ONLINE METHODS

Noncompetitive and competitive transplants. We performed noncompetitive transplants with bone marrow from 6- to 10-week-old F1 B6/129 *MSI2* inducible mice or rtTA littermate controls into B6SJL congenic CD45.1$^+$ recipients (Taconic Transgenics). We performed competitive transplants with 6- to 10-week-old F$_1$ B6/129 *MSI2* bone marrow mixed with wild-type competitor control (CD45.1$^+$) bone marrow at 1:1 or 3:1 ratios for a total of 1 million cells injected. We allowed the marrow to engraft for 4–6 weeks before administering doxycycline and assessing peripheral blood chimerism. The chimerism ratio was calculated by taking the percentage of CD45.2$^+$ cells for each mouse and normalizing it to the percentage of CD45.2$^+$ cells before doxycycline administration (**Fig. 2h**). The protocol was approved by the Institutional Animal Care and Use Committee (IACUC) at both the Massachusetts Institute of Technology and Children's Hospital Boston.

Colony-forming assays. Bone marrow and spleen cells were isolated, subjected to red cell lysis and resuspended in Iscove's modified Dulbecco's medium (IMDM) plus 10% FBS plus 5% (100 IU ml^{-1}) penicillin-streptomycin. (Cambrex, Biowhittaker). We plated cells in duplicate into M3434 methylcellulose medium (Stem Cell Technologies) at 1 × 10^4 cells per dish for bone marrow and 5 × 10^4 cells per dish for spleen cells. Colonies were scored after 7 d if at least 25 distinct colonies were observed per dish; the cells were replated in M3434 media at 1 × 10^4 cells per dish and then counted and replated every 7 d. Single-cytokine methylcellulose analysis was performed as described above with M3231 (Stem Cell Technologies), interleukin-3 (10 ng ml^{-1}) or granulocyte-macrophage colony–stimulating factor (20 ng ml^{-1}, Peprotech).

Western blotting. Whole-cell protein lysates were prepared from single-cell suspensions of splenocytes or cell lines. Immunoblotting was performed as previously described[31]. Antibodies used were pan-MSI (Cell Signaling Technologies, cat. no. 2154) and antibodies specific for MSI1 (Chemicon, cat. no. AB5977), glyceraldehyde-3-phosphate dehydrogenase (Santa Cruz, cat. no. sc-32233) and GATA-2 transcription factor (Santa Cruz, cat. no. Sc267).

Short hairpin RNA lentiviral acute myeloid leukemia and chronic myeloid leukemia cell line experiments. We transduced LAMA-84 and THP-1 (the German Collection of Microorganisms and Cell Cultures and Nomo1 and AR230 (gifts from S. Armstrong) with various pLKO.1puro lentiviral shRNA vectors targeting *MSI2* or a scrambled control shRNA as previously described[32]. We purchased *MSI2*-specific short hairpins through Open Biosystems: *MSI2*-1, 5′-CCCAACTTCGTGGCGACCTAT-3′ (TRCN62811); *MSI2*-2, 5′-CCAGCAAGTGTAGATAAAGTA-3′ (TRCN62808). RNA was isolated after 3 d of puromycin selection, and gene expression was profiled with the G4112F whole–human genome microarray (Agilent).

Human CD34$^+$ expansion. We thawed and plated human cord blood in serum free expansion medium (SFEM, StemCell Technology) medium with human cytokines Flt3 40 ng ml^{-1}, 100 ng ml^{-1} SCF and 50 ng ml^{-1} thrombopoietin (all from R&D Systems) for 5 d.

Msi2 knockdown. LSK cells from C57BL/6 mice were sorted and cultured in SFEM supplemented with 10 μg ml^{-1} heparin (Sigma), 10 ng ml^{-1} mouse SCF, 20 ng ml^{-1} thrombopoietin, insulin-like growth factor-2, (all from R&D Systems), 10 ng ml^{-1} human fibroblast growth factor-1 (Invitrogen) (STIF medium) at a concentration of 1 × 10^5 cells into a 96-well round bottom plate. LSK cells were infected twice at 24 and 48 h after sorting, and the percentage EGFP$^+$ cells was assessed before injection into syngeneic C57BL/6 mice with pSicoR Scramble and *Msi2* hairpins. We analyzed mice 6 weeks after engraftment.

Homing assay. Bone marrow cells from C57BL/6 mice were lineage-depleted (Lin$^-$) with Dynal beads (Invitrogen), cultured in STIF medium and infected as before with *Msi2*-specific shRNAs. Mice were lethally irradiated 72 h before transplantation and assessed for infection efficiency, and 3 × 10^6 cells were injected per mouse. Bone marrow was collected 17 h after injection and analyzed for EGFP homing.

Numb asymmetric immunofluorescence. We allowed mice to engraft for 6–10 weeks and then administered doxycycline to rtTA or *MSI2*-expressing mice for 5 d. LSKs were then sorted and cultured with STIF medium in 96-well round bottom plates for 16 h and treated with 10 nM of nocodazole (Sigma) for 24 h. We cytospun, fixed, methanol permeabilized and stained the cells with a Numb-specific antibody (Ab4147, Abcam) and goat-specific IgG Alexa Fluor 546–conjugated secondary antibody (Mol Probes) and counterstained with DAPI[14]. We determined symmetric versus asymmetric staining patterns on the basis of visual inspection of Numb only in cells undergoing division. Cells with an ambiguous staining pattern were omitted from our analysis.

Phospho-ERK analysis. Mice that were transplanted with MSI2-expressing marrow were administered doxycycline for 5 d, followed by isolation of Lin$^-$ cells, which were then serum starved for 1 h and stimulated with 100 μg ml^{-1} SCF. Cells were then fixed, permeabilized and stained for LSKs as described previously[33].

Statistical analyses. We computed *P* values for bar graphs with the unpaired two-tailed Student's *t* test, except where stated otherwise. Error bars reflect the s.e.m., except where stated otherwise. All statistical analyses were carried out with GraphPad Prism 4.0 and the R statistical environment. The prognostic value of *MSI2* was determined by comparing overall survival of *MSI2* expression-defined groups with Kaplan-Meier survival analysis.

Additional methods. Detailed methodology is described in the **Supplementary Methods**.

31. Rocnik, J.L. *et al.* Roles of tyrosine 589 and 591 in STAT5 activation and transformation mediated by FLT3-ITD. *Blood* **108**, 1339–1345 (2006).
32. Scholl, C. *et al.* Synthetic lethal interaction between oncogenic KRAS dependency and STK33 suppression in human cancer cells. *Cell* **137**, 821–834 (2009).
33. Kalaitzidis, D. & Neel, B.G. Flow-cytometric phosphoprotein analysis reveals agonist and temporal differences in responses of murine hematopoietic stem/progenitor cells. *PLoS One* **3**, e3776 (2008).

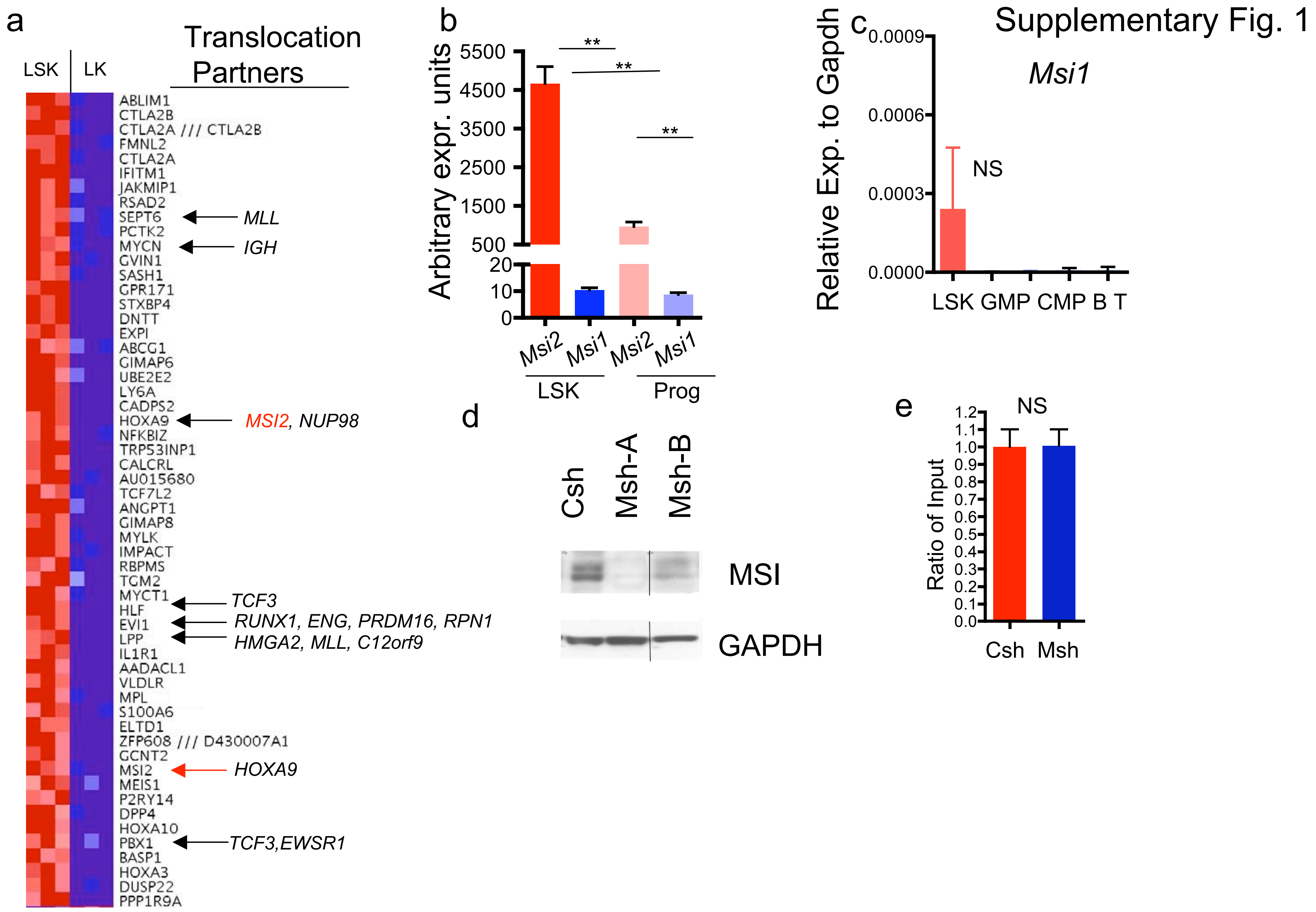
Supplementary Materials

Musashi-2 regulates normal hematopoiesis and promotes aggressive myeloid leukemia

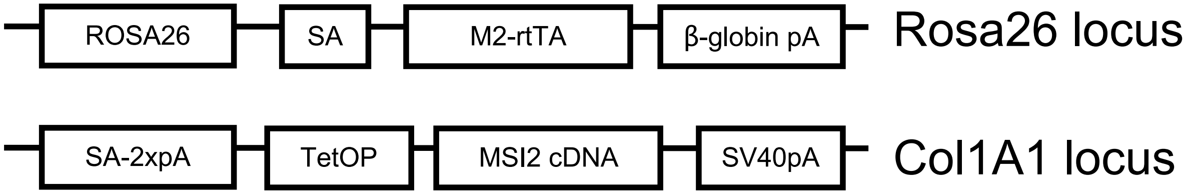
Michael G Kharas[1,2,15], Christopher J Lengner[3,15], Fatima Al-Shahrour[1,4], Lars Bullinger[5], Brian Ball[1], Samir Zaidi[6], Kelly Morgan[1], Winnie Tam[1], Mahnaz Paktinat[1], Rachel Okabe[1], Maricel Gozo[1], William S Einhorn[1,7], Steven W Lane[7], Claudia Scholl[5], Stefan Fröhling[5], Mark D. Fleming[8], Benjamin L Ebert[1,2], D Gary Gilliland[1,2,9], Rudolf Jaenisch[3,6] & George Q Daley[1,2,7,10-14]

[1]Division of Hematology, Department of Medicine, Brigham and Women's Hospital, Boston, Massachusetts, USA. [2]Harvard Medical School, Boston, Massachusetts, USA. [3]Whitehead Institute for Biomedical Research, Cambridge, Massachusetts, USA. [4]Broad Institute of Massachusetts Institute of Technology and Harvard, Cambridge, Massachusetts, USA. [5]Department of Internal Medicine III, University Hospital of Ulm, Ulm, Germany. [6]Department of Biology, Massachusetts Institute of Technology, Cambridge, Massachusetts, USA. [7]Division of Pediatric Hematology/Oncology, Children's Hospital, Boston, Massachusetts, USA. [8]Department of Pathology, Children's Hospital and Harvard Medical School, Boston, MA 02115, USA. [9]Merck Research Laboratories, North Wales, Pennsylvania, USA. [10]Howard Hughes Medical Institute, Boston, Massachusetts, USA. [11]Department of Biological Chemistry and Molecular Pharmacology, Harvard Medical School, Boston, Massachusetts, USA. [12]Stem Cell Transplantation Program, Children's Hospital and Dana Farber Cancer Institute, Boston, Massachusetts, USA. [13]Harvard Stem Cell Institute, Cambridge, Massachusetts, USA. [14]Manton Center for Orphan Disease Research, Children's Hospital, Boston, Massachusetts, USA. [15]These authors contributed equally to this work.

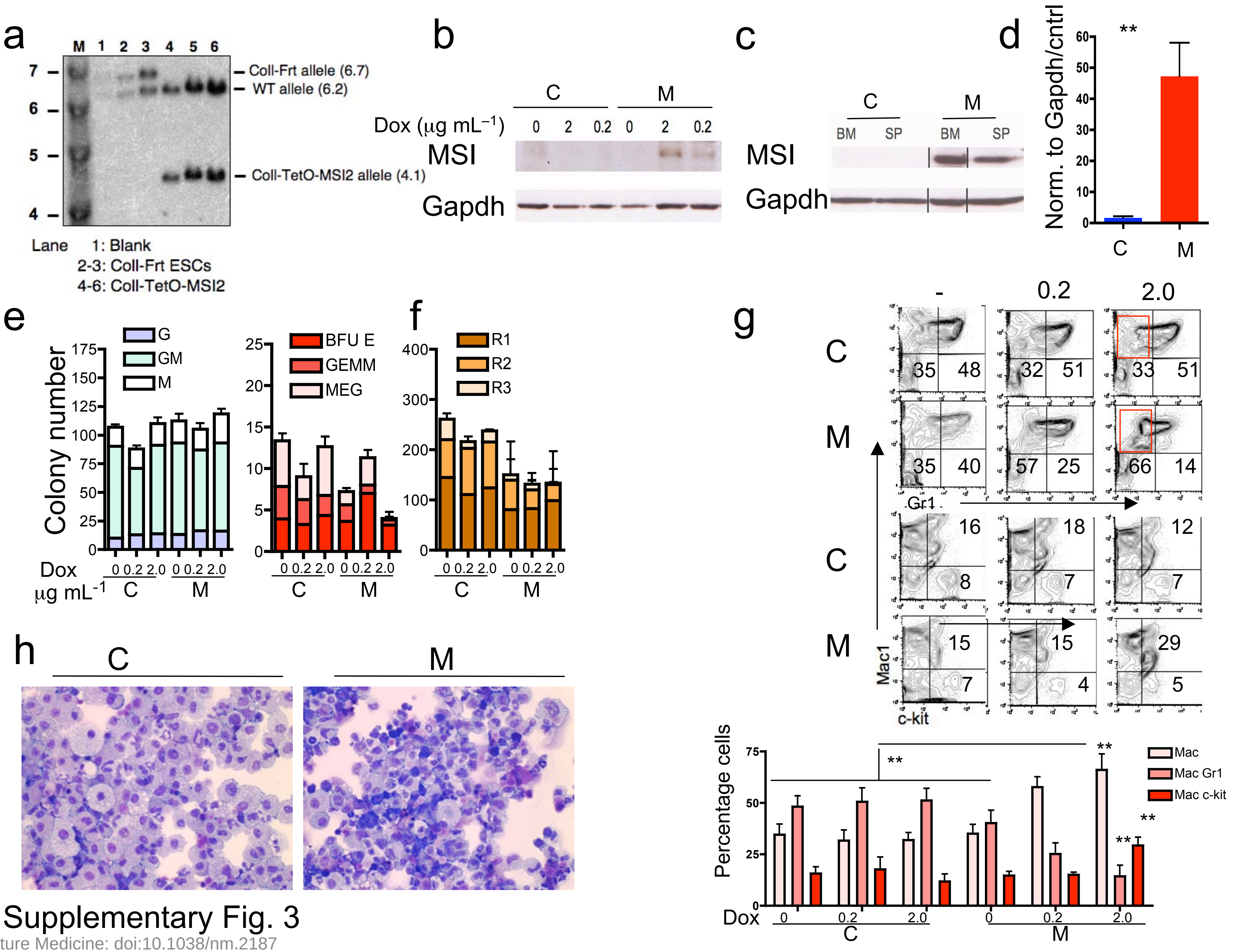
Supplementary Fig. 1



Supplementary Figure 1: Gene Expression Profiling in mouse adult bone marrow hematopoietic cells and *Msi2* knockdown. a, Murine LSK and LK cells were FACS purified followed by transcriptome analysis by microarray. Genes differentially expressed were ranked based on fold change and with an FDR less than 0.7. Arrows indicate genes preferentially expressed in LSK cells that are also known to be involved in chromosomal translocations observed in human hematopoietic cancers. Highlighted in red are translocations identified with *MSI2*. **b,** Gene expression from microarray from **a** (Arbitrary expression units in triplicates). **c,** QRT-PCR analysis and relative expression normalized to GAPDH in indicated sorted populations. **d,** Immunoblot in which human K562 CML cells were transduced with indicated vectors harboring two distinct hairpins targeting *MSI2* and co-expressing EGFP. Cells were sorted for EGFP expression and lysates blotted with indicated antibodies. *Msh*-A and *Msh*-B hairpins target both mouse and human *MSI2*. **e.** Lin$^-$ magnetically sorted bone marrow cells grown in cytokines for 72 hours and transduced with EGFP-expressing vectors containing Scramble (Csh) hairpins or hairpins targeting *MSI2* (Msh). EGFP+ cells were transplanted into lethally irradiated recipient mice which were then sacrificed 17 hours post transplant and the ratio of EGFP$^+$:EGFP$^-$ cells in the bone marrow was calculated and normalized to the ratio in the donor cell population indicating that both *MSI2* knockdown did not affect stem cell homing (ns= no significant difference, n=5 scramble, n=5 *MSI2*, n=5 *MSI2,* NS= not significant, **=$p<0.001$, *=$p<0.01$ and + =$p<0.05$)).



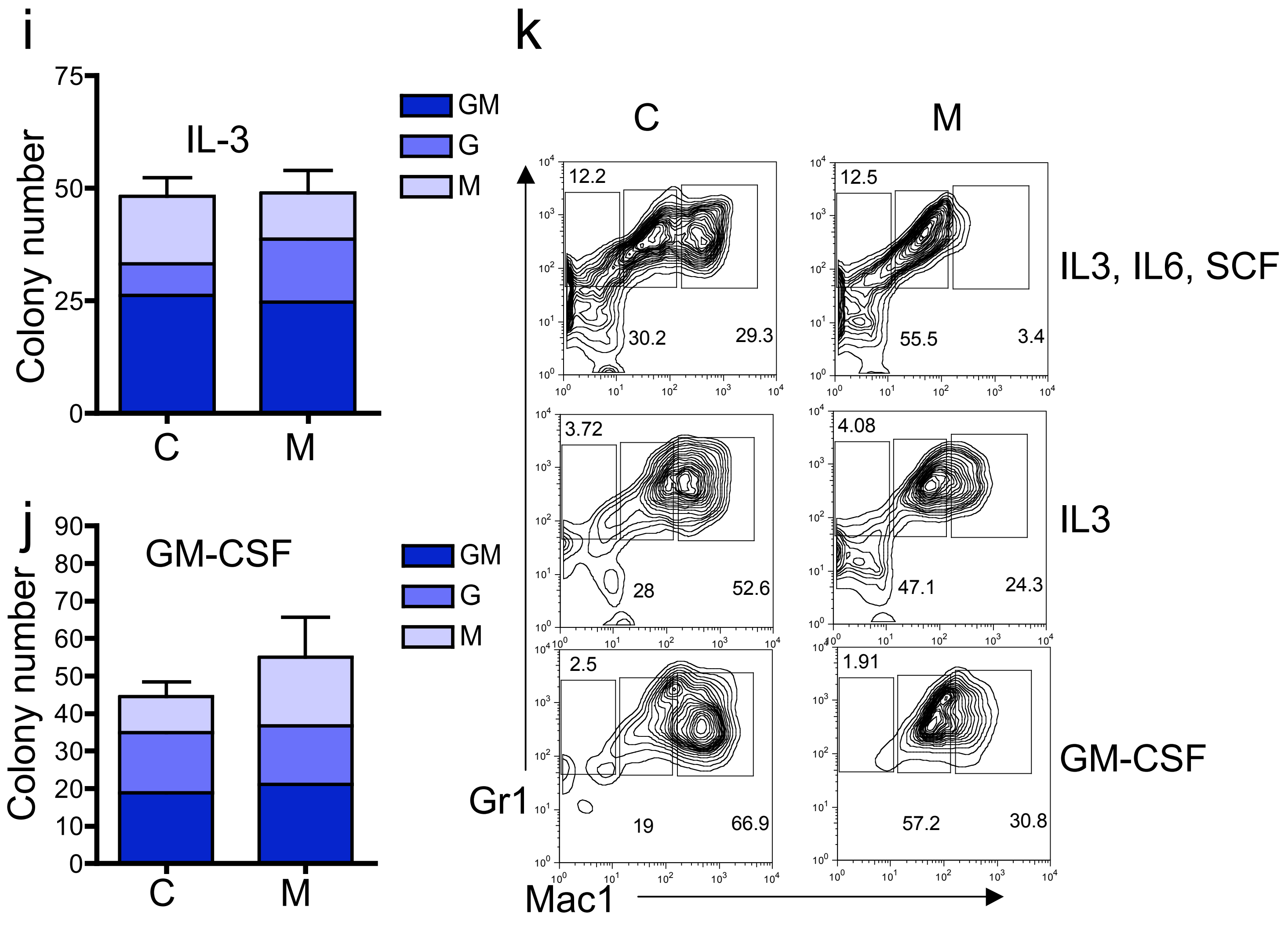
Supplementary Figure 2: Targeted MSI2-inducible expression system. Schematic of dox-inducible single copy transgenic system in which the M2 reverse tetracycline transactivator (M2rtTA) is constitutively expressed from the ROSA26 locus and the human *MSI2* cDNA under control of the tetracycline operator and promoter (TetOP) is targeted downstream of the Type I Collagen (Coll) locus. SA, splice acceptor; pA, polyadenylation signal.



Supplementary Fig. 3

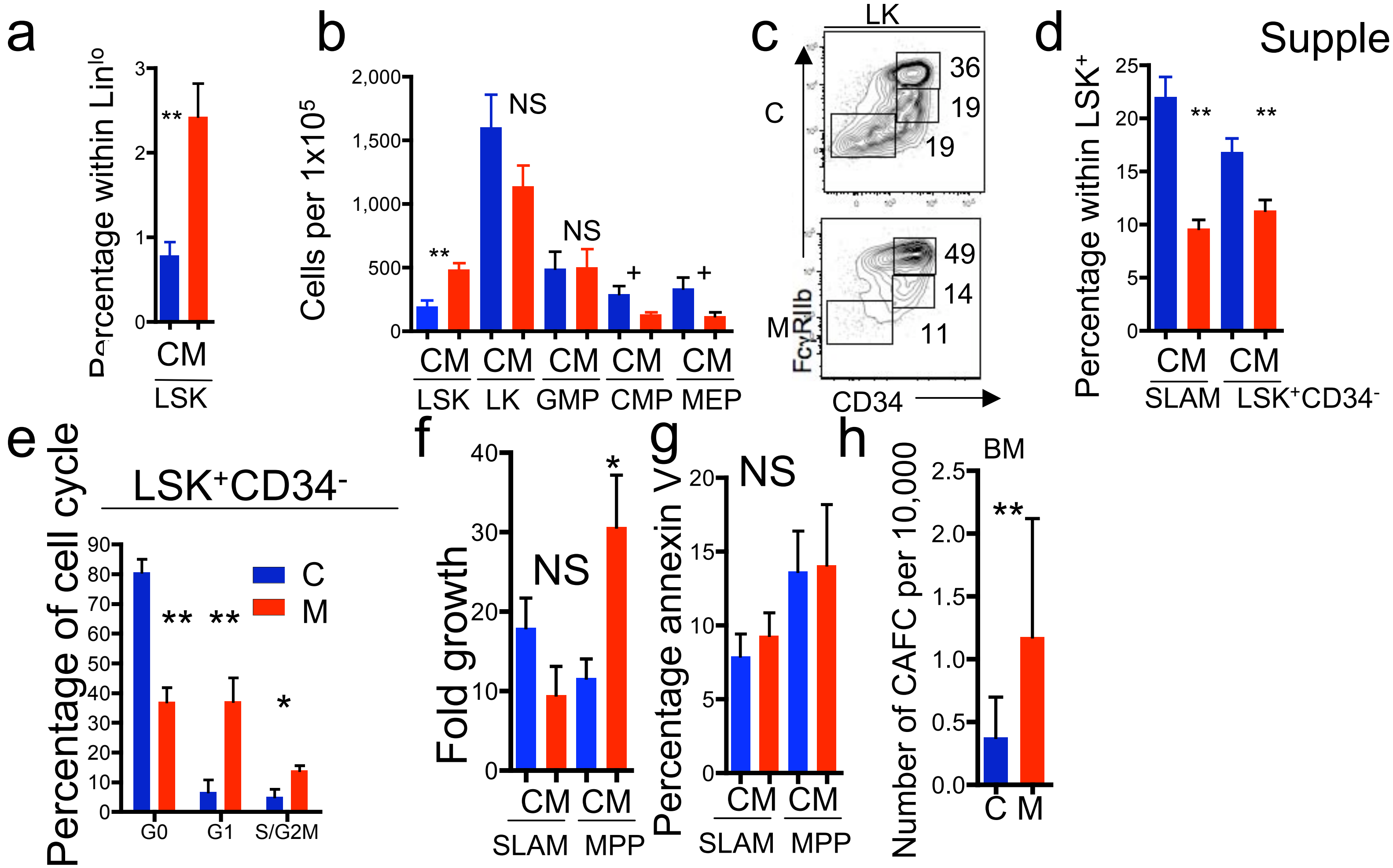
Nature Medicine: doi:10.1038/nm.2187

Supplementary Fig. 3



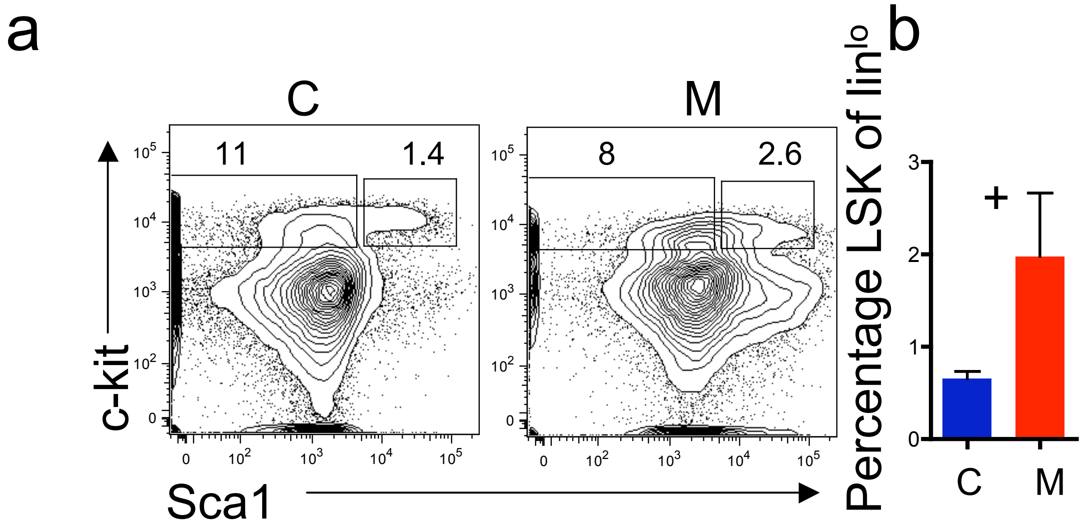
Supplementary Figure 3: Inducible expression of MSI2 *in vitro* attenuates myeloid differentiation. a, Southern blot analysis of genomic DNA from embryonic stem cell clones digested with SpeI demonstrating correct targeting of the Coll locus. **b,** Immunoblotting for MSI2 in control (C; ROSA26 rtTA) and MSI2 inducible (M; ROSA26rtTA, Coll-TetO-*MSI2*) bone marrow cells cultured with cytokines for 24hrs with indicated doses of dox (in μg/mL). **c,** Inducible MSI2 expression *in vivo* in indicated tissues after mice were administered 2 mg/mL dox for five days in the drinking water. **d,** Transplanted MSI2 inducible mice were treated with dox for 36 hours and LSKs were flow sorted. *MSI2* expression was determined by quantitative RT-PCR, relative to Gapdh (Representative of n=5 (C), and n=3 *MSI2* (M) induced LSKs, s.e.m **$p<0.001$). **e,** Methylcellulose colony-forming cells from the bone marrow were scored at 7 days post plating for indicated colony types [Granulocyte (G), Granulocyte Monocyte (GM), Monocyte (M), Burst forming Unit Erythroid (BFU-E), Megakaryocyte (MEG)] (error bars represent s.e.m. with indicated dox concentration in μg/mL). **f,** colonies were harvested and replated into methycellulose and counted over three rounds of replating (R1, R2 and R3) (differences between control (C) and MSI2-induction (M) were not statistically significant; n= at least 4 experiments). **g,** Methylcellulose colonies were analyzed by flow cytometry with indicated parameters after 1st round of replating (top panels: Mac1 vs. Gr1, red box indicates gate on the Mac1 population. Lower panels are representative Mac1 vs. c-Kit flow plots representative from at least 3 experiments, red box indicates gate on the $Mac^{+}c\text{-}Kit^{+}$ population. Data are quantified in bar graph at the bottom of the panel (** $p<0.001$). **h,** Histological analysis of cytospins stained with hematoxylin and eosin from 1st round of replating and representative image from 3 independent experiments. **i–j,** Methylcellulose colony-forming cells from the bone marrow were scored at 7 days post plating for indicated colony types as in **e** with only IL-3 (10ng/mL) or GM-CSF and (error bars represent s.e.m two independent experiments n=3 per genotype). **k,** Methylcellulose colonies were analyzed by flow cytometry with indicated parameters after 1st round of replating as in **g.** Data are representative of 2 independent experiments with n=3 per genotype, NS= not significant, **=$p<0.001$, *=$p<0.01$ and + =$p<0.05$).

Supplementary Fig. 4



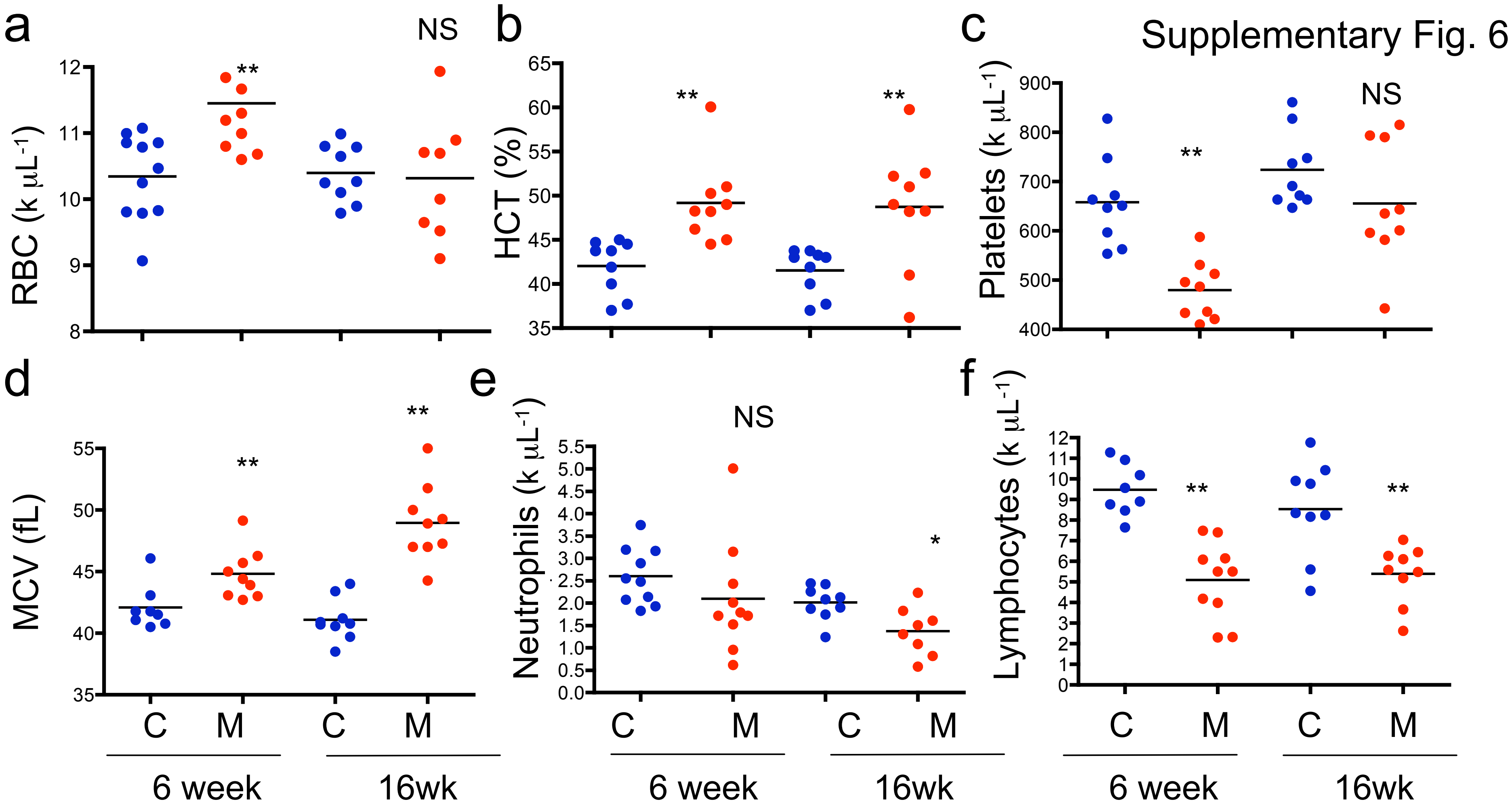
Supplementary Figure 4: Changes in frequency and proliferation of MSI2-expressing bone marrow cells. a, The percentage of LSK in the Lin^{low} compartment of the bone marrow in control (C) and MSI2 induced (M) cells. **b,** Numbers of bone marrow cells of specific phenotype, as indicated. Hematopoietic stem and progenitors cells (LSK); committed progenitors (LK); granulocyte monocyte progenitor (GMP); common myeloid progenitor (CMP); megakaryocyte-erythroid progenitors (MEP). **c,** Representative flow plot stained and gated on PI^{-}, Lineage^{Low} Kit^{+}, Sca^{-} progenitors with average percentages indicated in the plots. **d,** Frequency of long-term stem cells (SLAM; LSK^{+} CD150^{+} CD48^{-} or LSK^{+}CD34–) within the LSK compartment of the bone marrow; fractionation defined in methods. **e**, Cell cycle analysis was performed with Hoechst and pyronin gated on long term stem cells as in **Fig. 2c** (LSK^{+} CD34^{-}) and representative data from at least 7 mice and error bars represent s.e.m. **f**, Two thousand SLAM and MPP (LSK, CD48^{-}, CD150^{-}) cells were plated and counted after 5 days of proliferation (fold growth over day 0, n=4 control and n=3 MSI2). **g**, Flow cytometric apoptosis analysis gated on Annexin V/PI^{-} cells after 5 days of culture. **h**, Number of CAFC per 10,000 cells from whole bone-marrow plated for 2 weeks. Data are representative of two mice per genotype, NS= not significant, **=p<0.001, *=p<0.01 and + =p<0.05).

Supplementary Fig. 5



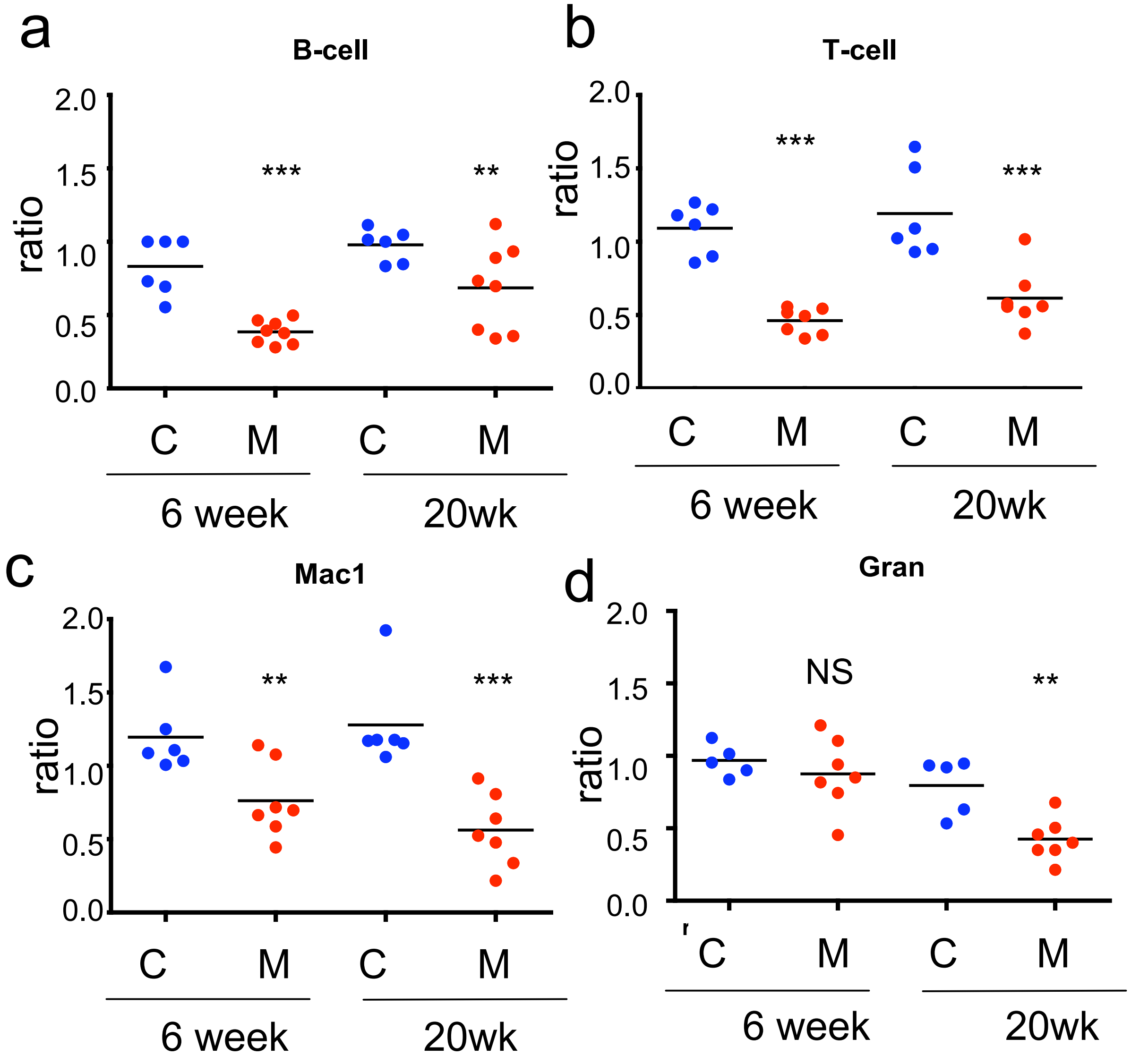
Supplementary Figure 5: MSI2 induction in primary animals leads to an expansion of hematopoietic stem cells and progenitor cells *in vivo*. a, Representative flow cytometry of primary rtTA control (C) and MSI2 induced bone marrow (M) five days after dox administration. **b,** Quantification of flow cytometry in panel **a**, data plotted as the percentage of LSK cells in the lineage^{low} fraction of the bone marrow (C=rtTA, M=MSI2. Representative of 3 independent experiments with at least 3 mice per condition, +: $p<0.05$)

Supplementary Fig. 6

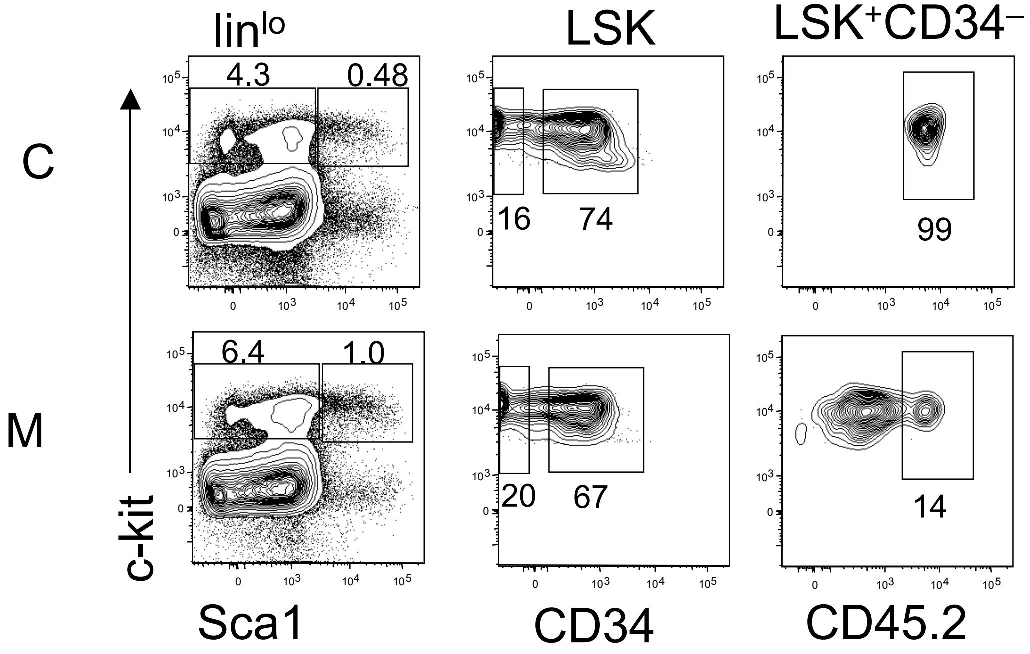


Supplementary Figure 6: Decreases in multiple hematopoietic populations of mice ectopically expressing MSI2 after long-term engraftment. **a–f,** Complete blood counts from non-competitive transplanted MSI2 inducible (M) and rtTA control (C) animals 6 and 16 weeks after dox administration. **a,** Red blood cells, **b,** Hematocrit, **c,** Platelets, **d,** Mean corpuscular volume, **e,** Neutrophils, and **f,** Lymphocytes, NS= not significant, **=p<0.001, *=p<0.01 and + =p<0.05.

Supplementary Fig. 7

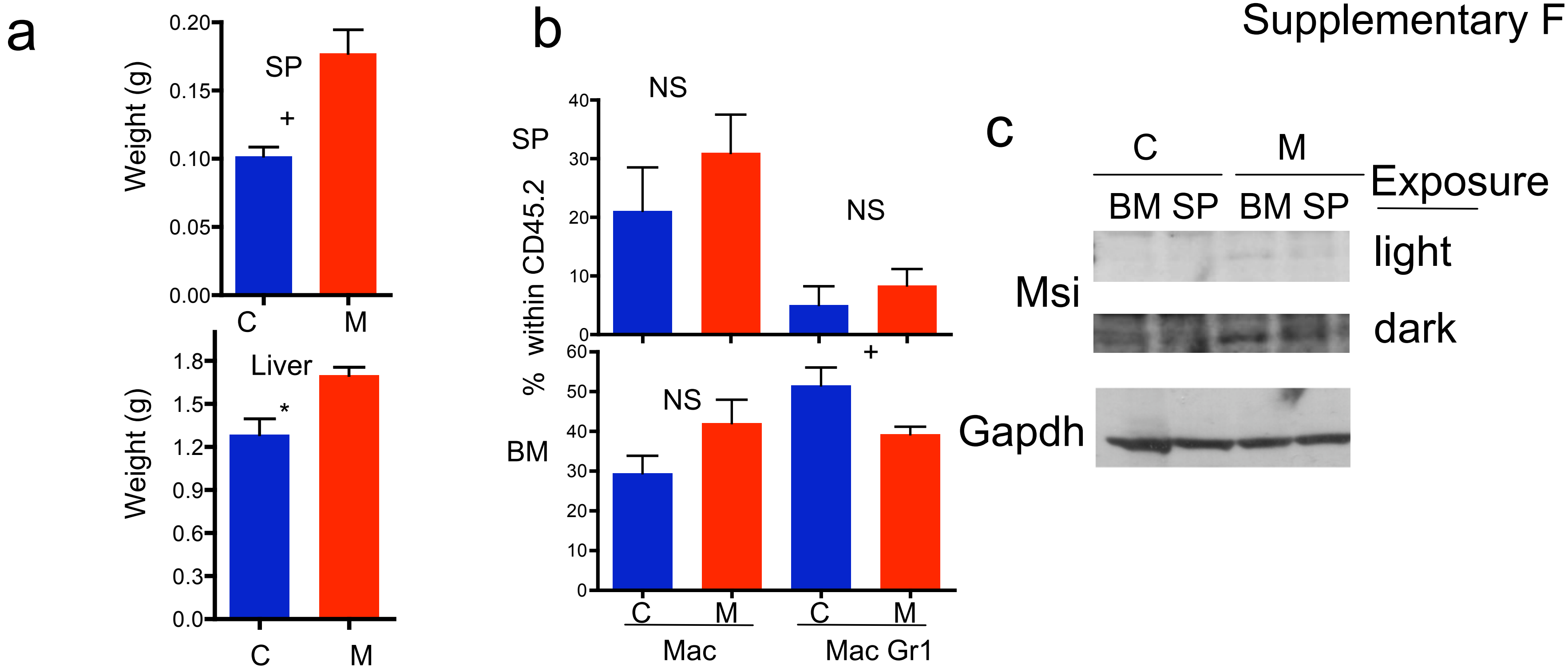


Supplementary Figure 7: Ectopic MSI2 expression decreases myeloid and lymphoid lineages in competitive long-term transplants. **a–d**, Individual contribution from the peripheral blood of competitive MSI2 inducible transplants (each dot represents an individual mouse, blue=rtTA; C, red=MSI2; M). Individual mice were allowed to engraft for 6 weeks and all the analysis was normalized to the initial, pre-dox treatment, then monitored at 6 and 29 weeks of dox treatment. Chimerism of peripheral blood B-cells (B220$^+$) T-cells (CD3 or CD4/CD8), Granulocytes (Mac1$^+$/Gr1$^+$), and macrophages (Mac1$^+$ Gr1$^-$), measured by flow cytometry NS= not significant, ***=p<0.001, **=p<0.001, *=p<0.01 and + =p<0.05.



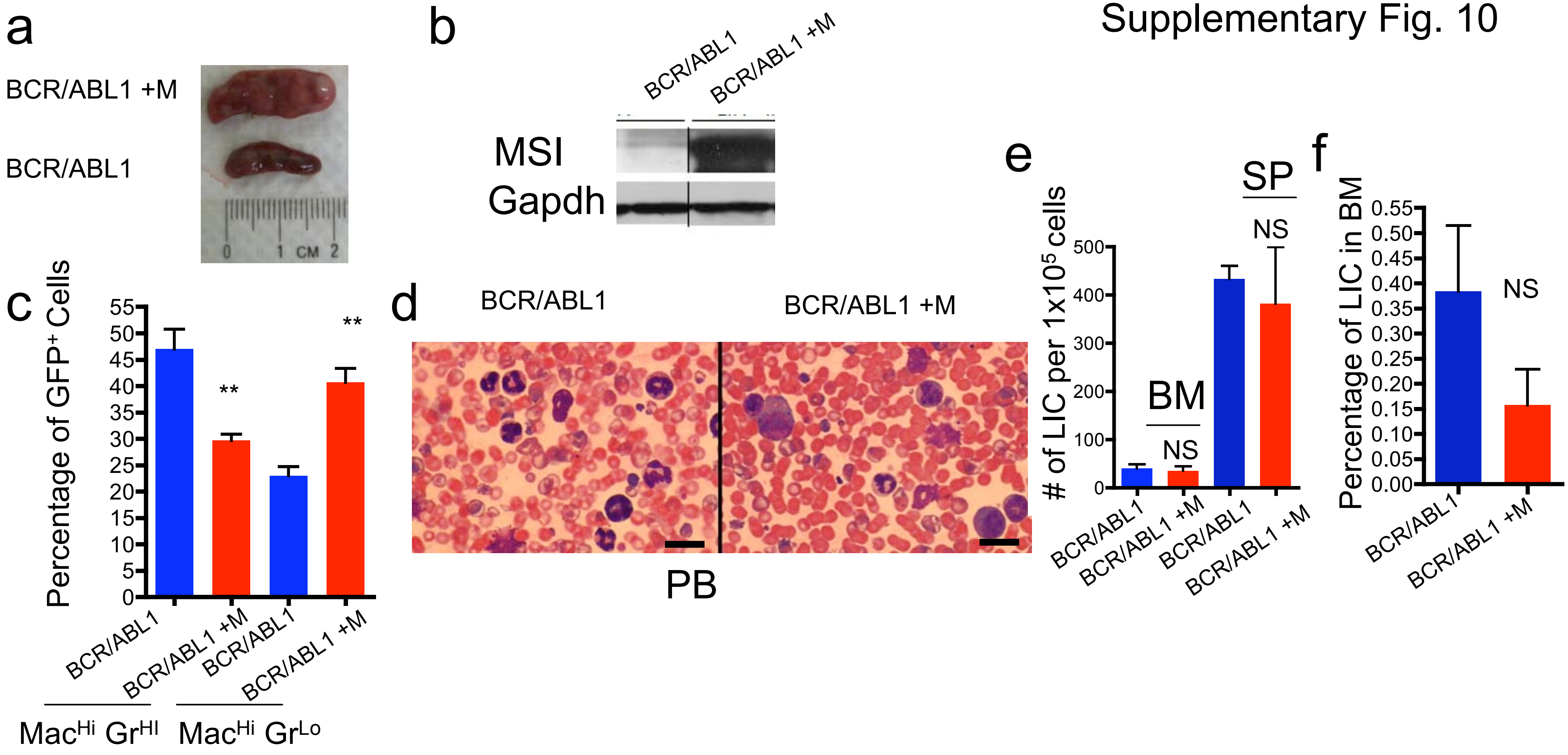
Supplementary Figure 8: Decreased long-term engraftment of CD34⁻ LSKs with ectopic MSI2 expression. Mice were competitively transplanted with a 3:1 ratio of MSI2- or rtTA-expressing (CD45.2):wildtype cells (CD45.1), allowed to engraft, then administered dox for 20 weeks. Bone marrow was then analyzed by flow cytometry and live, PI⁻ cells were gated and stained with indicated markers. (Representative flow cytometric plot for **Fig. 2i**).

Supplementary Fig. 9



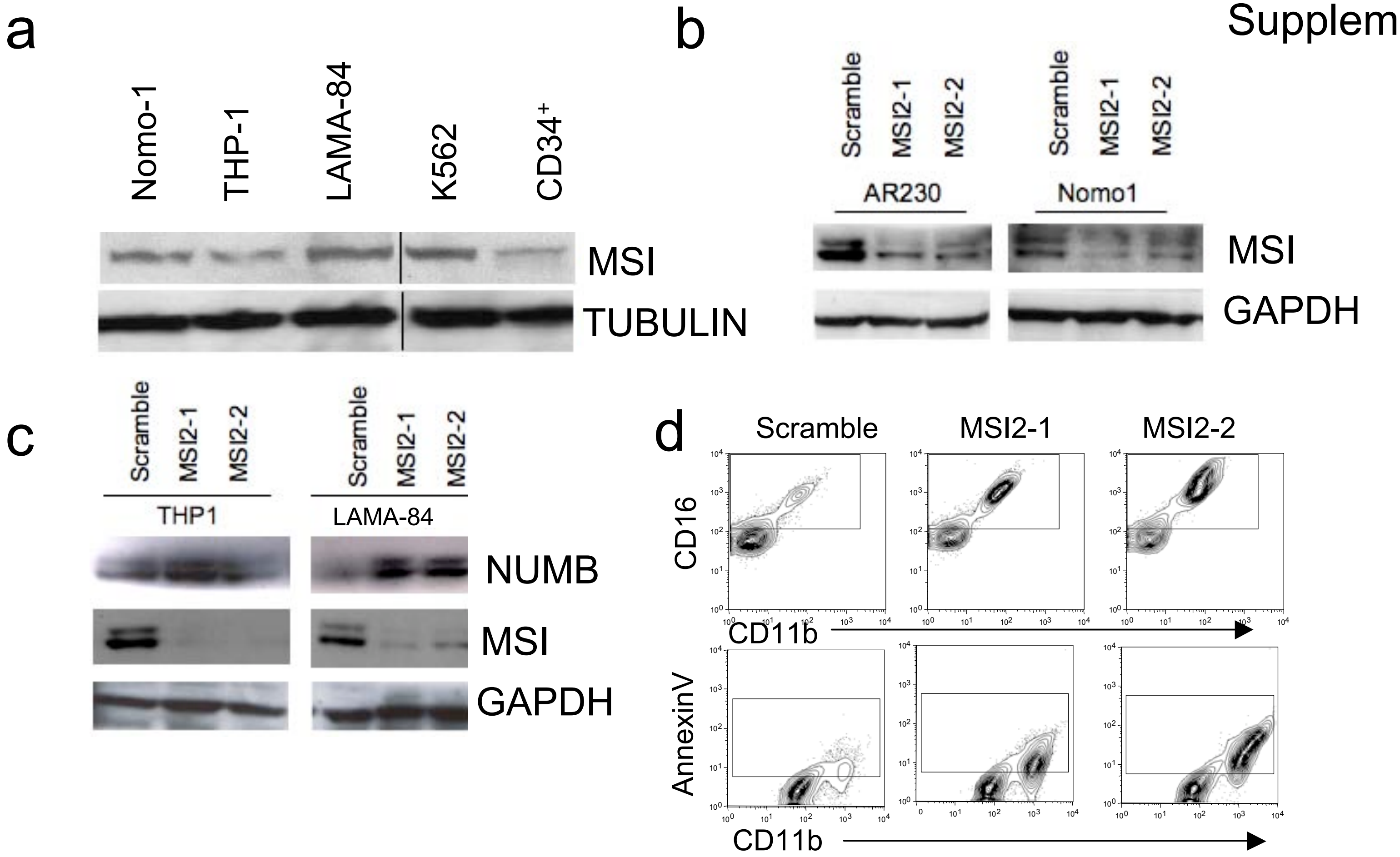
Supplementary Figure 9: Selection against MSI2 induction in long-term dox treated transplant recipients. **a,** Spleen and liver weights from at least 5 mice (+= $p<0.02$, *= $p<0.01$). **b,** Flow cytometric analysis with myeloid markers gated on CD45.2 congenic marker as in **Supplementary Fig. 3**. with indicated tissues and gating from at least 4 mice. **c,** Immunoblotting for MSI2 in the bone marrow of mice treated with doxycycline for 1 year after engraftment, NS= not significant, **=$p<0.001$, *=$p<0.01$ and + =$p<0.05$.

Supplementary Fig. 10

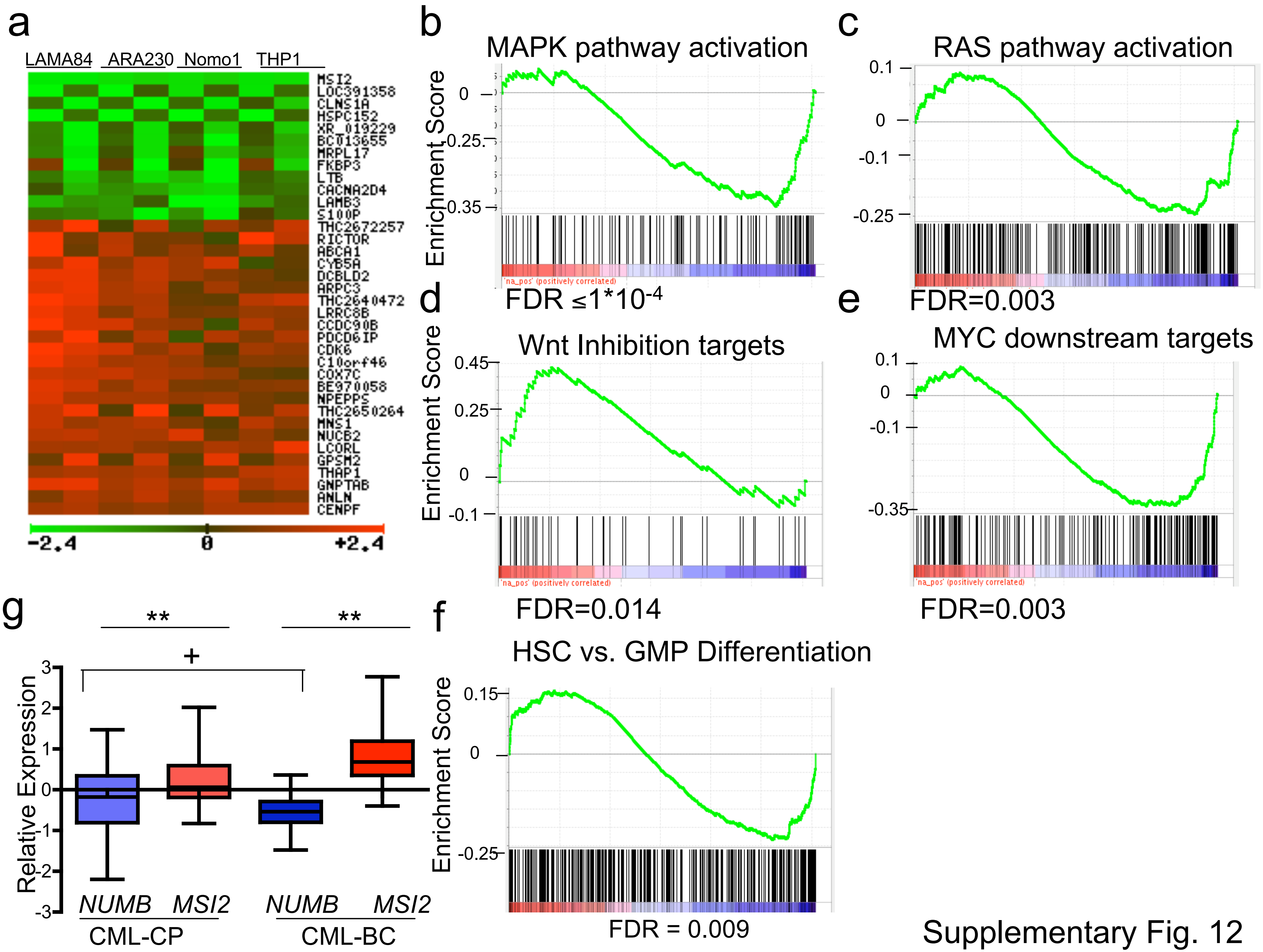


Supplementary Figure 10: Skewing towards a more immature myeloid BCR-ABL1 leukemia in MSI2 induced mice. a, Images of representative spleens from mice sacrificed at 14 days post transplantation of BCR-ABL1 with or without MSI2 (M). **b,** Immunoblot with indicated antibodies from control or MSI2 induced spleens from BCR/ABL1 diseased mice. **c,** Quantitation of GFP$^+$ cells of Mac1^{hi} Gr1^{hi} and Mac1^{hi} Gr1^{lo} from spleens of diseased mice. **d,** Representative peripheral blood smears of leukemic mice, black lines indicate scale 250 μm. **e–f,** Flow cytometric analysis of spleen (**e**) and bone marrow (**e, f**) from diseased mice were gated on leukemia initiating cells (PI$^-$, lineage^{low}, GPF$^+$ LSK in indicated tissues). Experiment from two independent experiments from at least 4 mice per condition, NS= not significant, **=p<0.001, *=p<0.01 and + =p<0.05.

Supplementary Fig. 11



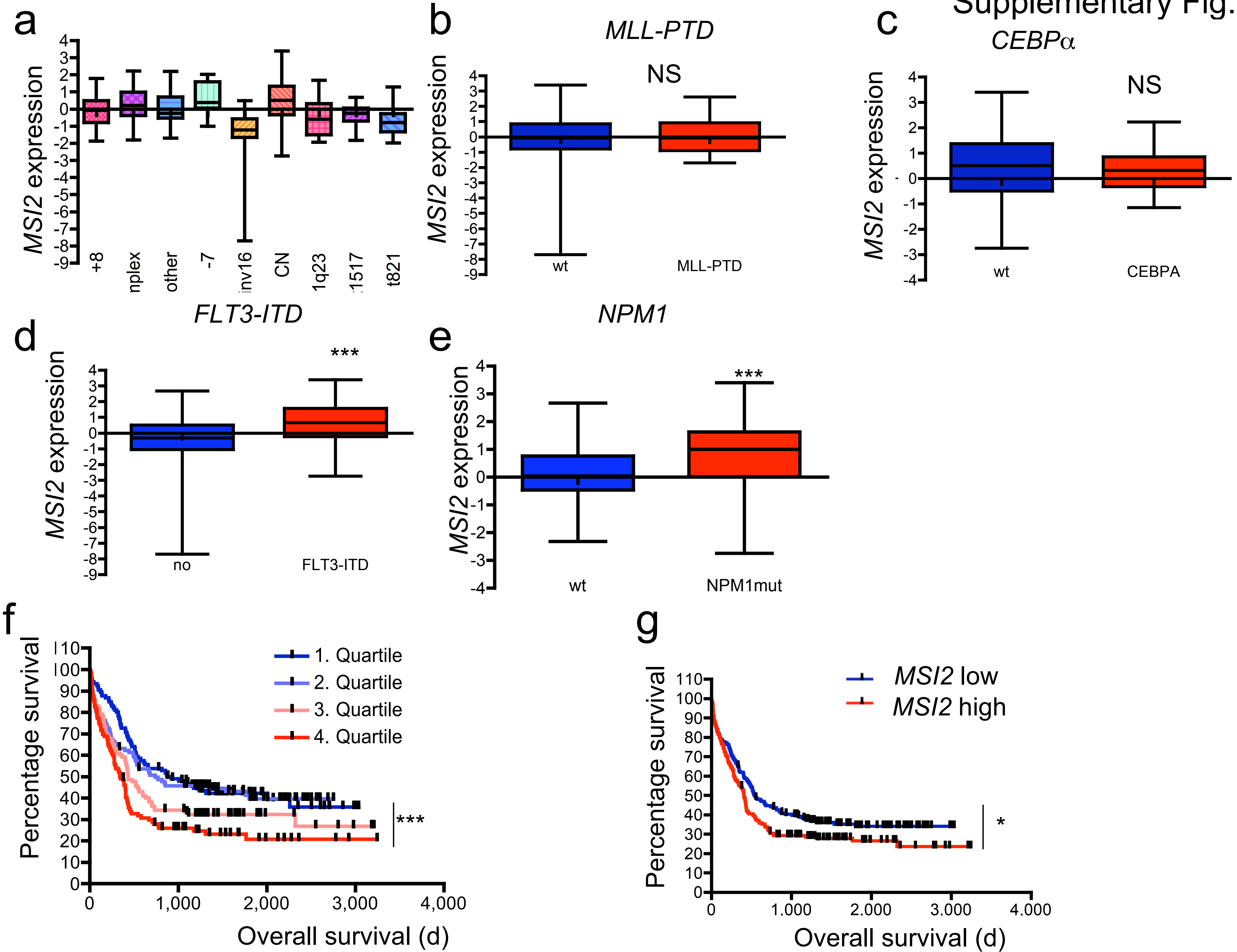
Supplementary Figure 11: Knockdown of MSI2 expression using shRNAs in myeloid leukemic cell lines and increased NUMB expression. a, Immunoblot of AML cell lines (Nomo-1, THP-1) and CML-BC cell lines (LAMA-84, K562) and human CD34$^+$ cord blood cells, probed with indicated antibodies. **b–c,** Indicated cell lines were infected with viruses harboring control (scramble) or two individual *MSI2* shRNAs along with a constitutively expressed puromycin resistance cassette, and analyzed for MSI2 and GAPDH protein levels (b) or NUMB, MSI2, and GAPDH protein levels (c) 3 days post puromycin selection. **d.** CD16 and CD11b surface antigen expression on LAMA-84 cells six days post- *MSI2* knockdown, indicating increased differentiation (representative flow plot from 3-4 independent experiments percentages presented in **Fig. 4d**, NS= not significant, **=$p<0.001$, *=$p<0.01$ and + =$p<0.05$



Supplementary Fig. 12

Supplementary Figure 12: Effects of MSI2 knockdown on global gene expression in human myeloid leukemic cell lines. **a,** Heat map of differentially expressed genes from MSI2 shRNA infected myeloid leukemic cell lines compared to scramble controls (FDR < 0.05 and Fold change ≥ 2), **b–f,** Gene set enrichment analysis using *MSI2* shRNA microarray data identifies genes targets activated by the MAPK pathway being suppressed (b), genes targets activated by the RAS pathway being suppressed (c), WNT pathway inhibition (d), MYC target genes being suppressed (f), and genes enriched in HSCs versus GMPs being suppressed by *MSI2* knockdown. **g,** Comparison of NUMB and *MSI2* expression in chronic phase (CP) and blast crisis (BC) CML, NS= not significant, **=p<0.001, *=p<0.01 and + =p<0.05.

Supplementary Fig. 13



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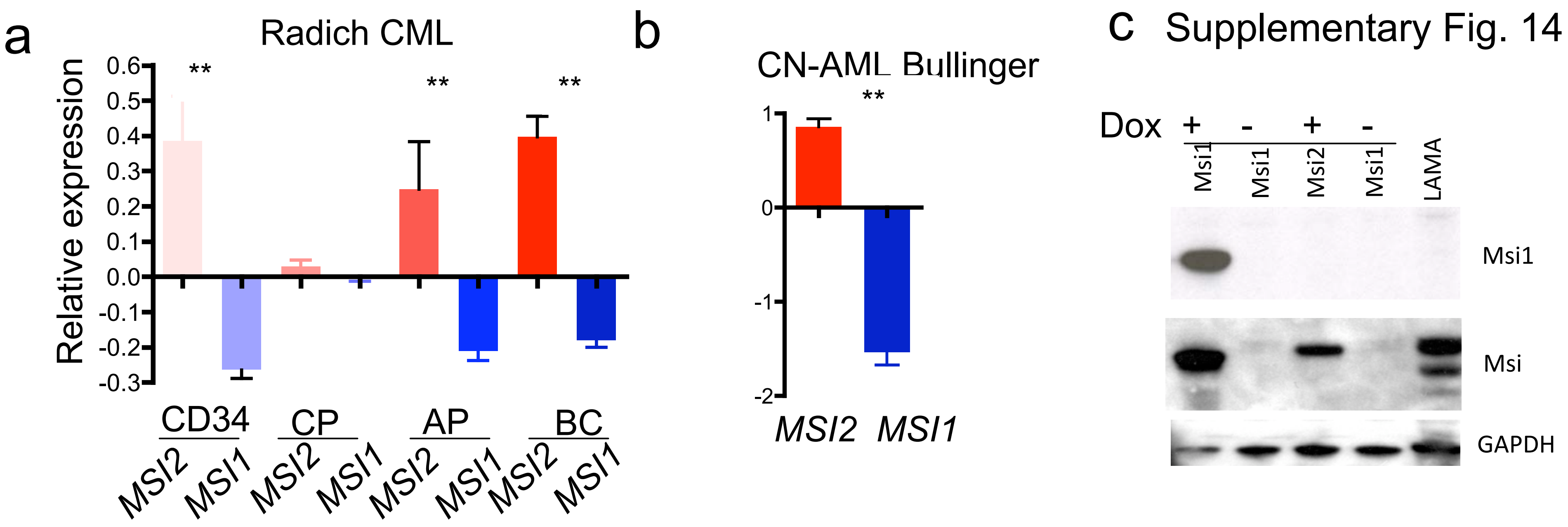
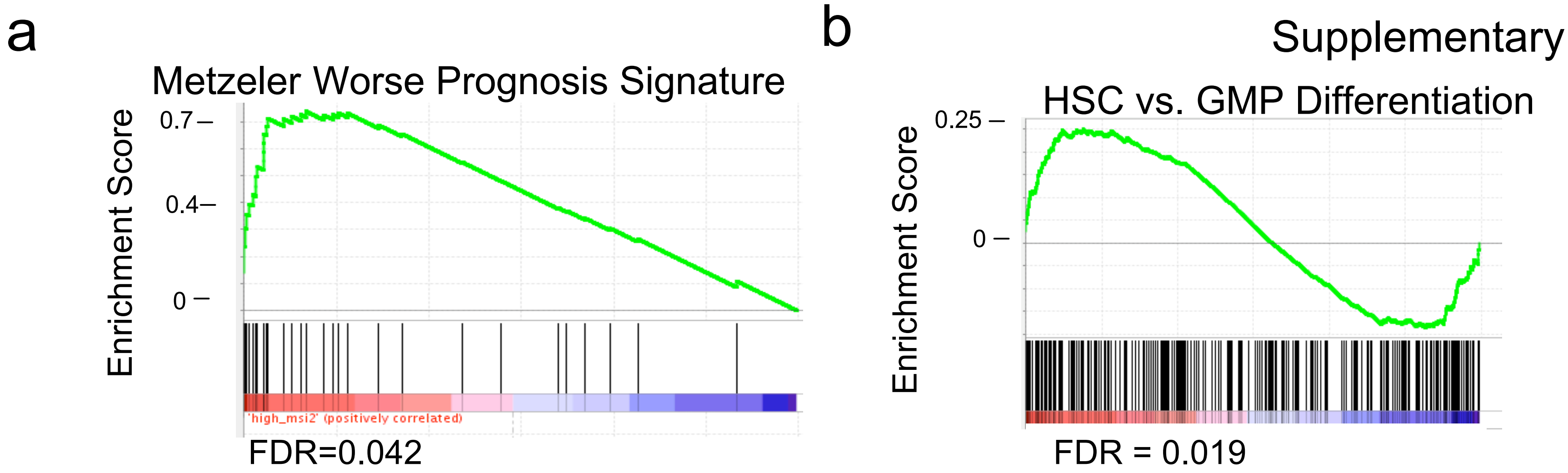
Supplementary Figure 13: Increased *MSI2* expression is associated with a worse prognosis leukemia and association with cytogenetic parameters and molecular markers. a–e, Levels of MSI2 mRNA expression obtained from Bullinger AML patient microarray data are segregated by molecular and cytogenetic markers (Oneway ANOVA g, NS= not significant, ***p<0.0001, **=p<0.001, *=p<0.01 and + =p<0.05).. **f,** Overall survival in AML patients segregated into quartiles based on *MSI2* expression. **g,** Overall survival of AML patients censoring inv16 and segregated by high and low *MSI2* expression.



Supplementary Figure 14: *MSI1* is not expressed in myeloid leukemias.

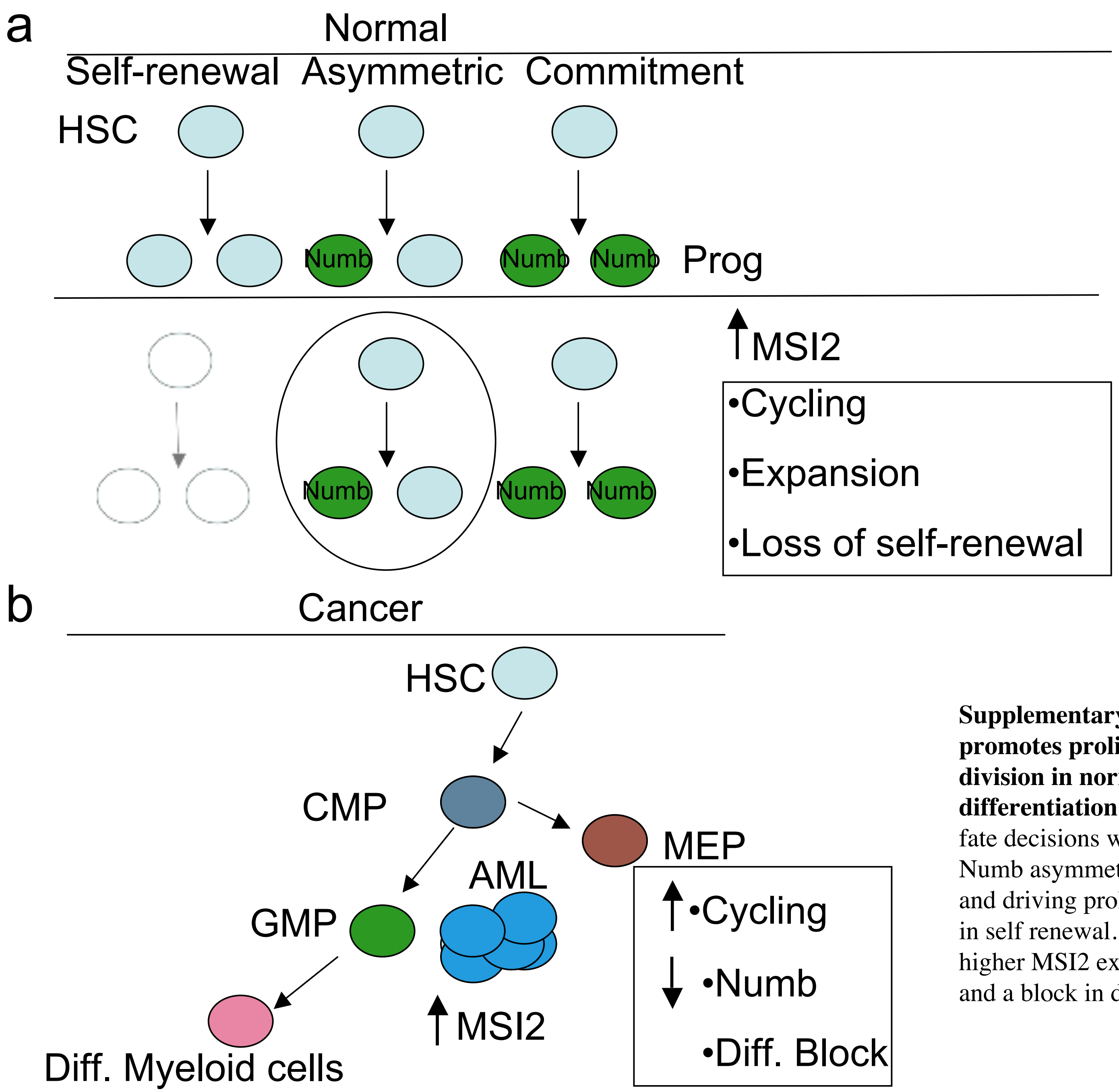
a, Analysis of Radich gene expression data comparing sorted human CD34$^+$ cells (n=7), chronic phase (CP, n=57), accelerated phase (AP, n=9), and myeloid blast crisis (BC, n=33) demonstrating significantly increased expression of *MSI2* (red) versus *MSI1* (blue) in CML blast crisis·. **b,** Analysis of normal karyotype Bullinger dataset CN-AML comparing *MSI1* (blue) and *MSI2* (red) expression. **c,** Immunoblot of MSI1- inducible embryonic stem cells and MSI2-inducible embryonic stem cells induced with doxocycline where indicated for 24 hours. The MSI1antibody is not cross-reactive to MSI2, while the pan-Msi antibody (middle blot) detects both family members (representative of two independent experiments, NS= not significant, **=$p<0.001$, *=$p<0.01$ and + =$p<0.05$).

Supplementary Fig. 15



Supplementary Figure 15: A worse prognosis and undifferentiated gene expression correlation in patients with high *MSI2* expression. a, CN-AML poor clinical prognosis gene signature was correlated with 15 AML patients selected for the highest *MSI2* expression of normal karyotype and 15 patients with the lowest *MSI2* expression (CN-AML High and Low *MSI2*). **b,** CN-AML High *MSI2* expression dataset positively correlates to the HSC versus GMP gene signature.

Supplementary Fig. 16



Supplementary Figure 16: MSI2 expression promotes proliferation and asymmetric division in normal HSCs and blocks differentiation in AML. a, Normal HSC cell fate decisions with MSI2 expression increasing Numb asymmetric segregation (large circle) and driving proliferation leading to a decrease in self renewal. **b**, In myeloid leukemic cells higher MSI2 expression maintains proliferation and a block in differentiation.

Table 1

MSI2 shRNA

NAME GENE SET	SIZE	NES	FDR	Upregulated in class	REFERENCE
ONCOGENIC SIGNATURES					
MAPK_UP_CREIGHTON	109	-1.71	<0.0001	MSI2shrna DN	Creighton et al 2008
MYC_UP_COLLER	239	-1.36	0.033	MSI2shrna DN	Coller et al 2000
CYCLIND1_UP_LAMB	190	-1.15	0.190	MSI2shrna DN	Lamb et al 2003
MYC_BILD	180	-1.84	0.003	MSI2shrna DN	Bild et al 2006
RAS_BILD	231	-1.36	0.047	MSI2shrna DN	Bild et al 2006
PROGNOSIS SIGNATURE					
METZELER_SURVIVALSIGNATURE_POSITIVESCORE	39	-1.66	0.046	MSI2shrna DN	Metzeler et al 2008
DIFFERENTIATION					
HSCVSGMP_UP	344	-1.39	0.009	MSI2shrna DN	Krivtsov et al 2006
WNT					
GUO_UP_WNT_INHIBITION	43	1.77	0.014	MSI2shrna UP	Guo et al. 2008
GUO_DN_WNT_INHIBITION	43	-1.62	0.077	MSI2shrna DN	Guo et al. 2008

CN-AML High and Low MSI2

NAME GENE SET	SIZE	NES	FDR	Upregulated in class	REFERENCE
DIFFERENTIATION					
HSCVSGMP_UP	298	1.32	0.019	high_msi2	Krivtsov et al 2006
HSCVSGMP_DN	171	-2.59	<0.0001	low_msi2	Krivtsov et al 2006

PROGNOSIS SIGNATURE					
METZELER_SURVIVALSIGNATURE_POSITIVESCORE	33	2.03	<0.0001	high_msi2	Metzeler et al 2008
GOOD_PROGNOSIS_AML_YAGI	28	-1.83	0.017	low_msi2	Yagi et al

LSK MSI2 overexpression

NAME GENE SET	SIZE	NES	FDR	Upregulated in class	REFERENCE
ONCOGENIC SIGNATURES					
MAPK_UP_CREIGHTON	95	-1.74	<0.0001	MSI2 overexpression	Creighton et al 2008
MYC_UP_COLLER	213	-1.44	0.01	MSI2 overexpression	Coller et al 2000
CYCLIND1_UP_LAMB	185	-1.49	0.01	MSI2 overexpression	Lamb et al 2003
RAF1_UP_CREIGHTON	489	-1.37	0.01	MSI2 overexpression	Creighton et al 2008
RAS_BILD	200	-2.04	<0.0001	MSI2 overexpression	Bild et al 2006

Supplementary Table 1: Gene set enrichment analysis summary.
GSEAs from indicated microarray datasets.

Table 2

Multivariate Cox Regression analysis of OS and EFS in AML (Bullinger dataset)

	Overall Survival (n =205)			Event-free Survival (n =205)		
Variable	HR (95% CI)	P		HR (95% CI)	P	
Age	1.04 (1.02-1.05	4.70E-007	***	1.02 (1.01-1.04	5.00E-004	***
FAB	1.02 (0.92-1.14	6.95E-001		0.96 (0.87-1.07	5.53E-001	
Cytogenetic group	0.98 (0.92-1.05	5.90E-001		0.98 (0.92-1.05	4.85E-001	
NPM1+/FLT3-	0.49 (0.31-0.79	3.20E-003	**	0.36 (0.23-0.58	1.90E-005	***
MSI2	1.22 (1.05-1.42	9.40E-003	**	1.11 (0.96-1.28	1.71E-001	

Table 3

Multivariate Cox Regression analysis of OS and EFS in AML (Bullinger dataset)

	Overall Survival (n =378)			Event-free Survival (n =376)		
Variable	HR (95% CI)	P		HR (95% CI)	P	
Age	1.03 (1.02-1.04	2.90E-010	***	1.02 (1.01-1.03	1.60E-006	***
FAB	0.97 (0.89-1.06	5.17E-001		0.92 (0.84-1.00	4.60E-002	*
Cytogenetic group	0.91 (0.88-0.96	1.60E-004	***	0.92 (0.88-0.96	3.30E-005	***
FLT3_ITD	1.90 (1.41-2.56	2.20E-005	***	1.55 (1.16-2.06	2.90E-003	**
MSI2	1.13 (1.00-1.27	4.81E-002	*	1.14 (1.02-1.28	1.99E-002	*

Table 4

Multivariate Cox Regression analysis of OS and EFS in Normal Karyotype AML (Metzeler dataset)

	Overall Survival (n =162)		
Variable	HR (95% CI)	P	
Age	1.03 (1.01-1.04	8.90E-004	***
FAB	0.94 (0.81-1.08	3.51E-001	
MSI2	1.41 (1.09-1.81	7.73E-003	**

Supplementary Table 2–4: *MSI2* is an independent prognostic marker in AML. Table. 2, *MSI2* expression was found to be significantly associated of a shorter overall survival with a hazard ratio of 0.122 (95% confidence interval 1.05 to 1.42 p=9.4e-03) considering age, FAB classification, FLT3-ITD and NPM1 mutational status (used as a binary variable), cytogenetic group and *MSI2* expression as a continuous variable. Age and NPM1$^+$/FLT3 ITD$^-$ status were found to be significant independents prognostic factors of overall and event free survival. **Table. 3,** Cytogenetic group was also found significant (p=2.2e-07) considering the same covariates except NPM1 status. **Table. 4,** Validation cohort of AML samples with normal karyotype showed a significant result for *MSI2* expression as a prognostic marker of worse prognosis (HR=1.41, 95 % CI =1.09-1.81 and p=7.73e-03) including age and FAB classification as variables in association with overall survival, NS= not significant, ***=*p<0.0001*, **=p<0.001, *=p<0.01 and + =p<0.05.

Supplementary Table 5: MSI2 shRNA signature from AML cell line.
List of the 480 probes used for unsupervised clustering in Fig. 4h.

ProbeName	GeneName	SystematicName	Description	logFC	AveExpr	t	P.Value	adj.P.Val
A_24_P281975	GNPTAB	NM_024312	ref|Homo sapiens N acetylglucosamine-1-phosphate transferase, alpha and beta subunits (GNPTAB), mRNA [NM_024312]	1.38	11.07	9.43	4.34E-06	0.01
A_32_P140153	THC2650264	THC2650264	thc|Q8CHC2_MOUSE (Q8CHC2) MKIAA0940 protein (Fragment), partial (57%) [THC2650264]	1.37	5.07	7.08	4.70E-05	0.02
A_24_P925191	THC2640472	THC2640472	thc|Q2M1U4_HUMAN (Q2M1U4) Catalase, partial (31%) [THC2640472]	1.35	8.13	5.53	0	0.03
A_24_P166663	CDK6	NM_001259	ref|Homo sapiens cyclin-dependent kinase 6 (CDK6), mRNA [NM_001259]	1.34	13.4	6.08	0	0.02
A_23_P162127	CCDC90B	NM_021825	ref|Homo sapiens coiled-coil domain containing 90B (CCDC90B), mRNA [NM_021825]	1.32	11.77	5.64	0	0.03
A_23_P204380	GNPTAB	NM_024312	ref|Homo sapiens N acetylglucosamine-1-phosphate transferase, alpha and beta subunits (GNPTAB), mRNA [NM_024312]	1.3	8.75	8.74	8.29E-06	0.01
A_32_P193322	RICTOR	NM_152756	ref|Homo sapiens rapamycin-insensitive companion of mTOR (RICTOR), mRNA	1.2	10.02	4.96	0	0.04
A_24_P137434	DCBLD2	NM_080927	ref|Homo sapiens discoidin, CUB and LCCL domain containing 2 (DCBLD2), mRNA [NM_080927]	1.17	9.86	5.35	0	0.03
A_32_P169679	LCORL	AL133031	gb|Homo sapiens mRNA; cDNA DKFZp434K087 (from clone DKFZp434K087). [AL133031]	1.16	6.38	8.76	8.16E-06	0.01
A_24_P167473	ARPC3	NM_005719	ref|Homo sapiens actin related protein 2/3 complex, subunit 3, 21kDa (ARPC3), mRNA [NM_005719]	1.14	15.89	5.47	0	0.03
A_23_P72643	ADAM9	NM_003816	ref|Homo sapiens ADAM metallopeptidase domain 9 (meltrin gamma) (ADAM9), transcript variant 1, mRNA [NM_003816]	1.13	9.89	4.65	0	0.05
A_24_P882914	C10orf46	NM_153810	ref|Homo sapiens chromosome 10 open reading frame 46 (C10orf46), mRNA [NM_153810]	1.13	8.97	6.1	0	0.02

A_24_P945194	PDCD6IP	NM_013374	ref|Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), mRNA [NM_013374]	1.11	9.26	5.65	0	0.03
A_24_P595460	NUCB2	AK097398	gb|Homo sapiens cDNA FLJ40079 fis, clone TESTI2001498, highly similar to DNA-BINDING PROTEIN NEFA PRECURSOR. [AK097398]	1.11	9.75	7.62	2.59E-05	0.01
A_23_P101208	CYB5A	NM_001914	ref|Homo sapiens cytochrome b5 type A (microsomal) (CYB5A), transcript variant 2, mRNA [NM_001914]	1.11	12.53	5.15	0	0.04
A_24_P235429	ABCA1	NM_005502	ref|Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 1 (ABCA1), mRNA [NM_005502]	1.09	9.53	4.98	0	0.04
A_24_P345131	LRRC8B	ENST00000330947	ens|Leucine-rich repeat-containing protein 8B (T-cell activation leucine repeat-rich protein). [Source:Uniprot/SWISSPROT;Acc:Q6P9F7] [ENST00000330947]	1.09	8.04	5.55	0	0.03
A_23_P134814	THAP1	NM_018105	THAP domain containing, apoptosis associated protein 1 (THAP1), transcript variant 1, mRNA [NM_018105]	1.09	11.22	9.33	4.74E-06	0.01
A_23_P110811	COX7C	NM_001867	cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA [NM_001867]	1.08	15.96	6.13	0	0.02
A_32_P131797	BE970058	BE970058	gb|BE970058 601680172F1 NIH_MGC_78 Homo sapiens cDNA clone IMAGE:3950464 5', mRNA sequence [BE970058]	1.08	9.56	6.39	0	0.02
A_32_P218671	THC2672257	THC2672257	Unknown	1.07	7.25	4.73	0	0.04
A_23_P401	CENPF	NM_016343	ref|Homo sapiens centromere protein F, 350/400ka (mitosin) (CENPF), mRNA [NM_016343]	1.03	13.45	12.48	3.76E-07	0
A_23_P84836	NPEPPS	NM_006310	ref|Homo sapiens aminopeptidase puromycin sensitive (NPEPPS), mRNA [NM_006310]	1.03	10.02	6.93	5.60E-05	0.02

A_23_P3302	MNS1	NM_018365	ref|Homo sapiens meiosis-specific nuclear structural 1 (MNS1), mRNA [NM_018365]	1.02	8.67	7.14	4.38E-05	0.02
A_24_P288979	GNPTAB	NM_024312	ref|Homo sapiens N-acetylglucosamine-1-phosphate transferase, alpha and beta subunits (GNPTAB), mRNA [NM_024312]	1.02	7.63	8.52	1.02E-05	0.01
A_24_P273132	GPSM2	NM_013296	ref|Homo sapiens G-protein signaling modulator 2 (AGS3-like, C. elegans) (GPSM2), mRNA [NM_013296]	1.01	8.37	8.91	7.06E-06	0.01
A_23_P356684	ANLN	NM_018685	ref|Homo sapiens anillin, actin binding protein (ANLN), mRNA [NM_018685]	1	10.66	10.36	1.93E-06	0.01
A_24_P188105	KIAA0280	D87470	gb|Homo sapiens mRNA for KIAA0280 gene, partial cds. [D87470]	0.99	7.52	5.26	0	0.04
A_24_P945147	RABEP1	NM_004703	ref|Homo sapiens rabaptin, RAB GTPase binding effector protein 1 (RABEP1), transcript variant 1, mRNA [NM_004703]	0.99	9.76	4.61	0	0.05
A_24_P941505	FAM120A	NM_014612	ref|Homo sapiens family with sequence similarity 120A (FAM120A), mRNA [NM_014612]	0.99	10.49	5.16	0	0.04
A_24_P18105	ASPH	NM_032466	ref|Homo sapiens aspartate beta-hydroxylase (ASPH), transcript variant 3, mRNA [NM_032466]	0.99	8.54	7.03	4.98E-05	0.02
A_24_P942786	DYRK2	AK024870	gb|Homo sapiens cDNA: FLJ21217 fis, clone COL00536. [AK024870]	0.99	8.47	6.09	0	0.02
A_32_P123743	KCNQ1OT1	NR_002728	ref|Homo sapiens KCNQ1 overlapping transcript 1 (non-protein coding) (KCNQ1OT1) on chromosome 11 [NR_002728]	0.99	9.53	4.67	0	0.05
A_24_P316305	AQR	AK001173	gb|Homo sapiens cDNA FLJ10311 fis, clone NT2RM2000359, highly similar to Homo sapiens mRNA for KIAA0560 protein. [AK001173]	0.98	9.59	5.06	0	0.04
A_23_P32903	OCRL	NM_000276	ref|Homo sapiens oculocerebrorenal syndrome of Lowe (OCRL), transcript variant a, mRNA [NM_000276]	0.98	11.23	6.53	8.89E-05	0.02

A_23_P349083	FCHO2	NM_138782	ref|Homo sapiens FCH domain only 2 (FCHO2), mRNA [NM_138782]	0.98	9.29	7.12	4.49E-05	0.02
A_23_P115167	LRRC8B	NM_015350	ref|Homo sapiens leucine rich repeat containing 8 family, member B (LRRC8B), mRNA [NM_015350]	0.97	9.54	5.85	0	0.03
A_32_P80678	ADAM9	NM_001005845	ref|Homo sapiens ADAM metallopeptidase domain 9 (meltrin gamma) (ADAM9), transcript variant 2, mRNA [NM_001005845]	0.97	8.08	5.16	0	0.04
A_32_P145385	AK001118	AK001118	gb|Homo sapiens cDNA FLJ10256 fis, clone HEMBB1000870. [AK001118]	0.97	5.97	4.72	0	0.04
A_23_P28797	THC2525955	THC2525955	thc|Q3T035_BOVIN (Q3T035) Actin related protein 2/3 complex, subunit 3, 21kDa, partial (53%) [THC2525955]	0.97	14.02	5.37	0	0.03
A_24_P96780	CENPF	NM_016343	ref|Homo sapiens centromere protein F, 350/400ka (mitosin) (CENPF), mRNA [NM_016343]	0.96	7.59	11.31	8.94E-07	0
A_23_P168669	CROT	NM_021151	ref|Homo sapiens carnitine O-octanoyltransferase (CROT), mRNA [NM_021151]	0.96	8.01	4.56	0	0.05
A_24_P373152	CFL2	NM_021914	ref|Homo sapiens cofilin 2 (muscle) (CFL2), transcript variant 1, mRNA [NM_021914]	0.96	8.06	5.03	0	0.04
A_24_P945000	FAM33A	NM_182620	family with sequence similarity 33, member A (FAM33A), transcript variant 1, mRNA [NM_182620]	0.95	10	5.77	0	0.03
A_24_P58647	LOC441131	XR_018731	ref|PREDICTED: Homo sapiens misc_RNA (LOC441131), miscRNA [XR_018731]	0.94	14.07	5.09	0	0.04
A_23_P3204	MAPK6	NM_002748	ref|Homo sapiens mitogen-activated protein kinase 6 (MAPK6), mRNA [NM_002748]	0.94	12.92	5.8	0	0.03
A_24_P46953	SGK3	NM_013257	ref|Homo sapiens serum/glucocorticoid regulated kinase family, member 3 (SGK3), transcript variant 1, mRNA [NM_013257]	0.94	11.01	8.41	1.14E-05	0.01
A_32_P170664	AK024898	AK024898	gb|Homo sapiens cDNA: FLJ21245 fis, clone COL01184. [AK024898]	0.94	8.72	4.89	0	0.04

A_24_P104278	ENST00000395606	ENST00000395606	ens|Probable phospholipase DDHD1 (EC 3.1.1.-) (DDHD domain protein 1) (Phosphatidic acid-preferring phospholipase A1 homolog) (PA-PLA1). [Source:Uniprot/SWISSPROT;Acc:Q8NEL9] [ENST00000395606]	0.93	7.81	5.21	0	0.04
A_32_P122285	BI013473	BI013473	gb|RC0-ET0185-220101-021-h02 ET0185 Homo sapiens cDNA, mRNA sequence [BI013473]	0.92	11.07	6.39	0	0.02
A_24_P642771	AK024956	AK024956	gb|Homo sapiens cDNA: FLJ21303 fis, clone COL02107. [AK024956]	0.92	5.73	4.77	0	0.04
A_23_P20852	AUH	NM_001698	ref|Homo sapiens AU RNA binding protein/enoyl-Coenzyme A hydratase (AUH), nuclear gene encoding mitochondrial protein, mRNA [NM_001698]	0.92	9.73	14.92	7.58E-08	0
A_24_P143888	C9orf86	NM_024718	ref|Homo sapiens chromosome 9 open reading frame 86 (C9orf86), mRNA [NM_024718]	0.92	11.07	4.97	0	0.04
A_23_P320897	C1orf218	NM_019049	ref|Homo sapiens chromosome 1 open reading frame 218 (C1orf218), mRNA [NM_019049]	0.91	8.72	6.65	7.74E-05	0.02
A_24_P255303	LOC391160	XR_018489	gb|PREDICTED: Homo sapiens similar to Actin-related protein 2 [XR_018489]	0.91	14.3	5.16	0	0.04
A_23_P92765	CCDC112	NM_001040440	ref|Homo sapiens coiled-coil domain containing 112 (CCDC112), transcript variant 1, mRNA [NM_001040440]	0.9	9.84	4.71	0	0.05
A_32_P155645	CCDC112	NM_001040440	ref|Homo sapiens coiled-coil domain containing 112 (CCDC112), transcript variant 1, mRNA [NM_001040440]	0.89	7.8	4.52	0	0.05
A_32_P83453	XR_018202	XR_018202	Homo sapiens similar to Tetratricopeptide repeat protein 3 (TPR repeat protein 3) (TPR repeat protein D) (LOC647768), mRNA	0.89	10.75	6.36	0	0.02

A_23_P102391	SLC40A1	NM_014585	ref|Homo sapiens solute carrier family 40 (iron-regulated transporter), member 1 (SLC40A1), mRNA [NM_014585]	0.89	11.44	5.4	0	0.03
A_32_P214471	BX116720	BX116720	gb|BX116720 Soares_testis_NHT Homo sapiens cDNA clone IMAGp998F241782 , mRNA sequence [BX116720]	0.88	7.37	4.88	0	0.04
A_32_P76156	RWDD4A	NM_152682	ref|Homo sapiens RWD domain containing 4A (RWDD4A), mRNA [NM_152682]	0.87	8.2	4.46	0	0.05
A_24_P895836	BC016022	BC016022	gb|Homo sapiens, clone IMAGE:4720764, mRNA. [BC016022]	0.87	6.91	4.67	0	0.05
A_23_P70746	AHI1	NM_017651	ref|Homo sapiens Abelson helper integration site 1 (AHI1), mRNA [NM_017651]	0.87	7.65	5.52	0	0.03
A_24_P261052	MTMR9	NM_015458	ref|Homo sapiens myotubularin related protein 9 (MTMR9), mRNA [NM_015458]	0.87	8.61	6.12	0	0.02
A_24_P137563	SCLT1	NM_144643	ref|Homo sapiens sodium channel and clathrin linker 1 (SCLT1), mRNA [NM_144643]	0.87	7.77	4.63	0	0.05
A_32_P5168	THC2717828	THC2717828	Unknown	0.87	6.03	4.75	0	0.04
A_23_P48669	CDKN3	NM_005192	ref|Homo sapiens cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase) (CDKN3), mRNA [NM_005192]	0.87	12.3	8.88	7.24E-06	0.01
A_32_P6682	BQ926066	BQ926066	gb|AGENCOURT_8878877 Lupski_sciatic_nerve Homo sapiens cDNA clone IMAGE:6202171 5', mRNA sequence [BQ926066]	0.87	8.78	5.64	0	0.03
A_23_P106241	TRIP11	NM_004239	ref|Homo sapiens thyroid hormone receptor interactor 11 (TRIP11), mRNA [NM_004239]	0.86	10.3	5.38	0	0.03
A_23_P160466	SLC19A2	NM_006996	ref|Homo sapiens solute carrier family 19 (thiamine transporter), member 2 (SLC19A2), mRNA	0.86	11.04	5.43	0	0.03
A_24_P925211	AK125129	AK125129	gb|Homo sapiens cDNA FLJ43139 fis, clone CTONG3007444. [AK125129]	0.86	5.19	4.73	0	0.04

A_24_P320880	SNX16	NM_022133	ref|Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, mRNA [NM_022133]	0.86	7.12	5.19	0	0.04
A_23_P88209	SCFD1	NM_016106	ref|Homo sapiens sec1 family domain containing 1 (SCFD1), transcript variant 1, mRNA [NM_016106]	0.86	11.37	5.02	0	0.04
A_23_P170280	ATP10D	NM_020453	ref|Homo sapiens ATPase, class V, type 10D (ATP10D), mRNA [NM_020453]	0.85	8.55	4.7	0	0.05
A_23_P258221	ABCC5	NM_005688	ref|Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 5 (ABCC5), transcript variant 1, mRNA [NM_005688]	0.85	10.95	5.67	0	0.03
A_32_P757733	CEP70	NM_024491	ref|Homo sapiens centrosomal protein 70kDa (CEP70), mRNA [NM_024491]	0.85	8.52	7.9	1.93E-05	0.01
A_32_P210202	E2F7	NM_203394	ref|Homo sapiens E2F transcription factor 7 (E2F7), mRNA [NM_203394]	0.85	10.51	4.64	0	0.05
A_32_P145355	BE156557	BE156557	gb|BE156557 QV0-HT0368-090200-099-d10 HT0368 Homo sapiens cDNA, mRNA sequence [BE156557]	0.85	7.81	6.25	0	0.02
A_23_P417974	AQP11	NM_173039	ref|Homo sapiens aquaporin 11 (AQP11), mRNA [NM_173039]	0.84	5.69	5.36	0	0.03
A_32_P157295	AK026338	AK026338	gb|Homo sapiens cDNA: FLJ22685 fis, clone HSI10917. [AK026338]	0.84	7.67	6.16	0	0.02
A_23_P144384	GALNT7	NM_017423	ref|Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7) (GALNT7), mRNA [NM_017423]	0.84	11.09	5.42	0	0.03
A_23_P258891	SNX16	NM_022133	ref|Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, mRNA [NM_022133]	0.84	8.58	6.4	0	0.02
A_24_P172768	GMFB	NM_004124	ref|Homo sapiens glia maturation factor, beta (GMFB), mRNA [NM_004124]	0.84	9.42	6.1	0	0.02
A_24_P246361	IQGAP2	NM_006633	ref|Homo sapiens IQ motif containing GTPase activating protein 2 (IQGAP2), mRNA [NM_006633]	0.83	8.62	10.68	1.48E-06	0.01
A_23_P89123	CFDP1	NM_006324	ref|Homo sapiens craniofacial development protein 1 (CFDP1), mRNA [NM_006324]	0.83	13.06	7.68	2.44E-05	0.01

A_23_P213661	HISPPD1	NM_015216	ref|Homo sapiens histidine acid phosphatase domain containing 1 (HISPPD1), mRNA [NM_015216]	0.83	11.89	4.71	0	0.05
A_23_P90659	LAPTM4A	NM_014713	ref|Homo sapiens lysosomal-associated protein transmembrane 4 alpha (LAPTM4A), mRNA [NM_014713]	0.83	14.17	5.08	0	0.04
A_23_P203009	CUL5	NM_003478	cullin 5 (CUL5), mRNA [NM_003478]	0.83	8.98	4.55	0	0.05
A_32_P165330	TTC3	NM_003316	ref|Homo sapiens tetratricopeptide repeat domain 3 (TTC3), transcript variant 1, mRNA [NM_003316]	0.83	8.69	5.79	0	0.03
A_23_P74799	SLC25A24	NM_213651	ref|Homo sapiens solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 24 (SLC25A24), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA [NM_213651]	0.82	11.86	4.89	0	0.04
A_24_P333663	MAPK6	NM_002748	ref|Homo sapiens mitogen-activated protein kinase 6 (MAPK6), mRNA [NM_002748]	0.82	9.65	6.96	5.42E-05	0.02
A_23_P213661	HISPPD1	NM_015216	ref|Homo sapiens histidine acid phosphatase domain containing 1 (HISPPD1), mRNA [NM_015216]	0.82	11.8	4.84	0	0.04
A_23_P136058	ATR	NM_001184	ref|Homo sapiens ataxia telangiectasia and Rad3 related (ATR), mRNA [NM_001184]	0.82	10.23	7.18	4.20E-05	0.02
A_23_P219188	C9orf86	NM_024718	ref|Homo sapiens chromosome 9 open reading frame 86 (C9orf86), mRNA [NM_024718]	0.82	12.95	5.18	0	0.04
A_23_P134925	BNIP3L	NM_004331	ref|Homo sapiens BCL2/adenovirus E1B 19kDa interacting protein 3-like (BNIP3L), mRNA [NM_004331]	0.82	12.99	5.51	0	0.03
A_24_P844995	AK054826	AK054826	gb|Homo sapiens cDNA FLJ30264 fis, clone BRACE2002613, moderately similar to Rattus norvegicus rsly1p mRNA. [AK054826]	0.82	10.64	5.05	0	0.04

A_23_P202029	ERLIN1	BC031791	gb|Homo sapiens ER lipid raft associated 1, mRNA (cDNA clone MGC:24915 IMAGE:4214940), complete cds. [BC031791]	0.81	13.27	4.8	0	0.04
A_32_P9253	THC2620541	THC2620541	thc|Q8WYP8_HUMAN (Q8WYP8) Mid-1-related chloride channel 4 (Mid-1-related chloride channel 1) (MCLC), partial (17%) [THC2620541]	0.81	5.17	4.48	0	0.05
A_23_P213661	HISPPD1	NM_015216	ref|Homo sapiens histidine acid phosphatase domain containing 1 (HISPPD1), mRNA [NM_015216]	0.81	11.63	4.73	0	0.04
A_23_P213661	HISPPD1	NM_015216	ref|Homo sapiens histidine acid phosphatase domain containing 1 (HISPPD1), mRNA [NM_015216]	0.81	11.68	4.78	0	0.04
A_24_P64241	ANKRD20A2	NM_001012421	ref|Homo sapiens ankyrin repeat domain 20 family, member A2 (ANKRD20A2), mRNA [NM_001012421]	0.81	6.76	4.9	0	0.04
A_23_P213661	HISPPD1	NM_015216	ref|Homo sapiens histidine acid phosphatase domain containing 1 (HISPPD1), mRNA [NM_015216]	0.81	11.97	4.83	0	0.04
A_23_P213661	HISPPD1	NM_015216	ref|Homo sapiens histidine acid phosphatase domain containing 1 (HISPPD1), mRNA [NM_015216]	0.81	11.91	4.72	0	0.04
A_24_P249824	DYRK2	NM_006482	ref|Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 (DYRK2), transcript variant 2, mRNA [NM_006482]	0.81	7.95	7.12	4.52E-05	0.02
A_32_P81092	THC2614876	THC2614876	Unknown	0.81	7.4	4.94	0	0.04
A_23_P213661	HISPPD1	NM_015216	ref|Homo sapiens histidine acid phosphatase domain containing 1 (HISPPD1), mRNA [NM_015216]	0.8	11.88	4.77	0	0.04
A_23_P213661	HISPPD1	NM_015216	ref|Homo sapiens histidine acid phosphatase domain containing 1 (HISPPD1), mRNA [NM_015216]	0.8	11.41	4.48	0	0.05
A_23_P376599	RALBP1	NM_006788	ref|Homo sapiens ralA binding protein 1 (RALBP1), mRNA [NM_006788]	0.8	14.13	4.79	0	0.04

A_32_P107219	THC2525583	THC2525583	thc|MUSIGHV01B Ig heavy chain precursor {Mus musculus} (exp=-1; wgp=0; cg=0), partial (26%) [THC2525583]	0.8	6.75	6.41	0	0.02
A_23_P303718	DST	NM_015548	ref|Homo sapiens dystonin (DST), transcript variant 1eA, mRNA [NM_015548]	0.8	7.99	6.1	0	0.02
A_23_P213661	HISPPD1	NM_015216	ref|Homo sapiens histidine acid phosphatase domain containing 1 (HISPPD1), mRNA [NM_015216]	0.79	11.83	4.7	0	0.05
A_23_P215070	TSGA14	NM_018718	ref|Homo sapiens testis specific, 14 (TSGA14), mRNA [NM_018718]	0.79	9.27	5.18	0	0.04
A_23_P51627	PPCS	NM_024664	ref|Homo sapiens phosphopantothenoylcysteine synthetase (PPCS), transcript variant 1, mRNA [NM_024664]	0.79	13.34	5.79	0	0.03
A_23_P213661	HISPPD1	NM_015216	ref|Homo sapiens histidine acid phosphatase domain containing 1 (HISPPD1), mRNA [NM_015216]	0.78	11.92	4.69	0	0.05
A_23_P207811	PAIP1	NM_006451	ref|Homo sapiens poly(A) binding protein interacting protein 1 (PAIP1), transcript variant 1, mRNA [NM_006451]	0.78	12.06	5.36	0	0.03
A_23_P162378	CCDC41	NM_016122	ref|Homo sapiens coiled-coil domain containing 41 (CCDC41), transcript variant 1, mRNA [NM_016122]	0.78	8.72	4.9	0	0.04
A_24_P227069	GPAM	NM_020918	glycerol-3-phosphate acyltransferase, mitochondrial (GPAM), nuclear gene encoding mitochondrial protein, mRNA [NM_020918]	0.78	9.31	6.85	6.10E-05	0.02
A_23_P18656	SCLT1	NM_144643	ref|Homo sapiens sodium channel and clathrin linker 1 (SCLT1), mRNA [NM_144643]	0.78	8.27	5.06	0	0.04
A_32_P524014	UTRN	NM_007124	utrophin (UTRN), mRNA [NM_007124]	0.78	10.09	7.21	4.07E-05	0.02
A_24_P549553	TTC3	NM_003316	ref|Homo sapiens tetratricopeptide repeat domain 3 (TTC3), transcript variant 1, mRNA [NM_003316]	0.78	7.61	6.19	0	0.02
A_23_P63402	GPSM2	NM_013296	ref|Homo sapiens G protein signaling modulator 2 (AGS3-like, C. elegans) (GPSM2), mRNA [NM_013296]	0.78	10.37	6.75	6.87E-05	0.02

A_24_P104174	TAOK3	NM_016281	ref|Homo sapiens TAO kinase 3 (TAOK3), mRNA [NM_016281]	0.78	14.08	8.58	9.69E-06	0.01
A_24_P84984	TTC3	NM_003316	ref|Homo sapiens tetratricopeptide repeat domain 3 (TTC3), transcript variant 1, mRNA [NM_003316]	0.77	9.79	6.63	7.89E-05	0.02
A_23_P52017	ASPM	NM_018136	ref|Homo sapiens asp (abnormal spindle) homolog, microcephaly associated (Drosophila) (ASPM), mRNA [NM_018136]	0.77	11.2	5.69	0	0.03
A_23_P105856	SLC46A3	NM_181785	ref|Homo sapiens solute carrier family 46, member 3 (SLC46A3), mRNA [NM_181785]	0.77	6.41	6.28	0	0.02
A_23_P369047	ENST00000324982	ENST00000324982	gb|Homo sapiens cDNA FLJ43379 fis, clone OCBBF2002626. [AK125369]	0.77	8.81	4.79	0	0.04
A_32_P204330	AK093982	AK093982	gb|Homo sapiens cDNA FLJ36663 fis, clone UTERU2002826. [AK093982]	0.77	8	7.95	1.82E-05	0.01
A_23_P118327	THUMPD1	NM_017736	ref|Homo sapiens THUMP domain containing 1 (THUMPD1), mRNA [NM_017736]	0.77	10.87	4.5	0	0.05
A_24_P296568	CBX1	NM_006807	ref|Homo sapiens chromobox homolog 1 (HP1 beta homolog Drosophila) (CBX1), mRNA	0.77	13.33	4.84	0	0.04
A_23_P21473	CEP70	NM_024491	ref|Homo sapiens centrosomal protein 70kDa (CEP70), mRNA [NM_024491]	0.77	9.42	6.12	0	0.02
A_23_P70660	FAM46A	NM_017633	ref|Homo sapiens family with sequence similarity 46, member A (FAM46A), mRNA [NM_017633]	0.77	13.82	4.64	0	0.05
A_23_P404211	FANCM	NM_020937	ref|Homo sapiens Fanconi anemia, complementation group M (FANCM), mRNA [NM_020937]	0.77	6.6	4.54	0	0.05
A_32_P399546	ARNTL2	AF256215	gb|Homo sapiens cycle-like factor CLIF mRNA, complete cds. [AF256215]	0.77	8.97	4.78	0	0.04
A_24_P210888	SMURF2	AK002019	gb|Homo sapiens cDNA FLJ11157 fis, clone PLACE1006961. [AK002019]	0.77	6.47	5.54	0	0.03
A_23_P72680	IFT81	NM_014055	ref|Homo sapiens intraflagellar transport 81 homolog (Chlamydomonas) (IFT81), transcript variant 1, mRNA [NM_014055]	0.76	6.47	6.91	5.71E-05	0.02

A_23_P102060	SSFA2	NM_006751	ref|Homo sapiens sperm specific antigen 2 (SSFA2), mRNA [NM_006751]	0.76	11.19	5.15	0	0.04
A_23_P392529	ENST00000344693	ENST00000344693	ens|Uncharacterized protein C21orf81. [Source:Uniprot/SWISSPROT;Acc:Q8NFU9] [ENST00000344693]	0.76	7.41	5	0	0.04
A_24_P713312	THC2639056	THC2639056	thc|ALU8_HUMAN (P39195) Alu subfamily SX sequence contamination warning entry, partial (10%) [THC2639056]	0.76	7.02	4.5	0	0.05
A_23_P363936	HSPA4L	NM_014278	ref|Homo sapiens heat shock 70kDa protein 4-like (HSPA4L), mRNA [NM_014278]	0.76	9.95	6.43	0	0.02
A_32_P106732	FANCM	NM_020937	ref|Homo sapiens Fanconi anemia, complementation group M (FANCM), mRNA [NM_020937]	0.76	8.91	5.4	0	0.03
A_23_P21230	TRIM37	NM_015294	ref|Homo sapiens tripartite motif-containing 37 (TRIM37), transcript variant 1, mRNA [NM_015294]	0.76	10.01	5.64	0	0.03
A_24_P910833	ZNF286A	AF086305	gb|Homo sapiens full length insert cDNA clone ZD50H12. [AF086305]	0.75	8.74	7.88	1.97E-05	0.01
A_24_P380132	G3BP2	NM_203505	ref|Homo sapiens GTPase activating protein (SH3 domain) binding protein 2 (G3BP2), transcript variant 1, mRNA [NM_203505]	0.75	13.9	5.28	0	0.04
A_24_P90878	THUMPD1	NM_017736	ref|Homo sapiens THUMP domain containing 1 (THUMPD1), mRNA [NM_017736]	0.75	9.83	4.51	0	0.05
A_24_P387869	PKN2	NM_006256	ref|Homo sapiens protein kinase N2 (PKN2), mRNA [NM_006256]	0.75	7.54	5.93	0	0.03
A_24_P868583	ANKRD20A2	NM_001012421	ref|Homo sapiens ankyrin repeat domain 20 family, member A2 (ANKRD20A2), mRNA [NM_001012421]	0.75	7.52	8.77	8.08E-06	0.01
A_24_P56240	CPNE8	NM_153634	copine VIII (CPNE8), mRNA [NM_153634]	0.75	9.72	6.27	0	0.02
A_24_P388632	PCGF3	NM_006315	ref|Homo sapiens polycomb group ring finger 3 (PCGF3), mRNA [NM_006315]	0.75	11.21	4.74	0	0.04
A_32_P229299	PHF6	NM_032458	ref|Homo sapiens PHD finger protein 6 (PHF6), transcript variant 2, mRNA [NM_032458]	0.75	11.68	6.59	8.33E-05	0.02

A_32_P177953	CR598364	CR598364	gb|full-length cDNA clone CS0CAP007YJ17 of Thymus of Homo sapiens (human). [CR598364]	0.75	11.24	6.04	0	0.02
A_23_P206228	VPS13C	NM_020821	ref|Homo sapiens vacuolar protein sorting 13 homolog C (S. cerevisiae) (VPS13C), transcript variant 2A, mRNA [NM_020821]	0.74	10.35	4.6	0	0.05
A_32_P123966	RPGRIP1L	NM_015272	ref|Homo sapiens RPGRIP1-like (RPGRIP1L), mRNA [NM_015272]	0.74	6.92	6.34	0	0.02
A_23_P53530	MTERFD3	NM_001033050	ref|Homo sapiens MTERF domain containing 3 (MTERFD3), transcript variant 1, mRNA [NM_001033050]	0.74	9.15	6.22	0	0.02
A_24_P236437	DYNC1LI2	NM_006141	ref|Homo sapiens dynein, cytoplasmic 1, light intermediate chain 2 (DYNC1LI2), mRNA [NM_006141]	0.74	11.45	5.58	0	0.03
A_23_P17503	KIF16B	NM_024704	ref|Homo sapiens kinesin family member 16B (KIF16B), mRNA [NM_024704]	0.74	7.69	5.25	0	0.04
A_23_P313728	FAM98A	NM_015475	ref|Homo sapiens family with sequence similarity 98, member A (FAM98A), mRNA [NM_015475]	0.74	9.85	5.23	0	0.04
A_32_P150012	CHD7	NM_017780	ref|Homo sapiens chromodomain helicase DNA binding protein 7 (CHD7), mRNA [NM_017780]	0.74	10.99	4.74	0	0.04
A_23_P350187	TET2	AB046766	gb|Homo sapiens mRNA for KIAA1546 protein, partial cds. [AB046766]	0.74	9.19	6.82	6.37E-05	0.02
A_32_P27706	BC008192	BC008192	gb|Homo sapiens HEAT repeat containing 2, mRNA (cDNA clone IMAGE:4213551), **** WARNING: chimeric clone ****. [BC008192]	0.73	10.38	4.53	0	0.05
A_23_P81463	DHX29	NM_019030	ref|Homo sapiens DEAH (Asp-Glu-Ala-His) box polypeptide 29 (DHX29), mRNA [NM_019030]	0.73	10.5	5.72	0	0.03
A_32_P103695	FAM92A1	NM_145269	ref|Homo sapiens family with sequence similarity 92, member A1 (FAM92A1), mRNA [NM_145269]	0.73	10.07	9.97	2.68E-06	0.01
A_23_P124476	CLCN3	NM_173872	ref|Homo sapiens chloride channel 3 (CLCN3), transcript variant e, mRNA [NM_173872]	0.73	9.57	5.6	0	0.03

A_24_P320970	C9orf41	ENST00000376834	ens|Uncharacterized protein C9orf41. [Source:Uniprot/SWISSPROT;Acc:Q8N4J0] [ENST00000376834]	0.73	9.55	4.47	0	0.05
A_24_P212072	ANKRD32	ENST00000255667	domain-containing protein 32. [Source:Uniprot/SWISSPROT;Acc:Q9BQI6] [ENST00000255667]	0.73	7.85	6.51	9.16E-05	0.02
A_23_P371966	KIAA1946	AB075826	mRNA for KIAA1946 protein. [AB075826]	0.73	7.9	8.11	1.56E-05	0.01
A_24_P256692	MIA3	NM_198551	ref|Homo sapiens melanoma inhibitory activity family, member 3 (MIA3), mRNA [NM_198551]	0.73	7.93	4.79	0	0.04
A_24_P364025	UBE2D1	NM_003338	ref|Homo sapiens ubiquitin-conjugating enzyme E2D 1 (UBC4/5 homolog, yeast) (UBE2D1), mRNA [NM_003338]	0.73	8.36	5.13	0	0.04
A_23_P65401	CFL2	NM_021914	ref|Homo sapiens cofilin 2 (muscle) (CFL2), transcript variant 1, mRNA [NM_021914]	0.72	9.43	6.47	9.63E-05	0.02
A_23_P259054	SNX14	NM_153816	ref|Homo sapiens sorting nexin 14 (SNX14), transcript variant 1, mRNA [NM_153816]	0.72	13.37	4.85	0	0.04
A_32_P131583	A_32_P131583	A_32_P131583	Unknown	0.72	7.09	5.9	0	0.03
A_23_P121825	FLJ13611	NM_024941	ref|Homo sapiens hypothetical protein FLJ13611 (FLJ13611), transcript variant 2, mRNA [NM_024941]	0.72	9.94	5.03	0	0.04
A_24_P138022	FAM120A	NM_014612	ref|Homo sapiens family with sequence similarity 120A (FAM120A), mRNA [NM_014612]	0.72	9.84	5.18	0	0.04
A_23_P133691	RRAGD	NM_021244	ref|Homo sapiens Ras-related GTP binding D (RRAGD), mRNA [NM_021244]	0.72	9.37	5.06	0	0.04
A_23_P41796	MAP3K1	NM_005921	ref|Homo sapiens mitogen-activated protein kinase kinase kinase 1 (MAP3K1), mRNA [NM_005921]	0.72	8.89	7.57	2.73E-05	0.01
A_24_P366315	KIF21A	NM_017641	ref|Homo sapiens kinesin family member 21A (KIF21A), mRNA [NM_017641]	0.72	9.45	5.53	0	0.03
A_24_P928038	IDE	BX648462	gb|Homo sapiens mRNA; cDNA DKFZp781M0420 (from clone DKFZp781M0420). [BX648462]	0.72	10.68	7.27	3.79E-05	0.02

A_23_P70998	tcag7.903	CR590623	gb|full-length cDNA clone CS0DF028YG12 of Fetal brain of Homo sapiens (human). [CR590623]	0.72	10.42	7.13	4.46E-05	0.02
A_23_P89327	ZNF286A	NM_020652	ref|Homo sapiens zinc finger protein 286A (ZNF286A), mRNA [NM_020652]	0.71	5.83	5.55	0	0.03
A_24_P230457	LOC131054	XR_019283	ref|PREDICTED: Homo sapiens misc_RNA (LOC131054), miscRNA [XR_019283]	0.71	12.66	4.95	0	0.04
A_23_P303810	DKFZp667G2110	NM_153605	ref|Homo sapiens hypothetical protein DKFZp667G2110 (DKFZp667G2110), mRNA [NM_153605]	0.71	10.13	6.93	5.57E-05	0.02
A_32_P196047	DPY19L4	NM_181787	ref|Homo sapiens dpy-19-like 4 (C. elegans) (DPY19L4), mRNA [NM_181787]	0.71	9.45	4.86	0	0.04
A_32_P50005	DBT	NM_001918	ref|Homo sapiens dihydrolipoamide branched chain transacylase E2 (DBT), nuclear gene encoding mitochondrial protein, mRNA [NM_001918]	0.71	8.35	5.55	0	0.03
A_23_P118544	CLTC	NM_004859	ref|Homo sapiens clathrin, heavy chain (Hc) (CLTC), mRNA [NM_004859]	0.71	15.28	5.27	0	0.04
A_24_P56270	DYRK2	NM_006482	ref|Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 (DYRK2), transcript variant 2, mRNA [NM_006482]	0.71	10.04	6.61	8.08E-05	0.02
A_32_P14201	XR_018202	XR_018202	Homo sapiens similar to Tetratricopeptide repeat protein 3 (TPR repeat protein 3) (TPR repeat protein D) (LOC647768), mRNA	0.71	8.47	6.16	0	0.02
A_23_P204090	PTPN11	NM_002834	ref|Homo sapiens protein tyrosine phosphatase, non-receptor type 11 (Noonan syndrome 1) (PTPN11), mRNA [NM_002834]	0.71	6.66	4.8	0	0.04
A_23_P56505	ITGA4	NM_000885	ref|Homo sapiens integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor) (ITGA4), mRNA [NM_000885]	0.71	10	6.72	7.16E-05	0.02
A_23_P126037	RLF	NM_012421	ref|Homo sapiens rearranged L-myc fusion (RLF), mRNA [NM_012421]	0.71	11.61	5.39	0	0.03

A_32_P120484	THC2647388	THC2647388	thc|Q4TD86_TETNG (Q4TD86) Chromosome undetermined SCAF6431, whole genome shotgun sequence. (Fragment), partial (9%) [THC2647388]	0.7	6.61	4.55	0	0.05
A_32_P55860	FAM33A	NM_182620	family with sequence similarity 33, member A (FAM33A), transcript variant 1, mRNA [NM_182620]	0.7	8.69	5.55	0	0.03
A_23_P160406	KCTD3	NM_016121	ref|Homo sapiens potassium channel tetramerisation domain containing 3 (KCTD3), mRNA [NM_016121]	0.7	11.46	6.36	0	0.02
A_23_P395075	JMJD1A	NM_018433	ref|Homo sapiens jumonji domain containing 1A (JMJD1A), mRNA [NM_018433]	0.7	9.21	6.59	8.27E-05	0.02
A_32_P69465	ENST00000340556	ENST00000340556	ens|MORN repeat-containing protein 2 (MORN motif protein in testis). [Source:Uniprot/SWISSPROT;Acc:Q502X0] [ENST00000340556]	0.7	9.97	5.76	0	0.03
A_24_P726336	PHACTR2	NM_001100164	ref|Homo sapiens phosphatase and actin regulator 2 (PHACTR2), transcript variant 1, mRNA [NM_001100164]	0.7	10.07	5.02	0	0.04
A_23_P346265	GNPTAB	NM_024312	ref|Homo sapiens N-acetylglucosamine-1-phosphate transferase, alpha and beta subunits (GNPTAB), mRNA [NM_024312]	0.7	8.26	5.06	0	0.04
A_32_P70875	CD239706	CD239706	gb|FNPBXF03 FNP Homo sapiens cDNA, mRNA sequence [CD239706]	0.7	8.04	4.56	0	0.05
A_23_P17269	CCDC88A	NM_018084	ref|Homo sapiens coiled-coil domain containing 88A (CCDC88A), mRNA [NM_018084]	0.7	8.14	4.51	0	0.05
A_23_P350045	REEP5	NM_005669	ref|Homo sapiens receptor accessory protein 5 (REEP5), mRNA [NM_005669]	0.7	11.38	4.67	0	0.05
A_24_P346587	MTFR1	NM_014637	ref|Homo sapiens mitochondrial fission regulator 1 (MTFR1), nuclear gene encoding mitochondrial protein, mRNA [NM_014637]	0.7	10.26	6.68	7.47E-05	0.02
A_23_P313734	KIAA1731	NM_033395	ref|Homo sapiens KIAA1731 (KIAA1731), mRNA [NM_033395]	0.7	10.68	4.6	0	0.05

A_32_P58937	MBTD1	NM_017643	ref|Homo sapiens mbt domain containing 1 (MBTD1), mRNA [NM_017643]	0.7	10.79	4.82	0	0.04
A_32_P176675	FAM92A1	NM_145269	ref|Homo sapiens family with sequence similarity 92, member A1 (FAM92A1), mRNA [NM_145269]	0.7	9.1	8.82	7.67E-06	0.01
A_24_P133085	CCDC90B	NM_021825	ref|Homo sapiens coiled-coil domain containing 90B (CCDC90B), mRNA [NM_021825]	0.7	11.3	5.16	0	0.04
A_23_P43150	ZHX1	NM_001017926	ref|Homo sapiens zinc fingers and homeoboxes 1 (ZHX1), transcript variant 1, mRNA [NM_001017926]	0.7	10.66	5.09	0	0.04
A_23_P120710	TTC3	NM_003316	ref|Homo sapiens tetratricopeptide repeat domain 3 (TTC3), transcript variant 1, mRNA [NM_003316]	0.69	9.98	6.49	9.36E-05	0.02
A_23_P54147	NIN	NM_016350	ref|Homo sapiens ninein (GSK3B interacting protein) (NIN), transcript variant 4, mRNA [NM_016350]	0.69	8.89	4.75	0	0.04
A_24_P360529	PDE7A	NM_002604	ref|Homo sapiens phosphodiesterase 7A (PDE7A), transcript variant 2, mRNA [NM_002604]	0.69	6.54	5.1	0	0.04
A_23_P205007	IPO5	NM_002271	importin 5 (IPO5), mRNA [NM_002271]	0.69	11.69	8.41	1.14E-05	0.01
A_23_P88331	DLG7	NM_014750	ref|Homo sapiens discs, large homolog 7 (Drosophila) (DLG7), mRNA	0.69	11.91	9.4	4.47E-06	0.01
A_23_P301079	FAM33A	NM_182620	family with sequence similarity 33, member A (FAM33A), transcript variant 1, mRNA [NM_182620]	0.69	9.19	5.64	0	0.03
A_23_P167905	DUSP22	AK000383	gb|Homo sapiens cDNA FLJ20376 fis, clone HUV01087. [AK000383]	0.69	8.14	4.8	0	0.04
A_24_P105761	JMJD1A	NM_018433	ref|Homo sapiens jumonji domain containing 1A (JMJD1A), mRNA [NM_018433]	0.69	10.52	6.5	9.24E-05	0.02
A_32_P152544	THC2775001	THC2775001	thc|Q96HI5_HUMAN (Q96HI5) HIG2 protein, partial (27%) [THC2775001]	0.69	4.68	5.82	0	0.03
A_32_P38426	C10orf46	NM_153810	ref|Homo sapiens chromosome 10 open reading frame 46 (C10orf46), mRNA [NM_153810]	0.69	10.59	6.14	0	0.02

A_24_P44341	UGCGL2	NM_020121	ref|Homo sapiens UDP-glucose ceramide glucosyltransferase-like 2 (UGCGL2), mRNA [NM_020121]	0.69	8.35	5.41	0	0.03
A_24_P277456	UBE2K	NM_005339	ref|Homo sapiens ubiquitin-conjugating enzyme E2K (UBC1 homolog, yeast) (UBE2K), transcript variant 1, mRNA [NM_005339]	0.69	11.89	4.73	0	0.04
A_23_P73114	PROS1	NM_000313	ref|Homo sapiens protein S (alpha) (PROS1), mRNA [NM_000313]	0.69	10.12	6.74	6.99E-05	0.02
A_23_P91900	SMC4	NM_005496	ref|Homo sapiens structural maintenance of chromosomes 4 (SMC4), transcript variant 1, mRNA [NM_005496]	0.69	12.54	4.65	0	0.05
A_24_P359165	SWAP70	BC000134	gb|Homo sapiens SWAP-70 protein, mRNA (cDNA clone IMAGE:2900736), containing frame-shift errors. [BC000134]	0.68	7.23	7.85	2.03E-05	0.01
A_23_P385126	DEPDC7	NM_139160	ref|Homo sapiens DEP domain containing 7 (DEPDC7), transcript variant 2, mRNA [NM_139160]	0.68	8.21	6.19	0	0.02
A_23_P53345	ARNTL2	NM_020183	ref|Homo sapiens aryl hydrocarbon receptor nuclear translocator-like 2 (ARNTL2), mRNA [NM_020183]	0.68	7.94	5.26	0	0.04
A_24_P342316	FRYL	NM_015030	FRY-like (FRYL), mRNA [NM_015030]	0.68	10.01	4.61	0	0.05
A_24_P328668	ARL13B	NM_182896	ref|Homo sapiens ADP-ribosylation factor-like 13B (ARL13B), transcript variant 1, mRNA [NM_182896]	0.68	8.71	5.04	0	0.04
A_23_P406438	SRPK2	NM_182691	ref|Homo sapiens SFRS protein kinase 2 (SRPK2), transcript variant 2, mRNA [NM_182691]	0.68	9.74	6.84	6.20E-05	0.02
A_23_P301051	PAIP2B	NM_020459	ref|Homo sapiens poly(A) binding protein interacting protein 2B (PAIP2B), mRNA [NM_020459]	0.68	8.61	5.62	0	0.03
A_24_P372553	C10orf137	NM_015608	ref|Homo sapiens chromosome 10 open reading frame 137 (C10orf137), mRNA [NM_015608]	0.68	8.84	4.87	0	0.04
A_23_P48295	CDADC1	NM_030911	ref|Homo sapiens cytidine and dCMP deaminase domain containing 1 (CDADC1), mRNA [NM_030911]	0.68	7.63	6.93	5.60E-05	0.02

A_24_P238836	XR_019164	XR_019164	Homo sapiens similar to RalA-binding protein 1 (RalBP1) (Ral-interacting protein 1) (76-kDa Ral-interacting protein) (Dinitrophenyl S-glutathione ATPase) (DNP-SG ATPase) (LOC129522), mRNA [XR_019164]	0.68	11.64	4.98	0	0.04
A_32_P177300	THC2692669	THC2692669	thc|ALU1_HUMAN (P39188) Alu subfamily J sequence contamination warning entry, partial (10%) [THC2692669]	0.68	8.6	4.8	0	0.04
A_23_P145984	TSPAN12	NM_012338	ref|Homo sapiens tetraspanin 12 (TSPAN12), mRNA [NM_012338]	0.68	6.13	6.81	6.44E-05	0.02
A_23_P396777	PCGF3	NM_006315	ref|Homo sapiens polycomb group ring finger 3 (PCGF3), mRNA [NM_006315]	0.68	7.44	5.24	0	0.04
A_24_P411899	RNF19A	NM_183419	ref|Homo sapiens ring finger protein 19A (RNF19A), transcript variant 1, mRNA [NM_183419]	0.67	9.1	4.88	0	0.04
A_23_P258037	JMJD1A	NM_018433	ref|Homo sapiens jumonji domain containing 1A (JMJD1A), mRNA [NM_018433]	0.67	10.01	6.14	0	0.02
A_24_P413941	FLJ38973	NM_153689	ref|Homo sapiens hypothetical protein FLJ38973 (FLJ38973), mRNA [NM_153689]	0.67	9.65	4.68	0	0.05
A_23_P87773	C12orf48	NM_017915	ref|Homo sapiens chromosome 12 open reading frame 48 (C12orf48), mRNA [NM_017915]	0.67	8.55	8.78	8.00E-06	0.01
A_23_P17269	CCDC88A	NM_018084	ref|Homo sapiens coiled-coil domain containing 88A (CCDC88A), mRNA [NM_018084]	0.67	8.22	4.49	0	0.05
A_23_P17269	CCDC88A	NM_018084	ref|Homo sapiens coiled-coil domain containing 88A (CCDC88A), mRNA [NM_018084]	0.67	8.3	4.59	0	0.05
A_23_P51397	ENAH	NM_001008493	ref|Homo sapiens enabled homolog (Drosophila) (ENAH), transcript variant 1, mRNA [NM_001008493]	0.67	8.76	5.35	0	0.03
A_32_P142991	AK026351	AK026351	gb|Homo sapiens cDNA: FLJ22698 fis, clone HSI12044. [AK026351]	0.67	12.66	4.53	0	0.05

A_24_P201323	ZMYND11	NM_006624	ref|Homo sapiens zinc finger, MYND domain containing 11 (ZMYND11), transcript variant 1, mRNA [NM_006624]	0.67	9.42	7.75	2.26E-05	0.01
A_23_P207940	PTPN2	NM_080422	ref|Homo sapiens protein tyrosine phosphatase, non-receptor type 2 (PTPN2), transcript variant 2, mRNA [NM_080422]	0.67	12.39	5.18	0	0.04
A_24_P391431	TAF9B	NM_015975	ref|Homo sapiens TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa (TAF9B), mRNA [NM_015975]	0.67	8.23	10.6	1.58E-06	0.01
A_24_P119141	PROS1	NM_000313	ref|Homo sapiens protein S (alpha) (PROS1), mRNA [NM_000313]	0.66	8.07	7.48	3.02E-05	0.02
A_24_P19810	PPCS	NM_024664	ref|Homo sapiens phosphopantothenoylcysteine synthetase (PPCS), transcript variant 1, mRNA [NM_024664]	0.66	11.67	6.05	0	0.02
A_23_P89755	RNF138	NM_016271	ref|Homo sapiens ring finger protein 138 (RNF138), transcript variant 1, mRNA [NM_016271]	0.66	12.97	4.61	0	0.05
A_23_P398836	TXNDC16	NM_020784	ref|Homo sapiens thioredoxin domain containing 16 (TXNDC16), mRNA [NM_020784]	0.66	9.02	7.85	2.04E-05	0.01
A_32_P164522	FAM33A	NM_182620	family with sequence similarity 33, member A (FAM33A), transcript variant 1, mRNA [NM_182620]	0.66	10.7	6.21	0	0.02
A_23_P433369	HEATR5A	NM_015473	ref|Homo sapiens HEAT repeat containing 5A (HEATR5A), mRNA [NM_015473]	0.66	7.62	6.23	0	0.02
A_23_P82738	RAD54B	NM_012415	ref|Homo sapiens RAD54 homolog B (S. cerevisiae) (RAD54B), mRNA [NM_012415]	0.66	9.18	9.4	4.46E-06	0.01
A_24_P477102	A_24_P477102	A_24_P477102	Unknown	0.66	8.78	4.78	0	0.04
A_24_P200162	HIGD1A	NM_014056	ref|Homo sapiens HIG1 domain family, member 1A (HIGD1A), transcript variant 3, mRNA	0.65	14.04	4.89	0	0.04
A_23_P82738	RAD54B	NM_012415	ref|Homo sapiens RAD54 homolog B (S. cerevisiae) (RAD54B), mRNA [NM_012415]	0.65	9.56	10.51	1.70E-06	0.01

A_23_P77079	MYEF2	NM_016132	ref|Homo sapiens myelin expression factor 2 (MYEF2), mRNA [NM_016132]	0.65	6.81	5.63	0	0.03
A_23_P68198	SH3YL1	NM_015677	ref|Homo sapiens SH3 domain containing, Ysc84-like 1 (S. cerevisiae) (SH3YL1), mRNA [NM_015677]	0.65	8.47	5.01	0	0.04
A_24_P281175	A_24_P281175	A_24_P281175	Unknown	0.65	8.08	6.13	0	0.02
A_24_P304636	RPS6KA5	NM_004755	ref|Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 5 (RPS6KA5), transcript variant 1, mRNA [NM_004755]	0.65	8.16	4.96	0	0.04
A_24_P187218	PCDH9	NM_020403	ref|Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA [NM_020403]	0.65	5.91	4.91	0	0.04
A_24_P236445	DYNC1LI2	NM_006141	ref|Homo sapiens dynein, cytoplasmic 1, light intermediate chain 2 (DYNC1LI2), mRNA [NM_006141]	0.64	8.91	5.58	0	0.03
A_23_P87556	CPNE8	NM_153634	copine VIII (CPNE8), mRNA [NM_153634]	0.64	8.14	5.8	0	0.03
A_24_P268196	LZIC	ENST00000377223	ens|Protein LZIC (Leucine zipper and ICAT homologous domain-containing protein) (Leucine zipper and CTNNBIP1 domain-containing protein). [Source:Uniprot/SWISSPROT;Acc:Q8WZA0] [ENST00000377223]	0.64	8.92	5.1	0	0.04
A_24_P684186	LOC647121	NR_003955	ref|Homo sapiens embigin homolog (mouse) pseudogene (LOC647121) on chromosome 1 [NR_003955]	0.64	10.75	5.06	0	0.04
A_23_P25403	HCFC2	NM_013320	ref|Homo sapiens host cell factor C2 (HCFC2), mRNA [NM_013320]	0.64	9.57	6.96	5.41E-05	0.02
A_24_P676259	A_24_P676259	A_24_P676259	Unknown	0.64	6.04	7.35	3.48E-05	0.02
A_24_P58381	CHD7	NM_017780	ref|Homo sapiens chromodomain helicase DNA binding protein 7 (CHD7), mRNA [NM_017780]	0.64	12.42	5.1	0	0.04
A_24_P409219	CCDC132	NM_017667	ref|Homo sapiens coiled-coil domain containing 132 (CCDC132), transcript variant 1, mRNA [NM_017667]	0.64	8.04	5.03	0	0.04

A_23_P400580	FNIP2	NM_020840	ref|Homo sapiens folliculin interacting protein 2 (FNIP2), mRNA [NM_020840]	0.64	9.17	6.02	0	0.02
A_32_P155043	A_32_P155043	A_32_P155043	Unknown	0.64	7.35	4.89	0	0.04
A_24_P803885	LOC149134	AK022825	gb|Homo sapiens cDNA FLJ12763 fis, clone NT2RP2001450. [AK022825]	0.64	7.99	5.35	0	0.03
A_24_P112087	ASF1A	NM_014034	ref|Homo sapiens ASF1 anti-silencing function 1 homolog A (S. cerevisiae) (ASF1A), mRNA [NM_014034]	0.64	8.52	5.37	0	0.03
A_32_P42780	ZNF271	NM_001112663	ref|Homo sapiens zinc finger protein 271 (ZNF271), transcript variant 1, mRNA [NM_001112663]	0.64	8.12	5.32	0	0.03
A_32_P74901	A_32_P74901	A_32_P74901	Unknown	0.64	7.41	4.97	0	0.04
A_24_P398130	USP6NL	NM_001080491	ref|Homo sapiens USP6 N-terminal like (USP6NL), mRNA [NM_001080491]	0.64	9.47	6.16	0	0.02
A_24_P450372	L40520	L40520	gb|Homo sapiens (clone DR3) mRNA fragment. [L40520]	0.64	7.41	4.51	0	0.05
A_23_P70007	HMMR	NM_012484	ref|Homo sapiens hyaluronan-mediated motility receptor (RHAMM) (HMMR), transcript variant 1, mRNA [NM_012484]	0.63	13.24	5.21	0	0.04
A_23_P171385	PHF6	NM_032335	ref|Homo sapiens PHD finger protein 6 (PHF6), transcript variant 3, mRNA [NM_032335]	0.63	7.76	5.25	0	0.04
A_24_P766204	MAP3K1	NM_005921	ref|Homo sapiens mitogen-activated protein kinase kinase kinase 1 (MAP3K1), mRNA [NM_005921]	0.63	8.43	6.64	7.83E-05	0.02
A_24_P28524	DBT	NM_001918	ref|Homo sapiens dihydrolipoamide branched chain transacylase E2 (DBT), nuclear gene encoding mitochondrial protein, mRNA [NM_001918]	0.63	7.34	6.59	8.34E-05	0.02
A_23_P147199	ZNF271	NM_006629	ref|Homo sapiens zinc finger protein 271 (ZNF271), transcript variant 2, mRNA [NM_006629]	0.63	8.86	5.59	0	0.03
A_23_P251421	CDCA7	NM_031942	ref|Homo sapiens cell division cycle associated 7 (CDCA7), transcript variant 1, mRNA [NM_031942]	0.63	12.81	5.06	0	0.04
A_23_P216071	A_23_P216071	A_23_P216071	Unknown	0.63	8.41	5.87	0	0.03

A_23_P82738	RAD54B	NM_012415	ref|Homo sapiens RAD54 homolog B (S. cerevisiae) (RAD54B), mRNA [NM_012415]	0.63	9.57	10.28	2.07E-06	0.01
A_23_P142918	FLJ38973	NM_153689	ref|Homo sapiens hypothetical protein FLJ38973 (FLJ38973), mRNA [NM_153689]	0.63	8.21	4.72	0	0.04
A_23_P92842	SAR1B	NM_001033503	ref|Homo sapiens SAR1 gene homolog B (S. cerevisiae) (SAR1B), transcript variant 1, mRNA [NM_001033503]	0.63	11.32	6.13	0	0.02
A_23_P151459	MYCBP2	NM_015057	ref|Homo sapiens MYC binding protein 2 (MYCBP2), mRNA [NM_015057]	0.63	11.3	4.53	0	0.05
A_24_P184769	WDR20	NM_181291	ref|Homo sapiens WD repeat domain 20 (WDR20), transcript variant 1, mRNA [NM_181291]	0.62	9.11	7.14	4.39E-05	0.02
A_23_P82738	RAD54B	NM_012415	ref|Homo sapiens RAD54 homolog B (S. cerevisiae) (RAD54B), mRNA [NM_012415]	0.62	9.62	9.95	2.74E-06	0.01
A_23_P157268	CLDN12	NM_012129	claudin 12 (CLDN12), mRNA [NM_012129]	0.62	9.17	5.46	0	0.03
A_23_P370635	MBOAT2	NM_138799	ref|Homo sapiens membrane bound O-acyltransferase domain containing 2 (MBOAT2), mRNA [NM_138799]	0.62	9.93	7.67	2.46E-05	0.01
A_23_P82738	RAD54B	NM_012415	ref|Homo sapiens RAD54 homolog B (S. cerevisiae) (RAD54B), mRNA [NM_012415]	0.62	9.45	9.74	3.28E-06	0.01
A_24_P95029	TAX1BP1	NM_006024	ref|Homo sapiens Tax1 (human T-cell leukemia virus type I) binding protein 1 (TAX1BP1), transcript variant 1, mRNA [NM_006024]	0.62	13.84	4.59	0	0.05
A_23_P16798	PFN4	NM_199346	ref|Homo sapiens profilin family, member 4 (PFN4), mRNA [NM_199346]	0.62	6.83	6.08	0	0.02
A_23_P349310	TNRC6A	NM_014494	ref|Homo sapiens trinucleotide repeat containing 6A (TNRC6A), mRNA [NM_014494]	0.62	9.99	4.73	0	0.04
A_24_P400507	C3orf64	NM_173654	ref|Homo sapiens chromosome 3 open reading frame 64 (C3orf64), mRNA [NM_173654]	0.62	6.79	4.98	0	0.04
A_24_P114255	MBOAT2	NM_138799	ref|Homo sapiens membrane bound O-acyltransferase domain containing 2 (MBOAT2), mRNA [NM_138799]	0.62	6.49	6.18	0	0.02

A_23_P99292	RAD51AP1	NM_006479	ref|Homo sapiens RAD51 associated protein 1 (RAD51AP1), mRNA [NM_006479]	0.62	11.39	6.38	0	0.02
A_24_P767901	LOC643014	XR_018450	gb|PREDICTED: Homo sapiens misc_RNA (LOC643014), miscRNA [XR_018450]	0.62	8.98	4.83	0	0.04
A_23_P82738	RAD54B	NM_012415	ref|Homo sapiens RAD54 homolog B (S. cerevisiae) (RAD54B), mRNA [NM_012415]	0.62	9.4	9.05	6.14E-06	0.01
A_32_P1445	PTPN2	NM_080423	ref|Homo sapiens protein tyrosine phosphatase, non-receptor type 2 (PTPN2), transcript variant 3, mRNA [NM_080423]	0.61	9.85	4.63	0	0.05
A_23_P88710	TMEM87A	NM_015497	ref|Homo sapiens transmembrane protein 87A (TMEM87A), transcript variant 1, mRNA [NM_015497]	0.61	13.36	8.52	1.03E-05	0.01
A_23_P40072	MTIF2	NM_001005369	ref|Homo sapiens mitochondrial translational initiation factor 2 (MTIF2), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA [NM_001005369]	0.61	11.97	4.48	0	0.05
A_23_P30377	DDX46	NM_014829	ref|Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 46 (DDX46), mRNA [NM_014829]	0.61	11.4	6.15	0	0.02
A_23_P82738	RAD54B	NM_012415	ref|Homo sapiens RAD54 homolog B (S. cerevisiae) (RAD54B), mRNA [NM_012415]	0.61	9.45	8.56	9.84E-06	0.01
A_23_P134078	CDYL	NM_170752	ref|Homo sapiens chromodomain protein, Y-like (CDYL), transcript variant 3, mRNA [NM_170752]	0.61	10.9	5.3	0	0.03
A_24_P525877	AK021840	AK021840	gb|Homo sapiens cDNA FLJ11778 fis, clone HEMBA1005911. [AK021840]	0.61	5.36	4.68	0	0.05
A_23_P82738	RAD54B	NM_012415	ref|Homo sapiens RAD54 homolog B (S. cerevisiae) (RAD54B), mRNA [NM_012415]	0.61	9.64	9.18	5.48E-06	0.01
A_24_P171549	CDCA7	NM_031942	ref|Homo sapiens cell division cycle associated 7 (CDCA7), transcript variant 1, mRNA [NM_031942]	0.61	9.88	4.46	0	0.05

A_23_P207981	SOCS6	NM_004232	ref|Homo sapiens suppressor of cytokine signaling 6 (SOCS6), mRNA [NM_004232]	0.61	8.68	6.03	0	0.02
A_23_P144684	ANKRD32	NM_032290	ref|Homo sapiens ankyrin repeat domain 32 (ANKRD32), mRNA [NM_032290]	0.61	10.19	5.81	0	0.03
A_23_P116980	TULP3	AF045583	gb|Homo sapiens tubby like protein 3 (TULP3) mRNA, complete cds. [AF045583]	0.6	6.39	5.11	0	0.04
A_24_P937855	RP5-1000E10.4	NM_001102396	ref|Homo sapiens suppressor of IKK epsilon (SIKE), transcript variant 1, mRNA [NM_001102396]	0.6	8.75	4.55	0	0.05
A_24_P217489	GLRB	NM_000824	ref|Homo sapiens glycine receptor, beta (GLRB), mRNA [NM_000824]	0.6	6.89	6.7	7.27E-05	0.02
A_32_P57140	JMJD1C	NM_032776	ref|Homo sapiens jumonji domain containing 1C (JMJD1C), transcript variant 1, mRNA [NM_032776]	0.6	7.81	5.25	0	0.04
A_32_P228183	LOC100127983	XM_001722571	gb|PREDICTED: Homo sapiens hypothetical protein LOC100127983 (LOC100127983), mRNA [XM_001722571]	0.6	7.21	5.1	0	0.04
A_23_P39050	ZNF823	NM_001080493	ref|Homo sapiens zinc finger protein 823 (ZNF823), mRNA [NM_001080493]	0.6	8.3	6.05	0	0.02
A_32_P186027	ANP32A	ENST00000267918	ens|Acidic leucine-rich nuclear phosphoprotein 32 family member A (Potent heat-stable protein phosphatase 2A inhibitor I1PP2A) (Acidic nuclear phosphoprotein pp32) (Leucine-rich acidic nuclear protein) (Lanp) (Putative HLA-DR-associated protein I) (PHAPI)	0.6	12.73	5.37	0	0.03
A_23_P142560	ZEB2	NM_014795	ref|Homo sapiens zinc finger E-box binding homeobox 2 (ZEB2), mRNA [NM_014795]	0.6	12.43	7.42	3.21E-05	0.02
A_23_P120644	A_23_P120644	A_23_P120644	Unknown	0.6	13.35	5.11	0	0.04
A_24_P128880	TBL1XR1	NM_024665	ref|Homo sapiens transducin (beta)-like 1 X-linked receptor 1 (TBL1XR1), mRNA [NM_024665]	0.6	11.42	4.6	0	0.05

A_24_P294124	SERTAD2	NM_014755	ref|Homo sapiens SERTA domain containing 2 (SERTAD2), mRNA [NM_014755]	0.6	10.46	5.79	0	0.03
A_23_P43071	MTERFD1	NM_015942	ref|Homo sapiens MTERF domain containing 1 (MTERFD1), mRNA [NM_015942]	0.6	11.61	6.11	0	0.02
A_32_P233304	LIN9	NM_173083	ref|Homo sapiens lin-9 homolog (C. elegans) (LIN9), mRNA [NM_173083]	0.6	11.78	4.82	0	0.04
A_24_P174775	THC2666103	THC2666103	Unknown	0.6	7.32	7.37	3.41E-05	0.02
A_23_P201918	ABCB10	NM_012089	ATP-binding cassette, sub-family B (MDR/TAP), member 10 (ABCB10), nuclear gene encoding mitochondrial protein, mRNA [NM_012089]	0.6	11.15	4.46	0	0.05
A_23_P105747	APPL2	NM_018171	ref|Homo sapiens adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 2 (APPL2), mRNA [NM_018171]	0.6	7.67	5.46	0	0.03
A_24_P329635	TSC1	NM_000368	ref|Homo sapiens tuberous sclerosis 1 (TSC1), transcript variant 1, mRNA [NM_000368]	0.6	10.44	4.5	0	0.05
A_24_P255314	SRP14P1	NR_003273	ref|Homo sapiens signal recognition particle 14kDa (homologous Alu RNA binding protein) pseudogene 1 (SRP14P1) on chromosome 12 [NR_003273]	0.6	13.69	4.51	0	0.05
A_24_P32411	CSPP1	NM_001077204	ref|Homo sapiens centrosome and spindle pole associated protein 1 (CSPP1), transcript variant 1, mRNA [NM_001077204]	0.6	6	4.7	0	0.05
A_32_P183218	ZNF367	AK091289	gb|Homo sapiens cDNA FLJ33970 fis, clone DFNES2001564. [AK091289]	0.6	7.94	5.26	0	0.04
A_23_P124427	NEK1	NM_012224	ref|Homo sapiens NIMA (never in mitosis gene a)-related kinase 1 (NEK1), mRNA [NM_012224]	0.6	7.31	5.06	0	0.04
A_32_P395879	C9orf93	NM_173550	ref|Homo sapiens chromosome 9 open reading frame 93 (C9orf93), mRNA [NM_173550]	0.6	5.36	6.64	7.86E-05	0.02
A_24_P323815	MYCBP2	NM_015057	ref|Homo sapiens MYC binding protein 2 (MYCBP2), mRNA [NM_015057]	0.6	9.15	4.65	0	0.05

A_24_P919399	ATP10D	NM_020453	ref|Homo sapiens ATPase, class V, type 10D (ATP10D), mRNA [NM_020453]	0.6	6.66	6.06	0	0.02
DOWN GENES								
ProbeName	GeneName	SystematicName	Description	logFC	AveExpr	t	P.Value	adj.P.Val
A_23_P44195	MSI2	NM_138962	ref|Homo sapiens musashi homolog 2 (Drosophila) (MSI2), transcript variant 1, mRNA [NM_138962]	-2.04	11.19	-30.99	9.14E-11	4.11E-06
A_24_P283814	HSPC152	NM_016404	ref|Homo sapiens hypothetical protein HSPC152 (HSPC152), mRNA [NM_016404]	-1.89	14.94	-13.08	2.47E-07	0
A_23_P12992	HSPC152	NM_016404	ref|Homo sapiens hypothetical protein HSPC152 (HSPC152), mRNA [NM_016404]	-1.83	15.03	-12.43	3.89E-07	0
A_23_P369479	MSI2	NM_170721	ref|Homo sapiens musashi homolog 2 (Drosophila) (MSI2), transcript variant 2, mRNA [NM_170721]	-1.46	8.79	-13.76	1.56E-07	0
A_23_P93348	LTB	NM_002341	ref|Homo sapiens lymphotoxin beta (TNF superfamily, member 3) (LTB), transcript variant 1, mRNA [NM_002341]	-1.34	12.48	-5.52	0	0.03
A_24_P280926	LOC391358	XM_372921	gb|PREDICTED: Homo sapiens similar to adrenal gland protein AD-001 (LOC391358), mRNA [XM_372921]	-1.33	13.38	-18.11	1.30E-08	0
A_23_P86012	LAMB3	NM_001017402	ref|Homo sapiens laminin, beta 3 (LAMB3), transcript variant 2, mRNA [NM_001017402]	-1.32	11.81	-4.53	0	0.05
A_23_P127995	CLNS1A	NM_001293	ref|Homo sapiens chloride channel, nucleotide-sensitive, 1A (CLNS1A), mRNA [NM_001293]	-1.28	14.78	-13.92	1.41E-07	0
A_24_P136641	BC013655	BC013655	gb|Homo sapiens, clone IMAGE:4152599, mRNA, partial cds. [BC013655]	-1.27	10.36	-8.4	1.15E-05	0.01
A_23_P117558	FKBP3	NM_002013	ref|Homo sapiens FK506 binding protein 3, 25kDa (FKBP3), mRNA [NM_002013]	-1.16	12.43	-6.53	8.94E-05	0.02

A_24_P255914	XR_019229	XR_019229	gb|PREDICTED: Homo sapiens similar to Methylosome subunit pICln (Chloride conductance regulatory protein ICln) (I(Cln)) (Chloride channel, nucleotide sensitive 1A) (Chloride ion current inducer protein) (ClCI) (Reticulocyte pICln) (LOC650438), mRNA [XR_01	-1.15	10.97	-12.1	4.94E-07	0
A_23_P87257	MRPL17	NM_022061	mitochondrial ribosomal protein L17 (MRPL17), nuclear gene encoding mitochondrial protein, mRNA [NM_022061]	-1.04	11.62	-8.13	1.53E-05	0.01
A_23_P353014	CACNA2D4	NM_172364	calcium channel, voltage-dependent, alpha 2/delta subunit 4 (CACNA2D4), mRNA [NM_172364]	-1.03	10.57	-5.31	0	0.03
A_23_P58266	S100P	NM_005980	ref|Homo sapiens S100 calcium binding protein P (S100P), mRNA [NM_005980]	-1.02	12.73	-4.47	0	0.05
A_23_P7932	TREML2	NM_024807	ref|Homo sapiens triggering receptor expressed on myeloid cells-like 2 (TREML2), mRNA [NM_024807]	-0.97	10.72	-7.2	4.09E-05	0.02
A_23_P204751	ACCN2	NM_020039	ref|Homo sapiens amiloride-sensitive cation channel 2, neuronal (ACCN2), transcript variant 1, mRNA [NM_020039]	-0.96	9.11	-7.97	1.79E-05	0.01
A_23_P12896	FANCF	NM_022725	ref|Homo sapiens Fanconi anemia, complementation group F (FANCF), mRNA [NM_022725]	-0.94	10.23	-5.42	0	0.03
A_23_P107963	FUT1	NM_000148	fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, H blood group) (FUT1), mRNA [NM_000148]	-0.94	8.65	-5.21	0	0.04
A_23_P250629	PSMB8	NM_004159	ref|Homo sapiens proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional peptidase 7) (PSMB8), transcript variant 1, mRNA [NM_004159]	-0.9	12.53	-7.59	2.67E-05	0.01
A_23_P37892	GPT2	NM_133443	ref|Homo sapiens glutamic pyruvate transaminase (alanine aminotransferase) 2 (GPT2), mRNA [NM_133443]	-0.89	10.21	-5.52	0	0.03

A_23_P166408	OSM	NM_020530	oncostatin M (OSM), mRNA [NM_020530]	-0.89	11.13	-6.09	0	0.02
A_23_P113212	TMEM45A	NM_018004	ref|Homo sapiens transmembrane protein 45A (TMEM45A), mRNA [NM_018004]	-0.86	10.79	-4.67	0	0.05
A_23_P114783	PARP1	NM_001618	ref|Homo sapiens poly (ADP-ribose) polymerase family, member 1 (PARP1), mRNA [NM_001618]	-0.85	14.92	-9.29	4.93E-06	0.01
A_23_P114783	PARP1	NM_001618	ref|Homo sapiens poly (ADP-ribose) polymerase family, member 1 (PARP1), mRNA [NM_001618]	-0.85	14.9	-8.29	1.29E-05	0.01
A_23_P114783	PARP1	NM_001618	ref|Homo sapiens poly (ADP-ribose) polymerase family, member 1 (PARP1), mRNA [NM_001618]	-0.85	14.87	-9.09	5.92E-06	0.01
A_23_P114783	PARP1	NM_001618	ref|Homo sapiens poly (ADP-ribose) polymerase family, member 1 (PARP1), mRNA [NM_001618]	-0.85	14.68	-8.96	6.70E-06	0.01
A_23_P114783	PARP1	NM_001618	ref|Homo sapiens poly (ADP-ribose) polymerase family, member 1 (PARP1), mRNA [NM_001618]	-0.84	15.04	-9.73	3.31E-06	0.01
A_23_P114783	PARP1	NM_001618	ref|Homo sapiens poly (ADP-ribose) polymerase family, member 1 (PARP1), mRNA [NM_001618]	-0.84	14.59	-9.24	5.18E-06	0.01
A_23_P14537	TMED10	NM_006827	ref|Homo sapiens transmembrane emp24-like trafficking protein 10 (yeast) (TMED10), mRNA [NM_006827]	-0.84	13.47	-6.16	0	0.02
A_23_P114783	PARP1	NM_001618	ref|Homo sapiens poly (ADP-ribose) polymerase family, member 1 (PARP1), mRNA [NM_001618]	-0.83	14.94	-8.85	7.46E-06	0.01
A_23_P114783	PARP1	NM_001618	ref|Homo sapiens poly (ADP-ribose) polymerase family, member 1 (PARP1), mRNA [NM_001618]	-0.83	15.1	-8.28	1.30E-05	0.01
A_23_P114783	PARP1	NM_001618	ref|Homo sapiens poly (ADP-ribose) polymerase family, member 1 (PARP1), mRNA [NM_001618]	-0.83	15.06	-8.37	1.19E-05	0.01
A_23_P114783	PARP1	NM_001618	ref|Homo sapiens poly (ADP-ribose) polymerase family, member 1 (PARP1), mRNA [NM_001618]	-0.83	14.91	-8.34	1.23E-05	0.01
A_23_P37702	TPSAB1	NM_003294	ref|Homo sapiens tryptase alpha/beta 1 (TPSAB1), mRNA [NM_003294]	-0.83	9.59	-4.91	0	0.04

A_24_P671842	THC2762149	THC2762149	thc|BC037545 poly(ADP-ribosyl)transferase {Homo sapiens} (exp=-1; wgp=0; cg=0), partial (24%) [THC2762149]	-0.82	12.81	-8.53	1.02E-05	0.01
A_23_P140207	PCK2	NM_004563	ref|Homo sapiens phosphoenolpyruvate carboxykinase 2 (mitochondrial) (PCK2), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA [NM_004563]	-0.82	14.94	-7.3	3.68E-05	0.02
A_23_P17430	RBM38	NM_017495	ref|Homo sapiens RNA binding motif protein 38 (RBM38), transcript variant 1, mRNA [NM_017495]	-0.81	11.26	-5.15	0	0.04
A_23_P42335	FANCE	NM_021922	ref|Homo sapiens Fanconi anemia, complementation group E (FANCE), mRNA [NM_021922]	-0.8	13.95	-6.59	8.33E-05	0.02
A_24_P800629	TMED10P	NR_002807	ref|Homo sapiens transmembrane emp24-like trafficking protein 10 (yeast) pseudogene (TMED10P) on chromosome 8 [NR_002807]	-0.8	10.72	-6.57	8.56E-05	0.02
A_23_P104692	PELI3	NM_145065	ref|Homo sapiens pellino homolog 3 (Drosophila) (PELI3), transcript variant 1, mRNA [NM_145065]	-0.79	10.28	-4.73	0	0.04
A_24_P236956	RAB3D	BC007960	gb|Homo sapiens RAB3D, member RAS oncogene family, mRNA (cDNA clone IMAGE:4301650), partial cds. [BC007960]	-0.78	11.23	-8.23	1.37E-05	0.01
A_23_P115862	COMTD1	NM_144589	ref|Homo sapiens catechol-O-methyltransferase domain containing 1 (COMTD1), mRNA [NM_144589]	-0.78	11.46	-5.01	0	0.04
A_23_P110879	TRAF3IP2	NM_147686	ref|Homo sapiens TRAF3 interacting protein 2 (TRAF3IP2), transcript variant 2, mRNA	-0.78	8.86	-4.64	0	0.05
A_23_P166336	ENST00000249122	ENST00000249122	gb|Homo sapiens mRNA; cDNA DKFZp434N035 (from clone DKFZp434N035). [AL136879]	-0.77	10.14	-5.41	0	0.03
A_24_P135856	RHD	NM_016124	ref|Homo sapiens Rh blood group, D antigen (RHD), mRNA [NM_016124]	-0.77	8.56	-5.4	0	0.03

A_23_P23765	ITGB3BP	NM_014288	ref|Homo sapiens integrin beta 3 binding protein (beta3-endonexin) (ITGB3BP), mRNA [NM_014288]	-0.77	10.28	-7.1	4.59E-05	0.02
A_23_P148162	ADI1	NM_018269	ref|Homo sapiens acireductone dioxygenase 1 (ADI1), mRNA [NM_018269]	-0.77	11.23	-6.35	0	0.02
A_23_P128817	PCK2	NM_004563	ref|Homo sapiens phosphoenolpyruvate carboxykinase 2 (mitochondrial) (PCK2), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA [NM_004563]	-0.77	10.69	-7.56	2.77E-05	0.01
A_24_P23995	RNF187	BC012758	gb|Homo sapiens ring finger protein 187, mRNA (cDNA clone IMAGE:3633225), partial cds. [BC012758]	-0.76	11.2	-6.06	0	0.02
A_24_P218265	TNFRSF10B	NM_003842	tumor necrosis factor receptor superfamily, member 10b (TNFRSF10B), transcript variant 1, mRNA [NM_003842]	-0.76	12.91	-6.14	0	0.02
A_23_P52676	CATSPER1	NM_053054	ref|Homo sapiens cation channel, sperm associated 1 (CATSPER1), mRNA [NM_053054]	-0.76	10.37	-5.32	0	0.03
A_23_P23765	ITGB3BP	NM_014288	ref|Homo sapiens integrin beta 3 binding protein (beta3-endonexin) (ITGB3BP), mRNA [NM_014288]	-0.75	10.26	-6.95	5.43E-05	0.02
A_32_P52911	ADI1	NM_018269	ref|Homo sapiens acireductone dioxygenase 1 (ADI1), mRNA [NM_018269]	-0.75	10.87	-6.76	6.81E-05	0.02
A_23_P90359	NRTN	NM_004558	neurturin (NRTN), mRNA [NM_004558]	-0.75	7.15	-6.8	6.49E-05	0.02
A_23_P23765	ITGB3BP	NM_014288	ref|Homo sapiens integrin beta 3 binding protein (beta3-endonexin) (ITGB3BP), mRNA [NM_014288]	-0.75	10.25	-7.05	4.84E-05	0.02
A_23_P253561	C20orf121	NM_024331	ref|Homo sapiens chromosome 20 open reading frame 121 (C20orf121), transcript variant 1, mRNA [NM_024331]	-0.74	11.67	-5.93	0	0.03
A_23_P23765	ITGB3BP	NM_014288	ref|Homo sapiens integrin beta 3 binding protein (beta3-endonexin) (ITGB3BP), mRNA [NM_014288]	-0.74	10.34	-7.44	3.15E-05	0.02

A_24_P386622	ARRB1	NM_004041	ref|Homo sapiens arrestin, beta 1 (ARRB1), transcript variant 1, mRNA [NM_004041]	-0.74	9.25	-4.45	0	0.05
A_23_P20437	TIGD5	NM_032862	ref|Homo sapiens tigger transposable element derived 5 (TIGD5), mRNA [NM_032862]	-0.74	11.53	-6.86	6.08E-05	0.02
A_23_P23765	ITGB3BP	NM_014288	ref|Homo sapiens integrin beta 3 binding protein (beta3-endonexin) (ITGB3BP), mRNA [NM_014288]	-0.74	10.2	-7.42	3.23E-05	0.02
A_23_P145904	H2AFV	NM_012412	ref|Homo sapiens H2A histone family, member V (H2AFV), transcript variant 1, mRNA [NM_012412]	-0.74	15.51	-5.03	0	0.04
A_23_P23765	ITGB3BP	NM_014288	ref|Homo sapiens integrin beta 3 binding protein (beta3-endonexin) (ITGB3BP), mRNA [NM_014288]	-0.74	10.33	-7.81	2.11E-05	0.01
A_23_P95823	NSMCE1	NM_145080	ref|Homo sapiens non-SMC element 1 homolog (S. cerevisiae) (NSMCE1), mRNA [NM_145080]	-0.73	12.82	-6.82	6.37E-05	0.02
A_23_P23765	ITGB3BP	NM_014288	ref|Homo sapiens integrin beta 3 binding protein (beta3-endonexin) (ITGB3BP), mRNA [NM_014288]	-0.73	10.29	-7.25	3.87E-05	0.02
A_23_P148984	DARS2	NM_018122	ref|Homo sapiens aspartyl-tRNA synthetase 2, mitochondrial (DARS2), nuclear gene encoding mitochondrial protein, mRNA [NM_018122]	-0.73	9.95	-6.76	6.78E-05	0.02
A_23_P203702	THC2707284	THC2707284	thc|Q214U3_RHOP A (Q214U3) Penicillin-binding protein 1C precursor, partial (3%)	-0.73	11.25	-5.92	0	0.03
A_23_P124962	FAM89B	NM_152832	family with sequence similarity 89, member B (FAM89B), transcript variant 2, mRNA [NM_152832]	-0.73	11.35	-5.92	0	0.03
A_23_P23765	ITGB3BP	NM_014288	ref|Homo sapiens integrin beta 3 binding protein (beta3-endonexin) (ITGB3BP), mRNA [NM_014288]	-0.73	10.05	-6.74	6.96E-05	0.02
A_23_P23765	ITGB3BP	NM_014288	ref|Homo sapiens integrin beta 3 binding protein (beta3-endonexin) (ITGB3BP), mRNA [NM_014288]	-0.73	10.29	-7.79	2.15E-05	0.01

A_23_P23765	ITGB3BP	NM_014288	ref|Homo sapiens integrin beta 3 binding protein (beta3-endonexin) (ITGB3BP), mRNA [NM_014288]	-0.72	10.17	-6.67	7.57E-05	0.02
A_23_P334709	FKBP9	NM_007270	ref|Homo sapiens FK506 binding protein 9, 63 kDa (FKBP9), mRNA [NM_007270]	-0.72	12.1	-5.23	0	0.04
A_23_P141315	NLE1	NM_001014445	ref|Homo sapiens notchless homolog 1 (Drosophila) (NLE1), transcript variant 2, mRNA [NM_001014445]	-0.72	12.5	-4.59	0	0.05
A_24_P156113	EHD2	NM_014601	ref|Homo sapiens EH-domain containing 2 (EHD2), mRNA [NM_014601]	-0.71	9.93	-4.64	0	0.05
A_23_P202881	FEZ1	NM_005103	ref|Homo sapiens fasciculation and elongation protein zeta 1 (zygin I) (FEZ1), transcript variant 1, mRNA [NM_005103]	-0.71	11.55	-5.48	0	0.03
A_24_P568645	XR_019461	XR_019461	gb|PREDICTED: Homo sapiens similar to Poly [ADP ribose] polymerase 1 (PARP-1) (ADPRT) (NAD(+) ADP-ribosyltransferase 1) (Poly[ADP-ribose] synthetase 1) (LOC649459), mRNA [XR_019461]	-0.71	12.17	-6.75	6.90E-05	0.02
A_23_P360626	LOC201164	NM_178836	ref|Homo sapiens similar to CG12314 gene product (LOC201164), mRNA [NM_178836]	-0.71	11.11	-4.52	0	0.05
A_23_P116809	COPZ1	NM_016057	ref|Homo sapiens coatomer protein complex, subunit zeta 1 (COPZ1), mRNA [NM_016057]	-0.71	10.48	-8.09	1.59E-05	0.01
A_23_P362712	ABHD11	NM_148912	ref|Homo sapiens abhydrolase domain containing 11 (ABHD11), mRNA [NM_148912]	-0.7	9.68	-5.09	0	0.04
A_23_P68851	KREMEN1	NM_001039570	ref|Homo sapiens kringle containing transmembrane protein 1 (KREMEN1), transcript variant 3, mRNA [NM_001039570]	-0.7	10.71	-6.3	0	0.02
A_24_P172990	AARS	NM_001605	ref|Homo sapiens alanyl-tRNA synthetase (AARS), mRNA [NM_001605]	-0.7	11.61	-6.29	0	0.02
A_23_P171336	NXF3	NM_022052	ref|Homo sapiens nuclear RNA export factor 3 (NXF3), mRNA [NM_022052]	-0.69	12.85	-4.49	0	0.05

A_23_P1043	C1orf106	NM_018265	ref|Homo sapiens chromosome 1 open reading frame 106 (C1orf106), mRNA [NM_018265]	-0.69	9	-5.66	0	0.03
A_23_P29684	VILL	NM_015873	villin-like (VILL), mRNA [NM_015873]	-0.69	9.28	-5.02	0	0.04
A_32_P107746	ENSA	NM_207042	ref|Homo sapiens endosulfine alpha (ENSA), transcript variant 1, mRNA [NM_207042]	-0.69	10.85	-10.46	1.78E-06	0.01
A_23_P148194	ADI1	NM_018269	ref|Homo sapiens acireductone dioxygenase 1 (ADI1), mRNA [NM_018269]	-0.69	12.08	-5.65	0	0.03
A_23_P16469	PLAUR	NM_001005377	ref|Homo sapiens plasminogen activator, urokinase receptor (PLAUR), transcript variant 3, mRNA [NM_001005377]	-0.68	11.08	-4.97	0	0.04
A_23_P55998	SLC1A5	NM_005628	ref|Homo sapiens solute carrier family 1 (neutral amino acid transporter), member 5 (SLC1A5), mRNA [NM_005628]	-0.68	10.9	-4.97	0	0.04
A_32_P37592	SCARNA17	NR_003003	ref|Homo sapiens small Cajal body-specific RNA 17 (SCARNA17) on chromosome 18 [NR_003003]	-0.68	10.69	-5.87	0	0.03
A_24_P118260	LOC100128203	XM_001715724	ref|PREDICTED: Homo sapiens similar to hCG2040272 (LOC100128203), mRNA [XM_001715724]	-0.68	8.59	-9.51	4.03E-06	0.01
A_23_P76882	CCNB1IP1	NM_182851	ref|Homo sapiens cyclin B1 interacting protein 1 (CCNB1IP1), transcript variant 3, mRNA	-0.68	13.41	-4.52	0	0.05
A_24_P50759	TNF	NM_000594	ref|Homo sapiens tumor necrosis factor (TNF superfamily, member 2) (TNF), mRNA	-0.67	8.31	-4.56	0	0.05
A_23_P156284	DBN1	NM_080881	ref|Homo sapiens drebrin 1 (DBN1), transcript variant 2, mRNA [NM_080881]	-0.67	12.68	-9.5	4.09E-06	0.01
A_24_P48856	CBS	NM_000071	ref|Homo sapiens cystathionine-beta-synthase (CBS), mRNA [NM_000071]	-0.67	9.81	-6.38	0	0.02
A_24_P50759	TNF	NM_000594	ref|Homo sapiens tumor necrosis factor (TNF superfamily, member 2) (TNF), mRNA	-0.67	8.3	-4.71	0	0.05
A_23_P58747	N4BP3	NM_015111	ref|Homo sapiens Nedd4 binding protein 3 (N4BP3), mRNA [NM_015111]	-0.67	9.33	-5.26	0	0.04

A_23_P500433	CARD9	NM_052813	ref|Homo sapiens caspase recruitment domain family, member 9 (CARD9), mRNA [NM_052813]	-0.67	11.77	-6.35	0	0.02
A_24_P335620	SLC7A5	NM_003486	ref|Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 5 (SLC7A5), mRNA [NM_003486]	-0.66	13.39	-5.7	0	0.03
A_24_P50759	TNF	NM_000594	ref|Homo sapiens tumor necrosis factor (TNF superfamily, member 2) (TNF), mRNA	-0.66	8.49	-5.05	0	0.04
A_23_P5831	HPCAL1	NM_134421	ref|Homo sapiens hippocalcin-like 1 (HPCAL1), transcript variant 2, mRNA [NM_134421]	-0.66	11.03	-6.11	0	0.02
A_23_P100344	ORC6L	NM_014321	ref|Homo sapiens origin recognition complex, subunit 6 like (yeast) (ORC6L), mRNA [NM_014321]	-0.66	11.69	-5.05	0	0.04
A_24_P50759	TNF	NM_000594	ref|Homo sapiens tumor necrosis factor (TNF superfamily, member 2) (TNF), mRNA	-0.66	8.37	-4.8	0	0.04
A_24_P250499	C20orf77	NM_021215	ref|Homo sapiens chromosome 20 open reading frame 77 (C20orf77), mRNA [NM_021215]	-0.66	11.09	-6.6	8.20E-05	0.02
A_23_P135015	RGP1	BC001725	gb|Homo sapiens RGP1 retrograde golgi transport homolog (S. cerevisiae), mRNA (cDNA clone MGC:755 IMAGE:3533857), complete cds. [BC001725]	-0.65	8.07	-4.89	0	0.04
A_23_P411296	CEBPB	NM_005194	ref|Homo sapiens CCAAT/enhancer binding protein (C/EBP), beta (CEBPB), mRNA [NM_005194]	-0.65	14.6	-4.5	0	0.05
A_24_P50759	TNF	NM_000594	ref|Homo sapiens tumor necrosis factor (TNF superfamily, member 2) (TNF), mRNA	-0.65	8.52	-5.1	0	0.04
A_24_P300777	ADAM8	NM_001109	ref|Homo sapiens ADAM metallopeptidase domain 8 (ADAM8), mRNA [NM_001109]	-0.65	12.88	-5.87	0	0.03
A_24_P225616	RRM2	NM_001034	ref|Homo sapiens ribonucleotide reductase M2 polypeptide (RRM2), mRNA [NM_001034]	-0.65	11.02	-6.75	6.87E-05	0.02

A_24_P73738	RPL13	ENST00000311528	protein L13 (Breast basic conserved protein 1). [Source:Uniprot/SWISSPROT;Acc:P26373] [ENST00000311528]	-0.65	12.75	-6.59	8.34E-05	0.02
A_23_P60683	STK24	NM_001032296	ref|Homo sapiens serine/threonine kinase 24 (STE20 homolog, yeast) (STK24), transcript variant 2, mRNA [NM_001032296]	-0.65	12.39	-7.74	2.29E-05	0.01
A_23_P411296	CEBPB	NM_005194	ref|Homo sapiens CCAAT/enhancer binding protein (C/EBP), beta (CEBPB), mRNA [NM_005194]	-0.65	14.41	-4.66	0	0.05
A_24_P192914	AMICA1	NM_153206	adhesion molecule, interacts with CXADR antigen 1 (AMICA1), transcript variant 2, mRNA [NM_153206]	-0.65	9.87	-5.34	0	0.03
A_23_P92349	FGFRL1	NM_001004356	ref|Homo sapiens fibroblast growth factor receptor-like 1 (FGFRL1), transcript variant 1, mRNA [NM_001004356]	-0.64	8.19	-7.21	4.05E-05	0.02
A_24_P195400	XR_019065	XR_019065	Homo sapiens similar to DNA replication complex GINS protein PSF2 (LOC391247), mRNA [XR_019065]	-0.64	10.41	-6.19	0	0.02
A_23_P127964	PRCP	NM_199418	ref|Homo sapiens prolylcarboxypeptidase (angiotensinase C) (PRCP), transcript variant 2, mRNA [NM_199418]	-0.64	13.53	-7.63	2.57E-05	0.01
A_23_P131676	CXCR7	NM_020311	ref|Homo sapiens chemokine (C-X-C motif) receptor 7 (CXCR7), mRNA [NM_020311]	-0.64	7.95	-4.63	0	0.05
A_23_P411296	CEBPB	NM_005194	ref|Homo sapiens CCAAT/enhancer binding protein (C/EBP), beta (CEBPB), mRNA [NM_005194]	-0.64	14.78	-4.73	0	0.04
A_23_P411296	CEBPB	NM_005194	ref|Homo sapiens CCAAT/enhancer binding protein (C/EBP), beta (CEBPB), mRNA [NM_005194]	-0.64	14.43	-4.64	0	0.05
A_23_P167674	F12	NM_000505	ref|Homo sapiens coagulation factor XII (Hageman factor) (F12), mRNA [NM_000505]	-0.64	10.93	-6.66	7.68E-05	0.02
A_24_P50759	TNF	NM_000594	ref|Homo sapiens tumor necrosis factor (TNF superfamily, member 2) (TNF), mRNA	-0.64	8.49	-4.61	0	0.05

A_23_P411296	CEBPB	NM_005194	ref|Homo sapiens CCAAT/enhancer binding protein (C/EBP), beta (CEBPB), mRNA [NM_005194]	-0.64	14.7	-4.56	0	0.05
A_24_P50759	TNF	NM_000594	ref|Homo sapiens tumor necrosis factor (TNF superfamily, member 2) (TNF), mRNA	-0.64	8.33	-4.52	0	0.05
A_23_P200901	ENSA	NM_004436	ref|Homo sapiens endosulfine alpha (ENSA), transcript variant 3, mRNA [NM_004436]	-0.64	11.36	-9.98	2.66E-06	0.01
A_24_P389959	COPZ1	NM_016057	ref|Homo sapiens coatomer protein complex, subunit zeta 1 (COPZ1), mRNA [NM_016057]	-0.64	12.71	-5.75	0	0.03
A_23_P388170	SLC39A3	NM_213568	solute carrier family 39 (zinc transporter), member 3 (SLC39A3), transcript variant 2, mRNA	-0.63	9.15	-4.71	0	0.05
A_23_P411296	CEBPB	NM_005194	ref|Homo sapiens CCAAT/enhancer binding protein (C/EBP), beta (CEBPB), mRNA [NM_005194]	-0.63	14.74	-4.52	0	0.05
A_23_P151368	N6AMT2	NM_174928	ref|Homo sapiens N 6 adenine-specific DNA methyltransferase 2 (putative) (N6AMT2), mRNA [NM_174928]	-0.63	10.21	-5.02	0	0.04
A_23_P118246	GINS2	NM_016095	ref|Homo sapiens GINS complex subunit 2 (Psf2 homolog) (GINS2), mRNA [NM_016095]	-0.63	13.06	-6.03	0	0.02
A_23_P215819	ZNF655	NM_024061	ref|Homo sapiens zinc finger protein 655 (ZNF655), transcript variant 2, mRNA [NM_024061]	-0.63	10.82	-4.83	0	0.04
A_23_P323943	SLC5A12	NM_178498	ref|Homo sapiens solute carrier family 5 (sodium/glucose cotransporter), member 12 (SLC5A12), mRNA [NM_178498]	-0.63	10.67	-5.31	0	0.03
A_24_P583007	BC039246	BC039246	gb|Homo sapiens cDNA clone IMAGE:5278517. [BC039246]	-0.63	10.75	-6.2	0	0.02
A_23_P78108	ALDOC	NM_005165	ref|Homo sapiens aldolase C, fructose-bisphosphate (ALDOC), mRNA [NM_005165]	-0.62	11.06	-4.45	0	0.05
A_23_P207058	SOCS3	NM_003955	ref|Homo sapiens suppressor of cytokine signaling 3 (SOCS3), mRNA [NM_003955]	-0.62	8.66	-5.52	0	0.03

A_24_P50759	TNF	NM_000594	ref|Homo sapiens tumor necrosis factor (TNF superfamily, member 2) (TNF), mRNA	-0.62	8.31	-4.52	0	0.05
A_32_P88349	CR620599	CR620599	gb|full-length cDNA clone CS0DF021YI14 of Fetal brain of Homo sapiens (human). [CR620599]	-0.62	11.41	-5.24	0	0.04
A_23_P253177	STK24	NM_001032296	ref|Homo sapiens serine/threonine kinase 24 (STE20 homolog, yeast) (STK24), transcript variant 2, mRNA [NM_001032296]	-0.61	12.97	-5.89	0	0.03
A_23_P65651	WARS	NM_004184	ref|Homo sapiens tryptophanyl-tRNA synthetase (WARS), transcript variant 1, mRNA [NM_004184]	-0.61	13.78	-4.68	0	0.05
A_24_P508012	TAF3	AK123254	gb|Homo sapiens cDNA FLJ41260 fis, clone BRAMY2034561. [AK123254]	-0.61	8.28	-6.58	8.41E-05	0.02
A_23_P64661	ARHGAP9	NM_032496	ref|Homo sapiens Rho GTPase activating protein 9 (ARHGAP9), transcript variant 1, mRNA [NM_032496]	-0.61	11.18	-4.6	0	0.05
A_23_P389391	SLC12A4	NM_005072	solute carrier family 12 (potassium/chloride transporters), member 4 (SLC12A4), mRNA [NM_005072]	-0.61	9.11	-4.62	0	0.05
A_32_P103131	THC2608658	THC2608658	thc|AF195969 rho GTPase activating protein 8 isoform 2 {Homo sapiens} (exp=-1; wgp=0; cg=0), partial (6%) [THC2608658]	-0.61	10.25	-7.12	4.51E-05	0.02
A_23_P55564	ZCCHC2	BC006340	gb|Homo sapiens zinc finger, CCHC domain containing 2, mRNA (cDNA clone IMAGE:4079754), complete cds. [BC006340]	-0.61	8.71	-4.66	0	0.05
A_23_P52939	SLC43A1	NM_003627	ref|Homo sapiens solute carrier family 43, member 1 (SLC43A1), mRNA [NM_003627]	-0.61	10.95	-4.75	0	0.04
A_23_P103919	B4GALT3	NM_003779	ref|Homo sapiens UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 3 (B4GALT3), mRNA [NM_003779]	-0.6	12.56	-4.94	0	0.04
A_24_P79955	RBM8A	NM_005105	ref|Homo sapiens RNA binding motif protein 8A (RBM8A), mRNA [NM_005105]	-0.6	11.74	-6.96	5.39E-05	0.02

A_23_P154566	TOX2	NM_032883	ref|Homo sapiens TOX high mobility group box family member 2 (TOX2), transcript variant 3, mRNA [NM_032883]	-0.6	13.03	-5.34	0	0.03
A_23_P42746	NCF1	NM_000265	ref|Homo sapiens neutrophil cytosolic factor 1, (chronic granulomatous disease, autosomal 1) (NCF1), mRNA [NM_000265]	-0.6	10.28	-4.83	0	0.04

Supplementary Materials and Methods:

Leukemic cell line MTS assays

Myeloid leukemic cell lines were infected with lentiviral vectors encoding anti- *MSI2* shRNAs and then selected based on puromycin resistance conferred by the lentiviral vectors. We plated $1*10^5$ infected cells and performed MTS proliferation assays with background absorbance values subtracted and normalized to day 0. Cell growth was assessed with the MTS reagent Promega as previously performed[1].

Human Patient Data

CML data was obtained from previously published studies[2, 3] through Oncomine.com and GEO. Previously published AML patient data was accessed through gene expression omnibus (GEO: GSE16432)[4,5]. In addition, RNA from adult AML patients with extensive clinical, cytogenetic and molecular genetic characterization was provided by the German-Austrian AML Study Group (AMLSG) with patient informed consent and institutional review board approval from all participating centers. CN-AML from this dataset was used to select the top 15 *MSI2* expressing samples and 15 lowest *MSI2* expressing samples and these were used for the "CN-AML High and Low *MSI2* dataset." Gene expression and clinical and outcome data for the 163 adult AML patients with normal cytogenetics (Affymetrix HG-U133B)[6] was downloaded from the Gene Expression Omnibus (GEO accession number GSE12417). This cohort was used as an independent dataset. We first normalized raw data using CEL files. *MSI2* probe intensities were collapsed into a single value using the highest intensity. The resulting value was log transformed (base2) and mean centered across arrays. Positive and negative *MSI2* expression levels for each individual were matched with survival data. Kaplan-Meier plot was created with Graphpad software.

Ba/F3 IL-3 Withdrawal Assay

We transduced BaF3 cells with retroviral vectors expressing indicated empty virus MSCVIRESEGFP (MIG) and *MSI2*, and sorted by flow cytometry for EGFP$^+$ cells. Cells were washed 3 times with 1X PBS after IL-3 was withdrawn and were counted at day 4 using a hemocytometer.

Quantitative PCR

mRNA was isolated from populations using TRIZOL and Qiagen RNEASY and reverse transcribed into cDNA with iSCRIPT (BioRad). Quantitative PCR was performed as previously described. Primers for *MSI1* and *MSI2* are *MSI1*(F) 5'-CACTTCCATGAAATCAACAACAA-3', (R) 5'-GGCTGGGCTTTCTTGCATT-3' MSI2 (F) 5'-ACGACTCCCAGCACGACC-3', (R) 5'-GCCAGCTCAGTCCACCGATA-3'.

MSI2 Inducible Knock-in Generation

Human *MSI2* cDNA from open biosystems clone ID#5942 Accession CV027635 in pDONR223 *MSI2* (CCDS 11596.1) was cloned into the unique EcoRI restriction site of the pBS31 vector containing a PGK promoter followed by an ATG start codon and an frt site, followed by a splice acceptor-double polyA cassette, the tetracycline operator with a CMV minimal promoter, the unique EcoRI site for cDNA insertion, and an SV40 polyA signal. The pBS31-*MSI2* vector was then electroporated along with a Flpe recombinase expressing vector into KH2 embryonic stem cells harboring the M2-rtTA at the *ROSA26* locus under control of the *ROSA26* promoter, as well as an frt-flanked PGK-neomycinR cassette followed by a promoterless, ATG-less hygromycinR cassette targeted downstream of the *Collagen1a1* locus. Selection for hygromycin resistance yielded numerous colonies which were verified for proper flip-in to the *Coll1a1* locus by digestion of genomic DNA followed by southern blotting with a 3' internal probe, yielding a 6.2 kb wildtype band, a 6.7 kb band for the frt-containing knockin allele, and a 4.1 kb band for the successfully flipped-in *MSI2* inducible allele. Activation of the *TetO-MSI2* allele was carried out in vivo by administration of 2mg/mL doxycycline hyclate (Sigma D9891) along with 10mg/mL sucrose in the drinking water. *In vitro* activation was performed by addition of 0.5-2ug/mL doxycycline to the culture media.

BCR-ABL1 Leukemia Assay

All mice were housed in a pathogen-free animal facility in microisolator cages, and experiments were conducted based on a protocol approved by the Institutional Animal Care and Use Committee (IACUC). Murine BMT experiments were performed as previously described[24]. We injected *MSI2* inducible 6-8 week old C57 Bl/6 SJL donor mice with a single IP injection of 5-FU (Sigma) at 0.15mg/g body weight on day -8. We sacrificed donor mice at day -2, and BM was then harvested. After red cell lysis in RBC lysis buffer (Puregene), the bone marrow was stimulated overnight in transplant media composed of RPMI/10%FBS and murine IL3, IL6, and SCF. The bone marrow was then transduced twice with the retroviral supernatant by spinfection with polybrene and HEPES and centrifuged at 2500RPM at 33^{o}C for 90 minutes. The transduced bone marrow was then washed and resuspended in Hank's solution. 6-8 week old C57 Bl/6 recipient mice were lethally irradiated with 2 doses of irradiation at 650 rads on day 0, and then we injected $1x10^6$ donor bone marrow cells into the tail vein of each mouse. We allowed the cells to home and lodge for 3 days prior to dox administration.

Hematopoietic Histopathology

Peripheral blood was collected from the retroorbital cavity using a heparinized glass capillary tube. Complete peripheral blood count analysis including a differential blood count was obtained using Hemavet (Drew Scientific). For histological analysis, peripheral blood smears were stained with Wright-Giemsa stain. We euthanized and collected the relevant organs, fixed in 10% formalin and paraffin embedded. The histopathology core facility (Brigham and Women's Hospital) provided 4μm sections that were stained by hematoxylin and eosin (H&E). We acquired digital images using a Nikon Eclipse E400 microscope equipped with a digital camera and analyzed them using Spot Advanced software.

Viral Supernatant Production

We maintained Ba/F3 cells in RPMI 1640 media with 10% FCS and either interleukin-3 (IL-3) (0.5 ng/mL; R&D Systems, Minneapolis, MN) or WEHI-conditioned media as a source of IL-3. We generated retroviral stocks by transfecting 293T cells with Fugene (Roche), and viral titers were then determined as previously described[2,7].

Flow Cytometry

We harvested bone marrow cells or splenocytes and subjected them to red cell lysis. We stained fresh or cryopreserved cells with the following antibodies: CD45.2-FITC and CD45.1-APC, Mac1-PE, Gr1-APC, c-Kit-APC, CD71-PE, Ter119-APC, B220-PE, and CD3-APC (Becton-Dickinson) and analyzed them on the BD FACSCalibur instrument. Staining for multiparameter flow cytometry was performed as previously described[8]. Lineage negative cocktail includes the following purified rat antibodies: (Lin^-; B220, CD4, CD8, CD3, Gr1, CD19, TER119). Mac1 was not included in the lineage cocktail. We depleted antibody-treated cells with rat-specific Dynal beads and then stained the cells with rat-specific PE-Cy5.5. Finally, we analyzed and sorted cells with the BD FACSAria instrument. For progenitor populations in **Fig. 1a** the populations were gated and sorted with indicated markers: GMP (LK, $Fc\gamma RIIb^{hi}$ $CD34^+$), CMP (LK, $Fc\gamma RIIb^{mid}$ $CD34^+$), MEP (LK, $Fc\gamma RIIb^{low}$ $CD34^-$), B-cells ($B220^+$) and T-cells ($CD3^+$).

Microarray Analysis in Primary AML cells

Gene expression profiling (GEP) was performed as previously described using the Stanford cDNA microarray platform[4]. Following Ficoll enrichment all samples contained at least 80% leukemic cells. Normalization and filtering of the data has been performed reported elsewhere[4]. The complete gene expression microarray dataset is available at the Stanford Microarray Database (http://smd.stanford.edu)[28].

Microarray Analysis in normal LSK and Progenitors

We hybridized RNA isolated from adult murine hematopoietic stem and progenitor cells ($Lineage^{Low}$, $Sca1^+$, Kit^+; LSK) and committed progenitor cells ($Lineage^{Low}$, $Sca1^-$, Kit^+;

LK) on mouse Expression Array 430A 2.0 (Affymetrix). Raw CEL data were normalized by RMA method. A t-test was used to determine significant differences in gene expression between the samples.

Microarray Analysis of *MSI2* Expression in Inducible Mice.

Hematopoietic stem and progenitor cells (Lineage^{Low}, Sca1^{+}, Kit^{+}; LSK) treated with doxycycline for 36 hours were sorted from control *rtTA* and *MSI2* mice. Cells were directly sorted into TRIZOL and then further isolated with QiagenRNEASY. RNA was then amplified using a NUGEN Pico amplification kit, fragmented and hybridized on Mouse Expression Array 430 2.0. Signal normalization was performed by RMA method. Data was analyzed using GSEA across the complete list of genes ranked by signal-to-noise ratio. (Microarray data is representative of n=3 rttA mice and n=2 *MSI2* doxycycline treated animals.)

Microarray Analysis in MSI2 knockdown

Agilent's Feature Extraction Software was used for array image analysis and the calculation of spot intensity measurements. We used the linear model for microarray data (LIMMA) Bioconductor package[9] to normalize the samples using loess and quantile methods within and between arrays respectively and empirical Bayes moderated t-statistics were used to detect genes differentially expressed. We considered genes regulated by *MSI2* knock-down with fold change > 1.5 and FDR p-value < 0.05 for components of *MSI2* gene expression signature. Then, we performed gene set enrichment analysis using GSEA across the complete list of genes ranked by t-statistic[10].

MSI2 signature and Survival Analysis

We matched *MSI2* signature genes to the corresponding probes id in AML dataset and log2 values were standardized by taking the mean value for each gene across the sample set. This *MSI2* signature was used to cluster the AML dataset using an unsupervised hierarchical method (by the ‘‘heatmap.plus’’ function of ‘‘gplots’’ package of R). We classified the two main clusters by positive or negative representation of the *MSI2* signature and then matched it with the survival data. Statistical significance was calculated by log rank test and Kaplan-Meier plots were created with Graphpad software (La Jolla, CA). We also examined the predictive value of *MSI2* expression when a validation cohort of CN-AML samples[6] was divided into low and high *MSI2* expression groups based on expression relative to the mean. Higher *MSI2* expression value was associated with worse overall survival (p=0.0004; Fig. 4h).

Multivariate Cox Regression analysis

We assessed the prognostic value of *MSI2* expression as an individual marker by a multivariate Cox-proportional hazard model analysis with overall survival and event-free survival as the dependant variable and FLT3-ITD/NPM1 status, age, FAB classification, cytogenetic group and continuous expression level of *MSI2* as directly assessed independent variables. We used the Wald test to assess the significance of each covariate in multivariate analysis. We performed a multivariate proportional-hazard analyses using the *coxph* function from R package *survival*.

Cobblestone area-forming Assay

We performed CAFC assays as descrined in [11]. In short, we plated bone-marrow cells in 96 flat bottom wells in limiting dilutions on top of confluent OP9 stroma at the indicated doses of bone marrow cells: $1x10^4$, $4x10^4$, $8x10^4$, 16x104 with 12 replicates per dose. The number of cobblestone positive wells per dose were enumerated and at 2 weeks post-plating. L-Calc software (StemCell Technologies) was used to calculate frequency and p-values between groups.

In vitro LT-HSC and MPP proliferation and apoptosis Assay

We sorted 2000 LT-HSC ($SLAM^+$) and MPP ($CD150^-$ $CD48^-$ LSK) into STIF medium in a round bottom plate and counted at day 5.Then we analyzed the cells stained for Annexin/PI to assess apoptosis.

Supplementary Methods Reference:

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