Supplementary information

Somatic *SETBP1* mutations in myeloid malignancies

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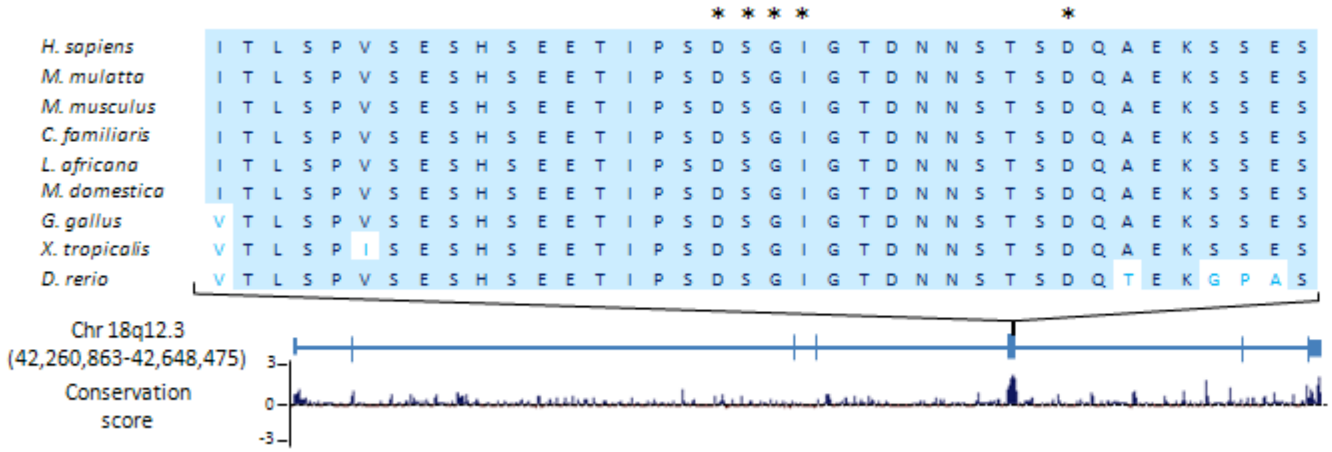
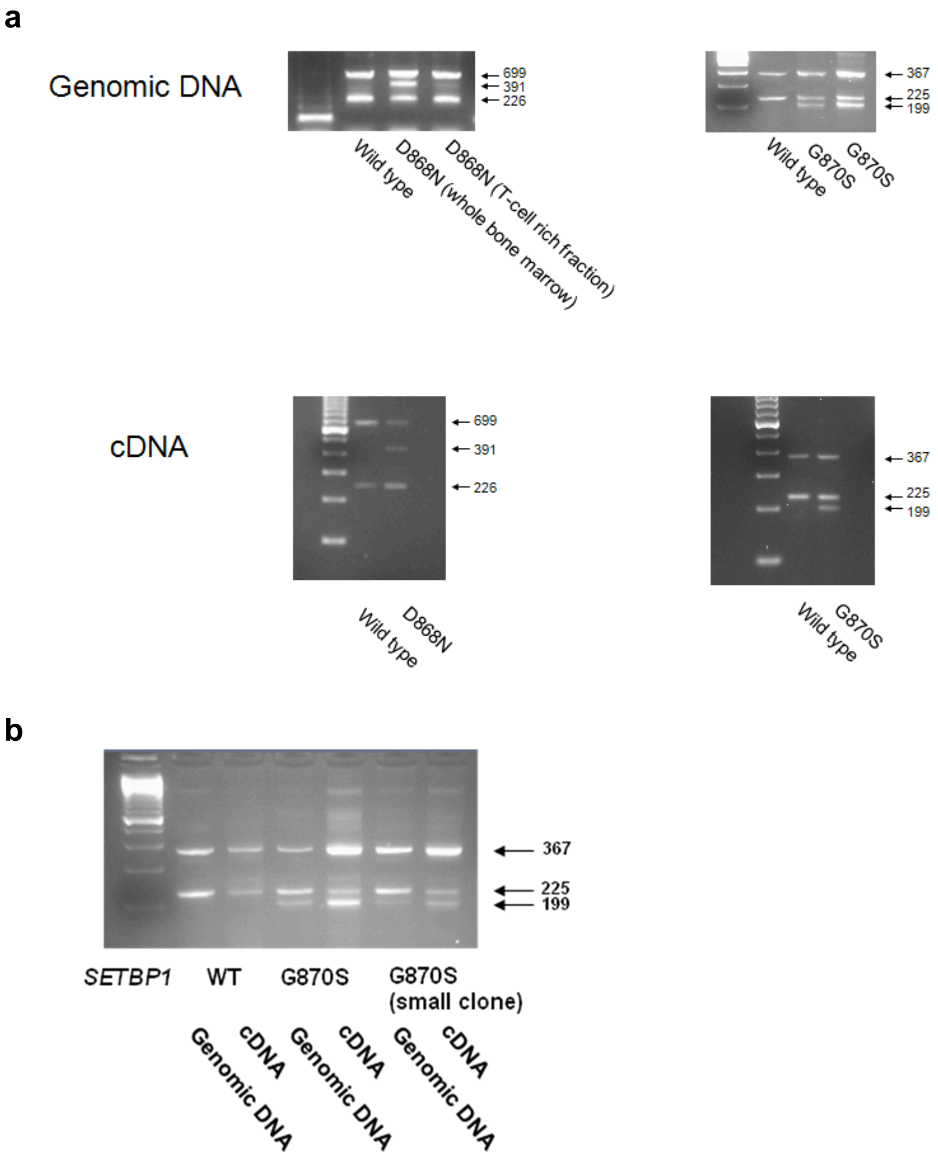


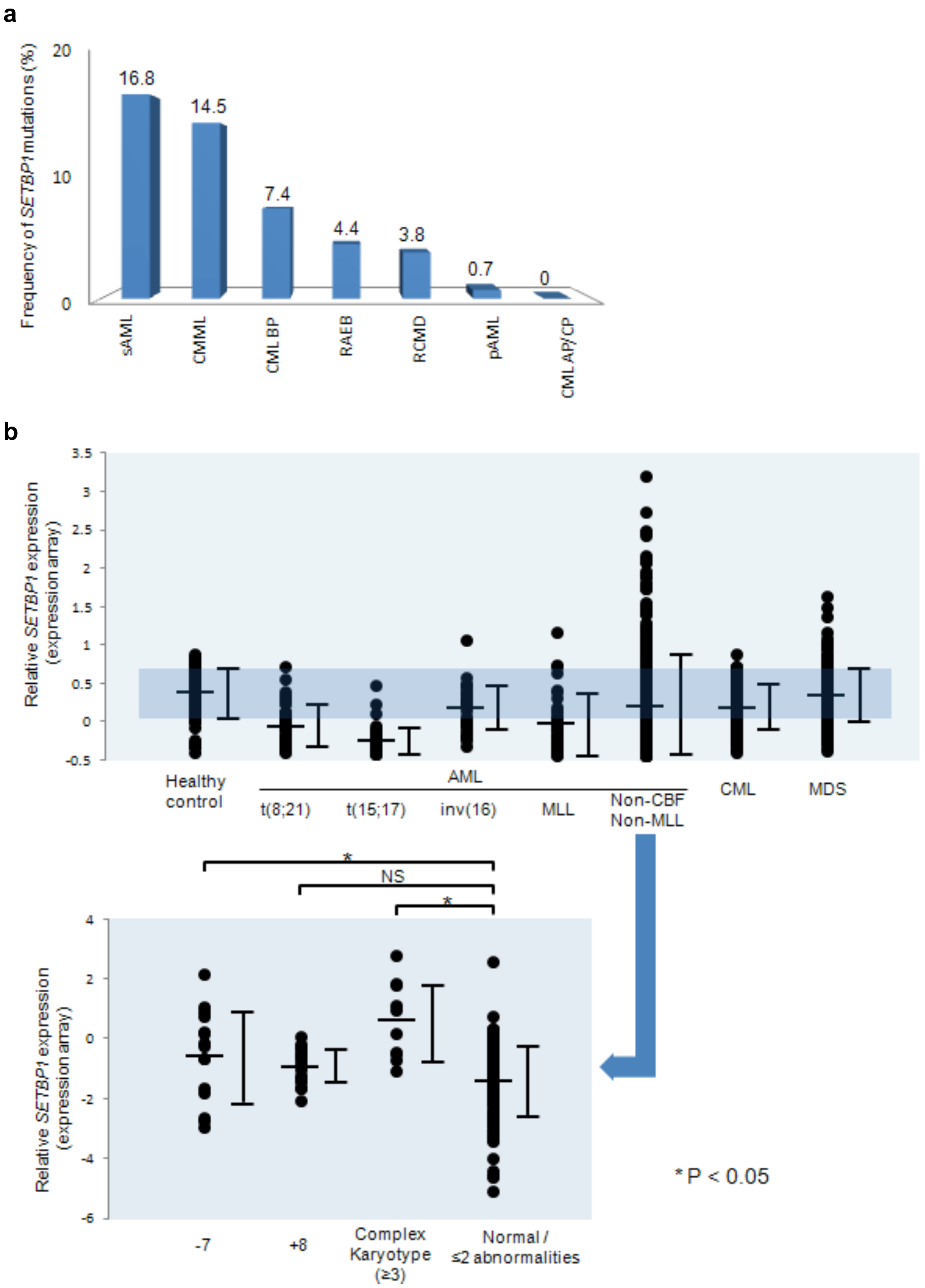
Supplementary Figure 1. Alignment of amino acids within the SKI domain of SETBP1 from different species.

Conserved amino acids are shown in dark blue with shadow. Mutated positions are indicated by asterisks. All affected residues are completely conserved throughout evolution (top). The conserved region of the whole *SETBP1* genome based on Placental Mammal Basewise Conservation by PhyloP (UCSC genome browser; http://genome.ucsc.edu/cgi-bin/hgGateway) (bottom).



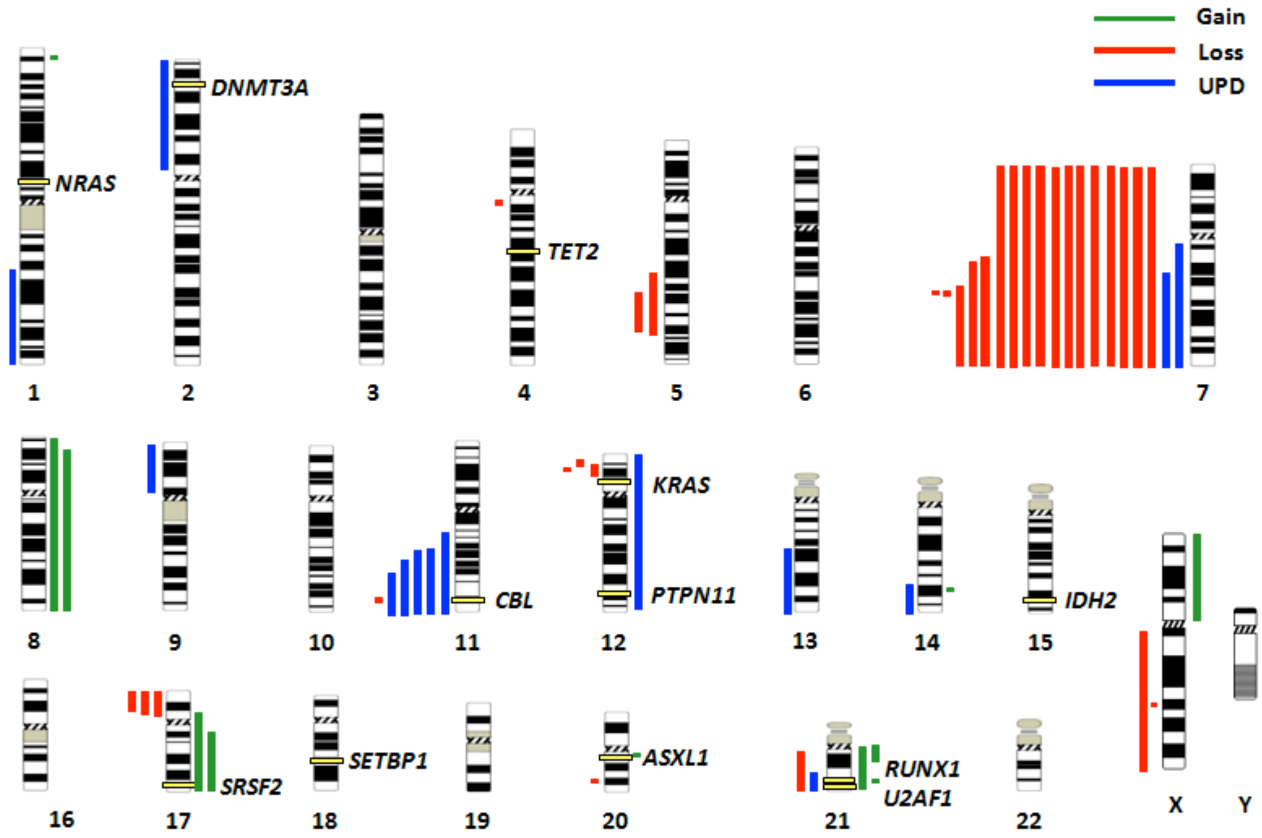
Supplementary Figure 2. Allele specific PCR for detecting *SETBP1* p.Asp868Asn and p.Gly870Ser alterations.

(a) Allele specific PCR was performed using genomic DNA (upper panel) and cDNA (lower panel) from cases with p.Asp868Asn or p.Gly870Ser alterations, and wild type *SETBP1*. Primer sets of each mutation are shown in Supplementary Table 14. For detection of p.Asp868Asn (c.2602G>A), product size by two outer primers was 699bp; A allele, 391bp; G allele, 226bp and for p.Gly870Ser (c.2608G>A), outer primers, 367bp; G allele, 225bp; A allele, 199bp. Mutant alleles were amplified using cDNA as genomic DNA. (b) In 2 cases with p.Gly870Ser alterations, genomic DNA and cDNA from the same cell fractions were tested in parallel.


a
Frequency of SETBP1 mutations (%)
20
10
0
16.8
14.5
7.4
4.4
3.8
0.7
0
sAML
CMML
CML BP
RAEB
RCMD
pAML
CML AP/CP
b
Relative SETBP1 expression (expression array)
3.5
3
2.5
2
1.5
1
0.5
0
-0.5
Healthy control
AML
t(8;21)
t(15;17)
inv(16)
MLL
Non-CBF Non-MLL
CML
MDS
*
NS
*
Relative SETBP1 expression (expression array)
4
2
0
-2
-4
-6
-7
+8
Complex Karyotype (≥3)
Normal / ≤2 abnormalities
*P < 0.05

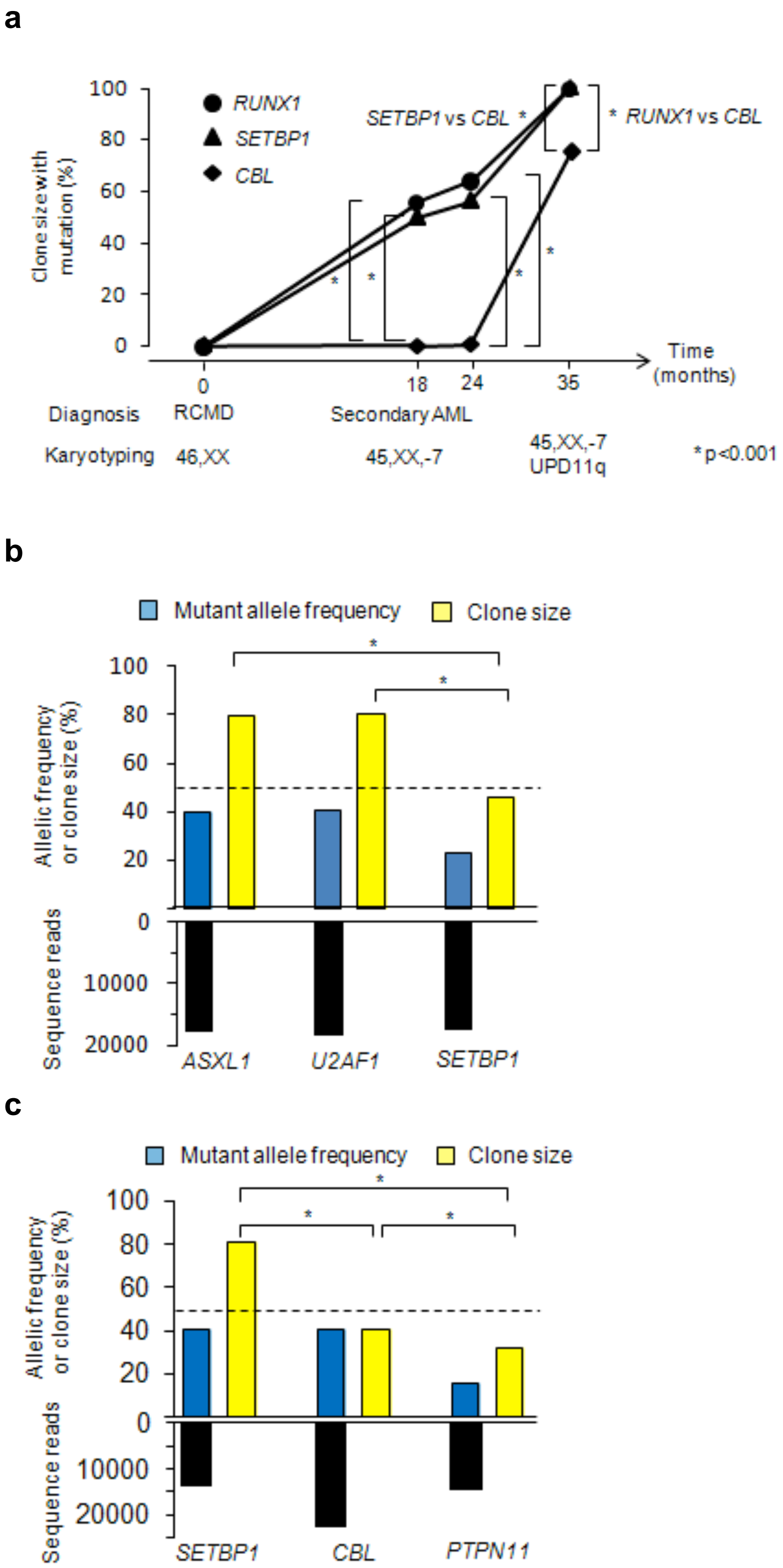
Supplementary Figure 3. Frequency and phenotypic association of *SETBP1* mutations and overexpression in myeloid malignancies.

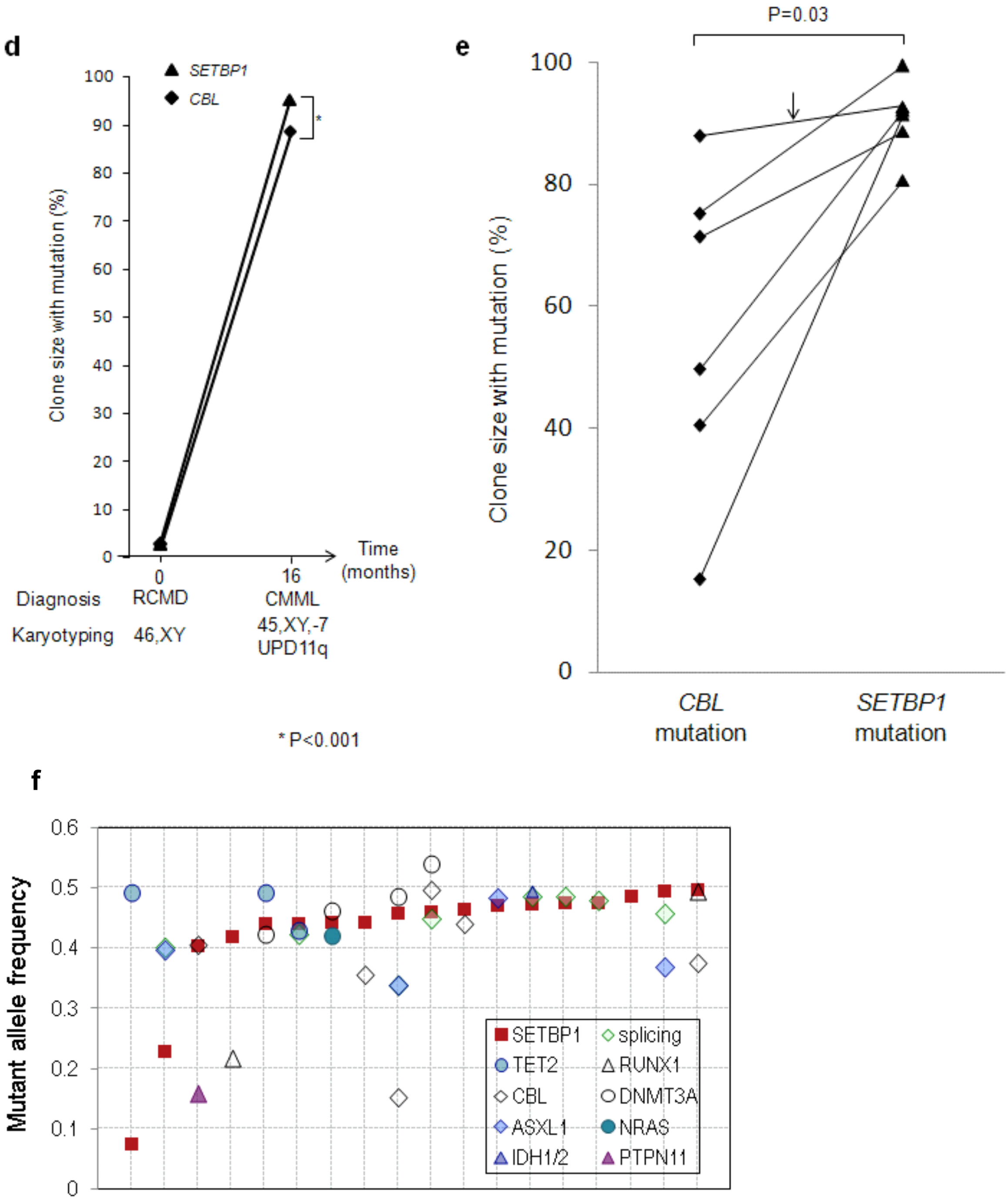
(a) In the cohort of 727 cases with myeloid malignancies, *SETBP1* mutations were present in 16.8% of sAML with a history of antecedent MDS (19/113), 13.9% of CMML (22/152) and 7.4% of CML in blast phase (2/27) as well as 4.4% of RAEB (4/90). Mutations were less frequent in 3.8% of lower-risk MDS (3/85) and 0.7% of primary AML (pAML) (1/145). No mutations were observed in CML chronic/accelerated phase (CP/AP). (b) Using expression array database (Oncomine; https://www.oncomine.org/), the *SETBP1* transcript was found to be expressed in the bone marrow of healthy donors and various myeloid malignancies. While *SETBP1* expression is not elevated in core binding factor (CBF) leukemia or AML with MLL rearrangement, this gene was found to be overexpressed in a proportion of cases of non-CBF pAML, sAML and MDS (upper panel). In particular, *SETBP1* expression was significantly increased in -7 ($P=0.03$) and cases with complex karyotype ($P<0.001$), but not in +8 ($P=0.39$) (lower panel). Horizontal bars in each disease category indicate mean values of *SETBP1* expression and error bars show mean±s.d. The blue area in the lower panel represents the range of mean±s.d. in healthy controls. Asterisks (*) indicate statistical significance ($P<0.05$) when individual disease categories were compared. NS; not significant.



Supplementary Figure 4. Karyotype analyses in cases with *SETBP1* mutations.

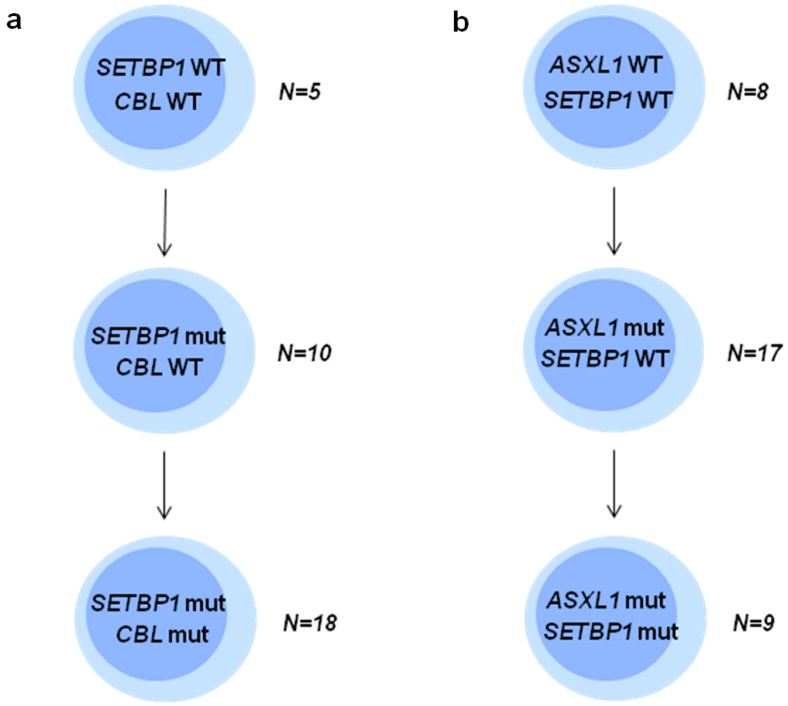
Each line represents chromosomal aberration: green - copy number gains, red - losses and blue - regions of UPD. Totally, 57 aberrations were detected by metaphase cytogenetics and/or single nucleotide polymorphism-array karyotyping in 46 cases with *SETBP1* mutations. Exact location of *NRAS*, *DNMT3A*, *TET2*, *CBL*, *KRAS*, *PTPN11*, *IDH2*, *SRSF2*, *SETBP1*, *ASXL1*, *RUNX1* and *U2AF1* were shown by yellow bars.


a
Clone size with mutation (%)
100
80
60
40
20
0
RUNX1
SETBP1
CBL
SETBP1 vs CBL *
* RUNX1 vs CBL
*
*
*
*
Time (months)
0
18
24
35
Diagnosis
RCMD
Secondary AML
Karyotyping
46,XX
45,XX,-7
45,XX,-7 UPD11q
* p<0.001
b
Mutant allele frequency
Clone size
*
*
Allelic frequency or clone size (%)
100
80
60
40
20
0
Sequence reads
10000
20000
ASXL1
U2AF1
SETBP1
c
Mutant allele frequency
Clone size
*
*
*
Allelic frequency or clone size (%)
100
80
60
40
20
0
Sequence reads
10000
20000
SETBP1
CBL
PTPN11

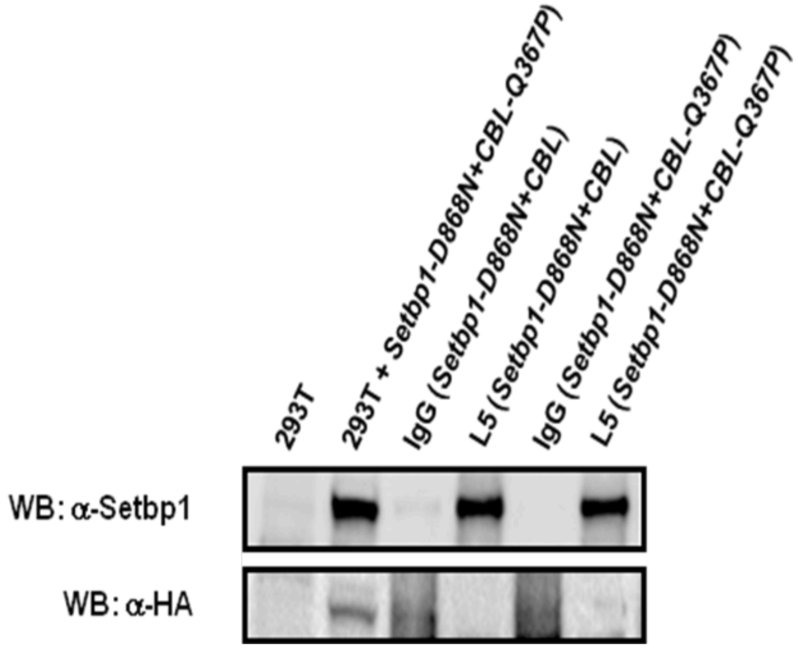

d
SETBP1
CBL
Clone size with mutation (%)
100
90
80
70
60
50
40
30
20
10
0
*
0
16
Time (months)
Diagnosis
RCMD
CMML
Karyotyping
46,XY
45,XY,-7
UPD11q
* P<0.001
e
P=0.03
100
80
60
40
20
0
Clone size with mutation (%)
CBL mutation
SETBP1 mutation
f
Mutant allele frequency
0.6
0.5
0.4
0.3
0.2
0.1
0
SETBP1
TET2
CBL
ASXL1
IDH1/2
splicing
RUNX1
DNMT3A
NRAS
PTPN11

Supplementary Figure 5. *SETBP1* and other concomitant mutations acquired in clinical course.

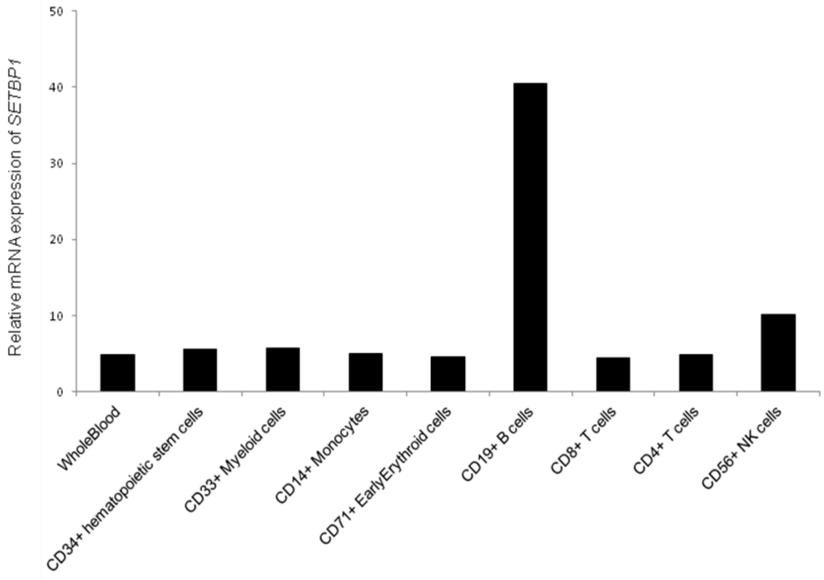
(a) The evaluation of an estimated mutated clone size defined by read counts as obtained in targeted deep sequencing helped to understand acquired molecular events. In a case of sAML, 4 serial samples were evaluated. While *RUNX1* and *SETBP1* mutations emerged at almost the same time in the leukemic evolution, a *CBL* mutation was observed in the later stage. (b) In a separate case with RCMD, the clone size of a *SETBP1* mutation was 46% (total sequence reads; 17516), while clone sizes of an *ASXL1* and *U2AF1* mutations were 79% (18230) and 80% (18230), respectively. The clone size of a *SETBP1* mutation was significantly smaller than that of *ASXL1* or *U2AF1* mutation, supporting the theory that *SETBP1* mutations were acquired in a subclone with *ASXL1* or *U2AF1* mutations. (c) In a RAEB case with *SETBP1* mutation, concomitant hemizygous *CBL* and heterozygous *PTPN11* mutations were found. By targeted deep sequencing, the clone size of a heterozygous *SETBP1* mutation was 81% (total reads; 13707), while the clone sizes of *CBL* and *PTPN11* mutations were 41% (22563) and 32 % (14511), respectively. The sizes of these 3 mutated clones were significantly different from each other ($P<0.001$, each). (d) In a case with CMML, leukemic evolution with -7 was observed 16 months after the initial presentation. *SETBP1* and *CBL* mutations were acquired during clonal expansion of CMML. By targeted deep sequencing, clone size based on allelic frequency of mutation was evaluated. Clone sizes were 88% (*CBL* mutation; 16536 total sequence reads) and 93% (*SETBP1* mutation; 22395 total sequence reads), which were significantly different ($P<0.001$). (e) Comparison of clone sizes based on allelic frequency and heterozygosity between *CBL* and *SETBP1* mutations showed that *CBL* mutation clones were smaller than that with *SETBP1* mutation in all tested cases (n=6). Paired statistical analysis confirmed significant difference between *CBL* and *SETBP1* mutation clone size. An arrow indicates the case presented in (d). (f) Remarkably, most of the *SETBP1* mutations examined (17/19) showed comparable or higher allele frequencies compared to other coexisting mutations, suggesting that these *SETBP1* mutations seemed to rapidly take over the dominant tumor population, even though many of them were thought to be acquired upon/during leukemic evolution.



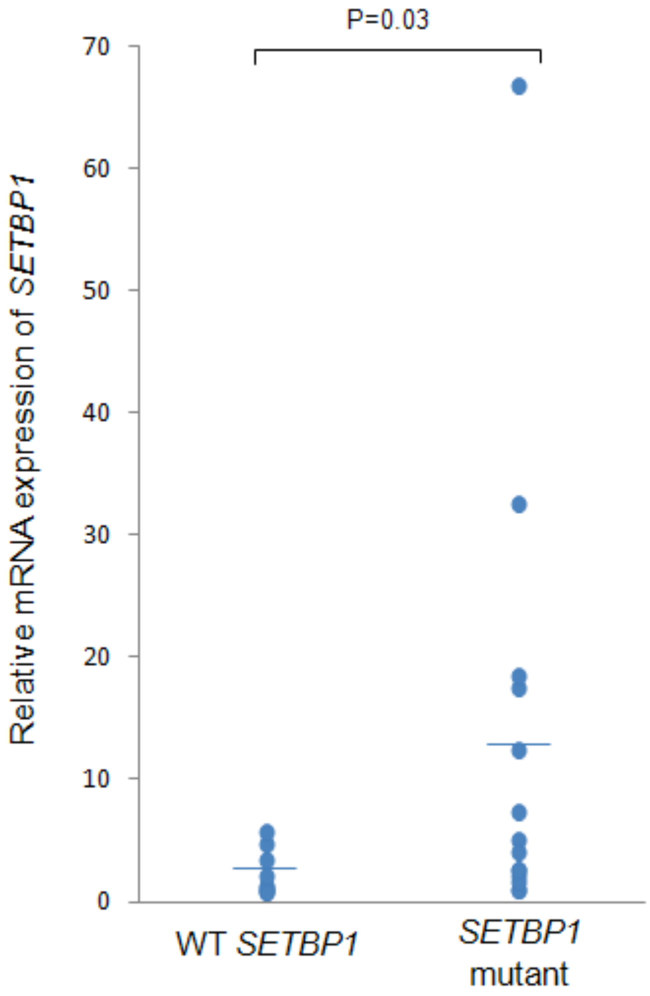
Supplementary Figure 6. Analysis of concomitant mutations in the cases with *SETBP1* mutation. Individual CFU-GMs were examined after culturing bone marrow mononuclear cells in semisolid media for 12 days in 2 cases with *SETBP1* mutation. We confirmed mutations in *SETBP1* as well as concomitant mutations by Sanger sequencing. (a) *SETBP1* Ile871Thr mutations were detected in 85% of examined colonies, while *CBL* frameshift mutations (at Gln409fs c.1227_1227del) were observed in the part (64%) of such colonies with *SETBP1* mutations. No colony represented the combination with WT *SETBP1* and mutant *CBL*, indicating that *CBL* mutation was acquired in the subclone with *SETBP1* mutation. (b) *ASXL1* frameshift mutations (at Arg634fs c.1900_1901del) were detected in main clone (76% of all colonies), and *SETBP1* p.Gly870Ser were observed in subclone with an *ASXL1* mutation (35% of *ASXL1*-mutated colonies).



Supplementary Figure 7. Absence of direct interaction between Setbp1 and CBL proteins. Immunoprecipitates prepared using control IgG or anti-FLAG L5 agarose beads (BioLegend) were analyzed by Western blotting analysis using antibodies specific for Setbp1 and HA tag. Whole-cell extracts from untransfected 293 T cells and 293T cells co-transfected with expression constructs of *Setbp1* and *CBL* mutations (encoding p.Asp868Asn and p.Gln367Pro) were included as controls. Immunoprecipitation was performed using Universal Co-IP Kit (Active Motif) from whole-cell extracts prepared from 293T cells at 48 hours after transfection with indicated combinations of FLAG-tagged mutant Setbp1 and HA-tagged wild-type and mutant *CBL* expression constructs.

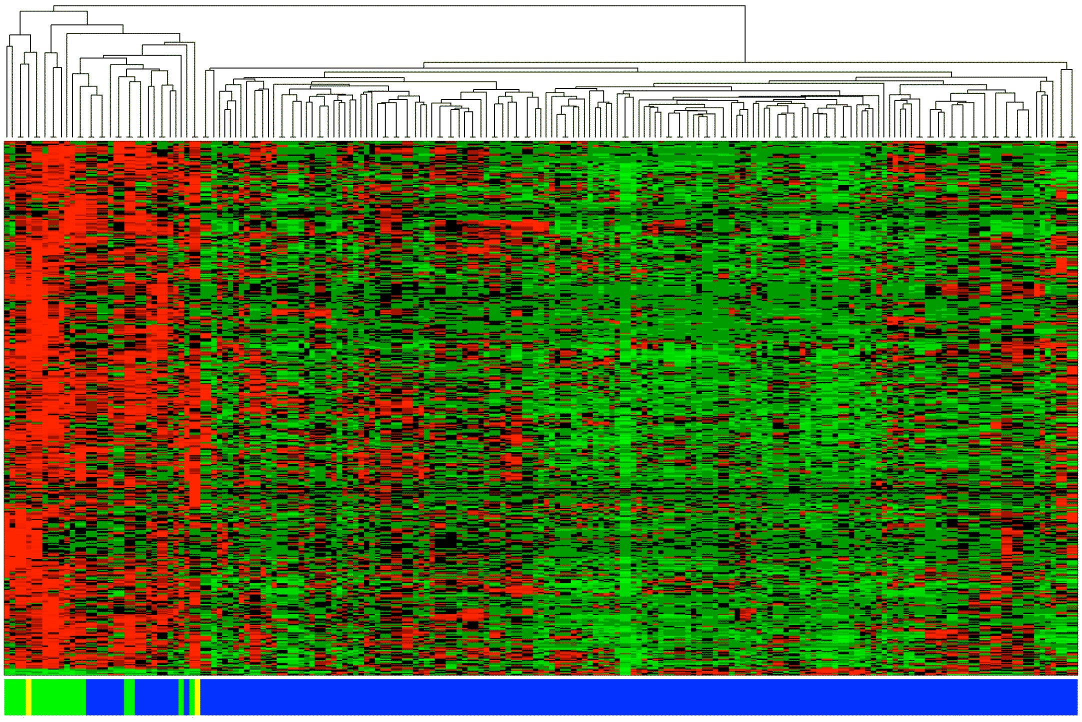


Supplementary Figure 8. Relative expression of *SETBP1* in hematopoietic cells.
SETBP1 mRNA expression in various fractions of hematopoietic cells were extracted from GeneAtlas U133A expression array results posted in BioGPS (http://biogps.org/).



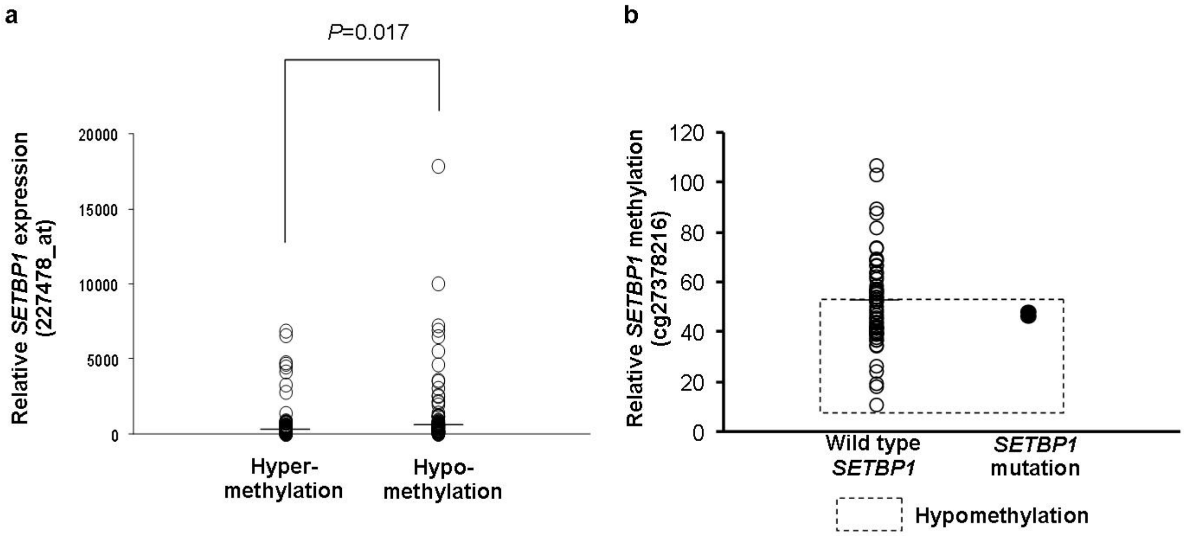
Supplementary Figure 9. mRNA expressions of *SETBP1* in bone marrow mononuclear cells.

mRNA expressions of *SETBP1* were assessed by quantitative real time PCR in myeloid malignancy cases with wild type *SETBP1* (N=9) and with *SETBP1* mutations (N=14). Mean of relative mRNA expression (horizontal bars in each group) was significantly higher in the group with *SETBP1* mutation than with WT *SETBP1* (P=0.03).

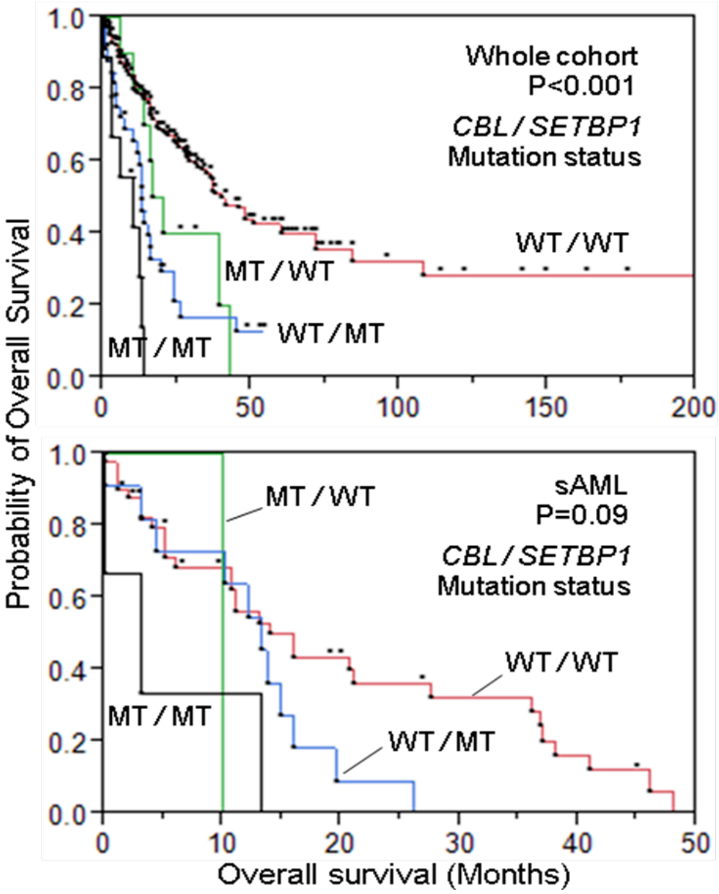


Supplementary Figure 10. Gene expression profiling associated with *SETBP1* mutation.

Expression array results were obtained from TCGA data portal (http://tcga-data.nci.nih.gov, LAML dataset). Samples were divided into two groups; high expresser cases were selected as top 10th percentile of *SETBP1* relative expression values (N=20) and remaining patients with WT *SETBP1* were assigned to normal/lower *SETBP1* expressers. Statistical significance between level of expression in high vs normal/low group was assessed using Student t-Test (p<0.05, Bonferroni adjusted, N=488). Cases were hierarchically clustered using complete Euclidean distance between patients. The color of grids represents expression levels, as red and green indicate higher and lower values. Yellow, green and blue colors at the bottom of the figure show the cases with *SETBP1* mutation, higher expression and normal/lower expression of WT *SETBP1*, respectively.

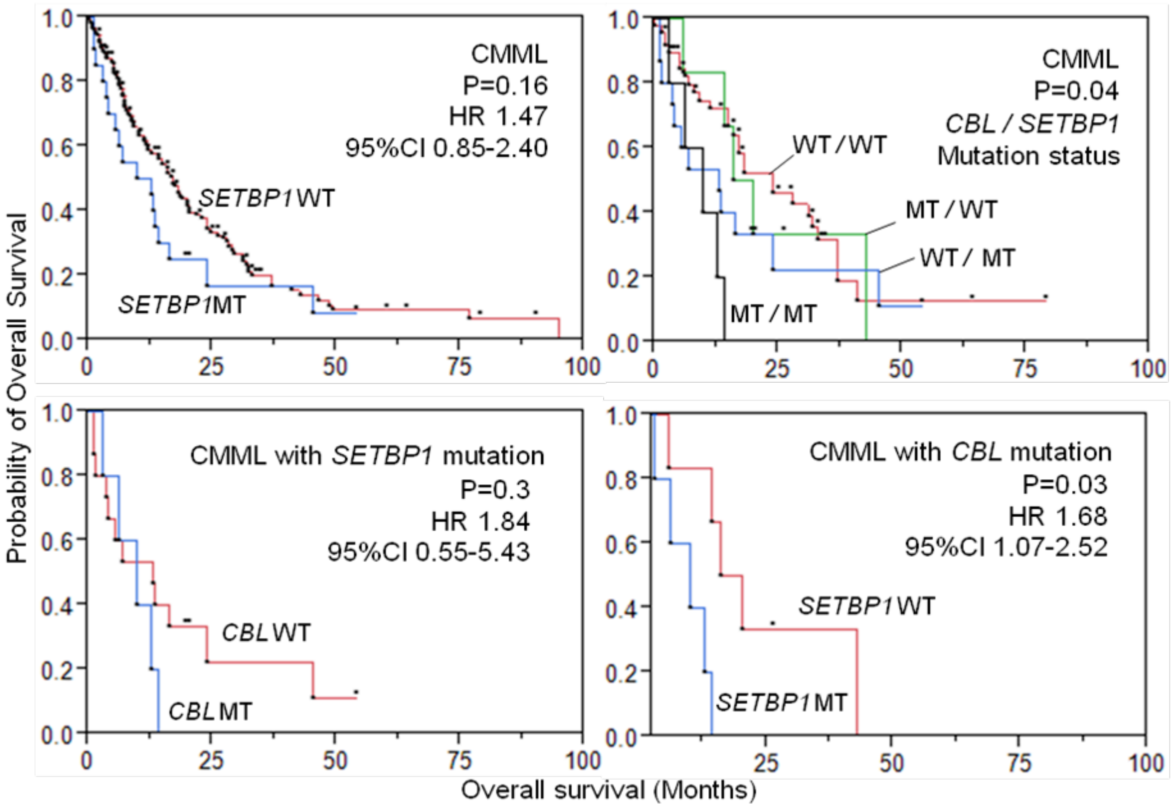


Supplementary Figure 11. Methylation levels associated with *SETBP1* overexpression and mutation.
(a) Methylation array and expression array results were obtained from TCGA database (http://cancergenome.nih.gov/). The values of methylation on a *SETBP1* CpG site (cg27378216) in AML (N=191) were dichotomized into hyper- and hypo-methylation groups by the median value. Statistical significance between levels of gene expression in hyper-/hypo-methylation groups was assessed using Wilcoxon test. The levels of *SETBP1* expression in the cases with hypo-methylation were significantly lower than in the hyper-methylation group (*P*=0.017). The bars indicate mean values of relative *SETBP1* expression. (b) Methylation array data of the independent cases with MDS, MDS/MPN and AML (N=63) on the identical probe demonstrated that methylation levels in the cases with *SETBP1* mutations (CMML and sAML; black) were lower than mean value of WT cases (white). The bar indicates the mean value of methylation levels in WT.



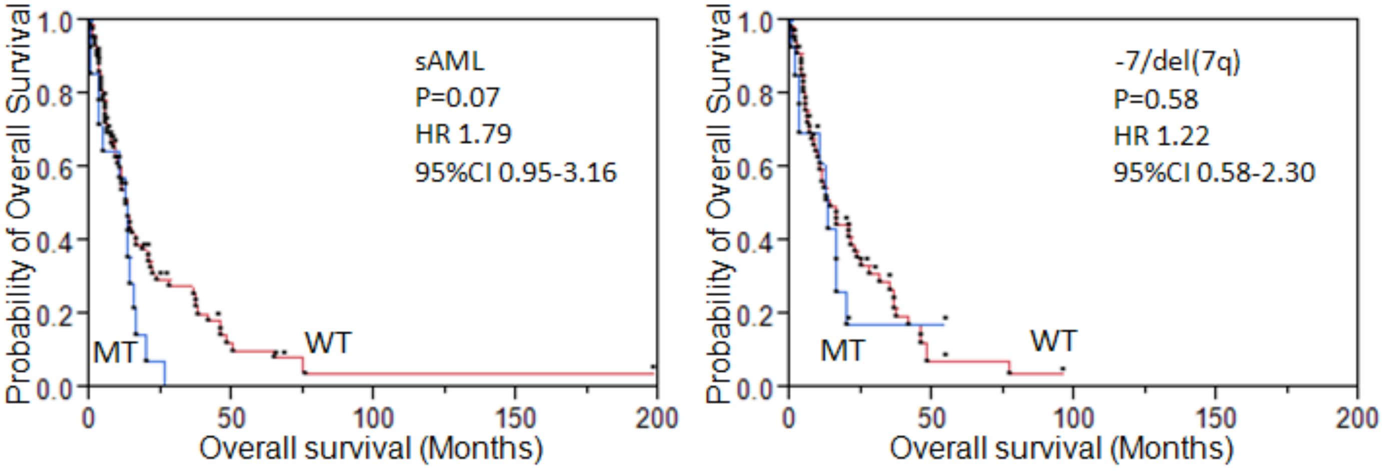
Supplementary Figure 12. Impact of *SETBP1* and *CBL* mutational status on overall survival in the whole cohort and sAML cohort.

Comparisons (overall survival analyses) in the cohorts of all cases and sAML cases between 4 groups with *SETBP1*^{WT}/*CBL*^{WT}, *SETBP1*^{WT}/*CBL*$^{mutation(mut)}$, *SETBP1*^{mut}/*CBL*^{WT} and *SETBP1*^{mut}/*CBL*^{mut}. In whole cohort, a statistically significant difference was detected (P<0.001), while in sAML cohort, there was no significant difference (P=0.09). Dots indicate events and censors.

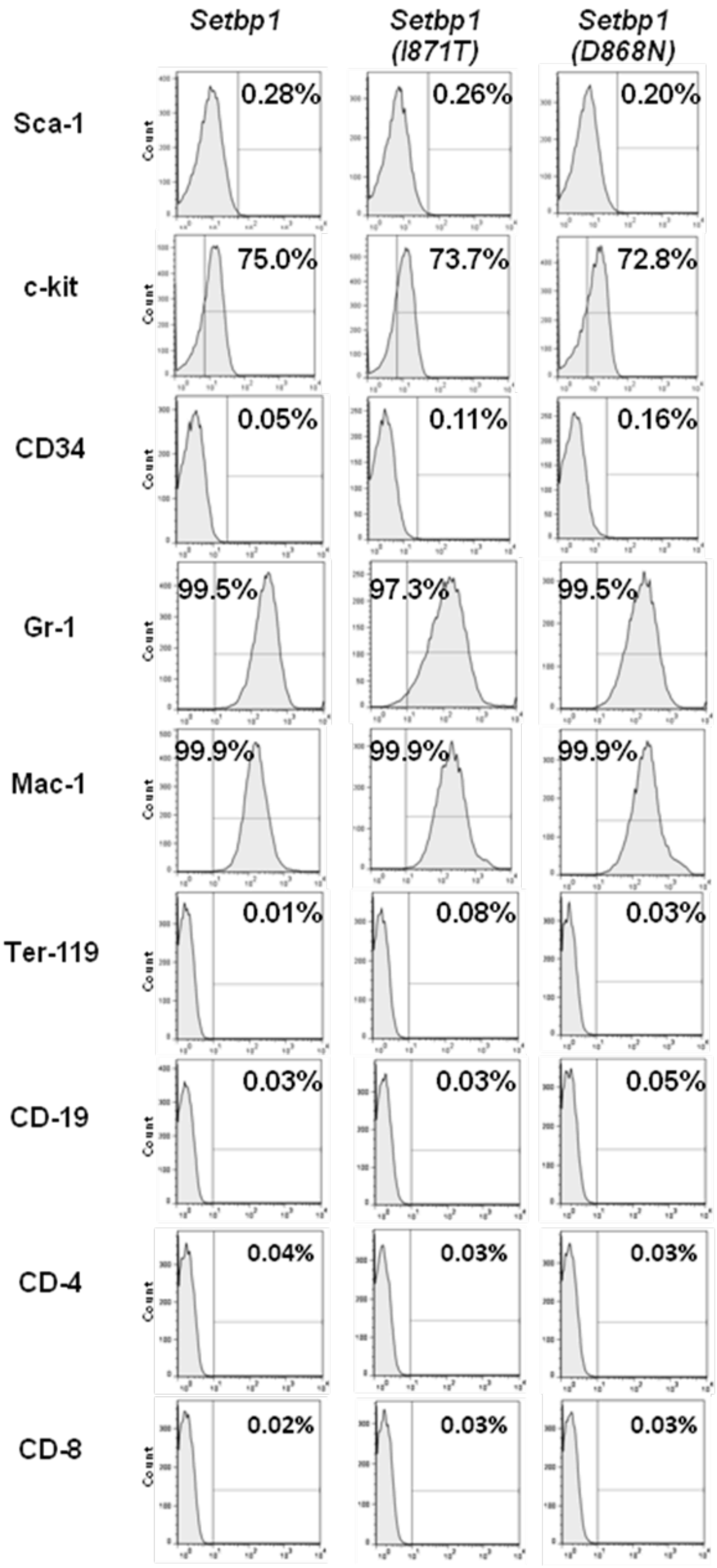


Supplementary Figure 13. Overall survival analysis in the CMML cohort.

All four panels represent comparisons (overall survival analyses) in the CMML cohort. While the upper left panel shows no significant difference between the cases with *SETBP1* wild type (WT) and mutation (MT), the upper right panel displays a statistically significant difference among 4 groups with *SETBP1*^{WT}/*CBL*^{WT}, *SETBP1*^{WT}/*CBL*$^{mutation(mut)}$, *SETBP1*^{mut}/*CBL*^{WT} and *SETBP1*^{mut}/*CBL*^{mut}. In the lower left, the analysis of isolated CMML cases with *SETBP1* mutation represents no survival impact of *CBL* mutation status, however, in the lower right, survival curves of CMML with *CBL* mutation demonstrate a statistically significant difference between the cases with *SETBP1* mutation (MT) and wild type (WT). Dots indicate events and censors.

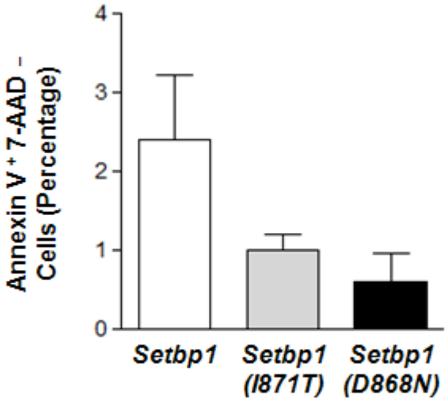


Supplementary Figure 14. Overall survival analysis in subgroups of myeloid malignancies. Comparisons (overall survival analyses) in the cohorts of sAML and -7/del(7q) between *SETBP1* mutations (MT) and wild type (WT). There was no significant difference of overall survival between MT and WT. Dots indicate events and censors.


Setbp1
Setbp1 (I871T)
Setbp1 (D868N)
Sca-1
0.28%
0.26%
0.20%
c-kit
75.0%
73.7%
72.8%
CD34
0.05%
0.11%
0.16%
Gr-1
99.5%
97.3%
99.5%
Mac-1
99.9%
99.9%
99.9%
Ter-119
0.01%
0.08%
0.03%
CD-19
0.03%
0.03%
0.05%
CD-4
0.04%
0.03%
0.03%
CD-8
0.02%
0.03%
0.03%
Count

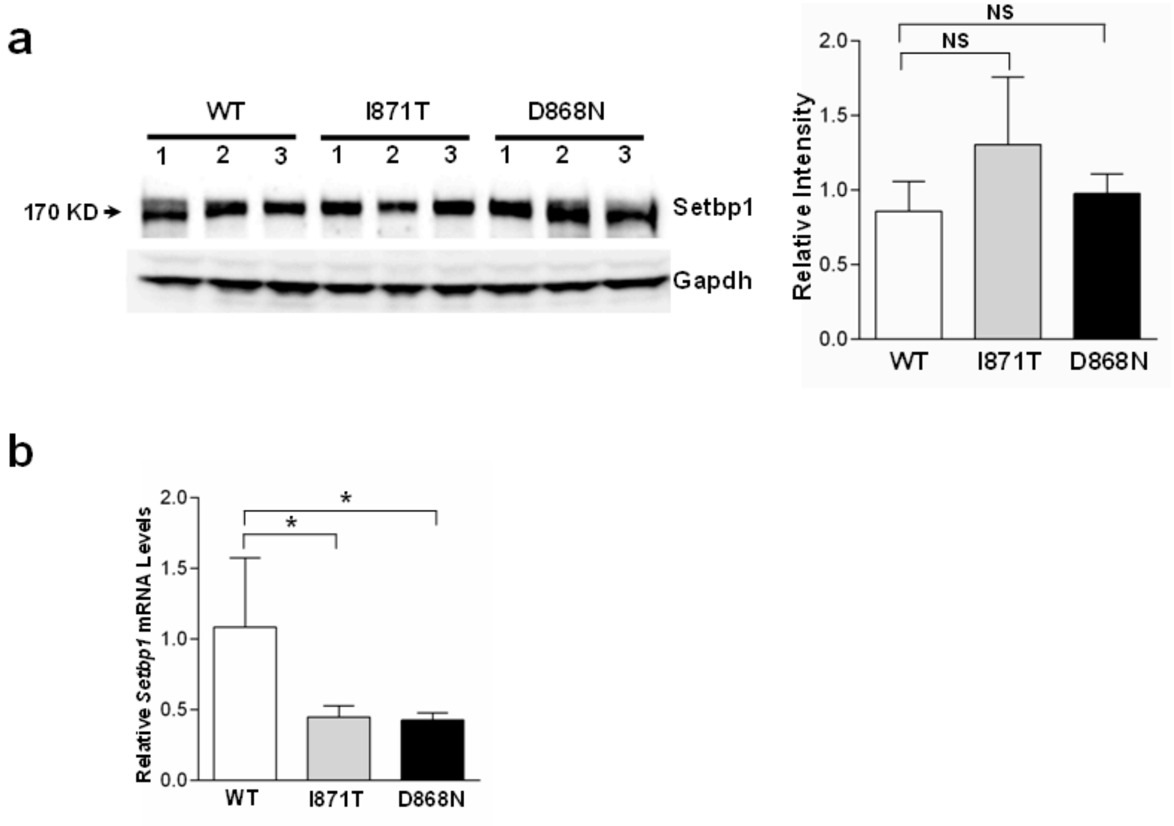
Supplementary Figure 15. Myeloid progenitors immortalized by wild type (WT) and mutant *Setbp1* share similar marker expression profiles.

FACS analysis of indicated marker expression by typical murine myeloid progenitors immortalized by WT and mutant *Setbp1.* Dead cells were excluded by staining with Sytox Blue (Invitrogen). All samples were analyzed on a BD LSRII flow cytometer.



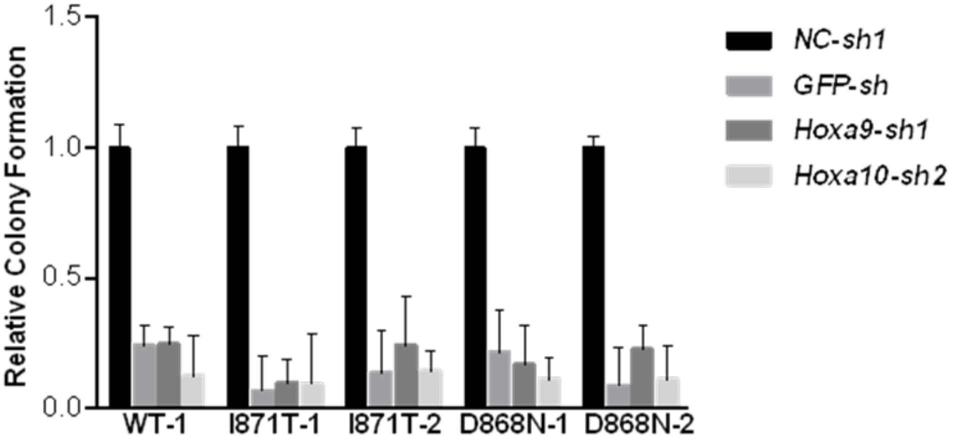
Supplementary Figure 16. Analysis of apoptosis in immortalized myeloid progenitors.

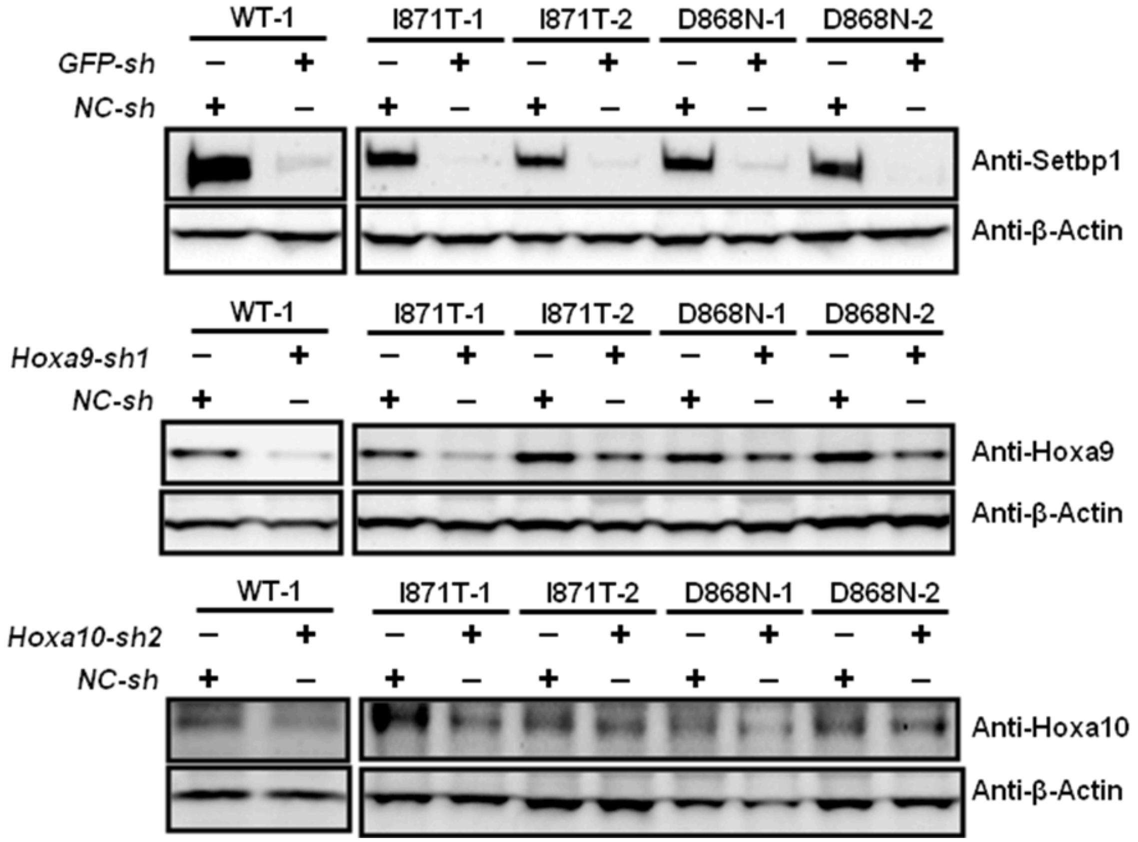
Analysis of apoptotic cells (Annexin V^{+}7-AAD^{-}) in myeloid progenitor populations immortalized by the expression of WT and mutant *Setbp1*. Mean and s.d. of percentage of apoptotic cells from three independently immortalized cell populations for each retroviral expression construct are shown.



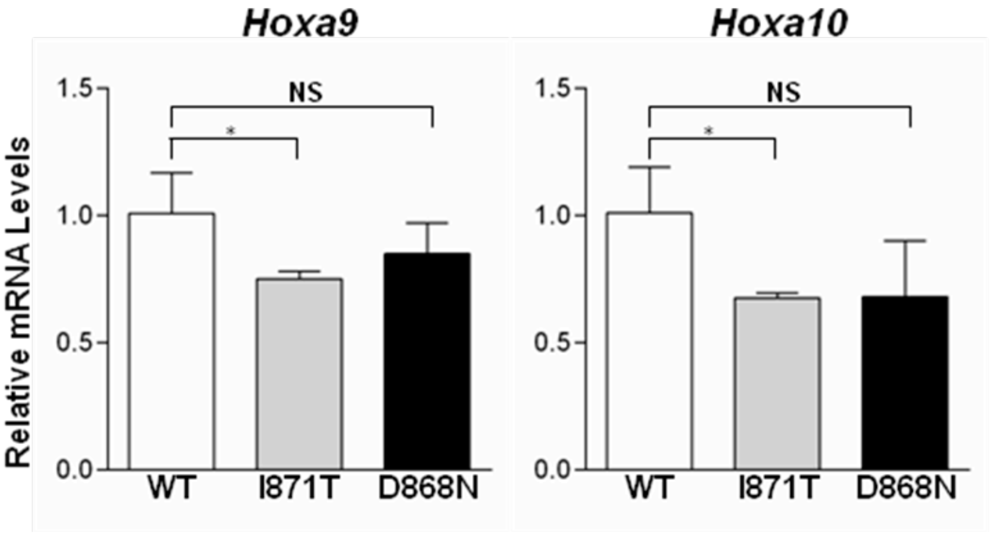
Supplementary Figure 17. Setbp1 protein levels are similar in myeloid progenitor cells immortalized by wild-type (WT) and mutant *Setbp1*.

(a) Left panel, Setbp1 protein expression was assessed by Western blotting analysis in myeloid progenitor populations independently immortalized by WT (WT-1-3) and mutant *Setbp1* (p.Ile871Thr-1-3 and p.Asp868Asn-1-3). Protein bands were visualized by incubation with SuperSignal West chemiluminescent substrate (Pierce). Setbp1 antibody has been described previously.[1] Right panel, quantification of Western blotting analysis shown in left panel. Relative Setbp1 protein levels in each immortalization group of cells after normalization to Gapdh levels (mean with s.d.) are shown. Protein bands were quantified using Quantity One data analysis software (Bio-Rad). NS, not significant. Note that no statistically significant difference was observed among groups. (b) Real-time RT-PCR analysis, using *Setbp1*-specific primers, of total RNA isolated from WT, p.I871T, and p.Asp868Asn groups of immortalized myeloid progenitor cells analyzed in (a). Relative mRNA levels were calculated after normalization to β-actin and represented as mean with s.d. *, $P<0.05$. Note that WT cells have significantly higher *Setbp1* mRNA levels than the other two groups. Given similar Setbp1 protein levels present in the three groups, this difference in transcript levels suggests that WT Setbp1 protein is less stable than mutant Setbp1 proteins.


Relative Colony Formation
0.0
0.5
1.0
1.5
WT-1
I871T-1
I871T-2
D868N-1
D868N-2
NC-sh1
GFP-sh
Hoxa9-sh1
Hoxa10-sh2

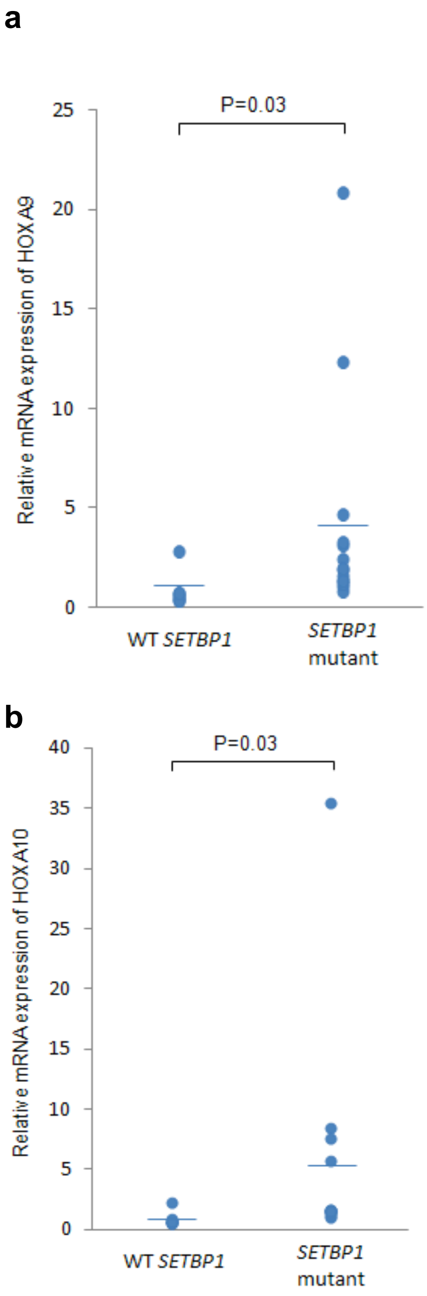

WT-1
I871T-1
I871T-2
D868N-1
D868N-2
GFP-sh – + – + – + – + – +
NC-sh + – + – + – + – + –
Anti-Setbp1
Anti-β-Actin
WT-1
I871T-1
I871T-2
D868N-1
D868N-2
Hoxa9-sh1 – + – + – + – + – +
NC-sh + – + – + – + – + –
Anti-Hoxa9
Anti-β-Actin
WT-1
I871T-1
I871T-2
D868N-1
D868N-2
Hoxa10-sh2 – + – + – + – + – +
NC-sh + – + – + – + – + –
Anti-Hoxa10
Anti-β-Actin

Supplementary Figure 18. *Setbp1*, *Hoxa9*, and *Hoxa10* knockdown in myeloid progenitor cells immortalized with wild-type (WT) and mutant Setbp1 reduces colony formation. Upper panel, mean and s.d. of colony formation potential of indicated immortalized cells in the presence of SCF and IL-3 at 48 hours after infection with shRNAs specific for exogenous *Setbp1* (*GFP-sh*), *Hoxa9* (*Hoxa9-sh1*), *Hoxa10* (*Hoxa10-sh2*) and control shRNA (*NC-sh*); lower panels, representative Western blotting analyses of Setbp1, Hoxa9, Hoxa10, and β-Actin protein in the infected cells of the upper panel at 72 hours after infection. All shRNA constructs and infection procedure were described previously (Oakley, et al.)[1].



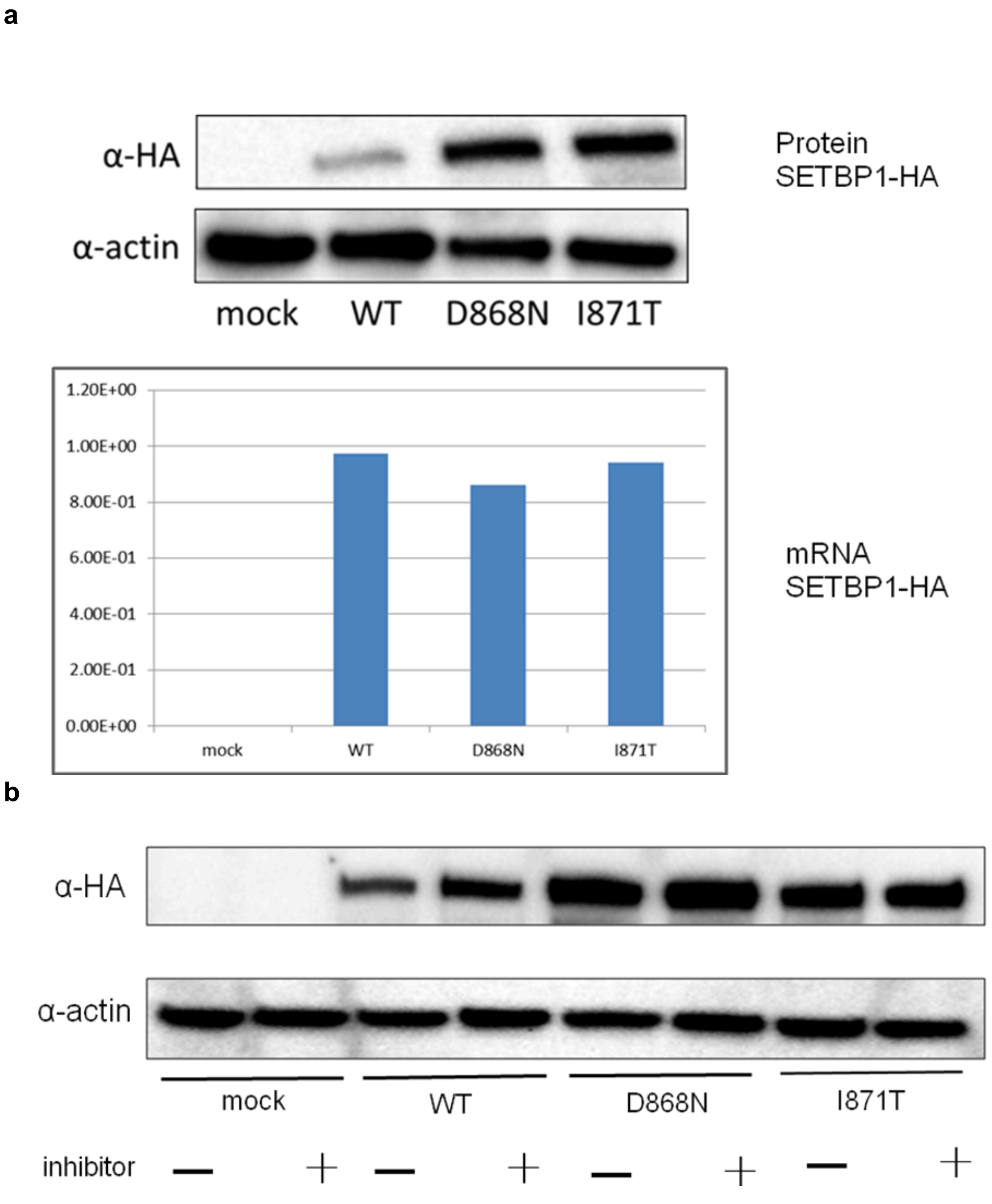
Supplementary Figure 19. Similar levels of *Hoxa9*, and *Hoxa10* mRNA are expressed in myeloid progenitor cells immortalized by wild-type (WT) and mutant *Setbp1*.

Real-time RT-PCR analysis, using gene-specific primers, of total RNA isolated from WT (n=3), p.Ile871Thr (n=3), and p.Asp868Asn (n=3) *Setbp1*-immortalized myeloid progenitor cells. Relative mRNA levels were calculated after normalization to β-actin and represented as mean with s.d. NS, not significant; *, P<0.05.

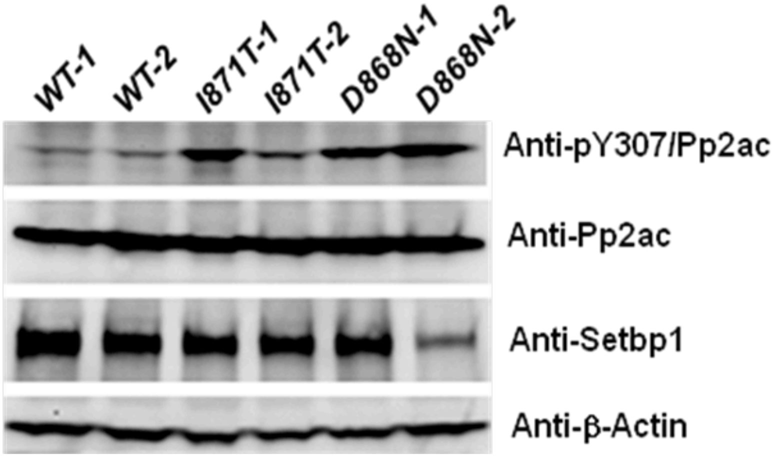


Supplementary Figure 20. mRNA expressions of *HOXA9* and *HOXA10* in bone marrow mononuclear cells.

Relative mRNA expressions of *HOXA9* (a) and *HOXA10* (b) were measured by quantitative real time PCR in myeloid malignancy cases with WT *SETBP1* (N=9) and with *SETBP1* mutations (N=14). In both analyses, there were significant differences between WT and mutant (P=0.03 and P=0.03, respectively). Horizontal bards indicate mean values.



Supplementary Figure 21. SETBP1 protein degradation associated with *SETBP1* mutational status. By Western blotting of Jurkat cells stably transduced with wild-type and mutant *SETBP1* by lentivirus-mediated gene transfer. (a) Mutant SETBP1 protein expressed higher than wild-type protein in spite of similar mRNA levels. (b) Wild-type SETBP1 protein level increased by adding proteasome inhibitor, and this effect was not seen in mutant protein.



Supplementary Figure 22. Myeloid cells immortalized by Setbp1 mutants have increased levels of Pp2ac phosphorylation.

Western blotting analysis using antibodies specific for p.Tyr307 phosphorylated Pp2ac, total Pp2ac, Setbp1 and β-Actin in whole cell extracts prepared from myeloid cells immortalized by wild-type *Setbp1* (WT-1 and -2) or 2 different *Setbp1* mutations (corresponding to p.Ile871Thr-1,-2 and p.Asp868Asn-1,-2).

Supplementary Table 1. Clinical characteristics of individual patients analyzed by next generation whole exome sequencing.

Case number for whole exome sequencing	Diagnosis	*SETBP1* mutation/alteration	Case number in supplementary Table 5
whole exome sequencing #1	sAML	Wild type	N/A
whole exome sequencing #2	sAML	Wild type	N/A
whole exome sequencing #3	CMML-1	Wild type	N/A
whole exome sequencing #4	RAEB-2	c.2602G>A, p.Asp868Asn	#11
whole exome sequencing #5	RCMD	Wild type	N/A
whole exome sequencing #6	PMF	Wild type	N/A
whole exome sequencing #7	CMML-2	Wild type	N/A
whole exome sequencing #8	sAML	Wild type	N/A
whole exome sequencing #9	RAEB-1	Wild type	N/A
whole exome sequencing #10	RARS	Wild type	N/A
whole exome sequencing #11	pAML	Wild type	N/A
whole exome sequencing #12	RARS-T	Wild type	N/A
whole exome sequencing #13	RAEB-2	c.2602G>A, p.Asp868Asn	#13
whole exome sequencing #14	RCMD	Wild type	N/A
whole exome sequencing #15	CMML-1	Wild type	N/A
whole exome sequencing #16	MDS/MPN-U	Wild type	N/A
whole exome sequencing #17	sAML*	Wild type	N/A
whole exome sequencing #18	RAEB-1	Wild type	N/A
whole exome sequencing #19	RCMD	Wild type	N/A
whole exome sequencing #20	MDS/MPN-U	Wild type	N/A

RCMD, refractory cytopenia with multilineage dysplasia; RARS, refractory anemia with ring sideroblasts; MDS/MPN-U, myelodysplastic syndrome/myeloproliferative neoplasms unclassifiable; CMML, chronic myelomonocytic leukemia; RARS-T, RARS associated with marked thrombocytosis; PMF, primary myelofibrosis; AML, acute myeloid leukemia; pAML, primary AML; sAML, secondary AML.

NE; not evaluated, N/A; not applicable.

* Therapy related AML.

Supplementary Table 2. Whole exome sequencing of an individual patient with *SETBP1* mutation (whole exome sequencing case #4).

Gene	Exonic Function	Amino acid Change	Chromosome	Start	End	Reference	Observation
CUX1	nonsynonymous SNV	NM_001202543:c.3920G>A:p.Arg1307*	chr7	101882864	101882864	G	A
TET2	stopgain SNV	NM_001127208:c.4618C>T:p.Gln1540*	chr4	106196285	106196285	C	T
TET2	nonsynonymous SNV	NM_001127208:c.4249G>T:p.Val1417Phe	chr4	106193787	106193787	G	T
SRSF2	nonsynonymous SNV	NM_003016:c.284C>T:p.Pro95Leu	chr17	74732959	74732959	G	A
SETBP1	nonsynonymous SNV	NM_015559:c.2602G>A:p.Asp868Asn	chr18	42531907	42531907	G	A

Supplementary Table 3. Whole exome sequencing of an individual patient with *SETBP1* mutation (whole exome sequencing case #13).

Gene	Exonic Function	Amino acid Change	Chromosome	Start	End	Reference	Observation
CBL	nonsynonymous SNV	NM_005188:c.1139T>C:p.Leu380Pro	chr11	119148919	119148919	T	C
SETBP1	nonsynonymous SNV	NM_015559:c.2602G>A:p.Asp868Asn	chr18	42531907	42531907	G	A
PTPN11	nonsynonymous SNV	NM_002834:c.181G>A:p.Asp61Asn	chr12	112888165	112888165	G	A
ASXL1	frameshift deletion	NM_015338:c.2095delC:p.Pro699fs	chr20	31022610	31022610	C	-

Supplementary Table 4. Whole exome sequencing of individual patients without *SETBP1* mutation.

Whole exome Case #	Gene	Exonic Function	Annotation	Chromosome	Observation	Amino acid change	Start	End
2	*EZH2*	nonsynonymous SNV	NM_001203249	chr7	c.1901G>A	p.Arg634His	148506443	148506443
2	*SGPP2*	nonsynonymous SNV	NM_152386	chr2	c.1016G>A	p.Arg339His	223423433	223423433
2	*TET2*	frameshift insertion	NM_001127208	chr4	c.2196_2197insT	p.Pro732fs	106157295	106157295
2	*TET2*	frameshift deletion	NM_001127208	chr4	c.3851delC	p.Ser1284fs	106180823	106180823
3	*CSF3R*	stopgain SNV	NM_000760	chr1	c.2245C>T	p.Gln749*	36932224	36932224
3	*TET2*	stopgain SNV	NM_001127208	chr4	c.3765C>A	p.Tyr1255*	106164897	106164897
3	*TET2*	stopgain SNV	NM_001127208	chr4	c.1648C>T	p.Arg550*	106156747	106156747
8	*DNMT3A*	frameshift deletion	NM_153759	chr2	c.418delG	p.Gly140fs	25470489	25470489
8	*LUC7L2*	stopgain SNV	NM_016019	chr7	c.79C>T	p.Arg27*	139060825	139060825
8	*U2AF1*	nonsynonymous SNV	NM_001025203	chr21	c.470A>G	p.Gln157Arg	44514777	44514777
10	*SF3B1*	nonsynonymous SNV	NM_012433	chr2	c.2098A>G	p.Lys700Glu	198266834	198266834
11	*PCBP2*	frameshift insertion	NM_001098620	chr12	c.505_506insC	p.Ser169fs	53856277	53856277
11	*PRPF8*	nonsynonymous SNV	NM_006445	chr17	c.3921G>A	p.Met1307Ile	1565301	1565301
11	*RIT1*	nonsynonymous SNV	NM_006912	chr1	c.245T>G	p.Phe82Cys	155874286	155874286
11	*STAG2*	frameshift insertion	NM_006603	chrX	c.3393_3394insTC	p.Arg1131fs	123224540	123224540
12	*SF3B1*	nonsynonymous SNV	NM_012433	chr2	c.1866G>C	p.Glu622Asp	198267491	198267491
14	*RAD21*	stopgain SNV	NM_006265	chr8	c.201T>A	p.Tyr67*	117875442	117875442
14	*TET2*	nonsynonymous SNV	NM_001127208	chr4	c.4138C>T	p.His1380Tyr	106190860	106190860
15	*ASXL1*	frameshift insertion	NM_015338	chr20	c.2253_2254insG	p.Val751fs	31022768	31022768
15	*CBL*	nonsynonymous SNV	NM_005188	chr11	c.1246T>C	p.Cys416Arg	119149238	119149238
15	*PTEN*	nonsynonymous SNV	NM_000314	chr10	c.353A>G	p.His118Arg	89692869	89692869
15	*RUNX1*	frameshift deletion	NM_001122607	chr21	c.393delT	p.Phe131fs	36252888	36252888
15	*SRSF2*	nonsynonymous SNV	NM_003016	chr17	c.284C>A	p.Pro95His	74732959	74732959
15	*TET2*	frameshift deletion	NM_001127208	chr4	c.4541delT	p.Leu1514fs	106196208	106196208
15	*TET2*	nonsynonymous SNV	NM_001127208	chr4	c.3862G>A	p.Gly1288Ser	106180834	106180834
17	*CDH23*	nonsynonymous SNV	NM_022124	chr10	c.4394G>A	p.Gly1465Glu	73499435	73499435
17	*GPR98*	nonsynonymous SNV	NM_032119	chr5	c.6269G>A	p.Arg2090His	89980007	89980007
18	*DNMT3A*	nonsynonymous SNV	NM_153759	chr2	c.2077C>T	p.Arg693Cys	25457243	25457243
19	*TP53*	nonsynonymous SNV	NM_001126116	chr17	c.263A>G	p.Tyr88Cys	7578190	7578190

SNV; single nucleotide variation

Supplementary Table 5. Clinical characteristics of patients with *SETBP1* mutation.

case	Age (years)	Sex	*SETBP1* mutation/alteration	Diagnosis	Karyotyping
1	67	F	c.2602G>A, p.Asp868Asn	sAML	No metaphase
2	81	M	c.2602G>A, p.Asp868Asn	sAML	No metaphase
3	63	M	c.2602G>A, p.Asp868Asn	RAEB	45,XY,-7[20]
4	71	M	c.2602G>A, p.Asp868Asn	sAML	46,XY[6]
5	57	M	c.2608G>A, p.Gly870Ser	CMML2	46,XY[20]
6	71	M	c.2608G>A, p.Gly870Ser	sAML	46,XY,del(7)(q11.2)[10]/46,XY,add(12)(q24.3)[7]/46,XY[3]
7	70	M	c.2602G>A, p.Asp868Asn	CMML2	46,XY,t(7;8)(q22;q24.3)[9]/46,XY[11]
8	77	M	c.2608G>A, p.Gly870Ser	RAEB	47,XY,+11[4]/47,sl,-17,+mar[8]/48,sdl1,+8[2]/46,XY[7]
9	77	M	c.2602G>A, p.Asp868Asn	sAML	46,XY[20]
10	56	M	c.2602G>A, p.Asp868Asn	CMML1	46,XY,del(20)(q11.2q13.3)[20]
11	63	F	c.2602G>A, p.Asp868Asn	RAEB	45,XX,-7[3]/46,XX,del(11)(q23)[8]/47,idem,+11[10]
12	83	M	c.2602G>A, p.Asp868Asn	CMML1	46,XY,del(7q)(q22)[18]/46,XY[2]
13	80	F	c.2602G>A, p.Asp868Asn	RAEB	46,XX,der(21)t(1;21)(q10;p10)[11]/46,XX[9]
14	79	F	c.2608G>A, p.Gly870Ser	CMML1	45,XX,-7[5]/46,XX[15]
15	N/A	M	c.2640C>A, p.Asp880Glu	sAML	46,XY[20]
16	67	M	c.2608G>A, p.Gly870Ser	CML BP	46,XY,t(9;22)(q34;q11.2)[20]
17	34	M	c.2602G>A, p.Asp868Asn	CMML2	45,XY,-7[20]
18	67	M	c.2608G>A, p.Gly870Ser	CMML1	46,XY[20]
19	72	F	c.2608G>A, p.Gly870Ser	sAML	45,XX,-7[20]
20	78	F	c.2602G>A, p.Asp868Asn	CMML2	47,XX,+8[20]
21	79	M	c.2638G>A, p.Asp880Asn	CMML1	47,XY,+21[4]/46,XY[22]
22	66	F	c.2602G>A, p.Asp868Asn	sAML	46,XX[cp20]
23	26	M	c.2612T>C, p.Ile871Thr	sAML	45,XY,-7[20]
24	48	M	c.2612T>C, p.Ile871Thr	sAML	45,XY,-7[20]
25	69	F	c.2612T>C, p.Ile871Thr	pAML	N/A
26	70	M	c.2602G>A, p.Asp868Asn	sAML	45,XY,-7[5]/46,XY[15]
27	61	F	c.2608G>A, p.Gly870Ser	sAML	46,XX,i(17)(q10)[7]/46,XX[18]
28	74	F	c.2602G>T, p.Asp868Tyr	CMML2	N/A
29	77	F	c.2602G>A, p.Asp868Asn	CMML1	No metaphase (-7 in SNP-array)

30	79	M	c.2602G>A, p.Asp868Asn	CMML1	46,XY[20]
31	67	F	c.2602G>A, p.Asp868Asn	CMML1	46,XX[20]
32	64	M	c.2608G>A, p.Gly870Ser	CMML1	46,XY,del(8)(p21p23)[6]/46,XY[14]
33	76	M	c.2602G>A, p.Asp868Asn	CMML2	46,XY,del(7)(q22;q36),t(7;12)(q22;p13)[20]
34	60	M	c.2602G>A, p.Asp868Asn	sAML	46,XY,del(17)(p13)[20]
35	56	M	c.2602G>A, p.Asp868Asn	CMML2	46,XY[24]/45,XY,t(8;10)(p12;p13)[1]
36	77	F	c.2608G>A, p.Gly870Ser	CMML1	46,XX[20]
37	79	M	c.2602G>A, p.Asp868Asn	CMML1	No metaphase
38	65	F	c.2608G>A, p.Gly870Ser	sAML	46,XX,del(21)(q11.2)[20]
39	64	M	c.2612T>C, p.Ile871Thr	sAML	45,XY,-7[20]
40	69	F	c.2608G>A, p.Gly870Ser	sAML	45,XX,-7[20]
41	50	M	c.2602G>A, p.Asp868Asn	RCMD	46,XY[20]
42	55	F	c.2602G>A, p.Asp868Asn	CMML2	45,XX,-7[20]
43	64	F	c.2608G>A, p.Gly870Ser	CMML1	46,XX[20]
44	79	F	c.2612T>C, p.Ile871Thr	RCMD	46,XX[20]
45	N/A	F	c.2608G>A, p.Gly870Ser	5q-syndrome	46,XX,del(5)(q??)[20]
46	N/A	F	c.2608G>A, p.Gly870Ser	PMF	46,XX[20]
47	68	M	c.2602G>A, p.Asp868Asn	CML BP	46,XY,t(9;22)(q34;q11.2)[20]
48	35	M	c.2602G>A, p.Asp868Asn	CMML1	46,XY[20]
49	N/A	F	c.2606G>A, p.Ser869Asn	sAML	N/A
50	73	F	c.2602G>A, p.Asp868Asn	sAML	46,XX[20]
51	64	M	c.2602G>A, p.Asp868Asn	sAML	46,XY[20]
52	77	F	c.2602G>A, p.Asp868Asn	CMML2	46,XX[20]

F; female, M; male

RAEB, refractory anemia with excess blasts; sAML, secondary acute myeloid leukemia;
CMML, chronic myelomonocytic leukemia; CML BP, chronic myelogenous leukemia blast phase.
pAML, primary AML; RCMD, refractory cytopenia with multilineage dysplasia; PMF; primary myelofibrosis,
N/A; not available.

Supplementary Table 6. Diagnosis of enrolled patients (N=727).*

MDS		**288**
	Low risk*	**85**
	RCUD / RCMD / 5q- / MDS-U	**75**
	RARS	**10**
	High risk*	**203**
	RAEB ½	**90**
	Secondary AML	**113**
MDS/MPN		**161**
	CMML	**152**
	MDS/MPN-U	**9**
MPN		**133**
	PV/PMF/ET	**70**
	CML	**63**
AML		
	Primary AML	**145**

* includes 4 cases with therapy related myeloid malignancies.

MDS, myelodysplastic syndromes; RCUD, refractory cytopenia with unilineage dysplasia; RCMD, refractory cytopenia with multilineage dysplasia; 5q-, MDS with isolated del(5q); MDS-U, MDS unclassifiable; RARS, refractory anemia with ring sideroblasts; RAEB, refractory anemia with excess blasts; AML, acute myeloid leukemia; MDS/MPN, MDS/myeloproliferative neoplasms; CMML, chronic myelomonocytic leukemia; PV, polycythemia vera; PMF, primary myelofibrosis; ET, essential thrombocytopenia; CML, chronic myelogenous leukemia.

Supplementary Table 7. *SETBP1* sequencing in myeloid cell lines.

Cell line	*SETBP1* mutation status
HEL	wild type
HL60	wild type
K562	wild type
KASUMI	wild type
KU812	wild type
MEGA2	wild type
MOLM13	wild type
MUTZ8	wild type
NKM1	wild type
SKM1	wild type
TF1	wild type
THP1	wild type
U937	wild type
UT7	wild type
KG1	wild type

Supplementary Table 8. List of genes and their annotation screened by Sanger sequencing.

Genes	Ensembl cDNA sequence	Amino acid	Coding exons	Sequenced exons
SETBP1	ENST00000282030	1596	2-6	2-6
RUNX1	ENST00000300305	480	2-9	2-9
ASXL1	ENST00000375687	1541	1-13	13
SRSF2	ENST00000392485	221	1-2	1
U2AF1	ENST00000291552	240	1-8	2, 6
CBL	ENST00000264033	906	1-16	8, 9
KRAS	ENST00000311936	188	2-5	2
NRAS	ENST00000369535	189	2-5	2
DNMT3A	ENST00000264709	912	2-23	2-23
TET2	ENST00000380013	2002	3-11	3-11
IDH1	ENST00000345146	414	3-10	4
IDH2	ENST00000330062	452	2-11	4
FLT3	ENST00000241453	993	1-24	14, 15, 20
NPM1	ENST00000296930	294	1-11	11

Supplementary Table 9. Concomitant mutational characteristics of myeloid malignancies with or without *SETBP1* mutations.

Mutated genes	Wild-type *SETBP1*	*SETBP1* mutant	P^a
RUNX1 % (no. of tested)	13.2 (159)	14.9 (47)	1
ASXL1 % (no. of tested)	16.9 (183)	35.6 (45)	0.12
SRSF2 % (no. of tested)	12.4 (234)	25.0 (52)	0.29
U2AF1 % (no. of tested)	8.6 (234)	7.7 (52)	1
CBL % (no. of tested)	5.5 (217)	24.5 (49)	**0.002**
KRAS % (no. of tested)	3.1 (129)	4.3 (47)	1
NRAS % (no. of tested)	1.6 (129)	2.1 (47)	1
DNMT3A % (no. of tested)	7.4 (175)	14.3 (42)	1
TET2 % (no. of tested)	24.4 (226)	14.3 (49)	1
IDH1/2 % (no. of tested)	2.7 (224)	4.2 (48)	1

a A Fisher's exact test was used to determine the *P* values. *P* values in multiple comparisons were evaluated by Bonferroni correction and statistically significant p values were indicated with bold font.

Supplementary Table 10a. Comparison of gene expression profiles between cases with activated *SETBP1* (high expression and mutation) and *SETBP1* lower expression.

Gene	ID	P-value	Bonferroni correction	Median (SETBP1 higher N=20)	Median (SETBP1 lower N=175)	SETBP1 mutant 1	SETBP1 mutant 2
SETBP1	227478_at	4.24764E-52	2.74452E-47	6548.612	361.284	4636.983	7241.875
SETBP1	205933_at	7.43583E-52	4.80452E-47	4733.851	285.7097	3213.413	6066.858
SETBP1	239544_at	9.98619E-42	6.45238E-37	2426.1645	317.3	1464.423	2808.191
SETBP1	234081_at	1.50558E-36	9.72798E-32	1176.07	200.3678	857.8883	1540.155
SETBP1	242901_at	5.89482E-36	3.80882E-31	1403.6335	201.2318	946.9578	1462.484
hopx	211597_s_at	8.71226E-24	5.62925E-19	35075.325	4334.313	14322.86	37723.21
sdk2	242064_at	1.96613E-23	1.27038E-18	4906.8825	501.5	6206.753	7408.785
C3orf50	234101_at	8.07924E-22	5.22024E-17	708.0427	167.6234	1516.864	1381.74
Pacsin1	227053_at	1.38882E-21	8.97357E-17	2115.3155	198.3	3138.909	377.7048
Gnai1	227692_at	1.92699E-21	1.24509E-16	8912.378	1606.9	4750.123	8868.102
tpm2	204083_s_at	3.28038E-21	2.11955E-16	2297.823	888.4855	1337.42	2194.81
C5orf56	230405_at	4.60273E-21	2.97396E-16	7354.6375	2045.9	7011.277	7697.998
SDK2	234073_at	1.2856E-20	8.30662E-16	1392.3165	278.8	2653.982	1991.224
SETBP1	236317_at	1.30384E-20	8.42449E-16	840.5025	226.3	717.1791	959.454
CARD11	243154_at	1.94368E-20	1.25587E-15	2032.695	603.0085	6136.117	1246.337
PPP1R16B	41577_at	8.90915E-20	5.75647E-15	3143.807	903.3415	3234.174	1222.571
C3orf50	1558411_at	1.31139E-19	8.47326E-15	3017.391	93.27065	5104.375	5444.332
KIAA1462	213316_at	2.70486E-19	1.74769E-14	1109.5741	143.7947	3900.839	1465.194
FLJ21443	233235_x_at	3.20869E-19	2.07323E-14	579.8981	87.0378	569.9943	781.7898
BCL11A	219498_s_at	1.24452E-18	8.04122E-14	12428.305	4882.4	15191.14	10790.76
BCL11A	222891_s_at	2.13906E-18	1.38211E-13	39166.18	14332.61	48026.52	36734.02
TCF4	212386_at	1.04004E-17	6.71999E-13	31485.74	8550.691	42977.59	13077.29
TCF4	212382_at	1.66712E-17	1.07717E-12	5513.164	1876.4	10684.52	2914.787
Gnai1	209576_at	3.21335E-17	2.07624E-12	7763.7745	1135.419	2350.505	4113.144
TCF4	222146_s_at	3.80234E-17	2.45681E-12	8222.6675	2498.8	12865.36	2206.889
TCF4	212387_at	6.59807E-17	4.26321E-12	10387.921	3414.4	16826.18	4823.588
HMGA2	208025_s_at	1.40995E-16	9.11008E-12	1910.1355	181.27	2878.35	2542.064
FMNL3	230640_at	1.72625E-16	1.11538E-11	672.4363	233.9072	774.9528	630.415
DNTT	1566363_at	2.21394E-16	1.43049E-11	85430.805	1187.5	103596	376.1903
TCF4	203753_at	2.46294E-16	1.59138E-11	13403.04	3900.4	16594.23	4722.487
FAM30A	220377_at	2.46837E-16	1.59489E-11	16589.76	3251.696	11033.2	12661.89
BCL11A	219497_s_at	3.18311E-16	2.0567E-11	24128.825	10304.18	29857.54	21174.87
GBP4	235175_at	4.40102E-16	2.84363E-11	2858.312	916.2	1729.073	5130.685
PPP1R16B	243771_at	5.22846E-16	3.37826E-11	1161.153	271.2	1349.659	1012.243
cobL	213050_at	5.92293E-16	3.82698E-11	223.66045	38.79073	4518.953	630.8448
BCL11A	1559078_at	1.58485E-15	1.02402E-10	10344.05	5202.7	24084.03	8864.822
PPP1R16B	212750_at	2.14054E-15	1.38307E-10	2235.744	844.6588	3364.438	1316.35
TCF4	212385_at	2.28401E-15	1.47577E-10	4204.7775	1651.969	10568.32	1793.049
NRIP1	202599_s_at	2.35958E-15	1.5246E-10	27198.855	8347.368	6123.393	75676.27
TCF4	213891_s_at	2.83332E-15	1.83069E-10	19520.28	5390.227	25775.6	8292.616
ATP10A	214255_at	2.89304E-15	1.86928E-10	4804.3015	1094.1	3661.393	4744.58
DNTT	1566362_at	5.43205E-15	3.50981E-10	3613.625	238.8	9847.621	127.1477
DNTT	210487_at	6.98692E-15	4.51446E-10	25338.525	217.1	46913.91	72.32637
Pfkfb2	226733_at	7.8227E-15	5.05448E-10	1689.653	578.3586	1937.122	851.749
KIAA1462	231841_s_at	8.67095E-15	5.60256E-10	504.5843	18.6	2072.045	680.7219
NRIP1	202600_s_at	1.03711E-14	6.7011E-10	37155.125	10139.15	8107.348	85631.81
rasd1	223467_at	1.55885E-14	1.00722E-09	3071.54	597.7	14801.37	228.3182
PRKD2	209282_at	1.7355E-14	1.12136E-09	4370.675	2191.4	4622.849	5161.89
Tcf7l2	236216_at	1.91893E-14	1.23988E-09	1137.0515	259.8587	1117.173	1729.938
foxo1	202724_s_at	2.25888E-14	1.45953E-09	3017.266	1202.157	5126.283	7223.057
TCF4	215164_at	2.40755E-14	1.55559E-09	2090.5565	551.6531	3968.74	822.6821
TCF4	228837_at	2.81736E-14	1.82038E-09	1163.214	356.7	3081.411	505.448
PRKD2	38269_at	3.2155E-14	2.07763E-09	8928.002	4212.167	10455.3	10991.62
STRBP	229513_at	3.28451E-14	2.12222E-09	6189.39	2488.921	11781.82	3978.828
GNG11	204115_at	3.90487E-14	2.52305E-09	5450.152	516.149	4304.874	325.9366
C5orf56	232253_at	4.21282E-14	2.72203E-09	5554.729	2239.954	6606.38	5554.729
C5orf56	1560128_x_at	5.73176E-14	3.70346E-09	5868.1645	2324.341	6626.744	6057.896
HMGA2	1567224_at	6.32317E-14	4.08559E-09	710.02685	159.936	1640.716	719.3384
JAKMIP2	205888_s_at	6.38624E-14	4.12634E-09	1292.324	349.6975	1317.631	1260.944
Fam129c	230983_at	6.39087E-14	4.12933E-09	1726.65	691.5782	8700.398	603.9232
glcci1	227525_at	7.24393E-14	4.68052E-09	8487.35	3210.8	9412.415	18957.62
SETBP1	240925_at	7.34119E-14	4.74337E-09	716.62415	287.6634	610.3551	770.1945
SMAD1	220450_at	7.97055E-14	5.15001E-09	883.8603	307.1	687.6315	718.6006
EVL	217838_s_at	1.10876E-13	7.164E-09	7760.5945	3090.8	5964.92	13007.14

MLLT3	1569652_at	1.21714E-13	7.86428E-09	3138.6405	843.0154	2040.222	4957.047
EVL	227232_at	1.26602E-13	8.18013E-09	3367.124	1633.041	4060.811	5921.8
SIPA1L1	202254_at	1.33072E-13	8.59818E-09	869.7167	464.6155	1030.668	2209.755
CHRDL1	209763_at	1.43907E-13	9.29827E-09	2634.323	308.2934	9688.823	1252.413
TNFRSF21	218856_at	1.6657E-13	1.07626E-08	4831.343	1019.712	5031.771	1907.734
BCL11A	210347_s_at	2.84136E-13	1.83589E-08	8127.6865	4225.916	11401.96	4188.416
IRF7	208436_s_at	3.33078E-13	2.15211E-08	6510.19	3371.827	12050.77	4476.307
Akt3	240568_at	3.50687E-13	2.2659E-08	1234.281	270.1	1071.31	1304.587
OSBPL3	209627_s_at	4.05881E-13	2.62252E-08	5276.254	1941.5	3259.768	10970.45
Fam171b	227370_at	5.18979E-13	3.35328E-08	1675.359	273.1929	1672.61	1675.359
Rbpms	209487_at	5.92617E-13	3.82908E-08	7247.6305	525.6	8029.771	4591.314
TNFRSF21	214581_x_at	7.21067E-13	4.65903E-08	1287.667	383.3771	2474.975	669.1055
Gna12	242514_at	7.41439E-13	4.79066E-08	1763.471	847.3047	2175.619	1250.13
SLC37A3	1569666_s_at	1.17133E-12	7.56834E-08	1100.764	378.1601	1083.324	1358.657
DLG3	212727_at	1.24199E-12	8.02487E-08	633.1099	206.1426	885.2161	1028.006
MLLT3	204918_s_at	1.75719E-12	1.13537E-07	2065.1115	616.8	1529.861	2574.109
Gna12	221737_at	1.91537E-12	1.23758E-07	1970.917	1183.866	2848.716	1440.945
C18orf8	221190_s_at	2.14E-12	1.38272E-07	4630.662	3323.6	4419.657	4254.427
Spib	205861_at	2.19187E-12	1.41624E-07	906.8437	461.0276	5570.792	251.3916
glcci1	225706_at	2.41662E-12	1.56145E-07	9891.75	3597.131	11172.64	17815.2
MLLT3	204917_s_at	2.50358E-12	1.61764E-07	2632.048	765.6987	2318.845	4508.693
Rbpms	241897_at	3.04562E-12	1.96786E-07	4406.825	497.7664	4454.44	4406.825
KIAA0125	206478_at	3.64503E-12	2.35516E-07	31420.105	5396.3	21607.8	17629.57
SYNE1	209447_at	3.87331E-12	2.50266E-07	3488.298	1499.5	2965.431	3488.298
SPON1	213994_s_at	3.96227E-12	2.56014E-07	1043.33305	119.4	2022.867	209.3076
Ldoc1	204454_at	5.59577E-12	3.61559E-07	1677.748	371	2030.208	1513.264
FUCA2	223120_at	5.71298E-12	3.69133E-07	1109.817	2651.091	1497.318	592.6191
PPP1R16B	1563473_at	6.08159E-12	3.9295E-07	7815.017	1882.5	3690.969	4187.259
LRRN2	205154_at	6.61616E-12	4.2749E-07	676.1514	113.216	1134.014	865.1028
gng7	228831_s_at	6.86266E-12	4.43417E-07	4558.129	1755.39	7958.043	5992.932
Spib	232739_at	6.89927E-12	4.45782E-07	356.8595	187.7863	1320.554	119.8602
SMAD1	208015_at	9.39678E-12	6.07154E-07	1171.664	610	1359.004	1171.664
cobL	1552496_a_at	9.52614E-12	6.15513E-07	97.85473	17.1	897.6827	14.50244
C5orf23	219054_at	1.02495E-11	6.62254E-07	21458.95	4323.1	7858.883	24553.15
TCF4	244480_at	1.09282E-11	7.06107E-07	726.2126	280.2284	747.192	397.8195
MTMR1	216095_x_at	1.21316E-11	7.83857E-07	6431.6535	4475.114	6562.836	5770.119
GZMB	210164_at	1.26398E-11	8.16695E-07	4245.4775	1070.149	7271.232	1057.192
Rbpms	209488_s_at	1.3943E-11	9.00897E-07	3991.758	401.6	4316.202	2637.906
TTC28	213058_at	1.398E-11	9.03291E-07	2933.291	1318.024	6504.276	1487.023
ARPC5L	226914_at	1.47274E-11	9.51582E-07	4023.55	2468.503	4192.137	3458.58
WWTR1	202133_at	1.52969E-11	9.88379E-07	369.1271	85.1	925.5596	2520.237
SPTBN1	212071_s_at	1.57723E-11	1.0191E-06	27150.305	11463.26	27837.06	35633.43
OPTN	202073_at	1.68588E-11	1.0893E-06	2733.34	658.4	2515.973	3330.893
tpm2	229911_at	1.85516E-11	1.19867E-06	146.21365	68.0223	232.8234	114.4999
C10orf10	209183_s_at	1.92761E-11	1.24549E-06	1519.5915	572.9	2396.272	1455.024
RIMKLB	229344_x_at	2.03238E-11	1.31318E-06	6128.6745	3342.1	4320.784	11520.52
Rbpms	207837_at	2.59259E-11	1.67515E-06	454.4621	142.8	251.4723	454.4621
tab2	212184_s_at	2.62839E-11	1.69828E-06	8899.9165	5740.426	5475.058	8820.133
CLEC4C	1552552_s_at	2.7985E-11	1.8082E-06	344.73655	174.8	1384.915	5.10475
Tcf7l2	216035_x_at	2.85598E-11	1.84533E-06	5456.423	2581.244	6009.965	5456.423
BAALC	218899_s_at	2.87457E-11	1.85735E-06	10481.0215	1042.5	13727.18	3064.515
MST1R	205455_at	2.91165E-11	1.88131E-06	491.8137	234.6312	743.7767	401.8979
tab2	1565889_at	2.99312E-11	1.93395E-06	2506.7835	1345.2	2608.327	2475.667
SH3BP4	222258_s_at	2.99634E-11	1.93602E-06	1929.6105	365.4827	2586.482	2532.917
LILRA4	210313_at	3.42701E-11	2.21429E-06	429.4768	264.3541	1712.929	79.90863
TNRC6B	1558142_at	4.16506E-11	2.69117E-06	12049.81	7465	9969.724	12049.81
Bach2	221234_s_at	4.627E-11	2.98964E-06	1576.895	496.16	5336.834	2058.531
MTMR1	213511_s_at	4.67901E-11	3.02325E-06	5837.9965	4180.06	6396.524	4689.628
ephb1	230425_at	4.72542E-11	3.05323E-06	197.0411	64.58678	1000.887	197.0411
GBP4	235574_at	5.59026E-11	3.61203E-06	1268.194	397.8	725.3029	999.0574
BAALC	222780_s_at	5.80797E-11	3.7527E-06	8483.259	821.0243	11264.08	1825.544
Tcf7l2	236094_at	6.282E-11	4.05899E-06	2258.102	789.5847	1524.44	3737.96
LOC283270	1556319_at	6.79498E-11	4.39044E-06	996.32955	646.7	836.4403	1151.355
ETS1	224833_at	6.8177E-11	4.40512E-06	15471.56	5383.046	14295.76	15798.81
PPM1J	229484_at	7.1551E-11	4.62313E-06	355.6619	161.1	420.9165	383.6357
pAG1	227354_at	7.3525E-11	4.75067E-06	6334.78	2971.9	9214.386	4518.123
LOC143286	1565644_at	7.78171E-11	5.028E-06	451.4683	214.7775	522.2742	461.7799
KIAA1462	231842_at	8.6628E-11	5.59729E-06	465.04065	97.2	1968.543	477.6249
foxo1	202723_s_at	8.72126E-11	5.63507E-06	1156.1995	346.5862	1915.93	1552.216
C13orf18	219471_at	8.86952E-11	5.73086E-06	1631.7015	798.436	8333.64	348.2334
CCDC50	228693_at	1.0036E-10	6.48456E-06	560.2482	462.8344	1994.267	488.1964
TSPYL2	218012_at	1.08456E-10	7.0077E-06	2510.6785	1286.149	2426.36	1473.199

Npas3	244172_at	1.10695E-10	7.15232E-06	2089.18	608	8758.05	168.0745
ZC3H12C	231899_at	1.15852E-10	7.48555E-06	5686.794	1879.397	3858.829	6338.455
HLF	204754_at	1.16473E-10	7.5257E-06	317.6431	47.5	87.7184	1921.332
CCDC50	226713_at	1.18994E-10	7.68858E-06	677.3531	591.1756	2364.537	676.4057
TNRC6B	230779_at	1.22789E-10	7.93379E-06	5338.5485	3199.959	3271.065	6271.468
pAG1	225626_at	1.43748E-10	9.28801E-06	10320.66	4610.2	11619.13	6890.248
OSBPL3	209626_s_at	1.47313E-10	9.51832E-06	3637.05	1587.4	1815.268	7124.505
COBLL1	243039_at	1.4929E-10	9.6461E-06	1548.735	537.1899	1637.481	388.873
KIAA1466	222139_at	1.50627E-10	9.73248E-06	1381.5	664.8577	516.785	773.6312
SLC38A1	218237_s_at	1.5247E-10	9.85156E-06	22265.22	8730.7	17226.23	15348.17
MAML2	235457_at	1.71708E-10	1.10946E-05	3090.306	1364.953	5029.091	2627.015
CYTH4	219183_s_at	1.89391E-10	1.22371E-05	7308.8125	3047.2	8996.578	4341.903
SLC38A1	224579_at	1.90644E-10	1.23181E-05	28156.57	11604.44	24447.13	18974.74
ISG20	204698_at	1.92274E-10	1.24234E-05	4647.6485	929.5	3537.32	1533.713
JAKMIP2	237100_at	1.93553E-10	1.2506E-05	701.1402	321.5949	649.2233	519.4354
NPR3	219789_at	2.1026E-10	1.35855E-05	11547.91	2511.5	3918.858	13887.26
FLNB	208614_s_at	2.21416E-10	1.43063E-05	6746.129	2097.1	7060.003	3705.847
SLC25A30	226782_at	2.34646E-10	1.51612E-05	4482.8495	2826.067	4394.19	3227.096
SMAD1	210993_s_at	2.3639E-10	1.52739E-05	5351.945	2652.45	4798.79	4485.935
herc6	239988_at	2.4046E-10	1.55368E-05	1089.6088	464.3	365.9442	1432.338
BLNK	207655_s_at	2.44476E-10	1.57963E-05	10462.04	1650.9	32896.01	165.1732
TCF4	240321_at	2.57009E-10	1.66061E-05	1326.2	448.8319	2067.14	608.581
MAN1A1	237849_at	2.63133E-10	1.70018E-05	8181.719	3059.826	7255.403	8181.719
DLGAP2	210227_at	2.84071E-10	1.83547E-05	352.8177	99.1	857.6971	145.697
SMAD1	227798_at	2.92918E-10	1.89263E-05	8068.639	3547.199	7616.84	6763.596
notch1	218902_at	2.99757E-10	1.93682E-05	5043.409	2919.3	5822.072	5043.409
FMNL3	227844_at	2.99919E-10	1.93786E-05	938.34805	443.4	765.4563	1206.647
Tcf7l2	212762_s_at	3.39252E-10	2.19201E-05	6960.8255	2205.6	6873.651	7211.316
Hs3st1	205466_s_at	3.42678E-10	2.21415E-05	741.5148	115.6852	2583.639	89.80471
Fam129c	1553369_at	3.65853E-10	2.36389E-05	275.521	69	956.4264	22.35111
SPANXA1	220922_s_at	4.23418E-10	2.73583E-05	123	39.07784	908.9677	38.44744
Tcf7l2	216037_x_at	4.26598E-10	2.75638E-05	4211.469	2422.07	5353.547	4211.469
glcci1	225700_at	4.29626E-10	2.77594E-05	1119.75	532.1161	1154.477	1352.177
SAPS2	202792_s_at	4.38912E-10	2.83595E-05	1922.392	1175.064	1658.525	2683.064
RERE	200940_s_at	4.53923E-10	2.93293E-05	6599.678	4318.995	5306.753	8592.482
C13orf18	44790_s_at	4.68244E-10	3.02546E-05	1864.9515	632.5472	12336.2	16.76657
JAKMIP2	205889_s_at	4.80471E-10	3.10446E-05	801.7969	178.3299	1263.666	801.7969
SPON1	209436_at	5.24171E-10	3.38683E-05	2647.7735	457.7826	3799.835	442.0873
CLEC4C	1555687_a_at	5.26969E-10	3.40491E-05	118.16405	105.3121	878.1563	12.67028
PRKCB	227817_at	5.56072E-10	3.59295E-05	8531.035	5065.3	7550.813	7356.734
stk24	1557316_at	5.68562E-10	3.67365E-05	1344.892	719.6	1388.263	2211.252
PTK2	241387_at	5.81338E-10	3.7562E-05	1273.0375	344.9088	2431.42	172.8458
Tcf7l2	232465_at	5.98889E-10	3.8696E-05	1472.692	666.2	1382.776	2247.946
ZNF154	217242_at	6.00535E-10	3.88024E-05	458.9955	162.3782	218.2753	483.7473
SPON1	213993_at	6.11315E-10	3.94989E-05	528.51255	56.4	808.9249	178.7689
npc1	202679_at	6.11548E-10	3.9514E-05	2660.296	1701.053	3355.202	1884.545
UGCG	224967_at	6.27997E-10	4.05768E-05	4461.628	3222.763	17111.46	3730.279
IL16	209827_s_at	6.38587E-10	4.1261E-05	6628.0275	4158.8	5069.886	4845.077
SNED1	213493_at	6.43224E-10	4.15606E-05	265.54965	53.2	207.3484	1584.421
STRBP	233252_s_at	7.05178E-10	4.55637E-05	3509.833	1888.803	5830.926	3079.685
LOC728743	225909_at	7.05837E-10	4.56062E-05	1387.061	859.8779	1838.952	1438.163
YPEL1	228788_at	7.23985E-10	4.67789E-05	2774.6355	1038.44	2248.417	3445.187
GBP2	242907_at	9.64461E-10	6.23167E-05	4525.334	1901.1	1652.754	4252.522
DGKE	238457_at	1.01639E-09	6.56721E-05	1299.674	639.6445	753.1713	3769.956
TAP2	225973_at	1.03698E-09	6.70024E-05	6405.664	4041	6970.757	6800.362
tlr9	223903_at	1.13205E-09	7.31449E-05	598.91595	537.5	1357.773	477.9331
PPP3CC	32541_at	1.15279E-09	7.44851E-05	2062.559	1258.648	2079.25	1663.873
PCDHGA1	211066_x_at	1.20403E-09	7.77957E-05	2339.403	1189.216	9116.334	4427.388
DTX3	235721_at	1.29746E-09	8.38325E-05	944.5634	264.03	878.0258	7043.124
Tcf7l2	216511_s_at	1.32309E-09	8.5489E-05	4642.97	2022.1	5152.487	4133.453
PPP3CC	207000_s_at	1.40585E-09	9.08363E-05	2167.3755	1332.8	2436.336	1680.415
PCDHGA1	205717_x_at	1.42858E-09	9.23051E-05	1399.343	830.7214	6302.753	2874.51
PTK2	239121_at	1.47687E-09	9.54248E-05	587.9573	233.2676	1302.044	147.2663
UGCG	204881_s_at	1.61741E-09	0.000104506	3926.305	3490.1	13105.25	3926.305
CARD11	223514_at	1.82104E-09	0.000117663	1217.7715	323.9	1577.679	1207.668
Rab11fip4	224482_s_at	1.87562E-09	0.00012119	538.829	193.4415	482.758	965.3473
Ptprs	226571_s_at	2.00671E-09	0.00012966	592.7755	234.6327	900.7805	642.3398
STRBP	233251_at	2.12914E-09	0.00013757	1425.5925	722.979	2434.996	1271.156
PPP1R16B	233813_at	2.26891E-09	0.000146601	963.25945	357	613.5356	481.37
Gna12	224681_at	2.28655E-09	0.000147741	6800.061	3289.5	9028.1	3439.561
nog	231798_at	2.43684E-09	0.000157452	3885.992	1227.4	5280.872	18968.48
FLJ46446	1556402_at	2.52482E-09	0.000163136	1016.505	217.8654	1072.989	6341.12

HAR1A	1557098_s_at	2.62856E-09	0.000169839	247.6632	55.2	652.4979	736.4958
ephb1	210753_s_at	2.84766E-09	0.000183996	274.96545	126.479	777.2672	164.0359
SNRPN	228370_at	2.86703E-09	0.000185247	3754.485	1581.8	2919.482	2852.273
TNFSF4	207426_s_at	2.87787E-09	0.000185948	5489.492	2244.314	2883.97	4669.884
CARD11	1562368_at	3.07477E-09	0.00019867	411.45955	221.5947	409.0917	362.9363
SEP9	208657_s_at	3.16772E-09	0.000204676	2036.556	1163.845	1510.526	1915.012
ST3GAL1	225033_at	3.20888E-09	0.000207335	5058.5515	2683.2	3273.744	4895.003
C21orf96	220918_at	3.28412E-09	0.000212197	15187.38	7581.835	9827.533	15187.38
Rcsd1	239328_at	3.31696E-09	0.000214319	7061.184	3253.205	3855.016	9761.096
Arl4c	202206_at	3.46788E-09	0.00022407	2796.847	1179.05	2405.501	2983.671
PCDHGA1	209079_x_at	3.61634E-09	0.000233663	1959.015	876.1	7894.268	2601.552
AJAP1	215790_at	3.7598E-09	0.000242932	13.964925	14.88708	9.80116	463.8555
STMN3	222557_at	3.8609E-09	0.000249464	5910.447	3362.6	5596.837	6377.118
SELL	204563_at	3.92629E-09	0.000253689	67493.405	29491.9	47254.13	80061.28
plxnc1	240638_at	4.2934E-09	0.000277409	1030.4	464.9635	1497.612	1124.204
runx3	204198_s_at	4.9648E-09	0.00032079	6106.3405	2610.9	6068.181	8170.055
psmb9	204279_at	5.09592E-09	0.000329262	12598.49	7136.5	14236.63	11457.36
Ncr1	207860_at	5.16833E-09	0.000333942	406.5276	184	359.1696	960.256
SNED1	235743_at	5.27097E-09	0.000340573	228.0999	78.4	124.8144	1083.206
Fam129c	1569422_at	5.54157E-09	0.000358058	461.41575	244.7513	1833.996	302.6234
GPRASP1	204793_at	5.57294E-09	0.000360084	1754.49	910.5	1653.639	5070.933
Cdh9	207729_at	5.6255E-09	0.00036348	363.3126	70.99381	736.7101	12213.79
gng7	1566643_a_at	6.10121E-09	0.000394218	772.6728	259.4579	1083.681	1358.43
SLC44A3	228221_at	6.13854E-09	0.00039663	207.28055	74.2	72.96017	2090.801
FLNB	1562416_at	6.70217E-09	0.000433047	1462.9505	659.3	1433.831	873.6851
FAR2	1557410_at	6.76891E-09	0.00043736	1753.4765	533.8	650.8967	5215.187
Ly9	210370_s_at	6.83071E-09	0.000441353	1146.401	403.7163	1983.496	222.0607
EVL	244375_at	6.95522E-09	0.000449397	1062.7915	478.9	1226.044	1870.081
IL28RA	244261_at	6.99268E-09	0.000451818	226.1215	90.24981	2425.2	7.57878
PTK2	1559529_at	7.06269E-09	0.000456342	731.7214	237.3531	3025.385	216.8663
RIMKLB	226164_x_at	7.53031E-09	0.000486556	3272.7815	1831.017	2459.501	5562.734
CAND2	213547_at	8.36471E-09	0.000540469	790.3	343.7015	1203.958	1333.698
Arl4c	202207_at	8.5097E-09	0.000549837	5809.026	2311.823	4182.288	5762.869
PTK2	208820_at	8.84584E-09	0.000571556	3461.6955	477.1532	9579.42	416.4796
stard10	223103_at	8.97737E-09	0.000580055	892.9255	399.9696	437.3618	1085.783
LOC100240735	241803_s_at	8.98879E-09	0.000580793	2056.6195	837.8	2376.014	2607.728
gats	1553971_a_at	9.08929E-09	0.000587286	1440.8905	786.542	1527.347	1666.602
Lsp1	203523_at	9.32586E-09	0.000602572	8456.7495	3652	8000.715	8847.199
IQGAP2	241723_at	9.45972E-09	0.000611221	2073.813	931.2	1020.96	1394.703
LPHN1	47560_at	9.64717E-09	0.000623332	1483.204	502.698	1504.007	1728.327
RERE	244625_at	9.95974E-09	0.000643529	4463.261	2237.87	2516.815	4421.457
SLC38A1	224580_at	1.04728E-08	0.000676678	2050.396	961.7859	2456.675	1633.346
PROM1	204304_s_at	1.14323E-08	0.000738678	28476.615	9429.681	21518.42	26943.17
Cobll1	203642_s_at	1.20093E-08	0.000775957	3194.563	745.6805	3548.579	669.7213
PTK2	242240_at	1.25793E-08	0.000812787	704.6238	475.3807	1566.756	449.0546
CD5	230489_at	1.28046E-08	0.000827343	1120.595	244.8644	279.5675	2783.418
Zmiz1	212124_at	1.34788E-08	0.000870906	24086.19	15385.14	21124.32	34811.59
KIAA1984	236518_at	1.36211E-08	0.000880103	940.3075	648.0353	1160.737	809.3305
ISG20	33304_at	1.42063E-08	0.000917911	4347.3305	1520.592	3758.953	1870.734
C12orf75	225105_at	1.44926E-08	0.00093641	5314.27	2171	6037.504	4591.036
Cobll1	203641_s_at	1.52059E-08	0.0009825	766.84715	365.0693	1029.022	317.6997
SLC2A5	204430_s_at	1.56006E-08	0.001008003	11372.125	5059.713	6990.166	4663.688
Rbpms	231961_at	1.62192E-08	0.001047973	581.89715	258.7235	935.719	643.4675
FLJ22536	236815_at	1.64949E-08	0.001065787	443.5828	124.8787	304.1255	995.4824
Sec61a2	219499_at	1.65489E-08	0.001069276	1074.932	731.2	1137.097	976.0063
GPR56	212070_at	1.65913E-08	0.001072012	9278.747	1912.147	3365.336	11734.83
PRKCH	218764_at	1.67792E-08	0.001084157	6760.104	2419.4	5019.121	3047.163
DLL1	224215_s_at	1.71074E-08	0.001105362	629.30955	131.8362	1429.684	447.3502
PRKCB	207957_s_at	1.73383E-08	0.00112028	12649.81	8556.13	11301.34	10303.88
TCF7	205255_x_at	1.73859E-08	0.001123353	15124.925	5376.924	7974.573	20162.1
HLF	204755_x_at	1.76416E-08	0.001139877	314.8969	61.8	25.21548	2163.95
CREBBP	228177_at	1.82199E-08	0.001177239	1606.85	1069.6	2477.062	1863.298
dusp5	209457_at	1.85624E-08	0.001199375	1743.674	997.9	1790.584	926.7944
PCDHGA1	215836_s_at	1.88147E-08	0.001215672	1891.3245	935.3807	5777.263	2116.617
lpin1	212276_at	1.89232E-08	0.001222683	7537.8175	3887.396	6802.836	5544.579
UBASH3B	244068_at	1.97525E-08	0.00127627	631.5942	347.2	796.2374	631.5942
HEG1	213069_at	2.03255E-08	0.001313291	839.02015	350.7	1262.759	2857.488
Pear1	228618_at	2.20064E-08	0.001421899	2197.5015	446.9233	1771.358	873.3049
GSTA4	235405_at	2.34368E-08	0.001514321	623.52225	219.9	862.4214	1752.651
GCOM1	228568_at	2.37357E-08	0.001533636	1070.7644	420.2128	1244.541	2913.765
C1orf21	223125_s_at	2.40199E-08	0.001552	3349.587	1515.31	3303.674	3720.804
STRBP	237195_at	2.40335E-08	0.001552878	1231.0875	667.5717	2603.402	1260.797

SEP9	41220_at	2.50687E-08	0.001619761	31836.69	20505.5	30347.88	30322.6
VAV3	218807_at	2.53544E-08	0.001638223	12775.1	6628.4	10496.65	7010.05
SLC15A4	225057_at	2.80362E-08	0.001811502	4690.764	3141.235	5672.875	5146.461
ANKRD6	204671_s_at	2.8348E-08	0.00183165	1606.187	646.3	1717.33	1928.239
naa15	1556382_a_at	2.99975E-08	0.001938226	1335.017	734.6522	1765.338	2778.404
GNB5	211871_x_at	3.17091E-08	0.00204882	1306.7115	719.6268	1014.689	1245.634
DGKE	238694_at	3.19523E-08	0.002064536	1829.283	997.8337	1159.743	8246.277
Ly9	215967_s_at	3.33162E-08	0.002152656	1929.7255	602.5	2734.042	523.8878
ANKRD13A	224810_s_at	3.39863E-08	0.002195959	17631.365	13851.99	20976.13	20638.24
skap1	205790_at	3.44415E-08	0.002225367	1493.645	674.1	1257.801	1119.774
C1orf21	223126_s_at	3.64297E-08	0.002353832	1107.785	503.856	1266.11	1105.017
PDE4DIP	212390_at	3.98579E-08	0.002575339	1051.12185	678.3051	838.2938	777.4952
tap1	202307_s_at	4.0676E-08	0.002628199	4893.417	3024.45	3890.291	8713.67
stk24	215188_at	4.1008E-08	0.002649649	1088.04035	472.9818	1756.858	1243.467
fam125a	1556643_at	4.10193E-08	0.002650379	2606.09	1549.496	2387.26	3243.243
MEF2C	209200_at	4.41121E-08	0.002850218	9501.182	4820.192	9536.697	18952.34
TFPI	215447_at	4.52487E-08	0.002923653	4553.2565	1808.585	1620.631	3976.708
Tcf7l2	212761_at	4.71836E-08	0.003048676	16156.41	7678.092	17229.53	13796.08
VAV3	218806_s_at	4.77733E-08	0.003086774	4366.126	2271.1	2847.239	2025.17
PARP12	218543_s_at	4.89092E-08	0.003160172	5668.896	2705.376	5006.416	5668.896
TMEM63A	228549_at	5.00491E-08	0.003233821	2544.75	1308	2666.528	1892.13
Irf1	238725_at	5.23169E-08	0.003380349	5604.165	3850.448	8747.866	8737.503
C9orf91	221865_at	5.2355E-08	0.003382812	2368.9505	1303.086	2566.03	1934.725
CACNA2D2	229636_at	5.31885E-08	0.003436672	432.80335	86.3	742.5579	337.3527
FLJ22536	229280_s_at	5.32051E-08	0.00343774	2031.316	540.0753	1048.093	5314.44
PAN3	239393_at	5.37103E-08	0.003470381	8382.337	5683.247	11878.37	7552.801
FLJ10489	1562433_at	5.61094E-08	0.003625395	2300.26	428.5277	2644.662	317.3395
LRRN2	216167_at	5.61134E-08	0.003625654	209.9545	48.4	205.5258	418.7487
FLJ43663	215330_at	5.68901E-08	0.00367584	2923.202	999.8376	860.345	2244.399
HLF	204753_s_at	5.84426E-08	0.003776154	346.1246	72.7	32.48095	1945.349
SPON1	209437_s_at	5.94403E-08	0.003840617	691.8448	266.2196	1013.159	164.0557
ERN1	235745_at	6.61351E-08	0.004273187	1352.523	811.7681	844.5643	2313.497
AMIGO2	222108_at	6.87704E-08	0.004443465	2008.522	497.9654	1083.429	805.6061
SLC37A3	223304_at	6.99292E-08	0.004518337	974.888	378.9	1572.468	914.077
Fam158a	1558938_at	7.04056E-08	0.004549117	1262.8025	971.3481	2315.274	2915.033
PHF11	221816_s_at	7.153E-08	0.004621771	13285.48	9301.013	16900.53	14819.92
SNED1	213488_at	7.24106E-08	0.004678663	434.1301	278.4666	423.8784	5365.883
Lrch1	226795_at	7.33729E-08	0.004740844	2541.0865	1866.917	2567.973	3140.452
runx3	204197_s_at	7.62712E-08	0.004928113	6287.232	2514.8	4184.854	6925.287
dsp	200606_at	7.73685E-08	0.004999008	253.8687	112.039	122.7944	294.4374
PLCL2	213309_at	7.87846E-08	0.005090507	6285.743	3809.2	5804.944	15489.82
Sec61a2	228747_at	8.1416E-08	0.005260535	1466.987	900.8	1485.553	1278.418
Crim1	233073_at	8.48219E-08	0.005480596	427.0772	223.8373	366.8815	276.1537
Med13l	212207_at	9.18388E-08	0.00593398	4305.609	2928.616	5179.091	4007.263
MYST3	226547_at	9.52293E-08	0.006153053	10385.445	7204.531	10402.09	14284.33
UBASH3B	238587_at	9.91057E-08	0.006403518	3987.598	1814.5	7151.163	3054.906
PAQR6	219236_at	9.98098E-08	0.006449013	820.95875	597.0081	625.5258	708.5505
CXXC5	233955_x_at	9.9856E-08	0.006451997	19909.51	9243.5	21167.96	24594.5
TNRC6B	240044_x_at	1.05124E-07	0.006792379	6161.5765	4177.101	5979.615	5919.146
C5orf41	235556_at	1.06548E-07	0.006884379	3165.837	2146.2	2269.594	3165.837
PTK2	242485_at	1.07366E-07	0.00693724	819.84945	292.5	1878.325	148.4933
SP4	236265_at	1.07578E-07	0.006950921	5165.8865	3245.731	5159.573	4494.241
LOC100131096	239062_at	1.0837E-07	0.00700211	836.5332	532.5914	742.7665	2092.512
Prkce	216766_at	1.10636E-07	0.007148507	2372.7175	1343.206	3790.317	1971.684
C6orf201	242739_at	1.12351E-07	0.007259365	1131.8435	689.8401	1181.74	1143.128
DMRTC1	1553998_at	1.13588E-07	0.007339263	547.9939	258.6437	918.7449	498.3428
PRIC285	232517_s_at	1.14441E-07	0.00739435	668.1588	380.9	848.9899	410.2219
mfap4	212713_at	1.14833E-07	0.007419695	366.0533	57.9701	4816.192	366.0533
AFF3	244696_at	1.15109E-07	0.007437511	3227.3195	1546.6	5695.445	1802.46
Sbf2	233914_s_at	1.15272E-07	0.007448054	3110.2025	1827.686	4155.027	3124.418
c19orf66	53720_at	1.1902E-07	0.007690207	3955.588	2499.338	3195.178	5818.677
PYCR2	224855_at	1.20991E-07	0.007817564	2737.9535	1926.974	2502.32	2794.422
Rcsd1	225763_at	1.21056E-07	0.007821798	15783.305	10138.4	12183.28	15366.06
MAP3K14	205192_at	1.23923E-07	0.008007034	1283.99	742.0333	1427.448	1283.99
Arrdc2	226055_at	1.34744E-07	0.008706244	4417.363	2738.297	6034.053	4989.073
TSPAN7	202242_at	1.37764E-07	0.008901344	3143.6845	423.556	6573.717	6657.558
Rbpms	207836_s_at	1.38878E-07	0.008973309	2257.3575	375.1986	2244.621	1387.733
DLG3	212728_at	1.45554E-07	0.009404676	570.44635	141.7106	596.6323	606.6147
stk24	208855_s_at	1.47865E-07	0.009554022	30486.95	19505.2	41590.79	33942.58
AFF3	1566880_at	1.49191E-07	0.009639653	923.0582	655.329	2664.979	682.1981
LOC284551	1563802_at	1.49657E-07	0.009669762	453.4412	284.2	696.2508	263.2229
C9orf142	226070_at	1.50849E-07	0.0097468	1489.0695	1095.656	1550.596	1537.431

ZNF496	1557616_at	1.55284E-07	0.010033351	758.9481	355.5	82.63664	913.9084
YPEL1	213996_at	1.56791E-07	0.010130715	1970.305	916.297	1066.766	1970.305
SPTBN1	226765_at	1.60625E-07	0.010378474	1610.692	753.4096	2114.65	3638.039
PLCXD2	235230_at	1.60964E-07	0.01040039	1213.8595	623.5619	2364.764	1089.038
STRBP	223246_s_at	1.67386E-07	0.010815342	1629.05	999.3	2693.449	1501.376
gnl1	228857_at	1.72305E-07	0.011133128	1184.974	676.3943	1440.769	1964.974
TMEM63A	214833_at	1.73034E-07	0.011180274	2862.9085	1483.659	2119.576	3355.57
GBP2	202748_at	1.78948E-07	0.011562382	4571.076	3478.531	3483.26	4571.076
Sh2d3c	1552667_a_at	1.79218E-07	0.011579817	2483.683	1408.373	2774.904	2565.575
GIMAP2	232024_at	1.79265E-07	0.011582848	13678.185	8402.7	12482.36	14874.01
CCDC50	235051_at	1.80023E-07	0.011631846	232.2935	282.8	1371.201	18.16394
AFF3	232286_at	1.8599E-07	0.012017395	3431.919	2084.6	7760.057	3397.628
L3mbtl4	228557_at	1.90994E-07	0.012340683	927.0143	225.5434	711.7726	1135.77
STAMBPL1	231891_at	1.92423E-07	0.012433056	431.10055	222.1116	367.2011	66.47868
DLK1	209560_s_at	1.96055E-07	0.012667725	391.80285	194.8472	154.5353	76735.45
C1orf55	244103_at	1.97341E-07	0.012750782	14586.62	9350.4	13379.25	11385.26
DAPK1	239162_at	2.00578E-07	0.012959957	4766.531	2307.405	4422.627	4766.531
NSUN3	1564248_at	2.11591E-07	0.013671547	1419.8795	746.6	721.1292	1631.871
LYSMD2	226748_at	2.12524E-07	0.013731789	17073.525	12135.1	14793.92	17012.25
ZNF530	232228_at	2.1878E-07	0.014136047	492.4497	317.0514	589.6146	734.4698
OPTN	202074_s_at	2.19351E-07	0.014172917	4021.886	882.7687	2311.664	4329.157
Kcnk10	220727_at	2.19999E-07	0.014214822	352.2769	186.9956	715.812	41.18683
STARD9	227108_at	2.2001E-07	0.014215522	1331.9155	609.5635	1281.838	1171.965
PLCG1	202789_at	2.20586E-07	0.014252718	2124.791	824.7	2873.279	1103.61
f2rl1	213506_at	2.20852E-07	0.014269914	5141.893	720.4365	4161.759	7913.146
Tox	204529_s_at	2.22045E-07	0.014347011	6390.938	2595.416	4841.873	6390.938
KLHL6	1560396_at	2.23212E-07	0.0144224	5089.7475	2802.3	3668.247	4989.954
Sh2d1a	210116_at	2.2483E-07	0.014526964	3118.7465	1084.591	857.2443	7787.659
ltbp3	227308_x_at	2.2639E-07	0.014627719	1414.8335	737.2755	952.2715	1403.648
rab40b	204547_at	2.26435E-07	0.014630641	1652.6675	865.7269	2785.824	3732.944
SCN3A	210432_s_at	2.39092E-07	0.015448482	4044.465	74.1	5050.752	755.9534
LOC730102	241607_at	2.39582E-07	0.015480088	254.0298	770.3235	173.1736	259.853
C12orf23	224759_s_at	2.46648E-07	0.015936674	6873.152	3793.8	7591.22	4953.094
TMEM204	219315_s_at	2.53561E-07	0.016383336	2049.3065	660.4689	1677.133	2411.564
Prpf40a	226687_at	2.53902E-07	0.016405352	3482.932	2738.1	4456.699	4246.32
INHBA	210511_s_at	2.5981E-07	0.016787072	142.4702	49.8	13.99243	142.4702
Cd6	1566448_at	2.62407E-07	0.016954881	549.0609	179.8033	82.24481	2450.134
CXXC5	222996_s_at	2.63654E-07	0.017035451	12055.65	5307.53	15596.1	13565.65
KLHL3	221221_s_at	2.64707E-07	0.017103519	1483.628	827.3987	1866.369	2650.954
PTK2	207821_s_at	2.6849E-07	0.017347943	1425.262	499.4	3397.166	240.5396
fam168a	36612_at	2.75416E-07	0.017795428	1908.026	1360.162	2577.026	1570.112
TTC28	215146_s_at	2.84078E-07	0.018355156	2544.68	1298.719	6209.663	1149.478
MEF2A	212535_at	3.00861E-07	0.019439529	9706.6445	5396.622	11887.77	5440.895
macrod2	1563209_a_at	3.0785E-07	0.019891129	184.3303	38.09488	508.0417	18.85816
MIR600HG	223522_at	3.08557E-07	0.019936824	1407.56	1042.167	3069.487	1041.736
CEP135	207286_at	3.08913E-07	0.019959818	1298.132	717.6	1271.266	1637.935
ddit4	202887_s_at	3.10287E-07	0.020048597	11809.72	3345.546	23647.19	5434.229
APOBEC3G	204205_at	3.13436E-07	0.020252014	5731.4565	4699.4	6028.846	4787.343
PLCB1	244726_at	3.15233E-07	0.020368157	10502.86	6360.3	10379.51	13070.96
macrod2	235278_at	3.17235E-07	0.02049748	661.23945	305.8	1525.727	74.49471
MAST4	225613_at	3.23528E-07	0.020904088	3701.5815	1926.656	2429.349	5106.149
Slc23a1	223732_at	3.25742E-07	0.021047197	608.27305	255.5773	1287.001	629.1973
Cobll1	229598_at	3.29551E-07	0.021293285	244.4438	68.84483	366.6297	5.6476
CDH4	206866_at	3.39061E-07	0.021907723	350.3036	138.6076	882.6906	1689.195
SEP9	1559025_at	3.39532E-07	0.021938184	2289.037	1383.718	2538.581	2448.755
FAM134B	218532_s_at	3.46551E-07	0.022391711	2120.439	451.9	2280.438	1154.616
ADI1	222400_s_at	3.5628E-07	0.023020302	5656.9645	10340.9	4628.521	5006.411
Irf1	202531_at	3.59671E-07	0.023239408	4888.347	3477.7	6176.209	6660.018
AKAP13	243450_at	3.70279E-07	0.023924817	2011.4395	1338.5	2094.872	1690.914
PTAR1	226110_at	3.7224E-07	0.024051535	7710.517	5827.46	9080.488	7686.483
PRKCH	233411_at	3.74117E-07	0.024172843	2504.242	1193.79	3232.133	1389.637
GSTA4	202967_at	3.76774E-07	0.024344508	1526.474	754.8	1552.284	5132.125
igf2bp3	203820_s_at	3.84227E-07	0.02482607	1293.566	548.2443	797.7154	335.7602
ST3GAL1	215874_at	3.97665E-07	0.025694347	1804.316	1087.914	779.171	1777.879
NIPAL2	227001_at	4.12725E-07	0.026667383	1945.9	3685.332	931.9128	2907.076
ANKRD6	204672_s_at	4.18963E-07	0.027070456	890.8073	375.5977	1301.673	1307.545
SH3TC1	219256_s_at	4.21485E-07	0.027233426	4362.881	1774.769	4871.644	1738.034
ERICH1	1563315_s_at	4.24589E-07	0.027433967	3163.609	2006.416	3315.286	3107.118
ZNF418	243439_at	4.30844E-07	0.027838141	1095.074	687.9389	1007.506	2139.717
cib2	205008_s_at	4.3161E-07	0.027887644	982.1022	519.9543	1064.565	791.604
FLJ43663	222378_at	4.3371E-07	0.028023319	1405.8975	592.9	543.7585	1067.471
polB	203616_at	4.43161E-07	0.028633989	7437.467	6060.9	7988.343	5455.857

csh1	206885_x_at	4.47926E-07	0.028941861	366.6388	95.21268	1142.51	241.6674
HOOK1	225792_at	4.5153E-07	0.029174696	610.21885	149.781	505.5481	2245.486
HLA-DRB3	221491_x_at	4.53328E-07	0.029290905	4915.5225	1067.105	6277.734	1498.757
ST3GAL1	208322_s_at	4.54563E-07	0.029370705	1437.99	962.9939	1258.839	1119.31
DDR1	1007_s_at	4.55679E-07	0.029442799	1969.948	733.6422	4455.432	787.7904
LIMS1	1570259_at	4.6474E-07	0.030028255	1116.7265	601.9	1093.262	1434.241
RGPD1	235597_s_at	4.73181E-07	0.03057362	264.7367	57.1	30.08063	192.5548
usp18	219211_at	4.78972E-07	0.030947843	1044.03645	414.1576	1233.56	1193.462
AFF3	227198_at	4.8722E-07	0.031480768	5071.447	2485.509	14389.12	3653.184
C16orf67	219442_at	4.90257E-07	0.031676947	1367.021	631.3	1378.442	1115.088
CBX7	212914_at	4.99423E-07	0.032269227	2010.134	1157.7	1863.379	1430.652
mll	226981_at	5.12865E-07	0.033137735	8016.59	5672.225	6824.888	8016.59
Crim1	202552_s_at	5.2055E-07	0.033634296	1258.79	561.7	766.3839	725.4421
S1PR5	230464_at	5.3293E-07	0.034434214	751.8	187.1531	786.3992	262.4233
brd4	202103_at	5.36822E-07	0.034685676	1632.335	1018.679	2515.933	3131.76
SHANK3	227923_at	5.50524E-07	0.035570976	5291.186	1508.471	3050.542	5166.972
TSPAN7	234245_at	5.5645E-07	0.035953896	1042.70895	377.0579	2729.242	1845.77
LOC374443	240572_s_at	5.57488E-07	0.036020997	2692.3355	1657.559	1159.518	1342.185
stt3b	238303_at	5.58905E-07	0.036112545	6919.3345	4168.7	5947.376	11319.4
NOVA1	205794_s_at	5.62696E-07	0.03635745	178.09525	135.9988	572.5845	1278.603
BEND7	227341_at	5.80952E-07	0.037537075	98.295595	40.88484	115.4169	1014.277
INHBA	227140_at	5.85487E-07	0.037830076	417.48225	184.8	434.0577	269.4488
fam171a1	212771_at	5.90876E-07	0.038178256	2383.466	647.6708	1111.526	2383.466
MARCH9	226454_at	6.23652E-07	0.040296054	1089.262	714.9005	1553.886	1467.659
Fnbp1	213940_s_at	6.27492E-07	0.040544128	8431.902	6390.808	5679.768	15355.64
FAIM3	221601_s_at	6.34696E-07	0.041009596	6396.264	1804.123	8598.693	7093.788
YWHAZ	214848_at	6.38813E-07	0.041275595	1214.7195	834.0923	1022.822	1938.981
PRKCH	206099_at	6.41125E-07	0.04142502	2653.46	1050.9	2229.518	1120.454
NCOA7	243807_at	6.41555E-07	0.041452767	1071.7695	670.9133	778.2184	1182.657
C17orf58	226901_at	6.48149E-07	0.041878821	781.42185	1512.6	880.4255	957.9495
Golga1	214997_at	6.55561E-07	0.042357776	1345.392	864.095	1115.999	1934.302
Smpd3	219695_at	6.75307E-07	0.043633626	403.52195	205.4355	1161.458	128.0978
KLHL6	228167_at	6.76196E-07	0.04369108	6270.619	3934.025	6479.031	5572.73
TNRC6B	238468_at	6.84022E-07	0.044196741	4371.362	3118.958	3385.481	4896.129
TRBV27	241133_at	6.87658E-07	0.04443167	21048.435	6380.6	19427.26	1399.316
stk24	208854_s_at	6.92434E-07	0.044740266	5569.3235	3499.5	7785.897	6071.486
NCRNA00118	230488_s_at	7.01127E-07	0.0453019	499.10015	312.7134	694.5419	365.4315
FLJ38379	1556474_a_at	7.09844E-07	0.045865163	1373.063	334.8	2998.249	2232.324
sntb2	241613_at	7.24453E-07	0.046809085	950.912	510.5316	1478.808	976.3358
Rftn1	215630_at	7.37384E-07	0.047644584	704.1537	445.236	727.7794	779.6472
C10orf11	223703_at	7.38849E-07	0.047739218	948.37295	2581.4	2112.798	1491.595
Prr5l	233379_at	7.44247E-07	0.048088052	423.164	227.3703	144.9773	423.164
Ngfr	205858_at	7.46763E-07	0.048250603	162.61095	44.18648	56.90435	21.46637
Tcf7l2	232522_at	7.6091E-07	0.049164679	2921.256	1282.05	2881.312	3739.292
Wasf2	221725_at	7.62448E-07	0.049264058	7593.046	5756.447	7690.483	7899.498

Supplementary Table 10b. Comparison of gene expression profiles between cases with high expression of wild-type *SETBP1* and *SETBP1* mutation.

Gene	ID	p-value	Bonferroni correction	median exp (SETBP1 high N=20)	SETBP1 mutant 1	SETBP1 mutant 2
KDM5D	206700_s_at	0.694282289	1	3950.28735	56.95809	9.1635
RPS4Y1	201909_at	0.401287823	1	15494.85	327.0542	62.22238
USP9Y	206624_at	0.415171421	1	335.488655	8.40325	7.06499
ST18	206135_at	0.545446641	1	312.49585	4.37063	11.93833
EIF1AY	204409_s_at	0.97594039	1	2285.6651	40.93431	116.4617
SLITRK4	230680_at	0.010398631	1	796.318	6.15691	53.04463
HOXB-AS3	236892_s_at	0.047174024	1	708.6851	49.16701	5.63805
ZC2HC1A	1560197_at	0.64223214	1	84.35035	2.48795	6.29364
TXLNG2P	232618_at	0.431965027	1	631.161845	15.45823	56.28426
DDX3Y	205000_at	0.564735949	1	1579.07465	81.65151	104.0446
TXLNG2P	236694_at	0.759508076	1	1354.0336	119.9828	48.09658
USP9Y	228492_at	0.322965555	1	685.1364	64.63863	20.76821
IPP	1554739_at	0.146811343	1	91.088595	6.74536	4.84344
EMC1	215991_s_at	0.512830468	1	344.80715	23.29783	21.03433
KALRN	236651_at	0.784421452	1	110.53695	7.29411	7.07766
CTLA4	236341_at	0.015178253	1	385.6943	28.34627	28.55128
TCP11L2	1565525_a_at	0.050399062	1	289.08295	26.57042	16.83651
TYR	1555504_at	0.482264643	1	32.885545	2.45915	2.70304
CDNF	1568696_at	0.42175654	1	127.37345	9.44728	10.82112
LOC286114	244255_at	0.46981675	1	172.5834	11.04292	17.21869
STK4	205411_at	0.129046988	1	384.2496	45.13301	18.21531
WDR67	1556429_a_at	0.4345484	1	162.35745	17.79659	9.05263
LOC100506403	210805_x_at	0.011920703	1	324.5641	14.90729	41.32024
UNC80	230220_at	0.095964805	1	99.36672	5.15287	12.07671
LOC339862	1557534_at	0.396995968	1	41.139325	2.61847	4.65641
PLEKHS1	1554190_s_at	0.695979903	1	59.89347	7.30014	3.54738
LOC339803	227941_at	0.27161552	1	793.37205	43.97814	99.81873
RNF144B	239704_at	0.389067723	1	313.66575	36.84151	20.01058
NCRNA00185	207063_at	0.247737736	1	219.7637	33.87719	6.01839
TMEM74	1552521_a_at	0.059130802	1	41.367875	4.66356	2.8933
ERC2	213938_at	0.113019184	1	106.40885	6.89018	12.57117
SOX2-OT	231898_x_at	0.334816068	1	30.967425	2.39182	3.46735
TXLNG2P	214131_at	0.933013752	1	1822.2607	161.4	183.5214
ATPBD4	1560404_a_at	0.704902406	1	55.049815	8.66979	2.04723
LOC100287177	1569086_at	0.009502012	1	214.07455	24.46805	17.72807
ZNF208	208542_x_at	0.876515332	1	143.90845	22.76942	5.91458
XIRP2	228794_at	6.27986E-05	1	473.7516	9.51278	85.59518
BDNF-AS	1567359_at	0.362325216	1	23.45391	3.28424	1.43675
TAS2R45	234108_at	0.31486983	1	97.63135	12.28737	7.49223
BMP2	205290_s_at	0.099308865	1	238.46605	38.15946	10.7758
PRKAA2	238441_at	0.864818799	1	38.342	3.01337	4.87106
LOC401098	1556609_at	0.586084535	1	84.479715	3.2565	14.52406
MCF2L2	215112_x_at	0.413194452	1	67.44387	3.05926	11.19275
CDKN2A	207039_at	0.307497586	1	134.09055	16.08363	12.47932
LOC440704	1562558_at	0.732604135	1	106.401125	15.84239	6.84002
LOC283665	1557328_at	0.764349043	1	111.1512	11.16007	12.56351
LOC100506274	1556454_a_at	0.901633137	1	103.5542	11.91982	10.26362
EIF1AY	204410_at	0.676518875	1	763.93095	15.86957	147.9288
SLC6A2	239394_at	0.141438933	1	168.207	23.67383	13.55427
RGS7	1554500_a_at	0.867414621	1	132.75695	12.07841	17.46778
ZFY	230760_at	0.804834933	1	481.3893	36.31574	70.92482
TECR	231556_at	0.526909702	1	130.21375	4.26118	24.76296
FUT2	208505_s_at	0.883544029	1	249.3283	17.66437	38.33484
ZFY-AS1	237225_at	0.379307879	1	126.2353	23.13581	5.96523
C12orf40	1561721_a_at	0.599153665	1	58.29828	7.57043	5.90774
SLC22A25	1561094_a_at	0.445121901	1	43.24749	3.36556	6.66478
KLHL32	1553765_a_at	0.130101137	1	70.93369	7.74474	8.80209
OPRM1	211359_s_at	0.884323676	1	180.567	18.56617	23.74603
PPM1H	233911_s_at	0.020070964	1	160.1089	19.23838	18.53878
LOC100130815	1564471_at	0.015510992	1	93.33892	8.96081	13.10095
SPTSSB	238702_at	0.512746983	1	164.9367	18.71618	20.32869
RGS13	1568751_at	0.492607919	1	15.942815	1.28658	2.49384
FLJ43663	238986_at	0.141015685	1	185.9799	15.7086	28.58955
CTNNA3	1554235_at	0.428913891	1	14.369455	163.739	11.12904
MET	203510_at	4.30956E-05	1	91.66215	176.0489	941.9171

TDGF1	206286_s_at	0.238469902	1	40.04949	162.8736	327.1857
CTSG	205653_at	0.008374887	1	1250.9925	1434.405	13963.19
CLDN22	218775_s_at	0.55070041	1	110.0715	121.5448	1236.271
DTX3	49049_at	0.751180754	1	74.03656	61.62205	854.5587
DCLK2	227666_at	0.457465964	1	60.829495	160.831	592.4784
FCER2	206760_s_at	0.068101875	1	44.938975	512.267	45.57795
STOM	201062_at	0.954524308	1	28.81282	108.3661	249.3313
LOC285095	238196_at	0.714571173	1	19.28284	16.79646	223.562
PRLR	227629_at	0.298945354	1	194.57575	2078.009	349.0263
BAZ1B	229658_at	0.968867841	1	42.73939	264.2034	269.0831
SGCE	204688_at	0.075642531	1	174.111	2169.923	18.98523
CYP2A13	208327_at	0.881248872	1	36.65	23.77455	437.0986
DAB1	228329_at	0.126543275	1	193.23405	187.9007	2247.104
OR7E19P	216536_at	0.27834837	1	14.94293	10.92663	178.1505
COL1A1	1556499_s_at	0.550632916	1	202.25735	2397.893	168.6384
HOMER3	204647_at	0.003340761	1	1035.707	7523.668	5629.84
CDA	205627_at	0.12929175	1	200.7428	727.1459	1822.332
COL4A1	211980_at	0.543689949	1	268.5126	338.2607	3094.672
FOXC1	1553613_s_at	0.250999752	1	363.75	602.7963	4056.996
ACACB	214584_x_at	0.21529864	1	44.58628	232.3079	339.0359
RGS6	214538_x_at	0.669018009	1	43.49628	72.34594	486.9131
DOHH	213949_s_at	0.432439362	1	36.977275	48.15561	427.9115
CWH43	220724_at	0.214603549	1	9.54621	11.57761	112.4661
CTNND2	209617_s_at	0.023725903	1	146.8363	103.7435	1807.521
LOC100505912	239174_at	0.100466989	1	37.76308	196.3377	295.5211
EREG	1569583_at	0.904159189	1	641.44635	70.62656	8351.661
PTPRD	213362_at	0.501867295	1	174.87195	190.51	2106.601
NPW	243110_x_at	0.701303593	1	45.10223	549.1476	45.10223
PBX1	212148_at	0.03618469	1	463.8481	334.4008	5778.286
MYBPH	206304_at	0.701250668	1	48.55	90.57813	553.2309
FLJ30901	1552388_at	0.688517651	1	196.13985	881.0526	1721.197
DPPA4	241199_x_at	0.903405925	1	50.38533	383.0499	286.6878
SNED1	213488_at	7.24106E-08	0.004678663	434.1301	423.8784	5365.883
LOC728613	1568762_at	0.481421476	1	30.538345	187.2971	222.0731
SIGLEC9	210569_s_at	0.16078621	1	59.607135	775.5965	29.45751
DEFB1	210397_at	0.305025226	1	297.78345	2547.231	1477.959
GREB1	205862_at	0.305787364	1	19.311285	11.4797	249.8863
GNA14	220108_at	0.258500347	1	69.3	256.8393	695.3547
POFUT2	207448_at	0.549728496	1	29.77904	312.0954	98.0475
MAF	1566323_at	0.335336579	1	10.25	32.06108	109.3402
HFM1	241469_at	0.15454546	1	23.02079	20.29171	303.2304
POF1B	1555383_a_at	0.295315533	1	16.177545	34.13367	193.6236
LMO3	231348_s_at	0.460676377	1	22.56743	146.3394	171.7613
CCDC158	1554846_at	0.079583224	1	24.32471	189.1486	153.7652
MFAP4	212713_at	1.14833E-07	0.007419695	366.0533	4816.192	366.0533
MYCN	209756_s_at	0.947166229	1	35.51606	120.1987	386.6899
LOC100506328	1560679_at	0.271235802	1	63.04544	858.0397	43.61737
PPP1R9A	228494_at	0.012067794	1	276.1807	3668.806	287.6614
TTC40	220539_at	0.678145117	1	34.25	195.7945	295.3887
MFSD7	214269_at	0.481362757	1	36.94467	149.5118	380.4905
TMPRSS3	223948_s_at	0.05812293	1	91.20225	36.8482	1272.964
TMEM98	223170_at	0.02939274	1	88.77728	56.6215	1229.672
PRR16	1554867_a_at	0.470570984	1	141.423	370.526	1684.391
PCDHGC4	231753_s_at	0.350471617	1	22.06688	39.47215	284.8542
KCNV1	220294_at	0.402279979	1	11.934645	13.34305	162.6318
DAZ1	207912_s_at	0.932172143	1	7.68542	19.90165	93.56784
PLA2G5	215871_at	0.70003935	1	43.83697	236.53	411.3802
ELOVL2	213712_at	0.588591268	1	27.245805	375.0946	27.99161
NRG1	208241_at	0.113404263	1	166.7164	290.4274	2178.883
GDF10	206159_at	0.035979206	1	157.7163	211.0802	2135.699
TRH	206622_at	0.662034376	1	457.726	442.2906	6401.701
LGALS12	223828_s_at	0.022158442	1	83.85	197.6549	1064.186
CFHR5	208088_s_at	0.802635761	1	12.83327	11.2021	184.743
IRGQ	242183_at	0.824778903	1	28.28006	335.643	96.30032
PEG10	212094_at	0.161084496	1	164.6711	2502.282	19.8959
DAPL1	229290_at	0.304976897	1	63.75171	44.54243	934.5373
LRRN1	226884_at	1.58138E-06	0.102177522	232.55515	724.4062	2849.184
LPAL2	210909_x_at	0.531809403	1	29.59075	169.8038	288.1998
FAM110B	221959_at	0.406790746	1	44.931	28.5734	672.0267
MCAM	211340_s_at	3.10091E-05	1	314.1494	192.4118	4706.34
ZNF503	227195_at	0.056315874	1	402.0958	2074.858	4263.116
NAV3	204823_at	0.356022094	1	51.473345	51.64669	765.46
MEG3	210794_s_at	0.871004759	1	59.51261	33.99963	916.4865
CXCL14	222484_s_at	0.958636114	1	28.76687	449.4167	11.1258

CYP1B1	202434_s_at	0.489849582	1	21.37931	296.6472	46.74595
GPC5	207174_at	7.76552E-06	0.501753548	84.07935	93.23876	1261.136
AKR1C1	217626_at	0.063589904	1	109.594	81.89236	1684.444
DOK6	241729_at	0.691735321	1	19.74645	24.06806	296.1346
CABLES1	1558621_at	0.573803487	1	92.2921	63.94252	1433.456
LOC100653010	221576_at	0.847590266	1	19.834185	18.86837	304.5097
TNFSF14	207907_at	0.374064511	1	50.423725	800.0702	30.8491
IGLV6-57	215035_at	0.434225412	1	38.709735	620.7621	19.46989
FGF18	206987_x_at	0.095767997	1	47.85511	74.73234	728.9922
GFRA1	227550_at	0.578069579	1	36.243205	239.0594	378.8635
NTRK1	208605_s_at	0.444332476	1	22.750795	22.52724	366.3514
RXFP1	231804_at	0.056054269	1	601.5537	2944.267	7527.572
FAM124A	230519_at	0.071197989	1	68.157225	1072.339	124.5355
WWTR1	202134_s_at	0.51965969	1	21.4923	20.44323	360.217
LOC100292909	241535_at	0.012956052	1	64.31009	72.6214	1068.224
NCR1	217088_s_at	0.483525015	1	20.726045	18.64233	350.131
PTPN14	226282_at	0.030192002	1	64.197605	75.59521	1097.888
LOC283484	1556940_at	0.364016144	1	8.54403	135.5416	20.79093
IL23R	1561853_a_at	0.965520723	1	20.94094	137.1936	249.3713
CDC25C	216914_at	0.400559648	1	36.227895	278.4731	402.3666
AQP4	210067_at	0.962084964	1	8.35662	3.8675	154.0581
PIR	207469_s_at	0.868957137	1	147.03155	128.7971	2651.371
LOX	215446_s_at	0.071017165	1	249.777	178.8047	4572.884
DSG2	217901_at	9.63658E-07	0.062264867	384.11015	323.6422	7040.605
CTNND2	209618_at	0.004684009	1	42.45	23.32869	797.3202
TMEM176B	220532_s_at	0.575716985	1	690.1432	13478.97	193.6421
EREG	205767_at	0.659062241	1	591.1	103.0895	11778.15
COL4A1	211981_at	0.906112353	1	30.54406	133.2209	483.0608
RXFP1	238206_at	0.036132257	1	801.2228	4957.771	11496.3
MARC1	218865_at	0.014656409	1	86.334885	1136.568	643.5128
ORM1	205040_at	0.998040616	1	27.869145	33.4669	552.8414
RORB	206443_at	0.002978052	1	76.28813	14.48909	1596.267
LDLR	217103_at	0.353301087	1	14.0832	11.82386	286.1098
RHBDL3	233409_at	0.9035715	1	54.1446	21.15967	1153.435
NXF3	220110_s_at	0.027052112	1	24.50322	10.10868	523.7061
AKR1C1	1555854_at	9.5103E-05	1	118.4809	243.8284	2371.156
HOMER3	222222_s_at	0.012843678	1	103.8974	1233.067	1086.415
LOC728052	1558795_at	0.918192309	1	67.04861	1443.038	67.04861
COBL	213050_at	5.92293E-16	3.82698E-11	223.66045	4518.953	630.8448
TNFSF11	210643_at	3.17393E-05	1	114.7185	13.3786	2641.208
FCAR	211306_s_at	0.253547359	1	40.06374	781.4969	149.1304
POU1F1	207846_at	0.031510149	1	42.1	56.66555	950.2228
VWF	202112_at	0.985536917	1	137.2257	155.8757	3130.01
DEFA1	205033_s_at	0.552215636	1	906.269	324.4041	21729.49
PHLDB2	1554778_at	0.473657912	1	8.00607	72.73761	122.5171
INSM1	206502_s_at	0.631012237	1	20.902245	378.9745	132.7847
DHCR24	200862_at	0.208707009	1	650.8766	705.5933	15311.75
AKR1C2	211653_x_at	0.041955073	1	800.64615	1024.793	18969.19
EPPK1	232165_at	8.39451E-06	0.542394251	100.62455	206.1347	2339.213
PTPRD	214043_at	0.068770232	1	247.492	280.1789	5994.5
PTPRB	230250_at	0.058179005	1	103.33167	78.56194	2560.212
BEX1	218332_at	0.760963738	1	958.7485	444.2147	24302.87
PTPRN2	203030_s_at	0.216522464	1	48.03874	704.1254	563.6624
LRCH2	227688_at	0.07393975	1	17.72734	17.75468	477.9551
FGFR2	203638_s_at	0.001090214	1	26.507925	57.31082	684.7302
RGS6	236726_at	0.035540697	1	17.33636	34.35672	457.1668
ZFP57	231236_at	0.875307623	1	42.463715	48.12743	1169.301
AKR1C1	216594_x_at	0.032798302	1	920.34995	1426.874	26040.73
AKR1C1	204151_x_at	0.0004906	1	1475.6795	1478.819	43167.59
TMPRSS3	223949_at	0.001685861	1	87.713995	103.753	2581.522
ERVFRD-1	1555880_at	0.231672795	1	28.410385	25.72077	850.3707
IGSF11	228375_at	0.219220335	1	33.03913	183.9509	854.4152
VMO1	235751_s_at	0.136633716	1	12.079845	12.72739	367.7864
EDIL3	225275_at	0.560862286	1	272.677	257.7331	8908.313
AJAP1	215790_at	3.7598E-09	0.000242932	13.964925	9.80116	463.8555
CDH9	207729_at	5.6255E-09	0.00036348	363.3126	736.7101	12213.79
TMPRSS3	220177_s_at	3.04874E-05	1	150.41735	134.8985	5291.198
PGBD5	219225_at	0.039080446	1	64.01736	120.7576	2232.37
SLC44A5	235763_at	0.226846007	1	71.723335	1853.608	939.6198
PRR16	220014_at	0.503304743	1	123.8413	878.8698	4677.579
MECOM	226420_at	0.850435406	1	135.56635	142.5754	6543.227
LEMD1-AS1	1561280_at	0.030888566	1	7.551805	8.07607	392.0937
ABCA8	204719_at	0.000109841	1	150.1717	8712.473	16.18574
LOC643401	1557765_at	0.104257777	1	24.15258	42.82973	1375.846

MECOM	221884_at	0.859796781	1	107.146675	80.59335	6381.95
MDGA2	239935_at	0.021074252	1	19.27102	34.73853	1416.207
EPPK1	232164_s_at	0.000136348	1	40.25406	20.37426	3290.186
AKR1C2	209699_x_at	0.0005914	1	380.11	1196.589	32451.79
SLITRK6	235976_at	0.69996096	1	6.25738	2.64845	609.7662
RORB	242385_at	7.09796E-05	1	154.2135	23.05367	26245.1
DLK1	209560_s_at	1.96055E-07	0.012667725	391.80285	154.5353	76735.45
KCNK12	220448_at	0.016518957	1	37.83076	14507.24	15.13075

Supplementary Table 11. Univariate and multivariate analyses of overall survival.

Whole cohort of myeloid malignancies (N= 547)

Univariate	Variable*	Hazard ratio	95% CI	P value**
	Male sex	1.53	1.20-1.96	**<0.001**
	Age (>60 years)	1.92	1.48-2.51	**<0.001**
	Increased bone marrow blast (>10%)	1.52	1.21-1.91	**<0.001**
	-7/del(7q)	2.05	1.53-2.70	**<0.001**
	Complex karyotype (≥3)	1.35	0.95-1.87	0.09
	SETBP1 mutation	2.30	1.58-3.25	**<0.001**
	RUNX1 mutation	1.45	0.87-2.29	0.15
	ASXL1 mutation	2.15	1.40-3.24	**<0.001**
	SRSF2 mutation	2.09	1.33-3.19	**0.002**
	U2AF1 mutation	1.94	0.92-3.60	0.05
	CBL mutation	2.50	1.42-4.13	**0.002**
	KRAS mutation	1.49	0.46-3.57	0.46
	NRAS mutation	2.24	0.37-7.21	0.32
	DNMT3A mutation	2.66	1.41-4.60	**0.004**
	TET2 mutation	1.31	0.88-1.89	0.18
	IDH1/2 mutation	0.85	0.26-2.02	0.75
Multivariate	Variable*	Hazard ratio	95% CI	P value**
	Male sex	1.98	1.25-3.19	**0.004**
	Age (>60 years)	2.86	1.58-5.41	**<0.001**
	Increased bone marrow blast (>10%)	1.37	0.85-2.23	0.20
	-7/del(7q)	1.32	0.69-2.42	0.39
	SETBP1 mutation	2.90	1.71-4.83	**<0.001**
	ASXL1 mutation	1.75	1.03-2.96	**0.04**
	SRSF2 mutation	1.14	0.63-2.02	0.65
	CBL mutation	2.15	1.05-4.09	**0.04**
	DNMT3A mutation	3.59	1.57-7.40	**0.004**

MDS and CMML (WBC<12,000/µl) cohort (N=317)

Univariate	Variable*	Hazard ratio	95% CI	P value**
	Male sex	1.44	1.06-1.99	**0.02**
	Age (>60 years)	1.5	1.09-2.10	**0.01**
	Increased bone marrow blast (>10%)	2.35	1.76-3.16	**<0.001**
	IPSS			**<0.001**
	low vs int-1	0.95	0.56-1.68	0.84
	low vs int-2	1.67	0.97-2.98	0.06
	low vs high	2.07	1.26-3.63	**0.004**
	int-1 vs int-2	1.76	1.19-2.60	**0.005**
	int-1 vs high	2.19	1.55-3.13	**<0.001**

	int-2 vs high	1.25	0.87-1.81	0.24
	SETBP1 mutation	1.92	1.20-2.94	**0.008**
	RUNX1 mutation	0.73	0.38-1.29	0.29
	ASXL1 mutation	1.28	0.71-2.19	0.4
	SRSF2 mutation	0.91	0.47-1.62	0.76
	U2AF1 mutation	1.01	0.42-2.04	0.99
	CBL mutation	1.26	0.61-2.34	0.51
	KRAS mutation	0.31	0.017-1.47	0.17
	NRAS mutation	1.36	0.07-6.45	0.77
	DNMT3A mutation	2.37	1.08-4.63	**0.03**
	TET2 mutation	0.9	0.50-1.53	0.72
	IDH1/2 mutation	0.42	0.02-1.91	0.32
Multivariate	Variable*	Hazard ratio	95% CI	P value**
	Male sex	1.74	1.05-2.99	**0.03**
	Age (>60 years)	1.19	0.67-2.21	0.56
	Increased bone marrow blast (>10%)	2.12	1.06-4.22	**0.03**
	IPSS			0.95
	SETBP1 mutation	1.83	1.04-3.12	**0.04**
	DNMT3A mutation	1.92	0.81-4.13	0.13

*Some data are not available. **Statistically significant p values were indicated with bold font.

Supplementary Table 12. IPSS score in myeloid malignancies with or without *SETBP1* mutations.

	SETBP1 mutation	WT *SETBP1*	P[a]
IPSS; no. (%)			0.31
Low	30 (11.32)	2 (7.14)	
INT-1	89 (33.58)	8 (28.57)	
INT-2	62 (23.4)	4 (14.29)	
HIGH	84 (31.7)	14 (50)	

a A Fisher's exact test was used to determine the P values.

Supplementary Table 13. Prognostic significance according to *SETBP1* and *CBL* mutation status.

Whole cohort of myeloid malignancies (N= 256)

SETBP1	*CBL*	VS	*SETBP1*	*CBL*	Hazard ratio	95% CI	P value*
wild type	mutation		wild type	wild type	1.97	0.87-3.82	0.1
mutation	wild type		wild type	wild type	2.86	1.80-4.39	**<0.001**
mutation	wild type		wild type	mutation	1.45	0.69-3.44	0.3
mutation	mutation		wild type	wild type	6.55	2.85-13.17	**<0.001**
mutation	mutation		wild type	mutation	3.33	1.21-9.20	**0.02**
mutation	mutation		mutation	wild type	2.29	0.96-4.92	0.06

CMML (N= 74)

SETBP1	*CBL*	VS	*SETBP1*	*CBL*	Hazard ratio	95% CI	P value*
wild type	mutation		wild type	wild type	1.19	0.40-2.85	0.7
mutation	wild type		wild type	wild type	1.54	0.75-3.00	0.2
mutation	wild type		wild type	mutation	1.3	0.48-4.09	0.6
mutation	mutation		wild type	wild type	3.81	1.25-9.65	**0.02**
mutation	mutation		wild type	mutation	3.19	0.86-11.92	0.08
mutation	mutation		mutation	wild type	2.46	0.76-7.03	0.1

Secondary AML (N= 56)

SETBP1	*CBL*	VS	*SETBP1*	*CBL*	Hazard ratio	95% CI	P value
wild type	mutation		wild type	wild type	3.36	0.18-17.00	0.3
mutation	wild type		wild type	wild type	1.93	0.89-3.93	0.09
mutation	wild type		wild type	mutation	0.57	0.11-10.65	0.6
mutation	mutation		wild type	wild type	4.02	0.93-12.11	0.06
mutation	mutation		wild type	mutation	1.19	0.15-24.50	0.9
mutation	mutation		mutation	wild type	2.09	0.47-6.81	0.3

*Statistically significant p values were indicated with bold font.

Supplementary Table 14. Primers for *SETBP1* sequencing and PCR specific for mutant alleles.

SETBP1 Sequencing	
Exon2_Forward	TCACCTTTCCCTTTTCCC
Exon2_Reverse	CCCTAAGAAGTTGAGGATAAAATG
Exon3_Forward	TGGTAAGTCCATTGCTGGTC
Exon3_Reverse	ATCCAAGGTTCGGGTTTCTG
Exon4_1_Forward	CATGCTCATCTTTGTTTCTCTCTC
Exon4_1_Reverse	ATGCTTTCTGGGCATTCTTG
Exon4_2_Forward	CCCCAGAACCACCTACGG
Exon4_2_Reverse	TTTGGATGCTGGATTTCTGG
Exon4_3_Forward	CCCAGGAGGTGTGTCTAAGC
Exon4_3_Reverse	CTTTTGCCTTCAGAGCAACG
Exon4_4_Forward	AGAAAGTTGGAAAGCTCGGC
Exon4_4_Reverse	GGACAGCGTGATTTCCTTTAG
Exon4_5_Forward	ACACAGTGGAACCTGGAAGC
Exon4_5_Reverse	AGGCCTACCACGCTTCTTC
Exon4_6_Forward	ACCACGAGAATCCATATCCC
Exon4_6_Reverse	CTTTGTCTGCGCTACTCAGC
Exon4_7_Forward	CACAAGCATAAGCACAAGGAAG
Exon4_7_Reverse	ATGTGTCTGAGGTGCAAAGC
Exon5_Forward	TGTTGTCTATCTTCCTGTTCCC
Exon5_Reverse	TCAACAGGCCATTCTCAGTG
Exon6_1_Forward	AGAGGCTGAGTTGAAGGCAC
Exon6_1_Reverse	GGTGGCCATGATGGTGTC
Exon6_2_Forward	GACCTGCCCAGCAAAAGAG
Exon6_2_Reverse	CGCTTCCCACGTGTCAG
Allele specific PCR (p.Asp868Asn)	
SETBP1_D868N_OF	TTCAGTCACTTGTGGCGTCT
SETBP1_D868N_OR	ATGGCACCGGGTAATAGTGA
SETBP1_D868N_FA	GGAGACGATCCCCAGCA
SETBP1_D868N_RG	TCCCAATGCCGCTGTC
Allele specific PCR (p.Gly870Ser)	
SETBP1_G870S_FA	AGTGAGGAGACGATCCCCAGCGACATCA
SETBP1_G870S_RG	GAAGTGCTGTTGTTGTCTGTCCCAATTCC
SETBP1_G870S_OF	TATGCCAAATCTCCAGCCCATCAGTGCT
SETBP1_G870S_OR	GTTGTCCACAATGAGATGCTTTTGCCGG

1. **Oakley, K. et al. Setbp1 promotes the self-renewal of murine myeloid progenitors via activation of Hoxa9 and Hoxa10. *Blood* 119, 6099-108 (2012).**