

Figure 1. The phylogenetic relationship of species used in this study and their lifespan phenotypes. a. the phylogenetic relationship of 74 mammals used in this study and their LQ values. LQ value is the ratio of the observed maximum lifespan to the expected lifespan. The expected lifespan was calculated according to their body weight following the formula *expect lifespan (years) = 3.34 * (adult weight (g)^0.193)*. Detail information can be seen in **Supplementary Table 1**. b) the observed maximum lifespan correlates significantly with their adult body weight. Data were obtained from the HAGR database.

Figure 2. The most significantly correlated genes between the relative evolutionary rates of protein and the changed of LQ value. a-c. the top 3 of most negatively correlated genes. d-f. the top 3 of most positively correlated genes. *P*-value was calculated according to Pearson's correlation. Circles represent the terminal branches while triangles represent the internal branches. Red color labels the lineages leading to the most long-lived mammals or their ancestors. Blue color labels the branch leading to the most short-lived mammals or their ancestors. Rho, the correlation between relative evolutionary rates of genes and the evolution of traits across a phylogeny.

Figure 3. Evolutionary driving forces of the significantly correlative genes. a. The ratio of intensively selected genes (positively selected genes) in long-lived mammals was significantly lower in positively correlated genes than negatively correlated genes or non-significantly correlative genes. b. The ratio of relaxed selected genes in long-lived

mammals was significantly higher in positively correlated genes than negatively correlated genes or non-significantly correlative genes.

Figure 4. The over-represented categories of GO biological process among significantly correlative genes. a. The over-represented categories of GO biological process in negatively correlated genes. b. The over-represented categories of GO biological process in positively correlated genes. All orthologous genes mean the 13381 one-to-one orthologous genes used to identify significantly correlative genes.

Figure 5. The closed relative or adverse categories of the GO biological process that over-represented by negatively correlated genes and positively correlated genes, simultaneously. a. Categories involved in oxygen utilization. b. Categories involved in purine metabolic/biosynthetic process and purinergic nucleotide receptor signaling pathway.

Figure 6. Comprehensive network analyses of significantly correlative genes.

Supplementary Figure 1. Comparison of the one-to-one orthologous genes before and after filtration. a. The distribution of the number of species in each one-to-one orthologous gene before and after filtration. b. The distribution of protein alignment length in each one-to-one orthologous before and after filtration.

Supplementary Figure 2. The changed value of LQ for each branch in the phylogenetic tree of 74 mammals. The values in the bracket were the LQ values for each existing species or the ancestor nodes. The values above the lineage were the changed LQ values in each branch, red means LQ value increase while blue means the LQ value decrease. Branches leading to the species with the top 10 largest or smallest LQ values or their ancestor were marked as red and blue, respectively.

Supplementary Figure 3. The ratio of positively selected genes was lower in positively correlated genes than negatively correlated genes. Positively selected genes in long-lived mammals were identified by PAML branch-site model.

Figure 1

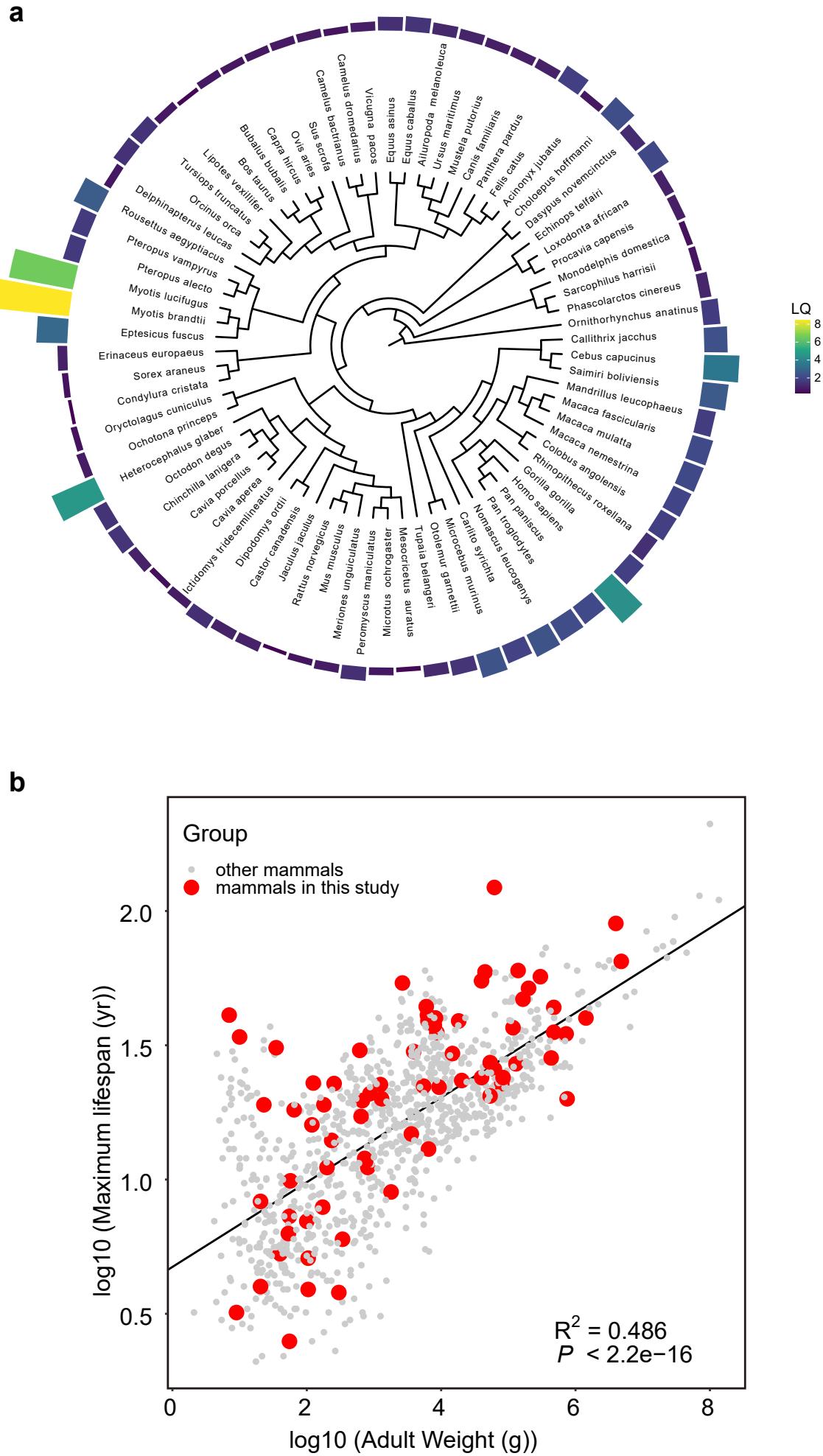


Figure 2

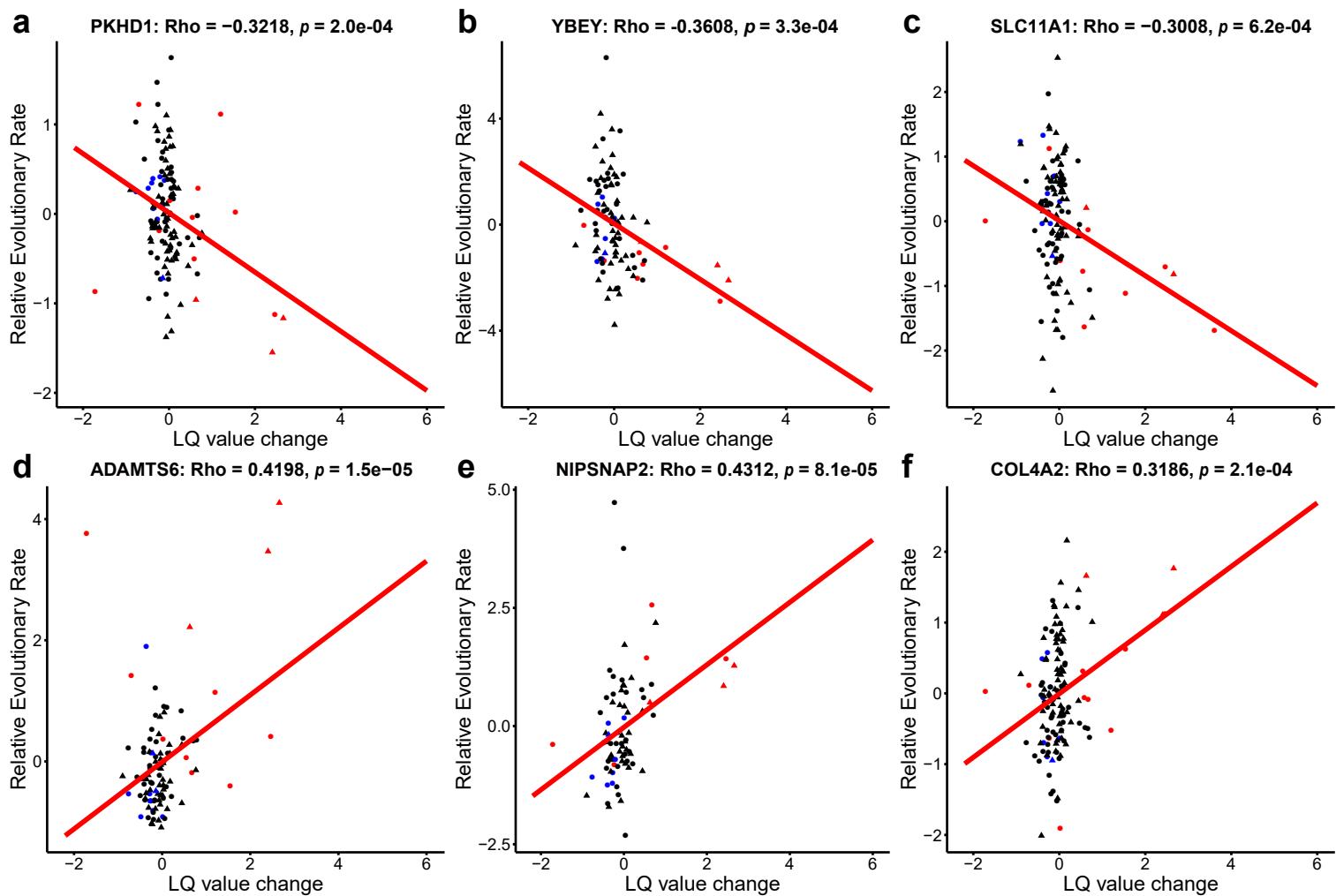


Figure 3

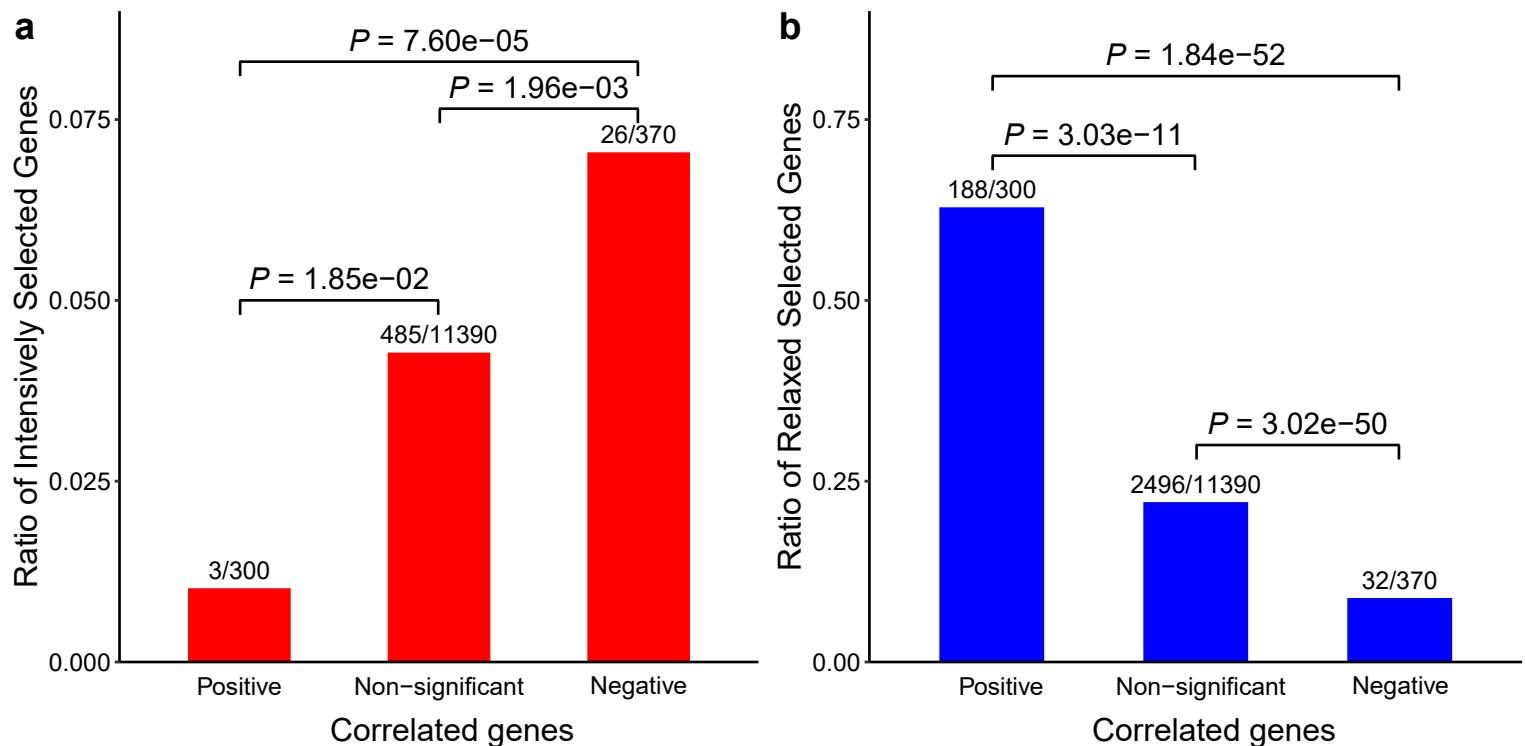
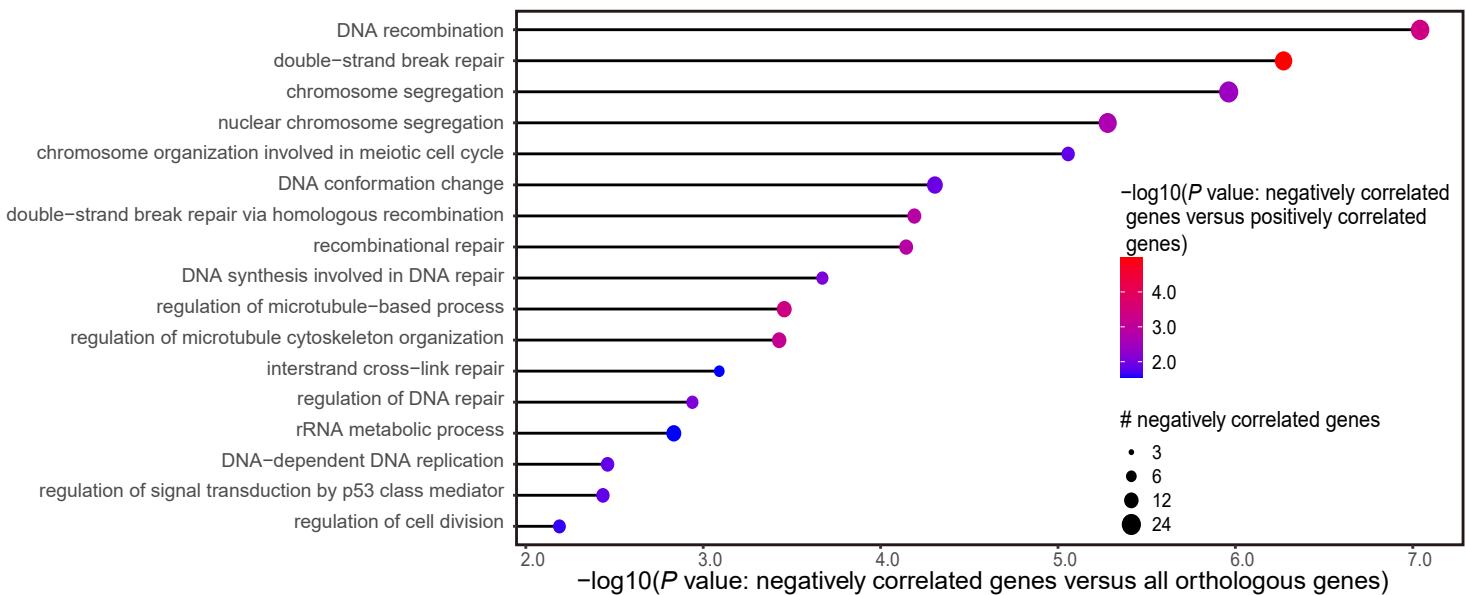


Figure 4

a



b

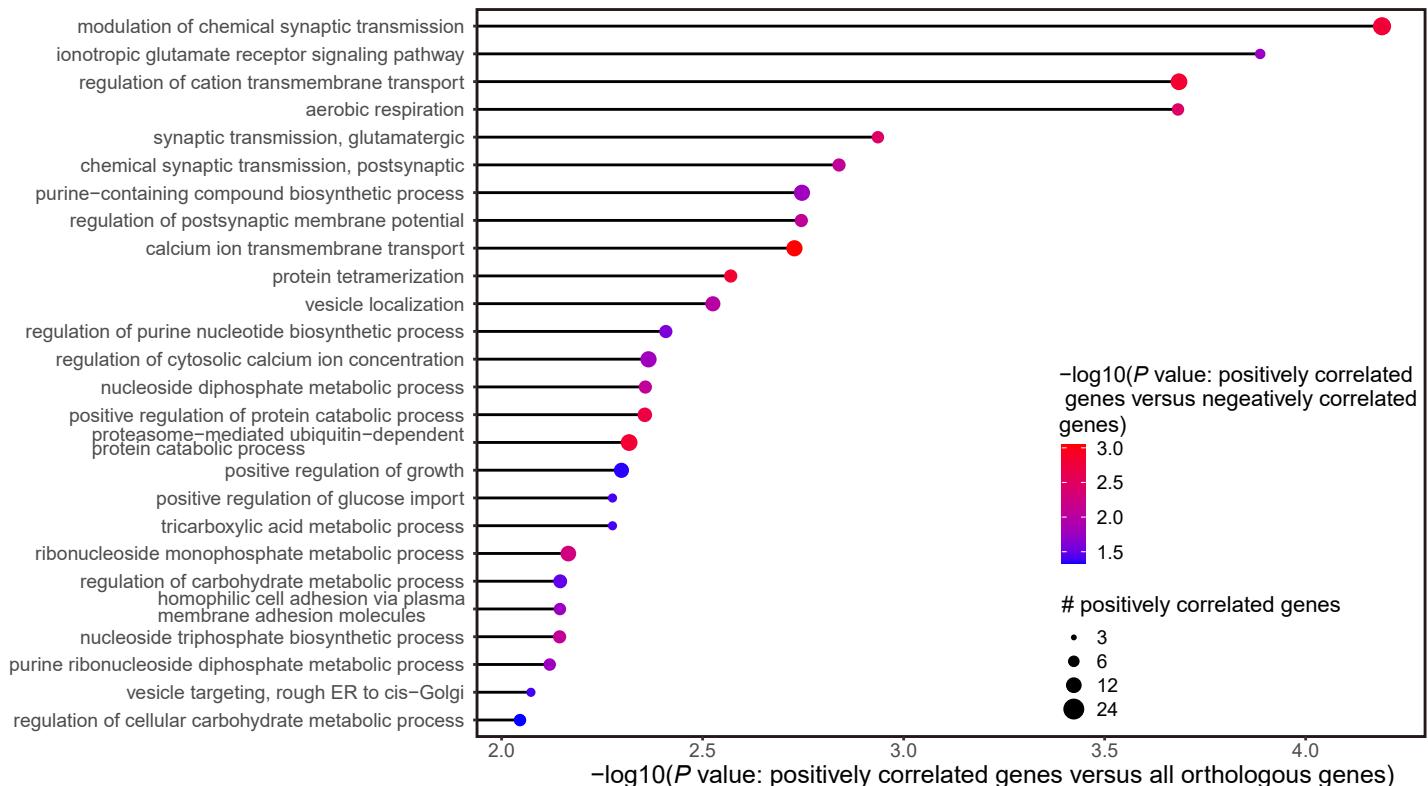


Figure 5

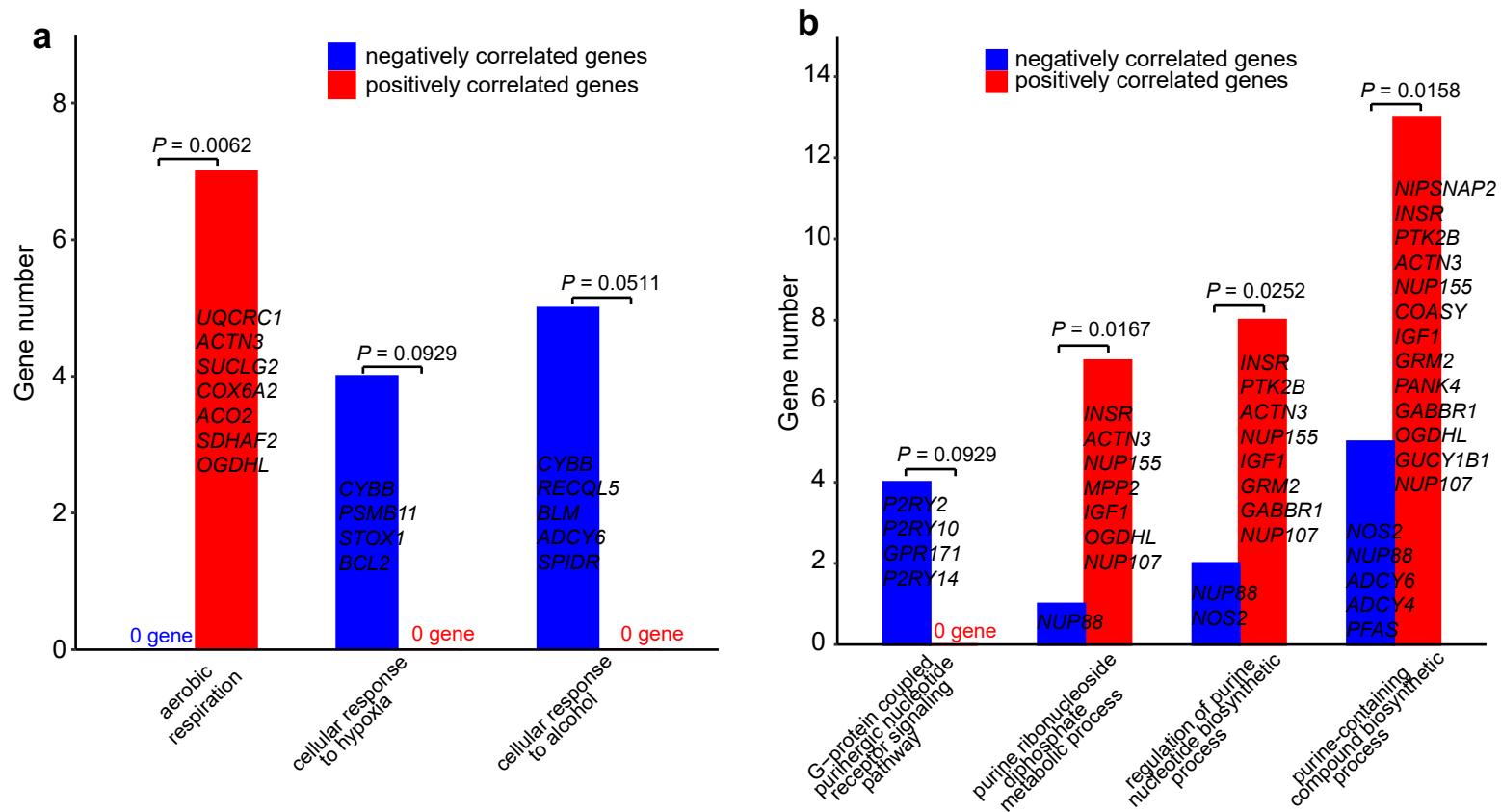
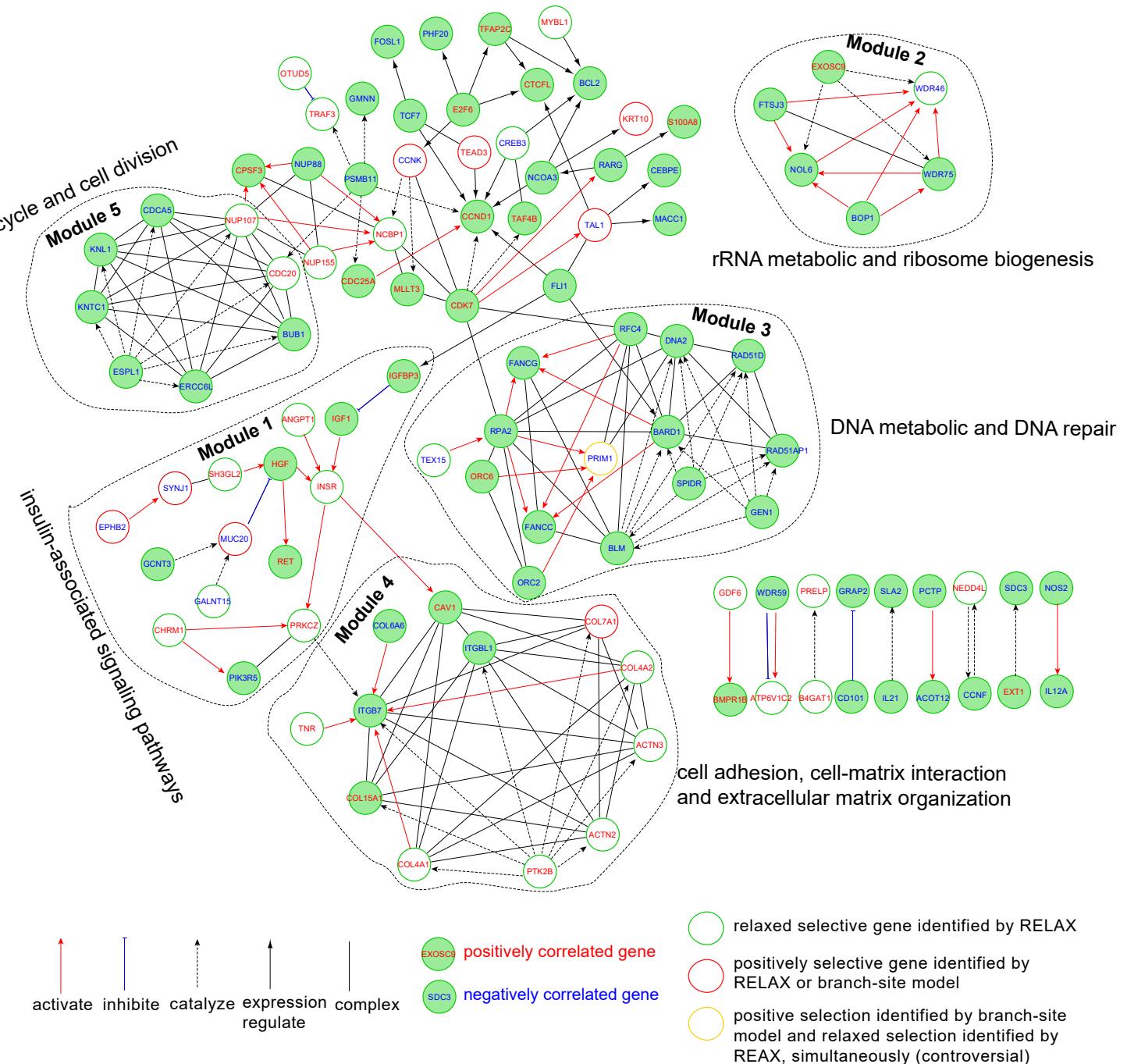
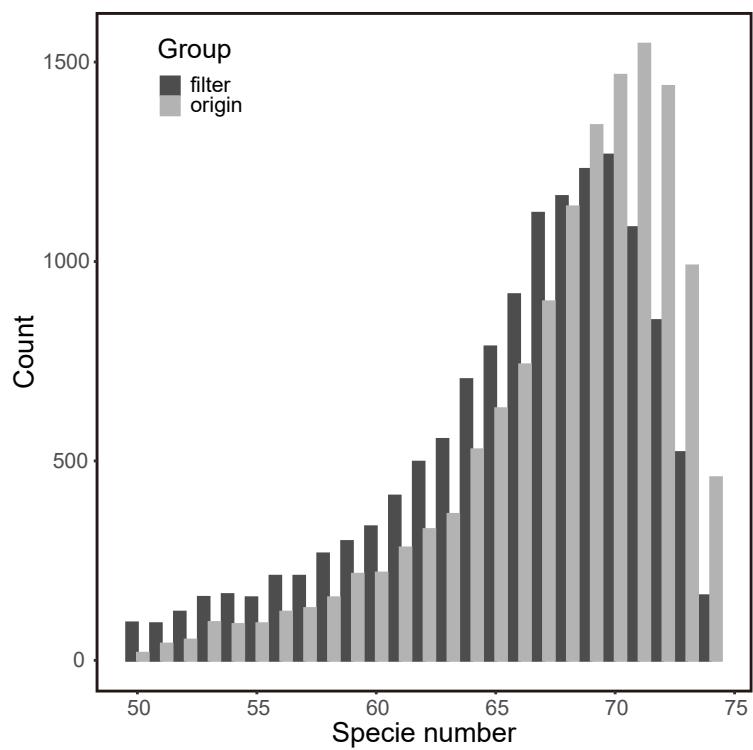


Figure 6

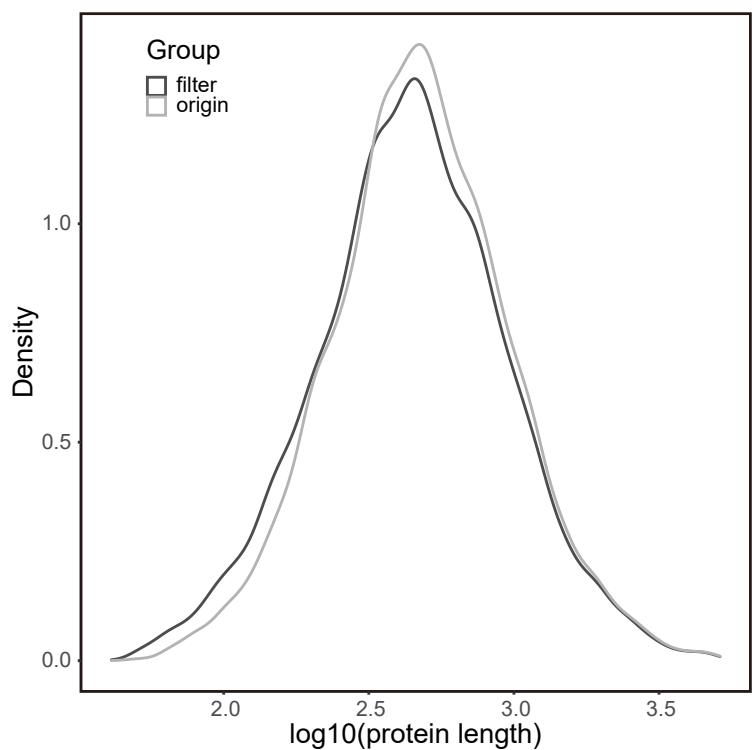


Supplementary Figure 1

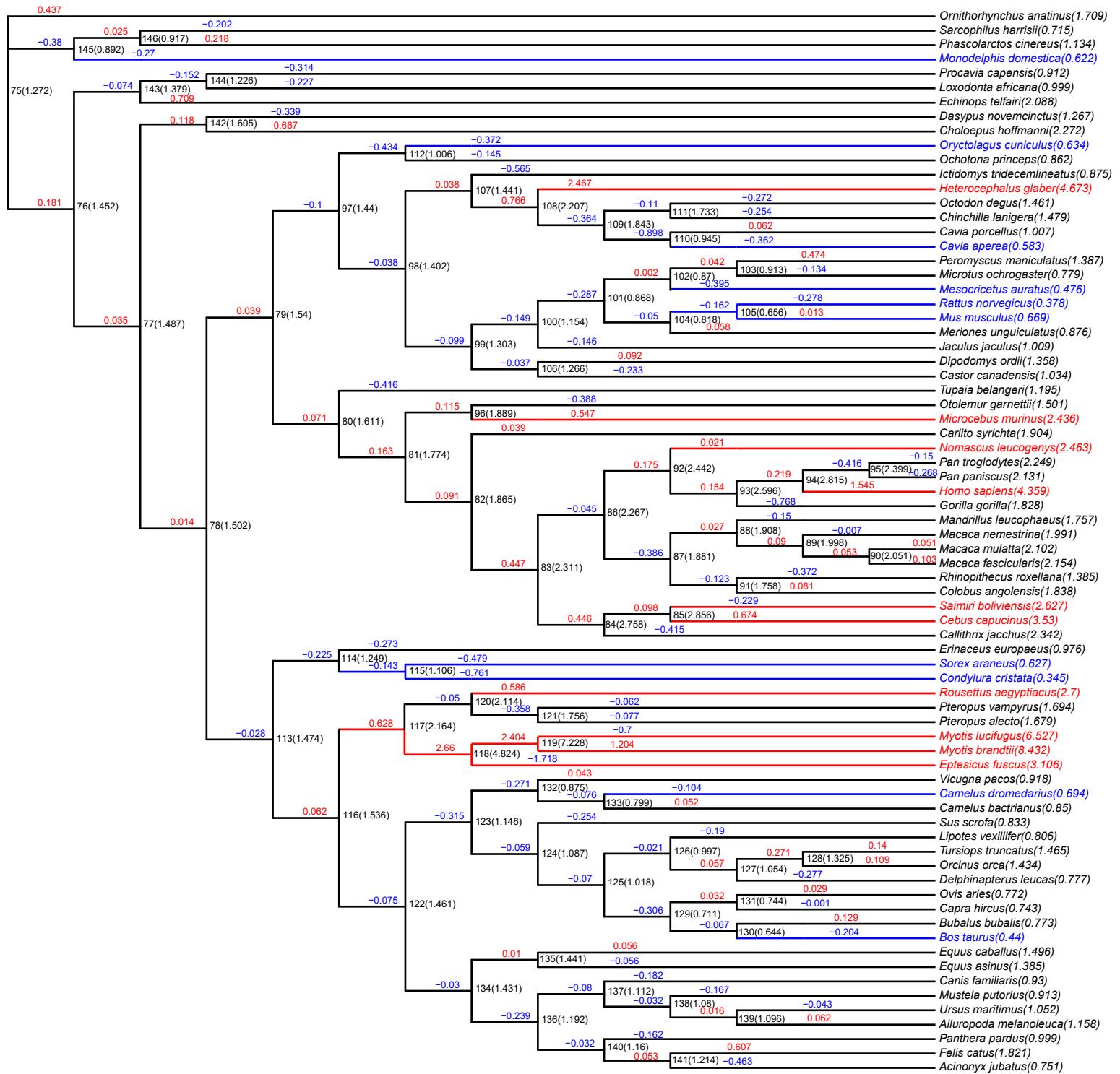
a



b



Supplementary Figure 2



Supplementary Figure 3

