450s also involved in the biodegradation
218 of DHBP by *P. sordida* YK-624 under non-ligninolytic conditions.

219 **DHBP metabolite determination and mechanism of BPF**

220 To determine the metabolites of DHBP, large-scale cultures of *P. sordida* YK-624
221 incubated in PDB medium were for 7 days. The molecular formula of DHBP metabolites was

222 calculated to be C₁₃H₉O₄ by Q-TOF-MS, which molecular ion was *m/z* 229.1180 [M-H]⁻. The
223 molecular formula of metabolite was increased by 16 from DHBP, and it is conjectured that an
224 O atom was inserted into one of the phenolic rings in DHBP. Moreover, the metabolite was
225 further characterized by ¹H-NMR analysis, which is the same as the HPHB standard (Fig. S4).
226 The metabolite was determined as HPHB (Fig. 4).

227 The time course of BPF metabolism was investigated to evaluate the transformation of
228 BPF (Fig. 1f). The metabolite DHBP was first detected at 1 day, and the concentration of DHBP
229 increased during the first 3 days. Then, DHBP gradually decreased, and HPHB was detected
230 starting at 3 days. HPHB was almost completely degraded by *P. sordida* YK-624 after 6 days
231 of incubation (Fig. 1e). Bacterium *S. yanoikuyae* strain FM-2 could degrade HPHB to 4-
232 hydroxybenzoate and 1,4-hydroquinone, and they were directly mineralized (Inoue et al., 2008).
233 It is suggested that *P. sordida* YK-624 could metabolize BPF to DHBP and then transform to
234 HPHB (Fig. 4). This reaction was followed by further metabolism.

235 **Effects of BPF and its metabolites on the expression of reproductive neuroendocrine-** 236 **related genes**

237 Here, 2 hpf zebrafish embryos were exposed to BPF and its metabolite for 96 h, and the
238 expression profiles of several reproductive neuroendocrine-related genes in zebrafish larvae
239 were further examined to reveal the differential endocrine-disrupting activities. The results
240 showed that BPF exposure did not significantly alter the expression levels of genes encoding
241 kisspeptin (*kiss1* and *kiss2*), gonadotropin-releasing hormone (*gnrh3*), or the estrogen receptor
242 (ER) isoforms Er α (*era*) and Er β 2 (*er β 2*); however, it upregulated the expression levels of the
243 follicle-stimulating hormone beta gene (*fsh β*) and the Er β 1 gene (*er β 1*) (Fig. 5). Meanwhile,

244 degradation to DHBP showed an alleviative effect on BPF-induced neuroendocrine toxicity, as
245 indicated by the downregulated expression of *fsh β* in zebrafish larvae exposed to DHBP
246 compared to BPF (Fig. 5d). Conversely, degradation to HPHB upregulated the expression levels
247 of *gnrh3*, *fsh β* and *er β 1* to a greater extent than BPF exposure (Fig. 5c, d, f).

Discussion

248 Our results shown that BPF could be completely removed by *P. sordida* YK-624 after 7 d
249 incubation (Fig. 1a). Some studies have reported that some enzymes of white-rot fungi have
250 huge capacity in the degradation of BPF. Under ligninolytic conditions, with the action of lignin
251 peroxidases (LiPs) and manganese peroxidases (MnPs), *P. sordida* YK-624 could completely
252 degrade BPF after 4 days of incubation (Wang et al. 2021). BPF could be removed by *Pleurotus*
253 *eryngii*, and laccase was involved in degrading BPF (Chang and Chang 2016). The complete
254 removal of BPF could be observed by laccase treatment at a 1 mM concentration within 90 min
255 (Nicolucci et al. 2011). Zdarta et al. first structured a new biopolymeric material with spongin
256 and laccase from *Trametes versicolor*, and 96% of BPF was removed by this immobilized
257 laccase in 24 h (Zdarta et al. 2018).

258 Cytochrome P450 enzymes are heme *b* containing monooxygenases defined as a distinct
259 class of haemoproteins (Klingenberg 1958). Several studies have reported that cytochrome
260 P450s are powerful biocatalysts that can catalyse a variety of oxidation reactions. Cytochrome
261 P450 enzymes are distributed in a number of organisms and have been widely identified in
262 white-rot fungi (Hirosue et al. 2011). In our previous studies, cytochrome P450s were involved
263 in the metabolism of some environmental pollutants by the white-rot fungus *P. sordida* YK-624
264 (Mori et al. 2017; Wang et al. 2011, 2013a, 2019). In the current research, PB, as a classic

265 inhibitor, was chosen to verify the oxidation of cytochrome P450s on BPF and its metabolite
266 DHBP degradation. It is indicated that cytochrome P450s were involved in the degradation of
267 BPF (Fig. 1b; 1d).

268 Degradation mechanism of BPF by *P. sordida* YK-624 has been studied by metabolites
269 determination and RNA-seq analysis. Firstly, a BPF metabolite DHBP was determined, it is
270 usually used as a UV filter to protect cosmetics, personal care products and packaging materials
271 from sunlight. DHBP has received growing attention as an emerging bisphenol analogue;
272 however, it has an endocrine-disrupting effect similar to BPA (Chen et al. 2002; Han et al. 2021).
273 DHBP was noticed with a high detection frequency of 55.8% in China's sludge from 30 cities
274 owing to its wide application (Song et al. 2014). However, there have been no studies assessing
275 its biodegradation. DHBP degradation by *P. sordida* YK-624 was further performed, and a
276 metabolite HPHB was determined (Fig. 4). The endocrine-disrupting activity of BPF and its
277 metabolites was used for evaluating the metabolites toxicity. Similar to the well-known
278 endocrine-disrupting chemical BPA, BPF has also been shown to be oestrogenic, androgenic,
279 and thyroidogenic (Rochester and Bolden 2015), even though its endocrine-disrupting activity
280 is much lower than that of BPA (Qiu et al. 2021). Our results were in conformity with previous
281 findings that *fsh β* and *er β 1* were the most sensitive among the various reproductive
282 neuroendocrine-related genes in zebrafish larvae in response to BPF exposure (Qiu et al. 2021).
283 It has demonstrated that HPHB had the highest endocrine-disrupting activity among these three
284 chemicals, followed by BPF and DHBP (Fig. 5). These results suggested that biotransformation
285 of BPF to DHBP, rather than to HPHB, might have a better application for environmental
286 remediation of BPF.

287 RNA-seq was used to research the functional genes of BPF degradation by *P. sordida* YK-
288 624. Seven upregulated DEGs encoded cytochrome P450s, and the enriched MF terms
289 correlated with cytochrome P450s according to the GO analysis (Fig. 3a). These results
290 illustrated that cytochrome P450s were involved in BPF biodegradation under non-ligninolytic
291 conditions, combined with the results of the cytochrome P450 inhibition experiment. Eleven
292 upregulated DEGs in BPF degradation were enriched in “biosynthesis of secondary metabolites”
293 pathways (KEGG ID: pco01110), including glycosyltransferase family 20, survival protein
294 SurE, malate synthase, 1,4- α -glucan branching enzyme, phosphatidylserine decarboxylase,
295 aldose 1-epimerase, and sterol 14 α -demethylase (Table S1). Sterol 14 α -demethylase play an
296 important role in the fungal-specific ergosterol biosynthesis, ergosterol is the major fungal
297 membrane sterol (Rosam et al. 2020; Yang et al. 2015). Glycosyltransferases play a central role
298 in glycans synthesis, fungi produce glycans for cell structure maintains and energy storage
299 (Hashimoto et al. 2009; Yang et al. 2019). It is reported that SurE of *Escherichia coli* might be
300 involved in the stress response (Caturegli et al. 2014), suggesting that the addition of BPF can
301 be a cause of stress for *P. sordida* YK-624. 1,4- α -glucan branching enzyme is classified as
302 glycoside hydrolase, it can break down carbohydrates and polysaccharides (Ban et al. 2020;
303 Rafiei et al. 2021). Meanwhile, *S*-transferase was upregulated in BPF degradation condition, it
304 might be related to conjugation reactions in glutathione metabolism (Uno et al. 2020).
305 Additionally, white-rot fungi secrete carbohydrate active enzymes (CAZymes) that act on
306 cellulose and hemicellulose (Hori et al. 2014). Carbohydrate-related enriched GO terms suggest
307 that *P. sordida* YK-624 might secrete more CAZymes in BPF-degrading conditions. It is
308 interesting that the “metabolism” pathway was annotated both in GO terms and KEGG

309 pathways (Fig. 3). It has been reported that white-rot fungi can use organic pollutants as carbon
310 sources (Zhang et al. 2019). We speculated that BPF might be used as a carbon source for *P.*
311 *sordida* YK-624 growth and metabolism based on the GO and KEGG analysis results.

312 The BPF mechanism by *P. sordida* YK-624 was proposed based on the results of
313 metabolite determination, cytochrome P450 inhibition experiments and RNA-seq analysis.
314 Cytochrome P450s can catalyse a great quantity of oxidation reactions, such as epoxidation of
315 C=C double bonds, aromatic hydroxylation, deamination and dehalogenation, C-C and C-O
316 phenol coupling, cleavage of C-C bonds, Baeyer-Villiger oxidation, and rearrangement
317 reactions (Urlacher and Girhard 2012). In the present study, BPF was transformed to DHBP
318 and further transformed to HPHB via the Baeyer-Villiger oxidation by cytochrome P450s in *P.*
319 *sordida* YK-624 (Fig. 4). This degradation pathway was mostly consistent with the degradation
320 of BPF by *Arthrobacter* sp. Strain YC-RL1 (Ren et al. 2016). In other studies, BPF was first
321 transformed to bis(4-hydroxyphenyl) methanol, which was further oxidized to DHBP (Inoue et
322 al. 2008; Lu et al. 2016). However, this transformation was not observed in this study. Baeyer-
323 Villiger monooxygenase is remarkable biocatalysts for the Baeyer-Villiger oxidation, it has
324 been found in fungi and bacteria (Mascotti et al. 2015; Zhang et al. 2021). Two other
325 monooxygenases (uncharacterized lactate 2-monooxygenase and leukotriene-B₄ 20-
326 monooxygenase) were upregulated in BPF degradation condition, but no Baeyer-Villiger
327 monooxygenase was found. Extensive genomic analysis of *P. sordida* YK-624 should be
328 performed.

329 In conclusion, *P. sordida* YK-624 could completely degrade BPF within 7 d of incubation
330 under non-ligninolytic conditions. A metabolite DHBP was determined, and more than 90% of

331 DHBP was degraded after 7 d of incubation. The results of cytochrome P450 inhibition
332 experiments and RNA-seq analysis suggested that cytochrome P450s involved in the
333 biotransformation of BPF. Further research showed that *P. sordida* YK-624 had efficient
334 capacity in degrading DHBP, and the metabolite HPHB was determined. The results of
335 exposure experiments demonstrated that the endocrine-disrupting activity between BPF and its
336 metabolites was HPHB > BPF > DHBP. The proposed degradation pathway of BPF suggested
337 that BPF was transformed to DHBP and further to HPHB catalysed by cytochrome P450s.
338 Additionally, *P. sordida* YK-624 could degrade HPHB, and it might be mineralized.

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343 **Author contribution statement:** JW, HH, RY and XZ conceived and designed the research.

344 RY, XZ, BW, and JJ conducted the experiments. RY, NW and PS analyzed the data. RY and
345 XZ wrote the manuscript. PX, TX and BY revised the manuscript. All authors read and approved
346 the manuscript.

347 **Data availability:** The sequence information that supports the findings of this study is
348 available in the National Microbiology Data Center (NMDC) with the accession number
349 NMDC10017948.

350 **Declarations**

351 **Ethics approval and consent to participate:** All applicable international, national, and/or
352 institutional guidelines for the care and use of animals were followed.

353 **Consent to participate:** Not applicable.

354 **Consent for publication:** Not applicable.

355 **Conflict of interest:** The authors declare no competing interests.

356

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528 **Figures Legends**

529 **Fig. 1.** Degradation of BPF and its metabolites by *P. sordida* YK-624 under non-ligninolytic
530 conditions: (a) Degradation of BPF; (b) The effect of a cytochrome P450 inhibitor on BPF
531 degradation; (c) Degradation of DHBP; (d) The effect of a cytochrome P450 inhibitor on DHBP
532 degradation; (e) Degradation of HPHB; (f) Biotransformation of BPF. (a), (c), (e): Triangle:
533 control without inoculation; diamond: treatment with *P. sordida* YK-624; (b), (d): Red circle:
534 control; yellow diamond: 0.01 mM PB; blue triangle: 0.1 mM; dark-blue square: 1 mM PB; (f):
535 Red circle: BPF; blue triangle: DHBP; yellow square: HPHB. Values are the means \pm SD of
536 triplicate samples.

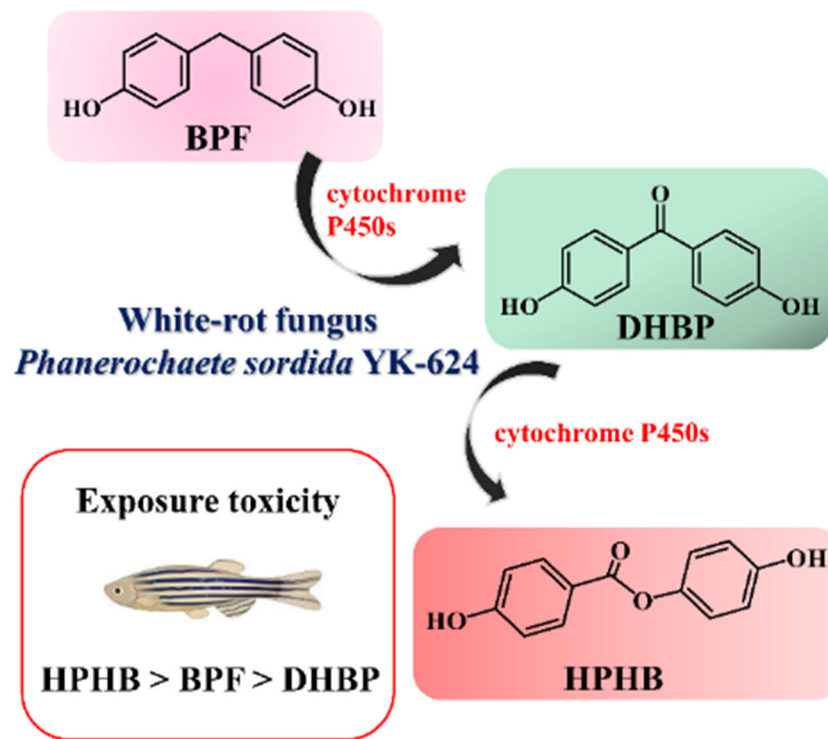
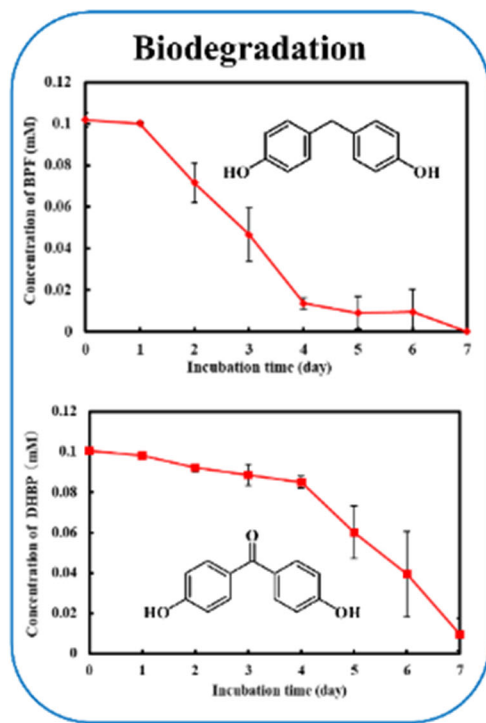
537 **Fig. 2.** Correlation analysis between qPCR and RNA-seq results for upregulated DEGs that were
538 characterized as cytochrome P450s. The details are shown in Table S4. Black bars: qPCR results;
539 grey line: RNA-seq results. Values are the means \pm SD of triplicate samples.

540 **Fig. 3.** GO (a) and KEGG (b) enrichment analyses of upregulated DEGs involved in BPF
541 degradation.

542 **Fig. 4.** Proposed pathway for the biodegradation of BPF by *P. sordida* YK-624 under non-
543 ligninolytic conditions. DHBP: 4,4'-dihydroxybenzophenone; HPHB: 4-hydroxyphenyl 4-
544 hydroxybenzoate.

545 **Fig. 5.** Effects of BPF, DHBP and HPHB (2.5 μ M) on the expression levels of reproductive
546 neuroendocrine-related genes in zebrafish larvae after 96 h of exposure. The abundances of
547 genes encoding kisspeptin [*kiss1* and *kiss2* (a-b)], gonadotropin-releasing hormone [*gnrh3* (c)],
548 β -subunit of gonadotropin [*fsh β* (d)] and estrogen receptors [*era*, *er β 1* and *er β 2* (e-g)] were
549 determined by qPCR. Data are shown as the means \pm standard deviation (n = 6), with a single

550 data point presented. Asterisks (*) indicate significant differences ($p < 0.05$) in comparison with
551 the vehicle control or between two linked groups with folding lines.



Graphical Abstract

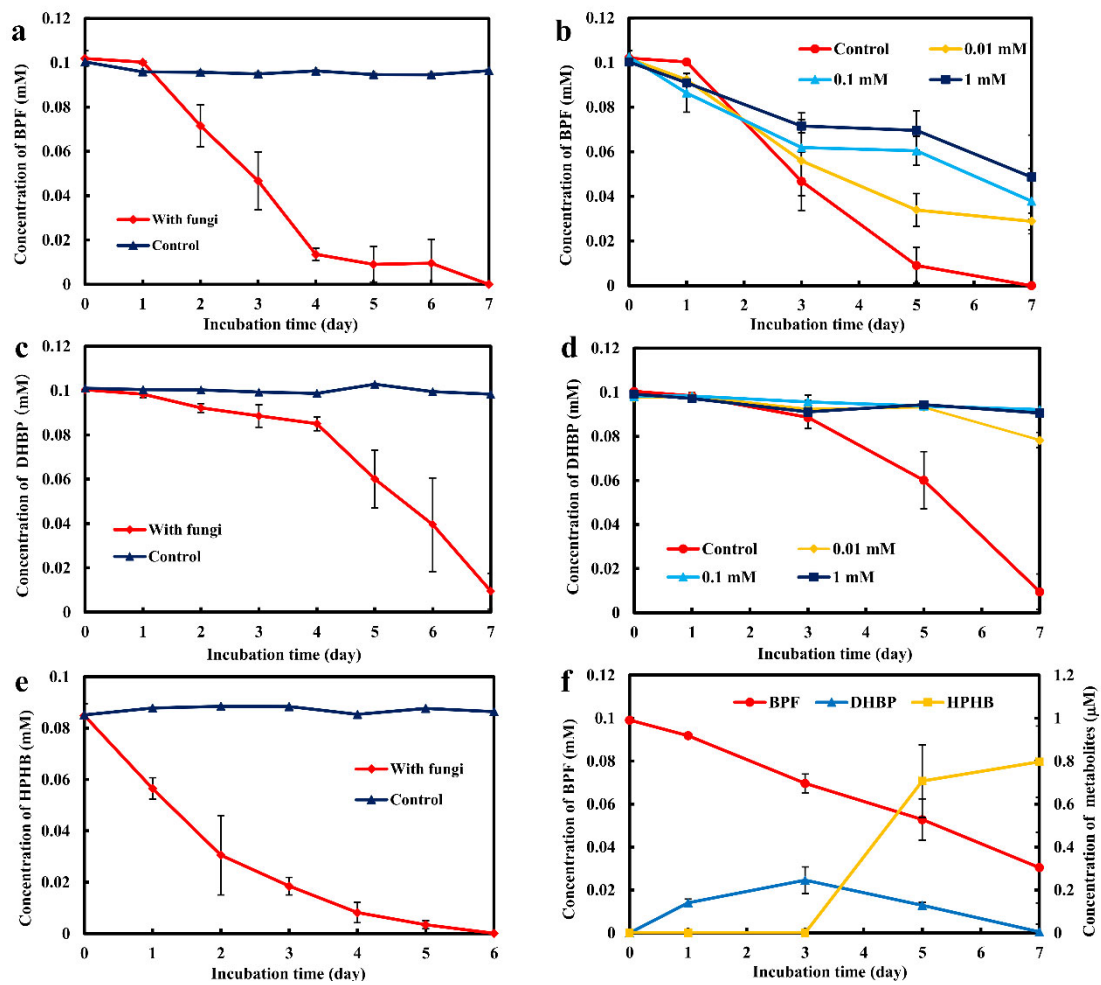


Fig. 1

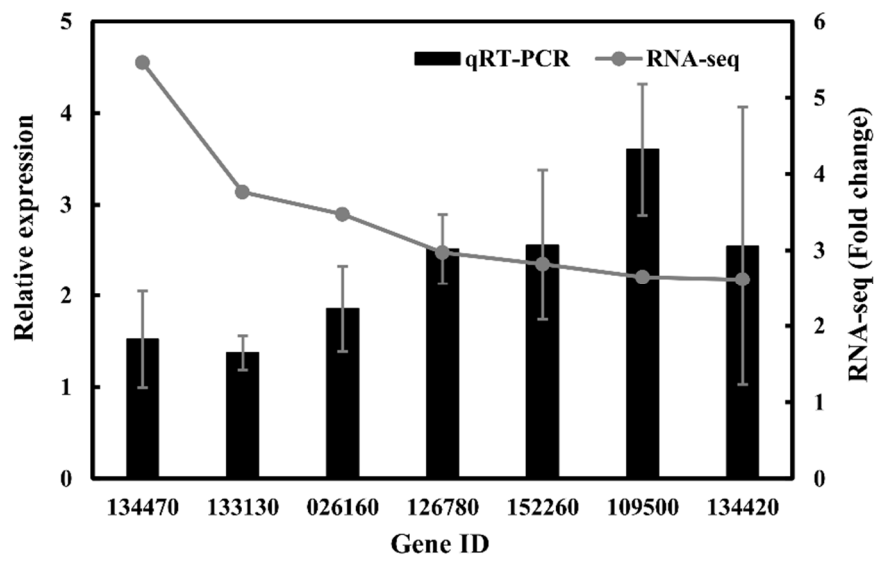


Fig. 2

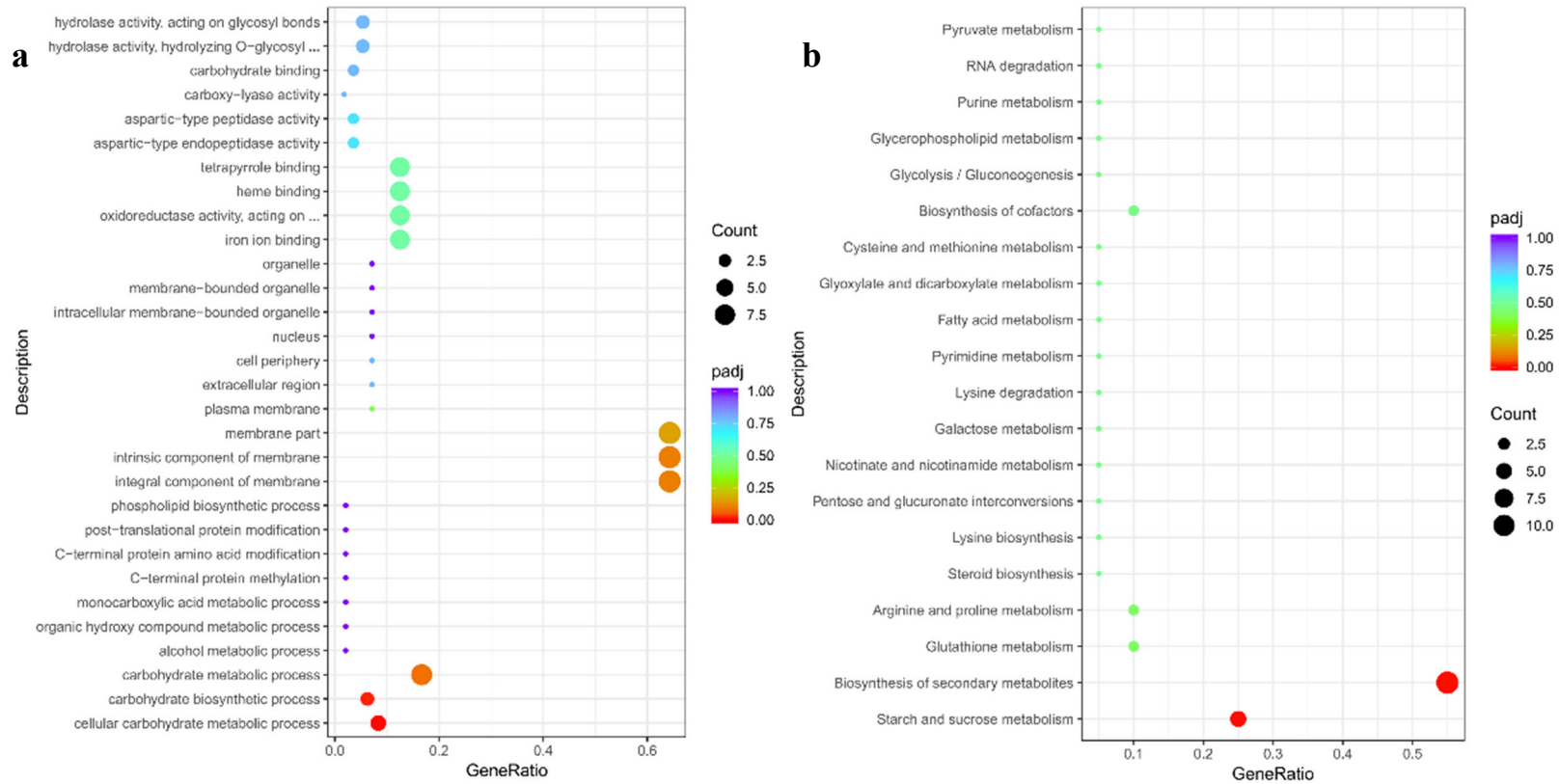


Fig. 3

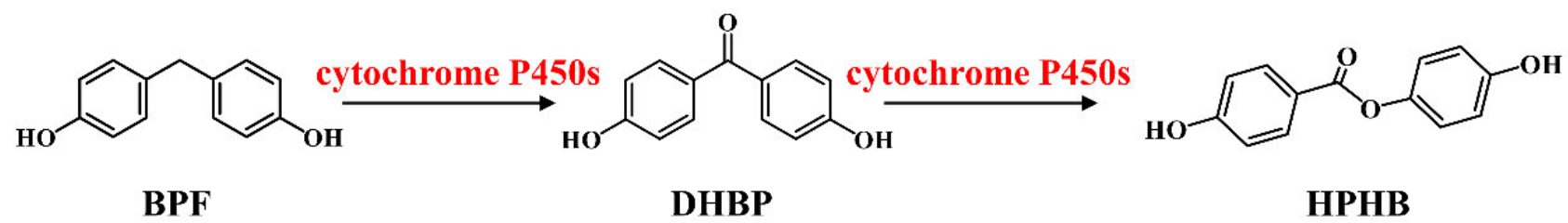


Fig. 4

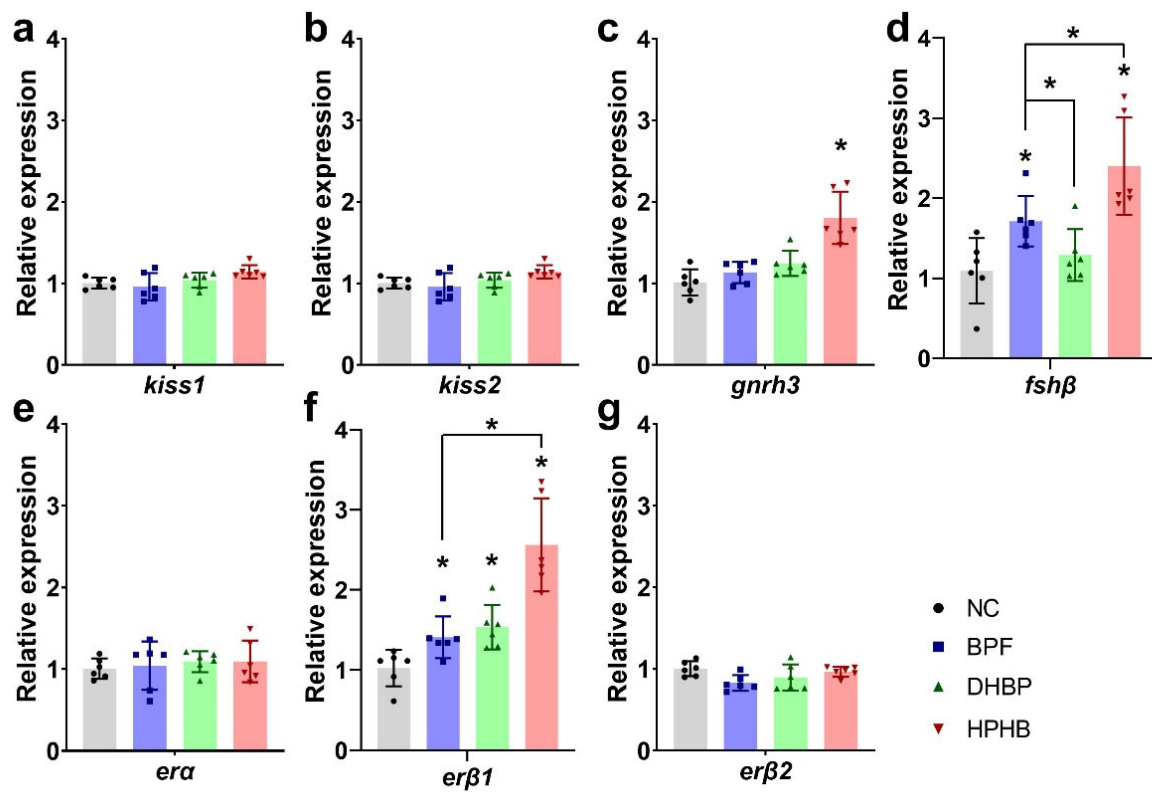


Fig. 5

**Biotransformation of bisphenol F by white-rot fungus *Phanerochaete sordida* YK-624
under non-ligninolytic condition**

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Table S1. Data for *P. sordida* YK-624 transcripts

gene_id	BPF_P	P_c	log2FoldChange	pvalue	padj	gene_length	gene_description
gene-PsYK624_160000	217.9988	2.105089	6.717235	0.000186	0.014149	336	-
gene-PsYK624_159990	58.71169	1.120186	5.637251	1.97E-05	0.002607	720	-
gene-PsYK624_125110	9405.437	216.6504	5.439092	2.29E-12	6.24E-09	825	P24665.1 RecName: Full=Aspergillopepsin-2; AltName: Full=Acid protease A; AltName: Full=Aspergillopepsin II; AltName: Full=Proctase A; Contains: RecName: Full=Aspergillopepsin-2 light chain; AltName: Full=Aspergillopepsin II light chain; Contains: RecName: Full=Aspergillopepsin-2 heavy chain; AltName: Full=Aspergillopepsin II heavy chain; Flags: Precursor && PF01828:Peptidase A4 family
gene-PsYK624_075980	63.8662	2.33815	4.797259	0.00021	0.015491	1161	-
gene-PsYK624_143540	7818.685	311.2152	4.65011	1.08E-11	1.36E-08	978	P30887.2 RecName: Full=Acid phosphatase; Flags: Precursor && PF01975:Survival protein SurE
gene-PsYK624_109090	200.9832	9.956011	4.328418	3.83E-06	0.000729	675	-
gene-PsYK624_081250	6141.75	345.4857	4.153697	1.66E-24	1.36E-20	2649	PF13632:Glycosyl transferase family group 2
gene-PsYK624_112600	73.16758	3.959403	4.1199	6.12E-12	9.11E-09	2244	-
gene-PsYK624_056710	3755.789	251.5699	3.900369	1.05E-07	3.61E-05	612	-
gene-PsYK624_159590	7350.905	527.427	3.800971	3.35E-07	9.98E-05	432	PF14200:Ricin-type beta-trefoil lectin domain-like

gene-PsYK624_095330	2374.609	176.7793	3.747308	1.16E-06	0.000292	1329	Q9HDX2.1 RecName: Full=Uncharacterized lactate 2-monooxygenase PB1A11.03 && PF01070:FMN-dependent dehydrogenase
gene-PsYK624_095160	2153.725	164.8945	3.705723	3.35E-08	1.34E-05	1296	PODJD7.1 RecName: Full=Pepsin A-4; AltName: Full=Pepsinogen-4; Flags: Precursor && PF00026:Eukaryotic aspartyl protease
gene-PsYK624_130100	3178.543	260.8948	3.606561	5.93E-30	9.70E-26	1254	PF02469:Fasciclin domain
gene-PsYK624_114330	33623.13	3199.488	3.393582	0.001003	0.044095	519	-
gene-PsYK624_168010	17001.08	1636.434	3.376698	8.94E-05	0.008213	1143	Q01752.1 RecName: Full=Aryl-alcohol dehydrogenase [NADP(+)]; Short=AAD && PF00248:Aldo/keto reductase family
gene-PsYK624_076870	1930.077	201.75	3.257006	7.80E-06	0.001238	759	Q5BH34.1 RecName: Full=Short chain dehydrogenase mdpC; AltName: Full=Monodictyphenone synthesis protein C && PF00106:short chain dehydrogenase
gene-PsYK624_056290	30.34646	3.171577	3.215145	0.00109	0.046937	348	PF10346:Conidiation protein 6
gene-PsYK624_117590	205.3274	23.12968	3.138995	1.50E-07	4.81E-05	957	-
gene-PsYK624_077130	680.353	79.89534	3.090791	1.45E-06	0.00034	783	PF03188:Eukaryotic cytochrome b561
gene-PsYK624_143870	545.2483	65.49858	3.060826	1.79E-08	8.11E-06	876	A0A097ZPE8.1 RecName: Full=Short chain dehydrogenase andI; AltName: Full=Anditomin synthesis protein I && PF00106:short chain dehydrogenase
gene-PsYK624_137730	24703.09	3004.111	3.039599	0.000211	0.015491	666	O59827.1 RecName: Full=Glutathione S-transferase 2; AltName: Full=GST-II && PF02798:Glutathione S-transferase, N-terminal

							domain PF00043:Glutathione S-transferase, C-terminal domain
gene-PsYK624_078140	873.6745	110.7766	2.978093	0.000369	0.02148	870	O74628.1 RecName: Full=Uncharacterized oxidoreductase C162.03 && PF00106:short chain dehydrogenase
gene-PsYK624_109210	744.5869	94.85288	2.973111	0.000679	0.033035	666	-
gene-PsYK624_029300	1313.512	167.4936	2.970871	0.000243	0.016469	684	PF00127:Copper binding proteins, plastocyanin/azurin family
gene-PsYK624_004470	6406.316	822.0135	2.962217	0.000181	0.013989	2049	Q8NKE1.2 RecName: Full=1,4-alpha-glucan-branching enzyme; AltName: Full=Glycogen-branching enzyme && PF00128:Alpha amylase, catalytic domain PF02922:Carbohydrate-binding module 48 (Isoamylase N-terminal domain) PF02806:Alpha amylase, C-terminal all-beta domain
gene-PsYK624_068710	4319.528	562.4657	2.940244	0.000264	0.017565	852	O13848.1 RecName: Full=NAD/NADP-dependent indole-3-acetaldehyde reductase; AltName: Full=AKR3C2 && PF00248:Aldo/keto reductase family
gene-PsYK624_058500	32.24456	4.476178	2.900026	0.000734	0.034883	336	-
gene-PsYK624_045360	8230.807	1123.608	2.872795	0.000859	0.039302	1302	P17576.1 RecName: Full=Polyporopepsin; AltName: Full=Aspartic proteinase && PF00026:Eukaryotic aspartyl protease

gene-PsYK624_121290	1362.146	186.9903	2.862696	1.15E-06	0.000292	1068	-
gene-PsYK624_001660	56.43754	7.476004	2.861384	1.79E-05	0.0025	495	-
gene-PsYK624_034690	180.6831	24.68105	2.856895	0.000226	0.016116	300	-
gene-PsYK624_150090	1026.819	150.6032	2.770359	7.05E-06	0.001142	741	-
gene-PsYK624_092250	7048.541	1075.028	2.713147	1.10E-10	1.13E-07	1305	PF00651:BTB/POZ domain
gene-PsYK624_013940	19552.28	3066.126	2.673046	2.32E-11	2.71E-08	2775	P78875.2 RecName: Full=Trehalose-phosphatase; AltName: Full=Trehalose-6-phosphate phosphatase; Short=TPP && PF00982:Glycosyltransferase family 20 PF02358:Trehalose-phosphatase
gene-PsYK624_042700	1421.376	224.751	2.661978	9.43E-10	6.71E-07	777	Q9HK58.2 RecName: Full=L-rhamnose 1-dehydrogenase (NADP(+)); Short=RHAD && PF00106:short chain dehydrogenase
novel.345	83.02279	13.64132	2.634287	7.93E-08	2.95E-05	712	-
gene-PsYK624_139620	8971.643	1477.625	2.602107	2.08E-06	0.000445	1620	P28344.3 RecName: Full=Malate synthase, glyoxysomal && PF01274:Malate synthase
gene-PsYK624_168050	1394.724	240.4342	2.535373	2.09E-05	0.002729	963	P23641.1 RecName: Full=Mitochondrial phosphate carrier protein; AltName: Full=Mitochondrial import receptor; AltName: Full=Phosphate transport protein; Short=PTP; AltName: Full=mPic 1; AltName: Full=p32; Contains: RecName: Full=Mitochondrial phosphate carrier protein, N-terminally processed && PF00153:Mitochondrial carrier protein
gene-PsYK624_164620	115.9762	19.96876	2.523691	2.71E-06	0.000548	423	-

gene-PsYK624_140830	17319.22	3045.407	2.50786	1.50E-06	0.000344	1725	Q7Z9I0.2 RecName: Full=Uncharacterized MFS-type transporter SPBC409.08 && PF07690:Major Facilitator Superfamily
gene-PsYK624_076840	76.87868	14.07498	2.464458	3.73E-05	0.004391	906	PF04140:Isoprenylcysteine carboxyl methyltransferase (ICMT) family
gene-PsYK624_052850	7456.227	1355.248	2.459811	0.000161	0.012631	456	-
gene-PsYK624_134470	1986.2	363.5762	2.449736	1.06E-07	3.61E-05	1677	P78329.1 RecName: Full=Phylloquinone omega-hydroxylase CYP4F2; AltName: Full=20-hydroxyeicosatetraenoic acid synthase; Short=20-HETE synthase; AltName: Full=Arachidonic acid omega-hydroxylase; AltName: Full=CYP1VF2; AltName: Full=Cytochrome P450 4F2; AltName: Full=Cytochrome P450-LTB-omega; AltName: Full=Leukotriene-B(4) 20-monooxygenase 1; AltName: Full=Leukotriene-B(4) omega-hydroxylase 1; Flags: Precursor && PF00067:Cytochrome P450
gene-PsYK624_057210	214.1077	39.15981	2.447817	0.000726	0.034618	645	-
gene-PsYK624_125280	360.6932	70.79247	2.346629	1.34E-06	0.000322	840	PF01828:Peptidase A4 family
gene-PsYK624_058770	1305.659	258.7326	2.335246	0.000329	0.020062	2037	PF08030:Ferric reductase NAD binding domain PF08022:FAD-binding domain PF01794:Ferric reductase like transmembrane component
gene-PsYK624_157640	96.01597	19.26197	2.325416	0.00086	0.039302	504	-

gene-PsYK624_062910	97.42058	19.56548	2.315521	1.03E-05	0.001569	2958	-
gene-PsYK624_018310	168.4005	34.07973	2.295213	0.001152	0.048817	351	-
gene-PsYK624_114930	28143.21	5799.589	2.278866	1.13E-05	0.001621	1677	Q8N0N3.1 RecName: Full=Beta-1,3-glucan-binding protein; Short=GBP; Flags: Precursor && PF00722:Glycosyl hydrolases family 16
gene-PsYK624_066280	2611.977	543.4704	2.265368	1.98E-05	0.002607	1407	O59711.1 RecName: Full=Saccharopine dehydrogenase [NADP(+), L-glutamate-forming]; AltName: Full=Saccharopine reductase && PF03435:Saccharopine dehydrogenase NADP binding domain PF16653:Saccharopine dehydrogenase C-terminal domain
gene-PsYK624_030080	311751.1	65236.61	2.256645	1.61E-06	0.000361	861	O74631.1 RecName: Full=Protein FDD123; AltName: Full=CvHSP30/1 && PF01036:Bacteriorhodopsin-like protein
gene-PsYK624_059620	5082.189	1069.458	2.249066	0.000295	0.01887	1137	-
gene-PsYK624_136440	74.23523	15.60912	2.244646	0.00079	0.036718	468	PF14200:Ricin-type beta-trefoil lectin domain-like
gene-PsYK624_017690	4404.842	930.4866	2.243367	2.12E-08	9.38E-06	930	P02723.1 RecName: Full=ADP,ATP carrier protein; AltName: Full=ADP/ATP translocase; AltName: Full=Adenine nucleotide translocator; Short=ANT && PF00153:Mitochondrial carrier protein
gene-PsYK624_067860	2518.535	533.9002	2.237462	3.01E-05	0.003621	2823	-
gene-PsYK624_045050	24.75203	5.166226	2.234871	0.000519	0.027146	285	-
gene-PsYK624_124870	1380.455	295.9864	2.221072	1.95E-05	0.002607	2121	-

gene-PsYK624_157620	333.4567	71.8782	2.213515	0.000362	0.021299	372	-
gene-PsYK624_050620	1544.59	338.703	2.186764	5.83E-07	0.000156	222	PF00172:Fungal Zn(2)-Cys(6) binuclear cluster domain
gene-PsYK624_111510	12602.1	2771.573	2.185051	0.000312	0.019655	231	-
gene-PsYK624_029490	3820.077	850.5653	2.167558	2.70E-06	0.000548	1527	-
gene-PsYK624_105970	1615.194	371.4026	2.119576	1.21E-06	0.000299	1509	P25346.1 RecName: Full=Probable metabolite transport protein GIT1 && PF00083:Sugar (and other) transporter
gene-PsYK624_080400	2211.151	510.1485	2.115172	1.15E-05	0.001621	963	O95154.2 RecName: Full=Aflatoxin B1 aldehyde reductase member 3; AltName: Full=AFB1 aldehyde reductase 2; Short=AFB1-AR 2 && PF00248:Aldo/keto reductase family
gene-PsYK624_088180	169.8789	39.93753	2.088169	5.73E-05	0.006051	327	-
gene-PsYK624_116240	12499.28	2940.163	2.08806	0.000187	0.014149	807	-
gene-PsYK624_162340	1417.728	336.6274	2.073623	0.000256	0.017148	888	-
gene-PsYK624_167910	113.9802	27.06376	2.063633	3.46E-06	0.000673	588	-
gene-PsYK624_015540	106.0963	25.27885	2.0599	0.000149	0.012085	1008	Q0CQL9.1 RecName: Full=Metacaspase-1B; Flags: Precursor && PF00656:Caspase domain
gene-PsYK624_074840	507.904	122.6938	2.052431	1.97E-09	1.29E-06	1029	Q9C0Y6.1 RecName: Full=Zinc-type alcohol dehydrogenase-like protein PB24D3.08c && PF16884:N-terminal domain of oxidoreductase PF00107:Zinc-binding dehydrogenase
gene-PsYK624_110950	10164.87	2451.074	2.052313	7.49E-12	1.02E-08	555	PF06687:SUR7/PaII family

gene-PsYK624_143630	1282.534	309.3453	2.052171	3.25E-06	0.00064	771	Q3SZ16.1 RecName: Full=Isoamyl acetate-hydrolyzing esterase 1 homolog && PF00657:GDSL-like Lipase/Acylhydrolase
gene-PsYK624_074250	254.3596	61.43025	2.049949	3.50E-10	3.37E-07	1425	A1YPR2.1 RecName: Full=2-epi-5-epi-valiolone synthase; Short=EEVS && PF01761:3-dehydroquinone synthase
gene-PsYK624_114680	108.805	26.7532	2.040968	1.25E-07	4.10E-05	606	-
gene-PsYK624_128180	740.7308	180.0016	2.038224	0.001188	0.049434	1527	Q9US44.1 RecName: Full=Uncharacterized transporter C1002.16c && PF07690:Major Facilitator Superfamily
gene-PsYK624_099270	4029.29	982.603	2.036472	1.31E-08	6.31E-06	1035	Q4R0J7.1 RecName: Full=D-arabinitol dehydrogenase 1; AltName: Full=NADP-dependent D-arabitol dehydrogenase && PF00107:Zinc-binding dehydrogenase PF08240:Alcohol dehydrogenase GroES-like domain
gene-PsYK624_039490	228.1287	56.06238	2.023359	7.90E-05	0.007526	243	-
gene-PsYK624_067340	57.40288	14.5173	2.001583	0.000128	0.010808	216	-
gene-PsYK624_137350	1517.216	381.7577	1.991101	8.26E-07	0.000218	1938	-
gene-PsYK624_052840	1094.384	276.2729	1.985977	6.85E-06	0.001142	204	-
gene-PsYK624_152310	2029.328	517.8045	1.97071	4.64E-05	0.00516	381	-
gene-PsYK624_122930	10630.26	2771.242	1.939381	8.84E-10	6.71E-07	1395	Q8X176.1 RecName: Full=Acid phosphatase; Flags: Precursor && PF04185:Phosphoesterase family
gene-PsYK624_136590	80.07662	20.79915	1.933503	0.000341	0.020535	939	-
gene-PsYK624_093050	331.3038	87.44635	1.918741	2.35E-08	9.84E-06	447	-

gene-PsYK624_133130	691.5215	183.892	1.913269	9.22E-10	6.71E-07	1563	Q27517.1 RecName: Full=Putative cytochrome P450 CYP13A3 && PF00067:Cytochrome P450
gene-PsYK624_074640	6549.919	1755.462	1.899643	0.000576	0.029272	762	PF01738:Dienelactone hydrolase family
gene-PsYK624_131780	387.3894	103.7454	1.899516	1.20E-08	6.20E-06	843	-
gene-PsYK624_131730	5793.561	1554.896	1.897788	7.68E-06	0.001232	666	Q92429.1 RecName: Full=Superoxide dismutase [Mn], mitochondrial; AltName: Full=Mn-SOD; Flags: Precursor && PF02777:Iron/manganese superoxide dismutases, C-terminal domain PF00081:Iron/manganese superoxide dismutases, alpha-hairpin domain
gene-PsYK624_169790	428.197	114.8565	1.89759	0.001178	0.049154	540	-
gene-PsYK624_065010	1339.358	359.9992	1.894219	0.001166	0.048905	984	-
gene-PsYK624_066270	1327.479	358.353	1.888469	6.93E-06	0.001142	915	-
gene-PsYK624_160640	693.4211	187.2147	1.886451	8.57E-05	0.008011	1641	Q7RVX9.2 RecName: Full=Repressible high-affinity phosphate permease && PF00083:Sugar (and other) transporter
gene-PsYK624_001650	64.58086	17.47001	1.885766	6.75E-06	0.001137	891	-
gene-PsYK624_096620	1209.806	334.5088	1.85447	0.000322	0.01986	1026	Q5AK66.1 RecName: Full=Phosphatidylserine decarboxylase proenzyme 2; Contains: RecName: Full=Phosphatidylserine decarboxylase 2 beta chain; Contains: RecName: Full=Phosphatidylserine decarboxylase 2 alpha chain && PF02666:Phosphatidylserine decarboxylase

gene-PsYK624_097580	2355.851	655.8012	1.844349	0.000367	0.021467	1875	Q54EW2.1 RecName: Full=Putative bifunctional amine oxidase DDB_G0291301; Includes: RecName: Full=Putative sarcosine oxidase; Short=PSO; Includes: RecName: Full=Putative L-amino-acid oxidase && PF01593:Flavin containing amine oxidoreductase
gene-PsYK624_071100	6553.324	1845.076	1.828696	2.16E-05	0.002805	4785	Q06625.1 RecName: Full=Glycogen debranching enzyme; AltName: Full=Glycogen debrancher; Includes: RecName: Full=4-alpha-glucanotransferase; AltName: Full=Oligo-1,4-1,4-glucantransferase; Includes: RecName: Full=Amylo-alpha-1,6-glucosidase; Short=Amylo-1,6-glucosidase; AltName: Full=Dextrin 6-alpha-D-glucosidase && PF06202:Amylo-alpha-1,6-glucosidase PF14702:central domain of human glycogen debranching enzyme PF14701:glucanotransferase domain of human glycogen debranching enzyme PF14699:N-terminal domain from the human glycogen debranching enzyme
gene-PsYK624_145690	4385.242	1246.492	1.814253	0.000227	0.016116	1158	-
gene-PsYK624_033870	1060.321	304.9244	1.800049	6.08E-05	0.006336	870	O34678.1 RecName: Full=Uncharacterized oxidoreductase YtbE && PF00248:Aldo/keto reductase family

gene-PsYK624_163570	1304.774	374.6266	1.799816	0.000115	0.009898	471	-
gene-PsYK624_013090	285.005	81.76023	1.799691	0.000443	0.024219	846	- && O34678.1 RecName: Full=Uncharacterized oxidoreductase YtbE && PF00248:Aldo/keto reductase family
gene-PsYK624_121590	102.4496	29.31175	1.797351	0.000502	0.026856	270	-
gene-PsYK624_026160	2167.605	624.2971	1.796588	3.85E-12	7.73E-09	1518	B8NHY4.1 RecName: Full=O-methylsterigmatocystin oxidoreductase; Short=OMST oxidoreductase; AltName: Full=Aflatoxin B synthase; AltName: Full=Aflatoxin biosynthesis protein Q; AltName: Full=Cytochrome P450 64 >P0CT93.1 RecName: Full=O-methylsterigmatocystin oxidoreductase; Short=OMST oxidoreductase; AltName: Full=Aflatoxin B synthase; AltName: Full=Aflatoxin biosynthesis protein Q; AltName: Full=Cytochrome P450 64 && PF00067:Cytochrome P450
gene-PsYK624_022090	54669.44	15802.59	1.79061	0.000394	0.022617	2694	O94641.1 RecName: Full=Heat shock protein 104; AltName: Full=Protein aggregation-remodeling factor hsp104 && PF10431:C-terminal, D2-small domain, of ClpB protein PF00004:ATPase family associated with various cellular activities (AAA) PF07724:AAA domain (Cdc48

							subfamily) PF02861:Clp amino terminal domain, pathogenicity island component
gene-PsYK624_124600	869.4547	251.8134	1.787759	0.000254	0.017071	1884	O23461.1 RecName: Full=L-arabinokinase; Short=AtISA1 && PF13528:Glycosyl transferase family 1
gene-PsYK624_066970	1192.142	350.2501	1.765224	0.000633	0.031478	2481	-
gene-PsYK624_132130	167.8474	49.52471	1.756444	0.000668	0.032824	1620	-
gene-PsYK624_007990	4770.16	1412.364	1.756034	7.14E-05	0.007164	1884	O94547.1 RecName: Full=Serine/threonine-protein kinase srk1; AltName: Full=Sty1-regulated kinase 1 && PF00069:Protein kinase domain
gene-PsYK624_092810	806.6887	242.416	1.73234	0.000413	0.023283	447	-
gene-PsYK624_080490	10818.64	3268.766	1.72685	0.000103	0.009197	840	- && - && PF14259:RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)
gene-PsYK624_077980	973.4561	295.9606	1.719542	1.89E-05	0.002575	1296	-
gene-PsYK624_080050	3823.733	1162.567	1.717784	3.82E-05	0.004461	1230	Q06816.2 RecName: Full=Putative epoxide hydrolase; AltName: Full=Epoxide hydratase; Flags: Precursor && PF06441:Epoxide hydrolase N terminus
gene-PsYK624_112150	443.9621	135.8022	1.710538	3.46E-07	0.000101	735	PF14234:Domain of unknown function (DUF4336)

gene-PsYK624_045920	262.0147	80.16382	1.706402	5.70E-06	0.001019	1101	-
gene-PsYK624_004020	7480.239	2293.091	1.706066	1.83E-05	0.002509	1830	PF13840:ACT domain
gene-PsYK624_036190	1925.156	590.8125	1.704904	0.000176	0.013739	1068	Q9P7F4.1 RecName: Full=Zinc-type alcohol dehydrogenase-like protein C2E1P3.01 && PF00107:Zinc-binding dehydrogenase
gene-PsYK624_039970	2383.747	737.1223	1.694256	4.57E-05	0.005115	1203	Q10088.1 RecName: Full=Putative agmatinase 1; AltName: Full=Agmatine ureohydrolase 1; Short=AUH 1; Flags: Precursor && PF00491:Arginase family
gene-PsYK624_130770	734.9303	230.3076	1.674214	6.26E-05	0.006444	2013	-
novel.668	117.8744	36.91438	1.671991	7.92E-05	0.007526	2083	Q7MGG3.1 RecName: Full=Riboflavin biosynthesis protein VVA0006; Includes: RecName: Full=Riboflavin biosynthesis intermediates N-glycosidase; Includes: RecName: Full=GTP cyclohydrolase-2; AltName: Full=GTP cyclohydrolase II && -
novel.88	2228.443	701.5117	1.667471	3.87E-05	0.004492	1113	Q6BVN0.1 RecName: Full=Plasma membrane proteolipid 3 && PF01679:Proteolipid membrane potential modulator
gene-PsYK624_114960	336.2298	106.0273	1.662112	0.000124	0.01064	1065	-
gene-PsYK624_117380	6730.419	2131.7	1.658269	2.09E-06	0.000445	1041	Q9P7U2.1 RecName: Full=Putative aryl-alcohol dehydrogenase C977.14c && PF00248:Aldo/keto reductase family
gene-PsYK624_076500	3781.247	1212.245	1.641602	5.85E-10	5.04E-07	915	P39315.1 RecName: Full=Quinone oxidoreductase 2 && PF05368:NmrA-like family

gene-PsYK624_077950	129.1829	41.68894	1.641219	0.000765	0.036084	966	-
gene-PsYK624_067330	199.2509	64.0526	1.638814	5.66E-05	0.006015	537	-
gene-PsYK624_018850	750.4983	241.2174	1.637808	0.000345	0.020622	573	A0A097ZPE6.1 RecName: Full=Anditomin synthesis protein L && PF01741:Large-conductance mechanosensitive channel, MscL
gene-PsYK624_084100	42654.79	13738.63	1.634428	0.00027	0.017801	987	PF02839:Carbohydrate binding domain PF11901:Protein of unknown function (DUF3421)
gene-PsYK624_157320	836.7759	269.4459	1.633217	4.06E-05	0.004607	1290	-
gene-PsYK624_010250	645.8301	208.2215	1.633056	6.88E-05	0.007027	195	-
gene-PsYK624_072340	1193.908	394.2794	1.598437	5.85E-06	0.001029	2244	O74839.1 RecName: Full=Uncharacterized MscS family protein C1183.11 && PF00924:Mechanosensitive ion channel
gene-PsYK624_070780	394.3942	130.452	1.597799	1.10E-05	0.001602	1542	-
gene-PsYK624_152360	188.9472	62.96134	1.58605	0.000452	0.024669	984	PF03547:Membrane transport protein
gene-PsYK624_126780	2224.293	748.004	1.571614	7.05E-06	0.001142	1545	Q16678.2 RecName: Full=Cytochrome P450 1B1; AltName: Full=CYP1B1 && PF00067:Cytochrome P450
novel.1034	73.96884	24.9085	1.565816	3.97E-05	0.004543	2791	-
gene-PsYK624_110620	1483.106	504.8016	1.55503	0.000587	0.029751	1200	P35182.1 RecName: Full=Protein phosphatase 2C homolog 1; Short=PP2C-1 && PF00481:Protein phosphatase 2C
gene-PsYK624_067710	1203.366	410.2968	1.552886	0.000428	0.023758	2700	Q9UVG5.2 RecName: Full=Pheromone-regulated membrane protein 10 && PF06738:Putative threonine/serine

							exporter PF12821:Threonine/Serine exporter, ThrE
gene-PsYK624_107170	7777.629	2655.527	1.550486	3.83E-06	0.000729	1680	Q00075.1 RecName: Full=Alpha,alpha-trehalose-phosphate synthase [UDP-forming] 1; AltName: Full=Trehalose-6-phosphate synthase; AltName: Full=UDP-glucose-glucosephosphate glucosyltransferase && PF00982:Glycosyltransferase family 20
gene-PsYK624_128250	63.11714	21.62953	1.539741	0.000974	0.043039	1329	PF01636:Phosphotransferase enzyme family
gene-PsYK624_009290	2018.105	696.2905	1.535382	0.000224	0.016082	615	PF13462:Thioredoxin
gene-PsYK624_040740	198.757	70.05426	1.511638	4.99E-05	0.005444	654	-
gene-PsYK624_117200	1539.382	540.5531	1.508314	4.83E-05	0.005338	1017	O95154.2 RecName: Full=Aflatoxin B1 aldehyde reductase member 3; AltName: Full=AFB1 aldehyde reductase 2; Short=AFB1-AR 2 && PF00248:Aldo/keto reductase family
gene-PsYK624_152260	649.5025	229.9563	1.496762	0.0006	0.030012	1518	O46658.3 RecName: Full=Vitamin D(3) 25-hydroxylase; AltName: Full=CYP11D25; AltName: Full=Cytochrome P450 2D25 && PF00067:Cytochrome P450
gene-PsYK624_067350	8649.507	3069.636	1.494381	0.000187	0.014149	1437	D4B1P2.1 RecName: Full=Uncharacterized FAD-linked oxidoreductase ARB_02372; Flags: Precursor && PF01565:FAD binding domain

gene-PsYK624_113790	2745.38	988.335	1.474023	0.000215	0.015659	3621	Q8TF05.1 RecName: Full=Serine/threonine-protein phosphatase 4 regulatory subunit 1 && -
gene-PsYK624_121700	347.6432	125.4849	1.467196	0.00011	0.009567	1686	Q54410.1 RecName: Full=Tripeptidyl aminopeptidase; Short=Tap; Flags: Precursor && PF00561:alpha/beta hydrolase fold PF08386:TAP-like protein
gene-PsYK624_051240	2287.461	844.8365	1.436882	4.43E-05	0.004997	1053	O94564.1 RecName: Full=Zinc-type alcohol dehydrogenase-like protein C1773.06c && PF08240:Alcohol dehydrogenase GroES-like domain PF00107:Zinc-binding dehydrogenase
gene-PsYK624_102250	21842.85	8114.131	1.42873	0.000266	0.017618	624	-
gene-PsYK624_019680	1785.192	664.8082	1.424797	0.001175	0.049154	1464	-
gene-PsYK624_146000	179.0956	66.88068	1.419975	0.000714	0.034173	2220	Q5U752.1 RecName: Full=Interferon-induced GTP-binding protein Mx; AltName: Full=Interferon-inducible Mx protein && PF00350:Dynamin family PF01031:Dynamin central region
gene-PsYK624_107940	306.3764	115.3769	1.408879	0.000131	0.011051	450	-
gene-PsYK624_109500	5488.457	2072.5	1.405177	0.001117	0.047809	1653	P49602.1 RecName: Full=Lanosterol 14-alpha demethylase; AltName: Full=CYP4I; AltName: Full=Cytochrome P450 51; AltName: Full=Cytochrome P450-14DM; AltName: Full=Cytochrome P450-LIA1; AltName: Full=Sterol 14-alpha demethylase && PF00067:Cytochrome P450

gene-PsYK624_100230	1287.651	488.9874	1.396761	0.000513	0.026932	1743	-
gene-PsYK624_121010	99.84329	38.2722	1.391136	2.68E-05	0.003293	729	-
gene-PsYK624_134420	833.7278	318.445	1.389075	0.000413	0.023283	1656	P33270.2 RecName: Full=Cytochrome P450 6a2; AltName: Full=CYPVIA2; AltName: Full=Cytochrome P450-B1 && PF00067:Cytochrome P450
gene-PsYK624_144860	125.7556	48.23021	1.380879	6.12E-05	0.006338	726	PF13419:Haloacid dehalogenase-like hydrolase
gene-PsYK624_086580	120.9547	46.46863	1.368634	0.000865	0.039393	1785	-
gene-PsYK624_117190	40837.13	15960	1.355444	4.30E-07	0.00012	1146	Q8CG76.3 RecName: Full=Aflatoxin B1 aldehyde reductase member 2; AltName: Full=Succinic semialdehyde reductase; Short=SSA reductase && PF00248:Aldo/keto reductase family
novel.547	604.2208	237.6071	1.346635	6.92E-05	0.007027	1562	-
gene-PsYK624_051130	5707.08	2281.48	1.322769	0.000367	0.021467	2784	O14081.1 RecName: Full=Putative alpha,alpha-trehalose-phosphate synthase [UDP-forming] 106 kDa subunit; AltName: Full=Trehalose-6-phosphate synthase; AltName: Full=UDP-glucose-glucosephosphate glucosyltransferase && PF00982:Glycosyltransferase family 20 PF02358:Trehalose-phosphatase
gene-PsYK624_030280	1920.854	777.1675	1.306524	0.000475	0.025643	1119	-
gene-PsYK624_053750	111.5268	45.1625	1.302079	0.00043	0.023758	429	-

gene-PsYK624_019640	792.8089	322.3392	1.29933	0.000328	0.020062	921	P10281.2 RecName: Full=Ribonuclease T2; Short=RNase T2; Flags: Precursor && PF00445:Ribonuclease T2 family
gene-PsYK624_063020	254.6861	104.1173	1.291425	6.47E-06	0.001102	2961	-
gene-PsYK624_041630	1133.734	466.2558	1.283009	2.80E-06	0.000558	768	O94628.1 RecName: Full=Uncharacterized methyltransferase C1347.09 && PF13489:Methyltransferase domain
gene-PsYK624_112550	1244.424	521.8282	1.255351	3.34E-05	0.003986	2241	-
gene-PsYK624_081110	1228.151	515.8026	1.250517	0.000291	0.018705	492	-
gene-PsYK624_040400	135.3607	56.6496	1.250039	8.19E-05	0.007696	534	-
gene-PsYK624_039060	97.09216	40.95032	1.244063	0.000926	0.041503	489	-
gene-PsYK624_103580	96.54516	40.64176	1.241289	0.000212	0.015491	210	-
gene-PsYK624_160180	724.591	307.6968	1.235306	0.000508	0.026901	756	PF12766:Pyridoxamine 5'-phosphate oxidase
gene-PsYK624_105430	4199.455	1803.663	1.219371	0.001039	0.045306	930	-
gene-PsYK624_102040	3348.884	1442.304	1.215853	0.000377	0.021882	1077	P0C1E8.1 RecName: Full=Uncharacterized protein Cgl2355/cg2587 && PF02826:D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain
gene-PsYK624_040730	120.1795	51.92009	1.211674	0.000148	0.012085	615	-
gene-PsYK624_041250	930.2605	401.9296	1.211177	0.001164	0.048905	534	Q31CS5.1 RecName: Full=CinA-like protein && PF02464:Competence-damaged protein
gene-PsYK624_048760	1098.114	476.3684	1.205929	0.000152	0.012223	762	P50161.2 RecName: Full=Versicolorin reductase 1; Short=VER-1; AltName: Full=Aflatoxin biosynthesis protein M && PF00106:short chain dehydrogenase

gene-PsYK624_058510	3020.537	1347.727	1.164535	0.000878	0.039651	1299	Q9GKX6.1 RecName: Full=Aldose 1-epimerase; AltName: Full=Galactose mutarotase && PF01263:Aldose 1-epimerase
gene-PsYK624_100520	322.5116	144.6294	1.160682	0.000148	0.012085	864	PF07264:Etoposide-induced protein 2.4 (EI24)
gene-PsYK624_017190	1333.275	597.6221	1.157037	4.32E-07	0.00012	1401	A1TFU9.1 RecName: Full=FAD-dependent urate hydroxylase; AltName: Full=Flavoprotein urate hydroxylase && PF01494:FAD binding domain
gene-PsYK624_042390	1144.053	514.9895	1.152478	0.000242	0.016469	1347	PF07247:Alcohol acetyltransferase
gene-PsYK624_075430	908.4146	410.0804	1.148742	0.000774	0.036285	792	-
gene-PsYK624_009130	18644.3	8581.388	1.119509	0.000341	0.020535	327	PF12585:Protein of unknown function (DUF3759)
gene-PsYK624_114370	397.3906	183.7527	1.114433	0.000157	0.012374	618	-
gene-PsYK624_074200	5545.908	2589.318	1.098871	0.000154	0.012256	1692	-
gene-PsYK624_075320	13163.12	6306.698	1.061679	0.000857	0.039302	2001	Q5B0C0.1 RecName: Full=Heat shock 70 kDa protein; Flags: Precursor && PF00012:Hsp70 protein PF10712:NAD-specific glutamate dehydrogenase
gene-PsYK624_020450	261.4999	128.9474	1.019552	0.001062	0.045961	948	-
gene-PsYK624_138800	1899.053	936.958	1.018801	0.000105	0.009371	864	Q4W946.2 RecName: Full=2-oxoglutarate-Fe(II) type oxidoreductase; AltName: Full=Endocrocin synthesis protein D && PF14226:non-haem dioxygenase in morphine synthesis N-terminal PF03171:2OG-Fe(II) oxygenase superfamily

gene-PsYK624_091350	526.535	260.3396	1.01617	7.71E-05	0.007419	3297	-
gene-PsYK624_059460	722.2375	357.8414	1.012375	0.00043	0.023758	618	-
gene-PsYK624_040100	816.8179	405.5096	1.010552	5.23E-05	0.005664	1212	-
gene-PsYK624_160600	7708.371	3853.256	1.000524	0.000933	0.04159	1920	O42943.1 RecName: Full=Uncharacterized ABC transporter ATP-binding protein C16H5.08c && PF12848:ABC transporter PF00005:ABC transporter PF07673:Protein of unknown function (DUF1602)
gene-PsYK624_123940	2255.579	4528.659	-1.005804	0.000389	0.022475	1986	P64264.1 RecName: Full=Uncharacterized GMC-type oxidoreductase Mb1310 >P9WMV4.1 RecName: Full=Uncharacterized GMC-type oxidoreductase MT1316 >P9WMV5.1 RecName: Full=Uncharacterized GMC-type oxidoreductase Rv1279 && PF00732:GMC oxidoreductase PF05199:GMC oxidoreductase
gene-PsYK624_157740	16850.2	33911.21	-1.009016	3.94E-05	0.004536	3003	P40036.1 RecName: Full=GLC7-interacting protein 2 && PF03370:Carbohydrate/starch-binding module (family 21)
gene-PsYK624_145170	633.1062	1279.207	-1.014546	0.000659	0.032494	696	Q2T0M6.2 RecName: Full=Pyridoxine/pyridoxamine 5'-phosphate oxidase; AltName: Full=PNP/PMP oxidase; Short=PNPOx; AltName: Full=Pyridoxal 5'-phosphate synthase && PF01243:Pyridoxamine 5'-phosphate

							oxidase PF10590:Pyridoxine 5'-phosphate oxidase C-terminal dimerisation region
gene-PsYK624_071590	5652.886	11678.38	-1.046835	0.000993	0.043759	705	-
gene-PsYK624_098480	2463.955	5102.53	-1.05035	0.000212	0.015491	1671	P23501.2 RecName: Full=Dihydrosphingosine 1-phosphate phosphatase YSR3; AltName: Full=Long-chain base protein 2; AltName: Full=Sphingolipid resistance protein 3 && PF01569:PAP2 superfamily
gene-PsYK624_158660	333.2254	690.9388	-1.052484	0.000297	0.018877	555	F4K265.1 RecName: Full=Autophagy-related protein 101 && PF07855:Protein of unknown function (DUF1649)
gene-PsYK624_133450	1695.172	3524.417	-1.055701	0.000689	0.033341	2403	P40317.2 RecName: Full=Protein SOK1 && PF05794:T-complex protein 11
gene-PsYK624_115430	166.3603	345.9106	-1.056712	0.001151	0.048817	1098	-
gene-PsYK624_007430	152.8422	326.0775	-1.095786	0.000108	0.009448	1506	-
gene-PsYK624_108200	642.0528	1372.828	-1.096113	0.000257	0.017148	924	P45856.1 RecName: Full=Probable 3-hydroxybutyryl-CoA dehydrogenase; AltName: Full=Beta-hydroxybutyryl-CoA dehydrogenase; Short=BHBD && PF02737:3-hydroxyacyl-CoA dehydrogenase, NAD binding domain PF00725:3-hydroxyacyl-CoA dehydrogenase, C-terminal domain

gene-PsYK624_158460	755.8194	1617.715	-1.098284	0.000422	0.023628	1335	O94221.1 RecName: Full=Probable alpha-galactosidase B; AltName: Full=Melibiose B; Flags: Precursor && PF16499:Alpha galactosidase A
gene-PsYK624_049950	192.0958	412.1741	-1.101218	0.00051	0.026901	702	PF01753:MYND finger
gene-PsYK624_143270	80.24281	173.5702	-1.113223	0.000431	0.023758	1743	PF12937:F-box-like
gene-PsYK624_077610	58.64064	127.6645	-1.12423	0.000392	0.022555	1851	Q88CW6.1 RecName: Full=Oxygen-dependent choline dehydrogenase; Short=CDH; Short=CHD; AltName: Full=Betaine aldehyde dehydrogenase; Short=BADH && PF00732:GMC oxidoreductase PF05199:GMC oxidoreductase
gene-PsYK624_017560	783.2282	1712.472	-1.128628	2.68E-07	8.43E-05	1206	Q9D379.2 RecName: Full=Epoxide hydrolase 1; AltName: Full=Epoxide hydratase; AltName: Full=Microsomal epoxide hydrolase && PF06441:Epoxide hydrolase N terminus
gene-PsYK624_142270	2031.858	4493.038	-1.145108	0.000308	0.019556	1941	Q9SHD3.1 RecName: Full=Cyclin-U2-1; Short=CycU2;1; AltName: Full=Cyclin-P3.1; Short=CycP3;1 && PF08613:Cyclin
gene-PsYK624_146100	4025.633	9011.219	-1.16264	0.000838	0.038724	3639	-
gene-PsYK624_036210	275.7147	625.9859	-1.183859	0.000328	0.020062	933	PF00106:short chain dehydrogenase

gene-PsYK624_002260	215.9372	498.4441	-1.205304	0.000334	0.020226	1530	B8NHY4.1 RecName: Full=O-methylsterigmatocystin oxidoreductase; Short=OMST oxidoreductase; AltName: Full=Aflatoxin B synthase; AltName: Full=Aflatoxin biosynthesis protein Q; AltName: Full=Cytochrome P450 64 >P0CT93.1 RecName: Full=O-methylsterigmatocystin oxidoreductase; Short=OMST oxidoreductase; AltName: Full=Aflatoxin B synthase; AltName: Full=Aflatoxin biosynthesis protein Q; AltName: Full=Cytochrome P450 64 && PF00067:Cytochrome P450
gene-PsYK624_093500	535.4393	1237.042	-1.207963	2.59E-05	0.003224	240	PF02935:Cytochrome c oxidase subunit VIIc
gene-PsYK624_157730	82.60015	192.1812	-1.219835	0.000654	0.032394	489	-
gene-PsYK624_053790	682.0441	1603.29	-1.233621	2.46E-05	0.003111	1473	Q32PP9.1 RecName: Full=Transcription factor Sox-14 && PF00505:HMG (high mobility group) box
gene-PsYK624_154980	473.3509	1130.575	-1.256695	0.000292	0.018705	588	-
gene-PsYK624_021610	487.1051	1174.679	-1.270699	0.001084	0.046763	1245	P09110.2 RecName: Full=3-ketoacyl-CoA thiolase, peroxisomal; AltName: Full=Acetyl-CoA acyltransferase; AltName: Full=Beta-ketothiolase; AltName: Full=Peroxisomal 3-oxoacyl-CoA thiolase; Flags: Precursor && PF00108:Thiolase, N-terminal domain PF02803:Thiolase, C-terminal domain

gene-PsYK624_002310	2116.07	5108.434	-1.271712	5.32E-06	0.000977	1530	G3Y420.1 RecName: Full=Cytochrome P450 monooxygenase yanH; AltName: Full=Yanuthone D synthesis protein H; Flags: Precursor && PF00067:Cytochrome P450
gene-PsYK624_143200	52.83407	128.312	-1.27376	0.000966	0.042835	1680	-
gene-PsYK624_077630	165.7608	399.9747	-1.274016	0.000408	0.023271	777	PF11937:Protein of unknown function (DUF3455)
gene-PsYK624_033950	41.6671	101.3506	-1.2803	0.000219	0.015883	468	-
gene-PsYK624_038300	424.5875	1039.333	-1.291859	3.69E-05	0.004378	738	-
gene-PsYK624_063440	61.09651	149.6771	-1.292143	0.000759	0.03586	1020	-
gene-PsYK624_043800	60.6941	148.4358	-1.293066	0.000321	0.01986	621	-
gene-PsYK624_131330	25.57847	62.51245	-1.301254	0.000799	0.037021	522	-
gene-PsYK624_075480	258.4902	638.1227	-1.303078	0.000133	0.011115	1170	PF08939:Domain of unknown function (DUF1917)
gene-PsYK624_051180	1340.133	3331.248	-1.313529	0.000361	0.021299	1212	A2QBQ3.1 RecName: Full=Probable endo-1,3(4)-beta-glucanase An02g00850; AltName: Full=Mixed-linked glucanase An02g00850; Flags: Precursor && -
gene-PsYK624_013500	102.4243	256.5181	-1.322764	9.00E-05	0.008223	678	-
gene-PsYK624_002130	186.9466	469.8614	-1.331609	0.000505	0.026901	1362	-
gene-PsYK624_161550	35.22042	88.71137	-1.334498	0.000223	0.016079	1155	-

gene-PsYK624_008500	295.9247	753.5602	-1.348141	7.47E-05	0.007319	1353	Q12618.1 RecName: Full=Acyl-CoA desaturase; AltName: Full=Delta(9)-desaturase; Short=Delta-9 desaturase; AltName: Full=Fatty acid desaturase; AltName: Full=Stearoyl-CoA desaturase && PF00487:Fatty acid desaturase PF00173:Cytochrome b5-like Heme/Steroid binding domain
gene-PsYK624_136370	289.4298	736.4772	-1.348592	0.000228	0.016116	1032	A8DRH7.1 RecName: Full=L-threo-3-deoxy-hexulosonate aldolase; AltName: Full=L-threo-3-deoxy-hexulosonate aldolase && PF00701:Dihydrodipicolinate synthetase family
gene-PsYK624_145810	56.43093	143.8497	-1.350128	0.000576	0.029272	531	-
gene-PsYK624_145010	105.3045	269.7971	-1.36048	0.000529	0.027579	1623	Q8J0I9.1 RecName: Full=Endo-1,6-beta-D-glucanase BGN16.3; AltName: Full=Beta-1,6-glucanase BGN16.3; AltName: Full=Glucan endo-1,6-beta-glucosidase BGN16.3; Flags: Precursor && PF02055:O-Glycosyl hydrolase family 30
gene-PsYK624_068940	645.0332	1657.479	-1.361287	5.30E-05	0.005699	795	PF11274:Protein of unknown function (DUF3074)
gene-PsYK624_090640	2740.615	7059.208	-1.365047	4.79E-06	0.000901	1008	-
gene-PsYK624_088840	445.3624	1146.503	-1.365166	2.44E-08	1.00E-05	2610	-

gene-PsYK624_016550	596.2126	1540.864	-1.369738	0.000178	0.013784	2331	Q55A09.1 RecName: Full=Probable serine/threonine-protein kinase DDB_G0272254 && PF07714:Protein tyrosine kinase
gene-PsYK624_166500	34.79934	89.92276	-1.370819	0.001057	0.04594	1119	-
gene-PsYK624_034520	203.5443	529.2105	-1.376917	9.04E-06	0.001409	3324	-
gene-PsYK624_154970	290.039	759.4127	-1.3897	0.000332	0.020168	372	-
gene-PsYK624_106920	28.72611	75.56655	-1.393436	0.000191	0.014399	363	-
gene-PsYK624_012610	221.2089	583.3361	-1.398158	1.08E-06	0.000281	2205	-
gene-PsYK624_024010	135.9241	358.4052	-1.401607	0.000567	0.029067	2268	Q32PJ3.1 RecName: Full=Origin recognition complex subunit 3 && PF07034:Origin recognition complex (ORC) subunit 3 N-terminus
gene-PsYK624_042210	1360.726	3619.45	-1.411717	0.001059	0.04594	1872	O59726.1 RecName: Full=Vacuolar membrane amino acid uptake transporter fnx2 && PF07690:Major Facilitator Superfamily
gene-PsYK624_062080	52.37806	139.6837	-1.415347	0.001033	0.045188	1698	PF12937:F-box-like
gene-PsYK624_089190	576.2017	1546.118	-1.423467	2.98E-05	0.003607	786	PF09729:Gti1/Pac2 family
gene-PsYK624_007180	2540.29	6846.952	-1.430609	7.27E-05	0.007207	1908	P22121.1 RecName: Full=Heat shock factor protein; Short=HSF; AltName: Full=Heat shock transcription factor; Short=HSTF && PF00447:HSF-type DNA-binding
gene-PsYK624_029360	347.6282	937.001	-1.431268	0.000283	0.018496	1689	P42535.4 RecName: Full=Pentachlorophenol 4-monooxygenase; AltName: Full=Pentachlorophenol hydroxylase && PF01494:FAD binding domain

gene-PsYK624_035120	349.6467	946.1506	-1.436245	0.000715	0.034173	888	-
gene-PsYK624_036420	1238.272	3369.806	-1.444343	0.000184	0.014092	1698	Q9M0X9.1 RecName: Full=4-coumarate--CoA ligase-like 7; AltName: Full=4-coumarate--CoA ligase isoform 6; Short=At4CL6 && PF13193:AMP-binding enzyme C-terminal domain PF00501:AMP-binding enzyme
novel.978	103.1021	289.5554	-1.490359	0.000744	0.035264	3880	-
gene-PsYK624_050300	61.07722	172.9538	-1.503875	0.000867	0.039393	1782	S0EEY7.1 RecName: Full=Efflux pump FUS6; AltName: Full=Fusarin biosynthesis protein 6 && PF07690:Major Facilitator Superfamily
gene-PsYK624_039320	1663.114	4734.11	-1.509235	2.27E-05	0.002899	1335	-
gene-PsYK624_073020	74.96983	213.7443	-1.513023	5.73E-06	0.001019	342	-
gene-PsYK624_072190	573.4377	1642.407	-1.517737	0.000313	0.019655	924	PF05705:Eukaryotic protein of unknown function (DUF829)
gene-PsYK624_047020	440.9842	1262.978	-1.518564	0.000514	0.026932	672	O59827.1 RecName: Full=Glutathione S-transferase 2; AltName: Full=GST-II && PF02798:Glutathione S-transferase, N-terminal domain PF00043:Glutathione S-transferase, C-terminal domain
gene-PsYK624_025140	110.2725	316.1413	-1.522922	0.000768	0.036121	774	-
gene-PsYK624_135140	215.2031	620.8018	-1.528862	0.000458	0.024902	357	PF03795:YCII-related domain
gene-PsYK624_005370	1419.974	4098.272	-1.528976	0.0001	0.009118	912	Q54BF3.1 RecName: Full=Fumarylacetoacetate hydrolase domain-containing protein 2 homolog && PF01557:Fumarylacetoacetate (FAA) hydrolase family

gene-PsYK624_128210	13.62201	38.93692	-1.532578	0.001203	0.049828	477	-
gene-PsYK624_158980	139.7711	405.6608	-1.538005	1.24E-06	0.000302	1500	-
gene-PsYK624_157690	94.04508	274.1879	-1.546428	0.000125	0.010646	393	-
gene-PsYK624_004170	1915.726	5625.616	-1.554219	0.000138	0.011459	1761	P26585.1 RecName: Full=HMG1/2-like protein; AltName: Full=Protein SB11 && PF00505:HMG (high mobility group) box
gene-PsYK624_055530	2156.765	6342.942	-1.556413	1.96E-05	0.002607	1191	PF03473:MOSC domain PF03476:MOSC N-terminal beta barrel domain
gene-PsYK624_065530	295.3014	870.3965	-1.559885	0.000152	0.012223	798	-
gene-PsYK624_158450	39.29359	116.5261	-1.567843	0.00116	0.048896	825	-
gene-PsYK624_149430	23.22417	69.22596	-1.580069	0.000343	0.02056	219	-
gene-PsYK624_158990	29.4315	88.01074	-1.583428	0.000552	0.028465	243	-
gene-PsYK624_106230	719.9115	2179.566	-1.598696	0.000684	0.03319	762	PF04140:Isoprenylcysteine carboxyl methyltransferase (ICMT) family
gene-PsYK624_155130	50.43997	153.9025	-1.613493	0.00023	0.016174	594	-
gene-PsYK624_152710	66.87423	204.9903	-1.618055	0.00066	0.032494	294	-
gene-PsYK624_065630	27.3672	84.17395	-1.625891	0.000314	0.019655	945	PF11937:Protein of unknown function (DUF3455)
gene-PsYK624_148560	471.0119	1462.444	-1.635112	6.22E-06	0.001071	1077	-
gene-PsYK624_001370	1719.505	5406.293	-1.652668	0.000164	0.012848	846	PF12695:Alpha/beta hydrolase family
gene-PsYK624_161570	234.1333	747.1497	-1.674053	0.000842	0.038776	711	PF04140:Isoprenylcysteine carboxyl methyltransferase (ICMT) family
gene-PsYK624_129970	52.14799	166.869	-1.678841	0.000697	0.033517	321	-
gene-PsYK624_052890	586.7751	1912.346	-1.704741	0.000435	0.023851	918	C3K630.1 RecName: Full=L-amino acid amidase && PF00561:alpha/beta hydrolase fold

gene-PsYK624_139140	3186.361	10438.04	-1.711918	5.43E-05	0.005801	4266	Q9R6X3.1 RecName: Full=Cyanobacterial phytochrome B && PF00360:Phytochrome region PF01590:GAF domain PF00512:His Kinase A (phospho-acceptor) domain PF08446:PAS fold PF00072:Response regulator receiver domain PF02518:Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase
gene-PsYK624_090050	60.92499	200.0682	-1.716743	0.00021	0.015491	1089	Q76NT9.1 RecName: Full=1-aminocyclopropane-1-carboxylate oxidase; Short=ACC oxidase; Short=Ddaco; AltName: Full=Ethylene-forming enzyme; Short=EFE >A6BM06.1 RecName: Full=1-aminocyclopropane-1-carboxylate oxidase; Short=ACC oxidase; Short=Dmaco; AltName: Full=Ethylene-forming enzyme; Short=EFE && PF14226:non-haem dioxygenase in morphine synthesis N-terminal PF03171:2OG-Fe(II) oxygenase superfamily
gene-PsYK624_151360	859.3596	2853.569	-1.731801	8.62E-05	0.008013	228	-
gene-PsYK624_068280	156.715	525.687	-1.746816	0.000102	0.009181	924	PF00651:BTB/POZ domain
gene-PsYK624_010550	216.0035	742.3696	-1.78219	1.52E-06	0.000344	249	-
gene-PsYK624_013380	2039.383	7015.175	-1.782535	9.39E-06	0.001449	1203	Q58D31.3 RecName: Full=Sorbitol dehydrogenase; AltName: Full=L-iditol 2-dehydrogenase && PF08240:Alcohol

							dehydrogenase GroES-like domain PF00107:Zinc-binding dehydrogenase
gene-PsYK624_115240	651.5281	2247.372	-1.787027	3.16E-07	9.57E-05	1299	-
gene-PsYK624_114980	792.4612	2756.57	-1.798687	7.00E-05	0.007069	1821	-
gene-PsYK624_041290	334.7165	1195.978	-1.837345	9.76E-08	3.47E-05	771	Q028J4.1 RecName: Full=CinA-like protein && PF02464:Competence-damaged protein
gene-PsYK624_114990	550.7749	2028.648	-1.881366	7.65E-05	0.007403	945	-
gene-PsYK624_157680	624.7343	2365.824	-1.921603	1.14E-05	0.001621	1356	Q53552.1 RecName: Full=Salicylate hydroxylase; AltName: Full=Salicylate 1-monooxygenase && PF01494:FAD binding domain
gene-PsYK624_083890	14.97321	57.05345	-1.925577	0.000897	0.040328	678	POCT87.1 RecName: Full=4-O-methyl-glucuronoyl methylesterase 1; AltName: Full=Glucuronoyl esterase 1; Short=GE1; Flags: Precursor && PF00734:Fungal cellulose binding domain
gene-PsYK624_102850	1074.036	4081.345	-1.926162	1.21E-08	6.20E-06	2946	Q5PRA2.2 RecName: Full=Probable 2-oxoglutarate dehydrogenase E1 component DHKTD1, mitochondrial; AltName: Full=Dehydrogenase E1 and transketolase domain-containing protein 1; Flags: Precursor && PF02779:Transketolase, pyrimidine binding domain PF16870:2-oxoglutarate dehydrogenase C-

							terminal PF00676:Dehydrogenase E1 component
gene-PsYK624_161770	146.5051	559.2251	-1.934232	2.60E-05	0.003224	333	O74300.1 RecName: Full=Hydrophobin-6; Flags: Precursor && PF01185:Fungal hydrophobin
gene-PsYK624_099280	659.3071	2537.212	-1.944366	7.47E-05	0.007319	528	Q9USV7.1 RecName: Full=Copper transport protein ctr6; Short=Copper transporter 6 && PF04145:Ctr copper transporter family
novel.698	36.55921	140.6265	-1.948798	8.79E-05	0.008123	1032	-
gene-PsYK624_058290	1542.195	5963.177	-1.951325	0.000241	0.016469	2406	-
gene-PsYK624_112480	307.7348	1199.094	-1.961352	0.000545	0.0282	1536	Q0CJ61.1 RecName: Full=Efflux pump atB; AltName: Full=Terreic acid biosynthesis cluster protein B && PF07690:Major Facilitator Superfamily
gene-PsYK624_166760	140.7728	554.6841	-1.98033	4.94E-05	0.005423	825	O13871.1 RecName: Full=Uncharacterized methyltransferase C1B3.06c && PF08241:Methyltransferase domain
gene-PsYK624_010560	824.3207	3271.382	-1.988693	8.64E-08	3.14E-05	564	O94363.1 RecName: Full=GTP-binding protein rhb1; AltName: Full=GTP-binding protein Rheb homolog; Flags: Precursor && PF00071:Ras family
gene-PsYK624_034430	37.64917	151.1849	-2.0057	0.000108	0.009448	1674	-

gene-PsYK624_054210	29.33425	117.3022	-2.008517	2.23E-05	0.002877	1365	-
gene-PsYK624_086510	1104.164	4443.878	-2.008801	1.44E-06	0.00034	339	-
gene-PsYK624_156510	6.747446	26.69341	-2.008813	0.00057	0.029115	642	-
gene-PsYK624_007570	163.7635	660.9877	-2.013004	7.56E-05	0.007356	1533	Q0CJ61.1 RecName: Full=Efflux pump atB; AltName: Full=Terreic acid biosynthesis cluster protein B && PF07690:Major Facilitator Superfamily
gene-PsYK624_070130	185.5346	780.3398	-2.074839	1.11E-08	6.20E-06	705	-
gene-PsYK624_093690	640.6682	2738.072	-2.095443	5.97E-05	0.006255	1989	PF00172:Fungal Zn(2)-Cys(6) binuclear cluster domain PF04082:Fungal specific transcription factor domain
gene-PsYK624_040520	163.5833	704.4658	-2.106227	0.00054	0.028021	222	-
gene-PsYK624_010510	104.6996	452.3245	-2.112684	0.000608	0.030303	1011	PF13417:Glutathione S-transferase, N-terminal domain
gene-PsYK624_009110	232.5429	1039.065	-2.159423	1.82E-05	0.002509	744	Q12335.1 RecName: Full=Protoplast secreted protein 2; Flags: Precursor && PF03358:NADPH-dependent FMN reductase
gene-PsYK624_115000	219.9927	993.6194	-2.176269	2.32E-06	0.000486	384	-
gene-PsYK624_151490	37.0858	169.111	-2.187809	5.25E-06	0.000976	279	-
gene-PsYK624_109370	2782.265	12705.68	-2.19119	0.000201	0.015102	441	PF07249:Cerato-platanin
gene-PsYK624_140460	802.7871	3691.207	-2.200972	1.09E-05	0.001602	762	-
gene-PsYK624_029700	100.0231	464.1125	-2.214301	0.001148	0.048817	1059	O42909.1 RecName: Full=Zinc-type alcohol dehydrogenase-like protein C16A3.02c && PF13602:Zinc-binding dehydrogenase
gene-PsYK624_133460	109.3055	509.6349	-2.222527	1.14E-05	0.001621	717	PF13417:Glutathione S-transferase, N-terminal domain

gene-PsYK624_098100	156.8349	757.3353	-2.273217	1.90E-06	0.000415	942	-
gene-PsYK624_161400	636.4048	3098.581	-2.283396	5.98E-06	0.00104	1041	G3XMB9.1 RecName: Full=Ketoreductase azaE; AltName: Full=Azaphilone biosynthesis cluster protein azaE && PF01370:NAD dependent epimerase/dehydratase family
gene-PsYK624_088370	66.90042	330.272	-2.300279	1.37E-08	6.41E-06	1290	Q556W1.1 RecName: Full=D-aspartate oxidase; Short=DASOX; AltName: Full=DDO && PF01266:FAD dependent oxidoreductase
gene-PsYK624_009950	114.9743	570.9528	-2.314568	3.74E-07	0.000107	1632	Q9VXY0.1 RecName: Full=Probable cytochrome P450 4s3; AltName: Full=CYP1VS3 && PF00067:Cytochrome P450
gene-PsYK624_155950	1000.93	5009.892	-2.323644	0.000202	0.015117	621	-
gene-PsYK624_092150	239.5168	1212.363	-2.340395	0.000251	0.016983	1659	O74923.1 RecName: Full=Uncharacterized transporter C757.13 && PF07690:Major Facilitator Superfamily
gene-PsYK624_046330	3883.834	19811.01	-2.350772	7.96E-05	0.007526	1332	P50125.2 RecName: Full=Homocysteine synthase; AltName: Full=O-acetylhomoserine sulfhydrylase; Short=OAH SHL; Short=OAH sulfhydrylase && PF01053:Cys/Met metabolism PLP-dependent enzyme
gene-PsYK624_093840	295.6219	1564.226	-2.404745	2.03E-12	6.24E-09	948	O13780.1 RecName: Full=Uncharacterized protein C17G6.02c && PF04479:RTA1 like protein

gene-PsYK624_046510	91.91331	486.709	-2.404943	2.53E-06	0.000524	1059	Q5AUY5.1 RecName: Full=Zinc-binding alcohol dehydrogenase domain-containing protein cipB; AltName: Full=Concanamycin-induced protein B && PF08240:Alcohol dehydrogenase GroES-like domain PF00107:Zinc-binding dehydrogenase
gene-PsYK624_152080	109.7379	584.545	-2.413301	0.000111	0.009567	1320	-
gene-PsYK624_161220	441.331	2353.628	-2.415272	0.000487	0.02621	1002	P43549.1 RecName: Full=Uncharacterized membrane protein YFL054C && PF00230:Major intrinsic protein
gene-PsYK624_124820	153.99	824.863	-2.421604	0.000229	0.016116	1044	-
gene-PsYK624_100840	2915.943	15717.66	-2.430409	3.04E-07	9.38E-05	1392	P08159.2 RecName: Full=6-hydroxy-D-nicotine oxidase; Short=6-HDNO && PF01565:FAD binding domain PF08031:Berberine and berberine like
novel.695	6.264415	33.92169	-2.435294	0.000237	0.016381	384	O43122.1 RecName: Full=Hydrophobin-B; Flags: Precursor [Agaricus bisporus] && PF01185:Fungal hydrophobin
gene-PsYK624_070160	831.0195	4639.707	-2.480917	0.000146	0.012031	1011	O14027.1 RecName: Full=Probable pyridoxal 5'-phosphate synthase subunit PDX1; Short=PLP synthase subunit PDX1 && PF01680:SOR/SNZ family
gene-PsYK624_054200	13.62578	77.14428	-2.509141	1.90E-06	0.000415	450	-
gene-PsYK624_120470	1063.58	6189.593	-2.541101	5.68E-06	0.001019	414	O43122.1 RecName: Full=Hydrophobin-B; Flags: Precursor [Agaricus bisporus] && PF01185:Fungal hydrophobin

gene-PsYK624_115810	25.79779	153.6052	-2.572747	0.000466	0.025233	672	PF11937:Protein of unknown function (DUF3455)
gene-PsYK624_130190	14.69681	88.5316	-2.575129	0.000288	0.01864	798	PF01828:Peptidase A4 family
gene-PsYK624_024410	358.0026	2240.894	-2.646586	1.06E-05	0.001602	912	-
gene-PsYK624_040510	185.1702	1195.232	-2.6902	0.000154	0.012252	783	-
gene-PsYK624_079210	386.5437	2642.348	-2.773528	8.33E-06	0.001311	1104	-
gene-PsYK624_065340	47.83676	337.1099	-2.816406	0.000787	0.036668	780	PF11937:Protein of unknown function (DUF3455)
gene-PsYK624_015860	45.14787	336.3291	-2.898194	0.000234	0.016199	1632	A1CP08.1 RecName: Full=Probable mannosyl-oligosaccharide alpha-1,2-mannosidase 1B; AltName: Full=Class I alpha-mannosidase 1B; AltName: Full=Man(9)-alpha-mannosidase 1B; Flags: Precursor && PF01532:Glycosyl hydrolase family 47
gene-PsYK624_158880	19.9106	149.8617	-2.919691	5.19E-07	0.000142	1026	-
gene-PsYK624_157750	1543.919	12446.21	-3.011039	2.47E-05	0.003111	1569	W7N2B4.2 RecName: Full=Efflux pump FUB11; AltName: Full=Fusaric acid biosynthesis protein 11 && PF07690:Major Facilitator Superfamily
gene-PsYK624_084020	212.0943	1823.515	-3.104505	1.10E-07	3.68E-05	1044	-
gene-PsYK624_074080	210.4993	1842.257	-3.129642	4.47E-12	7.73E-09	618	PF01753:MYND finger
novel.826	29.444	261.2915	-3.153172	0.000241	0.016469	1745	-
gene-PsYK624_138980	22.91569	205.109	-3.166118	0.001212	0.049946	282	-
gene-PsYK624_157700	429.7923	3857.513	-3.166458	1.30E-08	6.31E-06	951	-
gene-PsYK624_101630	10.80205	96.51476	-3.167739	1.09E-05	0.001602	282	PF11779:Protein of unknown function (DUF3317)

gene-PsYK624_037870	882.8523	7969.198	-3.174521	6.92E-08	2.66E-05	195	-
gene-PsYK624_024000	78.0605	743.3314	-3.252873	4.73E-12	7.73E-09	1602	Q91WG0.1 RecName: Full=Acylcarnitine hydrolase; Short=ACH M1; AltName: Full=Carboxylesterase 2; Short=CES 2; AltName: Full=Peroxisome proliferator-inducible acylcarnitine hydrolase; Flags: Precursor && PF00135:Carboxylesterase family
gene-PsYK624_077420	1254.66	12480.28	-3.314366	2.50E-09	1.52E-06	1059	PF00172:Fungal Zn(2)-Cys(6) binuclear cluster domain
gene-PsYK624_027340	87.29295	884.8196	-3.341615	6.50E-10	5.31E-07	1461	B8NHY4.1 RecName: Full=O-methylsterigmatocystin oxidoreductase; Short=OMST oxidoreductase; AltName: Full=Aflatoxin B synthase; AltName: Full=Aflatoxin biosynthesis protein Q; AltName: Full=Cytochrome P450 64 >P0CT93.1 RecName: Full=O-methylsterigmatocystin oxidoreductase; Short=OMST oxidoreductase; AltName: Full=Aflatoxin B synthase; AltName: Full=Aflatoxin biosynthesis protein Q; AltName: Full=Cytochrome P450 64 && PF00067:Cytochrome P450

gene-PsYK624_021640	461.3715	4718.819	-3.354527	0.000136	0.011341	2502	PF02884:Polysaccharide lyase family 8, C-terminal beta-sandwich domain PF02278:Polysaccharide lyase family 8, super-sandwich domain PF08124:Polysaccharide lyase family 8, N terminal alpha-helical domain
gene-PsYK624_112590	176.5326	1811.269	-3.35903	2.84E-05	0.003469	2055	-
gene-PsYK624_054480	71.97248	746.823	-3.379931	3.29E-13	1.35E-09	1818	O23024.1 RecName: Full=Probable indole-3-pyruvate monooxygenase YUCCA3; AltName: Full=Flavin-containing monooxygenase YUCCA3 && PF13738:Pyridine nucleotide-disulphide oxidoreductase
gene-PsYK624_065510	88.36978	949.9563	-3.428155	3.90E-09	2.28E-06	792	PF11937:Protein of unknown function (DUF3455)
gene-PsYK624_127210	2.155392	22.91642	-3.459475	0.00036	0.021299	192	PF00067:Cytochrome P450
gene-PsYK624_014180	21.54408	243.0132	-3.498781	7.24E-05	0.007207	468	PF01124:MAPEG family
gene-PsYK624_008130	23.19034	263.4697	-3.507994	0.00089	0.040088	639	-
gene-PsYK624_075810	73.61073	866.8436	-3.558273	6.99E-08	2.66E-05	777	Q8GYM1.1 RecName: Full=Glutathione S-transferase U22; Short=AtGSTU22; AltName: Full=GST class-tau member 22 && PF13417:Glutathione S-transferase, N-terminal domain PF16865:Glutathione S-transferase, C-terminal domain

gene-PsYK624_093510	201.122	2386.427	-3.569083	0.000151	0.012212	1419	Q5B6Q3.1 RecName: Full=Glucan endo-1,6-beta-glucosidase B; AltName: Full=Beta-1,6-glucanase B; AltName: Full=Endo-1,6-beta-D-glucanase B; AltName: Full=Endo-1,6-beta-glucanase B; Flags: Precursor && PF00150:Cellulase (glycosyl hydrolase family 5)
gene-PsYK624_065560	103.38	1710.482	-4.047766	3.78E-11	4.12E-08	795	PF11937:Protein of unknown function (DUF3455)
gene-PsYK624_066750	113.4556	1984.757	-4.129538	1.14E-08	6.20E-06	1017	-
gene-PsYK624_068130	15.42812	283.1632	-4.202081	4.43E-10	4.03E-07	789	PF13302:Acetyltransferase (GNAT) domain
gene-PsYK624_164010	221.3822	4209.491	-4.24907	1.84E-09	1.25E-06	675	O59827.1 RecName: Full=Glutathione S-transferase 2; AltName: Full=GST-II && PF00043:Glutathione S-transferase, C-terminal domain PF02798:Glutathione S-transferase, N-terminal domain
gene-PsYK624_083300	215.414	4144.55	-4.266154	2.68E-12	6.27E-09	708	Q01490.1 RecName: Full=Peptidyl-prolyl cis-trans isomerase B; Short=PPIase B; AltName: Full=Cyclophilin B; AltName: Full=Rotamase B; Flags: Precursor && PF00160:Cyclophilin type peptidyl-prolyl cis-trans isomerase/CLD
gene-PsYK624_151220	2.162194	41.8699	-4.294794	0.000234	0.016199	297	-
gene-PsYK624_076580	272.3085	6408.392	-4.556806	2.24E-08	9.66E-06	516	PF03625:Domain of unknown function DUF302
gene-PsYK624_068140	14.03041	344.1203	-4.61394	7.10E-16	3.87E-12	789	PF13302:Acetyltransferase (GNAT) domain

gene-PsYK624_139040	79.16738	2121.874	-4.744965	2.43E-09	1.52E-06	1524	Q00557.2 RecName: Full=Cytochrome P450 1A1; AltName: Full=CYP1A1; AltName: Full=Cytochrome P-450MC && PF00067:Cytochrome P450
gene-PsYK624_145270	231.16	11955.48	-5.692698	0.000102	0.009181	951	P61869.1 RecName: Full=Mono- and diacylglycerol lipase; Short=MDGL; Flags: Precursor >P61870.1 RecName: Full=Mono- and diacylglycerol lipase; Short=MDGL; Flags: Precursor && PF01764:Lipase (class 3)

Table S2. Primers used for qPCR

Primer	Sequence (5'-3')	Product (bp)	NR description
134470-F 134470-R	TCGGTCCTCGTCGGAATATG CGCGACTTCCTCCAATGAAC	172	Cytochrome P450
133130-F 133130-R	GCCACAAGCTGTCGTTCAAG TTCGTCGGTGCGAACTTCC	100	Cytochrome P450
026160-F 026160-R	TAGCCGCCATACACACCTTC AGGTAGGCAGACGTTTCGTTTC	108	Cytochrome P450
126780-F 126780-R	GGGGCGTGCTATACCTTTCA GTAGTGCGGCGAGTCTAACA	160	Cytochrome P450
152260-F 152260-R	ATCCGCAAATCTCTCGCACA CCGGGTATGTTTCGGGATCG	109	Cytochrome P450
109500-F 109500-R	TCTGCTGAGGACGCATACAC CGACGTATTGACGCAGGTTG	142	Cytochrome P450
134420-F 134420-R	ACTATGGGCAGGTCGTGAAG TGAGCAGTTTTCCGATTGCG	147	Cytochrome P450
ActinF ActinR	AGCACGGTATCGTCACCAAC AGCGAAACCCTCGTAGATGG		

Table S3. Summary of transcripts information

Sample	Raw Reads	Clean Reads	Clean Bases	Error (%)	Q20 (%)	Q30 (%)	GC Content (%)
P_c1	48081496	46651480	7.0 G	0.02	98.54	95.8	62.07
P_c2	48110798	46582956	6.99 G	0.02	98.41	95.53	61.86
P_c3	60043026	58625892	8.79 G	0.02	98.44	95.55	61.81
BPF_P1	57418896	56758682	8.51 G	0.02	98.38	95.35	61.72
BPF_P2	50580470	49105572	7.37 G	0.02	98.4	95.49	61.77
BPF_P3	46594462	45137014	6.77 G	0.02	98.51	95.74	61.7

Table S4. Details of cytochrome P450s in BPF degradation by *P. sordida* YK-624.

gene_id	BPF_P_c_r eadcount	P_c_rea dcount	log ₂ Fold Change	<i>P</i> - value	Padj	Gene Length	Gene Descriptio n
gene- PsYK624_13 4470	1986.2	363.576 2	2.449735 597	1.06 E-07	3.61 E-05	1677	cytochro me P450
gene- PsYK624_13 3130	691.5215	183.892	1.913268 88	9.22 E-10	6.71 E-07	1563	cytochro me P450
gene- PsYK624_02 6160	2167.605	624.297 1	1.796587 744	3.85 E-12	7.73 E-09	1518	cytochro me P450
gene- PsYK624_12 6780	2224.293	748.004	1.571613 92	7.05 E-06	0.00 1142	1545	cytochro me P450
gene- PsYK624_15 2260	649.5025	229.956 3	1.496761 957	0.00 06	0.03 0012	1518	cytochro me P450
gene- PsYK624_10 9500	5488.457	2072.5	1.405177 281	0.00 1117	0.04 7809	1653	cytochro me P450
gene- PsYK624_13 4420	833.7278	318.445	1.389075	0.00 0413	0.02 3283	1656	cytochro me P450

Log₂Fold change: values of transcripts upregulated in BPF addition is represented by positive numbers and downregulated is represented by negative numbers.

Padj: adjust *P*-value

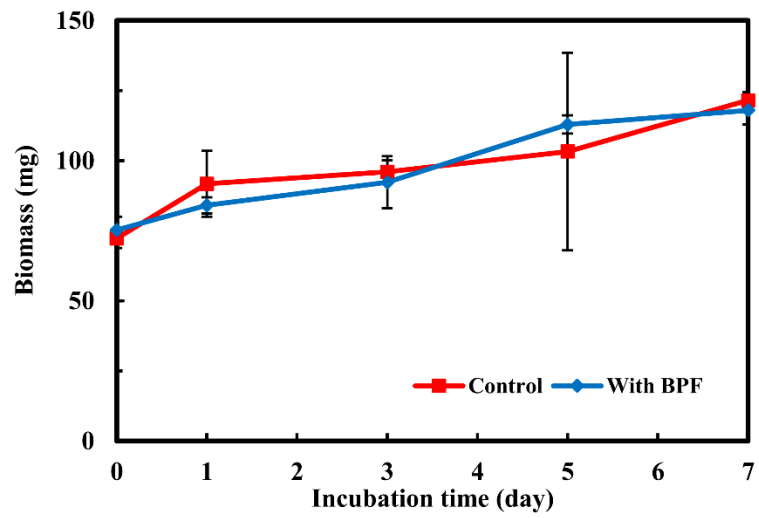


Fig. S1. The change of biomass of *P. sordida* YK-624 with incubation time (red square: samples with BPF; blue diamond: control).

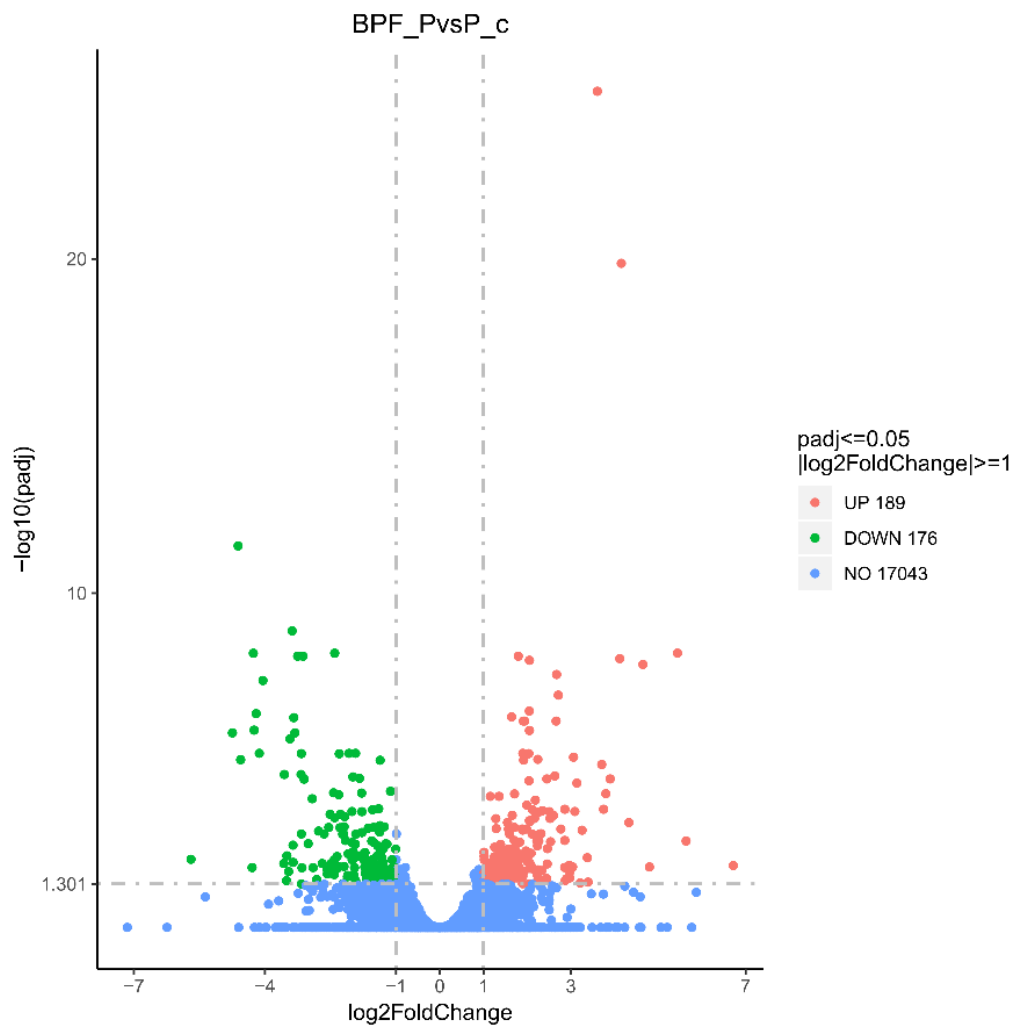


Fig. S2. DEGs involved in BPF biodegradation by *P. sordida* YK-624 under non-ligninolytic conditions. Red: upregulated DEGs; green: downregulated DEGs

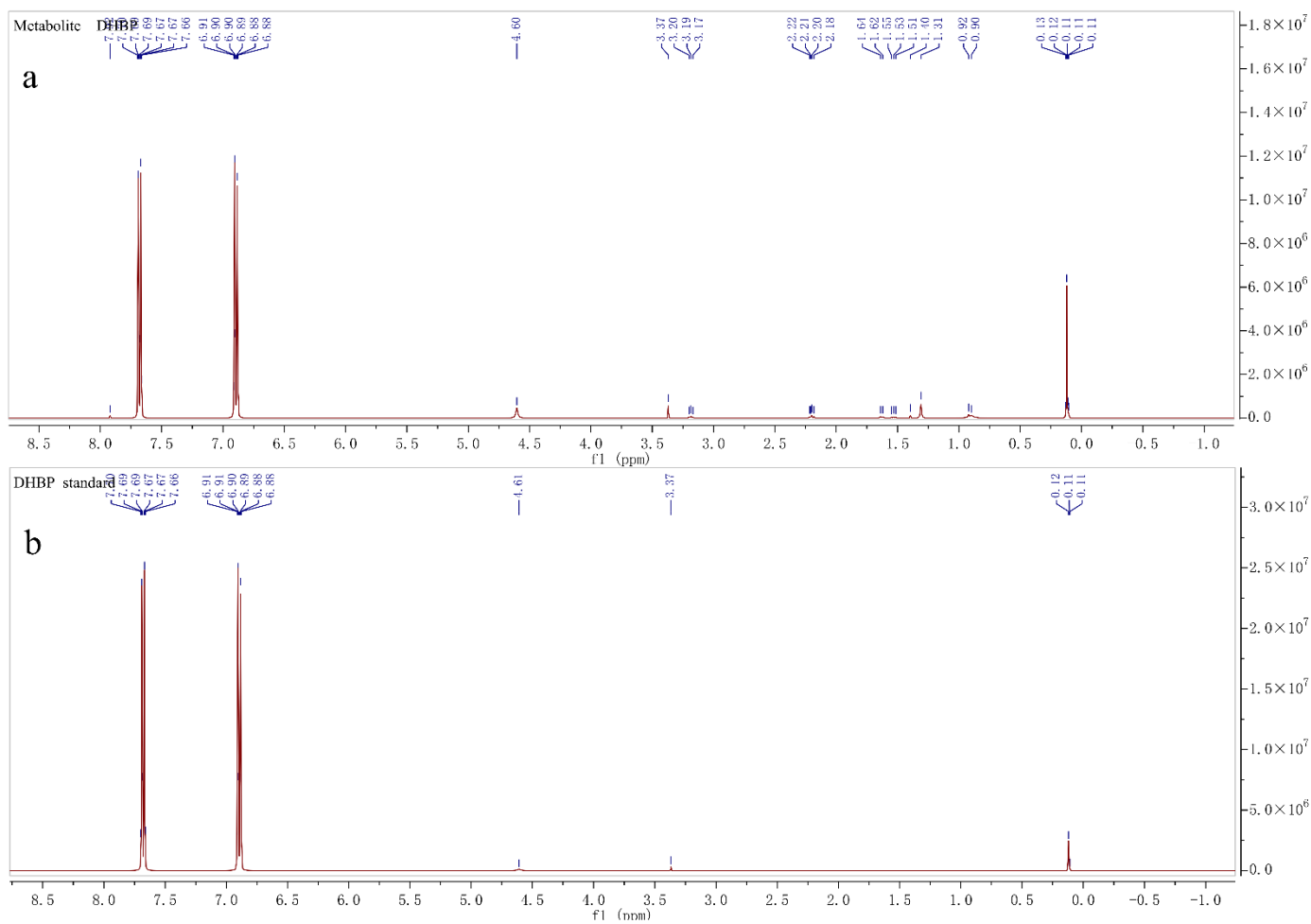


Fig. S3. $^1\text{H-NMR}$ spectra of metabolite DHBP and the purchased standard compound.; a: metabolite DHBP; b: DHBP standard.

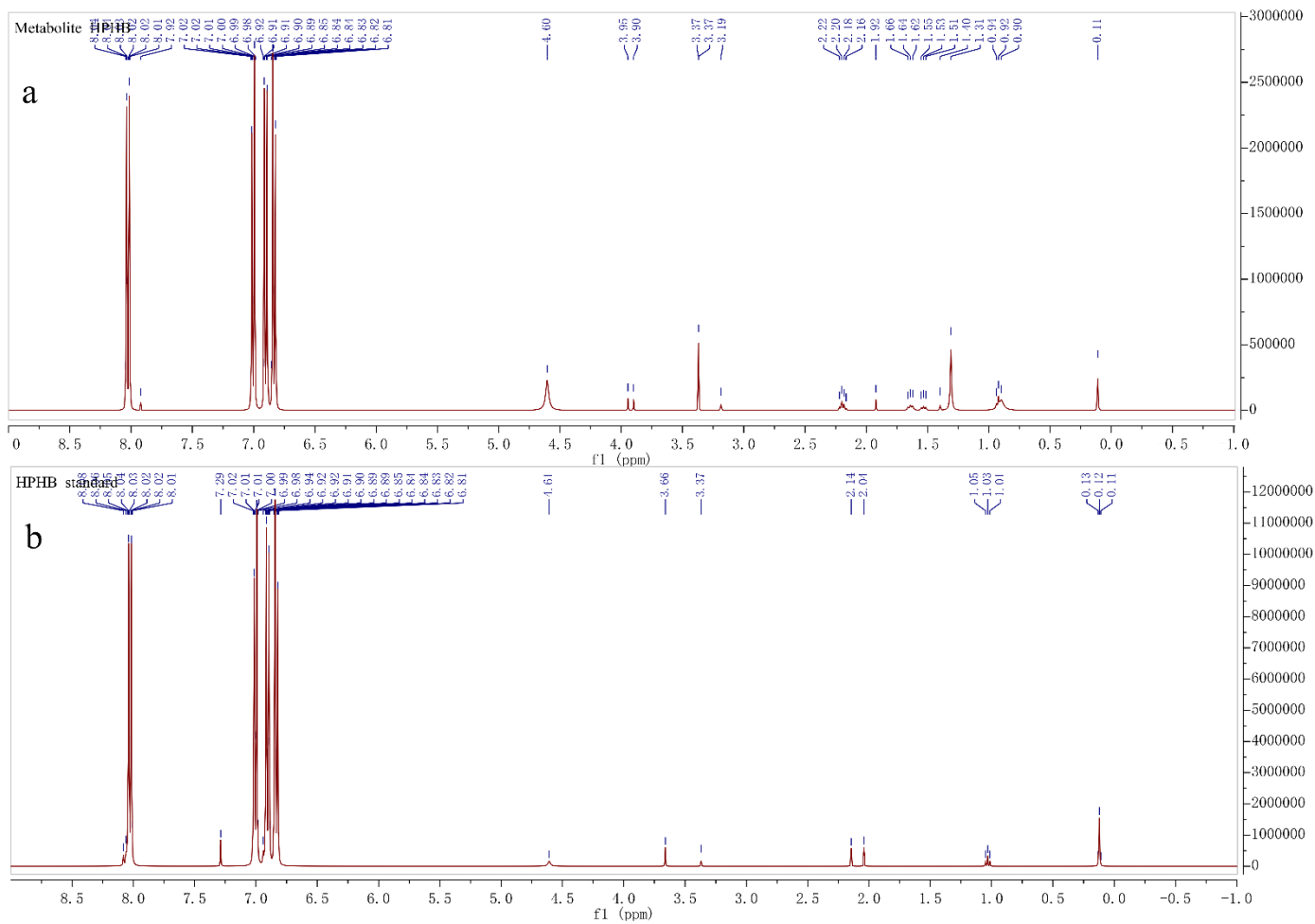


Fig. S4. ¹H-NMR spectra of metabolite HPHB and the purchased standard compound. a: metabolite HPHB; b: HPHB standard.

Sequence information of functional genes

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