Article

Whole-Genome Resequencing and Evolutionary Analysis of Wild Morel Mushroom *Morchella* sp.

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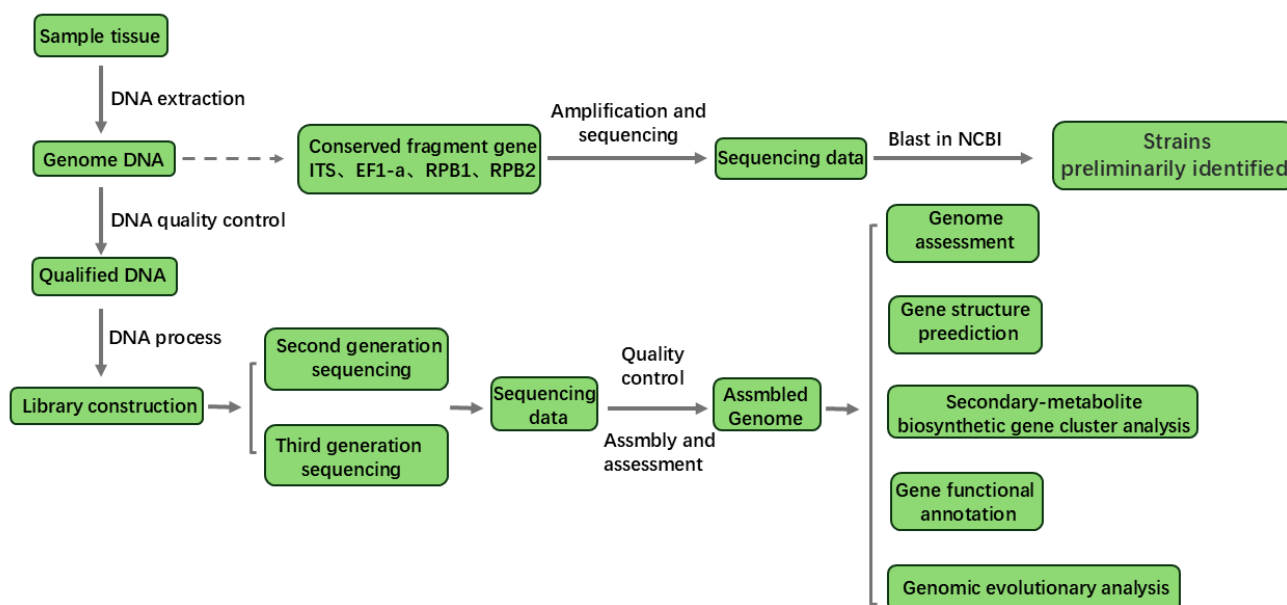
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Supplementary materials

Figures

Figure S1. The protocol of current study.

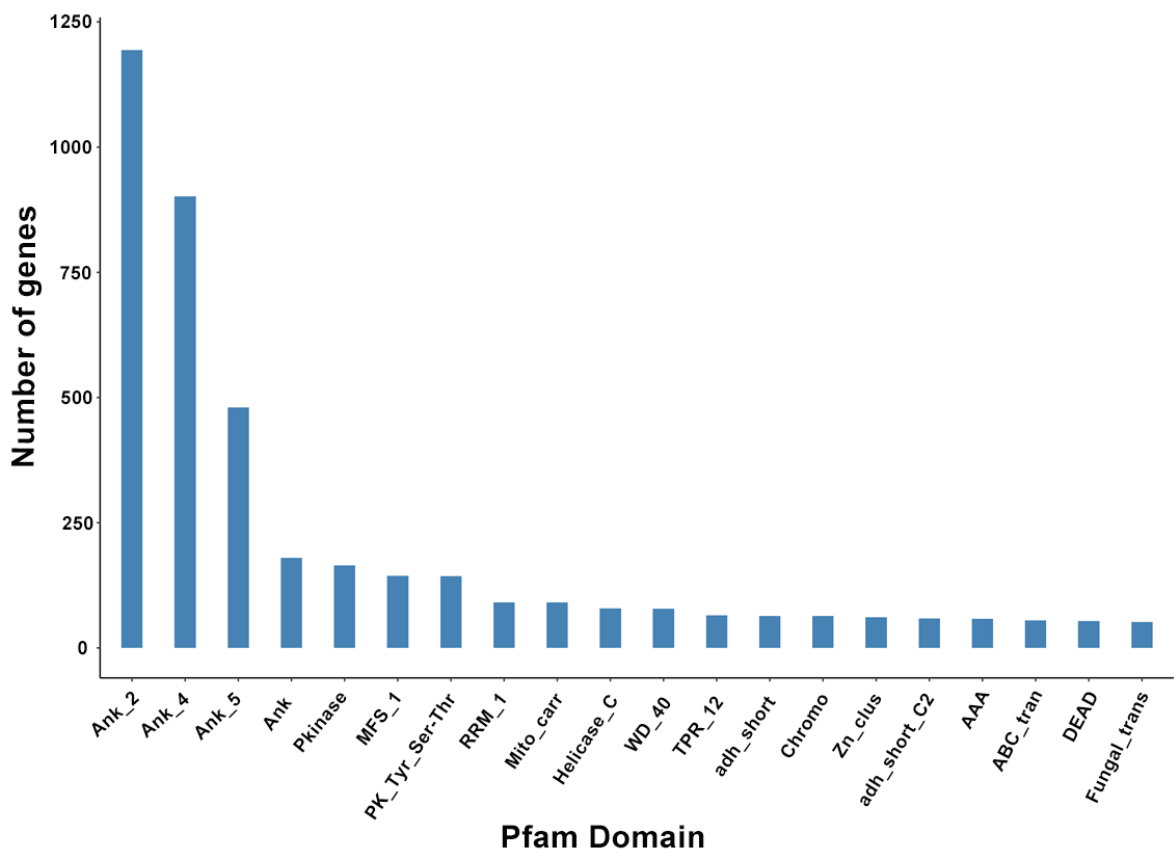**Figure S2.** The fruit body of wild morels *Morchella* sp. (*Mosp*).

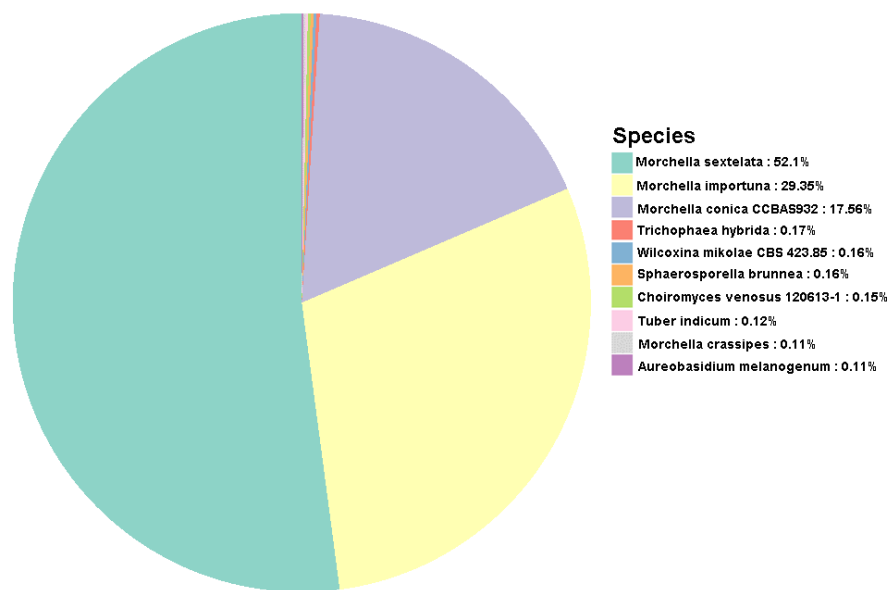**Figure S3.** The statistical histogram of gene functional annotation in Pfam database.

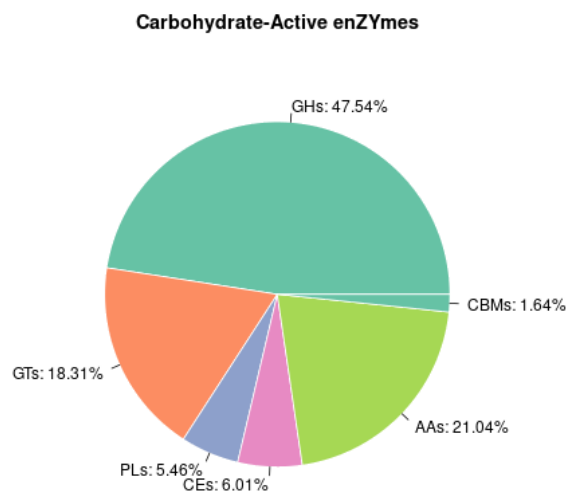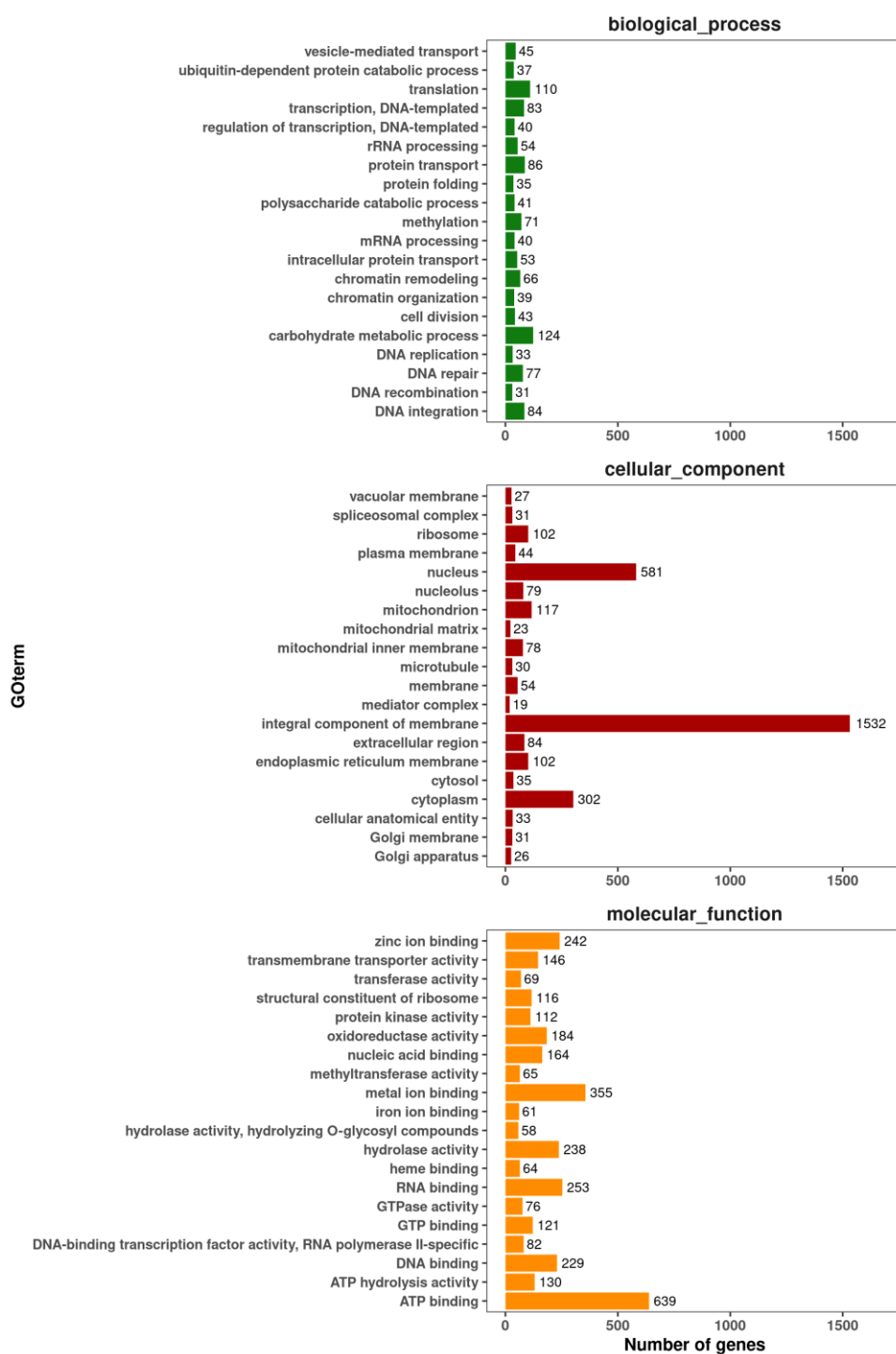**Figure S4.** The pie chart of gene alignment in Nr database.

Figure S5. The distribution and classification of 336 genes annotated in CAZyme database.

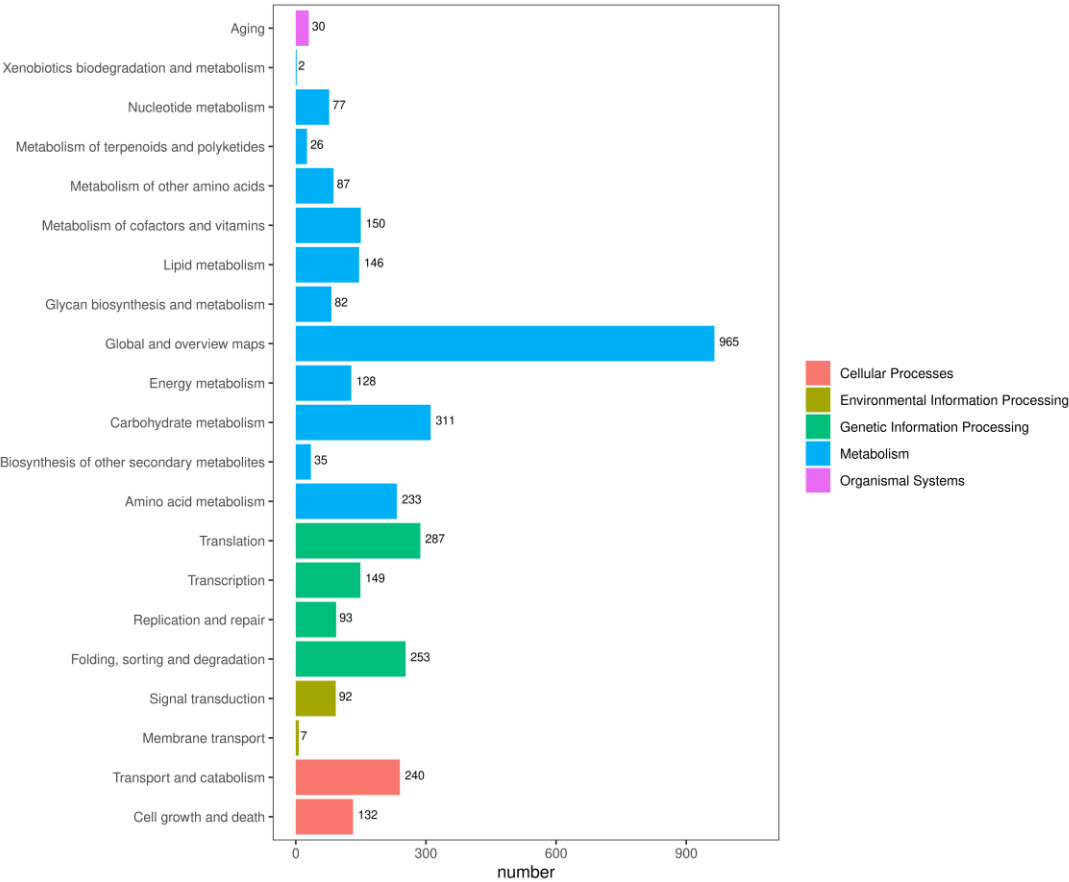**Figure S6.** The GO enrichment of annotated genes.

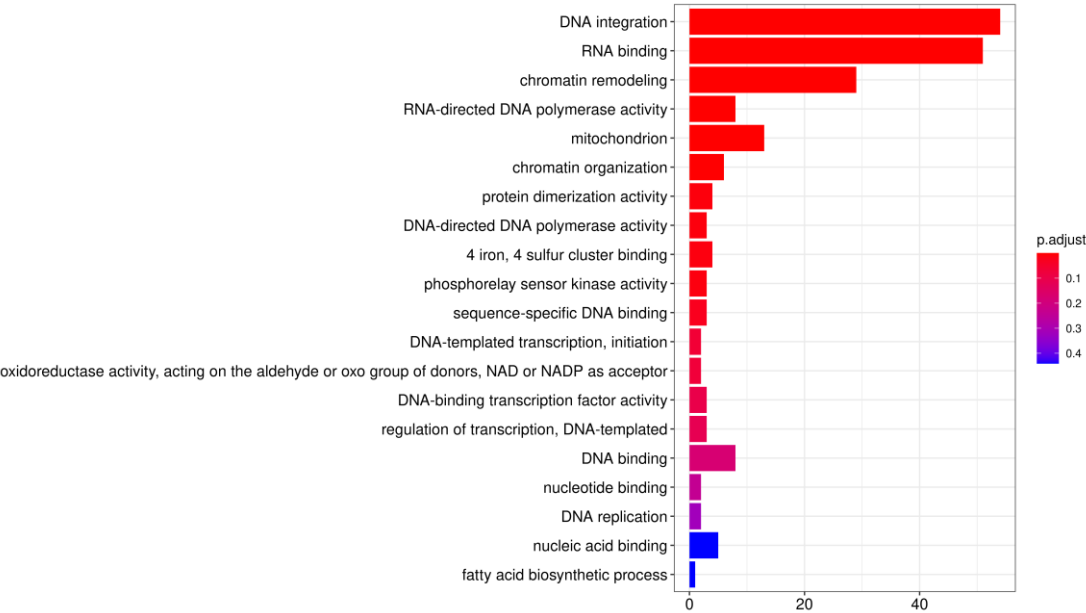**Figure S7.** The KEGG enrichment of annotated genes.

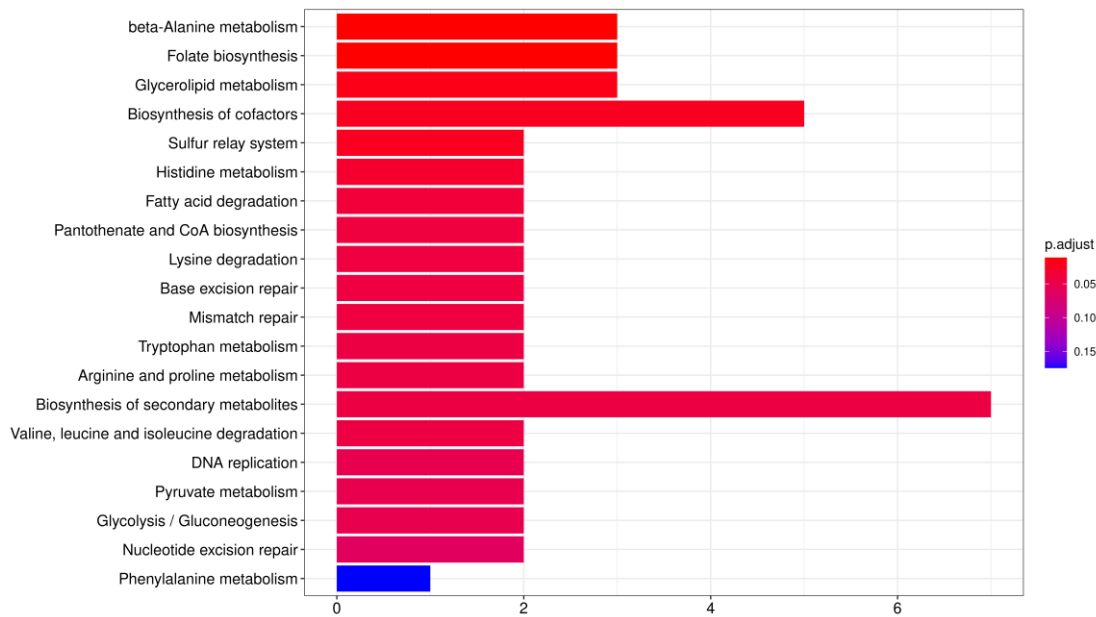**Figure S8.** The GO enrichment of specific genes.

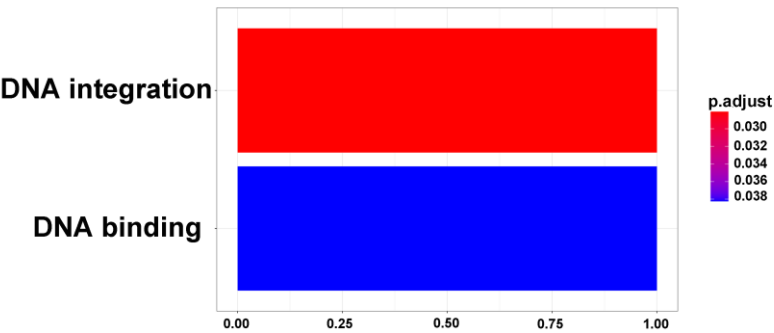**Figure S9.** The KEGG enrichment of specific genes.

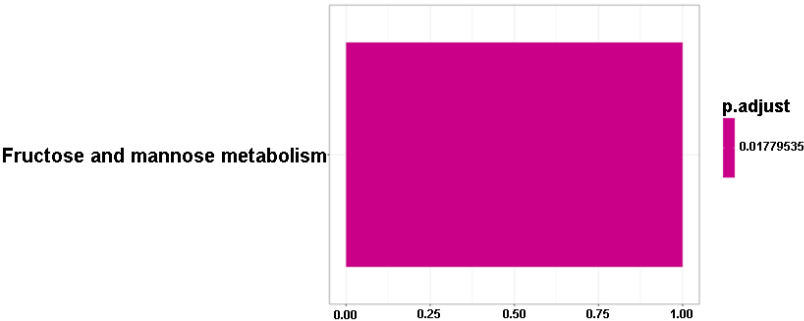**Figure S10.** The GO enrichment of contraction genes.

Figure S11. The KEGG enrichment of contraction genes.
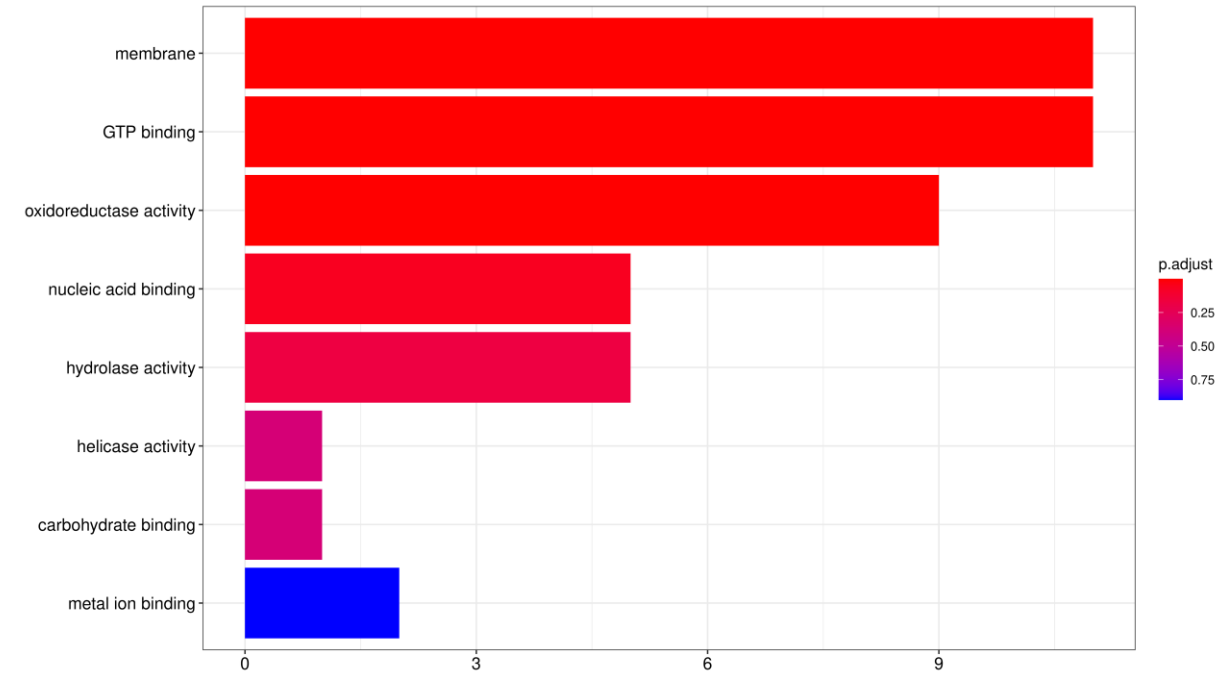
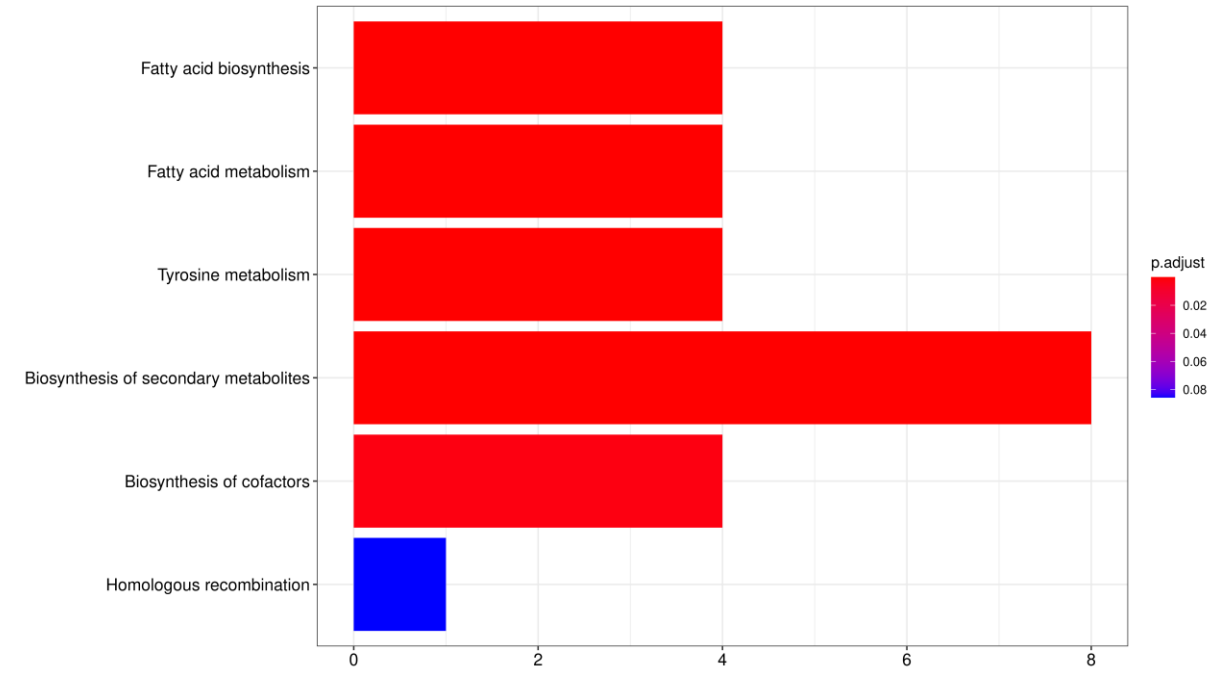**Figure S12.** The GO enrichment of expansion genes.

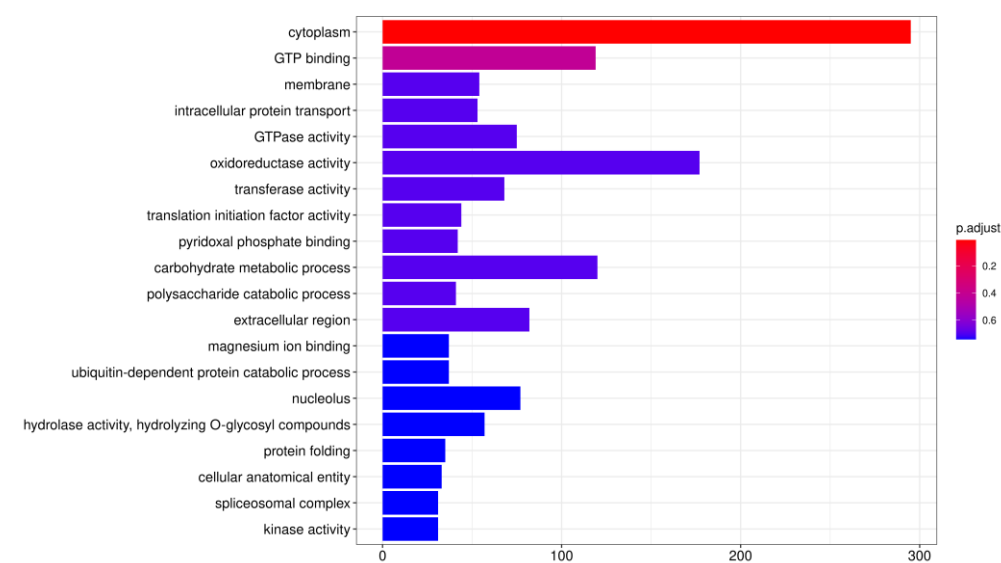**Figure S13.** The KEGG enrichment of expansion genes.

Figure S14. The GO enrichment of common gene family.

Figure S15. The KEGG enrichment of common gene family.

Figure S16. The GO enrichment of *Morchella* sp. unique gene family.

Figure S17. The KEGG enrichment of *Morchella* sp. unique gene family.

Tables

Table S1. The genome information of morels.

Species	Clade	Total length (bp)	N50 (bp)	GC content (%)	GenBank
Morchella importuna	Elata clade （Black morels）	50.9 Mb	958.7 kb	47.5	GCA_003444635.2
Morchella sextelata	Elata clade （Black morels）	52.9 Mb	1.6 Mb	47.5	GCA_020137385.1
Morchella septimelata	Elata clade （Black morels）	50.8 Mb	1.9 Mb	47	GCA_024713935.1

Morchella synderi	Elata clade （Black morels）	54.8 Mb	1.3 Mb	47.5	GCA_024521645.1
Morchella conica	Elata clade （Black morels）	52.4 Mb	742.5 kb	47.5	GCA_008079325.1
Morchella eohespera	Elata clade （Black morels）	53.8 Mb	1.9 Mb	47.7	---
Morchella crassipes	Esculenta clade (Yellow morels)	56.8 Mb	814.1. kb	47.3	GCA_009192285.1
Morchella rufobrunnea	Rufubrunnea clade	57.2 Mb	1.9 Mb	46.5	GCA_024713595.1

--- means no information collected.

Table S2. The statistics of third-generation sequencing data.

	Total base	Total reads	Max length	Average length	N50	L50	N90	L90	Mean Q
All	6,920,758,119	1,144,416	271,015	604,741	16,364	103,606	2,289	616,242	10.92
Pass	6,584,353,825	1,075,597	188,191	612,158	16,593	97,616	2,307	579,693	11.22

Table S3. The statistics of second-generation sequencing data.

Type	Number of sequences	Sum of length	GC content (%)	Q20 (%)	Q30 (%)
Raw data	36,809,500	5,521,425,000	49.70	96.72	92.56
Clean data	36,001,878	5,069,861,067	49.26	97.71	93.88