



Integrative analysis of physiology, transcriptome, and metabolome reveals the alterations in fat deposition, metabolism and immunity of triploid rainbow trout (*Oncorhynchus mykiss*) with different body weights

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BACKGROUND:

Oncorhynchus mykiss is an artificially bred sterile fish that has the advantages of fast growth rate, strong resistance to disease, and delicious meat quality.

Oncorhynchus mykiss is mainly raised in Xinjiang and Qinghai and other places, where the water quality is excellent and the water supply is abundant, making it suitable for the growth of cold-water fish.

The body size of aquatic animals has multiple impacts on their physiological functions, including antioxidant capacity, gene expression, and metabolic activity. The adjustment of these physiological functions helps aquatic animals adapt to different environmental conditions and survival needs.

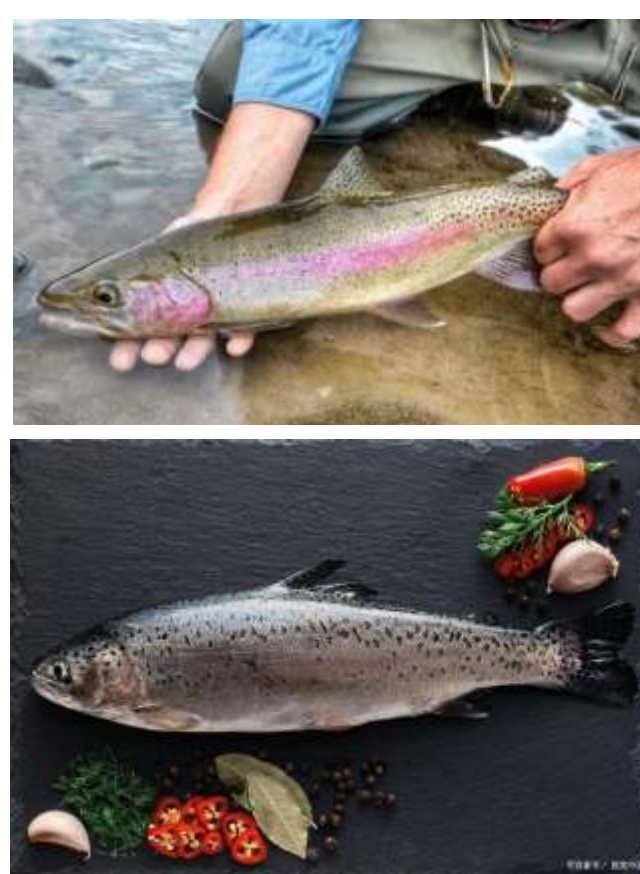


Figure 1 *Oncorhynchus mykiss*

EXPERIMENT DESING:

Body size is an evident and significant property of fish, and body weight is one of the major elements influencing fish metabolism. In this study, the serum biochemical parameters, transcriptomes and metabolomes of *Oncorhynchus mykiss* with different body weights (SRT, 0.61 ± 0.19 kg; MRT, 1.39 ± 0.27 kg; LRT, 2.58 ± 0.38 kg) were examined.

RESULTS:

The results revealed that the SOD content in the SRT group was significantly greater than that in the LRT group ($P < 0.05$), and the protein carbonyl level was significantly lower than that in the LRT group ($P > 0.05$).

SRT group were significantly enriched in the “serotonin synapse” pathway ($P < 0.05$). In SRT group were significantly enriched in the “serotonin synapse” pathway ($P < 0.05$). In the MRT vs. SRT group, differentially abundant metabolites were significantly enriched in pathways such as “fatty acid metabolism” and “fatty acid degradation” ($P < 0.05$). Integrated transcriptomics and metabolomics analyses revealed that differentially expressed genes and differentially abundant metabolites were significantly enriched in the “amino acid biosynthesis” and “cysteine and methionine metabolism” pathways in the LRT vs. MRT and LRT vs. SRT groups ($P < 0.05$).

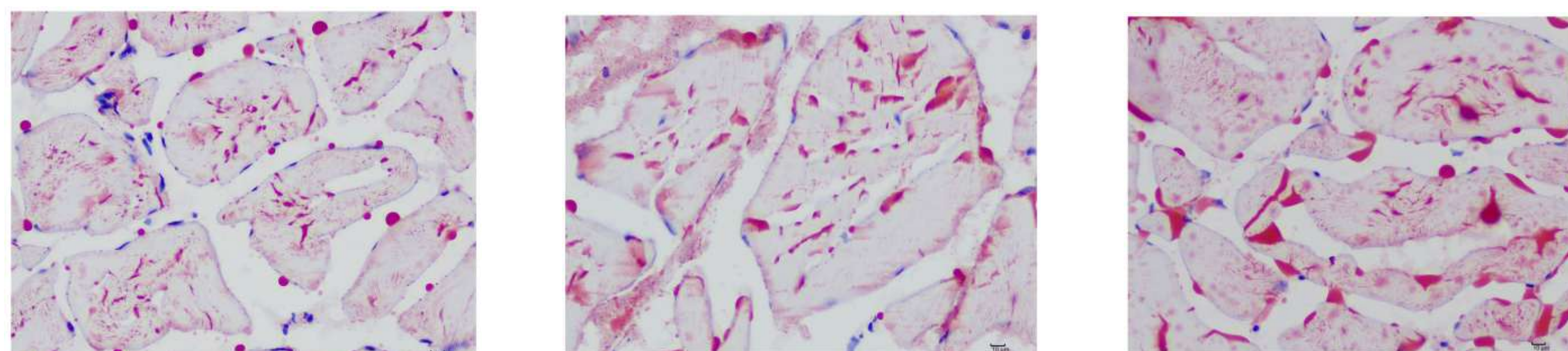


Figure 2 Oil red O staining of liver tissues of triploid rainbow trout with different body weights. A. Oil red O staining of liver tissues of LRT. B. Oil red O staining of liver tissues of MRT. C. Oil red O staining of liver tissues of SRT.

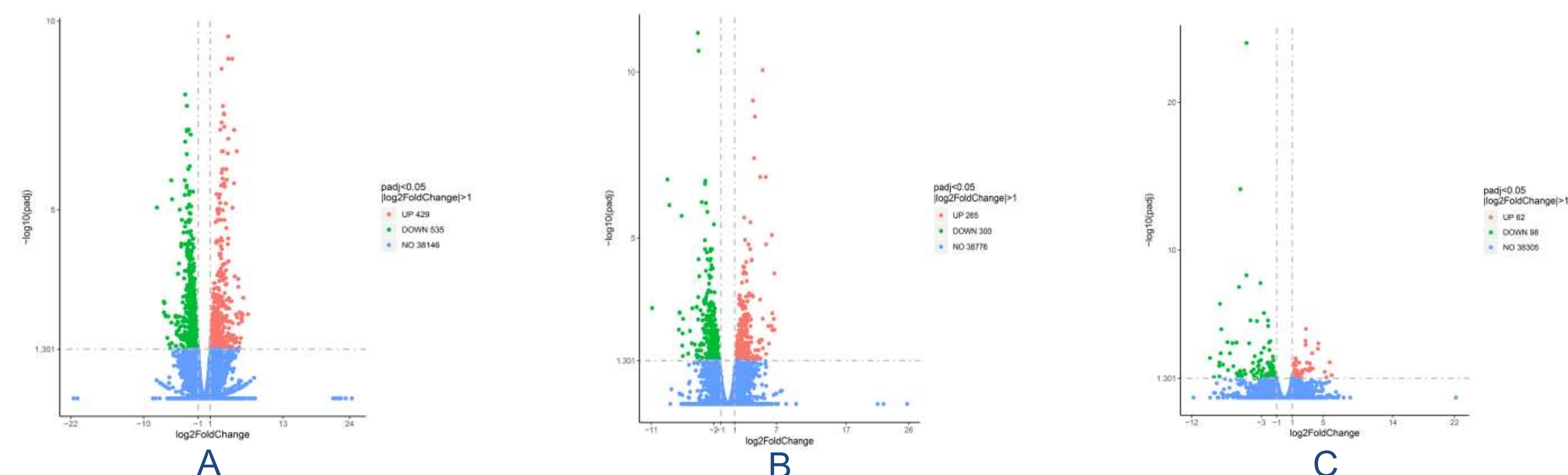


Figure 3 Volcano diagram of differentially expressed genes in triploid rainbow trout with different body weights. The abscissa represents the fold change, and the farther away from the center, the larger the fold difference. The ordinate represents the P -value, and the closer the point to the top, the more significant the difference between the two groups. Green color indicates down-regulated metabolites, red color indicates up-regulated metabolites, and gray color indicates metabolites have no difference between the two groups. A. LRT vs. MRT group. B. LRT vs. SRT group. C. MRT vs. SRT group.

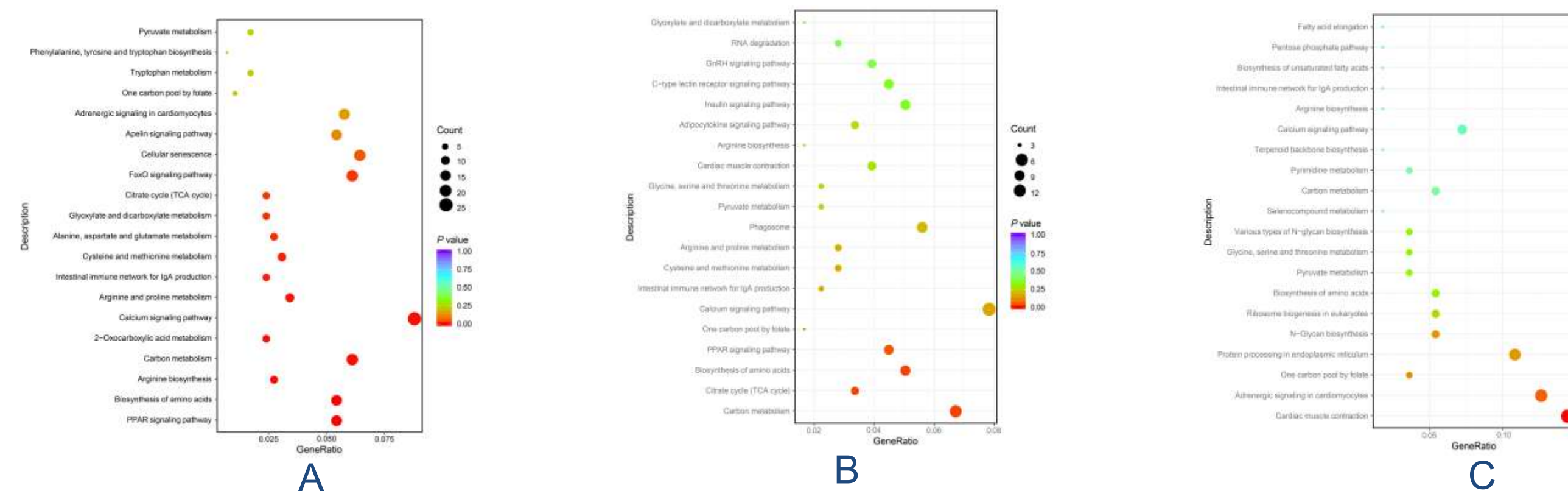


Figure 4 KEGG enrichment of differentially expressed genes in triploid rainbow trout with different body weights. Each circle represents a pathway, the ordinate indicates the name of the pathway, and the abscissa is the enrichment factor. The color of the circle represents the P value, and the circle size indicates the number of genes enriched in the go term or pathway. Pathways with redder colors and larger circles had greater reference values. Twenty pathways with minimum P values are displayed in this study. A. KEGG enrichment of all differentially expressed genes in LRT vs. MRT group. B. KEGG enrichment of all differentially expressed genes in LRT vs. SRT group. C. KEGG enrichment of all differentially expressed genes in MRT vs. SRT group.

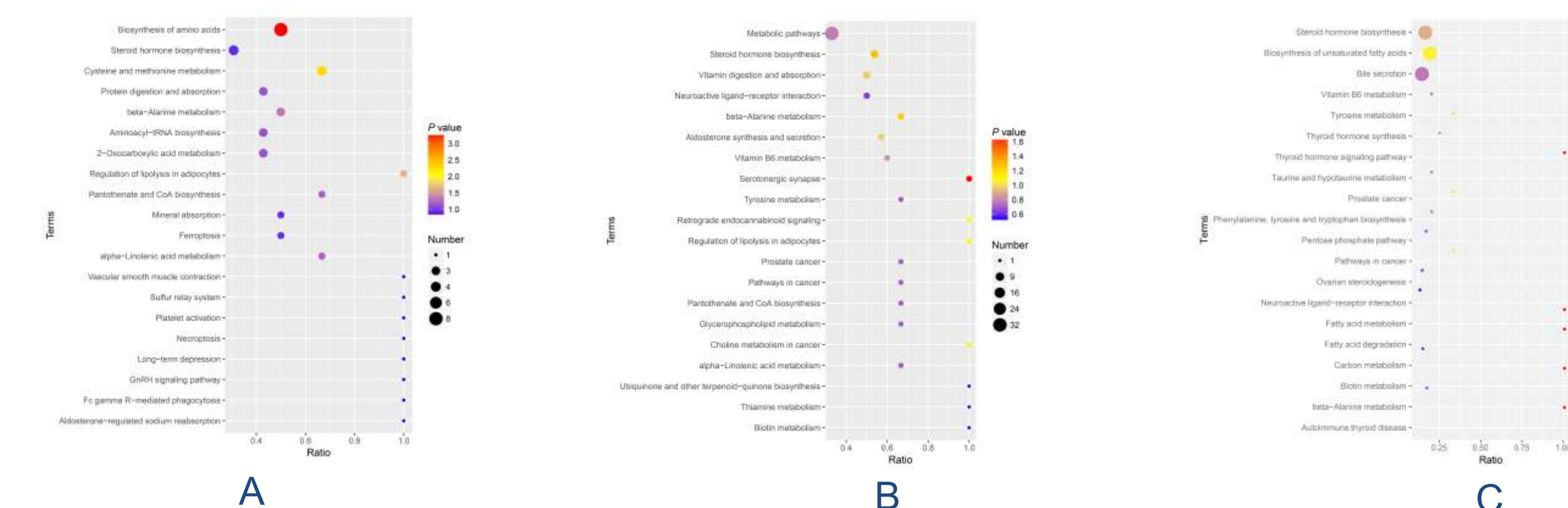


Figure 5 KEGG enrichment of differentially abundant metabolites in different comparison groups. A. KEGG enrichment of all differentially abundant metabolites in LRT vs. MRT group. B. KEGG enrichment of all differentially abundant metabolites in LRT vs. SRT group. C. KEGG enrichment of all differentially abundant metabolites in MRT vs. SRT group.

CONCLUSION:

In summary, integrated physiological, transcriptomic and metabolomic analyses revealed that SRT had greater antioxidant and immune capacity, whereas LRT had greater metabolic and fat deposition capacity. *Oncorhynchus mykiss* is accompanied by alterations in the active biosynthesis, metabolism of amino acids and fatty acids and immunity, which ensures rapid growth, fat deposition, and response to environmental stress.