

Supplementary Information

The role of cardiac transcription factor *NKX2-5* in regulating the human cardiac miRNAome.

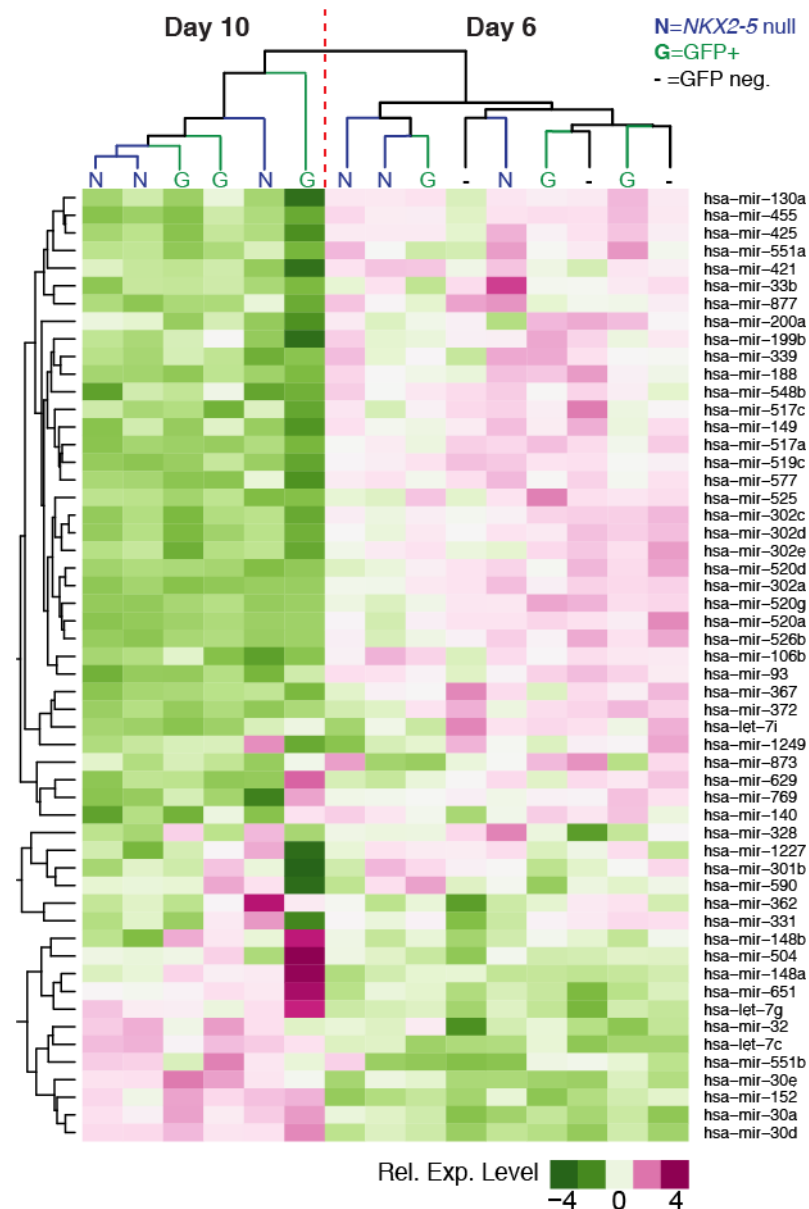
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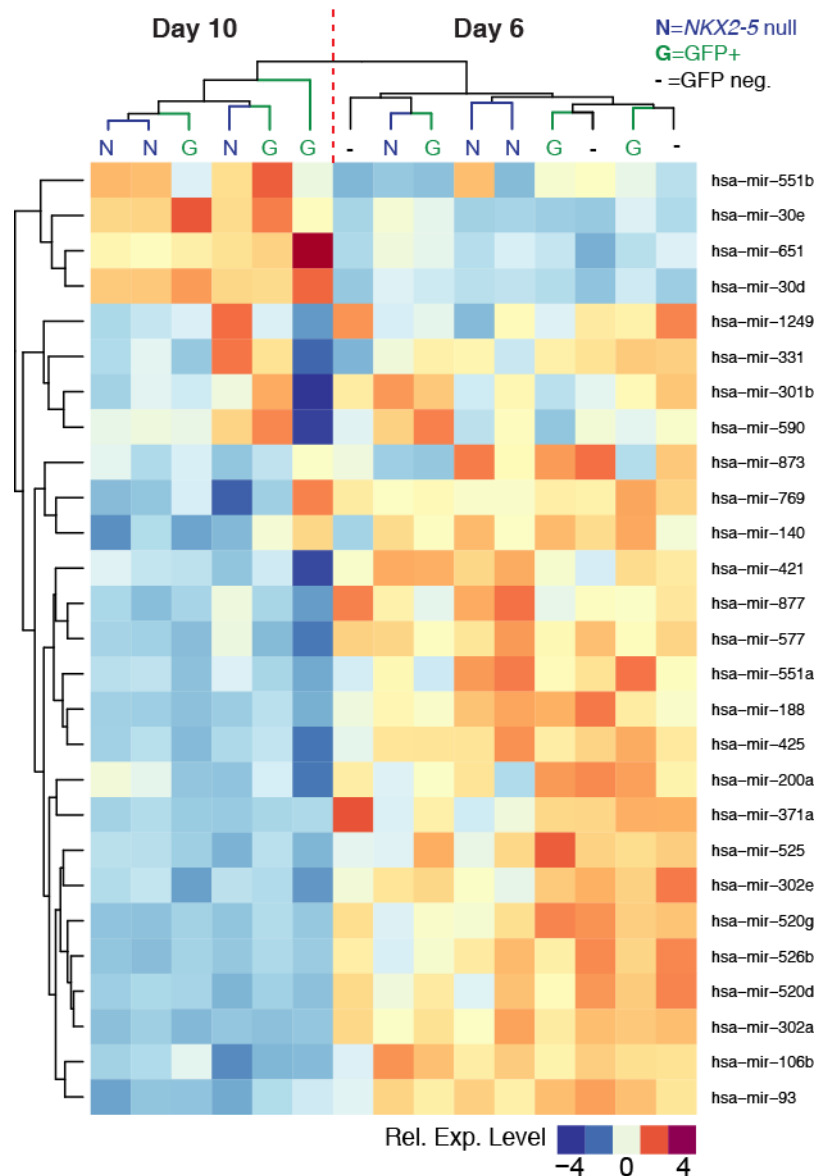
Supplementary Table 1. Summary of small RNA sequencing data.

Sample	miRNA reads	% reads miRNA	snoRNA reads	% reads snoRNAs
d6 GFP ^{neg}	2061961	22	403256	4.3
d6 GFP ^{neg}	1814338	25	124178	1.7
d6 GFP ^{neg}	2141959	22	431677	4.4
d6 GFP ⁺	1822388	24.5	138515	1.9
d6 GFP ⁺	1550786	23.5	91198	1.4
d6 GFP ⁺	154552	21.9	124484	1.7
d10 GFP ⁺	2271422	27.5	141034	1.7
d10 GFP ⁺	2521212	36.8	173173	2.5
d10 GFP ⁺	2272235	30.6	166257	2.2

Supplementary Figures.



Supplementary Figure 1. Day 6 NKX2-5 positive cells are enriched for microRNAs associated with cell proliferation. Heat map of unsupervised hierarchical clustering of microRNA sequence profile from day 6 and day 10 cells based on microRNA associated with cell proliferation ($\log_2$ RPM values). Samples cluster more closely according to day of differentiation than *NKX2-5* genotype. Differential microRNA profiles suggest the day 6 samples are more proliferative than day 10. *NKX2-5* knockout cells are indicated in blue, while the *NKX2-5*^{eGFP} positive cells are shown in green and negative cells in black.



Supplementary Figure 2. Differential expression of miRNAs in the Hippo/YAP pathway during cardiac differentiation. Heat map of unsupervised hierarchical clustering of day 6 and day 10 samples based on microRNAs involved in the Hippo/YAP pathway ($\log_2$ RPM values). Samples cluster more closely according to day of differentiation than *NKX2-5* genotype. Differential microRNA profiles suggest the day 6 samples have higher levels of Hippo/YAP signalling. *NKX2-5* knockout cells are indicated in blue, while the *NKX2-5*^{eGFP} positive cells are shown in green and negative cells in black.