CARFMAP: a curated pathway map of cardiac fibroblasts

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S1 Appendix. Transcription factor analyses based on ChIP-Seq and text mining.

We denote "cardiac-specific" as genes having strongly up- or down-regulated expression in CFb, as compared to TFb. We used public ChIP-Seq datasets to identify the binding targets of cardiac-specific transcription factors. The overlap targets of two cardiac-specific TFs (Figure S3A) also include multiple cardiac-specific genes (strongly yellow or strongly red nodes). Replicating this process further, we identified 9 common targets of 7 cardiac-specific transcription factors (Figure S3B). Alternative to ChIP-Seq dataset, we also performed literature mining to collect the target genes of cardiac-specific TFs (Figure S3C). From this analysis, we collected 5 genes that are regulated by two or more TFs. It is also important to note that there are 5 cardiac-specific TFs that have no known binding targets from either ChIP-Seq database or the literature (orphans). The genes of interest are summarised in Figure S3D, which may serve as candidates for further experimental validation.