

## Supplementary files

**Table S1.** Summary of the transcriptome sequencing of the isonuclear alloplasmic strain of *F. filiformis*.

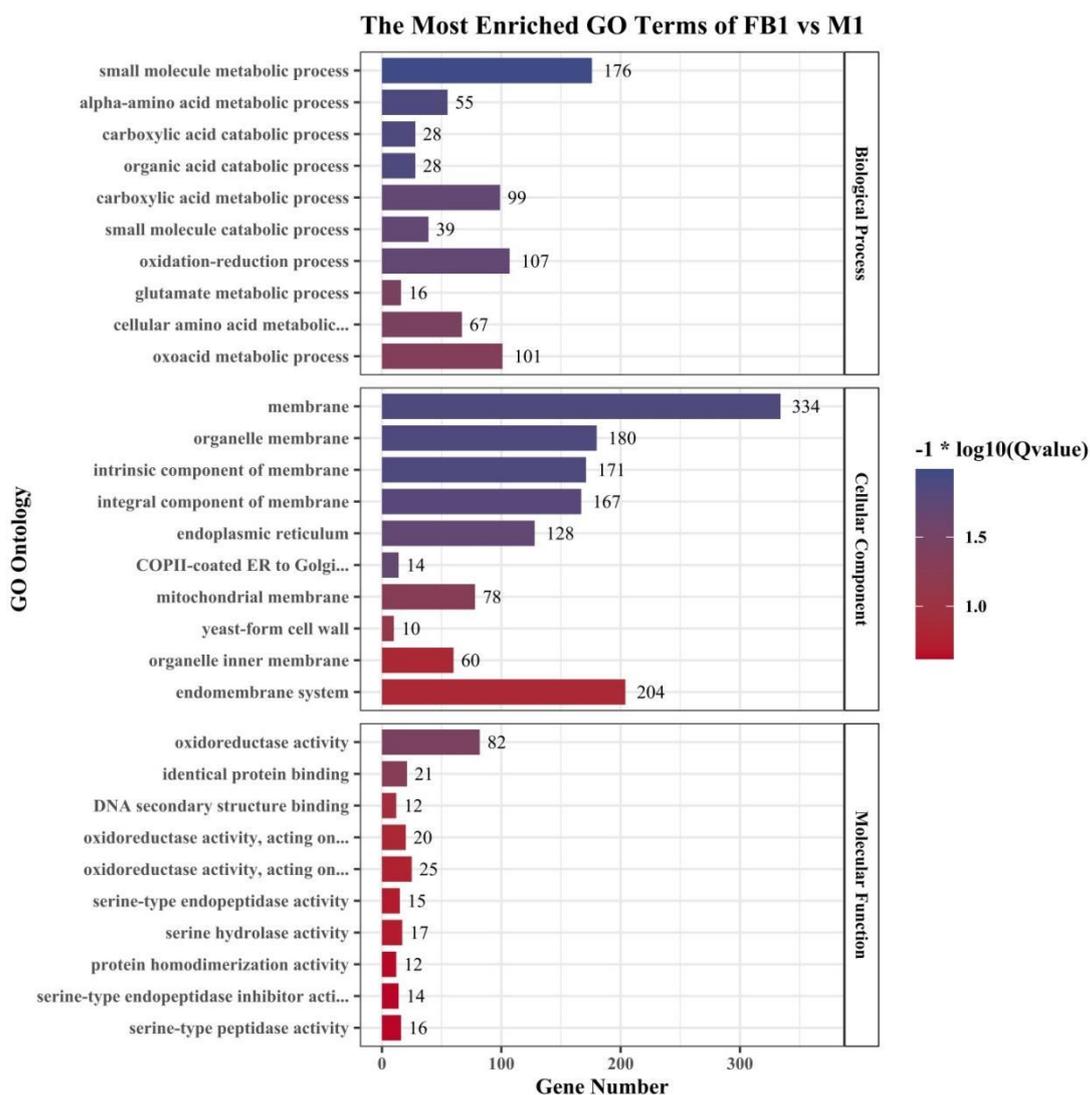
Sample	Total Raw Reads	Total Clean Reads (%)	Clean Bases	GC (%)
M1_1	20,017,959	20,016,738(99.99%)	6,004,832,502	53.49
M1_2	22,499,971	22,498,684(99.99%)	6,749,364,512	53.5
M1_3	21,379,105	21,377,917(99.99%)	6,413,137,206	53.61
M2_1	21,661,185	21,660,514(99.99%)	6,497,803,936	53.85
M2_2	22,637,497	22,636,726(99.99%)	6,790,823,350	53.54
M3_3	21,099,320	21,098,578(99.99%)	6,329,364,908	53.78
P1_1	20,669,020	20,666,662(99.99%)	6,199,635,280	53.77
P1_2	22,308,253	22,305,678(99.99%)	6,691,454,632	53.72
P1_3	19,855,093	19,852,433(99.99%)	5,955,486,738	53.63
P2_1	18,468,051	18,466,017(99.99%)	5,539,499,546	53.79
P2_2	20,343,988	20,341,430(99.99%)	6,102,103,252	53.75
P3_3	23,600,733	23,597,952(99.99%)	7,078,892,378	53.32
YF1_1	18,480,730	18,478,637(99.99%)	5,543,341,450	53.6
YF1_2	17,691,296	17,689,015(99.99%)	5,306,455,422	53.72
YF1_3	22,983,749	22,980,902(99.99%)	6,893,918,224	53.76
YF2_1	20,515,219	20,512,806(99.99%)	6,153,457,682	53.64
YF2_2	18,751,383	18,749,226(99.99%)	5,624,437,498	53.56
YF3_3	20,532,445	20,529,936(99.99%)	6,158,637,704	53.71
FB1_1	25,374,941	25,373,457(99.99%)	7,611,735,016	53.87
FB1_2	23,593,251	23,591,888(99.99%)	7,077,256,998	53.89
FB1_3	20,873,905	20,872,049(99.99%)	6,260,361,860	53.95
FB2_1	22,139,555	22,138,256(99.99%)	6,641,206,138	53.76
FB2_2	21,433,113	21,431,780(99.99%)	6,429,276,578	53.83
FB3_3	19,161,190	19,159,932(99.99%)	5,747,798,844	53.81

Note: M1\_1, M1\_2, M1\_3 is the three independent biological replicates of *F. filiformis* strain J1-Y33 during mycelium growth stage; M2\_1, M2\_2, M3\_3 is the three independent biological replicates of *F. filiformis* strain Y33-J1 during mycelium growth stage; P1\_1, P1\_2, P1\_3 is the three independent biological replicates of J1-Y33 during primordia formation stage; P2\_1, P2\_2, P3\_3 is the three independent biological replicates of Y33-J1 during primordia formation stage; YF1\_1, YF1\_2, YF1\_3 is the three independent biological replicates of J1-Y33 during young mushroom stage; YF2\_1, YF2\_2, YF3\_3 is the three independent biological replicates of Y33-J1 during young mushroom stage; FB1\_1, FB1\_2, FB1\_3 is the three independent biological replicates of J1-Y33 during fruiting body stage; FB2\_1, FB2\_2, FB3\_3 is the three independent biological replicates of Y33-J1 during fruiting body stage.

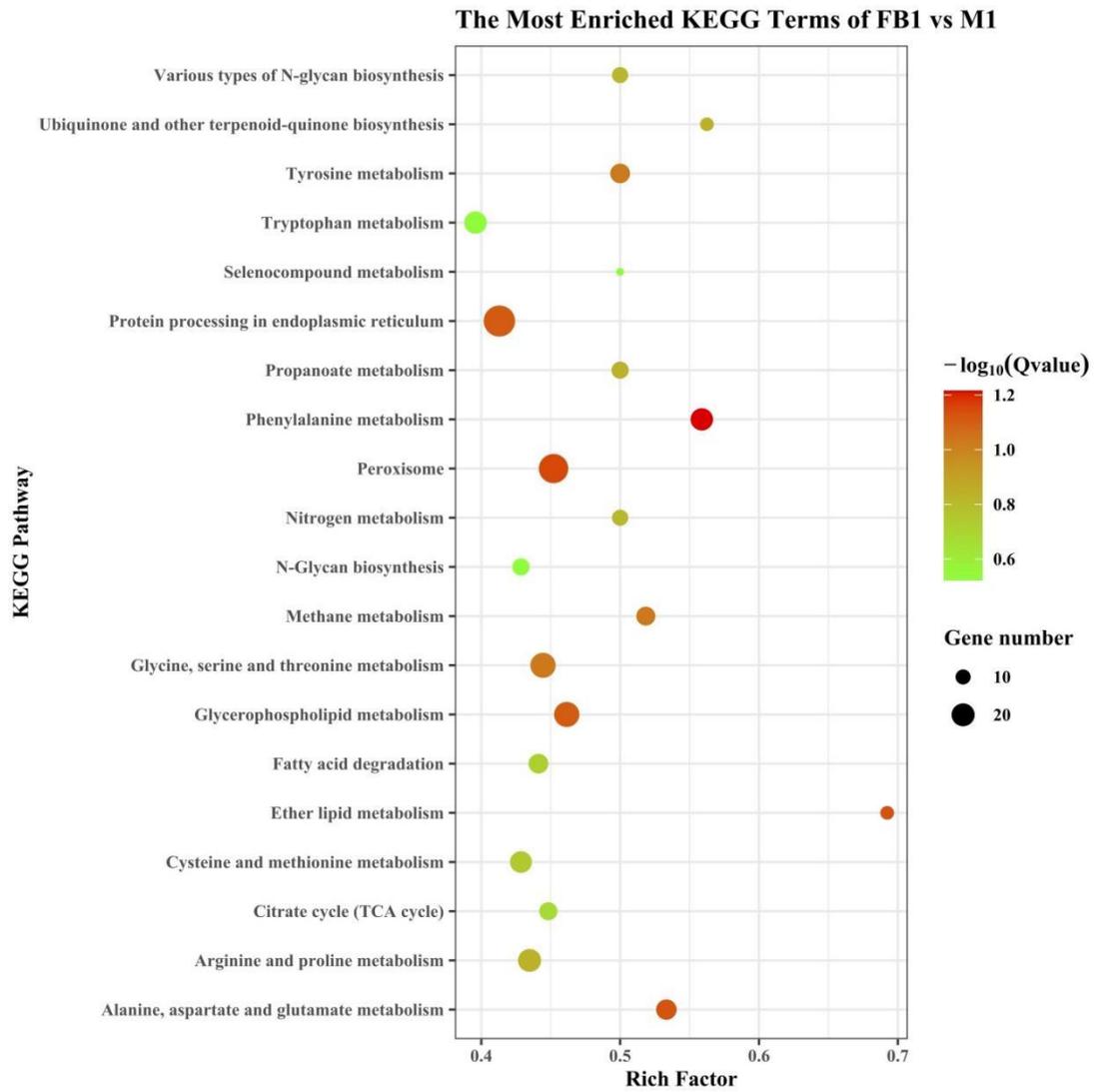
**Table S2.** The primers used in this study.

Gene	Primer Name	Primer Sequence
GB008257	GB008257-F	TCTACGACAGGCAACGAACC
	GB008257-R	AGCGCCAGATATCAAGCCAA
GB007198	GB007198-F	ATTCGCGGTCGTGATCAACT
	GB007198-R	CGCGTCGAATAAACTCGCAG
GB009214	GB009214-F	CTTCGATATCCACCCCGACG
	GB009214-R	ACGACAGTGGTAACGCCATT
GB009768	GB009768-F	TATCCCGCTTTCCTACCGC
	GB009768-R	CCTTCCATCCGCCTTGAGT
GB006100	GB006100-F	CGCTTCGCAAGACGTACAAG
	GB006100-R	TGGTTCGTAGAAACCCAGCC
GB004373	GB004373-F	TCGGTATCGCCGCTTAGTC

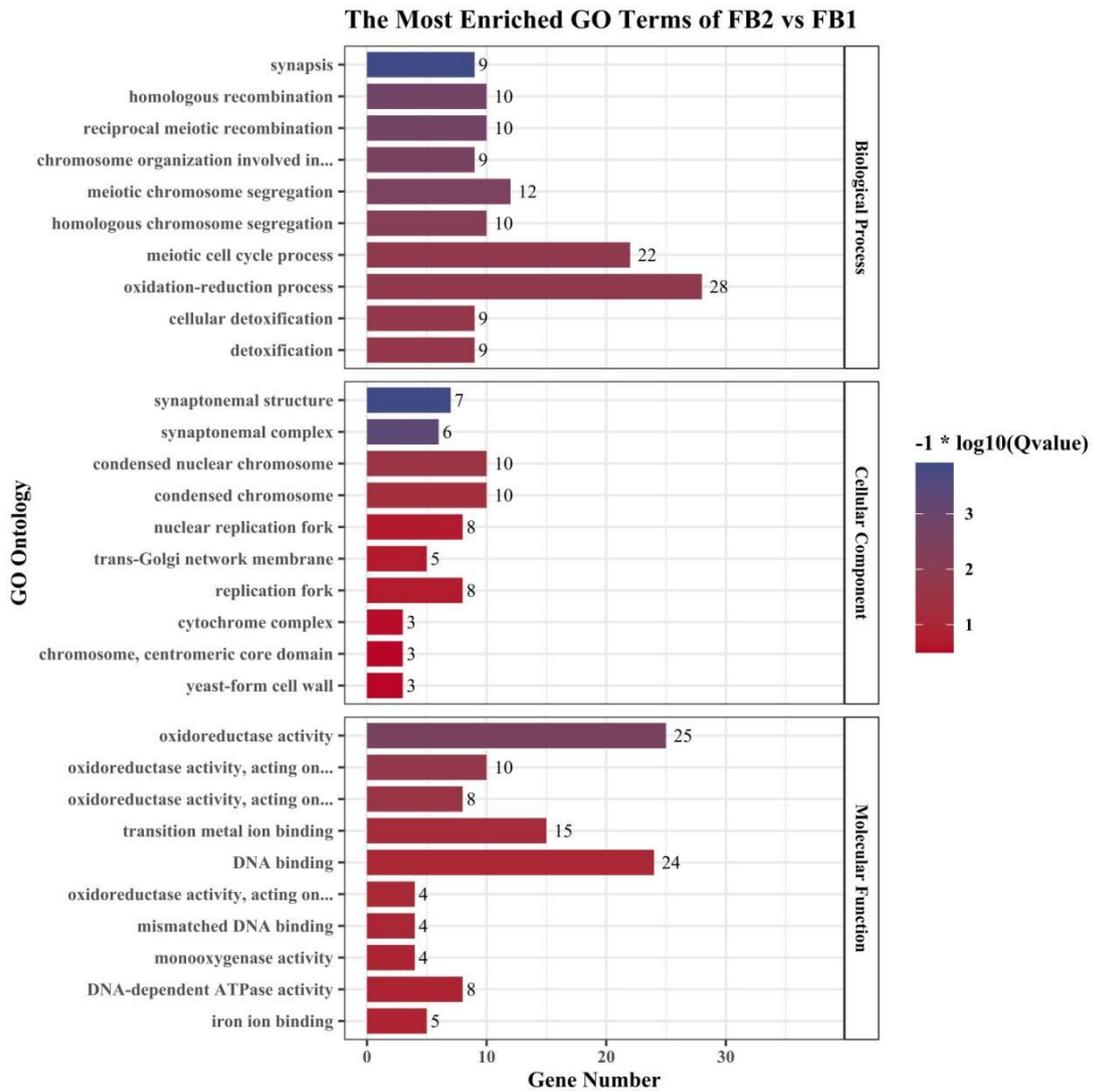
	GB004373-R	CTCTTGCCTGGGAGTCAAGT
GB006766	GB006766-F	AACCAAACATTTTCGCGCACA
	GB006766-R	GAGGTACTCGTATTGCGGGG
GB005431	GB005431-F	TACAGACGTTGAAGGGTGCC
	GB005431-R	AGAGGGTTGGATGAGCAAGC
GB001767	GB001767-F	GAGGCAACATCAACGAAGGC
	GB001767-R	ACAAAATCGCACCCCTTTGCC
GB005682	GB005682-F	GCTTCCCGAGAGTACGGATG
	GB005682-R	GACCGAAAAGGGACGGAAGC
GB006651	GB006651-F	TGACACGGAAGGAAAGCCTC
	GB006651-R	CTTGTTGGTGCTCGAGTCCT



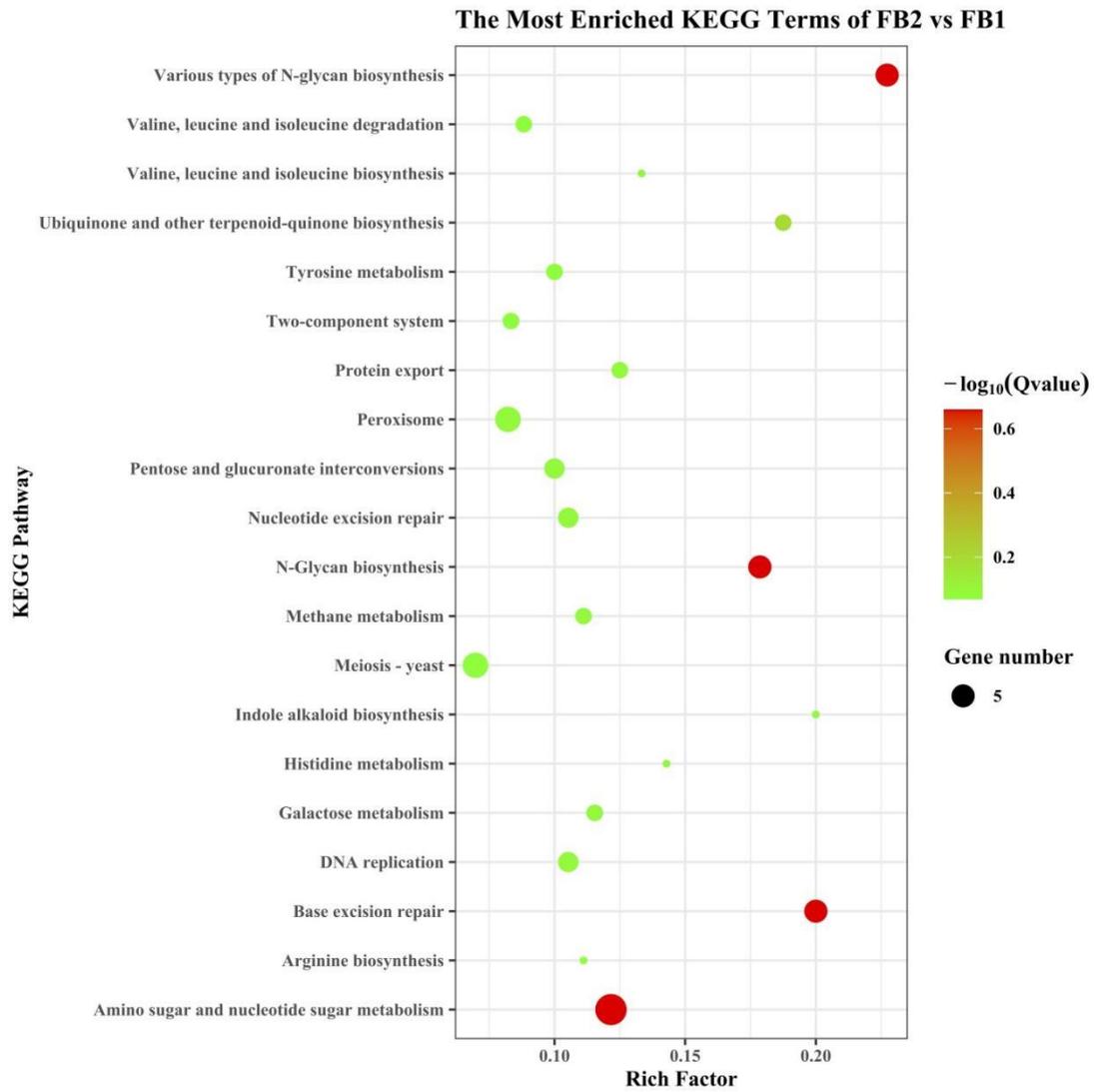
**Figure S1.** The Gene Ontology (GO) enrichment analysis of the differentially expressed genes (DEGs) between the fruiting body stage of *F. filiformis* J1-Y33 (FB1) and the mycelium growth stage of *F. filiformis* J1-Y33 (M1) was conducted. The results were summarized in three main GO categories, namely Biological Process, Cellular Component and Molecular Function. The x-axis denoted the number of differentially expressed genes annotated in the GO category, while the y-axis indicated the GO term. The color of each GO category represented the  $-\log_{10}(Q\text{-value})$ . This value is a measure of the statistical significance of the GO term which is used to investigate the biological relevance of the DEGs.



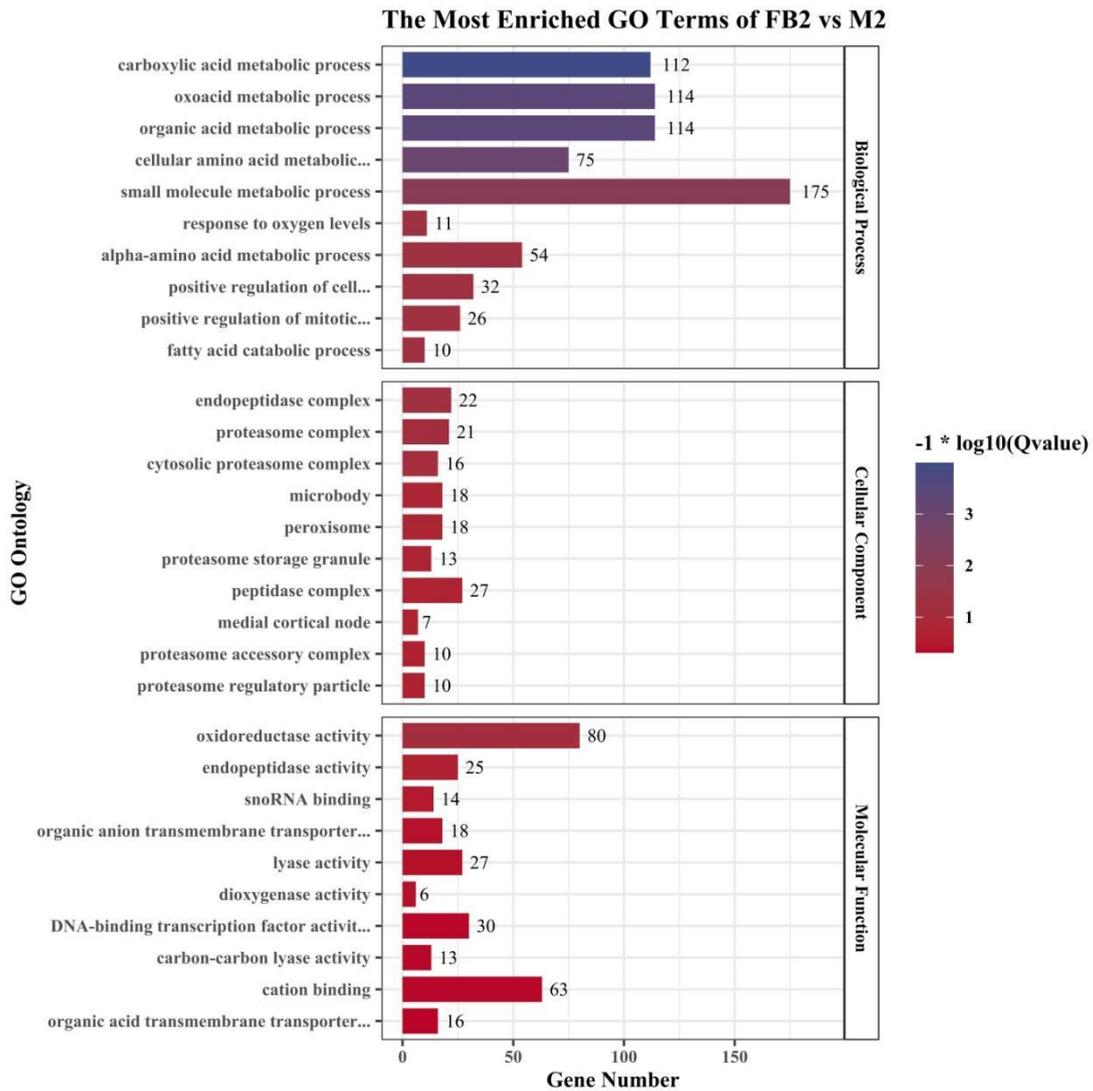
**Figure S2.** KEGG enrichment analysis of the differentially expressed genes (DEGs) between the fruiting body stage of *F. filiformis* J1-Y33 (FB1) and the mycelium growth stage of *F. filiformis* J1-Y33 (M1) is presented. The x-axis of the figure displays the rich factor, while the y-axis reflects the KEGG pathway. The count indicates the number of DEGs enriched in the pathway, and the color implies the  $-\text{Log}_{10}(Q\text{-value})$  of each pathway.



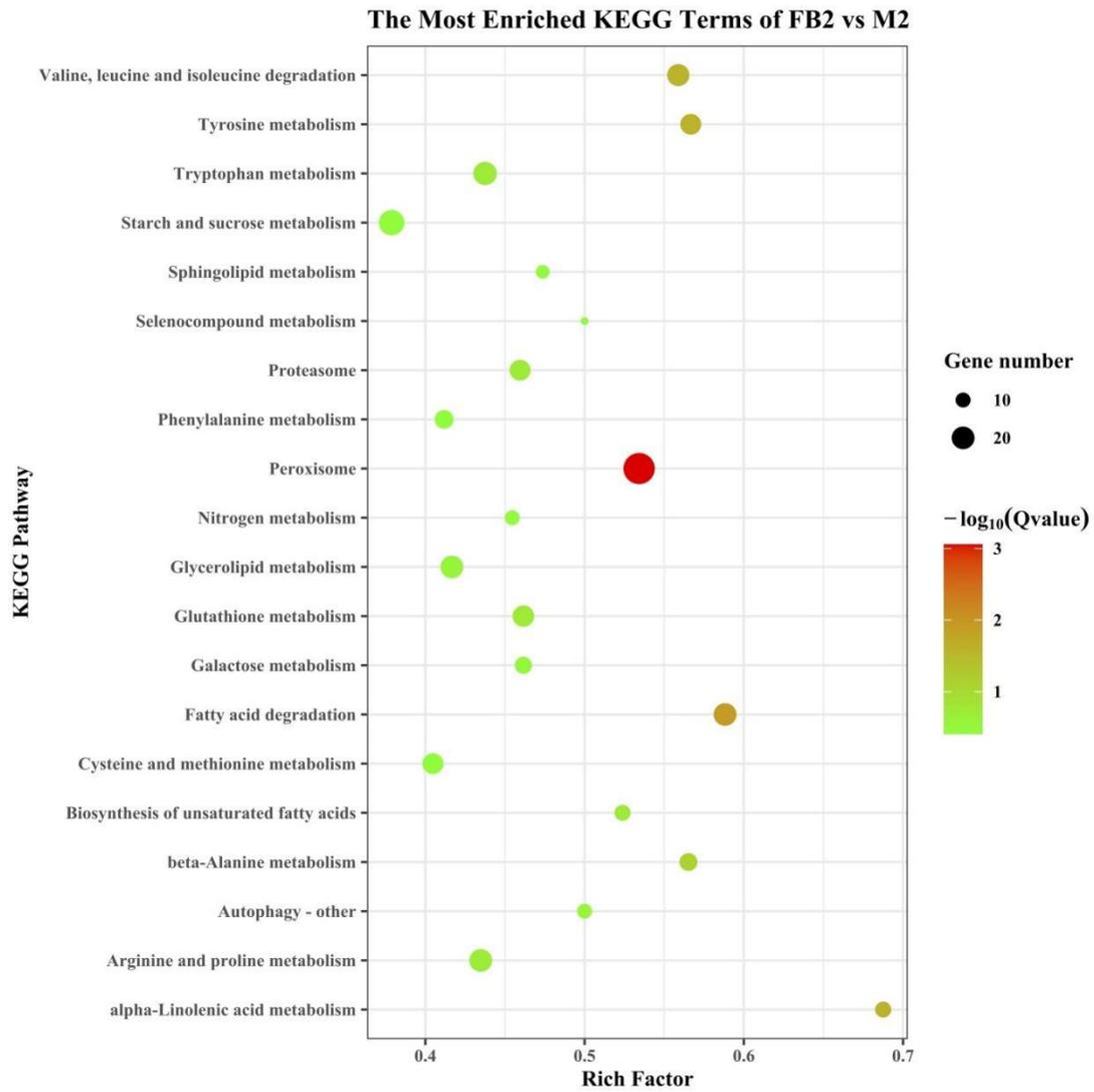
**Figure S3.** The Gene Ontology (GO) enrichment analysis of the differentially expressed genes (DEGs) between the fruiting body stage of *F. filiformis* Y33-J1 (FB2) and the fruiting body stage of *F. filiformis* J1-Y33 (FB1) was conducted. The results were summarized in three main GO categories, namely Biological Process, Cellular Component and Molecular Function. The x-axis denoted the number of differentially expressed genes annotated in the GO category, while the y-axis indicated the GO term. The color of each GO category represented the  $-\log_{10}(Q\text{-value})$ . This value is a measure of the statistical significance of the GO term which is used to investigate the biological relevance of the DEGs.



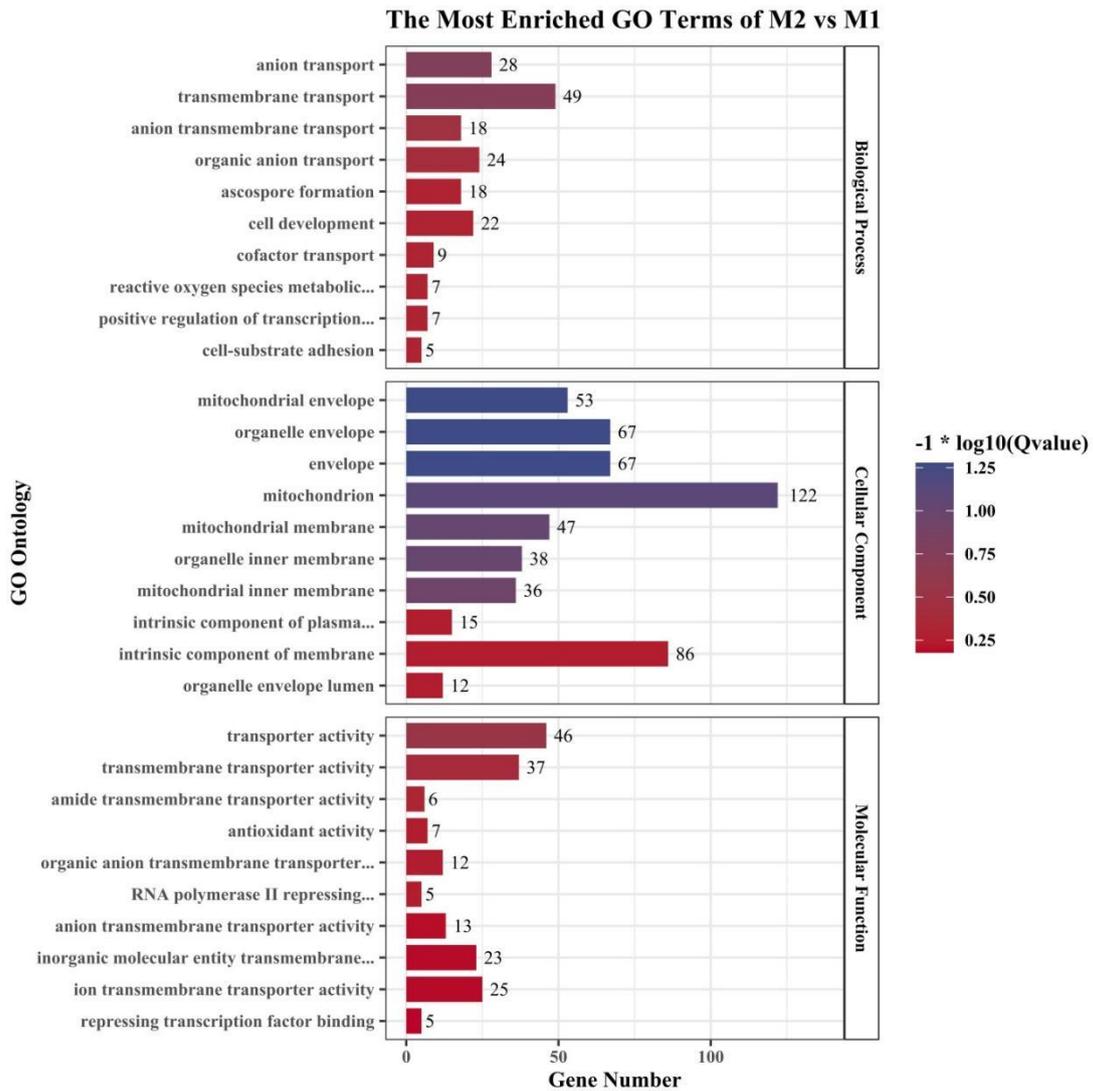
**Figure S4.** KEGG enrichment analysis of the differentially expressed genes (DEGs) between the fruiting body stage of *F. filiformis* Y33-J1 (FB2) and the fruiting body stage of *F. filiformis* J1-Y33 (FB1) is presented. The x-axis of the figure displays the rich factor, while the y-axis reflects the KEGG pathway. The count indicates the number of DEGs enriched in the pathway, and the color implies the  $-\text{Log}_{10}(\text{Q-value})$  of each pathway.



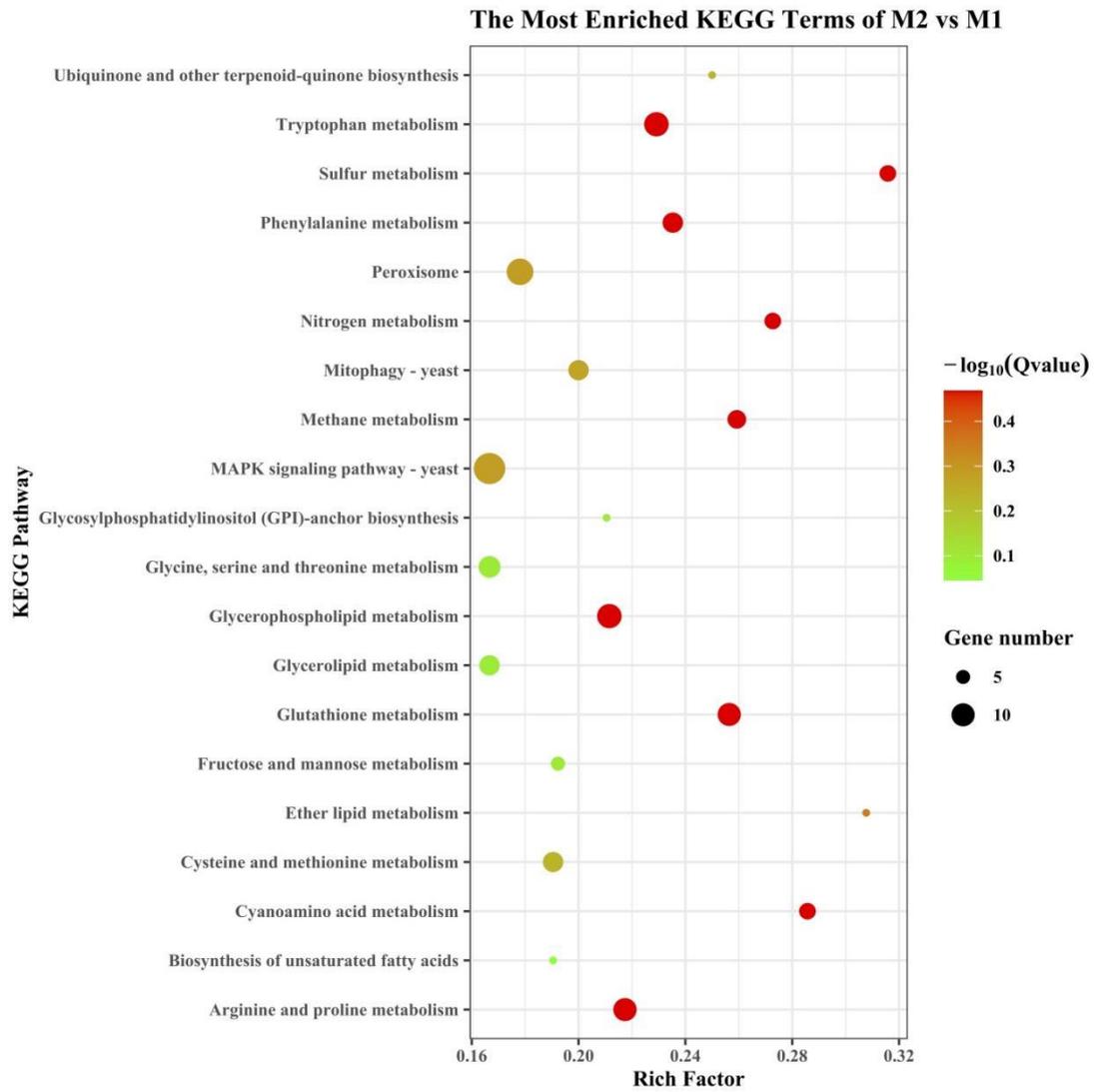
**Figure S5.** The Gene Ontology (GO) enrichment analysis of the differentially expressed genes (DEGs) between the fruiting body stage of *F. filiformis* Y33-J1 (FB2) and the mycelium growth stage of *F. filiformis* J1-Y33 (FB1) was conducted. The results were summarized in three main GO categories, namely Biological Process, Cellular Component and Molecular Function. The x-axis denoted the number of differentially expressed genes annotated in the GO category, while the y-axis indicated the GO term. The color of each GO category represented the  $-\log_{10}(Q\text{-value})$ . This value is a measure of the statistical significance of the GO term which is used to investigate the biological relevance of the DEGs.



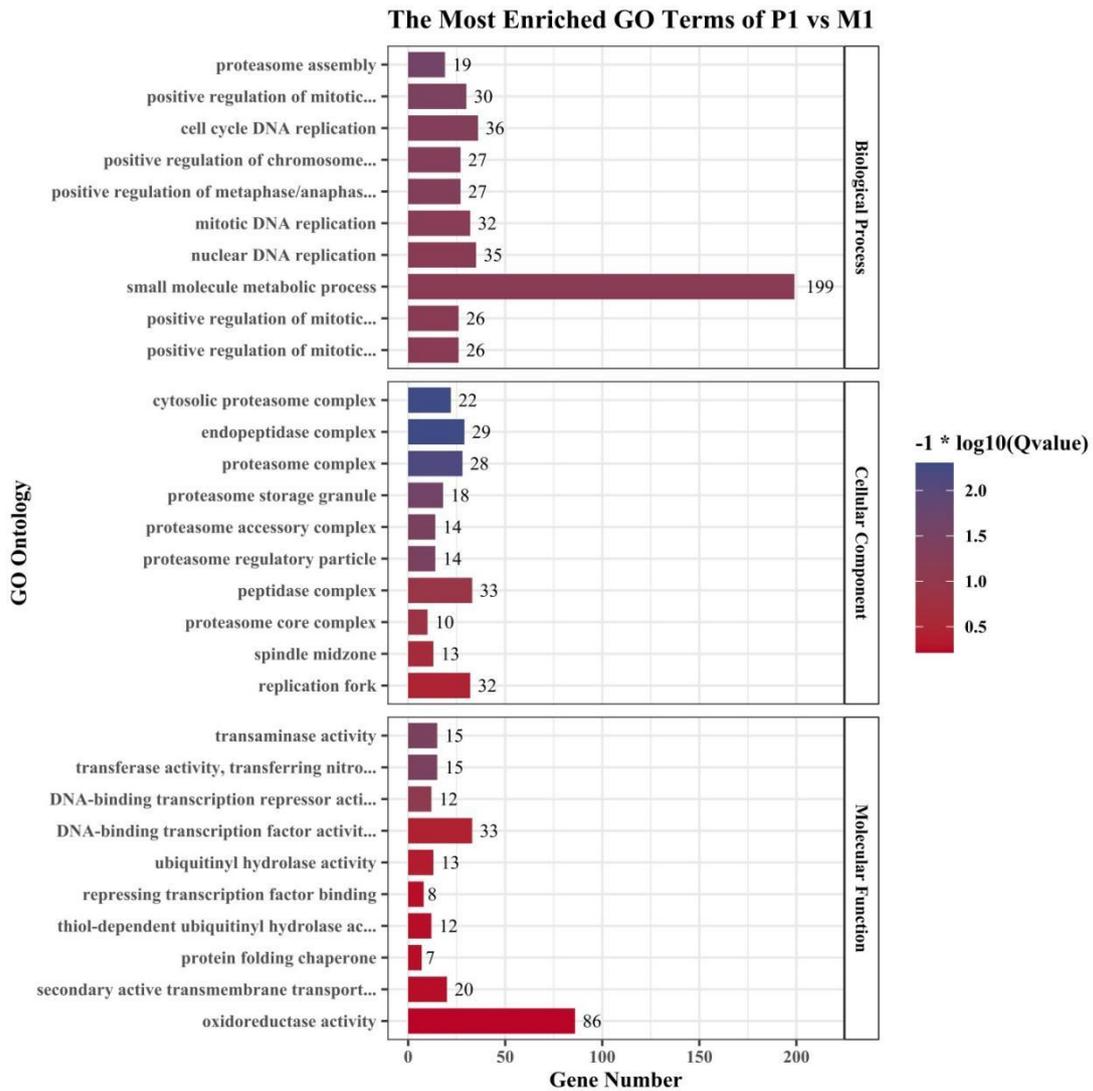
**Figure S6.** KEGG enrichment analysis of the differentially expressed genes (DEGs) between the fruiting body stage of *F. filiformis* Y33-J1 (FB2) and the mycelium growth stage of *F. filiformis* J1-Y33 (FB1) is presented. The x-axis of the figure displays the rich factor, while the y-axis reflects the KEGG pathway. The count indicates the number of DEGs enriched in the pathway, and the color implies the  $-\text{Log}_{10}(Q\text{-value})$  of each pathway.



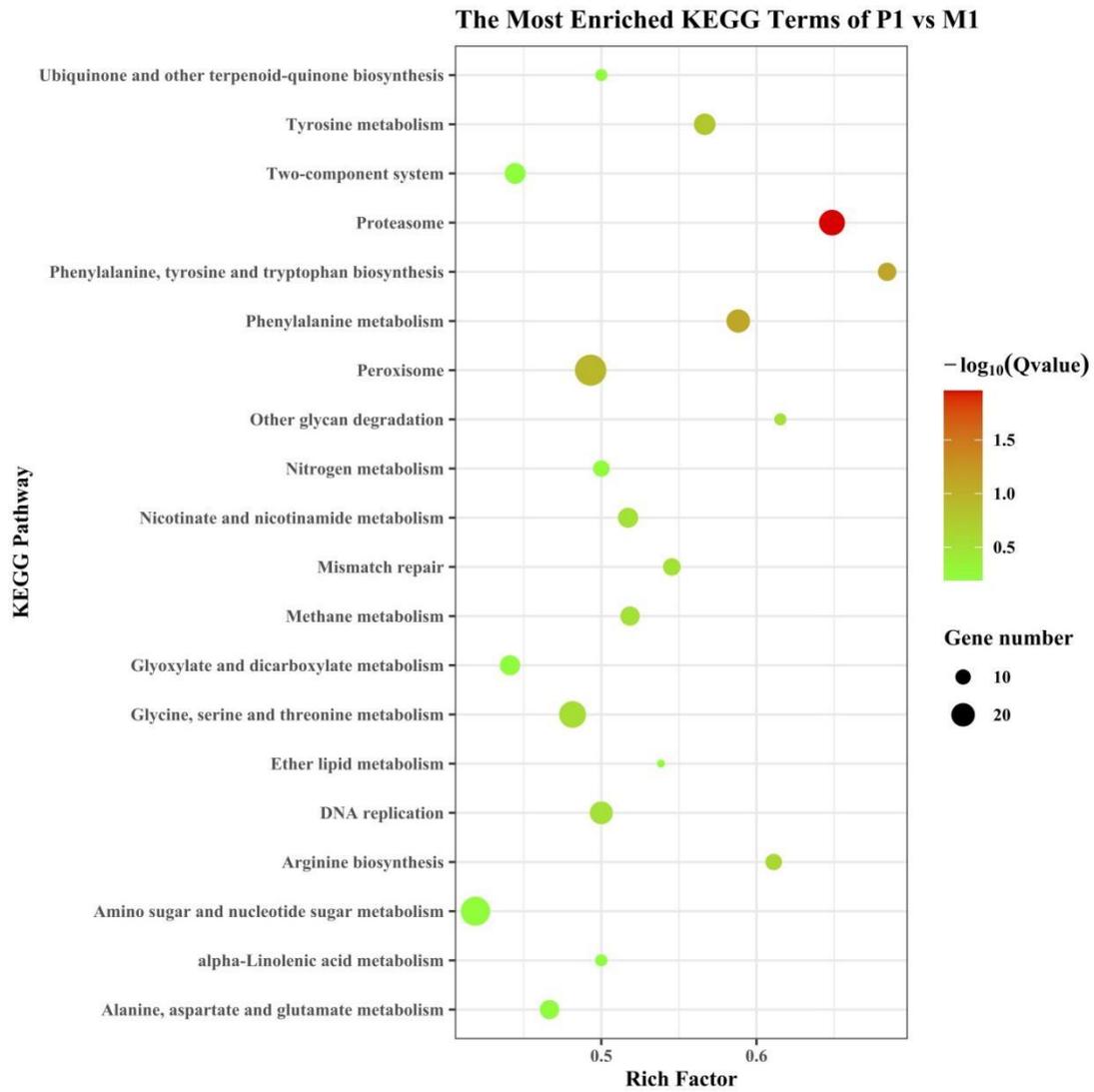
**Figure S7.** The Gene Ontology (GO) enrichment analysis of the differentially expressed genes (DEGs) between the mycelium growth stage of *F. filiformis* Y33-J1 (M2) and the mycelium growth stage of *F. filiformis* J1-Y33 (M1) was conducted. The results were summarized in three main GO categories, namely Biological Process, Cellular Component and Molecular Function. The x-axis denoted the number of differentially expressed genes annotated in the GO category, while the y-axis indicated the GO term. The color of each GO category represented the  $-\log_{10}(Q\text{-value})$ . This value is a measure of the statistical significance of the GO term which is used to investigate the biological relevance of the DEGs.



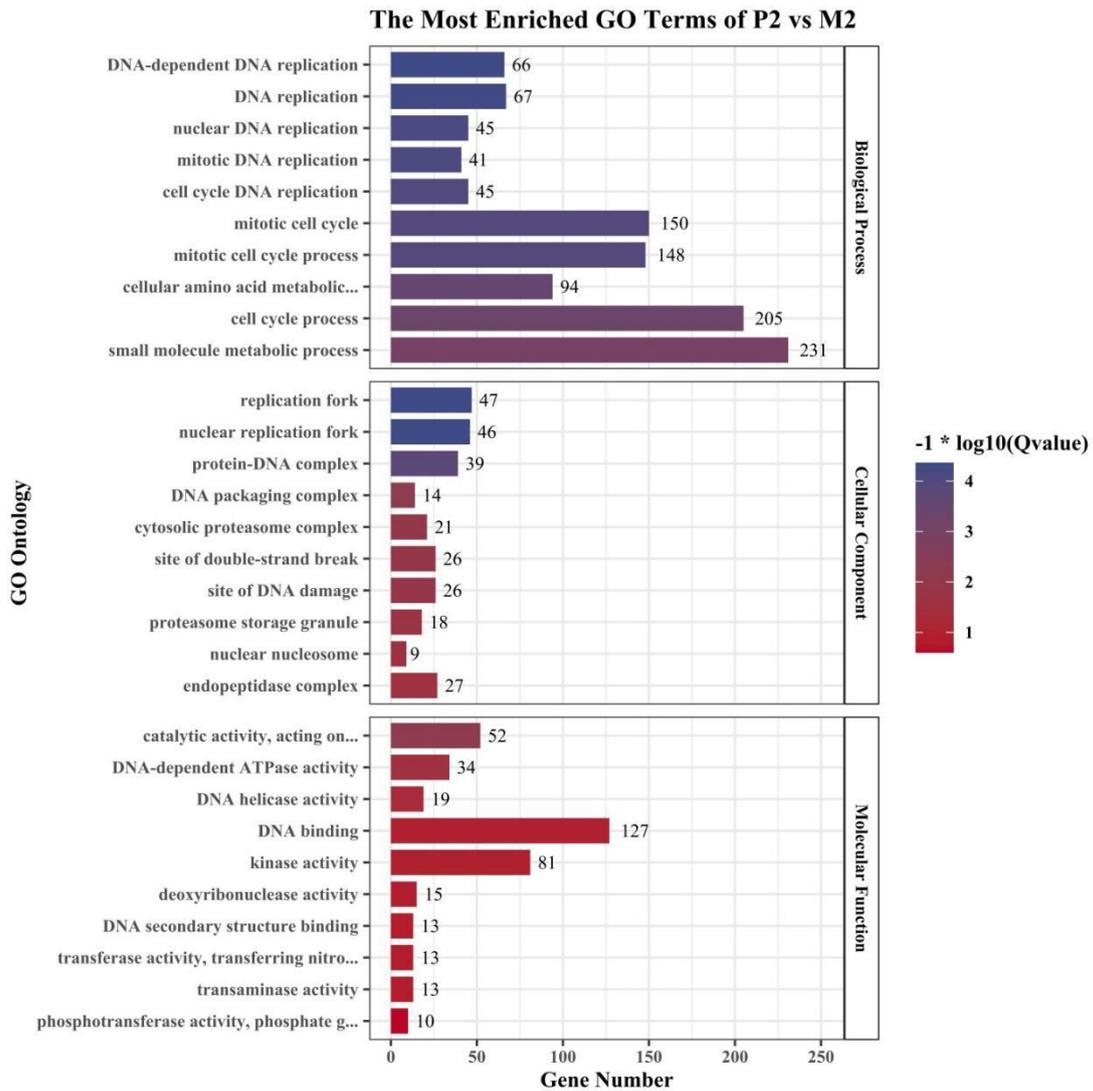
**Figure S8.** KEGG enrichment analysis of the differentially expressed genes (DEGs) between the mycelium growth stage of *F. filiformis* Y33-J1 (M2) and the mycelium growth stage of *F. filiformis* J1-Y33 (M1) is presented. The x-axis of the figure displays the rich factor, while the y-axis reflects the KEGG pathway. The count indicates the number of DEGs enriched in the pathway, and the color implies the  $-\text{Log}_{10}(Q\text{-value})$  of each pathway.



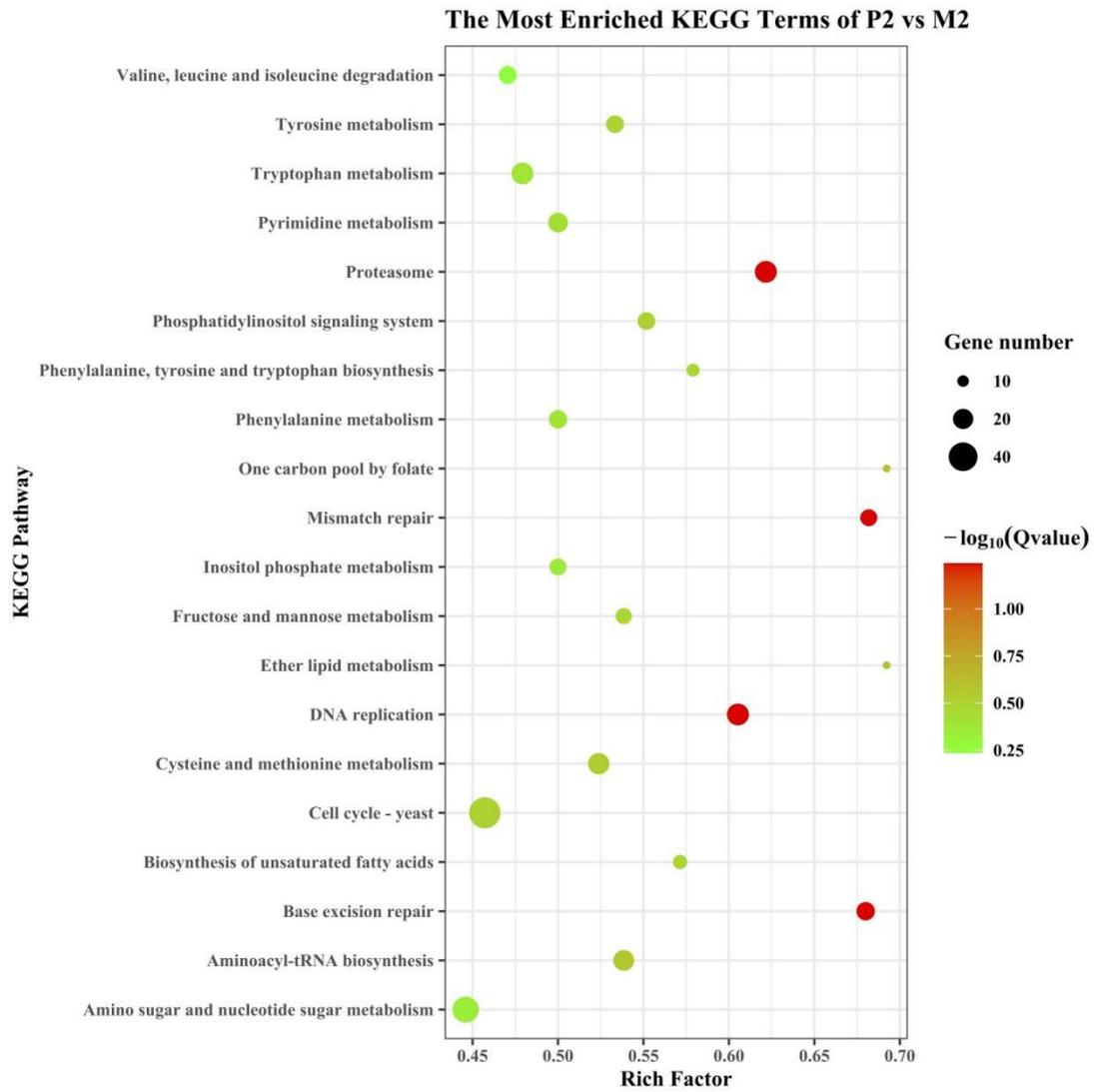
**Figure S9.** The Gene Ontology (GO) enrichment analysis of the differentially expressed genes (DEGs) between the primordia formation stage of *F. filiformis* J1-Y33 (P1) and the mycelium growth stage of *F. filiformis* J1-Y33 (M1) was conducted. The results were summarized in three main GO categories, namely Biological Process, Cellular Component and Molecular Function. The x-axis denoted the number of differentially expressed genes annotated in the GO category, while the y-axis indicated the GO term. The color of each GO category represented the  $-\log_{10}(Q\text{-value})$ . This value is a measure of the statistical significance of the GO term which is used to investigate the biological relevance of the DEGs.



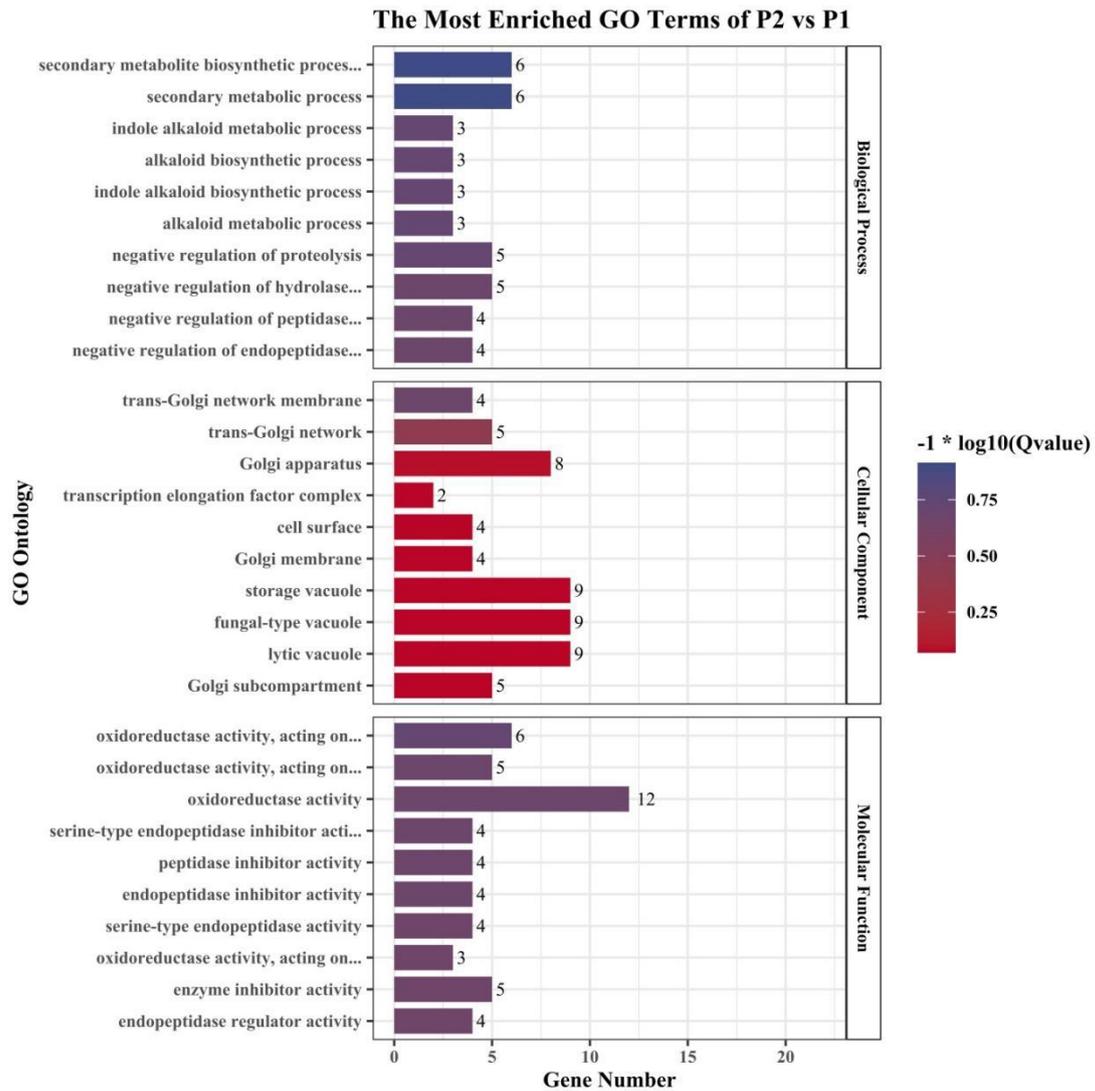
**Figure S10.** KEGG enrichment analysis of the differentially expressed genes (DEGs) between the primordia formation stage of *F. filiformis* J1-Y33 (P1) and the mycelium growth stage of *F. filiformis* J1-Y33 (M1) is presented. The x-axis of the figure displays the rich factor, while the y-axis reflects the KEGG pathway. The count indicates the number of DEGs enriched in the pathway, and the color implies the  $-\log_{10}(Q\text{-value})$  of each pathway.



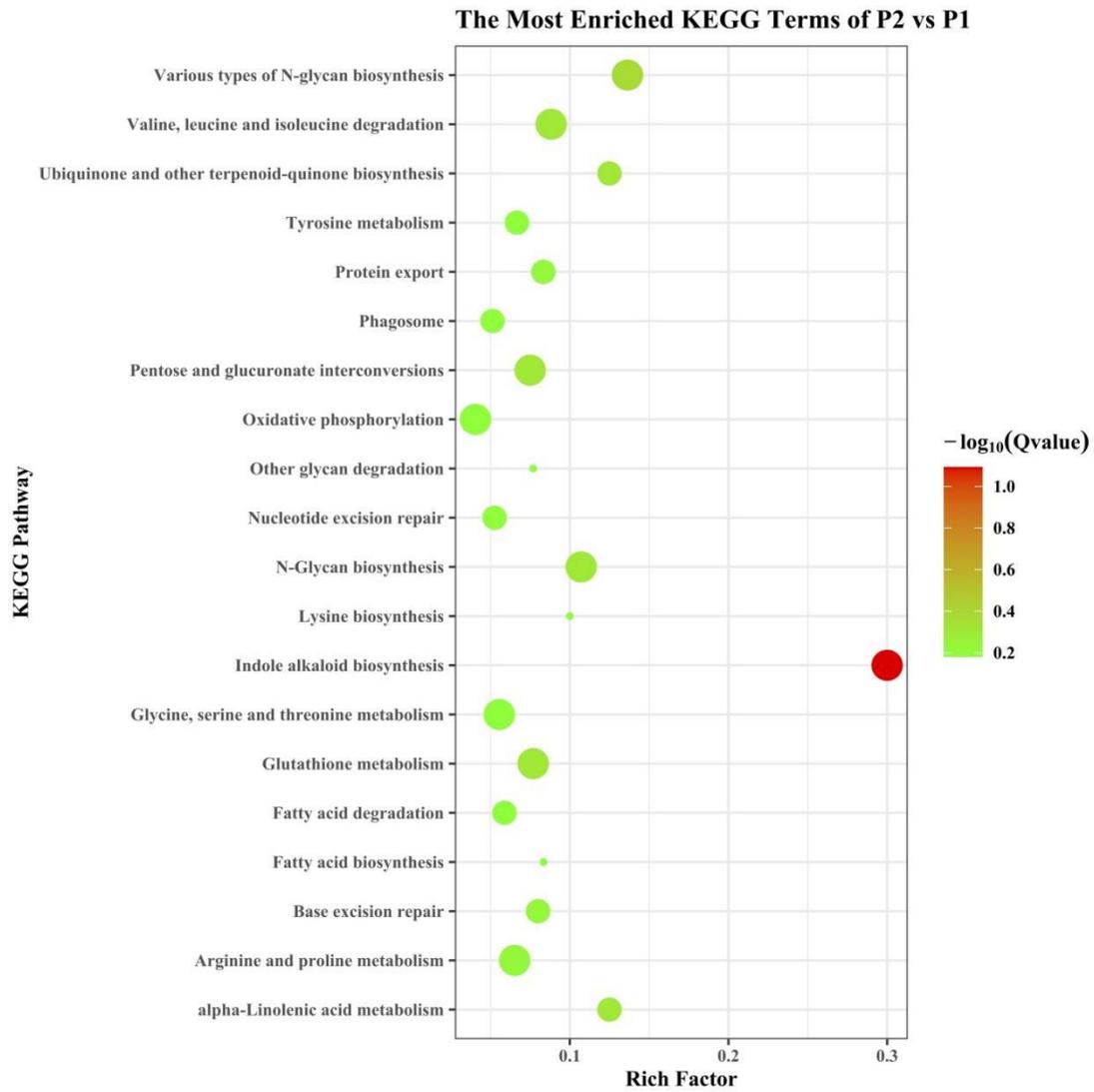
**Figure S11.** The Gene Ontology (GO) enrichment analysis of the differentially expressed genes (DEGs) between the primordia formation stage of *F. filiformis* Y33-J1 (P2) and the mycelium growth stage of *F. filiformis* Y33-J1 (M2) was conducted. The results were summarized in three main GO categories, namely Biological Process, Cellular Component and Molecular Function. The x-axis denoted the number of differentially expressed genes annotated in the GO category, while the y-axis indicated the GO term. The color of each GO category represented the  $-\log_{10}(Q\text{-value})$ . This value is a measure of the statistical significance of the GO term which is used to investigate the biological relevance of the DEGs.



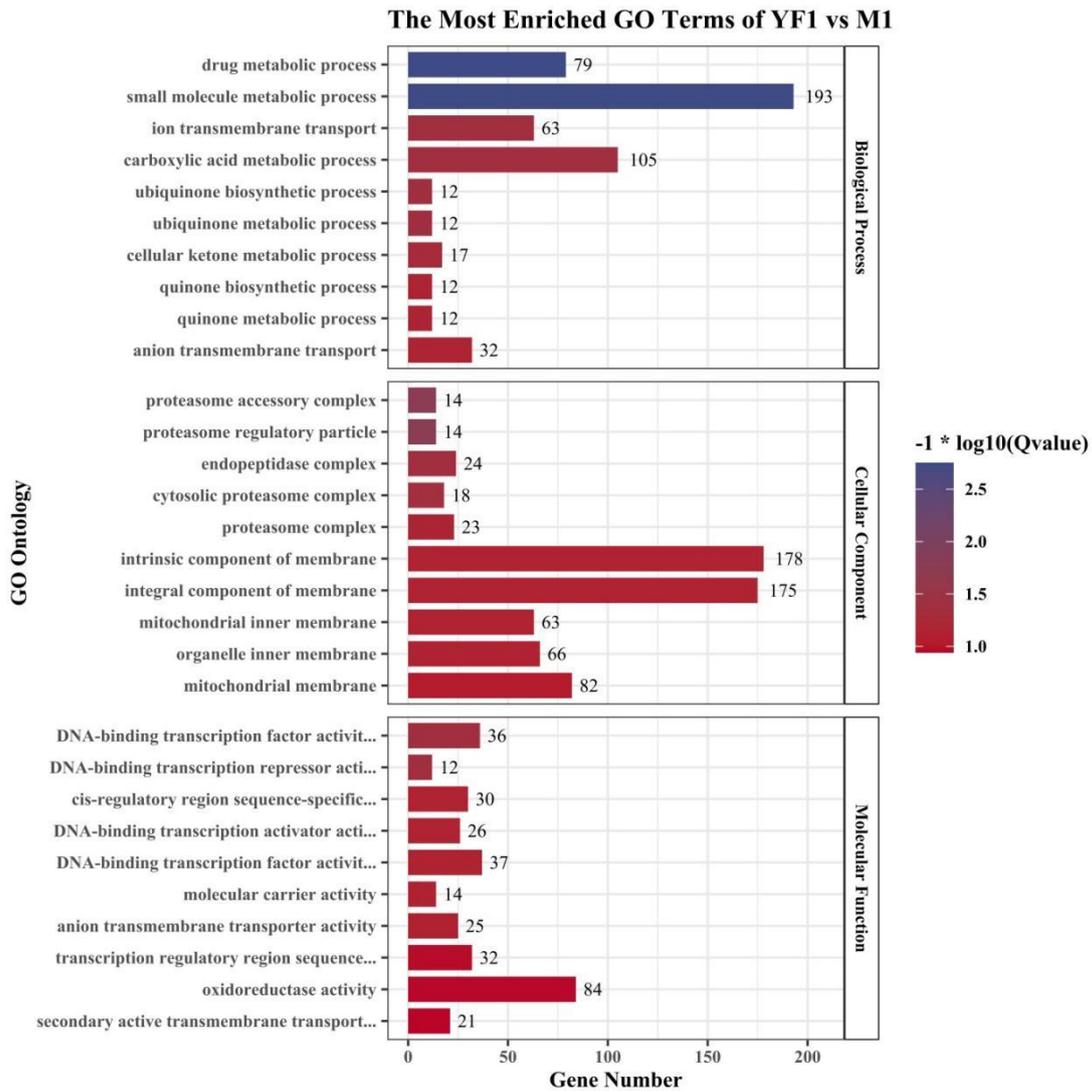
**Figure S12.** KEGG enrichment analysis of the differentially expressed genes (DEGs) between the primordia formation stage of *F. filiformis* Y33-J1 (P2) and the mycelium growth stage of *F. filiformis* Y33-J1 (M2) is presented. The x-axis of the figure displays the rich factor, while the y-axis reflects the KEGG pathway. The count indicates the number of DEGs enriched in the pathway, and the color implies the  $-\log_{10}(Q\text{-value})$  of each pathway.



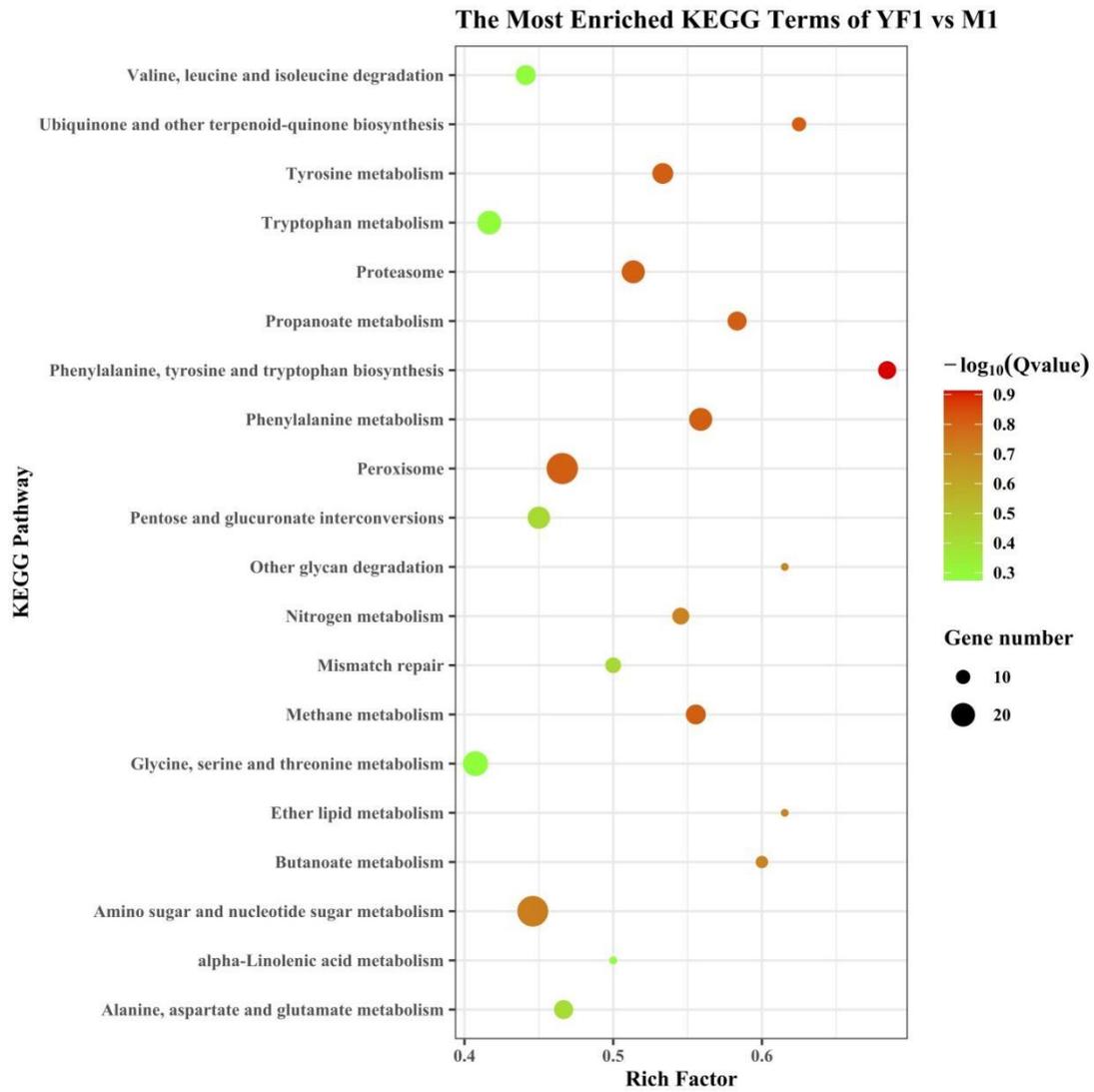
**Figure S13.** The Gene Ontology (GO) enrichment analysis of the differentially expressed genes (DEGs) between the primordia formation stage of *F. filiformis* Y33-J1 (P2) and the primordia formation stage of *F. filiformis* J1-Y33 (P1) was conducted. The results were summarized in three main GO categories, namely Biological Process, Cellular Component and Molecular Function. The x-axis denoted the number of differentially expressed genes annotated in the GO category, while the y-axis indicated the GO term. The color of each GO category represented the  $-\log_{10}(Q\text{-value})$ . This value is a measure of the statistical significance of the GO term which is used to investigate the biological relevance of the DEGs.



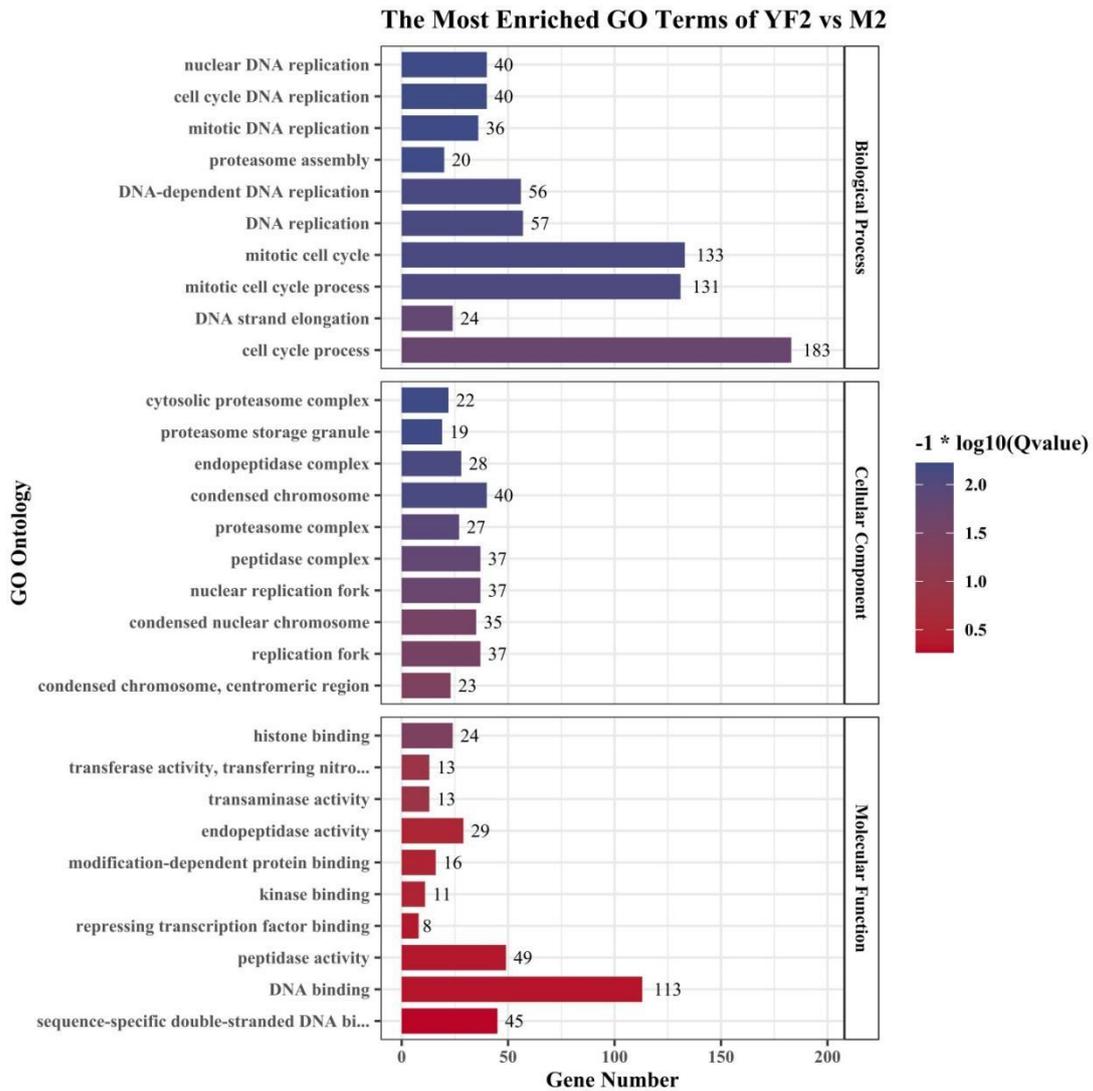
**Figure S14.** KEGG enrichment analysis of the differentially expressed genes (DEGs) between the primordia formation stage of *F. filiformis* Y33-J1 (P2) and the primordia formation stage of *F. filiformis* J1-Y33 (P1) is presented. The x-axis of the figure displays the rich factor, while the y-axis reflects the KEGG pathway. The count indicates the number of DEGs enriched in the pathway, and the color implies the  $-\text{Log}_{10}(\text{Q-value})$  of each pathway.



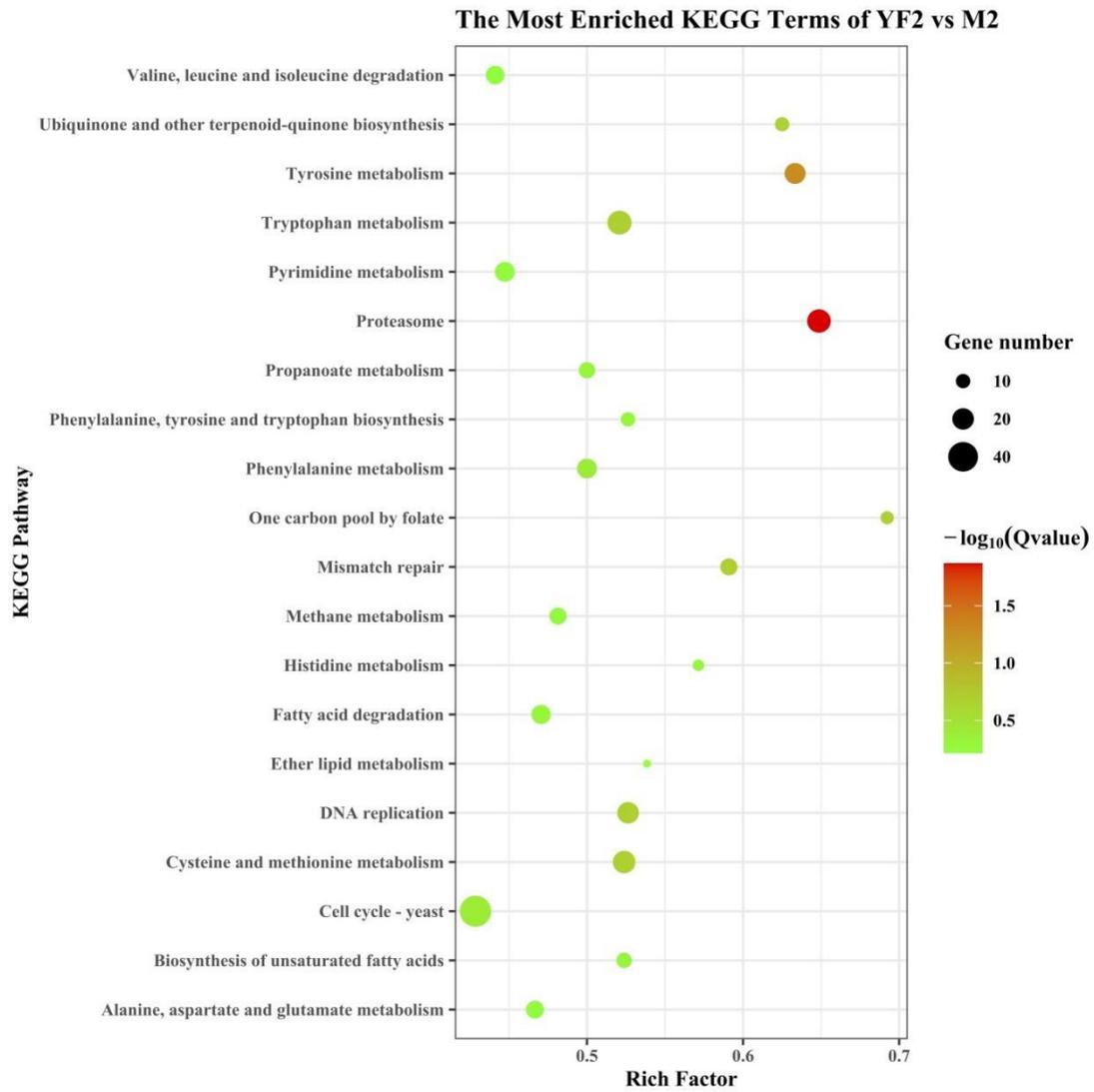
**Figure S15.** The Gene Ontology (GO) enrichment analysis of the differentially expressed genes (DEGs) between the young mushroom stage of *F. filiformis* J1-Y33 (YF1) and the mycelium growth stage of *F. filiformis* J1-Y33 (M1) was conducted. The results were summarized in three main GO categories, namely Biological Process, Cellular Component and Molecular Function. The x-axis denoted the number of differentially expressed genes annotated in the GO category, while the y-axis indicated the GO term. The color of each GO category represented the  $-\log_{10}(Q\text{-value})$ . This value is a measure of the statistical significance of the GO term which is used to investigate the biological relevance of the DEGs.



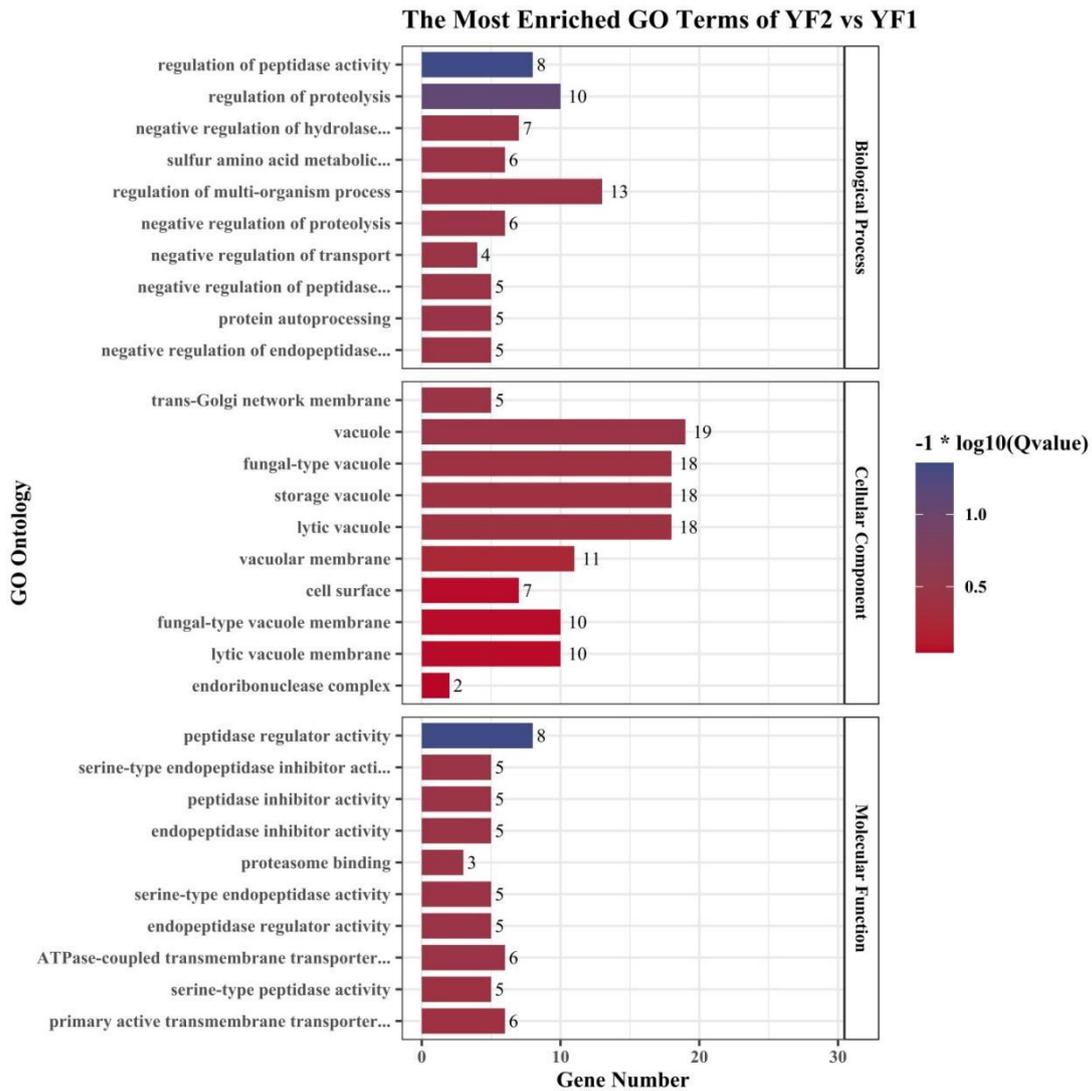
**Figure S16.** KEGG enrichment analysis of the differentially expressed genes (DEGs) between the young mushroom stage of *F. filiformis* J1-Y33 (YF1) and the mycelium growth stage of *F. filiformis* J1-Y33 (M1) is presented. The x-axis of the figure displays the rich factor, while the y-axis reflects the KEGG pathway. The count indicates the number of DEGs enriched in the pathway, and the color implies the  $-\text{Log}_{10}(Q\text{-value})$  of each pathway.



**Figure S17.** The Gene Ontology (GO) enrichment analysis of the differentially expressed genes (DEGs) between the young mushroom stage of *F. filiformis* Y33-J1 (YF2) and the mycelium growth stage of *F. filiformis* Y33-J1 (M2) was conducted. The results were summarized in three main GO categories, namely Biological Process, Cellular Component and Molecular Function. The x-axis denoted the number of differentially expressed genes annotated in the GO category, while the y-axis indicated the GO term. The color of each GO category represented the  $-\log_{10}(Q\text{-value})$ . This value is a measure of the statistical significance of the GO term which is used to investigate the biological relevance of the DEGs.

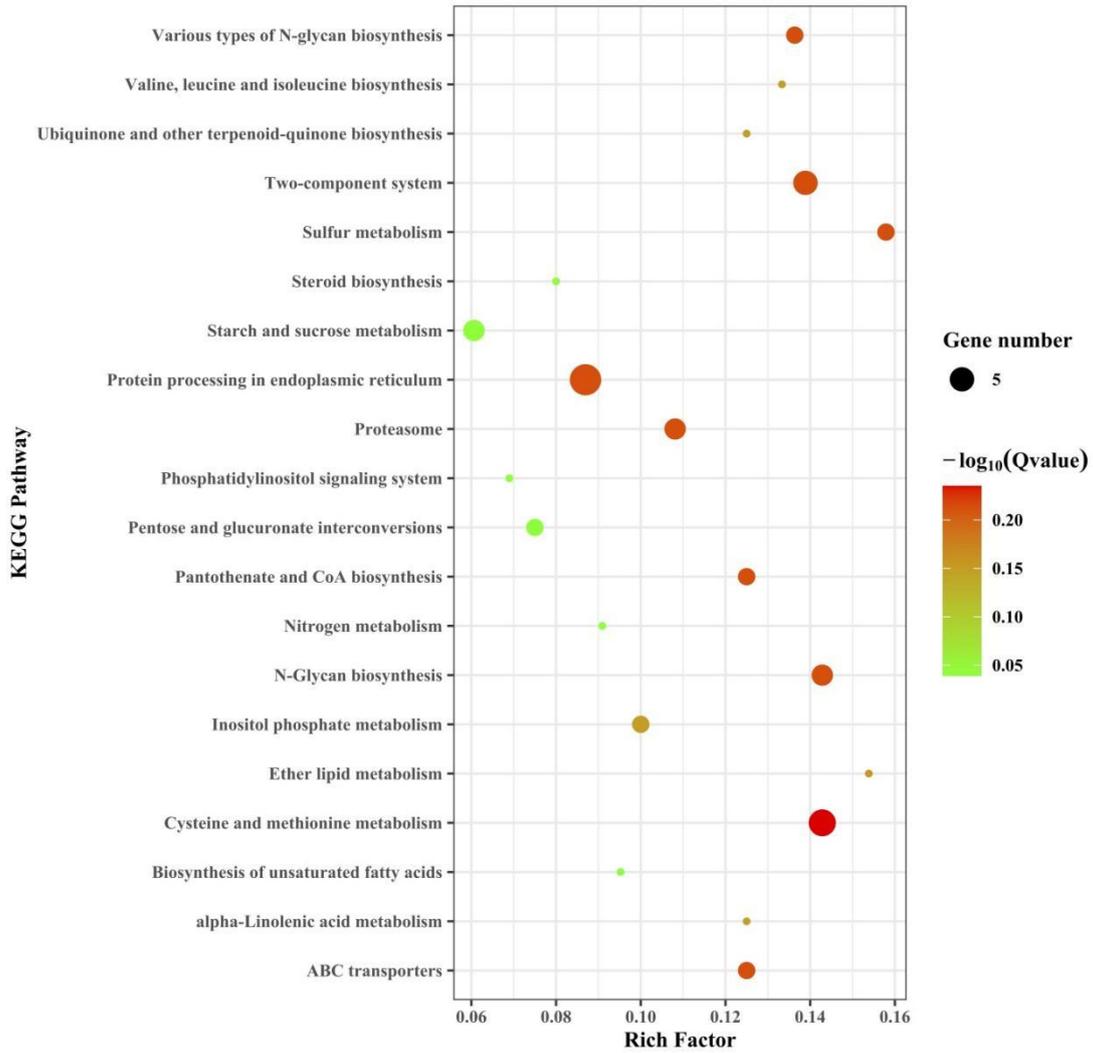


**Figure S18.** KEGG enrichment analysis of the differentially expressed genes (DEGs) between the young mushroom stage of *F. filiformis* Y33-J1 (YF2) and the mycelium growth stage of *F. filiformis* Y33-J1 (M2) is presented. The x-axis of the figure displays the rich factor, while the y-axis reflects the KEGG pathway. The count indicates the number of DEGs enriched in the pathway, and the color implies the  $-\log_{10}(Q\text{-value})$  of each pathway.



**Figure S19.** The Gene Ontology (GO) enrichment analysis of the differentially expressed genes (DEGs) between the young mushroom stage of *F. filiformis* Y33-J1 (YF2) and the young mushroom stage of *F. filiformis* J1-Y33 (YF1) was conducted. The results were summarized in three main GO categories, namely Biological Process, Cellular Component and Molecular Function. The x-axis denoted the number of differentially expressed genes annotated in the GO category, while the y-axis indicated the GO term. The color of each GO category represented the  $-\log_{10}(Q\text{-value})$ . This value is a measure of the statistical significance of the GO term which is used to investigate the biological relevance of the DEGs.

### The Most Enriched KEGG Terms of YF2 vs YF1



**Figure S20.** KEGG enrichment analysis of the differentially expressed genes (DEGs) between the young mushroom stage of *F. filiformis* Y33-J1 (YF2) and the young mushroom stage of *F. filiformis* J1-Y33 (YF1) is presented. The x-axis of the figure displays the rich factor, while the y-axis reflects the KEGG pathway. The count indicates the number of DEGs enriched in the pathway, and the color implies the  $-\text{Log}_{10}(\text{Q-value})$  of each pathway.