



Comparative transcriptome analysis of mixed tissues of black porgy (*Acanthopagrus schlegelii*) with differing growth rates



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Introduction

- Black porgy belongs to the order *Perciformes*, the family *Sparidae*, and the genus *Acanthopagrus*. It is an essential marine aquaculture fish (Haomiao Zhu et al., 2014).
- The quality of skeletal muscle has an important impact on an individual's development (Eldem V et al., 2015; Lanmei Wang et al., 2020).
- The transcriptome is altered with changes in growth and development stages, physiological conditions, and the external environment (Hui Luo et al., 2015), which can reveal critical regulatory genes and pathways in related aspects in a targeted manner.

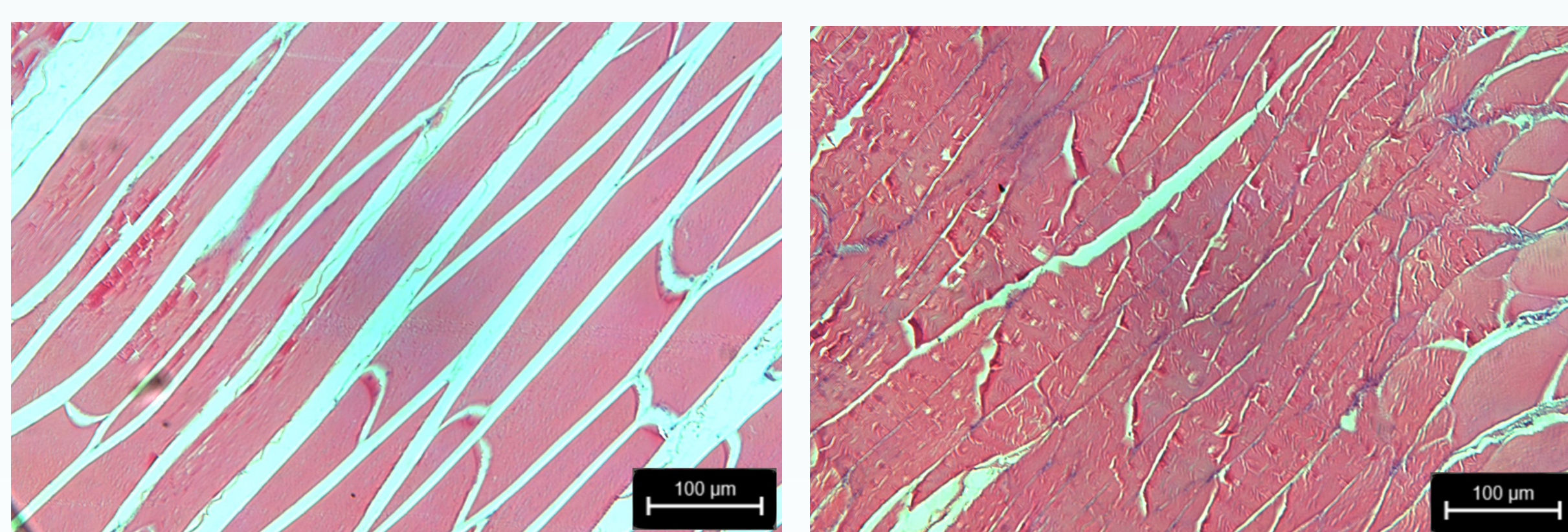
Objectives

We hoped to find candidate genes and regulatory pathways involved in the growth of black porgy through the detection of differentially expressed genes of black porgy at different growth rates, and ultimately to provide a theoretical reference for breeding black porgy strains with excellent growth characteristics.

Methods

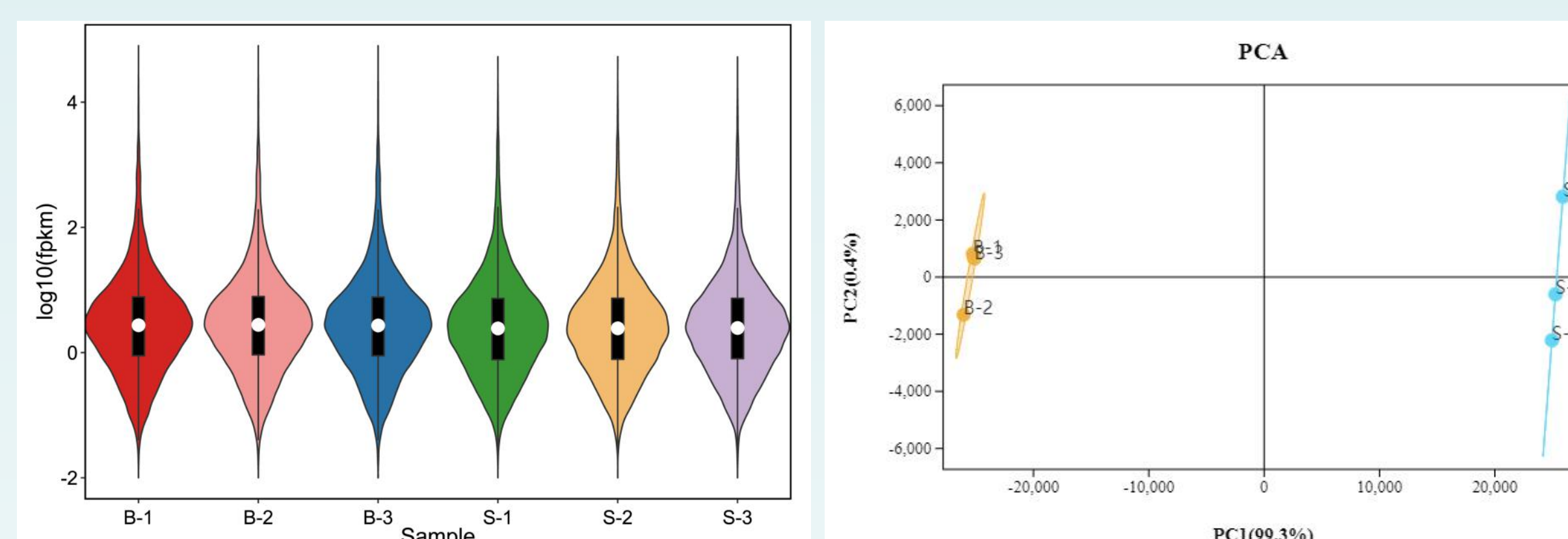
- Muscle tissue section and morphological observation
- RNA extraction, library construction and transcriptome sequencing
- According to $FDR < 0.05$, and absolute fold change ≥ 2 (Lou L. et al., 2021), DEGs were screened out.
- Principal Component Analysis
- GO and KEGG enrichment Analysis

Results 1

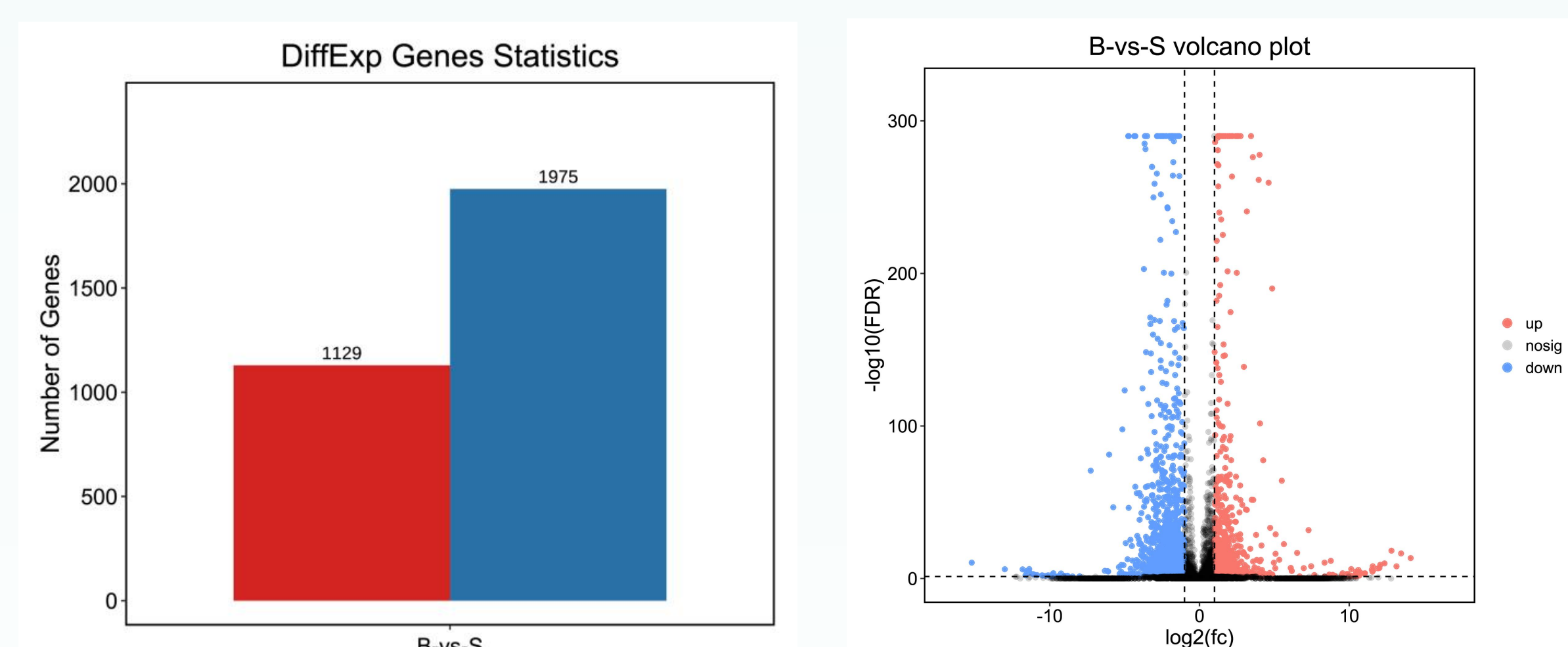


Observation of back muscle tissue of black porgy with different growth. the muscle fibers of the fast-growing black porgy (left picture) were thicker and the intercellular spaces were larger; while the muscle fibers of the slow-growing black porgy (right picture) were arranged tightly, and some cells were polygonal.

Results 2

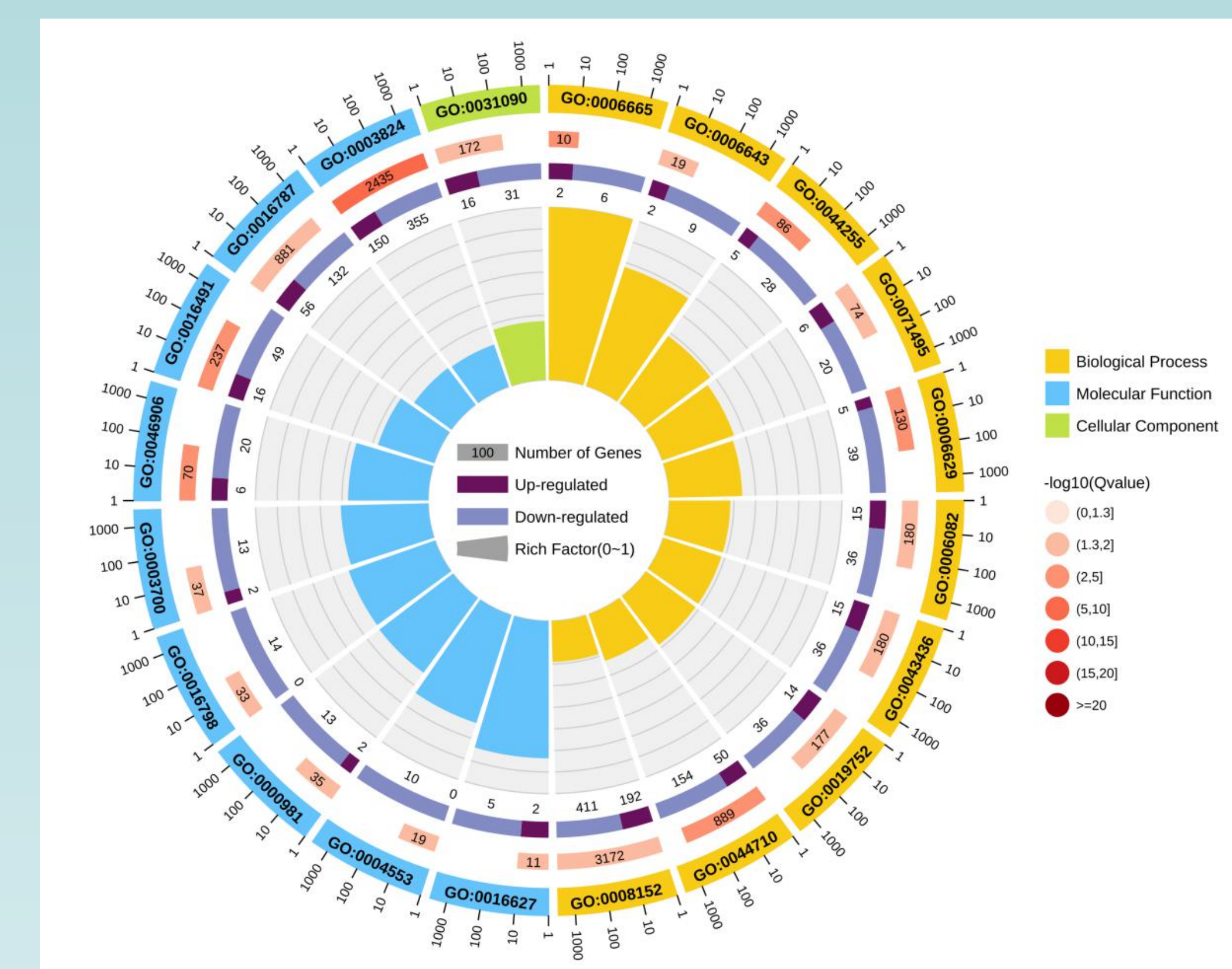


- The expression violin plot results reflect the differences in genes in individuals with different growth rates.
- From PCA result, the composition of the samples had significant differences, and the samples within the group have good repeatability.

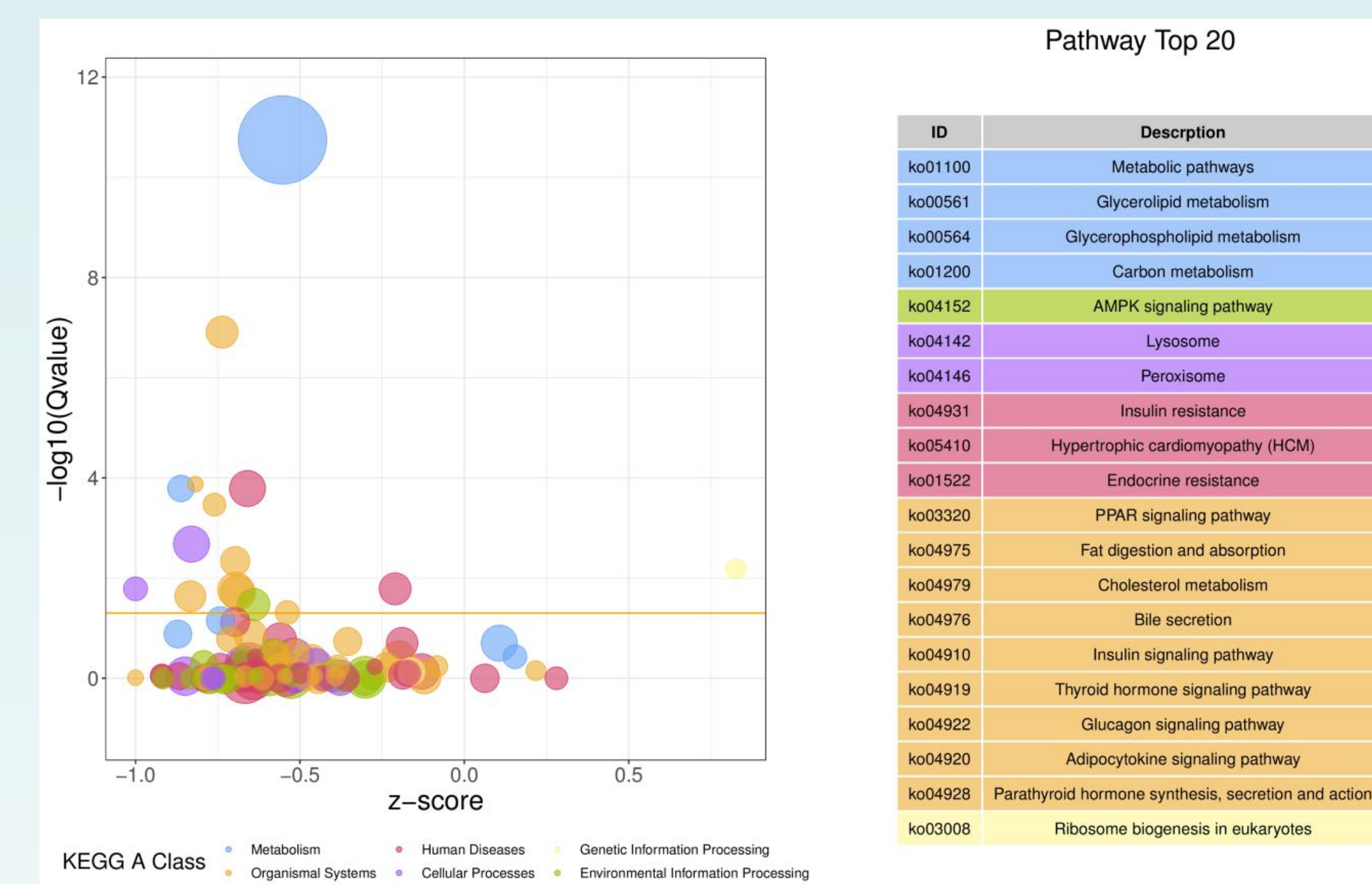


Through the analysis of the transcriptome data of group B and S, and 3104 significantly DEGs were found, of which 1129 were up-regulated genes and 1975 were down-regulated genes, including MYH4, IGF, Myl3, MYH6, Mb, GHR1 and other key genes involved in the regulation of muscle growth.

Results 3



We identified a total of 25 extremely significant GO enrichment terms ($FDR < 0.1$), focusing on material metabolism, enzyme activity regulation, and hormone-mediated signal pathway regulation.



According to the results of KEGG pathway analysis, we screened 39 significant related pathways from 336 enriched pathways. For example, metabolic pathways, thyroid signaling pathways, PPAR signaling pathways.

References

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