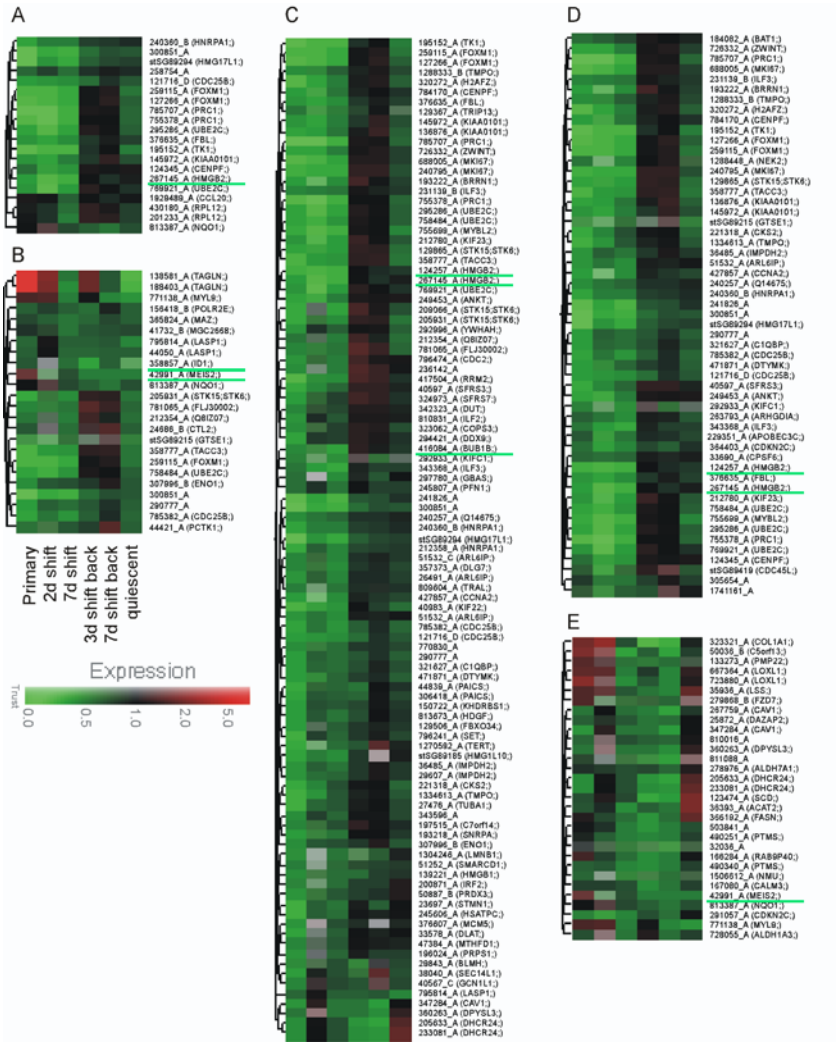

A
147469_B (IGFBP4;)
273587_A (IGFBP4;)
33937_A (GAS6;)
42497_A (GAS6;)
222589_A (DUSP1;)
146239_A (DUSP1;)
427808_A (RGS3;)
269815_A (NR4A3;)
323346_C (RGS3;)
114213_A (RGS3;)
310449_A (PLOD2;)
785655_A (MME;)
B
296513_B (DCN;)
205645_A (DCN;)
323181_A (FAP;)
345996_A (IFITM1;)
810449_A (MMP2;)
30206_A (SERPINE2;)
361744_A (LUM;)
813823_A (LUM;)
1574238_B (IL6ST;)
151523_A (WNT5A;)
129059_A (IL7R;)
22936_A (AFAP;)
120106_C (CASP1;)
346080_B
23767_A (RAB14;)
293270_A (AKR1C2;)
783679_A (LTBP1;)
788591_A (LTBP1;)
24858_A (TGFBR2;)
299497_B (TXNIP;)
788143_A (SAT;)
299204_A (IGFBP7;)
785655_A (MME;)
200914_A (MME;)
241959_A (MME;)
324901_A (WNT5A;)
127340_A (MSX2;)
667451_A (PBEF;)
760201_A (PBEF;)
49109_A (ATP2B1;)
788098_A (TNFAIP6;)
212078_A (ITGA1;)
154007_A (STC1;)
156520_A (TNFAIP6;)
122274_A
357031_A (TNFAIP6;)
341038_A (ATP6IP2;)
42127_A (SLC1A3;)
1074540_A (CSF3;)
1667001_A (CSF3;)
40851_A (DUSP6;)
stSG89454 (LIF;)
51689_A (PRNP;)
324655_B (IL1B;)
1674777_A (PHLDA1;)
153589_A (STC1;)
342570_A (COL7A1;)
153342_A (CXCL2;)
153340_A (CXCL2;)
Primary
2d shift
7d shift
3d shift back
7d shift back
quiescent
Expression
Tuple
0.0
0.5
1.0
2.0
5.0
C
324061_A (FN1;)
361256_A (PEA15;)
788143_A (SAT;)
359721_A (TXNIP;)
301777_A (ZFP36L1;)
114043_A (MEG3;)
246147_A (CSPG2;)
197712_A (PSAP;)
stSG89160 (HMOX1;)
136059_A (SSR4;)
152315_A (SSR4;)
191550_A (SSR4;)
756630_A (CDKN1A;)
610331_A (FLJ23867;)
296325_A (TIMP1;)
270187_A (TIMP1;)
232638_A (ADM;)
796005_A (CDH11;)
770859_A (ITGB5;)
175182_B
273587_A (IGFBP4;)
147469_B (IGFBP4;)
249977_A (TIMP3;)
788581_A (LTBP1;)
783679_A (LTBP1;)
23767_A (RAB14;)
299204_A (IGFBP7;)
1323860_A (APLP2;)
258070_A (SERPINE2;)
30206_A (SERPINE2;)
322180_A (IFITM2;)
345996_A (IFITM1;)
810449_A (MMP2;)
33937_A (GAS6;)
42497_A (GAS6;)
323181_A (FAP;)
296513_B (DCN;)
205645_A (DCN;)
D
297848_A
357158_B (PIGPC1;)
322096_B
774491_A (GPX1;)
783648_A (GPC1;)
213136_A (BTG2;)
471099_A (CYFIP2;)
47670_A
47475_A (CYFIP2;)
795275_B (PIG3;)
149319_A (G1P2;)
299204_A (IGFBP7;)
37721_A (HERPUD1;)
249193_A (XPC;)
163572_A (APLP1;)
143356_A (PLAU;)
324655_B (IL1B;)
323783_B (VEGF;)
666367_A (SERPINE1;)
345996_A (IFITM1;)
49164_A (C1orf8;)
33683_A (C1orf8;)
342410_A (P4HA2;)
142621_A (DGKA;)
124554_A (CSF1;)
756630_A (CDKN1A;)
153137_A
153114_A (PLXNB2;)
stSG89300
304879_A (PAM;)
784928_A (SRPX;)
139059_A (SSR4;)
191550_A (SSR4;)
197712_A (PSAP;)
246147_A (CSPG2;)
114043_A (MEG3;)
175182_B
147469_B (IGFBP4;)
273587_A (IGFBP4;)
249977_A (TIMP3;)
30206_A (SERPINE2;)
258070_A (SERPINE2;)
300737_A (WYLK;)
42497_A (GAS6;)
810449_A (MMP2;)
359721_A (TXNIP;)
E
796005_A (CDH11;)
273587_A (IGFBP4;)
147469_B (IGFBP4;)
stSG89160 (HMOX1;)
361305_A (HIST2H2AB;)
297596_A (PTP4A1;)
342410_A (P4HA2;)
49454_A (HIST3H2A;)
38048_A (SRPX;)
811740_A (ITGA2;)
24858_A (TGFBR2;)
788591_A (LTBP1;)
783679_A (LTBP1;)
154007_A (STC1;)
726576_A (ATP6V0B;)
109989_A (VEGFC;)
288649_A (ANXA1;)
300484_A (ANXA1;)
45138_A (VEGFC;)
262752_A (CD44;)
221587_A (PHLDA1;)
241985_A (BTG3;)
34852_C (BIRC2;)
34852_A (BIRC2;)
246304_C (BTG3;)
33501_A (ATP6V1C1;)
22790_B (PLAUR;)
323783_B (VEGF;)
38832_A (ATP6V1G1;)
299995_A (ATP6V1G1;)
252443_A (DUSP4;)
32170_A
24033_A (STAT1;)
stSG89454 (LIF;)
269815_A (NR4A3;)
26599_A (STAT1;)
49681_A (PRNP;)
812048_A (PRNP;)
51689_A (PRNP;)
38821_A (KAB;)
1187505_A (PTGS2;)
1851583_A (PTGS2;)
503931_B (IL1B;)
580874_B (TFPI2;)
37045_A (ATP6V1G1;)
470769_A (RIL;)
324655_B (IL1B;)
249092_A (IER3;)
259649_A (IER3;)
1674777_A (PHLDA1;)
153589_A (STC1;)
24927_A (DDB2;)
753447_B (DDB2;)
240183_A (SLC8A1;)
30272_A (SLC8A1;)
37721_A (HERPUD1;)
753184_A (SOX9;)
505118_B (STAC;)
3109800_A (DJA1;)
300419_A (SOX9;)
810331_A
296325_A (TIMP1;)
270187_A (TIMP1;)
323185_A (GNG11;)
282781_A
788143_A (SAT;)
363151_A (PEA15;)
298387_A (TXNIP;)
359721_A (TXNIP;)
299497_B (TXNIP;)
308187_B (SOX9;)
361256_A (PEA15;)
418223_B (RABGGTB;)
246304_A (BTG3;)
129932_A (BIRC3;)
273180_A
321426_A (STX3A;)
297803_B (BRD2;)
282914_A (TIEG;)
3830012_A (PPP1R15A;)
115383_A (GADD45A;)
310141_A (GADD45A;)
415112_A (GADD45A;)
823885_A
222589_A (DUSP1;)
146239_A (DUSP1;)
470979_A
770670_A (TNFAIP3;)
309943_A (TNFAIP3;)
32485_A (SPRY2;)
33285_A (DUSP5;)
383387_A (TSC22;)
273190_A (ATF3;)
143356_A (PLAU;)
147834_A (ZNF217;)
1568015_A (AREG;)
668944_A (KLF4;)
343273_A (NFIL3;)
197479_A (DUSP5;)
470756_A (DTR;)
302434_A (DTR;)
222129_A (NR1D1;)
383083_A
68999_A (RELB;)
324122_B (LDHA;)
1351002_A (CEBPG;)
278252_A
278203_A
823850_A (SNAPC1;)
201890_A (BIRC3;)
40262_A (SPRY2;)
stSG89188
1074540_A (CSF3;)
1667001_A (CSF3;)
153342_A (CXCL2;)
153340_A (CXCL2;)


A
B
C
D
E
Primary
2d shift
7d shift
3d shift back
7d shift back
quiescent
Expression
Trust
0.0
0.5
1.0
2.0
5.0

Sup Fig. 1: **A selection of the genes/clones significantly up-regulated after 7 days LT inactivation, compared to cells cultured at 33°C**. Clustered according to their expression in primary cells, quiescent cells, cells shifted for 2 days and cells shifted to 39°C for 7 days and then shifted back to 33°C (all compared directly to proliferating cells at 33°C). Genes are grouped according to whether they were also up-regulated in serially passaged primary cells (A), quiescence (B), after 2 days at 39°C (D), or when LT is re-activated for 7 days (E) or if they were down-regulated with immortalisation (C). Genes chosen for further analysis by western or RNAi are underlined.

Sup Fig. 2: **A selection of the genes/clones significantly down-regulated after 7 days LT inactivation, compared to cells cultured at 33°C**. Clustered according to their expression in primary cells, quiescent cells, cells shifted for 2 days and cells shifted to 39°C for 7 days and then shifted back to 33°C (all compared directly to proliferating cells at 33°C). Genes are grouped according to whether they were also down-regulated in serially passaged primary cells (A), quiescence (B), after 2 days at 39°C (D), or when LT is re-activated for 7 days (E) or if they were up-regulated with immortalisation (C). Genes chosen for further analysis by western blotting are underlined.