Supplementary Figures

Zhou Wu *et al.*

*Corresponding author. Email: zhou.wu@roslin.ed.ac.uk

Supplementary Figures

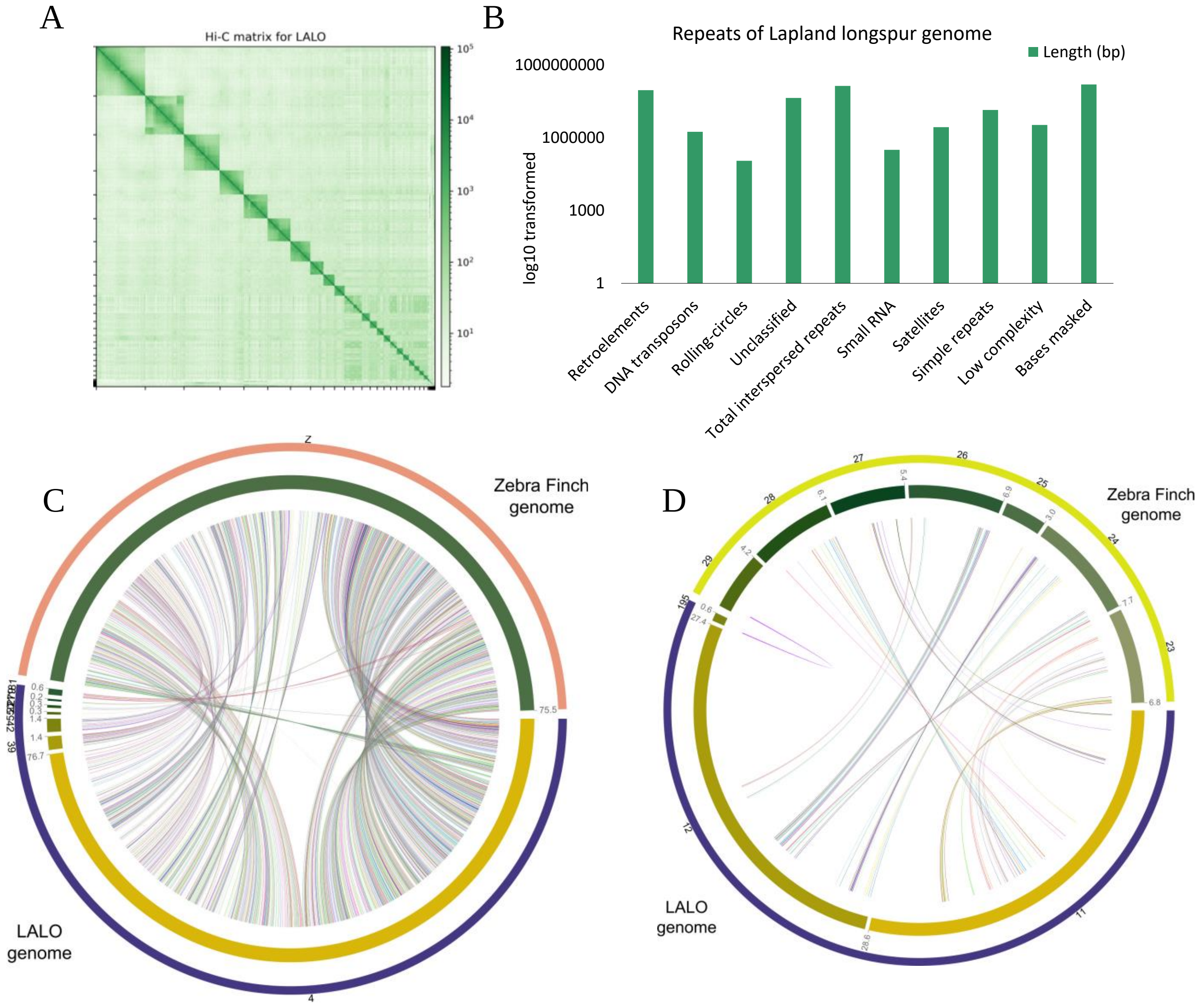

Fig. S1. Genome assembly of Lapland longspur (*C. lapponicus*). (**A**) The interaction matrix shows the Omni-C results for the genome assembly. (**B**) Repeat content of the Lapland longspur genome. The x axis denotes the repeat category, the y axis denotes the length of the repeat elements (log10 transformed). (**C**) Alignment between zebra finch chromosomes and Lapland longspur scaffolds for Z chromosome and (**D**) micro-chromosomes.

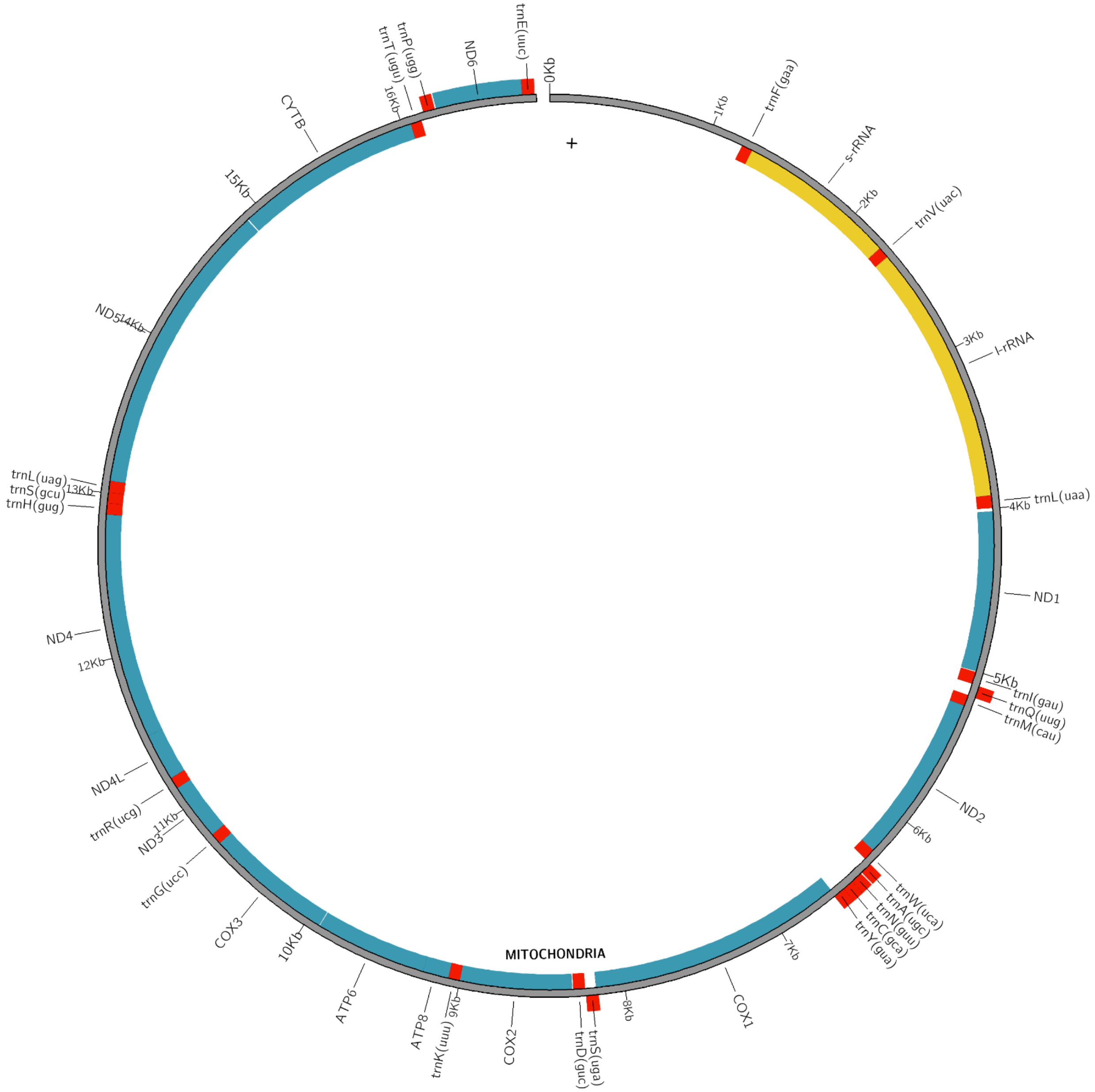

Fig. S2. **Mitochondrial genome and gene annotation of the Lapland longspur genome.**

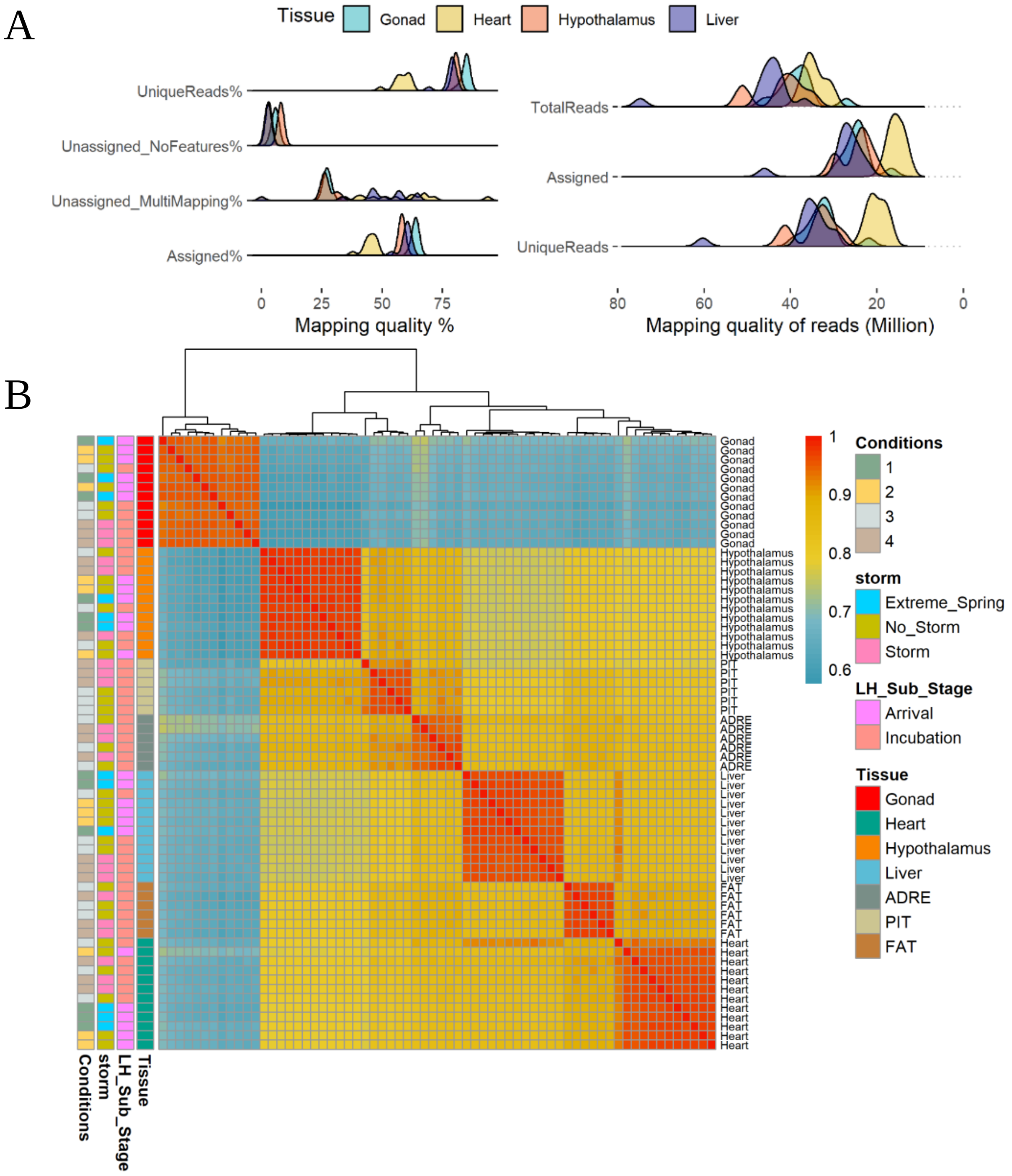

Fig. S3. Expression profile of RNA-seq data. (**A**) RNA mapping quality summarised by tissue. (**B**) Heatmap shows the correlation between all RNA-seq samples, demonstrating a tissue-specific pattern. The basic information for each sample is displayed on the right.

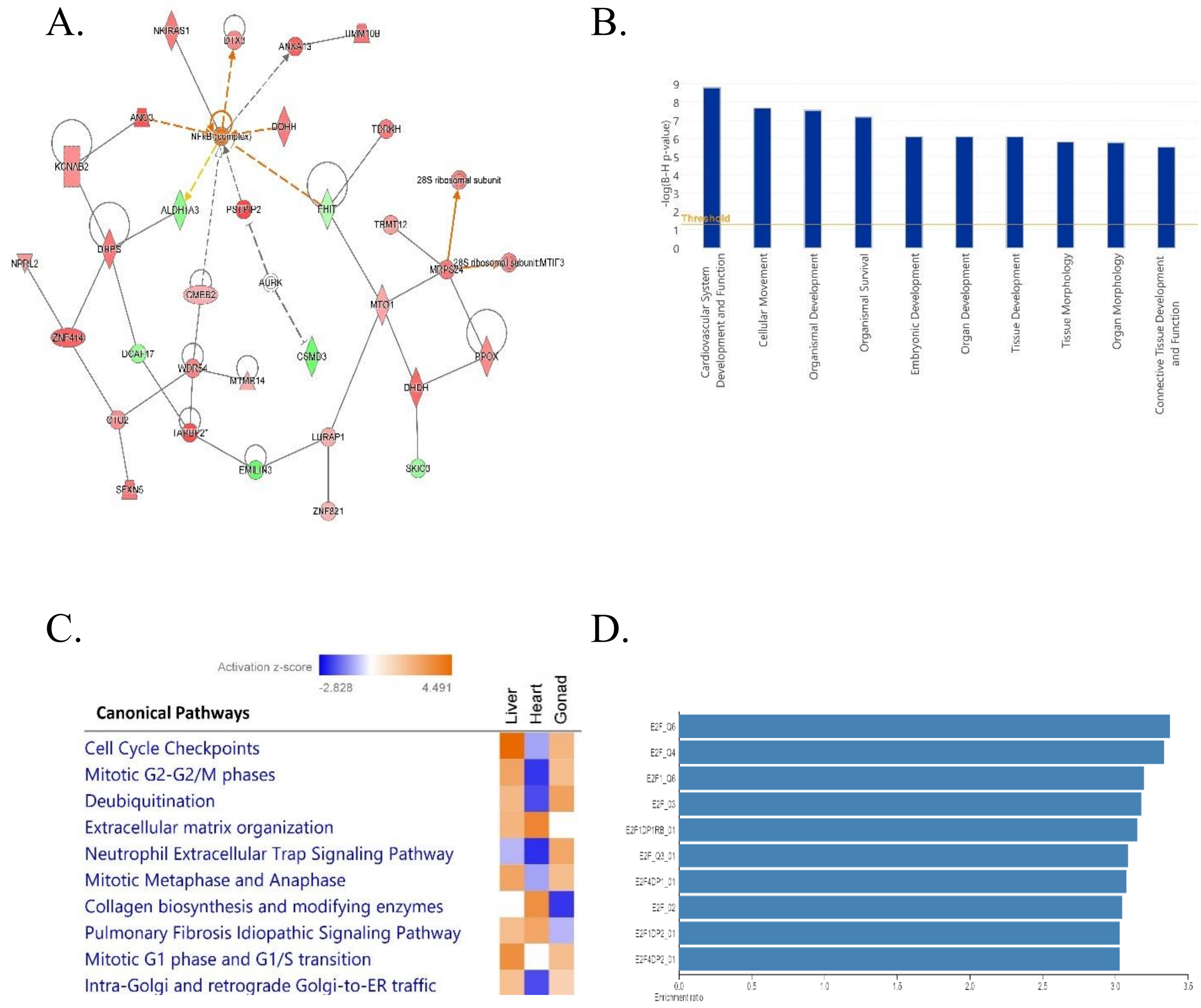

Fig. S4. Enriched pathways, networks and transcription factor binding sites of genes differentially expressed under normal conditions. (**A**) Significant network in gonad was identified using DEGs detected between benign life history stages (LHS). (**B**) Top 10 enriched molecular functions detected in heart (benign LHS). (**C**) Overview of significant canonical pathways across three tissues (benign LHS). (**D**) The significant transcription factor targets that are overrepresented in the liver (benign LHS).

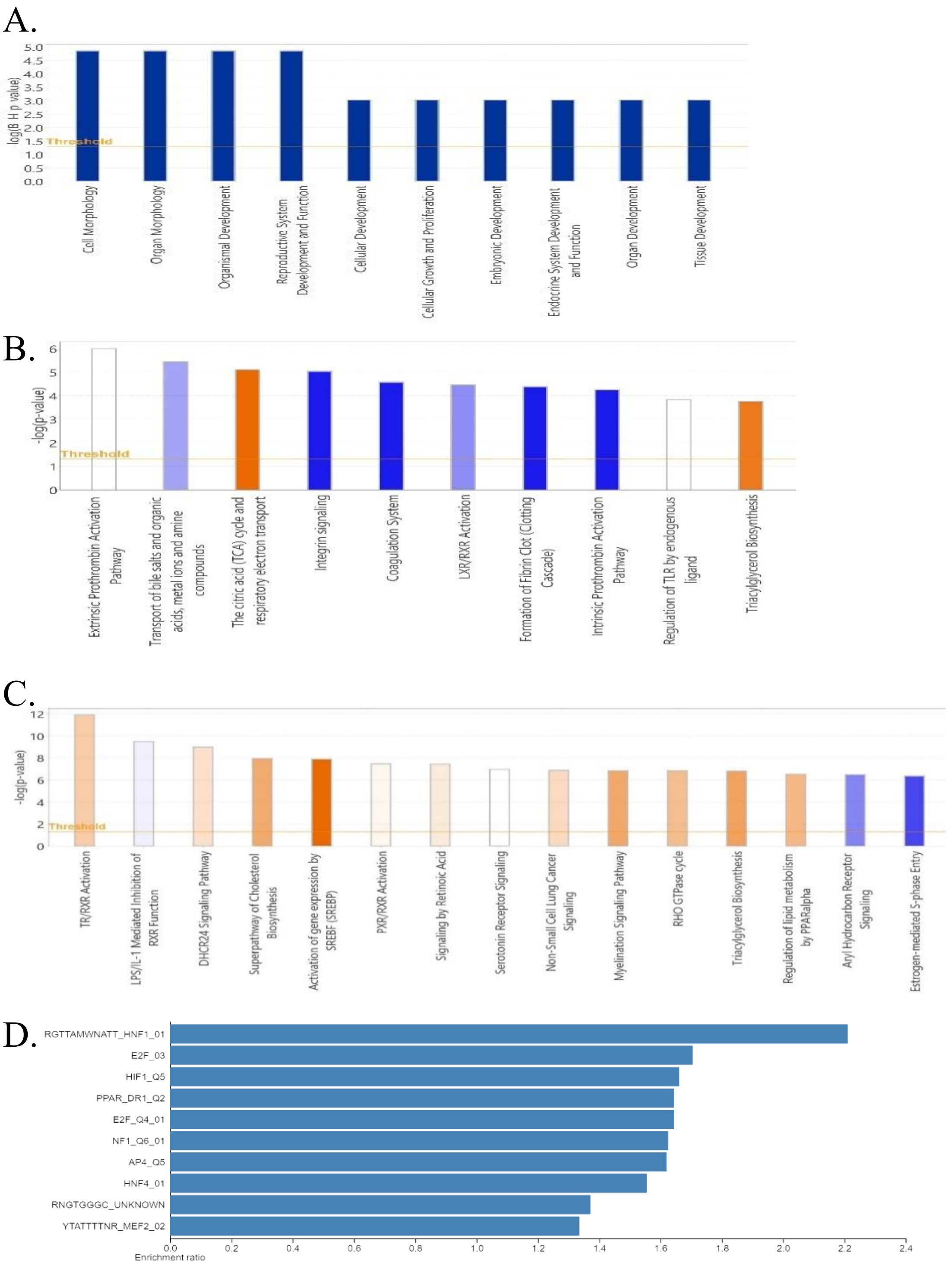

Fig. S5. Enriched pathways and transcription factor binding sites of genes differentially expressed under extreme conditions. (**A**) Top 10 molecular functions detected in gonad (extreme spring). (**B**) Most significant pathways detected in the liver (extreme spring). (**C**) Most significant pathways detected in liver (snowstorm). (**D**) The significant transcription factor targets that are overrepresented in liver (snowstorm).

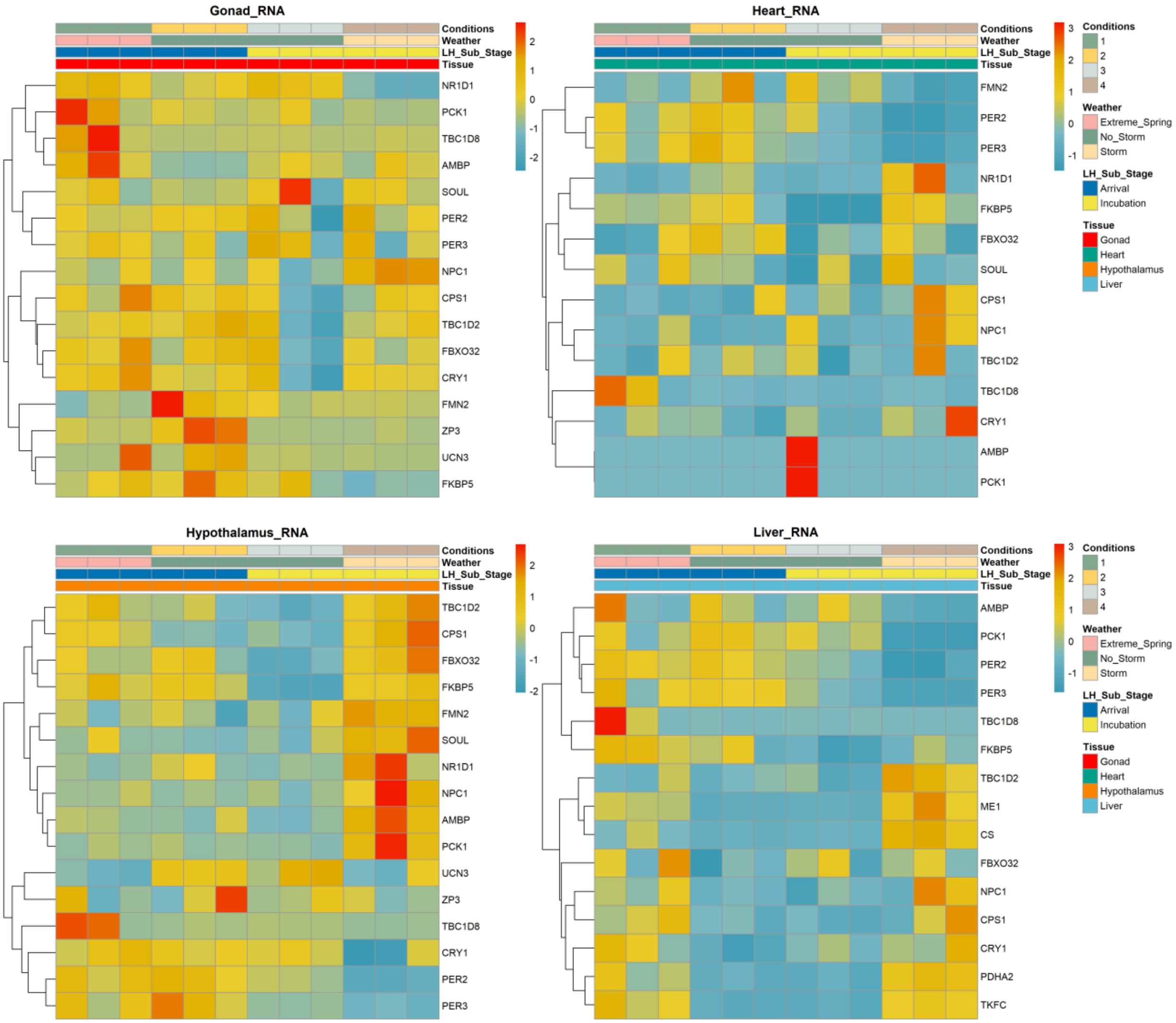

Fig. S6. Expression of genes of interest in each of the four tissues tested in the two extreme weather events.

Tissues are shown in the title of each grid, with each row showing a gene of interest, and each column showing an individual. The colour of the cell shows the relative expression level. The weather condition and the life-history stages of individuals are shown by colours at the top of each grid.

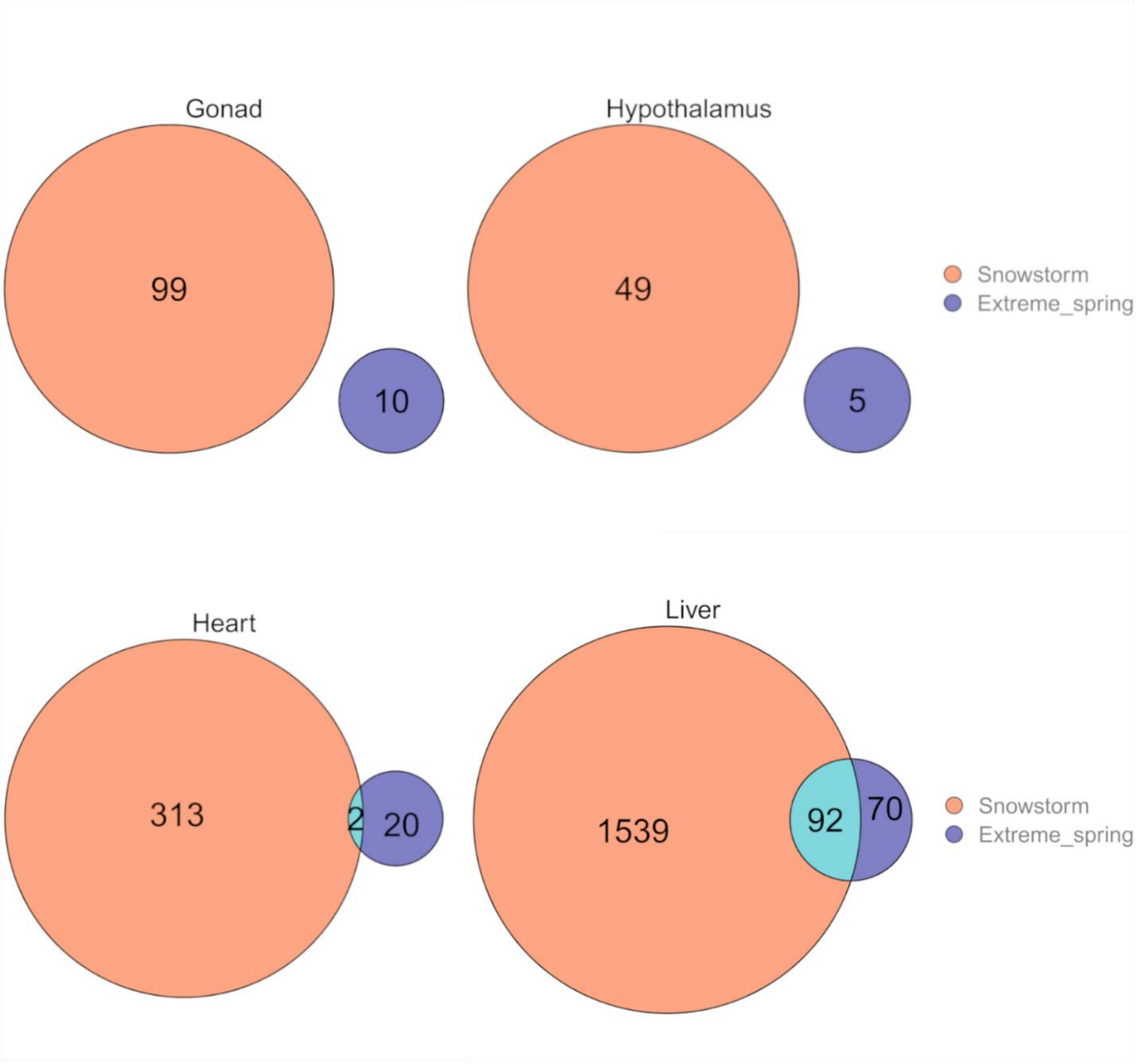

Fig. S7. Comparison of the tissue-specific differentially expressed genes.
Venn diagrams show the DEGs between the two extreme weather conditions in each tissue.

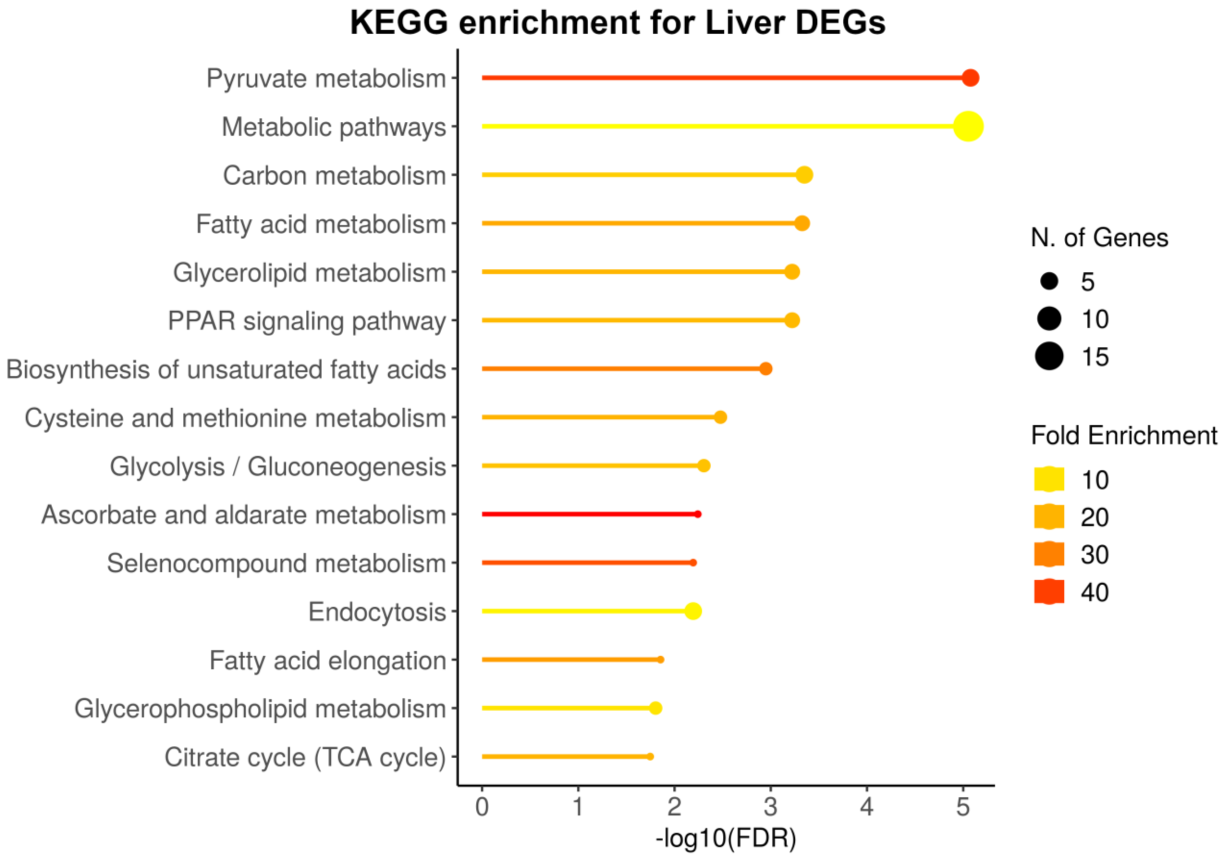

Fig. S8. **Function of Differentially Expressed Genes in liver.** KEGG pathway enrichment for liver DEGs that were identified in both extreme weather events (i.e., the extreme spring and the snowstorm).