**Supplementary figure titles and legends**

**Supp. Fig. 1. RNA-Seq experiment general statistics.**

(**A**) Boxplots indicate the number of sequenced (dark grey) and uniquely mapped (light grey) reads per sample. (**B**) An example of the quality scores per base across all sequenced reads. (**C**) On the left, raw counts' density plots for each sample are shown. Details of the colored lines are shown in the legend. On the right, density plots of normalized and filtered counts are shown. (**D**) Multidimensional scaling analysis to confirm high correlation and reproducibility among individual samples of each group. (**E**) Principal component analysis (PCA) on normalized and filtered gene expression values. It revealed that healthy individuals (H1, H2, H3 and H4) were consistently separate from HF patients (DCM1, DCM2, RCM1 and RCM2).

**Supp. Fig. 2 Analysis of differential gene expression in RNA-Seq datasets**

**(A-B)** MDS plots indicating the two biological replicates per condition DCM **(A)** and RCM **(B)** (both in blue colour), compared to healthy (CTR) individuals (red color). **(C)** Heatmap of expression values for genes differentially expressed (NOI-Seq posterior probability P≥0.95) between DCM and RCM patients. **(D)** Boxplot summarizing the results of the pathway analysis carried out on genes differentially expressed between the two pathologic conditions (DCM vs RCM).

**Supp. Fig.3. Validation of RNA**-Seq **data by qRT-PCR.**

In the figure is shown the expression profiles of up- and down-regulated DEGs (randomly selected) analyzed by qRT-PCR to validate the RNA-Seq results. Light-grey columns represent the expression values of HF vs HD detected by RNA-Seq (CPM) and dark-grey columns the expression values of HF vs HD detected by qRT-PCR (2-ΔΔCt).