

Supporting Information

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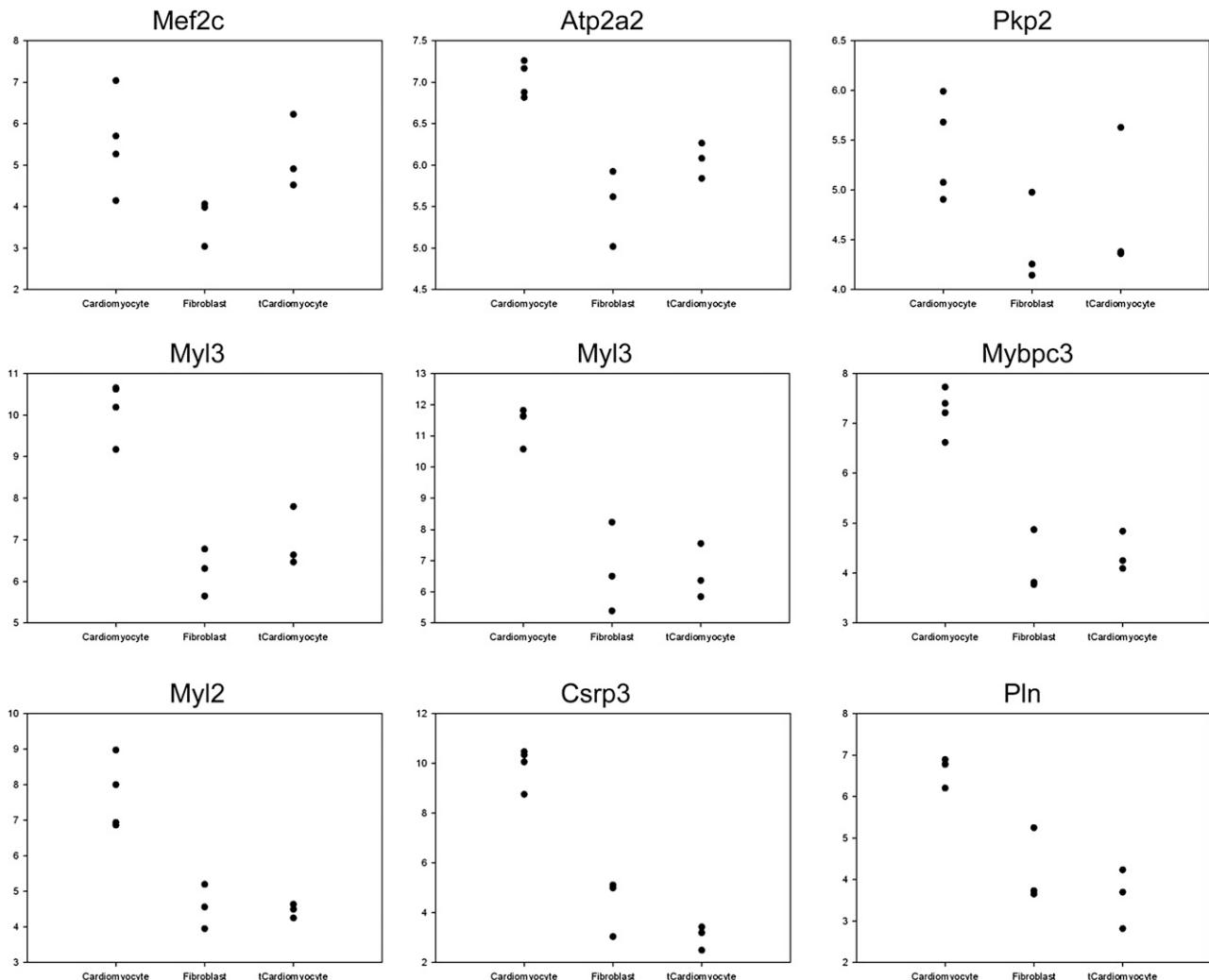


Fig. S1. The gene expression levels of selected individual genes display intercellular variability within a cell type. The expression levels of selected individual genes (log₂ scale) are plotted by cell types. Mef2c, myocyte enhancer factor 2c; Atp2a2, calcium-transporting ATPase sarcomeric reticulum type 2; Pkp2, plakophilin; Myl3, myosin, light chain 3; Mybpc3, cardiac myosin-binding protein C; Myl2, myosin, light chain 2; Csrp3, cysteine and glycine-rich protein 3; Pln, cardiac phospholamban.

Table S1. Top 25 Gene Ontology categories enriched in cardiomyocyte-specific genes that are up-regulated in tCardiomyocytes (*n* = 262)

Category	Term	Description	Count	Fold enrichment	P value	Benjamini P
BP_FAT	GO:0030900	Forebrain development	8	4.62	1.71E-03	8.83E-01
BP_FAT	GO:0010604	Positive regulation of macromolecule metabolic process	16	2.44	2.22E-03	7.52E-01
MF_FAT	GO:0016563	Transcription activator activity	10	3.44	2.46E-03	5.30E-01
BP_FAT	GO:0045893	Positive regulation of transcription, DNA-dependent	12	2.78	3.84E-03	8.00E-01
BP_FAT	GO:0045944	Positive regulation of transcription from RNA polymerase II promoter	11	2.96	3.94E-03	7.10E-01
BP_FAT	GO:0051254	Positive regulation of RNA metabolic process	12	2.76	4.05E-03	6.39E-01
BP_FAT	GO:0006357	Regulation of transcription from RNA polymerase II promoter	15	2.35	4.51E-03	6.11E-01
MF_FAT	GO:0000166	Nucleotide binding	38	1.55	4.76E-03	5.18E-01
BP_FAT	GO:0010557	Positive regulation of macromolecule biosynthetic process	13	2.36	8.64E-03	7.89E-01
BP_FAT	GO:0045941	Positive regulation of transcription	12	2.43	1.01E-02	7.95E-01
BP_FAT	GO:0010628	Positive regulation of gene expression	12	2.37	1.21E-02	8.18E-01
BP_FAT	GO:0009891	Positive regulation of biosynthetic process	13	2.25	1.25E-02	7.93E-01
MF_FAT	GO:0017076	Purine nucleotide binding	32	1.53	1.39E-02	7.61E-01
BP_FAT	GO:0051329	Interphase of mitotic cell cycle	4	7.87	1.40E-02	7.99E-01
MF_FAT	GO:0030528	Transcription regulator activity	23	1.70	1.43E-02	6.67E-01
BP_FAT	GO:0016311	Dephosphorylation	6	4.10	1.53E-02	8.01E-01
BP_FAT	GO:0051325	Interphase	4	7.56	1.55E-02	7.80E-01
BP_FAT	GO:0046632	α - β T-cell differentiation	3	15.22	1.61E-02	7.66E-01
BP_FAT	GO:0045935	Positive regulation of nucleobase, nucleoside, nucleotide, and nucleic acid metabolic process	12	2.27	1.64E-02	7.49E-01
BP_FAT	GO:0006796	Phosphate metabolic process	17	1.89	1.65E-02	7.30E-01
BP_FAT	GO:0006793	Phosphorus metabolic process	17	1.89	1.65E-02	7.30E-01
MF_FAT	GO:0016791	Phosphatase activity	8	3.00	1.72E-02	6.54E-01
CC_FAT	GO:0005886	Plasma membrane	41	1.39	1.75E-02	9.81E-01
BP_FAT	GO:0007292	Female gamete generation	4	6.88	1.99E-02	7.74E-01
BP_FAT	GO:0051173	Positive regulation of nitrogen compound metabolic process	12	2.20	2.01E-02	7.57E-01

Table S2. Top 25 Gene Ontology categories enriched in fibroblast-specific genes that are down-regulated in tCardiomyocytes (*n* = 136)

Category	Term	Description	Count	Fold enrichment	P value	Benjamini P
MF_FAT	GO:0003735	Structural constituent of ribosome	7	7.51	3.14E-04	5.14E-02
CC_FAT	GO:0005840	Ribosome	7	7.01	4.34E-04	6.46E-02
MF_FAT	GO:0019787	Small conjugating protein ligase activity	6	7.78	9.84E-04	7.94E-02
CC_FAT	GO:0043232	Intracellular non-membrane-bounded organelle	21	2.11	1.03E-03	7.65E-02
CC_FAT	GO:0043228	Non-membrane-bounded organelle	21	2.11	1.03E-03	7.65E-02
MF_FAT	GO:0016881	Acid-amino acid ligase activity	6	5.86	3.42E-03	1.74E-01
BP_FAT	GO:0006412	Translation	8	4.01	3.56E-03	8.44E-01
MF_FAT	GO:0016879	Ligase activity, forming carbon-nitrogen bonds	6	5.04	6.45E-03	2.38E-01
BP_FAT	GO:0032446	Protein modification by small protein conjugation	4	8.09	1.29E-02	9.66E-01
BP_FAT	GO:0019941	Modification-dependent protein catabolic process	9	2.83	1.31E-02	8.99E-01
BP_FAT	GO:0043632	Modification-dependent macromolecule catabolic process	9	2.83	1.31E-02	8.99E-01
CC_FAT	GO:0031974	Membrane-enclosed lumen	13	2.13	1.48E-02	5.36E-01
CC_FAT	GO:0005739	Mitochondrion	14	2.04	1.51E-02	4.44E-01
BP_FAT	GO:0051603	Proteolysis involved in cellular protein catabolic process	9	2.69	1.72E-02	8.96E-01
BP_FAT	GO:0044257	Cellular protein catabolic process	9	2.68	1.78E-02	8.45E-01
MF_FAT	GO:0005198	Structural molecule activity	8	2.88	1.97E-02	4.88E-01
BP_FAT	GO:0030163	Protein catabolic process	9	2.59	2.14E-02	8.47E-01
MF_FAT	GO:0004842	Ubiquitin-protein ligase activity	4	6.23	2.56E-02	5.16E-01
CC_FAT	GO:0034399	Nuclear periphery	3	11.78	2.60E-02	5.56E-01
BP_FAT	GO:0070647	Protein modification by small protein conjugation or removal	4	6.15	2.65E-02	8.65E-01
CC_FAT	GO:0070013	Intracellular organelle lumen	12	2.04	2.76E-02	5.13E-01
CC_FAT	GO:0043233	Organelle lumen	12	2.03	2.81E-02	4.66E-01
CC_FAT	GO:0030529	Ribonucleoprotein complex	7	2.91	3.04E-02	4.48E-01
BP_FAT	GO:0044265	Cellular macromolecule catabolic process	9	2.36	3.43E-02	8.97E-01
BP_FAT	GO:0009057	Macromolecule catabolic process	9	2.20	4.87E-02	9.45E-01

Table S3. Single-cell analyses to determine tCardiomyocytes

Experiment	Immunocytochemistry	Single-cell microarray	Electrophysiology	Any analysis	Age
10X		+		+	3 wk
10A	-			-	
10B	-			-	
10C	-	+	-	+	4 wk
10D			-	-	
10E	-		+	+	5.5 wk
10F	+		+	+	3, 5, 8 wk
10G	-			-	
10H					
10I					
10J	-		+	+	3 wk
10JB					
10K					
10L					
10M					
10N	-			-	
10O	+			+	2 wk
10P	-			-	
10Q					
10R					
10S					
10T					

+, confirmed tCardiomyocyte from experiments. -, no tCardiomyocyte confirmation from experiments. Cell morphology was initially observed before taking any single-cell analysis.