Supplemental Material

**Data S1.**

Supplemental Methods

Statistics – Network analysis

We explored the global multivariate patterns by comparing differences across the architectures of the GE networks. The network´s nodes are variables confirmed in both statistical and machine-learning steps. The edges between nodes are the absolute values of the Pearson correlation coefficients if the FDR-adjusted *p*-values were significant. The graph was computed using the stress-majorization layout [14]. To facilitate the visualization of important nodes, two filters were used: a) the node-degree > 2, and normalized centrality-betweenness > 20%.

Table S1. Primer for RT-qPCR.

HPRT1	
Foward	GGACTTGAATCATGTTTGTG
Reverse	CAGATGTTTCCAAACTCAAC
GAPDH	
Foward	ACCAGGGCTGCTTTTAACTCTG
Reverse	TTCTCCATGGTCGTGAAGACAC
CASP1	
Foward	GCAGAAGCAAGCGTGACAGC
Reverse	TGGCATCAAAAGCTGCACATAC
RAD51B	
Foward	ACTCTGTCGCTTCTGTGGTAA
Reverse	ACATCAAGATCAGCTCCCAC
FAM104A	
Foward	CAAGGCCCGTACTTCCACAT
Reverse	CACAGAAGGCAAGAAACCGC

**Figure S1. Troponin kenetics dring maintenance perfusion.**
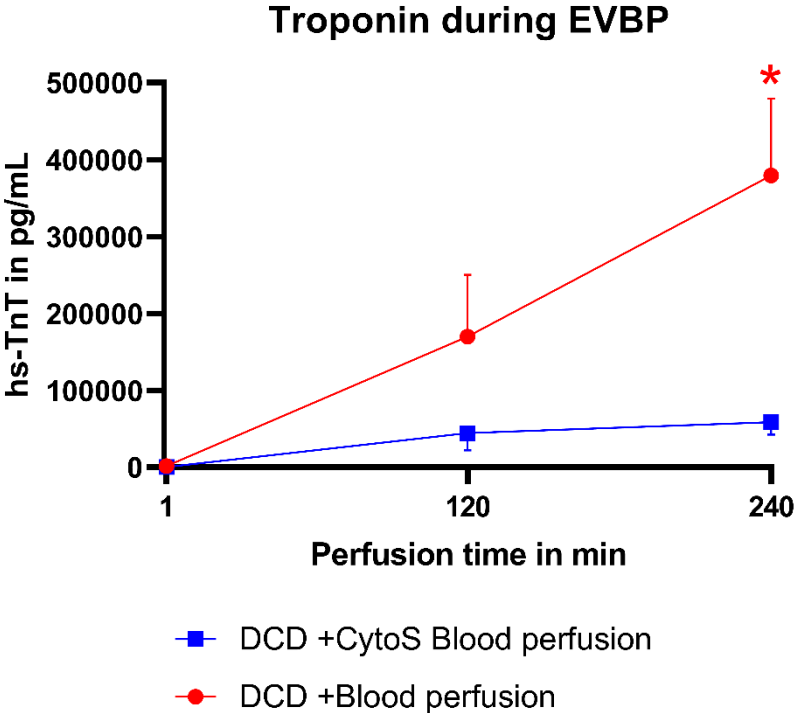
Timepoint 1 and 120 min: Samples of 3-4 pigs per group. Timepoint 240 min: Samples from 8 pigs per group.

Figure S2. Network analysis.
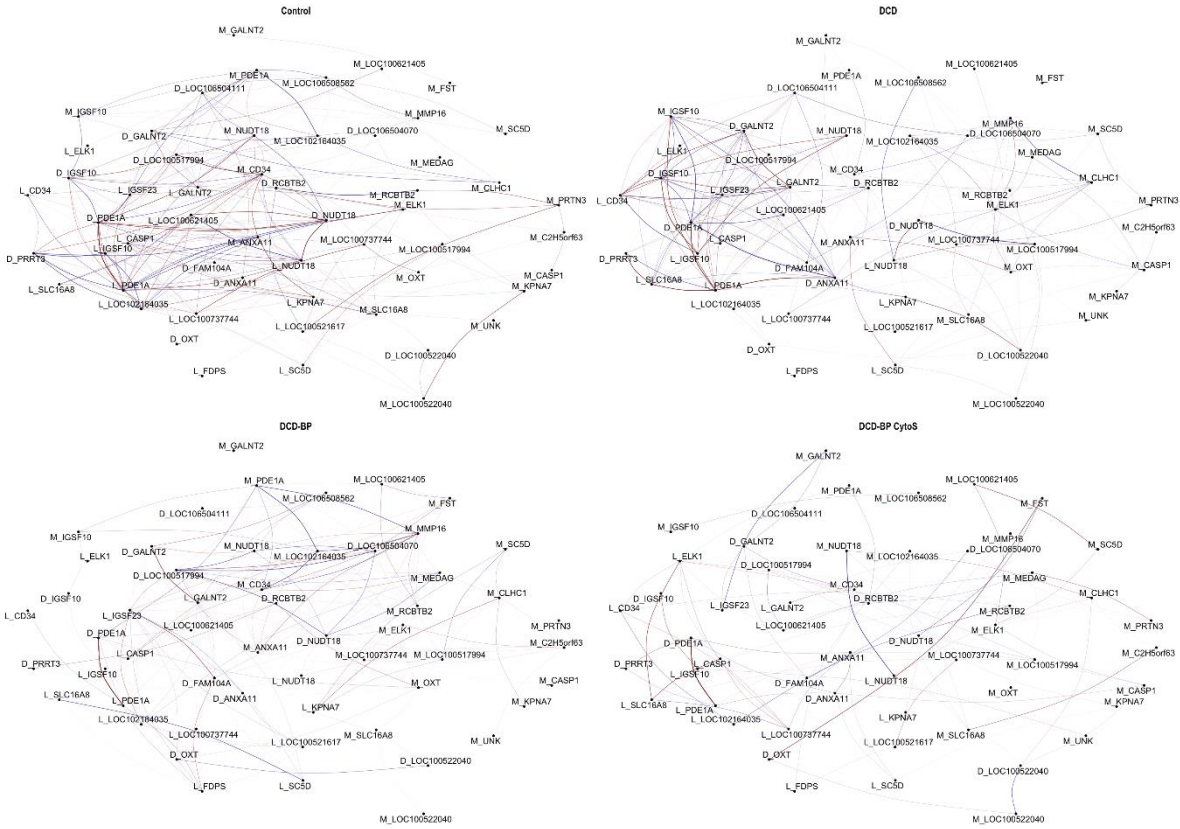
The edges between nodes are the absolute values of the Pearson correlation coefficients if the FDR-adjusted *p*-values were significant. To facilitate the visualization of important nodes, two filters [42] were used: a) the node-degree > 2, and normalized centrality-betweenness > 20%." BP: Blood perfusion. CytoS: CytoSorb. DCD: Donation after circulatory death. LAD: Left anterior descending. M, L, and D combined with gene symbols reflect the myocardial expression, LAD expression, or expression difference between both tissues. A positive correlation is shown in blue. A negative correlation is shown in red.

Figure S3. Pathway analysis for tissue comparison.
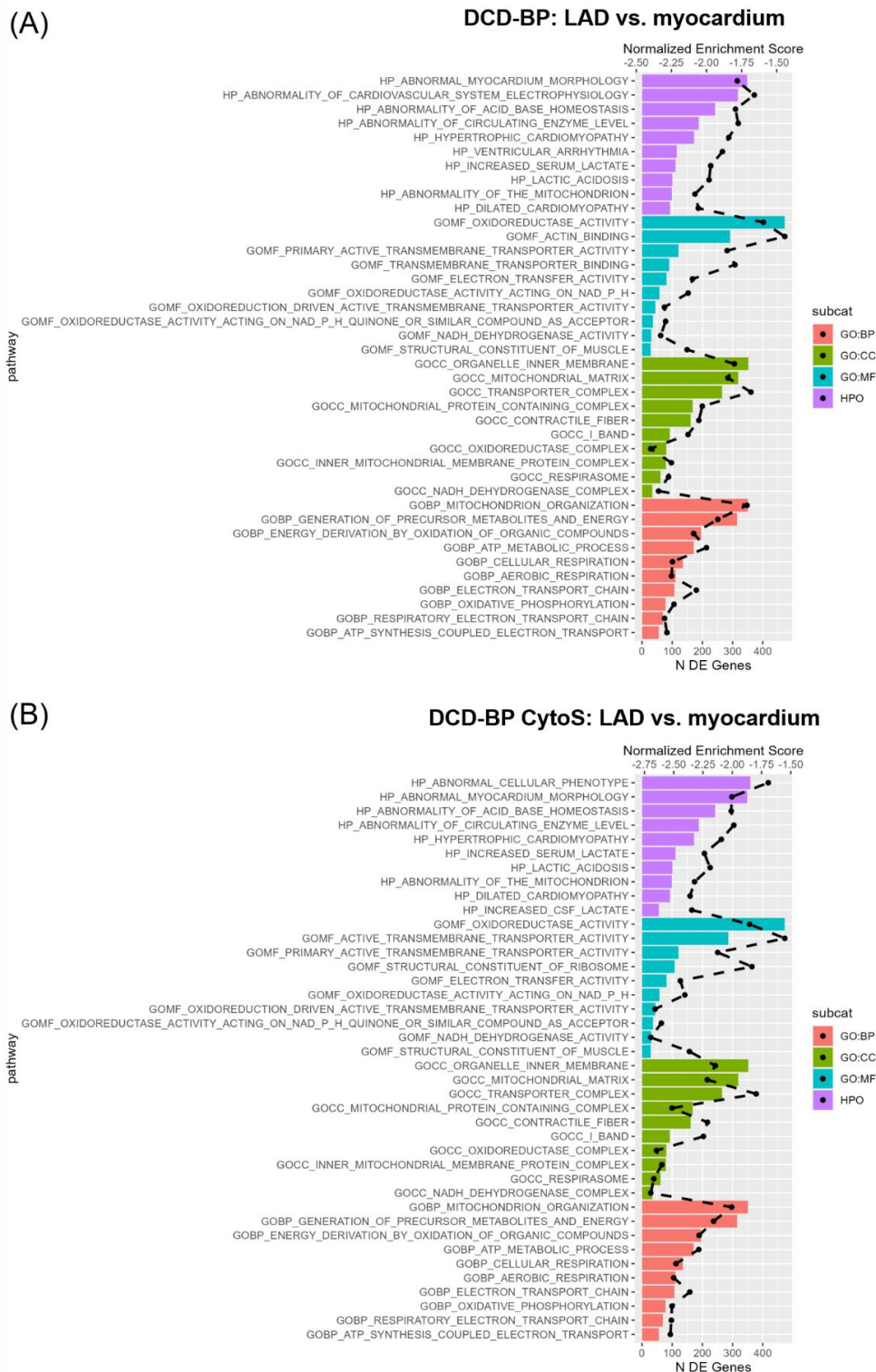
BP: biological process. DE: differentially expressed. CC: cellular component. GO: Gene ontology. HPO: human phenotype ontology. MF: molecular function. The dashed black line represents the normalized enrichment score. All plotted pathways are p<0.05.