**Supplementary Figures**

**The Cardiac Endothelial Cell Transcriptome in Neonatal, Adult, and Remodeling Hearts**

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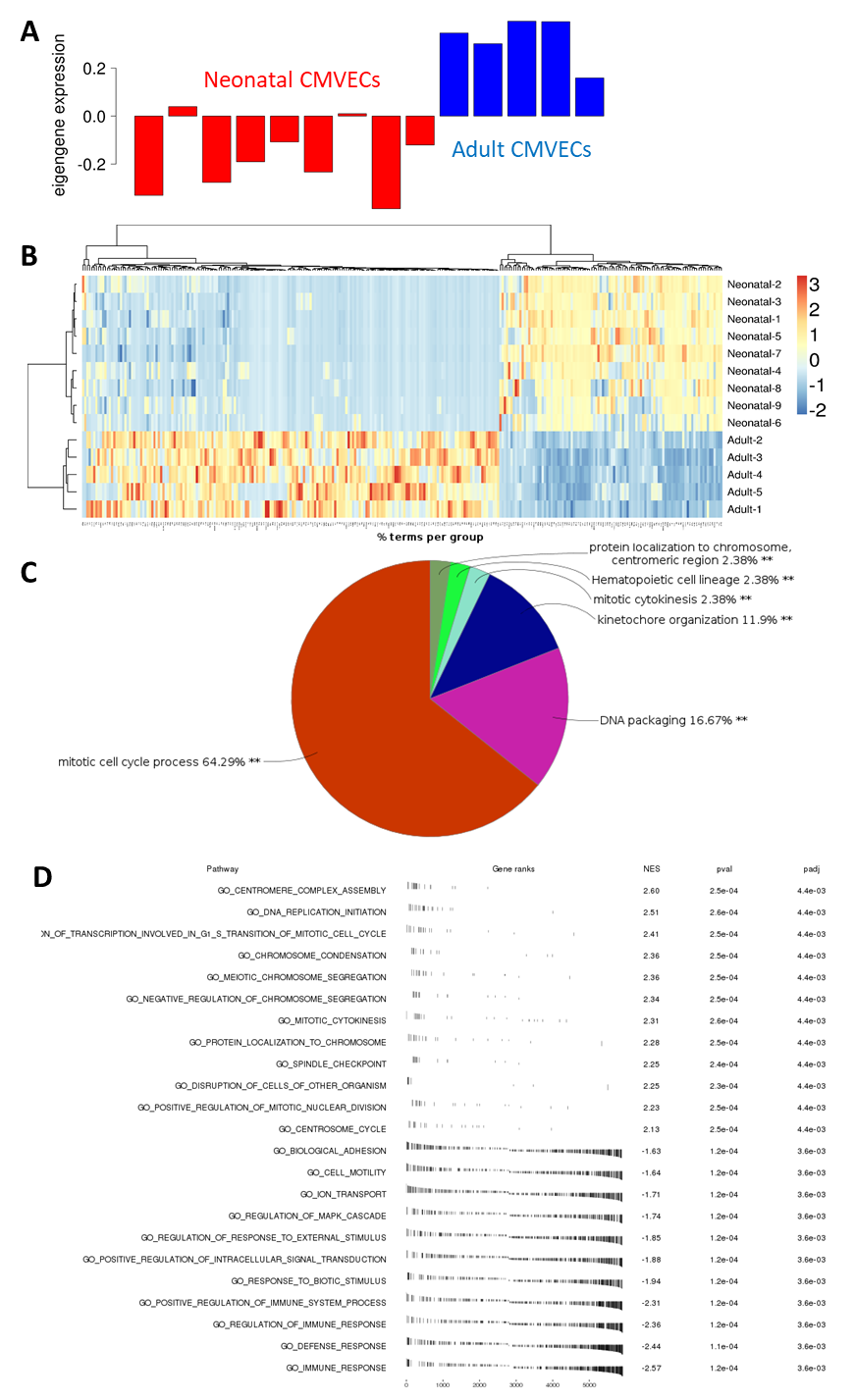
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**Supplementary Figure 1**

**Supplementary Figure 1.** **Pathway analysis of the brown module generated by co-expression network analysis. A)** Eigengene expression in 9 neonatal CMVEC samples and 5 adult CMVEC samples. The eigengene is the first principal component of the module and serves as a summary of the expression profiles of all genes in the brown module. **B)** Heatmap of all significantly up- or down-regulated genes in the brown module. **C)** ClueGO pathway analysis showing all pathways related to the differential gene expression between neonatal and adult CMVECs in the brown module. **D)** fGSEA pathway analysis showing most relevant gene ontology pathways related to the differential gene expression between neonatal and adult CMVECs in the brown module. The upper part of the table relates to pathways up-regulated in neonatal CMVECs, whereas the lower part of the table relates to pathways up-regulated in adult CMVECs.

**Supplementary Figure 2**

**Supplementary Figure 2.** **Pathway analysis of the turquoise module generated by co-expression network analysis. A)** Eigengene expression in 9 neonatal CMVEC samples and 5 adult CMVEC samples. The eigengene is the first principal component of the module and serves as a summary of the expression profiles of all genes in the turquoise module. **B)** Heatmap of all significantly up- or down-regulated genes in the turquoise module. **C)** ClueGO pathway analysis showing all pathways related to the differential gene expression between neonatal and adult CMVECs in the turquoise module. **D)** fGSEA pathway analysis showing most relevant gene ontology pathways related to the differential gene expression between neonatal and adult CMVECs in the turquoise module. The upper part of the table relates to pathways up-regulated in neonatal CMVECs, whereas the lower part of the table relates to pathways up-regulated in adult CMVECs.

**Supplementary Figure 3**

**Supplementary Figure 3.** **Pathway analysis of the grey module generated by co-expression network analysis. A)** Heatmap of all significantly up- or down-regulated genes in the grey module. **B)** ClueGO pathway analysis showing all pathways related to the differential gene expression between neonatal and adult CMVECs in the grey module. **C)** fGSEA pathway analysis showing most relevant gene ontology pathways related to the differential gene expression between neonatal and adult CMVECs in the grey module. The upper part of the table relates to pathways up-regulated in neonatal CMVECs, whereas the lower part of the table relates to pathways up-regulated in adult CMVECs.