Pseudo-mutant P53 is a unique phenotype of *DNMT3A*-mutated pre-leukemia

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Received: November 9, 2021.
Accepted: January 19, 2022.
Prepublished: February 24, 2022.

https://doi.org/10.3324/haematol.2021.280329

Supplemental information for Tuval A et al, Pseudo-mutant P53 is a unique phenotype of *DNMT3A*-mutated pre-leukemia

Samples:

All samples were collected, Ficoll separated and viably frozen. CD3 cells were separated (EasySep™, StemCell Technologies, Vancouver, Canada) and expanded *in vivo* as previously described[1]. Mobilized peripheral blood mononuclear cells (PBMCs) and cord blood samples were also enriched for $CD34^+$ cells (CD34 MicroBead Kit, Miltenyi Biotec, Bergisch Gladbach, Germany).

Mass cytometry:

Staining procedure was performed at room temperature (20°C). Briefly, $5x10^6$ Cells were incubated in Maxpar® PBS containing 1.25µM Cell-ID™ Cisplatin (Fluidigm, San Francisco, CA) at room temperature for 1 min, followed by incubation with antibodies directed at cell surface proteins (Supplemental tables S2A, S2B and S2C) for 30 min at room temperature in Maxpar® Cell Staining Buffer (Fluidigm, San Francisco, CA). Cells were washed, fixed and permeabilized using the Maxpar® Nuclear Antigen Staining Buffer Set (Fluidigm, San Francisco, CA), and then incubated with antibodies directed at intra-nuclear proteins for 30 minutes at room temperature. Cells were washed and fixed in 4% Paraformaldehyde (Thermo Fisher Scientific, Waltham, MA) overnight at 4°C. Following this, cells were incubated in 125nM Cell-ID™ Intercalator-Ir solution (Fluidigm, San Francisco, CA), washed, resuspended in Maxpar® Water containing 1:10 EQ™ Four Element Calibration Beads (Fluidigm, San Francisco, CA) and acquired via a CyTOF- Helios™ mass cytometer (Fluidigm, San Francisco, CA). Data were normalized and concatenated using CyTOF Software v.6.7.1014 and analyzed (i.e. gating, multidimensional analyses and unbiased analyses) using Cytobank (Cytobank Inc.[2] Beckman Coulter, Brea, CA, USA). viSNE[3] and FlowSOM analyses were performed using all surface markers.

Maxpar® X8 Antibody Labeling Kit (Fluidigm, San Francisco, CA, USA) was used to conjugate antibodies to heavy metals. In cases where intra-cellular antibodies were of different batches, they were combined and the titer of the pool was validated (with the first calibrated batch serving as a reference) using a primary AML sample harboring *TP53*^{P151A} mutation. Since cadmium and zinc chelators can influence the conformation of P53[4], all the reagents that were used for the intra-cellular staining did not contain zinc chelators, and antibodies were not conjugated to cadmium.

Xenotransplantation assays and *in vivo* pharmacologic treatment:

We used the following mouse strains of immune-deficient NSG (NOD/SCID/IL-2Rgc-null) mice: NSG (Stock No: 005557), NSG-hSCF (Stock No: 017830), that transgenically express human SCF, and NSG-SGM3 (Stock No: 013062), that transgenically express human IL-3, GM-CSF and SCF (all from The Jackson Laboratory, Bar-Harbor, ME, USA).

1-2.5x10^6 CD3 depleted mononuclear cells were injected intra-femoraly (right femur) into 8 to 12-week-old female mice. Mice were sub-lethally irradiated (200 cGy) 6–24 hours before human cells' injection.

pCAP-250 and the control peptide were delivered by implanting subcutaneous micro-osmotic pumps that excrete the peptides at a rate of 19 mg/kg/day (over a period of 14 days), achieving blood concentrations of approximately 6 ugr/mL[5].

Mice were sacrificed on day 56 (three weeks following pump implantation). The bone marrows of the injected bone (right femur) and the non-injected bones (left femur, tibiae) were flushed with Iscove's Modified Dulbecco's Medium (IMDM) (Cat: 01-058-1A, Biological Industries, Beit Ha'emek, Israel). Cells were extracted from both injected and non-injected bones to increase the yield of human cells. Cells were filtered through a 35µm cell strainer (Cat: 352235, Corning, Corning, NY, USA) to obtain a single-cell suspension.

Human engraftment was assessed by flow cytometry, as described below.

Experiments that included RNA sequencing or mass cytometry analyses of engrafting cells were performed as follows: eight weeks following human AML sample injection, mice were IV injected with a single dose of either pCAP-250 or the scrambled peptide (16.6 mg/kg). Mice were sacrificed 12 hours later. Bone marrows were harvested as described.

Flow Cytometry:

Analyses were performed using antibody panel (supplemental table S3), on Cytoflex (Beckman Coulter, Brea, CA, USA), using CytExpert software v 2.4.0.28 (Beckman Coulter, Brea, CA, USA).

Deep targeted DNA Sequencing:

Sequencing of mononuclear hematopoietic cells and of expanded T cells from each sample was performed in duplicates following genomic DNA extraction (DNeasy kit, Qiagen, Hilden, Germany).

We used a panel of single molecule Molecular Inversion Probes (smMIPs)[6] (designed with MIPgen software[7] that covers recurrently mutated AML "hotspots" in 33 genes (supplemental table S4).

For deep targeted DNA sequencing of engrafting human cells, cells retrieved from bone marrows of sacrificed mice were sorted by FACS BD FACSAria™ III Cell Sorter (BD Biosciences, San Jose, CA, USA) according to the main engrafting sub-populations using a panel of monoclonal antibodies (supplemental table S5). See supplemental figures S6 and S7 for examples of the sorting outline. Sorted cells underwent whole genome amplification (Repli-G, Qiagen, Hilden, Germany).

Libraries were prepared using a panel of smMIPs that was designed to capture mutations known to be present in the original injected samples (supplemental table S6).

Validation of sequencing results of *DNMT3A*^{R882} was performed when the coverage depth of the targets was insufficient (less than 100X). This was done by preparing a different library using an amplicon-based approach. This approach was used also when only a single target was of interest (i.e.: for *DNMT3A*^{R882} mutated clonal hematopoiesis samples).
Primary PCR for *DNMT3A* (exon 23) was performed with the following primers:
Forward:CTACACGACGCTCTTCCGATCTTAACTTTGTGTCGCTACCTC
Reverse:CAGACGTGTGCTCTTCCGATCTTTTTCTCCCCCAGGGTATTTG
Secondary PCR was performed with the following primers:

Forward primer:
AATGATACGGCGACCACCGAGATCTACAC[Fw_Index_D5XX]ACACTCTTTCCCTACACGACGCTCTTCCG;

Reverse primer:
CAAGCAGAAGACGGCATACGAGAT[Rev_Index_D7XX]GTGACTGGAGTTCAGACGTGTGCTCTTCCG;

All Sequencing were performed with MiSeq, MiniSeq and NovaSeq sequencers (Illumina, San Diego, CA, USA).

Data pre-processing and variant calling:

Paired-end 2 X 151bp sequencing data were converted to fastq format. Reads were merged using BBmerge v38.62[8] with default parameters, followed by trimming of the ligation and extension arm using Cutadapt v2.10[9]. Unique Molecular Identifiers (UMIs) were trimmed and assigned to each read header. Processed reads were aligned using BWA-MEM[10] to a custom reference genome, comprised of the appropriate smMIP panel sequences ± 150 bases extracted from broad hg19. Aligned files were sorted, converted to BAM (SAMTools V1.9[11]) followed by Indel realignment using AddOrReplaceReadGroups (Picard tools) and later IndelRealigner (GATK v.3.7[12]). Variant calling was done using mpileup and MuTect2 (in a tumor-only mode, GATK 3.7[12] (for the single nucleotide variant (SNVs), and Varscan2 v2.3.9[13] and Platypus[14] for indels. Variants were annotated using ANNOVAR[15]. This bioinformatics pipeline can identify variants as low as 0.005 (manuscript under preparation).

Single cell RNA sequencing (scRNAseq):

Libraries were prepared using 10X Genomics Chromium Single Cell 3′ Reagent Kits v3 (10X Genomics, Pleasanton, CA, USA) according to manufacturer's protocol. Libraries were prepared twice, using biological duplicates. Sequencing was performed with Illumina NextSeq sequencer (Illumina, San Diego, CA, USA).

Demultiplexing, alignment, filtering, barcode counting, and UMI counting were performed using Cell-Ranger (version 3.1.0) bioinformatics pipeline.

In order to exclude contamination of mice cells in the samples that were obtained following engraftment, the pipeline was run twice with different genomes: once with a joint genome of mm10 and hg38 and the other with only hg38. Cells were determined to be of murine origin if the expression of mouse genes was above 20% from the total gene expression in the joint analysis (mm10 & hg38).
Altogether, 80-120 cells were excluded from each sample.

The output from the hg38 genome was used for further analysis with R version 3.6.0 and Seurat version 3.1.1[16].

Cell filtering was based on the total number of genes or UMI counts per cell (high or low 5 percentiles were removed), and the percentage of mitochondria genes (filtered out when higher than 20%). The number of cells after filtering ranged between 2203 and 3779 per sample. 26 clusters were created with 2000 variable genes and 20 principal components (PCs).
Additionally, Somatic variants were called for genes that are known to be mutated in the samples.

Gene set enrichment analyses:

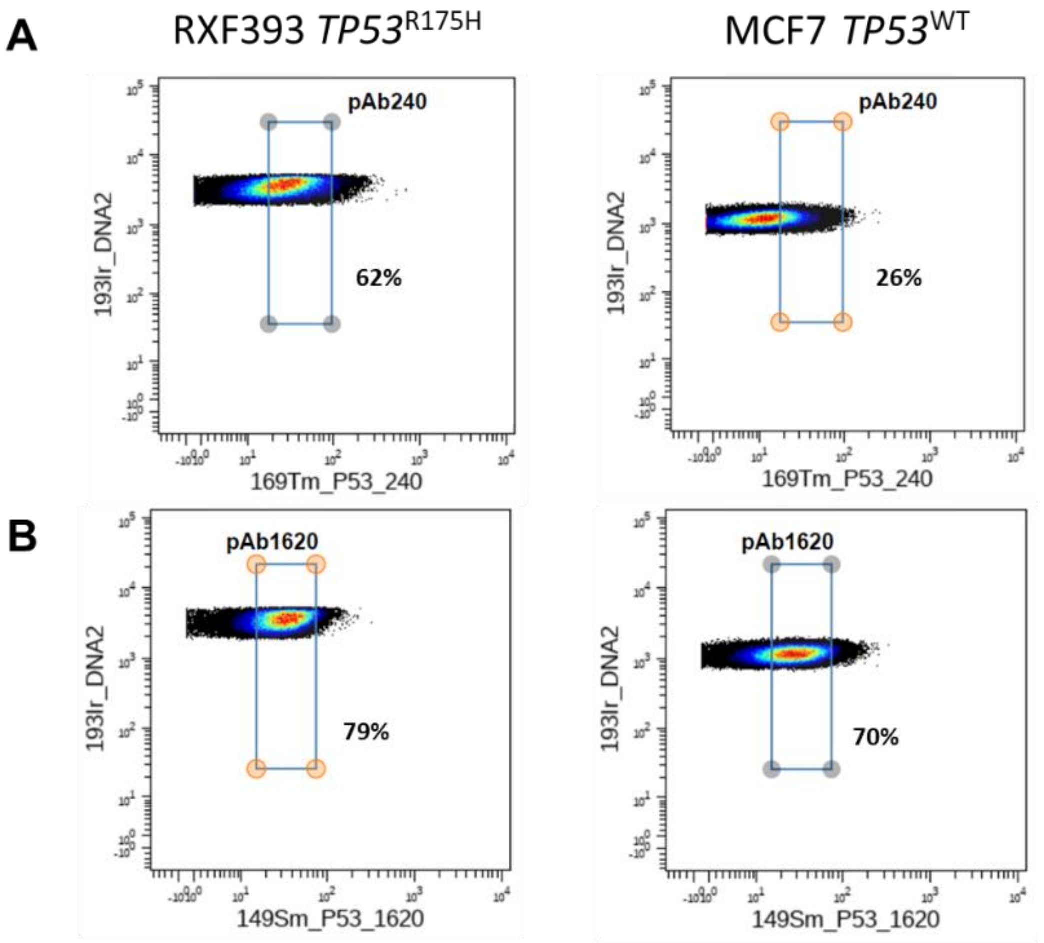
An overrepresentation analysis (ORA)[17] was employed. The gene sets associated with a blood or immune cell types, were downloaded from PanglaoDB database[18] and compared to the differentially positive expressed cluster markers filtered with criteria of $\ln FC \geq 1$ and $padj \leq 0.05$. To test for overrepresentation of successes in the sample, the hypergeometric p value was calculated using R function phyper with lower tail= false as the probability of randomly drawing k or more successes from the population in n total draws[19]. The FDR was achieved by adjusting the p value using Benjamini and Hochberg[20]. In addition, Enrichr was used to identify enrichment of cluster marker genes with various molecular pathways[21,22].

Statistical analyses:

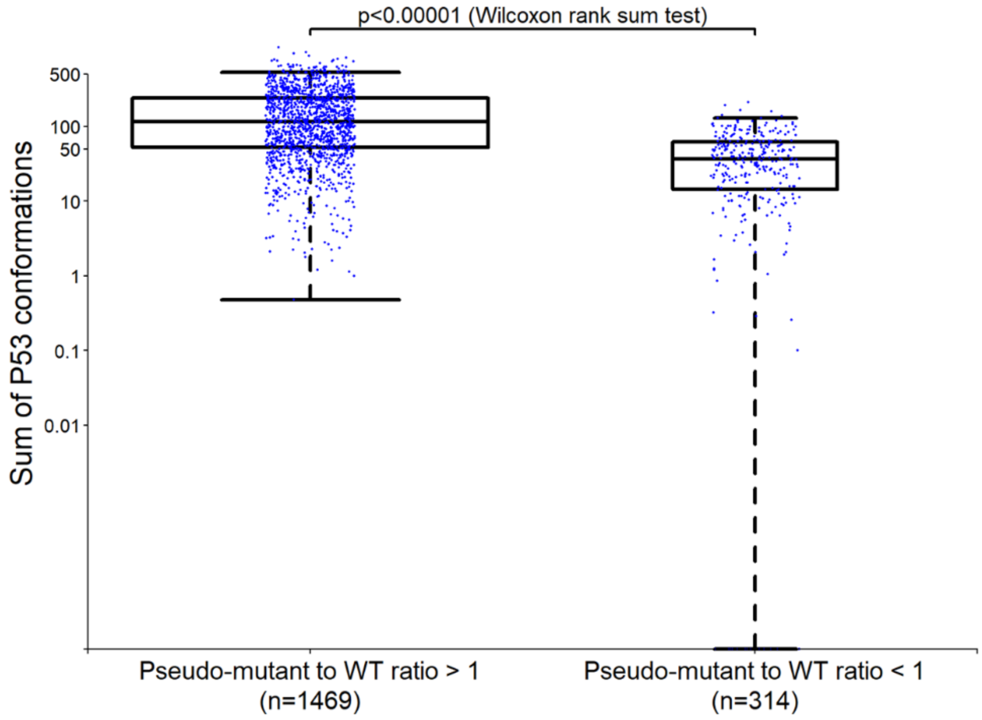
The dependency between treatment and the size of each cluster was determined by chi square test for independence. For a two-by-two table the Yates continuity correction was applied. A post-hoc standardized residuals analysis with Bonferroni correction for multiple comparisons was used to find out which clusters had a significantly different size than expected. The same statistical analyses were performed also for unbiased analyses of mass cytometry data of engrafting human cells.

Supplemental figures

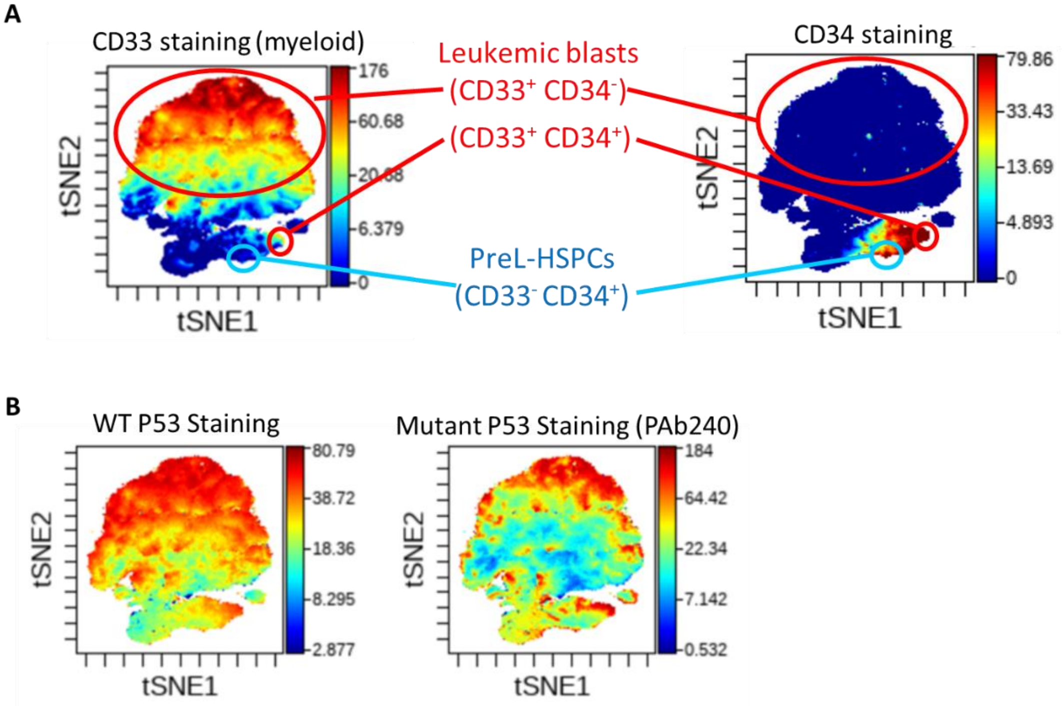
Supplemental Figure S1: Calibration of intracellular monoclonal antibodies



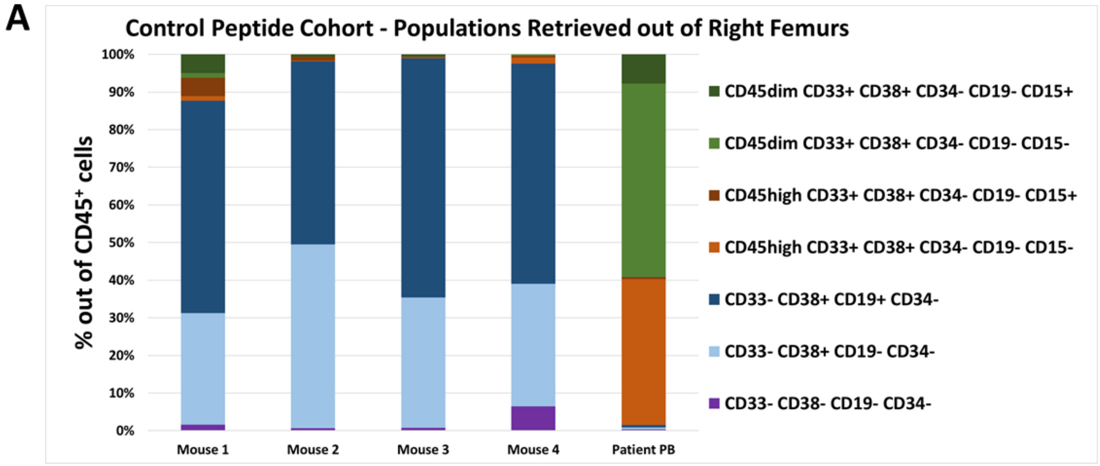
Supplemental Figure S2: Total P53 expression in preL-HSPCs according to their pseudo-mutant to WT ratio

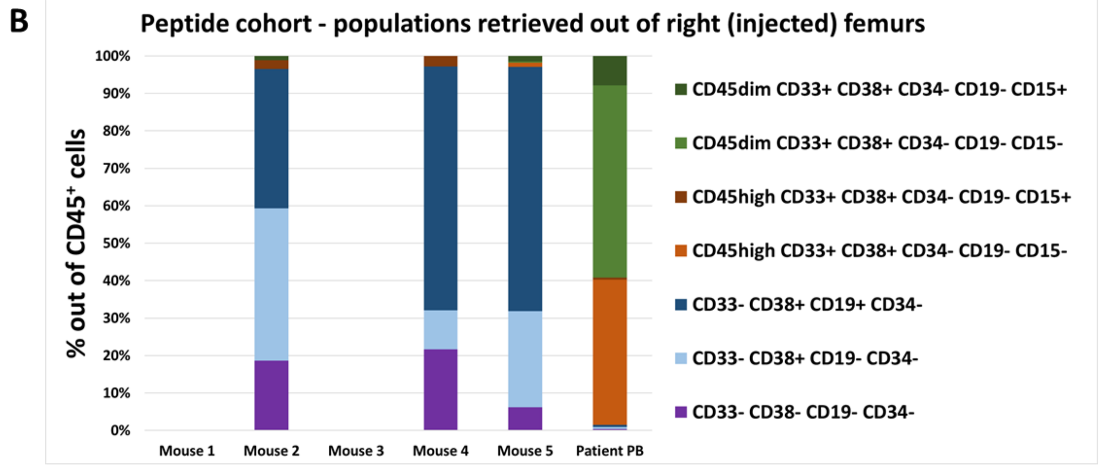


Supplemental Figure S3: Mass cytometry of a *TP53*^{R248Q} AML sample

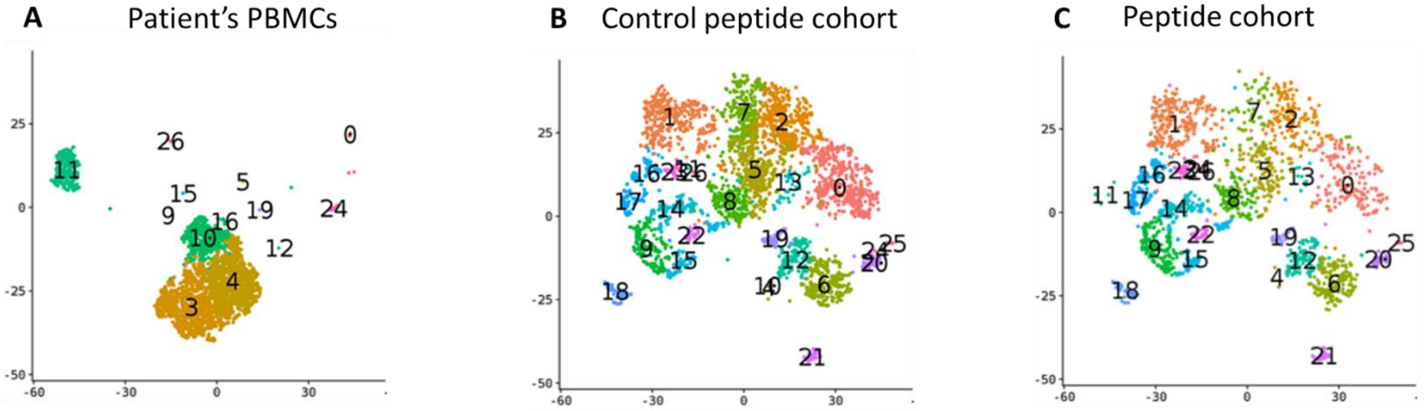


Supplemental Figure S4:
Flow cytometry analyses of representative engrafting sub-populations of sample #160005





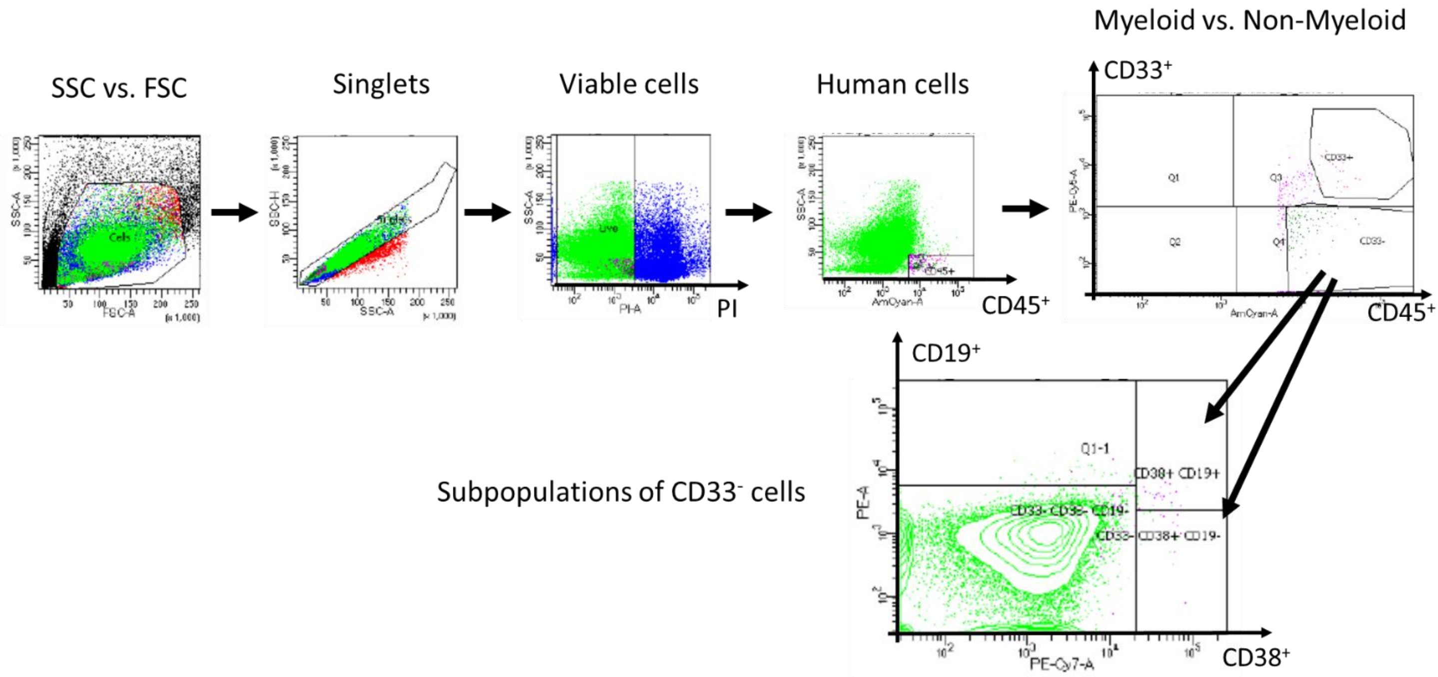
Supplemental Figure S5:
Single cell RNA sequencing of *DNMT3A*^{R882H}, *NPM1*c AML blasts and of this sample's patient-derived *DNMT3A*^{R882H} pre-leukemic xenografts


A Patient's PBMCs

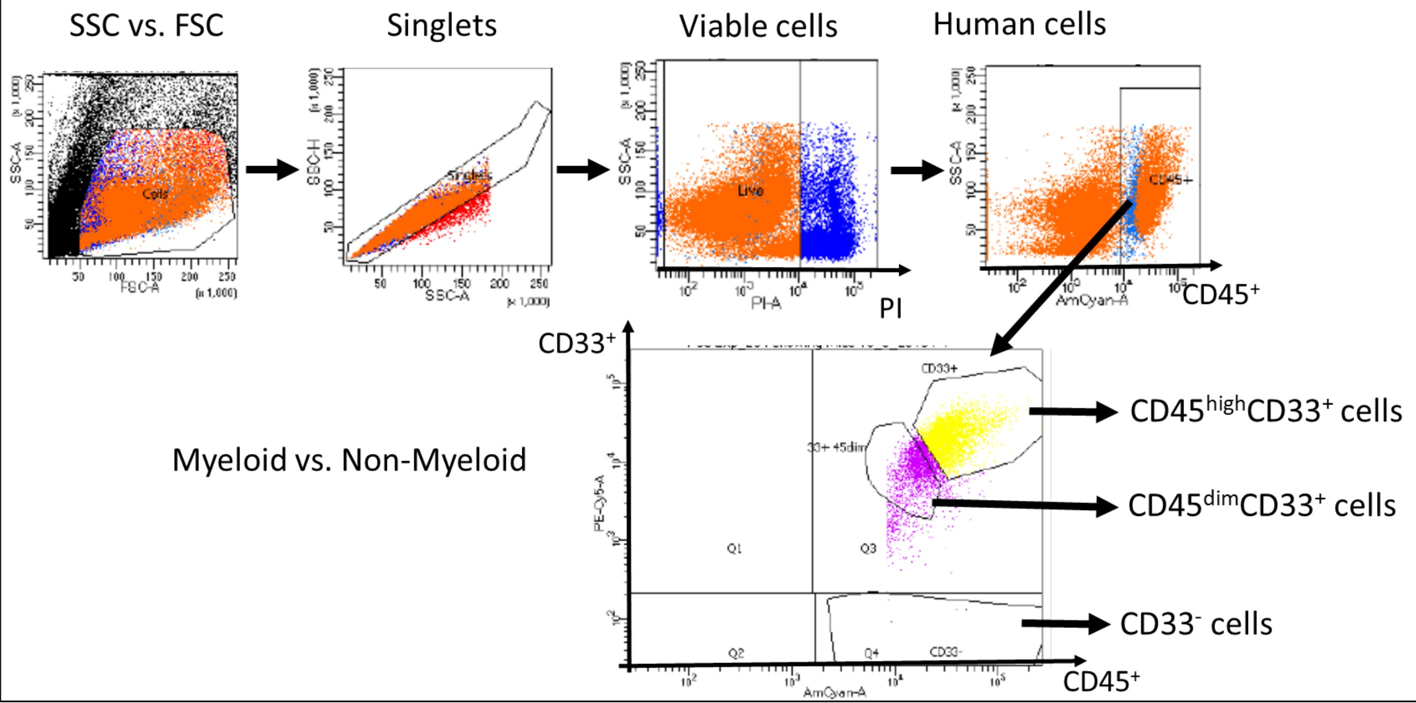
B Control peptide cohort

C Peptide cohort

Supplemental Figure S6: Example of the sorting outline of a multi-lineage engraftment sample



Supplemental Figure S7: Example of the sorting outline of a myeloid (leukemic) engraftment



Legends for supplemental figures

Supplemental Figure S1: Calibration of intracellular monoclonal antibodies

The staining titer (per 1 X 10^6 cells) of the intra-cellular antibodies was calibrated using MCF 7 cells line (*TP53* WT) and RXF 393 cell line (*TP53*^{R175H}). Staining was performed while using the two P53 conformation-specific monoclonal antibodies simultaneously.
Y-axis represents viable cells (Iridium positive).
Positively stained cells are gated.
Percentage of gated cells is presented next to each gate.

(A) Staining with PAb240 (targeting the mutant conformation of P53 or its denatured conformation). Most MCF 7 cells are negative for this staining (as expected).
Reactivity of some MCF 7 cells with PAb240 can represent background staining, that might result from denatured P53 or binding of MDM2 to p53[23].
Overall, denaturation caused by the staining protocol is minimal.

(B) Staining with PAb1620 (targeting the WT conformation of P53).
Both cell lines show a similar staining.
Of note, although RXF 393 is homozygous for R175H mutation, it was found to be reactive with PAb1620.
This can represent background staining or protein in its wild type conformation.
A similar observation was previously reported in other homozygous cell lines[24,25].
This can be attributed to the relatively low temperatures used while performing the staining procedure [25, 26].

Supplemental Figure S2:
Total P53 expression in preL-HSPCs according to their pseudo-mutant to WT ratio

Estimate of the total expression of P53 (sum of the intensities of PAb240 and PAb1620 staining) in each immunophenotypic pre-leukemic hematopoietic stem and progenitor cell (preL-HSPC) of 9 AML samples.
Cells were divided into two cohorts: cells in which the pseudo-mutant to wild type (WT) conformation ratio (PM/WT-CR) of P53 was greater than 1, and cells in which this ratio was less than 1.
n denotes the number of cells in each cohort.
Cells with a high PM/WT-CR had a higher total expression of P53 (median total intensity of 116.3) when compared with cells with a low PM/WT-CR (median total intensity of 36.4).

Box plot centers, hinges and whiskers represent the median, first and third quartiles and 1.5 X interquartile range, respectively.
Boxes are drawn with widths proportional to the square-roots of the number of observations in each group.
The two-tailed, non-paired, nonparametric Wilcoxon rank sum test was used with 95% confidence interval and continuity correction.

Supplemental Figure S3: Mass cytometry of a *TP53*^{R248Q} AML sample

Single cell analysis of P53 conformations in a primary human *TP53*^{R248Q}-mutated AML sample (#161632) was performed by mass cytometry similar to Figure 1.

(A) viSNE analysis of mass cytometry single cell data showing CD33 staining (left panel) and C34 staining (right panel) in the peripheral blood mononuclear cells.
Leukemic blasts (CD33$^+$ CD34$^-$) are clustered in the upper part of the plot (circled in red).
CD34$^+$ cells are clustered in the lower part of the plot.
Some of them are leukemic blasts (CD33$^+$ CD34$^+$, circled in red) and some are pre-leukemic HSPCs (CD33$^-$ CD34$^+$, circled in blue).

(B) P53 staining for the two conformations of P53 (as detected by the monoclonal antibodies PAb1620 for the wild type conformation and PAb240 for the mutant conformation) superimposed on the same viSNE analysis.
TP53^{R248Q} has a stronger reactivity with PAb1620 than with PAb240.
As expected, most leukemic blasts are PAb1620-positive

Supplemental Figure S4:
Flow cytometry analyses of representative engrafting sub-populations of sample #160005

Injected peripheral blood mononuclear cells appear in the right bars (Patient PB).
Only human CD45$^+$ cells that were extracted from the right femurs of the mice are presented. PB – peripheral blood

(A) Cells retrieved from control peptide cohort mice

(B) Cells retrieved from pCAP-250-treated mice (peptide cohort)

Most engrafting cells are non-myeloid (blue colors) as opposed to the injected blasts, reflecting their differentiation capacity and their non-leukemic origin.

Supplemental Figure S5:
Single cell RNA sequencing of *DNMT3A*$^{\mathbf{R882H}}$, *NPM1*c AML blasts and of this sample's patient-derived *DNMT3A*$^{\mathbf{R882H}}$ pre-leukemic xenografts

t-distributed stochastic neighbor-embedding (tSNE) analyses of single cell RNA sequencing data. Unbiased clustering was performed on all samples together.
PBMCs - peripheral blood mononuclear cells.

(A) *DNMT3A*^{R882H}, *NPM1*c AML blasts (sample #160005).

(B) Engrafting *DNMT3A*^{R882H} pre-leukemic cells from the control peptide cohort.

(C) Engrafting *DNMT3A*^{R882H} pre-leukemic cells from the pCAP-250-treated cohort.

Blasts are represented by four clusters (3,4,10,11). Somatic variant calling of RNA sequencing data revealed the *NPM1*c mutation in this sample. Cluster 24 represents B cells. In contrast, engrafting cells have a preserved differentiation capacity as reflected by 22 different clusters that represent them. Clusters that represent blasts are not found among the engrafting cells. Somatic variant calling of RNA sequencing data revealed only the *DNMT3A* mutation in the engrafting cells, without *NPM1*c.

Supplemental Figure S6:
Example of the sorting outline of a multi-lineage engraftment sample

A multi-lineage engraftment was defined when a subpopulation of B cell progenitors ($CD33^-CD3^-$ cells expressing $CD38^+$ and $CD19^+$) could be identified and comprised more than 10% of the engrafting human cells.
Human cells were then sorted to three main sub-populations: $CD33^+$, $CD33^-CD38^+CD19^+$ and $CD33^-CD38^+CD19^-$ cells.
First, cells were gated according to their side scatter and forward scatter characteristics. Singlets were identified as those having linear proportions between their side scatter height and their side scatter area. Next, viable cells were identified as being PI negative. Out of the viable cells, human cells of interest are those stained as human CD45 positive. Human cells were divided into two main groups according to their CD33 staining.
CD33 negative cells were further divided to progenitors ($CD33^-CD38^+CD19^-$) and B-lineage progenitors ($CD33^-CD38^+CD19^+$).

Supplemental Figure S7:
Example of the sorting outline of a myeloid (leukemic) engraftment.

When a myeloid (leukemic) engraftment was noted (defined when more than 90% of the human cells were $CD33^+$), engrafting human cells were sorted to immature myeloid cells ($CD45^{dim}$ $CD33^+$) and mature myeloid cells ($CD45^{high}$ $CD33^+$).

Supplemental tables

Supplemental Table S1: Clinical characteristics of primary samples

sample	Gender	Sample Type	Diagnosis	Age (years)	Blasts immunophenotype
161632	Male	PB	AML	57	CD34: 91%, CD 117: 89%, HLA-DR: 90%, CD38: 97%, CD33: 98%, CD13: 93%, CD36: 17%, CD64: 19%, CD71: 85%, MPO: 75%
151296	Female	PB	AML	77	MPO+, CD33+, CD117+, CD38+, partial CD123+, partial CD13+, partial CD11c+, partial CD64+, partial CD56+, CD34-, HLA DR-, CD11b-, CD65-, CD16-, CD10-, CD15-, CD36-, CD14-, CD4-, CD7-, CD2-, CD19-, CD71-, CD235-, TdT-
160436	Female	PB	AML	51	CD34-, partial CD117+, HLA-DR-, CD2-, CD4-, CD7-, CD10-, CD11b-, subset partial dim CD11c+, partial CD13+, CD14-, CD15-, CD16-, homogeneous CD33+, CD36-, heterogeneous CD38+, partial subset CD56+, partial CD64+, CD65-, dim CD71+, equivocal dim CD123+ and CD235a-. cCD3-, CD19-, cCD22-, cCD79a-, MPO+ and TdT-.
151050	Female	PB	AML	79	CD34-,CD117+, CD33+, CD13-, CD11b-, CD11c, CD64+ dim and partial. HLA-DR -, CD65-, CD16-, CD56-, CD36-, CD10-, CD15- and CD123-. No expression of lymphoid markers.
151044	Male	PB	AML	70	84% CD117+/CD34- myeloid precursors with: CD45+, CD34 -, CD117 dim+, HLA-DR-, CD38+, CD123 dim+, CD11b-, CD11c+, CD13-, CD14-,CD15-, CD33+, CD36-, CD64-, CD65-, CD71+, CD235-, cyMPO+, Tdt- and CD56-/+ small subset+. Negative for: CD2, cyCD3, CD4, CD7, CD19, cyCD22, cyCD79a. Besides the blast population, there are monocytes that are slightly left shifted with a subset being negative for CD14 and dim positive for CD36. The CD14+ monocytes are dim positive for CD123, partly positive for CD16 and CD56.
160005	Male	PB	AML	38	CD117+, CD13+, CD38+, CD11b-, CD15-, CD64-, CD33+, HLA-DR+, CD123-, CD34-, MPO+. cyCD19=0% ,cyCD3=0% ,CD64=0% ,CD123=0%, CD10-
150279	Female	PB	AML	63	Positive for CD117 (dim equivocal), CD11b (predominantly negative, subset dim), CD33, CD38 (dim), CD71 (equivocal), CD123, CD11c, CD64 (very dim), with myeloperoxidase. Negative for CD13, CD14, CD15, CD16, CD36, CD56, CD65, HLA-DR, CD235a, CD19, CD10, cCD22, cCD79a, cCD3,CD2, CD4, CD7, or nTdT
160537	Male	PB	AML	78	Blasts are heterogeneous CD34+ and CD117+. Additional markers show: CD2-, CD4-, CD7-, dimCD11b+, homogeneous CD11c+, CD13+, CD14-, CD15-, CD16-, CD33+, CD36-, CD38+, CD56-, CD64+, partial subset CD65+, dim CD71+, dim CD123+, CD235a-, partial subset HLA-DR+ and TdT-. cCD3-, CD10-,CD19-, cCD22-, cCD79a- and MPO+.
160406	Female	PB	AML	64	CD34- and partial CD117+, CD2-, partial dim CD4+, CD7-, CD10-, partial CD11b+, CD11c+, CD13+, CD14+, partial dim CD15+, subset CD16+, CD33+, bimodal CD36+,CD38+, partial dim CD56+, bimodal CD64+, CD65+, dim CD71+, partial dim CD123+, CD235a- and HLA-DR+, cCD3-, CD19-, cCD22-, cCD79a-, MPO+, TdT-.
150491	Female	PB	AML	43	CD33+ , CD13+, CD11c+ ; Partial: MPO+, CD117+, CD71, HLA DR+, CD38+, CD123+ (21%), CD34+ (20%), CD11b+ , CD15+, CD36+, CD64+, CD7+ ; Negative: CD65-, CD16-, CD10-, CD14-, CD4-, CD2-, CD19-, CD56-, CD235-, TdT-, cCD3-, CD79a-, cCD22-
141467	Male	Mobilized PBMCs	Multiple myeloma	61	
141164	Female	Mobilized PBMCs	Healthy AlloBMT donor	63	
141464	Female	Mobilized PBMCs	Non Hodgkin's lymphoma, following chemotherapy	58	
Cord Blood					

Supplemental Table S1: Clinical characteristics of primary samples

sample	Cytogenetics	mutations in specifed genes			
		TP53	*DNMT3A*	*NPM1* c	*FLT3*
161632	**46,XY,del(3)(p21),+del(3)(q21),+del(6)(q21),del(7)(q22q32),-11,-14,-17,+mar[9]**	**R248Q (VAF=94%)**	**none**	**none**	**none**
151296		**none**	**D702Y**	**positive**	**ITD (low allelic ratio)**
160436	**Normal Karyotype**	**none**	**G722D**	**positive**	**ITD**
151050	**Normal**	**none**	**N717fs**	**positive**	**TKD**
151044		**none**	**R882C**	**positive**	**ITD**
160005	**46 XY [8]**	**none**	**R882H**	**positive**	**none**
150279		**none**	**R882C**	**positive**	**ITD**
160537	**normal karyotype**	**none**	**R882H**	**positive**	**none**
160406		**none**	**R882C**	**positive**	**ITD (low allelic ratio)**
150491		**none**	**R882H**	**positive**	**none**
141467		**none**	**R882H (VAF = 19.7%)**	**none**	**none**
141164		**none**	**R882H (VAF = 34%)**	**none**	**none**
141464		**none**	**R882H (VAF = 69%)**	**none**	**none**
Cord Blood		**none**	**none**	**none**	**none**

Supplemental Table S2A:
Antibodies used for mass cytometry of primary human samples

Antibody	label	clone	Catalogue number (Fluidigm, San Francisco, CA, USA) (unless stated otherwise)
Surface			
CD38	172Yb	HIT2	3172007B
CD184 (CXCR4)	175Lu	12G5	3175001B
CD117 (ckit)	143Nd	104D2	3143001B
CD33	158Gd	WM53	3158001B
CD19	142Nd	HIB19	3142001B
CD11b (Mac-1)	209Bi	ICRF44	3209003B
CD34	166Er	581	3166012B
CD15 (SSEA-1)	164Dy	W6D3	3164001B
CD123 (IL-3R)	151Eu	6H6	3151001B
CD45	154Sm	HI30	3154001B
CD45RA	153Eu	HI100	3153001B
CD90	161Dy	5 E 10	3161009B
CD133/1	165Ho	REA753	Miltenyi Biotec, Bergisch Gladbach, Germany
CD133/2	155Gd	REA816	Miltenyi Biotec, Bergisch Gladbach, Germany
CD49d	141Pr	9F10	3141004B
CD16	148Nd	3G8	3148004B
CD79b	162Dy	CB3-1	3162008B
CD3	170Er	UCHT1	3170001B
Intranuclear			
Mutant P53	169Tm	pAb240	OP29 (Merck, Kenilworth, NJ, USA)
WT P53	149Sm	pAb1620	OP33 (Merck, Kenilworth, NJ, USA); MABE339 (Sigma-Adlrich, St. Louis, MO, USA)
p21 Waf1/Cip1	159Tb	12D1	3159026A

Supplemental Table S2B: Antibodies used for mass cytometry of *DNMT3A* -mutated AML patient-derived xenografts			
Anti human antibody	**label**	**clone**	**Catalogue number (Fluidigm, San Francisco, CA, USA) (unless stated otherwise)**
Surface			
CD38	**172Yb**	**HIT2**	**3172007B**
CD184 (CXCR4)	**175Lu**	**12G5**	**3175001B**
CD117 (ckit)	**143Nd**	**104D2**	**3143001B**
CD33	**158Gd**	**WM53**	**3158001B**
CD19	**142Nd**	**HIB19**	**3142001B**
CD11b (Mac-1)	**209Bi**	**ICRF44**	**3209003B**
CD34	**166Er**	**581**	**3166012B**
CD15 (SSEA-1)	**164Dy**	**W6D3**	**3164001B**
CD123 (IL-3R)	**151Eu**	**6H6**	**3151001B**
CD45	**154Sm**	**HI30**	**3154001B**
CD3	**170Er**	**UCHT1**	**3170001B**
CD44	**171Yb**	**IM7**	**3171003B**
HLA DR	**174Yb**	**L243**	**3174001B**
CD64	**146Nd**	**10.1**	**3146006B**
CD7	**147Sm**	**CD7-6B7**	**3147006B**
Intracellular			
Mutant P53	**169Tm**	**pAb240**	**OP29 (Merck, Kenilworth, NJ, USA)**
WT P53	**149Sm**	**pAb1620**	**OP33 (Merck, Kenilworth, NJ, USA); MABE339 (Sigma-Adlrich, St. Louis, MO, USA)**
p21 Waf1/Cip1	**159Tb**	**12D1**	**3159026A**

Supplemental Table S2C: Antibodies used for mass cytometry of *TP53* -mutated AML patient-derived xenografts

Anti human antibody (unless stated otherwise)	label	clone	Catalogue number (Fluidigm, San Francisco, CA, USA) (unless stated otherwise)	Titer ($uL/10^6$ cells)
Surface				
Anti mouse CD45	89Y	30-F11	3089005B	0.4
Anti mouse MHC class I (H-$2D^b$)	144Nd	28-14-8	3144016B	0.4
CD38	172Yb	HIT2	3172007B	0.4
CD184 (CXCR4)	175Lu	12G5	3175001B	0.4
CD117 (ckit)	143Nd	104D2	3143001B	0.4
CD33	158Gd	WM53	3158001B	0.4
CD19	142Nd	HIB19	3142001B	0.4
CD11b (Mac-1)	209Bi	ICRF44	3209003B	0.4
CD34	166Er	581	3166012B	0.4
CD15 (SSEA-1)	164Dy	W6D3	3164001B	0.4
CD123 (IL-3R)	151Eu	6H6	3151001B	0.4
CD45	154Sm	HI30	3154001B	0.2
CD45RA	153Eu	HI100	3153001B	0.4
CD90	161Dy	5 E 10	3161009B	0.4
CD133/1	165Ho	REA753	Miltenyi Biotec, Bergisch Gladbach, Germany	0.4
CD133/2	155Gd	REA816	Miltenyi Biotec, Bergisch Gladbach, Germany	0.4
CD49d	141Pr	9F10	3141004B	0.4
CD16	148Nd	3G8	3148004B	0.4
CD79b	162Dy	CB3-1	3162008B	0.4
CD3	170Er	UCHT1	3170001B	0.4
CD44	171Yb	IM7	3171003B	0.4
HLA DR	174Yb	L243	3174001B	0.4
CD64	146Nd	10.1	3146006B	0.4
CD7	147Sm	CD7-6B7	3147006B	0.4
Intracellular				
Mutant p53	169Tm	pAb240	OP29 (Merck, Kenilworth, NJ, USA)	2.1
WT p53	149Sm	pAb1620	OP33 (Merck, Kenilworth, NJ, USA); MABE339 (Sigma-Adlrich, St. Louis, MO, USA)	2
p21 Waf1/Cip1	159Tb	12D1	3159026A	2

Supplemental Table S2D: Antibodies used for mass cytometry of *DNMT3A* ^{R882H} clonal hematopoiesis mouse model

Anti mouse antibody	label	clone	Catalogue number (Fluidigm, San Francisco, CA, USA) (unless stated otherwise)	Titer (uL/10^6 cells)
Surface				
CD45.2	147Sm	104-2	3147004B	1
B220 (CD45R)	176Yb	RA3-6B2	3176002B	1
CD3e	152Sm	145-2C11	3152004B	1
CD8	146Nd	53-6.7	3146003B	1
CD19	166Er	6D5	3166015B	1
Ly-6G/C/Gr-1	141Pr	RB6-8C5	3141005B	0.5
TER119	154Sm	TER-119	3154005B	0.5
CD4	172Yb	RM4-5	3172003B	1
CD11b	148Nd	M1/70	3148003B	0.5
Ly-6A/E (Sca1)	164Dy	D7	3164005B	1
CKIT	173Yb	2B8	3173004B	1
CD150 (SLAM)	167Er	TC15-12F12.2	3167004B	1
CD48	156Gd	HM48-1	3156012B	0.5
FLT3 (CD135)	165Ho	A2F10.1	14-1351-82 eBioscience	1
CD16/32 (FCR II/III)	144Nd	93	3144009B	1
CD34	175Lu	RAM34	14-0341-82 eBioscience	1
CD127 (IL-7Ra)	174Yb	A7R34	3174013B	1
CD41	143Nd	MWReg30	3143009B	1
CD49b	170Er	HMalpha2	3170008B	1
Intracellular				
KI-67	161Dy	B56	3161007B	2
CyclinB1	153Eu	GNS-1	3153009A	2
Mutant p53	169Tm	pAb240	OP29 (Merck, Kenilworth, NJ, USA)	2.1
WT p53	149Sm	pAb1620	OP33 (Merck, Kenilworth, NJ, USA); MABE339 (Sigma-Adlrich, St. Louis, MO, USA)	2
p21 Waf1/Cip1	159Tb	F5	SC-6246 (Santa Cruz Biotechnology Inc., Dallas, TX, USA)	2

Supplemental Table S3: Antibodies and viability staining used for flow cytometry

Antibody	Manufacturer	Clone/Catalogue number	Titer
CD45-BV510	BioLegend, San Diego, CA, USA	HI30	1:200
CD33-APC	BD Biosciences, San Jose, CA, USA	WM53	1:100
CD34-APC Cy7	BioLegend, San Diego, CA, USA	581	1:100
CD15-BV421	BioLegend, San Diego, CA, USA	W6D3	1:100
CD38-PE Cy7	BioLegend, San Diego, CA, USA	HIT2	1:100
CD3-FITC	BD Biosciences, San Jose, CA, USA	UCHT1	1:100
CD19-PE	BD Biosciences, San Jose, CA, USA	HIB19	1:200
PI	BD Biosciences, San Jose, CA, USA	556463	1:100

Supplemental Table S4: smMIP panel covering recurrently mutated AML “hotspots” in 33 genes

Gene	Chromosome	Location (GRCh37/hg19)	smMIP sequence
ASXL1	20	31021069 to 31021258	GCTCTCGGCCAGATCTCCGAACCAGANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGTGATTTTGATTTGCAG
ASXL1	20	31022483 to 31022677	GCCATGTCCAGAGCTAGGAGAGAGGACCTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGAGGGAGGTGGCAGA
ASXL1	20	31023428 to 31023617	CAATGTCCACCTGTTGACAGTAACTGCCANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTTCTCATCCTTGTCC
ASXL1	20	31024719 to 31024818	CAGAAGGGCAAGTCCATGACAAAGGGCATNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGAGTTGGGAGGGGAG
ASXL1	20	31015935 to 31016124	GCTGGATGGCGAGACCACTGCAGGGCATNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAAGAGAGGAAAATAAA
ASXL1	20	31023378 to 31023547	GCCTCTGACTTTGAAGGTCACCTCACGGANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGCCTTACTTCACTCT
ASXL1	20	31016106 to 31016295	CAGGTATAAGGCAAGATCCCTCCTTCTCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCTTTATTTTCCTCTCT
ASXL1	20	31024627 to 31024791	GCCAGGGAAGGGGCTCAGTGAGCCTCTGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGACTTTTGTGGGGGG
ASXL1	20	31022594 to 31022768	GAGGATAAGGCGGCAGTAGTTGTGTTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAACGGGGAGTTGGGAGG
ASXL1	20	31024734 to 31024908	CGGGGTAATTTCCAGAAGGGCAAGTCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGGAAAGGTGGGAGAG
ASXL1	20	31022238 to 31022417	ACCCAGGGTGGTTTGATACGTGAAAGTTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCTATGGCAGTGGTGA
ASXL1	20	31022328 to 31022427	CCACTGCCATAGAGAGGCGGCCANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGCCGGGGTTGGACTGGCG
ASXL1	20	31022332 to 31022451	GCCATCGGAGGGGGGGGTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGGGTTGGACTGGCGCCAGGA
ASXL1	20	31022686 to 31022885	GCATCCGGATGTTAGAACTGAATGTGAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGAGAAAGGAGGAAAG
ASXL1	20	30946433 to 30946607	GCGAGGTCTCGGGTGCGGCCGGGGAGAANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCCTTCTTCTTCTTCTG
ASXL1	20	30946538 to 30946657	TGGTGAGGCGGACAGCCGAGGGGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGAGGTCCCGCGTGGA
ASXL1	20	30946569 to 30946688	TGGGGCCCGGGGTGGGGGGGGCTCGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGGGAGAAGGATGAAGGAC
ASXL1	20	30954152 to 30954316	GCTTAACATGAGGGTTTCATAGGATATGTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGCACACTGAAATTAG
ASXL1	20	30956795 to 30956959	GTGATATGAACTCTCTTTTGGTGCAGTGANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCCATTCTTTTGTGGT
ASXL1	20	31015888 to 31016052	GCCAGCACTGTGAGTGGTGAAAACGATGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTTGTAGGGTTTTGTT
ASXL1	20	31017109 to 31017273	ACTCATGGTTGTGATGCTTTTTCCTCAGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGGCTCTCTTTTGTT
ASXL1	20	31017642 to 31017806	GCGCTGCTATTCGTGGCCAGGCCGAGGTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGTCTGAGAGCCATGG
ASXL1	20	31017761 to 31017930	GCAGGCCTAGTGAGAAGATGATGTCTTCTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCTCTCTGGCCCTGGG
ASXL1	20	31019081 to 31019255	GCAAGGTATAGATTTCAGCTTTTTAAAAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCTGCTGCTGGAAGTG
ASXL1	20	31019174 to 31019343	GCACGGAGGTTGGTGTTGACAAGAATGGANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAAAGAGAACAGAAGC
ASXL1	20	31019361 to 31019525	CATCTCGGACGGCTTGCGACGCACCTGTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTTTTTTCCCCCTTGAT
ASXL1	20	31020603 to 31020767	GTCTTATGGACAGCTGAATCTCCCAGTTTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAGAACTTTTCTTTCC
ASXL1	20	31020733 to 31020897	GTGTTGGACAAGAATGTGGAGATTGCAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAAAAGAAGGTGGAACA
ASXL1	20	31020999 to 31021183	GCTTGTGTGTCCCAGGAGAATCAGTGCGTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATCTGTGTTTCTGGGT
ASXL1	20	31021165 to 31021269	GCTGTATACGCACTGATTCTCCTGGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTCCTTCTGGCTCTGG
ASXL1	20	31021184 to 31021348	GCTGTCGGGTGGCTGGACCACGCTGTATNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTAGAGGGGAACATCT
ASXL1	20	31021236 to 31021340	TGCAAAATCTGTGGCCTCAGATGTTCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTCGGCCAGATCTCCGAA
ASXL1	20	31021275 to 31021334	GCTAAGGATGCAAAATCTGTGGCCTCAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACAAAAAACAGGAGTCA
ASXL1	20	31021284 to 31021368	ACCCCTGCTTGTTCTGACTCCTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTCTTAGCCTCCCCATCCTTGT
ASXL1	20	31021289 to 31021488	GCATCCTTAGCAACCCCTGCTTGTTCTGANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTGTCTGGCTCAGCCT
ASXL1	20	31021392 to 31021576	GCTGCAGAGGATGTGCCTGGCAGATGGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTTCCTCTTCTGATCC
ASXL1	20	31021488 to 31021687	GCAGAGGCACGTGCCAAGTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGGCTGTGGCTTTTCGGTGTG
ASXL1	20	31021599 to 31021773	GCCGGGGCTTCTTTTCGGGAAAGGATGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACCCTCAAAGAAAACC
ASXL1	20	31022180 to 31022364	ACTGACTGGGTGATCTGACCTAGGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGTCTGCGAGGGTCCTGG
ASXL1	20	31022914 to 31023098	GCAGGAACGGTGGGTCCTTGCTCCTCATNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGCTCTGTTCTGCAGG
ASXL1	20	31022349 to 31022523	GCAGTGGTGATGGTGGTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGGACCCTCGCAGACATTAAAG
ASXL1	20	31022389 to 31022533	GTGGTGATGGTGGTGAGGCCTGTGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAGGGGCGAGAGGTCA
ASXL1	20	31022395 to 31022499	GCCTCTCTATGGCAGTGGTGACCTCTCGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTCTGCCACCTCCCTC
ASXL1	20	31022409 to 31022523	GCAGTGGTGATGGTGGTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGCCATAGAGAGGCGGCCACCA
ASXL1	20	31022822 to 31023001	GCTGCTCCACTAATCTCTCAGCTACTGAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGCCAGTTCCTTTCT
ASXL1	20	31023005 to 31023184	GATCCTTCATAGTGGGATGACTGTCAAGANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGAGCCTTGGTTTTCA
ASXL1	20	31023140 to 31023304	GTTGAGCCCCAGGTTGGAGAGGAGTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAGGGAAAGTGATACTAGA
ASXL1	20	31023250 to 31023429	GCCATCTCGAGGAGGCAGTGACAGCAATGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAACCAGAATCCAGAGA
ASXL1	20	31023556 to 31023730	GCTGGGTGTCTCGAGTATGTGCGGTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTGAGGCTGACACTAGAGAA
ASXL1	20	31023602 to 31023786	GCTGGCCAGTACTGAGTACCAGCCAAGAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGACAAGGATGAGAAA
ASXL1	20	31023729 to 31023893	GTAGGGAATCTGGGATCTTTTGGCGGACNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTGGGCTGGTGGAAGA
ASXL1	20	31023832 to 31024001	GCTACCCTGCAGCAACTGCATCACAAGTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAACCATGCCACTGTTT
ASXL1	20	31023931 to 31024120	GCGTAGCGAGCCATGGCTCTGGTCTTTTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTTTGGGGTGCTCCAG
ASXL1	20	31024053 to 31024222	GCAAGACCAGTGCCTGTTTCACAGCTATCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAGAACTGCTCTTTGG
ASXL1	20	31024155 to 31024344	GAGGATGTAATGGGATTTGTCACTGGATGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAGATGAGAAACGAGG
ASXL1	20	31024273 to 31024437	GCTCTTTCCTGGAGCAGCATTTGAATTACNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCAGAGCCAAAAAGCTT
ASXL1	20	31024384 to 31024548	GCCTGTAACATTGCTCTGATCACCCAGGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGAGTTTGTGCTTGG
ASXL1	20	31024501 to 31024680	GCAAATGCCGAGAACAGGAAAGCTACTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCCCTCCAGTTTTTCC
ASXL1	20	31024778 to 31024902	AGAAGAAGGCTCCAGAGGCTCACTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGGTGGGAGAGCTAGAGG
ASXL1	20	31024821 to 31024950	GAAAGCTTCCCATAAAATGCCTGCTTGATNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTGCTTTGTGGCTCAG
ASXL1	20	31024849 to 31025033	GCTGGTGGAACTCAGTTGGAGTTTAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACACTGGAGCGAGATG
ASXL1	20	31024975 to 31025139	GCTCTGTGTATTGTGCCTTGTGGTGAGATNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCACTTTCCTTGCAAAT
ASXL1	20	31025080 to 31025269	GGGTCCAATACAGTCATCGTGACAGANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTGGGGGAAGGCAAGAGTG

Supplemental Table S4: smMIP panel covering recurrently mutated AML "hotspots" in 33 genes

Gene	Chromosome	Location (GRCh37/hg19)	smMIP sequence
BRAF	7	140452994 to 140453158	GCTGAGTTACTAGAAAGTCATTGAAGGTCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGTGATTTTGGTCTAG
CALR	19	13054464 to 13054628	GAGGAGGAGGAGGCAGAGGACAAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGATGTCGGGGGCGGG
CALR	19	13054464 to 13054583	CGAGGAGCAGAGGCTTAAGGAGGAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGATGTCGGGGGCGGG
CALR	19	13054541 to 13054640	GCAGAGGACAAGGAGGATGATGAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAATGAAGGACAAACAGGA
CALR	19	13054574 to 13054748	GCTGTAGAGAGGCCTGCCTCCAGGGCTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTAAGGAGGAGGAAGAAG
CBL	11	119145524 to 119145688	GCAGGTCAGTTCAATGACGCAAAGAGATTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTGATCTTGTTTCTTT
CBL	11	119148841 to 119149005	CATGTGCACATCCTGTCTTACATCCTGGCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCAACTAATAGTCTTT
CBL	11	119103269 to 119103458	GCAGGTCTGTGACTGCCTGAATGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAGGGGAAGATGGAGACACT
CBL	11	119156017 to 119156211	GCCTGGTGTACAAGGCAAGGGGCGTCTTTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGGGCAATGAAAATGG
CBL	11	119170185 to 119170354	GCCTCACCTCAGCTCTCCAGTGAGATCGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTCTTTCCTATTTCTTC
CBL	11	119148946 to 119149110	GGGGTGGCCTGGCTTTTGGGGTTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGGATGTAAAGATTGAG
CBL	11	119077049 to 119077248	GCGAGGGAGAGAAGCAGGGCGTGAAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGTGGTGGTGGTGGTGCG
CBL	11	119077187 to 119077366	GCTGTTGCAGGGTGGGCGTGGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGGTTCGGGTGGCCTGATTGG
CBL	11	119103107 to 119103286	GCTATTACTTGGAGAATTTTAAGGACAGCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGTCTCCATCTTCCCC
CBL	11	119103216 to 119103380	GCTGGTAGGTATCTGGTAGCAGGTCTANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTCTTTCTTTTCCCTCCT
CBL	11	119142413 to 119142587	GCGGAATTTTGGAGAAAAGCTTTTGGGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTGTTTAATTATTGCA
CBL	11	119142524 to 119142698	GCTTTAGTAATCCGAAATGTGTCTCCCTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTTTTCTCAGAGTTCC
CBL	11	119144497 to 119144676	GCCATGGCTCTGAAATCCACTATTGATCTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCCTTCCTTTCCTTGA
CBL	11	119144571 to 119144740	GCTCTTCCAAGGGACTATTGTCCTGGGGANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCCTACCTGAAAGAGT
CBL	11	119144633 to 119144797	GCTACTTCGGTGAAGAGAAAGCTTTTTTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGTTCTGGGCTGGAGG
CBL	11	119145621 to 119145785	GCAATAGCCAAGGTTCTGCAATAGGATTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAGTGAAAGCTCGGCT
CBL	11	119146656 to 119146820	GCTTTAGTAGATTATGCTGGTATTACGGTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGTGCTTGGAAGAGAG
CBL	11	119146736 to 119146900	GTCTGGGAACTTAGGGGCTGTCCAACNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGGTCAGTGGGCTATTGG
CBL	11	119148430 to 119148594	GTAACCAACCCTGGGTTTTATTTAAGCCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGTGTCCAGTGATATG
CBL	11	119149087 to 119149251	AAAAGCCAGGCCACCCCTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCGGCAGAAAGGACAGCCCTGACCTTCT
CBL	11	119149203 to 119149367	GCTCCCTCCCCAAATTATGATGATGATGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTTGCTTCTTCTGCAG
CBL	11	119149296 to 119149460	GCAGTTTAGGAGACTGGCAAAATCCATTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATCCTAGAGGGAGTGG
CBL	11	119155626 to 119155790	GATTACTTTCGTTTGGGGAAATGGCATCTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCAGAAGCACTTGAGGG
CBL	11	119155691 to 119155855	GCTTGTGGGGCCATGGAGAATGGAGAAGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACACAGCAAAGAATCC
CBL	11	119155863 to 119156027	GCAGGGTGAAAGCAAATCAGTAAAAACCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGGGCGTCTTTGAGGT
CBL	11	119155946 to 119156085	GCGGTGGTGGTGGAAGATCTCGAAGTGTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTAGAGGGGACAGGGGG
CBL	11	119156161 to 119156330	GCCGGTTGGTTAATTCTCTTCCTGTCCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCTGGCCCACACATATT
CBL	11	119158535 to 119158699	GCTATATTTTGTACAGTGGAGTTGTTACTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTTTCAACACTTTTCT
CBL	11	119167497 to 119167661	GTGCCAAAACTGCCACCTGGGGAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATAGTTCCCTAGGTGAC
CBL	11	119167612 to 119167776	GGTTCACAACAACCCTTTTTGGGCCCTATNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATTCTTCATCTTCCAG
CBL	11	119168048 to 119168212	GCCATAATGATCTTTGGAAATAGAACTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGTAGCAGAATGGCAA
CBL	11	119169050 to 119169234	GCTCCTCCTTTGGCTGGTTGTCTCTGGATNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCACTCATTTTTCTCC
CBL	11	119169137 to 119169306	GCCGGCACAGGTGGCTTTGGGACATCATNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAACATACAGGCCACA
CBL	11	119170294 to 119170478	GCAGCAGAGGCGGCAGGACCACTACCTTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGGCAGGAGAAGAAA
CBL	11	119170412 to 119170586	GTTTTTGGCCATCTCGATGTTGTTCTGGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAAGTCACCAAAGGAA
CEBPA	19	33793185 to 33793284	GGTGGCTGCTCATCGGGGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTGGGGCGGGAGGCTGCGCGGG
CEBPA	19	33792127 to 33792291	GCCGTGCGAGCCAGGACTAGGAGATTCCGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCAGCTGCCAGAGAGCT
CEBPA	19	33792242 to 33792386	GTCAAGGCCATGGGCAACTGCGCGTGAGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGAAGGTGCTGGAGCT
CEBPA	19	33792258 to 33792447	GCGGCTCTTGCGCACCGCGATGTTGTTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCATGGCCTTGACCAA
CEBPA	19	33792344 to 33792448	GCGCACCGCGATGTTGTTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTGCGCAGGCGGTCATTGTCACTGG
CEBPA	19	33792361 to 33792525	GCAGAAGGTGCTGGAGCTGACCAGTGACNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGTGGCGGCAGCGGCG
CEBPA	19	33792464 to 33792563	CGGTGGACAAGAACAGCAACGAGTACCGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCAAGGGGCTGGGCGC
CEBPA	19	33792492 to 33792686	GCAGGTGCATGGTGGTCTGGCCGCAGTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACTTCTTGGCCTTGCCC
CEBPA	19	33792527 to 33792636	TGCGGGCTGGGCACGGGCGTGGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCGCGGAGGTCGGGGTG
CEBPA	19	33792560 to 33792664	GTGGGGTGACCGGGCTGCAGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTGAGCGCGCTGCCAGGGC
CEBPA	19	33792611 to 33792710	CCCACGCCCGTGCCCAGCCCGCACCCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCGCACCTGCAGTTCCA
CEBPA	19	33792644 to 33792843	CTCCTCGCGGGGCTCCTGCTTGATNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTGGGGTGACCGGGCT
CEBPA	19	33792649 to 33792848	TGCACCTGCAGCCCGGTCACNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGTGATCAAGCAGGAGCCCCGC
CEBPA	19	33792652 to 33792751	GCCAGACCACCATGCACCTGCAGCCCGGTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCACCCGCACCCGCAC
CEBPA	19	33792718 to 33792862	CCGCCGCCCGCGCACCTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGCGCTGCGGCCGCTGGTGATC
CEBPA	19	33792734 to 33792853	GCGGGGCTCCTGCTTGATCACCAGCGGCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGGTGCGGGTGCGGGT
CEBPA	19	33792734 to 33792858	GCTTGATCACCAGCGGCCGCAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGGTGCGGGTGCGGGTGCG
CEBPA	19	33792773 to 33792942	GCGCAGCCGTAGCCGGGCGGGGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGCTGGTAAGGGAAGAG
CEBPA	19	33792813 to 33792912	GCAGGAGCCCCGCGAGGAGGATGAAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGCTACCTGGACGGCAGG
CEBPA	19	33792870 to 33792969	TCCCCCGGGCATGACGGCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCGACGCGCTCGTACAGGGGCTCC
CEBPA	19	33792888 to 33793052	CCTGGACGGCAGGCTGGAGCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGGCCAAGGCGGCCGTGGGC
CEBPA	19	33792907 to 33793026	TGCGCGGCCGCCGGCTACNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGCGGCGGCGGCGGCGGCGACTTTGAC
CEBPA	19	33792913 to 33793022	TACGGCTGCGCGGCCGCCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCGGCGGCGGCGGCGACTTTGAC
CEBPA	19	33792944 to 33793063	GCCGTCATGCCCGGGGGAGCGCACGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCAGCAGGAGAAGGCC
CEBPA	19	33792961 to 33793065	GGGCCCCGGCGGCGCCGTCATGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCGGCAGCAGGAGAAGGCC
CEBPA	19	33792995 to 33793159	GGACGTCTCGTGCTCGCAGATGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGGTAGTCAAAGTCGCCGC
CEBPA	19	33793029 to 33793143	GGCGCTGATGTCGATGGACGTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGGGCCCACGGCCGCCTT
CEBPA	19	33793043 to 33793162	CGATGGACGTCTCGTGCTCGCAGATGCCGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCCTTGGCCTTCTCCT
CEBPA	19	33793046 to 33793165	TGCTCGCAGATGCCGCCCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTGGCCTTCTCCTGCTGCCGGCTGTG

Supplemental Table S4: smMIP panel covering recurrently mutated AML "hotspots" in 33 genes

Gene	Chromosome	Location (GRCh37/hg19)	smMIP sequence
CEBPA	19	33793067 to 33793166	TTCCTGGCCGACCTGTTCCAGCACAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGGCGGCATCTGCGAGC
CEBPA	19	33793071 to 33793235	TTCCTGGCCGACCTGTTCCAGCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCGCCTTCGGCTTTCCCC
CEBPA	19	33793100 to 33793199	CCTACATCGACCCGGCCGCCTTCAANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGCCTCCCGCCCCACCT
CEBPA	19	33793151 to 33793250	GGCGGCGCTGCTGGGCGCGTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCGCAGATGCCGCCCAGCGGCT
CEBPA	19	33793184 to 33793348	GGGGGAGTTAGAGTTCTCCCGGCATGGCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGTGGGGCGGGAGGCT
CEBPA	19	33793238 to 33793337	TGCAGAGCCCCCCGCACGCGCCCAGCAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGAACTCTAACTCCCCC
CEBPA	19	33793239 to 33793408	CCACCCGGAGACCCTGCTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGCTGGGCGCGTGCGGGGGGCTCT
CEBPA	19	33793291 to 33793405	GTCGGCCGACTTCTACGAGGCGGAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGGGTCTCCGGGTGGG
CEBPA	19	33793353 to 33793492	AGGCTGGAGGCCGCCGAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGGGGCGACGCGGCCTGCCGGG
DNMT3A	2	25457085 to 25457249	GCCTCGCCAAGCGGCTCATNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTTTGTGTTTTTTGTTTGTTTGTTT
DNMT3A	2	25468067 to 25468231	GCAGAGGGAGGGGATGGGGTGAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGAAGGCCGAAGGGCCGG
DNMT3A	2	25469921 to 25470085	GCAAAGCCATCTACGAGGTCCTGCANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGGGTGGGTGCTTGC
DNMT3A	2	25470411 to 25470595	GCCTGGGGTGGGGGAAGGTTCTTGATNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGAGCTGGTGTGGGGG
DNMT3A	2	25463136 to 25463305	CCAGCAACCTTGGTTTGGCCAGCTCACTANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTCTTCTTTGAGTTCT
DNMT3A	2	25463477 to 25463641	GCAACGTGATGGGCCTGCTGTCCAGGGANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGAGAAGGTGGAGGGG
DNMT3A	2	25463217 to 25463381	GCTGTCTGCATAGGACAGTGGTGTGGCTCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACCACATTCTCAAAGA
DNMT3A	2	25470445 to 25470594	GCAAATTCTCAGTGGTAAGTTGTGGGGTTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAGCTGGTGTGGGGGA
DNMT3A	2	25467375 to 25467539	GCTGTTGTGGCCTCCAGTGGTCTCCTTAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTTCCCGCTGCTGTCT
DNMT3A	2	25457194 to 25457373	GCCGGTCATGGAGCGTGCCAGTCATNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGGTCCTGCTGTGTGG
DNMT3A	2	25497750 to 25497864	CGTCCCGCTTGCGCTTGCTGATGTAGTAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCACTTCTGGTTTTCC
DNMT3A	2	25469513 to 25469632	CTGGGGGGCTTCCAGCCTTCTGGCCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCGCGGGGAAGCTGTT
DNMT3A	2	25464406 to 25464570	GTATGTCCATGCTGTGGGGCGCAGCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGTGCTGAAGGACTTGGG
DNMT3A	2	25464465 to 25464629	GCGGCACCAGGGGAAGATCATGTANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGGGTGCCAGGGAGATGG
DNMT3A	2	25464471 to 25464570	GGCATGGTGCGGCACCAGGGGAAGATNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGTGCTGAAGGACTTGGG
DNMT3A	2	25467037 to 25467236	CGGCTCCAGATGTTCTTCGCTAATAACCANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCTCCTCTGCTCACTG
DNMT3A	2	25469011 to 25469185	GTAGGGATTCTTCTCTTCTGGAGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCAGAAGCAGGCCAACTA
DNMT3A	2	25458532 to 25458696	GCATCTGGCTGCGGTGTGGCTGTTCTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGTTCAGCAAAGTGAGG
DNMT3A	2	25459756 to 25459920	ACTGTAACAACAGAAACCTGGATAACAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCTTCCTTCTCCCTGCC
DNMT3A	2	25461977 to 25462141	GCCAAGGAGGAGCATGAAACAGCGCCGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGGCCCAGGAGCTTTC
DNMT3A	2	25464295 to 25464459	TTCTGTGTGACGCTGCGGACGTCCCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAGGAGAAAAAGAGGCTGGG
DNMT3A	2	25464407 to 25464526	GTATGTCCATGCTGTGGGGCGCAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCGGAGGTGTGTGAGG
DNMT3A	2	25470444 to 25470508	CCACATGACCCAGCGGGTGCCTTCANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAACCCCACAACTTACCACT
DNMT3A	2	25466634 to 25466798	GCGATTCCATCAAAGAGAGACAGCACCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGCTTCCCCTTTGGGA
DNMT3A	2	25466714 to 25466823	GCTGGCCGCCTTGTCCCAGGATGGGGGAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCAGCTGAGAAGAGGAA
DNMT3A	2	25466745 to 25466909	GTGAGGGGTGCAGGCCCAAGAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGGTGGGAGCTTGGGACA
DNMT3A	2	25466771 to 25466870	GGGTGCTGTCTCTCTTTGATGGAATCGCTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGTTGTGCTCACTGCT
DNMT3A	2	25466811 to 25466910	TGTCCCAAGCTCCCACCCANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTCTTCTCAGCTGGGACAGGTGGGTA
DNMT3A	2	25466938 to 25467122	GCTGTGCGCAGGGTGTGTGGGTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATGTGCGGGCACAAGGGT
DNMT3A	2	25470520 to 25470684	GCATTGTGTCTTGGTGGATGACGGGCCGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGGGGGATCAGGGTG
DNMT3A	2	25458600 to 25458764	CACCAGCCAACACTGGTCATGCGTCTACCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATGTCCTCTTTCTCAT
DNMT3A	2	25468851 to 25469015	GCCTGGGAACTCTGGCACTCCTAGTGTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTCTGGAGAGGGTGGC
DNMT3A	2	25470525 to 25470684	GCCGCATTGTGTCTTGGTGGATGACGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGGGGGATCAGGGTG
DNMT3A	2	25469127 to 25469301	GTGTACACGGACATGTGGGTGGAACCTGANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTAGAGTTGGGAGGTGG
DNMT3A	2	25469134 to 25469248	AGTGTACACGGACATGTGGGTGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGGGTGGGGGAAGGGGCT
DNMT3A	2	25469423 to 25469602	GCCTTGGCAGTGTCACTCTCATCGCTGTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTCCCAGCCCTGGTGT
DNMT3A	2	25469448 to 25469627	TTTCTGGGACCCCTGCCCGCCANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGGGAAGCTGTTCCCGGTGTG
DNMT3A	2	25469480 to 25469579	GGGCCTGGAGCCACCAGAAGGTAAATGAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAGGCCGTGGAGGTGC
DNMT3A	2	25469524 to 25469628	TGGGCCCTGGGGGGCTTCCANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGGGAAGCTGTTCCCGGTGTG
DNMT3A	2	25469549 to 25469713	GCTGGAAGGCAGATGGGTCAGGCTCAAGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCATGGGCTTGTTCTG
DNMT3A	2	25469867 to 25470031	GAGGAGGAGCCTAGAGCACTAGGAGGCCTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCAGGTGTGTGTTGAG
DNMT3A	2	25470814 to 25471013	GTGGGGGATGCGGGGTCAGTGGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGGAGATGGAGAGAGGAG
DNMT3A	2	25470816 to 25471000	TCTCCTCTCTCCATCTCCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCATCCCCCACTGTGGCTACCACGCCT
DNMT3A	2	25470540 to 25470599	CCCCCACACCAGCTCCCCAANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACACAATGCGGCCTGGCCACCAGGA
DNMT3A	2	25470928 to 25471117	GCTGGGGACAAGAATGCCACCAAAGCAGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGAAGAAAGCCAAGGT
DNMT3A	2	25470958 to 25471137	GCTACCACGCCTGAGCCCGTGGGGTCCGANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTTTTTGTTTCCCCAG
DNMT3A	2	25470973 to 25471142	ATCCCCCACTGTGGCTACCACGCCTGANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTTTGTTTTTTGTTTCCC
DNMT3A	2	25471051 to 25471120	CAGGGGCCCGGGGAGTCTCANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTGAGAAGAAAGCCAAGGTC
DNMT3A	2	25497694 to 25497868	GCTTGCGCTTGCTGATGTAGTAGGGGTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATTAAGAGGCTCCCAG
DNMT3A	2	25497756 to 25497935	GCCCGTCCTGCAGAACTGGAAAACCAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGTGGCTTGGGCTGGG
DNMT3A	2	25497804 to 25497978	GCTGGCACGCTGGAAAAGGGAGGTGAGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAATGTCTGTCTCTCTG
DNMT3A	2	25497806 to 25497935	GCTGGCACGCTGGAAAAGGGAGGTGANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGTGGCTTGGGCTGGG
DNMT3A	2	25497848 to 25497977	GCGGGGGACCCCTACTACATCAGCAAGCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATGTCTGTCTCTCTGTC
DNMT3A	2	25497919 to 25498033	CCCACCAAGGAGGCACTCGCCTCAAACACNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCCCAGCCCAAGCCAC
DNMT3A	2	25498319 to 25498483	GCTCTGTGGATCCTGATTCTAGAAGAAGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGGGCCTGTGAGCCA
DNMT3A	2	25505221 to 25505400	GCTTCAGGCAGGGTCTCAGCTGCACCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTCCTGGGACCTGCTG
DNMT3A	2	25505306 to 25505410	GCCGAGGAGCCCCTGCAGAAGCGGGTGANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGAGGGAGAGGGTGCAG
DNMT3A	2	25505317 to 25505436	GGAGGGCCGAGGAGCCCCTGCANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGGGGGCAGAAGGGCGGG
DNMT3A	2	25505355 to 25505544	GCCTGAAGCCTCAAGAGCAGTGGAAAATGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATCTCCAAGTCCCCAT

Supplemental Table S4: smMIP panel covering recurrently mutated AML "hotspots" in 33 genes

Gene	Chromosome	Location (GRCh37/hg19)	smMIP sequence
DNMT3A	2	25505473 to 25505657	GCCTGTTTTGGATCATTGACCGCTCTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTTCTCCAAGTCCCCAT
DNMT3A	2	25505488 to 25505607	ACTCAGGCGCCTCAGAGCTATTACCCAATNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCTTGTGTATCTTTCT
DNMT3A	2	25522965 to 25523129	CTACACACCCTCCTGTGCACACACACAACNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGTGTCTGTGCCTGCA
DNMT3A	2	25536644 to 25536823	GCTCACGACAGGGTGTGGGACCATCACATNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGACACCAGCAGCTCTG
DNMT3A	2	25536669 to 25536858	GCTGGAGGGCATGGCGGGCATCTGGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAGCACTGAGTGATGCG
DNMT3A	2	25536681 to 25536820	GCTCCTCATACTGAGTGCATGACCGCATNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACCAGCAGCTCTGCTG
DNMT3A	2	25536682 to 25536881	GCTCCTCATACTGAGTGCATGACCGCANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCAGCCCCAGCCTGCCT
DNMT3A	2	25536781 to 25536980	TCCCGGTGTTGAGCCCTCTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCTTTCGGTCCTCCTCCCGCTC
EZH2	7	148515038 to 148515212	GCAGCAGCAAACTCCTTTGCTCCCTCCTANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCCCTGCTTCCCTATC
EZH2	7	148506102 to 148506266	AGGGCTTTTTCTACTGGATTGTGAACTCTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCAGTGTGTCTCTTTG
EZH2	7	148523529 to 148523718	GCCTGGGAGCTGCTGTTCGGTGAGTTCTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGAAAATGAAAACGTAC
EZH2	7	148526780 to 148526944	GCTTCTTCTCTTGGAAAAAGGGGCTAAAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTAGGTGGAAGATGAA
EZH2	7	148543505 to 148543669	ATCATCATCTTTTGGTTTATGCTATTGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCAGAAAATTTTGGAAAG
EZH2	7	148544249 to 148544413	GCCCATGATTATTCTAAAAGCAATGGTTTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATTTTCACAAAAGATA
EZH2	7	148507361 to 148507525	GTTGCATGTGGCAGCCTTCTGCCGGCCGANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCTGTGTCTTTCTTTT
EZH2	7	148511985 to 148512149	GAGGAGCCGTCTGAGTAAAGATAACATCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATCAAAGCAACAAATAC
EZH2	7	148506351 to 148506515	GGAACTCCCTTTTCAGTCCTGTGATGANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTCACTGGGCTGTGCTT
EZH2	7	148514347 to 148514526	GCACTTACTATGACAATTTCTGTGCCATTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTTCCAATCATTTCTT
EZH2	7	148544318 to 148544482	CGGAAGCGTGTAAAATCAGAGTACATGCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGTTAGTTTGCTGCGG
EZH2	7	148504673 to 148504847	GCCTTAGCTTCAGGAACCTCGAGTACTGTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATGTTGGATGGGTGGC
EZH2	7	148508688 to 148508852	GTAAGGCACTGATAACCTGTATTCAGGTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCCTCCTTTTTTGATG
EZH2	7	148508624 to 148508788	GGTAAGTCTGTGGGTTTGANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTGGCAGGCTGGGGGATTTTT
EZH2	7	148511017 to 148511201	GCACTGCTTGGTGTTGCACTGTGCTTTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACAAACAATCTTCCAGA
EZH2	7	148511145 to 148511344	GCTACCTGGCTGTCCGAGAGTGTGANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGTGGTTGTGAGGGTT
EZH2	7	148512083 to 148512247	CCTGTGGAGTGTAGCTGGCCTGCCTTTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCGTGGATGATCACAGGG
EZH2	7	148512536 to 148512700	GCGGGAAGCTACAAATCCAACAGAGAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAACAAATGAAAACAAAGC
EZH2	7	148513733 to 148513897	GCTCCTTAGAGAAGTCAACATAGATAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGCTCTGTGACTGTG
EZH2	7	148514258 to 148514422	AAGAGCTTCAAACATAGAGATAAAACTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGTGGAGTGGAGTGGTG
EZH2	7	148514935 to 148515099	GCACATTAATGGTGGGGGTGCTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAACAGTAAAACCCAGTTA
EZH2	7	148515145 to 148515314	GCCAGGTTAGTCAAAAAATGTATCACNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGACGTTTTGGTGGGG
EZH2	7	148516637 to 148516801	CAGAGGGTACTTGAGAGGACTTTGCACNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTTTGTTTCATTTATTTT
EZH2	7	148523379 to 148523578	ATTGCACTTACGATGTAGGAAGCAGTCATNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGAGCAATCCTCAAGC
EZH2	7	148523595 to 148523764	GCTTACACTCCTTTCATACGCTTTTCTGTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTGTTTCATGTTTACT
EZH2	7	148524217 to 148524381	GTTCCTTTGAGGCAATCTTGCCCTGTATGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCCTTTCATATTCTCC
EZH2	7	148525778 to 148525947	GTAGCCATTACAGCTTTCTTTCAAAAACANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTTTGTGGAGTTGGTG
EZH2	7	148525900 to 148526064	GCCCTTGGTCAATATAATGATGATGACGANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCTATGCCTGTTTTGT
EZH2	7	148526886 to 148527050	GTGTACATGTCTTTACCCAGTTCTCCAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTAAAACTTCATCTCCC
EZH2	7	148529695 to 148529859	GGTCACCGAACACTAAAACAGAAAAAATANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCAAATAAGCAGAAGAT
EZH2	7	148529742 to 148529906	AGGACAACCTTAAGCTGTAGCCATCANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGGGGAGACCAAGAATACA
EZH2	7	148543559 to 148543723	GCTCATTGCGCGGGACTAGGGAGGTTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCTCCTTTCCTCTCCTTC
FLT3	13	28592550 to 28592714	GTGACAAGCACGTTCCTGGCGGCCAGGTCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAACGACACAACACAAA
FLT3	13	28602281 to 28602445	CCACTTCCACGAAAATCACCTCATCAAAANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAATGCTCCTTTCTTTG
FLT3	13	28607881 to 28608075	GCTAAAAATGGAGTGGATTGGGGTGTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGAATTAGCAAAACAGGAG
FLT3	13	28607972 to 28608136	CACCTGATCCTAGTACCTTCCCTGCAAAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGTGCCTCCCATTTTT
FLT3	13	28608059 to 28608223	GCAACAGCTTATGGAATTAGCAAAACAGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTTTGGTAAGAATGGA
FLT3	13	28608170 to 28608334	GCCGGTCACCTGTACCATCTGTAGCTGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCAATGGAAAAGAAATG
FLT3	13	28608264 to 28608458	GCTTTTACCTTTTTGTACTTGTGACAAATNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCATATTCTCTGAAATC
FLT3	13	28608393 to 28608562	GGGAAGGGGCCTGCAACAAAAGAGTGTCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTGCAGATAGAGGAAAG
FLT3	13	28608516 to 28608695	CCACTCTACATATACTCTACTCCCCACAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGATGTTGTCTTGGATG
GNAS1	20	57484354 to 57484518	GGATCTCACCAAAGCCAACCGAAACAGTANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCATGATCTCTGTTAT
GNAS1	20	57484965 to 57485129	GCCGTGTGAATGCTTGGGAGAAGCGCGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGGAGTAGTGTAGCGAG
GNAS1	20	57485020 to 57485184	GCTGGCTGTTCATTGCGGTGGTTCTTTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCTCTGTGATCCTGTT
GNB1	1	1747205 to 1747369	GATCTACGCCATGCACTGGGGCANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAGGATGGGTGATGAGGAG
GNB1	1	1737867 to 1738031	CAGTACCGCACAACACAGAAAGTGTANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGTTTCCTGGGTTGGT
IDH1	2	209113079 to 209113243	GCTTATGGGGATCAAGTAAGTCATGTTGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAAACAAATGTGGAAA
IDH2	15	90631896 to 90632060	CTGTCTTCCGGGAGCCCATCANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGCTGTGTTGTTGCTTGGGGT
IDH2	15	90631740 to 90631904	GCGTGGGATGTTTTTGCAGATGATGGGCTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAGACAAGAGGATGGC
JAK2	9	5073673 to 5073837	GCCTTTCTCAGAGCATCTGTTTTTGTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCTTTGTACTTTTTTTTTT
JAK2	9	5069972 to 5070136	GCCTCTGTAATGTTGGTGAGGTTGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCAATGTCACATGAATGTAA

Supplemental Table S4: smMIP panel covering recurrently mutated AML "hotspots" in 33 genes

Gene	Chromosome	Location (GRCh37/hg19)	smMIP sequence
KIT	4	55599208 to 55599372	GTGGTTAAAGGAAACGTGAGTACCCATTCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGTTTTCTTTTCTCCT
KRAS	12	25380201 to 25380365	GCTTTCTTTGTGTATTTGCCATAAATAANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGTGTTTCTCCCTTCT
KRAS	12	25398250 to 25398414	GCAAGAGTGCCTTGACGATACAGCTANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGTACTGGTGGAGTATTTG
MPL	1	43817850 to 43818014	GAAGGAAGAGAAGCAGACTGAGCCATGGCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCAGGGTTGGTGGTGGG
MYD88	3	38182567 to 38182731	GCCCTTGCCCCATGGTGGGACAAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTGGTGCAGGGGTTGGTG
NMP1	5	170837409 to 170837573	CATTCTACCACCAGAGAGTTAACTCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTTCTTAAAGAGACTTCCTC
NMP1	5	170837522 to 170837686	GCCAGAGATCTTGAATAGCCTGGAAAAANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATCAAACACGGTAGGGA
NOTCH1	9	139390913 to 139391037	GCTGCATCTGTAAGTTTTGTGGCTGCANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCTGGCTGCTGAGCTC
NOTCH1	9	139391562 to 139391726	GCTGCTGGGCTTGCGGACCTTCTTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGGTAGCCATGGGGTG
NOTCH1	9	139391221 to 139391400	GCAGAGCGGCATGGTGCCGAACCAATACANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGCCTTTGAGACTGG
NOTCH1	9	139390487 to 139390671	GGGGACGGGGTGAGGAAGGGGTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGGAAAGGAAGCCGGGG
NOTCH1	9	139390567 to 139390641	GCGGGGACGAGCTGGACCACTGGTCAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGTGGGAGGGCTGGAG
NOTCH1	9	139390567 to 139390736	GCGAGGAGTAGCTGTGCTGCGAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGTGGGAGGGCTGGAG
NOTCH1	9	139390603 to 139390707	GCTGGTGGCTGGGGGTGTTGTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGACGTTGGAATGCGGGGA
NOTCH1	9	139390649 to 139390758	TTCCTCACCCCGTCCCCTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCAGCCCAGTTCCTGACGCCCCCCTC
NOTCH1	9	139390689 to 139390788	CAACACCCCCAGCCACCANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGCCATCCTCGCTGGTCCCACCC
NOTCH1	9	139390726 to 139390825	GGGCGGGGCTCTCCTGGGGCAGAATNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGTGCTGCGAGGGGGG
NOTCH1	9	139390779 to 139390848	GTGTGCACCGCCAGGCTGCTGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAGGATGGCAGCGACGTGGG
NOTCH1	9	139390780 to 139390959	GCGGCTGTGGTGGTGGTGGTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGGATGGCAGCGACGTGGG
NOTCH1	9	139390806 to 139390905	TTCTGCCCCAGGAGAGCCCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGGCCGGAGCTTCCTGAGTGG
NOTCH1	9	139390810 to 139390899	GCGGTGCACACTATTCTGCCCCAGGAGANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGAGCTTCCTGAGTGG
NOTCH1	9	139390866 to 139391035	GCTGCTGCATCTGTAAGTTTTGTGGCTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCTGCCTGGCTCGGCT
NOTCH1	9	139390970 to 139391154	GCAAGGCTACTGTGCAGCGGGCCTACCANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCTTTGCTGCTGCTGG
NOTCH1	9	139390981 to 139391115	GCAGAACCTGCAGCCAGCAAACATCCAGCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGTCCCAGATGATGAG
NOTCH1	9	139391054 to 139391238	GCAGAGGGTTGTATTGGTTCGGCACCANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCAGGTGAGGCTGGGTG
NOTCH1	9	139391056 to 139391185	GCTGCAGGGAGGGGGCCTGTGTGCTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGTGAGGCTGGGTGGC
NOTCH1	9	139391125 to 139391239	GCAGAGGGTTGTATTGGTTCGGCACCATNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCAGCAAGGCTACTGTG
NOTCH1	9	139391148 to 139391312	GCCCCCTCCCTGCAGCATGGCATGGTAGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCTGAATTTCACTGTG
NOTCH1	9	139391191 to 139391310	GGGGGAGTGTGGCACCAGGCCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGAATTTCACTGTGGGCGGG
NOTCH1	9	139391216 to 139391375	GCGGCATGGTGCCGAACCAATACAACCCTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCTCTCCCACCTGCCT
NOTCH1	9	139391360 to 139391529	GCACGGACGGAGACTGCTGGAACGGGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGGCAGGTGGGAGAGA
NOTCH1	9	139391459 to 139391518	GAGGGGCACGGACGGAGACTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGATGCCCAGGTGGGTGTCGGG
NOTCH1	9	139391478 to 139391542	CCACCTGCCTGGGATGCCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCACTGCTGCCCTCCCCGTTCC
NOTCH1	9	139391487 to 139391681	GTGCCTTGAGGTCCTTGGCCTCCTTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGCAGGTGGTTGAGGG
NOTCH1	9	139391496 to 139391605	CTCCGTCCGTGCCCCTCAANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATGCTCTCGCCCGTGGACTCCCT
NOTCH1	9	139391517 to 139391616	CGGGCGAGAGCATGCCGGAGCTGTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGCTGGAACGGGGAGGG
NOTCH1	9	139391520 to 139391589	GCCATGGGGTGACTCCAGGGAGTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGAACGGGGAGGGCAG
NOTCH1	9	139391598 to 139391722	GCTGCTGGGCTTGCGGACCTTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAGAGCATGCCGGAGCTGT
NOTCH1	9	139391638 to 139391737	GCTTGCGGACCTTCTTGCCCTGCACGCCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCTGGGACTTCTTCCT
NOTCH1	9	139391657 to 139391776	GCCGTTGGGCGAGCAGAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGCCTTGAGGTCCTTGGCCTCC
NOTCH1	9	139391667 to 139391861	GCCTGTGGAAGCAAGGAGGCCAAGGANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAGGCTGCTGGACGAG
NOTCH1	9	139391813 to 139391947	GTCCCGGTTGGCAAAGTGGTCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCCGTGCAGCTGCGGGCTG
NOTCH1	9	139391835 to 139391959	GTGAGGCTGCTGGACGAGTACAACCTGGTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAGGTGCTGCTGGACC
NOTCH1	9	139391910 to 139392094	GCCAACCGGGACATCACGGATCATATGGANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTGCTTCCTCTGGTGA
NRAS	1	115258635 to 115258799	CAGTGGTAGCCCGCTGACCTGATCCTGTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGTTCTTGCTGGTGTG
NRAS	1	115256462 to 115256626	GGTGTGGAGGGTAAGGGGGCAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGCAAATACACAGAGGAA
PPM1D	17	58700888 to 58701087	GCTAGGAAGACCCGTCATAGTCTTTGGCCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTCTCTTTCCTTGGGA
PPM1D	17	58740574 to 58740743	GTCCAATTCTGGCCCCCTGATGAAGAAGCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCTTCCAATTGGCCTT
PPM1D	17	58740663 to 58740832	GTTGGAGGGGTTCTTTCAATTTCTTGGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGTGAGTTTAACAGAG
PPM1D	17	58740446 to 58740620	GCCTACTAATTCAACAAACACTGTCATGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAGGTTTCAGCTGAGA
PPM1D	17	58740337 to 58740516	GTCATACCCTCAAAAGATCCAGAACCACTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTACCTTCTTATTTTT
PPM1D	17	58677959 to 58678143	GCCCGGGAGCACTTGTGGGGTTTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAAGTCTCGGGGAAAGG
PPM1D	17	58725301 to 58725500	GAGTGTGGACACTTGTGTCTGGTTCAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCAGAAGTACCAAAACAA

Supplemental Table S4: smMIP panel covering recurrently mutated AML “hotspots” in 33 genes

Gene	Chromosome	Location (GRCh37/hg19)	smMIP sequence
PPM1D	**17**	**58734109 to 58734273**	**GCTGTCAGTCAGGTTCAGGTATAACTCANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTTTCCAGGTGACGCT**
PPM1D	**17**	**58677653 to 58677812**	**GCTGTACTCGCTGGGAGTGAGCGTCTTCTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCCCCCTCCCCCTTCT**
PPM1D	**17**	**58677729 to 58677893**	**CCGACGGCTGAAGAAAAGCCCTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGATTCGGCGGGCTGCGTGGG**
PPM1D	**17**	**58677824 to 58677998**	**GCGGTGGCAGCCCGAGAGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGGAGGAAGTACATGGAGGACG**
PPM1D	**17**	**58677826 to 58677975**	**GCGGCGAAGTCTCGGGGAAAGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAGGAAGTACATGGAGGACG**
PPM1D	**17**	**58677905 to 58678014**	**GCGGAGGCAACGGCTGAGACAGCGANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGGAGAGGGTCGCGAG**
PPM1D	**17**	**58677977 to 58678096**	**TCTCGGGCTGCCACCGCTGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTGCCCGTCGCACACGGCGA**
PPM1D	**17**	**58678056 to 58678190**	**CGTCCGAGCCGGCTAAGGTTTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCCGTTCCTCCGTGGCCTTTT**
PPM1D	**17**	**58678072 to 58678251**	**GCCGTGCCCGTCGCACACGGCGAAAAAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTACCCAGTTTCTTCC**
PPM1D	**17**	**58678186 to 58678350**	**CGGATGGCAGCGCAAACCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTTGGTTGCGCTCTGGGTGCCGGGGG**
PPM1D	**17**	**58700761 to 58700960**	**GCCAGTGTGGTCATCATTCGGGGCATGAANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAATTGTTTCCTGTGCT**
PPM1D	**17**	**58701048 to 58701247**	**GTTCTGGCTTATGGTCCTGTGTCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCATCAGACAAACTAAAAAACC**
PPM1D	**17**	**58711195 to 58711359**	**GCACTTGGTAAGTAGGACTTAATTTGGTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTGAACTCTTTATTTTT**
PPM1D	**17**	**58711293 to 58711457**	**GCCAGAAAAGGAATCTGGTCAATAACTGTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCATGATATCTCTACCC**
PPM1D	**17**	**58725225 to 58725404**	**CCACCACAAGATGCCATCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCTTGCTTTTTCTGCTCCCTTCCCCCA**
PPM1D	**17**	**58733927 to 58734091**	**GCATCTCTCCAGAAGTGGACAATCAGGGANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTACTTTCCTTCTCCT**
PPM1D	**17**	**58734029 to 58734193**	**GGCACTAGTGTTATCTGCTCGGAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGTGTAGAACATGGGGAAGG**
PPM1D	**17**	**58740785 to 58740949**	**GCTGTGAGGTTGTGGGGAGACTTGCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCTAAGTTTGGAAAAACC**
PTPN11	**12**	**112919860 to 112920024**	**CAAAGGTTGGACAAGTAAGTATATTGTCGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTTTCTGATCTCTTCC**
PTPN11	**12**	**112926879 to 112927048**	**GCTAGGCCTCTTGGATACGCTCTCCTTTTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGAGGTCAGGGATGGT**
PTPN11	**12**	**112926786 to 112926955**	**GCGGTCCAGCATTATATTGAAACACTANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTCTGCAGTTTCTCTTT**
PTPN11	**12**	**112892443 to 112892607**	**TCAGCCTCCATGTACCCATTGCAGCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCTATGGTGGAAACATTGG**
PTPN11	**12**	**112856894 to 112857058**	**GGGTCGGGGTTGGGGGCCGGTTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGAGCCGGAGGGCGGGAG**
PTPN11	**12**	**112884036 to 112884200**	**GTAACCCTGGAGACTTCACACTTTCCGTTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCAGTGTCTTGTTTTTT**
PTPN11	**12**	**112884123 to 112884287**	**GCTTGGATAGCTTGCTGCCTGCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTGTTGACAAGAGGAGTTGATGG**
PTPN11	**12**	**112890955 to 112891129**	**GATTTTGTTCTTTCTGTGCGCACTGGTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCCATAGTAGAGCTAAA**
PTPN11	**12**	**112891070 to 112891249**	**GGGTGGCTCTGGCTCTCTCGTACAAGAANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCAGAAAAATCACCCAAA**
PTPN11	**12**	**112892348 to 112892512**	**GGTGAGCAGATTGGAAAGCTCAAGCTTTCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCATGTGTTTATCTTG**
PTPN11	**12**	**112893736 to 112893900**	**GTTATTAAAAAACTGTTTTTACGTGAGTTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACTGCTGTACTCGATC**
PTPN11	**12**	**112910726 to 112910890**	**GCTCAGTAATAGTCACTCTTGGAGATTTTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATTGACTTTTCTTTCT**
PTPN11	**12**	**112915402 to 112915566**	**GCTTTGCTTTTCACAGTGTTTTCTGACCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTTTTCCTGAAGCAGT**
PTPN11	**12**	**112915628 to 112915812**	**GAAGAAAATCCTTCAAACACCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTCTCCACTTCTTTCGTTGTCATG**
PTPN11	**12**	**112915695 to 112915864**	**GCCTTGTGTGGCAATGTAACTCTTTTTGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATACTTTAAAAACAGT**
PTPN11	**12**	**112919896 to 112920060**	**GAGACTTTGGGAACTGTTGATGGTGTGTANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGCCTGATGAGTATG**
PTPN11	**12**	**112924256 to 112924425**	**GCATCATGGATGCAGGGCCGGTCGTGGTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGTTTTTCTTGGCTCT**
PTPN11	**12**	**112924364 to 112924543**	**GCTTATGGTGCACCTCCTCCAGGAAGTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATTAAATTCTTCCTAC**
PTPN11	**12**	**112926198 to 112926362**	**GCAGGGACAACAGAATCATTCATGGGGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATAAACTAAAAACAGAA**
PTPN11	**12**	**112942472 to 112942636**	**GCAAGTGCTCTATTGGTTAATTGTTTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATGTCTTTCTTTTTCTTTT**
PTPN11	**12**	**112888068 to 112888267**	**GCAAGGGGACAAATAAAGAGTTACACCAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCATCTCCATTCTTCTC**
PTPN11	**12**	**112939802 to 112939966**	**GACGGGTTGAGAATACTGATACATTGACCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCCCTTTCCTCTTGCT**
PTPN11	**12**	**112939932 to 112940096**	**GTGCTGAAGGAAATTCTTTTTACCTGGTCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTCTTCCAAATTTCAG**
PTPN11	**12**	**112888195 to 112888359**	**GTGACCACAAAGTCTGCTGCTCCCTTGTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTTGCCACTTTGGCTG**
RUNX1	**21**	**36171577 to 36171761**	**GTGGGGATGGTTGGATCTGCCTTGTATCTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNATGTGTTTTCAAGTGG**
RUNX1	**21**	**36231740 to 36231904**	**GTGCATCCACTTGGGGCTGGTACACCCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNCTGTTTTGTTCTCTATC**
RUNX1	**21**	**36164649 to 36164753**	**CCTCCTACCACCTGTACTACGGCGCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCACGCGCTACCACACCT**
RUNX1	**21**	**36164661 to 36164760**	**GGTGTGGTAGCGCGTGGCCGAGCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGGTGGTAGGAGGGCGAG**
RUNX1	**21**	**36206614 to 36206793**	**GCGTGGGGGCTGGGTGGTGTGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGTTGGTCTGGGAAGGTGTG**
RUNX1	**21**	**36206733 to 36206917**	**GCCTCCCTGAACCACTCCACTGCCTTTAANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCCCTGCTCCCCACAA**
RUNX1	**21**	**36206742 to 36206931**	**GCAGGGAGGGGAGGGGATGGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGTGGAGTGGTTCAGGGAGG**
RUNX1	**21**	**36164275 to 36164459**	**GCCCGACGGCCAGGATCTCGCTGTAGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGGAGGAGGCCGTGTGG**
RUNX1	**21**	**36164425 to 36164549**	**GCTCTGGTTCGGGAGGCTGGGGTTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGCGCCTCAGTAGGG**

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Gene	Chromosome	Location (GRCh37/hg19)	smMIP sequence
RUNX1	21	36164425 to 36164594	GCGTTGGTGCAGGGCGGCAGGATGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNTGGCGCCTCAGTAGGG
RUNX1	21	36164475 to 36164594	GCGTTGGTGCAGGGCGGCAGGATGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGCCATGTTGGTGGGGG
RUNX1	21	36164480 to 36164584	GTGGAGGCGTTGGTGCAGGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTTGGTGGGGGAGTTGCTGT
RUNX1	21	36164535 to 36164639	CTCCGCGCTGCTCAACCCCAGCCTCCCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTCCTACCAGTTCTCC
RUNX1	21	36164535 to 36164674	GCGCCGTAGTACAGGTGGTAGGAGGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGGGAGGCTGGGGTTGA
RUNX1	21	36164662 to 36164856	GCATGCGGGGGTCGGAGATGGAGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGGTGGTAGGAGGGCGAG
RUNX1	21	36164605 to 36164704	TTGGAACGGGCCTCCCTGCGCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGCGCTCGCCGCCCACCAT
RUNX1	21	36171709 to 36171888	GTATGTGGCCTATGTACCAGGGTTTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGGTAGGACTGATCGTAGG
RUNX1	21	36164717 to 36164821	GCGTCGGGGAGTAGGTGAAGGCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGGGTAGGGCGGCGGCAGG
RUNX1	21	36164737 to 36164901	GCGGGTCGCTGAACGCTGTCAGGTCGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNAGGTGTGGTAGCGCGTG
RUNX1	21	36164763 to 36164862	GCGGGGGTCGGAGATGGAGGGCAGCGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATGGCCGACATGCCGA
RUNX1	21	36164803 to 36164937	CCTTCACCTACTCCCCGANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTCCGCTCCGTTCTCTTGCCCGCCCT
RUNX1	21	36164839 to 36165023	CGCCTAGGAGGATGGGAAGCCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGGGGGTCGGAGATGGAGGG
RUNX1	21	36164884 to 36165023	GCAGCGGCACCCGACCTGACAGCGTTCANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGCTTCCCATCCTCCT
RUNX1	21	36206617 to 36206751	GCTGAGGGTTAAAGGCAGTGGAGTGGTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGTCTGGGAAGGTGTG
RUNX1	21	36206684 to 36206793	GTTGGGCGTGGGGGCTGGGTGGTGTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGTGGGCTCCATCTGGT
RUNX1	21	36206764 to 36206933	GCAGGGAGGGGAGGGGATGGGGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGAGGGTTGGGCGTGGGGG
RUNX1	21	36259107 to 36259286	CGGAGAGGGTGGTGGGAGGACAGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGGCAAGCTGAGGAGCG
RUNX1	21	36259197 to 36259376	GCGCGGTGGAAGGCGGCGTGAAGCGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAGGAAGTTGGGGCTG
RUNX1	21	36252803 to 36252977	GCTTGAAACACGTTTCATGGCAACAAACCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNCTGGTCACTGTGATGG
RUNX1	21	36252869 to 36253043	GCAAGATTTAATGACCTCAGGTTTGTCGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGATGTCTGCATTTGTC
RUNX1	21	36259121 to 36259285	TCGCCGCTCCTCAGCTTGCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNACCCTCTCCGGGCCAGTACCTT
RUNX1	21	36164564 to 36164748	GCGGCGGCAGGTAGGTGTGGTAGCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGGTGGAGGCGTTGGTG
RUNX1	21	36265179 to 36265343	TCCCCCGACTTTTTTTTTTTTGCTAGCTCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGGTGTGTACTTTATTT
RUNX1	21	36421051 to 36421215	GCAGCTTGTTTCACCTCGGTGCAGAGATGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGCATTTTCAGGAGGAA
RUNX1	21	36421138 to 36421302	TCACTGTTTCAGCCTCACCCCTCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNCCTCTCATGAAGCACTGTGGGT
RUNX1	21	36259105 to 36259259	CGGAGAGGGTGGTGGGAGGACAGGCGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATGGTGGAGGTGCTGG
RUNX1	21	36259109 to 36259258	GCCCGGAGAGGGTGGTGGGAGGACANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNTGGTGGAGGTGCTGGC
RUNX1	21	36259313 to 36259457	AGGCGTTGCCGCTGGGCGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGTCTGGTAGGAGCTGTTTGCAGGG
RUNX1	21	36259334 to 36259453	GAGTTAGGACCCTGCAAACAGCTCCTACCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCATCTTGCCTGGGCT
RUNX1	21	36206842 to 36206941	GAGGGGAGGGGATGGGGGGAGGGAAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCTCGGAAAAGGACAAG
SETBP1	18	42531878 to 42532042	GCTGGGGATCGTCTCCTCACTGTGGGACTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCTTTGTGCTGGTGTC
SF3B1	2	198266704 to 198266868	GCTCATCCACAAGACCTACAAAACCAAACNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTTACCTTTCCTCTGT
SF3B1	2	198267235 to 198267399	GTCTCGCTTGCCAGGACTTCTTGCTTTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTCCTAAAGAAAAAAAAA
SF3B1	2	198267412 to 198267576	GCATTCCTTCTTTATTGCCCTTCTTAANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTGTCCTTTCTTTGTT
SMC1A	X	53432084 to 53432253	GCTTTCTCATCCCAGCGCCGTGCCTTGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGAAGGGAACAAGAAAGA
SMC1A	X	53423351 to 53423520	GCCATGGTCTCATCTATGATCTTCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNCTCTATCTACGTCCTCCCACC
SMC1A	X	53406965 to 53407129	CTAAGCTGTCCCTCTCCCAATCTCTGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNCTTTTTCTCCCTCCTCCT
SMC1A	X	53407483 to 53407647	CTACTCCCTGCCTGATTTCCCAGGGCAGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNCAAATTACATCAAGGA
SMC1A	X	53407592 to 53407756	GCAGAAGAGGTAGGGTAGGGAGAGGAAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGAGAGAGATGACGATGG
SMC1A	X	53407877 to 53408041	GCCCCCAGGTCGGGGTTGGGTTTCAGGGANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNTCAGTGTCAGCTCACC
SMC1A	X	53409109 to 53409288	GCCATCCAAGTAGGGCTCTTCAGGGTTCTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNTCAGTTCAGTCTCTTC
SMC1A	X	53409201 to 53409365	GCTTCCGGCCTATGGACAACTTGTCAGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNTTCCTGTCCCTATCTC
SMC1A	X	53409402 to 53409571	GCTTGGCCTTCTTTGCTCGCTTTCGGGCTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGGTTGGGTAAGGGGCT
SMC1A	X	53409436 to 53409600	AGATCTATAAGGCCCTGTCCCGCAATAGCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNCTGTCTTTCTTTCTGG
SMC1A	X	53409966 to 53410150	GCCTACGATGAGGACAAGAGGCTAAGGGTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNAAGCAAGAGATGAACA
SMC1A	X	53410032 to 53410196	GCTGGAAAGTGTCCGAGACAAGTTCCANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNTTGCTGGGCCTGGGGCTT
SMC1A	X	53421655 to 53421819	GTGTGGTGGGGGTGGGGGTTGGGTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNTGCCATTGCAGGGTAG
SMC1A	X	53421724 to 53421888	GCACGAGAGGCCCTCATTGAGATTGACTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNTGAAGGCTGCAAAGGA
SMC1A	X	53423049 to 53423213	GCAACTTAATGTCCTGCATCTTACAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNATCTTTCTCTCTCTCAC
SMC1A	X	53423123 to 53423287	GTGAGTATTGTGGCTGGTGGTGGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNTTACAGAAGGAGGTGAC
SMC1A	X	53423195 to 53423374	GCTACAGGCCTGTAAGATGCAGGACATTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNTGGGGTGGGAGGACGT
SMC1A	X	53423416 to 53423590	GACAAGAATCATGAGATGGAGGAGATTCGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGGTAAGATGGGGAAAG
SMC1A	X	53426461 to 53426625	AGACAGACTAATAACTGGGAGGAAAAATGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNCTTGGGCATTCAGTTG
SMC1A	X	53426542 to 53426706	CACTCATAATCTCATCAGCCAGAGATAACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNTTTTTCACTGTCTGCT
SMC1A	X	53430459 to 53430623	GGATTGGTAGAAGAGATTGGCATGCCCTTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNCCCTGGCTTCTCTTCT
SMC1A	X	53430660 to 53430824	GCGTGTGTGTCAGGGCAGGACTGGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNAAAAATCCAAGCTGGAGAG
SMC1A	X	53430734 to 53430898	GAGAAAAAGCTACCTTGACTGCATTGGCCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNTTCATTTCCCTCTCTC
SMC1A	X	53431842 to 53432006	GTTCTAGGTCACTCTGGGAGTACTTGAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGGAGGAGACGGGGAAG
SMC1A	X	53431916 to 53432080	GTGGGGCCTGGCCTTCAGCCCTGTTCTCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNAGCAGATGAAGGCAAA
SMC1A	X	53431967 to 53432131	GCTAGGTGGTAAGGTGGTGGCTGACCTANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGTGTCTTGGTCTGTTC
SMC1A	X	53432169 to 53432333	CGCTTGACAGAGGAGCTGAAAGTAAGCCANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNCTGTGTGTAGACAGTG

Supplemental Table S4: smMIP panel covering recurrently mutated AML “hotspots” in 33 genes

Gene	Chromosome	Location (GRCh37/hg19)	smMIP sequence
SMC1A	X	53432213 to 53432382	GCTGGGATGAGAAAGCAGTAGACAAGTTGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNACTGGAGATTCATTTG
SMC1A	X	53432391 to 53432560	GCTCATAGCGAATCACATCAATCACTAGCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNTGTCCAGCTCCAGCCT
SMC1A	X	53432474 to 53432643	GCTTGTGGCAATGCCCTTGTCTGTGACAANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNCTGTTTGTGTTCTGCC
SMC1A	X	53432581 to 53432775	GCTCCTTGATATACTGAATACAGTCCCGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGAGTTTCTCATCTGTA
SMC1A	X	53432680 to 53432859	GTGAGGCTTGTTGGGGATTGGGTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNCACACAAAAGAAGTATCAG
SMC1A	X	53432748 to 53432917	GCCGGGACTGTATTCAGTATATCAAGGAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNCTTCAGTTTTCCCTTC
SMC1A	X	53435959 to 53436158	GCAGAGAGGGAACTCATTTCCTGAGCACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNAGAGGAGGTGGAGATG
SMC1A	X	53436083 to 53436257	GCTGAACCAGGTGATGGAGCAGCTAGGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGAGCCAGGAGTATTTT
SMC1A	X	53436289 to 53436453	GGCCTGTTCTTGTGACCCTACCTACATGCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNTGGAATGTTTGTTTCC
SMC1A	X	53438679 to 53438848	GCTTCTTCTTTCAACCGGTGGTATTTCTTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNCCATCATCCCTAATCT
SMC1A	X	53438761 to 53438930	GCTGGAGAAATTCAATCGAGACCAGAAAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGGGTTGGCAGGGAGGA
SMC1A	X	53438886 to 53439050	GATCCCTGGGCTGACATCTGCTGACTTGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGGAGAAGGAGATGCTG
SMC1A	X	53439004 to 53439168	GTGGAGAAGGCTCGGCAGGAGTTTGAAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNAGTACATCAAAGCCAA
SMC1A	X	53439116 to 53439290	GCTTTTCACCCAAAGGAGAGCTTGAGCCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNTGCTTCCAGCTTCTTG
SMC1A	X	53439818 to 53439997	GAGGCAGACCTGGGCCTGCAACTTGTGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNAGAAGCTCAACAAGGAA
SMC1A	X	53439959 to 53440138	GCAGGGGTGCATCGATAAGGCACTGGCTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNTCTCCTTGTTCTTTGA
SMC1A	X	53440118 to 53440282	CAGGATGGAGCCAGTGCCTTATCGATGCANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNAGAAGGAAATGGTGAA
SMC1A	X	53440158 to 53440322	GTAGGTGGCCAAGCTACCTCTTGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNAGTCGTTCTGGGGAGCTG
SMC1A	X	53440243 to 53440432	GTGAAGGCTGAAGAGGACACACAGTTTAANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNTGGGTTGGCTGGGGTC
SMC1A	X	53441674 to 53441838	GCGTTTTTAACAGTTATTGGCTATCTGGTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNCTCATGCATTGTCTTG
SMC1A	X	53441882 to 53442076	GCTCTCCTTGGGTCCTGGGAGGTGGCTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNAAAAAACCAGCAACCT
SMC1A	X	53442000 to 53442179	GCTCCTGTGGGCAAGCCAGCTGCCAACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNTTCCTTTTCCTCTCCTCT
SMC1A	X	53449389 to 53449553	ACGTCCCGGCCTGGACCCCTTATNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNCGTCATGGGGTTCCTGAAACTG
SMC1A	X	53449462 to 53449636	CGGACCATTTCAGAGGTTCACCGCCANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNTTGCACTGCGGCGTTTCCC
SMC3	10	112337572 to 112337736	GTACTTAAATAGAGATGGGGTATTGCTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGCTTTTACATTTTTTC
SMC3	10	112338370 to 112338534	GAGTAATTCTTGAGTGATGAATTTGGTTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCATTGTTTGTCAACAG
SMC3	10	112343189 to 112343368	GTTCAGGTGAGTAGCAACTGTAGAAGACNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAAAGAAGAAAAAGAAC
SMC3	10	112349618 to 112349782	GCAGGTTCTTTTCATCACCTCTGTTTACANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAATTAAAGACAGTCT
SMC3	10	112327449 to 112327613	GCAGGTAAGGCCTTCGCGTCCCTCCACCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTTTGTTTGGCTGAGG
SMC3	10	112327479 to 112327648	GCCGGTAAGGGCCGCTCCTTGAGGCGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTTGGGGGAGGGGTCG
SMC3	10	112328651 to 112328815	ACTCGGTCATATTTATAGTCTATACAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTTTTTTTGTGGGGTGG
SMC3	10	112333401 to 112333520	ACTTTTTTTATGGTAGGTGTTGCTTTTTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGTAAACAGTTTTAAT
SMC3	10	112333441 to 112333560	GACCTGGGTATCTTAGGGTAGATNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTTGTACTTTTTGAAATTTTCC
SMC3	10	112333441 to 112333605	GCCCACTGGAAAATTTCAAAAAGTACAAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGGTTTCATGAATAC
SMC3	10	112335016 to 112335180	CTTATTTATAACTTCCCACACCTCAATAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTAAAGCAGTCTCACT
SMC3	10	112337157 to 112337321	GTTTAGCTGATTTTCTTCATACTTTGAAANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTCTCACTTCTTTCAT
SMC3	10	112337170 to 112337334	CACGAGGACCAGTACCTTCCTAAAAATGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAAGCTTAAAAAGTTTC
SMC3	10	112338256 to 112338420	GATGTGATGAACCTCCTTGAAAGCGCTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAGGATGATACAGATGG
SMC3	10	112342302 to 112342466	ACTTTTGAGACAGGGTCTTGTTCTGTCANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGTTGTTTTTTTTCTTA
SMC3	10	112340619 to 112340783	GCATCTCCTTAATGAAAGAAACAGGTAANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGAGGCTACAGCTATG
SMC3	10	112340677 to 112340841	GCTTTAATCTCTGAGAATCTGGTGCTGTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCACTCTGTCACAAAAAC
SMC3	10	112341663 to 112341827	CCTGGAATATACCATTTACAATCAGGAACNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTCCCCATTTCTTTTA
SMC3	10	112341738 to 112341912	GCTAGTTCTTCCTTTTCTTCCTCTAGAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCAAATTCATAAAAACAA
SMC3	10	112343111 to 112343290	GCCAAGGATTTACAAGATGAACTAGCAGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCCTTATTTTCTGTTT
SMC3	10	112343578 to 112343742	GCTAGGTCTGAGAACTTTCACCAACACNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCATTTTTACTTTGTTT
SMC3	10	112343632 to 112343796	ACTAGGTTGTCCGAGGAGCTCAATTANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAAAAAATAGAAGAAAAGC
SMC3	10	112343923 to 112344117	GCTGCTATACATAAGGATTTGGAAGACACNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGCTTCTATTTTGTGT
SMC3	10	112344035 to 112344204	GCCTGATCTAAAGACTTGAGTTCCTTTTTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCATTTATCTCTTCTGA
SMC3	10	112349249 to 112349413	GTCAAAGCTCGAGTAGAAGAACTGGACNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCCTCCCTCACCTTTTG
SMC3	10	112349351 to 112349515	GCATTAATGTTTTCAGTAATGTTCGTTACNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTATTTCCATAGAAAC
SMC3	10	112350151 to 112350320	GCTTTCTACACATGCGTGGAAGTCACTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCATTTCTGACAACTTAC
SMC3	10	112350214 to 112350378	CATGCTGGTTTATTCCTTTTCGACGGAAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCTTATTCCCTCTTCT
SMC3	10	112350698 to 112350867	TCTTTATTGGTACTCAGGGTCTCCCTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCCTGACATCTAACTTGTT
SMC3	10	112350818 to 112350987	GCTAGTGCCCAGGCACTATACACTGGGANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCTTCCTGGAGAGGTT
SMC3	10	112352791 to 112352955	CAACCCAGCTGGCCCGTGCTTTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTGTGTTGTGATCTCTCTGTTG
SMC3	10	112352891 to 112353065	CATATAATCTGGCTGGGCGCAGTGGCTCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCATGTGTTTGGAAAGAC
SMC3	10	112356126 to 112356300	GCAAAGCTCAATGAAAACCTGCGCAGAAANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACAGACCTATTACATA
SMC3	10	112356174 to 112356348	GCATAGTGATAGATATTGTGGGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGGGTGCTCTAACTGGGG
SMC3	10	112357877 to 112358046	GCAGCAGTCAGAGAAAACCTTCATGCCTANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTTTCCTTAGCCTTGT
SMC3	10	112357927 to 112358091	GCTGGGTCTCGATCTGTTGCATTTGGTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAATCTGTAACAATCGATC
SMC3	10	112359368 to 112359532	CATTTATTAGTAAGGTATTAGCCACTGTANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTCTCTTCTGATCTTC
SMC3	10	112359476 to 112359640	GCTATTGTGAAAAGGGCCTTTCTTGCTANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAGCAGAACTGGGAACT
SMC3	10	112360140 to 112360304	GCATGTACATTTCACACACAGGAATGGTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTGTTCTACTTGGTCC
SMC3	10	112360243 to 112360407	GCTCTGATTGAAAGCATGGGCTTTGGGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTACTCGAGTAGAGAC
SMC3	10	112360740 to 112360904	GCACGATCAGAAGGTGAATTTTTATGTAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTAACATTTGAAACTAA
SMC3	10	112360819 to 112360983	GCTTCAAGTTCTGATGTTGTGGCTGTGAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTAGCATATGCTTCTGC
SMC3	10	112361375 to 112361549	GATGACAAATCGGCAAGGCATGCTATTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTTGTTTCCCCCCATCT
SMC3	10	112361465 to 112361639	GCATCCATATGTTCTTTTTCCATATTTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTTGAGGCTCAGTGTCTG

Supplemental Table S4: smMIP panel covering recurrently mutated AML "hotspots" in 33 genes

Gene	Chromosome	Location (GRCh37/hg19)	smMIP sequence
SMC3	10	112361581 to 112361755	GCTTCCTGGGGAAGTGATCCAAGTTCTCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCTGTGTTGCACTGCT
SMC3	10	112361701 to 112361865	GCGTCAAGAAGAGTTAGATAGGGGTTACANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAATACATATTTTCTC
SMC3	10	112361812 to 112361991	ACACACAGAGGACAAAAGCTTCCAGCTCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCGAGCAGAAAGAAAAG
SMC3	10	112362214 to 112362408	GCAGTGTCCCATCAGTTGACCAGTTTACTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATCTGCTTTTGTTTTA
SMC3	10	112362332 to 112362516	GCAAATCTGATTGGTGCATTATATGCAAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATGAAGGAGAAGGGAG
SMC3	10	112362529 to 112362698	CCTAAAGGGCAGAATCACCACCATCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGAGCCGGGTCACATTTCTG
SMC3	10	112362619 to 112362793	ATTTCTGTCCACCTGAAAGCTGTTGCATNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAATACAAAACCAAAAC
SMC3	10	112362876 to 112363040	GCTGACAAATTCTATGGTGTAAAGTTCANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGTTGCTTTTTAAATTT
SMC3	10	112362946 to 112363110	ACTGAGCATGTACAGCAAGTTCCATAATCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCAGAATTCAACAAAT
SMC3	10	112363930 to 112364094	GTTAATTACATCAGTGTTTACATTGTATANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTACATCTCCCAAACCA
SMC3	10	112364022 to 112364186	GTGGTATCATCTTCTACAAAGTCTTTGGCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAAAGGACTATGATGC
SRSF2	17	74732928 to 74732987	GCGCGCCATTTGCACCCGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCGGTCCCCGGCGGCTGTGGTGTGAG
SRSF2	17	74732928 to 74732987	GCGCGCCATTTGCACCCGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCGGTCCCCGGCGGCTGTGGTGTGAGT
SRSF2	17	74732937 to 74732996	TTGCACCCGCAGCTCGCGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCGGCTGTGGTGTGAGTCCGGG
SRSF2	17	74732940 to 74732999	CCCGGACTCACACCACAGCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGCCGCGAGCTGCGGGTGCAA
STAG2	X	123202356 to 123202520	ACTGTTAAGGAACAGGTTAGTAATTACTANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNAGAAATGCTGAATTGT
STAG2	X	123184021 to 123184185	GCTATCGCATCACTGAATGGGGGAAGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGAAGCAGTCTGAAGGG
STAG2	X	123195585 to 123195749	GGGTATGCCAATCAATGTCTTTTCAATNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNCTTTCTGACTTTTTTTTT
STAG2	X	123195680 to 123195844	CTTCCCACGGGAGGATGACATTCAGCCGCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNAAGCAAAGGTTGTCTG
STAG2	X	123171358 to 123171522	ATCAGCAGCTCTCAAATAGTCACTTCGTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNTTTTTTCCCTCTGCTGT
STAG2	X	123156445 to 123156609	GCATTAACTTCAGTTAAATTTCCTTCTGCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNTGACATTGAGGTGTTC
STAG2	X	123159658 to 123159822	ACAGAAAGATAAGAATTAAAACCCTTCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNTGTGTGTGTGTGAGATCT
STAG2	X	123184014 to 123184178	GCATGATAAGGTAAGATGTGCCCTTCAGANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNCGTTTTTCCTTCCCCC
STAG2	X	123164886 to 123165055	GTTGGTGATGACCATTCATTCGGTTTGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNAAAAATCAGAGCTACAC
STAG2	X	123176381 to 123176545	GCAAATGTCAGAAGTTAATATATGGTGTGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGTCAAGATAAACATGC
STAG2	X	123178990 to 123179174	CAGTCATTTCACTTCTTACAGGATTGTCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNTGCTGTTTTAAATTTTT
STAG2	X	123179076 to 123179250	GCCGTACTAACACGCCAATGAATTCACAANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNACAATATGCAGAAAAT
STAG2	X	123181178 to 123181342	GCCAATGAGAGGCTAGAACTCCTGCTACANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNACCATACTTTTACTCT
STAG2	X	123181224 to 123181403	ATTTAGGCTATTGTGTGACCAACTTGGTCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNTTGGTGAATGTGGCAC
STAG2	X	123182797 to 123182961	GTTGTGACAGTTTTTTTCATAAATAGCATNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGGTGTTCATTTGGTTG
STAG2	X	123164781 to 123164950	GCATAAAAAAATACGAGGTGGTTAAGTTANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNACAACTTCAAACAACA
STAG2	X	123184840 to 123185004	TGTTTCATACCATAGCATTCCTTCAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGAGCAGTAAGACATTTGAG
STAG2	X	123184966 to 123185130	GTCATTTGCAAACACTTTTCTCTTGCTTTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNTTTAGCAAGGTGAAGT
STAG2	X	123185099 to 123185263	GCAAGAGAAAAGTGTTTGCAAATGACAAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGCAACAAATACATACT
STAG2	X	123189938 to 123190102	GCAGTAACAGGTGCTTTTAGTAACGTCCTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNCAGATATATAGATTTA
STAG2	X	123191675 to 123191839	CTTTCTAGAAAGTGAGGTTAGTTGATAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGTTGTTGTTGTCGTAA
STAG2	X	123191730 to 123191894	TTCCATCCTCCTCTGGATCTCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNTGCCTCATTTTAACCCCTTTTCC
STAG2	X	123195030 to 123195194	GCAATGTGGTCTTAGACAATTATCATACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNTACCTTCCTCTCCACT
STAG2	X	123195103 to 123195267	GCAGCTCAGTAGCACAGTCCCACATGCTANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGGACAAATAAATGGAA
STAG2	X	123196731 to 123196895	GTGTTACTAAGAAATGAGTTTTTTTTCCCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGAAGTCTTTCTGTTCC
STAG2	X	123196881 to 123197045	CTGTGAGGCATTTAGGGAAAAAAAACTCANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNCGTCCAGTGGTATATA
STAG2	X	123196968 to 123197132	GTTAGTCACCTTTTCTGCATCTACAGAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGAAATATAAACAAACGC
STAG2	X	123197661 to 123197845	CAACAGAGTAGATATTTCAAGAAGTCAACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNTGCCTTAGTTTTGATG
STAG2	X	123197784 to 123197953	GTGAACTCTTCATTACAGAGTGCATGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNTGCAGTAGAGGGGCTC
STAG2	X	123199663 to 123199827	GTGAAAACTCCTAGGCTATCAAAATGTCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNAAGAAAACAGGAACTTC
STAG2	X	123199948 to 123200112	GCTAAGCCTAATGACAATTGTTTTGGACTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNCTGCTCAGGCATGTCT
STAG2	X	123200029 to 123200193	GCAAATAAATCCCACTTTGAAAGGTCATGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNTCAAAGGATACAGTTA
STAG2	X	123200155 to 123200319	GTGGTGGTTCAGTAGTGTTTTTATTAGACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGAAGTCTTGTGACTTT
STAG2	X	123202405 to 123202569	GCAACCTTTATAAAATCTGAACTAATGTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNTTTTTCAAGGAGGACT
STAG2	X	123202464 to 123202628	GTATTCACGTTGGTCAGGTAATGTTGANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNACATAGGCAGATACAAGA
STAG2	X	123204970 to 123205134	GCTCAGCTTTATTTTGGATCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGCTTTCCTCTTTTTTTTTTTTTT
STAG2	X	123205055 to 123205224	ACACTAATGGCTCTAACATGTCACGCCCTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNTTTGATTTTATGGTGG
STAG2	X	123210134 to 123210298	GTGGTGGAGATGAATACAGCTGCAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGGTTGAAATAAAATACAAGA
STAG2	X	123210241 to 123210405	GCATGGCTGCCATTGAATTCTTTAAGGGCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNCTTGCAGCATTTTGTA
STAG2	X	123211778 to 123211942	CATTAAGAGTACCAACTTTAGCTAACACANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNAGCTCTAATTTGTACA
STAG2	X	123215208 to 123215377	ACAAGAGAAGCCATTGCCATGCTACACANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNTGCTTTCTTTCTTTCCA
STAG2	X	123215293 to 123215457	GCAAAACGTCGAGCAAGTTCTTTTATGCCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNCCAAATGAAAGGGCTA
STAG2	X	123217157 to 123217321	CTTCCTTTGCCAAGCTTTTAATTTGAGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNTGGCTCTCCCCTTGCGG
STAG2	X	123217255 to 123217419	GAACAGTGTATGTATTTGCTGGAAATGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNTTGTTTTCCTTTGCAG
STAG2	X	123217291 to 123217455	GCTCTCCCCTTGCGGATTAGGCTCTTTAANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNTTGCCCTTAAGAATCC
STAG2	X	123220355 to 123220519	GCTGGTGGTGATGATGACACCATGTCAGTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNAGATTTCTGTATCAAA
STAG2	X	123220441 to 123220610	CGGAAAGTGGTTGAGGGCATGCAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGAAGAGAGGATGTGTGGCTTC
STAG2	X	123220529 to 123220693	CGTACTGTTGACCCCCGGCTGCTGATTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNAAGGTGAACCTTAATGAC
STAG2	X	123224376 to 123224540	CGAGGTTTAGTCACTAATTTTGACTATTCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNTCTTTTGGGCTCTCTC
STAG2	X	123224478 to 123224642	GTGGTGTCTGCATCATAACAGGGGTGTGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNAGTACAGAAAATGATCA

Supplemental Table S4: smMIP panel covering recurrently mutated AML “hotspots” in 33 genes

Gene	Chromosome	Location (GRCh37/hg19)	smMIP sequence
STAG2	X	123224674 to 123224838	GCCATGTAAGTGAGAGTGCCTTATTGTCTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGTTAAAAGAGGAATAA
STAG2	X	123224756 to 123224920	CTCATTGCTGCTCTCTCCTGCTGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGGTTACTCTAGAGAGTTTGCTG
STAG2	X	123227821 to 123227985	GAGGGAATGGATTTTGACACCATGGATNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNAGTCACGACATTAGTTCA
STAG2	X	123227925 to 123228089	TCCTCCCTTCTGAGGACATCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNTCTCTTGGTAAGTATTTCTCTACTC
STAG2	X	123229106 to 123229270	GAGAGAACAGAACTGAAGCCTGATTTCTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGTGTCAGGTACACTTGG
STAG2	X	123229205 to 123229369	GTATAGGCAGTCTCTCAGTTTGAGGTTGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNTTCCTTTTTTCCTTTAG
STAG2	X	123234398 to 123234597	GCTTACCAAGATCAAGTGCATTGAGGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNTTTCTCCCCTCTCTCTCT
TET2	4	106156790 to 106156974	GTGAAAACGAGGGGCCTTCAATTCAATCCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGTTGTTTTCTGGGTG
TET2	4	106157280 to 106157464	GTGAACTCTGGGATGGTTGTGTTTGTGCTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTTCACCATGAAAACA
TET2	4	106157404 to 106157593	GCCAAAGAATGATCCTTCTCTTTGCTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCTGTATTTTGCATGC
TET2	4	106157799 to 106157998	GTTGACCAGACATATCTTGGTTTCTATTTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCTGTGTTTGCTGCTG
TET2	4	106158325 to 106158504	GCTGCTCTAAAGCTGGGGTGTGGCTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACATCTGCAAGATGGGAAA
TET2	4	106155252 to 106155421	TTCTCTCTCTGGGCTCCTTCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCACCAAGTGGCACTCTTTCAAAAGT
TET2	4	106190713 to 106190877	GCGAAAGTAGTTAGTTTTACTCTTACACCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCAAGTCTCTGTGGGCA
TET2	4	106190820 to 106190984	GCAGTGACCCCTGAGAATGGANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTACCCAGTCTTGCATATGTCTTT
TET2	4	106155360 to 106155554	GCGTTTTATTCCTCCATTTTGCAAACACNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTCACAGATTCTTTCTT
TET2	4	106196241 to 106196420	GCTTCTGTAGAGGCTGGGGCTGCTGGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGTGTGAAGAGTTTGG
TET2	4	106196565 to 106196729	GCAGTTGTCCACTGATAGGTTTCCATTGCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCTGGCTATTTCCAAA
TET2	4	106155606 to 106155795	GCTCTGGATTTTCAGGCCCACTGCAGTTANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTGAGACAGTGTTTTT
TET2	4	106162460 to 106162624	GCAAAGGCACAGGGCAGATTAACGTTTATNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAGGTCTAAAATAATA
TET2	4	106197193 to 106197362	GCTCGCTGTCTGACCAGACCTCATCGTTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGGAGATCCTGGTGGG
TET2	4	106155841 to 106156005	GCCTGACTGTTAATGGCATTTATGTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATCAGCATCATCAGCATCA
TET2	4	106197074 to 106197253	GCTTTCTGGATCCTGACATTGGGGGAGTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCTCTTAACCATGATA
TET2	4	106196942 to 106197121	GCACTGTAGTTATGGATTATGTGAGAAGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTTGTGTAAGCCTCCT
TET2	4	106180817 to 106180981	GCTTTATTTTTCATAGAGAATTCATTAGCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTGCCTCCTTCTCTTT
TET2	4	106180720 to 106180889	GCTATGGATAGCATTATATAGGCTGTGCANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGGATCTTGCTTCTGG
TET2	4	106157165 to 106157329	CACTGGGGACATAAGTTTTTCAGTTTGGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTTGCTGGTTTTGAGG
TET2	4	106196117 to 106196286	GAAGGCTAGTGAGGATACTTAAATGTAGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGCTGGGGCTGTGGTG
TET2	4	106155888 to 106156067	GCCCTGAGGTATGCGATGGGTGAGTGATCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGTAGTTGTTCTGGTT
TET2	4	106156656 to 106156850	GCGGAATCCCATCTAAAACGTAATGAGGCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGTAGCAGTGGAGAG
TET2	4	106156916 to 106157100	GCCCCCCAGGCATGTTGGAATTTCCAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATGGTCTGTTTTGGAG
TET2	4	106157058 to 106157222	GTGCACCTGGTGTGAGGGTTTTTGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAAGCCTGTTGATTCAAGTG
TET2	4	106157549 to 106157748	GATTTCATGGTCTGACTATAAGGGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAAGCACCTGTGAAGAAGA
TET2	4	106157950 to 106158114	GCTTCTGTAAGAGATGCCACCTTAGAGCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTTTTTCCATGTTTTG
TET2	4	106158064 to 106158228	GTGGTGCTGTGTGCATACAGGCATGTGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATGGTCAAATAACGAC
TET2	4	106156062 to 106156261	GCTTACTTCAAGCAAAGCTCAGTGTTCANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACTACAACAACAAAAAT
TET2	4	106155089 to 106155258	GTTCTATCCTGTTCCATCAGGCTTGCTTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTTGGTGTCTCCATTT
TET2	4	106158182 to 106158381	GGCGTGAAACTGCTTCAGATGCTGCTCCANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTTGGTTGGTGTCTTT
TET2	4	106164689 to 106164853	GTGGGAAGGAATCCCGCTGTCTCTGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGTGGGGGTGTTTGGGA
TET2	4	106164795 to 106164959	GAGTAAGTGAAGCCCAGGGCCTCTCCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGAGGCTGCAGTGATTGTG
TET2	4	106196464 to 106196628	GAACCTGCAGCTTGAGATGAGGTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGAGACTGGGGAGAATAGG
TET2	4	106196604 to 106196798	GCAGGGAGATGGTTTCAGCAGTTGTACCANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGGTTCCTATTCTCC
TET2	4	106155032 to 106155201	GCCAGACAGAACCTCTGGCTACAAAGCTCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTTTTGTTTCCATGCT
TET2	4	106155187 to 106155351	GCTTCCATTCTGGAGCTTTGTAGCCAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCCTCTACTTTCTTGT
TET2	4	106182964 to 106183128	GCATCAGGTGCAAGTTTCTTATATGTTGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCAACAATTAAGAGGAA
TET2	4	106155970 to 106156134	GAAAATAACATCCAGGGAACCACAAAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTGGTGAGTGAGGCCTG
TET2	4	106156177 to 106156341	GTTCAGAGCTGCCACCAGGAGCTTGCAANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTGTGGAAGAGGAGGAG
TET2	4	106156268 to 106156432	CCACTACCCCAACCAAAGTAACACAACACNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATTCCTTTTCTGCCAC
TET2	4	106156309 to 106156483	GTAAACCTGAGGCACCACCTTCCCAGANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTGCTTCTTTCTCCCC
TET2	4	106156407 to 106156606	AGTGTTGTGTTACTTTGGTTGGGGTAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCAGAACACAATGGAACAG
TET2	4	106156415 to 106156514	TCCATCTACACATGTATGCAGCCCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACCAAAGTAACACAACACTT
TET2	4	106156475 to 106156539	GCCCTTCTCCGATGCTTTCTGAAAGGCCTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTTCCCAGAGTCCTAA
TET2	4	106156482 to 106156546	TGCATACATGTGTAGATGGATTAGGACTCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTATTCTGAGGCCTTTC
TET2	4	106156517 to 106156646	CAATGTCAGAACACCTCAAGCATAACCCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTCCGATGCTTTCTGAA
TET2	4	106156553 to 106156717	CCCTGCAGTCTGTATGTCATTCCTGTTCANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCTCTTGCTCTTTGTT
TET2	4	106193677 to 106193856	GACATTACAGCCTCAACTACAGGTCCCAANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTTTTTTCTCCTCCTG
TET2	4	106157689 to 106157858	GCTGCGCAACTTGCTCAGCAAAGGTACTTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCACATGCAATATTTTC
TET2	4	106193749 to 106193918	GCGAAAAGTCAGGATGTTAGCAGAGCCANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAGAATTTGGAGGAAAA
TET2	4	106158375 to 106158539	GTGCCAGAAATGTACTGAGACACATGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAACCAAAAGAACAGCTGC
TET2	4	106193823 to 106193987	GCAGCTGAAAAGCTTTCCTCCCTGGAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTTGGGAGTGTGGAAGCT
TET2	4	106163961 to 106164125	GCCTTTGGTCTTAAATCTTGGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGTGTGTGTGTTTCTGTGG

Supplemental Table S4: smMIP panel covering recurrently mutated AML “hotspots” in 33 genes

Gene	Chromosome	Location (GRCh37/hg19)	smMIP sequence
TET2	4	106193931 to 106194110	GCTTTCTTGGCTTCTAGTTTCCTTTGTCGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCACATTTATCTACAAA
TET2	4	106164917 to 106165081	GCCTGTTTGGCAGTCATGCGATAAGAAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGTGTGCCTTGAATGA
TET2	4	106182867 to 106183031	CAGGTAAGTTTAAATAATCATTGGCAGCANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAGAAAATGGACTTAG
TET2	4	106155486 to 106155665	GTTGACTGCTTTCACCTGGATTTCTTTCTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTTTCCCCTCCTGCT
TET2	4	106196360 to 106196524	TGGGCCGTCTCATGTATGGATTGGTGGANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGGGTAAGGGTTCATGG
TET2	4	106196687 to 106196851	CCTTGGCTGGTAAAGTGTATGGATGGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTCATGAGTGGGATAAGG
TET2	4	106196801 to 106197000	GCTCCGGGCATGTTCAACAGCTCTCTTCANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGACCAAATGTACATC
TET2	4	106155748 to 106155912	AGGAGTTCACCATGTGTGTGTTCCACGGANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGAGGTATGCGATGGG
TET2	4	106197290 to 106197459	GTTGTGGCATGCAGCTCACGCTTTGCACANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCTTCCTCTTTCTCAC
TET2	4	106197408 to 106197572	CAGAGCCCACTTACCTGCGTTTCATCANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGCTCTTTGGGAAGCC
TET2	4	106197522 to 106197721	GTTTCATGTGGCTCAGCAGGCTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGTTGTGGTCTTTTCAAGTGAGG
TP53	17	7578348 to 7578447	GCGATGGTGAGCAGCTGGGGCTGGAGAGANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCATCTACAAGCAGTCA
TP53	17	7578378 to 7578577	GCCCCCACCATGAGCGCTGCTCAGATNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTGTCTCCTTCCTCTTC
TP53	17	7577472 to 7577636	GGAGATAACACAGGCCCAAGATGAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGTGCAGGGTGGCAAGTGG
TP53	17	7578140 to 7578304	GCAACTGGGGTCTCTGGGAGGAGGGGTTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACTGATTGCTCTTAGG
TP53	17	7579583 to 7579742	GCTCTTTTCACCCATCTACAGTCCCCCTTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTTTCTGCTCTTGTCT
TP53	17	7572865 to 7573034	GCTGTAGGAGACAGAAGCAGGGAGGAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATGGCAGGGGAGGGAGAG
TP53	17	7578391 to 7578490	GCCGGGCGGGGGTGTGGAATCAANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCATGGTGGGGGCAGCG
TP53	17	7578188 to 7578352	CGACATAGTGTGGTGGTGCCCTATGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGAGACGACAGGGCTGGTTG
TP53	17	7579269 to 7579433	GCCAGGAGGGGGCTGGTGCAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGCATTGAAGTCTCATGGAAG
TP53	17	7578436 to 7578620	GCACAAGTGAACAGATAAAGCAACTGGAANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGCTTGTAGATGGCCA
TP53	17	7572830 to 7572999	GCGGGAGGTAGACTGACCCTTTTTGGACNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATTGCAAGCAAGGGTT
TP53	17	7572872 to 7573036	GACAGAAGCAGGGAGGAGAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGGAGGGAGAGATGGGGGTG
TP53	17	7572992 to 7573091	GTGCCCCTTTTCCCTGACCAATGCTTTGANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTTTGGACTTCAGGTG
TP53	17	7578471 to 7578635	GCAACTGGAAGACGGCAGCAAAGAANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGGCGGGGGTGTGGAA
TP53	17	7573894 to 7574058	GTGACCTCAGCCCCTTCCTGGCCCTACTCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTCTCCCCCTCCTCTG
TP53	17	7576963 to 7577127	GGAGACCAAGGGTGCAGTTATGCCTCAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAGGTGCGTGTTTGTG
TP53	17	7576782 to 7576946	CTAACACTCAAAATGCCGTTTTCTTCTTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTTCCTTGCCTCTTTCC
TP53	17	7577075 to 7577239	CCCATTTAAAAAACCAGGCTCCATCTANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTCTCTTCCTCTGTGC
TP53	17	7578247 to 7578436	CCTCACAACCTCCGTCATGTGCTGTGACTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAATTTCCTTCCACTC
TP53	17	7579374 to 7579433	CCCAGAAAACCTACCAGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTGCACCAGCCCCCTCCTGGCCCCT
TP53	17	7579376 to 7579570	CGTCCGGGGACAGCATCAAATCATCCATTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGTAGGTTTTCTGGG
TP53	17	7579392 to 7579561	GTTCAATATCGTCCGGGGACAGCATCAAANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAGGGACAGAAGATGA
TP53	17	7579484 to 7579648	GTCCAGATGAAGCTCCCAGAATGCCAGANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGGGGGCTGGGGGGCT
TP53	17	7579504 to 7579603	GCAAGGGGGACTGTAGATGGGTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATCTGGACCTGGGTCTTCAGTG
TP53	17	7579509 to 7579568	AATGGTTCACTGAAGACCCAGGTCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGATGATTTGATGCTGTCC
TP53	17	7579529 to 7579648	GCTGTCCCCGGACGATATTGAACAATGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGGGGGCTGGGGGGCTG
TP53	17	7579674 to 7579778	GACAAGGGTTGGGCTGGGGACNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGAGACCTGTGGGAAGCGA
TP53	17	7579678 to 7579842	GCCCTTCCAATGGATCCACTCACAGTTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCAGCCCAACCCTTGT
TP53	17	7579716 to 7579815	GTTGGGGTGGGGGTGGTGGGCCTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGAAGTCTGAAAGACAAGAGCA
TP53	17	7579776 to 7579895	GAGGGGGCTCGACGCTAGGATCTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCTGCTAGGGGGCTGGG
TP53	17	7579798 to 7579962	ATTGGAAGGGCAGGCCCACCACCCCCACCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATCCCCACTTTTCCTC

Supplemental Table S4: smMIP panel covering recurrently mutated AML "hotspots" in 33 genes

Gene	Chromosome	Location (GRCh37/hg19)	smMIP sequence
U2AF1	21	44524406 to 44524570	GCTGGGAAGATATCAAACACATGGAATANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGAAAAAAAGGCAAACAA
U2AF1	21	44514722 to 44514886	GCCAGTGACGTGACTGAGCACAGTTCGGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAAGATGCGGAAAAGG
WT1	11	32410582 to 32410776	GCTTTGAGGGGTCTCCCTCGGGGACCGTTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGTGCCTGTCTCTTTG
WT1	11	32421472 to 32421636	GAAAAAGGCTCAGTGTGGCTCACAGTCGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGGGCCTGTCTGTGT
WT1	11	32410449 to 32410643	GCTGGAGTTTGGTCATGTTTCTCTGATGCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTAGTTTCCAGAAGCA
WT1	11	32413497 to 32413661	GCCTCGGCCCTAACAATGTGGGCACAGTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGTGAAGAAAAGTTTA
WT1	11	32414079 to 32414243	GTCTCCTTTGGTGTCTTTTGAGCTGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATGGGGGGAAAATACTG
WT1	11	32414184 to 32414348	GTTTGTAGGTTCACTTCTCATTGCTGGCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCCCTTTTCCAGTATCA
WT1	11	32417757 to 32417921	CACTGGTCTCAGATGCCGACCGTACAAGANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCTCTTGAACCATGTT
WT1	11	32417812 to 32417981	GCTGTCCCACTTACAGATGCACAGCAGGANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTCCCTTCCTCTTACT
WT1	11	32437995 to 32438159	GCGGAGATGGCAAAGCAAATGGCGTAGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTCTGGGATCTGGGGG
WT1	11	32439077 to 32439241	CCATTGCCTTTCCACAGTAACTTATACCTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTGTGGTTATGTGTTT
WT1	11	32449383 to 32449482	CTGCGGGCATGCAGGGTCTTGGANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGCGTCTGGGTCCTTGGG
WT1	11	32449412 to 32449531	GCGGACTTGGGAACGCCCCAGCCGGGCAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGCTTTGCTGCTGAGG
WT1	11	32449432 to 32449531	CGGAGGGGACGCATGAGCCGGCGGACTTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGCTTTGCTGCTGAGG
WT1	11	32449493 to 32449622	GCTGCTCACCTGCAGAGAGAACCGAAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCTTCCTACCTGCTGT
WT1	11	32449548 to 32449647	CAGCTGAGCGAGTGCGCCCCAAGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGTCGGTGGGGGTGTGG
WT1	11	32449548 to 32449677	GTGCGAGGCTGCGGGCAGGGGTTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGTCGGTGGGGGTGTGG
WT1	11	32449598 to 32449697	GCAGGGGTTGGGGGAGACACGAGATCCTGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGCTCACCTGCAGAGA
WT1	11	32449980 to 32450144	GCGTGTGACCGTAGCTGGGCGTCCCGTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGGGAGAGGAGGAT
WT1	11	32450079 to 32450243	GCAGTGGGTCTGAACCAGCCACGGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGAATGAGTGGTTGGG
WT1	11	32456154 to 32456293	CCCCCCTCTCCTACCCCTTTTGACCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCTACCTGCCCAGCTGCCT
WT1	11	32456162 to 32456356	GCTGGGCGGAGGAGGACCGAAGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGGGTAGGAGAGGGGGG
WT1	11	32456250 to 32456349	GCCTGGCTGGGCGGAGGAGGANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATTGCGAATAGCGGGCTGG
WT1	11	32456279 to 32456403	GCTGTGCCAGTGAACTGGCCGGAAAAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGCTGGGCAGGTAGGG
WT1	11	32456279 to 32456488	GCTCCTGTTTGATGAAGGAGTGAGGCGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGCTGGGCAGGTAGGG
WT1	11	32456303 to 32456487	GCGTCATCCGGCCAGGCCAGGATGTTTCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCCTCACTCCTTCATC
WT1	11	32456397 to 32456496	GCCTGAGCGCCTTCACTGTCCACTTTTCCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCCGCCGCCGCCTCAC
WT1	11	32456425 to 32456589	TCCAGCACCGGCGCCCACNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCACTGCTCCTCGTGCGGCTCCGC
WT1	11	32456450 to 32456589	TCCAGCACCGGCGCCCACNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCGCCCCAGCTCGGCTCCTGTTTG
WT1	11	32456477 to 32456596	GTCCAGCACCGGCGCCCACTGCGCCGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGGAGTGAGGCGGCGG
WT1	11	32456530 to 32456694	GCTTACGGGTCGTTGGGCGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCAGCAAATGGGCTCCGACG
WT1	11	32456536 to 32456635	CGGGCGCTTCGGCTTACGGGTCGTTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGGTGGCGGCGGCGG
WT1	11	32456603 to 32456702	CGTCGGAGCCCATTTGCTGCGGCTCAGANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCACAGGCAGGGCACA
WT1	11	32456649 to 32456818	GCGGGACCTGAACGCGCTGCTGCCCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTACAGCAGCCAGAGCA
WT1	11	32456653 to 32456752	TGCGGGACCTGAACGCGCTGCTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGGCCAGCGCTGAACGTCTCC
WT1	11	32456684 to 32456818	GCGTCCGGGTCTGAGCCGCAGCAAATGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTACAGCAGCCAGAGCA
WT1	11	32456719 to 32456818	ACTCCCTGCTGCTCTGGCTGCTGTANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTCCTCCGGCCCTGGAG
WT1	11	32456729 to 32456903	GCCGAGGCCAGCGCTGAACGTCTCCAGGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGACTTCCTCTTGCTGC
WT1	11	32456764 to 32456903	GCCGGGTCCTGCAGCAAGAGGAAGTCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAACTTGGCCCAGATGC
WT1	11	32456803 to 32456922	GAGGAAGTCCAGGATCGCGGCGAGGAGANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGCTCTGGCTGCTGTA
WT1	11	32456833 to 32456982	GCTCTGGGTGGGTGGGTGGGTGAATGANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAGCGGAGCGTGTGCTG
WT1	11	32456837 to 32457006	GTAGGTGGGAGGGAGGGCGGGAAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGAGCGTGTGCTGAGA
WT1	11	32456864 to 32456983	GCTCTGGGTGGGTGGGTGGGTGAATGAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGACACACGTGGAAGC

Supplemental Table S5: Antibodies and viability staining used for sorting

Antibody	Manufacturer	Clone/Catalogue number	Titer
CD45-BV510	**BioLegend, San Diego, CA, USA**	**HI30**	**1:20**
CD33-PECy5	**BD Biosciences, San Jose, CA, USA**	**WM53**	**1:20**
CD38-PECy7	**BioLegend, San Diego, CA, USA**	**HIT2**	**1:20**
CD19-PE	**BD Biosciences, San Jose, CA, USA**	**HIB19**	**1:20**
PI	**BD Biosciences, San Jose, CA, USA**	**556463**	**1:50**

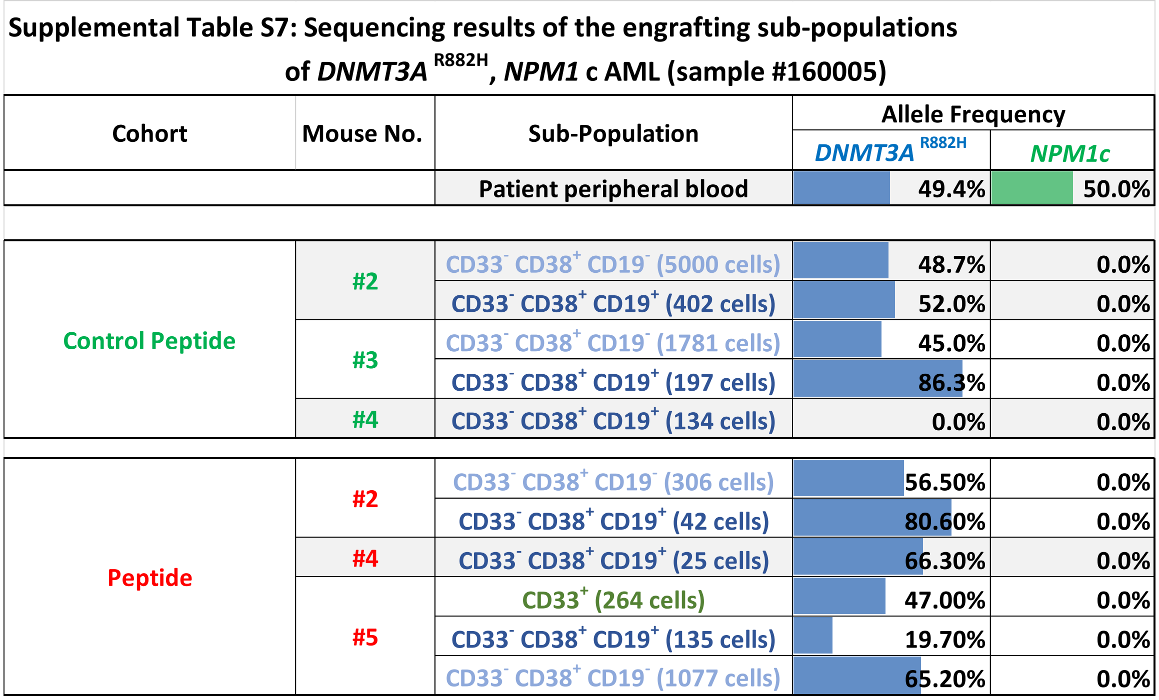
Supplemental Table S6: smMIP panel covering mutations known to be present in the injected primary human samples

Target (gene and location)	Chromosome	location (GRCh37/hg19)	smMIP sequence (RED - Extension Arm, BLUE - Ligation arm, Green -Linker)
FLT3 Exon 20	**chr13**	**28592637 to 28592645**	**GCGGCCAGGTCTCTGTGAACACACTGTCANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGACACAACACAAAATA**
FLT3 Exons 14,15 intron 14	**chr13**	**28608024 to 28608352**	**GCTGCAGAAACATTTGGCACATTCCATTCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTTGTTGCTGTCCTTC**
			CATTATCTGAGGAGCCGGTCACCTGTACCNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGTGAGTACGTGCATT
			GCAGGGTTAAAACGACAATGAAGAGGAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAAATCAACGTAGAAG
DNMT3A Exon 23	**chr2**	**25457242 to 25457254**	**GCGTGTGTGTAAGGGACATGGGGGCAAANNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTCTCTGCCTTTTCTCC**
NPM1 Exon 12	**chr5**	**170837540 to 170837563**	**GCCTGGAAAAAAAAAAAAAGAAATGTGGTNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAACACGGTAGGGAAA**
DNMT3A Exon 18	**chr2**	**25463477 to25463646**	**GTGATGGGCCTGCTGTCCAGGGACAGAGNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGAGAAGGTGGAGGGG**

Supplemental Table S7:

Sequencing results of the engrafting sub-populations of *DNMT3A*^{R882H}, *NPM1*c AML (sample #160005, Figure 4B, supplemental figure S4)

The number of sorted cells in each sub-population is presented.
The patient’s (injected) cells are presented in the first row.
Except for a single sub-population, all engrafting cells are pre-leukemic harboring only *DNMT3A*^{R882H} mutation, without *NPM1*c mutation.

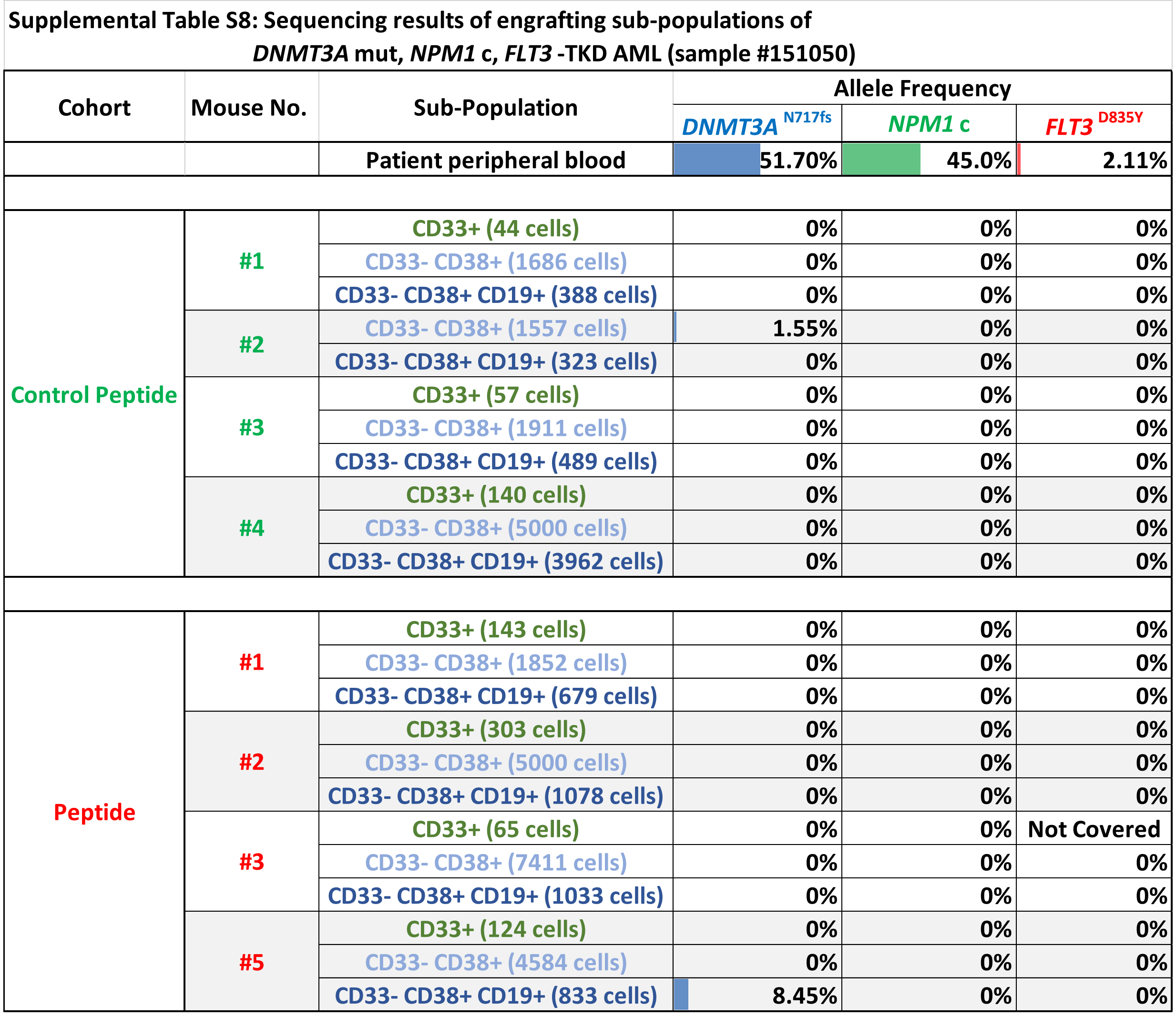


Supplemental Table S7: Sequencing results of the engrafting sub-populations of *DNMT3A* ^{R882H}, *NPM1* c AML (sample #160005)

Cohort	Mouse No.	Sub-Population	Allele Frequency	
			DNMT3A ^{R882H}	*NPM1c*
		Patient peripheral blood	49.4%	50.0%
Control Peptide	#2	CD33$^-$ CD38$^+$ CD19$^-$ (5000 cells)	48.7%	0.0%
		CD33$^-$ CD38$^+$ CD19$^+$ (402 cells)	52.0%	0.0%
	#3	CD33$^-$ CD38$^+$ CD19$^-$ (1781 cells)	45.0%	0.0%
		CD33$^-$ CD38$^+$ CD19$^+$ (197 cells)	86.3%	0.0%
	#4	CD33$^-$ CD38$^+$ CD19$^+$ (134 cells)	0.0%	0.0%
Peptide	#2	CD33$^-$ CD38$^+$ CD19$^-$ (306 cells)	56.50%	0.0%
		CD33$^-$ CD38$^+$ CD19$^+$ (42 cells)	80.60%	0.0%
	#4	CD33$^-$ CD38$^+$ CD19$^+$ (25 cells)	66.30%	0.0%
	#5	CD33$^+$ (264 cells)	47.00%	0.0%
		CD33$^-$ CD38$^+$ CD19$^+$ (135 cells)	19.70%	0.0%
		CD33$^-$ CD38$^+$ CD19$^-$ (1077 cells)	65.20%	0.0%

Supplemental Table S8: Sequencing results of engrafting sub-populations of *DNMT3A*mut, *NPM1*c, *FLT3*-TKD AML (sample #151050, Figure 4D)

The number of sorted cells in each sub-population is presented.
This sample gave rise to a multi-lineage graft. Except for a few, rare cells, most engrafting cells do not harbor any of the mutations that were found in the injected, leukemic cells (first row). Therefore, engrafting cells originated from a non-pre-leukemic clone (or clones).

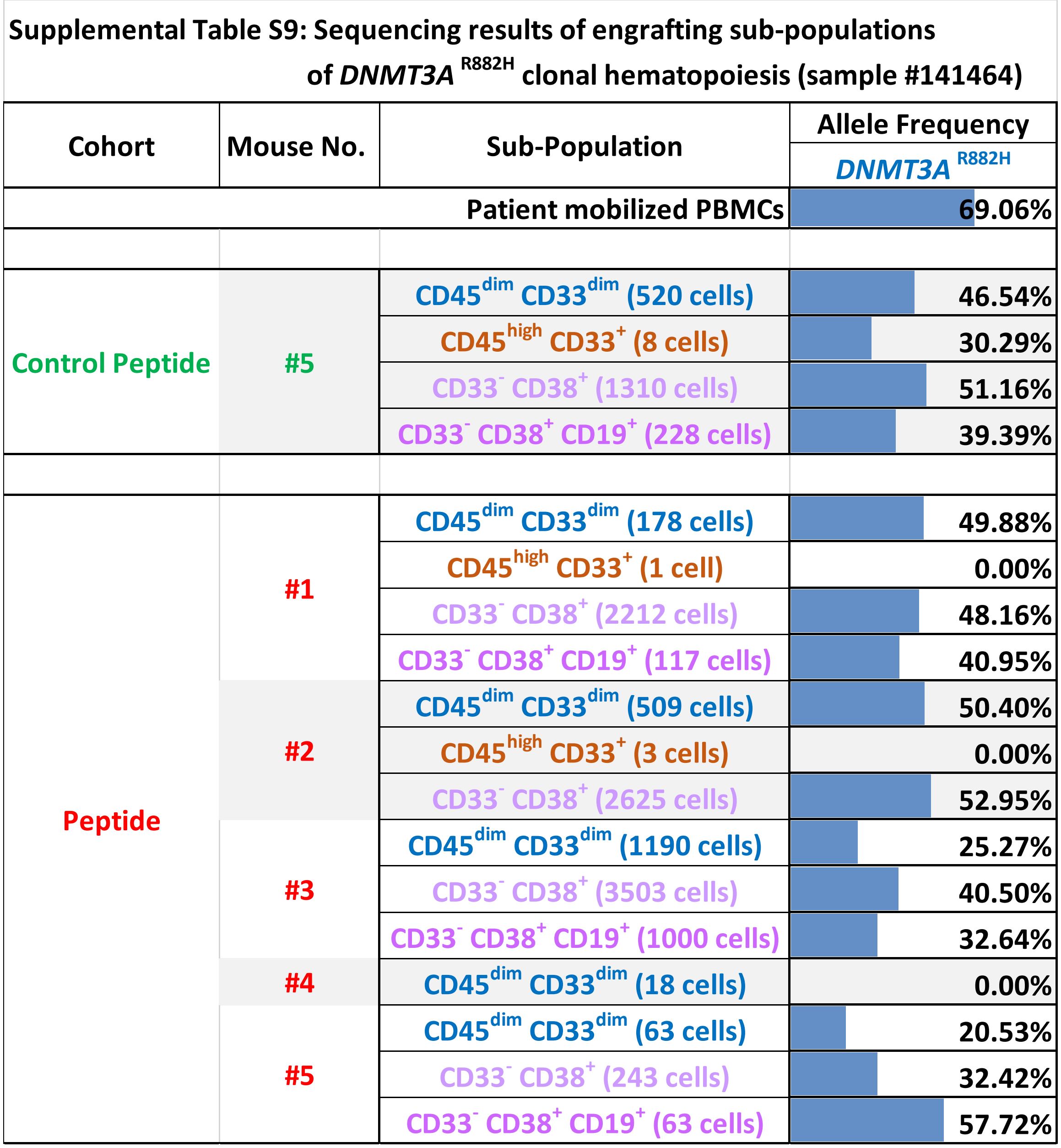


Supplemental Table S8: Sequencing results of engrafting sub-populations of
***DNMT3A* mut, *NPM1* c, *FLT3* -TKD AML (sample #151050)**

Cohort	Mouse No.	Sub-Population	Allele Frequency		
			DNMT3A ^{N717fs}	*NPM1* c	*FLT3* ^{D835Y}
		Patient peripheral blood	51.70%	45.0%	2.11%
Control Peptide	#1	CD33+ (44 cells)	0%	0%	0%
		CD33- CD38+ (1686 cells)	0%	0%	0%
		CD33- CD38+ CD19+ (388 cells)	0%	0%	0%
	#2	CD33- CD38+ (1557 cells)	1.55%	0%	0%
		CD33- CD38+ CD19+ (323 cells)	0%	0%	0%
	#3	CD33+ (57 cells)	0%	0%	0%
		CD33- CD38+ (1911 cells)	0%	0%	0%
		CD33- CD38+ CD19+ (489 cells)	0%	0%	0%
	#4	CD33+ (140 cells)	0%	0%	0%
		CD33- CD38+ (5000 cells)	0%	0%	0%
		CD33- CD38+ CD19+ (3962 cells)	0%	0%	0%
Peptide	#1	CD33+ (143 cells)	0%	0%	0%
		CD33- CD38+ (1852 cells)	0%	0%	0%
		CD33- CD38+ CD19+ (679 cells)	0%	0%	0%
	#2	CD33+ (303 cells)	0%	0%	0%
		CD33- CD38+ (5000 cells)	0%	0%	0%
		CD33- CD38+ CD19+ (1078 cells)	0%	0%	0%
	#3	CD33+ (65 cells)	0%	0%	Not Covered
		CD33- CD38+ (7411 cells)	0%	0%	0%
		CD33- CD38+ CD19+ (1033 cells)	0%	0%	0%
	#5	CD33+ (124 cells)	0%	0%	0%
		CD33- CD38+ (4584 cells)	0%	0%	0%
		CD33- CD38+ CD19+ (833 cells)	8.45%	0%	0%

Supplemental Table S9: Sequencing results of engrafting sub-populations of *DNMT3A*$^{\text{R882H}}$ clonal hematopoiesis (sample #141464, Figure 4E)

The number of sorted cells in each sub-population is presented.
Except for a few sub-populations, all engrafting cells harbor the *DNMT3A*$^{\text{R882H}}$ mutation.
PBMCs – peripheral blood mononuclear cells.

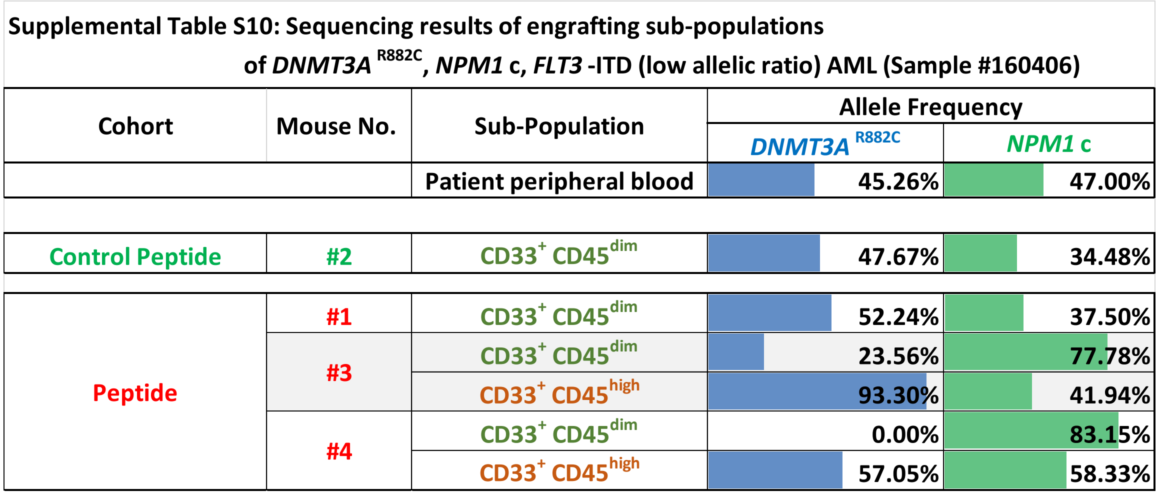


Supplemental Table S9: Sequencing results of engrafting sub-populations of *DNMT3A*$^{\text{R882H}}$ clonal hematopoiesis (sample #141464)

Cohort	Mouse No.	Sub-Population	Allele Frequency *DNMT3A*$^{\text{R882H}}$
		Patient mobilized PBMCs	69.06%
Control Peptide	#5	CD45$^{\text{dim}}$ CD33$^{\text{dim}}$ (520 cells)	46.54%
		CD45$^{\text{high}}$ CD33^{+} (8 cells)	30.29%
		CD33^{-} CD38^{+} (1310 cells)	51.16%
		CD33^{-} CD38^{+} CD19^{+} (228 cells)	39.39%
Peptide	#1	CD45$^{\text{dim}}$ CD33$^{\text{dim}}$ (178 cells)	49.88%
		CD45$^{\text{high}}$ CD33^{+} (1 cell)	0.00%
		CD33^{-} CD38^{+} (2212 cells)	48.16%
		CD33^{-} CD38^{+} CD19^{+} (117 cells)	40.95%
	#2	CD45$^{\text{dim}}$ CD33$^{\text{dim}}$ (509 cells)	50.40%
		CD45$^{\text{high}}$ CD33^{+} (3 cells)	0.00%
		CD33^{-} CD38^{+} (2625 cells)	52.95%
	#3	CD45$^{\text{dim}}$ CD33$^{\text{dim}}$ (1190 cells)	25.27%
		CD33^{-} CD38^{+} (3503 cells)	40.50%
		CD33^{-} CD38^{+} CD19^{+} (1000 cells)	32.64%
	#4	CD45$^{\text{dim}}$ CD33$^{\text{dim}}$ (18 cells)	0.00%
	#5	CD45$^{\text{dim}}$ CD33$^{\text{dim}}$ (63 cells)	20.53%
		CD33^{-} CD38^{+} (243 cells)	32.42%
		CD33^{-} CD38^{+} CD19^{+} (63 cells)	57.72%

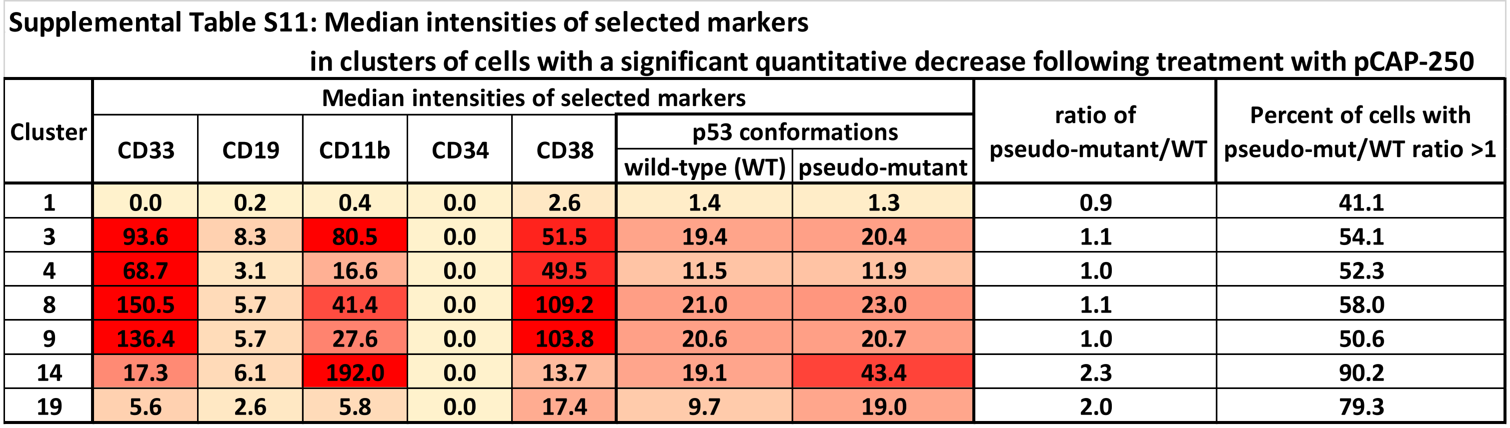
Supplemental Table S10:
Sequencing results of engrafting sub-populations of *DNMT3A*^{R882C}, *NPM1*c, *FLT3*-ITD (low allelic ratio) AML (Sample #160406, Figure 4F).

5000 cells were sorted from each sub-population.
Engrafting cells originated from leukemic stem cells since they all harbor *NPM1*c mutations, similar to the injected cells (first row).



Supplemental Table S10: Sequencing results of engrafting sub-populations of *DNMT3A*^{R882C}, *NPM1* c, *FLT3* -ITD (low allelic ratio) AML (Sample #160406)

Cohort	Mouse No.	Sub-Population	Allele Frequency	
			DNMT3A ^{R882C}	*NPM1* c
		Patient peripheral blood	45.26%	47.00%
Control Peptide	#2	CD33^{+} CD45^{dim}	47.67%	34.48%
Peptide	#1	CD33^{+} CD45^{dim}	52.24%	37.50%
	#3	CD33^{+} CD45^{dim}	23.56%	77.78%
		CD33^{+} CD45^{high}	93.30%	41.94%
	#4	CD33^{+} CD45^{dim}	0.00%	83.15%
		CD33^{+} CD45^{high}	57.05%	58.33%

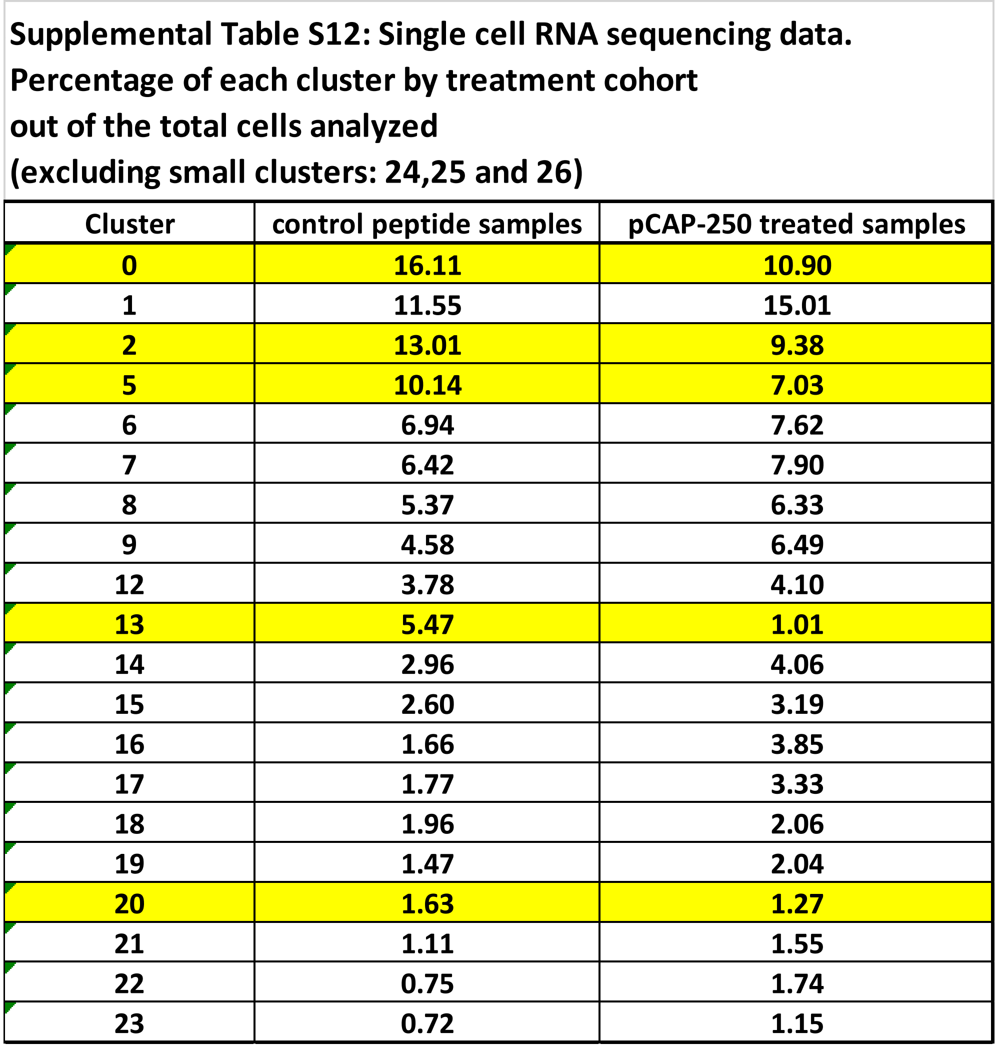


Supplemental Table S11: Median intensities of selected markers in clusters of cells with a significant quantitative decrease following treatment with pCAP-250

Cluster	Median intensities of selected markers							ratio of pseudo-mutant/WT	Percent of cells with pseudo-mut/WT ratio >1
	CD33	CD19	CD11b	CD34	CD38	p53 conformations			
						wild-type (WT)	pseudo-mutant		
1	0.0	0.2	0.4	0.0	2.6	1.4	1.3	0.9	41.1
3	93.6	8.3	80.5	0.0	51.5	19.4	20.4	1.1	54.1
4	68.7	3.1	16.6	0.0	49.5	11.5	11.9	1.0	52.3
8	150.5	5.7	41.4	0.0	109.2	21.0	23.0	1.1	58.0
9	136.4	5.7	27.6	0.0	103.8	20.6	20.7	1.0	50.6
14	17.3	6.1	192.0	0.0	13.7	19.1	43.4	2.3	90.2
19	5.6	2.6	5.8	0.0	17.4	9.7	19.0	2.0	79.3

Supplemental Table S12:
Single cell RNA sequencing data. Percentage of each cluster by treatment cohort out of the total cells analyzed.

Small clusters (24,25 and 26) and clusters that represent leukemic blasts (3,4,10,11) were excluded. Clusters that decreased quantitatively are highlighted.



Supplemental Table S12: Single cell RNA sequencing data.
Percentage of each cluster by treatment cohort
out of the total cells analyzed
(excluding small clusters: 24,25 and 26)

Cluster	control peptide samples	pCAP-250 treated samples
0	16.11	10.90
1	11.55	15.01
2	13.01	9.38
5	10.14	7.03
6	6.94	7.62
7	6.42	7.90
8	5.37	6.33
9	4.58	6.49
12	3.78	4.10
13	5.47	1.01
14	2.96	4.06
15	2.60	3.19
16	1.66	3.85
17	1.77	3.33
18	1.96	2.06
19	1.47	2.04
20	1.63	1.27
21	1.11	1.55
22	0.75	1.74
23	0.72	1.15

Supplemental Table S13: Single cell RNA sequencing data.

Cell type of each cluster according to its statistically significant positively expressed genes by pangloadb[18].

Cluster	Cell type	p-value	Genes	FDR
0	B cells:Immune system	4.37261E-06	CD72; SPIB	0.000170532
0	B cells memory:Immune system	2.53789E-06	SPIB; CD72	0.000123722
0	B cells naive:Immune system	3.37305E-06	CD72; SPIB	0.000138473
0	Plasma cells:Immune system	0.000480767	IGLC7	0.008764445
0	Plasmacytoid dendritic cells:Immune system	0.000200587	SPIB	0.005047037
1	B cells:Immune system	1.26957E-09	IGLL1; DNTT; VPREB3; VPREB1	1.65043E-07
1	B cells memory:Immune system	0.000797421	VPREB3	0.012958092
1	B cells naive:Immune system	0.000959656	VPREB3	0.013861694
1	Plasmacytoid dendritic cells:Immune system	0.000476069	IGLL1	0.008764445
2	Basophils:Immune system	0.000358281	HIST1H2AC	0.007984553
2	Plasma cells:Immune system	0.000424721	IGLC7	0.008764445
3	Dendritic cells:Immune system	0.000770664	FCGR3A; LYZ	0.012789744
3	Monocytes:Immune system	3.19738E-08	GBP1; CXCL10; FCGR3A; FCN1	3.11744E-06
3	Myeloid-derived suppressor cells:Immune system	0.000381256	FCGR3A	0.008260537
3	Neutrophils:Immune system	0.000109002	FCGR3A; LYZ	0.003281092
3	Plasmacytoid dendritic cells:Immune system	0.003615332	TNFSF13B	0.037585294
3	Platelets:Blood	0.00081873	FCGR2A; STX11	0.013032845
4	Dendritic cells:Immune system	0.000156335	CD163; LYZ	0.004064722
4	Macrophages:Immune system	0.002797217	CD163	0.030303189
4	Monocytes:Immune system	0.001352414	CD163	0.017751085
4	Neutrophils:Immune system	0.001352414	LYZ	0.017751085
4	Plasmacytoid dendritic cells:Immune system	0.001245943	TNFSF13B	0.017354209
6	Macrophages:Immune system	0.000342177	LILRA5; FPR1	0.007849932
6	Monocytes:Immune system	0.000113576	PADI4; FCN1	0.003281092
6	Neutrophils:Immune system	0.000113576	LYZ; PTGS2	0.003281092
9	Gamma delta T cells:Immune system	0.000152051	UBE2C	0.004064722
9	Plasmacytoid dendritic cells:Immune system	0.002695129	IGLL1	0.030031434
10	Dendritic cells:Immune system	5.64641E-05	CD163; LYZ	0.002001907
10	Macrophages:Immune system	0.001433293	CD163	0.018327356
10	Monocytes:Immune system	0.000689832	CD163	0.011957093
10	Neutrophils:Immune system	0.000689832	LYZ	0.011957093
11	Platelets:Blood	0.00094756	ANGPT1	0.013861694
12	Dendritic cells:Immune system	0.000909388	LYZ	0.013861694
12	Eosinophils:Immune system	9.84745E-05	RNASE2	0.00320042
12	Neutrophils:Immune system	1.56208E-06	LYZ; AZU1	8.1228E-05
13	Monocytes:Immune system	1.08125E-07	OAS1; MX1	8.43377E-06
14	B cells:Immune system	0.001136436	IGLL1	0.016116726
14	Plasmacytoid dendritic cells:Immune system	0.000476069	IGLL1	0.008764445

Supplemental Table S13: Single cell RNA sequencing data.

Cell type of each cluster according to its statistically significant positively expressed genes by pangloadb[18].

Cluster	Cell type	p-value	Genes	FDR
15	B cells:Immune system	0.003093285	IGLL1	0.032872606
15	Gamma delta T cells:Immune system	2.0712E-07	UBE2C; TROAP	1.34628E-05
15	Plasmacytoid dendritic cells:Immune system	0.001305727	IGLL1	0.017751085
16	B cells:Immune system	0.000480767	DNTT	0.008764445
17	B cells:Immune system	0.000128013	IGLL1; DNTT	0.00356608
17	Basophils:Immune system	0.003662157	HIST1H1D	0.037585294
17	Plasmacytoid dendritic cells:Immune system	0.001832446	IGLL1	0.021989349
18	Basophils:Immune system	0.000483168	CPA3; MS4A2	0.008764445
18	Eosinophils:Immune system	0.00232858	CPA3	0.026710184
18	Mast cells:Immune system	1.28402E-16	CPA3; CMA1; TPSAB1; IL1RL1; MAOB; TPSB2; RGS13; MS4A2; VWA5A; SLC45A3	5.00766E-14
18	NK cells:Immune system	0.000441976	CMA1; KLRG1	0.008764445
18	Nuocytes:Immune system	6.04854E-05	IL1RL1	0.002051244
18	T helper cells:Immune system	0.000299891	TNF; IL1RL1	0.007088339
19	Eosinophils:Immune system	3.04036E-06	RNASE3; RNASE2	0.000131749
19	Neutrophils:Immune system	0.000939816	AZU1	0.013861694
20	B cells:Immune system	0.001942765	HLA-DQA1	0.022959947
20	B cells memory:Immune system	0.001365468	CD1C	0.017751085
20	B cells naive:Immune system	0.001641912	CD1C	0.020328436
20	Basophils:Immune system	0.001641912	FCER1A	0.020328436
20	Dendritic cells:Immune system	2.22733E-10	CD1C; HLA-DQA1; CLEC10A; FCER1A; HLA-DRB5	3.47463E-08
20	Macrophages:Immune system	3.46131E-05	JAML; CLEC10A	0.001285628
20	Mast cells:Immune system	0.003118683	FCER1A	0.032872606
20	Neutrophils:Immune system	0.000886817	JAML	0.013834352
21	Plasmacytoid dendritic cells:Immune system	6.72688E-15	LILRA4; IL3RA; CLEC4C; PTCRA; DERL3; ZFAT; SLC15A4	1.74899E-12
22	B cells:Immune system	0.000240261	IGLL1; DNTT	0.005856369
22	Gamma delta T cells:Immune system	6.64912E-07	UBE2C; TROAP	3.70451E-05
22	Plasmacytoid dendritic cells:Immune system	0.002781378	IGLL1	0.030303189
24	B cells:Immune system	1.42329E-07	TNFRSF13C; HLA-DQA1; BANK1	1.00924E-05
24	B cells memory:Immune system	0.00073682	BANK1	0.012493906
24	B cells naive:Immune system	1.00204E-07	BANK1; TNFRSF13C; LINC00926	8.43377E-06
24	Dendritic cells:Immune system	0.001763368	HLA-DQA1	0.021491045
25	B cells:Immune system	0.004837305	HLA-DQA1	0.049001268
25	Dendritic cells:Immune system	2.25302E-07	HLA-DQA1; CLEC9A; BATF3; HLA-DRB5	1.35181E-05
25	Monocytes:Immune system	0.002226391	IDO1	0.025919182
25	T cells:Immune system	0.002407596	BATF3	0.027216297
26	Gamma delta T cells:Immune system	2.69058E-09	PRF1; KLRF1; TRDC	2.99807E-07
26	Natural killer T cells:Immune system	2.77812E-06	KLRB1; PRF1	0.000127467
26	NK cells:Immune system	9.60766E-22	KLRB1; KLRC1; KLRF1; GZMH; GZMM; PRF1; SAMD3; XCL2; TRDC; XCL1; GZMK	7.49397E-19
26	T cells:Immune system	3.81844E-14	GZMM; GZMH; GZMK; CD160; TRDC; KLRB1; CCL4L2	7.44595E-12

Supplemental Table S14: Median intensities of selected markers in sub-populations from a normal cord blood sample

	CD45	CD33	CD19	CD3	CD38	CD34	CD45RA	p53 conformations	
								wild type	mutant
Myeloid	216.0	27.9	0.0	0.0	17.7	0.0	3.8	40.8	13.1
B Cells	183.5	0.0	71.2	0.0	34.8	0.0	32.4	22.3	15.7
T Cells	431.2	0.0	0.0	133.1	75.4	0.0	26.9	33.0	26.4
HSPCs	7.0	0.0	0.0	0.0	0.6	5.3	0.0	21.0	20.8
Progenitors	26.7	0.0	0.0	0.0	19.7	26.3	7.2	43.1	46.0

Supplemental Table S15: Clusters of cells with a significant quantitative decrease following treatment with pCAP-250

Cluster	Number of events in control peptide sample	Number of events in pCAP-250 treated sample	Percentage of decrease	p-value for significance of quantitative decrease
1	25793	8677	66.36	0
3	4262	3702	13.14	9.11435E-06
4	4424	2426	45.16	0
8	4518	2021	55.27	0
9	2607	1885	27.69	2.59792E-14
14	15300	3122	79.59	0
19	4289	428	90.02	0

Supplemental Table S16:
Median intensities of suface markers in clusters of cells that quantitatively decreased following treatment with pCAP-250 (sensitive) in *TP53* ^{R248H}-mutated AML patient-derived xenograft model

Cluster	Median intensities of selected markers				
	CD33	CD11b	CD38	CD34	CD19
4	0	1.07	0.36	0	0
5	18.87	121.84	53.12	0	0.35
6	36.5	153.45	31.74	0	0.04
7	14.62	94.41	20.37	0	0.13
9	52.85	141.03	66.75	0	0.92
10	17.53	124.88	27.6	0	0.11
11	1.15	9.9	2.99	0	3.49
15	28.93	207.18	44.33	0	4.61

Supplemental Table S17:
Median intensities of suface markers in clusters of cells that quantitatively increased following treatment with pCAP-250 (resistant) in *TP53* ^{R248H}-mutated AML patient-derived xenograft model

Cluster	Median intensities of selected markers				
	CD33	CD11b	CD38	CD34	CD19
1	29.17	253.49	65.53	0	0.46
8	21.87	0.78	39.2	23.28	1.38
12	13.98	202.84	24.48	0	0
13	31.09	322.87	61.59	0	0.29
14	9.84	128.58	19.83	0	0.37
16	18.17	118.93	28.01	0	0.3
17	65.07	251.09	201.69	0	0.74
18	22.06	141.88	34.19	0	0.28
19	36.87	236.82	111.25	0	0.02
20	29.78	275.24	76.55	0	0

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