Supplementary Material

Insights into the seasonal adaptive mechanisms of Chinese alligators (*Alligator sinensis*) from transcriptomic analyses

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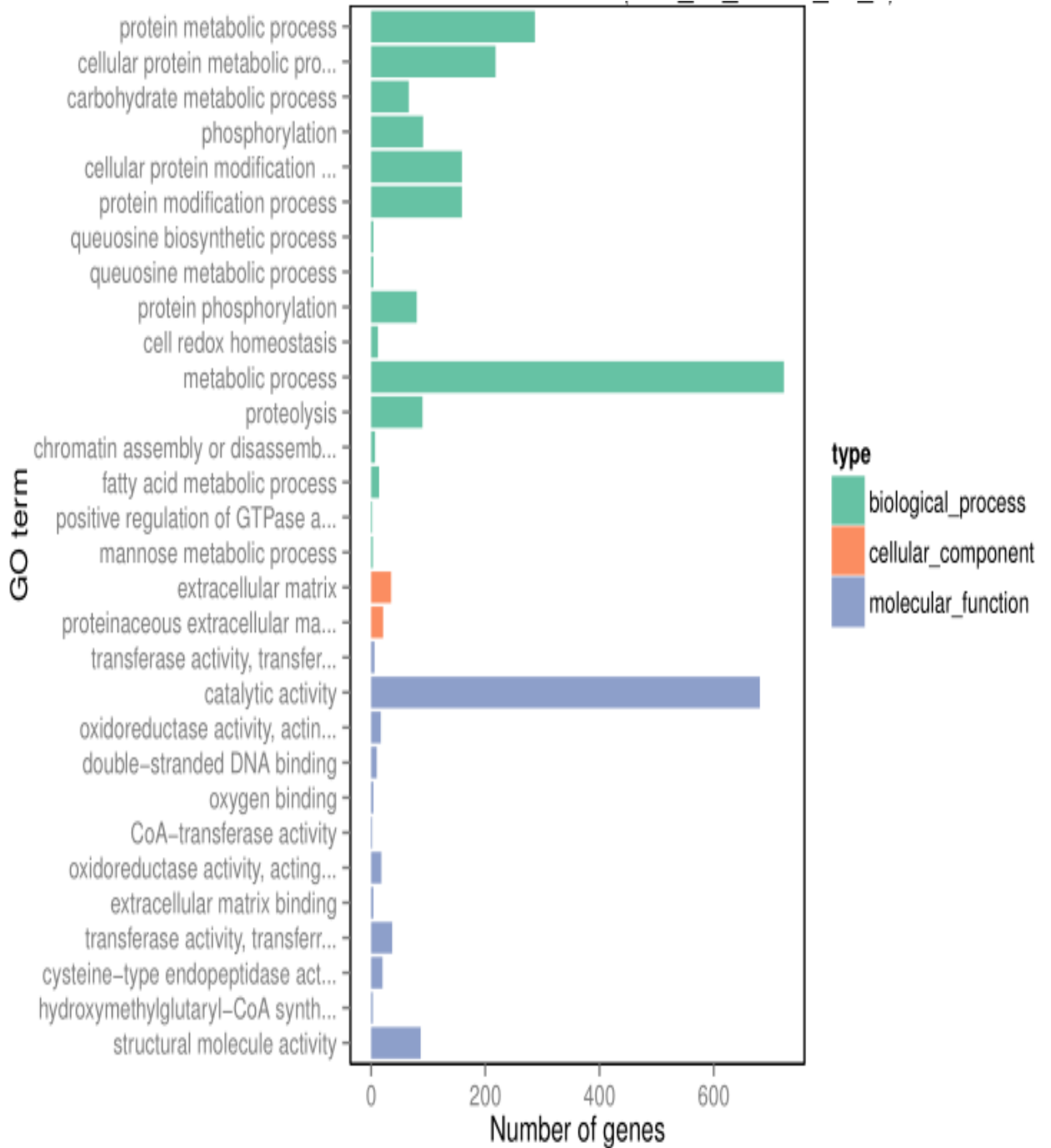
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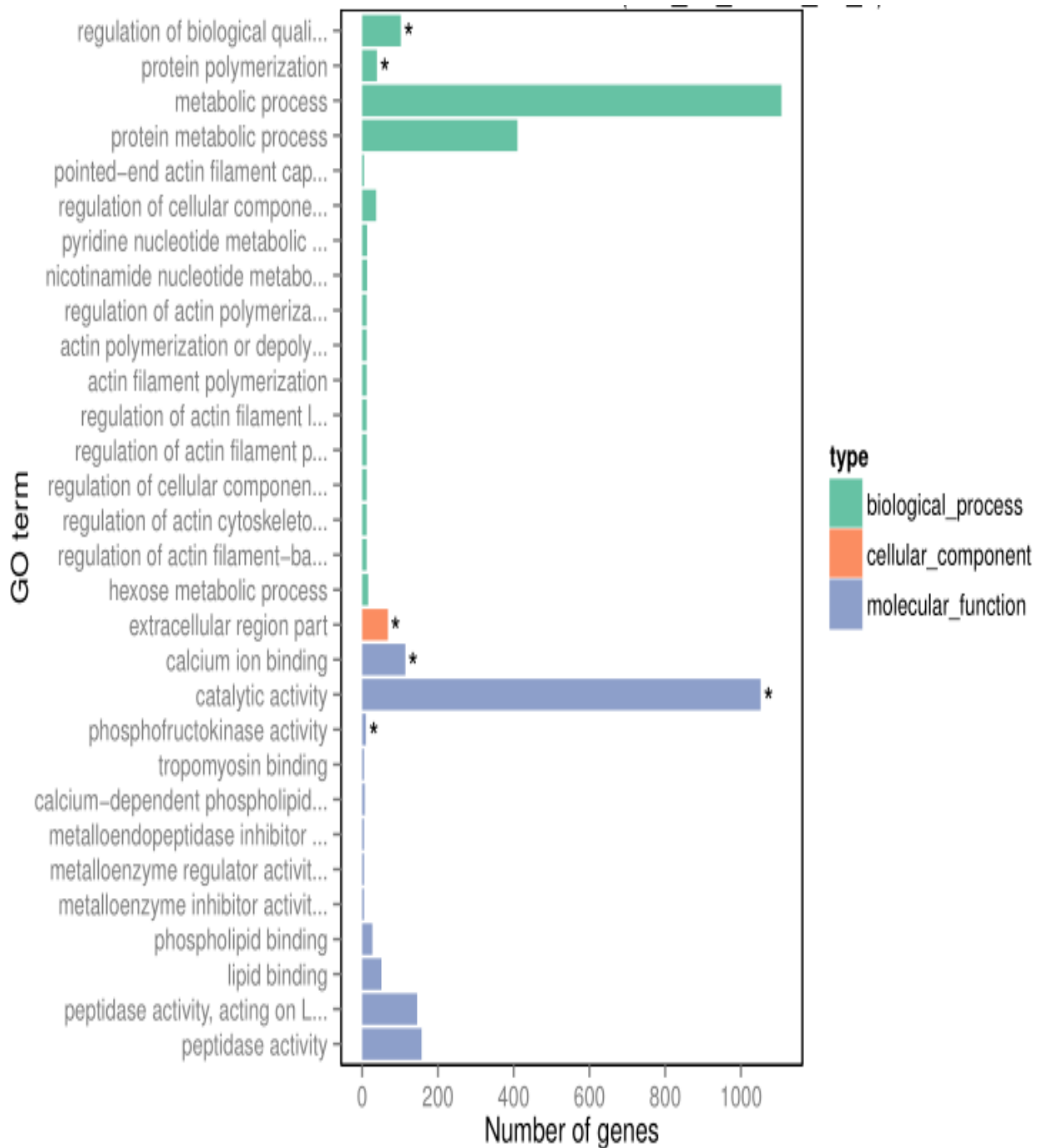
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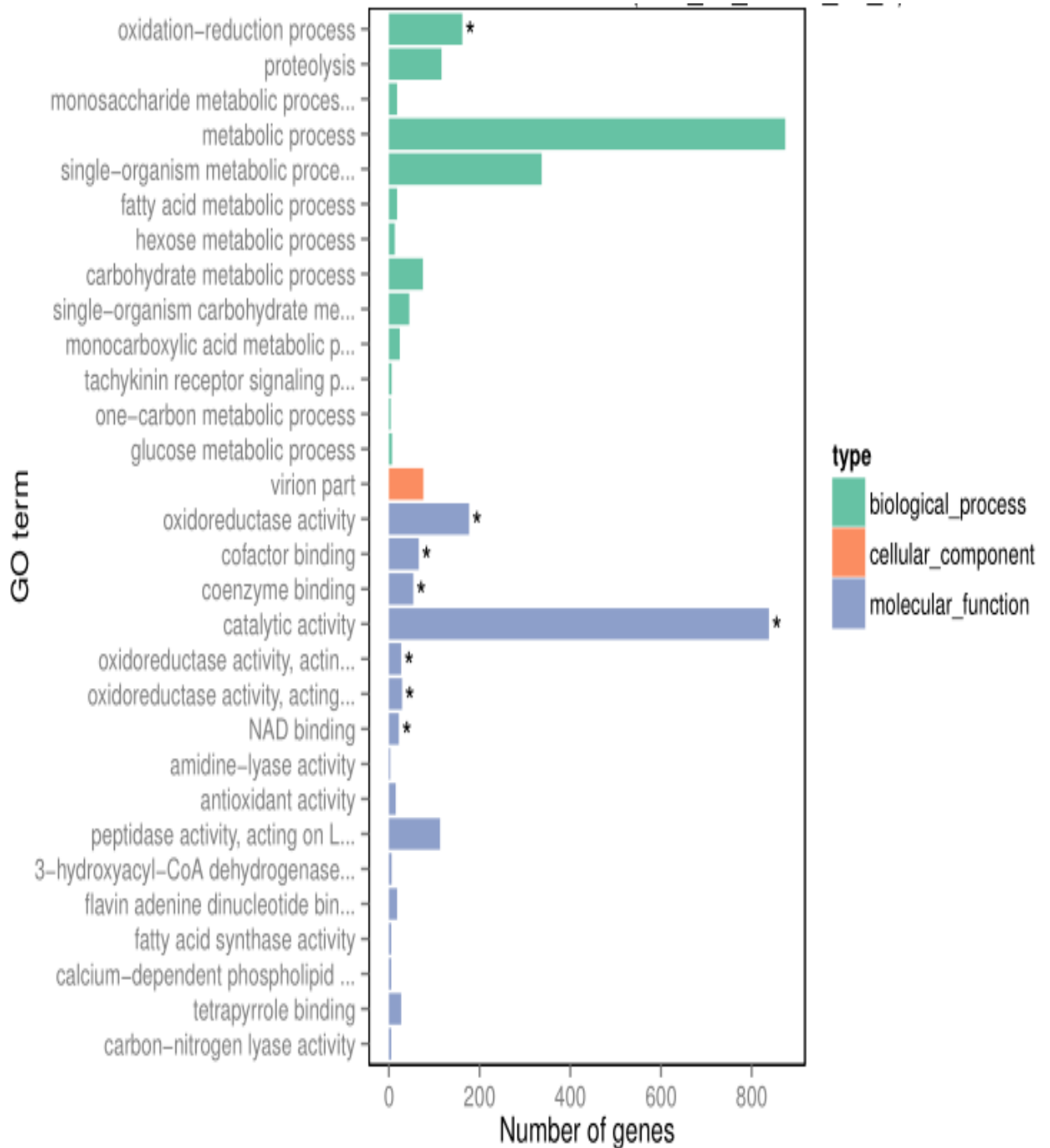
The Most Enriched GO Terms (H_A vs H_H)

The Most Enriched GO Terms (S_A vs S_H)

# The Most Enriched GO Terms (K_A vs K_H)

Supplementary figure S1. GO enrichment bar chart of differentially expressed genes. Y-axis denotes enriched GO term, X-axis denotes the number of differentially expressed genes. Different colours distinguish between biological process, cellular component and molecular function, with the "*" is significantly enriched GO term (Corrected p-value < 0.05). Specific sample name: H_H: Heart_Hibernation; S_H: Skeletal muscle_Hibernation; K_H: Kidney_Hibernation; H_A: Heart_Activity; S_A: Skeletal muscle_Activity; K_A: Kidney_Activity.
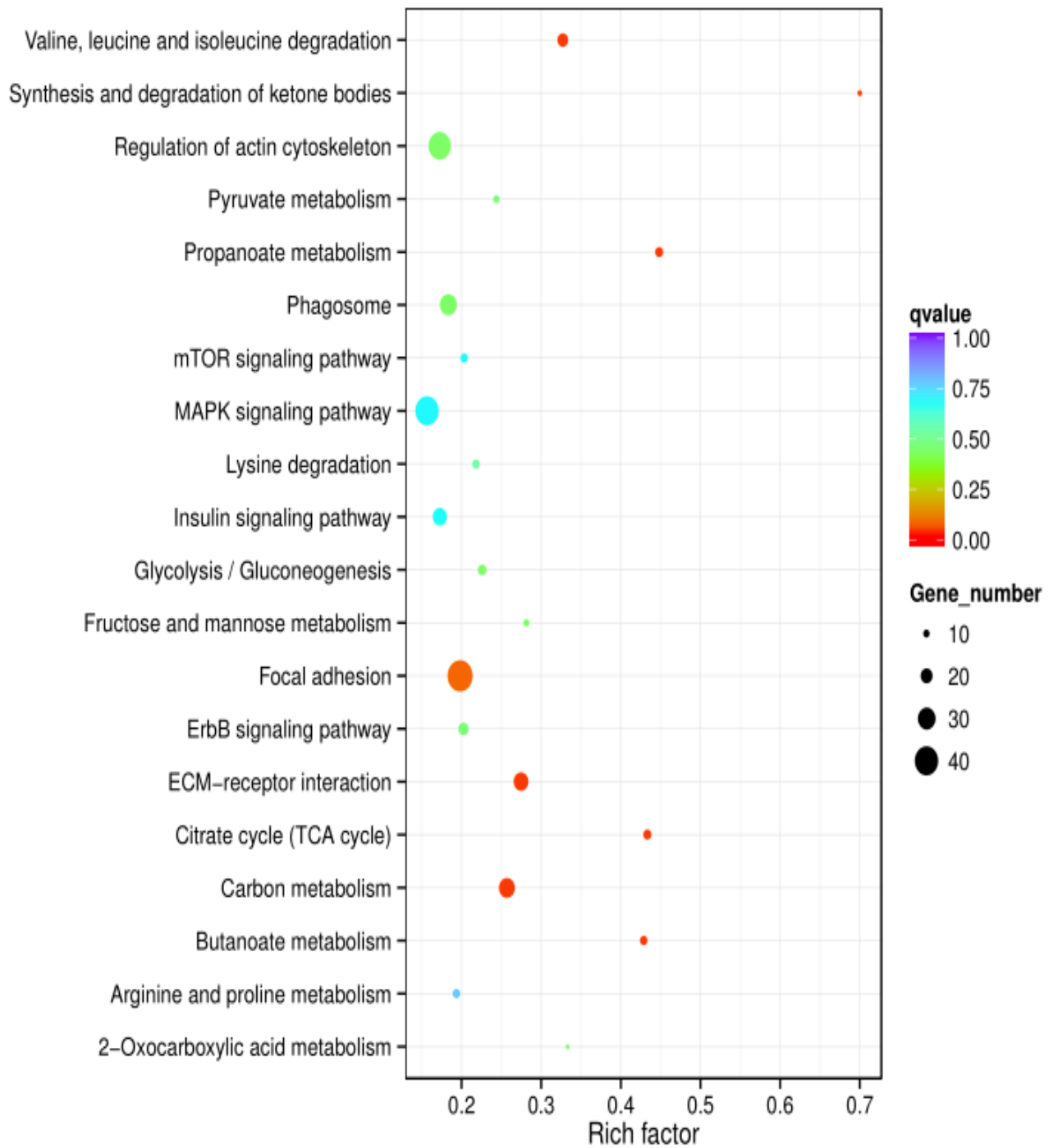
H_A vs H_H

Statistics of Pathway Enrichment
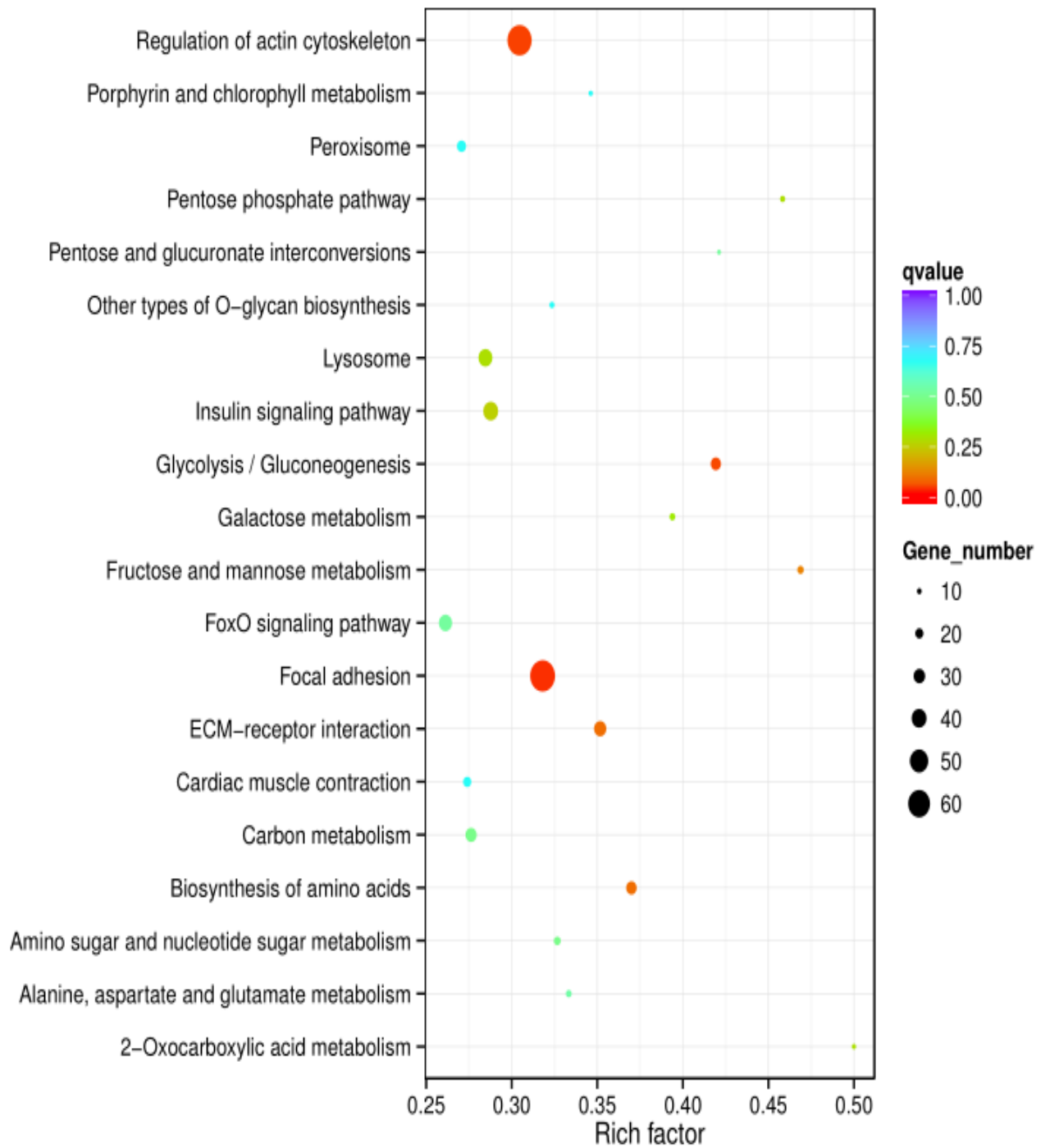
S_A vs S_H

Statistics of Pathway Enrichment

K_A vs K_H

Supplementary figure S2. KEGG enrichment scattered plot of differentially expressed genes. Y-axis represents the name of the pathway, and x-axis represents Rich factor. Rich factor is the ratio of differentially expressed genes counts to this pathway in the annotated genes counts. The size of the dots indicates the number of differentially expressed genes in this pathway, and the colour of the dots corresponding to different ranges of q-value [0,1]. The more the q-value is close to zero, the more significant enrichment.