

## Supplementary File

# The Molecular Mechanism of Mycelial Incubation time effects on Primordium Formation of *Pleurotus tuoliensis* through Transcriptome and Lipidomic Analyses

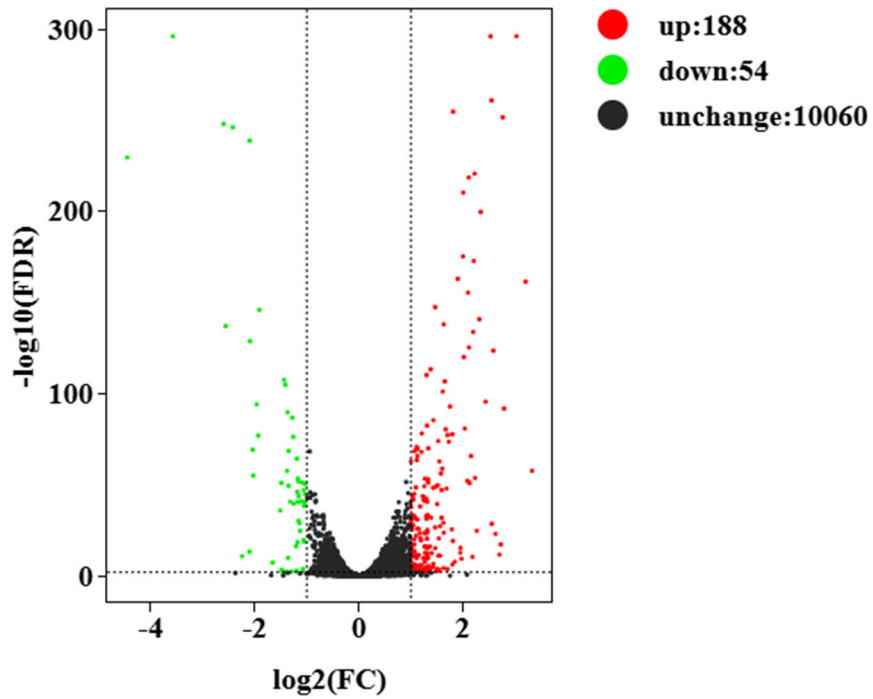
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**Table S1.** Primers for qRT-PCR of 25 DEGs.

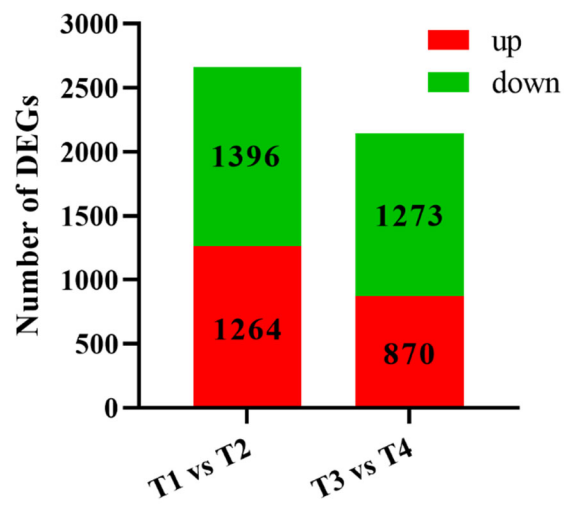
Sample	Positive sequence (5'-3')	Reverse sequence (5'-3')	Gene function
newGene 1669	AGAAATCCTAGCCATCAACCAG	CATGAAAACCGTGCCATTCTG	$\alpha$ -galactosidase
P1A2676	CAGAAGCGGGATGAAGAGTC	TGGTGAGCGGATTTAGTTTGG	$\alpha$ -galactosidase
P1A1532	TCAAGCTCTTTCACCGACG	CAATGCCACAAGTTCACCAG	fatty acid synthase subunit alpha
P1A7381	CGAAACCTGTATACGCTCTGG	ATCATTCACTTCTCCCGCAC	glycerol kinase
newGene 2541	GTGACTCGGGAACCTTAGAAGG	CGAATGAAGGCGAAATGGAC	phosphatidylserine decarboxylase
P1A6700	GTTCAACGAGATCTTCCGAGAG	GTTGAGGACCGAAGTGGAG	phosphatidylserine decarboxylase
P1A7387	TTGGTGTCGCTGGTGATG	AGCATTCTGTCGTAGGTGAAG	3-oxoacyl-[acyl-carrier protein] reductase
P1A5499	TCCTGCTCTGATCATTGGAAC	ATTCGTGACCAGCATCTCC	3-oxoacyl-[acyl-carrier protein] reductase
P1A7966	CACAAAGGAAAGTAAGCACGG	GGTAGGCTCGATGAAATATCCG	aldehyde dehydrogenase (NAD <sup>+</sup> )
P1A5682	CAAACCAACTACACGCCAATG	GGACGGCTTTGATGTTTGTG	aldehyde dehydrogenase (NAD <sup>+</sup> )
P1A1158	AGGTGTAGGAGAAATTGTCCG	CTTGAGGCAGTTTTGTTCCG	alcohol dehydrogenase
P1A3336	CTTTGGAGAAGGTATGCTTGC	CGAGGGATGAAGTTGAGATGAC	alcohol dehydrogenase
P1A4217	CATCCCCTCCGTTAAAACCTAC	ATGCGTATGATAACCCCTCTGC	phosphatidate phosphatase LPIN
P1A2381	CCACCGACTTTCTCCATTACTC	ACAGGAAGATGAAGGCCAAG	phosphatidylserine synthase 2
P1A2354	TTGCCTCATAACGTGGATACC	GTCCTCATCCGCTTCATTCTC	phospholipase D
P1A1213	CGATTGGCTGGAATTGACATC	ATTCCCACTTCGTCTTCGTC	lysophospholipase I
P1A6588	AATCCAGTCATTGCTACCGG	GGTGTAGGTATCTTGTTAGGCTG	C-4 methyl sterol oxidase
P1A3757	CGATACCTGTTTCATGGCTACTG	AAAACCTCCTGCCCTCATGG	squalene monooxygenase
newGene 1706	GACGTCAAGATGCCCCCTTC	GCAGGAACGAATTTGGCATG	squalene monooxygenase
P1A6656	GATTATATCTGGAAGGTGACGGG	GGTGTGCGGGTACTTGTG	transcriptional enhancer factor Tec1
newGene 4823	CAGACTACATTTTCAAGGCGAC	GTGCTGAACCTCCAAATCGG	transcriptional enhancer factor Tec1
P1A3282	AAAAGCCTGAGACGGAAGAG	GAGATACTCCACCTTCGCTTG	transcription factor Sko1
newGene 4303	CCAGTACATTCTCAGAGTTTCGG	AGAGGAAATCGAGCCAGTTG	transcription factor RLM1
P1A1038	CACCTCCGAACCTATCCCAAC	AGAAAGACAATCAGATGGCACC	SHO1 osmosensor
newGene 3847	ACCGGGAAGTACAACGTTATG	ACTAATCTTCGCCAGACCTTG	protein kinase A
$\beta$ -actin	AGTCGGTGCCTTGTTAT	ATACCGACCATCACACCT	$\beta$ -actin

**Table S2.** Statistical analysis of the number of sequencing reads.

Samples	Clean reads	Clean bases	GC Content	% $\geq$ Q30	Mapped Reads
T1A	21,657,002	6,467,838,148	52.84%	95.04%	38,256,792 (88.32%)
T1B	21,266,375	6,349,328,454	52.83%	95.07%	37,559,799 (88.31%)
T1C	21,596,161	6,448,273,398	52.84%	95.45%	38,151,136 (88.33%)
T2A	21,665,019	6,475,839,802	52.78%	94.83%	37,655,790 (86.90%)
T2B	22,550,603	6,744,909,426	53.01%	94.44%	39,046,010 (86.57%)
T2C	23,351,508	6,983,964,152	53.22%	94.93%	41,849,231 (89.61%)
T3A	20,937,567	6,245,015,624	52.72%	95.17%	37,009,441 (88.38%)
T3B	25,677,555	7,653,048,468	53.37%	95.29%	47,233,814 (91.97%)
T3C	23,264,575	6,969,377,810	52.92%	94.69%	41,432,682 (89.05%)
T4A	21,077,406	6,305,920,772	52.43%	94.69%	36,906,095 (87.55%)
T4B	22,302,687	6,677,620,318	52.98%	94.33%	39,799,202 (89.23%)
T4C	22,881,666	6,836,773,504	53.29%	94.79%	41,681,338 (91.08%)



**Figure S1.** Volcano plot analysis of DEGs with different incubation time.



**Figure S2.** The DEGs were changed in the mycelia cultured for 4 days in dark and then stimulated (T1 vs T2), The DEGs were changed in the mycelia cultured for 6 days in dark and then stimulated (T3 vs T4).