

## Supplementary Table 4

### Involution Day 1 Transcription Factor Binding

#	Annotation	Total Genes With Ann	ln(Bayes factor)	neg ln(p value)	FE: neg ln(p value)	FE: neg ln(FDR)
<b>UP in Wild Type at Involution Day 1 (&gt;2 fold compared to E2F3 Het)</b>						
1	E2F_Q6: E2F	67	5.48	9.33	9.49	3.78
2	E2F_Q4: E2F	40	5.02	8.98	8.82	3.78
3	E2F1_Q6: E2F-1	52	4.38	8.28	8.18	3.55
4	OCT1_Q6: octamer-binding factor 1	26	3.23	7.1	0	0
5	HNF4_Q1_B: Hepatocyte nuclear factor 4	6	2.51	6.27	3.22	0.53
6	VMW65_Q6	19	2.28	6.06	0	0
7	GATA_C: GATA binding site	22	2.23	5.99	0	0
8	HNF1_Q1: hepatic nuclear factor 1	4	2.23	5.99	0	0
9	E2F1_Q3_Q1	32	2.08	5.84	5.73	1.56
10	E2F_Q6_Q1	17	1.89	5.63	5.69	1.56
11	TEF_Q6	15	1.57	5.24	0	0
12	FOXD3_Q1: fork head box D3	54	1.56	5.19	0	0
13	OCT1_Q2: octamer factor 1	14	1.42	5.07	0	0
14	GATA1_Q5: GATA-binding factor 1	9	1.26	4.91	1.96	0
15	AHR_Q5: aryl hydrocarbon / dioxin receptor	9	1.18	4.79	1.88	0
<b>UP in E2F3 Het at Involution Day 1 (&gt;2 fold compared to Wild Type control)</b>						
1	SREBP1_Q6	40	1.82	5.57	5.55	0.15
2	IRF7_Q1: interferon regulatory factor 7	36	1.21	4.84	0	0
3	HAND1E47_Q1: Hand1:E47 heterodimer	60	1.16	4.79	4.88	0.15
4	AP1_Q4: activator protein 1	59	1.01	4.63	0	0
5	EBF_Q6	34	0.84	4.4	4.51	0.15
6	ARNT_Q1: AhR nuclear translocator homodimers	1	0.55	4.03	0	0
7	POLY_C: Retroviral Poly A signal	5	0.5	3.97	4.73	0.15
8	SMAD4_Q6	45	0.39	3.85	3.97	0.03
9	GATA1_Q2: GATA-binding factor 1	40	0.38	3.85	3.99	0.03
10	BRN2_Q1: POU factor Brn-2	26	0.33	3.79	0.01	0
11	FOXO4_Q1: fork head box O4	49	0.12	3.55	0.01	0
12	PIT1_Q6	55	0.05	3.49	0.01	0
13	MYOGNF1_Q1: myogenin / nuclear factor 1 or related factors	26	0.05	0	3.69	0.03
14	DR3_Q4: direct repeat 3	19	0.04	0	3.79	0.03
15	MAZR_Q1: MAZ related factor	44	0.03	0	3.56	0.01

#### E2F Target Gene List

1110020C13Rik 1110064N10Rik 2510040D07Rik 9630015D15Rik Actg2 Anxa1 Anxa3 Anxa5 Apobec1 Arf4 Arrdc4 Atf4 Atf5 BC006779 BC018371 Bcar1 Bcl2l1 Brf2 Cap1 Ccna2 Cd24a Cnot2 Cryab Cyr61 FKSG24 Flnb Fosl2 Fus Gli3r2 Hist1h2bc Hsp105 Hspb1 Igk-V8 Kdelr3 Klf5 Klf6 Krt1-15 Krt2-8 Lasp1 Lpgat1 Ltbp2 Mapkapk2 Mit1 Mt2 Myc Npn3 Nupl1 Nupr1 Plekha4 Pou3f3 Pscdbp Pvr12 Rhob Riok1 S100a10 S100a11 Slc20a1 Slc30a4 Sprr2h Ssh2 Tcf12 Tead1 Tead3 Tgfr Tnc Tnfrsf12a Tubb6 Ywhah Zfp3612 Zyx

#### E2F Target Gene List From Involution Day 2

Ascc2 Col16a1 Coro1c Gja1 Hist1h2bc Hist1h3i Lgmn Lpl Metrnl Mid1ip1 Pea15 Rnase4 Rpa3 Sgpl1 Tcfe2a 2310046G15Rik 6330406L22Rik Aacs Ascc2 Col16a1 Coro1c Hexb Lgals3 Lpl Mmd Mmp14 Rpa3

## Validated Chromatin IP Target Genes

Gene	E2F Sites	Asynchronous		Apoptosis	
	(-250 to +50)	Fold Elevation	p-value	Fold Elevation	p-value
Trp53lnp1	2	2.76	0.0125	5.56	0.0135
MAP3K4	1	1.81	0.0255	4.56	0.0217
HexB	2	1.91	0.0479	2.47	0.0141
RhoB	2	1.25	NS	1.88	0.0371
Grim19	4	1.61	NS	1.60	NS
MT1	4	1.34	NS	1.65	NS
RR2 (Control)	Established	6.41	0.002	3.07	0.0169