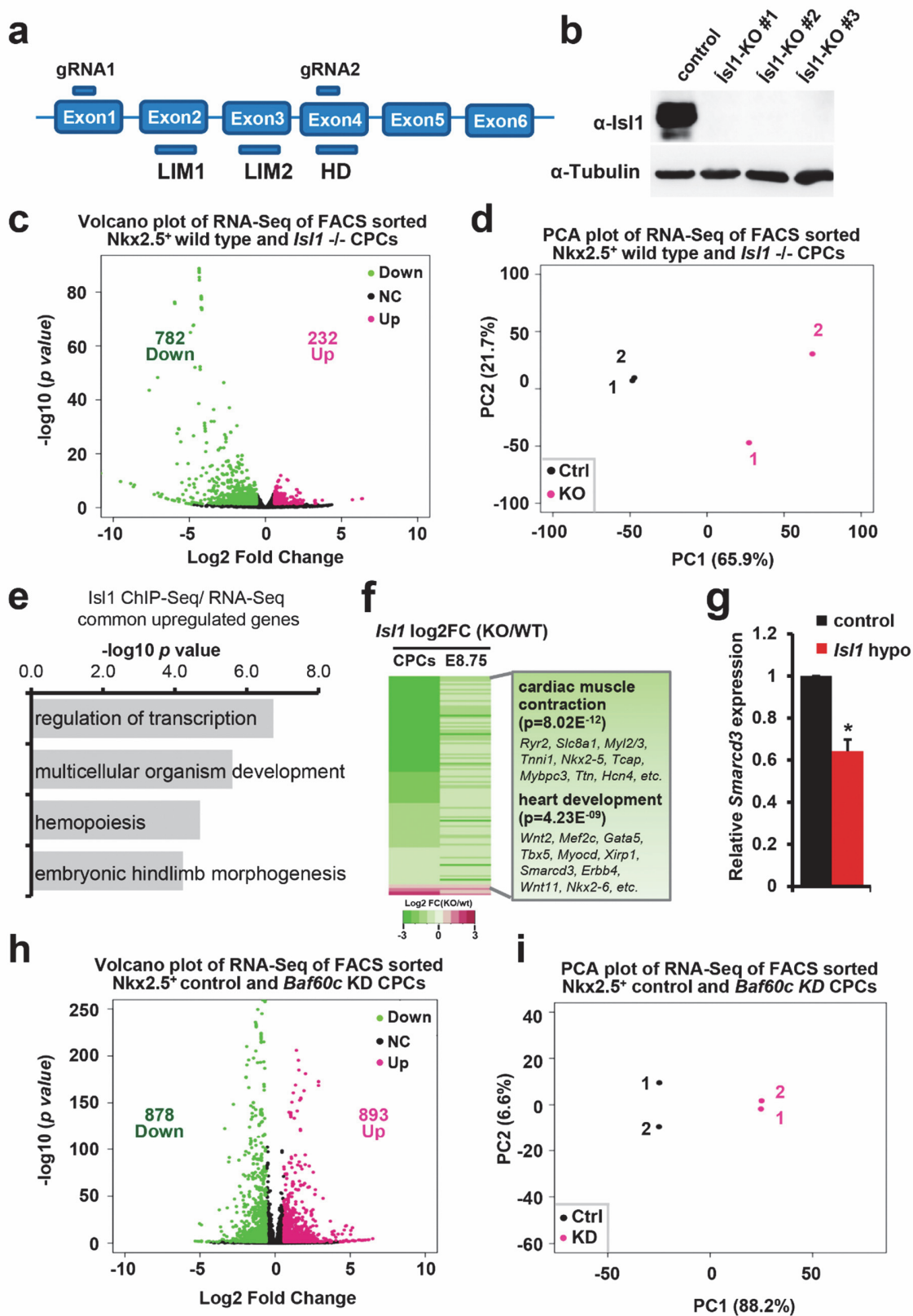




Supplementary information, Figure S4 | Gene expression changes in control, *Isl1*^{-/-} and *Baf60c* KD mESC-derived CPCs. (a) Schematic representation of the strategy used to generate *Isl1*^{-/-} mESCs using the CRISPR/Cas9 gene editing technology. (b) Western blot analysis of protein extracts from control and *Isl1*^{-/-} CPCs (day 5) derived from control and *Isl1*^{-/-} mESCs. Tubulin served as a loading control. (c) Volcano plot of RNA-Seq analysis of FACS-sorted Nkx2.5⁺ CPCs derived from two independent control and *Isl1*^{-/-} mESC clones. Down- and upregulated genes (n=2, fold change > 1.5; log2 fold change < -0.58, >0.58; p-value < 0.05) are reported as green and magenta dots, respectively. Not differentially expressed genes are represented as black dots. (d) Principal component analysis (PCA) of variance stabilized transformed RNA-Seq read counts of top 10,000 genes of control and *Isl1*^{-/-} Nkx2.5⁺ CPCs (n=2). (e) GO terms enriched in genes bound by Isl1 in ESC-derived CPCs and upregulated in *Isl1*^{-/-} CPCs. (f) Heatmap of genes bound by Isl1 and deregulated in both RNA-Seq analysis, of dissected pharyngeal mesoderm and hearts of wild-type and E8.75 Isl1 knockout embryos (n=4) and of control and *Isl1*^{-/-} Nkx2.5⁺ CPCs (n=2) (fold change > 1.5, p < 0.05). Representative genes and enriched GO terms are presented on the right side. (g) Relative mRNA expression of *Baf60c* (*Smarcd3*) in dissected OFT and RV of E10.5 control and Isl1 hypomorphic embryos. Data represent mean ± SEM, n=3. (h) Volcano plot of RNA-Seq analysis of FACS-sorted control and *Baf60c* KD Nkx2.5⁺ CPCs. Down- and upregulated genes (n=2, fold change > 1.5; log2 fold change < -0.58, >0.58; p-value < 0.05) are reported as green and magenta dots, respectively. Not differentially expressed genes are represented as black dots. (i) Principal component analysis (PCA) of variance stabilized transformed RNA-Seq read counts of top 10,000 genes of control and *Baf60c* KD Nkx2.5⁺ CPCs (n=2).