Table S1. Gene ontology classification of differentially expressed genes based on molecular and cellular functions. The top functional categories enriched in the 3 gene subsets indicated in Figure 4A identified using Ingenuity Pathway Analysis are shown. Significant associations with functional categories were identified using Fisher's exact test at a cutoff p-value of 0.01.

Gene set i : Genes upregulated in D2 WT cells but unaffected in Myc-GFPhigh cells

Molecular and Cellular functions	Genes
Cellular Growth and Proliferation	MBP, TCIRG1, BCL6, CTSS, OSM, CD274, MXI1, STK17B, MED7 (includes EG:9443), TP53INP1, BTG1, SH3BP2, BMX, STX2, FYB, WWP2, HDAC5, TLR2, BCL2L1, CSF2RB, CD9, NDFIP1, DOK1, PRDX2, B2M, OSR2, CD55, CD74, JAK2, LOC643751, EP300, CDC25B, SLFN1, IGF1, ANXA1, STAT1, TNFRSF10A (includes EG:8797), HGS, IL4, APOBEC1, COL4A3BP, MDM2, STK3, MSI2, CSF1R, XPA, ISG15, LY6A, LY96, CAPNS1, GRAP2, KLF5, CDKN1A, BNIP3L, CDKN1B, PAFAH1B1, PRKCB
Cell Death	DYRK1B, AHSP, PDPK1, BCL6, TNIP1, UBE2B, CTSS, PPP1R13B, OSM, CD274, GPX4, STK17B, MED7 (includes EG:9443), SHISA5, TP53INP1, DNASE2, DDIT4, ASAH1, WWP2, TLR2, BCL2L1, CD9, STRADB, USE1, ALDOA, HIST1H1C, USP18, ZFP36, JAK2, EP300, CDC25B, IGF1, AKT3, MAP1LC3B, STAT1, TNFRSF10A (includes EG:8797), IL4, MDM2, STK3, AXL, SOAT1, NFE2L1, XPA, LY6A, ROCK1, PGLYRP1, ATP6AP2, GNAS, LAMP2, CAPNS1, GRAP2, CDKN1A, KLF5, BNIP3L, CDKN1B, PAFAH1B1, PRKCB
Cell Cycle	JAK2, BCL6, LOC643751, EP300, CDC25B, SLFN1, IGF1, ANXA1, DSTN, OSM, CD274, STAT1, MXI1, IL4, TP53INP1, SH3BP2, MDM2, STX2, CSF1R, XPA, FZR1, GNAS, BCL2L1, CCNG2, CDKN1A, CDKN1B
Cellular Development	B2M, HIST1H1C, ZFP36, AHSP, MBP, CD55, PDPK1, CD74, JAK2, BCL6, LOC643751, IDH1, EP300, TOP1, SLFN1, IGF1, UBE2B, OSM, STAT1, HGS, STK17B, IL4, MED7 (includes EG:9443), DNASE2, AP3D1, SCD2, MDM2, STX2, AXL, CSF1R, WWP2, TLR2, LY6A, BCL2L1, GNAS, CAPNS1, CD9, GRAP2, CDKN1A, ADD1, CDKN1B, PRKCB, PRDX2
Molecular Transport	B2M, ASPSCR1, AHSP, HEXA, PDPK1, CD74, SLC2A3, IDH1, RFFL, USO1, ANXA1, AP2M1, AP3D1, RAB10, SOAT1, CSF1R, NFE2L1, CHIC2, TLR2, UROD, CSF2RB, ARF5, FABP5, USE1, CDKN1A, SLC6A4, CDKN1B, SLC11A1, PRDX2
Protein Trafficking	USO1, AP2M1, ASPSCR1, ARF5, AP3D1, USE1, RAB10, CD74, SOAT1, CHIC2, RFFL
Cellular Movement	TCIRG1, CD55, LOC643751, AXL, CSF1R, TLR2, ROCK1, CSF2RB, IGF1, NDEL1, OSM, PAFAH1B1, IL4
Cell Morphology	ATG12, ULK1, AHSP, PDPK1, HBP1, LOC643751, PSME3, ISG15, ROCK1, TLR2, BCL2L1, ST5, CAPNS1, IGF1, STRADB, ANXA1, CDKN1A, IRGM, CDKN1B, PAFAH1B1, HGS, STK17B, IL4, PRDX2

Gene set ii : Genes unchanged in D2 WT cells but perturbed in Myc-GFPlow cells

Molecular and Cellular Functions	Genes
Cell-To-Cell Signaling and Interaction	SELL, ADRBK1, ELANE, PRF1, SPHK2, PIK3CG, ATG5 (includes EG:9474), PTPN6, PTPRE, TIAM1, MIF, PSMB5, PLEC1, IFNGR1, IRF1, F2RL3, PRDX3, GP5, PRTN3, LAT, CLCN7, GP1BB, ELMO1, AOC3, ITGA2B (includes EG:3674), F2RL2, PSMB10, CTNNA1, P2RX1, MFGE8, BECN1, OGT, RASSF5, CASP8, MAPKAPK2, CALR, RAB21, FCGR2A, VWF, VIM, ALS2, SELPLG, CCL9, CEBPE, PSME1, MAPK14, SWAP70, CORO1A, CD44, AP3B1, PIK3CB
Cellular Movement	GBX2, AOC3, RAF1, ITGA2B (includes EG:3674), SELL, PLCB2, ADRBK1, ELANE, PDPK1, TGFBR2, PRF1, ST8SIA4, SPHK2, PIK3CG, IRS2, RASSF5, GSK3B, MAPKAPK2, FRS2, CALR, TIMP3, PTPN6, TIAM1, RAB21, FCGR2A, PLEC1, IFNGR1, BAX, SELPLG, CEBPE, IL16, SWAP70, MAPK14, CYTIP, PRTN3, MYL12B, PPIA (includes EG:268373), CORO1A, ARHGEF6, CD44, PIK3CB
Cellular Function and Maintenance	CTNNA1, ELANE, MFGE8, IKZF1, BECN1, RICTOR, DEF6, TGFBR2, PRF1, PIK3CG, IRS2, MAPKAPK2, CASP8, ATG5, CALR, FCGR2A, IFNGR1, BAX, IER3, HSPA2, MLST8, IRF1, CEBPE, MAPK14, ST3GAL1, LAT, CORO1A, CD44, AP3B1, PIK3CB, ELMO1, LGALS1
Cellular Development	PHC2, ELANE, IKZF1, DEF6, TGFBR2, GPC1, PRF1, PIK3CG, ATF4, ARID3A, CASP8, HIPK2, TIAM1, IFNGR1, BAX, IER3, HSPA2, CEBPE, MAPK14, ST3GAL1, LAT, CD44, AP3B1, PML, LGALS1
Carbohydrate Metabolism	F2RL2, MECP2, GM2A, H6PD, PIP4K2B, GCLC, PFKL, TPI1, F2RL3, MAPK14, HK2, CHKA, IRS2
Cell Cycle	MIF, PHC2, BAX, BECN1, GRB10, GPC1, MAPK14, SPHK2, XPC, ARID3A, RASSF5, POLK, PML, PLAC8
Molecular Transport	F2RL2, FCGR2A, RAB2A, P2RX1, F2RL3, TMED10, GLB1, AP3B1, SGPP1, CHMP5, GSK3B, SLC19A2, NAPA, PPP3CA
Small Molecule Biochemistry	F2RL2, PDIA3, FCGR2A, GM2A, P2RX1, H6PD, GCLC, GNAZ, PFKL, BAX, F2RL3, PRDX3, SPHK2, GLB1, PIK3CG, PAPSS1 (includes EG:9061), PAOX (includes EG:196743), NCOR1, IRS2, SGPP1, SLC19A2, HSD17B4, AIFM1

Gene set iii : Genes downregulated in D2 WT cells but unchanged in Myc-GFPhigh cells

Molecular and Cellular Functions	Genes
Gene Expression	NARG1, YWHAE, NPM3, CD3EAP, TCOF1, POLR1E, HMGA1, HMGN1, PARP1
RNA Post-Transcriptional Modification	QTRT1, NPM1 (includes EG:18148), SRPK1, BOP1, NPM3, WDR55, SFRS13A, IMP4, RSRC1
Cell Death	CLNS1A, SMN1, PRPF19, DUSP1, TRIM28, HSF1, HMGA1, KRT10, NDN, PARP1, AIFM1
Cellular Assembly and Organization	NPM1 (includes EG:18148), C14ORF169, HDAC2, AATF, HSF1, ABCA3, SRF, RBBP7, RANBP1, HMGN1, TPP2, SKP2, PARP1, PES1, BOP1, TFAM, SFRS13A, KIF11, RTEL1
DNA Replication, Recombination, and Repair	MCM6, C14ORF169, HDAC2, HSF1, RBBP7, PSMC3IP, RAD54L, HMGN1, POLD1, TPP2, MCM4, SKP2, PARP1, MND1, QTRT1, PRMT7, TFAM, XRCC6, HUS1, MSH6, KIF11, RTEL1, UNG, MCM7
Cell Cycle	C14ORF169, HDAC2, COX10, HSF1, RBBP7, PSMC3IP, DDX3X, RANBP1, HMGN1, SKP2, PARP1, MYBL2, PPP5C, KIF11
Cellular Compromise	PPID, SMN1, EXT2, HSF1, MEF2C, SMARCC1, UNG, PARP1
Post-Translational Modification	HSPA8, PDSS1, PFDN2, HSP90AA1

Table S2. qRT-PCR Primer sequences. Primers sequences were obtained from PrimerBank website[1,2] (http://pga.mgh.harvard.edu/primerbank) or previous studies[3], or were designed using Primer Express 3.0 software (Applied Biosystems).

Gene	Sense primer	Antisense primer
Hbb-b1	GCACCTGACTGATGCTGAGAA	TTCATCGGCGTTCACCTTTCC
Hbb-b2	GCACCTGACTGATGCTGAGAA	ACTTCATCGGGGTTCACCTTT
Hba-a1	CACCACCAAGACCTACTTTCC	CAGTGGCTCAGGAGCTTGA
Spna1	AGAAATCCAACACCGAAGAGC	TCCAGGTCATCTGCGTCTCTC
GypA	ACTGTAGGTAACCCAAATCAGCA	GGAAAATCGTGTTGCACTTCAG
GATA1	TGGGGACCTCAGAACCCTTG	GGCTGCATTTGGGGAAGTG
Prkcd	TGGGGGTGACCTGATGTTC	CCAGCACCAACAATACCTGTAA
Jak2	TTGTGGTATTACGCCTGTGTATC	ATGCCTGGTTGACTCGTCTAT
Akt3	TGGGTTCAGAAGAGGGGAGAA	AGGGGATAAGGTAAGTCCACATC
Bcl-X_L	GACAAGGAGATGCAGGTATTGG	TCCCGTAGAGATCCACAAAAGT
Rac2	GACAGTAAGCCGGTGAACCTG	CTGACTAGCGAGAAGCAGATG
Ccng2	CCCCGGAGAATGATAACACTTT	CCACTTTGGCATTTCTCAGTCT
ccne1	GTGGCTCCGACCTTTCAGTC	CACAGTCTTGTCAATCTTGGCA
cdc25a	ACAGCAGTCTACAGAGAATGGG	GATGAGGTGAAAGGTGTCTTGG
Hras	CGTGAGATTCGGCAGCATAAA	GACAGCACACATTTGCAGCTC
Ebp1	CAGCAGGAGCAAACTATCGC	GGCATCACCTTTCTCACACAAG
p27	TGCCTCCTGAGTGCTGAGATT	AGTACCCAGAGGTGATGGCACA
CBP	GGCTTCTCCGCGAATGACAA	GTTTGGACGCAGCATCTGGA
Elp3	CAGTCCCTCCTCACTATCGAA	TCTGTGGGGTTTGCACATCAC
p300	CAGAACCAGCAGATGCTCAA	GAGGTGCTTGGCTGTTCTTC
GCN5	AAGGCCAATGAAACCTGCAAG	CTCACAGCTACGGCACAACTC
Hat1	AAGTGTAACACCAACACAGCA	CGAAAGCAGTTTCATCATCCCC
PCAF	CGGATCGCCGTGAAGAAGG	CATTGCATTTACAGGACTCCTCT
Tip60	CGAGCGGCTGGACTTAAAGAA	GGGCGGGACCCAGGAA
Hdac1	GGTCTCTACCGAAAAATGGAGA	TCATCACTGTGGTACTTGGTCA
Hdac2	CTCCACGGGTGGTTCAGT	CCCAATTGACAGCCATATCA
Hdac3	TCAACGTGGGTGATGACTG	TGTTGCTCCTTGCAGAGATG
Hdac4	AATCCTGCCCGTGTGAAC	GTAGGGGCCACTTGCAGA
Hdac5	GAGTCCAGTGCTGGTTACAAAA	TACACCTGGAGGGGCTGTAA
Hdac6	GAAGGAGGAGCTGATGTTGG	TCATGTACTGGGTTGTCTCCAT
Hdac8	GCAGCTGGCAACTCTGATT	GTCAAGTATGTCCAGCAACGAG
Hdac10	CGACTGCTCTGGGATGACCC	CAGGCACCTTTCTTCCAGGC

ChIP qRT-PCR primer sequences:

Binding site relative to Gcn5 TSS	Sense primer	Antisense primer
-1596 to -1690	CACTCTACCAGTGAGGCTGCT	AGCGAAACCTTGGGCATC
-44 to -142	CGATGGGAGTCGTAGTCTTCC	GCTCAACCAAGCGACATTTG
-3 to -96	GCAACCGGCGCACAG	GTATGGAAGGCCAAAGGATG

Supplementary References:

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3. Popova EY, Krauss SW, Short SA, et al. Chromatin condensation in terminally differentiating mouse erythroblasts does not involve special architectural proteins but depends on histone deacetylation. Chromosome Res. 2009;17:47-64.