

## 10 SUPPLEMENTARY DATA

## 10.1 Supplementary A: Gene Ontology Tables

Supplementary Table 1. GO association of genes upregulated in C2C12 differentiated cells compared to undifferentiated cells. BP - Biological Process, CC - Cellular Component

ID	p value	Odds Ratio	Expected Count	Observed Count	Size	Term	Ontology
GO:0006937	2.1E-06	31.74	1	6	10	regulation of muscle contraction	BP
GO:0006986	7.3E-04	9.39	1	5	16	response to unfolded protein	BP
GO:0005861	1.2E-08	Inf	0	6	6	troponin complex	CC
GO:0030017	9.7E-06	10.75	1	8	24	sarcomere	CC
GO:0005783	1.2E-05	4.52	5	16	100	endoplasmic reticulum	CC
GO:0043292	2.6E-05	9.03	1	8	27	contractile fiber	CC
GO:0015629	2.9E-05	5.83	3	11	53	actin cytoskeleton	CC

Supplementary Table 2. GO association of genes downregulated in C2C12 differentiated cells compared to undifferentiated cells. BP - Biological Process, CC - Cellular Component

ID	p value	Odds Ratio	Expected Count	Observed Count	Size	Term	Ontology
GO:0000279	9.0E-12	18.05	2	16	29	M phase	BP
GO:0000278	6.6E-11	14.63	3	16	32	mitotic cell cycle	BP
GO:0006260	1.6E-09	12.01	3	15	33	DNA replication	BP
GO:0051301	2.7E-09	15.31	2	13	31	cell division	BP
GO:0043283	7.9E-07	3.09	17	40	264	biopolymer metabolism	BP
GO:0007067	1.5E-06	13.51	1	9	21	mitosis	BP
GO:0007059	2.5E-05	19.65	1	6	10	chromosome segregation	BP
GO:0051241	3.0E-05	Inf	0	4	4	negative regulation of organismal physiological process	BP
GO:0006334	9.8E-05	13.08	1	6	12	nucleosome assembly	BP
GO:0007160	1.0E-04	21.61	1	5	8	cell-matrix adhesion	BP
GO:0006333	1.1E-04	9.23	1	7	17	chromatin assembly or disassembly	BP
GO:0006268	1.4E-04	51.38	0	4	5	DNA unwinding during replication	BP
GO:0051726	2.2E-04	4.20	4	12	51	regulation of cell cycle	BP
GO:0006270	4.0E-04	25.67	0	4	6	DNA replication initiation	BP
GO:0000910	4.0E-04	25.67	0	4	6	cytokinesis	BP
GO:0007126	4.0E-04	12.94	1	5	10	meiosis	BP
GO:0051321	4.0E-04	12.94	1	5	10	meiotic cell cycle	BP

GO:0007088	4.1E-04	Inf	0	3	3	regulation of mitosis	BP
GO:0007001	4.4E-04	5.00	3	9	33	chromosome organization and biogenesis (sensu Eukaryota)	BP
GO:0006323	5.7E-04	4.79	3	9	34	DNA packaging	BP
GO:0006461	6.6E-04	7.82	1	6	28	protein complex assembly	BP
GO:0006139	8.2E-04	2.10	20	37	310	nucleobase, nucleoside, nucleotide and nucleic acid metabolism	BP
GO:0005694	4.9E-08	7.63	4	16	54	chromosome	CC
GO:0043228	2.4E-07	3.47	14	35	208	non-membrane-bound organelle	CC
GO:0005634	5.3E-07	2.98	23	50	378	nucleus	CC
GO:0000793	9.1E-07	80.55	1	6	7	condensed chromosome	CC
GO:0000776	1.3E-04	52.49	0	4	5	kinetochore	CC
GO:0000786	1.9E-04	16.55	1	5	9	nucleosome	CC
GO:0005876	3.9E-04	Inf	0	3	3	spindle	CC
GO:0005657	8.2E-04	17.47	1	4	7	microtubule replication fork	CC

**Supplementary Table 3. GO association of genes upregulated in HL-1 cells compared to undifferentiated C2C12 cells. BP - Biological Process, CC - Cellular Component**

ID	p value	Odds Ratio	Expected Count	Observed Count	Size	Term	Ontology
GO:0006941	2.0E-04	34.15	1	5	6	striated muscle contraction	BP
GO:0015980	2.0E-04	3.96	6	14	39	energy derivation by oxidation of organic compounds	BP
GO:0044275	2.7E-04	6.25	3	9	19	cellular carbohydrate catabolism	BP
GO:0006096	3.8E-04	6.92	2	8	16	glycolysis	BP
GO:0005975	6.8E-04	2.95	8	17	58	carbohydrate metabolism	BP

**Supplementary Table 4. GO association of genes downregulated in HL-1 cells compared to undifferentiated C2C12 cells. BP - Biological process, CC - Cellular component**

ID	p value	Odds Ratio	Expected Count	Observed Count	Size	Term	Ontology
GO:0007275	2.5E-07	2.66	29	56	235	development	BP
GO:0007155	4.0E-07	4.41	9	24	65	cell adhesion	BP
GO:0000902	3.5E-06	4.88	6	18	45	cellular morphogenesis	BP
GO:0007160	4.1E-06	48.78	1	7	8	cell-matrix adhesion	BP
GO:0042060	5.1E-05	11.18	2	8	13	wound healing	BP
GO:0006817	1.2E-04	12.16	2	7	11	phosphate transport	BP
GO:0007399	1.5E-04	3.34	8	18	57	nervous system development	BP
GO:0001525	1.7E-04	4.72	4	12	30	angiogenesis	BP
GO:0009887	1.9E-04	3.13	9	19	63	organ morphogenesis	BP
GO:0030216	2.8E-04	Inf	1	4	4	keratinocyte differentiation	BP
GO:0001568	3.5E-04	3.69	6	14	41	blood vessel development	BP
GO:0048637	8.7E-04	6.93	2	7	14	skeletal muscle development	BP
GO:0031012	2.5E-08	6.11	7	22	47	extracellular matrix	CC
GO:0005576	2.7E-06	2.42	30	54	223	extracellular region	CC
GO:0005581	1.4E-04	19.26	1	6	8	collagen	CC
GO:0005604	3.8E-04	9.02	2	7	12	basement membrane	CC
GO:0005615	4.5E-04	1.99	27	44	201	extracellular space	CC

**Supplementary Table 5. Biological process GO association of genes regulated by Gata4 in HL-1 cells according to ChIP-chip data.**

ID	p value	Odds Ratio	Expected Count	Observed Count	Size	Term
GO:0007507	2.1E-06	4.45	5	17	113	heart development
GO:0007519	1.9E-05	4.69	3	13	82	striated muscle development
GO:0048741	2.6E-05	6.93	2	9	41	skeletal muscle fiber development
GO:0008284	2.9E-05	3.94	4	15	110	positive regulation of cell proliferation
GO:0006936	4.4E-05	7.56	1	8	34	muscle contraction
GO:0007155	5.5E-05	2.40	14	30	349	cell adhesion
GO:0045823	6.4E-05	Inf	0	3	3	positive regulation of heart contraction
GO:0006937	9.4E-05	10.47	1	6	20	regulation of muscle contraction
GO:0002520	1.1E-04	2.92	7	19	182	immune system development
GO:0048731	1.3E-04	1.77	41	64	1026	system development
GO:0048518	1.5E-04	1.92	27	47	686	positive regulation of biological process
GO:0008016	1.5E-04	13.54	1	5	14	regulation of heart contraction
GO:0002026	1.6E-04	24.29	0	4	8	cardiac inotropy
GO:0055008	2.5E-04	72.65	0	3	4	cardiac muscle morphogenesis
GO:0030097	3.9E-04	2.91	6	16	153	hemopoiesis
GO:0035051	4.4E-04	16.19	0	4	10	cardiac cell differentiation
GO:0008217	4.6E-04	7.32	1	6	26	blood pressure regulation
GO:0045822	6.0E-04	36.32	0	3	5	negative regulation of heart contraction
GO:0014032	7.3E-04	8.70	1	5	19	neural crest cell development
GO:0048869	8.6E-04	1.64	41	61	1033	cellular developmental process
GO:0045670	9.7E-04	12.14	0	4	12	regulation of osteoclast differentiation

**Supplementary Table 6. Biological process GO association of genes regulated by Mef2a in HL-1 cells according to ChIP-chip data.**

ID	p value	Odds Ratio	Expected Count	Observed Count	Size	Term
GO:0006936	1.0E-08	6.55	4	19	54	muscle contraction
GO:0030036	1.2E-06	3.31	10	27	126	actin cytoskeleton organization and biogenesis
GO:0007010	2.4E-06	2.30	23	47	298	cytoskeleton organization and biogenesis
GO:0007512	5.6E-06	35.50	1	6	8	adult heart development
GO:0007507	6.8E-06	3.30	8	23	107	heart development
GO:0008015	7.9E-06	4.46	5	16	59	circulation
GO:0048738	5.4E-05	29.53	1	5	7	cardiac muscle development
GO:0008284	1.1E-04	2.83	9	21	110	positive regulation of cell proliferation
GO:0002026	1.4E-04	19.68	1	5	8	cardiac inotropy
GO:0045214	1.4E-04	19.68	1	5	8	sarcomere organization
GO:0032502	3.1E-04	1.41	134	168	1700	developmental process
GO:0001568	3.3E-04	2.35	12	25	153	blood vessel development
GO:0055002	4.0E-04	8.87	1	6	14	striated muscle cell development
GO:0050789	4.6E-04	1.36	189	225	2398	regulation of biological process
GO:0045823	4.8E-04	Inf	0	3	3	positive regulation of heart contraction
GO:0035050	5.3E-04	11.81	1	5	10	embryonic heart tube development
GO:0006357	5.5E-04	1.89	23	39	289	regulation of transcription from RNA polymerase II promoter
GO:0042692	6.8E-04	3.73	4	11	46	muscle cell differentiation
GO:0048628	9.3E-04	7.09	1	6	16	myoblast maturation

**Supplementary Table 7. Biological process GO association of genes regulated by Nkx2.5 in HL-1 cells according to ChIP-chip data.**

ID	p value	Odds Ratio	Expected Count	Observed Count	Size	Term
GO:0007507	1.6E-06	4.79	4	16	123	heart development
GO:0002026	6.5E-05	30.76	0	4	8	cardiac inotropy
GO:0007155	1.2E-04	2.50	11	25	349	cell adhesion
GO:0014032	2.6E-04	11.02	1	5	19	neural crest cell development
GO:0006936	2.8E-04	5.42	2	8	54	muscle contraction
GO:0045822	3.1E-04	45.95	0	3	5	negative regulation of heart contraction
GO:0030282	4.1E-04	15.37	0	4	12	bone mineralization
GO:0001947	4.1E-04	15.37	7	4	12	heart looping
GO:0006928	4.3E-04	2.77	7	17	212	cell motility
GO:0008015	5.3E-04	4.88	2	8	59	circulation
GO:0048771	5.3E-04	4.88	2	8	59	tissue remodeling
GO:0031214	6.6E-04	5.43	2	7	47	biomineral formation
GO:0008284	7.4E-04	3.48	4	11	110	positive regulation of cell proliferation
GO:0065007	8.0E-04	1.56	78	101	2437	biological regulation
GO:0045893	8.9E-04	2.67	7	16	206	positive regulation of transcription, DNA-dependent
GO:0006357	9.1E-04	2.37	9	20	289	regulation of transcription from RNA polymerase II promoter

**Supplementary Table 8. Biological process GO association of genes regulated by Srf in HL-1 cells according to ChIP-chip data.**

ID	p value	Odds Ratio	Expected Count	Observed Count	Size	Term
GO:0065007	1.7E-06	1.41	307	369	2437	biological regulation
GO:0050794	2.5E-06	1.42	272	332	2164	regulation of cellular process
GO:0006350	4.9E-06	1.47	173	224	1379	transcription
GO:0048869	9.1E-06	1.51	130	174	1033	cellular developmental process
GO:0006936	1.6E-05	3.83	7	19	54	muscle contraction
GO:0008016	1.6E-05	6.49	3	12	25	regulation of heart contraction
GO:0019222	2.0E-05	1.41	191	240	1522	regulation of metabolic process
GO:0006355	3.6E-05	1.43	160	204	1272	regulation of transcription, DNA-dependent
GO:0019219	4.0E-05	1.41	171	216	1361	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
GO:0032774	4.4E-05	1.42	162	206	1290	RNA biosynthetic process
GO:0007512	8.7E-05	20.99	1	6	8	adult heart development
GO:0043283	9.8E-05	1.32	327	378	2602	biopolymer metabolic process
GO:0015980	1.7E-04	2.56	12	25	94	energy derivation by oxidation of organic compounds
GO:0042787	2.5E-04	Inf	1	4	4	protein ubiquitination during ubiquitin-dependent protein catabolic process
GO:0050793	2.7E-04	1.97	24	41	189	regulation of developmental process
GO:0035239	4.0E-04	2.71	9	20	72	tube morphogenesis
GO:0035050	5.2E-04	10.49	1	6	10	embryonic heart tube development
GO:0048519	6.2E-04	1.47	80	107	635	negative regulation of biological process
GO:0048731	6.2E-04	1.37	129	162	1026	system development
GO:0048771	6.8E-04	2.85	7	17	59	tissue remodeling
GO:0030036	7.6E-04	2.11	16	29	126	actin cytoskeleton organization and biogenesis
GO:0048468	7.8E-04	1.44	87	114	688	cell development
GO:0008284	9.2E-04	2.19	14	26	110	positive regulation of cell proliferation

**Supplementary Table 9. Biological process GO terms overrepresented for genes at which binding of more than one TF was observed.**

Binding TFs	ID	P value	OddsR atio	ExpCo unt	Co unt	Size	Term
Gata4 & Mef2a	GO:0008015	1.80E-07	9.42	1	11	59	circulation
	GO:0006936	7.10E-07	9.29	1	10	54	muscle contraction
	GO:0008284	3.20E-06	5.54	3	13	110	positive regulation of cell proliferation
	GO:0007507	1.40E-05	5.19	3	12	107	heart development
	GO:0045823	1.60E-05	Inf	0	3	3	positive regulation of heart contraction
	GO:0007155	1.80E-05	3	9	23	349	cell adhesion
	GO:0002026	2.50E-05	39.68	0	4	8	cardiac inotropy
	GO:0035051	7.20E-05	26.44	0	4	10	cardiac cell differentiation
	GO:0051146	1.40E-04	12.45	1	5	21	striated muscle cell differentiation
	GO:0045822	1.50E-04	59.19	0	3	5	negative regulation of heart contraction
	GO:0035295	2.60E-04	4.32	3	10	104	tube development
	GO:0048738	5.10E-04	29.59	0	3	7	cardiac muscle development
	GO:0051891	6.30E-04	Inf	0	2	2	positive regulation of cardioblast differentiation
	GO:0007512	8.00E-04	23.67	0	3	8	adult heart development
GO:0048518	8.30E-04	2.02	17	31	686	positive regulation of biological process	
Gata4 & Nkx2.5	GO:0006936	2.20E-06	11.16	1	8	54	muscle contraction
	GO:0022610	3.10E-06	3.95	6	19	349	biological adhesion
	GO:0002026	4.50E-06	62.24	0	4	8	cardiac inotropy
	GO:0007507	4.60E-06	6.42	2	11	123	heart development
	GO:0045822	4.20E-05	92.54	0	3	5	negative regulation of heart contraction
	GO:0016337	4.20E-05	5.49	2	10	128	cell-cell adhesion
Gata4 & Srf	GO:0008015	4.40E-05	8.55	1	7	59	circulation
	GO:0008015	2.80E-07	10.31	1	10	59	circulation
	GO:0008284	2.40E-06	6.24	2	12	110	positive regulation of cell proliferation
	GO:0048518	7.20E-06	2.69	14	32	686	positive regulation of biological process
	GO:0045823	8.70E-06	Inf	0	3	3	positive regulation of heart contraction
	GO:0035051	3.30E-05	32.45	0	4	10	cardiac cell differentiation
	GO:0006936	5.90E-05	10.55	1	6	34	muscle contraction
	GO:0048869	1.90E-04	2.1	21	38	1033	cellular developmental process
	GO:0065007	2.50E-04	1.83	50	71	2437	biological regulation
	GO:0051891	4.20E-04	Inf	0	2	2	positive regulation of cardioblast differentiation
	GO:0002026	4.50E-04	29	0	3	8	cardiac inotropy
	GO:0007512	4.50E-04	29	0	3	8	adult heart development
	GO:0008283	4.80E-04	2.76	7	17	333	cell proliferation
	GO:0014032	5.30E-04	12.96	0	4	19	neural crest cell development
	GO:0006937	6.60E-04	12.15	0	4	20	regulation of muscle contraction
	GO:0009887	7.20E-04	2.65	7	17	345	organ morphogenesis
	GO:0048731	7.40E-04	1.96	21	36	1026	system development
	GO:0051146	8.00E-04	11.43	0	4	21	striated muscle cell differentiation
GO:0006357	8.80E-04	2.78	6	15	289	regulation of transcription from RNA polymerase II promoter	
GO:0035050	9.30E-04	20.71	0	3	10	embryonic heart tube development	
Mef2a & Nkx2.5	GO:0022610	5.30E-06	3.38	8	22	349	biological adhesion
	GO:0007507	1.10E-05	5.8	2	11	102	heart development
	GO:0002026	1.40E-05	46.32	0	4	8	cardiac inotropy
	GO:0008015	3.50E-05	7.42	1	8	59	circulation
	GO:0007010	7.10E-05	3.16	6	18	298	cytoskeleton organization and biogenesis
	GO:0045822	9.70E-05	69.03	0	3	5	negative regulation of heart contraction
	GO:0006936	1.50E-04	7	1	7	54	muscle contraction
	GO:0006357	1.60E-04	3.05	6	17	289	regulation of transcription from RNA polymerase II promoter
	GO:0048738	3.30E-04	34.51	0	3	7	cardiac muscle development
	GO:0030036	3.80E-04	4.09	3	10	126	actin cytoskeleton organization and biogenesis
	GO:0035295	4.00E-04	4.48	2	9	104	tube development
	GO:0016337	4.30E-04	4.02	3	10	128	cell-cell adhesion
	GO:0030511	4.70E-04	Inf	0	2	2	positive regulation of transforming growth factor beta receptor signaling pathway
	GO:0008284	6.00E-04	4.21	2	9	110	positive regulation of cell proliferation
	GO:0014032	6.40E-04	12.33	0	4	19	neural crest cell development
	GO:0006928	6.60E-04	3.13	5	13	212	cell motility
	GO:0048731	9.40E-04	1.91	22	37	1026	system development

*Supplementary Data*

	GO:0003007	9.50E-04	10.88	0	4	21	heart morphogenesis
Mef2a & Srf	GO:0006936	4.70E-11	11.6	2	16	54	muscle contraction
	GO:0007512	6.40E-08	79.81	0	6	8	adult heart development
	GO:0008015	1.60E-07	7.68	2	13	59	circulation
	GO:0030036	3.40E-06	4.27	5	17	126	actin cytoskeleton organization and biogenesis
	GO:0065007	7.40E-06	1.76	90	124	2437	biological regulation
	GO:0008284	1.10E-05	4.3	4	15	110	positive regulation of cell proliferation
	GO:0035050	1.50E-05	26.49	0	5	10	embryonic heart tube development
	GO:0007155	3.20E-05	2.53	13	29	349	cell adhesion
	GO:0045823	5.00E-05	Inf	0	3	3	positive regulation of heart contraction
	GO:0045445	5.40E-05	8.88	1	7	28	myoblast differentiation
	GO:0001944	5.40E-05	3.36	6	17	155	vasculature development
	GO:0048514	7.70E-05	3.57	5	15	129	blood vessel morphogenesis
	GO:0055002	1.00E-04	14.71	1	5	14	striated muscle cell development
	GO:0002026	1.10E-04	26.39	0	4	8	cardiac inotropy
	GO:0045214	1.10E-04	26.39	0	4	8	sarcomere organization
	GO:0048731	1.40E-04	1.8	38	60	1026	system development
	GO:0007010	1.50E-04	2.5	11	24	288	cytoskeleton organization and biogenesis
	GO:0007519	2.00E-04	4.16	3	11	82	striated muscle development
	GO:0050794	2.10E-04	1.6	80	107	2164	regulation of cellular process
	GO:0048628	2.10E-04	12.03	1	5	16	myoblast maturation
	GO:0035239	2.90E-04	4.32	3	10	72	tube morphogenesis
	GO:0007507	3.00E-04	3.67	4	12	100	heart development
	GO:0048869	3.10E-04	1.74	38	59	1033	cellular developmental process
	GO:0030865	3.20E-04	17.59	0	4	10	cortical cytoskeleton organization and biogenesis
	GO:0035051	3.20E-04	17.59	0	4	10	cardiac cell differentiation
	GO:0048518	3.50E-04	1.89	25	43	686	positive regulation of biological process
	GO:0016049	5.00E-04	4	3	10	77	cell growth
	GO:0014032	5.10E-04	9.45	1	5	19	neural crest cell development
	GO:0048747	6.70E-04	5.47	2	7	41	muscle fiber development
	GO:0001947	7.20E-04	13.19	0	4	12	heart looping
GO:0016477	8.30E-04	2.69	7	16	177	cell migration	
GO:0051674	8.30E-04	2.52	8	18	212	localization of cell	
GO:0009892	8.70E-04	2.38	9	20	249	negative regulation of metabolic process	
GO:0006357	1.00E-03	2.25	11	22	289	regulation of transcription from RNA polymerase II promoter	
Mef2a & Nkx2.5	GO:0014033	1.60E-05	20.31	0	5	19	neural crest cell differentiation
	GO:0001947	4.40E-05	28.23	0	4	12	heart looping
	GO:0006936	4.50E-05	8.57	1	7	54	muscle contraction
	GO:0014031	5.60E-05	14.96	0	5	24	mesenchymal cell development
	GO:0050789	7.40E-05	2.03	43	64	2398	regulation of biological process
	GO:0001755	1.20E-04	20.52	0	4	15	neural crest cell migration
	GO:0007507	1.80E-04	5.02	2	9	113	heart development
	GO:0002026	3.00E-04	33.61	0	3	8	cardiac inotropy
	GO:0006928	4.00E-04	3.53	4	12	212	cell motility
	GO:0045944	4.00E-04	4.07	3	10	153	positive regulation of transcription from RNA polymerase II promoter
	GO:0007155	4.70E-04	2.87	6	16	349	cell adhesion
	GO:0048514	4.90E-04	4.34	2	9	129	blood vessel morphogenesis
	GO:0008015	6.10E-04	6.46	1	6	59	circulation
	GO:0035050	6.20E-04	24	0	3	10	embryonic heart tube development
	GO:0045941	6.40E-04	3.15	5	13	256	positive regulation of transcription
GO:0006366	7.10E-04	2.85	6	15	327	transcription from RNA polymerase II promoter	
GO:0007010	8.60E-04	2.91	5	14	298	cytoskeleton organization and biogenesis	
GO:0050801	9.00E-04	5.01	2	7	87	ion homeostasis	
Gata4 & Mef2a & Nkx2.5	GO:0007507	1.20E-06	7.45	2	11	123	heart development
	GO:0022610	1.80E-06	4.33	5	18	349	biological adhesion
	GO:0002026	2.70E-06	71.46	0	4	8	cardiac inotropy
	GO:0006936	1.00E-05	10.92	8	7	54	muscle contraction
	GO:0016337	1.30E-05	6.35	2	10	128	cell-cell adhesion
	GO:0008015	1.90E-05	9.86	1	7	59	circulation
GO:0045822	2.80E-05	106.11	0	3	5	negative regulation of heart contraction	
GO:0008284	9.70E-04	4.94	2	7	110	positive regulation of cell proliferation	
Gata4 & Nkx2.5 & Srf	GO:0006936	1.80E-06	14.55	1	7	54	muscle contraction
	GO:0007507	7.30E-06	7.86	1	9	123	heart development
	GO:0002026	7.00E-05	55.8	0	3	8	cardiac inotropy
	GO:0022610	1.00E-04	3.96	4	13	349	biological adhesion
	GO:0008284	2.00E-04	6.59	1	7	110	positive regulation of cell proliferation

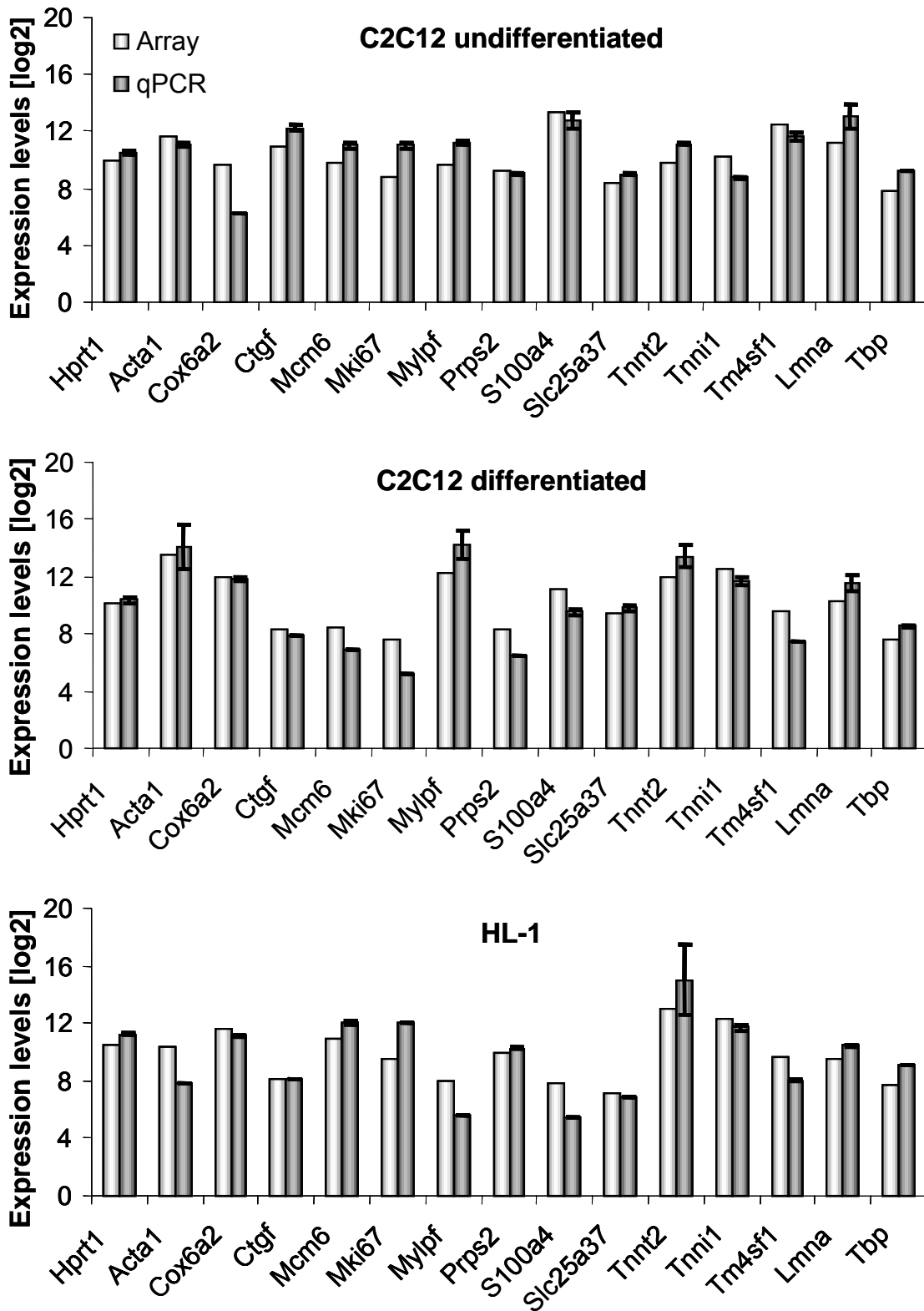
Cardiac Transcription Networks

	GO:0045893	4.10E-04	4.49	2	9	206	positive regulation of transcription; DNA-dependent
	GO:0008015	4.60E-04	8.79	1	5	59	circulation
	GO:0048731	4.90E-04	2.5	11	23	1026	system development
	GO:0016337	5.00E-04	5.59	1	7	128	cell-cell adhesion
	GO:0009991	5.40E-04	23.23	0	3	15	response to extracellular stimulus
	GO:0050919	7.10E-04	91.8	0	2	4	negative chemotaxis
	GO:0006366	8.60E-04	3.47	4	11	327	transcription from RNA polymerase II promoter
	GO:0035295	9.70E-04	5.85	1	6	104	tube development
	GO:0008283	9.90E-04	3.4	4	11	333	cell proliferation
	GO:0007155	8.40E-05	3.58	5	15	349	cell adhesion
	GO:0006936	9.40E-05	9.37	1	6	54	muscle contraction
	GO:0014032	1.20E-04	19.65	0	4	19	neural crest cell development
	GO:0002026	1.40E-04	43.8	0	3	8	cardiac inotropy
	GO:0008015	1.60E-04	8.48	1	6	59	circulation
	GO:0007507	1.60E-04	5.79	2	8	113	heart development
	GO:0007010	2.30E-04	3.57	4	13	298	cytoskeleton organization and biogenesis
Mef2a	GO:0035050	2.90E-04	31.28	0	3	10	embryonic heart tube development
&	GO:0030036	3.50E-04	5.14	2	8	126	actin cytoskeleton organization and biogenesis
Nkx2.5	GO:0048762	3.60E-04	14.02	0	4	25	mesenchymal cell differentiation
&	GO:0035239	4.70E-04	6.79	1	6	72	tube morphogenesis
Srf	GO:0001947	5.30E-04	24.32	0	3	12	heart looping
	GO:0048731	5.80E-04	2.27	14	27	1026	system development
	GO:0006357	6.30E-04	3.36	4	12	289	regulation of transcription from RNA polymerase II promoter
	GO:0051674	6.90E-04	3.79	3	10	212	localization of cell
	GO:0050789	7.50E-04	1.96	33	49	2398	regulation of biological process
	GO:0016477	7.60E-04	4.08	2	9	177	cell migration
	GO:0008284	8.10E-04	5.11	2	7	110	positive regulation of cell proliferation
	GO:0048878	8.50E-04	5.06	2	7	111	chemical homeostasis
	GO:0007507	3.70E-06	8.63	1	9	123	heart development
	GO:0006936	1.60E-05	13.16	1	6	54	muscle contraction
	GO:0022610	4.20E-05	4.37	4	13	349	biological adhesion
	GO:0002026	5.50E-05	60.78	0	3	8	cardiac inotropy
Gata4	GO:0008284	1.20E-04	7.21	1	7	110	positive regulation of cell proliferation
&	GO:0048731	1.30E-04	2.81	10	23	1026	system development
Mef2a	GO:0016337	3.00E-04	6.12	1	7	128	cell-cell adhesion
&	GO:0008015	3.10E-04	9.59	1	5	59	circulation
Nkx2.5	GO:0006366	4.20E-04	3.82	3	11	327	transcription from RNA polymerase II promoter
&	GO:0009991	4.20E-04	25.3	0	3	15	response to extracellular stimulus
Srf	GO:0050919	6.10E-04	99.87	0	2	4	negative chemotaxis
	GO:0035295	6.30E-04	6.4	1	6	104	tube development
	GO:0014032	8.80E-04	18.96	0	3	19	neural crest cell development
	GO:0045944	8.80E-04	5.05	2	7	153	positive regulation of transcription from RNA polymerase II promoter

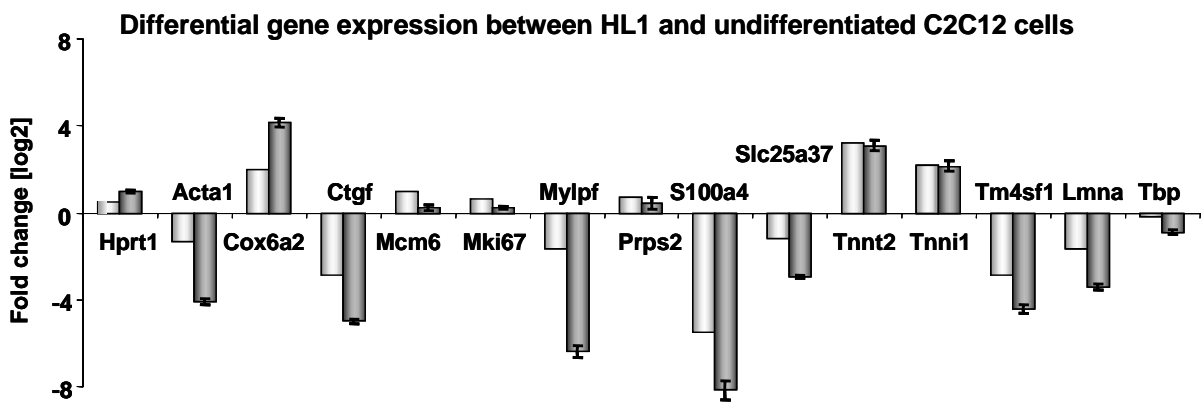
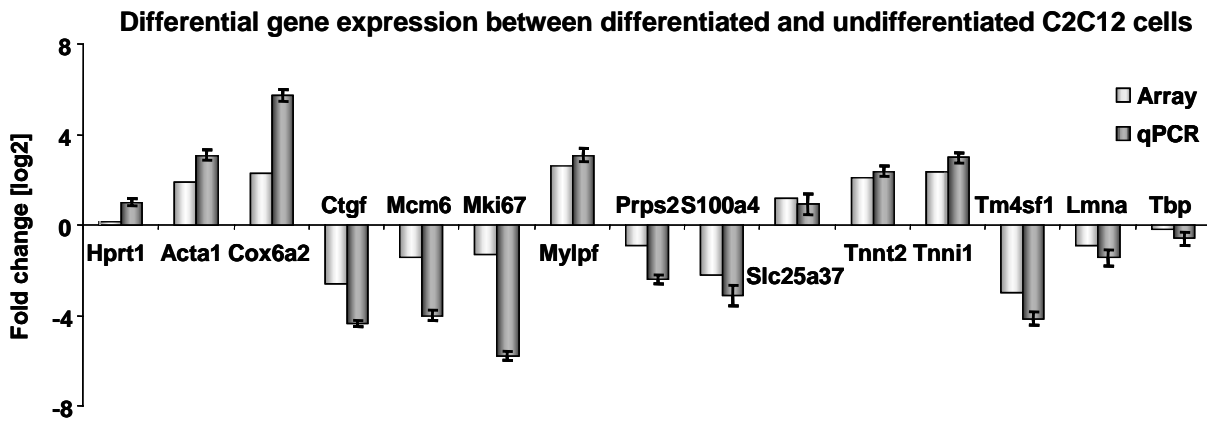


## 10.2 Supplementary B: qPCR Controls

## Verification of Expression Arrays

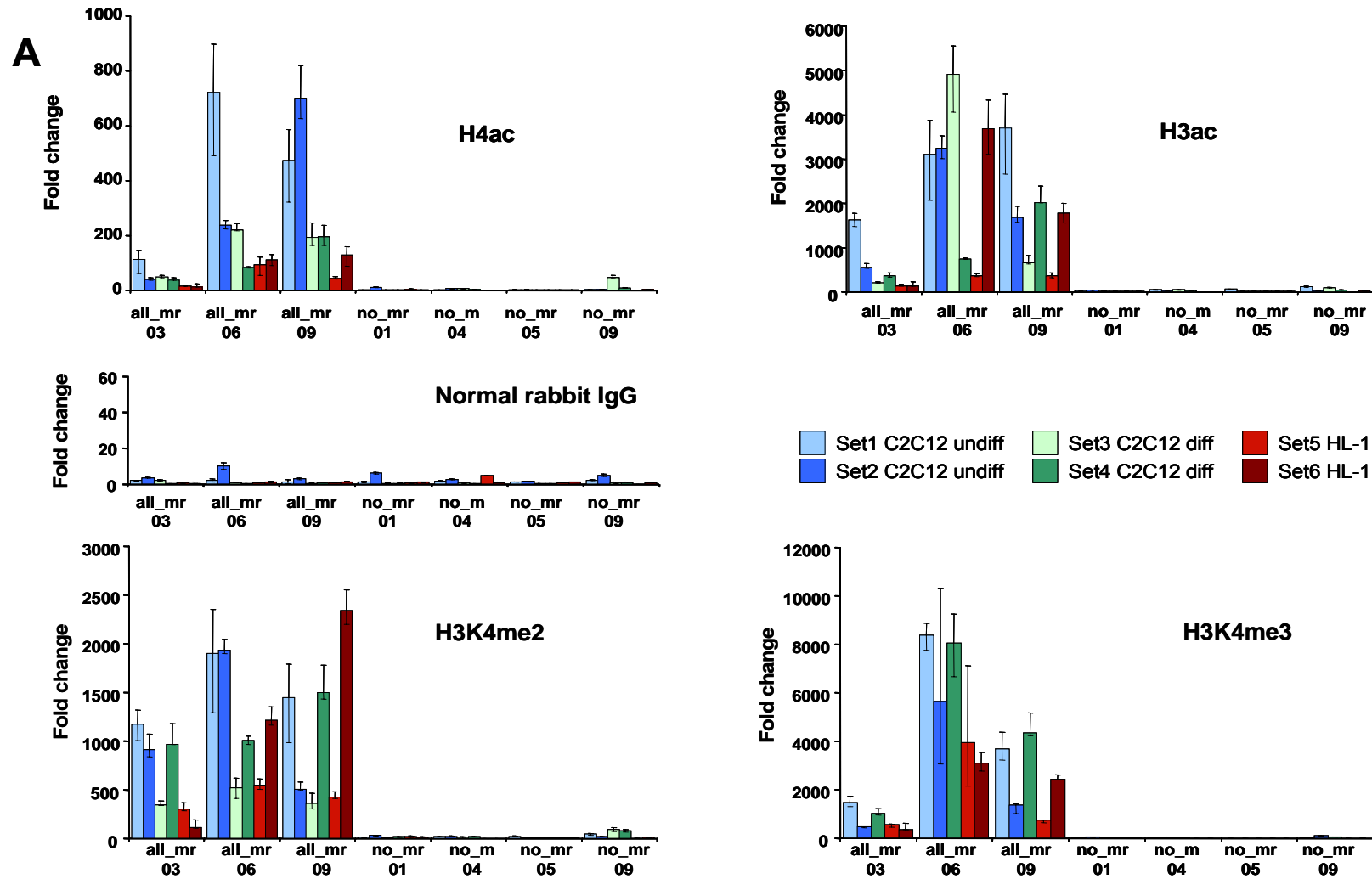


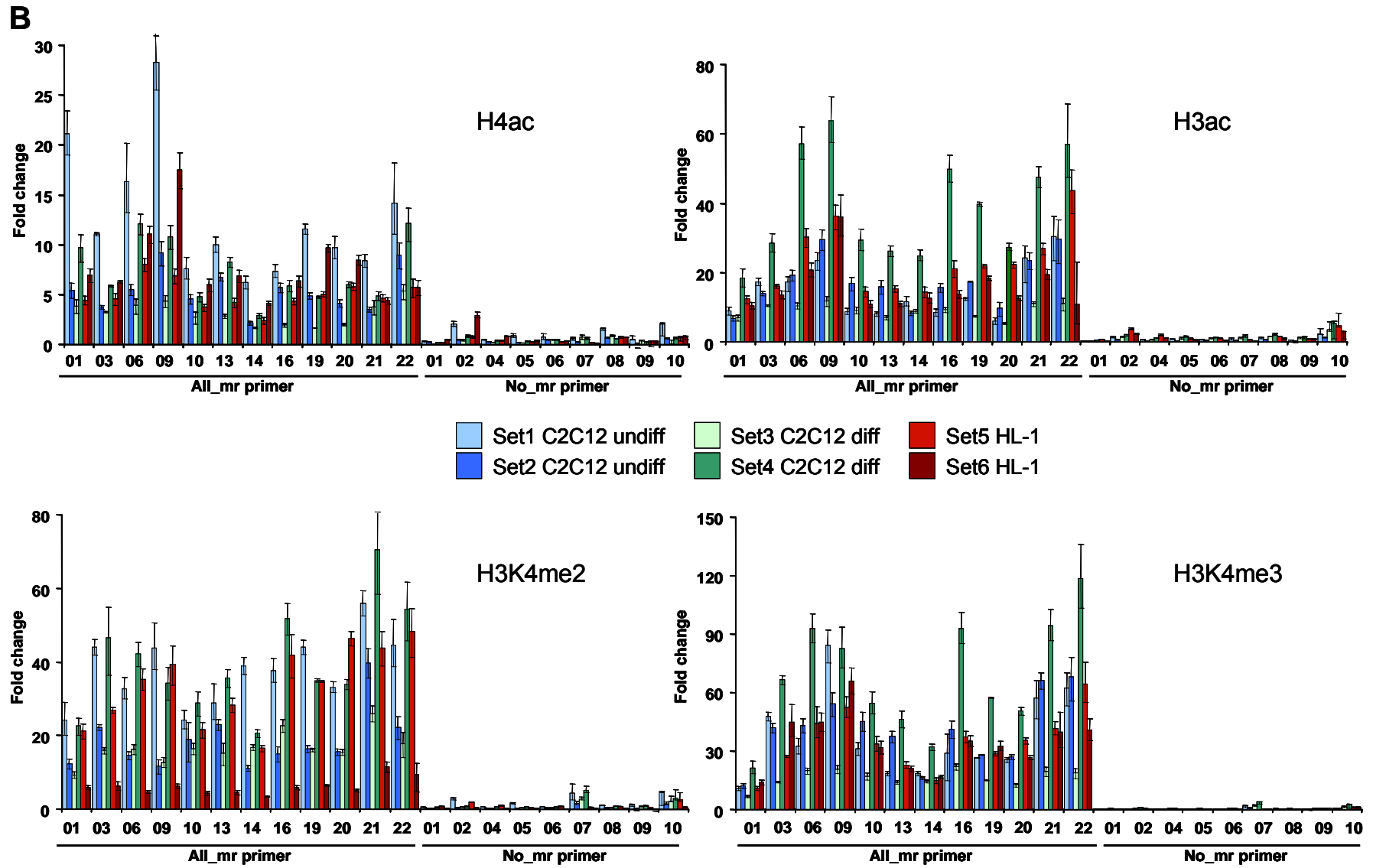
Supplementary Figure 1. Comparison of intensities as determined from expression arrays and by real-time PCR. Shown are log<sub>2</sub> intensities over two biological replicates normalized to Hprt1.



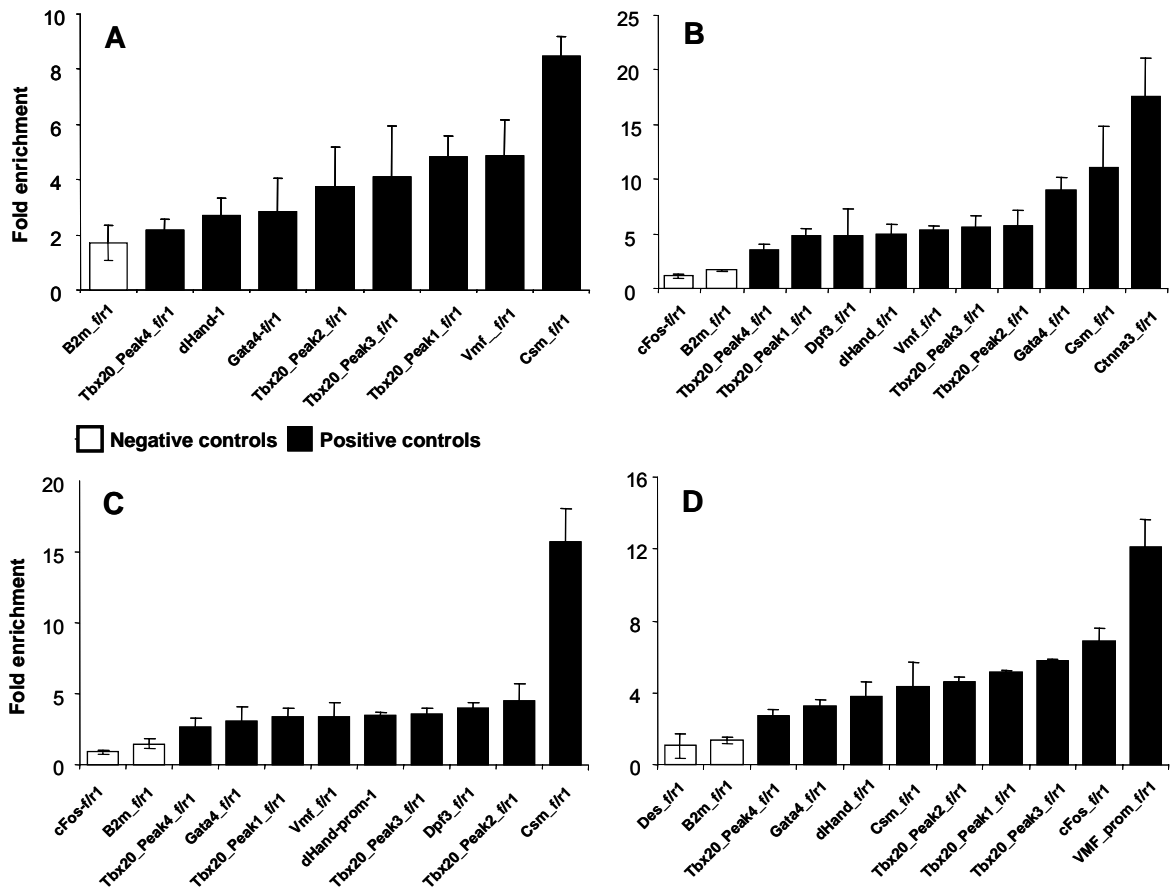
Supplementary Figure 2. Comparison of  $\log_2$  fold-changes of differentially expressed transcripts as determined from microarray analysis and by real-time PCR. Shown are values as calculated from two independent biological replicates. Real-time PCR data was normalized to Hprt1.

Supplementary Figure 3. qPCR controls of verification of Histone Modification ChIP arrays From each cell type two biological replicates (set1 and set2) were analyzed for each histone modification. Fold changes were calculated relative to input. Primers named “all\_mr” were designed for sites showing enrichment on arrays (positive controls), primers named “no\_mr” were designed for non-enriched sites (negative controls). (A) Validation of ChIP enrichment before linear amplification. Normal rabbit IgG ChIP was analyzed as control. ChIP with normal rabbit IgG showed no enrichment over input at any tested site. (B) Validation of modified sites identified by ChIP-chip using amplified material.





Confirmation of TF ChIP-chip Results



Supplementary Figure 4. Confirmation of known target genes as well as binding sites at the Tbx20 promoter by qPCR of A) Gata4, B) Mef2a C) Nkx2.5 and D) Srf.

### 10.3 Supplement C: Immunofluorescence Time Course of siRNA Treated Cells

Supplementary Figure 5. Indirect Immunofluorescence (IF) on HL-1 cells showing decreased protein levels of the transcription factors Gata4, Mef2a, Nkx2.5, and Srf after treatment with two siRNAs directed against each TF for 48h or 72h. TFs are stained red (*Alexa Fluor*<sup>®</sup> 594), nuclei were counterstained blue using 4',6-diamidino-2-phenylindole (*DAPI*). Scale bars are 50  $\mu$ m.

