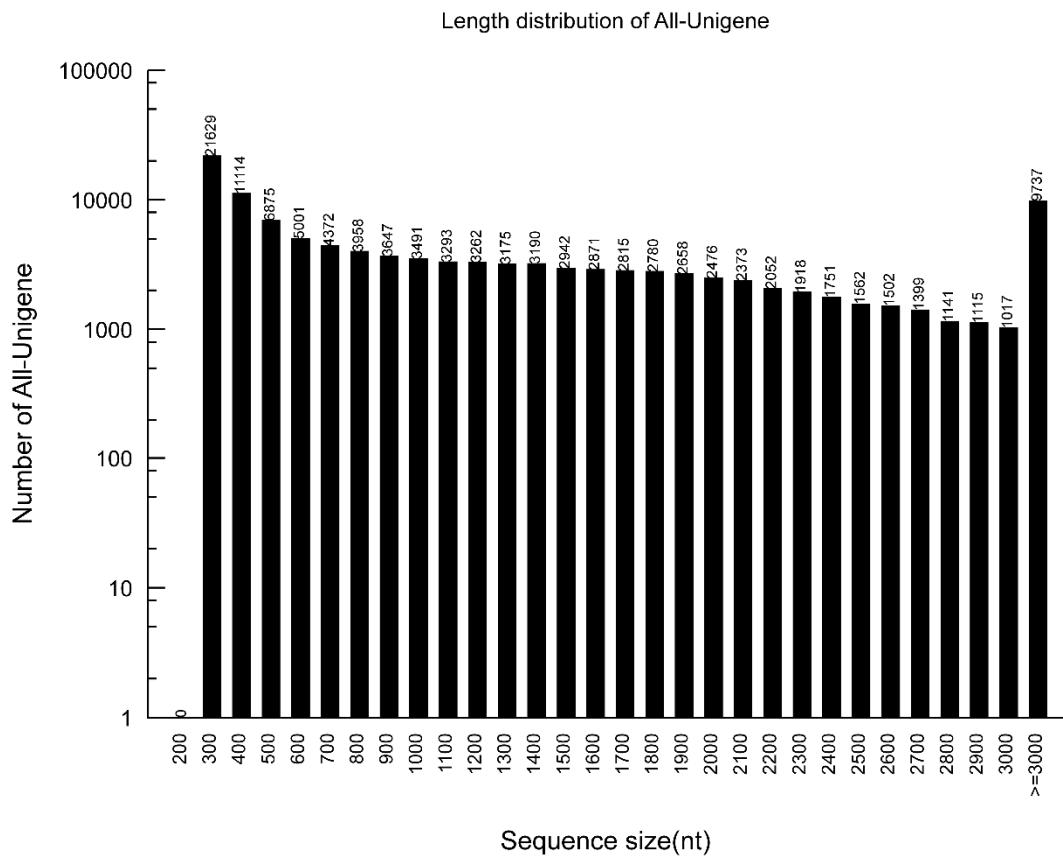
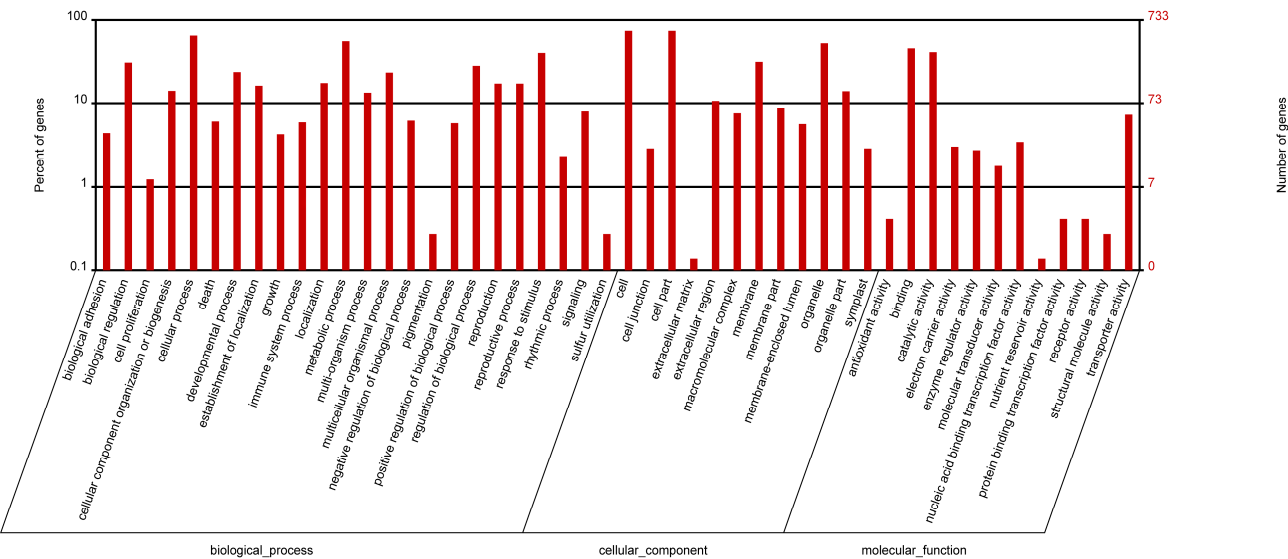


# Supplementary Information

**Figure S1.** Distribution of all-unigene lengths in the transcriptome of *P. fortunei*.



**Figure S2.** Gene ontology (GO) classification of the *P. fortunei* DEGs. Final DEGs were annotated and categorized into 48 function groups.



**Table S1.** KEGG pathway analysis results for the *P. fortunei* all-unigenes.

#	Pathway	Count (46,381)	Pathway ID
1	Metabolic pathways	10,325	ko01100
2	Biosynthesis of secondary metabolites	4713	ko01110
3	Plant-pathogen interaction	2734	ko04626
4	Plant hormone signal transduction	2418	ko04075
5	Spliceosome	1754	ko03040
6	RNA transport	1561	ko03013
7	Glycerophospholipid metabolism	1405	ko00564
8	Protein processing in endoplasmic reticulum	1350	ko04141
9	Endocytosis	1332	ko04144
10	Starch and sucrose metabolism	1242	ko00500
11	Ether lipid metabolism	996	ko00565
12	mRNA surveillance pathway	965	ko03015
13	Ubiquitin mediated proteolysis	913	ko04120
14	Purine metabolism	900	ko00230
15	RNA degradation	806	ko03018
16	Pyrimidine metabolism	772	ko00240
17	Ribosome	743	ko03010
18	Ribosome biogenesis in eukaryotes	703	ko03008
19	Phenylpropanoid biosynthesis	662	ko00940
20	ABC transporters	601	ko02010
21	Circadian rhythm - plant	549	ko04712
22	Glycolysis / Gluconeogenesis	519	ko00010
23	Amino sugar and nucleotide sugar metabolism	517	ko00520
24	Galactose metabolism	500	ko00052
25	Phosphatidylinositol signaling system	472	ko04070
26	Pentose and glucuronate interconversions	469	ko00040
27	Peroxisome	427	ko04146
28	Oxidative phosphorylation	424	ko00190
29	Aminoacyl-tRNA biosynthesis	383	ko00970
30	RNA polymerase	382	ko03020
31	Basal transcription factors	364	ko03022
32	Other glycan degradation	363	ko00511
33	Pyruvate metabolism	360	ko00620
34	Inositol phosphate metabolism	359	ko00562
35	Nucleotide excision repair	358	ko03420
36	Flavonoid biosynthesis	356	ko00941
37	Homologous recombination	348	ko03440
38	Carotenoid biosynthesis	345	ko00906
39	Cyanoamino acid metabolism	332	ko00460
40	Phagosome	326	ko04145
41	Porphyrin and chlorophyll metabolism	324	ko00860
42	Stilbenoid, diarylheptanoid and gingerol biosynthesis	322	ko00945
43	Arginine and proline metabolism	321	ko00330

**Table S1. Cont.**

#	Pathway	Count (46,381)	Pathway ID
44	N-Glycan biosynthesis	315	ko00510
45	Valine, leucine and isoleucine degradation	313	ko00280
46	Glutathione metabolism	312	ko00480
47	Glycosylphosphatidylinositol(GPI)-anchor biosynthesis	305	ko00563
48	Terpenoid backbone biosynthesis	304	ko00900
49	Zeatin biosynthesis	301	ko00908
50	Glycerolipid metabolism	294	ko00561
51	Regulation of autophagy	290	ko04140
52	Sphingolipid metabolism	288	ko00600
53	Ascorbate and aldarate metabolism	287	ko00053
54	Pentose phosphate pathway	285	ko00030
55	Natural killer cell mediated cytotoxicity	278	ko04650
56	Fatty acid metabolism	276	ko00071
57	Cysteine and methionine metabolism	274	ko00270
58	Glycine, serine and threonine metabolism	265	ko00260
59	Limonene and pinene degradation	248	ko00903
60	Fructose and mannose metabolism	247	ko00051
61	Carbon fixation in photosynthetic organisms	245	ko00710
62	Glycosaminoglycan degradation	241	ko00531
63	Tyrosine metabolism	237	ko00350
64	alpha-Linolenic acid metabolism	232	ko00592
65	Phenylalanine metabolism	229	ko00360
66	Alanine, aspartate and glutamate metabolism	225	ko00250
67	DNA replication	220	ko03030
68	Base excision repair	219	ko03410
69	Mismatch repair	218	ko03430
70	Nitrogen metabolism	206	ko00910
71	Protein export	199	ko03060
72	Phenylalanine, tyrosine and tryptophan biosynthesis	198	ko00400
73	Propanoate metabolism	196	ko00640
74	Photosynthesis	184	ko00195
75	Glyoxylate and dicarboxylate metabolism	178	ko00630
76	Citrate cycle (TCA cycle)	175	ko00020
77	SNARE interactions in vesicular transport	175	ko04130
78	Pantothenate and CoA biosynthesis	168	ko00770
79	Cutin, suberine and wax biosynthesis	167	ko00073
80	Steroid biosynthesis	165	ko00100
81	Proteasome	161	ko03050

**Table S1. Cont.**

#	Pathway	Count (46,381)	Pathway ID
82	Glycosphingolipid biosynthesis - ganglio series	159	ko00604
83	Tryptophan metabolism	159	ko00380
84	Ubiquinone and other terpenoid-quinone biosynthesis	146	ko00130
85	Butanoate metabolism	143	ko00650
86	Fatty acid biosynthesis	141	ko00061
87	$\beta$ -Alanine metabolism	141	ko00410
88	Lysine degradation	139	ko00310
89	Flavone and flavonol biosynthesis	137	ko00944
90	Diterpenoid biosynthesis	134	ko00904
91	Brassinosteroid biosynthesis	122	ko00905
92	Lysine biosynthesis	113	ko00300
93	Linoleic acid metabolism	110	ko00591
94	Valine, leucine and isoleucine biosynthesis	110	ko00290
95	Riboflavin metabolism	108	ko00740
96	Biosynthesis of unsaturated fatty acids	106	ko01040
97	Histidine metabolism	104	ko00340
98	Isoquinoline alkaloid biosynthesis	100	ko00950
99	One carbon pool by folate	97	ko00670
100	Nicotinate and nicotinamide metabolism	95	ko00760
101	Fatty acid elongation	88	ko00062
102	Sulfur metabolism	84	ko00920
103	Tropane, piperidine and pyridine alkaloid biosynthesis	82	ko00960
104	Folate biosynthesis	81	ko00790
105	Selenocompound metabolism	78	ko00450
106	Circadian rhythm-mammal	75	ko04710
107	Benzoxazinoid biosynthesis	71	ko00402
108	Taurine and hypotaurine metabolism	67	ko00430
109	Vitamin B6 metabolism	67	ko00750
110	Sesquiterpenoid and triterpenoid biosynthesis	63	ko00909
111	Monoterpenoid biosynthesis	62	ko00902
112	Arachidonic acid metabolism	59	ko00590
113	Glucosinolate biosynthesis	56	ko00966
114	Thiamine metabolism	54	ko00730
115	Isoflavonoid biosynthesis	53	ko00943
116	Photosynthesis-antenna proteins	52	ko00196
117	Glycosphingolipid biosynthesis-globo series	50	ko00603
118	Sulfur relay system	46	ko04122
119	Non-homologous end-joining	42	ko03450

**Table S1. Cont.**

#	Pathway	Count (46,381)	Pathway ID
120	C5-Branched dibasic acid metabolism	39	ko00660
121	Other types of <i>O</i> -glycan biosynthesis	39	ko00514
122	Indole alkaloid biosynthesis	39	ko00901
123	Synthesis and degradation of ketone bodies	39	ko00072
124	Lipoic acid metabolism	22	ko00785
125	Biotin metabolism	22	ko00780
126	Anthocyanin biosynthesis	7	ko00942
127	Caffeine metabolism	2	ko00232
128	Betalain biosynthesis	2	ko00965

**Table S3.** KEGG pathway analysis results for the *P. fortunei* DEGs. Top 10 pathways are in Table 4.

#	Pathway	DEGswith Pathway Annotation	<i>p</i> -Value	<i>Q</i> Value	Pathway ID
11	Flavonoid biosynthesis	13 (2.43%)	0.000294	$2.21 \times 10^{-3}$	ko00941
12	Pentose and glucuronateinterconversions	15 (2.8%)	0.000425	$2.94 \times 10^{-3}$	ko00040
13	Zeatin biosynthesis	11 (2.06%)	0.000835	$5.33 \times 10^{-3}$	ko00908
14	Flavone and flavonol biosynthesis	7 (1.31%)	0.001108	$6.57 \times 10^{-3}$	ko00944
15	Metabolic pathways	147 (27.48%)	0.002526	$1.40 \times 10^{-2}$	ko01100
16	Sulfur metabolism	5 (0.93%)	0.002929	$1.52 \times 10^{-2}$	ko00920
17	Cutin, suberine and wax biosynthesis	7 (1.31%)	0.0034	$1.66 \times 10^{-2}$	ko00073
18	Glucosinolate biosynthesis	4 (0.75%)	0.004004	$1.85 \times 10^{-2}$	ko00966
19	Cysteine and methionine metabolism	8 (1.5%)	0.014881	$6.50 \times 10^{-2}$	ko00270
20	Diterpenoid biosynthesis	5 (0.93%)	0.019914	$8.26 \times 10^{-2}$	ko00904
21	Lysine biosynthesis	4 (0.75%)	0.042247	$1.67 \times 10^{-1}$	ko00300
22	Phenylalanine metabolism	6 (1.12%)	0.050661	$1.91 \times 10^{-1}$	ko00360
23	Inositol phosphate metabolism	8 (1.5%)	0.058159	$2.10 \times 10^{-1}$	ko00562
24	Other glycan degradation	8 (1.5%)	0.061211	$2.12 \times 10^{-1}$	ko00511
25	Valine, leucine and isoleucine degradation	7 (1.31%)	0.072313	$2.40 \times 10^{-1}$	ko00280
26	SNARE interactions in vesicular transport	4 (0.75%)	0.144865	$4.52 \times 10^{-1}$	ko04130
27	Phenylpropanoid biosynthesis	11 (2.06%)	0.146939	$4.52 \times 10^{-1}$	ko00940
28	Brassinosteroid biosynthesis	3 (0.56%)	0.167226	$4.82 \times 10^{-1}$	ko00905
29	Arginine and proline metabolism	6 (1.12%)	0.168565	$4.82 \times 10^{-1}$	ko00330
30	Galactose metabolism	8 (1.5%)	0.222831	$6.08 \times 10^{-1}$	ko00052
31	Selenocompound metabolism	2 (0.37%)	0.227163	$6.08 \times 10^{-1}$	ko00450
32	Starch and sucrose metabolism	17 (3.18%)	0.269985	$7.00 \times 10^{-1}$	ko00500
33	Glycosphingolipid biosynthesis-ganglio series	3 (0.56%)	0.278167	$7.00 \times 10^{-1}$	ko00604
34	Isoquinoline alkaloid biosynthesis	2 (0.37%)	0.320879	$7.83 \times 10^{-1}$	ko00950
35	Regulation of autophagy	4 (0.75%)	0.430279	1.00	ko04140
36	Plant hormone signal transduction	29 (5.42%)	0.44149	1.00	ko04075
37	Mismatch repair	3 (0.56%)	0.460996	1.00	ko03430
38	Ubiquitin mediated proteolysis	11 (2.06%)	0.484156	1.00	ko04120

Table S3. *Cont.*

#	Pathway	DEGs with Pathway Annotation	<i>p</i> -Value	<i>Q</i> Value	Pathway ID
39	Fatty acid biosynthesis	2 (0.37%)	0.485025	1.00	ko00061
40	Sesquiterpenoid and triterpenoid biosynthesis	1 (0.19%)	0.518772	1.00	ko00909
41	Phagosome	4 (0.75%)	0.519833	1.00	ko04145
42	Glycosaminoglycan degradation	3 (0.56%)	0.527311	1.00	ko00531
43	Vitamin B6 metabolism	1 (0.19%)	0.540624	1.00	ko00750
44	Fructose and mannose metabolism	3 (0.56%)	0.543859	1.00	ko00051
45	Spliceosome	20 (3.74%)	0.552954	1.00	ko03040
46	Benzoxazinoid biosynthesis	1 (0.19%)	0.561486	1.00	ko00402
47	Glyoxylate and dicarboxylate metabolism	2 (0.37%)	0.610346	1.00	ko00630
48	Phosphatidylinositol signaling system	5 (0.93%)	0.636256	1.00	ko04070
49	Sphingolipid metabolism	3 (0.56%)	0.647326	1.00	ko00600
50	Glycosylphosphatidylinositol(GPI)-anchor biosynthesis	3 (0.56%)	0.685028	1.00	ko00563
51	Histidine metabolism	1 (0.19%)	0.701191	1.00	ko00340
52	Alanine, aspartate and glutamate metabolism	2 (0.37%)	0.734255	1.00	ko00250
53	Tyrosine metabolism	2 (0.37%)	0.759972	1.00	ko00350
54	Lysine degradation	1 (0.19%)	0.801127	1.00	ko00310
55	Glycine, serine and threonine metabolism	2 (0.37%)	0.811724	1.00	ko00260
56	Ether lipid metabolism	9 (1.68%)	0.813014	1.00	ko00565
57	ABC transporters	5 (0.93%)	0.824141	1.00	ko02010
58	Natural killer cell mediated cytotoxicity	2 (0.37%)	0.832185	1.00	ko04650
59	Pentose phosphate pathway	2 (0.37%)	0.842353	1.00	ko00030
60	Terpenoid backbone biosynthesis	2 (0.37%)	0.867194	1.00	ko00900
61	Oxidative phosphorylation	3 (0.56%)	0.868532	1.00	ko00190
62	Citrate cycle (TCA cycle)	1 (0.19%)	0.869212	1.00	ko00020
63	Plant-pathogen interaction	26 (4.86%)	0.869223	1.00	ko04626
64	Pyrimidine metabolism	6 (1.12%)	0.881902	1.00	ko00240
65	Photosynthesis	1 (0.19%)	0.882228	1.00	ko00195
66	Endocytosis	11 (2.06%)	0.902846	1.00	ko04144
67	Nitrogen metabolism	1 (0.19%)	0.908857	1.00	ko00910
68	Homologous recombination	2 (0.37%)	0.911529	1.00	ko03440
69	Base excision repair	1 (0.19%)	0.921672	1.00	ko03410
70	DNA replication	1 (0.19%)	0.92258	1.00	ko03030
71	RNA polymerase	2 (0.37%)	0.935848	1.00	ko03020
72	Amino sugar and nucleotide sugar metabolism	3 (0.56%)	0.938431	1.00	ko00520
73	Glycerophospholipid metabolism	10 (1.87%)	0.963808	1.00	ko00564
74	Purine metabolism	5 (0.93%)	0.97865	1.00	ko00230
75	Nucleotide excision repair	1 (0.19%)	0.984542	1.00	ko03420
76	Basal transcription factors	1 (0.19%)	0.98559	1.00	ko03022
77	Ribosome biogenesis in eukaryotes	3 (0.56%)	0.988163	1.00	ko03008
78	Aminoacyl-tRNA biosynthesis	1 (0.19%)	0.988461	1.00	ko00970

**Table S3. Cont.**

#	Pathway	DEGs with Pathway Annotation	<i>p</i> -Value	<i>Q</i> Value	Pathway ID
79	RNA transport	9 (1.68%)	0.993872	1.00	ko03013
80	Glycolysis/Gluconeogenesis	1 (0.19%)	0.997655	1.00	ko00010
81	Ribosome	2 (0.37%)	0.998349	1.00	ko03010
82	mRNA surveillance pathway	3 (0.56%)	0.999043	1.00	ko03015
83	Protein processing in endoplasmic reticulum	4 (0.75%)	0.999893	1.00	ko04141

**Table S4.** Primers of quantitative RT-PCR analysis of candidate defence genes. -r represents reverse primers.

Potential Gene Function	Gene Name	Size (bp)	Up/Down *	Primer	Sequence
WRKY protein	<i>WRKY29</i>	1081	Up	CL3202.Contig3_All CL3202.Contig3_All-r	TGAGGAACAACCACTTTAGC GCAGAACACAGCCATAGC
histidine kinase	<i>CRE1</i>	1848	Up	Unigene12008_All Unigene12008_All-r	GAGGGTATATTGGAAGCATTGTC CAGGATAAGCATAAGCAGTAAGG
histidine-containing phosphor transfer protein	<i>AHP</i>	915	Down	CL8962.Contig1_All CL8962.Contig1_All-r	GCACACAATTTCAAGAATACTG ACGACAATAAAGCAACGATTAG
abscisic acid receptor	<i>PYL</i>	533	Up	CL12775.Contig1_All CL12775.Contig1_All-r	AGTGTAATATGTGCTTGTAACC CCTATTAAGTCTGTGAAGTATCG
ABA responsive element binding factor	<i>ABF</i>	818	Up	CL2960.Contig1_All CL2960.Contig1_All-r	GGTCCTCAAGTTCTCCAAGTG GCGTAGGCGTATGGTATCG
Adenylate isopentenyl transferase	<i>IPT</i>	1130	Up	Unigene27866_All Unigene27866_All-r	AAGGTTACTGATGAGGAATG CCAGCAATGATAGGAAGC
cytokinin trans-hydroxylase	<i>CYP735A</i>	1848	Down	CL4119.Contig2_All CL4119.Contig2_All-r	GGAATACATCAGTTACGAAGG TTTGGAGGGTGAAGAATGG
serine/threonine-protein kinase	<i>PBS1</i>	1644	Down	CL2490.Contig6_All CL2490.Contig6_All-r	CCGAACTCTTGGACAACC AACAACTGCGAATGATGATG
circadian clock associated 1	<i>CCA1</i>	2362	Up	CL4203.Contig5_All CL4203.Contig5_All-r	GTCAGGCAGAGAAGATATG GGAACAGGAGAACCAATC
GIGANTEA	<i>GI</i>	4520	Down	Unigene30581_All Unigene30581_All-r	CCAGCACCATTAGCAACAG TACTCGCAGCACCTCTTG
plasma intrinsic protein 2		611	Up	Unigene10760_All Unigene10760_All-r	ATTGGATTTGCTGTGTTC CCTTAGGATGAATTGATGG
plasma membrane H <sup>+</sup> -ATPase LilHA2		413	Up	Unigene14837_All Unigene14837_All-r	AGACCATCCAGCAGCATTAC GCTCTTTCTTGCCTCATTCC

\* Up or down regulation indicated the expression in the PFI vs. PF comparison. In the PFI-60 vs. PFI comparison, the tendencies were opposite.



**Table S5.** Parameters and versions of softwares and databases in this study.

Software	Version	Parameters	Database	Version
filter_fq	in house	–	–	–
Trinity	release-20121005	--seqType fq --min_contig_length 100; --group_pairs_distance 250 --min_kmer_cov 2	–	–
TGICL	v2.1	-l 40 -c 10 -v 20	–	–
Phrap	Release 23.0	-repeat_stringency 0.95 -minmatch 35; -minscore 35	–	–
BLAST	v2.2.26+x64-linux	-F F -e 1e-5 -p blastn; -F F -e 1e-5 -p blastx	nt	release-20121005
			nr	release-20121005
			KEGG	release 63.0
			Swiss-Prot	release-2012_08
			COG	release-20090331
Blast2GO	v2.5.0	Default	GO	release 2012-10-01
Path_finder	in house	–	KEGG	release 63.0
ESTScan	v3.0.2	–	–	–
fpkm	in house	–	–	–
SOAP	Release 2.21	-m 0 -x 500 -s 40 -l 35 -v 5 -r 1	–	–
GO-TermFinder	v0.86	–	GO	release 1 October 2012