

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	CTTCGATATCCACCCGACG
	GB009214-R	ACGACAGTGGTAACGCCATT
GB009768	GB009768-F	TATCCCCGCTTTCCTACCGC
	GB009768-R	CCTTTCATCCGCCTTGAGT
GB006100	GB006100-F	CGCTTCGCAAGACGTACAAG
	GB006100-R	TGGTTCGTAGAAACCCAGCC
GB004373	GB004373-F	TCGGTATCGCCGCTTTAGTC

	GB004373-R	CTCTTGCGTGGGAGTCAAGT
GB006766	GB006766-F	AACCAAACATTTGCGGCACA
	GB006766-R	GAGGTACTCGTATTGCGGGG
GB005431	GB005431-F	TACAGACGTTGAAGGGTGCC
	GB005431-R	AGAGGGTTGGATGAGCAAGC
GB001767	GB001767-F	GAGGCAACATCAACGAAGGC
	GB001767-R	ACAAAATCGCACCCCTTTGCC
GB005682	GB005682-F	GCTTCCCGAGAGTACGGATG
	GB005682-R	GACCGAAAAGGGACGGAAC
GB006651	GB006651-F	TGACACGGAAGGAAAGCCTC
	GB006651-R	CTTGTTGGTGCTCGAGTCCT

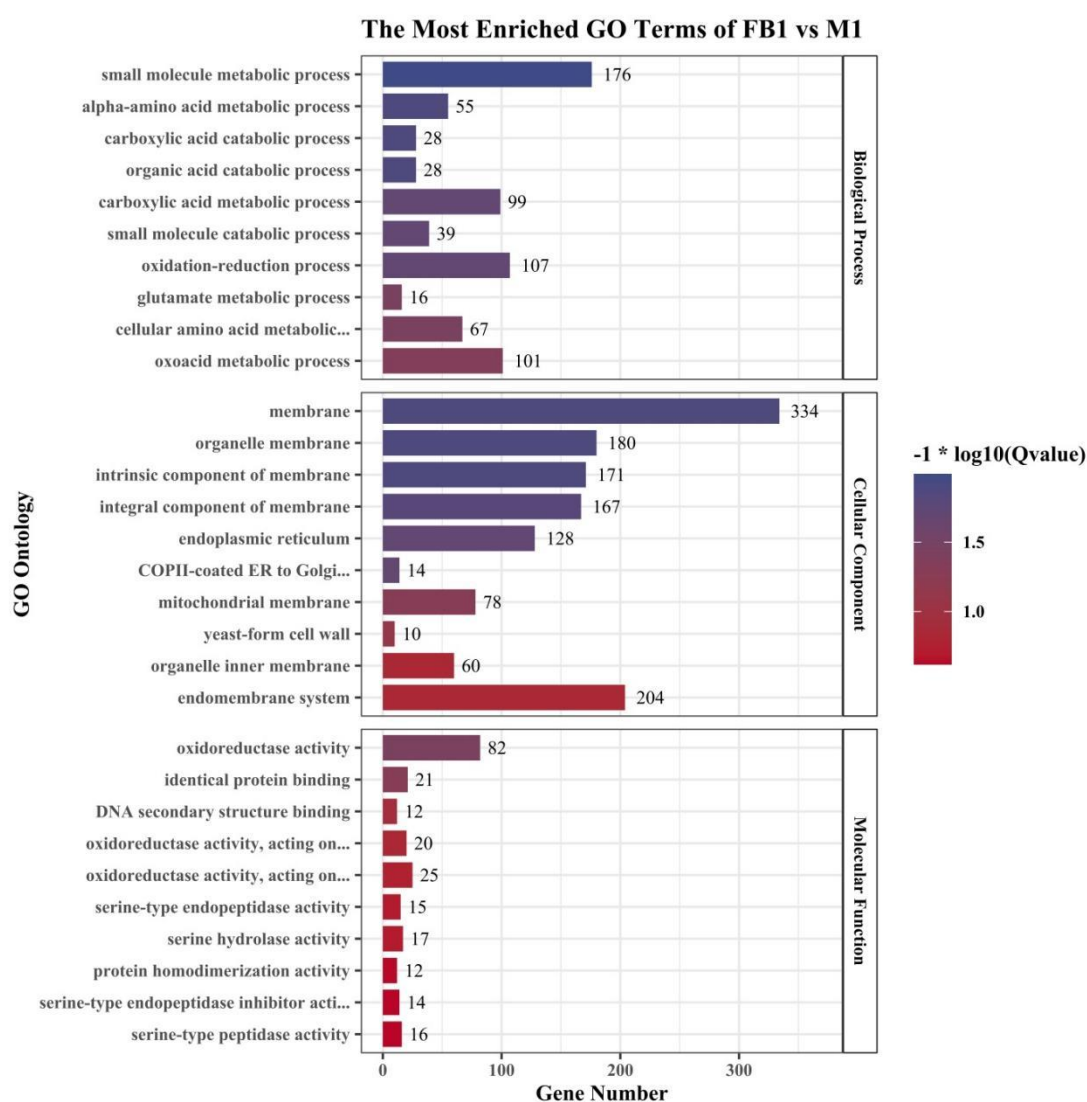


Figure S1. The Gene Ontology (GO) enrichment analysis of the differentially expressed genes (DEGs) between the fruiting body stage of *F. filiformis* J1-Y33 (FB1) and the mycelium growth stage of *F. filiformis* J1-Y33 (M1) was conducted. The results were summarized in three main GO categories, namely 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.

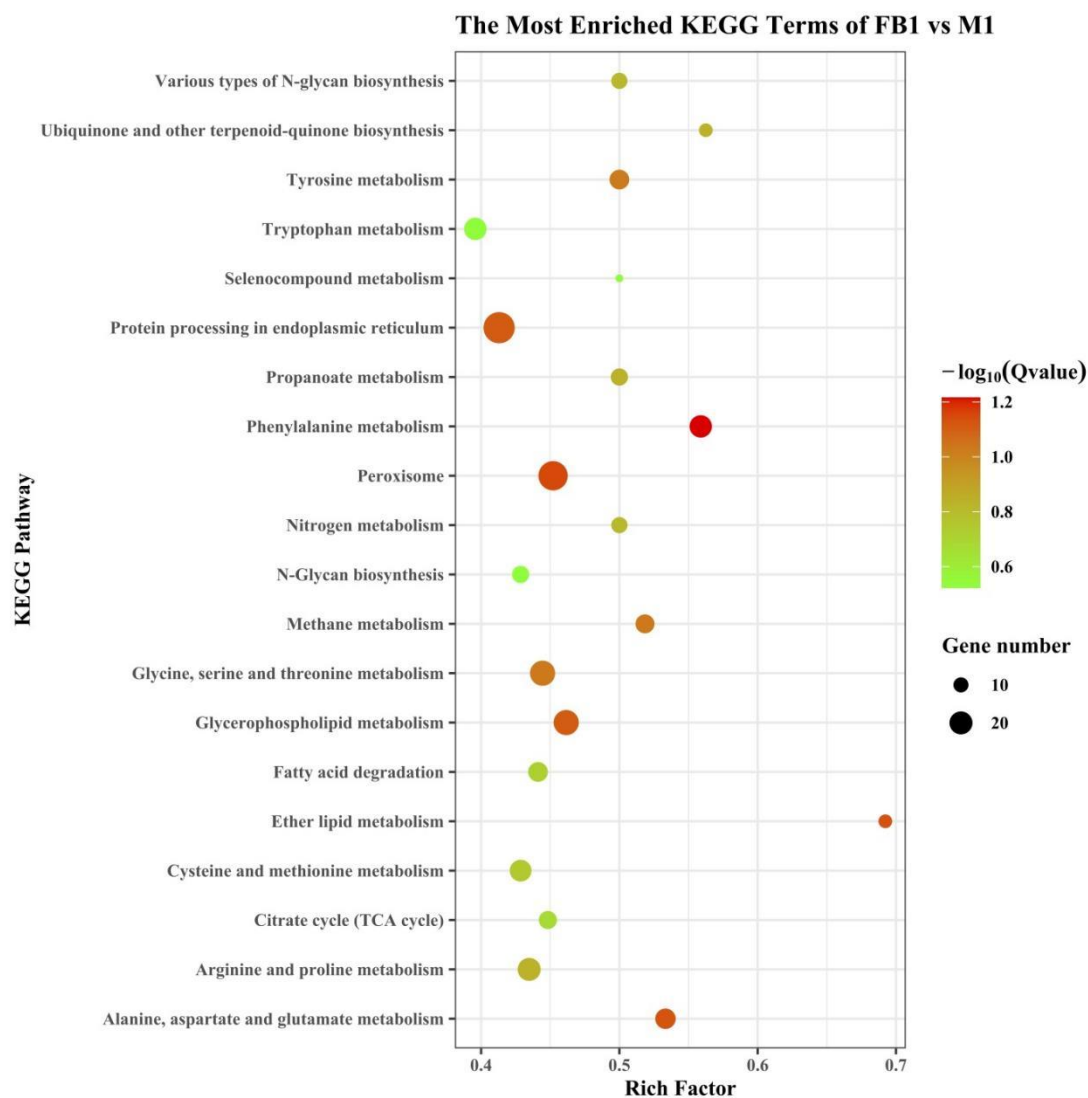


Figure S2. KEGG enrichment analysis of the differentially expressed genes (DEGs) between the fruiting body stage of *F. filiformis* J1-Y33 (FB1) and the mycelium growth stage of *F. filiformis* J1-Y33 (M1) is presented. The x-axis of the figure displays the rich factor, while the y-axis reflects the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

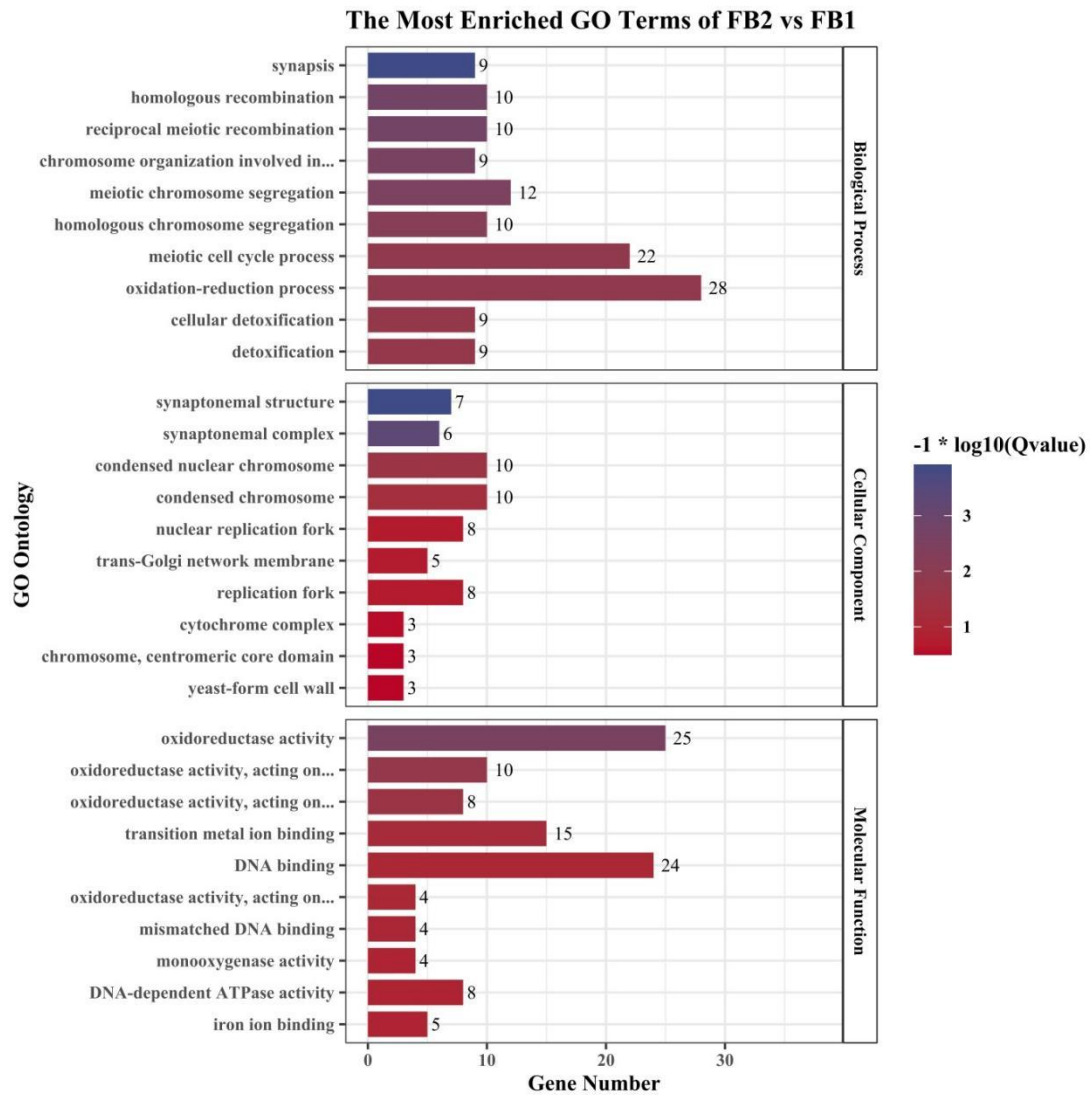


Figure S3. The Gene Ontology (GO) enrichment analysis of the differentially expressed genes (DEGs) between the fruiting body stage of *F. filiformis* Y33-J1 (FB2) and the fruiting body stage of *F. filiformis* J1-Y33 (FB1) was conducted. The results were summarized in three main GO categories, namely 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.

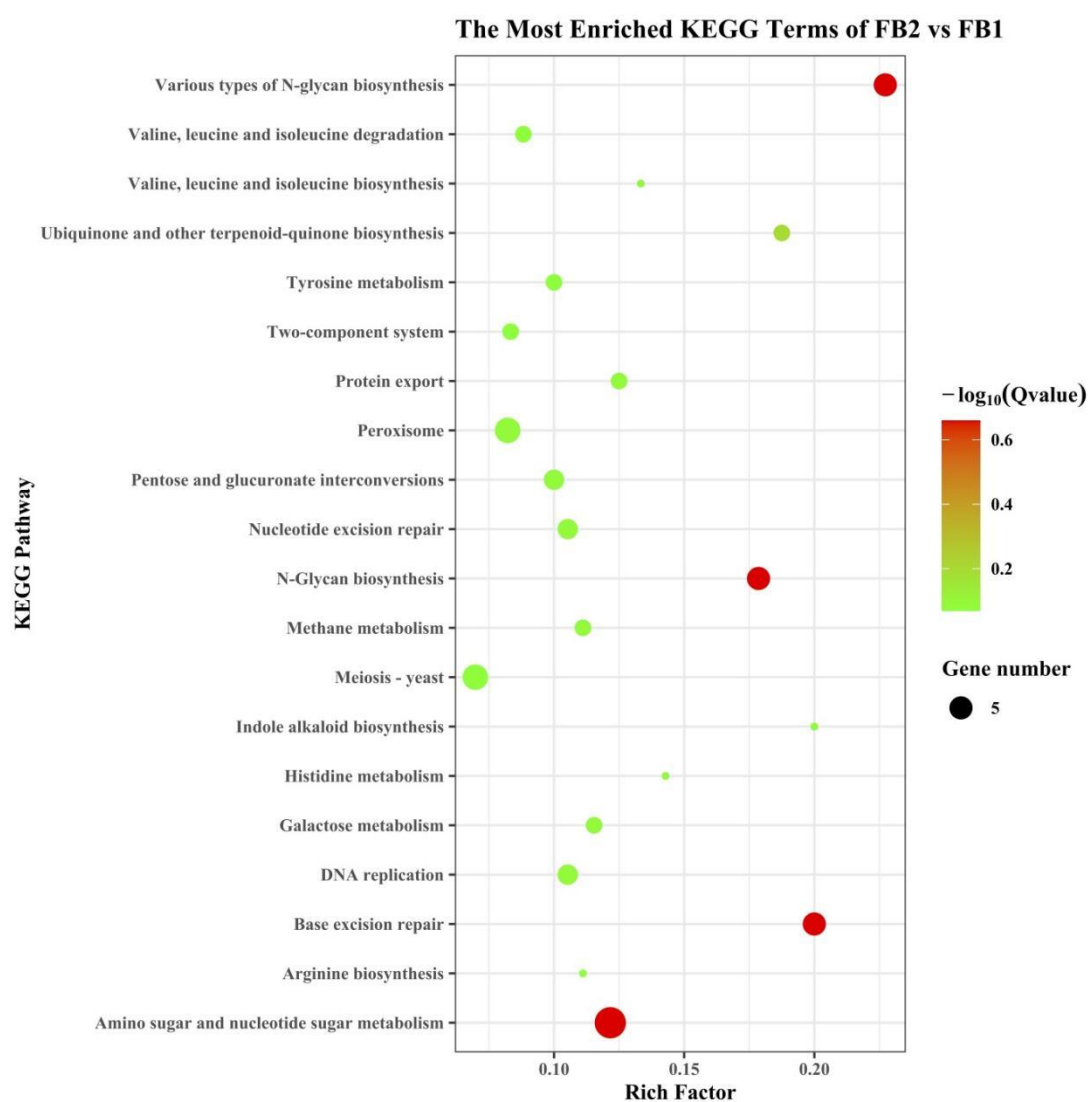


Figure S4. KEGG enrichment analysis of the differentially expressed genes (DEGs) between the fruiting body stage of *F. filiformis* Y33-J1 (FB2) and the fruiting body stage of *F. filiformis* J1-Y33 (FB1) is presented. The x-axis of the figure displays the rich factor, while the y-axis reflects the KEGG 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.

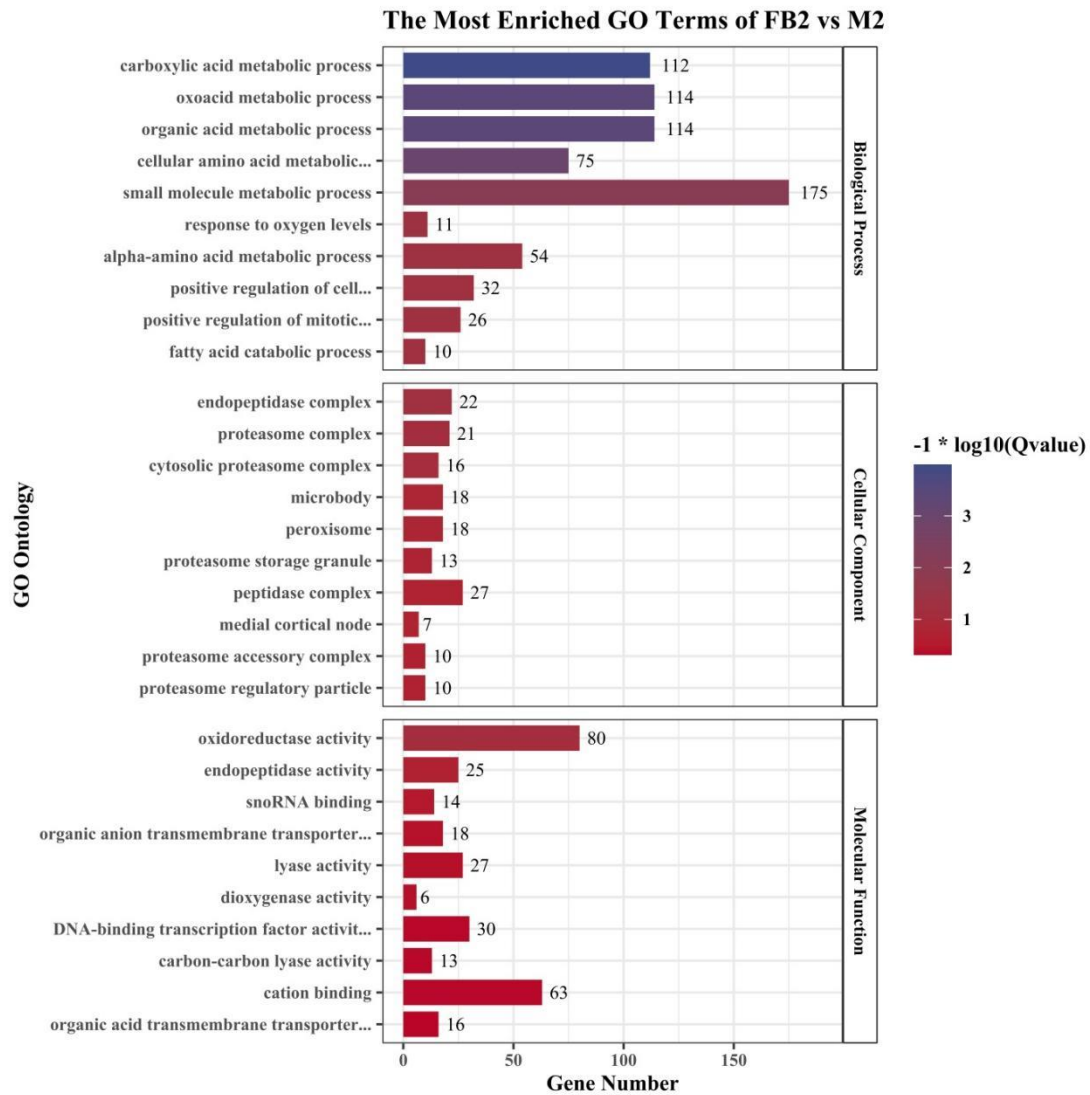


Figure S5. The Gene Ontology (GO) enrichment analysis of the differentially expressed genes (DEGs) between the fruiting body stage of *F. filiformis* Y33-J1 (FB2) and the mycelium growth stage of *F. filiformis* J1-Y33 (FB1) was conducted. The results were summarized in three main GO categories, namely 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.

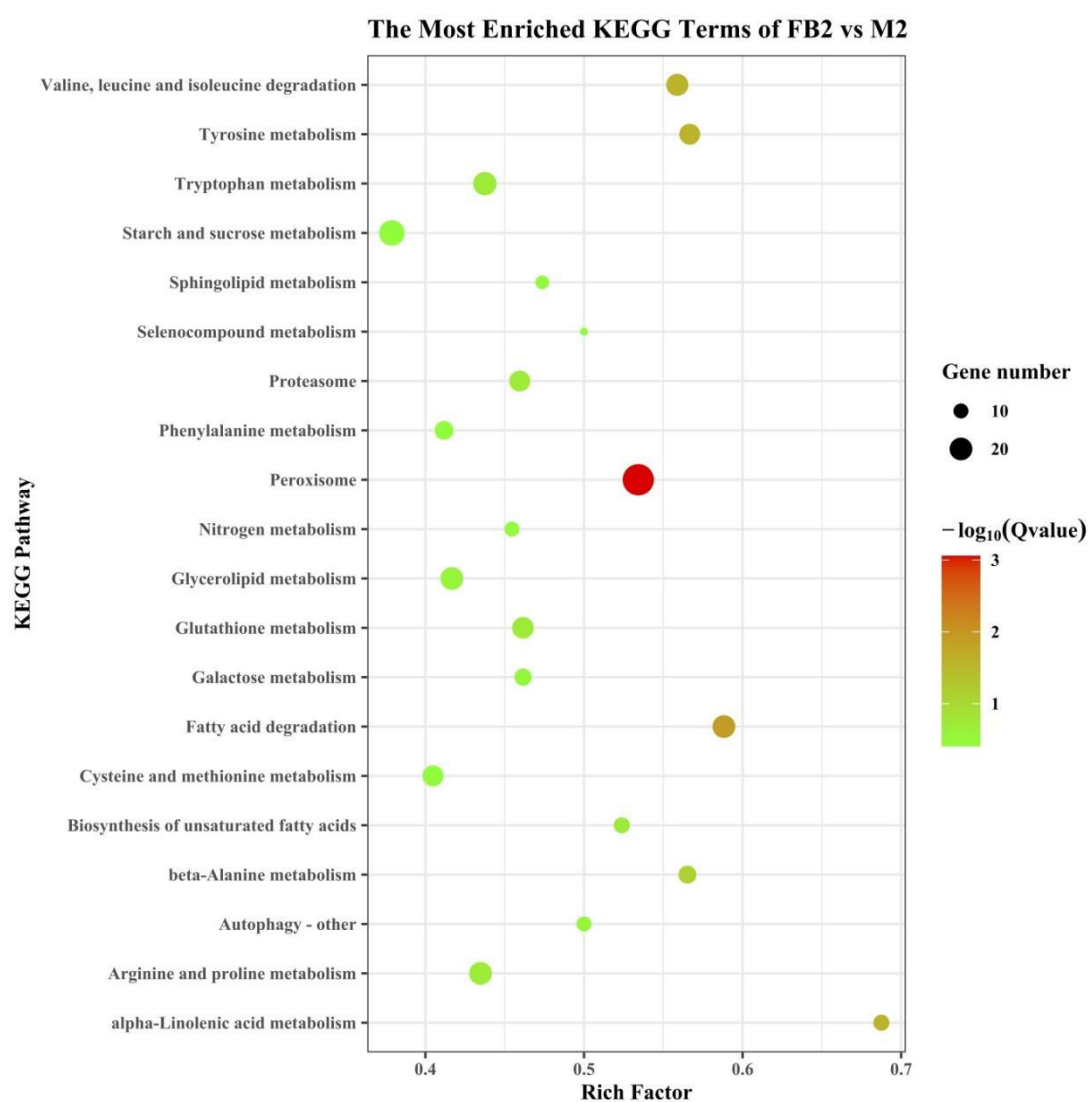


Figure S6. KEGG enrichment analysis of the differentially expressed genes (DEGs) between the fruiting body stage of *F. filiformis* Y33-J1 (FB2) and the mycelium growth stage of *F. filiformis* J1-Y33 (FB1) is presented. The x-axis of the figure displays the rich factor, while the y-axis reflects the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

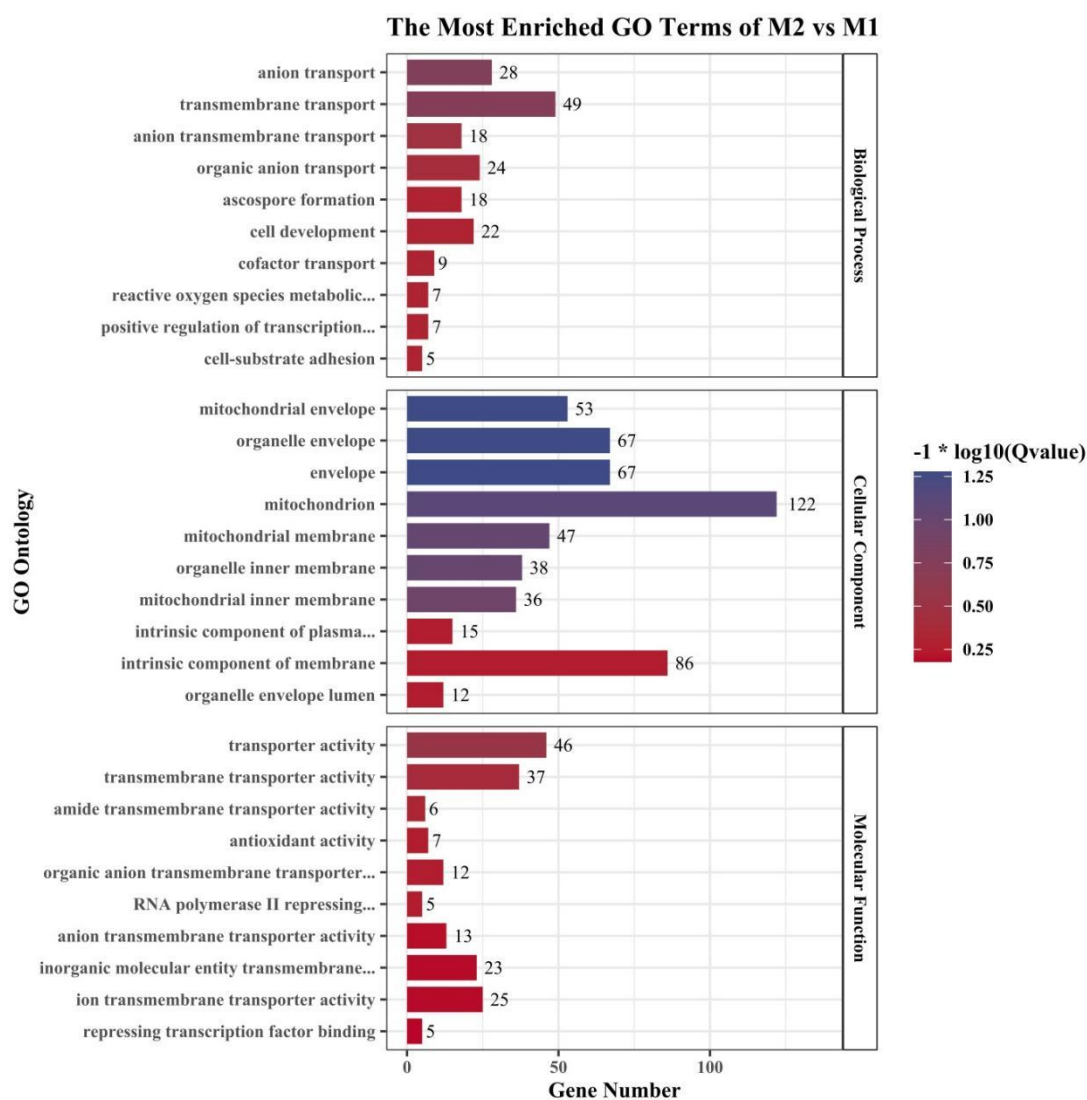


Figure S7. The Gene Ontology (GO) enrichment analysis of the differentially expressed genes (DEGs) between the mycelium growth stage of *F. filiformis* Y33-J1 (M2) and the mycelium growth stage of *F. filiformis* J1-Y33 (M1) was conducted. The results were summarized in three main GO categories, namely 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.

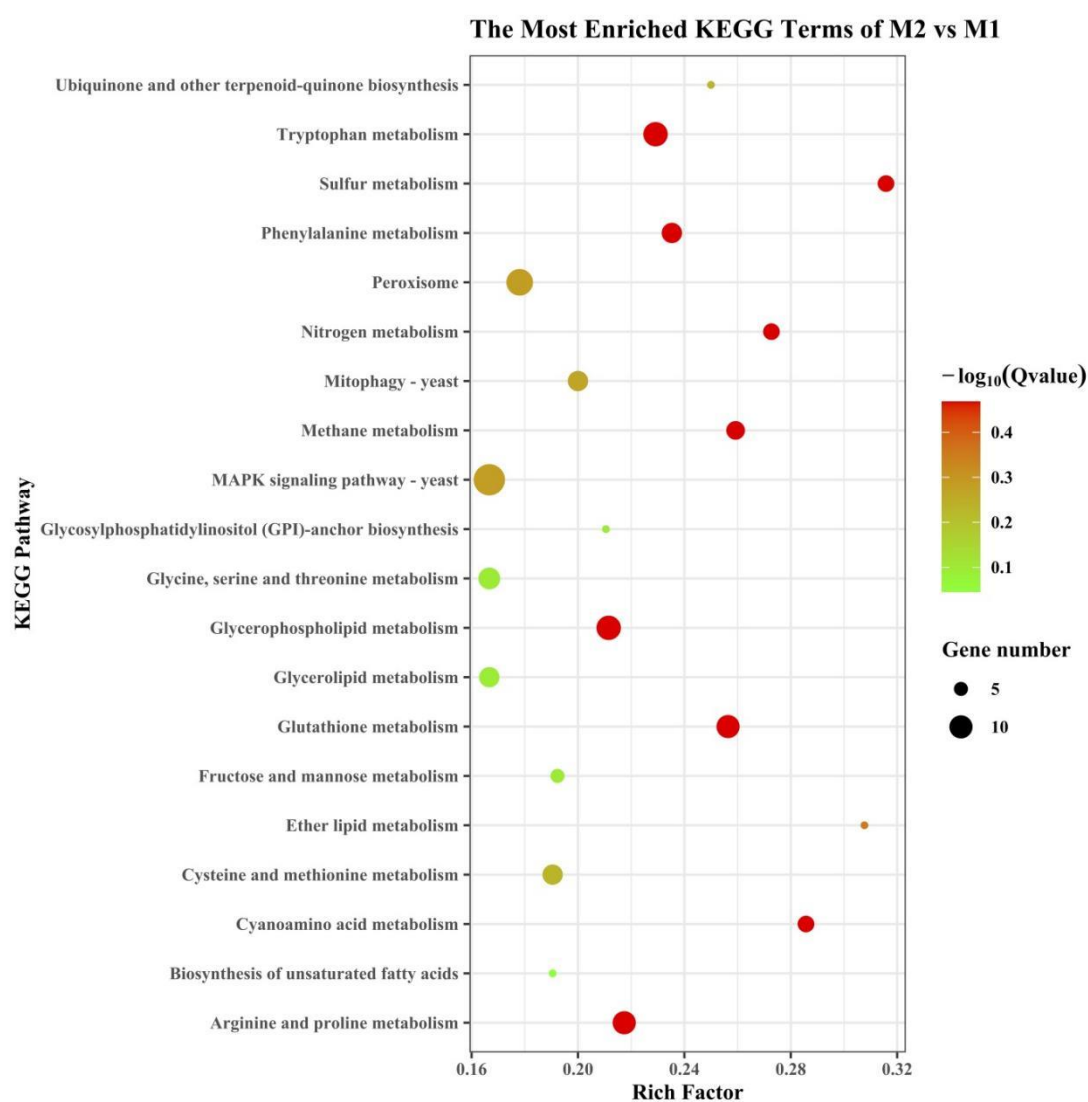


Figure S8. KEGG enrichment analysis of the differentially expressed genes (DEGs) between the mycelium growth stage of *F. filiformis* Y33-J1 (M2) and the mycelium growth stage of *F. filiformis* J1-Y33 (M1) is presented. The x-axis of the figure displays the rich factor, while the y-axis reflects the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

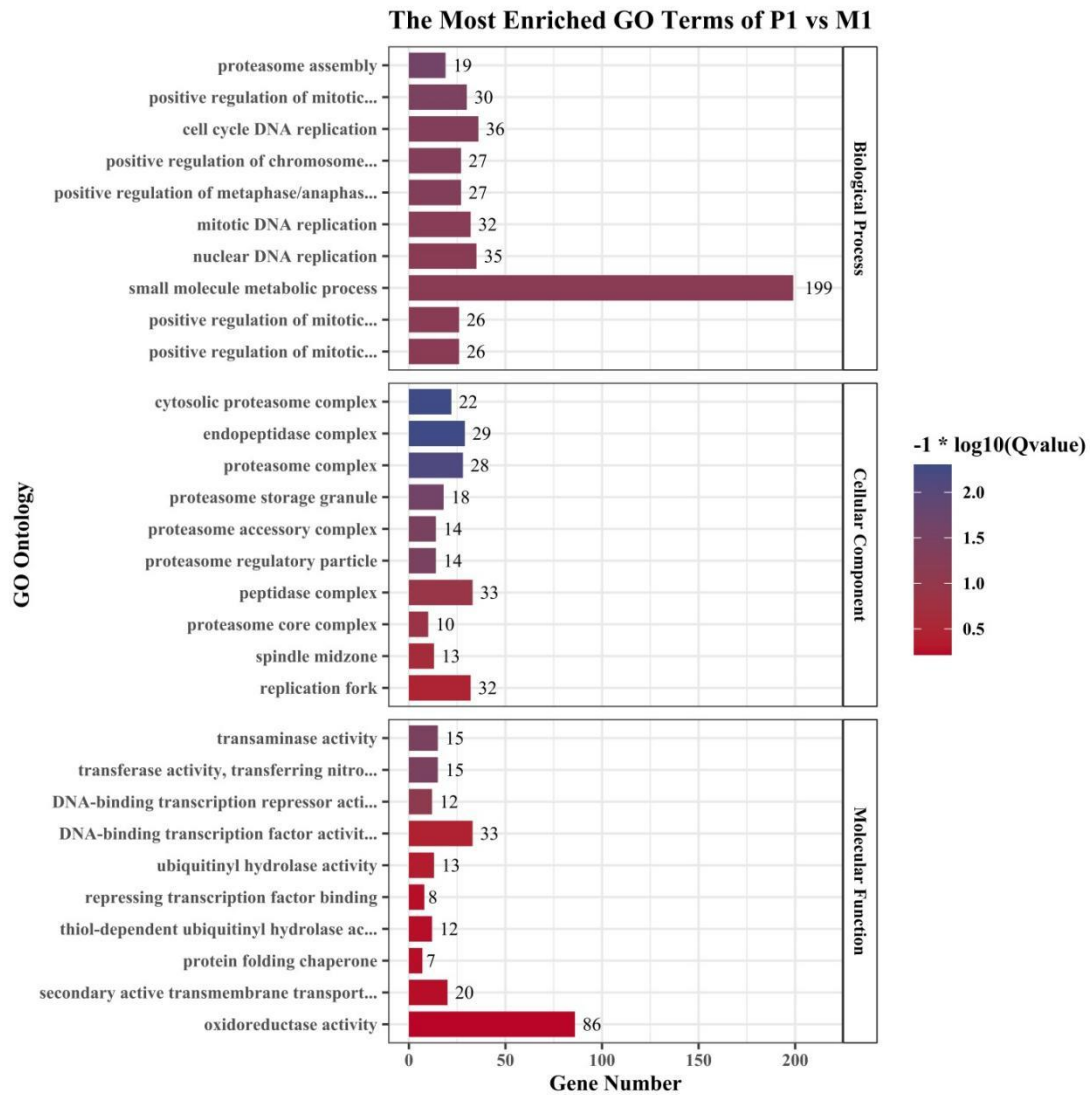


Figure S9. The Gene Ontology (GO) enrichment analysis of the differentially expressed genes (DEGs) between the primordia formation stage of *F. filiformis* J1-Y33 (P1) and the mycelium growth stage of *F. filiformis* J1-Y33 (M1) was conducted. The results were summarized in three main GO categories, 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.

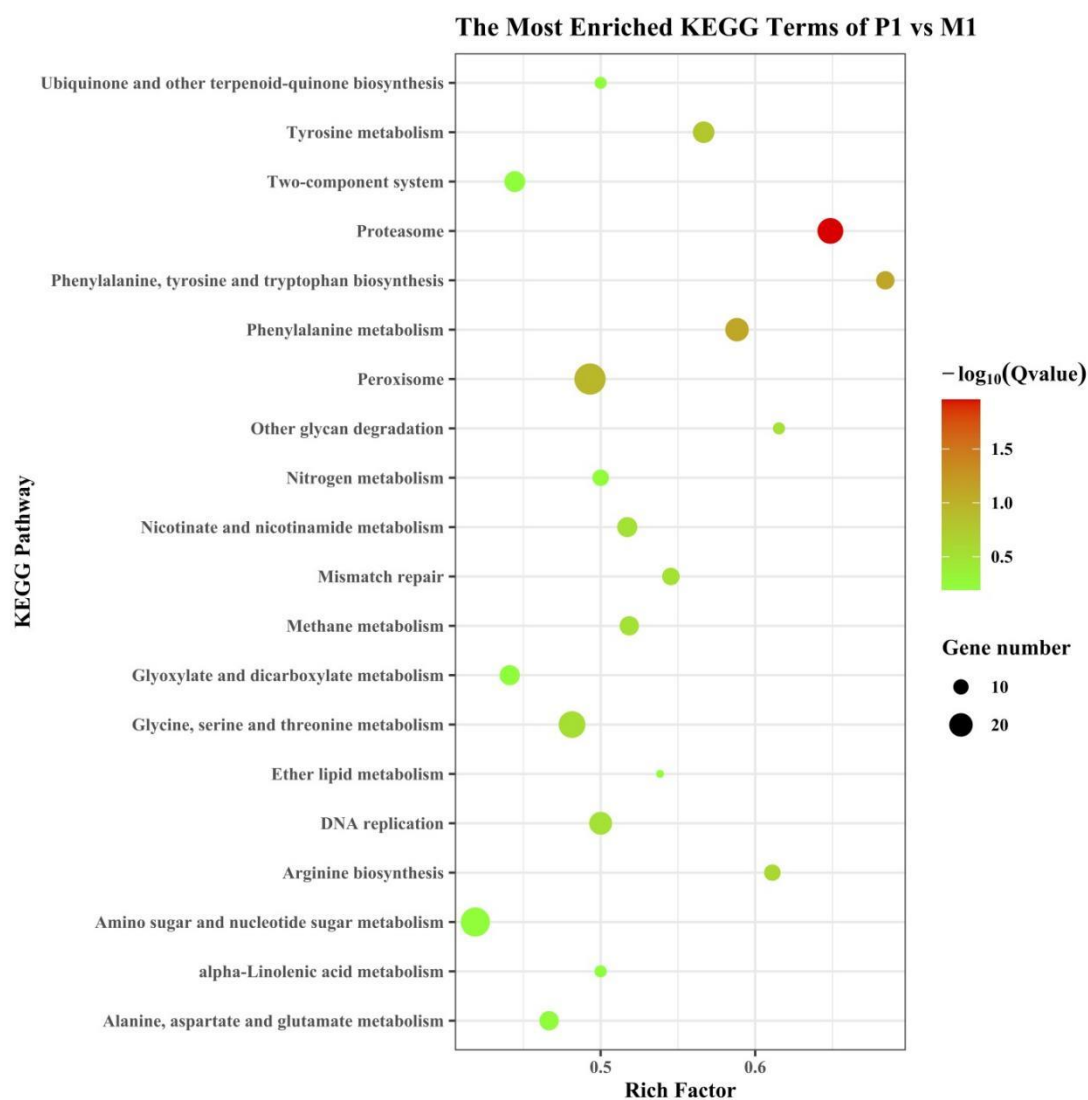


Figure S10. KEGG enrichment analysis of the differentially expressed genes (DEGs) between the primordia formation stage of *F. filiformis* J1-Y33 (P1) and the mycelium growth stage of *F. filiformis* J1-Y33 (M1) is presented. The x-axis of the figure displays the rich factor, while the y-axis reflects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

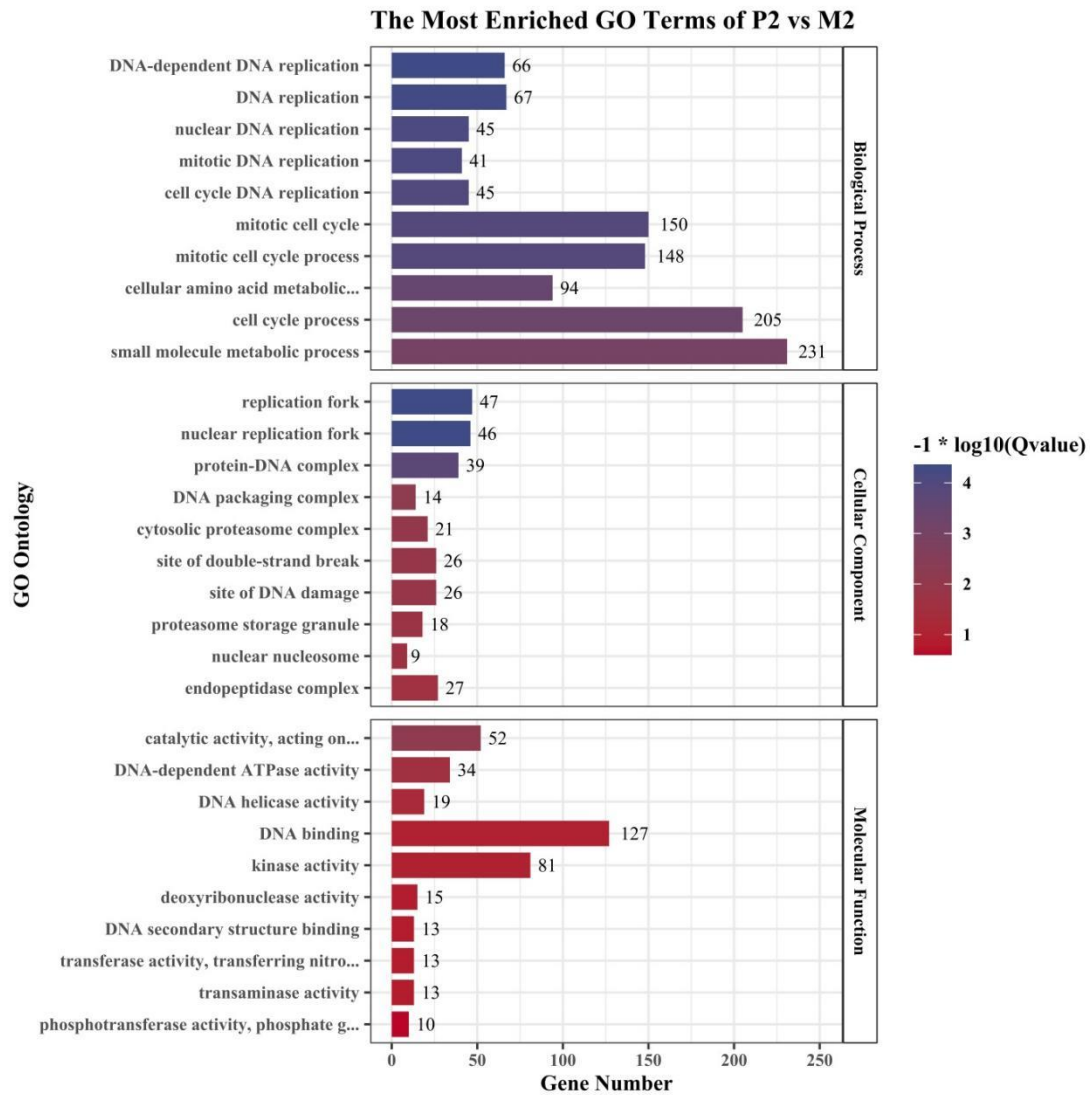


Figure S11. The Gene Ontology (GO) enrichment analysis of the differentially expressed genes (DEGs) between the primordia formation stage of *F. filiformis* Y33-J1 (P2) and the mycelium growth stage of *F. filiformis* Y33-J1 (M2) was conducted. The results were summarized in three main GO categories, 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 $-\log_{10}(\text{Q-value})$. This value is a measure of the statistical significance of the GO term which is used to investigate the biological relevance of the DEGs.

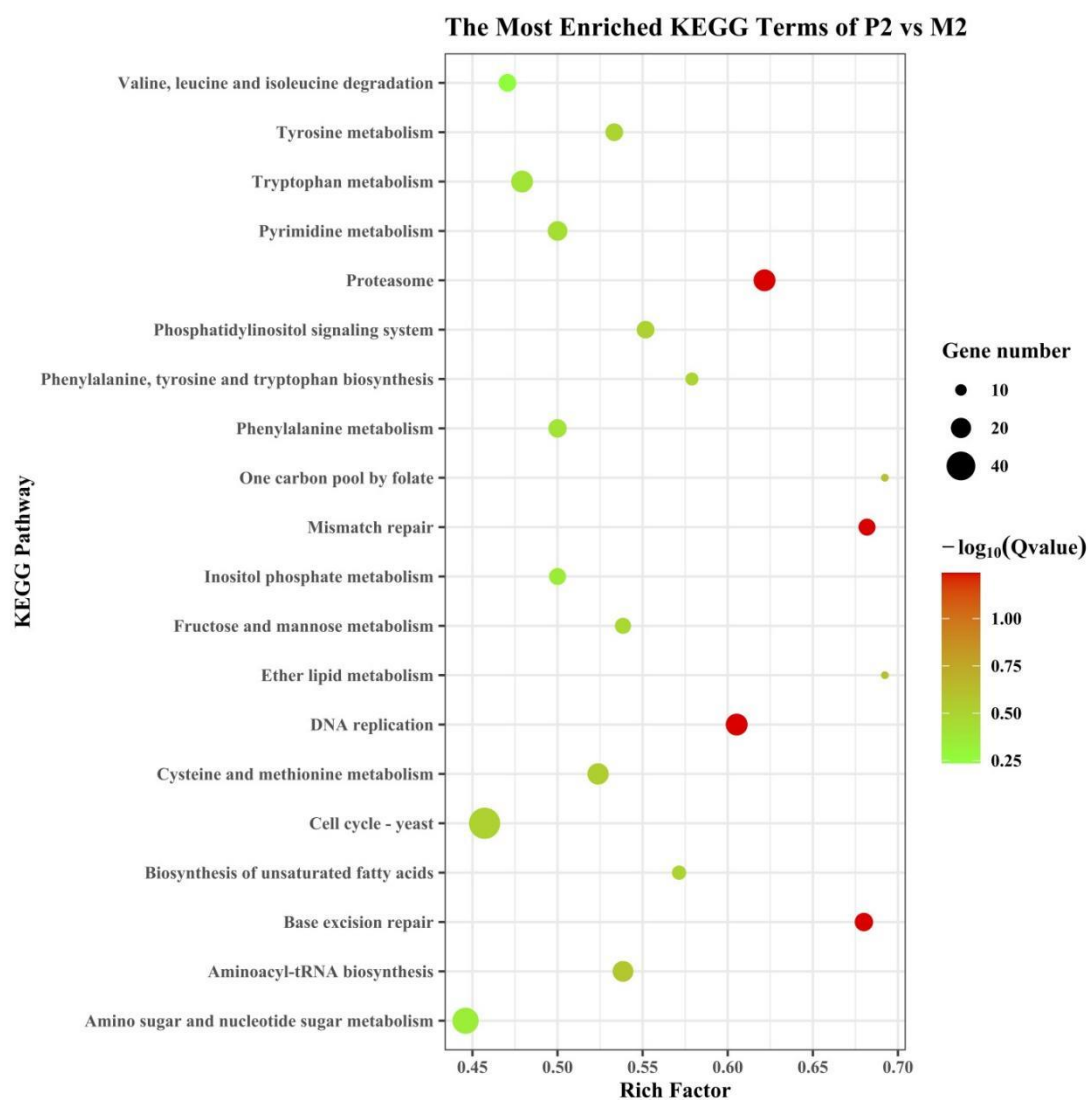


Figure S12. KEGG enrichment analysis of the differentially expressed genes (DEGs) between the primordia formation stage of *F. filiformis* Y33-J1 (P2) and the mycelium growth stage of *F. filiformis* Y33-J1 (M2) is presented. The x-axis of the figure displays the rich factor, while the y-axis reflects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

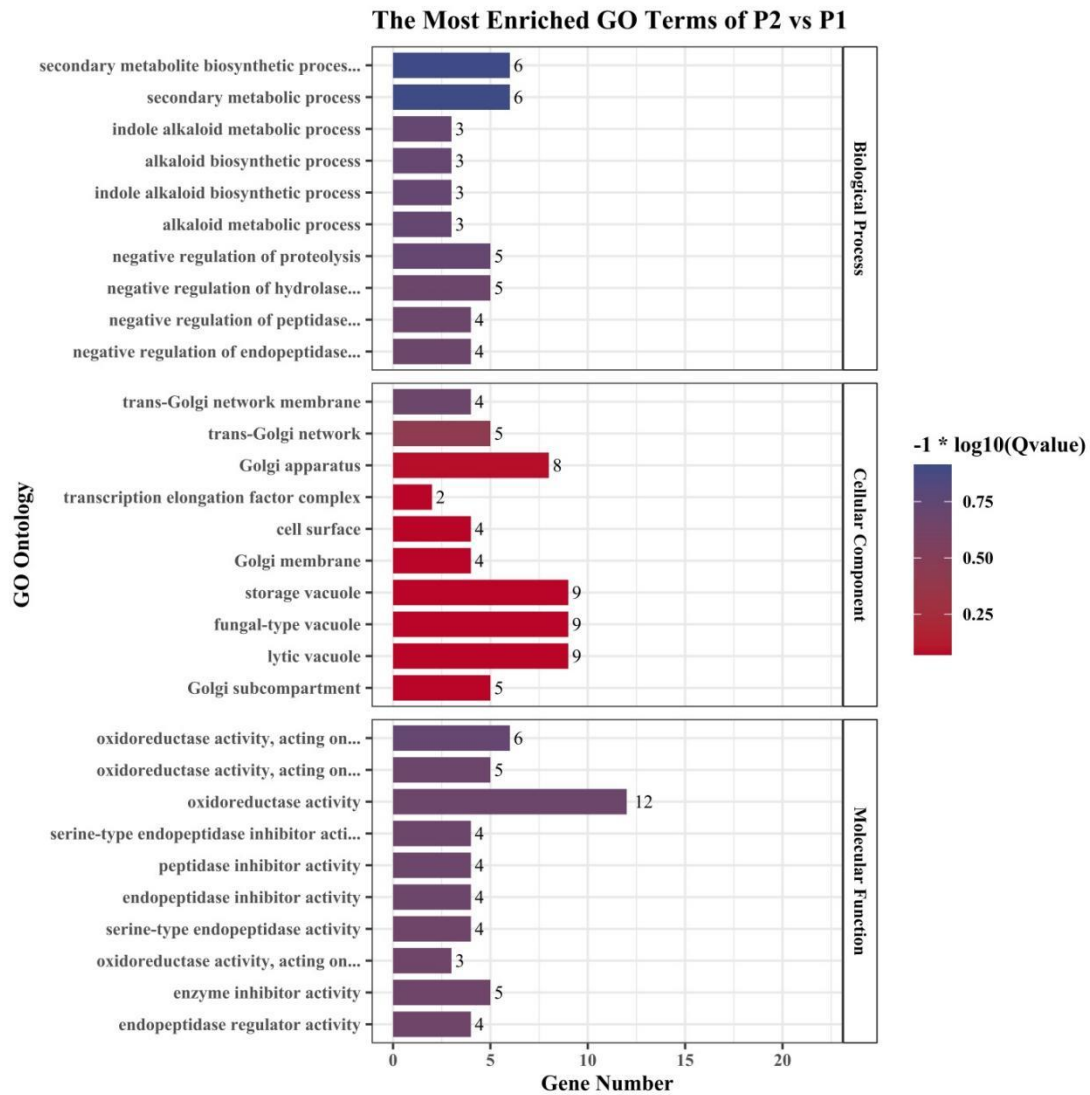


Figure S13. The Gene Ontology (GO) enrichment analysis of the differentially expressed genes (DEGs) between the primordia formation stage of *F. filiformis* Y33-J1 (P2) and the primordia formation stage of *F. filiformis* J1-Y33 (P1) was conducted. The results were summarized in three main GO categories, 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.

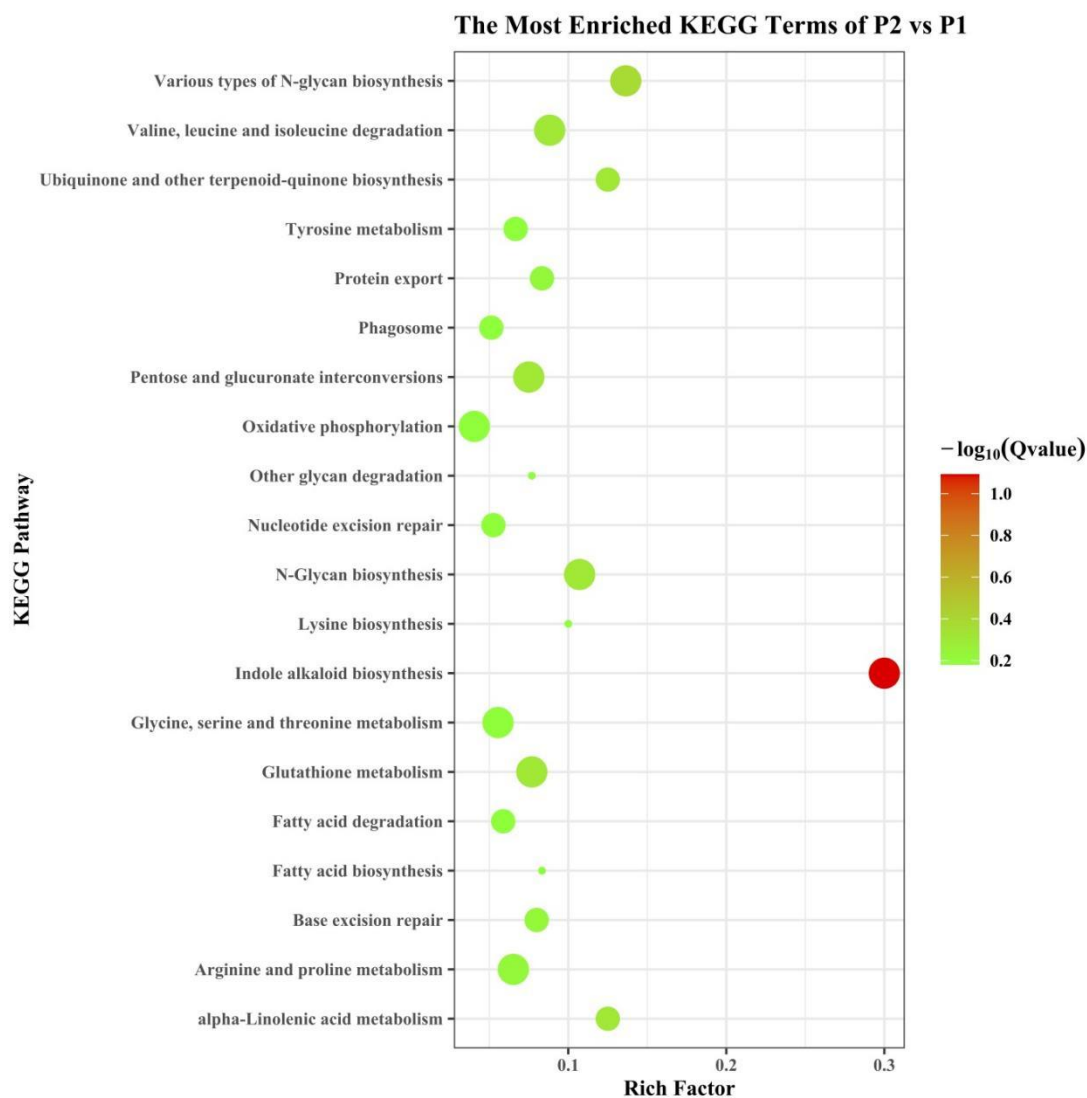


Figure S14. KEGG enrichment analysis of the differentially expressed genes (DEGs) between the primordia formation stage of *F. filiformis* Y33-J1 (P2) and the primordia formation stage of *F. filiformis* J1-Y33 (P1) is presented. The x-axis of the figure displays the rich factor, while the y-axis reflects 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.

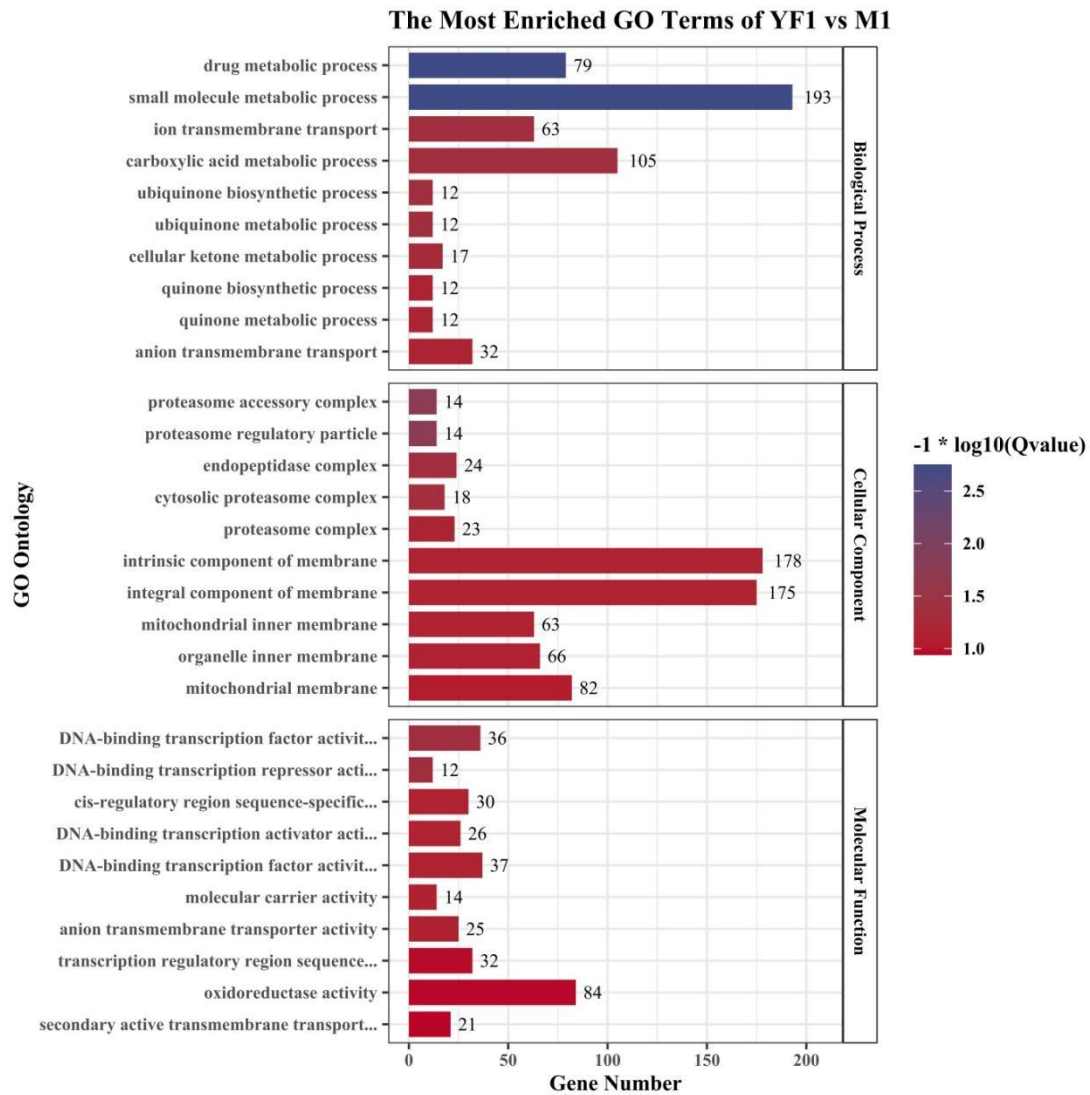


Figure S15. The Gene Ontology (GO) enrichment analysis of the differentially expressed genes (DEGs) between the young mushroom stage of *F. filiformis* J1-Y33 (YF1) and the mycelium growth stage of *F. filiformis* J1-Y33 (M1) was conducted. The results were summarized in three main GO categories, namely 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.

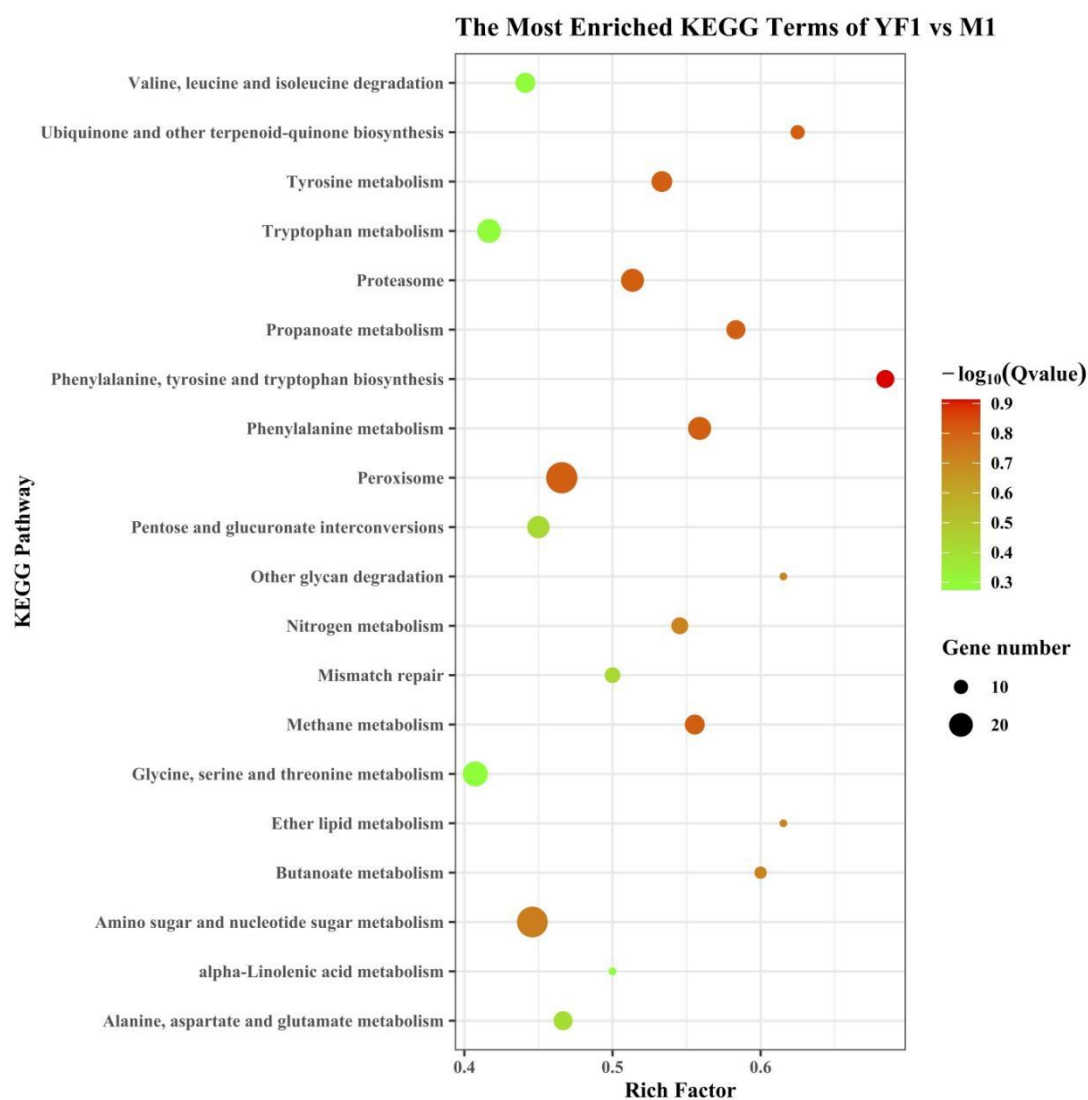


Figure S16. KEGG enrichment analysis of the differentially expressed genes (DEGs) between the young mushroom stage of *F. filiformis* J1-Y33 (YF1) and the mycelium growth stage of *F. filiformis* J1-Y33 (M1) is presented. The x-axis of the figure displays the rich factor, while the y-axis reflects the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

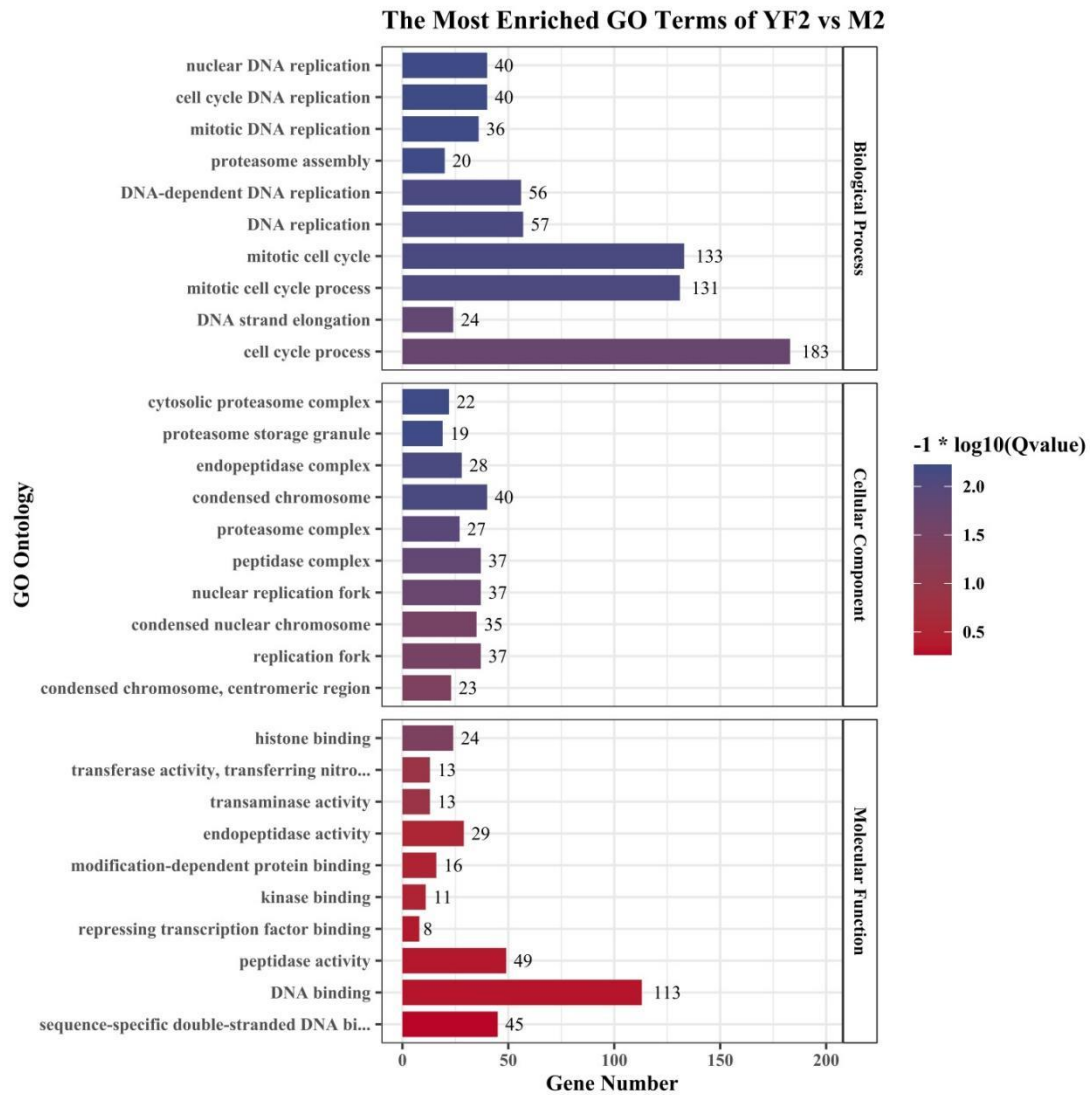


Figure S17. The Gene Ontology (GO) enrichment analysis of the differentially expressed genes (DEGs) between the young mushroom stage of *F. filiformis* Y33-J1 (YF2) and the mycelium growth stage of *F. filiformis* Y33-J1 (M2) was conducted. The results were summarized in three main GO categories, namely 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.

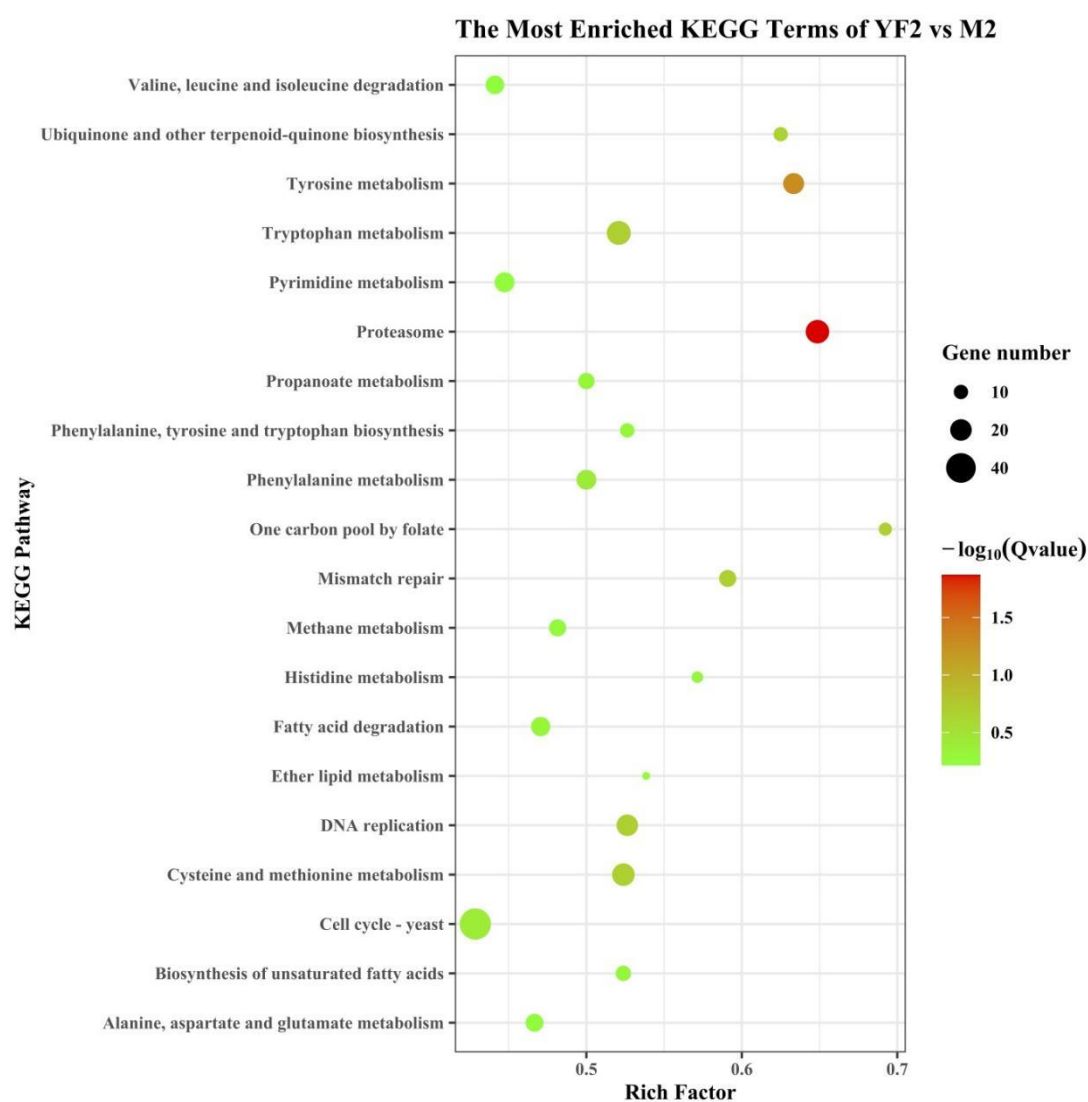


Figure S18. KEGG enrichment analysis of the differentially expressed genes (DEGs) between the young mushroom stage of *F. filiformis* Y33-J1 (YF2) and the mycelium growth stage of *F. filiformis* Y33-J1 (M2) is presented. The x-axis of the figure displays the rich factor, while the y-axis reflects the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

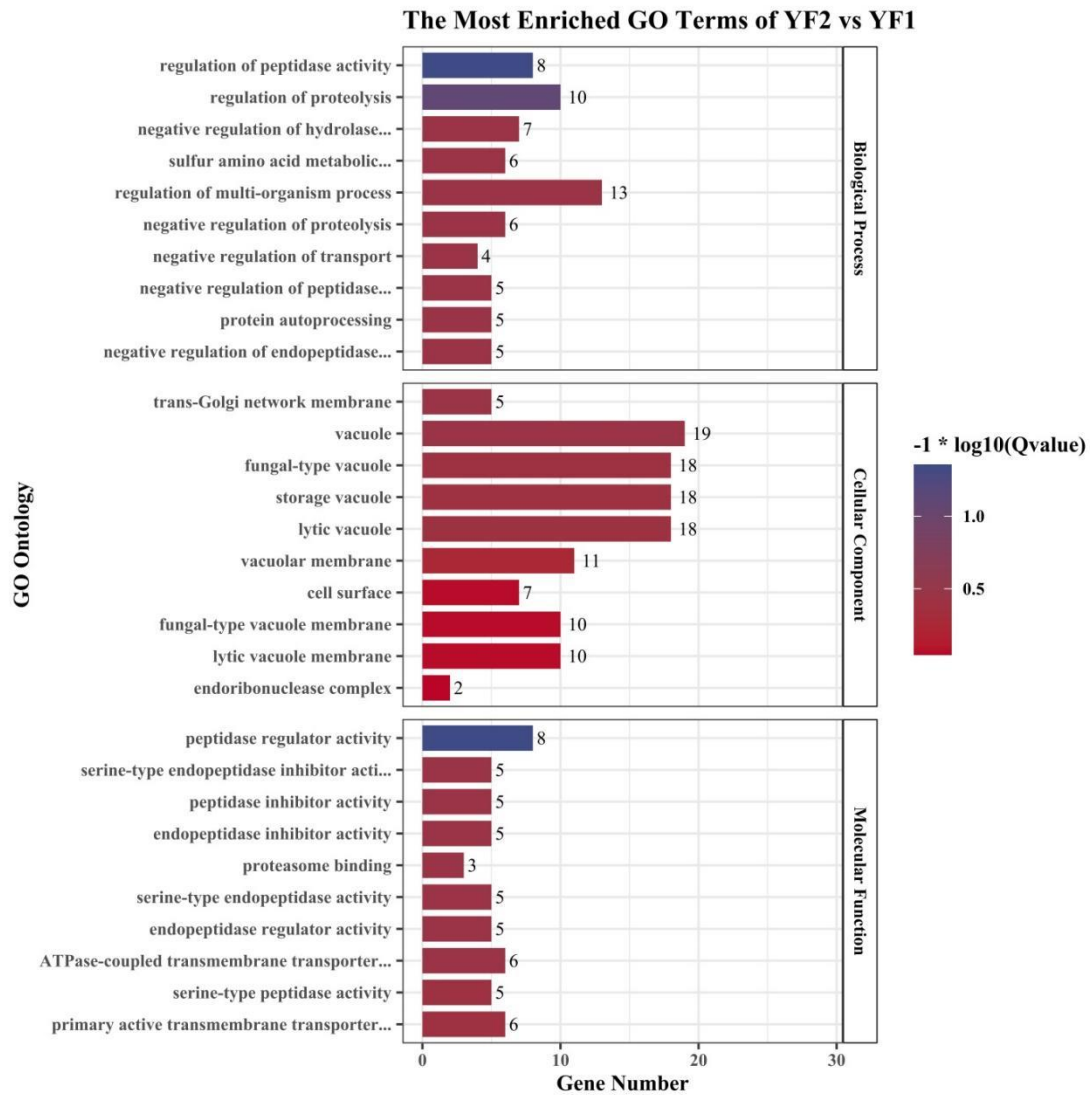


Figure S19. The Gene Ontology (GO) enrichment analysis of the differentially expressed genes (DEGs) between the young mushroom stage of *F. filiformis* Y33-J1 (YF2) and the young mushroom stage of *F. filiformis* J1-Y33 (YF1) was conducted. The results were summarized in three main GO categories, namely 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.

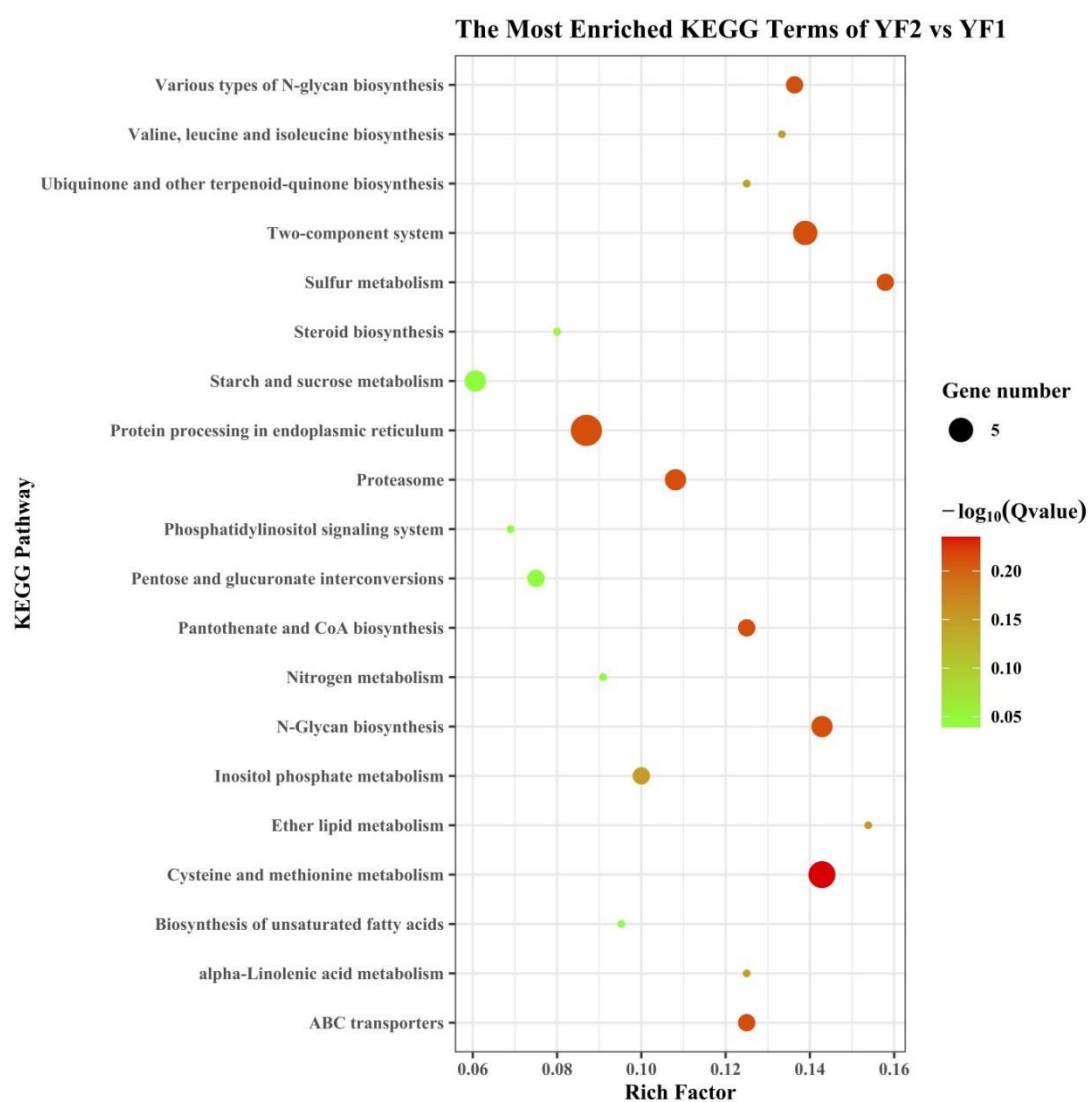


Figure S20. KEGG enrichment analysis of the differentially expressed genes (DEGs) between the young mushroom stage of *F. filiformis* Y33-J1 (YF2) and the young mushroom stage of *F. filiformis* J1-Y33 (YF1) is presented. The x-axis of the figure displays the rich factor, while the y-axis reflects the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