

Wirt et al., <http://www.jcb.org/cgi/content/full/jcb.201003048/DC1>

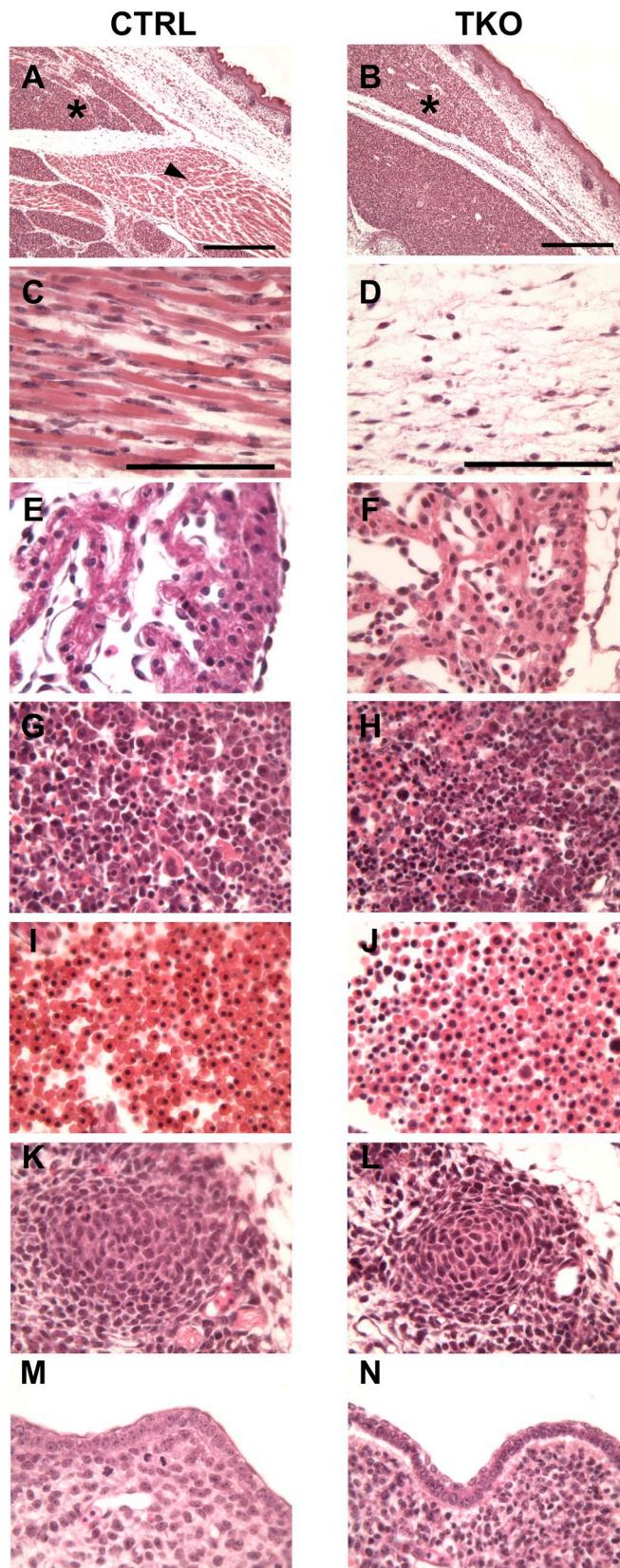


Figure S1. Histopathological analysis of representative control (CTRL) and *Mox2*^{+/-}TKO embryos. An E15.5 CTRL embryo has developing skeletal muscle (arrowhead) and adipose tissue (asterisks; A and C), whereas a TKO littermate lacks skeletal muscle completely (B and D). Other tissues examined include the heart muscle (E and F), liver (G and H), blood (I and J), developing rib (K and L), and skin (M and N). Sections were counterstained with hematoxylin and eosin. This figure is related to Fig. 1. Bars: (A and B) 500 μ m; (C–N) 150 μ m.

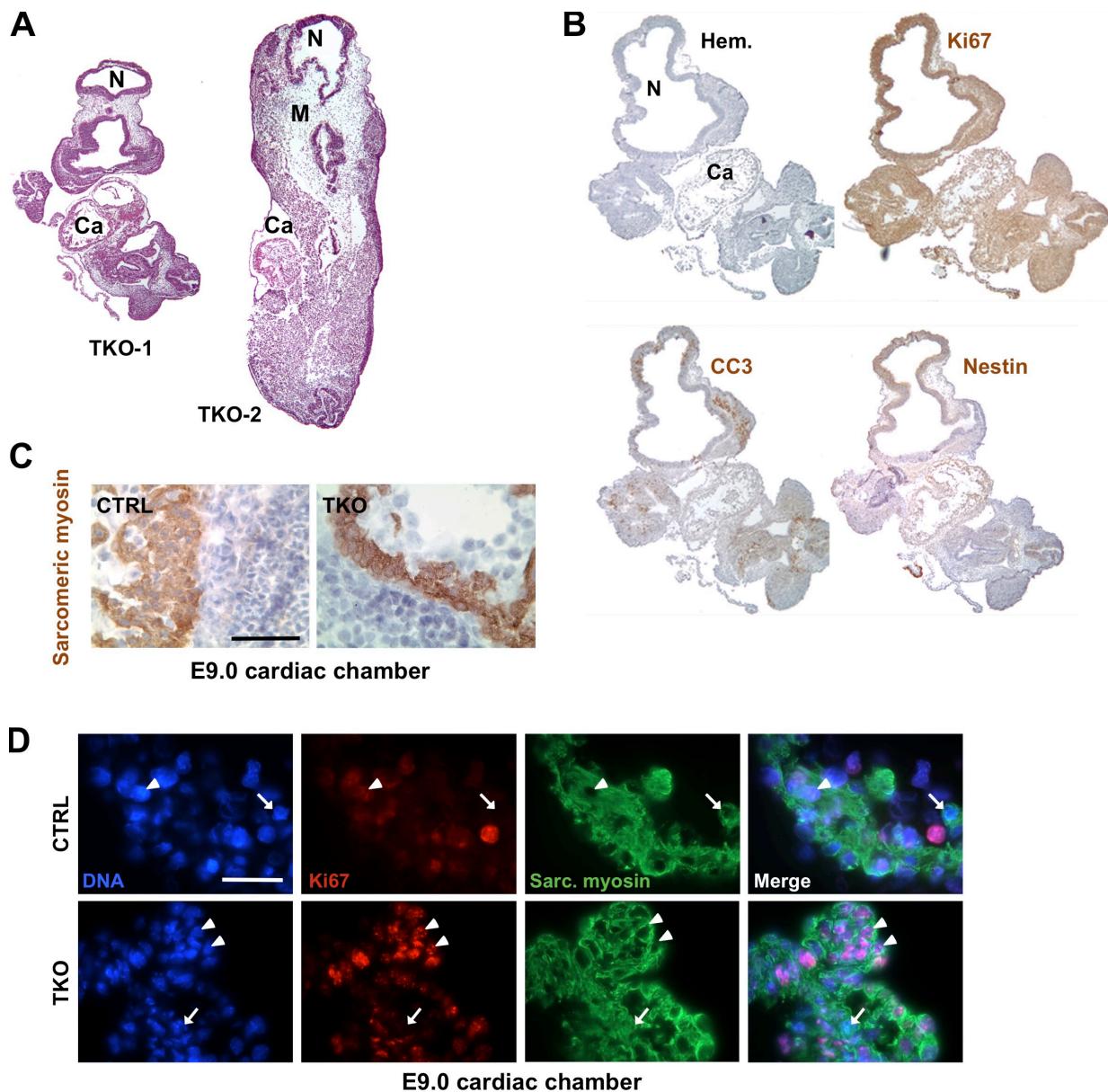


Figure S2. Histopathological analysis of E9 TKO tetraploid embryos. (A) Hematoxylin and eosin staining of representative sections from TKO tetraploid embryos, showing neural tube (N), cardiac cavity (Ca), and mesenchyme (M). Magnification is 50x. (B) Immunostaining for Ki67, CC3, and nestin staining (brown) in representative sections of TKO tetraploid embryos. (C) Immunohistochemistry for sarcomeric myosin (brown) in control (CTRL) and TKO E9 cardiac chambers. Bar, 100 µm. (D) Immunostaining for the cell cycle marker Ki67 (red) and sarcomeric myosin (green) in the cardiac chamber of CTRL and TKO embryos. Arrowheads point to cardiac cells that are double positive for Ki67 and sarcomeric myosin, arrows point to cells that are negative for Ki67 but positive for sarcomeric myosin. This figure is related to Fig. 2. Bar, 100 µm.

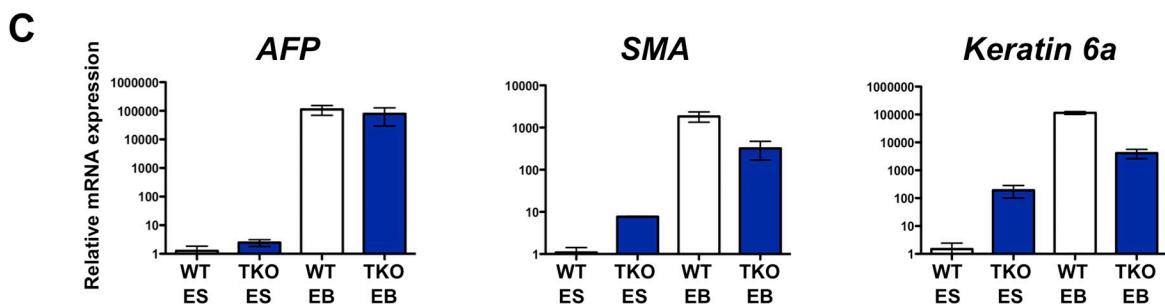
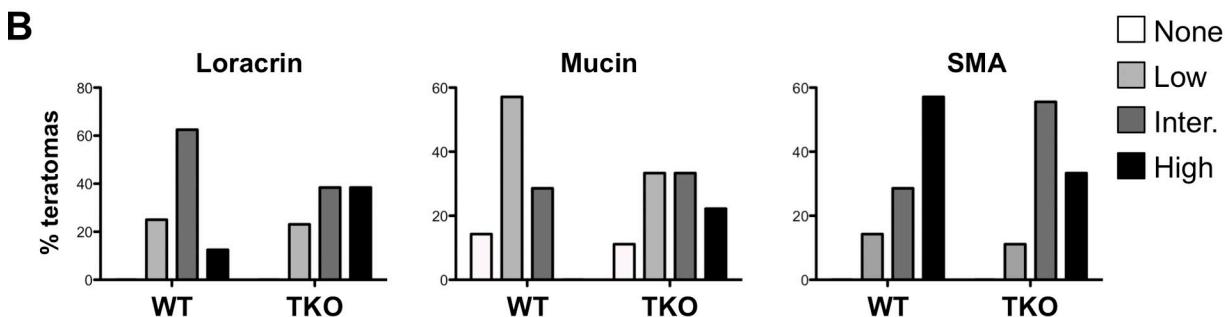
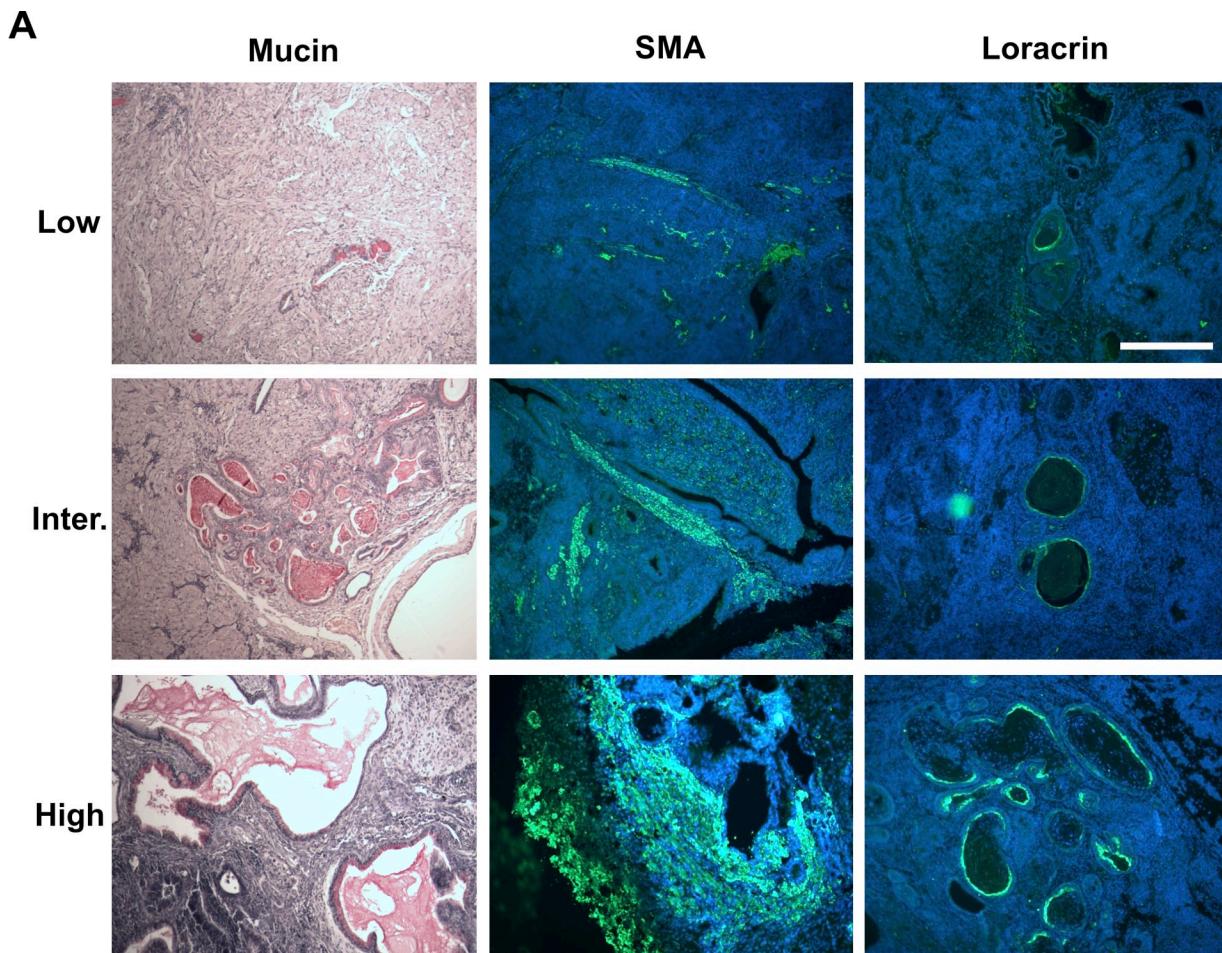


Figure S3. Immunostaining for markers of each of the three germ cell layers in WT and TKO teratomas. (A) Teratomas were stained for mucin (endoderm), SMA (mesoderm), and loracrin (ectoderm). 8 WT and 13 TKO teratomas were stained for each marker. Representative images are shown indicating presence of low, intermediate, or high levels of staining. Bar, 500 μ m. (B) Quantification of A. (C) Expression of genes associated with differentiation in WT and TKO mESCs and EBs assessed by quantitative RT-PCR. Relative mRNA expression is shown for three genes representing each of the three germ layers: *AFP* (endoderm), *SMA* (mesoderm), and *Keratin 6a* (ectoderm). Y axes represent relative mRNA expression on a log₁₀ scale. Means \pm SEM are shown; $n \geq 4$ for each genotype. This figure is related to Figs. 5 and 6.

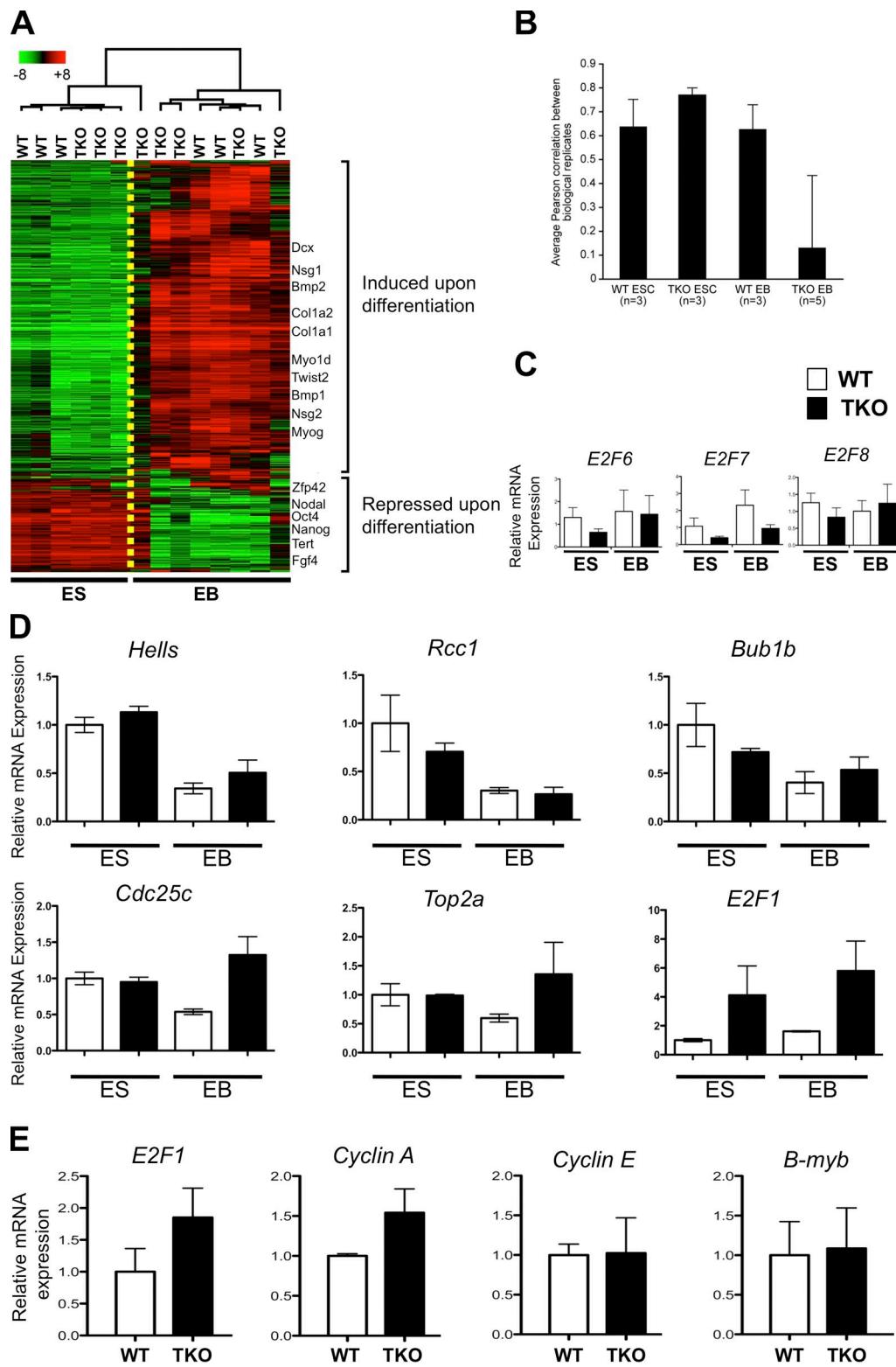


Figure S4. Gene expression analysis of WT and TKO mESCs and EBs. (A) Unsupervised hierarchical clustering of WT and TKO undifferentiated mESCs (ES) and re-plated EBs. Individual genes are indicated on the right. (B) Variability of gene expression in *Rb* family TKO mESCs undergoing differentiation in culture. A Pearson correlation of all genes was determined for each pairwise set of biological replicates to determine the extent of variability between samples. Shown is the mean Pearson correlation (\pm SD) for each cell type. Although little variation is observed within the WT mESC and EB samples and TKO mESC samples, TKO EB samples show less similarity between biological replicates and much greater variability. (C) Quantitative RT-PCR measurement of mRNA levels for the atypical E2Fs E2F6, E2F7, and E2F8 in WT and TKO mESCs and EBs. (D) Quantitative RT-PCR measurement of E2F target genes in WT and TKO ES and EB populations. (top) *Hells*, *Rcc1*, and *Bub1b* are E2F targets belonging to the Rb family-independent group that are repressed upon differentiation. (bottom) *Cdc25c*, *Top2a*, and *E2F1* are de-repressed during differentiation and are Rb family dependent. (E) Quantitative RT-PCR measurement of E2F target genes in WT and TKO ES and EB populations generated from the protocol described in Fig. 4 (enrichment in cortical neurons) whose expression is Rb family dependent (*E2F1* and *Cyclin A*) or independent (*MCM3* and *Cyclin E*). Means \pm SEM are shown (error bars).

Table S1. Generation of TKO and control embryos using the tetraploid complementation method

mESC genotype	Number of embryos implanted	Number of placentas observed	Number of embryos (alive)
<i>p107^{-/-};p130^{-/-}</i>	24	4	4 (4)
TKO-1	38	12	0 (0)
TKO-2	36	20	9 (3)
TKO-3	11	4	1 (0)

Pregnancies were terminated at E10.5–E11.5. While the development of double knockout embryos corresponded to this stage, live and dead TKO embryos from three independent mouse ES cell clones were all developmentally delayed (E8.5–E9).

Table S2. GO term enrichment analysis (p<0.001) on genes identified in the clusters shown in Fig. 9 A and Table S2

Set	Enriched set	P-value	Set hits	Set size	Set hits	Total hits	Total size	Total hits
Cluster D1	Lipid metabolism	1.19×10^{-6}	11	63	17.47	400	14,300	2.8
Cluster D1	Lipid transport	2.09×10^{-6}	5	63	7.94	48	14,300	0.34
Cluster D1	Cellular lipid metabolism	1.08×10^{-5}	9	63	14.29	322	14,300	2.26
Cluster D1	Fatty acid metabolism	8.47×10^{-5}	5	63	7.94	102	14,300	0.72
Cluster D1	Organic acid metabolism	4.70×10^{-4}	7	63	11.12	317	14,300	2.22
Cluster D1	Isomerase activity	6.86×10^{-4}	4	63	6.35	91	14,300	0.64
Cluster D2	Microtubule cytoskeleton organization and biogenesis	5.40×10^{-5}	4	83	4.82	36	14,300	0.26
Cluster D2	Protein depolymerization	2.68×10^{-4}	3	83	3.62	22	14,300	0.16
Cluster D2	Microtubule	3.90×10^{-4}	5	83	6.03	107	14,300	0.75
Cluster D2	Cytoskeleton	4.93×10^{-4}	10	83	12.05	486	14,300	3.4
Cluster D3	DNA metabolism	5.71×10^{-14}	24	117	20.52	427	14,300	2.99
Cluster D3	DNA replication	2.42×10^{-12}	14	117	11.97	129	14,300	0.91
Cluster D3	M phase	4.36×10^{-10}	13	117	11.12	156	14,300	1.1
Cluster D3	Nuclear part	4.76×10^{-9}	19	117	16.24	455	14,300	3.19
Cluster D3	Mitosis	4.59×10^{-8}	10	117	8.55	119	14,300	0.84
Cluster D3	Biopolymer metabolism	1.00×10^{-7}	35	117	29.92	1,681	14,300	11.76
Cluster D3	Nuclear membrane	1.32×10^{-7}	7	117	5.99	49	14,300	0.35
Cluster D3	Cell cycle	1.99×10^{-7}	18	117	15.39	517	14,300	3.62
Cluster D3	Organelle part	2.82×10^{-7}	29	117	24.79	1,275	14,300	8.92
Cluster D3	DNA repair	5.86×10^{-7}	10	117	8.55	156	14,300	1.1
Cluster D3	Mitotic cell cycle	7.40×10^{-7}	10	117	8.55	160	14,300	1.12
Cluster D3	DNA-directed DNA polymerase activity	1.26×10^{-6}	5	117	4.28	24	14,300	0.17
Cluster D3	Nuclear chromosome	1.44×10^{-6}	6	117	5.13	44	14,300	0.31
Cluster D3	Nuclear envelope	2.14×10^{-6}	7	117	5.99	73	14,300	0.52
Cluster D3	Response to endogenous stimulus	3.52×10^{-6}	10	117	8.55	190	14,300	1.33
Cluster D3	Nucleotidyltransferase activity	4.69×10^{-6}	7	117	5.99	82	14,300	0.58
Cluster D3	Nuclear pore	1.19×10^{-5}	5	117	4.28	37	14,300	0.26
Cluster D3	DNA-dependent DNA replication	1.22×10^{-5}	6	117	5.13	63	14,300	0.45
Cluster D3	Microtubule	2.72×10^{-5}	7	117	5.99	107	14,300	0.75
Cluster D3	Microtubule cytoskeleton	2.87×10^{-5}	8	117	6.84	148	14,300	1.04
Cluster D3	Nuclear chromosome part	4.71×10^{-5}	4	117	3.42	25	14,300	0.18
Cluster D3	Cell division	7.75×10^{-5}	7	117	5.99	126	14,300	0.89
Cluster D3	Chromosome	9.41×10^{-5}	8	117	6.84	175	14,300	1.23
Cluster D3	Sister chromatid segregation	1.11×10^{-4}	3	117	2.57	12	14,300	0.09
Cluster D3	Nucleic acid binding	1.37×10^{-4}	28	117	23.94	1,662	14,300	11.63
Cluster D3	DNA integrity checkpoint	1.44×10^{-4}	3	117	2.57	13	14,300	0.1
Cluster D3	Cell cycle checkpoint	1.45×10^{-4}	4	117	3.42	33	14,300	0.24
Cluster D3	Envelope	1.92×10^{-4}	8	117	6.84	194	14,300	1.36
Cluster D3	Replication fork	2.77×10^{-4}	3	117	2.57	16	14,300	0.12
Cluster D3	DNA binding	2.93×10^{-4}	22	117	18.81	1,211	14,300	8.47
Cluster D3	Cytoskeletal part	3.93×10^{-4}	9	117	7.7	272	14,300	1.91
Cluster D3	Microtubule-based movement	4.11×10^{-4}	4	117	3.42	43	14,300	0.31
Cluster D3	Condensed chromosome	4.70×10^{-4}	3	117	2.57	19	14,300	0.14
Cluster D3	Microtubule-based process	5.87×10^{-4}	5	117	4.28	83	14,300	0.59
Cluster D3	Nucleotide binding	6.04×10^{-4}	21	117	17.95	1,190	14,300	8.33
Cluster D3	Nuclear transport	6.91×10^{-4}	5	117	4.28	86	14,300	0.61
Cluster D3	Cellular localization	7.49×10^{-4}	11	117	9.41	427	14,300	2.99
Cluster D3	Chromosome segregation	9.53×10^{-4}	3	117	2.57	24	14,300	0.17
Cluster D3	Cytoskeleton-dependent intracellular transport	9.82×10^{-4}	4	117	3.42	54	14,300	0.38
Cluster II	Enzyme linked receptor protein signaling pathway	4.82×10^{-5}	10	197	5.08	152	14,300	1.07
Cluster II	Regulation of cellular process	8.03×10^{-5}	51	197	25.89	2,194	14,300	15.35
Cluster II	Transmembrane receptor protein ser/thr kinase signaling pathway	8.18×10^{-5}	5	197	2.54	33	14,300	0.24
Cluster II	Embryonic development	2.44×10^{-4}	6	197	3.05	64	14,300	0.45

Table S2. GO term enrichment analysis (p.001) on genes identified in the clusters shown in Fig. 9 A and Table S2 (Continued)

Set	Enriched set	P-value	Set hits	Set size	Set hits	Total hits	Total size	Total hits
Cluster I1	Transforming growth factor β receptor signaling pathway	2.99×10^{-4}	4	197	2.04	24	14,300	0.17
Cluster I1	Cytoskeletal protein binding	3.36×10^{-4}	11	197	5.59	229	14,300	1.61
Cluster I1	Transcription	4.06×10^{-4}	33	197	16.76	1,298	14,300	9.08
Cluster I1	Cytoskeleton	4.06×10^{-4}	17	197	8.63	486	14,300	3.4
Cluster I1	Protein modification	4.29×10^{-4}	27	197	13.71	980	14,300	6.86
Cluster I1	Primary metabolism	5.26×10^{-4}	80	197	40.61	4,220	14,300	29.52
Cluster I1	Diacylglycerol binding	5.52×10^{-4}	4	197	2.04	28	14,300	0.2
Cluster I1	Cell communication	5.80×10^{-4}	47	197	23.86	2,134	14,300	14.93
Cluster I1	Kinase binding	9.38×10^{-4}	5	197	2.54	55	14,300	0.39
Cluster I1	Endosome	9.38×10^{-4}	5	197	2.54	55	14,300	0.39
Cluster I2	Intracellular part	4.21×10^{-6}	88	185	47.57	4,532	14,300	31.7
Cluster I2	Biopolymer metabolism	7.60×10^{-6}	43	185	23.25	1,681	14,300	11.76
Cluster I2	Primary metabolism	4.51×10^{-5}	80	185	43.25	4,220	14,300	29.52
Cluster I2	Nuclear part	8.77×10^{-5}	17	185	9.19	455	14,300	3.19
Cluster I2	Cellular protein metabolism	1.87×10^{-4}	40	185	21.63	1,740	14,300	12.17
Cluster I2	Nucleolus	2.43×10^{-4}	6	185	3.25	68	14,300	0.48
Cluster I2	RNA binding	2.79×10^{-4}	14	185	7.57	364	14,300	2.55
Cluster I2	Nucleotide binding	3.00×10^{-4}	30	185	16.22	1,190	14,300	8.33
Cluster I2	Protein modification	3.68×10^{-4}	26	185	14.06	980	14,300	6.86
Cluster I2	Nucleic acid binding	6.37×10^{-4}	37	185	20	1,662	14,300	11.63
Cluster I2	Nuclear lumen	7.64×10^{-4}	11	185	5.95	269	14,300	1.89
Cluster I2	Organelle lumen	9.63×10^{-4}	13	185	7.03	366	14,300	2.56

Table S3. TF motifs search (p.01) on genes identified in the clusters shown in Fig. 9 A and Table S2

Cluster	Enriched set	P-value	Set hits	Set size	Set hits	Total hits	Total size	Total hits
D1	TGCCAAR.NF.1.wttx@WGGAATGY.TEF.1.wttx	5.30×10^{-5}	3	63	4.77	17	14,300	0.12
D1	TGTTTG.Y.HNF.3.wttx@V_IRF1_01.wttx	4.82×10^{-4}	3	63	4.77	35	14,300	0.25
D1	GCCATNTTG.YY1.wttx@V_STAT1_02.wttx	5.25×10^{-4}	3	63	4.77	36	14,300	0.26
D1	V_FREACT7_01.wttx	1.06×10^{-3}	14	63	22.23	1272	14,300	8.9
D1	V_AP2GAMMA_01.wttx@V_IRF_Q6_01.wttx	2.92×10^{-3}	6	63	9.53	323	14,300	2.26
D1	V_NRF2_Q4.wttx	2.94×10^{-3}	12	63	19.05	1109	14,300	7.76
D1	V_PITX2_Q2.wttx	3.19×10^{-3}	7	63	11.12	442	14,300	3.1
D1	V_FOXJ2_01.wttx	5.03×10^{-3}	16	63	25.4	1836	14,300	12.84
D1	V YY1_Q6.wttx	8.78×10^{-3}	11	63	17.47	1114	14,300	7.8
D1	V_HNF3_Q6_01.wttx	9.74×10^{-3}	17	63	26.99	2145	14,300	15
D2	RCGCANGCGY.NRF.1.wttx@V ETF_Q6.wttx	1.20×10^{-3}	5	83	6.03	137	14,300	0.96
D2	AAGWWRNYGGC.wttx@V_KROX_Q6.wttx	5.32×10^{-3}	3	83	3.62	61	14,300	0.43
D2	V_HMEF2_Q6.wttx@V_KROX_Q6.wttx	6.89×10^{-3}	4	83	4.82	130	14,300	0.91
D2	V_ICSBP_Q6.wttx@V_NFKAPPAB65_01.wttx	9.09×10^{-3}	3	83	3.62	74	14,300	0.52
D3	SGCGSSAAA.E2F.1.DP.2.wttx	2.39×10^{-5}	11	117	9.41	288	14,300	2.02
D3	CGGAARNNGCNG.wttx@V_TBP_01.wttx	7.34×10^{-4}	3	117	2.57	22	14,300	0.16
D3	V_E2F1_Q4_01.wttx	1.02×10^{-3}	6	117	5.13	140	14,300	0.98
D3	V_KROX_Q6.wttx@V_POU1F1_Q6.wttx	1.64×10^{-3}	7	117	5.99	209	14,300	1.47
D3	SGCGSSAAA.E2F.1.DP.2.wttx@V_PAX2_02.wttx	2.03×10^{-3}	3	117	2.57	31	14,300	0.22
D3	V_E2F4DP2_01.wttx	2.28×10^{-3}	6	117	5.13	164	14,300	1.15
D3	V_E2F4DP1_01.wttx	3.26×10^{-3}	5	117	4.28	122	14,300	0.86
D3	V ETF_Q6.wttx@V_POU1F1_Q6.wttx	4.82×10^{-3}	6	117	5.13	191	14,300	1.34
D3	V_E2F_Q6_01.wttx	5.17×10^{-3}	5	117	4.28	136	14,300	0.96
D3	CCAATNNNSNNNGCG.wttx	7.28×10^{-3}	8	117	6.84	344	14,300	2.41
D3	GKCGCN>NNNNNNNTGAYG.wttx	7.99×10^{-3}	5	117	4.28	151	14,300	1.06
D4	TCCATTKW.wttx@WGTTNNNNNAAA.wttx	2.37×10^{-4}	4	112	3.58	39	14,300	0.28
D4	CCGNMNNNTNACG.wttx	9.61×10^{-4}	7	112	6.25	199	14,300	1.4
D4	CCGNMNNNTNACG.wttx@V_STAT4_01.wttx	1.19×10^{-3}	3	112	2.68	27	14,300	0.19
D4	V_MEIS1AHGX9_01.wttx	1.24×10^{-3}	10	112	8.93	403	14,300	2.82
D4	V_AP2_Q6_01.wttx@V_CDX_Q5.wttx	9.42×10^{-3}	6	112	5.36	230	14,300	1.61
I1	GGGCGGR.SP1.wttx@V_NFY_01.wttx	9.54×10^{-4}	7	197	3.56	113	14,300	0.8
I1	V ETF_Q6.wttx@V_FOXO4_01.wttx	1.89×10^{-3}	10	197	5.08	241	14,300	1.69
I1	GATTGGY.NFY.wttx@V ETF_Q6.wttx	2.28×10^{-3}	5	197	2.54	67	14,300	0.47
I1	V_NFY_01.wttx@YATGNWAAT.OCT.X.wttx	2.85×10^{-3}	3	197	1.53	21	14,300	0.15
I1	V ETF_Q6.wttx@V_HNF3ALPHA_Q6.wttx	2.88×10^{-3}	12	197	6.1	343	14,300	2.4
I1	KTGGYRSGAA.wttx@V_TFIII_Q6.wttx	2.88×10^{-3}	7	197	3.56	137	14,300	0.96
I1	KTGGYRSGAA.wttx@V_MAZ_Q6.wttx	3.15×10^{-3}	8	197	4.07	177	14,300	1.24
I1	V ETF_Q6.wttx@V_NFY_01.wttx	4.41×10^{-3}	8	197	4.07	187	14,300	1.31

Table S3. TF motifs search (p.01) on genes identified in the clusters shown in Fig. 9 A and Table S2 (Continued)

Cluster	Enriched set	P-value	Set hits	Set size	Set hits	Total hits	Total size	Total hits
I1	GGGCGR.SP1.wttx@MCAATNNNNNGCG.wttx	4.74×10^{-3}	3	197	1.53	25	14,300	0.18
I1	GGGCGR.SP1.wttx@MYAATNNNNNNNGGC.wttx	4.74×10^{-3}	3	197	1.53	25	14,300	0.18
I1	CTTTAAR.wttx	7.01×10^{-3}	20	197	10.16	798	14,300	5.59
I1	V_HFH3_01.wttx@V_KROX_Q6.wttx	8.00×10^{-3}	8	197	4.07	207	14,300	1.45
I1	V_POU3F2_01.wttx@V_SP1_Q6_01.wttx	8.42×10^{-3}	7	197	3.56	167	14,300	1.17
I1	V_FOXJ2_01.wttx@V_MAZR_01.wttx	9.17×10^{-3}	8	197	4.07	212	14,300	1.49
I1	GGGCGR.SP1.wttx@V_ALPHACP1_01.wttx	9.34×10^{-3}	4	197	2.04	60	14,300	0.42
I1	V_AP2_Q6_01.wttx@V_HNF3ALPHA_Q6.wttx	9.76×10^{-3}	10	197	5.08	305	14,300	2.14
I2	V_AP2_Q6_01.wttx@YNGTTNNNATT.wttx	1.53×10^{-4}	7	185	3.79	89	14,300	0.63
I2	RCGCANGCGY.NRF.1.wttx	7.42×10^{-4}	20	185	10.82	700	14,300	4.9
I2	V_E2F_Q6_01.wttx	1.94×10^{-3}	7	185	3.79	136	14,300	0.96
I2	SCGGAAGY.ELK.1.wttx	2.35×10^{-3}	16	185	8.65	556	14,300	3.89
I2	V_PPARG_01.wttx	2.91×10^{-3}	8	185	4.33	186	14,300	1.31
I2	V_FOXJ2_01.wttx@V_SP1_Q6_01.wttx	3.33×10^{-3}	14	185	7.57	472	14,300	3.31
I2	V_AP3_Q6.wttx@V_STAT5B_01.wttx	5.53×10^{-3}	4	185	2.17	55	14,300	0.39
I2	V_AP2GAMMA_01.wttx@YNGTTNNNATT.wttx	5.90×10^{-3}	4	185	2.17	56	14,300	0.4
I2	GCCATNTTG.YY1.wttx@RCGCANGCGY.NRF.1.wttx	7.34×10^{-3}	3	185	1.63	31	14,300	0.22
I2	V_AP2ALPHA_01.wttx@YNGTTNNNATT.wttx	7.52×10^{-3}	4	185	2.17	60	14,300	0.42
I2	V_SP1_Q6_01.wttx@YNGTTNNNATT.wttx	8.78×10^{-3}	6	185	3.25	137	14,300	0.96
I2	V_KROX_Q6.wttx@YNGTTNNNATT.wttx	9.61×10^{-3}	5	185	2.71	100	14,300	0.7

Table S4. List of genes found in the two clusters identified in Fig. 9 B

Entrez gene	Gene symbol
Rb family dependent	
15270	H2afx
12236	Bub1b
58184	Rqcd1
53890	Sart3
98415	Nucks1
17215	Mcm3
237911	Brip1
78656	Brd8
71846	Syce2
21973	Top2a
70472	Atad2
70454	Cenpl
12316	Aspm
12545	Cdc7
76843	Dtl
71804	2610016C23Rik
208628	Kntc1
12144	Blm
12704	Cit
102920	Cenpi
19891	Rpa2
19348	Kif20a
52276	Cdca8
218977	Dlgap5
19366	Rad54l
12532	Cdc25c
66442	Spc25
20630	Snrpc
68612	Ube2c
21853	Timeless
60411	Cenpk
20877	Aurkb
66471	Anp32e
228482	Arhgap11a
19362	Rad51ap1
23834	Cdc6
15382	Hnrnpa1
67196	Ube2t
71151	Exod1
78833	Gins3
18005	Nek2
22223	Uchl1
16563	Kif2a
210035	Tmem194
67967	Pold3
53761	Bat2
22225	Usp5
26885	Casp8ap2
52563	Cdc23
Rb family independent	
70640	Dcp2
14670	Gna-rs1
22278	Usf1
381921	Taok2
68277	2310057M21Rik
56433	Vps29
66687	Tbc1d15
353190	Edc3
228410	Cstf3
78913	Zfp294
212127	2810046L04Rik
19646	Rbbp4
52202	Rbm34
70359	Gtpbp3

Table S4. List of genes found in the two clusters identified in Fig. 9 B
(Continued)

Entrez gene	Gene symbol
69962	2810422O20Rik
20871	Aurkc
76454	Fbxo31
17687	Msh5
238831	Ppwd1
66870	Serbp1
107071	Wdr74
234138	BC019943
68252	A030007L17Rik
231724	Rad9b
30795	Fkbp3
53607	Snrpa
15193	Hdgfrp2
20674	Sox2
68646	1110020G09Rik
228829	Phf20
75430	3200002M19Rik
68926	Ubap2
22608	Ybx1
70769	Nolc1
56351	Ptges3
11637	Ak2
13619	Phc1
100088	Rcc1
67223	Rrp15
17350	Mlh1
66953	Cdca7
56306	Tera
66667	Hspbap1
225348	Wdr36
20585	Hlf
103284	Zc3h10
71991	Ercc8
76781	Mettl4
72556	Zfp566
66497	2610528E23Rik
226539	Dars2
74195	Eip3
22294	Uxt
99100	Cep152
226442	Zfp281
56380	Arid3b
16549	Khsrp
18477	Prdx1
11702	Amd1
66973	Mrps18b
20768	Seph2
18160	Npr1
67487	Dhx40
14055	Ezh1
224619	Traf7
14415	Gad1
208691	Eif5a2
71781	Slc16a14
319651	Usp37
68107	Cntd1
21454	Nudt15
214254	Gpr4
319197	Hist1h4c
319155	Elov13
12686	Fdps
110196	Mtap
66902	

Table S5. Primers for quantitative RT-PCR analysis of gene expression

Primer	Forward	Reverse
AFP	5'-CATGCTGCAAAGCTGACAA-3'	5'-CTTGCAATGGATGCTCTT-3'
SMA	5'-AGGACTTCTCACACCCCTGG-3'	5'-GTGGTCTCTCTCACACATGG-3'
Keratin 6a	5'-AGTTGCCTCCTCATCGAC-3'	5'-TGCTAAACATAGGCTCCAG-3'
MCM3	5'-CAGGACTCCCAGAAAGTCCA-3'	5'-TAAGAGGGCCGCCCTAAAAA-3'
Hells	5'-ACCCTTCACAACCAAAGC-3'	5'-CCATTTCCCAAAGCATCC-3'
Rcc1	5'-ATGCTGTGTCCAAGGATGGT-3'	5'-CACAGGACTCCAGGCATCTT-3'
B-myb	5'-TTAAATGGACCCACGAGGAG-3'	5'-TTCCAGTCTGCTGTCCAAA-3'
Cyclin E	5'-CTGAGAGATGAGCACTTCTGC-3'	5'-GAGCTTATAGACTTCGCACACCT-3'
Bub1b	5'-TTACGCCGTACGTGGAAGA-3'	5'-GCTCAATCTGCATGGTGTC-3'
Cdc25c	5'-GGAAACACCCGGACTGAA-3'	5'-ACTTCCAGACAGCAAAGCAG-3'
Top2a	5'-CAAAAGAGTCATCCCCAAG-3'	5'-GGGGTACCCCTAACGTTTC-3'
E2F1	5'-TGCCAAGAAGTCCAAGAATCA-3'	5'-CTTCAAGCCGCTTACCAATC-3'
TBP	5'-CGGTCGCGTCATTCTC-3'	5'-GGGTTATCTTCACACACCATGA-3'

Table S6 lists genes found in the six clusters identified in Fig. 9 A, and is available as a PDF file.