Supplementary Appendix

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<u>**Supplementary Appendix Table of Contents**</u>

1. Supplementary Methods

1.1 Patient samples

This study used patient samples approved by the institutional review board at Washington University in St. Louis under protocol 201011766 and was conducted in accordance with the provisions of the Declaration of Helsinki. All samples were obtained from patients either known or suspected to have a diagnosis of AML or MDS who consented to genomic studies and were seen at Washington University in St. Louis. Samples were selected for sequencing for three specific purposes: 1) WGS performance assessment, 2) Establishing diagnostic yield and clinical feasibility, and 3) Evaluation of risk prediction in patients with unsuccessful or incomplete cytogenetic studies. To achieve these objectives, a combination of retrospective and prospective patient cohorts was used, descriptions of which are provided below.

Retrospective cohort (N=146)

Retrospective samples from AML and MDS patients consented under the abovementioned protocol were obtained from the Siteman Cancer Center Tissue Procurement Core and included DNA extracted from either cryopreserved bone marrow (N=133) or peripheral blood (N=13) specimens. For WGS performance evaluation, 111 samples were selected based on DNA availability and results from conventional cytogenetic studies in order to include a wide range of chromosomal abnormalities, including risk-defining translocations, copy number alterations (CNAs), and either a complex or normal karyotype. Separately, to determine whether WGS could be used to predict outcomes for patients with unknown cytogenetics, 35 retrospective samples were selected from patients treated with induction chemotherapy and for whom cytogenetics was unknown, unsuccessful, or inconclusive at diagnosis (see **Section 1.3** for definitions). Of note, samples with successful cytogenetic studies from the prospective cohort below were also used for WGS performance evaluation, and likewise, prospective samples with unsuccessful or inconclusive cytogenetics were used for the analysis of WGS-based risk prediction in patients with unknown cytogenetics.

Prospective cohort (N=117)

Evaluation of the feasibility and diagnostic yield of WGS compared to standard testing used samples from a cohort of 117 prospective patients. These samples included bone marrow aspirate (N=116) or peripheral blood (N=1) specimens from 117 consecutive, unselected patients for whom clinical cytogenetic analysis via karyotyping in the Cytogenomics and Molecular Pathology Laboratory was requested between May 2019 and February 2020. The only selection criteria for these patients were that they were consented under the abovementioned protocol and there was sufficient remaining specimen left after standard cytogenetic analysis to be used for sequencing (some samples required the addition of RPMI-based media to wash residual material out of the sodium heparin tubes prior to DNA extraction). Samples were transported from the Cytogenomics laboratory to the CLIA-licensed Environment (CLE) clinical sequencing laboratory at the McDonnell Genome Institute (MGI) for DNA extraction and sequencing. As stated above, this cohort included patients with both successful and unsuccessful cytogenetic studies, and therefore contributed to WGS performance evaluation and WGS-based risk prediction analysis for patients with unknown cytogenetics.

1.2 WGS procedures

Tumor-only WGS was performed in the CLIA-licensed environment clinical sequencing laboratory in the McDonnell Genome Institute at Washington University School of Medicine (MGI-CLE; CLIA ID #26D2092546, CAP #9047655, David H. Spencer MD, PhD, Medical Director). No normal tissue comparator was used for this assay in order to reduce time, complexity, and cost, and because the purpose is to identify clearly pathogenic somatic events that generally do not require a germline control. All samples were accessioned into the MGI laboratory information management system (LIMS) upon receipt prior to DNA extraction (for prospective samples) or library preparation (for retrospective samples received as DNA). DNA from prospective peripheral blood or bone marrow aspirate specimens was extracted using 200 uL of material with the QIAamp DNA mini kit (Qiagen, Hilden, Germany) as detailed in the package insert, followed by quantification with the Qubit 1.0 fluorometer High Sensitivity dsDNA assay (ThermoFisher, Waltham, MA). Subsequent WGS procedures are described below.

Library preparation

WGS library preparation used the Nextera Flex library preparation kit (cat# 20015804, Illumina, Inc, San Diego, CA) along with dual unique index library adapters (cat# 20015881). This on-bead tagmentation-based library construction method was selected because it is fast, simple, and automatable, and thus fits well in a clinical testing environment where training of laboratory staff and turnaround time are important considerations. For this study, library construction was performed in a single day in batches of 2 to 16 samples by individual laboratory staff who followed the protocol detailed in the package insert without modification. In general, 500 ng of input DNA was used for library construction, although as little as 35 ng was used when DNA amounts were limiting. Completed libraries were accessioned into the LIMS, then assessed for size using an Agilent 2100 Bioanalyzer with a DNA High Sensitivity chip (Agilent, Santa Clara, CA), and quantified via Qubit (ThermoFisher, Waltham, MA). Final libraries were optionally quantified further via qPCR (generally on a subsequent day) using Kapa SYBR Fast qPCR library quantification (Roche, Basel Switzerland), and then diluted to 1 nM for equimolar pooling prior to sequencing.

Sequencing

Sequencing was performed on NovaSeq 6000 sequencing instruments (Illumina) using either S1 or S4 flowcells and 2x150 sequencing chemistry. Retrospective samples were sequenced on S4 flowcells in pools of 16 (or pools of 4 samples on one S4 lane using the XP lane loader) and prospective ‘real-time’ sequencing used S1 flow cells in pools of 3 samples, which is designed to yield >133 Gbp of raw sequence and 60x genome coverage per sample. Flowcell loading and sequencing were performed as recommended by the manufacturer. Times for sequencing are 25 and 44 hours for S1 and S4 flowcells, respectively, and were documented in the MGI LIMS system.

Data processing

Completed sequencing runs were processed into aligned CRAM files using the GRCh38 human reference genome via two approaches:

- *Local processing:* For retrospective samples, instrument data were processed and demultiplexed into FASTQ files using bcl2fastq (Illumina) via the in-house LIMS. Data were then aligned via a local installation of the DRAGEN (version 3.5.7) hardware-accelerated sequence processing software suite using default alignment parameters. Processing time with this approach for S4 flowcells were generally 47 hours for sequencing data transfer and 12 hours for demultiplexing. Alignment times using DRAGEN ranged from 20-40 minutes depending on coverage.
- *BaseSpace processing:* To speed the processing of prospective samples, data generated on S1 flowcells were streamed from the NovaSeq instrument to the cloud-based BaseSpace sequence analysis platform. This saved time at both the sequencing and data processing steps, owing to the shorter run time for S1 flowcells and ‘on-demand’ rapid data processing. After the sequencing run completed, demultiplexing and FASTQ generation was automatically launched in BaseSpace. Data were then aligned via manual launching of the DRAGEN Germline (alignment only) BaseSpace App (version 3.2.8, see

https://basespace.illumina.com/apps/6840834/DRAGEN-Germline-Pipeline), which completed in about the same amount of time as the local DRAGEN installation. We note that the manual step of launching DRAGEN can be automated via the BaseSpace API to further reduce turnaround time.

Alignments in CRAM format generated using both the in-house and cloud-based procedures were used as input for the variant analysis workflow described below.

Variant analysis and reporting

Tumor-only variant analysis used a custom analysis workflow ('ChromoSeq') specified in the WDL workflow language and executed using the Cromwell workflow engine[1] in dockerized compute containers, which is available for public use as a custom application on BaseSpace (https://basespace.illumina.com/apps/6984978/Chromoseq -- pending BaseSpace approval for public release). Analysis involves three components: CNA identification, SV identification, and gene-level variant identification. All three of these components are subject to targeted analysis and filtering to yield variants that may be clinically relevant.

CNA identification

Cytogenetically evident CNAs greater than 5 Mbp, which are of a size potentially detectable by karyotype analysis, are identified via a read-depth approach using a previously published purity and subclone-aware Hidden Markov Model, ichorCNA[2]; https://github.com/GavinHaLab/ichorCNA). The input for this script is a file with read counts in 500,000 bp nonoverlapping windows across the genome, either generated using bedtools[3] or outputted directly from the DRAGEN mapping software during alignment using the command:

```
dragen -r $obj->{_dragenref} --fastq-list $fastqfile --fastq-list-sample-id $samplename --enable-cnv true --cnv-target-bed /staging/garza_testing/reference/all_sequences.fa.bed --cnv-interval-width 500000 --output-directory $cramout --output-file-prefix $sample --output-format CRAM --enable-bam-indexing true --enable-duplicate-marking true
```

Binned read counts are supplied to ichorCNA for normalization for GC content, mappability, and using a 'panel of normals' normalization file generated from 20 normal karyotype cases per the instructions on the ichorCNA github repo. Outputs from ichorCNA were text-processed via a custom PERL script (available upon request) to retain CNAs >5 Mbp and converted to VCF format, and then combined with SV calls (below) for input into the ChromoSeq reporting script. CNA abundance as a percentage was calculated using the equation:

$$\text{Abundance} = (2^{L2R} - 1.0) / ((CN/2.0 - 1.0)))*100$$

Where L2R is the log2 normalized coverage ratio vs. a panel of normals and CN is the estimated copy number for the event.

SV identification

SV identification is performed with the break-end caller Manta[4] and broken into two 'tiers', with recurrrent and risk defining events are detected with a high sensitivity approach, and novel SVs are subject to more rigorous filtering. Manta is run directly from the aligned CRAM file in 'tumor' mode and with custom parameters to increase the sensitivity and limit calls to those that are at least 100 kbp in length to reduce the number of calls with unknown clinical significance. SVs are then filtered to identify translocations, deletions, duplications, and inversions that overlap a curated list of 612 recurrent and/or risk-defining SVs obtained from published sources, including the WHO and the Atlas of Genetics and Cytogenetics in Oncology **(see Table S2)**. Genomic events where both ends overlap one of these recurrent SVs are reported as ‘top-level’ findings in ChromoSeq without additional filtering. Although the remaining SVs will rarely be clinically relevant, they could include patient-specific events or identify cytogenetically cryptic rearrangements involving genes relevant for AML or MDS. We therefore perform rigorous annotation and filtering using a custom PERL script (available upon request) and report the remaining high-quality novel events as secondary findings. The following criteria must be met to yield a passing call: 1) at least 2 ‘paired and 2 ‘split’ reads supporting the break-ends, 2) absence of an overlapping call from a large set of SVs identified from >17,795 human genomes[5], 3) coverage depth of deletion or duplication call must be <0.8 or >1.3 compared to the background[6], respectively, and 4) a defined breakpoint must be identified and the spanning contig generated by Manta must map back to the reported breakpoints. This procedure dramatically reduces the number of reported calls. For example, the mean number of raw Manta calls per case is >5,000; after filtering we reported a mean of 11 calls across all 263 cases in this study (including recurrent SVs). SVs are then converted to VCF format, combined with CNA calls (from above), and annotated with VEP[7] using Ensembl version 90, prior to reporting with the ChromoSeq reporting script.

Gene-level variant identification

Gene mutations are identified in ~85 kbp targeting 40 genes and gene hotspots that are recurrently mutated in AML or MDS[8]. This target space was selected to be identical to that of the targeted gene panel used for clinical testing of these patients at our institution, and is relatively small so that rare inherited variants (i.e., variants of uncertain significance (VUS)), are minimized. The primary variant caller is Varscan2[9], which is run in SNV and indel mode using custom parameters to enhance sensitivity. The indel caller Pindel[10] and Manta are also run on exons 13-15 of *FLT3* to identify *FLT3* ITD alleles[11]. In addition, a read count based ‘hotspot’ analysis is performed on 66 recurrently mutated positions to recover low abundance variants that are not detected by Varscan2 (a minimum variant read count of 3 is required to report these hotspot positions). Variant calls identified via these approaches are merged and harmonized using a custom python script (available upon request), and annotated with VEP using Ensembl version 90 prior to reporting.

Final report

Annotated CNA, SV, and gene mutation calls are combined with coverage QC information to generate a final text report using a custom python script (available upon request). This report includes the CNAs, recurrent SVs, and gene mutations identified by the above steps as ‘top-level’ results. The remaining SVs that remained after filtering are reported in two categories. The first includes high-quality novel SVs that affect (overlap) a gene that is included in either the recurrent SV or gene mutation target space. The second category is all other high-quality novel SVs. Additional coverage QC metrics are also reported. This text file **(see Figure S1A)** is copied to the final case directory along with data files (CRAM, and VCF) and graphical coverage plots from ichorCNA. The final text report is also used to generate a graphical ChromoSeq report, as shown in **Figure S1B**.

WGS analysis for study patients

All retrospective samples were sequenced on S4 flowcells and processed using in-house demultiplexing, aligned with the local DRAGEN server, and analyzed on a local compute cluster with the ChromoSeq workflow. Prospective samples were sequenced on S1 flowcells and initially analyzed using the cloud-based approach on BaseSpace to record failure rates and turnaround times. ChromoSeq reports with QC metrics and variants for the prospective patients were reviewed in 1 hour sessions by board-certified molecular pathologists (D.H.S., E.J.D.) and a board-certified cytogeneticist and molecular geneticist (M.C.S.) without prior knowledge of the results from conventional testing. Exact times for processing steps shown in Figure 3A were obtained from the MGI LIMS system and from the timestamp in the ChromoSeq text report. A final ChromoSeq analysis was performed on all prospective samples at the end of the study to harmonize the results and file formats (which changed over the course of the study) with the outputs from the retrospective samples. These final results were used for the analysis and figures in the main text. See **Table S3** for all harmonized WGS results.

1.3 Conventional cytogenetic studies

Cytogenetics and FISH were performed in the Cytogenomics and Molecular Pathology Laboratory at Washington University School of Medicine in St. Louis per standard clinical protocols. Culture of cells from bone marrow or leukemic peripheral blood samples was performed per standard clinical protocols, followed by harvest, slide dropping, G-banding with trypsin/Wright stain, and analysis. Cytogenetic events were considered clonal if they occurred in at least two metaphases (at least three metaphases for monosomies). For the purposes of this study, cytogenetic analysis was called 'unsuccessful' if no metaphases were obtained for analysis, and 'inconclusive' if fewer than 20 metaphases were analyzed without detection of clonal abnormalities, which is similar to approaches taken by other studies[12–14]. [15]FISH results used for risk stratification and calculation of the yield of WGS in the prospective cohort were obtained from clinical reports performed at diagnosis. For AML patients, most FISH studies (60 of 68 patients) included the ELN-recommended panel of *PML-RARA* (LSI PML/RARA Dual Color, Dual Fusion, Abbot/Vysis) CBFB-MYH11 (LSI CBFB Dual Color, Break Apart Rearrangement Probe, Abbot/Vysis), *RUNX1-RUNX1T1* (LSI RUNX1T1/RUNX1 Dual Color, Dual Fusion, Vysis), del(5q) (D5S630/D5S2064 Dual Color Probe, Cytocell/Aquarius), and del(7q) (LSI D7S486/D7Z1 Dual Color Probe, Abbot/Vysis). Additional FISH assays were also performed to confirm WGS findings but were not used to for risk group assignments.

1.4 Targeted sequencing

Gene mutations were obtained as part of standard diagnostic testing using a commercially available PCR-based assay for the *FLT3* internal tandem duplication mutation (ITD) (Invivoscribe, San Diego, CA), in-house testing for the NPM1c mutation, and/or a laboratory-developed clinical sequencing assay, including either clinical tumor/normal exome sequencing[16] or a clinical gene panel that targets 40 recurrently mutated genes or gene hotspots in AML and MDS (Myeloseq; Department of Pathology and Immunology, Washington University School of Medicine, **see Table S1**) performed in the CLIA-Licensed Environment Clinical Sequencing Laboratory at the McDonnell Genome Institute at Washington University in St. Louis.

1.5 Comparison and confirmation procedures

WGS results were compared to conventional cytogenetics and FISH to determine the sensitivity and positive predictive value for detecting recurrent SVs and CNAs. These comparisons used the following approaches:

- <u>SVs:</u> Cases with successful cytogenetics (at least 3 metaphases analyzed, N=235) were used to evaluate SV performance. SVs identified by WGS were manually compared to ISCN karyotypes obtained from clinical testing to identify true positives. Breakpoints were required to occur within 1 chromosome band. New SVs that were not reported by conventional cytogenetics were subject to confirmation using either FISH, PCR for SV breakpoints, or analysis of existing RNA-seq data for fusion transcripts (see below).

- CNAs: CNAs from WGS were compared to ISCN karyotypes using 143 cases with conclusive cytogenetic results (i.e., 20 metaphases) and no ambiguous findings, such as composite karyotypes, marker chromosomes, or additional unidentifiable material, as these preclude definitive comparisons. ISCN cytogenetic karyotypes were transformed into a matrix of gains and losses for each chromosome band using published software[17], which were then converted with a custom PERL script to BEDPE format using band coordinates based on the GRCh38 human reference. The bedtools program was then used to compare CNAs between WGS and cytogenetics using at least 1 bp of overlap to identify concordant events. New CNAs were subject to confirmation using either FISH or chromosomal microarrays (CMA).

Every effort was made to confirm all novel findings, although priority was given to findings in the prospective cohort and for risk-defining events. Specific confirmation procedures are described below.

FISH

WGS findings not present in the karyotype or confirmed by diagnostic FISH results were confirmed using FISH studies where possible **(see Table S4)**. FISH was the primary means of confirmation for new SVs and CNAs when appropriate probes were available and clinical specimens were available for testing. All FISH studies were performed in the Cytogenomics and Molecular Pathology Laboratory using validated probes and standard clinical procedures using 200 cells and were reviewed by board certified cytogeneticists. The presence of an abnormal result in the specified study was considered as support for the genomic event identified by WGS. For example, we considered an abnormal result for the *KMT2A* dual color/dual fusion FISH assay as confirmation of an SV involving *KTM2A* in the WGS data.

PCR

Selected SVs that could not be confirmed via FISH because of insufficient or inadequate samples were confirmed via PCR from DNA using primers spanning the SV breakends identified by Manta when FISH studies could not be performed due to limited material and/or lack of appropriate FISH probes **(see Table S4)**. PCR primers were designed from breakpoint-spanning sequence contigs generated from Manta and were used in standard PCR reactions with human genomic DNA. Amplified fragments were excised, purified, sequenced with Sanger sequencing, and analyzed with Blat to verify localization to the breakpoint region.

CMA

CNAs were confirmed via chromosomal microarray (CMA) for cases with available DNA but insufficient material or probe for FISH assays **(see Table S5)**. CMAs were performed in the Washington University School of Medicine Cytogenetics Core per standard methods using the CytoScan HD platform (ThermoFisher) with subsequent analysis in Chromosome Analysis Suite (ThermoFisher). Data were reviewed and interpreted by a board-certified cytogeneticist and molecular geneticist (M.C.S.)

RNA-seq

SVs in two cases with *KMT2A* rearrangements (380949 and 410324, **see Table S4**) were confirmed using existing RNA-seq data that was published as part of the TCGA AML study (see Supplemental Table 1 in ref. [18], which can be accessed here: https://api.gdc.cancer.gov/data/b9196563-a05d-40b8-80dc-640ec712eb06; samples 380949 and 410324). We note that clinical FISH using a *KMT2A* breakapart probe for these cases was also abnormal, and the identification of a fusion transcript via RNA-seq provided the definitive confirmation of the translocation partner.

1.6 Risk stratification

Conventional

Cytogenetics, FISH (for the panel described above, when performed, see section 1.3), and molecular results were used to assign patients to established genomic risk categories, which used the 2017 ELN guidelines for AML patients[12] and the cytogenetic component of the IPSS-R scoring system for MDS patients[19], both without modification **(see Table S9)**. Cytogenetic abnormalities were required to meet the abovementioned criteria to be considered clonal. For AML patients, risk group assignment was performed using cytogenetic results, *FLT3* ITD mutation allele ratio from PCR (or presence/absence if the allelic ratio was not available), and the mutation status for *CEBPA*, *NPM1*, *TP53*, *RUNX1*, and *ASXL1* from either clinical tumor/normal exome sequencing (N=12) or gene panel sequencing (using Myeloseq, N=71, see above, or a commercial assay, N=1). Sequencing assays were not performed for 6 retrospective patients who were either assigned to a risk group using only *NPM1* and *FLT3* ITD mutation status (N=3), or they were assigned to intermediate risk (N=3). Patients with a normal karyotype and <20 metaphases were not assigned to a risk group with unless there was an unequivocal result from either FISH or targeted sequencing (e.g., a positive *PML-RARA* or del(5q) by FISH, or a TP53 mutation by targeted sequencing). IPSS-R risk groups do not involve gene mutations and is therefore performed using cytogenetics alone.

WGS

WGS results were used to assign patients to risk groups using the identical guidelines as above for both AML and MDS patients **(see Tables S9, S10)**. For AML patients, risk assignment used CNAs, recurrent SVs, and gene mutations. *FLT3* ITD mutation results from PCR were used instead of the WGS result (even though ITD alleles can be detected) because the PCR assay is an FDA-cleared companion diagnostic for the *FLT3* targeted therapy midostaurin. For both AML and MDS patients, the clinically important classifications of normal karyotype and complex karyotype used only CNAs and recurrent SVs and not SVs reported as secondary findings. A normal karyotype was designated if no variants in either category were identified, and a complex karyotype was designated if at least 3 chromosomal abnormalities were identified, including recurrent SVs (not WHO category-defining events) or CNAs greater than 5 Mbp that were identified by copy number analysis and that involved separate chromosome arms. All but 3 of the patients with a complex karyotype could be assigned to this category based on CNAs alone, which indicates that copy number gains and losses are defining features of this phenotype.

1.7 Statistics

Survival analyses of 139 AML patients (and subgroups thereof) were performed using death as the endpoint. Censoring of patients in these analyses was random and occurred because of limited follow-up time. Survival analyses of patients with defined cytogenetic risk (N=71 non-transplanted patients; N=101 total patients) was pre-planned using patients within our cohort (i.e., they were not selected specifically for outcome analysis) and was performed by Kaplan-Meier analyses using the log-rank test for equal survival across the groups. Cox proportional-hazards regression was used to calculate hazard ratios and test for equal survival between the adverse risk group and either intermediate, favorable, or a combined intermediate/favorable ‘not adverse’ risk group. All log-rank tests performed in the paper were adjusted for multiple comparisons using the method of Benjamini and Hochberg (1995). Cox regression was adjusted for age (binned by decade), which was significantly associated with overall survival in the 71 non-transplanted patients with defined risk stratified by conventional risk groups (HR: 1.46, 95% CI 1.05-2.05) but not WGS-based risk groups (HR: 1.29, 95% CI 0.92-1.81). The log of the white blood cell count was also used as a covariate with ELN risk, but was not significant in any analysis ($P>0.05$ in all analyses) and therefore was not included in the model. The proportional hazards assumption was found to be tenable for all Cox models.

The same approaches were used for AML patients with undefined cytogenetic risk (N=27 non-transplanted patients; N=38 total patients). Prior to this pre-planned analysis, we performed a power calculation to estimate the sample size necessary to observe a difference in survival among ELN risk groups in this cohort. This used the Power and Sample Size task in SAS/Studio software along with the observed survival in the defined cytogenetic risk cohort above (N=71), which was largely consistent with published data on a mixture of older (60 and over) and younger (less than 60) patients[14]. The power calculation used a median survival of 3600 days of survival for the favorable group and 346 for the adverse group, with a minimum follow-up interval of 279 days and a total number of days (accrual + follow-up) of 750 days. This demonstrated 80% power to detect a survival difference between favorable and adverse risk at a sample size of 12 (per group) using an alpha of 0.05. Additional exploratory analyses were performed but not presented, including log-rank tests for differences in survival among all three risk groups (rather than not adverse vs. adverse) and unadjusted Cox regression tests, which yielded similar results to those shown here. Survival statistics were obtained using SAS for Windows, Version 9.4. The survminer package in R was used for visualization.

1.8 Cost analysis

Conventional testing: cytogenetics, FISH, and targeted gene sequencing

The cost estimate for conventional testing was based on the Centers for Medicare and Medicaid Services 2019 and 2020 laboratory and professional reimbursement fee schedule (https://www.cms.gov/Medicare/Medicare-Fee-for-Service-Payment/ClinicalLabFeeSched). We assumed that genomic testing for new AML and MDS patients would include targeted gene sequencing, karyotyping for 20 metaphases, 6 FISH assays using 10 probes (4 breakapart assays with 2 probes each and 2 single probe assays for del(5q) and del(7), interpretation and reporting. Based on this testing, the following CPT codes would be billed at the CMS rates shown below.

CPT code	Description	Rate	Quantity	Cost
81450	Targeted genomic seq analysis	$ 759.53	1	$ 759.53
88264	Chromosome analysis 20-25	$ 144.61	1	$ 144.61
88237	Tissue culture bone marrow	$ 143.75	1	$ 143.75
88271	Cytogenetics dna probe	$ 21.42	10	$ 214.20
88275	Cytogenetics 100-300	$ 51.19	6	$ 307.14
88291	Cyto/molecular report	$ 33.88	1	$ 33.88
			Total	$ 1,603.11

Of course, this is the reimbursement by CMS and not the laboratory cost. However, this amount is likely close to the laboratory cost given that laboratories are unlikely to generate sizeable profits from CMS for a single case, nor are they likely to run at a tremendous loss because many AML and MDS patients are over 65 and covered by Medicare. If one were to assume that the laboratory generates up to 10% profit or runs at a loss of up to 20% relative to the CMS reimbursement amount for these tests, then the aggregate cost for these assays would be:

Lower bound: $1,603.11 / 120% = $1,335.92

Upper bound: $1,603.11 * 120% = $2,003.89

These calculations are consistent with internal data on laboratory costs at Washington University as well as previous studies of the cost of diagnostic testing for new AML patients[20]. We note that this estimate includes a relatively small set of FISH studies. Expanding these would obviously increase the cost of conventional testing.

Cost of WGS

The total cost of WGS analysis was estimated using current reagent costs and labor. As stated in the main text of the article, the cost of WGS is driven mostly by sequencing, which is highly dependent on volume. This relationship relates both to the volume at the time of sequencing (i.e., the ‘flow cell’ used to sequence a particular batch of samples), and the overall volume in a laboratory, which determines the reagent cost per billion base pairs (Gbp) of sequence data generated. We therefore considered these variables in our cost calculations. We used costs from 2 sources. The first is the list price for Illumina flow cells that we combined with the minimum throughput for each flow cell to arrive at a cost per Gbp of sequence data generated. The second is the cost of commodity sequencing tracked by the National Human Genome Research Institute (NHGRI)[21]. The cost for WGS at 60x coverage (using a very conservative estimate of 150 Gbp of raw sequence data) using these sources is shown in the table below:

Cost model / flow cell	Flow cell throughput (Gbp)	Cost	Cost / Gbp	Cost for 150 Gbp
SP	200	$ 3,000	$ 15.00	$ 2,250.00
S1	400	$ 5,250	$ 13.13	$ 1,968.75
S2	1000	$ 9,600	$ 9.60	$ 1,440.00
S4	2400	$ 14,400	$ 6.00	$ 900.00
Mean across flow cells	N/A		$ 10.93	$ 1,639.69
NHRGI commodity cost*	N/A		$ 6.74	$ 1,011.00

* NHGRI tracked cost of commodity sequencing, see https://www.genome.gov/about-genomics/fact-sheets/DNA-Sequencing-Costs-Data.

Additional costs for WGS include reagents for library preparation and QC, data processing and analysis, and technologist labor. These amounts are summarized below, assuming a mean of 2 samples are prepared per batch:

Item	Quantity	Cost	Cost per sample

Nextera DNA Flex LPK (24)	24 libraries	$ 1,038.00	$ 43.25
Nextera DNA CD Idx (24)	24 libraries	$ 124.00	$ 5.17
Library QC*	1	$ 12.50	$ 12.50
Library quantification*	1	$ 17.00	$ 17.00
Technologist labor†	12 hours/batch	$ 30.00/hour	$ 180.00
Data processing/analysis on BaseSpace‡	1	$ 25.00	$ 15.60
		Total	**$ 273.52**

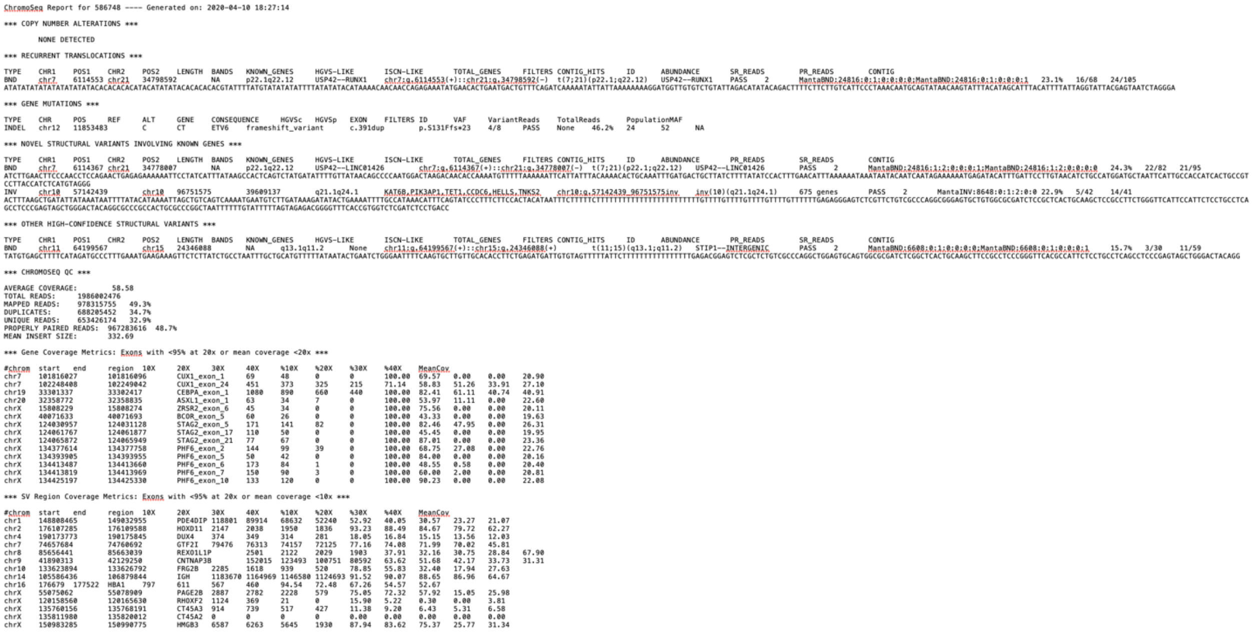
* Values are established based on current costs for Agilent TapeStation, Qubit, and qPCR reagents.
† Labor includes library preparation, QC/quantification, and loading of sequencer
‡ Assumes DRAGEN alignment (2 hours) and ChromoSeq analysis (2 hours) using BaseSpace Apps

Combined with the raw sequencing cost, the current marginal cost range for WGS would be:

Lower (NHGRI commodity cost): $1,284.52
Mean (mean list flowcell cost): $1,913.21
Upper (highest list flowcell cost): $2,523.52

These estimates do not include additional overhead, such as amortized instrument cost, service contracts, proficiency testing and alternative assessments required by CAP, etc. However, in many laboratories some of these costs can be distributed over additional aspects of laboratory operations that laboratory-specific and difficult to model (e.g., other sequencing assays, research sequencing, etc). In addition, the assumptions here are that batch sizes will be small and a handled by a single technician who is dedicated to WGS, which results in higher labor cost. While imperfect, these estimates nonetheless provide a rough idea of the marginal cost of WGS compared to standard testing.

2. Supplementary Figures



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ChromoSeq Report for 586748 ---- Generated on: 2020-04-10 18:27:14

*** COPY NUMBER ALTERATIONS ***

        NONE DETECTED

*** RECURRENT TRANSLOCATIONS ***

TYPE    CHR1    POS1    CHR2    POS2    LENGTH  BANDS   KNOWN_GENES     HGVS-LIKE       ISCN-LIKE       TOTAL_GENES     FILTERS CONTIG_HITS     ID      ABUNDANCE       SR_READS        PR_READS        CONTIG
BND     chr7    6114553 chr21   34798592        NA      p22.1q22.12     USP42--RUNX1    chr7:g.6114553(+)::chr21:g.34798592(-)  t(7;21)(p22.1;q22.12)   USP42--RUNX1    PASS    2       MantaBND:24816:0:1:0:0:0:0;MantaBND:24816:0:1:0:0:0:1   23.1%   16/68   24/105
ATATATATATATATATATATACACACACACATACATATATACACACACACGTATTTTATGTATATATATTTTATATATACATAAAACAACAACCAGAGAAATATGAACACTGAATGACTGTTTCAGATCAAAAATATTATTAAAAAAAAAGGATGGTTGTGTCTGTATTAGACATATACAGACTTTTCTTCTTGTCATTCCCTAAACAATGCAGTATAACAAGTATTTACATAGCATTTACATTTTATTAGGTATTACGAGTAATCTAGGGA

*** GENE MUTATIONS ***

TYPE    CHR     POS     REF     ALT     GENE    CONSEQUENCE     HGVSc   HGVSp   EXON    FILTERS ID      VAF     VariantReads    TotalReads      PopulationMAF
INDEL   chr12   11853483        C       CT      ETV6    frameshift_variant      c.391dup        p.S131Ffs*23    4/8     PASS    None    46.2%   24      52      NA

*** NOVEL STRUCTURAL VARIANTS INVOLVING KNOWN GENES ***

TYPE    CHR1    POS1    CHR2    POS2    LENGTH  BANDS   KNOWN_GENES     HGVS-LIKE       ISCN-LIKE       TOTAL_GENES     FILTERS CONTIG_HITS     ID      ABUNDANCE       PR_READS        SR_READS        CONTIG
BND     chr7    6114367 chr21   34778007        NA      p22.1q22.12     USP42--LINC01426        chr7:g.6114367(+)::chr21:g.34778007(-)  t(7;21)(p22.1;q22.12)   USP42--LINC01426        PASS    2       MantaBND:24816:1:2:0:0:0:1;MantaBND:24816:1:2:0:0:0:0   24.3%   22/82   21/95
ATCTTGAACTTCCCAACCTCCAGAACTGAGAGAAAAAATTCCTATCATTTATAAGCCACTCAGTCTATGATATTTTGTTATAACAGCCCCAATGGACTAAGACAACACCAAAATGTTTTTAAAAAAATTCATTATTTACAAAACACTGCAAATTTGATGACTGCTTATCTTTTATATCCACTTTGAACATTTAAAAAATAAATAATACAATCAATAGAAAAAATGAGATACATTTGATTCCTTGTAACATCTGCCATGGATGCTAATTCATTGCCACCATCACTGCCGT
CCTTACCATCTCATGTAGGG
INV     chr10   57142439        chr10   96751575        39609137        q21.1q24.1      KAT6B,PIK3AP1,TET1,CCDC6,HELLS,TNKS2    chr10:g.57142439_96751575inv    inv(10)(q21.1q24.1)     675 genes       PASS    2       MantaINV:8648:0:1:2:0:0 22.9%   5/42    14/41
ACTTTAAGCTGATATTATAAATAATTTTATACATAAAATTAGCTGTCAGTCAAAATGAATGTCTTGATAAAGATATACTGAAAATTTTGCCATAAACATTTCAGTATCCCTTTCTTCCACTACATAATTTCTTTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTGTTTTGTTTTGTTTTGTTTTGTTTTTTGAGAGGGAGTCTCGTTCTGTCGCCCAGGCGGGAGTGCTGTGGCGCGATCTCCGCTCACTGCAAGCTCCGCCTTCTGGGTTCATTCCATTCTCCTGCCTCA
GCCTCCCGAGTAGCTGGGACTACAGGCGCCCGCCACTGCGCCCGGCTAATTTTTTGTATTTTTAGTAGAGACGGGGTTTCACCGTGGTCTCGATCTCCTGACC

*** OTHER HIGH-CONFIDENCE STRUCTURAL VARIANTS ***

TYPE    CHR1    POS1    CHR2    POS2    LENGTH  BANDS   KNOWN_GENES     HGVS-LIKE       ISCN-LIKE       TOTAL_GENES     FILTERS CONTIG_HITS     ID      ABUNDANCE       PR_READS        SR_READS        CONTIG
BND     chr11   64199567        chr15   24346088        NA      q13.1q11.2      None    chr11:g.64199567(+)::chr15:g.24346088(+)        t(11;15)(q13.1;q11.2)   STIP1--INTERGENIC       PASS    2       MantaBND:6608:0:1:0:0:0:0;MantaBND:6608:0:1:0:0:0:1     15.7%   3/30    11/59
TATGTGAGCTTTTCATAGATGCCCTTTGAAATGAAGAAAGTTCTCTTATCTGCCTAATTTGCTGCATGTTTTTATAATACTGAATCTGGGAATTTTCAAGTGCTTGTTGCACACCTTCTGAGATGATTGTGTAGTTTTTATTCTTTTTTTTTTTTTTTTTGAGACGGAGTCTCGCTCTGTCGCCCAGGCTGGAGTGCAGTGGCGCGATCTCGGCTCACTGCAAGCTTCCGCCTCCCGGGTTCACGCCATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGG

*** CHROMOSEQ QC ***

AVERAGE COVERAGE:       58.58
TOTAL READS:    1986002476
MAPPED READS:   978315755   49.3%
DUPLICATES:     688205452   34.7%
UNIQUE READS:   653426174   32.9%
PROPERLY PAIRED READS:  967283616  48.7%
MEAN INSERT SIZE:       332.69

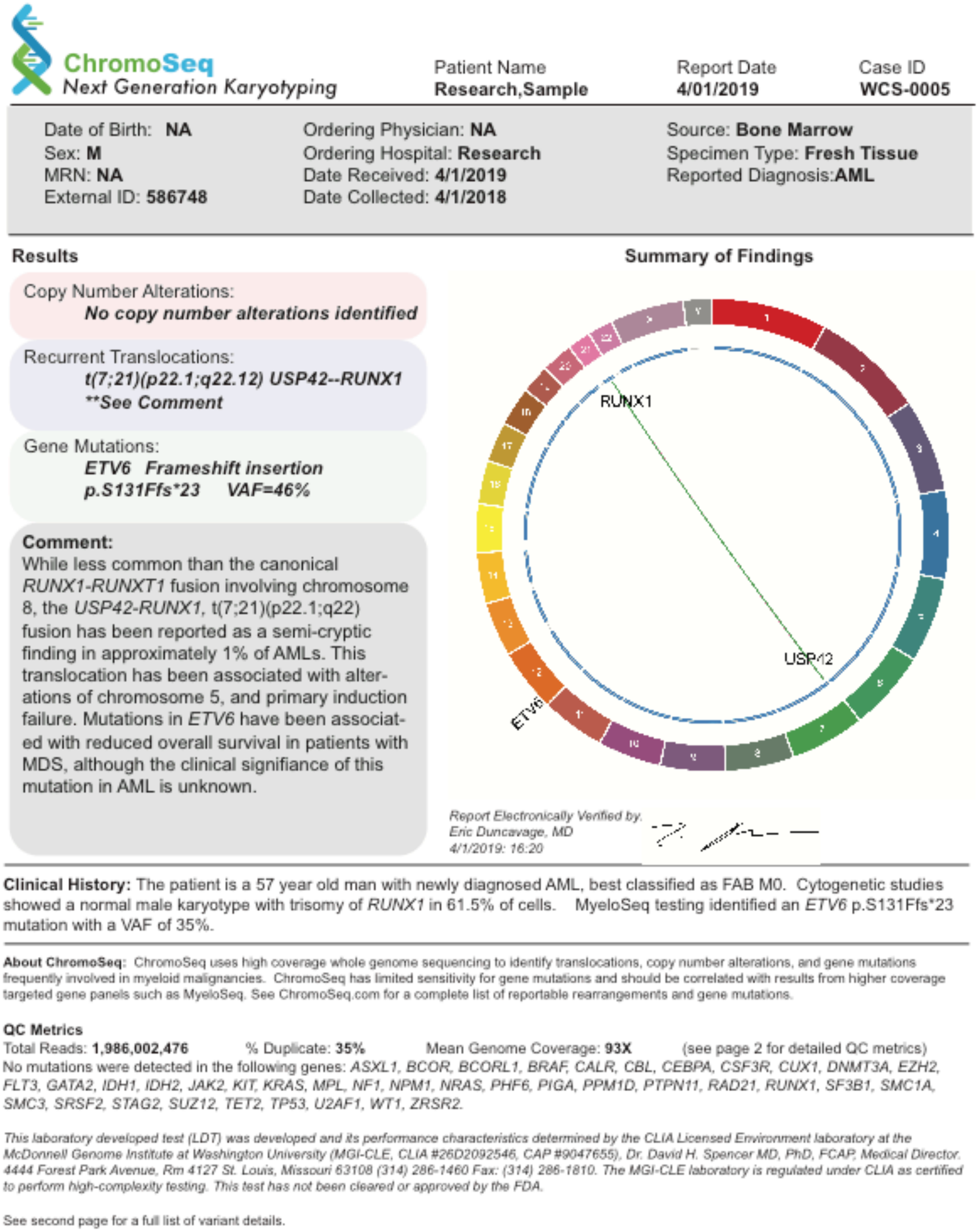
*** Gene Coverage Metrics: Exons with <95% at 20x or mean coverage <20x ***

#chrom  start   end     region  10X     20X     30X     40X     %10X    %20X    %30X    %40X    MeanCov
chr7    101816027       101816096       CUX1_exon_1     69      48      0       0       100.00  69.57   0.00    0.00    20.90
chr7    102248408       102249042       CUX1_exon_24    451     373     325     215     71.14   58.83   51.26   33.91   27.10
chr19   33301337        33302417        CEBPA_exon_1    1080    890     660     440     100.00  82.41   61.11   40.74   40.91
chr20   32358772        32358835        ASXL1_exon_1    63      34      7       0       100.00  53.97   11.11   0.00    22.60
chrX    15808229        15808274        ZRSR2_exon_6    45      34      0       0       100.00  75.56   0.00    0.00    20.11
chrX    40071633        40071693        BCOR_exon_5     60      26      0       0       100.00  43.33   0.00    0.00    19.63
chrX    124030957       124031128       STAG2_exon_5    171     141     82      0       100.00  82.46   47.95   0.00    26.31
chrX    124061767       124061877       STAG2_exon_17   110     50      0       0       100.00  45.45   0.00    0.00    19.95
chrX    124065872       124065949       STAG2_exon_21   77      67      0       0       100.00  87.01   0.00    0.00    23.36
chrX    134377614       134377758       PHF6_exon_2     144     99      39      0       100.00  68.75   27.08   0.00    22.76
chrX    134393905       134393955       PHF6_exon_5     50      42      0       0       100.00  84.00   0.00    0.00    20.16
chrX    134413487       134413660       PHF6_exon_6     173     84      1       0       100.00  48.55   0.58    0.00    20.40
chrX    134413819       134413969       PHF6_exon_7     150     90      3       0       100.00  60.00   2.00    0.00    20.81
chrX    134425197       134425330       PHF6_exon_10    133     120     0       0       100.00  90.23   0.00    0.00    22.08

*** SV Region Coverage Metrics: Exons with <95% at 20x or mean coverage <10x ***

#chrom  start   end     region  10X     20X     30X     40X     %10X    %20X    %30X    %40X    MeanCov
chr1    148808465       149032955       PDE4DIP 118801  89914   68632   52240   52.92   40.05   30.57   23.27   21.07
chr2    176107285       176109588       HOXD11  2147    2038    1950    1836    93.23   88.49   84.67   79.72   62.27
chr4    190173773       190175845       DUX4    374     349     314     281     18.05   16.84   15.15   13.56   12.03
chr7    74657684        74760692        GTF2I   79476   76313   74157   72125   77.16   74.08   71.99   70.02   45.81
chr8    85656441        85663039        REXO1L1P        2501    2122    2029    1903    37.91   32.16   30.75   28.84   67.90
chr9    41890313        42129250        CNTNAP3B        152015  123493  100751  80592   63.62   51.68   42.17   33.73   31.31
chr10   133623894       133626792       FRG2B   2285    1618    939     520     78.85   55.83   32.40   17.94   27.63
chr14   105586436       106879844       IGH     1183670 1164969 1146580 1124693 91.52   90.07   88.65   86.96   64.67
chr16   176679  177522  HBA1    797     611     567     460     94.54   72.48   67.26   54.57   52.67
chrX    55075062        55078909        PAGE2B  2887    2782    2228    579     75.05   72.32   57.92   15.05   25.98
chrX    120158560       120165630       RHOXF2  1124    369     21      0       15.90   5.22    0.30    0.00    3.81
chrX    135760156       135768191       CT45A3  914     739     517     427     11.38   9.20    6.43    5.31    6.58
chrX    135811980       135820012       CT45A2  0       0       0       0       0.00    0.00    0.00    0.00    0.00
chrX    150983285       150990775       HMGB3   6587    6263    5645    1930    87.94   83.62   75.37   25.77   31.34
```

Figure S1A. Sample WGS text report.
Text output of the ChromoSeq workflow showing CNAs, recurrent SVs, gene mutations, then novel SVs. QC data on overall coverage and coverage of specific genes appears at the bottom of the report.



ChromoSeq
Next Generation Karyotyping

Patient Name	Report Date	Case ID
Research,Sample	**4/01/2019**	**WCS-0005**

Date of Birth: **NA**
Sex: **M**
MRN: **NA**
External ID: **586748**

Ordering Physician: **NA**
Ordering Hospital: **Research**
Date Received: **4/1/2019**
Date Collected: **4/1/2018**

Source: **Bone Marrow**
Specimen Type: **Fresh Tissue**
Reported Diagnosis:**AML**

Results

Copy Number Alterations:
No copy number alterations identified

Recurrent Translocations:
t(7;21)(p22.1;q22.12) USP42--RUNX1
*****See Comment***

Gene Mutations:
ETV6 Frameshift insertion
p.S131Ffs*23 VAF=46%

Comment:
While less common than the canonical *RUNX1-RUNXT1* fusion involving chromosome 8, the *USP42-RUNX1*, t(7;21)(p22.1;q22) fusion has been reported as a semi-cryptic finding in approximately 1% of AMLs. This translocation has been associated with alterations of chromosome 5, and primary induction failure. Mutations in *ETV6* have been associated with reduced overall survival in patients with MDS, although the clinical signifiance of this mutation in AML is unknown.

Summary of Findings

Report Electronically Verified by.
Eric Duncavage, MD
4/1/2019: 16:20

Clinical History: The patient is a 57 year old man with newly diagnosed AML, best classified as FAB M0. Cytogenetic studies showed a normal male karyotype with trisomy of *RUNX1* in 61.5% of cells. MyeloSeq testing identified an *ETV6* p.S131Ffs*23 mutation with a VAF of 35%.

About ChromoSeq: ChromoSeq uses high coverage whole genome sequencing to identify translocations, copy number alterations, and gene mutations frequently involved in myeloid malignancies. ChromoSeq has limited sensitivity for gene mutations and should be correlated with results from higher coverage targeted gene panels such as MyeloSeq. See ChromoSeq.com for a complete list of reportable rearrangements and gene mutations.

QC Metrics
Total Reads: **1,986,002,476** % Duplicate: **35%** Mean Genome Coverage: **93X** (see page 2 for detailed QC metrics)
No mutations were detected in the following genes: *ASXL1, BCOR, BCORL1, BRAF, CALR, CBL, CEBPA, CSF3R, CUX1, DNMT3A, EZH2, FLT3, GATA2, IDH1, IDH2, JAK2, KIT, KRAS, MPL, NF1, NPM1, NRAS, PHF6, PIGA, PPM1D, PTPN11, RAD21, RUNX1, SF3B1, SMC1A, SMC3, SRSF2, STAG2, SUZ12, TET2, TP53, U2AF1, WT1, ZRSR2.*

This laboratory developed test (LDT) was developed and its performance characteristics determined by the CLIA Licensed Environment laboratory at the McDonnell Genome Institute at Washington University (MGI-CLE, CLIA #26D2092546, CAP #9047655), Dr. David H. Spencer MD, PhD, FCAP, Medical Director. 4444 Forest Park Avenue, Rm 4127 St. Louis, Missouri 63108 (314) 286-1460 Fax: (314) 286-1810. The MGI-CLE laboratory is regulated under CLIA as certified to perform high-complexity testing. This test has not been cleared or approved by the FDA.

See second page for a full list of variant details.

Figure S1B. Graphical WGS report.
Page 1 of a graphical ChromoSeq report highlighting the clinically significant findings in the genome sequence of an AML patient.

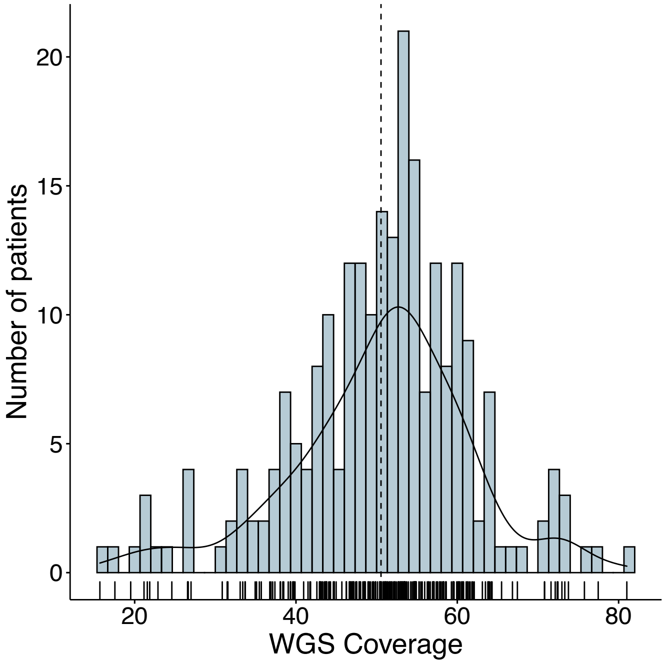


Figure S1C. Distribution of genome coverage.
Histogram of the genome-wide coverage depth in unique reads for 235 WGS cases.

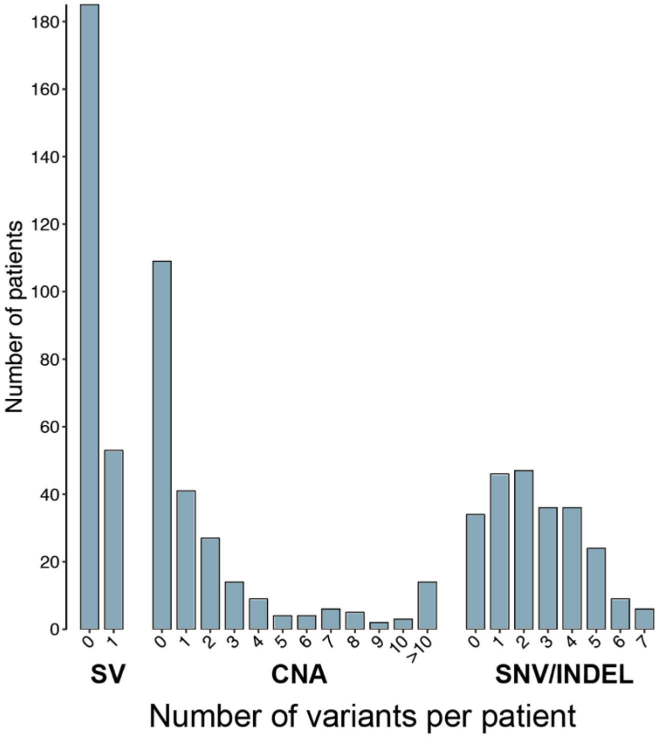


Figure S1D. Variants detected per patient.
Number distribution of SVs, CNAs, and gene mutations detected in 235 patients.

***KMT2A* breakapart FISH confirmation of *KMT2A* rearrangements**

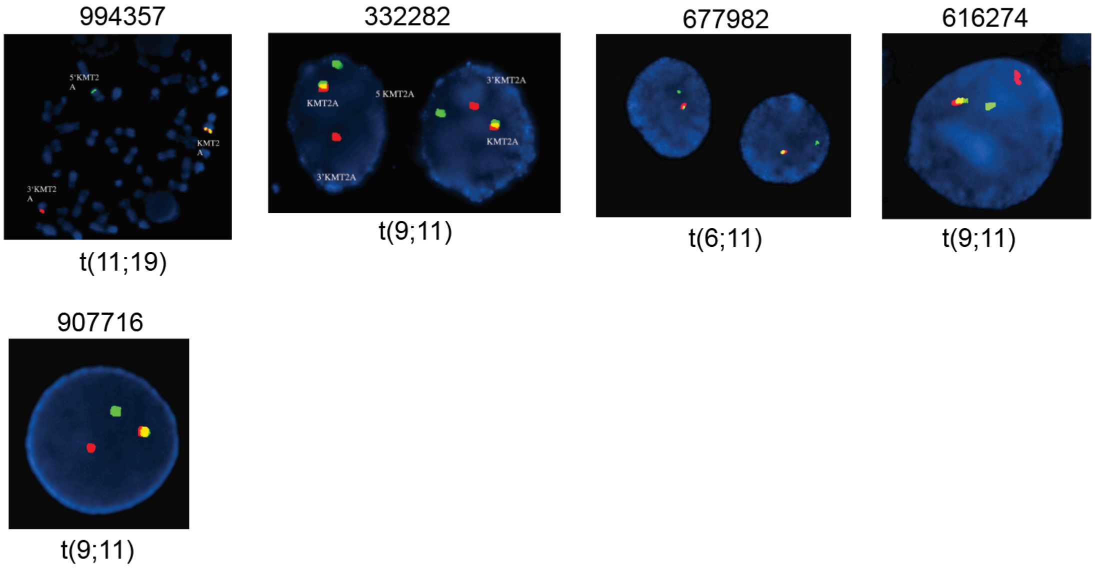


Figure S2A. Confirmation of SVs.

FISH results from metaphase and interphase FISH analysis utilizing a dual color, breakapart probe targeting *KMT2A* (manufactured by Vysis). A normal signal hybridizaiton pattern is 2Y. Rearrangement of a *KMT2A* locus generates a separation of the green signal, which encompasses the 5’ segment of *KMT2A* and surrounding region, and the red signal, which encompasses the 3’ segment of *KMT2A* and surrounding region.

994357) ish t(11;19)(5’KMT2A+,3’KMT2A-;3'KMT2A+) shown by WGS to have a t(11;19)(q23.3;p13.11)

332282) nuc ish(KMT2Ax2)(5’KMT2A sep 3’KMT2A)x1 in sample shown by WGS to have a t(9;11)(p21.3;q23.3)

677982) nuc ish(5’KMT2Ax2,3’KMT2Ax1)(5’KMT2A con 3’KMT2Ax1) in a sample shown by WGS to have a t(6;11)(q27;q23.3)

616274) nuc ish(KMT2Ax2)(5’KMT2A sep 3’KMT2A)x1 in sample shown by WGS to have a t(9;11)(p21.3;q23.3)

907716) nuc ish(KMT2Ax2)(5’KMT2A sep 3’KMT2A)x1 in sample shown by WGS to have a t(9;11)(p21.3;q23.3)

```
  ACTIONS      QUERY   SCORE START   END QSIZE IDENTITY  CHROM  STRAND  START        END   SPAN
-----------------------------------------------------------------------------------------------
browser details YourSeq   128    18   152   153  100.0%  chr11   +   118485815 118485950   136
browser details YourSeq   117    18   152   153   96.2%  chr11   +    31328531  31328675   145
browser details YourSeq   117    18   152   153   96.2%  chr1    +   155369176 155369314   139
browser details YourSeq   116    18   152   153   95.4%  chr14   -    21139482  21139616   135
```

```
  ACTIONS      QUERY   SCORE START   END QSIZE IDENTITY  CHROM  STRAND  START        END   SPAN
-----------------------------------------------------------------------------------------------
browser details YourSeq    79     1    79   122  100.0%  chr10   -    21631312  21631390    79
```

```
  ACTIONS      QUERY   SCORE START   END QSIZE IDENTITY  CHROM  STRAND  START        END   SPAN
-----------------------------------------------------------------------------------------------
browser details YourSeq   119    54   172   627  100.0%  chr7    -     6114251   6114369   119
browser details YourSeq    59     2    84   627   84.4%  chr21   +    34777953  34778023    71
```

Figure S2A, continued. PCR confirmation of t(10,11) in 451513 and t(7;21) in 586748. PCR using primers flanking the SV breakpoint were used to amplify across the breakpoint region, followed by Sanger sequencing and mapping to the GRCh38 reference using Blat.

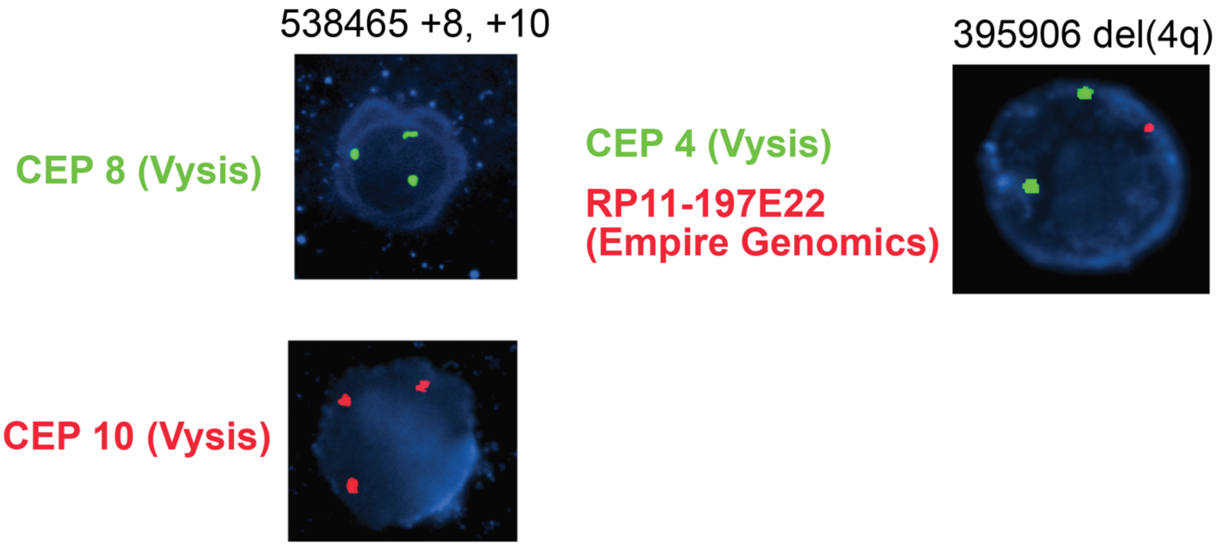
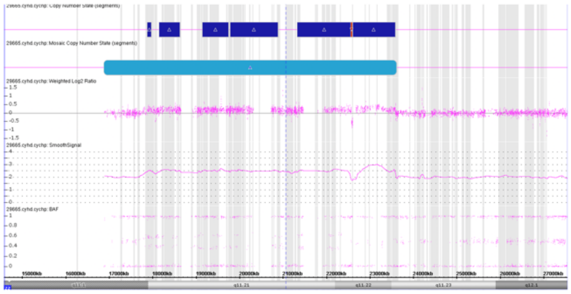


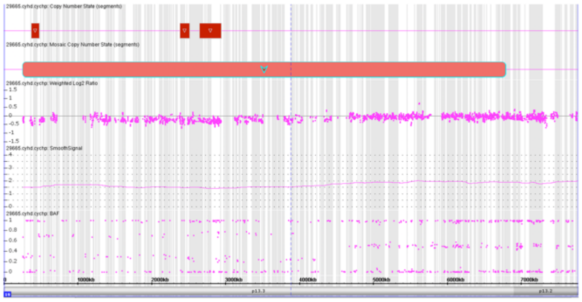
Figure S2B. Confirmation of CNAs
Confirmation of selected CNAs by FISH. See also Table S5.
<u>538465)</u> nuc ish(D8Z2x3)[44/20],(CEP10x3)[29/200]
<u>395906)</u> nuc ish(RP11-197E22x1,4cenx2)[161/200]



arr[GRCh37] 22q11.1q11.23(16888899_23615801)x2-3

UPN 905177

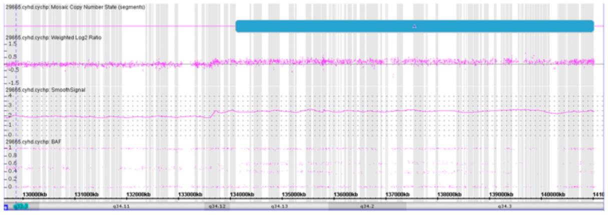
Chromoseq calls:
gain(22)(q11.21q11.23)[54.9%]



arr[GRCh37] 19p13.3(260911_6791879)x1-2

UPN 905177

Chromoseq calls:
del(19)(p13.3pter)[53.8%],

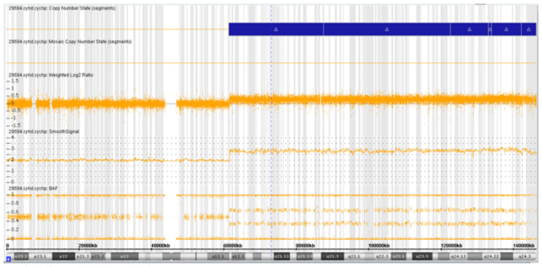


arr[GRCh37] 9q34.13q34.3(134108368_141020389)x2-3

UPN 905177

Chromoseq calls:
Gain(9)(q34.12qter)[58.2%],

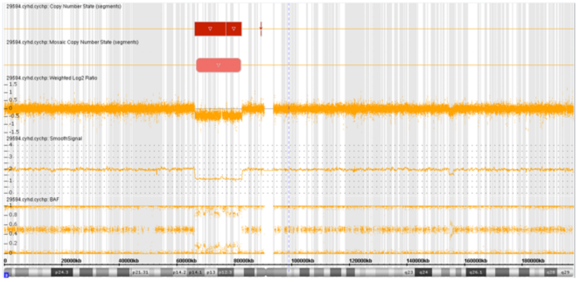
Figure S2B, continued. Confirmation of CNAs.
Confirmation of selected CNAs by CMA. See also Table S5.



arr[GRCh37] 8q24.22(133208518_134024374)x3
arr[GRCh37] 8q24.3(142246437_146295771)x3
arr[GRCh37] 8q24.22q24.3(134034960_142233759)x3
arr[GRCh37] 8q24.13q24.22(122681401_133202844)x3
arr[GRCh37] 8q12.1q21.3(61503566_87645437)x3
arr[GRCh37] 8q21.3q24.13(87650621_122664826)x3

UPN 155912

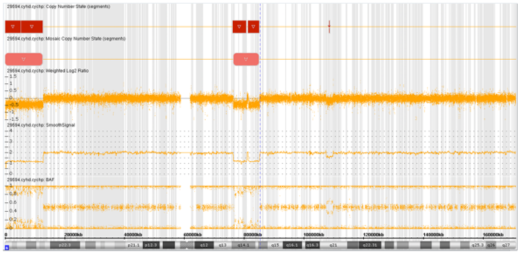
Chromoseq calls:
gain(8)(q12.1qter)[72.8%]



arr[GRCh37] 3p14.1p12.2(66972250_82402319)x1-2

UPN 155912

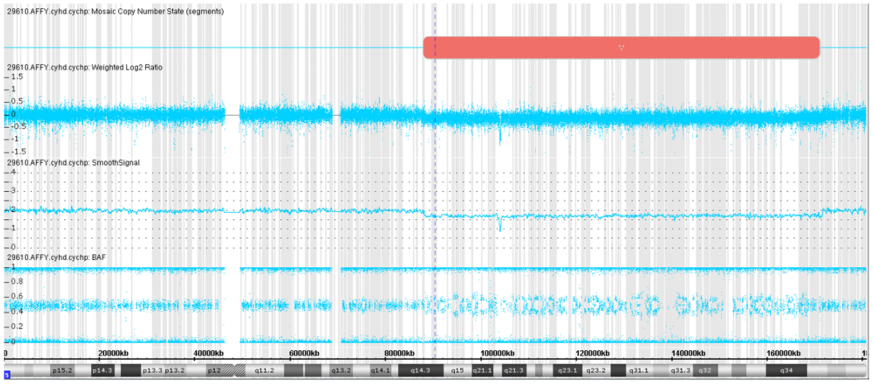
Chromoseq calls:
del(3)(p12.2p14.1)[76.6%]



arr[GRCh37] 6q14.1q14.3(76560018_84992750)x1-2
arr[GRCh37] 6p25.3p24.1(156974_12592062)x1-2

UPN 155912

Chromoseq calls:
del(6)(p24.1pter)[75.1%],
del(6)(q14.1q14.3)[77.6%]



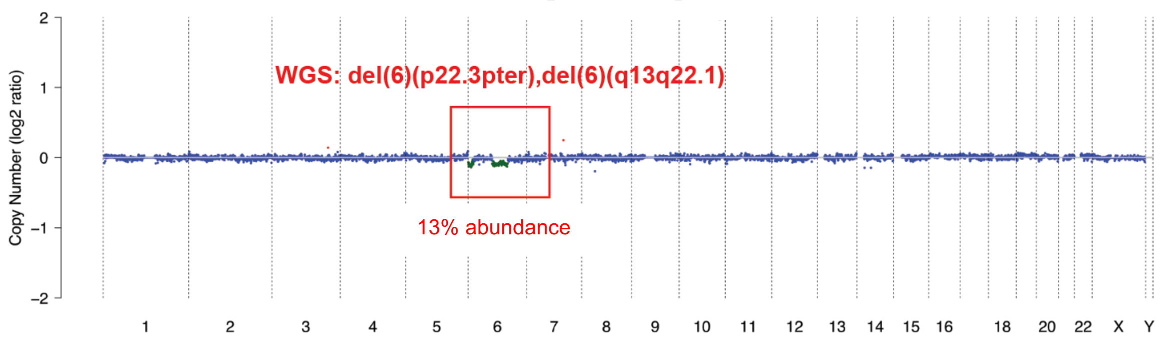
UPN 984418

By Chromoseq:
del(5)(q14.3q35.1)[24.4%]

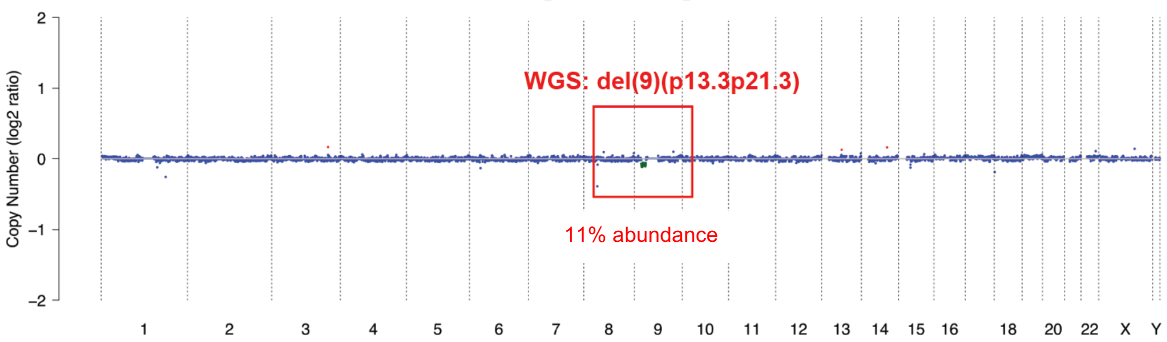
arr[GRCh37] 5q14.3q35.1(88111710_171208088)x1-2

Figure S2B, continued. Confirmation of CNAs.
Confirmation of selected CNAs by CMA. See also Table S5.

455499
AML
46,XX,t(15;17)(q22;q21)[12]/46,XX[8]



578200
AML
46,XY[20]



714148
AML
46,XY[20]

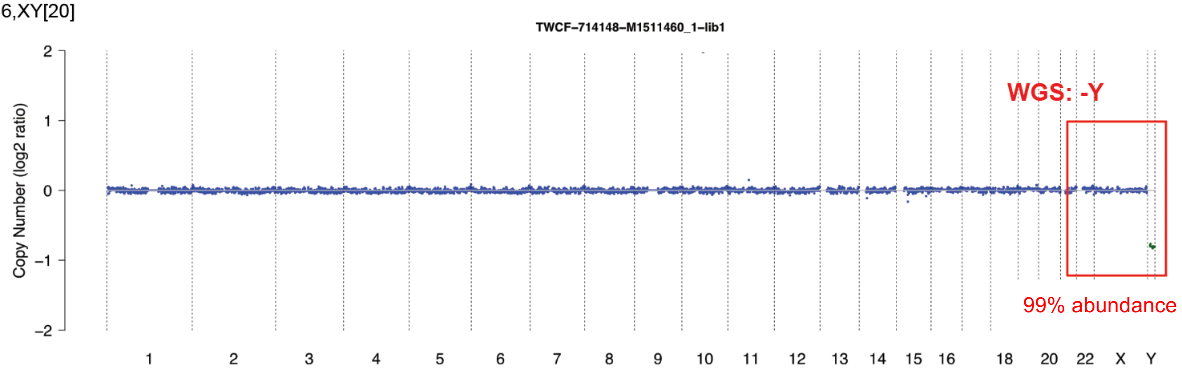
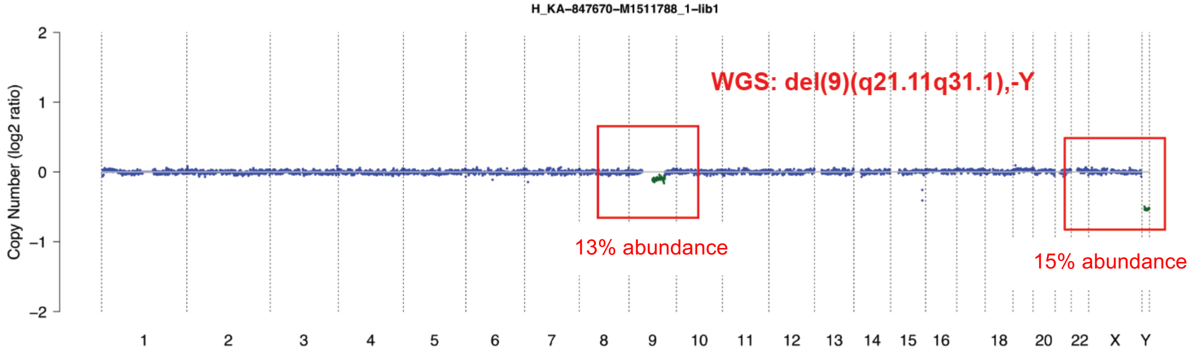


Figure S2C. WGS-only CNAs
Normalized coverage plots of WGS results for CNAs that were detected by WGS but could not be confirmed because of their small size, low abundance, lack of FISH probes, or lack of material.

847670

AML
46,XY,der(X)t(8;21)(q22;q22)t(X;21)(q28;?q22),
der(8)t(8;21)(q22;q22),
der(21)t(8;21)(q22;q22)t(X;21)(q28;?q22)[18]/46,XY[2]



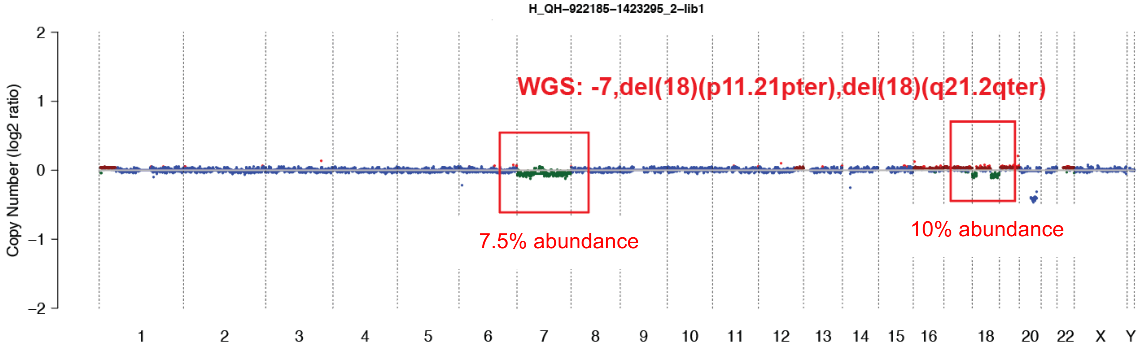
WGS: del(9)(q21.11q31.1),-Y

13% abundance

15% abundance

922185

MDS
46,XY,**del(20)(q11.2)[13]**/46,XY[7]



WGS: -7,del(18)(p11.21pter),del(18)(q21.2qter)

7.5% abundance

10% abundance

* Note for 922185, a del(20q) was also present, but was not discordant between WGS and cytogenetics.

Figure S2C, continued. WGS-only CNAs.

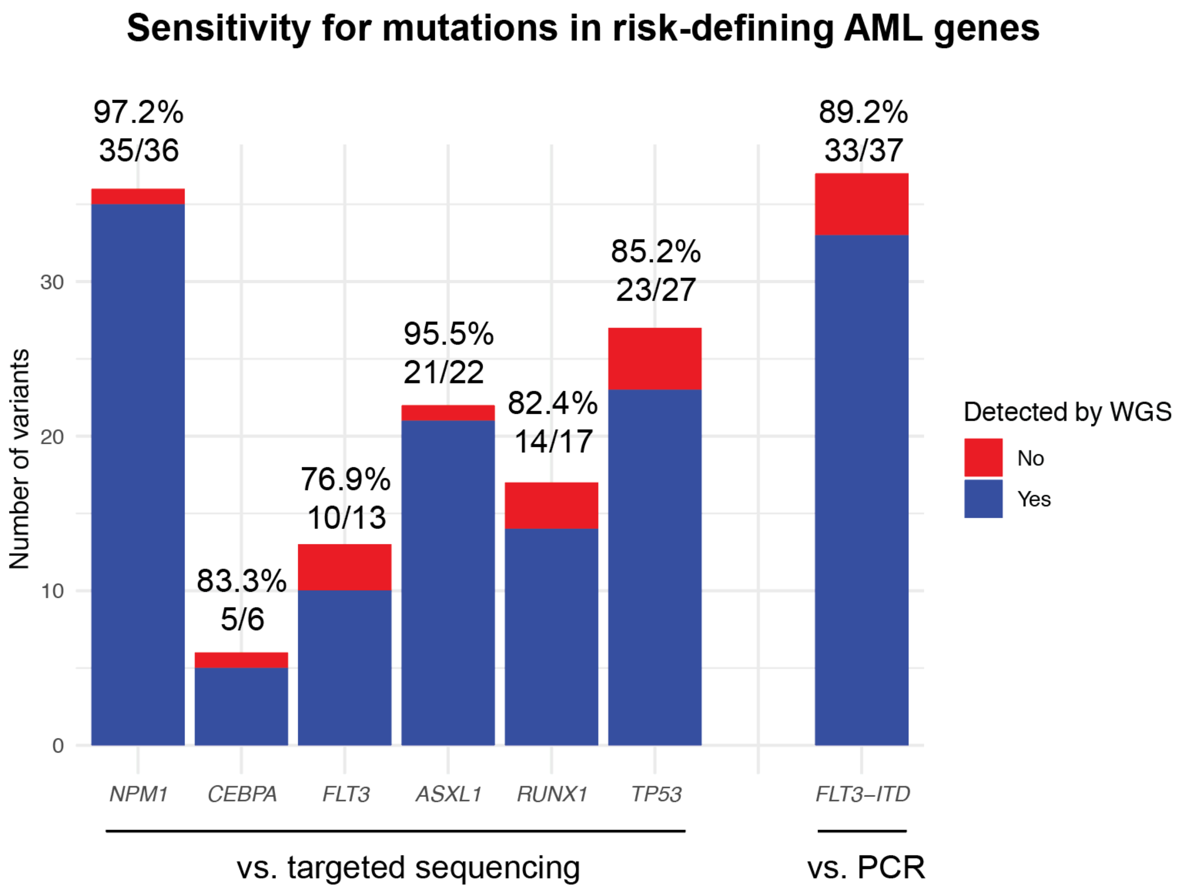
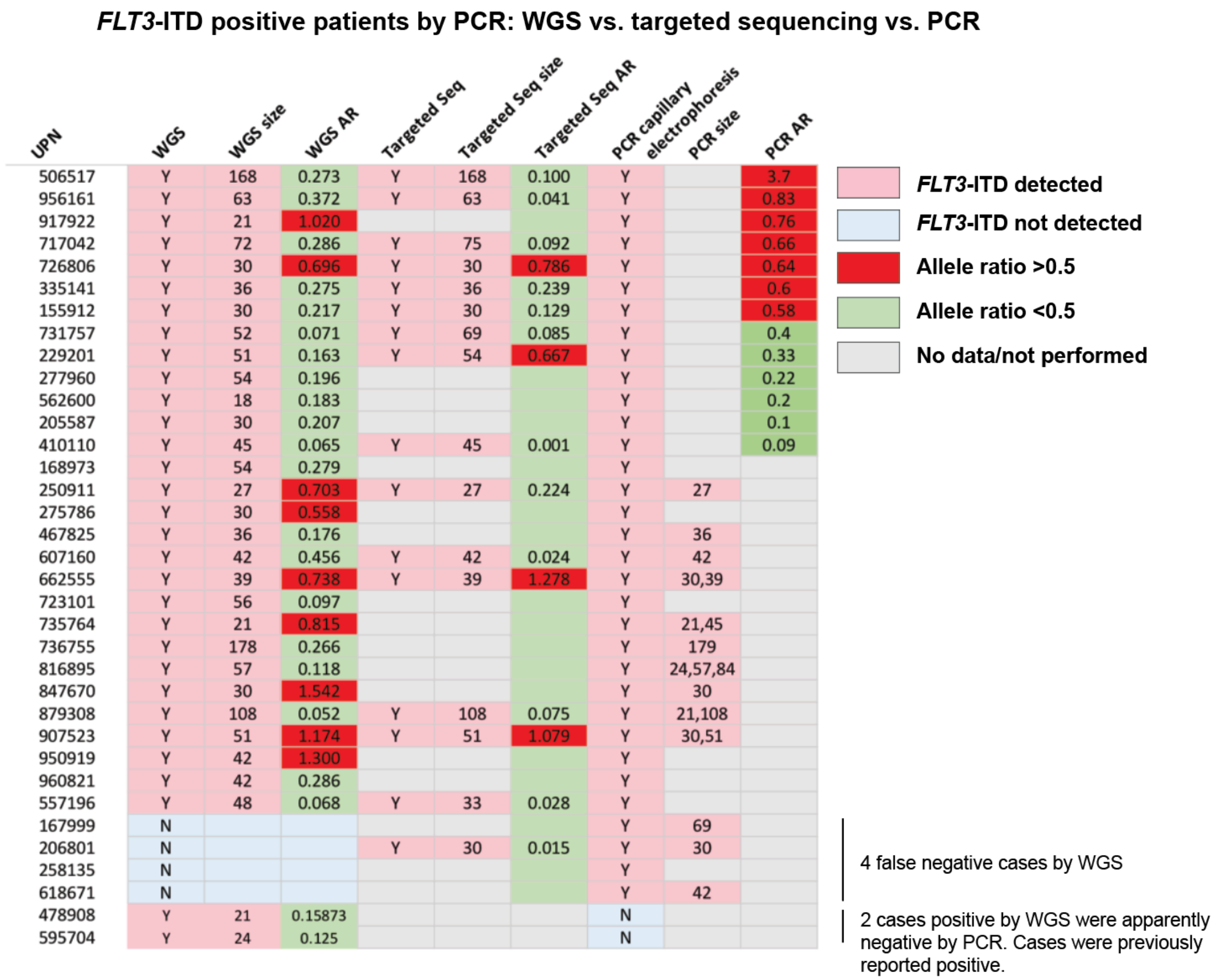


Figure S2D. Sensitivity of WGS for mutations in AML risk-defining genes. Gold standard mutations *NPM1* (NPM1c only), *CEBPA*, *FLT3* (non-ITD mutations), *RUNX1*, and *TP53* were obtained from targeted sequencing (>500x coverage) using a clinical assay (N=103 patients). *FLT3*-ITD mutations were obtained from clinical testing via PCR and capillary electrophoresis (N=104 patients). Numbers above each bar indicate the sensitivity (TP/(TP+FN) x 100) and the number of true positives and total positives by the gold standard assay.



***FLT3*-ITD positive patients by PCR: WGS vs. targeted sequencing vs. PCR**

UPN	WGS	WGS size	WGS AR	Targeted Seq	Targeted Seq size	Targeted Seq AR	PCR capillary electrophoresis	PCR size	PCR AR
506517	Y	168	0.273	Y	168	0.100	Y		3.7
956161	Y	63	0.372	Y	63	0.041	Y		0.83
917922	Y	21	1.020				Y		0.76
717042	Y	72	0.286	Y	75	0.092	Y		0.66
726806	Y	30	0.696	Y	30	0.786	Y		0.64
335141	Y	36	0.275	Y	36	0.239	Y		0.6
155912	Y	30	0.217	Y	30	0.129	Y		0.58
731757	Y	52	0.071	Y	69	0.085	Y		0.4
229201	Y	51	0.163	Y	54	0.667	Y		0.33
277960	Y	54	0.196				Y		0.22
562600	Y	18	0.183				Y		0.2
205587	Y	30	0.207				Y		0.1
410110	Y	45	0.065	Y	45	0.001	Y		0.09
168973	Y	54	0.279				Y		
250911	Y	27	0.703	Y	27	0.224	Y	27	
275786	Y	30	0.558				Y		
467825	Y	36	0.176				Y	36	
607160	Y	42	0.456	Y	42	0.024	Y	42	
662555	Y	39	0.738	Y	39	1.278	Y	30,39	
723101	Y	56	0.097				Y		
735764	Y	21	0.815				Y	21,45	
736755	Y	178	0.266				Y	179	
816895	Y	57	0.118				Y	24,57,84	
847670	Y	30	1.542				Y	30	
879308	Y	108	0.052	Y	108	0.075	Y	21,108	
907523	Y	51	1.174	Y	51	1.079	Y	30,51	
950919	Y	42	1.300				Y		
960821	Y	42	0.286				Y		
557196	Y	48	0.068	Y	33	0.028	Y		
167999	N						Y	69	
206801	N			Y	30	0.015	Y	30	
258135	N						Y		
618671	N						Y	42	
478908	Y	21	0.15873				N		
595704	Y	24	0.125				N		

🟪 ***FLT3*-ITD detected**

🟦 ***FLT3*-ITD not detected**

🟥 **Allele ratio >0.5**

🟩 **Allele ratio <0.5**

⬜ **No data/not performed**

4 false negative cases by WGS

2 cases positive by WGS were apparently negative by PCR. Cases were previously reported positive.

Figure S2E. *FLT3*-ITD detection by WGS vs. PCR. Results for 35 patients with *FLT3*-ITD mutations detected by either PCR and capillary electrophoresis or WGS. Rows show results for each patient with a positive ITD assay, including WGS, a clinical targeted sequencing assay, and PCR. The ITD allele sizes and allele ratios are indicated for each assay. Allele sizes and ratios were available for all positive results. Data from PCR include an in-house laboratory developed test (LDT) and the commercial FDA companion diagnostic assay, and therefore the allele size and ratios were not always reported. Note that ITD alleles were detected by WGS in two patients for whom the in-house LDT assay was negative (in 2002). ITD alleles were also detected in these patients in the AML TCGA study (see Supplementary Table 1 in reference[18]).

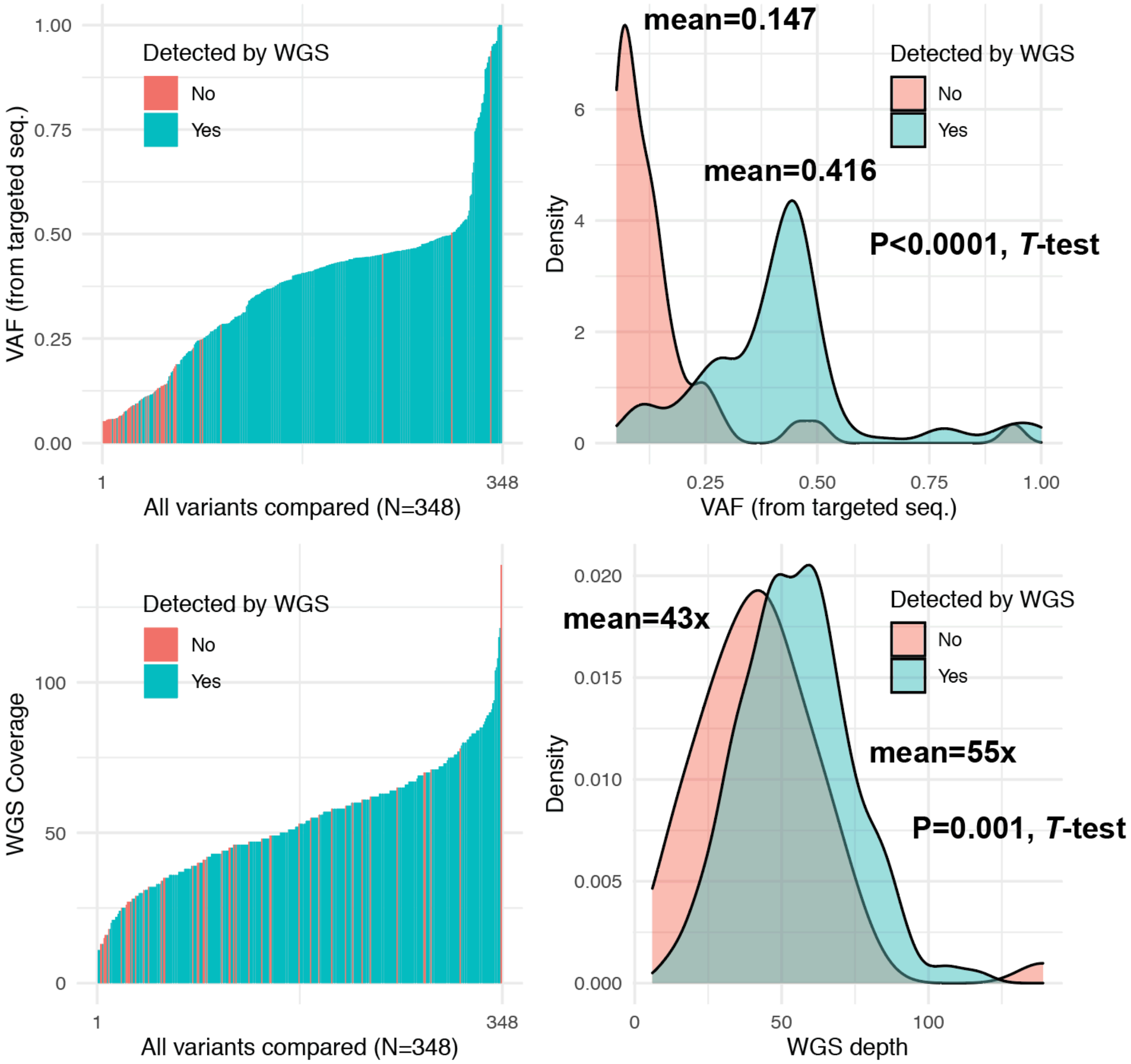


Figure S2F. Abundance and coverage depth of gene mutations in WGS data. Shown are the VAFs from deep targeted sequencing and WGS coverage for 348 variants detected in 102 patients using a clinical targeted sequencing assay. Left panels show the VAF from targeted sequencing (top) and WGS coverage for variants detected (N=300, in blue) and missed (N=48, in orange) by WGS. Right panels show the distribution of VAFs and WGS coverage for detected and missed variants. This analysis demonstrates the mutations not detected by WGS were significantly lower in abundance (top left; mean VAF by targeted sequencing of 14.7% vs. 41.6%, P < 0.0001, T-test), and occurred at positions with significantly less coverage (top right) in the WGS data compared to those that were detected (mean WGS coverage of 43x vs. 55x, P=0.001, T-test), such that false negatives are likely due to sampling statistics[22] (see Figure S2G below).

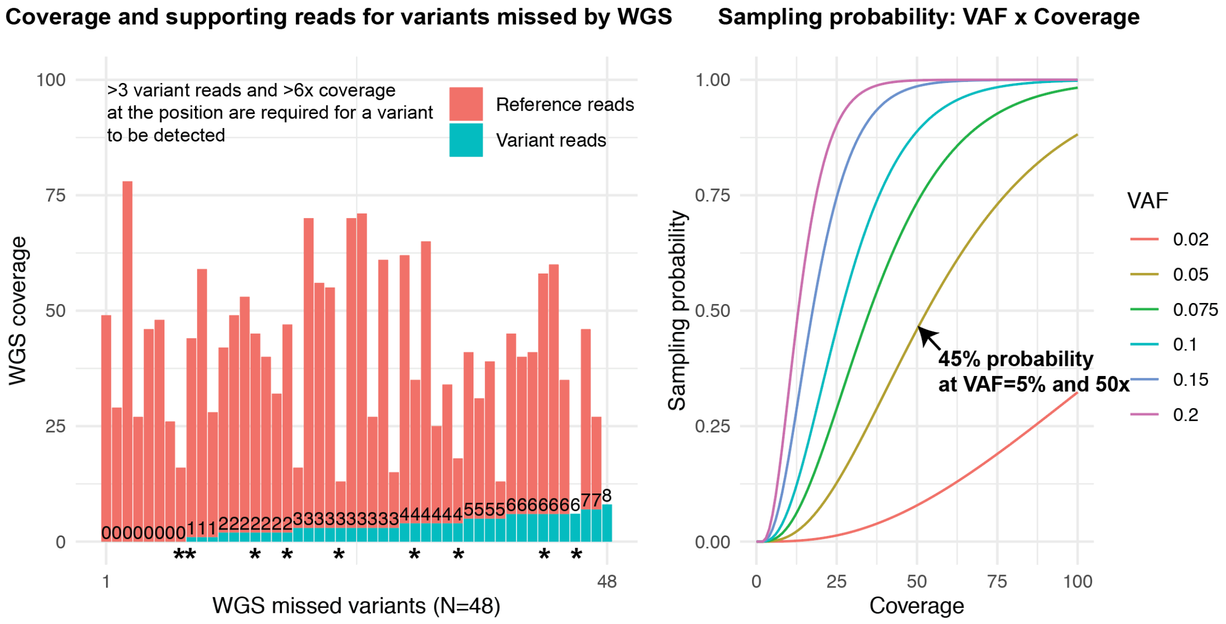


Figure S2G. Coverage metrics and for false negative gene mutations. Left panel shows WGS coverage (indicated by the height of the bar) and variant supporting reads (height of the blue bar) for 48 variants that were detected by clinical targeted sequencing but missed by WGS. Most of the variants (41/48) were present in the WGS data, but at very low frequency. Detection of gene variants required >3 variant-supporting reads and >6x total coverage. Variants highlighted by the asterisk were subsequently detected upon top-up sequencing of 4 cases. Right panel demonstrates the theoretical binomial sampling probability for detecting variants at VAFs ranging from 2% to 20% and coverage levels from 0 to 100x. Note that at 50x coverage (the mean obtained for this study), there is a 45% probability of sampling a variant >3 times if the true abundance is 5%. This is consistent with previous work showing that ‘standard coverage’ WGS is inadequate for robust detection of low frequency variants, but this can be improved with by increasing coverage depth[22] (see also Figure S2H).

						Original sequencing run			After additional sequencing		
Patient	Chromosome	Position	Gene	P syntax	Gene panel VAF	Total reads	Variant reads	WGS VAF	Total reads	Variant reads	WGS VAF
312088	chr1	114716123	*NRAS*	p.Gly13Asp	7.7%	39	3	7.7%	72	7	9.7%
312088	chr5	171410539	*NPM1*	p.Trp288CysfsTer12	38.4%	24	7	24.2%	84	29	34.5%
312088	chr8	116854320	*RAD21*	p.Met362SerfsTer8	42.6%	27	10	32.3%	62	26	41.9%
312088	chr11	32435332	*WT1*	p.Ala5Val	47.6%	21	7	33.3%	39	17	43.6%
312088	chr11	32435333	*WT1*	p.Ala5Thr	47.7%	23	9	39.1%	41	19	46.3%
312088	chr2	25234374	*DNMT3A*	p.Arg882Cys	44.7%	32	17	53.1%	62	36	58.1%
312088	chr12	25227342	*KRAS*	p.Gln61Leu	8.8%	32	2	NOT DETECTED	66	7	10.6%
312088	chr12	112450359	*PTPN11*	p.Gly60Val	18.8%	34	4	NOT DETECTED	61	10	16.4%
681540	chr20	32434599	*ASXL1*	p.Glu635ArgfsTer15	10.6%	62	3	9.9%	171	16	9.4%
681540	chr21	34886941	*RUNX1*	p.His85ThrfsTer38	44.3%	50	24	50.5%	150	76	50.70%
681540	chr4	105275394	*TET2*	p.Tyr1628Ter	5.8%	45	6	NOT DETECTED	101	9	8.90%
681540	chr4	105276142	*TET2*	p.Arg1878Cys	6.5%	53	2	NOT DETECTED	125	7	5.60%
681540	chrX	15818643	*ZRSR2*	splice	24.7%	13	5	NOT DETECTED	31	6	NOT DETECTED
416413	chr1	114716126	*NRAS*	p.Gly12Asp	27.3%	11	3	27.3%	76	21	27.6%
416413	chr20	32434638	*ASXL1*	p.Gly646TrpfsTer12	41.5%	32	11	35.9%	114	44	38.6%
416413	chr11	119278568	*CBL*	p.Ile429Asn	43.9%	22	9	40.9%	70	35	50.0%
416413	chr17	7673773	*TP53*	p.Arg283Cys	46.6%	11	6	54.5%	61	37	60.7%
416413	chr19	33301429	*CEBPA*	p.Glu329GlyfsTer74	14.2%	16	0	NOT DETECTED	72	7	9.7%
416413	chr4	105235633	*TET2*	p.Trp564Ter	50.3%	18	4	NOT DETECTED	60	25	41.7%
416413	chr4	105236832	*TET2*	p.Gln964Ter	45.2%	15	3	NOT DETECTED	71	28	39.4%
416413	chrX	124081379	*STAG2*	splice	93.8%	6	6	NOT DETECTED	27	27	100.0%
262878	chr12	25245350	*KRAS*	p.Gly12Asp	5.7%	60	7	11.7%	121	13	10.7%
262878	chr8	116849009	*RAD21*	p.Gly547AlafsTer65	36.2%	55	20	33.9%	126	38	30.2%
262878	chr5	171410539	*NPM1*	p.Trp288CysfsTer12	37.9%	60	23	35.2%	139	52	37.4%
262878	chr17	31221870	*NF1*	p.Gln554His	42.0%	47	24	51.1%	95	43	45.3%
262878	chr12	25245347	*KRAS*	p.Gly13Asp	5.2%	59	1	NOT DETECTED	122	5	NOT DETECTED
262878	chr13	28018505	*FLT3*	p.Asp835His	13.1%	60	6	NOT DETECTED	121	18	14.9%

Figure S2H. Additional variants detected after top-up sequencing. WGS missed 11 gene variants from patients 312088, 681540, 416413, and 262878 that were either present at low abundance in targeted sequencing data (<20% VAF, N=7) or occurred at position with low coverage in the WGS data (<25x, N=4). Additional sequencing of these samples increased the coverage for these samples from a mean of 35x (range: 17x-58x) to 83x (range: 59x-121x), and resulted in the detection of 9 of the 11 missed variants. The remaining 2 variants were present at low frequency in the WGS data but were not detected by the variant analysis pipeline.

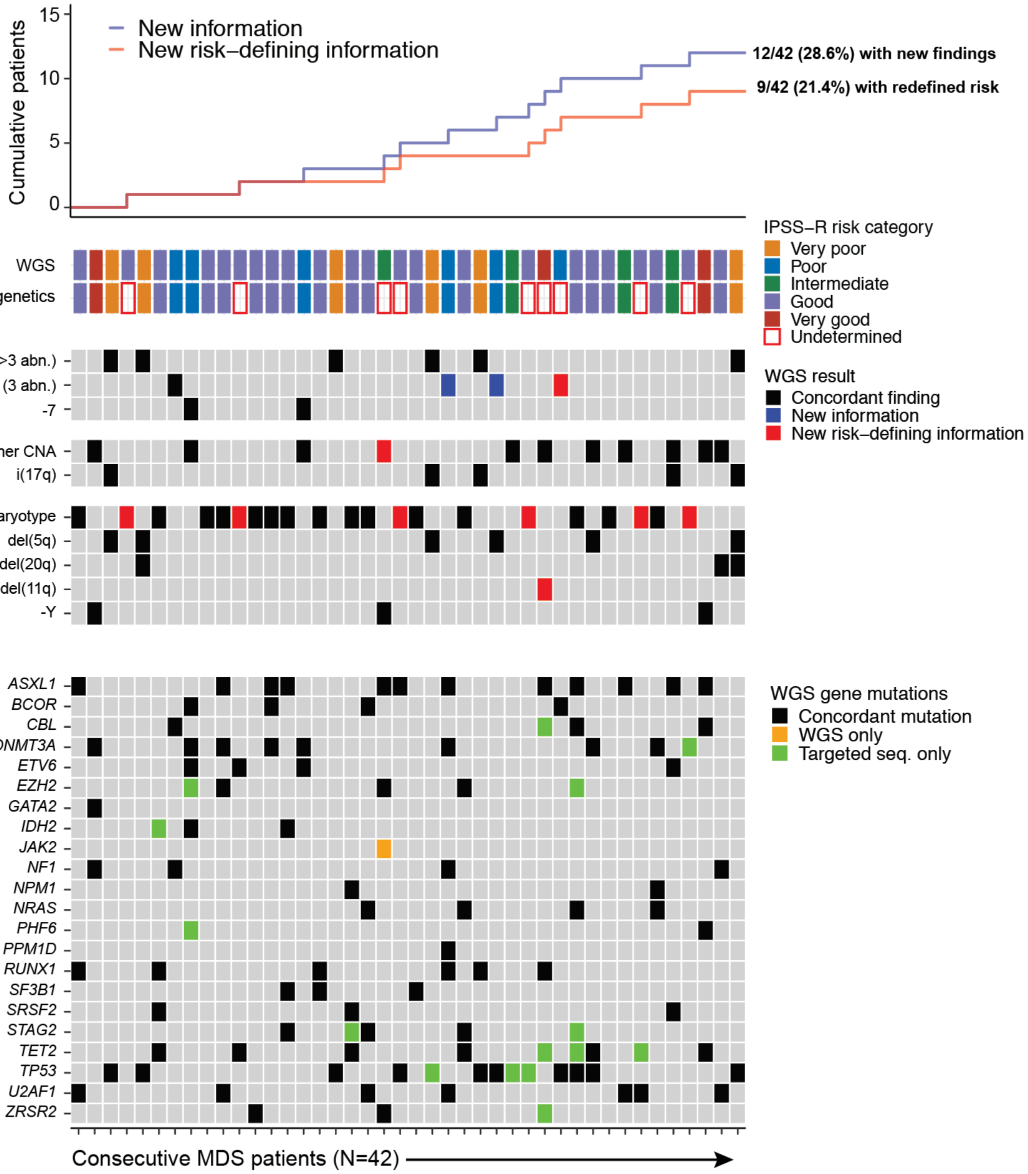


Figure S3. Diagnostic yield from prospective sequencing of MDS patients. Diagnostic yield of WGS in 42 consecutive MDS patients. Figure is organized as in Figure 3B. Consecutive MDS patients were sequenced from April 2019 to February 2020 to estimate the diagnostic yield of WGS compared to standard testing. Top panel shows the cumulative number of patients with new findings (in blue) and the cumulative number of patients with findings that changed the IPSS-R cytogenetic risk score. IPSS-R from cytogenetics and sequencing are shown in the middle panel. Middle panels show chromosomal abnormalities obtained from WGS and indicates new findings (in blue) and findings that changed the IPSS-R category. Bottom panel shows mutations in MDS-associated genes referenced in NCCN guidelines, with concordance between WGS and targeted sequencing indicated by the color (concordant in black, WGS only in orange, and targeted sequencing only in green). Note that the yield in risk-defining events in this cohort is due entirely to cases where cytogenetics was unsuccessful or inconclusive, resulting in an undetermined IPSS-R risk category.

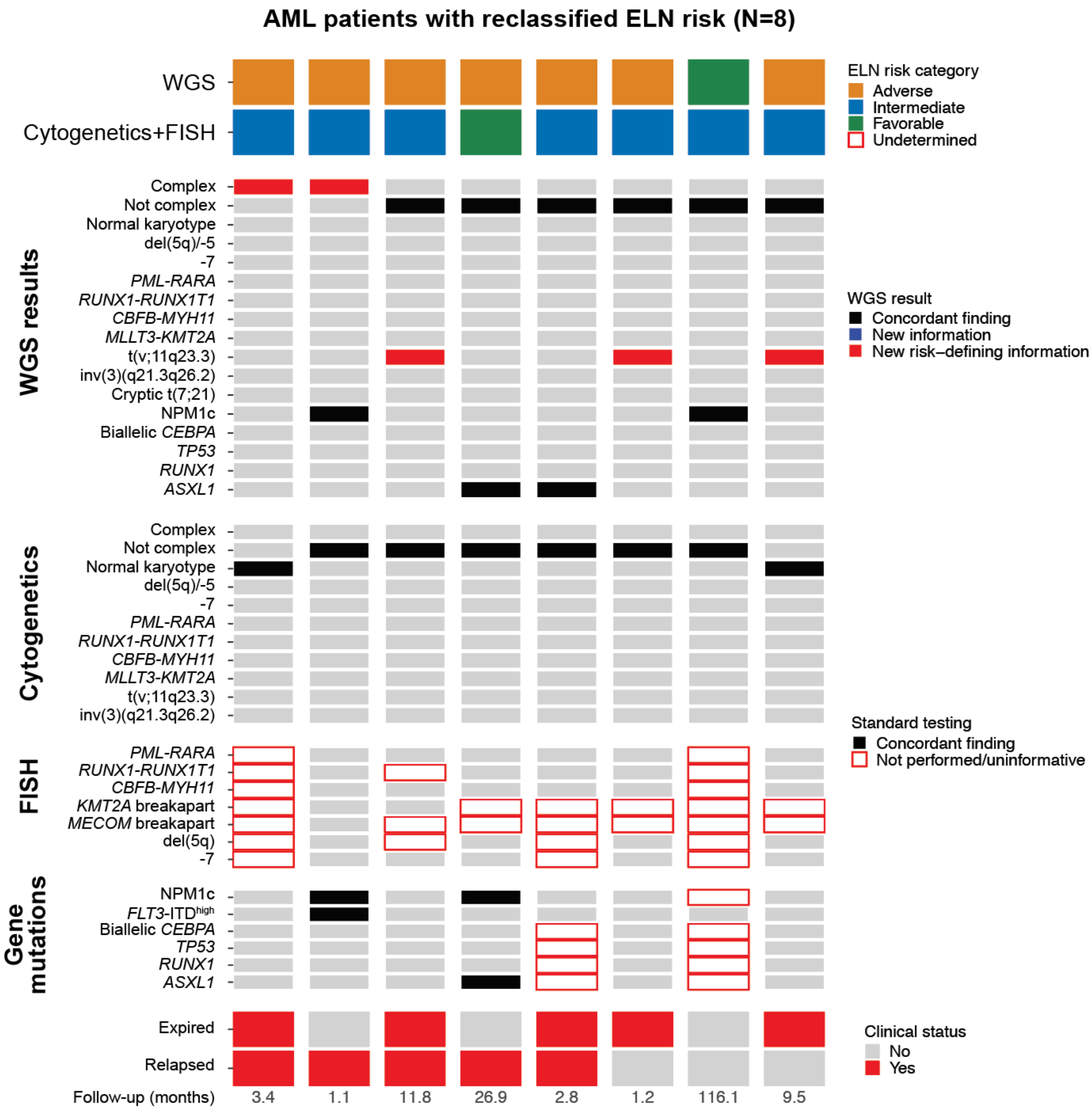


Figure S4A. AML patients with reclassified risk groups by WGS. AML patients included in the outcome analysis with defined cytogenetic risk that were reclassified by WGS. Top panel shows the ELN risk groups by cytogenetics combined with FISH for *PML-RARA*, *RUNX1-RUNX1T1*, *CBFB-MYH11*, del(5q), and del(7q) (bottom), and gene mutation testing either via targeted sequencing or PCR, and WGS and *FLT3*-ITD PCR only (top). Lower panels show WGS results (with the risk-defining event highlighted in red), and results from cytogenetics, FISH, and gene mutation analysis. *FLT3*-ITD mutation status by PCR was used for both WGS and conventional risk group assignments. Cells outlined in red indicate that testing was either not performed or failed. Also shown is the clinical status of each patient, including whether they expired or relapsed, and the follow-up time in months from diagnosis. WGS identified new adverse risk findings in 5 patients, while 3 patients had differences in gene mutations in *ASXL1* and *NPM1* and either due to lack of testing at diagnosis (N=2) or a missed low abundance NPM1c mutation by WGS (N=1).

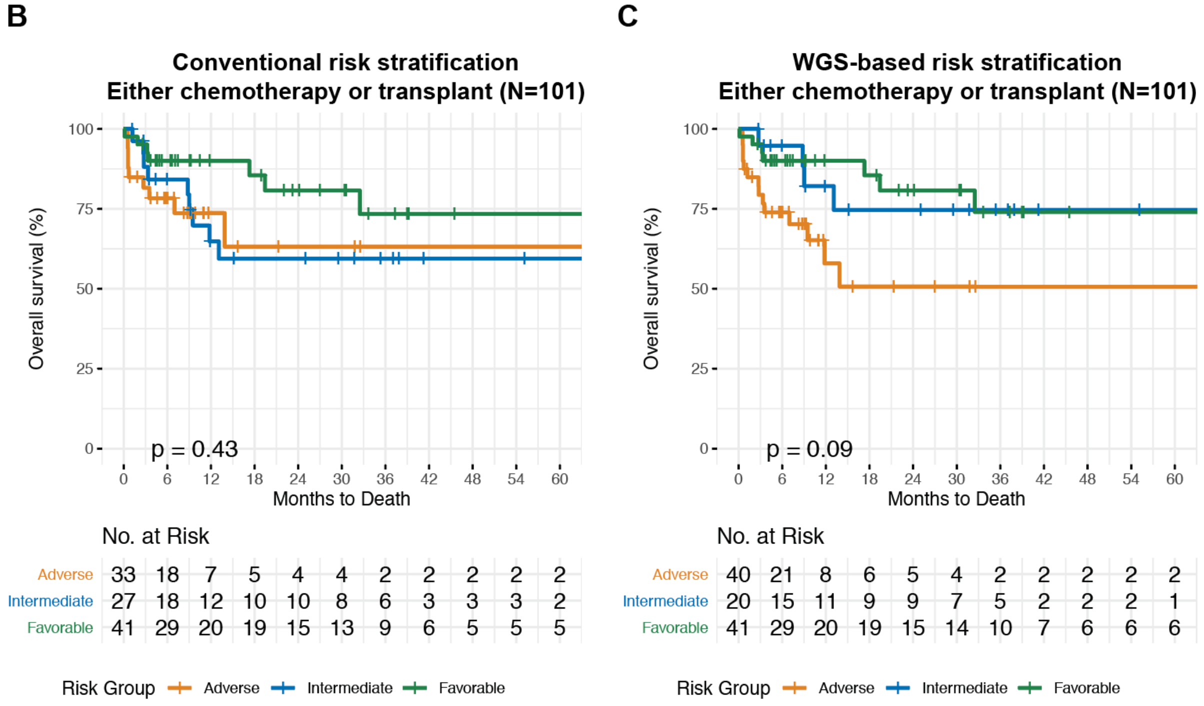


Figure S4B,C. Survival analysis of 101 AML patients with defined risk.

Panel B) Kaplan Meier survival curves using death as the endpoint for 101 AML patients treated with either post-remission chemotherapy alone (N=71) or allogeneic stem cell transplant (N=30) stratified by ELN risk groups from cytogenetics, targeted sequencing, and *FLT3* ITD mutation testing. Log-rank test for equal survival across the groups, adjusted P=0.43. Age-adjusted Cox regression for death in not adverse vs. adverse cytogenetic risk groups: 1.06, 95% CI 0.45 to 2.50.

Panel C) Kaplan Meier survival curves using death as the endpoint for 101 AML patients treated with either post-remission chemotherapy alone (N=71) or allogeneic stem cell transplant (N=30) stratified by ELN risk groups from WGS and *FLT3* ITD mutation testing. Log-rank test for equal survival across the groups, adjusted P=0.09. Age-adjusted Cox regression for death in not adverse and adverse WGS-based risk groups: 0.59, 95% CI 0.26 to 1.36.

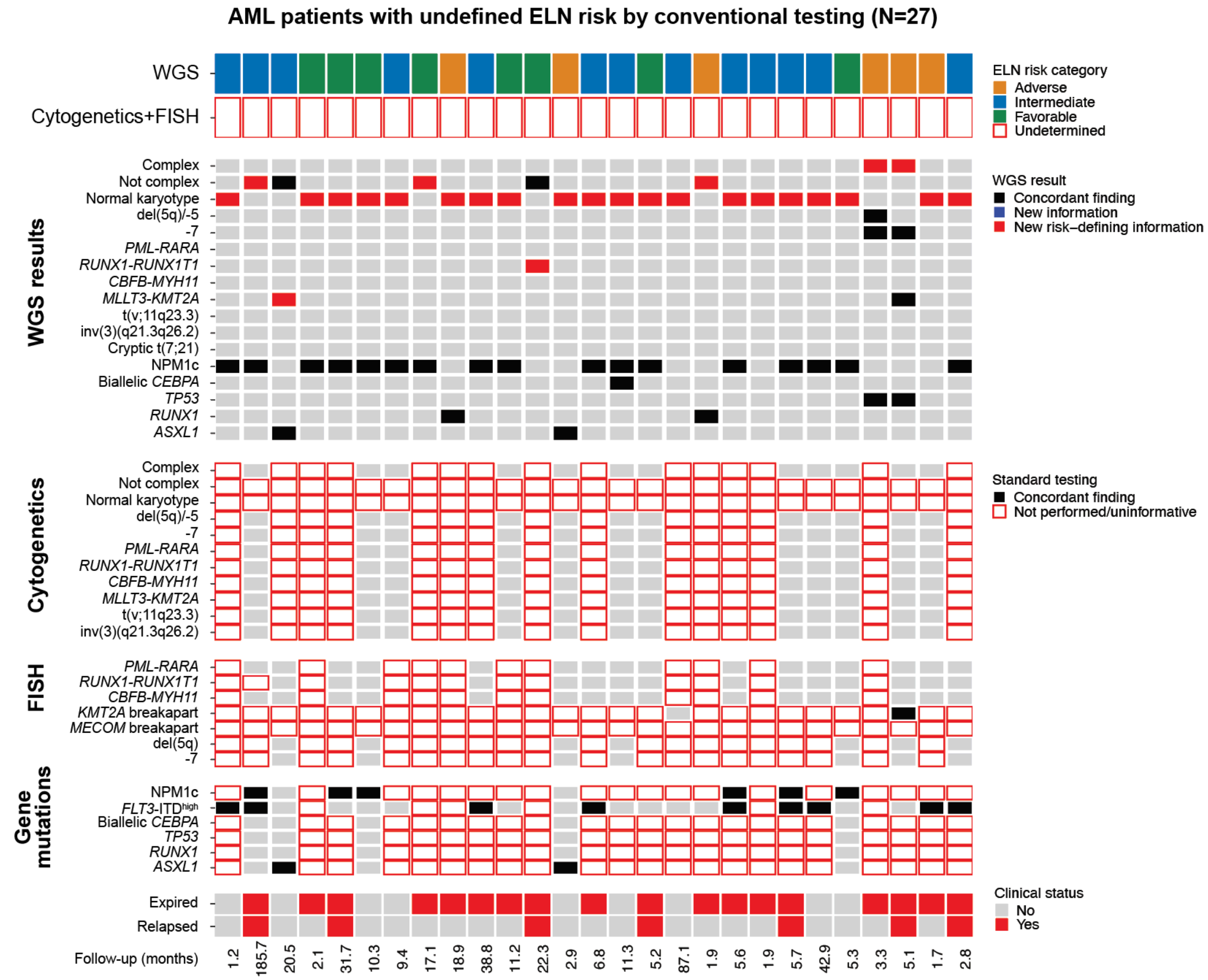


Figure S4D. WGS results for AML patients with inconclusive cytogenetics. Patients with unsuccessful (N=6), inconclusive (N=13), or unknown (N=8) cytogenetic and FISH studies that precluded definitive genomic risk assignment. WGS-based ELN risk group is shown in the top panel. Results from WGS, cytogenetics, FISH, and gene mutation testing are shown below. *FLT3*-ITD mutation status was determined by PCR and was used for risk stratification according to ELN criteria using an allele ratio cutoff of 0.5, or presence/absence if an allele ratio was not available. Bottom panel shows clinical status and follow-up time in months. WGS identified risk-defining chromosomal abnormalities in four patients, including *KMT2A* and *RUNX1-RUNX1T1* rearrangements (N=1 each) and a complex karyotype (N=2). The remaining 23 patients were assigned to ELN risk groups based on gene mutations.

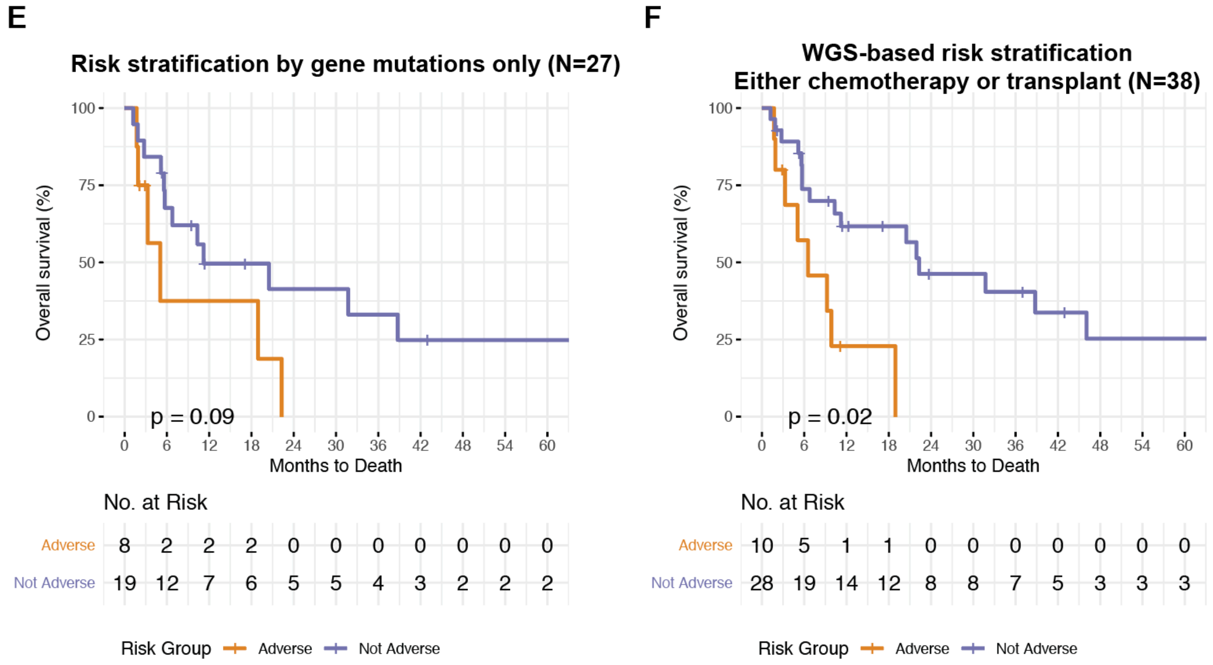


Figure S4E,F. Survival analysis of AML patients with inconclusive cytogenetics.
Panel E) Kaplan Meier survival curve for 27 AML patients with unsuccessful for inconclusive cytogenetics stratified by gene mutations only. Patients were considered intermediate risk unless favorable risk or adverse risk gene mutations were identified. Log-rank test for equal survival across the groups, adjusted P=0.09. Age-adjusted Cox regression hazard ratio for death in not adverse vs. adverse risk, 0.4; 95% CI, 0.14 to 1.1.
Panel F) Kaplan Meier survival curves using death as the endpoint for the above cohort of 38 patients stratified by ELN risk groups from WGS and *FLT3* ITD mutation testing. Median survival for this expanded cohort was 22.3 months, 95% CI, 6.8 to 46.1. Log-rank test for equal survival across the groups, adjusted P=0.02. Age-adjusted Cox regression hazard ratio for death in not adverse vs. adverse risk, 0.28; 95% CI, 0.11 to 0.71.

3. Supplementary Tables

Table S1. Target list for gene mutation identification.

Chrom	Start	End	Exon	Strand	GeneName	GeneID	TranscriptID
chr1	114713797	114713981	NRAS_exon_3	-	NRAS	ENSG00000213281	ENST00000369535
chr1	114716047	114716163	NRAS_exon_2	-	NRAS	ENSG00000213281	ENST00000369535
chr1	36466356	36466911	CSF3R_exon_17	-	CSF3R	ENSG00000119535	ENST00000373103
chr1	36467226	36467314	CSF3R_exon_16	-	CSF3R	ENSG00000119535	ENST00000373103
chr1	36467554	36467654	CSF3R_exon_15	-	CSF3R	ENSG00000119535	ENST00000373103
chr1	36467818	36467965	CSF3R_exon_14	-	CSF3R	ENSG00000119535	ENST00000373103
chr1	36468071	36468224	CSF3R_exon_13	-	CSF3R	ENSG00000119535	ENST00000373103
chr1	36469152	36469260	CSF3R_exon_12	-	CSF3R	ENSG00000119535	ENST00000373103
chr1	36469648	36469843	CSF3R_exon_11	-	CSF3R	ENSG00000119535	ENST00000373103
chr1	36471429	36471649	CSF3R_exon_10	-	CSF3R	ENSG00000119535	ENST00000373103
chr1	36472062	36472142	CSF3R_exon_9	-	CSF3R	ENSG00000119535	ENST00000373103
chr1	36472234	36472394	CSF3R_exon_8	-	CSF3R	ENSG00000119535	ENST00000373103
chr1	36472513	36472689	CSF3R_exon_7	-	CSF3R	ENSG00000119535	ENST00000373103
chr1	36473431	36473625	CSF3R_exon_6	-	CSF3R	ENSG00000119535	ENST00000373103
chr1	36473760	36473890	CSF3R_exon_5	-	CSF3R	ENSG00000119535	ENST00000373103
chr1	36475373	36475676	CSF3R_exon_4	-	CSF3R	ENSG00000119535	ENST00000373103
chr1	36479429	36479499	CSF3R_exon_3	-	CSF3R	ENSG00000119535	ENST00000373103
chr1	43349260	43349362	MPL_exon_10	+	MPL	ENSG00000117400	ENST00000372470
chr10	110567813	110567834	SMC3_exon_1	+	SMC3	ENSG00000108055	ENST00000361804
chr10	110568934	110569016	SMC3_exon_2	+	SMC3	ENSG00000108055	ENST00000361804
chr10	110573703	110573748	SMC3_exon_3	+	SMC3	ENSG00000108055	ENST00000361804
chr10	110575332	110575406	SMC3_exon_4	+	SMC3	ENSG00000108055	ENST00000361804
chr10	110577417	110577495	SMC3_exon_5	+	SMC3	ENSG00000108055	ENST00000361804
chr10	110577831	110577917	SMC3_exon_6	+	SMC3	ENSG00000108055	ENST00000361804
chr10	110578624	110578709	SMC3_exon_7	+	SMC3	ENSG00000108055	ENST00000361804
chr10	110580900	110581024	SMC3_exon_8	+	SMC3	ENSG00000108055	ENST00000361804
chr10	110581919	110582101	SMC3_exon_9	+	SMC3	ENSG00000108055	ENST00000361804
chr10	110582558	110582645	SMC3_exon_10	+	SMC3	ENSG00000108055	ENST00000361804
chr10	110583380	110583551	SMC3_exon_11	+	SMC3	ENSG00000108055	ENST00000361804
chr10	110583837	110583965	SMC3_exon_12	+	SMC3	ENSG00000108055	ENST00000361804
chr10	110584179	110584399	SMC3_exon_13	+	SMC3	ENSG00000108055	ENST00000361804
chr10	110589601	110589711	SMC3_exon_14	+	SMC3	ENSG00000108055	ENST00000361804
chr10	110589888	110589994	SMC3_exon_15	+	SMC3	ENSG00000108055	ENST00000361804
chr10	110590408	110590575	SMC3_exon_16	+	SMC3	ENSG00000108055	ENST00000361804
chr10	110590987	110591135	SMC3_exon_17	+	SMC3	ENSG00000108055	ENST00000361804
chr10	110593069	110593226	SMC3_exon_18	+	SMC3	ENSG00000108055	ENST00000361804
chr10	110596394	110596553	SMC3_exon_19	+	SMC3	ENSG00000108055	ENST00000361804
chr10	110598135	110598293	SMC3_exon_20	+	SMC3	ENSG00000108055	ENST00000361804
chr10	110599650	110599815	SMC3_exon_21	+	SMC3	ENSG00000108055	ENST00000361804
chr10	110600435	110600549	SMC3_exon_22	+	SMC3	ENSG00000108055	ENST00000361804
chr10	110601018	110601133	SMC3_exon_23	+	SMC3	ENSG00000108055	ENST00000361804
chr10	110601633	110601887	SMC3_exon_24	+	SMC3	ENSG00000108055	ENST00000361804
chr10	110601962	110602181	SMC3_exon_25	+	SMC3	ENSG00000108055	ENST00000361804
chr10	110602470	110602668	SMC3_exon_26	+	SMC3	ENSG00000108055	ENST00000361804
chr10	110602821	110603005	SMC3_exon_27	+	SMC3	ENSG00000108055	ENST00000361804
chr10	110603180	110603293	SMC3_exon_28	+	SMC3	ENSG00000108055	ENST00000361804
chr10	110604227	110604302	SMC3_exon_29	+	SMC3	ENSG00000108055	ENST00000361804
chr11	119278163	119278300	CBL_exon_8	+	CBL	ENSG00000110395	ENST00000264033
chr11	119278507	119278716	CBL_exon_9	+	CBL	ENSG00000110395	ENST00000264033
chr11	32389057	32389182	WT1_exon_10	-	WT1	ENSG00000184937	ENST00000332351
chr11	32391968	32392067	WT1_exon_9	-	WT1	ENSG00000184937	ENST00000332351
chr11	32392662	32392758	WT1_exon_8	-	WT1	ENSG00000184937	ENST00000332351
chr11	32396253	32396410	WT1_exon_7	-	WT1	ENSG00000184937	ENST00000332351
chr11	32399944	32400047	WT1_exon_6	-	WT1	ENSG00000184937	ENST00000332351
chr11	32416486	32416543	WT1_exon_5	-	WT1	ENSG00000184937	ENST00000332351
chr11	32417573	32417657	WT1_exon_4	-	WT1	ENSG00000184937	ENST00000332351
chr11	32427952	32428061	WT1_exon_3	-	WT1	ENSG00000184937	ENST00000332351
chr11	32428493	32428622	WT1_exon_2	-	WT1	ENSG00000184937	ENST00000332351
chr11	32434696	32435348	WT1_exon_1	-	WT1	ENSG00000184937	ENST00000332351
chr12	112450315	112450515	PTPN11_exon_3	+	PTPN11	ENSG00000179295	ENST00000351677
chr12	112489021	112489178	PTPN11_exon_13	+	PTPN11	ENSG00000179295	ENST00000351677
chr12	112502141	112502259	PTPN11_exon_14	+	PTPN11	ENSG00000179295	ENST00000351677
chr12	11650124	11650163	ETV6_exon_1	+	ETV6	ENSG00000139083	ENST00000396373
chr12	11752446	11752582	ETV6_exon_2	+	ETV6	ENSG00000139083	ENST00000396373
chr12	11839136	11839307	ETV6_exon_3	+	ETV6	ENSG00000139083	ENST00000396373
chr12	11853423	11853564	ETV6_exon_4	+	ETV6	ENSG00000139083	ENST00000396373
chr12	11869420	11869972	ETV6_exon_5	+	ETV6	ENSG00000139083	ENST00000396373
chr12	11884441	11884590	ETV6_exon_6	+	ETV6	ENSG00000139083	ENST00000396373
chr12	11885922	11886029	ETV6_exon_7	+	ETV6	ENSG00000139083	ENST00000396373
chr12	11890937	11891046	ETV6_exon_8	+	ETV6	ENSG00000139083	ENST00000396373
chr12	25227231	25227415	KRAS_exon_3	-	KRAS	ENSG00000133703	ENST00000256078
chr12	25245271	25245387	KRAS_exon_2	-	KRAS	ENSG00000133703	ENST00000256078
chr13	28018463	28018592	FLT3_exon_20	-	FLT3	ENSG00000122025	ENST00000241453
chr13	28033884	28033994	FLT3_exon_15	-	FLT3	ENSG00000122025	ENST00000241453
chr13	28034079	28034217	FLT3_exon_14	-	FLT3	ENSG00000122025	ENST00000241453
chr13	28034298	28034410	FLT3_exon_13	-	FLT3	ENSG00000122025	ENST00000241453
chr15	90088584	90088750	IDH2_exon_4	-	IDH2	ENSG00000182054	ENST00000330062
chr17	31095306	31095372	NF1_exon_1	+	NF1	ENSG00000196712	ENST00000358273
chr17	31155979	31156129	NF1_exon_2	+	NF1	ENSG00000196712	ENST00000358273
chr17	31159006	31159096	NF1_exon_3	+	NF1	ENSG00000196712	ENST00000358273
chr17	31163182	31163379	NF1_exon_4	+	NF1	ENSG00000196712	ENST00000358273
chr17	31169887	31170000	NF1_exon_5	+	NF1	ENSG00000196712	ENST00000358273
chr17	31181418	31181492	NF1_exon_6	+	NF1	ENSG00000196712	ENST00000358273
chr17	31181706	31181788	NF1_exon_7	+	NF1	ENSG00000196712	ENST00000358273
chr17	31182504	31182668	NF1_exon_8	+	NF1	ENSG00000196712	ENST00000358273
chr17	31200418	31200598	NF1_exon_9	+	NF1	ENSG00000196712	ENST00000358273
chr17	31201033	31201162	NF1_exon_10	+	NF1	ENSG00000196712	ENST00000358273
chr17	31201407	31201488	NF1_exon_11	+	NF1	ENSG00000196712	ENST00000358273
chr17	31206236	31206374	NF1_exon_12	+	NF1	ENSG00000196712	ENST00000358273
chr17	31214447	31214588	NF1_exon_13	+	NF1	ENSG00000196712	ENST00000358273
chr17	31219001	31219121	NF1_exon_14	+	NF1	ENSG00000196712	ENST00000358273
chr17	31221846	31221932	NF1_exon_15	+	NF1	ENSG00000196712	ENST00000358273
chr17	31223440	31223570	NF1_exon_16	+	NF1	ENSG00000196712	ENST00000358273
chr17	31225091	31225253	NF1_exon_17	+	NF1	ENSG00000196712	ENST00000358273
chr17	31226431	31226687	NF1_exon_18	+	NF1	ENSG00000196712	ENST00000358273
chr17	31227214	31227294	NF1_exon_19	+	NF1	ENSG00000196712	ENST00000358273
chr17	31227519	31227609	NF1_exon_20	+	NF1	ENSG00000196712	ENST00000358273
chr17	31229021	31229468	NF1_exon_21	+	NF1	ENSG00000196712	ENST00000358273
chr17	31229831	31229977	NF1_exon_22	+	NF1	ENSG00000196712	ENST00000358273
chr17	31230256	31230385	NF1_exon_23	+	NF1	ENSG00000196712	ENST00000358273
chr17	31230838	31230928	NF1_exon_24	+	NF1	ENSG00000196712	ENST00000358273
chr17	31232069	31232192	NF1_exon_25	+	NF1	ENSG00000196712	ENST00000358273
chr17	31232696	31232884	NF1_exon_26	+	NF1	ENSG00000196712	ENST00000358273
chr17	31232998	31233216	NF1_exon_27	+	NF1	ENSG00000196712	ENST00000358273
chr17	31235607	31235775	NF1_exon_28	+	NF1	ENSG00000196712	ENST00000358273
chr17	31235914	31236024	NF1_exon_29	+	NF1	ENSG00000196712	ENST00000358273
chr17	31248980	31249122	NF1_exon_30	+	NF1	ENSG00000196712	ENST00000358273
chr17	31252934	31253003	NF1_exon_31	+	NF1	ENSG00000196712	ENST00000358273
chr17	31258340	31258505	NF1_exon_32	+	NF1	ENSG00000196712	ENST00000358273
chr17	31259028	31259132	NF1_exon_33	+	NF1	ENSG00000196712	ENST00000358273
chr17	31260365	31260518	NF1_exon_34	+	NF1	ENSG00000196712	ENST00000358273
chr17	31261707	31261860	NF1_exon_35	+	NF1	ENSG00000196712	ENST00000358273
chr17	31265225	31265342	NF1_exon_36	+	NF1	ENSG00000196712	ENST00000358273
chr17	31325816	31326255	NF1_exon_37	+	NF1	ENSG00000196712	ENST00000358273
chr17	31327495	31327842	NF1_exon_38	+	NF1	ENSG00000196712	ENST00000358273
chr17	31330292	31330501	NF1_exon_39	+	NF1	ENSG00000196712	ENST00000358273
chr17	31334834	31335034	NF1_exon_40	+	NF1	ENSG00000196712	ENST00000358273
chr17	31336329	31336476	NF1_exon_41	+	NF1	ENSG00000196712	ENST00000358273

chr17	31336631	31336917	NF1_exon_42	+	NF1	ENSG00000196712	ENST00000358273
chr17	31337364	31337585	NF1_exon_43	+	NF1	ENSG00000196712	ENST00000358273
chr17	31337815	31337883	NF1_exon_44	+	NF1	ENSG00000196712	ENST00000358273
chr17	31338021	31338142	NF1_exon_45	+	NF1	ENSG00000196712	ENST00000358273
chr17	31338700	31338808	NF1_exon_46	+	NF1	ENSG00000196712	ENST00000358273
chr17	31340501	31340648	NF1_exon_47	+	NF1	ENSG00000196712	ENST00000358273
chr17	31343005	31343138	NF1_exon_48	+	NF1	ENSG00000196712	ENST00000358273
chr17	31349116	31349254	NF1_exon_49	+	NF1	ENSG00000196712	ENST00000358273
chr17	31350179	31350321	NF1_exon_50	+	NF1	ENSG00000196712	ENST00000358273
chr17	31352253	31352417	NF1_exon_51	+	NF1	ENSG00000196712	ENST00000358273
chr17	31356456	31356585	NF1_exon_52	+	NF1	ENSG00000196712	ENST00000358273
chr17	31356956	31357093	NF1_exon_53	+	NF1	ENSG00000196712	ENST00000358273
chr17	31357265	31357372	NF1_exon_54	+	NF1	ENSG00000196712	ENST00000358273
chr17	31358476	31358625	NF1_exon_55	+	NF1	ENSG00000196712	ENST00000358273
chr17	31358965	31359018	NF1_exon_56	+	NF1	ENSG00000196712	ENST00000358273
chr17	31360483	31360706	NF1_exon_57	+	NF1	ENSG00000196712	ENST00000358273
chr17	31374009	31374155	NF1_exon_58	+	NF1	ENSG00000196712	ENST00000358273
chr17	31937243	31937523	SUZ12_exon_1	+	SUZ12	ENSG00000178691	ENST00000322652
chr17	31940282	31940335	SUZ12_exon_2	+	SUZ12	ENSG00000178691	ENST00000322652
chr17	31940418	31940489	SUZ12_exon_3	+	SUZ12	ENSG00000178691	ENST00000322652
chr17	31947613	31947688	SUZ12_exon_4	+	SUZ12	ENSG00000178691	ENST00000322652
chr17	31966143	31966199	SUZ12_exon_5	+	SUZ12	ENSG00000178691	ENST00000322652
chr17	31973142	31973234	SUZ12_exon_6	+	SUZ12	ENSG00000178691	ENST00000322652
chr17	31975478	31975716	SUZ12_exon_7	+	SUZ12	ENSG00000178691	ENST00000322652
chr17	31976517	31976617	SUZ12_exon_8	+	SUZ12	ENSG00000178691	ENST00000322652
chr17	31982995	31983107	SUZ12_exon_9	+	SUZ12	ENSG00000178691	ENST00000322652
chr17	31988316	31988500	SUZ12_exon_10	+	SUZ12	ENSG00000178691	ENST00000322652
chr17	31993238	31993336	SUZ12_exon_11	+	SUZ12	ENSG00000178691	ENST00000322652
chr17	31993861	31994011	SUZ12_exon_12	+	SUZ12	ENSG00000178691	ENST00000322652
chr17	31994560	31994724	SUZ12_exon_13	+	SUZ12	ENSG00000178691	ENST00000322652
chr17	31995560	31995765	SUZ12_exon_14	+	SUZ12	ENSG00000178691	ENST00000322652
chr17	31996794	31996880	SUZ12_exon_15	+	SUZ12	ENSG00000178691	ENST00000322652
chr17	31998654	31999003	SUZ12_exon_16	+	SUZ12	ENSG00000178691	ENST00000322652
chr17	60662991	60663552	PPM1D_exon_6	+	PPM1D	ENSG00000170836	ENST00000305921
chr17	7669608	7669693	TP53_exon_11	-	TP53	ENSG00000141510	ENST00000269305
chr17	7670605	7670718	TP53_exon_10	-	TP53	ENSG00000141510	ENST00000269305
chr17	7673531	7673611	TP53_exon_9	-	TP53	ENSG00000141510	ENST00000269305
chr17	76736796	76737163	SRSF2_exon_1	-	SRSF2	ENSG00000161547	ENST00000392485
chr17	7673697	7673840	TP53_exon_8	-	TP53	ENSG00000141510	ENST00000269305
chr17	7674177	7674293	TP53_exon_7	-	TP53	ENSG00000141510	ENST00000269305
chr17	7674855	7674974	TP53_exon_6	-	TP53	ENSG00000141510	ENST00000269305
chr17	7675049	7675239	TP53_exon_5	-	TP53	ENSG00000141510	ENST00000269305
chr17	7675990	7676275	TP53_exon_4	-	TP53	ENSG00000141510	ENST00000269305
chr17	7676378	7676406	TP53_exon_3	-	TP53	ENSG00000141510	ENST00000269305
chr17	7676517	7676597	TP53_exon_2	-	TP53	ENSG00000141510	ENST00000269305
chr19	12943710	12943913	CALR_exon_9	+	CALR	ENSG00000179218	ENST00000316448
chr19	33301337	33302417	CEBPA_exon_1	-	CEBPA	ENSG00000245848	ENST00000498907
chr2	197392302	197392464	SF3B1_exon_25	-	SF3B1	ENSG00000115524	ENST00000335508
chr2	197392968	197393191	SF3B1_exon_24	-	SF3B1	ENSG00000115524	ENST00000335508
chr2	197396052	197396331	SF3B1_exon_23	-	SF3B1	ENSG00000115524	ENST00000335508
chr2	197397981	197398119	SF3B1_exon_22	-	SF3B1	ENSG00000115524	ENST00000335508
chr2	197398457	197398584	SF3B1_exon_21	-	SF3B1	ENSG00000115524	ENST00000335508
chr2	197400051	197400169	SF3B1_exon_20	-	SF3B1	ENSG00000115524	ENST00000335508
chr2	197400248	197400437	SF3B1_exon_19	-	SF3B1	ENSG00000115524	ENST00000335508
chr2	197400711	197400939	SF3B1_exon_18	-	SF3B1	ENSG00000115524	ENST00000335508
chr2	197401396	197401528	SF3B1_exon_17	-	SF3B1	ENSG00000115524	ENST00000335508
chr2	197401738	197401891	SF3B1_exon_16	-	SF3B1	ENSG00000115524	ENST00000335508
chr2	197401981	197402133	SF3B1_exon_15	-	SF3B1	ENSG00000115524	ENST00000335508
chr2	197402552	197402829	SF3B1_exon_14	-	SF3B1	ENSG00000115524	ENST00000335508
chr2	197402945	197403038	SF3B1_exon_13	-	SF3B1	ENSG00000115524	ENST00000335508
chr2	197403581	197403767	SF3B1_exon_12	-	SF3B1	ENSG00000115524	ENST00000335508
chr2	197405072	197405180	SF3B1_exon_11	-	SF3B1	ENSG00000115524	ENST00000335508
chr2	197405271	197405475	SF3B1_exon_10	-	SF3B1	ENSG00000115524	ENST00000335508
chr2	197407994	197408122	SF3B1_exon_9	-	SF3B1	ENSG00000115524	ENST00000335508
chr2	197408365	197408584	SF3B1_exon_8	-	SF3B1	ENSG00000115524	ENST00000335508
chr2	197409766	197410010	SF3B1_exon_7	-	SF3B1	ENSG00000115524	ENST00000335508
chr2	197416737	197416914	SF3B1_exon_6	-	SF3B1	ENSG00000115524	ENST00000335508
chr2	197418505	197418591	SF3B1_exon_5	-	SF3B1	ENSG00000115524	ENST00000335508
chr2	197420424	197420545	SF3B1_exon_4	-	SF3B1	ENSG00000115524	ENST00000335508
chr2	197421025	197421136	SF3B1_exon_3	-	SF3B1	ENSG00000115524	ENST00000335508
chr2	197423804	197423977	SF3B1_exon_2	-	SF3B1	ENSG00000115524	ENST00000335508
chr2	197434968	197435002	SF3B1_exon_1	-	SF3B1	ENSG00000115524	ENST00000335508
chr2	208248366	208248663	IDH1_exon_4	-	IDH1	ENSG00000138413	ENST00000415913
chr2	25234278	25234423	DNMT3A_exon_23	-	DNMT3A	ENSG00000119772	ENST00000264709
chr2	25235703	25235828	DNMT3A_exon_22	-	DNMT3A	ENSG00000119772	ENST00000264709
chr2	25236932	25237008	DNMT3A_exon_21	-	DNMT3A	ENSG00000119772	ENST00000264709
chr2	25239126	25239218	DNMT3A_exon_20	-	DNMT3A	ENSG00000119772	ENST00000264709
chr2	25240298	25240453	DNMT3A_exon_19	-	DNMT3A	ENSG00000119772	ENST00000264709
chr2	25240636	25240733	DNMT3A_exon_18	-	DNMT3A	ENSG00000119772	ENST00000264709
chr2	25241558	25241710	DNMT3A_exon_17	-	DNMT3A	ENSG00000119772	ENST00000264709
chr2	25243894	25243985	DNMT3A_exon_16	-	DNMT3A	ENSG00000119772	ENST00000264709
chr2	25244151	25244341	DNMT3A_exon_15	-	DNMT3A	ENSG00000119772	ENST00000264709
chr2	25244536	25244655	DNMT3A_exon_14	-	DNMT3A	ENSG00000119772	ENST00000264709
chr2	25245249	25245335	DNMT3A_exon_13	-	DNMT3A	ENSG00000119772	ENST00000264709
chr2	25246016	25246067	DNMT3A_exon_12	-	DNMT3A	ENSG00000119772	ENST00000264709
chr2	25246156	25246312	DNMT3A_exon_11	-	DNMT3A	ENSG00000119772	ENST00000264709
chr2	25246616	25246779	DNMT3A_exon_10	-	DNMT3A	ENSG00000119772	ENST00000264709
chr2	25247047	25247161	DNMT3A_exon_9	-	DNMT3A	ENSG00000119772	ENST00000264709
chr2	25247587	25247752	DNMT3A_exon_8	-	DNMT3A	ENSG00000119772	ENST00000264709
chr2	25248033	25248255	DNMT3A_exon_7	-	DNMT3A	ENSG00000119772	ENST00000264709
chr2	25274937	25275090	DNMT3A_exon_6	-	DNMT3A	ENSG00000119772	ENST00000264709
chr2	25275496	25275546	DNMT3A_exon_5	-	DNMT3A	ENSG00000119772	ENST00000264709
chr2	25282437	25282714	DNMT3A_exon_4	-	DNMT3A	ENSG00000119772	ENST00000264709
chr2	25300135	25300246	DNMT3A_exon_3	-	DNMT3A	ENSG00000119772	ENST00000264709
chr2	25313909	25313987	DNMT3A_exon_2	-	DNMT3A	ENSG00000119772	ENST00000264709
chr20	32358772	32358835	ASXL1_exon_1	+	ASXL1	ENSG00000171456	ENST00000375687
chr20	32366380	32366469	ASXL1_exon_2	+	ASXL1	ENSG00000171456	ENST00000375687
chr20	32367723	32367732	ASXL1_exon_3	+	ASXL1	ENSG00000171456	ENST00000375687
chr20	32369011	32369126	ASXL1_exon_4	+	ASXL1	ENSG00000171456	ENST00000375687
chr20	32428124	32428251	ASXL1_exon_5	+	ASXL1	ENSG00000171456	ENST00000375687
chr20	32428321	32428425	ASXL1_exon_6	+	ASXL1	ENSG00000171456	ENST00000375687
chr20	32429334	32429434	ASXL1_exon_7	+	ASXL1	ENSG00000171456	ENST00000375687
chr20	32429897	32430056	ASXL1_exon_8	+	ASXL1	ENSG00000171456	ENST00000375687
chr20	32431317	32431487	ASXL1_exon_9	+	ASXL1	ENSG00000171456	ENST00000375687
chr20	32431579	32431682	ASXL1_exon_10	+	ASXL1	ENSG00000171456	ENST00000375687
chr20	32432876	32432988	ASXL1_exon_11	+	ASXL1	ENSG00000171456	ENST00000375687
chr20	32433280	32433920	ASXL1_exon_12	+	ASXL1	ENSG00000171456	ENST00000375687
chr20	32434428	32437338	ASXL1_exon_13	+	ASXL1	ENSG00000171456	ENST00000375687
chr21	34792134	34792613	RUNX1_exon_8	-	RUNX1	ENSG00000159216	ENST00000300305
chr21	34799297	34799465	RUNX1_exon_7	-	RUNX1	ENSG00000159216	ENST00000300305
chr21	34834406	34834604	RUNX1_exon_6	-	RUNX1	ENSG00000159216	ENST00000300305
chr21	34859470	34859581	RUNX1_exon_5	-	RUNX1	ENSG00000159216	ENST00000300305
chr21	34880553	34880716	RUNX1_exon_4	-	RUNX1	ENSG00000159216	ENST00000300305
chr21	34886839	34887099	RUNX1_exon_3	-	RUNX1	ENSG00000159216	ENST00000300305
chr21	34892921	34892966	RUNX1_exon_2	-	RUNX1	ENSG00000159216	ENST00000300305
chr21	35048838	35048902	RUNX1_exon_1	-	RUNX1	ENSG00000159216	ENST00000300305
chr21	43094652	43094791	U2AF1_exon_6	-	U2AF1	ENSG00000160201	ENST00000291552
chr21	43104312	43104405	U2AF1_exon_2	-	U2AF1	ENSG00000160201	ENST00000291552
chr3	128481018	128481321	GATA2_exon_6	-	GATA2	ENSG00000179348	ENST00000341105
chr3	128481815	128481947	GATA2_exon_5	-	GATA2	ENSG00000179348	ENST00000341105
chr3	128483856	128484008	GATA2_exon_4	-	GATA2	ENSG00000179348	ENST00000341105
chr3	128485723	128486371	GATA2_exon_3	-	GATA2	ENSG00000179348	ENST00000341105
chr3	128486799	128487034	GATA2_exon_2	-	GATA2	ENSG00000179348	ENST00000341105
chr4	105233939	105237354	TET2_exon_3	+	TET2	ENSG00000168769	ENST00000540549
chr4	105241335	105241432	TET2_exon_4	+	TET2	ENSG00000168769	ENST00000540549
chr4	105242830	105242930	TET2_exon_5	+	TET2	ENSG00000168769	ENST00000540549

chr4	105243566	105243781	TET2_exon_6	+	TET2	ENSG00000168769	ENST00000540549
chr4	105259615	105259772	TET2_exon_7	+	TET2	ENSG00000168769	ENST00000540549
chr4	105261755	105261851	TET2_exon_8	+	TET2	ENSG00000168769	ENST00000540549
chr4	105269606	105269750	TET2_exon_9	+	TET2	ENSG00000168769	ENST00000540549
chr4	105272560	105272921	TET2_exon_10	+	TET2	ENSG00000168769	ENST00000540549
chr4	105275044	105276519	TET2_exon_11	+	TET2	ENSG00000168769	ENST00000540549
chr4	54695509	54695784	KIT_exon_2	+	KIT	ENSG00000157404	ENST00000288135
chr4	54723581	54723701	KIT_exon_8	+	KIT	ENSG00000157404	ENST00000288135
chr4	54725854	54726053	KIT_exon_9	+	KIT	ENSG00000157404	ENST00000288135
chr4	54727215	54727327	KIT_exon_10	+	KIT	ENSG00000157404	ENST00000288135
chr4	54727413	54727545	KIT_exon_11	+	KIT	ENSG00000157404	ENST00000288135
chr4	54728008	54728124	KIT_exon_13	+	KIT	ENSG00000157404	ENST00000288135
chr4	54733067	54733195	KIT_exon_17	+	KIT	ENSG00000157404	ENST00000288135
chr5	171410524	171410565	NPM1_exon_11	+	NPM1	ENSG00000181163	ENST00000296930
chr7	101816027	101816096	CUX1_exon_1	+	CUX1	ENSG00000257923	ENST00000360264
chr7	101916111	101916228	CUX1_exon_2	+	CUX1	ENSG00000257923	ENST00000360264
chr7	102028094	102028148	CUX1_exon_3	+	CUX1	ENSG00000257923	ENST00000360264
chr7	102070335	102070420	CUX1_exon_4	+	CUX1	ENSG00000257923	ENST00000360264
chr7	102097360	102097504	CUX1_exon_5	+	CUX1	ENSG00000257923	ENST00000360264
chr7	102104332	102104462	CUX1_exon_6	+	CUX1	ENSG00000257923	ENST00000360264
chr7	102111694	102111777	CUX1_exon_7	+	CUX1	ENSG00000257923	ENST00000360264
chr7	102115203	102115276	CUX1_exon_8	+	CUX1	ENSG00000257923	ENST00000360264
chr7	102158556	102158611	CUX1_exon_9	+	CUX1	ENSG00000257923	ENST00000360264
chr7	102170442	102170553	CUX1_exon_10	+	CUX1	ENSG00000257923	ENST00000360264
chr7	102178465	102178660	CUX1_exon_11	+	CUX1	ENSG00000257923	ENST00000360264
chr7	102189809	102189874	CUX1_exon_12	+	CUX1	ENSG00000257923	ENST00000360264
chr7	102193838	102193893	CUX1_exon_13	+	CUX1	ENSG00000257923	ENST00000360264
chr7	102195503	102195606	CUX1_exon_14	+	CUX1	ENSG00000257923	ENST00000360264
chr7	102196630	102197308	CUX1_exon_15	+	CUX1	ENSG00000257923	ENST00000360264
chr7	102198798	102198870	CUX1_exon_16	+	CUX1	ENSG00000257923	ENST00000360264
chr7	102200067	102200175	CUX1_exon_17	+	CUX1	ENSG00000257923	ENST00000360264
chr7	102201356	102202207	CUX1_exon_18	+	CUX1	ENSG00000257923	ENST00000360264
chr7	102204387	102204559	CUX1_exon_19	+	CUX1	ENSG00000257923	ENST00000360264
chr7	102205110	102205173	CUX1_exon_20	+	CUX1	ENSG00000257923	ENST00000360264
chr7	102227363	102227672	CUX1_exon_21	+	CUX1	ENSG00000257923	ENST00000360264
chr7	102234048	102234243	CUX1_exon_22	+	CUX1	ENSG00000257923	ENST00000360264
chr7	102239316	102239587	CUX1_exon_23	+	CUX1	ENSG00000257923	ENST00000360264
chr7	102248408	102249042	CUX1_exon_24	+	CUX1	ENSG00000257923	ENST00000360264
chr7	140753272	140753396	BRAF_exon_15	-	BRAF	ENSG00000157764	ENST00000288602
chr7	148807645	148807709	EZH2_exon_20	-	EZH2	ENSG00000106462	ENST00000320356
chr7	148809067	148809158	EZH2_exon_19	-	EZH2	ENSG00000106462	ENST00000320356
chr7	148809306	148809393	EZH2_exon_18	-	EZH2	ENSG00000106462	ENST00000320356
chr7	148810329	148810417	EZH2_exon_17	-	EZH2	ENSG00000106462	ENST00000320356
chr7	148811621	148811723	EZH2_exon_16	-	EZH2	ENSG00000106462	ENST00000320356
chr7	148813955	148814140	EZH2_exon_15	-	EZH2	ENSG00000106462	ENST00000320356
chr7	148814910	148815042	EZH2_exon_14	-	EZH2	ENSG00000106462	ENST00000320356
chr7	148815502	148815549	EZH2_exon_13	-	EZH2	ENSG00000106462	ENST00000320356
chr7	148816680	148816781	EZH2_exon_12	-	EZH2	ENSG00000106462	ENST00000320356
chr7	148817218	148817394	EZH2_exon_11	-	EZH2	ENSG00000106462	ENST00000320356
chr7	148817873	148818120	EZH2_exon_10	-	EZH2	ENSG00000106462	ENST00000320356
chr7	148819592	148819690	EZH2_exon_9	-	EZH2	ENSG00000106462	ENST00000320356
chr7	148826450	148826635	EZH2_exon_8	-	EZH2	ENSG00000106462	ENST00000320356
chr7	148827160	148827269	EZH2_exon_7	-	EZH2	ENSG00000106462	ENST00000320356
chr7	148828736	148828883	EZH2_exon_6	-	EZH2	ENSG00000106462	ENST00000320356
chr7	148829724	148829851	EZH2_exon_5	-	EZH2	ENSG00000106462	ENST00000320356
chr7	148832630	148832753	EZH2_exon_4	-	EZH2	ENSG00000106462	ENST00000320356
chr7	148846466	148846601	EZH2_exon_3	-	EZH2	ENSG00000106462	ENST00000320356
chr7	148847178	148847301	EZH2_exon_2	-	EZH2	ENSG00000106462	ENST00000320356
chr8	116847499	116847694	RAD21_exon_14	-	RAD21	ENSG00000164754	ENST00000297338
chr8	116848942	116849032	RAD21_exon_13	-	RAD21	ENSG00000164754	ENST00000297338
chr8	116850614	116850770	RAD21_exon_12	-	RAD21	ENSG00000164754	ENST00000297338
chr8	116851944	116852099	RAD21_exon_11	-	RAD21	ENSG00000164754	ENST00000297338
chr8	116852545	116852711	RAD21_exon_10	-	RAD21	ENSG00000164754	ENST00000297338
chr8	116854241	116854471	RAD21_exon_9	-	RAD21	ENSG00000164754	ENST00000297338
chr8	116856162	116856291	RAD21_exon_8	-	RAD21	ENSG00000164754	ENST00000297338
chr8	116856642	116856774	RAD21_exon_7	-	RAD21	ENSG00000164754	ENST00000297338
chr8	116857263	116857476	RAD21_exon_6	-	RAD21	ENSG00000164754	ENST00000297338
chr8	116858348	116858461	RAD21_exon_5	-	RAD21	ENSG00000164754	ENST00000297338
chr8	116861837	116861943	RAD21_exon_4	-	RAD21	ENSG00000164754	ENST00000297338
chr8	116863126	116863262	RAD21_exon_3	-	RAD21	ENSG00000164754	ENST00000297338
chr8	116866582	116866732	RAD21_exon_2	-	RAD21	ENSG00000164754	ENST00000297338
chr9	5069922	5070055	JAK2_exon_12	+	JAK2	ENSG00000096968	ENST00000381652
chr9	5073695	5073788	JAK2_exon_14	+	JAK2	ENSG00000096968	ENST00000381652
chrX	124022624	124022674	STAG2_exon_3	+	STAG2	ENSG00000101972	ENST00000218089
chrX	124025836	124025921	STAG2_exon_4	+	STAG2	ENSG00000101972	ENST00000218089
chrX	124030957	124031128	STAG2_exon_5	+	STAG2	ENSG00000101972	ENST00000218089
chrX	124037523	124037626	STAG2_exon_6	+	STAG2	ENSG00000101972	ENST00000218089
chrX	124042565	124042648	STAG2_exon_7	+	STAG2	ENSG00000101972	ENST00000218089
chrX	124045160	124045371	STAG2_exon_8	+	STAG2	ENSG00000101972	ENST00000218089
chrX	124047350	124047508	STAG2_exon_9	+	STAG2	ENSG00000101972	ENST00000218089
chrX	124049001	124049081	STAG2_exon_10	+	STAG2	ENSG00000101972	ENST00000218089
chrX	124050182	124050312	STAG2_exon_11	+	STAG2	ENSG00000101972	ENST00000218089
chrX	124051117	124051222	STAG2_exon_12	+	STAG2	ENSG00000101972	ENST00000218089
chrX	124051311	124051397	STAG2_exon_13	+	STAG2	ENSG00000101972	ENST00000218089
chrX	124056124	124056238	STAG2_exon_14	+	STAG2	ENSG00000101972	ENST00000218089
chrX	124057862	124057980	STAG2_exon_15	+	STAG2	ENSG00000101972	ENST00000218089
chrX	124061220	124061344	STAG2_exon_16	+	STAG2	ENSG00000101972	ENST00000218089
chrX	124061767	124061877	STAG2_exon_17	+	STAG2	ENSG00000101972	ENST00000218089
chrX	124062898	124062997	STAG2_exon_18	+	STAG2	ENSG00000101972	ENST00000218089
chrX	124063112	124063208	STAG2_exon_19	+	STAG2	ENSG00000101972	ENST00000218089
chrX	124063844	124064054	STAG2_exon_20	+	STAG2	ENSG00000101972	ENST00000218089
chrX	124065872	124065949	STAG2_exon_21	+	STAG2	ENSG00000101972	ENST00000218089
chrX	124066171	124066265	STAG2_exon_22	+	STAG2	ENSG00000101972	ENST00000218089
chrX	124066352	124066439	STAG2_exon_23	+	STAG2	ENSG00000101972	ENST00000218089
chrX	124068560	124068659	STAG2_exon_24	+	STAG2	ENSG00000101972	ENST00000218089
chrX	124071145	124071326	STAG2_exon_25	+	STAG2	ENSG00000101972	ENST00000218089
chrX	124076328	124076474	STAG2_exon_26	+	STAG2	ENSG00000101972	ENST00000218089
chrX	124077953	124078061	STAG2_exon_27	+	STAG2	ENSG00000101972	ENST00000218089
chrX	124081376	124081531	STAG2_exon_28	+	STAG2	ENSG00000101972	ENST00000218089
chrX	124083417	124083552	STAG2_exon_29	+	STAG2	ENSG00000101972	ENST00000218089
chrX	124086543	124086773	STAG2_exon_30	+	STAG2	ENSG00000101972	ENST00000218089
chrX	124090571	124090767	STAG2_exon_31	+	STAG2	ENSG00000101972	ENST00000218089
chrX	124090850	124090967	STAG2_exon_32	+	STAG2	ENSG00000101972	ENST00000218089
chrX	124094014	124094147	STAG2_exon_33	+	STAG2	ENSG00000101972	ENST00000218089
chrX	124095368	124095452	STAG2_exon_34	+	STAG2	ENSG00000101972	ENST00000218089
chrX	124100570	124100597	STAG2_exon_35	+	STAG2	ENSG00000101972	ENST00000218089
chrX	130005228	130005320	BCORL1_exon_1	+	BCORL1	ENSG00000085185	ENST00000540052
chrX	130012574	130012671	BCORL1_exon_2	+	BCORL1	ENSG00000085185	ENST00000540052
chrX	130012946	130016216	BCORL1_exon_3	+	BCORL1	ENSG00000085185	ENST00000540052
chrX	130020981	130021153	BCORL1_exon_4	+	BCORL1	ENSG00000085185	ENST00000540052
chrX	130022893	130022980	BCORL1_exon_5	+	BCORL1	ENSG00000085185	ENST00000540052
chrX	130024986	130025382	BCORL1_exon_6	+	BCORL1	ENSG00000085185	ENST00000540052
chrX	130028631	130028864	BCORL1_exon_7	+	BCORL1	ENSG00000085185	ENST00000540052
chrX	130037363	130037536	BCORL1_exon_8	+	BCORL1	ENSG00000085185	ENST00000540052
chrX	130039133	130039285	BCORL1_exon_9	+	BCORL1	ENSG00000085185	ENST00000540052
chrX	130050713	130050797	BCORL1_exon_10	+	BCORL1	ENSG00000085185	ENST00000540052
chrX	130051856	130052019	BCORL1_exon_11	+	BCORL1	ENSG00000085185	ENST00000540052
chrX	130055850	130056136	BCORL1_exon_12	+	BCORL1	ENSG00000085185	ENST00000540052
chrX	134377614	134377758	PHF6_exon_2	+	PHF6	ENSG00000156531	ENST00000332070
chrX	134378001	134378109	PHF6_exon_3	+	PHF6	ENSG00000156531	ENST00000332070
chrX	134393497	134393637	PHF6_exon_4	+	PHF6	ENSG00000156531	ENST00000332070
chrX	134393905	134393955	PHF6_exon_5	+	PHF6	ENSG00000156531	ENST00000332070
chrX	134413487	134413660	PHF6_exon_6	+	PHF6	ENSG00000156531	ENST00000332070
chrX	134413819	134413969	PHF6_exon_7	+	PHF6	ENSG00000156531	ENST00000332070
chrX	134415012	134415123	PHF6_exon_8	+	PHF6	ENSG00000156531	ENST00000332070
chrX	134417165	134417305	PHF6_exon_9	+	PHF6	ENSG00000156531	ENST00000332070

chrX	134425197	134425330	PHF6_exon_10	+	PHF6	ENSG00000156531	ENST00000332070
chrX	15321505	15321775	PIGA_exon_6	-	PIGA	ENSG00000165195	ENST00000333590
chrX	15324661	15324874	PIGA_exon_5	-	PIGA	ENSG00000165195	ENST00000333590
chrX	15325016	15325155	PIGA_exon_4	-	PIGA	ENSG00000165195	ENST00000333590
chrX	15325910	15326049	PIGA_exon_3	-	PIGA	ENSG00000165195	ENST00000333590
chrX	15331212	15331933	PIGA_exon_2	-	PIGA	ENSG00000165195	ENST00000333590
chrX	15790492	15790539	ZRSR2_exon_1	+	ZRSR2	ENSG00000169249	ENST00000307771
chrX	15790930	15791016	ZRSR2_exon_2	+	ZRSR2	ENSG00000169249	ENST00000307771
chrX	15799868	15799956	ZRSR2_exon_3	+	ZRSR2	ENSG00000169249	ENST00000307771
chrX	15803684	15803799	ZRSR2_exon_4	+	ZRSR2	ENSG00000169249	ENST00000307771
chrX	15804107	15804200	ZRSR2_exon_5	+	ZRSR2	ENSG00000169249	ENST00000307771
chrX	15808229	15808274	ZRSR2_exon_6	+	ZRSR2	ENSG00000169249	ENST00000307771
chrX	15809196	15809321	ZRSR2_exon_7	+	ZRSR2	ENSG00000169249	ENST00000307771
chrX	15815673	15815893	ZRSR2_exon_8	+	ZRSR2	ENSG00000169249	ENST00000307771
chrX	15818583	15818645	ZRSR2_exon_9	+	ZRSR2	ENSG00000169249	ENST00000307771
chrX	15820203	15820319	ZRSR2_exon_10	+	ZRSR2	ENSG00000169249	ENST00000307771
chrX	15822727	15823242	ZRSR2_exon_11	+	ZRSR2	ENSG00000169249	ENST00000307771
chrX	40052108	40052403	BCOR_exon_15	-	BCOR	ENSG00000183337	ENST00000378444
chrX	40053882	40054045	BCOR_exon_14	-	BCOR	ENSG00000183337	ENST00000378444
chrX	40054252	40054336	BCOR_exon_13	-	BCOR	ENSG00000183337	ENST00000378444
chrX	40055364	40055516	BCOR_exon_12	-	BCOR	ENSG00000183337	ENST00000378444
chrX	40057151	40057324	BCOR_exon_11	-	BCOR	ENSG00000183337	ENST00000378444
chrX	40062135	40062396	BCOR_exon_10	-	BCOR	ENSG00000183337	ENST00000378444
chrX	40062742	40063074	BCOR_exon_9	-	BCOR	ENSG00000183337	ENST00000378444
chrX	40063604	40063955	BCOR_exon_8	-	BCOR	ENSG00000183337	ENST00000378444
chrX	40064332	40064602	BCOR_exon_7	-	BCOR	ENSG00000183337	ENST00000378444
chrX	40070969	40071162	BCOR_exon_6	-	BCOR	ENSG00000183337	ENST00000378444
chrX	40071633	40071693	BCOR_exon_5	-	BCOR	ENSG00000183337	ENST00000378444
chrX	40072345	40075183	BCOR_exon_4	-	BCOR	ENSG00000183337	ENST00000378444
chrX	40076450	40076535	BCOR_exon_3	-	BCOR	ENSG00000183337	ENST00000378444
chrX	40077840	40077932	BCOR_exon_2	-	BCOR	ENSG00000183337	ENST00000378444
chrX	53380102	53380189	SMC1A_exon_25	-	SMC1A	ENSG00000072501	ENST00000322213
chrX	53380616	53380733	SMC1A_exon_24	-	SMC1A	ENSG00000072501	ENST00000322213
chrX	53381014	53381090	SMC1A_exon_23	-	SMC1A	ENSG00000072501	ENST00000322213
chrX	53382228	53382386	SMC1A_exon_22	-	SMC1A	ENSG00000072501	ENST00000322213
chrX	53382502	53382663	SMC1A_exon_21	-	SMC1A	ENSG00000072501	ENST00000322213
chrX	53383093	53383256	SMC1A_exon_20	-	SMC1A	ENSG00000072501	ENST00000322213
chrX	53394774	53394891	SMC1A_exon_19	-	SMC1A	ENSG00000072501	ENST00000322213
chrX	53396223	53396383	SMC1A_exon_18	-	SMC1A	ENSG00000072501	ENST00000322213
chrX	53396468	53396620	SMC1A_exon_17	-	SMC1A	ENSG00000072501	ENST00000322213
chrX	53399585	53399733	SMC1A_exon_16	-	SMC1A	ENSG00000072501	ENST00000322213
chrX	53403562	53403675	SMC1A_exon_15	-	SMC1A	ENSG00000072501	ENST00000322213
chrX	53403773	53403896	SMC1A_exon_14	-	SMC1A	ENSG00000072501	ENST00000322213
chrX	53405008	53405152	SMC1A_exon_13	-	SMC1A	ENSG00000072501	ENST00000322213
chrX	53405241	53405394	SMC1A_exon_12	-	SMC1A	ENSG00000072501	ENST00000322213
chrX	53405489	53405675	SMC1A_exon_11	-	SMC1A	ENSG00000072501	ENST00000322213
chrX	53405767	53405959	SMC1A_exon_10	-	SMC1A	ENSG00000072501	ENST00000322213
chrX	53409058	53409272	SMC1A_exon_9	-	SMC1A	ENSG00000072501	ENST00000322213
chrX	53409417	53409506	SMC1A_exon_8	-	SMC1A	ENSG00000072501	ENST00000322213
chrX	53411757	53411904	SMC1A_exon_7	-	SMC1A	ENSG00000072501	ENST00000322213
chrX	53411991	53412256	SMC1A_exon_6	-	SMC1A	ENSG00000072501	ENST00000322213
chrX	53412896	53413141	SMC1A_exon_5	-	SMC1A	ENSG00000072501	ENST00000322213
chrX	53413228	53413438	SMC1A_exon_4	-	SMC1A	ENSG00000072501	ENST00000322213
chrX	53414754	53414873	SMC1A_exon_3	-	SMC1A	ENSG00000072501	ENST00000322213
chrX	53414977	53415172	SMC1A_exon_2	-	SMC1A	ENSG00000072501	ENST00000322213
chrX	53422488	53422603	SMC1A_exon_1	-	SMC1A	ENSG00000072501	ENST00000322213

Coordinates are based on the GRCh38 human reference

Downloadable version can be found here: https://wustl.box.com/v/rapidclinicalwgs-tables1

Table S2. Recurrent SVs in AML and MDS.

Chrom1	Start1	End1	Chrom2	Start2	End2	Gene_Pair	Gene1_Strand	Gene2_Strand
chr1	3069210	3438621	chr1	2228694	2310119	PRDM16_SKI	+	+
chr1	110338505	110346677	chr22	40410280	40636685	RBM15_MRTFA	+	-
chr1	148808465	149032955	chr5	150113836	150155860	PDE4DIP_PDGFRB	+	-
chr1	154157317	154192058	chr5	150113836	150155860	TPM3_PDGFRB	-	-
chr1	186311651	186375325	chr8	38411138	38468834	TPR_FGFR1	-	-
chr1	221701423	221742176	chr1	3069210	3438621	DUSP10_PRDM16	-	+
chr1	234604268	234609525	chr17	40309193	40356796	IRF2BP2_RARA	-	+
chr10	134464	254626	chr17	51177424	51260066	ZMYND11_MBTD1	+	-
chr10	21524674	21743630	chr9	41890313	42129250	MLLT10_CNTNAP3B	+	-
chr10	21524674	21743630	chrX	41333347	41364472	MLLT10_DDX3X	+	+
chr10	32009009	32056431	chr4	54229096	54298247	KIF5B_PDGFRA	-	+
chr10	59788762	59906656	chr5	150113836	150155860	CCDC6_PDGFRB	-	-
chr10	74824935	75032284	chr16	3725053	3880726	KAT6B_CREBBP	+	-
chr10	94501433	94602098	chr8	2938098	4994972	HELLS_CSMD1	+	-
chr10	101130504	101137789	chr7	142299010	142813287	TLX1_TRB	+	+
chr10	102394109	102402529	chr6	117288299	117425855	NFKB2_ROS1	+	-
chr11	925808	1012245	chr14	52004802	52069228	AP2A2_NID2	+	-
chr11	3675009	3797792	chr11	3675009	3797792	NUP98_NUP98	-	-
chr11	3675009	3797792	chr11	108665024	108940930	NUP98_DDX10	-	+
chr11	3675009	3797792	chr11	118436463	118526832	NUP98_KMT2A	-	+
chr11	3675009	3797792	chr12	280128	389454	NUP98_KDM5A	-	-
chr11	3675009	3797792	chr17	7235027	7239506	NUP98_PHF23	-	-
chr11	3675009	3797792	chr2	176092890	176095938	NUP98_HOXD13	-	+
chr11	3675009	3797792	chr2	176107285	176109588	NUP98_HOXD11	-	+
chr11	3675009	3797792	chr20	41028817	41124487	NUP98_TOP1	-	+
chr11	3675009	3797792	chr3	87259403	87276587	NUP98_POU1F1	-	-
chr11	3675009	3797792	chr3	100401192	100456319	NUP98_LNP1	-	+
chr11	3675009	3797792	chr5	177133078	177300210	NUP98_NSD1	-	+
chr11	3675009	3797792	chr6	138773508	138793317	NUP98_CCDC28A	-	+
chr11	3675009	3797792	chr7	27162434	27165530	NUP98_HOXA9	-	-
chr11	3675009	3797792	chr7	27181514	27185216	NUP98_HOXA11	-	-
chr11	3675009	3797792	chr7	27194363	27200106	NUP98_HOXA13	-	-
chr11	3675009	3797792	chr8	38269696	38382272	NUP98_NSD3	-	-
chr11	3675009	3797792	chr9	15464065	15511019	NUP98_PSIP1	-	-
chr11	3675009	3797792	chr9	129665640	129722674	NUP98_PRRX2	-	+
chr11	3675009	3797792	chrX	150983285	150990775	NUP98_HMGB3	-	+
chr11	3855701	4093209	chr5	177133078	177300210	STIM1_NSD1	+	+
chr11	8106092	8169043	chr7	142299010	142813287	RIC3_TRB	-	+
chr11	8106092	8169043	chr7	142801040	142802748	RIC3_TRBC2	-	+
chr11	20156154	20160613	chr9	36833274	37034185	DBX1_PAX5	-	-
chr11	34051682	34101156	chr5	150113836	150155860	CAPRIN1_PDGFRB	+	-
chr11	59142747	59155039	chr6	135181314	135219171	FAM111A_MYB	+	+
chr11	62559600	62573973	chr6	73368554	73395093	EEF1G_OOEP	-	-
chr11	72002864	72080693	chr17	40309193	40356796	NUMA1_RARA	-	+
chr11	72814405	72843674	chr11	118436463	118526832	ATG16L2_KMT2A	+	+
chr11	85957687	86069097	chr10	21524674	21743630	PICALM_MLLT10	-	+
chr11	101451563	101583928	chr8	109240918	109334385	TRPC6_NUDCD1	-	-
chr11	114059592	114250676	chr17	40309193	40356796	ZBTB16_RARA	+	+
chr11	117427772	117797261	chr11	118436463	118526832	DSCAML1_KMT2A	-	+
chr11	117836980	117877486	chr11	118436463	118526832	FXYD6_KMT2A	-	+
chr11	118436463	118526832	chr1	51354262	51519328	KMT2A_EPS15	+	-
chr11	118436463	118526832	chr1	151057757	151068497	KMT2A_MLLT11	+	+
chr11	118436463	118526832	chr10	20783905	21174187	KMT2A_NEBL	+	-
chr11	118436463	118526832	chr10	21524674	21743630	KMT2A_MLLT10	+	+
chr11	118436463	118526832	chr10	26746595	26861087	KMT2A_ABI1	+	-
chr11	118436463	118526832	chr10	68560655	68694482	KMT2A_TET1	+	+
chr11	118436463	118526832	chr11	73308288	73369091	KMT2A_ARHGEF17	+	+
chr11	118436463	118526832	chr11	85957687	86069097	KMT2A_PICALM	+	-
chr11	118436463	118526832	chr11	95976597	96343180	KMT2A_MAML2	+	-
chr11	118436463	118526832	chr11	118436463	118526832	KMT2A_KMT2A	+	+
chr11	118436463	118526832	chr11	119206275	119308149	KMT2A_CBL	+	+
chr11	118436463	118526832	chr11	120337077	120489936	KMT2A_ARHGEF12	+	+
chr11	118436463	118526832	chr12	55757273	55817756	KMT2A_SARNP	+	-
chr11	118436463	118526832	chr14	66507406	67181803	KMT2A_GPHN	+	+
chr11	118436463	118526832	chr14	104865279	104896742	KMT2A_CEP170B	+	+
chr11	118436463	118526832	chr15	40594019	40664342	KMT2A_KNL1	+	+
chr11	118436463	118526832	chr15	40807088	40815084	KMT2A_ZFYVE19	+	+
chr11	118436463	118526832	chr16	3725053	3880726	KMT2A_CREBBP	+	-
chr11	118436463	118526832	chr17	9913849	10198551	KMT2A_GAS7	+	-
chr11	118436463	118526832	chr17	38705541	38729803	KMT2A_MLLT6	+	+
chr11	118436463	118526832	chr17	38869858	38921770	KMT2A_LASP1	+	+
chr11	118436463	118526832	chr17	40309193	40356796	KMT2A_RARA	+	+
chr11	118436463	118526832	chr19	4360369	4400547	KMT2A_SH3GL1	+	-
chr11	118436463	118526832	chr19	6210378	6279948	KMT2A_MLLT1	+	-
chr11	118436463	118526832	chr19	18442662	18522127	KMT2A_ELL	+	-
chr11	118436463	118526832	chr2	203328218	203447723	KMT2A_ABI2	+	+
chr11	118436463	118526832	chr22	41091785	41180079	KMT2A_EP300	+	+
chr11	118436463	118526832	chr3	48673843	48685927	KMT2A_NCKIPSD	+	-
chr11	118436463	118526832	chr3	108549868	108589452	KMT2A_CIP2A	+	-
chr11	118436463	118526832	chr3	155870535	155944026	KMT2A_GMPS	+	+
chr11	118436463	118526832	chr3	188212932	188890671	KMT2A_LPP	+	+
chr11	118436463	118526832	chr4	39822862	39977956	KMT2A_PDS5A	+	-
chr11	118436463	118526832	chr4	48497362	48780299	KMT2A_FRYL	+	-
chr11	118436463	118526832	chr4	52590971	52659335	KMT2A_USP46	+	-
chr11	118436463	118526832	chr4	76949808	77040384	KMT2A_SEPT11	+	+
chr11	118436463	118526832	chr4	86935001	87141054	KMT2A_AFF1	+	+
chr11	118436463	118526832	chr4	185585443	185956368	KMT2A_SORBS2	+	-
chr11	118436463	118526832	chr5	127517608	127555089	KMT2A_PRRC1	+	+
chr11	118436463	118526832	chr5	139274103	139331671	KMT2A_MATR3	+	+
chr11	118436463	118526832	chr5	142770376	143229011	KMT2A_ARHGAP26	+	+
chr11	118436463	118526832	chr5	160251656	160312928	KMT2A_CCNJL	+	-
chr11	118436463	118526832	chr6	70667775	70862015	KMT2A_SMAP1	+	+
chr11	118436463	118526832	chr6	89829899	89871412	KMT2A_CASP8AP2	+	+
chr11	118436463	118526832	chr6	108559834	108684774	KMT2A_FOXO3	+	+
chr11	118436463	118526832	chr6	136557046	136792518	KMT2A_MAP3K5	+	-
chr11	118436463	118526832	chr6	167826990	167972020	KMT2A_AFDN	+	+
chr11	118436463	118526832	chr7	5306789	5423546	KMT2A_TNRC18	+	-
chr11	118436463	118526832	chr7	87628412	87832296	KMT2A_RUNDC3B	+	+
chr11	118436463	118526832	chr9	20341664	20622543	KMT2A_MLLT3	+	-
chr11	118436463	118526832	chr9	96450200	96491336	KMT2A_HABP4	+	+
chr11	118436463	118526832	chr9	121567101	121785528	KMT2A_DAB2IP	+	+
chr11	118436463	118526832	chr9	129887186	130043194	KMT2A_FNBP1	+	-
chr11	118436463	118526832	chr9	131009081	131093059	KMT2A_LAMC3	+	+
chr11	118436463	118526832	chrX	71096196	71103535	KMT2A_FOXO4	+	+
chr11	118436463	118526832	chrX	119615723	119693370	KMT2A_SEPT6	+	-
chr11	118436463	118526832	chrX	135760156	135768191	KMT2A_CT45A3	+	-
chr11	118436463	118526832	chrX	135811980	135820012	KMT2A_CT45A2	+	-
chr11	118436463	118526832	chrX	154348525	154374638	KMT2A_FLNA	+	-
chr11	119206275	119308149	chr9	470290	746105	CBL_KANK1	+	+
chr11	122655674	122814473	chr7	23504779	23532041	UBASH3B_TRA2A	+	-
chr12	991207	1495933	chr5	150113836	150155860	ERC1_PDGFRB	+	-
chr12	6666476	6689510	chr5	64165881	64372869	ZNF384_RNF180	-	+
chr12	10158300	10172138	chrX	123859811	123913976	OLR1_XIAP	-	+
chr12	10170541	10191785	chrX	123859811	123913976	TMEM52B_XIAP	+	+
chr12	11649853	11895402	chr1	3069210	3438621	ETV6_PRDM16	+	+
chr12	11649853	11895402	chr1	179099326	179229601	ETV6_ABL2	+	-
chr12	11649853	11895402	chr10	99396869	99431569	ETV6_GOT1	+	-
chr12	11649853	11895402	chr12	11649853	11895402	ETV6_ETV6	+	+
chr12	11649853	11895402	chr12	56595595	56636366	ETV6_BAZ2A	+	-
chr12	11649853	11895402	chr12	70638081	70920843	ETV6_PTPRR	+	-
chr12	11649853	11895402	chr15	87859750	88256747	ETV6_NTRK3	+	-
chr12	11649853	11895402	chr17	8144054	8156360	ETV6_PER1	+	-
chr12	11649853	11895402	chr18	44680886	45068510	ETV6_SETBP1	+	+

chr12	11649853	11895402	chr3	41194740	41239949	ETV6_CTNNB1	+	+
chr12	11649853	11895402	chr3	169084760	169663470	ETV6_MECOM	+	-
chr12	11649853	11895402	chr4	54009788	54064690	ETV6_CHIC2	+	-
chr12	11649853	11895402	chr4	54229096	54298247	ETV6_PDGFRA	+	+
chr12	11649853	11895402	chr5	131949975	132011914	ETV6_ACSL6	+	-
chr12	11649853	11895402	chr5	150113836	150155860	ETV6_PDGFRB	+	-
chr12	11649853	11895402	chr5	158695919	159099761	ETV6_EBF1	+	-
chr12	11649853	11895402	chr6	115931148	116060758	ETV6_FRK	+	-
chr12	11649853	11895402	chr6	124962544	125092633	ETV6_RNF217	+	+
chr12	11649853	11895402	chr7	36389805	36453791	ETV6_ANLN	+	+
chr12	11649853	11895402	chr7	36854360	37449249	ETV6_ELMO1	+	-
chr12	11649853	11895402	chr8	55879834	56014168	ETV6_LYN	+	+
chr12	11649853	11895402	chr8	98454694	98942571	ETV6_STK3	+	-
chr12	11649853	11895402	chr9	4985244	5128183	ETV6_JAK2	+	+
chr12	11649853	11895402	chr9	90801786	90898549	ETV6_SYK	+	+
chr12	11649853	11895402	chr9	130713945	130885683	ETV6_ABL1	+	+
chr12	14365631	14502935	chr9	4985244	5128183	ATF7IP_JAK2	+	+
chr12	26938382	26966553	chr8	38411138	38468834	FGFR1OP2_FGFR1	+	-
chr12	48935722	48957551	chr6	149317533	149411395	ARF3_TAB2	-	+
chr12	49018974	49055324	chr4	82819010	82900538	KMT2D_SEC31A	-	-
chr12	51281281	51324668	chr5	150113836	150155860	BIN2_PDGFRB	-	-
chr12	53452101	53481161	chr9	131394092	131500197	PCBP2_PRRC2B	+	+
chr12	65824130	65966295	chr12	65824130	65966295	HMGA2_HMGA2	+	+
chr12	69239536	69274358	chr8	38411138	38468834	CPSF6_FGFR1	+	-
chr12	71754873	71800285	chr12	71839717	71927248	RAB21_TBC1D15	+	+
chr12	104456970	104762014	chrX	120362084	120383249	CHST11_ATP1B4	+	+
chr12	108522579	108561389	chr5	150113836	150155860	SART3_PDGFRB	-	-
chr12	109929801	109996389	chr5	150113836	150155860	GIT2_PDGFRB	-	-
chr12	117453053	117968983	chr3	4303303	4317567	KSR2_SETMAR	-	+
chr12	121429098	121581015	chr5	132875378	132963634	KDM2B_AFF4	-	-
chr12	121429098	121581015	chrY	13248378	13480673	KDM2B_UTY	-	-
chr12	124324414	124535603	chr6	117288299	117425855	NCOR2_ROS1	-	-
chr12	132489550	132585188	chr9	36833274	37034185	FBRSL1_PAX5	+	-
chr13	19958669	20091829	chr8	38411138	38468834	ZMYM2_FGFR1	+	-
chr13	48303725	48481890	chr7	15200317	15562015	RB1_AGMO	+	-
chr14	21621903	22552132	chr14	95709966	95714196	TRA_TCL1A	+	-
chr14	21621903	22552132	chr6	118460780	118710075	TRA_CEP85L	+	-
chr14	21621903	22552132	chr7	142299010	142813287	TRA_TRB	+	+
chr14	21621903	22552132	chr9	21968104	21995301	TRA_CDKN2A	+	-
chr14	21621903	22552132	chr9	136494432	136545786	TRA_NOTCH1	+	-
chr14	21621903	22552132	chrX	155065320	155147775	TRA_MTCP1	+	-
chr14	22422545	22466577	chr14	95709966	95714196	TRD_TCL1A	+	-
chr14	22422545	22466577	chr5	170861869	171300015	TRD_RANBP17	+	+
chr14	22422545	22466577	chr5	171309283	171312134	TRD_TLX3	+	+
chr14	22422545	22466577	chr5	173232108	173235357	TRD_NKX2-5	+	-
chr14	22422545	22466577	chr8	127736068	127741434	TRD_MYC	+	+
chr14	22422545	22466577	chr8	127890627	128101253	TRD_PVT1	+	+
chr14	22422545	22466577	chr9	77716086	78031458	TRD_GNAQ	+	-
chr14	30893798	31026401	chr9	4985244	5128183	STRN3_JAK2	-	+
chr14	50719762	50831121	chr5	150113836	150155860	NIN_PDGFRB	-	-
chr14	73958009	74015928	chr6	135283531	135497745	ENTPD5_AHI1	-	-
chr14	91271324	91417777	chr5	150113836	150155860	CCDC88C_PDGFRB	-	-
chr14	91965990	92040059	chr5	150113836	150155860	TRIP11_PDGFRB	-	-
chr14	99169286	99271485	chr14	99169286	99271485	BCL11B_BCL11B	-	-
chr14	99169286	99271485	chr5	173232108	173235357	BCL11B_NKX2-5	-	-
chr14	105586436	106879844	chr3	187721376	187745727	IGH_BCL6	-	-
chr14	105586436	106879844	chr4	190173773	190175845	IGH_DUX4	-	+
chr14	105586436	106879844	chr5	1253166	1295047	IGH_TERT	-	-
chr14	105586436	106879844	chr5	112976735	113020970	IGH_DCP2	-	+
chr14	105586436	106879844	chr5	158695919	159099761	IGH_EBF1	-	-
chr14	105586436	106879844	chr6	391738	411447	IGH_IRF4	-	+
chr14	105586436	106879844	chr7	55019100	55211628	IGH_EGFR	-	+
chr14	105586436	106879844	chr7	92468379	92477915	IGH_ERVW-1	-	-
chr14	105586436	106879844	chr7	110663053	111562517	IGH_IMMP2L	-	-
chr14	105586436	106879844	chr8	47736908	47739086	IGH_CEBPD	-	-
chr14	105586436	106879844	chr9	36833274	37034185	IGH_PAX5	-	-
chr14	105586436	106879844	chr9	124011609	124033301	IGH_LHX2	-	+
chr15	43407208	43510614	chr5	150113836	150155860	TP53BP1_PDGFRB	-	-
chr15	43510957	43531620	chr9	128947698	129007096	MAP1A_NUP188	+	+
chr15	73994728	74047812	chr17	40309193	40356796	PML_RARA	+	+
chr15	75370932	75455783	chr9	33524393	33573001	SIN3A_ANKRD18B	-	+
chr15	80947328	80989828	chrX	41514933	41923169	MESD_CASK	-	-
chr15	91853855	92172435	chr7	36854360	37449249	SLCO3A1_ELMO1	+	-
chr16	176679	177522	chr5	150401669	150412929	HBA1_CD74	+	-
chr16	3725053	3880726	chr7	142645960	142646467	CREBBP_TRBV23-1	-	+
chr16	3725053	3880726	chr8	41929478	42052026	CREBBP_KAT6A	-	-
chr16	10877197	10936388	chr9	5450502	5470566	CIITA_CD274	+	+
chr16	10877197	10936388	chr9	5510569	5571254	CIITA_PDCD1LG2	+	+
chr16	10877197	10936388	chr9	133097719	133149334	CIITA_RALGDS	+	-
chr16	11976737	12574289	chr9	4985244	5128183	SNX29_JAK2	+	+
chr16	15643266	15726353	chr5	150113836	150155860	NDE1_PDGFRB	+	-
chr16	31180109	31194871	chr21	38380029	38661780	FUS_ERG	+	-
chr16	31180109	31194871	chr9	128683654	128696400	FUS_SET	+	+
chr16	67029146	67101058	chr16	15703171	15857011	CBFB_MYH11	+	-
chr16	88874857	88977204	chr16	4314760	4339597	CBFA2T3_GLIS2	-	+
chr17	5282299	5385812	chr5	150113836	150155860	RABEP1_PDGFRB	+	-
chr17	16029156	16215549	chr8	55879834	56014168	NCOR1_LYN	-	+
chr17	17042759	17192648	chr5	150113836	150155860	MPRIP_PDGFRB	+	-
chr17	20009362	20314138	chr5	150113836	150155860	SPECC1_PDGFRB	+	-
chr17	27456469	27626435	chrX	124375902	124963817	KSR1_TENM1	+	-
chr17	29071123	29180412	chr5	150113836	150155860	MYO18A_PDGFRB	-	-
chr17	29071123	29180412	chr8	38411138	38468834	MYO18A_FGFR1	-	-
chr17	42199167	42276406	chr17	40309193	40356796	STAT5B_RARA	-	+
chr17	50183288	50201632	chr5	150113836	150155860	COL1A1_PDGFRB	-	-
chr17	50962173	51120865	chr9	4985244	5128183	SPAG9_JAK2	-	+
chr17	57256533	57684685	chr17	57256533	57684685	MSI2_MSI2	+	+
chr17	57256533	57684685	chr7	27162434	27165530	MSI2_HOXA9	+	-
chr17	68515399	68551319	chr17	40309193	40356796	PRKAR1A_RARA	+	+
chr17	80260867	80398786	chr8	127736068	127741434	RNF213_MYC	+	+
chr17	82519714	82604607	chr7	74289474	74405943	FOXK2_CLIP2	+	+
chr18	2847029	2915993	chr9	36833274	37034185	EMILIN2_PAX5	+	-
chr18	12785477	12884338	chr5	159263080	159286040	PTPN2_UBLCP1	-	+
chr18	58671385	58754477	chr3	47850695	48088839	MALT1_MAP4	+	-
chr19	2360237	2426239	chr9	36833274	37034185	TMPRSS9_PAX5	+	-
chr19	10718092	10831884	chr7	93188585	93226524	DNM2_HEPACAM2	+	-
chr19	13099032	13102867	chr7	142299010	142813287	LYL1_TRB	-	+
chr19	19385832	19508931	chr8	55879834	56014168	GATAD2A_LYN	+	+
chr19	21020619	21060050	chr9	4985244	5128183	ZNF430_JAK2	+	+
chr19	34172565	34229515	chr9	130713945	130885683	LSM14A_ABL1	+	+
chr19	44748546	44760044	chr8	127736068	127741434	BCL3_MYC	+	+
chr19	58183028	58213562	chr9	4985244	5128183	ZNF274_JAK2	+	+
chr19	58305318	58315663	chr8	38411138	38468834	ERVK3-1_FGFR1	+	-
chr2	32946971	33399359	chr2	32357027	32618899	LTBP1_BIRC6	+	+
chr2	43230835	43596046	chr3	169084760	169663470	THADA_MECOM	-	-
chr2	54456316	54671445	chr5	150113836	150155860	SPTBN1_PDGFRB	+	-
chr2	60450519	60554467	chr3	169084760	169663470	BCL11A_MECOM	-	-
chr2	108719480	108785811	chr2	29192773	29921566	RANBP2_ALK	+	-
chr2	108719480	108785811	chr8	38411138	38468834	RANBP2_FGFR1	+	-
chr2	108719480	108785811	chr9	130713945	130885683	RANBP2_ABL1	+	+
chr2	191678135	191696659	chr17	40309193	40356796	NABP1_RARA	+	+
chr2	237627575	237780315	chr8	38411138	38468834	LRRFIP1_FGFR1	+	-
chr20	18587892	18763917	chr5	150113836	150155860	DTD1_PDGFRB	+	-
chr20	32277663	32335011	chr7	142299010	142813287	KIF3B_TRB	+	+
chr20	34714773	34825649	chr8	70051650	70071327	NCOA6_PRDM14	-	-
chr20	44496223	44522085	chr9	37120538	37358149	SERINC3_ZCCHC7	-	+
chr20	47209213	47356889	chr5	150113836	150155860	ZMYND8_PDGFRB	-	-

chr20	52051662	52191779	chr21	34787800	35049344	ZFP64_RUNX1	-	-
chr21	14961234	15065000	chr3	169084760	169663470	NRIP1_MECOM	-	-
chr21	15730024	15880069	chr9	4985244	5128183	USP25_JAK2	+	+
chr21	29024628	29054488	chr21	34787800	35049344	USP16_RUNX1	+	-
chr21	34516483	34615142	chr4	123396794	123403760	RCAN1_SPRY1	-	+
chr21	34787800	35049344	chr1	3069210	3438621	RUNX1_PRDM16	-	+
chr21	34787800	35049344	chr1	28736620	28769774	RUNX1_YTHDF2	-	+
chr21	34787800	35049344	chr1	86424085	86456558	RUNX1_CLCA2	-	+
chr21	34787800	35049344	chr1	151282311	151291903	RUNX1_ZNF687	-	+
chr21	34787800	35049344	chr11	33542274	33674102	RUNX1_KIAA1549L	-	+
chr21	34787800	35049344	chr11	58526870	58578166	RUNX1_LPXN	-	-
chr21	34787800	35049344	chr11	63998557	64166061	RUNX1_MACROD1	-	-
chr21	34787800	35049344	chr16	88874857	88977204	RUNX1_CBFA2T3	-	-
chr21	34787800	35049344	chr21	34787800	35049344	RUNX1_RUNX1	-	-
chr21	34787800	35049344	chr3	169084760	169663470	RUNX1_MECOM	-	-
chr21	34787800	35049344	chr3	169483670	169484080	RUNX1_RPL22P1	-	-
chr21	34787800	35049344	chr4	151120286	151325632	RUNX1_SH3D19	-	-
chr21	34787800	35049344	chr5	127517608	127555089	RUNX1_PRRC1	-	+
chr21	34787800	35049344	chr5	129460264	129738683	RUNX1_ADAMTS19	-	+
chr21	34787800	35049344	chr6	17582033	17582305	RUNX1_SUMO2P13	-	+
chr21	34787800	35049344	chr7	6104883	6161564	RUNX1_USP42	-	+
chr21	34787800	35049344	chr7	27242699	27247825	RUNX1_EVX1	-	+
chr21	34787800	35049344	chr8	91954966	92103226	RUNX1_RUNX1T1	-	-
chr21	34787800	35049344	chr8	105318691	105804532	RUNX1_ZFPM2	-	+
chr21	34787800	35049344	chr8	115408495	115669001	RUNX1_TRPS1	-	-
chr21	34787800	35049344	chrX	23667445	23686399	RUNX1_PRDX4	-	+
chr21	38380029	38661780	chr4	190173773	190175845	ERG_DUX4	-	+
chr21	42653749	42775509	chr8	85656441	85663039	PDE9A_REXO1L1P	+	-
chr22	22026075	22922913	chr4	1793292	1808872	IGL_FGFR3	+	+
chr22	22026075	22922913	chr6	391738	411447	IGL_IRF4	+	+
chr22	22026075	22922913	chr6	41934933	42050357	IGL_CCND3	+	-
chr22	22026075	22922913	chr8	127890627	128101253	IGL_PVT1	+	+
chr22	23180209	23318037	chr4	54229096	54298247	BCR_PDGFRA	+	+
chr22	23180209	23318037	chr8	38411138	38468834	BCR_FGFR1	+	-
chr22	23180209	23318037	chr9	4985244	5128183	BCR_JAK2	+	+
chr22	23180209	23318037	chr9	126914773	127223164	BCR_RALGPS1	+	+
chr22	23180209	23318037	chr9	130713945	130885683	BCR_ABL1	+	+
chr22	41091785	41180079	chr7	27153715	27156677	EP300_HOXA7	+	-
chr3	9397718	9478154	chr7	50304668	50405101	SETD5_IKZF1	+	+
chr3	10115591	10127190	chr3	10141007	10152220	BRK1_VHL	+	+
chr3	12583600	12664226	chr3	12734706	12769457	RAF1_TMEM40	-	-
chr3	15560703	15601852	chr3	15450132	15521751	HACL1_COLQ	-	-
chr3	15667235	15859771	chr11	3675009	3797792	ANKRD28_NUP98	-	-
chr3	16315855	16513706	chr8	127890627	128101253	RFTN1_PVT1	-	+
chr3	28241594	28325142	chr3	27372720	27484420	CMC1_SLC4A7	+	-
chr3	30606501	30694134	chr19	4044363	4066945	TGFBR2_ZBTB7A	+	-
chr3	37243176	37366751	chr5	150113836	150155860	GOLGA4_PDGFRB	+	-
chr3	37988058	38007188	chr9	137007233	137028922	VILL_ABCA2	+	-
chr3	39051997	39096388	chr5	150113836	150155860	WDR48_PDGFRB	+	-
chr3	47016688	47163967	chr3	46921730	46982010	SETD2_CCDC12	-	-
chr3	47585271	47781917	chr17	47970533	47981772	SMARCC1_CDK5RAP3	-	+
chr3	47850695	48088839	chr18	58671385	58754477	MAP4_MALT1	-	+
chr3	48599002	48610037	chr3	43365847	43622068	UQCRC1_ANO10	-	-
chr3	48673843	48685927	chr3	48636468	48662915	NCKIPSD_CELSR3	-	-
chr3	49940006	50077249	chr5	150053290	150113372	RBM6_CSF1R	+	-
chr3	100609588	100695479	chr3	100709360	100748942	ADGRG7_TFG	+	+
chr3	100709360	100748942	chr3	100609588	100695479	TFG_ADGRG7	+	+
chr3	101324204	101513184	chr12	11649853	11895402	SENP7_ETV6	-	+
chr3	121663202	121749767	chr13	28003273	28100592	GOLGB1_FLT3	-	-
chr3	121663202	121749767	chr5	150113836	150155860	GOLGB1_PDGFRB	-	-
chr3	128479426	128493185	chr3	169084760	169663470	GATA2_MECOM	-	-
chr3	128479426	128493185	chr7	27162434	27165530	GATA2_HOXA9	-	-
chr3	128479426	128493185	chr7	27171219	27180261	GATA2_HOXA10	-	-
chr3	128571999	128576086	chr3	169084760	169663470	LINC01565_MECOM	-	-
chr3	128620158	128681075	chr1	3069210	3438621	RPN1_PRDM16	-	+
chr3	128620158	128681075	chr3	169084760	169663470	RPN1_MECOM	-	-
chr3	134157132	134250744	chr21	33903452	33915980	RYK_ATP5PO	-	-
chr3	136148921	136195846	chr3	177019354	177196478	MSL2_TBL1XR1	-	-
chr3	152268039	152465779	chr9	36833274	37034185	MBNL1_PAX5	+	-
chr3	152268039	152465779	chr9	130713945	130885683	MBNL1_ABL1	+	+
chr3	160494994	160565588	chr9	109640787	109946703	KPNA4_PALM2	-	+
chr3	169084760	169663470	chr21	34787800	35049344	MECOM_RUNX1	-	-
chr3	169084760	169663470	chr3	169084760	169663470	MECOM_MECOM	-	-
chr3	169084760	169663470	chr7	92604920	92833917	MECOM_CDK6	-	-
chr3	169084760	169663470	chr7	142299010	142813287	MECOM_TRB	-	+
chr3	172040553	172401665	chr3	169084760	169663470	FNDC3B_MECOM	+	-
chr3	177019354	177196478	chr17	40309193	40356796	TBL1XR1_RARA	-	+
chr3	177019354	177196478	chr3	139357405	139389732	TBL1XR1_COPB2	-	-
chr3	177019354	177196478	chr3	189631426	189897279	TBL1XR1_TP63	-	+
chr3	177019354	177196478	chr5	150053290	150113372	TBL1XR1_CSF1R	-	-
chr3	180912301	180982753	chr3	177019354	177196478	FXR1_TBL1XR1	+	-
chr3	186147200	186362237	chr4	15703095	15732787	DGKG_BST1	-	+
chr3	187721376	187745727	chr13	46125919	46211348	BCL6_LCP1	-	-
chr3	187721376	187745727	chr16	10877197	10936388	BCL6_CIITA	-	+
chr3	187721376	187745727	chr19	6677703	6720682	BCL6_C3	-	-
chr3	187721376	187745727	chr3	152268039	152465779	BCL6_MBNL1	-	+
chr3	187721376	187745727	chr6	37170202	37175426	BCL6_PIM1	-	+
chr3	187721376	187745727	chr8	66562174	66613249	BCL6_MYBL1	-	-
chr3	188212932	188890671	chr3	187721376	187745727	LPP_BCL6	+	-
chr3	189631426	189897279	chr3	177019354	177196478	TP63_TBL1XR1	+	-
chr4	1009978	1026891	chr4	1211447	1249137	FGFRL1_CTBP1	+	-
chr4	1289850	1340137	chr4	1211447	1249137	MAEA_CTBP1	+	-
chr4	1347315	1395989	chr4	1289850	1340137	UVSSA_MAEA	+	+
chr4	26860690	27025381	chr7	50304668	50405101	STIM2_IKZF1	+	+
chr4	53377644	53459668	chr17	40309193	40356796	FIP1L1_RARA	+	+
chr4	53377644	53459668	chr4	54229096	54298247	FIP1L1_PDGFRA	+	+
chr4	54009788	54064690	chr12	11649853	11895402	CHIC2_ETV6	-	+
chr4	54229096	54298247	chr10	91798311	91865276	PDGFRA_TNKS2	+	+
chr4	54229096	54298247	chr12	11649853	11895402	PDGFRA_ETV6	+	+
chr4	67468747	67545606	chr9	130713945	130885683	CENPC_ABL1	-	+
chr4	78776377	78912185	chr12	6666476	6689510	BMP2K_ZNF384	+	-
chr4	81087369	81215117	chr5	150113836	150155860	PRKG2_PDGFRB	-	-
chr4	86935001	87141054	chr11	117427772	117797261	AFF1_DSCAML1	+	-
chr4	86935001	87141054	chr11	117836980	117877486	AFF1_FXYD6	+	-
chr4	86935001	87141054	chr11	118998141	119015745	AFF1_CCDC84	+	+
chr4	86935001	87141054	chr14	67819828	68730218	AFF1_RAD51B	+	+
chr4	88592422	88708542	chr4	88709788	88730103	HERC3_FAM13A-AS1	+	+
chr4	108047544	108168956	chr6	42050521	42087461	LEF1_TAF8	-	+
chr4	139716752	140154184	chr4	77157150	77170059	MAML3_CCNG2	-	+
chr4	150264658	151015727	chr4	151120286	151325632	LRBA_SH3D19	-	-
chr4	158124473	158173050	chr4	158210248	158255411	FAM198B_TMEM144	-	+
chr4	190173773	190175845	chr10	133623894	133626792	DUX4_FRG2B	+	-
chr4	190173773	190175845	chr14	105586436	106879844	DUX4_IGH	+	-
chr4	190173773	190175845	chr21	38380029	38661780	DUX4_ERG	+	-
chr4	190173773	190175845	chr4	118467589	118554100	DUX4_CEP170P1	+	+
chr5	864272	892824	chr15	34343314	34357737	BRD9_NUTM1	-	+
chr5	35856848	35879603	chr7	142801040	142802748	IL7R_TRBC2	+	+
chr5	36876758	37066413	chr12	11649853	11895402	NIPBL_ETV6	+	+
chr5	36876758	37066413	chr17	48621158	48626356	NIPBL_HOXB9	+	-
chr5	36876758	37066413	chr7	27162434	27165530	NIPBL_HOXA9	+	-
chr5	40759378	40798198	chr5	40512332	40755908	PRKAA1_TTC33	-	-
chr5	55307759	55425581	chr11	116843401	117098421	MTREX_SIK3	+	-
chr5	56815573	56896152	chr16	58157906	58197920	MAP3K1_CSNK2A2	+	-
chr5	64165881	64372869	chr15	85380714	85749355	RNF180_AKAP13	+	+
chr5	65517765	65563171	chr11	118436463	118526832	CENPK_KMT2A	-	+
chr5	81413020	81751253	chr5	108747821	109196841	SSBP2_FER	-	+

chr5	81413020	81751253	chr5	150053290	150113372	SSBP2_CSF1R	-	-
chr5	83940553	84384793	chr7	131110095	131487844	EDIL3_MKLN1	-	+
chr5	88718240	88904257	chr11	118436463	118526832	MEF2C_KMT2A	-	+
chr5	98853984	98928957	chr21	34787800	35049344	CHD1_RUNX1	-	-
chr5	112976735	113020970	chr14	61695539	61748258	DCP2_HIF1A	+	+
chr5	122774995	122830108	chr9	130713945	130885683	SNX2_ABL1	+	+
chr5	132060528	132063204	chr14	105586436	106879844	IL3_IGH	+	-
chr5	134148934	134177038	chr5	132875378	132963634	SKP1_AFF4	-	-
chr5	140691425	140699318	chr5	140700333	140706676	HARS2_ZMAT2	+	+
chr5	141639301	141651419	chr7	140719326	140924810	FCHSD1_BRAF	-	-
chr5	144158158	144170659	chr5	143277930	143435512	YIPF5_NR3C1	-	-
chr5	150113836	150155860	chr14	91271324	91417777	PDGFRB_CCDC88C	-	-
chr5	150113836	150155860	chr14	91965990	92040059	PDGFRB_TRIP11	-	-
chr5	150113836	150155860	chr17	29071123	29180412	PDGFRB_MYO18A	-	-
chr5	150113836	150155860	chr20	18587892	18763917	PDGFRB_DTD1	-	+
chr5	150401669	150412929	chr5	150113836	150155860	CD74_PDGFRB	-	-
chr5	151029948	151087158	chr5	150113836	150155860	TNIP1_PDGFRB	-	-
chr5	157785742	157859145	chr5	88718240	88904257	CLINT1_MEF2C	-	-
chr5	158695919	159099761	chr9	4985244	5128183	EBF1_JAK2	-	+
chr5	170861869	171300015	chr14	22422545	22466577	RANBP17_TRD	+	+
chr5	171309283	171312134	chr14	99169286	99271485	TLX3_BCL11B	+	-
chr5	171387115	171410883	chr17	40309193	40356796	NPM1_RARA	+	+
chr5	171387115	171410883	chr19	10350532	10380676	NPM1_TYK2	+	-
chr5	171387115	171410883	chr3	158571162	158606460	NPM1_MLF1	+	+
chr5	172983756	173035445	chr12	62260337	62416389	ATP6V0E1_USP15	+	+
chr5	173056351	173139284	chr14	96392110	96489427	CREBRF_AK7	+	+
chr5	177133078	177300210	chr11	3675009	3797792	NSD1_NUP98	+	-
chr5	177133078	177300210	chr11	61792636	61797244	NSD1_FEN1	+	+
chr5	177331561	177351852	chr14	96502372	96567111	LMAN2_PAPOLA	-	+
chr5	177331561	177351852	chr5	177133078	177300210	LMAN2_NSD1	-	+
chr5	179614178	179624669	chr10	21524674	21743630	HNRNPH1_MLLT10	-	+
chr5	179614178	179624669	chr21	38380029	38661780	HNRNPH1_ERG	-	-
chr5	179820758	179838078	chr8	38411138	38468834	SQSTM1_FGFR1	+	-
chr5	179820758	179838078	chr9	131125560	131234670	SQSTM1_NUP214	+	+
chr6	5998001	6007605	chr19	2511218	2702709	NRN1_GNG7	-	-
chr6	17615034	17706834	chr9	130713945	130885683	NUP153_ABL1	-	+
chr6	18223867	18264823	chr9	131125560	131234670	DEK_NUP214	-	+
chr6	31676739	31680377	chr6	31686948	31703444	LY6G5C_ABHD16A	-	-
chr6	33620364	33696574	chr6	36243202	36308595	ITPR3_PNPLA1	+	+
chr6	39299000	39314553	chr6	39329989	39725405	KCNK17_KIF6	-	-
chr6	41934933	42050357	chr12	11649853	11895402	CCND3_ETV6	-	+
chr6	44219504	44234151	chr6	44246165	44253888	SLC29A1_HSP90AB1	+	+
chr6	45898450	46080348	chr6	44828731	45377933	CLIC5_SUPT3H	-	-
chr6	69675950	69867236	chr20	41402100	41618494	LMBRD1_CHD6	-	-
chr6	75602046	75718278	chr6	123804140	124825657	SENP6_NKAIN2	+	+
chr6	85660949	85678748	chr6	85505495	85593913	SNHG5_SNX14	-	-
chr6	89926528	90296908	chr11	19117128	19176415	BACH2_ZDHHC13	-	+
chr6	106969830	106975465	chrX	48574523	48579066	CD24_RBM3	-	+
chr6	115931148	116060758	chr12	11649853	11895402	FRK_ETV6	-	+
chr6	124962544	125092633	chr12	11649853	11895402	RNF217_ETV6	+	+
chr6	130013698	130141449	chr6	127968778	128520674	L3MBTL3_PTPRK	+	-
chr6	135181314	135219171	chr16	89644430	89657845	MYB_CHMP1A	+	-
chr6	135181314	135219171	chr5	71455614	71567820	MYB_BDP1	+	+
chr6	135181314	135219171	chr6	135283531	135497745	MYB_AHI1	+	-
chr6	135181314	135219171	chr6	143940301	144064599	MYB_PLAGL1	+	-
chr6	135181314	135219171	chr7	156994050	157009075	MYB_MNX1	+	-
chr6	135181314	135219171	chrX	48786553	48794308	MYB_GATA1	+	+
chr6	138773508	138793317	chr11	3675009	3797792	CCDC28A_NUP98	+	-
chr6	143060853	143340290	chr17	30477361	30527592	AIG1_GOSR1	+	+
chr6	144291828	144853034	chr14	73958009	74015928	UTRN_ENTPD5	+	-
chr6	156776019	157210779	chr12	6666476	6689510	ARID1B_ZNF384	+	-
chr6	166999181	167052713	chr10	43077026	43130351	FGFR1OP_RET	+	+
chr6	166999181	167052713	chr8	38411138	38468834	FGFR1OP_FGFR1	+	-
chr6	167826990	167972020	chr11	118436463	118526832	AFDN_KMT2A	+	+
chr7	876551	896434	chr7	5306789	5423546	GET4_TNRC18	+	-
chr7	2631950	2664802	chr7	1815793	2233243	TTYH3_MAD1L1	+	-
chr7	5190187	5233826	chr12	112013315	112023451	WIPI2_ERP29	+	+
chr7	6374522	6403977	chr6	75084325	75206051	RAC1_COL12A1	+	-
chr7	10931950	10940256	chr7	12570685	12660179	NDUFA4_SCIN	-	+
chr7	16646130	16706523	chr7	65960683	65982314	BZW2_GUSB	+	-
chr7	27162434	27165530	chr8	107251511	107336522	HOXA9_ANGPT1	-	-
chr7	27168898	27171915	chr6	109366513	109382812	HOXA10-AS_CD164	+	-
chr7	27171219	27180261	chr19	1086578	1095357	HOXA10_POLR2E	-	-
chr7	27171219	27180261	chr7	142299010	142813287	HOXA10_TRB	-	+
chr7	27181514	27185216	chr7	16646130	16706523	HOXA11_BZW2	-	+
chr7	27184670	27189169	chr7	92604920	92833917	HOXA11-AS_CDK6	+	-
chr7	27201843	27207259	chr3	18347939	18438773	HOTTIP_SATB1	+	-
chr7	30289793	30289890	chr7	30284306	30367692	MIR550A1_ZNRF2	+	+
chr7	34928875	35038041	chr7	27181514	27185216	DPY19L1_HOXA11	-	-
chr7	37683871	37741374	chr15	52756988	52790012	GPR141_ONECUT1	+	-
chr7	38240023	38368055	chr14	95709966	95714196	TRG_TCL1A	-	-
chr7	40126022	40134652	chr6	27866848	27867529	MPLKIP_HIST1H1B	-	-
chr7	43112598	43566001	chr5	150113836	150155860	HECW1_PDGFRB	+	-
chr7	45736786	45765812	chr7	56011066	56051604	SEPT7P2_PSPH	-	-
chr7	50304668	50405101	chr1	3069210	3438621	IKZF1_PRDM16	+	+
chr7	50304668	50405101	chr12	11649853	11895402	IKZF1_ETV6	+	+
chr7	50304668	50405101	chr12	55966768	55972784	IKZF1_CDK2	+	+
chr7	50304668	50405101	chr15	34343314	34357737	IKZF1_NUTM1	+	+
chr7	50304668	50405101	chr17	16415541	16437003	IKZF1_TRPV2	+	+
chr7	50304668	50405101	chr3	9397718	9478154	IKZF1_SETD5	+	+
chr7	50304668	50405101	chr7	48171459	48647495	IKZF1_ABCA13	+	+
chr7	50590062	50793462	chr7	3301447	4269000	GRB10_SDK1	-	+
chr7	66114604	66154561	chr10	96593311	96720514	CRCP_PIK3AP1	+	-
chr7	74657684	74760692	chr17	40309193	40356796	GTF2I_RARA	+	+
chr7	75533299	75738947	chr5	150113836	150155860	HIP1_PDGFRB	-	-
chr7	92560792	92590393	chr7	92604920	92833917	FAM133B_CDK6	-	-
chr7	92604920	92833917	chr11	118436463	118526832	CDK6_KMT2A	-	+
chr7	92604920	92833917	chr14	36516416	36521149	CDK6_NKX2-1	-	-
chr7	92604920	92833917	chr3	169084760	169663470	CDK6_MECOM	-	-
chr7	92604920	92833917	chr5	171309283	171312134	CDK6_TLX3	-	+
chr7	92604920	92833917	chr7	27269356	27269678	CDK6_RPL35P4	-	-
chr7	99472892	99503650	chr7	99493239	99500297	ZNF789_ZNF394	+	-
chr7	100852752	100867008	chr6	135181314	135219171	SLC12A9_MYB	+	+
chr7	101815903	102283958	chr4	73436162	73456174	CUX1_AFP	+	+
chr7	101815903	102283958	chr7	149126415	149182802	CUX1_ZNF398	+	+
chr7	101815903	102283958	chr8	38411138	38468834	CUX1_FGFR1	+	-
chr7	107923817	108003255	chr7	116862472	116922049	LAMB1_CAPZA2	-	+
chr7	116862472	116922049	chr19	58544468	58550716	CAPZA2_TRIM28	+	+
chr7	138460333	138589993	chr8	38411138	38468834	TRIM24_FGFR1	+	-
chr7	139043519	139109648	chr13	42272152	42323267	ZC3HAV1_AKAP11	-	+
chr7	142299010	142813287	chr10	101130504	101137789	TRB_TLX1	+	+
chr7	142299010	142813287	chr11	8224313	8268716	TRB_LMO1	+	-
chr7	142299010	142813287	chr14	95709966	95714196	TRB_TCL1A	+	-
chr7	142299010	142813287	chr22	37125837	37149990	TRB_IL2RB	+	-
chr7	142299010	142813287	chr3	169084760	169663470	TRB_MECOM	+	-
chr7	142299010	142813287	chr7	27162434	27165530	TRB_HOXA9	+	-
chr7	142299010	142813287	chr7	27181514	27185216	TRB_HOXA11	+	-
chr7	142299010	142813287	chr8	127736068	127741434	TRB_MYC	+	+
chr7	142299010	142813287	chrX	108732481	108736409	TRB_IRS4	+	-
chr7	148697913	148800582	chr7	153887096	154894285	CUL1_DPP6	+	+
chr7	152134924	152436005	chr7	152759748	152855378	KMT2C_ACTR3B	-	+
chr7	156994050	157009075	chr12	11649853	11895402	MNX1_ETV6	-	+
chr7	158730994	158829628	chr20	3471039	3651122	ESYT2_ATRN	-	+
chr8	17922856	18029944	chr9	4985244	5128183	PCM1_JAK2	+	+
chr8	23385782	23457695	chr8	18527300	19013686	ENTPD4_PSD3	-	-
chr8	28890403	29053270	chr9	4985244	5128183	HMBOX1_JAK2	+	+

chr8	38411138	38468834	chr5	179820758	179838078	FGFR1_SQSTM1	-	+
chr8	38411138	38468834	chr7	101815903	102283958	FGFR1_CUX1	-	+
chr8	38411138	38468834	chr8	38411138	38468834	FGFR1_FGFR1	-	-
chr8	41929478	42052026	chr16	3725053	3880726	KAT6A_CREBBP	-	-
chr8	41929478	42052026	chr19	39776594	39786135	KAT6A_LEUTX	-	+
chr8	41929478	42052026	chr2	25733752	25878516	KAT6A_ASXL2	-	-
chr8	41929478	42052026	chr20	47501901	47656877	KAT6A_NCOA3	-	+
chr8	41929478	42052026	chr22	41091785	41180079	KAT6A_EP300	-	+
chr8	41929478	42052026	chr8	41929478	42052026	KAT6A_KAT6A	-	-
chr8	41929478	42052026	chr8	70109761	70403805	KAT6A_NCOA2	-	-
chr8	42338454	42371808	chr8	132571952	132675617	POLB_LRRC6	+	-
chr8	42896931	43030539	chr8	38411138	38468834	HOOK3_FGFR1	+	-
chr8	51817574	51899186	chr7	549196	727341	PCMTD1_PRKAR1B	-	-
chr8	56160903	56211279	chr7	142797455	142797502	PLAG1_TRBJ2-7	-	+
chr8	99013265	99877580	chrX	123961313	124102656	VPS13B_STAG2	+	+
chr8	123219956	123241398	chr7	27184670	27189169	C8orf76_HOXA11-AS	-	+
chr8	127736068	127741434	chr6	44828731	45377933	MYC_SUPT3H	+	-
chr8	127736068	127741434	chr9	37120538	37358149	MYC_ZCCHC7	+	+
chr8	127736068	127741434	chr9	37438113	37465399	MYC_ZBTB5	+	-
chr8	127890627	128101253	chr13	34942286	35672735	PVT1_NBEA	+	+
chr8	127890627	128101253	chr3	169084760	169663470	PVT1_MECOM	+	-
chr8	127890627	128101253	chr8	125091852	125367120	PVT1_NSMCE2	+	+
chr8	127890627	128101253	chr8	130052106	130443660	PVT1_ASAP1	+	-
chr8	127890627	128101253	chr9	37120538	37358149	PVT1_ZCCHC7	+	+
chr8	143833720	143840974	chr9	109015151	109119945	NRBP2_TMEM245	-	-
chr9	470290	746105	chr5	150113836	150155860	KANK1_PDGFRB	+	-
chr9	2015185	2193620	chr12	6666476	6689510	SMARCA2_ZNF384	+	-
chr9	2015185	2193620	chr9	2621833	2660053	SMARCA2_VLDLR	+	+
chr9	3218301	3526001	chr9	4985244	5128183	RFX3_JAK2	-	+
chr9	4985244	5128183	chr16	11976737	12574289	JAK2_SNX29	+	+
chr9	4985244	5128183	chr5	158695919	159099761	JAK2_EBF1	+	-
chr9	15464065	15511019	chr11	3675009	3797792	PSIP1_NUP98	-	-
chr9	21968104	21995301	chr14	21621903	22552132	CDKN2A_TRA	-	+
chr9	21968104	21995301	chr9	21455483	21456049	CDKN2A_IFNWP19	-	+
chr9	21968104	21995301	chr9	21802648	21937651	CDKN2A_MTAP	-	+
chr9	33041763	33076659	chr9	4985244	5128183	SMU1_JAK2	-	+
chr9	34179012	34252523	chr9	34086386	34126773	UBAP1_DCAF12	+	-
chr9	35812959	35815021	chr9	35792153	35809732	HINT2_NPR2	-	+
chr9	36833274	37034185	chr10	7818503	8016627	PAX5_TAF3	-	+
chr9	36833274	37034185	chr11	33542274	33674102	PAX5_KIAA1549L	-	+
chr9	36833274	37034185	chr12	132489550	132585188	PAX5_FBRSL1	-	+
chr9	36833274	37034185	chr14	76310711	76498475	PAX5_ESRRB	-	+
chr9	36833274	37034185	chr16	88874857	88977204	PAX5_CBFA2T3	-	-
chr9	36833274	37034185	chr16	89720984	89740903	PAX5_ZNF276	-	+
chr9	36833274	37034185	chr17	47896149	47928957	PAX5_SP2	-	+
chr9	36833274	37034185	chr20	32277663	32335011	PAX5_KIF3B	-	+
chr9	36833274	37034185	chr20	32358329	32439319	PAX5_ASXL1	-	+
chr9	36833274	37034185	chr20	32443061	32584890	PAX5_NOL4L	-	-
chr9	36833274	37034185	chr20	46060984	46089952	PAX5_NCOA5	-	-
chr9	36833274	37034185	chr3	152268039	152465779	PAX5_MBNL1	-	+
chr9	36833274	37034185	chr6	10747830	10759774	PAX5_TMEM14B	-	+
chr9	36833274	37034185	chr7	86643913	86864884	PAX5_GRM3	-	+
chr9	36833274	37034185	chr9	470290	746105	PAX5_KANK1	-	+
chr9	36833274	37034185	chr9	20341664	20622543	PAX5_MLLT3	-	-
chr9	36833274	37034185	chr9	36336403	36401198	PAX5_RNF38	-	-
chr9	36833274	37034185	chr9	37120538	37358149	PAX5_ZCCHC7	-	+
chr9	36833274	37034185	chr9	113165519	113221361	PAX5_FKBP15	-	-
chr9	36833274	37034185	chrX	1462571	1537107	PAX5_P2RY8	-	-
chr9	36833274	37034185	chrX	40051245	40177329	PAX5_BCOR	-	-
chr9	36833274	37034185	chrX	120158560	120165630	PAX5_RHOXF2	-	+
chr9	37120538	37358149	chr20	44496223	44522085	ZCCHC7_SERINC3	+	-
chr9	37120538	37358149	chr9	36833274	37034185	ZCCHC7_PAX5	+	-
chr9	37422665	37436990	chr19	6677703	6720682	GRHPR_C3	+	-
chr9	37919133	38069211	chr11	118747765	118791136	SHB_DDX6	-	-
chr9	71683365	71768884	chr8	27311481	27459390	CEMIP2_PTK2B	-	+
chr9	92711362	92764812	chr9	4985244	5128183	BICD2_JAK2	-	+
chr9	95875700	95968840	chr19	41330322	41353911	ERCC6L2_TGFB1	+	-
chr9	100302083	100352939	chr9	97674908	97697357	TEX10_XPA	-	-
chr9	105662456	105663112	chr7	142299010	142813287	TAL2_TRB	+	+
chr9	109640787	109946703	chr9	110048695	110172512	PALM2_AKAP2	+	+
chr9	111525158	111577844	chr9	125261831	125367207	ZNF483_GAPVD1	+	+
chr9	111896765	111935369	chr8	127890627	128101253	UGCG_PVT1	+	+
chr9	120388868	120580170	chr4	54229096	54298247	CDK5RAP2_PDGFRA	-	+
chr9	121075011	121177608	chr4	54657917	54740715	CNTRL_KIT	+	+
chr9	121075011	121177608	chr8	38411138	38468834	CNTRL_FGFR1	+	-
chr9	123379653	123930107	chr9	37120538	37358149	DENND1A_ZCCHC7	-	+
chr9	124517274	124771277	chr9	133205279	133209250	NR6A1_OBP2B	-	-
chr9	128683654	128696400	chr9	131125560	131234670	SET_NUP214	+	+
chr9	129887186	130043194	chr11	118436463	118526832	FNBP1_KMT2A	-	+
chr9	130713945	130885683	chr17	74748651	74769353	ABL1_SLC9A3R1	+	+
chr9	130713945	130885683	chr22	23180209	23318037	ABL1_BCR	+	+
chr9	130713945	130885683	chr9	131394092	131500197	ABL1_PRRC2B	+	+
chr9	131125560	131234670	chr22	16783411	16821699	NUP214_XKR3	+	-
chr9	131125560	131234670	chr7	6374522	6403977	NUP214_RAC1	+	+
chr9	131125560	131234670	chr9	130713945	130885683	NUP214_ABL1	+	+
chr9	131394092	131500197	chr10	129467183	129768007	PRRC2B_MGMT	+	+
chr9	131394092	131500197	chr22	23180209	23318037	PRRC2B_BCR	+	+
chr9	136440096	136483759	chr9	136494432	136545786	SEC16A_NOTCH1	-	-
chr9	136494432	136545786	chr9	136862118	136866286	NOTCH1_EDF1	-	-
chr9	136658855	136672678	chr17	83079690	83095119	EGFL7_METRNL	+	+
chr9	136862118	136866286	chr9	136494432	136545786	EDF1_NOTCH1	-	-
chrX	1462571	1537107	chr9	36833274	37034185	P2RY8_PAX5	-	-
chrX	2691132	2741309	chr9	4985244	5128183	CD99_JAK2	+	+
chrX	13734744	13769353	chr9	4985244	5128183	OFD1_JAK2	+	+
chrX	40051245	40177329	chr17	40309193	40356796	BCOR_RARA	-	+
chrX	49028730	49043486	chrX	71283191	71301166	TFE3_NONO	-	+
chrX	55075062	55078909	chrX	55009054	55031064	PAGE2B_ALAS2	+	-
chrX	71118555	71142453	chr7	27162434	27165530	MED12_HOXA9	+	-
chrX	71283191	71301166	chr2	43222401	43226609	NONO_ZFP36L2	+	-
chrX	71283191	71301166	chrX	49028730	49043486	NONO_TFE3	+	-
chrX	100969710	100990806	chrX	101009345	101052116	ARL13A_TRMT2B	+	-
chrX	123859811	123913976	chr12	10158300	10172138	XIAP_OLR1	+	-
chrX	123961313	124102656	chr7	16646130	16706523	STAG2_BZW2	+	+
chrX	123961313	124102656	chrX	77504877	77786216	STAG2_ATRX	+	-
chrX	123961313	124102656	chrX	130384439	130385447	STAG2_GPR119	+	-
chrX	130064873	130110716	chr21	38380029	38661780	ELF4_ERG	-	-
chrX	138632677	139205023	chr6	134169245	134318058	FGF13_SGK1	-	-

Coordinates are based on the GRCh38 human reference

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Table S3. Cytogenetic and WGS results for 235 cases with successful cytogenetics.

UPN	Diagnosis	Cohort	Specimen	Cytogenetics.ISCN.Line	Normal.karyotype	Complex	Gene.mutations	WGS.CNAs	WGS.Recurrent.SVs	WGS.Gene.mutations	WGS.NK	WGS.Complex	CONFIRMATION STUDIES	New.information
103395	MDS	retrospective	BM	46,XY[20]	Y	N		0	0	ASXL1:p.E635Rfs*15[38.5%]	Y	N		N
104895	AML	retrospective	BM	46,XX,del(3)(q12)[16]/46,XX[4]	N	N	CUX1:p.Arg1259Gln[3.1%],FLT3:p.Asp835Tyr[2.5%],IDH2:p.Arg140Gln[45%],SRSF2:p.Pro95His[46.8%],STAG2:[35.5%]	del(3)(q13.11q26.33)[23.6%]	0	FLT3:p.D835Y[3.8%],IDH2:p.R140Q[42.3%],SRSF2:p.P95H[43.8%],STAG2:NA[45.1%]	N	N		N
142194	AML	retrospective	BM	46,XY,inv(16)(p13.1q22)[13]/46,XY[7]	N	N		0	inv(16)(q22.1p13.11)[29.8%],inv(16)(q22.1p13.11)[19.7%]	NRAS:p.G12C[35.7%],WT1:p.A382Vfs*4[37.2%]	N	N		N
142283	MDS	retrospective	BM	45,X,-Y[8]/46,XY[12]	N	N		-Y[manual review]	0	DNMT3A:p.G707S[13.7%]	N	N		N
142639	AML	retrospective	BM	46,XX[19]/46,XX,+mar[1]	Y	N	TET2:p.Arg1516Ter[4.1%],FLT3:p.Asp835Glu[30.2%]	del(7)(q22.1qter)[60.0%],del(10)(q22.2q22.3)[58.6%],gain(13)(q21.32qter)[56.6%]	0	TET2:p.R1516*[8.8%],FLT3:p.D835E[41.0%]	N	Y	CONFIRMED: del(7q) called nonclol in karyotype	Complex
146218	AML	retrospective	BM	46,XY,inv(16)(p13q22)[9]/46,XY[10]	N	N		0	inv(16)(q22.1p13.11)[24.8%],inv(16)(q22.1p13.11)[35.7%]	NRAS:p.Q61K[25.7%],NRAS:p.G13D[7.5%]	N	N		N
147444	MDS	retrospective	BM	44,XX,-5,-7,-20,+mar[15]/46,XX[5]	N	Y		del(5)(q11.2qter)[52.1%],-7[51.5%],del(12)(p12.3p13.2)[49.3%],del(20)(p12.1p12.2)[50.4%]	0	TP53:p.R213*[48.9%]	N	Y	CONFIRMED: Cs BY ARRAY	N
167152	AML	retrospective	BM	44-47,XY,add{3}{p1?3),add{4}{p14),-5,-7,-10,-15,add{17}(p1?1.2),-18,-20,+22,+3-5mar[cp19]/46,XY[1]	N	Y		gain(2)(p14pter)[154.8%],+2[71.7%],del(3)(p22.3p26.1)[82.6%],del(3)(p12.3p14.2)[82.3%],+3[75.3%],del(4)(p12pter)[82.6%],del(5)(q11.2qter)[82.7%],del(7)(p15.3p21.2)[83.6%],del(10)(q11.22q25.3)[82.1%],del(15)(q14q15.3)[80.4%],del(17)(p11.2pter)[75.7%],del(20)(p11.21pter)[80.6%]	0	ETV6:p.R210H[41.7%],TP53:p.R282W[68.6%],CALR:p.A382Qfs*48[20.8%]	N	Y		N
167999	AML	retrospective	BM	46,XY[12]	NA	N	None detected	del(13)(q21.2q21.31)[96.6%]	0	DNMT3A:p.R882H[39.3%],KRAS:p.Q61L[41.7%],NPM1:p.W288Cfs*12[27.9%]	N	N		Not Complex
168973	AML	retrospective	PB	46,XX[11]	NA	N		0	0	DNMT3A:p.R882H[42.9%],TET2:p.E1874Sfs*13[10.0%],TET2:p.Y1998Sfs*25[34.4%],KRAS:p.G13D[15.9%],NPM1:p.W288Cfs*12[41.7%],FLT3:p.D593_L610dup[21.8%]	Y	N		NK
179016	AML	retrospective	BM	46,XY,del(9)(q13q22),t(11;21)(p13;q22),t(15;17)(q22;q21)[20]	N	N		del(9)(q21.11q31.1)[87.3%],del(11)(p12p14.3)[87.6%]	t(15;17)(q24.1;q21.2)[35.0%],t(15;17)(q24.1;q21.2)[32.5%]	0	N	N	CONFIRMED: del(11p) by Sequence breakpoints	del(11)(p12p14.3)[87.6%]
189012	MDS	retrospective	BM	46,XY,del(5)(q15q33)[16]/46,XY[3]/46,XY,del(5)(q12q33),del(7)(q21q32)[1]	N	N		del(5)(q14.3q34)[41.8%]	0	SF3B1:p.K700E[10.3%]	N	N		N
190938	MDS	retrospective	BM	46,XY,-5[17],del(7)(q32q36)[6],del(7)(q22q36)[6],-11[17],-12[17],-16[6],-17[17],-20[6],add(20)(p12)[6],+2~5mar[cp17]/46,XY[3]	N	Y		del(5)(q13.3q33.3)[70.5%],del(7)(q21.2q22.1)[70.0%],del(7)(q31.2qter)[69.4%],del(12)(p12.1p13.2)[70.1%],del(12)(q21.2qter)[68.8%],del(17)(p13.1pter)[63.7%],del(20)(q11.22q13.13)[66.4%]	0	TP53:p.Y220C[61.5%]	N	Y		N
199019	MDS	retrospective	BM	45-49,XX,+1,add(3)(p11),del(5)(q13q33)del(10)(q24q26),add(18)(q21),+19,-20,+21,+1-2mar[cp20]	N	Y		+1[26.1%],del(3)(p22.2pter)[62.7%],del(3)(p11.2p14.2)[57.3%],gain(3)(q11.2qter)[13.0%],del(5)(q21.1q32)[62.6%],del(10)(q21.3q22.2)[61.5%],del(18)(q22.3qter)[61.0%],+19[26.3%],del(20)(q11.23q13.2)[58.5%],gain(21)(q11.2qter)[24.9%]	0	TET2:p.E452*[26.3%],TP53:p.I162N[65.9%]	N	Y		N
199994	AML	retrospective	BM	41-42,X,-Y,add(2)(q21),add(4)(q32),add(5)(q35),-7,-13,-17,-21,-22,+1-2mar[cp7]/46,XY[1]	N	Y		del(4)(q21.22q31.1)[60.8%],-7[60.2%],gain(13)(q12.11q14.11)[56.2%],del(13)(q14.11q21.31)[60.9%],-17[55.0%],gain(21)(q11.2qter)[58.9%],-X[98.5%]	0	DNMT3A:p.L637R[30.9%],TP53:p.R337C[32.6%]	N	Y		N
200915	AML	retrospective	BM	46,XY[20]	Y	N	None detected	0	0	0	Y	N		N
206801	AML	retrospective	BM	46,XX[20]	Y	N	FLT3:p.Asp586_Arg595dup[1.5%],IDH2:p.Arg140Gln[35.5%],CEBPA:p.Ile62HisfsTer46[54.4%]	0	0	IDH2:p.R140Q[27.7%],CEBPA:p.I62Hfs*46[53.7%]	Y	N		N
221833	MDS	retrospective	BM	47,XY,+2[2]/48,idem,t(3;21)(q26.2;q22),+der(21)t(3;21)[18]	N	Y		+2[83.5%],gain(3)(q25.33qter)[74.7%],gain(21)(q11.2q22.11)[71.9%]	0	TET2:p.C484Vfs*2[23.8%],TET2:p.K1243Nfs*10[38.2%],PHF6:NA[83.3%]	N	Y		N
242129	AML	retrospective	BM	44~46,XX,del(11)(q23),der(19)?t(11;19)(q23;p13.1)[cp11]/44~45,XX,-19[cp4]/46,XX[5]	N	N		0	t(11;19)(q23.3;p13.11)[29.8%]	KRAS:p.G12V[20.4%]	N	N	CONFIRMED: NO Cs BY ARRAY	Not Complex; No CNAs on chr11 or chr19
250911	AML	retrospective	BM	46,XY[20]	Y	N	NPM1:p.Trp288CysfsTer12[45.9%],FLT3:p.Glu611_Phe612insLeuGluPheProArgGluAsnLeuGlu[29.1%],IDH2:p.Arg140Gln[49.1%]	0	0	IDH2:p.R140Q[46.9%],NPM1:p.W288Cfs*12[37.7%],FLT3:p.E611_F612insLEFPRENLE[41.3%]	Y	N		N
258135	AML	retrospective	BM	46,XX,inv(16)(p13q22)[5]/46,idem,t(3;3)(p13;q?28)[5]/46,XX[6]	N	N		gain(11)(q23.3qter)[15.0%]	inv(16)(q22.1p13.11)[36.5%]	CBL:NA[20.0%],PTPN11:p.A72V[20.6%]	N	N		gain(11)(q23.3qter)[15.0%]
263578	AML	retrospective	BM	46,XX,t(8;21)(q22;q22)[17]/46,XX[3]	N	N		0	t(8;21)(q21.3;q22.12)[21.4%],t(8;21)(q21.3;q22.12)[32.5%]	KIT:p.T417delinsIP[41.7%]	N	N		N
266995	MDS	retrospective	BM	45,XX,-7[2]/46,XX[18]	N	N		-7[13.6%]	0	GATA2:p.A411V[55.0%]	N	N		N
270086	MDS	retrospective	BM	39~43,XY,-3,add(3)(p13),der(4)t(4;11)(q31;q13),del(5)(q15q33),add(7)(q11.2),inv(9)(p12q13),-10,add(10)(q25),-11,add(12)(q14),der(12)t(12;13)(p11.2;q12),-13,-13,add(17)(p11.2),-19,-21,+1~3mar[cp12]/46,XY,inv(9)(p12q13)[8]	N	Y		del(5)(q14.3qter)[8.1%],del(7)(q11.23qter)[7.6%],gain(13)(q12.11q13.1)[21.9%],+19[6.1%]	0	0	N	Y		N
272341	AML	retrospective	BM	47,XX,+8[20]	N	N		+8[69.4%]	0	TET2:p.C1289F[95.2%],CUX1:p.E824D[42.6%],NF1:NA[35.9%],NF1:NA[32.6%],SRSF2:p.P95L[43.4%],RUNX1:p.A352Rfs*249[26.7%],ASXL1:p.G646Wfs*12[36.5%]	N	N		N
272848	MDS	retrospective	BM	46,XX,-7,del(13)(q12q14),+mar[18]46,XX[1]/47,XX,+15[1]	N	Y		del(7)(p12.3pter)[82.5%],del(7)(q11.23qter)[82.2%],del(13)(q14.11q21.1)[83.5%]	0	0	N	Y		N

275786	AML	retrospective	BM	45,X,-Y,t(8;21)(q22;q22)[19]/46,XY[1]	N	N		-Y[38.7%]	t(8;21)(q21.3;q22.12)[26.6%],t(8;21)(q21.3;q22.12)[19.5%]	CSF3R:p.S810Qfs*6[9.8%],FLT3:p.E598_Y599insVAYVDFREYE[35.8%]	N	N		N
277960	AML	retrospective	BM	46,XX[11]	NA	N		0	0	TET2:p.L615Sfs*24[36.4%],TET2:p.L1244Qfs*25[38.9%],TET2:p.R1572W[39.6%],BCOR:p.R763Q[50.0%],NPM1:p.W288Cfs*12[55.4%],FLT3:p.R595_F612dup[16.4%]	Y	N		NK
285982	AML	retrospective	BM	46,XY,t(16;22)(q22;q13)[10]	N	N		0	inv(16)(q22.1p13.11)[33.3%]	NRAS:p.G13D[11.8%],FLT3:p.D835Y[8.3%]	N	N	CONFIRMED: inv(16) FISH showed rearrangement	inv(16)(q22.1p13.11)[33.3%]
300777	AML	retrospective	BM	46,XY,inv(16){p13q22)[20]	N	N		+Y[39.4%],del(Y)(q11.221q11.223)[19.1%]	inv(16)(q22.1p13.11)[6.1%],inv(16)(q22.1p13.11)[6.6%]	0	N	N		N
307995	MDS	retrospective	BM	46,XY,der(1;7)(q10;p10)[9]	N	N		gain(1)(q21.2qter)[35.3%],del(7)(q11.21qter)[36.9%]	0	RUNX1:p.D123Gfs*11[18.2%]	N	N	CONFIRMED: Cs BY ARRAY	N
319590	AML	retrospective	BM	87,<4n>,XXXX,-2,-5,-8,-11,-12,-14,-16,+2mar[1]/46,XX[19] FISH:tetrasomy9q(41.5%),tetrasomy22q(41.5%),tetrasomy15q(45%),trisomy16q(46%),tetrasomy17q(45%)	N	Y		gain(1)(p12p34.3)[24.2%],gain(1)(q25.2qter)[25.7%],del(2)(q34qter)[50.8%],del(5)(q31.3q33.2)[53.2%],gain(5)(q33.2q34)[48.6%],del(5)(q35.1qter)[44.3%],gain(6)(q22.33qter)[50.7%],del(9)(p13.1pter)[52.2%],del(11)(q12.2qter)[50.2%],del(12)(q23.1q24.21)[49.4%],del(13)(q12.11q31.1)[28.0%],gain(13)(q31.1qter)[23.5%],del(14)(q12q21.3)[51.9%]	0	ASXL1:p.S1064Dfs*24[24.2%]	N	Y		N
325191	AML	retrospective	BM	46,XX,t(11;20)(p15;q11.2)[20]	N	N	NRAS:p.Gly12Cys[18.4%],FLT3:p.Asp835His[15.5%],CEBPA:p.Ile294ThrfsTer25[19.5%],CEBPA:p.Pro23GlnfsTer81[13.1%]	0	t(11;20)(p15.4;q12)[31.2%],t(11;20)(p15.4;q12)[25.5%]	NRAS:p.G13D[4.2%],NRAS:p.G12C[27.8%],FLT3:p.D835H[18.3%],CEBPA:p.I294Tfs*25[29.5%],CEBPA:p.P23Qfs*81[10.6%]	N	N		N
327472	AML	retrospective	BM	46,XX,t(9;11)(p21;q23)[10]/47,idem,+21[7]/46,XX[3]	N	N		gain(21)(q11.2qter)[33.8%]	t(9;11)(p21.3;q23.3)[22.8%],t(9;11)(p21.3;q23.3)[28.2%]	0	N	N		N
332923	AML	retrospective	PB	46,XY[8]	NA	N		0	0	NRAS:p.Q61K[25.0%],DNMT3A:p.R729W[34.4%],DNMT3A:p.A357Pfs*50[36.9%],NPM1:p.W288Cfs*12[25.5%]	Y	N		NK
347494	AML	retrospective	BM	47,XY,+8[5]/47,idem,inv(16)(p13.1q22)[15]	N	N		+8[86.8%]	inv(16)(q22.1p13.11)[26.2%],inv(16)(q22.1p13.11)[26.5%]	NRAS:p.G12D[42.4%],FLT3:p.D835Y[9.3%]	N	N		N
350719	MDS	retrospective	BM	45,XX,der(5;17)(p10;q10)[11]/46,XX,del(13)(q12q22)[1]/46,XX[8]	N	N		del(5)(q11.2qter)[11.8%],del(13)(q12.3q14.3)[10.9%]	0	TP53:p.C238Y[6.9%]	N	N		N
353053	MDS	retrospective	BM	46,XX,+1,der(1;7)(q10;p10)[19]/46,XX[1]	N	N		gain(1)(q21.2qter)[18.6%],del(7)(q11.21qter)[18.9%]	0	TET2:p.Y1964H[60.6%],RUNX1:p.E422*[18.6%]	N	N	CONFIRMED: Cs BY ARRAY	N
377158	MDS	retrospective	BM	46,XX[19]/46,XX,del(9)(q13)[1]	N	N		0	0	ASXL1:p.E635Rfs*15[23.8%],RUNX1:p.R204Q[39.0%],U2AF1:p.Q157P[59.5%]	Y	N		N
378511	MDS	retrospective	BM	46,XY,+1,der(1;7)(q10;p10),del(13)(q12q21.3)[17]/46,XY[2]/46,XY,t(2;16)(p11.2;q12.1)[1]	N	N		gain(1)(q21.2qter)[70.2%],del(7)(q11.21qter)[73.0%],del(13)(q13.1q21.32)[73.9%]	0	U2AF1:p.Q157R[8.9%],ETV6:p.L416Ffs*10[47.6%]	N	Y		N
380949	AML	retrospective	BM	45,X,-X[21]/46,XX[9]	N	N	None detected	-X[88.4%]	t(10;11)(p12.31;q23.3)[32.1%]	CUX1:p.G1121R[47.4%]	N	N	CONFIRMED: KMT2A breakapart FISH abnormal; R-seq positive	t(10;11)(p12.31;q23.3)[32.1%]
387082	AML	retrospective	BM	44-47,XY,del(5)(q13q33),-7,add(12)(p11.1),t(12;13)(p11.2;q12),+1-3der(13)t(12;13),del(16)(q22),add(17)(p13),-19[cp2O)	N	Y		del(5)(q15q34)[66.2%],-7[55.8%],del(12)(p12.1pter)[61.3%],gain(13)(q12.11q12.3)[188.9%],del(13)(q12.3q14.13)[65.9%],del(16)(q22.1qter)[64.1%],del(17)(p11.2pter)[62.5%],del(19)(q12q13.13)[63.1%]	0	TP53:p.S37Cfs*9[45.3%]	N	Y		N
391518	AML	retrospective	BM	46,XY[21]	Y	N	SRSF2:p.Pro95Arg[46.7%],NPM1:p.Trp288CysfsTer12[35.3%],FLT3:p.Asp835Tyr[37.9%]	0	0	FLT3:p.D835Y[35.4%],SRSF2:p.P95R[48.8%],NPM1:p.W288Cfs*12[47.5%]	Y	N		N
395344	MDS	retrospective	BM	47,XY,+8[1]/47,idem,del(5)(q22q35)[19]	N	N		del(5)(q22.2q34)[70.8%],+8[80.1%]	0	TP53:p.A63G[44.7%],ASXL1:p.G646Wfs*12[48.6%],RUNX1:p.R166Q[47.1%],U2AF1:p.S34F[34.1%]	N	N		N
407992	AML	retrospective	BM	46,XY,t(11;19)(q23;p13)[17]/46,XY,t(11;19)(q23;p13),inv(12)(p12p13)[3]	N	N		0	t(11;19)(q23.3;p13.11)[27.9%]	FLT3:p.D835E[21.9%]	N	N		N
410324	AML	retrospective	BM	52~54,XY,+2,+4,+6,+8,del(11)(q23),+19,+19,+21[17]/46,XY[3]	N	Y		+2[59.0%],+4[56.4%],+6[57.7%],+8[59.0%],gain(11)(q23.3qter)[71.0%],+19[146.2%],gain(21)(q11.2qter)[60.6%]	t(6;11)(q27;q23.3)[37.9%],t(6;11)(q27;q23.3)[32.7%]	0	N	Y	CONFIRMED: KMT2A breakapart FISH abnormal; R-seq positive	t(6;11)(q27;q23.3)[37.9%]
429745	MDS	retrospective	BM	48,XX,+8,+8,del(8)(q11.23q21.2)x3,del(12)(p13),add(17)(p13),del(22)(q13)[20]	N	Y		gain(8)(p11.22pter)[160.7%],-8[82.0%],gain(8)(q12.3qter)[155.8%]	0	BCOR:p.Y985*[31.9%],RUNX1:p.T148Rfs*17[32.7%]	N	N		Not Complex; No CNAs on chr12,chr17,chr22
430998	MDS	retrospective	BM	47,XY,+14[5]/46,XY,i(14)(q10)[5]/46,XY[10]	N	N		gain(14)(q11.2qter)[51.4%]	0	SF3B1:p.K700E[28.1%],FLT3:p.Y591_F612dup[8.3%]	N	N		N
439820	MDS	retrospective	BM	46,XY,del(7)(q22),del(20)(?q13.1)[12]/46,idem,?add(17)(p13)[4]/46,idem,add(17)(q25)[4]	N	Y		del(7)(q21.3qter)[89.7%],gain(19)(p13.2pter)[96.8%],del(20)(q11.23q13.2)[85.4%]	0	TP53:p.R248Q[54.0%],U2AF1:p.Q157P[34.4%],PHF6:p.D25Qfs*10[61.3%],ASXL1:p.G646Wfs*12[45.6%]	N	Y		N
447649	AML	retrospective	BM	46,XY,t(15;17)(q22;q21)[20]	N	N		0	t(15;17)(q24.1;q21.2)[21.8%],t(15;17)(q24.1;q21.2)[25.7%]	FLT3:p.Y597_K602dup[41.9%]	N	N		N
455499	AML	retrospective	BM	46,XX,t(15;17)(q22;q21)[12]/46,XX[8]	N	N		del(6)(p22.3pter)[13.1%],del(6)(q13q22.1)[12.2%]	t(15;17)(q24.1;q21.2)[15.1%],t(15;17)(q24.1;q21.2)[19.5%]	0	N	N		del(6)(p22.3pter)[13.1%],del(6)(q13q22.1)[12.2%]
455981	AML	retrospective	BM	43-46,XX,-3,add(3)(p12),del(5)(q15q33),-6,add(9)(q12),-17,-18,-19,-20,-22,add(22)(p11.2),+1-5mar[cp14]/46,XX[6	N	Y		del(3)(p11.2p24.1)[49.8%],del(5)(q22.1q34)[50.8%],del(6)(p12.1pter)[49.5%],del(6)(q13q14.1)[50.5%],gain(9)(p13.1pter)[35.5%],del(17)(p11.2pter)[46.6%],gain(22)(q11.21qter)[27.7%]	0	TP53:NA[44.4%],TP53:p.P250L[20.7%]	N	Y		N
459785	AML	retrospective	BM	46,XX[11]	NA	N		0	0	FLT3:p.D835V[36.5%],STAG2:NA[57.7%]	Y	N		NK
461513	AML	retrospective	BM	47,XX,+8[1]/46,XX[4]	NA	N	NRAS:p.Gly12Asp[40.9%]	+8[84.9%]	t(10;11)(p12.31;q23.3)[37.0%]	NRAS:p.G12D[25.0%],ASXL1:p.G646Wfs*12[25.5%],ASXL1:p.E1370G[49.2%]	N	N	CONFIRMED: PCR	t(10;11)(p12.31;q23.3)[37.0%]
463352	AML	retrospective	BM	45,X,-Y,t(8;21)(q22;q22)[13]/45,idem,del(9)(q22q32)[7]	N	N		del(9)(q21.11q31.1)[70.5%],-X[99.5%]	t(8;21)(q21.3;q22.12)[23.1%],t(8;21)(q21.3;q22.12)[19.7%]	ASXL1:p.G646Wfs*12[41.7%],RAD21:p.E453Vfs*12[50.0%]	N	N		N
463763	MDS	retrospective	BM	47,XY,+Y[6]/46,XY[14]	N	N		+Y[18.4%]	0	BCOR:p.P663Lfs*6[12.5%],U2AF1:p.S34F[13.8%]	N	N		N
465146	AML	retrospective	BM	47,XY,+8[19]/46,XY[1]	N	N	NPM1:p.Trp288CysfsTer12[31.2%],KRAS:p.Gly13Asp[3%]	+8[67.3%]	0	NPM1:p.W288Cfs*12[22.6%]	N	N		N
467825	AML	retrospective	BM	47,XX,del(7)(q22),+8[20]	N	N		del(7)(q21.3q36.1)[92.7%],+8[66.1%]	0	SF3B1:p.K666N[41.5%],RUNX1:p.R162S[33.9%],FLT3:p.R607_E608insQNEYDLKWEFPR[15.0%]	N	N		N

478908	AML	retrospective	BM	46,XY,t(15;17)(q22;q21)[20]	N	N		0	t(15;17)(q24.1;q21.2)[19.4%],t(15;17)(q24.1;q21.2)[17.8%]	FLT3:p.F594_D600dup[13.7%]	N	N		N
480109	MDS	retrospective	BM	45~48,XX,t(1;14)(q12;q32),-2,add(5)(q11.2),dic(6;7)(q25;p15),add(12)(p11.2),-13,add(17)(q11.2),-22,+r,+2~6mar[cp15]/46,XX[7].	N	Y		del(5)(q14.1q33.3)[59.3%],del(12)(p11.21pter)[58.4%],gain(13)(q12.11q12.12)[151.6%],del(13)(q12.13q22.1)[58.2%],gain(13)(q22.1qter)[116.7%],del(13)(q34qter)[60.3%]	0	JAK2:p.V617F[34.1%],TP53:p.C275Y[32.1%]	N	Y		N
489196	MDS	retrospective	BM	45,XX,t(13;17)(q25;p11.2),-20[1]/44-45,XX,del(1)(p36.1),add(2)(q33),t(3;17)(q25;p11.2),add(4)(q21),-7,add(11)(p11.2),-20,+mar[cp17]/46,XX[2]	N	Y		gain(1)(p31.1p35.2)[37.8%],del(2)(q37.1qter)[41.8%],gain(3)(q21.1q27.3)[58.9%],del(4)(q24qter)[42.1%],-7[57.3%],del(11)(p15.4pter)[58.8%],del(17)(p13.1pter)[54.2%],gain(17)(q22qter)[59.6%],gain(19)(q13.33qter)[103.9%],+20[56.0%],del(20)(q11.23q13.2)[57.3%]	0	TP53:p.P177R[85.7%]	N	Y		N
491309	MDS	retrospective	BM	44~45,XX,der(3)t(3;12)(p25;q13)del(3)(q21q24),add(5)(q11.2),del(8)(p11.2),-12,add(15)(p11.2)[cp3]/46,XX[17]	N	Y		del(3)(p12.3pter)[5.9%],del(5)(q11.2q33.2)[7.2%],+19[6.1%]	0	TP53:NA[60.0%]	N	Y		N
493129	AML	retrospective	BM	44-46,X,-X,der{1)del{1){p?13p?22)del{1){q12q25),-5,-7,add{11){q14),del{12){p12),-16,-18,+2-5mar[cp17]/90-91,idemx2[2]/46,XX[1]	N	Y		del(5)(q14.2q33.3)[86.8%],del(7)(p21.1pter)[85.8%],del(7)(q34qter)[86.9%],gain(11)(q21qter)[225.9%],del(12)(p11.21p13.2)[87.1%],del(18)(q12.1q22.3)[86.1%],del(X)(p11.3p22.2)[86.2%]	0	TP53:p.R175G[85.9%]	N	Y		N
494166	AML	retrospective	BM	47,XY,add(2)(p13),del(5)(q22q33),-7,+8,del(8)(q11.2q21.2),+mar[20]	N	Y		del(5)(q14.2q31.2)[96.8%],del(7)(q21.3q36.1)[96.9%],+8[93.3%]	0	DNMT3A:p.M315L[35.0%],NF1:p.K2169_V2175del[42.9%]	N	Y		N
499829	AML	retrospective	BM	47,XY,+8[2]/46,XY[18]	N	N	TET2:p.Lys1243SerfsTer9[40.2%],TET2:p.Gln1274Ter[51.8%],NPM1:p.Trp288CysfsTer12[5.2%],CBL:p.Phe418Ser[95.4%],SRSF2:p.Pro95Leu[46.2%],ASXL1:p.Arg693Ter[34.8%]	gain(3)(q13.33qter)[8.1%],+8[8.4%]	0	TET2:p.K1243Sfs*9[41.2%],TET2:p.Q1274*[52.8%],CBL:p.F418S[97.7%],SRSF2:p.P95L[50.8%],ASXL1:p.R693*[39.4%]	N	N	CONFIRMED: FISH for +8 and +MECOM sigl	gain(3)(q13.33qter)[8.1%],+8[8.4%]
501944	AML	retrospective	BM	46,XX,t(15;17)(q22;q21.1)[19]/47,idem,+8[1]	N	N		+19[5.6%]	t(15;17)(q24.1;q21.2)[21.9%],t(15;17)(q24.1;q21.2)[25.7%]	0	N	N		N
502635	MDS	retrospective	BM	45~48,XY,-3,del(4)(q25q31),add(5)(q13),-7,add(7)(p22),-8,del(9)(q22),idic(12)(p12),add(20)(q13.3),+21,+2~5mar[cp12]/46,XY[8]	N	Y		del(5)(q14.3q33.2)[16.2%],gain(5)(q33.2q34)[12.8%],del(5)(q34q34)[17.1%],del(7)(p11.2p14.3)[14.4%],gain(7)(q11.21q11.23)[10.9%],del(7)(q31.1q31.33)[14.6%],del(8)(p21.3p22)[15.0%],del(8)(p12p12)[16.7%],gain(8)(p11.21p12)[17.0%],del(8)(q11.21q11.23)[15.4%],gain(8)(q11.23q23.1)[11.8%],del(8)(q23.1q23.3)[15.3%],del(9)(q21.11q21.32)[13.5%],gain(20)(q13.2qter)[16.0%],gain(X)(p22.2pter)[12.7%]	0	0	N	Y		N
504394	AML	retrospective	BM	47,XY,+8[8]	N	N		+8[85.8%]	0	TET2:p.Q742*[38.1%],TET2:p.Q1348*[54.2%],CBL:p.Y371N[27.0%],STAG2:p.R1012*[92.0%],EZH2:p.K17Sfs*3[80.0%],ASXL1:p.G646Wfs*12[43.2%],NRAS:p.G13D[6.5%]	N	N		N
507696	AML	retrospective	BM	46,XY,inv(16)(p13q22)[20]	N	N		0	inv(16)(q22.1p13.11)[30.4%],inv(16)(q22.1p13.11)[32.8%]	KIT:p.T417Lfs*6[19.1%],KIT:p.Y418Vfs*30[7.7%],KIT:p.Y418*[25.0%]	N	N		N
509179	AML	retrospective	BM	46,XY[20]	Y	N	TET2:p.Arg1452Gln[49.5%],NPM1:p.Trp288CysfsTer12[40.7%],WT1:p.Ser381Ter[47.6%],PTPN11:p.Glu76Ala[52.9%]	0	0	GATA2:p.K390del[2.9%],TET2:p.R1452Q[51.7%],WT1:p.S381*[41.3%],PTPN11:p.E76A[47.6%],NPM1:p.W288Cfs*12[23.2%]	Y	N		N
514066	AML	retrospective	BM	46,XX,t(8;21)(q22;q22)[20]	N	N		0	t(8;21)(q21.3;q22.12)[12.6%],t(8;21)(q21.3;q22.12)[29.3%]	KIT:p.D816V[47.7%],TET2:p.F125Lfs*3[73.0%],TET2:p.T556Nfs*11[18.4%]	N	N		N
521733	AML	retrospective	BM	39~43,XY,-Y,-5,?dic(7;11)(q36;p15),add(8)(q24.3),-9,-11,-13,add(14)(p13),-17,-18,add(18)(p11.2),?der(18)t(11;18)(?q11.2;?q22),-20,add(20)(q13.3),-21,-22,+r,+1~6mar[cp14]/46,XY[6]	N	Y		del(5)(q15q21.2)[65.5%],del(5)(q31.1qter)[60.0%],-9[62.8%],del(11)(p15.4pter)[56.8%],gain(13)(q12.11q14.11)[63.3%],del(13)(q14.11q21.31)[63.9%],gain(13)(q21.31q32.1)[119.2%],del(17)(p13.1pter)[58.8%],del(17)(q25.1qter)[61.2%],del(18)(p11.21pter)[59.9%],del(20)(q11.22q13.2)[60.4%],gain(21)(q11.2qter)[46.4%]	0	TP53:p.T125%3D[53.3%]	N	Y		N
544583	AML	retrospective	PB	46,XX[11]	NA	N		0	t(11;19)(q23.3;pter)[18.0%]	NF1:p.R1509H[54.0%]	N	N	CONFIRMED: PCR	t(11;19)(q23.3;pter)[18.0%]
562600	AML	retrospective	PB	46,XY[9]	NA	N		0	0	DNMT3A:p.R882C[39.7%],IDH2:p.R140W[11.3%],CEBPA:p.Q41*[17.0%],CEBPA:p.H24Afs*84[10.2%],NPM1:p.W288Cfs*12[51.5%],FLT3:p.R595_E596insDYVDFR[15.5%]	Y	N		NK
570755	AML	retrospective	BM	46,XY,t(11;19)(q23;p13)[20]	N	N		0	t(11;19)(q23.3;p13.11)[25.7%],t(11;19)(q23.3;p13.11)[25.3%]	SMC1A:p.R96H[93.8%],WT1:p.S381Lfs*71[28.8%],FLT3:NA[36.8%],FLT3:p.Y597_E598insR**VLLR*FQRI*I*SQMGVSKRKFRVW*[5.6%]	N	N		N
578200	AML	retrospective	BM	46,XY[20]	Y	N	CEBPA:p.Asp301_Lys302del[28.7%],CEBPA:p.Ala93GlyfsTer15[40.3%]	del(9)(p13.3p21.3)[11.6%]	0	CEBPA:p.D301_K302del[43.2%],CEBPA:p.A93Gfs*15[65.8%]	N	N		del(9)(p13.3p21.3)[11.5%]
578613	AML	retrospective	BM	46,XY[8]	NA	N		0	0	TET2:p.S794*[38.9%],TET2:p.D1425*[42.6%],SUZ12:p.I525V[53.7%],NPM1:p.W288Cfs*12[42.4%]	Y	N		NK
595704	AML	retrospective	BM	46,XX,inv(16)(p13q22)[19]/46,XX[1]	N	N		0	inv(16)(q22.1p13.11)[31.5%],inv(16)(q22.1p13.11)[38.3%]	KIT:p.Y418_D419insFF[6.9%],WT1:p.G191S[49.1%],FLT3:p.V592_Y599dup[11.1%]	N	N		N
596762	MDS	retrospective	BM	46,XY,t(6;9)(p23;q34)[4]/46,XY[16]	N	N		0	t(6;9)(p22.3;q34.13)[20.6%],t(6;9)(p22.3;q34.13)[14.8%]	0	N	N		N
607160	AML	retrospective	BM	46,XX[20]	Y	N	DNMT3A:p.Val649Met[40.4%],NPM1:p.Trp288CysfsTer12[41%],IDH2:p.Arg140Gln[41.9%],FLT3:p.Ser584_Tyr597dup[1%]	0	0	DNMT3A:p.V649M[36.6%],IDH2:p.R140Q[52.7%],NPM1:p.W288Cfs*12[37.7%],FLT3:p.S584_Y597dup[31.3%]	Y	N		N
611521	AML	retrospective	BM	49,XY,+3mar[2]/46,XY[2]	NA	N		0	0	SMC3:p.G1118V[41.5%],FLT3:p.D835Y[55.8%],CEBPA:p.Q83Pfs*25[11.9%],NPM1:p.W288Cfs*12[41.7%]	Y	N		NK
616274	AML	retrospective	BM	47,XX,+8[7]/46,XX[13]	N	N	FLT3:p.Ile836del[14.2%]	+8[23.6%]	t(9;11)(p21.3;q23.3)[19.7%],t(9;11)(p21.3;q23.3)[20.8%]	FLT3:p.I836del[10.7%]	N	N	CONFIRMED: KMT2A breakapart FISH	t(9;11)(p21.3;q23.3)[19.7%],t(9;11)(p21.3;q23.3)[20.8%]
618671	AML	retrospective	BM	46,XX[20]	Y	N	CEBPA:p.Gln312dup[28.9%],CEBPA:p.Pro39SerfsTer119[26.7%],FLT3:p.Ser585_Glu598dup[0.4%]	0	0	CEBPA:p.Q312dup[40.0%],CEBPA:p.P39Sfs*119[20.9%]	Y	N		N
623930	AML	retrospective	BM	46,XX[20]	Y	N	NRAS:p.Gly12Cys[9%],DNMT3A:p.Arg635Gln[44.4%],NPM1:p.Trp288CysfsTer12[38.5%],SMC1A:p.Lys500Glu[46.3%]	0	0	DNMT3A:p.R635Q[47.8%],RUNX1:p.Y407S[12.5%],SMC1A:p.K500E[51.7%],NPM1:p.W288Cfs*12[42.9%]	Y	N		N

627844	MDS	retrospective	BM	46,XY,t(17;17)(p13;q11.2)[9]/46,XY[11]	N	N		0	0	RUNX1:p.V79Wfs*44[33.1%]	Y	N		N
639691	MDS	retrospective	BM	44~46,XX,del(5)(q12q33),del(7)(q22q34),add(12)(p13),dic(12;18)(p13;p11.3),del(13)(q12q14),del(17)(p11.2),-19[cp19]/46,XX[1].	N	Y		del(5)(q13.2qter)[35.5%],del(7)(q22.1q36.1)[34.9%],del(12)(p12.3p13.32)[35.7%],del(13)(q13.3q14.3)[37.3%],del(13)(q21.33q22.3)[36.0%],del(13)(q32.1qter)[34.8%],del(17)(p11.2p13.1)[32.8%],del(19)(q12q13.12)[30.9%],gain(19)(q13.2qter)[44.1%]	0	TP53:p.F113C[18.4%]	N	Y		N
662555	AML	retrospective	BM	46,XY[20]	Y	N	DNMT3A:p.Arg882His[49.7%],NPM1:p.Leu287IlefsTer13[43.9%],NPM1:p.Trp288CysfsTer12[43.9%],FLT3:p.Phe594_Pro606dup[29.5%],FLT3:p.Glu604_Phe605insValProPheArgGluTyrGluTyrAspLeuLysTrpGlu[51.1%],FLT3:p.Glu604delinsAspSerGluAsnMetAsnMetIleSerAsnGlySerPheGln[51.1%],FLT3:p.Lys602_Trp603insCysAspPheProPheArgGluTyrGluTyrAspLeuLys[51.1%],FLT3:p.Lys602_Trp603insLeuTerPheProLeuArgGluTyrGluTyrAspLeuTer[51.1%],FLT3:p.Phe594_Pro606dup[51.1%],FLT3:p.Leu601_Lys602insIleTrpGluPheProPheArgGluTyrGluTyrAspLeu[51.1%],FLT3:p.Val592_Leu601dup[50.7%],FLT3:p.Asp600_Leu601insPheLysTrpGluPheProPheArgGluTyrGluTyrAsp[51.4%],FLT3:p.Glu596_Tyr597insAspGluTyrAspLeuLysTrpGluPheProPheArgGlu[51.4%],FLT3:p.Phe594_Arg595insIleGluTyrGluTyrAspLeuLysLeuGluPheProPhe[51.4%],DNMT3A:p.Arg882His[47.6%],NPM1:p.Trp288CysfsTer12[42.4%],FLT3:p.Phe594_Pro606dup[32.5%],FLT3:p.Pro606_Arg607insPheArgGluTyrGluSerAspLeuLysTrpGluPhePro[55.5%],FLT3:p.Trp603_Glu604insAspPheProPheArgGluTyrGluSerAspLeuLysTrp[55.6%],FLT3:p.Lys602_Trp603insSerGluPheProPheArgGluTyrGluTyrAspLeuLys[55.6%],FLT3:p.Leu601_Lys602insIleTrpTerPheProPheIleTerTyrTerTyrAspLeu[55.6%],FLT3:p.Leu601_Lys602insGluTrpGluPheProPheArgGluTyrGluCysAspLeu[55.6%],FLT3:p.Tyr599_Asp600insTyrLeuLysLeuGluPheProPheArgGluTyrGluTyr[56%],FLT3:p.Phe594_Pro606dup[56%],FLT3:p.Glu596_Tyr597insTer[56%],FLT3:p.Arg595_Glu596insGlyTyrGluTyrAspLeuLysTrpGluPheProPheArg[56%]	0	0	DNMT3A:p.R882H[39.6%],NPM1:p.W288Cfs*12[28.8%],FLT3:p.F594_P606dup[42.5%]	Y	N		N
668971	AML	retrospective	BM	45~47,XY,+8[cp10]	N	N		0	0	0	Y	N		NK
672014	AML	retrospective	BM	46,XY[20]	Y	N	DNMT3A:p.Arg882His[48.4%],FLT3:p.Asp835Tyr[35.6%],NPM1:p.Trp288CysfsTer12[32%],SMC1A:p.Arg790Gln[91.5%]	0	0	DNMT3A:p.R882H[38.1%],FLT3:p.D835Y[34.7%],SMC1A:p.R790Q[95.7%],NPM1:p.W288Cfs*12[42.3%]	Y	N		N
675128	AML	retrospective	BM	46~49,XY,add(5)(q13),del(5)(q33),+6,add(6)(q13),-7,+8,+9,+10,-17,+19,+1~2mar[cp19]/46/XY[1]	N	Y		del(7)(q21.11qter)[82.3%],-17[78.2%],gain(17)(q22qter)[51.8%],+20[42.5%],del(20)(q11.21q13.32)[79.2%]	0	DNMT3A:p.R749H[41.0%],FLT3:p.Y842C[36.5%],TP53:p.Y234H[81.2%]	N	Y		N
680763	AML	retrospective	BM	45,XY,del(5)(q13q33),-7[19]/46,XY[1]	N	N		del(5)(q21.1qter)[70.8%],-7[71.0%],del(12)(p12.3p13.2)[70.9%]	0	NF1:p.L2730V[36.0%],PPM1D:p.K535*[34.9%],ASXL1:p.G646Wfs*12[36.5%]	N	Y	CONFIRMED: del(12p) by Sequencing breakpoints	Complex
692900	AML	retrospective	BM	47,XY,del(5)(q22q33),+5,t(10;11)(p13~p15;q22~23),i(17)(q10)[3]/46,XY[17]	N	Y		+4[72.1%],del(5)(q31.1q33.1)[77.6%],del(17)(p11.2pter)[72.2%],gain(17)(q11.2qter)[89.0%]	t(10;11)(p12.31;q14.2)[18.0%],t(10;11)(p12.31;q14.2)[17.1%]	RAD21:NA[47.6%]	N	Y		N
706350	AML	retrospective	BM	46,XX[20]	Y	N	DNMT3A:p.Arg882His[31.5%],IDH1:p.Arg132Cys[28.0%]	0	0	DNMT3A:p.R882H[34.9%],IDH1:p.R132C[33.9%]	Y	N		N
708869	AML	retrospective	BM	43,XX,del(5)(q22q35),-7,+3mar[cp2]/46,XX[2]	N	Y		-5[28.0%],del(7)(p11.2p14.1)[25.6%],del(7)(q11.22qter)[27.3%],del(12)(p12.1pter)[26.6%],gain(13)(q12.11q12.3)[41.8%],del(13)(q12.3q22.2)[19.5%],gain(13)(q31.1q32.3)[46.5%],del(17)(p13.1pter)[23.1%]	0	TP53:p.E286K[14.3%]	N	Y		N
714148	MDS	retrospective	BM	46,XY[20]	Y	N		-Y[21.4%]	0	DNMT3A:p.E756K[26.1%],KIT:p.V532I[42.9%]	N	N		new -Y
723101	AML	retrospective	BM	46,XY[15]	NA	N		0	0	DNMT3A:p.R736H[51.9%],DNMT3A:p.G646V[39.2%],IDH2:p.R140Q[39.7%],FLT3:p.D600Gfs*30[8.8%]	Y	N		NK
735764	AML	retrospective	PB	46,XY[12]	NA	N		0	0	DNMT3A:p.R882H[50.0%],FLT3:p.Y597_W603dup[44.9%],FLT3:p.V592_D593insGEVGAGSSDNEYFYV[60.9%],NPM1:p.W288Cfs*12[52.4%]	Y	N		NK
736755	AML	retrospective	BM	46,XY[20]	Y	N		0	0	DNMT3A:p.R882H[43.5%],SMC3:p.R661P[41.3%],WT1:p.R462W[38.3%],NPM1:p.W288Cfs*12[41.0%],FLT3:NA[26.6%]	Y	N		N
761809	AML	retrospective	BM	46,XY,-8,+r(?)[19]/46,XY[1]	N	N		del(8)(p12pter)[70.5%],gain(8)(p11.21p12)[289.4%],gain(8)(q12.3q24.21)[152.9%],del(8)(q24.21qter)[69.6%]	0	DNMT3A:p.R882H[39.1%],DNMT3A:p.T671Rfs*34[8.3%],TET2:p.C1271Wfs*29[21.8%],TET2:p.K1488*[37.2%]	N	N		N
769516	MDS	retrospective	BM	46,XY,-7,del(20)(q11.2),+21[3]/48,idem,+13,+21[9]/46,XY[8]	N	Y		-7[55.8%],gain(13)(q12.11qter)[26.3%],del(20)(q11.21q13.2)[53.9%],gain(21)(q11.2qter)[78.1%]	0	CUX1:p.K54N[66.7%],SRSF2:p.P95R[33.3%]	N	Y		N
791810	AML	retrospective	BM	46,XY,inv(16)(p13.1q22)[7]/47,idem,+22[9]/46,XY[4]	N	N		gain(22)(q11.21qter)[41.2%]	inv(16)(q22.1p13.11)[18.9%],inv(16)(q22.1p13.11)[25.8%]	CBL:NA[12.5%]	N	N		N
796518	MDS	retrospective	BM	46,XY,+1,der(1;7)(q10;p10)[20]	N	N		gain(1)(q21.2qter)[58.5%],del(7)(q11.21qter)[59.4%]	0	0	N	N	CONFIRMED: Cs BY ARRAY	N
812077	MDS	retrospective	BM	44~45,XX,-2,del(5)(q13q33),-7,add(7)(p21),add(7)(q11.1),+8,-16,-17,-19,+der(21)t(17;21)(q11.2;p13),add(22)(q12), +mar[cp12]/46,XX[8]	N	Y		del(5)(q13.2q13.3)[82.3%],del(5)(q21.3q33.2)[82.5%],del(7)(p21.3pter)[77.3%],del(7)(q11.23qter)[82.3%],+8[44.6%],del(12)(p13.1p13.2)[79.9%],-16[79.6%],del(17)(p12p13.1)[78.5%]	0	GATA2:p.L375F[16.2%],GATA2:p.G200Vfs*18[3.8%],CUX1:p.S1134C[76.5%],TP53:p.T81Nfs*42[70.5%]	N	Y		N
816895	AML	retrospective	PB	46,XX[5]	NA	N		0	0	IDH2:p.R140Q[53.8%],NPM1:p.W288Cfs*12[45.3%],CEBPA:p.D80Gfs*28[50.0%],FLT3:p.V592_L610dup[10.5%],FLT3:p.F594_D600dup[9.8%]	Y	N		NK

827494	MDS	retrospective	BM	46,XX,del(5)(q22q35)[8]/46,XX[12]	N	N		del(5)(q15q33.3)[33.6%]	0	SF3B1:p.K700E[16.7%]	N	N		N
839903	MDS	retrospective	BM	46,XX,t(6;9)(p23;q34)[2]/46,XX[6]	N	N		0	t(6;9)(p22.3;q34.13)[25.7%],t(6;9)(p22.3;q34.13)[27.0%]	NRAS:p.G12D[15.1%],PIGA:p.V397%3D[46.5%]	N	N		N
847670	AML	retrospective	BM	46,XY,der(X)t(8;21)(q22;q22)t(X;21)(q28;?q22),der(8)t(8;21)(q22;q22),der(21)t(8;21)(q22;q22)t(X;21)(q28;?q22)[18]/46,XY[2]	N	N		del(9)(q21.11q31.1)[13.2%],-Y[15.4%]	t(8;21)(q21.3;q22.12)[26.5%],t(8;21)(q21.3;q22.12)[27.9%]	FLT3:p.E596_Y597insEYYFYVDFRE[60.7%]	N	N		del(9)(q21.11q31.1)[13.2%],-Y[30.8%]
856550	MDS	retrospective	BM	46,XX[20]	Y	N		0	0	NRAS:p.G12D[33.3%],EZH2:p.N673S[47.1%],RUNX1:p.G122R[88.1%],PHF6:p.E139*[35.7%]	Y	N		N
856681	AML	retrospective	BM	46,XX,del(7)(q32)[4]	N	N		+7[92.3%],del(7)(q11.21qter)[93.8%]	0	NRAS:p.G12D[41.8%],DNMT3A:p.C497Y[98.8%],EZH2:p.Q28Tfs*9[83.7%],IDH2:p.R172K[50.7%],BCOR:p.P1648Tfs*4[43.8%]	N	N		N
879308	AML	retrospective	BM	46,XY[20]	Y	N	DNMT3A:p.Arg882His[39.1%], NPM1:p.Trp288CysfsTer12[43.4%],WT1:p.Pro136dup[53.5%], FLT3:p.Gln577_Phe612dup[3.9%],FLT3:p.Phe594_Asp600dup[0.3%],FLT3:p.Tyr589_Phe590insArgTrpAsrgTerProAlaThrGlnIleMetSerThrSerThrLeuIleSerGluAsnMetAsnMetIleSerAsnGlySerPheGlnGluLysIleTerSerPhe[0.6%],FLT3:p.Glu588delinsAspArgCysTyrMetTerProAlaProGlnIleMetSerThrSerThrLeuIleSerGluAsnMetAsnMetIleSerAsnGlySerPheGlnGluLysIleTerSerLeu[0.7%],FLT3:p.Asn587_Glu588insGlnLysValGlnValThrGlySerSerAspAsnGluTyrPheTyrValAspPheArgGluTyrGluTyrAspLeuLysTrpGluPheProArgGluAsnLeuGluPhe[1.5%]	0	0	DNMT3A:p.R882H[36.7%],WT1:p.P136dup[37.3%],NPM1:p.W288Cfs*12[35.6%],FLT3:p.Q577_F612dup[4.9%]	Y	N		N
898627	AML	retrospective	PB	46,XX[5]	NA	N		-7[80.9%],+8[83.2%],del(12)(p12.2pter)[78.2%]	t(9;11)(p21.3;q23.3)[19.3%],t(9;11)(p21.3;q23.3)[18.4%]	CBL:p.D459_D460del[46.9%], TP53:p.P152Rfs*18[70.1%]	N	Y	CONFIRMED: KMT2A breakapart FISH positive	t(9;11)(p21.3;q23.3)[19.3%],t(9;11)(p21.3;q23.3)[18.4%]; Complex
907471	MDS	retrospective	BM	46,XX,del(5)(?q12q33)[1]/46,XX[19]	N	N		del(5)(q14.1q34)[10.7%],+19[5.5%]	0	0	N	N		N
907523	AML	retrospective	BM	46,XY[20]	Y	N	DNMT3A:p.Met674Val[44%],DNMT3A:p.Met548Thr[45%],NPM1:p.Trp288CysfsTer12[43.4%],FLT3:p.Asp593 Asn609dup[51.9%]	0	0	DNMT3A:p.M674V[55.4%],DNMT3A:p.M548T[48.6%],NPM1:p.W288Cfs*12[37.5%],FLT3:p.D593 N609dup[54.0%],FLT3:p.K602delinsRFQRI*I*SQMGVSKRK*[15.4%]	Y	N		N
907716	AML	retrospective	BM	47,XY+8[17]/46,XY[3]	N	N	EZH2:p.Asn693Thr[5.1%]	+8[74.5%]	t(9;11)(p21.3;q23.3)[32.7%],t(9;11)(p21.3;q23.3)[34.0%]	SRSF2:p.P95_R102del[5.5%]	N	N	CONFIRMED: KMT2A breakapart FISH	t(9;11)(p21.3;q23.3)[32.7%],t(9;11)(p21.3;q23.3)[34.0%]
922185	MDS	retrospective	BM	46,XY,del(20)(q11.2)[13]/46,XY[7]	N	N		-7[7.5%],del(18)(p11.21pter)[10.1%],del(18)(q21.2qter)[10.1%],+19[5.3%]	0	0	N	Y		-7[7.5%],del(18)(p11.21pter)[10.1%],del(18)(q21.2qter)[10.1%],+19[5.3%]
922771	AML	retrospective	BM	46,XY,der(8)t(8;21}(q22;q22),der(12)t(8;12)(q22;p13)[6]	N	N		0	t(8;21)(q21.3;q22.12)[32.6%]	ASXL1:p.Y591delins*[36.9%]	N	N		N
938927	AML	retrospective	BM	46,XX[20]	Y	N	NRAS:p.Gly12Asp[43.6%],DNMT3A:p.Phe752del[46.1%],NPM1:p.Trp288CysfsTer12[38.1%],IDH2:p.Arg140Gln[42.6%]	0	0	NRAS:p.G12D[35.8%],DNMT3A:p.F752del[29.2%],CBL:p.D460del[4.7%],IDH2:p.R140Q[35.4%],NPM1:p.W288Cfs*12[46.6%]	Y	N		N
950919	AML	retrospective	BM	47,XY,+4[20]	N	N	DNMT3A:p.Arg882His[49.7%], NPM1:p.Trp288CysfsTer12[33.1%],FLT3:p.Tyr591_Val592insThrAspProValThrGlySerSerAspAsnGluTyrPheTyr[21.1%]	+4[88.0%]	0	NRAS:p.G13D[5.3%],DNMT3A:p.R882H[48.9%],NPM1:p.W288Cfs*12[38.5%],FLT3:p.Y591_V592insTDPVTGSSDNEYFY[56.5%]	N	N		N
960821	AML	retrospective	BM	46,XY[10]	NA	N		0	0	DNMT3A:p.R736H[54.7%],TET2:p.D162Vfs*9[45.3%],RAD21:p.Q613R[47.4%],U2AF1:p.S34F[42.4%],FLT3:p.W603_E604insDYVDFREYEYDLKW[22.2%]	Y	N		NK
971297	MDS	retrospective	BM	41~42,XY,del(5)(q13q33),dup(11)(q13q25),-12,del(16)(q11.2),der(17;21)(p10;q10),-18,dic(13;20)(p12;q11.2)[cp20]	N	Y		del(5)(q15q33.3)[85.1%],del(11)(q14.2q21)[82.7%],del(11)(q22.1q22.3)[82.8%],del(12)(p12.3p13.31)[81.6%],del(12)(p11.21p11.23)[78.7%],del(12)(q21.32q23.1)[82.8%],-16[54.1%],del(17)(p11.2pter)[80.0%],-18[75.5%],del(20)(q11.21q13.32)[79.4%]	0	TP53:p.L344P[86.2%]	N	Y		N
976116	AML	retrospective	BM	41~43,XY,der(1)t(1;17)(q12;q11.2),add(3)(p?13),add(5)(q11.2),add(5)(q11.2),-7,t(14;17)q(11.2;p13),-17,-18,add(19)(p13.3)add(21)(p11.2)[cp20]	N	Y		del(1)(p13.2p13.3)[71.6%],del(3)(p21.1pter)[71.6%],del(5)(q13.3q33.3)[72.8%],-7[71.6%],del(17)(p13.2pter)[68.2%],-18[71.5%],del(19)(p13.12p13.2)[66.6%],gain(19)(p13.11p13.12)[149.2%]	0	TP53:p.R273H[73.2%],NF1:p.R1870Q[65.3%],ASXL1:p.V1072I[44.2%]	N	Y		N
978141	AML	retrospective	BM	46,XX[20]	Y	N	DNMT3A:p.Arg882Cys[47.3%], NPM1:p.Trp288CysfsTer12[34.1%],PHF6:p.His42GlnfsTer41[2.9%]	0	0	NRAS:p.G12D[6.5%],DNMT3A:p.R882C[41.9%],NPM1:p.W288Cfs*12[52.3%]	Y	N		N
984418	AML	retrospective	BM	46,XX[20]	Y	N		del(5)(q14.3q35.1)[24.4%]	0	SF3B1:p.K700E[19.0%],IDH1:p.R132C[7.5%],ETV6:p.V285M[57.1%]	N	N	CONFIRMED: Cs BY ARRAY	del(5)(q14.3q35.1)[24.4%]
988638	MDS	retrospective	BM	46,XY,del(12)(q21q24.1)[13]/46,XY[7]	N	N		del(12)(q21.2q23.3)[44.7%]	0	SRSF2:p.P95H[11.4%],ASXL1:p.G646Wfs*12[12.2%]	N	N		N
991140	MDS	retrospective	BM	44,XY,-7,psudic(12;15)(p13;p13),-18,+mar[13]/44,Y,t(X;19)(q11.2;p13.1),add(3)(p?23),add(5)(q13),add(7)(p13),-18[3]/46,XY[4	N	Y		-7[47.7%],del(12)(p12.1p13.31)[48.7%],del(18)(q21.1qter)[52.6%]	0	TP53:p.C176G[26.9%],TP53:p.L111Q[31.1%]	N	Y		N
991679	AML	retrospective	BM	45,X,-Y[2]/45,idem,del(9)(q21q22)[3]	N	N		del(9)(q21.11q21.33)[23.2%],-X[95.9%]	0	FLT3:p.D835Y[41.5%],SMC1A:p.R363I[83.3%],NPM1:p.W288Cfs*12[38.3%]	N	N		N
780327	AML	prospective	BM	46,XY[5]	NA	N	NPM1:p.Trp288CysfsTer12[36.5%],CUX1:p.Leu173Phe[50.3%],CUX1:p.Gly709Val[45.5%],IDH2:p.Arg140Gln[42.9%]	0	0	CUX1:p.L173F[46.0%],CUX1:p.G709V[48.0%],IDH2:p.R140Q[41.2%],NPM1:p.W288Cfs*12[51.9%]	Y	N		NK
776603	MDS	prospective	BM	46,XY[20]	Y	N	ASXL1:p.Gly646TrpfsTer12[24.5%],RUNX1:p.Ile342HisfsTer258[14.9%],RUNX1:p.Val238GlyfsTer23[5.7%],RUNX1:p.Arg162Lys[17.2%],U2AF1:p.Ser34Phe[32.7%]	0	0	ASXL1:p.G646Wfs*12[38.5%], RUNX1:p.I342Hfs*258[14.0%], RUNX1:p.R162K[24.4%],U2AF1:p.S34F[52.2%]	Y	N		N

994357	AML	prospective	BM	46,XX[20]	Y	N	None detected	0	t(11;19)(q23.3;p13.11)[23.6%],t(11;19)(q23.3;p13.11)[28.5%]	0	N	N	CONFIRMED: KMT2A breakapart FISH	t(11;19)(q23.3;p13.11)[23.6%],t(11;19)(q23.3;p13.11)[28.5%]
586748	AML	prospective	BM	46,XY[20]	Y	N	ETV6:p.Ser131PhefsTer23[35.7%]	0	t(7;21)(p22.1;q22.12)[23.1%]	ETV6:p.S131Ffs*23[46.3%]	N	N	CONFIRMED: PCR	t(7;21)(p22.1;q22.12)[23.1%]
651844	MDS	prospective	BM	45,X,-Y[8]/46,XY[12]	N	N		-Y[11.8%]	0	DNMT3A:NA[17.2%],NF1:p.V1909Afs*16[8.8%],GATA2:p.K390del[2.8%]	N	N		N
553306	MDS	prospective	BM	46,XX,del(X)(p11.2),?t(2;4)(q33;q31),t(3;10)(p21;p15),del(5)(q13q33),del(6)(q13q23),del(7)(p11.2p13),del(10)(q22),-11,add(12)(p11.1),+15,add(15)(p11.1),-16,add(17)(p11.2),add(21)(q22)[20]	N	YY	TP53:p.Arg273His[83.5%]	del(2)(q33.3q34)[85.0%],del(2)(q36.1q37.1)[85.2%],del(3)(p21.31p22.1)[82.6%],del(4)(q13.1q13.2)[85.8%],del(4)(q31.3q32.2)[83.3%],del(5)(q14.3q34)[86.0%],del(11)(q13.4q22.1)[76.7%],gain(11)(q24.2qter)[303.4%],del(11)(q25qter)[78.4%],del(12)(p12.2p13.2)[85.3%],gain(15)(q15.3qter)[70.7%],-16[87.1%],del(17)(p13.1p13.2)[82.4%]	0	TP53:p.R273H[80.0%]	N	YY		N
677322	AML	prospective	BM	46,XY[20]	Y	N	DNMT3A:p.Met548Thr[43.7%],IDH1:p.Arg132His[42.5%],EZH2:p.Glu392Lys[49.2%],CEBPA:p.Pro196TrpfsTer117[76.6%],CEBPA:p.Arg35ProfsTer126[34.5%],SMC1A:p.Arg586Trp[89.4%],PHF6:p.His43ProfsTer2[8.0%],PHF6:p.Glu293Ter[5.7%]	0	0	DNMT3A:p.M548T[42.5%],IDH1:p.R132H[28.9%],EZH2:p.E392K[56.5%],SMC1A:p.R586W[89.7%],CEBPA:p.P196Wfs*117[33.3%],CEBPA:p.R35Pfs*126[49.0%]	Y	N		N
281935	PNH	prospective	BM	46,XY[20]	Y	N	PIGA:p.Tyr43ThrfsTer18[3.9%]	0	0	0	Y	N		N
902503	AML	prospective	BM	46,XY[20]	Y	N	IDH2, SRSF2, TET2, RUNX1	0	0	IDH2:p.R140Q[54.1%],SRSF2:p.P95H[50.7%],RUNX1:p.R232W[59.5%]	Y	N		N
504451	MDS	prospective	BM	46,XY,add(5)(q11.2),-13,der(15)t(13;15)(q14;p11.2),-20[10]/46,XY,add(7)q11.2[5]/46,XY[5]	N	YY	TP53:p.Arg273His[81.2%]	del(5)(q11.2qter)[43.3%],del(7)(q11.22qter)[36.7%],del(13)(q12.13q14.3)[42.3%],del(20)(q11.22q13.31)[39.9%],gain(21)(q11.2q21.2)[67.1%],gain(21)(q22.13qter)[67.5%]	0	TP53:p.R273H[84.4%]	N	YY		N
410110	AML	prospective	BM	48,XX,+13,+13[7]/50,idem,+X,-13,+15,+19[2]/46,XX[7]	N	Y	DNMT3A:p.Arg882Cys[45.6%],SRSF2:p.Pro95His[48.4%],RUNX1:p.Arg166Ter[44.9%],RUNX1:p.Asp123GlyfsTer15[39.0%],FLT3:p.Phe612_Gly613insValTyrAspLeuLysTrpGluPheProArgGluAsnLeuGluPhe[0.1%]	gain(13)(q12.11qter)[87.1%],gain(15)(q11.2qter)[38.2%],+19[38.3%],+X[32.8%]	0	DNMT3A:p.R882C[54.3%],SRSF2:p.P95H[37.0%],RUNX1:p.R166*[49.3%],RUNX1:p.D123Gfs*15[55.3%],FLT3:p.F612_G613insVYDLKWEFPRENLEF[6.5%]	N	Y		N
296442	AML	prospective	BM	46~52,XY,-3,?add(5)(q3?3),del(7)(q22q34),-10,-13,-22,+2~9mar[cp20]	N	Y	TP53:[47.0%],TP53:p.Cys238Tyr[43.1%]	del(3)(p11.2pter)[94.2%],del(3)(q12.2q13.12)[89.9%],del(3)(q13.32q23)[93.7%],del(3)(q25.33q26.2)[93.8%],del(3)(q27.3qter)[94.1%],del(7)(q21.11qter)[94.3%],gain(13)(q12.11q14.11)[443.9%],del(13)(q14.11q21.33)[87.9%],gain(13)(q21.33q31.3)[476.9%],del(13)(q31.3qter)[93.4%]	0	TP53:NA[46.7%],TP53:p.C238Y[45.7%]	N	Y		N
889663	AML	prospective	BM	46,XX,del(5)(q22q35)[10]/46,XX[10]	N	N	WT1:p.Arg380ThrfsTer5[9.4%],RUNX1:p.Arg107Cys[8.3%],BCOR:[14.0%],BCORL1:p.Ser1143TrpfsTer82[5.9%]	del(5)(q21.1q33.3)[36.8%]	0	0	N	N		N
508617	MDS	prospective	BM	46,XX[20]	Y	N	TET2:p.Asp162ArgfsTer9[36.1%],TET2:p.Asn1118LysfsTer12[4.9%],IDH2:p.Arg140Gln[2.3%],SRSF2:p.Pro95His[45.7%],RUNX1:p.Gly165Ser[25.2%]	0	0	TET2:p.D162Rfs*9[51.8%],TET2:p.Q866*[28.6%],SRSF2:p.P95H[42.2%],RUNX1:p.G165S[27.3%]	Y	N		N
437892	MDS	prospective	BM	46,XX,add(1)(p13),der(6)t(1;6)(p32;q12),del(11)(q21)[8]/46,XX[12]	N	Y	CBL:p.Ile383Leu[22.0%],NF1:p.Arg897Gln[44.4%]	del(1)(p12p32.3)[53.8%],del(6)(q12q23.3)[53.9%],del(11)(q14.1q23.3)[53.3%]	0	CBL:p.I383L[32.8%],NF1:p.R897Q[59.7%]	N	Y		N
726806	AML	prospective	BM	46,XX[20]	Y	N	CSF3R:p.Gly366Arg[51.6%],TET2:p.Asn439ThrfsTer8[52.3%],NPM1:p.Trp288CysfsTer12[46.4%],FLT3:p.Trp603_Glu604insAspArgGluTyrGluTyrAspLeuLysTrp[23.4%],ASXL1:p.Gly219Val[44.0%]	0	0	CSF3R:p.G366R[63.3%],TET2:p.N439Tfs*8[37.7%],FLT3:p.W603_E604insDREYEYDLKW[41.0%],ASXL1:p.G219V[50.0%],NPM1:p.W288Cfs*12[48.1%]	Y	N		N
375074	AML	prospective	BM	45,XY,del(1)(p36.2),-7[18]/46,XY[2]	N	N	TET2:p.Val1180Asp[78.0%],NPM1:p.Trp288CysfsTer12[30.9%],IDH2:p.Arg140Gln[48.7%],SRSF2:p.Pro95Arg[44.8%]	del(1)(p35.1p36.32)[56.8%],-7[63.2%]	0	TET2:p.V1180D[83.7%],IDH2:p.R140Q[39.0%],SRSF2:p.P95R[52.2%],NPM1:p.W288Cfs*12[20.3%]	N	N		N
557196	AML	prospective	BM	46,XY[20]	Y	N	NRAS:p.Gly12Asp[3.8%],NRAS:p.Gly12Ser[23.6%],DNMT3A:p.Glu733Ter[37.7%],DNMT3A:p.Cys710Tyr[40.9%],TET2:[37.2%],KRAS:p.Ala18Asp[5.8%],FLT3:p.Lys602_Phe612dup[0.4%],FLT3:p.Tyr589_Glu604dup[0.8%],FLT3:p.Phe594_Glu598dup[0.5%],FLT3:p.Val581_Arg595dup[1.0%],ZRSR2:p.Glu133GlyfsTer11[74.6%],BCORL1:p.Cys908Ter[79.1%]	0	0	NRAS:p.G12S[16.3%],DNMT3A:p.E733*[44.4%],DNMT3A:p.C710Y[32.5%],TET2:NA[45.5%],ZRSR2:p.E133Gfs*11[37.9%],BCORL1:p.C908*[77.8%],FLT3:p.Y589_E604dup[6.3%]	Y	N		N
271002	MDS	prospective	BM	45,XY,-7[14]/46,XY[6]	N	N	DNMT3A:p.Arg882Cys[41.1%],EZH2:p.Gln612Ter[9.5%],ETV6:p.Val158ProfsTer10[11.6%],IDH2:p.Arg140Gln[38.9%],BCORL1:p.Asn1481Ser[99.5%],PHF6:p.Ser246Thr[13.6%],PHF6:p.Ser247Tyr[13.6%],PHF6:p.Arg342Ter[5.7%]	-7[76.5%]	0	DNMT3A:p.R882C[42.5%],IDH2:p.R140Q[44.7%],BCORL1:p.N1481S[100.0%],ETV6:p.V158Pfs*10[12.2%]	N	N		N
259112	AML	prospective	BM	46,XY[20]	Y	N	DNMT3A:p.Arg882His[89.7%],IDH2:p.Arg140Gln[44.3%],SRSF2:p.Pro95His[49.5%]	0	0	DNMT3A:p.R882H[94.8%],IDH2:p.R140Q[51.7%],SRSF2:p.P95H[43.8%]	Y	N		N
819978	AML	prospective	BM	60~65<3n>,XXYY,+1,-2,-4,+6,add(6)(p22),-7,-8,-11,-12,add(12)(p11.2),-13x3,-14,-15,-17,-18,-19,+20,+21,-22,-22,+1~4mar[cp13]/86<4n>,XXXXYYY,-2,-3,-4x2,+6,add(6)(p22),-7x2,-8,-10x2,-11,-13x2,-14,-15,+16,+3mar[1]/46,XY[6]	N	Y	NRAS:p.Gly13Asp[9.0%],KRAS:p.Gly13Asp[10.6%],IDH2:p.Arg140Gln[41.0%],TP53:p.Lys132Arg[77.8%],NF1:p.Gln985Ter[4.8%],SRSF2:p.Pro95Leu[51.0%]	+1[55.9%],-2[27.8%],-4[30.9%],+6[57.3%],-7[27.7%],-8[16.7%],-11[28.5%],-12[25.0%],del(13)(q12.11qter)[35.3%],del(15)(q11.2qter)[30.4%],gain(21)(q11.2qter)[36.7%],del(22)(q11.21qter)[18.5%],+Y[27.2%]	0	NRAS:p.G13D[9.0%],IDH2:p.R140Q[36.2%],TP53:p.K132R[72.2%],SRSF2:p.P95L[54.7%]	N	Y		N
895870	AML	prospective	BM	46,XX[20]	Y	N	NPM1:p.Leu287IlefsTer13[27.5%],NPM1:p.Trp288CysfsTer12[28.0%],NPM1:p.Trp288CysfsTer12[28.1%],FLT3:p.Val592Gly[27.1%],IDH2:p.Arg140Gln[48.9%],SRSF2:p.Arg94dup[45.9%],ASXL1:p.Gly646TrpfsTer12[11.1%],STAG2:p.Ala956PhefsTer4[9.0%]	0	0	FLT3:p.V592G[38.6%],IDH2:p.R140Q[37.5%],SRSF2:p.R94dup[48.9%],NPM1:p.W288Cfs*12[30.0%]	Y	N		N
992091	AML	prospective	BM	44,XY,add(2)(p?14),add(3)(q21),add(5)(q31),-6,-7,i(8)(q10)x2,add(12)(q13),add(15)(p11.2),-16,-17,-18,add(22)(q13),+1~4mar[cp13]/46,XY[7]	N	Y	DNMT3A:p.Gly532Ser[2.4%],TP53:p.Arg342Ter[67.1%],ASXL1:p.Leu1413Ser[34.8%]	del(2)(p23.3pter)[78.3%],del(3)(q13.11q13.31)[83.5%],del(4)(q26q28.3)[80.3%],del(5)(q23.3qter)[77.0%],-6[83.1%],del(7)(q11.23qter)[82.6%],del(8)(p11.22pter)[81.1%],+8[212.1%],del(12)(q13.2q14.2)[82.3%],del(12)(q21.32q22)[82.2%],-16[77.6%],-17[74.2%],del(18)(q11.2qter)[83.2%]	0	TP53:p.R342*[71.9%],NF1:p.I679Dfs*21[71.7%],ASXL1:p.L1413S[44.9%]	N	Y		N

150377	MDS	prospective	BM	46,XX[20]	Y	N	None detected	0	0	0	Y	N		N
438506	MDS	prospective	BM	46,XY[20]	Y	N		0	0	DNMT3A:p.M406Dfs*2[24.8%],EZH2:p.P132L[39.5%],ASXL1:p.Y591*[44.8%],ASXL1:p.L1304V[46.7%],U2AF1:p.Q157P[33.3%]	Y	N		N
333171	MDS	prospective	BM	46,XY[10]	NA	N	TET2:p.Tyr1964His[47.9%],ETV6:p.Arg353Gln[49.7%],KRAS:p.Gly12Ala[37.0%],SMC1A:p.Arg96His[28.6%]	0	0	TET2:p.Y1964H[40.4%],ETV6:p.R353Q[50.8%],KRAS:p.G12A[40.5%],SMC1A:p.R96H[21.2%]	Y	N		NK
606753	MDS	prospective	BM	46,XY[20]	Y	N	ZRSR2:p.R442dup[100%]	0	0	ZRSR2:p.R442dup[68.0%]	Y	N		N
704854	AML	prospective	BM	46,XY[20]	Y	N	DNMT3A:p.Arg899Cys[42.0%],DNMT3A:p.Arg598Ter[45.9%],GATA2:p.Thr387_Lys389del[30.2%],EZH2:p.Ile744Thr[5.3%],PTPN11:p.Gly503Val[25.8%],ASXL1:p.Ala640GlyfsTer60[4.3%],ASXL1:p.Pro808LeufsTer10[41.1%]	0	0	DNMT3A:p.R899C[40.6%],DNMT3A:p.R598*[36.8%],PTPN11:p.G507V[31.2%],ASXL1:p.P808Lfs*10[20.8%],GATA2:p.T387_K389del[29.8%]	Y	N		N
952492	MDS	prospective	BM	46,XY[20]	Y	N	DNMT3A:p.Thr44Met[48.3%],ASXL1:p.Gln428ThrfsTer10[21.9%],BCOR:p.Val11Ala[100.0%]	0	0	DNMT3A:p.T44M[52.5%],ASXL1:p.Q428Tfs*10[32.9%],BCOR:p.V11A[100.0%]	Y	N		N
312088	AML	prospective	BM	47,XY,+21[17]/46,XY[3]	N	N	NRAS:p.Gly13Asp[7.7%],NRAS:p.Gly12Ser[2.4%],DNMT3A:p.Arg882Cys[44.7%],NPM1:p.Trp288CysfsTer12[38.4%],NPM1:p.Trp288CysfsTer12[38.4%],RAD21:p.Met362SerfsTer8[42.6%],WT1:p.Ala5Val[47.6%],WT1:p.Ala5Thr[47.7%],KRAS:p.Gln61Leu[8.8%],PTPN11:p.Gly60Val[18.8%]	gain(21)(q11.2qter)[88.6%]	0	NRAS:p.G13D[7.7%],DNMT3A:p.R882C[53.1%],WT1:p.A5V[33.3%],WT1:p.A5T[39.1%],NPM1:p.W288Cfs*12[24.2%],RAD21:p.M362Sfs*8[32.3%]	N	N		N
430826	AML	prospective	BM	46,XY,t(15;17)(q24;q21)[5]/46,XY[1]	N	N		gain(2)(q14.1qter)[23.6%],gain(7)(p12.3p14.1)[23.6%],-7[21.5%],del(9)(p21.1pter)[17.4%],gain(9)(q22.33qter)[21.4%],del(10)(p11.21pter)[23.8%],gain(10)(q11.21qter)[22.1%],del(13)(q12.11qter)[20.7%],del(16)(q23.1qter)[21.7%],del(18)(p11.21pter)[15.2%],gain(19)(p12pter)[21.7%],gain(20)(q11.21qter)[35.8%]	t(15;17)(q24.1;q21.2)[3.3%],t(15;17)(q24.1;q21.2)[4.1%]	0	N	Y		Complex
570496	MDS	prospective	BM	46,XY[20]	Y	N	SF3B1:p.Glu592Lys[41.2%],IDH2:p.Arg140Gln[49.4%],CEBPA:p.Glu284Ter[2.7%],ASXL1:p.Gly646TrpfsTer12[46.3%],STAG2:p.Arg216Ter[40.4%],STAG2:p.Arg614Ter[35.4%]	0	0	SF3B1:p.E592K[46.6%],IDH2:p.R140Q[43.5%],ASXL1:p.G646Wfs*12[36.3%],STAG2:p.R216*[52.0%],STAG2:p.R614*[32.1%]	Y	N		N
994807	None	prospective	BM	46,XY[20]	Y	N	None detected	0	0	0	Y	N		N
229201	AML	prospective	BM	46,XY[5]	NA	N	NPM1:p.Trp288CysfsTer12[26.2%],FLT3:p.Leu601_Lys602insGlySerAspAsnGluTyrPheTyrValAspPheArgGluTyrGluTyrAspLeu[7.3%],FLT3:p.Leu601_Lys602insGlySerAspAsnGluTyrPheTyrValAspPheArgGluTyrGluTyrAspLeu[7.0%],FLT3:p.Arg595_Glu596insTer[12.3%],FLT3:p.Asp593_Phe594insLeuArgAspPheGluTyrAspLeuValSerAspAsnGluTyrPheTyrPheAsp[8.9%],IDH2:p.Arg140Gln[37.0%]	0	0	IDH2:p.R140Q[37.7%],NPM1:p.W288Cfs*12[15.5%],FLT3:p.S585_L601dup[14.0%]	Y	N		NK
983349	AML	prospective	BM	42~43,XY,add(3)(q10),add(5)(q13),-7,-9,add(11)(p10),der(11)hsr(11)(q23),-12,add(16)(p11.2),add(16)(q12),-17,-18,+mar[cp20]	N	Y	TP53:p.Tyr126Cys[53.5%],SMC1A:p.Ile1062Met[100.0%]	del(3)(q11.2q24)[41.7%],gain(3)(q26.1qter)[34.1%],+5[30.3%],del(5)(q11.2q12.3)[79.7%],del(5)(q31.1qter)[74.3%],-7[41.3%],gain(9)(p13.3pter)[102.6%],del(11)(p11.2pter)[36.4%],gain(11)(q23.2qter)[110.4%],del(12)(q23.1q24.13)[77.2%],del(16)(q23.3qter)[75.1%],del(17)(p13.1pter)[75.3%],del(17)(q11.2q21.33)[29.8%],-18[46.0%],+19[36.6%],gain(21)(q11.2qter)[61.4%]	0	TP53:p.Y126C[71.8%],SMC1A:p.I1062M[100.0%]	N	Y		N
534164	MDS	prospective	BM	45,XY,-7[20]	N	N	DNMT3A:p.Arg326Cys[44.2%],RAD21:p.Gly273Cys[13.2%],ETV6:p.Ala377Val[40.4%]	-7[83.9%],del(13)(q14.2q14.3)[85.3%]	0	DNMT3A:p.R326C[50.9%],ETV6:p.A377V[37.9%]	N	N	CONFIRMED: del(19p) by Sequence breakpoints	del(13)(q14.2q14.3)[85.3%]
931622	MDS	prospective	BM	46,XY,del(10)(p1?3)[2]/46,XY,t(1;3)(p36.3;q21)[1]/46,XY[17]	N	N		0	0	SF3B1:p.K700E[34.2%],RUNX1:p.G170Rfs*43[23.2%]	Y	N	CONFIRMED: FISH for 10p: normal result	N
925086	AML	prospective	BM	46,XX[20]	Y	N	DNMT3A:p.Arg882His[40.1%],NPM1:p.Trp288CysfsTer12[40.6%],ASXL1:p.Thr1498Met[50.6%],BCOR:p.Asn790Ser[49.6%]	0	0	DNMT3A:p.R882H[42.9%],ASXL1:p.T1498M[46.6%],BCOR:p.N790S[52.7%],NPM1:p.W288Cfs*12[40.3%]	Y	N		N
875579	AML	prospective	BM	47,XX,t(3;21)(q26;q22),del(7)(q32),+14[19]/46,XX[1]	N	Y	CSF3R:p.Gln770Ter[28.6%],U2AF1:p.Gln157Pro[28.2%]	del(7)(q33q36.2)[46.7%],gain(14)(q11.2qter)[46.2%]	t(3;21)(q26.2;q22.12)[6.5%],t(3;21)(q26.2;q22.12)[11.4%]	CSF3R:p.Q770*[15.7%],U2AF1:p.Q157P[14.8%]	N	Y	CONFIRMED: Cyto	N
679540	AML	prospective	BM	46,XX,inv(3)(q21q26.1)[3]/45,sl,der(16;17)(p10;q10)[4]/46,sdl,+13[5]/46,XX[8]	N	N	SF3B1:p.His662Asp[24.4%],TP53:p.Met160_Ala161del[38.7%],NF1:p.Arg816Ter[11.5%]	del(16)(q11.2qter)[81.4%],-17[78.9%]	inv(3)(q21.3q26.2)[29.2%],inv(3)(q21.3q26.2)[30.6%]	SF3B1:p.H662D[39.7%],TP53:p.M160_A161del[67.2%],NF1:p.R816*[43.3%]	N	N		N
477377	AML	prospective	BM	46,XY[20]	Y	N	NRAS:p.Gly12Asp[4.6%],NRAS:p.Gly12Ser[6.5%],IDH2:p.Arg140Gln[44.5%],SRSF2:p.Pro95_Arg102del[44.3%],SMC1A:p.Arg790Gln[81.4%]	0	0	IDH2:p.R140Q[50.8%],SRSF2:p.P95_R102del[45.2%],SMC1A:p.R790Q[80.6%]	Y	N		N
493436	AML	prospective	BM	46,XX,t(2;15)(q23;q15)[11]/46,XX[9]	N	N	NRAS:p.Gly12Cys[36.9%],RUNX1:p.Pro294GlnfsTer12[36.8%],RUNX1:p.Ser141_Ala142insGlyPro[37.7%]	0	0	NRAS:p.G12C[45.8%],RUNX1:p.P294Qfs*12[22.4%],RUNX1:p.S141_A142insGP[21.3%]	Y	N		N
429293	AML	prospective	BM	47,XX,+8[7]/46,XX[13]	N	N	RAD21:p.Arg65Ter[20.9%],PTPN11:p.Gln79Arg[21.9%],IDH2:p.Arg140Gln[24.5%],RUNX1:[26.7%],RUNX1:p.Ala149Pro[22.8%],BCOR:[31.3%]	+8[50.3%]	0	RAD21:p.R65*[22.8%],PTPN11:p.Q79R[30.4%],IDH2:p.R140Q[19.6%],RUNX1:NA[25.9%],BCOR:NA[36.9%]	N	N		N
802619	MDS	prospective	BM	42~49,XX,add(1)(p13),add(1)(q12),del(1)(q32q44)x1~2,-2,der(14;15)(q10;q10),der(15;22)(q10;q10),-19,-20,-21,-22,+2 ~6mar[cp10]/46,XX[10]	N	YY	RAD21:[18.3%],TP53:p.Ile232Thr[24.9%],TP53:p.Ala86CysfsTer63[24.7%]	gain(1)(q31.1q41)[13.1%],gain(1)(q43qter)[14.7%],gain(19)(p12pter)[34.9%],gain(21)(q21.1q22.2)[18.0%]	0	TP53:p.A86Cfs*63[27.5%]	N	YY		N
294891	MDS	prospective	BM	46,XX[20]	Y	N	TET2:p.Thr1554AspfsTer24[18.8%],NPM1:p.Trp288CysfsTer12[26.7%],SRSF2:p.Pro95His[36.7%],STAG2:p.Ala520Asp[3.1%]	0	0	TET2:p.Q530Lfs*4[37.5%],TET2:p.T1554Dfs*24[49.2%],SRSF2:p.P95H[42.2%],NPM1:p.W288Cfs*12[7.3%]	Y	N		N
731757	AML	prospective	BM	46,XY[20]	Y	N	DNMT3A:p.Gly685Val[51.4%],NPM1:p.Trp288CysfsTer12[40.8%],NPM1:p.Trp288CysfsTer12[40.8%],SMC3:p.Gly655Asp[44.7%],FLT3:[10.8%],FLT3:[15.6%],FLT3:p.Lys602delinsAsnProProGluGlyGlyGlyIleTerIleTerSerGlnMetGlyValSerLysArgLysPheArgValTer[9.2%],FLT3:p.Leu601_Lys602insProProGluGlyGlyGlyIleTerIleTerSerGlnMetGlyValSerLysArgLysPheArgValCys[8.0%],FLT3:p.Leu601delinsProProAr	0	0	DNMT3A:p.G685V[45.6%],SMC3:p.G655D[45.5%],NPM1:p.W288Cfs*12[28.2%],FLT3:NA[7.1%]	Y	N		N

							gLysValGlyGluTyrGluTyrAspLeuLysTrpGluPheProArgGluAsnLeuGluPheVal[9.7%],FLT3:p.Asp600_Leu601insProProGlyArgTrpGlyAsnMetAsnMetIleSerAsnGlySerPheGlnGluLysIleTerSerLeu[9.7%],FLT3:p.Asp600_Leu601insProLysValGlnLeuThrGlySerSerAspTyrGluTerPheTerValAspPheArgGluTyrGluTyrAsp[10.1%],FLT3:p.Glu598_Tyr599insTer[16.5%],FLT3:p.Tyr597_Glu598insThrPheAspPheArgGluTyr[12.0%]							
335141	AML	prospective	BM	46,XY, add(2)(q37)[6]	N	N	DNMT3A:p.Arg882His[44.8%],SF3B1:p.Lys700Glu[44.4%],FLT3:p.Leu601_Lys602insAsnTyrValAspPheArgGluTyrGluTyrAspLeu[18.8%],FLT3:p.Phe594_Asp600dup[27.6%],FLT3:p.Arg595_Glu596insAspHisValAspPheArg[30.7%],FLT3:p.Val581_Phe594dup[31.8%],FLT3:p.Val592_Asp593insValPheValThrGlySerSerAspAsnGluTyrPheTyrVal[33.7%]	del(2)(q36.3qter)[89.1%],gain(11)(q13.4qter)[90.2%]	0	DNMT3A:p.R882H[52.1%],SF3B1:p.K700E[39.4%],FLT3:p.L601_K602insNYVDFREYEYDL[21.6%],FLT3:p.V581_F594dup[22.5%]	N	N		Not Complex
155912	AML	prospective	BM	46,XX,der(3)t(3;6)(q25;q13),der(6)t(3;6)(q25;q13)t(6;8)(p23;q13)[19]/46,XX[1]	N	N	DNMT3A:p.Cys557Arg[42.2%],NPM1:p.Trp288CysfsTer12[38.4%],WT1:p.Arg369GlyfsTer7[43.2%],PTPN11:p.Thr553Met[45.8%],FLT3:p.Phe605_Pro606insArgHisGluTyrAspLeuLysTrpGluPhe[12.9%],FLT3:p.Tyr597_Glu598insAspProAlaAspPheArgGluTyr[19.9%],NF1:p.Ile679AspfsTer21[2.4%]	del(3)(p12.2p14.1)[76.6%],del(6)(p24.1pter)[75.1%],del(6)(q14.1q14.3)[77.6%],gain(8)(q12.1qter)[72.8%]	0	DNMT3A:p.C557R[36.9%],PTPN11:p.T557M[47.6%],NPM1:p.W288Cfs*12[37.1%],WT1:p.R369Gfs*7[42.1%],FLT3:p.F605_P606insRHEYDLKWEF[17.9%]	N	Y	CONFIRMED: CS BY ARRAY	Complex
677982	AML	prospective	BM	47,XY,+i(21)(q10)[14]/47,XY,+21[2]/46,XY[4]	N	N	None detected	gain(21)(q11.2qter)[173.8%]	t(6;11)(q27;q23.3)[28.8%]	0	N	N	CONFIRMED: KMT2A breakapart FISH	t(6;11)(q27;q23.3)[28.8%]
103744	AML	prospective	BM	46,XX[3]	NA	N	TP53:p.Phe134Val[29.6%],NF1:p.Gln756Ter[4.3%]	del(3)(p11.2pter)[61.8%],+5[76.7%],del(5)(q11.2qter)[60.6%],-7[57.2%],+8[57.6%],+9[52.3%],gain(15)(q11.2qter)[43.2%],del(16)(q21qter)[58.5%],del(17)(p13.1pter)[53.0%],+18[43.5%],gain(22)(q11.21q12.3)[64.0%]	0	TP53:p.F134V[50.0%]	N	Y	CONFIRMED: FISH positive for TP53 and CEP17 deletion	Complex
956161	AML	prospective	BM	45,X,-Y[22]	N	N	SF3B1:p.Lys666Thr[44.9%],FLT3:p.Glu598_Tyr599insGluValGlnValThrGlySerSerAspAsnGluTyrTyrTyrAspAspPheArgTerTyrGlu[5.2%],FLT3:p.Val581_Glu596dup[6.8%],FLT3:p.Arg595_Glu596insAspGluValGlnLeuThrGlySerThrAspAsnGluTyrIleTyrValAspPheArgGluTyr[6.9%],FLT3:p.Tyr589_Phe590insLeuValGlnValThrGlySerSerAspAsnGluTyr[3.9%],FLT3:p.Glu588_Tyr589insPhePheTyrValAspPheArgAspTyrTerLeuValGlnValThrGlySerSerAspIleGlu[7.6%],FLT3:p.Asp586_Asn587insIleGluPhePheTyrValAspLeuArgGluTyrGluGluValGlnValThrGlySerSerAsp[7.6%],FLT3:p.Ser584_Ser585insTer[7.6%],STAG2:p.Ile790Phe[3.9%],STAG2:p.Ile794Phe[3.3%]	-Y[96.7%]	0	SF3B1:p.K666T[49.1%],FLT3:p.E598_Y599insEVQVTGSSDNEYFYVDFREYE[27.1%]	N	N		N
673325	MDS	prospective	BM	46,XY[20]	Y	N	NRAS:p.Gly13Asp[11.3%],NRAS:p.Gly12Asp[10.1%],FLT3:p.Arg595_Asp600dup[0.3%],FLT3:p.Leu576_Tyr589dup[0.2%],U2AF1:p.Ser34Phe[46.2%],BCOR:p.Arg976Ter[96.1%],STAG2:p.Glu849ArgfsTer23[94.9%]	0	0	NRAS:p.G13D[8.7%],NRAS:p.G12D[7.5%],U2AF1:p.S34F[40.6%],BCOR:p.R976*[95.0%],STAG2:p.E849Rfs*23[61.1%]	Y	N		N
451688	MDS	prospective	BM	46,XY[3]	NA	N	EZH2:p.Arg360ThrfsTer5[20.8%],ASXL1:p.Gly646TrpfsTer12[30.6%],ZRSR2:[59.5%]	del(4)(q21.1q25)[53.3%],-Y[27.1%]	0	ASXL1:p.G646Wfs*12[30.2%],ZRSR2:NA[68.0%],EZH2:p.R360Tfs*5[16.7%],JAK2:p.V617F[4.8%]	N	N	CONFIRMED: FISH and array positive for deletion of 4q22.1	Independent clones
905177	ALL	prospective	BM	46,XY,t(9;22)(q34;q11.2)[20]	N	N		gain(9)(q34.12qter)[58.2%],del(19)(p13.3pter)[53.8%],gain(22)(q11.21q11.23)[54.9%]	t(9;22)(q34.12;q11.23)[32.6%],t(9;22)(q34.12;q11.23)[43.8%]	0	N	Y	CONFIRMED: Cs BY ARRAY	gain(9)(q34.12qter)[58.2%],del(19)(p13.3pter)[53.8%],gain(22)(q11.21q11.23)[54.9%]
891309	MDS	prospective	BM	46,XY[5]	NA	N	TP53:p.Arg306Ter[22.4%],TP53:p.Met237Ile[2.4%],ASXL1:p.Glu635ArgfsTer15[18.8%],ASXL1:p.Trp796GlyfsTer22[5.9%]	0	0	TP53:p.R306*[19.5%],ASXL1:p.E635Rfs*15[8.2%]	Y	N		NK
869692	MDS	prospective	BM	46,XY[21]	Y	N		0	0	SF3B1:p.E622D[37.0%]	Y	N		N
572410	MDS	prospective	BM	41~47,X,add(X)(p11.2),+3,add(3)(q11.2),?add(5)(q11.2),-17,der(17)t(11;17)(q13;p12),-20,add(20)(q11.2),+21,i(21)(q10),+1~2mar[cp4]/46,XX[16]	N	YY	TP53:p.Arg213Ter[12%]	gain(1)(p21.2p36.32)[18.8%],del(5)(q13.1q34)[18.5%],gain(11)(q13.4qter)[17.3%],del(16)(q23.1qter)[16.8%],del(17)(p13.1pter)[16.6%],del(18)(q12.1qter)[16.7%],gain(22)(q11.21qter)[52.5%],gain(X)(p21.1pter)[11.7%]	0	0	N	YY		N
395906	MDS	prospective	BM	46,XY,del(3)(q12q25),+8[20]	N	N	DNMT3A:p.Arg882His[44.6%],NF1:p.Arg1534Ter[52.6%],PPM1D:p.Leu484Ter[45.0%],ASXL1:p.Ser921Phe[48.3%],RUNX1:p.Phe97Ser[43.1%],U2AF1:p.Ser34Phe[43.4%]	del(3)(q21.2q24)[83.4%],del(4)(q28.3q31.1)[65.6%],+8[82.7%]	0	DNMT3A:p.R882H[50.9%],NF1:p.R1534*[54.5%],PPM1D:p.L484*[47.2%],ASXL1:p.S921F[58.6%],RUNX1:p.F97S[35.2%],U2AF1:p.S34F[56.8%]	N	Y	CONFIRMED: 4q28.3 deletion by FISH	Complex
830563	ALL	prospective	BM	45~48,XX,+1,-4,-5,del(5)(q13q31),der(7)del(p?14)add(q32),+8,del(9)(p22),-13,?del(13)(q22),+15,add(15)(p11.2),-16,-19,-20,+21,-22,+1~4mar[cp20].	N	Y	TP53:p.Tyr220Cys[41.8%],TP53:p.Gln167LeufsTer15[42.4%]	del(4)(q23q24)[93.3%],del(5)(q14.2q34)[93.6%],del(7)(q32.3q36.1)[93.0%],gain(9)(p21.3pter)[227.4%],del(9)(p21.1p21.3)[88.0%],gain(9)(p13.1p21.1)[227.5%],-16[86.3%],del(20)(q11.21q13.13)[90.1%],gain(21)(q11.2qter)[45.3%]	0	TP53:p.Y220C[63.0%],TP53:p.Q167Lfs*15[47.8%]	N	Y		N
467399	AML	prospective	BM	46,XY[20]	Y	N	DNMT3A:p.Arg882His[45.4%],TET2:p.Val1213PhefsTer11[40.3%],TET2:p.Cys1271TrpfsTer29[24.0%],NPM1:p.Trp288CysfsTer12[41.7%],FLT3:p.Asn841Lys[15.9%]	0	0	DNMT3A:p.R882H[53.2%],TET2:p.V1213Ffs*11[43.4%],TET2:p.C1271Wfs*29[20.5%],FLT3:p.N841K[23.6%],NPM1:p.W288Cfs*12[43.2%]	Y	N		N
205587	AML	prospective	BM	46,XY,t(15;17)(q24;q21)[1]/47,sl,+8[1]/48,sdl,+21[18]/46,XY[2]	N	N		+8[47.6%],gain(21)(q11.2qter)[47.7%]	t(15;17)(q24.1;q21.2)[21.9%],t(15;17)(q24.1;q21.2)[12.9%]	FLT3:p.S584_D593dup[17.2%]	N	N		N
764488	AML	prospective	PB	46,XY[10]	NA	N	NRAS:p.Gly12Asp[3.5%],DNMT3A:[46.9%],TET2:p.His1380Tyr[49.0%],TET2:p.Ala1919ProfsTer31[45.3%],NPM1:p.Trp288CysfsTer12[30.4%],FLT3:p.Leu576Gln[14.0%],FLT3:p.Tyr572Cys[4.1%],CEBPA:p.Glu59ProfsTer102[25.1%]	+4[7.7%],gain(21)(q22.2qter)[10.7%]	0	DNMT3A:NA[52.4%],TET2:p.H1380Y[46.2%],TET2:p.A1919Pfs*31[36.1%],FLT3:p.L576Q[17.3%],CEBPA:p.E59Pfs*102[34.6%],NPM1:p.W288Cfs*12[33.3%]	N	N	CONFIRMED: FISH positive for trisomy 4	Not Complex

809382	AML	prospective	BM	46,XX[20]	Y	N	DNMT3A:p.Gln615Ter[43.0%],TET2:p.Lys824Ter[39.1%],TET2:p.Gln962Ter[43.2%],NPM1:p.Trp288CysfsTer12[36.5%],SRSF2:p.Pro95Arg[25.7%]	0	0	DNMT3A:p.Q615*[49.0%],TET2:p.K824*[47.6%],TET2:p.Q962*[46.1%],SRSF2:p.P95R[53.4%],NPM1:p.W288Cfs*12[44.6%]	Y	N		N
917922	AML	prospective	BM	46,XY, t(15;17)(q24;q21)[20]	N	N		0	t(15;17)(q24.1;q21.2)[26.9%],t(15;17)(q24.1;q21.2)[27.4%]	FLT3:p.W603_N609dup[50.5%]	N	N		N
211740	AML	prospective	BM	46,XX,t(3;3)(q21;q26.2)[20]	N	N	SF3B1:p.Lys666Glu[55.6%],WT1:p.Arg380ProfsTer2[2.7%],RUNX1:p.Gly199Arg[28.6%]	0	gain(3)(q21.3q26.2)[23.1%],del(3)(q21.3q26.2)[26.5%]	SF3B1:p.K666E[39.1%],WT1:p.R462W[17.2%],RUNX1:p.G199R[35.3%]	N	N		N
462268	AML	prospective	BM	46,XY,t(8;21)(q22;q22)[4]/46,idem,inv(18)(p11.2q21.3)[13]	N	N	SMC3:[43.9%]	0	t(8;21)(q21.3;q22.12)[26.3%],t(8;21)(q21.3;q22.12)[28.6%]	SMC3:NA[37.3%]	N	N		N
267935	AML	prospective	BM	46,XY,inv(16)(p13.1q22)[6]/46,XY[4]	N	N	NRAS:p.Gly13Arg[2.5%],KIT:p.Thr417del[11.3%],KIT:p.Asp419del[12.2%],KIT:p.Trp557Arg[3.8%],KIT:p.Asn655Lys[3.1%],WT1:p.Val371CysfsTer14[2.8%]	0	inv(16)(q22.1p13.11)[38.8%],inv(16)(q22.1p13.11)[25.3%]	0	N	N		N
491972	AML	prospective	BM	46,XY[20]	Y	N	DNMT3A:p.Gln886Glu[34.2%],TET2:p.Gln913Ter[29.0%],NPM1:p.Trp288CysfsTer12[27.3%]	0	0	DNMT3A:p.Q886E[48.1%],TET2:p.Q913*[46.5%],NPM1:p.W288Cfs*12[49.1%]	Y	N		N
783803	MDS	prospective	BM	46,XX[20]	Y	N		0	0	NRAS:p.G13V[47.8%],TET2:p.H1868Y[52.6%],TET2:p.H1881R[36.7%],EZH2:p.Y153D[92.0%],STAG2:p.R259*[46.5%]	Y	N		N
872523	MDS	prospective	BM	44~45,XY,add(5)(p13),del(7)(q32),-12,-16,add(17)(p11.2),-20,+21,+1~2mar[cp19]/46,XY[1]	N	YY	TP53:[44.3%],TP53:[43.6%],RUNX1:p.Arg233Leu[49.0%]	del(12)(p11.21pter)[89.0%],del(12)(q21.32qter)[85.8%],del(16)(q11.2qter)[85.6%],del(17)(p13.2pter)[65.9%],-17[83.5%]	0	TP53:NA[42.9%],TP53:NA[46.5%],RUNX1:p.R233L[60.7%]	N	YY		N
188798	AML	prospective	BM	47,XX,der(1)t(1;7)(q32;p13),del(5)(q22q35),-7,+8,del(12)(p11.2),der(13)del(13)(q14q14)inv(13)(p13q13),add(18)(p11.2),+19[4].	N	Y	TP53:p.Arg248Trp[20.5%],TP53:p.Leu145Pro[31.2%]	del(5)(q21.3q33.3)[47.1%],del(7)(q11.23q36.1)[47.5%],+8[41.3%],del(12)(p11.21p13.2)[42.2%],del(18)(p11.23pter)[38.7%],+19[37.5%]	0	TP53:p.R248W[27.7%],TP53:p.L145P[27.4%]	N	Y		N
739025	MDS	prospective	BM	46~47,XY,-5,del(7)(q22q34),+8,t(11;15)?(p15;q22),+mar[cp14]/46,XY[6]	N	Y	TP53:p.Cys275Tyr[75.3%]	del(5)(q11.2qter)[63.2%],del(7)(q21.2qter)[63.2%],+8[43.1%]	0	TP53:p.C275Y[75.9%]	N	Y		Complex
506517	AML	prospective	BM	46,XX[20]	Y	N	NPM1:p.Trp288CysfsTer12[48.2%],WT1:p.Glu384AspfsTer8[38.9%],BCOR:p.Pro678Ser[45.9%],BCORL1:p.Val329Leu[49.6%]	0	0	WT1:p.E384Dfs*8[51.4%],BCOR:p.P678S[52.6%],BCORL1:p.V329L[48.5%],NPM1:p.W288Cfs*12[42.2%],FLT3:p.F621_G622insEYEYDLKWEFPRENLEFGKNGMCQMFLQHFFSIGKSLKCTYSPFVFAGKVLGSGAF[21.4%]	Y	N		N
985517	MDS	prospective	BM	47,XY,+11[3]	N	N	SMC3:p.Gly1118Ter[6.2%],TP53:p.Tyr220Cys[8.5%]	+11[8.1%]	0	0	N	N		N
553902	AML	prospective	BM	49,XY,+1,del(5)(q13q33),+8,-16,add(17)(p13),der(17)del(17)(p12)del(17)(q11.1q12),+21,+21[18]/50,idem,+mar[2]	N	Y	None detected	gain(1)(p31.1p36.32)[82.9%],+1[67.1%],del(5)(q11.2q34)[82.9%],+8[80.5%],del(16)(q23.1qter)[83.1%],del(17)(p13.1pter)[78.8%],gain(21)(q11.2qter)[116.7%]	0	0	N	Y	CONFIRMED: Cs BY ARRAY	N
538465	AML	prospective	BM	46,XY,t(15;17)(q24;q21)[17]/46,XY[3]	N	N		+8[27.6%],+10[29.3%]	t(15;17)(q24.1;q21.2)[34.2%],t(15;17)(q24.1;q21.2)[28.8%]	0	N	N	CONFIRMED: +8 and +10 by FISH	Not Complex
537017	AML	prospective	BM	74<3N>,XXY,+1,?add(1)(p22),+2,+3,+6,-19,+21,+22[1]/82<4N>,XXYY,-1,?add(1)(p22),-2,-3,-4,-5,-7,-11,add(11)(q13),-12,-13,-14,-15,-16,-17,-18,-18,-19,add(19)(q13.3),-21,-22,+8mar[1]/46,XY[18].	N	Y	TP53:p.His168Arg[33.1%]	gain(1)(p32.1p35.2)[26.1%],-4[14.5%],-5[30.4%],+6[32.3%],-7[13.3%],gain(8)(q21.11qter)[18.8%],-11[21.3%],-12[11.3%],gain(13)(q12.11qter)[28.5%],-16[29.2%],del(17)(p12pter)[28.7%],+19[32.2%],gain(21)(q11.2qter)[17.8%]	0	TP53:p.H168R[43.2%]	N	Y		N
666013	AML	prospective	BM	46,XX,del(3)(?p24)[10]/46,XX[10]	N	N	DNMT3A:p.Asn797Ser[2.2%],DNMT3A:[30.2%],IDH1:p.Arg132Cys[11.6%],TET2:p.Ser1239Cys[2.1%],BCOR:p.Gln123ArgfsTer38[9.4%],PHF6:p.Arg277GlufsTer2[10.8%]	del(5)(q31.2q31.2)[10.1%]	0	DNMT3A:NA[54.2%],IDH1:p.R132C[23.8%],BCOR:p.Q123Rfs*38[22.7%],PHF6:p.R277Efs*2[32.1%]	N	N	CONFIRMED: FISH negative for 3p11.1 and 3p26.3 C or aneuploidy; small del(5q) by FISH	del(5)(q31.2q31.2)[10.1%]; Omitted from CNA performance comparisons due to size <5Mbp
967740	MDS	prospective	BM	46,XX[18]	NA	N	TP53:p.Tyr126His[2.7%]	0	0	0	Y	N		NK
887041	AML	prospective	BM	46,XY[20]	Y	N	NRAS:p.Gly13Asp[2.9%],NRAS:p.Gly13Arg[6.9%],DNMT3A:p.Arg598Ter[46.6%],DNMT3A:p.Thr65Lys[49.4%],IDH1:p.Arg132Leu[44.4%],FLT3:p.Asp835Glu[21.7%],SRSF2:p.Pro95His[46.5%],ASXL1:p.Gly646TrpfsTer12[38.8%],RUNX1:p.Arg162Lys[95.4%]	0	0	DNMT3A:p.R598*[50.7%],DNMT3A:p.T65K[51.6%],IDH1:p.R132L[55.3%],FLT3:p.D835E[17.4%],SRSF2:p.P95H[43.1%],ASXL1:p.G646Wfs*12[50.8%],RUNX1:p.R162K[96.3%]	Y	N		N
416413	MDS	prospective	BM	46,XY[20]	Y	N	NRAS:p.Gly12Asp[27.3%],TET2:p.Trp564Ter[50.3%],TET2:p.Gln964Ter[45.2%],EZH2:p.Val626Met[3.3%],CBL:p.Ile429Asn[43.9%],FLT3:p.Asn841Ile[2.3%],TP53:p.Arg283Cys[46.6%],CEBPA:p.Glu329GlyfsTer74[14.2%],ASXL1:p.Gly646TrpfsTer12[41.5%],STAG2:[93.8%]	0	0	NRAS:p.G12D[27.3%],CBL:p.I429N[40.9%],TP53:p.R283C[54.5%],ASXL1:p.G646Wfs*12[35.9%]	Y	N		N
218281	MDS	prospective	BM	46,XY,del(5)(q22q35)[20]	N	N		del(5)(q21.3q34)[95.9%]	0	DNMT3A:p.R882C[33.3%],TET2:p.S1284F[54.2%],TET2:p.K1468*[53.8%],PTPN11:p.E76K[72.0%],TP53:p.K132N[56.0%]	N	N		N
228950	MDS	prospective	BM	46,XY[20]	Y	N	None detected	0	0	0	Y	N		N
853337	AML	prospective	BM	46,XX[14]	NA	N	DNMT3A:p.Glu523Ter[44.4%],IDH1:p.Arg132His[5.7%],NPM1:p.Leu287IlefsTer13[40.5%],NPM1:p.Trp288CysfsTer12[42.7%],NPM1:p.Trp288CysfsTer12[42.7%],SMC3:[37.3%],ETV6:p.Leu117AsnfsTer7[4.1%],PTPN11:p.Asp61Gly[38.6%],NF1:p.Arg1306Ter[3.8%]	0	0	DNMT3A:p.E523*[43.3%],SMC3:NA[48.0%],PTPN11:p.D61G[45.6%],NPM1:p.W288Cfs*12[38.3%],CEBPA:p.M15Afs*84[37.3%]	Y	N		NK
800962	MDS	prospective	BM	47,XY,+19[19]/46,XY[1]	N	N	ASXL1:p.Gly646TrpfsTer12[11.1%],U2AF1:p.Gln157Pro[10.2%]	+19[74.9%]	0	U2AF1:p.Q157P[36.5%],ASXL1:p.G646Wfs*12[41.3%]	N	N		N
787399	MDS	prospective	BM	46,XY[3]	NA	N	TET2:p.Gln232Ter[5.0%],TET2:p.Asn535LysfsTer6[2.7%],U2AF1:p.Gln157Arg[20.6%],U2AF1:p.Ser34Tyr[21.4%]	0	0	U2AF1:p.Q157R[24.1%],U2AF1:p.S34Y[30.0%]	Y	N		NK
293825	AML	prospective	BM	46,XX[21]	Y	N	DNMT3A:p.Arg882Cys[29.3%],NPM1:p.Trp288CysfsTer12[30.4%],PTPN11:p.Gly60Ala[13.8%],IDH2:p.Arg140Leu[29.5%]	0	0	DNMT3A:p.R882C[33.3%],IDH2:p.R140L[30.2%],NPM1:p.W288Cfs*12[38.5%]	Y	N		N
541728	MDS	prospective	BM	46,XX[20]	Y	N	NRAS:p.Gln61Lys[42.8%],DNMT3A:p.Trp698Ter[47.8%],NPM1:p.Trp288CysfsTer12[44.5%]	0	0	NRAS:p.Q61K[43.3%],DNMT3A:p.W698*[45.9%],NPM1:p.W288Cfs*12[40.7%]	Y	N		N

632997	MDS	prospective	BM	46,XY,i(17)(q10)[15]/46,XY[5]	N	N	ETV6:p.Gly375Arg[44.5%],PTPN11:p.Gln510His[28.3%],SRSF2:p.Pro95His[59.2%],ASXL1:p.Glu635ArgfsTer15[45.3%]	del(17)(p11.2pter)[73.4%],+17[77.9%]	0	ETV6:p.G375R[61.5%],SRSF2:p.P95H[72.2%],ASXL1:p.E635Rfs*15[43.3%]	N	N		N
187885	AML	prospective	BM	46,XY[20]	Y	N	DNMT3A:p.Arg882Cys[48.6%],IDH1:p.Arg132His[36.8%],NPM1:p.Trp290ArgfsTer10[46.1%],FLT3:p.Asp835Ala[7.4%],FLT3:p.Val592Ala[13.2%]	0	0	DNMT3A:p.R882C[50.0%],IDH1:p.R132H[43.2%],FLT3:p.V592A[19.6%],NPM1:p.W290Rfs*10[50.9%]	Y	N		N
191374	MDS	prospective	BM	45,X,-Y[20]	N	N	TET2:p.Gln810Ter[45.7%],TET2:p.Ala911LeufsTer10[47.6%],CUX1:p.Glu398Ter[50.5%],RAD21:p.Gly481Arg[44.9%],CBL:[41.5%],ASXL1:p.Asn63Lys[45.9%],PHF6:p.Ile314Thr[92.5%]	-Y[96.0%]	0	TET2:p.Q810*[41.3%],TET2:p.A911Lfs*10[28.6%],CUX1:p.E398*[52.8%],RAD21:p.G481R[47.7%],CBL:NA[56.2%],ASXL1:p.N63K[50.0%],PHF6:p.I314T[96.0%]	N	N		N
314322	MDS	prospective	BM	46,XY,del(20)(q11.2)[19]/46,XY[1]	N	N	NF1:p.Gly772ArgfsTer16[64.6%],U2AF1:p.Ser34Phe[43.4%]	del(20)(q11.21qter)[81.8%]	0	NF1:p.G772Rfs*16[75.8%],NF1:NA[68.6%],U2AF1:p.S34F[46.9%]	N	N		N
480059	AML	prospective	BM	46,XX,t(4;7)(q25;q22)?c[20]	N	N	NPM1:p.Trp288CysfsTer12[28.5%],CBL:[3.1%],NF1:[28.5%],PPM1D:p.Cys478Ter[27.8%],SRSF2:p.Pro95Leu[53.3%],ASXL1:p.Gly646TrpfsTer12[41.7%]	del(7)(q22.1q22.1)[90.7%]	0	NF1:NA[34.9%],PPM1D:p.C478*[40.0%],SRSF2:p.P95L[49.1%],ASXL1:p.G646Wfs*12[46.4%],NPM1:p.W288Cfs*12[27.8%]	N	N		N
905861	AML	prospective	BM	44,XY,-3,del(5)(q23),add(7)(q11.2),-9 ,-10,-14,-15,del(16)(q21),der(19)t(4;19)(q11.2;q13.3),+1~3mar[cp17]/44,idem,+1,add(2)(p21),-del(16)(q21),+2~7mar[cp8]	N	Y	NRAS:p.Gly10dup[3.6%],GATA2:p.Arg362Gln[92.4%],TP53:p.Ser106Arg[95.6%]	-3[92.1%],del(5)(q11.2qter)[92.1%],del(7)(q11.23qter)[92.8%],del(15)(q21.2q22.32)[93.4%],gain(19)(q13.33qter)[90.2%]	0	GATA2:p.R362Q[87.9%],TP53:p.S106R[95.3%]	N	Y		N
654925	AML	prospective	BM	46,XY[20]	Y	N	NRAS:p.Gly12Asp[2.7%],DNMT3A:p.Met880IlefsTer26[34.0%],IDH1:p.Arg132Gly[40.9%],NPM1:p.Trp288CysfsTer12[40.7%],FLT3:p.Tyr842Cys[7.7%],FLT3:p.Val592Ala[16.1%]	0	0	DNMT3A:p.M880Ifs*26[44.1%],IDH1:p.R132G[42.1%],FLT3:p.Y842C[18.6%],NPM1:p.W288Cfs*12[35.1%]	Y	N		N
653268	AML	prospective	BM	46,XY[20]	Y	N	NRAS:p.Gly13Asp[6.6%],DNMT3A:p.Glu733_Phe734delinsVal[46.4%],NPM1:p.Trp288CysfsTer12[42.2%],KRAS:p.Gln61Pro[3.9%],PTPN11:p.Ser502Pro[12.4%],FLT3:p.Asp835Val[11.8%],FLT3:p.Val592_Tyr599dup[0.9%],FLT3:p.Asn587_Phe594dup[1.0%],NF1:p.Ile679AspfsTer21[2.0%]	0	0	NRAS:p.G13D[7.9%],DNMT3A:p.E733_F734delinsV[36.4%],PTPN11:p.S506P[15.9%],FLT3:p.D835V[14.7%],NPM1:p.W288Cfs*12[39.3%]	Y	N		N
888204	MDS	prospective	BM	43,XX,dic(3;8)(p11;p11.2),del(5)(q13),der(6)t(1;6)(p32;p22),inv(7)(p21q22),add(9)(q34),add(11)(p11.1),-12,-16,-17,add(17)(p11.2),del(20)(q11.2q13.1),add(22)(q13),+mar[21]	N	YY		gain(1)(p32.3p36.32)[91.9%],del(3)(p12.3p14.1)[93.4%],del(5)(q14.2qter)[93.1%],del(7)(p12.2p15.3)[90.8%],del(8)(p11.23pter)[96.4%],del(11)(p14.1p15.4)[92.5%],-12[92.9%],del(12)(q14.1q24.11)[93.3%],-16[94.2%],del(17)(p13.1pter)[92.5%],del(17)(q11.2q12)[90.9%],del(20)(q11.21q13.32)[92.5%],gain(22)(q11.21qter)[91.5%]	0	TP53:p.R175H[92.5%]	N	YY	CONFIRMED: Cs BY ARRAY	N
946179	AML	prospective	BM	46,XX[20]	Y	N	NRAS:p.Gly12Asp[47.0%],NPM1:p.Trp288CysfsTer12[44.5%]	0	0	NRAS:p.G12D[51.1%],NPM1:p.W288Cfs*12[56.9%]	Y	N		N
717042	AML	prospective	BM	46,XY[20]	Y	N	DNMT3A:p.Arg882His[45.5%],NPM1:p.Trp288CysfsTer12[40.2%],FLT3:p.Val579_Trp603dup[12.8%],FLT3:p.Trp603_Glu604insValGlnValThrGlySerSerAspAsnGluTyrPheTyrValAspPheArgGluTyrGluTyrAspLeuLysSer[12.3%],FLT3:p.Lys602_Trp603insGlyValGlnValThrGlySerSerAspAsnGluTyrPheTyrValAspPheArgGluTyrGluTyrAspLeuLys[12.6%],FLT3:p.Leu601_Lys602insGlnTrpValGlnValThrGlySerSerAspAsnGluTyrPheTyrValAspPheArgGluTyrGluTyrAspLeu[12.1%],FLT3:p.Lys602_Trp603insGlyValGlnValThrGlySerSerAspAsnGluTyrPheTyrValAspPheArgGluTyrGluTyrAspLeuLys[12.1%],FLT3:p.Asp600_Leu601insGlyValGlnLeuThrGlySerSerAspAslaAsnIleTyrValTyrIleIleTerAspGluTyrAspLeuAsn[4.5%],FLT3:p.Glu598delinsGlyGlyTyrArgTerGllaProGlnIleMetIleThrSerThrPheIleSerGluAsnMetAsnMetIleSerLys[4.3%],FLT3:p.Tyr597delinsTrpAlaLeuAsn[4.2%],FLT3:p.Val592_Asp593insMetAsnMetIleSerArgGlyTyrArgArgGlnHisProGlnIleLysSerThrSerThrLeuIleSerGluAsn[4.2%],FLT3:p.Phe590_Tyr591insTer[12.2%],FLT3:p.Val581_Phe590dup[1.0%]	0	0	DNMT3A:p.R882H[53.8%],NPM1:p.W288Cfs*12[41.7%],FLT3:p.V579_K602dup[22.2%]	Y	N		N
262878	AML	prospective	BM	46,XX[20]	Y	N	NPM1:p.Trp288CysfsTer12[37.9%],RAD21:p.Gly547AlafsTer65[36.2%],KRAS:p.Gly13Asp[5.2%],KRAS:p.Gly12Asp[5.7%],PTPN11:p.Asp61Val[2.5%],FLT3:p.Asp835His[13.1%],FLT3:p.Val592_Asp593insGluThrGlySerSerAspAsnGluTyrPheTyrVal[0.8%],NF1:p.Gln554His[42.0%]	0	0	KRAS:p.G12D[11.7%],NF1:p.Q554H[51.1%],NPM1:p.W288Cfs*12[35.2%],RAD21:p.G547Afs*65[33.9%]	Y	N		N
880398	ALL	prospective	BM	47,XX,+3[1]/48,idem,+X,t(9;22)(q34;q11.2)[1]/46,XX[1]	N	Y		+3[26.4%],del(7)(p11.2pter)[29.8%],+8[26.2%],del(13)(q12.3q33.1)[28.8%],gain(14)(q11.2qter)[27.3%],+X[29.3%]	t(9;22)(q34.12;q11.23)[8.1%],t(9;22)(q34.12;q11.23)[10.3%]	ASXL1:p.G646Wfs*12[11.0%]	N	Y	CONFIRMED: FISH positive for D13, CRLF2, BCL6	Complex
332282	AML	prospective	BM	47,XX,+8[20]	N	N	None detected	+8[77.9%]	t(9;11)(p21.3;q23.3)[34.5%],t(9;11)(p21.3;q23.3)[26.2%]	0	N	N	CONFIRMED: KMT2A breakapart FISH	t(9;11)(p21.3;q23.3)[34.5%],t(9;11)(p21.3;q23.3)[26.2%]
516070	AML	prospective	BM	46,XY[13]	NA	N	CUX1:p.Gln623Ter[4.3%],EZH2:p.Val626Met[4.9%],SRSF2:p.Phe62Val[4.6%],ASXL1:p.Gly646TrpfsTer12[5.8%]	0	0	CUX1:p.Q623*[8.7%],ASXL1:p.G646Wfs*12[4.8%]	Y	N		NK
869318	AML	prospective	BM	46,XX,?t(12;16)(q24.3;q22)[4]/46,XX[4]	N	N	KRAS:p.Gly13Asp[26.8%],KRAS:p.Gly12Asp[4.4%]	0	inv(16)(q22.1p13.11)[32.5%]	KRAS:p.G13D[38.7%]	N	N	CONFIRMED: inv(16) FISH showed rearrangement	inv(16)(q22.1p13.11)[31.1%]
736399	AML	prospective	BM	46,XX[20]	Y	N	TET2:p.Pro1367Gln[28.5%],TET2:p.Pro1741ThrfsTer11[47.9%],TET2:p.Pro1742Ser[46.6%],NPM1:p.Trp288CysfsTer12[46.5%],PPM1D:p.Glu476Ter[45.9%]	0	0	TET2:p.P1367Q[50.0%],TET2:p.P1741Tfs*11[41.9%],TET2:p.P1742S[57.9%],PPM1D:p.E476*[65.7%],NPM1:p.W288Cfs*12[39.2%]	Y	N		N
324214	ALL	prospective	BM	46,XX[20](hyperdiploid)	N	NA		+1[44.6%],-2[21.4%],-3[21.6%],-4[22.0%],del(5)(q21.2qter)[20.7%],+6[42.6%],-7[21.7%],+8[42.3%],-9[20.8%],-12[21.3%],del(13)(q12.11qter)[21.5%],del(15)(q11.2qter)[20.7%],-16[19.7%],-17[19.2%],+18[42.1%],+19[47.4%],-	0	TP53:p.R248W[31.2%]	N	Y		N

								20[19.1%],gain(21)(q11.2qter)[43.2%],-X[24.2%]					
924089	AML	prospective	BM	46,XX,t(9;11)(p22;q23)[20]	N	N	CBL:[16.9%],CBL:[25.6%],PTPN11:p.Ser502Leu[19.9%],FLT3:p.Tyr589_Val592del[18.8%]	0	t(9;11)(p21.3;q23.3)[27.3%],t(9;11)(p21.3;q23.3)[23.2%]	CBL:NA[26.0%],CBL:NA[26.2%],PTPN11:p.S506L[15.1%],FLT3:p.Y589_V592del[15.0%]	N	N	N
525644	AML	prospective	BM	46,Y,t(X;15)(q25;q22),der(3;21)(q10;q10),del(5)(q22q33),der(6)add(6)(p23)t(3;6)(q25;p21),del(12)(p13),+21[cp20]	N	Y	NRAS:p.Gly12Val[2.3%],PTPN11:p.Asn58Tyr[5.5%]	del(5)(q23.2q31.3)[80.6%],del(6)(p22.3p25.1)[82.1%],del(6)(q23.2q23.3)[82.9%],del(12)(p13.1p13.32)[80.7%],del(12)(q21.33q22)[81.3%]	0	0	N	Y	N
869658	ALL	prospective	BM	43~44,XY,add(4)(p16),-7,-9,t(9;22)(q34;q11.2),der(10)t(9;10)(q22;p11.2),?add(17p),add(19)(p13),-20,+1~2mar[cp20]. ish der(10)(ABL1+)[3/3]	N	Y	None detected	del(4)(p16.1pter)[93.4%],-7[97.5%],-9[79.6%],del(20)(q12qter)[92.8%]	t(9;22)(q34.12;q11.23)[39.9%],t(9;22)(q34.12;q11.23)[36.0%]	0	N	Y	N

See Supplementary Methods for more information.
Downloadable version with more complete information can be found here: https://wustl.box.com/v/rapidclinicalwgs-tables3

Table S4. New recurrent SVs

UPN	Diagnosis	Cytogenetics ISCN.Line	WGS Recurrent.SVs	New.information	CONFIRMATION STUDIES*
285982	AML	46,XY,t(16;22)(q22;q13)[10]	inv(16)(q22.1p13.11)[33.3%]	inv(16)(q22.1p13.11)[33.3%]	CONFIRMED: nuc ish(CBFBx2)(5'CBFB sep 3'CBFBx1)
332282	AML	47,XX,+8[20]	t(9;11)(p21.3;q23.3)[34.5%],t(9;11)(p21.3;q23.3)[26.2%]	t(9;11)(p21.3;q23.3)[34.5%],t(9;11)(p21.3;q23.3)[26.2%]	CONFIRMED: nuc ish(KMT2Ax2)(5'KMT2A sep 3'KMT2Ax1)
380949	AML	45,X,-X[21]/46,XX[9]	t(10;11)(p12.31;q23.3)[32.1%]	t(10;11)(p12.31;q23.3)[32.1%]	CONFIRMED: nuc ish(KMT2Ax2)(5'KMT2A sep 3'KMT2Ax1); RNA-seq positive
410324	AML	52~54,XY,+2,+4,+6,+8,del(11)(q23),+19,+19,+21[17]/46,XY[3]	t(6;11)(q27;q23.3)[37.9%],t(6;11)(q27;q23.3)[32.7%]	t(6;11)(q27;q23.3)[37.9%]	CONFIRMED nuc ish(KMT2Ax2)(5'KMT2A sep 3'KMT2Ax1); RNA-seq positive
461513	AML	47,XX,+8[1]/46,XX[4]	t(10;11)(p12.31;q23.3)[37.0%]	t(10;11)(p12.31;q23.3)[37.0%]	CONFIRMED: PCR
544583	AML	46,XX[11]	t(11;19)(q23.3;pter)[18.0%]	t(11;19)(q23.3;pter)[18.0%]	CONFIRMED: PCR
586748	AML	46,XY[20]	t(7;21)(p22.1;q22.12)[23.1%]	t(7;21)(p22.1;q22.12)[23.1%]	CONFIRMED: PCR
616274	AML	47,XX,+8[7]/46,XX[13]	t(9;11)(p21.3;q23.3)[19.7%],t(9;11)(p21.3;q23.3)[20.8%]	t(9;11)(p21.3;q23.3)[19.7%],t(9;11)(p21.3;q23.3)[20.8%]	CONFIRMED: nuc ish(KMT2Ax2)(5'KMT2A sep 3'KMT2Ax1)
677982	AML	47,XY,+i(21)(q10)[14]/47,XY,+21[2]/46,XY[4]	t(6;11)(q27;q23.3)[28.8%]	t(6;11)(q27;q23.3)[28.8%]	CONFIRMED: nuc ish(5,ÄôKMT2Ax2,3,ÄôKMT2Ax1)(5,ÄôKMT2A con 3,ÄôKMT2Ax1)
869318	AML	46,XX,?t(12;16)(q24.3;q22)[4]/46,XX[4]	inv(16)(q22.1p13.11)[32.5%]	inv(16)(q22.1p13.11)[31.1%]	CONFIRMED: nuc ish(CBFBx2)(5'CBFB sep 3'CBFBx1)
898627	AML	46,XX[5]	t(9;11)(p21.3;q23.3)[19.3%],t(9;11)(p21.3;q23.3)[18.4%]	t(9;11)(p21.3;q23.3)[19.3%],t(9;11)(p21.3;q23.3)[18.4%];Complex	CONFIRMED: nuc ish(KMT2Ax2)(5'KMT2A sep 3'KMT2Ax1)
907716	AML	47,XY+8[17]/46,XY[3]	t(9;11)(p21.3;q23.3)[32.7%],t(9;11)(p21.3;q23.3)[34.0%]	t(9;11)(p21.3;q23.3)[32.7%],t(9;11)(p21.3;q23.3)[34.0%]	CONFIRMED: nuc ish(KMT2Ax2)(5'KMT2A sep 3'KMT2Ax1)
994357	AML	46,XX[20]	t(11;19)(q23.3;p13.11)[23.6%],t(11;19)(q23.3;p13.11)[28.5%]	t(11;19)(q23.3;p13.11)[23.6%],t(11;19)(q23.3;p13.11)[28.5%]	CONFIRMED: nuc ish(KMT2Ax2)(5'KMT2A sep 3'KMT2Ax1)

* 'Confirmed' indicates the variant was supported by an orthogonal method, either clinical FISH studies performed at diagnosis, confirmation FISH studies, or PCR for sequence-defined breakpoints. See Figure S2A.
Downloadable version with more fields can be found here: https://wustl.box.com/v/rapidclinicalwgs-tables4

Table S5. New CNAs

UPN	Chrom	Start	End	Size	Type	Diagnosis	Cohort	Cytogenetics ISCN.Line	WGS.CNAs	WGS Recurrent.SVs	New.information	Confirmation	Comments
103744	chr16	61500000	90000000	28500000	DEL	AML	prospective	46,XX[3]	del(3)(p11.2pter)[61.8%],+5[76.7%],del(5)(q11.2qter)[60.6%],-7[57.2%],+8[57.6%],+9[52.3%],gain(15)(q11.2qter)[43.2%],del(16)(q21qter)[58.5%],del(17)(p13.1pter)[53.0%],+18[43.5%],gain(22)(q11.21q12.3)[64.0%]	0	Complex	Ambiguous or incomplete cytogenetics--did not attempt confirmation	
103744	chr17	500000	10500000	10000000	DEL	AML	prospective	46,XX[3]	del(3)(p11.2pter)[61.8%],+5[76.7%],del(5)(q11.2qter)[60.6%],-7[57.2%],+8[57.6%],+9[52.3%],gain(15)(q11.2qter)[43.2%],del(16)(q21qter)[58.5%],del(17)(p13.1pter)[53.0%],+18[43.5%],gain(22)(q11.21q12.3)[64.0%]	0	Complex	Ambiguous or incomplete cytogenetics--did not attempt confirmation	
103744	chr18	500000	80000000	79500000	DUP	AML	prospective	46,XX[3]	del(3)(p11.2pter)[61.8%],+5[76.7%],del(5)(q11.2qter)[60.6%],-7[57.2%],+8[57.6%],+9[52.3%],gain(15)(q11.2qter)[43.2%],del(16)(q21qter)[58.5%],del(17)(p13.1pter)[53.0%],+18[43.5%],gain(22)(q11.21q12.3)[64.0%]	0	Complex	Ambiguous or incomplete cytogenetics--did not attempt confirmation	
103744	chr22	17500000	36500000	19000000	DUP	AML	prospective	46,XX[3]	del(3)(p11.2pter)[61.8%],+5[76.7%],del(5)(q11.2qter)[60.6%],-7[57.2%],+8[57.6%],+9[52.3%],gain(15)(q11.2qter)[43.2%],del(16)(q21qter)[58.5%],del(17)(p13.1pter)[53.0%],+18[43.5%],gain(22)(q11.21q12.3)[64.0%]	0	Complex	Ambiguous or incomplete cytogenetics--did not attempt confirmation	
103744	chr3	1000000	87500000	86500000	DEL	AML	prospective	46,XX[3]	del(3)(p11.2pter)[61.8%],+5[76.7%],del(5)(q11.2qter)[60.6%],-7[57.2%],+8[57.6%],+9[52.3%],gain(15)(q11.2qter)[43.2%],del(16)(q21qter)[58.5%],del(17)(p13.1pter)[53.0%],+18[43.5%],gain(22)(q11.21q12.3)[64.0%]	0	Complex	Ambiguous or incomplete cytogenetics--did not attempt confirmation	
103744	chr5	1000000	52000000	51000000	DUP	AML	prospective	46,XX[3]	del(3)(p11.2pter)[61.8%],+5[76.7%],del(5)(q11.2qter)[60.6%],-7[57.2%],+8[57.6%],+9[52.3%],gain(15)(q11.2qter)[43.2%],del(16)(q21qter)[58.5%],del(17)(p13.1pter)[53.0%],+18[43.5%],gain(22)(q11.21q12.3)[64.0%]	0	Complex	Ambiguous or incomplete cytogenetics--did not attempt confirmation	
103744	chr5	52000000	181000000	129000000	DEL	AML	prospective	46,XX[3]	del(3)(p11.2pter)[61.8%],+5[76.7%],del(5)(q11.2qter)[60.6%],-7[57.2%],+8[57.6%],+9[52.3%],gain(15)(q11.2qter)[43.2%],del(16)(q21qter)[58.5%],del(17)(p13.1pter)[53.0%],+18[43.5%],gain(22)(q11.21q12.3)[64.0%]	0	Complex	Ambiguous or incomplete cytogenetics--did not attempt confirmation	
103744	chr7	500000	159000000	158500000	DEL	AML	prospective	46,XX[3]	del(3)(p11.2pter)[61.8%],+5[76.7%],del(5)(q11.2qter)[60.6%],-7[57.2%],+8[57.6%],+9[52.3%],gain(15)(q11.2qter)[43.2%],del(16)(q21qter)[58.5%],del(17)(p13.1pter)[53.0%],+18[43.5%],gain(22)(q11.21q12.3)[64.0%]	0	Complex	Ambiguous or incomplete cytogenetics--did not attempt confirmation	
103744	chr8	500000	145000000	144500000	DUP	AML	prospective	46,XX[3]	del(3)(p11.2pter)[61.8%],+5[76.7%],del(5)(q11.2qter)[60.6%],-7[57.2%],+8[57.6%],+9[52.3%],gain(15)(q11.2qter)[43.2%],del(16)(q21qter)[58.5%],del(17)(p13.1pter)[53.0%],+18[43.5%],gain(22)(q11.21q12.3)[64.0%]	0	Complex	Ambiguous or incomplete cytogenetics--did not attempt confirmation	
103744	chr9	500000	138000000	137500000	DUP	AML	prospective	46,XX[3]	del(3)(p11.2pter)[61.8%],+5[76.7%],del(5)(q11.2qter)[60.6%],-7[57.2%],+8[57.6%],+9[52.3%],gain(15)(q11.2qter)[43.2%],del(16)(q21qter)[58.5%],del(17)(p13.1pter)[53.0%],+18[43.5%],gain(22)(q11.21q12.3)[64.0%]	0	Complex	Ambiguous or incomplete cytogenetics--did not attempt confirmation	
103744	chr15	23500000	101500000	78000000	DUP	AML	prospective	46,XX[3]	del(3)(p11.2pter)[61.8%],+5[76.7%],del(5)(q11.2qter)[60.6%],-7[57.2%],+8[57.6%],+9[52.3%],gain(15)(q11.2qter)[43.2%],del(16)(q21qter)[58.5%],del(17)(p13.1pter)[53.0%],+18[43.5%],gain(22)(q11.21q12.3)[64.0%]	0	Complex	Ambiguous or incomplete cytogenetics--did not attempt confirmation	
142639	chr13	67000000	113500000	46500000	DUP	AML	retrospective	46,XX[19]/46,XX,+mar[1]	del(7)(q22.1qter)[60.0%],del(10)(q22.2q22.3)[58.6%],gain(13)(q21.32qter)[56.6%]	0	Complex	Ambiguous or incomplete cytogenetics--did not attempt confirmation	
142639	chr7	101500000	159000000	57500000	DEL	AML	retrospective	46,XX[19]/46,XX,+mar[1]	del(7)(q22.1qter)[60.0%],del(10)(q22.2q22.3)[58.6%],gain(13)(q21.32qter)[56.6%]	0	Complex	Ambiguous or incomplete cytogenetics--did not attempt confirmation	
142639	chr10	75000000	79500000	4500000	DEL	AML	retrospective	46,XX[19]/46,XX,+mar[1]	del(7)(q22.1qter)[60.0%],del(10)(q22.2q22.3)[58.6%],gain(13)(q21.32qter)[56.6%]	0	Complex	Ambiguous or incomplete cytogenetics--did not attempt confirmation	
167999	chr13	60500000	62500000	2000000	DEL	AML	retrospective	46,XY[12]	del(13)(q21.2q21.31)[96.6%]	0	Not Complex	Ambiguous or incomplete cytogenetics--did not	

												attempt confirmation
258135	chr11	117000000	135000000	18000000	DUP	AML	retrospective	46,XX,inv(16)(p13q22)[5]/46,idem,t(3;3)(p13;q?28)[5]/46,XX[6]	gain(11)(q23.3qter)[15.0%]	inv(16)(q22.1p13.11)[36.5%]	gain(11)(q23.3qter)[15.0%]	Ambiguous or incomplete cytogenetics--did not attempt confirmation
324214	chr1	3000000	248000000	245000000	DUP	ALL	prospective	46,XX[20](hyperdiploid)	+1[44.6%],-2[21.4%],-3[21.6%],-4[22.0%],del(5)(q21.2qter)[20.7%],+6[42.6%],-7[21.7%],+8[42.3%],-9[20.8%],-12[21.3%],del(13)(q12.11qter)[21.5%],del(15)(q11.2qter)[20.7%],-16[19.7%],-17[19.2%],+18[42.1%],+19[47.4%],-20[19.1%],gain(21)(q11.2qter)[43.2%],-X[24.2%]	0	N	Ambiguous or incomplete cytogenetics--did not attempt confirmation
324214	chr12	500000	133000000	132500000	DEL	ALL	prospective	46,XX[20](hyperdiploid)	+1[44.6%],-2[21.4%],-3[21.6%],-4[22.0%],del(5)(q21.2qter)[20.7%],+6[42.6%],-7[21.7%],+8[42.3%],-9[20.8%],-12[21.3%],del(13)(q12.11qter)[21.5%],del(15)(q11.2qter)[20.7%],-16[19.7%],-17[19.2%],+18[42.1%],+19[47.4%],-20[19.1%],gain(21)(q11.2qter)[43.2%],-X[24.2%]	0	N	Ambiguous or incomplete cytogenetics--did not attempt confirmation
324214	chr13	20000000	113500000	93500000	DEL	ALL	prospective	46,XX[20](hyperdiploid)	+1[44.6%],-2[21.4%],-3[21.6%],-4[22.0%],del(5)(q21.2qter)[20.7%],+6[42.6%],-7[21.7%],+8[42.3%],-9[20.8%],-12[21.3%],del(13)(q12.11qter)[21.5%],del(15)(q11.2qter)[20.7%],-16[19.7%],-17[19.2%],+18[42.1%],+19[47.4%],-20[19.1%],gain(21)(q11.2qter)[43.2%],-X[24.2%]	0	N	Ambiguous or incomplete cytogenetics--did not attempt confirmation
324214	chr15	23500000	101500000	78000000	DEL	ALL	prospective	46,XX[20](hyperdiploid)	+1[44.6%],-2[21.4%],-3[21.6%],-4[22.0%],del(5)(q21.2qter)[20.7%],+6[42.6%],-7[21.7%],+8[42.3%],-9[20.8%],-12[21.3%],del(13)(q12.11qter)[21.5%],del(15)(q11.2qter)[20.7%],-16[19.7%],-17[19.2%],+18[42.1%],+19[47.4%],-20[19.1%],gain(21)(q11.2qter)[43.2%],-X[24.2%]	0	N	Ambiguous or incomplete cytogenetics--did not attempt confirmation
324214	chr16	1500000	90000000	88500000	DEL	ALL	prospective	46,XX[20](hyperdiploid)	+1[44.6%],-2[21.4%],-3[21.6%],-4[22.0%],del(5)(q21.2qter)[20.7%],+6[42.6%],-7[21.7%],+8[42.3%],-9[20.8%],-12[21.3%],del(13)(q12.11qter)[21.5%],del(15)(q11.2qter)[20.7%],-16[19.7%],-17[19.2%],+18[42.1%],+19[47.4%],-20[19.1%],gain(21)(q11.2qter)[43.2%],-X[24.2%]	0	N	Ambiguous or incomplete cytogenetics--did not attempt confirmation
324214	chr17	500000	83000000	82500000	DEL	ALL	prospective	46,XX[20](hyperdiploid)	+1[44.6%],-2[21.4%],-3[21.6%],-4[22.0%],del(5)(q21.2qter)[20.7%],+6[42.6%],-7[21.7%],+8[42.3%],-9[20.8%],-12[21.3%],del(13)(q12.11qter)[21.5%],del(15)(q11.2qter)[20.7%],-16[19.7%],-17[19.2%],+18[42.1%],+19[47.4%],-20[19.1%],gain(21)(q11.2qter)[43.2%],-X[24.2%]	0	N	Ambiguous or incomplete cytogenetics--did not attempt confirmation
324214	chr18	500000	80000000	79500000	DUP	ALL	prospective	46,XX[20](hyperdiploid)	+1[44.6%],-2[21.4%],-3[21.6%],-4[22.0%],del(5)(q21.2qter)[20.7%],+6[42.6%],-7[21.7%],+8[42.3%],-9[20.8%],-12[21.3%],del(13)(q12.11qter)[21.5%],del(15)(q11.2qter)[20.7%],-16[19.7%],-17[19.2%],+18[42.1%],+19[47.4%],-20[19.1%],gain(21)(q11.2qter)[43.2%],-X[24.2%]	0	N	Ambiguous or incomplete cytogenetics--did not attempt confirmation
324214	chr19	1500000	58500000	57000000	DUP	ALL	prospective	46,XX[20](hyperdiploid)	+1[44.6%],-2[21.4%],-3[21.6%],-4[22.0%],del(5)(q21.2qter)[20.7%],+6[42.6%],-7[21.7%],+8[42.3%],-9[20.8%],-12[21.3%],del(13)(q12.11qter)[21.5%],del(15)(q11.2qter)[20.7%],-16[19.7%],-17[19.2%],+18[42.1%],+19[47.4%],-20[19.1%],gain(21)(q11.2qter)[43.2%],-X[24.2%]	0	N	Ambiguous or incomplete cytogenetics--did not attempt confirmation
324214	chr2	500000	242000000	241500000	DEL	ALL	prospective	46,XX[20](hyperdiploid)	+1[44.6%],-2[21.4%],-3[21.6%],-4[22.0%],del(5)(q21.2qter)[20.7%],+6[42.6%],-7[21.7%],+8[42.3%],-9[20.8%],-12[21.3%],del(13)(q12.11qter)[21.5%],del(15)(q11.2qter)[20.7%],-16[19.7%],-17[19.2%],+18[42.1%],+19[47.4%],-20[19.1%],gain(21)(q11.2qter)[43.2%],-X[24.2%]	0	N	Ambiguous or incomplete cytogenetics--did not attempt confirmation
324214	chr20	500000	64000000	63500000	DEL	ALL	prospective	46,XX[20](hyperdiploid)	+1[44.6%],-2[21.4%],-3[21.6%],-4[22.0%],del(5)(q21.2qter)[20.7%],+6[42.6%],-7[21.7%],+8[42.3%],-9[20.8%],-12[21.3%],del(13)(q12.11qter)[21.5%],del(15)(q11.2qter)[20.7%],-16[19.7%],-17[19.2%],+18[42.1%],+19[47.4%],-20[19.1%],gain(21)(q11.2qter)[43.2%],-X[24.2%]	0	N	Ambiguous or incomplete cytogenetics--did not attempt confirmation
324214	chr21	14000000	46500000	32500000	DUP	ALL	prospective	46,XX[20](hyperdiploid)	+1[44.6%],-2[21.4%],-3[21.6%],-4[22.0%],del(5)(q21.2qter)[20.7%],+6[42.6%],-7[21.7%],+8[42.3%],-	0	N	Ambiguous or incomplete cytogenetics--

									9[20.8%],-12[21.3%],del(13)(q12.11qter)[21.5%],del(15)(q11.2qter)[20.7%],-16[19.7%],-17[19.2%],+18[42.1%],+19[47.4%],-20[19.1%],gain(21)(q11.2qter)[43.2%],-X[24.2%]			did not attempt confirmation
324214	chr3	1000000	197500000	196500000	DEL	ALL	prospective	46,XX[20](hyperdiploid)	+1[44.6%],-2[21.4%],-3[21.6%],-4[22.0%],del(5)(q21.2qter)[20.7%],+6[42.6%],-7[21.7%],+8[42.3%],-9[20.8%],-12[21.3%],del(13)(q12.11qter)[21.5%],del(15)(q11.2qter)[20.7%],-16[19.7%],-17[19.2%],+18[42.1%],+19[47.4%],-20[19.1%],gain(21)(q11.2qter)[43.2%],-X[24.2%]	0	N	Ambiguous or incomplete cytogenetics--did not attempt confirmation
324214	chr4	500000	189500000	189000000	DEL	ALL	prospective	46,XX[20](hyperdiploid)	+1[44.6%],-2[21.4%],-3[21.6%],-4[22.0%],del(5)(q21.2qter)[20.7%],+6[42.6%],-7[21.7%],+8[42.3%],-9[20.8%],-12[21.3%],del(13)(q12.11qter)[21.5%],del(15)(q11.2qter)[20.7%],-16[19.7%],-17[19.2%],+18[42.1%],+19[47.4%],-20[19.1%],gain(21)(q11.2qter)[43.2%],-X[24.2%]	0	N	Ambiguous or incomplete cytogenetics--did not attempt confirmation
324214	chr5	104000000	181000000	77000000	DEL	ALL	prospective	46,XX[20](hyperdiploid)	+1[44.6%],-2[21.4%],-3[21.6%],-4[22.0%],del(5)(q21.2qter)[20.7%],+6[42.6%],-7[21.7%],+8[42.3%],-9[20.8%],-12[21.3%],del(13)(q12.11qter)[21.5%],del(15)(q11.2qter)[20.7%],-16[19.7%],-17[19.2%],+18[42.1%],+19[47.4%],-20[19.1%],gain(21)(q11.2qter)[43.2%],-X[24.2%]	0	N	Ambiguous or incomplete cytogenetics--did not attempt confirmation
324214	chr6	500000	170500000	170000000	DUP	ALL	prospective	46,XX[20](hyperdiploid)	+1[44.6%],-2[21.4%],-3[21.6%],-4[22.0%],del(5)(q21.2qter)[20.7%],+6[42.6%],-7[21.7%],+8[42.3%],-9[20.8%],-12[21.3%],del(13)(q12.11qter)[21.5%],del(15)(q11.2qter)[20.7%],-16[19.7%],-17[19.2%],+18[42.1%],+19[47.4%],-20[19.1%],gain(21)(q11.2qter)[43.2%],-X[24.2%]	0	N	Ambiguous or incomplete cytogenetics--did not attempt confirmation
324214	chr7	500000	159000000	158500000	DEL	ALL	prospective	46,XX[20](hyperdiploid)	+1[44.6%],-2[21.4%],-3[21.6%],-4[22.0%],del(5)(q21.2qter)[20.7%],+6[42.6%],-7[21.7%],+8[42.3%],-9[20.8%],-12[21.3%],del(13)(q12.11qter)[21.5%],del(15)(q11.2qter)[20.7%],-16[19.7%],-17[19.2%],+18[42.1%],+19[47.4%],-20[19.1%],gain(21)(q11.2qter)[43.2%],-X[24.2%]	0	N	Ambiguous or incomplete cytogenetics--did not attempt confirmation
324214	chr8	500000	145000000	144500000	DUP	ALL	prospective	46,XX[20](hyperdiploid)	+1[44.6%],-2[21.4%],-3[21.6%],-4[22.0%],del(5)(q21.2qter)[20.7%],+6[42.6%],-7[21.7%],+8[42.3%],-9[20.8%],-12[21.3%],del(13)(q12.11qter)[21.5%],del(15)(q11.2qter)[20.7%],-16[19.7%],-17[19.2%],+18[42.1%],+19[47.4%],-20[19.1%],gain(21)(q11.2qter)[43.2%],-X[24.2%]	0	N	Ambiguous or incomplete cytogenetics--did not attempt confirmation
324214	chr9	500000	138000000	137500000	DEL	ALL	prospective	46,XX[20](hyperdiploid)	+1[44.6%],-2[21.4%],-3[21.6%],-4[22.0%],del(5)(q21.2qter)[20.7%],+6[42.6%],-7[21.7%],+8[42.3%],-9[20.8%],-12[21.3%],del(13)(q12.11qter)[21.5%],del(15)(q11.2qter)[20.7%],-16[19.7%],-17[19.2%],+18[42.1%],+19[47.4%],-20[19.1%],gain(21)(q11.2qter)[43.2%],-X[24.2%]	0	N	Ambiguous or incomplete cytogenetics--did not attempt confirmation
324214	chrX	3000000	154000000	151000000	DEL	ALL	prospective	46,XX[20](hyperdiploid)	+1[44.6%],-2[21.4%],-3[21.6%],-4[22.0%],del(5)(q21.2qter)[20.7%],+6[42.6%],-7[21.7%],+8[42.3%],-9[20.8%],-12[21.3%],del(13)(q12.11qter)[21.5%],del(15)(q11.2qter)[20.7%],-16[19.7%],-17[19.2%],+18[42.1%],+19[47.4%],-20[19.1%],gain(21)(q11.2qter)[43.2%],-X[24.2%]	0	N	Ambiguous or incomplete cytogenetics--did not attempt confirmation
335141	chr11	72500000	135000000	62500000	DUP	AML	prospective	46,XY, add(2)(q37)[6]	del(2)(q36.3qter)[89.1%],gain(11)(q13.4qter)[90.2%]	0	Not Complex	Ambiguous or incomplete cytogenetics--did not attempt confirmation
335141	chr2	227500000	242000000	14500000	DEL	AML	prospective	46,XY, add(2)(q37)[6]	del(2)(q36.3qter)[89.1%],gain(11)(q13.4qter)[90.2%]	0	Not Complex	Ambiguous or incomplete cytogenetics--did not attempt confirmation
429745	chr8	500000	39500000	39000000	DUP	MDS	retrospective	48,XX,+8,+8,del(8)(q11.23q21.2)x3,del(12)(p13),add(17)(p13),del(22)(q13)[20]	gain(8)(p11.22pter)[160.7%],-8[82.0%],gain(8)(q12.3qter)[155.8%]	0	Not Complex; No CNAs on chr12,chr17,chr22	Ambiguous or incomplete cytogenetics--did not attempt confirmation
429745	chr8	39500000	64000000	24500000	DEL	MDS	retrospective	48,XX,+8,+8,del(8)(q11.23q21.2)x3,del(12)(p13),add(17)(p13),del(22)(q13)[20]	gain(8)(p11.22pter)[160.7%],-8[82.0%],gain(8)(q12.3qter)[155.8%]	0	Not Complex; No CNAs on chr12,chr17,chr22	Ambiguous or incomplete cytogenetics--did not attempt confirmation

429745	chr8	64000000	145000000	81000000	DUP	MDS	retrospective	48,XX,+8,+8,del(8)(q11.23q21.2)x3,del(12)(p13),add(17)(p13),del(22)(q13)[20]	gain(8)(p11.22pter)[160.7%],-8[82.0%],gain(8)(q12.3qter)[155.8%]	0	Not Complex; No CNAs on chr12,chr17,chr22	Ambiguous or incomplete cytogenetics--did not attempt confirmation
430826	chr18	500000	14000000	13500000	DEL	AML	prospective	46,XY,t(15;17)(q24;q21)[5]/46,XY[1]	gain(2)(q14.1qter)[23.6%],gain(7)(p12.3p14.1)[23.6%],-7[21.5%],del(9)(p21.1pter)[17.4%],gain(9)(q22.33qter)[21.4%],del(10)(p11.21pter)[23.8%],gain(10)(q11.21qter)[22.1%],del(13)(q12.11qter)[20.7%],del(16)(q23.1qter)[21.7%],del(18)(p11.21pter)[15.2%],gain(19)(p12pter)[21.7%],gain(20)(q11.21qter)[35.8%]	t(15;17)(q24.1;q21.2)[3.3%],t(15;17)(q24.1;q21.2)[4.1%]	Complex	Ambiguous or incomplete cytogenetics--did not attempt confirmation
430826	chr19	1500000	20000000	18500000	DUP	AML	prospective	46,XY,t(15;17)(q24;q21)[5]/46,XY[1]	gain(2)(q14.1qter)[23.6%],gain(7)(p12.3p14.1)[23.6%],-7[21.5%],del(9)(p21.1pter)[17.4%],gain(9)(q22.33qter)[21.4%],del(10)(p11.21pter)[23.8%],gain(10)(q11.21qter)[22.1%],del(13)(q12.11qter)[20.7%],del(16)(q23.1qter)[21.7%],del(18)(p11.21pter)[15.2%],gain(19)(p12pter)[21.7%],gain(20)(q11.21qter)[35.8%]	t(15;17)(q24.1;q21.2)[3.3%],t(15;17)(q24.1;q21.2)[4.1%]	Complex	Ambiguous or incomplete cytogenetics--did not attempt confirmation
430826	chr20	31500000	64000000	32500000	DUP	AML	prospective	46,XY,t(15;17)(q24;q21)[5]/46,XY[1]	gain(2)(q14.1qter)[23.6%],gain(7)(p12.3p14.1)[23.6%],-7[21.5%],del(9)(p21.1pter)[17.4%],gain(9)(q22.33qter)[21.4%],del(10)(p11.21pter)[23.8%],gain(10)(q11.21qter)[22.1%],del(13)(q12.11qter)[20.7%],del(16)(q23.1qter)[21.7%],del(18)(p11.21pter)[15.2%],gain(19)(p12pter)[21.7%],gain(20)(q11.21qter)[35.8%]	t(15;17)(q24.1;q21.2)[3.3%],t(15;17)(q24.1;q21.2)[4.1%]	Complex	Ambiguous or incomplete cytogenetics--did not attempt confirmation
430826	chr7	38500000	48000000	9500000	DUP	AML	prospective	46,XY,t(15;17)(q24;q21)[5]/46,XY[1]	gain(2)(q14.1qter)[23.6%],gain(7)(p12.3p14.1)[23.6%],-7[21.5%],del(9)(p21.1pter)[17.4%],gain(9)(q22.33qter)[21.4%],del(10)(p11.21pter)[23.8%],gain(10)(q11.21qter)[22.1%],del(13)(q12.11qter)[20.7%],del(16)(q23.1qter)[21.7%],del(18)(p11.21pter)[15.2%],gain(19)(p12pter)[21.7%],gain(20)(q11.21qter)[35.8%]	t(15;17)(q24.1;q21.2)[3.3%],t(15;17)(q24.1;q21.2)[4.1%]	Complex	Ambiguous or incomplete cytogenetics--did not attempt confirmation
430826	chr7	48000000	159000000	111000000	DEL	AML	prospective	46,XY,t(15;17)(q24;q21)[5]/46,XY[1]	gain(2)(q14.1qter)[23.6%],gain(7)(p12.3p14.1)[23.6%],-7[21.5%],del(9)(p21.1pter)[17.4%],gain(9)(q22.33qter)[21.4%],del(10)(p11.21pter)[23.8%],gain(10)(q11.21qter)[22.1%],del(13)(q12.11qter)[20.7%],del(16)(q23.1qter)[21.7%],del(18)(p11.21pter)[15.2%],gain(19)(p12pter)[21.7%],gain(20)(q11.21qter)[35.8%]	t(15;17)(q24.1;q21.2)[3.3%],t(15;17)(q24.1;q21.2)[4.1%]	Complex	Ambiguous or incomplete cytogenetics--did not attempt confirmation
430826	chr13	20000000	113500000	93500000	DEL	AML	prospective	46,XY,t(15;17)(q24;q21)[5]/46,XY[1]	gain(2)(q14.1qter)[23.6%],gain(7)(p12.3p14.1)[23.6%],-7[21.5%],del(9)(p21.1pter)[17.4%],gain(9)(q22.33qter)[21.4%],del(10)(p11.21pter)[23.8%],gain(10)(q11.21qter)[22.1%],del(13)(q12.11qter)[20.7%],del(16)(q23.1qter)[21.7%],del(18)(p11.21pter)[15.2%],gain(19)(p12pter)[21.7%],gain(20)(q11.21qter)[35.8%]	t(15;17)(q24.1;q21.2)[3.3%],t(15;17)(q24.1;q21.2)[4.1%]	Complex	Ambiguous or incomplete cytogenetics--did not attempt confirmation
430826	chr16	74500000	90000000	15500000	DEL	AML	prospective	46,XY,t(15;17)(q24;q21)[5]/46,XY[1]	gain(2)(q14.1qter)[23.6%],gain(7)(p12.3p14.1)[23.6%],-7[21.5%],del(9)(p21.1pter)[17.4%],gain(9)(q22.33qter)[21.4%],del(10)(p11.21pter)[23.8%],gain(10)(q11.21qter)[22.1%],del(13)(q12.11qter)[20.7%],del(16)(q23.1qter)[21.7%],del(18)(p11.21pter)[15.2%],gain(19)(p12pter)[21.7%],gain(20)(q11.21qter)[35.8%]	t(15;17)(q24.1;q21.2)[3.3%],t(15;17)(q24.1;q21.2)[4.1%]	Complex	Ambiguous or incomplete cytogenetics--did not attempt confirmation
430826	chr9	500000	32500000	32000000	DEL	AML	prospective	46,XY,t(15;17)(q24;q21)[5]/46,XY[1]	gain(2)(q14.1qter)[23.6%],gain(7)(p12.3p14.1)[23.6%],-7[21.5%],del(9)(p21.1pter)[17.4%],gain(9)(q22.33qter)[21.4%],del(10)(p11.21pter)[23.8%],gain(10)(q11.21qter)[22.1%],del(13)(q12.11qter)[20.7%],del(16)(q23.1qter)[21.7%],del(18)(p11.21pter)[15.2%],gain(19)(p12pter)[21.7%],gain(20)(q11.21qter)[35.8%]	t(15;17)(q24.1;q21.2)[3.3%],t(15;17)(q24.1;q21.2)[4.1%]	Complex	Ambiguous or incomplete cytogenetics--did not attempt confirmation
430826	chr2	118000000	242000000	124000000	DUP	AML	prospective	46,XY,t(15;17)(q24;q21)[5]/46,XY[1]	gain(2)(q14.1qter)[23.6%],gain(7)(p12.3p14.1)[23.6%],-7[21.5%],del(9)(p21.1pter)[17.4%],gain(9)(q22.33qter)[21.4%],del(10)(p11.21pter)[23.8%],gain(10)(q11.21qter)[22.1%],del(13)(q12.11qter)[20.7%],del(16)(q23.1qter)[21.7%],del(18)(p11.21pter)[15.2%],gain(19)(p12pter)[21.7%],gain(20)(q11.21qter)[35.8%]	t(15;17)(q24.1;q21.2)[3.3%],t(15;17)(q24.1;q21.2)[4.1%]	Complex	Ambiguous or incomplete cytogenetics--did not attempt confirmation
430826	chr9	99500000	138000000	38500000	DUP	AML	prospective	46,XY,t(15;17)(q24;q21)[5]/46,XY[1]	gain(2)(q14.1qter)[23.6%],gain(7)(p12.3p14.1)[23.6%],-7[21.5%],del(9)(p21.1pter)[17.4%],gain(9)(q22.33qter)[21.4%],del(10)(p11.21pter)[23.8%],gain(10)(q11.21qter)[22.1%],del(13)(q12.11qter)[20.7%],del(16)(q23.1qter)[21.7%],del(18)(p11.21pter)[15.2%],gain(19)(p12pter)[21.7%],gain(20)(q11.21qter)[35.8%]	t(15;17)(q24.1;q21.2)[3.3%],t(15;17)(q24.1;q21.2)[4.1%]	Complex	Ambiguous or incomplete cytogenetics--did not attempt confirmation
430826	chr10	500000	37000000	36500000	DEL	AML	prospective	46,XY,t(15;17)(q24;q21)[5]/46,XY[1]	gain(2)(q14.1qter)[23.6%],gain(7)(p12.3p14.1)[23.6%],-7[21.5%],del(9)(p21.1pter)[17.4%],gain(9)(q22.33qter)[21.4%],del(10)(p11.21pter)[23.8%],gain(10)(q11.21qter)[22.1%],del(13)(q12.11qter)[20.7	t(15;17)(q24.1;q21.2)[3.3%],t(15;17)(q24.1;q21.2)[4.1%]	Complex	Ambiguous or incomplete cytogenetics--did not attempt confirmation

									%],del(16)(q23.1qter)[21.7%],del(18)(p11.21pter)[15.2%],gain(19)(p12pter)[21.7%],gain(20)(q11.21qter)[35.8%]			
430826	chr10	43000000	133500000	90500000	DUP	AML	prospective	46,XY,t(15;17)(q24;q21)[5]/46,XY[1]	gain(2)(q14.1qter)[23.6%],gain(7)(p12.3p14.1)[23.6%],-7[21.5%],del(9)(p21.1pter)[17.4%],gain(9)(q22.33qter)[21.4%],del(10)(p11.21pter)[23.8%],gain(10)(q11.21qter)[22.1%],del(13)(q12.11qter)[20.7%],del(16)(q23.1qter)[21.7%],del(18)(p11.21pter)[15.2%],gain(19)(p12pter)[21.7%],gain(20)(q11.21qter)[35.8%]	t(15;17)(q24.1;q21.2)[3.3%],t(15;17)(q24.1;q21.2)[4.1%]	Complex	Ambiguous or incomplete cytogenetics--did not attempt confirmation
451688	chrY	7000000	21000000	14000000	DEL	MDS	prospective	46,XY[3]	del(4)(q21.1q25)[53.3%],-Y[27.1%]	0	Independent clones	Ambiguous or incomplete cytogenetics--did not attempt confirmation
451688	chr4	76000000	107000000	31000000	DEL	MDS	prospective	46,XY[3]	del(4)(q21.1q25)[53.3%],-Y[27.1%]	0	Independent clones	Ambiguous or incomplete cytogenetics--did not attempt confirmation
666013	chrX	3000000	9500000	6500000	DUP	AML	prospective	46,XX,del(3)(?p24)[10]/46,XX[10]	del(5)(q31.2q31.2)[10.1%]	0	del(5)(q31.2q31.2)[10.1%]; Omitted from CNA performance comparisons due to size <5Mbp	Ambiguous or incomplete cytogenetics--did not attempt confirmation
666013	chr5	137577914	139513006	1935093	DEL	AML	prospective	46,XX,del(3)(?p24)[10]/46,XX[10]	del(5)(q31.2q31.2)[10.1%]	0	del(5)(q31.2q31.2)[10.1%]; Omitted from CNA performance comparisons due to size <5Mbp	Ambiguous or incomplete cytogenetics--did not attempt confirmation
666013	chr19	2000000	58500000	56500000	DUP	AML	prospective	46,XX,del(3)(?p24)[10]/46,XX[10]	del(5)(q31.2q31.2)[10.1%]	0	del(5)(q31.2q31.2)[10.1%]; Omitted from CNA performance comparisons due to size <5Mbp	Ambiguous or incomplete cytogenetics--did not attempt confirmation
666013	chr5	1000000	30000000	29000000	DUP	AML	prospective	46,XX,del(3)(?p24)[10]/46,XX[10]	del(5)(q31.2q31.2)[10.1%]	0	del(5)(q31.2q31.2)[10.1%]; Omitted from CNA performance comparisons due to size <5Mbp	Ambiguous or incomplete cytogenetics--did not attempt confirmation
739025	chr7	92000000	159000000	67000000	DEL	MDS	prospective	46~47,XY,-5,del(7)(q22q34),+8,t(11;15)?(p15;q22),+mar[cp14]/46,XY[6]	del(5)(q11.2qter)[63.2%],del(7)(q21.2qter)[63.2%],+8[43.1%]	0	Complex	Ambiguous or incomplete cytogenetics--did not attempt confirmation
739025	chr8	500000	145000000	144500000	DUP	MDS	prospective	46~47,XY,-5,del(7)(q22q34),+8,t(11;15)?(p15;q22),+mar[cp14]/46,XY[6]	del(5)(q11.2qter)[63.2%],del(7)(q21.2qter)[63.2%],+8[43.1%]	0	Complex	Ambiguous or incomplete cytogenetics--did not attempt confirmation
739025	chr5	57500000	181000000	123500000	DEL	MDS	prospective	46~47,XY,-5,del(7)(q22q34),+8,t(11;15)?(p15;q22),+mar[cp14]/46,XY[6]	del(5)(q11.2qter)[63.2%],del(7)(q21.2qter)[63.2%],+8[43.1%]	0	Complex	Ambiguous or incomplete cytogenetics--did not attempt confirmation
764488	chr21	41000000	46500000	5500000	DUP	AML	prospective	46,XY[10]	+4[7.7%],gain(21)(q22.2qter)[10.7%]	0	Not Complex	Ambiguous or incomplete cytogenetics--did not attempt confirmation
764488	chr4	500000	189500000	189000000	DUP	AML	prospective	46,XY[10]	+4[7.7%],gain(21)(q22.2qter)[10.7%]	0	Not Complex	Ambiguous or incomplete cytogenetics--did not attempt confirmation
880398	chr13	31000000	104000000	73000000	DEL	ALL	prospective	47,XX,+3[1]/48,idem,+X,t(9;22)(q34;q11.2)[1]/46,XX[1]	+3[26.4%],del(7)(p11.2pter)[29.8%],+8[26.2%],del(13)(q12.3q33.1)[28.8%],gain(14)(q11.2qter)[27.3%],+X[29.3%]	t(9;22)(q34.12;q11.23)[8.1%],t(9;22)(q34.12;q11.23)[10.3%]	Complex	Ambiguous or incomplete cytogenetics--did not attempt confirmation
880398	chr8	500000	145000000	144500000	DUP	ALL	prospective	47,XX,+3[1]/48,idem,+X,t(9;22)(q34;q11.2)[1]/46,XX[1]	+3[26.4%],del(7)(p11.2pter)[29.8%],+8[26.2%],del(13)(q12.3q33.1)[28.8%],gain(14)(q11.2qter)[27.3%],+X[29.3%]	t(9;22)(q34.12;q11.23)[8.1%],t(9;22)(q34.12;q11.23)[10.3%]	Complex	Ambiguous or incomplete cytogenetics--did not attempt confirmation
880398	chrX	3000000	154000000	151000000	DUP	ALL	prospective	47,XX,+3[1]/48,idem,+X,t(9;22)(q34;q11.2)[1]/46,XX[1]	+3[26.4%],del(7)(p11.2pter)[29.8%],+8[26.2%],del(13)(q12.3q33.1)[28.8%],gain(14)(q11.2qter)[27.3%],+X[29.3%]	t(9;22)(q34.12;q11.23)[8.1%],t(9;22)(q34.12;q11.23)[10.3%]	Complex	Ambiguous or incomplete cytogenetics--did not attempt confirmation
880398	chr7	500000	54500000	54000000	DEL	ALL	prospective	47,XX,+3[1]/48,idem,+X,t(9;22)(q34;q11.2)[1]/46,XX[1]	+3[26.4%],del(7)(p11.2pter)[29.8%],+8[26.2%],del(13)(q12.3q33.1)[28.8%],gain(14)(q11.2qter)[27.3%],+X[29.3%]	t(9;22)(q34.12;q11.23)[8.1%],t(9;22)(q34.12;q11.23)[10.3%]	Complex	Ambiguous or incomplete cytogenetics--did not attempt confirmation

880398	chr14	20000000	105500000	85500000	DUP	ALL	prospective	47,XX,+3[1]/48,idem,+X,t(9;22)(q34;q11.2)[1]/46,XX[1]	+3[26.4%],del(7)(p11.2pter)[29.8%],+8[26.2%],del(13)(q12.3q33.1)[28.8%],gain(14)(q11.2qter)[27.3%],+X[29.3%]	t(9;22)(q34.12;q11.23)[8.1%],t(9;22)(q34.12;q11.23)[10.3%]	Complex	Ambiguous or incomplete cytogenetics--did not attempt confirmation	
880398	chr3	1000000	197500000	196500000	DUP	ALL	prospective	47,XX,+3[1]/48,idem,+X,t(9;22)(q34;q11.2)[1]/46,XX[1]	+3[26.4%],del(7)(p11.2pter)[29.8%],+8[26.2%],del(13)(q12.3q33.1)[28.8%],gain(14)(q11.2qter)[27.3%],+X[29.3%]	t(9;22)(q34.12;q11.23)[8.1%],t(9;22)(q34.12;q11.23)[10.3%]	Complex	Ambiguous or incomplete cytogenetics--did not attempt confirmation	
155912	chr3	66500000	82500000	16000000	DEL	AML	prospective	46,XX,der(3)t(3;6)(q25;q13),der(6)t(3;6)(q25;q13)t(6;8)(p23;q13)[19]/46,XX[1]	del(3)(p12.2p14.1)[76.6%],del(6)(p24.1pter)[75.1%],del(6)(q14.1q14.3)[77.6%],gain(8)(q12.1qter)[72.8%]	0	Complex	Array	Confirmed: arr[GRCh37] 3p14.1p12.2(66972250_82402319)x1-2 (at breakpoint of rearrangement)
155912	chr6	75500000	84500000	9000000	DEL	AML	prospective	46,XX,der(3)t(3;6)(q25;q13),der(6)t(3;6)(q25;q13)t(6;8)(p23;q13)[19]/46,XX[1]	del(3)(p12.2p14.1)[76.6%],del(6)(p24.1pter)[75.1%],del(6)(q14.1q14.3)[77.6%],gain(8)(q12.1qter)[72.8%]	0	Complex	Array	Confirmed: arr[GRCh37] 6q14.1q14.3(76560018_84992750)x1-2 (at breakpoints of rearrangement)
455499	chr6	70000000	115000000	45000000	DEL	AML	retrospective	46,XX,t(15;17)(q22;q21)[12]/46,XX[8]	del(6)(p22.3pter)[13.1%],del(6)(q13q22.1)[12.2%]	t(15;17)(q24.1;q21.2)[15.1%],t(15;17)(q24.1;q21.2)[19.5%]	del(6)(p22.3pter)[13.1%],del(6)(q13q22.1)[12.2%]	Array	did not confirm by array
455499	chr6	500000	16000000	15500000	DEL	AML	retrospective	46,XX,t(15;17)(q22;q21)[12]/46,XX[8]	del(6)(p22.3pter)[13.1%],del(6)(q13q22.1)[12.2%]	t(15;17)(q24.1;q21.2)[15.1%],t(15;17)(q24.1;q21.2)[19.5%]	del(6)(p22.3pter)[13.1%],del(6)(q13q22.1)[12.2%]	Array	did not confirm by array
578200	chr9	20500000	33500000	13000000	DEL	AML	retrospective	46,XY[20]	del(9)(p13.3p21.3)[11.6%]	0	del(9)(p13.3p21.3)[11.5%]	Array	did not confirm by array
922185	chr18	500000	13000000	12500000	DEL	MDS	retrospective	46,XY,del(20)(q11.2)[13]/46,XY[7]	-7[7.5%],del(18)(p11.21pter)[10.1%],del(18)(q21.2qter)[10.1%],+19[5.3%]	0	-7[7.5%],del(18)(p11.21pter)[10.1%],del(18)(q21.2qter)[10.1%],+19[5.3%]	Array	did not confirm by array
922185	chr18	55000000	80000000	25000000	DEL	MDS	retrospective	46,XY,del(20)(q11.2)[13]/46,XY[7]	-7[7.5%],del(18)(p11.21pter)[10.1%],del(18)(q21.2qter)[10.1%],+19[5.3%]	0	-7[7.5%],del(18)(p11.21pter)[10.1%],del(18)(q21.2qter)[10.1%],+19[5.3%]	Array	did not confirm by array
922185	chr7	500000	159000000	158500000	DEL	MDS	retrospective	46,XY,del(20)(q11.2)[13]/46,XY[7]	-7[7.5%],del(18)(p11.21pter)[10.1%],del(18)(q21.2qter)[10.1%],+19[5.3%]	0	-7[7.5%],del(18)(p11.21pter)[10.1%],del(18)(q21.2qter)[10.1%],+19[5.3%]	Array	did not confirm by array
984418	chr5	89000000	172000000	83000000	DEL	AML	retrospective	46,XX[20]	del(5)(q14.3q35.1)[24.4%]	0	del(5)(q14.3q35.1)[24.4%]	Array	Confirmed: arr[GRCh37] 5q14.3q35.1(88111710_171208088)x1-2
714148	chrY	7000000	21000000	14000000	DEL	MDS	retrospective	46,XY[20]	-Y[21.4%]	0	new -Y	Confirmation not attempted	
847670	chr9	68500000	105000000	36500000	DEL	AML	retrospective	46,XY,der(X)t(8;21)(q22;q22)t(X;21)(q28;?q22),der(8)t(8;21)(q22;q22),der(21)t(8;21)(q22;q22)t(X;21)(q28;?q22)[18]/46,XY[2]	del(9)(q21.11q31.1)[13.2%],-Y[15.4%]	t(8;21)(q21.3;q22.12)[26.5%],t(8;21)(q21.3;q22.12)[27.9%]	del(9)(q21.11q31.1)[13.2%],-Y[30.8%]	Confirmation not attempted	
847670	chrY	7000000	21000000	14000000	DEL	AML	retrospective	46,XY,der(X)t(8;21)(q22;q22)t(X;21)(q28;?q22),der(8)t(8;21)(q22;q22),der(21)t(8;21)(q22;q22)t(X;21)(q28;?q22)[18]/46,XY[2]	del(9)(q21.11q31.1)[13.2%],-Y[15.4%]	t(8;21)(q21.3;q22.12)[26.5%],t(8;21)(q21.3;q22.12)[27.9%]	del(9)(q21.11q31.1)[13.2%],-Y[30.8%]	Confirmation not attempted	
395906	chr4	134000000	139500000	5500000	DEL	MDS	prospective	46,XY,del(3)(q12q25),+8[20]	del(3)(q21.2q24)[83.4%],del(4)(q28.3q31.1)[65.6%],+8[82.7%]	0	Complex	FISH	Confirmed: nuc ish(RP11-197E22x1,CEP4x2)[161/200]
499829	chr3	119500000	197500000	78000000	DUP	AML	retrospective	47,XY,+8[2]/46,XY[18]	gain(3)(q13.33qter)[8.1%],+8[8.4%]	0	gain(3)(q13.33qter)[8.1%],+8[8.4%]	FISH	
538465	chr10	500000	133500000	133000000	DUP	AML	prospective	46,XY,t(15;17)(q24;q21)[17]/46,XY[3]	+8[27.6%],+10[29.3%]	t(15;17)(q24.1;q21.2)[34.2%],t(15;17)(q24.1;q21.2)[28.8%]	Not Complex	FISH	Confirmed: nuc ish(D8Z2x3)[44/20],(CEP10x3)[29/200]
538465	chr8	500000	145000000	144500000	DUP	AML	prospective	46,XY,t(15;17)(q24;q21)[17]/46,XY[3]	+8[27.6%],+10[29.3%]	t(15;17)(q24.1;q21.2)[34.2%],t(15;17)(q24.1;q21.2)[28.8%]	Not Complex	FISH	Confirmed: nuc ish(D8Z2x3)[44/20],(CEP10x3)[29/200]
905177	chr9	131000000	138000000	7000000	DUP	ALL	prospective	46,XY,t(9;22)(q34;q11.2)[20]	gain(9)(q34.12qter)[58.2%],del(19)(p13.3pter)[53.8%],gain(22)(q11.21q11.23)[54.9%]	t(9;22)(q34.12;q11.23)[32.6%],t(9;22)(q34.12;q11.23)[43.8%]	gain(9)(q34.12qter)[58.2%],del(19)(p13.3pter)[53.8%],gain(22)(q11.21q11.23)[54.9%]	FISH	Confirmed: arr[GRCh37] 9q34.13q34.3(134108368_141020389)x2-3
905177	chr22	17500000	23500000	6000000	DUP	ALL	prospective	46,XY,t(9;22)(q34;q11.2)[20]	gain(9)(q34.12qter)[58.2%],del(19)(p13.3pter)[53.8%],gain(22)(q11.21q11.23)[54.9%]	t(9;22)(q34.12;q11.23)[32.6%],t(9;22)(q34	gain(9)(q34.12qter)[58.2%],del(19)(p13.3	FISH	Confirmed: arr[GRCh37] 22q11.1q11.2

										.12;q11.23)[43.8%]	pter)[53.8%],gain(22)(q11.21q11.23)[54.9%]			3(16888899_23615801)x2-3
179016	chr11	23000000	42000000	19000000	DEL	AML	retrospective	46,XY,del(9)(q13q22),t(11;21)(p13;q22),t(15;17)(q22;q21)[20]	del(9)(q21.11q31.1)[87.3%],del(11)(p12p14.3)[87.6%]	t(15;17)(q24.1;q21.2)[35.0%],t(15;17)(q24.1;q21.2)[32.5%]	del(11)(p12p14.3)[87.6%]	Seq		has breakpoints and spans WT1
534164	chr13	47000000	53500000	6500000	DEL	MDS	prospective	45,XY,-7[20]	-7[83.9%],del(13)(q14.2q14.3)[85.3%]	0	del(13)(q14.2q14.3)[85.3%]	Seq		has breakpoints and spans RB1
680763	chr12	10000000	15500000	5500000	DEL	AML	retrospective	45,XY,del(5)(q13q33),-7[19]/46,XY[1]	del(5)(q21.1qter)[70.8%],-7[71.0%],del(12)(p12.3p13.2)[70.9%]	0	Complex	Seq		has breakpoints and spans ETV6

Coordinates are based on the GRCh38 human reference.
* ‘Confirmed’ indicates the variant was supported by an orthogonal method, either clinical FISH studies performed at diagnosis, confirmation FISH studies, CMA (array), or sequence-defined breakpoints.
Downloadable version can be found here: https://wustl.box.com/v/rapidclinicalwgs-tables5

Table S6. Gene mutation comparisons.

UPN	chr	pos	ref	alt	type	gene	vaf_wgs	vaf_genepanel	variant	WGS Detected	GenePanel Detected
104895	chr13	28018505	C	A	SNV	FLT3	0.038	0.0251451	p.Asp835Tyr	Y	Y
104895	chr17	76736877	G	T	SNV	SRSF2	0.438	0.46848	p.Pro95His	Y	Y
104895	chr15	90088702	C	T	SNV	IDH2	0.423	0.450396	p.Arg140Gln	Y	Y
104895	chrX	124051313	A	G	SNV	STAG2	0.451	0.355191		Y	Y
142639	chr4	105275056	C	T	SNV	TET2	0.088	0.040568	p.Arg1516Ter	Y	Y
142639	chr13	28018503	A	C	SNV	FLT3	0.41	0.301744	p.Asp835Glu	Y	Y
206801	chr15	90088702	C	T	SNV	IDH2	0.277	0.355402	p.Arg140Gln	Y	Y
206801	chr19	33302231	T	TG	INDEL	CEBPA	0.537	0.544199	p.Ile62HisfsTer46	Y	Y
250911	chr5	171410539	C	CTCTG	INDEL	NPM1	0.377	0.459245	p.Trp288CysfsTer12	Y	Y
250911	chr13	28034083	A	AAACTCTAAATTTTCTCTTGGAAACTCC	INDEL	FLT3	0.413	0.291209	p.Glu611_Phe612insLeuGluPheProArgGluAsnLeuGlu	Y	Y
250911	chr15	90088702	C	T	SNV	IDH2	0.469	0.491429	p.Arg140Gln	Y	Y
465146	chr5	171410543	G	GCAGA	INDEL	NPM1	0.226	0.312388	p.Trp288CysfsTer12	Y	Y
499829	chr17	76736877	G	A	SNV	SRSF2	0.508	0.461538	p.Pro95Leu	Y	Y
499829	chr4	105243699	GACAA	G	INDEL	TET2	0.412	0.402341	p.Lys1243SerfsTer9	Y	Y
499829	chr20	32434789	C	T	SNV	ASXL1	0.394	0.347645	p.Arg693Ter	Y	Y
499829	chr11	119278535	T	C	SNV	CBL	0.977	0.954214	p.Phe418Ser	Y	Y
499829	chr4	105259635	C	T	SNV	TET2	0.528	0.518291	p.Gln1274Ter	Y	Y
499829	chr5	171410539	C	CTCTG	INDEL	NPM1		0.0519943	p.Trp288CysfsTer12	N	Y
509179	chr5	171410540	T	TCTGC	INDEL	NPM1	0.232	0.407112	p.Trp288CysfsTer12	Y	Y
509179	chr3	128481291	CCTT	C	INDEL	GATA2	0.029			Y	N
509179	chr4	105272736	G	A	SNV	TET2	0.517	0.495419	p.Arg1452Gln	Y	Y
509179	chr12	112450407	A	C	SNV	PTPN11	0.476	0.529412	p.Glu76Ala	Y	Y
509179	chr11	32396364	G	T	SNV	WT1	0.413	0.47617	p.Ser381Ter	Y	Y
607160	chr15	90088702	C	T	SNV	IDH2	0.527	0.419328	p.Arg140Gln	Y	Y
607160	chr13	28034127	C	CATATTCTCTGAAATCAACGTAGAAGTACTCATTATCTGAGGA	INDEL	FLT3	0.313			Y	N
607160	chr2	25241699	C	T	SNV	DNMT3A	0.366	0.40448	p.Val649Met	Y	Y
607160	chr5	171410540	T	TCTGC	INDEL	NPM1	0.377	0.410256	p.Trp288CysfsTer12	Y	Y
623930	chr2	25243930	C	T	SNV	DNMT3A	0.478	0.443627	p.Arg635Gln	Y	Y
623930	chr21	34792358	T	G	SNV	RUNX1	0.125			Y	N
623930	chrX	53409109	T	C	SNV	SMC1A	0.517	0.46337	p.Lys500Glu	Y	Y
623930	chr1	114716127	C	A	SNV	NRAS		0.0903226	p.Gly12Cys	N	Y
623930	chr5	171410541	C	CTGTT	INDEL	NPM1	0.429	0.384615	p.Trp288CysfsTer12	Y	Y
662555	chr2	25234373	C	T	SNV	DNMT3A	0.396	0.49697	p.Arg882His	Y	Y
662555	chr13	28034100	T	TTGGAAACTCCCATTTGAGATCATATTCATATTCTCTGAA	INDEL	FLT3	0.425	0.29488	p.Phe594_Pro606dup	Y	Y

662555	chr5	171410539	C	CTCTG	INDEL	NPM1	0.288	0.439086	p.Trp288CysfsTer12	Y	Y
879308	chr2	25234373	C	T	SNV	DNMT3A	0.367	0.391036	p.Arg882His	Y	Y
879308	chr5	171410539	C	CTCTG	INDEL	NPM1	0.356	0.43364	p.Trp288CysfsTer12	Y	Y
879308	chr11	32434938	A	AGGC	INDEL	WT1	0.373	0.534884	p.Pro136dup	Y	Y
879308	chr13	28034082	C	CAAACTCTAAATTTTCTCTTGGAAACTCCCATTTGAGATCATATTCATATTCTCTGAAATCAACGTAGAAGTACTCATTATCTGAGGAGCCGGTCACCTGTACCATCTG	INDEL	FLT3	0.049	0.0393258	p.Gln577_Phe612dup	Y	Y
907523	chr13	28034091	A	AATTTTCTCTTGGAAACTCCCATTTGAGATCATATTCATATTCTCTGAAATC	INDEL	FLT3	0.54	0.519565	p.Asp593_Asn609dup	Y	Y
907523	chr2	25244564	A	G	SNV	DNMT3A	0.486	0.453353	p.Met548Thr	Y	Y
907523	chr2	25241624	T	C	SNV	DNMT3A	0.554	0.445946	p.Met674Val	Y	Y
907523	chr5	171410539	C	CTCTG	INDEL	NPM1	0.375	0.434664	p.Trp288CysfsTer12	Y	Y
907716	chr17	76736853	CGGCGGCTGTGGTGTGAGTCCGGGG	C	INDEL	SRSF2	0.055			Y	N
907716	chr7	148809342	T	G	SNV	EZH2		0.0514286	p.Asn693Thr	N	Y
938927	chr15	90088702	C	T	SNV	IDH2	0.354	0.426408	p.Arg140Gln	Y	Y
938927	chr11	119278645	TATG	T	INDEL	CBL	0.047			Y	N
938927	chr2	25240366	CAGA	C	INDEL	DNMT3A	0.292	0.461054	p.Phe752del	Y	Y
938927	chr1	114716126	C	T	SNV	NRAS	0.358	0.436117	p.Gly12Asp	Y	Y
938927	chr5	171410539	C	CTCTG	INDEL	NPM1	0.466	0.380805	p.Trp288CysfsTer12	Y	Y
780327	chr7	102104413	C	T	SNV	CUX1	0.46	0.503484	p.Leu173Phe	Y	Y
780327	chr15	90088702	C	T	SNV	IDH2	0.412	0.428571	p.Arg140Gln	Y	Y
780327	chr7	102201390	G	T	SNV	CUX1	0.48	0.454768	p.Gly709Val	Y	Y
780327	chr5	171410542	T	TGTAG	INDEL	NPM1	0.519	0.365108	p.Trp288CysfsTer12	Y	Y
776603	chr20	32434638	A	AG	INDEL	ASXL1	0.385	0.245179	p.Gly646TrpfsTer12	Y	Y
776603	chr21	34834502	A	AC	INDEL	RUNX1		0.0568966	p.Val238GlyfsTer23	N	Y
776603	chr21	34880580	C	T	SNV	RUNX1	0.244	0.171995	p.Arg162Lys	Y	Y
776603	chr21	34792554	T	TG	INDEL	RUNX1	0.14	0.149051	p.Ile342HisfsTer258	Y	Y
776603	chr21	43104346	G	A	SNV	U2AF1	0.522	0.326577	p.Ser34Phe	Y	Y
994357	chr21	34792313	T	G	SNV	RUNX1		0.333333	p.Glu422Ala	N	Y
586748	chr12	11853483	C	CT	INDEL	ETV6	0.463	0.357362	p.Ser131PhefsTer23	Y	Y
553306	chr17	7673802	C	T	SNV	TP53	0.8	0.835125	p.Arg273His	Y	Y
677322	chrX	134417211	G	T	SNV	PHF6		0.0566449	p.Glu293Ter	N	Y
677322	chr7	148817943	C	T	SNV	EZH2	0.565	0.492437	p.Glu392Lys	Y	Y
677322	chrX	53405648	G	A	SNV	SMC1A	0.897	0.894094	p.Arg586Trp	Y	Y
677322	chr2	208248388	C	T	SNV	IDH1	0.289	0.424589	p.Arg132His	Y	Y
677322	chr2	25244564	A	G	SNV	DNMT3A	0.425	0.436548	p.Met548Thr	Y	Y
677322	chrX	134377742	A	AC	INDEL	PHF6		0.0801457	p.His43ProfsTer2	N	Y
677322	chr19	33302311	C	CGG	INDEL	CEBPA	0.49	0.344923	p.Arg35ProfsTer126	Y	Y
677322	chr19	33301813	AGGTGCGCGGGCGGCGG	A	INDEL	CEBPA	0.333	0.765823	p.Pro196TrpfsTer117	Y	Y
504451	chr17	7673802	C	T	SNV	TP53	0.844	0.81203	p.Arg273His	Y	Y

410110	chr21	34880697	T	TC	INDEL	RUNX1	0.553	0.389922	p.Asp123GlyfsTer15	Y	Y
410110	chr13	28034081	C	CCAAACTCTAAATTTTCTCTTGGAAACTCCCATTTGAGATCATATA	INDEL	FLT3	0.065			Y	N
410110	chr21	34880569	G	A	SNV	RUNX1	0.493	0.449102	p.Arg166Ter	Y	Y
410110	chr17	76736877	G	T	SNV	SRSF2	0.37	0.484058	p.Pro95His	Y	Y
410110	chr2	25234374	G	A	SNV	DNMT3A	0.543	0.456156	p.Arg882Cys	Y	Y
296442	chr17	7673533	A	G	SNV	TP53	0.467	0.46994		Y	Y
296442	chr17	7674250	C	T	SNV	TP53	0.457	0.431262	p.Cys238Tyr	Y	Y
889663	chr21	34886875	G	A	SNV	RUNX1		0.0826211	p.Arg107Cys	N	Y
889663	chr11	32396368	G	GT	INDEL	WT1		0.0943396	p.Arg380ThrfsTer5	N	Y
889663	chrX	130016199	T	TGGGAGGGA	INDEL	BCORL1		0.0590062	p.Ser1143TrpfsTer82	N	Y
889663	chrX	40054335	T	C	SNV	BCOR		0.139896		N	Y
508617	chr4	105234422	T	TA	INDEL	TET2	0.518	0.361345	p.Asp162ArgfsTer9	Y	Y
508617	chr4	105236538	C	T	SNV	TET2	0.286			Y	N
508617	chr17	76736877	G	T	SNV	SRSF2	0.422	0.456767	p.Pro95His	Y	Y
508617	chr21	34880572	C	T	SNV	RUNX1	0.273	0.251938	p.Gly165Ser	Y	Y
437892	chr11	119278217	A	T	SNV	CBL	0.328	0.220177	p.Ile383Leu	Y	Y
437892	chr17	31229305	G	A	SNV	NF1	0.597	0.443627	p.Arg897Gln	Y	Y
343604	chr20	32434638	A	AG	INDEL	ASXL1	0.393	0.434307	p.Gly646TrpfsTer12	Y	Y
343604	chr7	148828882	T	C	SNV	EZH2	0.955	0.909953		Y	Y
343604	chr12	25245347	C	T	SNV	KRAS	0.35	0.350453	p.Gly13Asp	Y	Y
726806	chr4	105235256	CA	C	INDEL	TET2	0.377	0.522659	p.Asn439ThrfsTer8	Y	Y
726806	chr1	36471622	C	T	SNV	CSF3R	0.633	0.515625	p.Gly366Arg	Y	Y
726806	chr20	32429991	G	T	SNV	ASXL1	0.5	0.439655	p.Gly219Val	Y	Y
726806	chr5	171410539	C	CTCTG	INDEL	NPM1	0.481	0.464455	p.Trp288CysfsTer12	Y	Y
726806	chr13	28034107	C	CTCCCATTTGAGATCATATTCATATTCTCTG	INDEL	FLT3	0.41	0.233546	p.Trp603_Glu604insAspArgGluTyrGluTyrAspLeuLysTrp	Y	Y
375074	chr5	171410539	C	CTCTG	INDEL	NPM1	0.203	0.309175	p.Trp288CysfsTer12	Y	Y
375074	chr4	105242872	T	A	SNV	TET2	0.837	0.779874	p.Val1180Asp	Y	Y
375074	chr17	76736877	G	C	SNV	SRSF2	0.522	0.448009	p.Pro95Arg	Y	Y
375074	chr15	90088702	C	T	SNV	IDH2	0.39	0.486797	p.Arg140Gln	Y	Y
557196	chr2	25240427	C	CA	INDEL	DNMT3A	0.444	0.376923	p.Glu733Ter	Y	Y
557196	chrX	130015496	C	A	SNV	BCORL1	0.778	0.790909	p.Cys908Ter	Y	Y
557196	chr2	25240684	C	T	SNV	DNMT3A	0.325	0.4093	p.Cys710Tyr	Y	Y
557196	chr13	28034105	A	AACTCCCATTTGAGATCATATTCATATTCTCTGAAATCAACGTAGAAGT	INDEL	FLT3	0.063	0.00833649	p.Tyr589_Glu604dup	Y	Y
557196	chr12	25245332	G	T	SNV	KRAS		0.0575472	p.Ala18Asp	N	Y
557196	chr4	105269609	G	T	SNV	TET2	0.455	0.372362		Y	Y
557196	chr1	114716127	C	T	SNV	NRAS	0.163	0.235823	p.Gly12Ser	Y	Y
557196	chrX	15804193	AAG	A	INDEL	ZRSR2	0.379	0.746269	p.Glu133GlyfsTer11	Y	Y
271002	chrX	134415022	T	A	SNV	PHF6		0.136364	p.Ser246Thr	N	Y

271002	chr12	11869428	CTG	C	INDEL	ETV6	0.122	0.116187	p.Val158ProfsTer10	Y	Y
271002	chr7	148813976	G	A	SNV	EZH2		0.0950704	p.Gln612Ter	N	Y
271002	chr2	25234374	G	A	SNV	DNMT3A	0.425	0.411061	p.Arg882Cys	Y	Y
271002	chr15	90088702	C	T	SNV	IDH2	0.447	0.389437	p.Arg140Gln	Y	Y
271002	chrX	134425256	C	T	SNV	PHF6		0.0571429	p.Arg342Ter	N	Y
271002	chrX	134415026	C	A	SNV	PHF6		0.136364	p.Ser247Tyr	N	Y
271002	chrX	130037503	A	G	SNV	BCORL1	1	0.994764	p.Asn1481Ser	Y	Y
259112	chr2	25234373	C	T	SNV	DNMT3A	0.948	0.897436	p.Arg882His	Y	Y
259112	chr17	76736877	G	T	SNV	SRSF2	0.438	0.494824	p.Pro95His	Y	Y
259112	chr15	90088702	C	T	SNV	IDH2	0.517	0.442682	p.Arg140Gln	Y	Y
819978	chr15	90088702	C	T	SNV	IDH2	0.362	0.410135	p.Arg140Gln	Y	Y
819978	chr17	7675217	T	C	SNV	TP53	0.722	0.777619	p.Lys132Arg	Y	Y
819978	chr1	114716123	C	T	SNV	NRAS	0.09	0.0897305	p.Gly13Asp	Y	Y
819978	chr17	76736877	G	A	SNV	SRSF2	0.547	0.51005	p.Pro95Leu	Y	Y
819978	chr12	25245347	C	T	SNV	KRAS		0.105566	p.Gly13Asp	N	Y
895870	chr5	171410539	C	CTCTG	INDEL	NPM1	0.3	0.280462	p.Trp288CysfsTer12	Y	Y
895870	chr20	32434638	A	AG	INDEL	ASXL1		0.11126	p.Gly646TrpfsTer12	N	Y
895870	chrX	124081469	TGCTTTAAC	T	INDEL	STAG2		0.0900225	p.Ala956PhefsTer4	N	Y
895870	chr15	90088702	C	T	SNV	IDH2	0.375	0.488538	p.Arg140Gln	Y	Y
895870	chr13	28034144	A	C	SNV	FLT3	0.386	0.271178	p.Val592Gly	Y	Y
895870	chr17	76736879	G	GCGC	INDEL	SRSF2	0.489	0.458671	p.Arg94dup	Y	Y
992091	chr20	32436950	T	C	SNV	ASXL1	0.449	0.347531	p.Leu1413Ser	Y	Y
992091	chr17	31226459	A	AC	INDEL	NF1	0.717			Y	N
992091	chr17	7670685	G	A	SNV	TP53	0.719	0.670951	p.Arg342Ter	Y	Y
333171	chrX	53414992	C	T	SNV	SMC1A	0.212	0.28595	p.Arg96His	Y	Y
333171	chr12	11884493	G	A	SNV	ETV6	0.508	0.497291	p.Arg353Gln	Y	Y
333171	chr4	105276400	T	C	SNV	TET2	0.404	0.478554	p.Tyr1964His	Y	Y
333171	chr12	25245350	C	G	SNV	KRAS	0.405	0.369942	p.Gly12Ala	Y	Y
606753	chrX	15823117	C	CGCA	INDEL	ZRSR2	0.68	1	p.Arg442dup	Y	Y
704854	chr7	148807671	A	G	SNV	EZH2		0.0526316	p.Ile744Thr	N	Y
704854	chr2	25244214	G	A	SNV	DNMT3A	0.368	0.459297	p.Arg598Ter	Y	Y
704854	chr20	32435133	TC	T	INDEL	ASXL1	0.208	0.410985	p.Pro808LeufsTer10	Y	Y
704854	chr3	128481293	TTCTTCATGG	T	INDEL	GATA2	0.298	0.302291	p.Thr387_Lys389del	Y	Y
704854	chr12	112489084	G	T	SNV	PTPN11	0.312	0.258204	p.Gly503Val	Y	Y
704854	chr2	25234323	G	A	SNV	DNMT3A	0.406	0.420389	p.Arg899Cys	Y	Y
952492	chrX	40077898	A	G	SNV	BCOR	1	1	p.Val11Ala	Y	Y
952492	chr2	25300185	G	A	SNV	DNMT3A	0.525	0.482845	p.Thr44Met	Y	Y
952492	chr20	32433473	C	CA	INDEL	ASXL1	0.329	0.219272	p.Gln428ThrfsTer10	Y	Y

312088	chr2	25234374	G	A	SNV	DNMT3A	0.531	0.447244	p.Arg882Cys	Y	Y
312088	chr12	112450359	G	T	SNV	PTPN11		0.188153	p.Gly60Val	N	Y
312088	chr12	25227342	T	A	SNV	KRAS		0.0875445	p.Gln61Leu	N	Y
312088	chr11	32435332	G	A	SNV	WT1	0.333	0.476	p.Ala5Val	Y	Y
312088	chr1	114716123	C	T	SNV	NRAS	0.077	0.0765306	p.Gly13Asp	Y	Y
312088	chr5	171410539	C	CTCTG	INDEL	NPM1	0.242	0.383845	p.Trp288CysfsTer12	Y	Y
312088	chr11	32435333	C	T	SNV	WT1	0.391	0.477046	p.Ala5Thr	Y	Y
312088	chr8	116854320	CA	C	INDEL	RAD21	0.323	0.425532	p.Met362SerfsTer8	Y	Y
570496	chr15	90088702	C	T	SNV	IDH2	0.435	0.494118	p.Arg140Gln	Y	Y
570496	chrX	124063866	C	T	SNV	STAG2	0.321	0.353556	p.Arg614Ter	Y	Y
570496	chr20	32434638	A	AG	INDEL	ASXL1	0.363	0.462963	p.Gly646TrpfsTer12	Y	Y
570496	chr2	197402981	C	T	SNV	SF3B1	0.466	0.411936	p.Glu592Lys	Y	Y
570496	chrX	124045347	C	T	SNV	STAG2	0.52	0.404475	p.Arg216Ter	Y	Y
229201	chr13	28034115	T	TGAGATCATATTCATATTCTCTGAAATCAACGTAGAAGTACTCATTATCTGAGCC	INDEL	FLT3	0.14	0.0726788	p.Leu601_Lys602insGlySerAspAsnGluTyrPheTyrValAspPheArgGluTyrGluTyrAspLeu	Y	Y
229201	chr5	171410539	C	CTCTG	INDEL	NPM1	0.155	0.261972	p.Trp288CysfsTer12	Y	Y
229201	chr15	90088702	C	T	SNV	IDH2	0.377	0.369789	p.Arg140Gln	Y	Y
983349	chr17	7675235	T	C	SNV	TP53	0.718	0.535032	p.Tyr126Cys	Y	Y
983349	chrX	53382605	G	C	SNV	SMC1A	1	1	p.Ile1062Met	Y	Y
534164	chr8	116856286	C	A	SNV	RAD21		0.131579	p.Gly273Cys	N	Y
534164	chr12	11884565	C	T	SNV	ETV6	0.379	0.403968	p.Ala377Val	Y	Y
534164	chr2	25247629	G	A	SNV	DNMT3A	0.509	0.442248	p.Arg326Cys	Y	Y
925086	chrX	40072977	T	C	SNV	BCOR	0.527	0.495556	p.Asn790Ser	Y	Y
925086	chr2	25234373	C	T	SNV	DNMT3A	0.429	0.400607	p.Arg882His	Y	Y
925086	chr20	32437205	C	T	SNV	ASXL1	0.466	0.505505	p.Thr1498Met	Y	Y
925086	chr5	171410539	C	CTCTG	INDEL	NPM1	0.403	0.406479	p.Trp288CysfsTer12	Y	Y
875579	chr21	43094667	T	G	SNV	U2AF1	0.148	0.282226	p.Gln157Pro	Y	Y
875579	chr1	36466641	G	A	SNV	CSF3R	0.157	0.286447	p.Gln770Ter	Y	Y
679540	chr2	197402649	G	C	SNV	SF3B1	0.397	0.243719	p.His662Asp	Y	Y
679540	chr17	31229061	C	T	SNV	NF1	0.433	0.114583	p.Arg816Ter	Y	Y
679540	chr17	7675126	GATGGCC	G	INDEL	TP53	0.672	0.387312	p.Met160_Ala161del	Y	Y
477377	chr1	114716127	C	T	SNV	NRAS		0.065051	p.Gly12Ser	N	Y
477377	chr17	76736853	CGGCGGCTGTGGTGTGAGTCCGGGG	C	INDEL	SRSF2	0.452	0.442539	p.Pro95_Arg102del	Y	Y
477377	chrX	53403617	C	T	SNV	SMC1A	0.806	0.814241	p.Arg790Gln	Y	Y
477377	chr15	90088702	C	T	SNV	IDH2	0.508	0.445313	p.Arg140Gln	Y	Y
493436	chr21	34880640	G	GCCGGGC	INDEL	RUNX1	0.213	0.376623	p.Ser141_Ala142insGlyPro	Y	Y
493436	chr1	114716127	C	A	SNV	NRAS	0.458	0.369087	p.Gly12Cys	Y	Y
493436	chr21	34799371	TGCTGGGTGCACAGAAG	T	INDEL	RUNX1	0.224	0.368175	p.Pro294GlnfsTer12	Y	Y
429293	chr21	34880620	C	G	SNV	RUNX1		0.227561	p.Ala149Pro	N	Y

429293	chr15	90088702	C	T	SNV	IDH2	0.196	0.245259	p.Arg140Gln	Y	Y
429293	chr8	116863211	G	A	SNV	RAD21	0.228	0.209272	p.Arg65Ter	Y	Y
429293	chr21	34834409	C	T	SNV	RUNX1	0.259	0.267133		Y	Y
429293	chr12	112450416	A	G	SNV	PTPN11	0.304	0.219114	p.Gln79Arg	Y	Y
429293	chrX	40062137	A	C	SNV	BCOR	0.369	0.31338		Y	Y
802619	chr17	7674268	A	G	SNV	TP53		0.248775	p.Ile232Thr	N	Y
802619	chr17	7676114	A	AG	INDEL	TP53	0.275	0.247289	p.Ala86CysfsTer63	Y	Y
802619	chr8	116848945	C	T	SNV	RAD21		0.183246		N	Y
294891	chr4	105235529	C	CCT	INDEL	TET2	0.375	0.2	p.Gln530HisfsTer11¬†	Y	Y
294891	chr5	171410540	T	TCTGC	INDEL	NPM1	0.073	0.26672	p.Trp288CysfsTer12	Y	Y
294891	chr17	76736877	G	T	SNV	SRSF2	0.422	0.36695	p.Pro95His	Y	Y
294891	chr4	105275167	C	CA	INDEL	TET2	0.492	0.188356	p.Thr1554AspfsTer24	Y	Y
731757	chr13	28034122	A	ATATTCATATTCGCCCAGCTTCCGGGGGGCATACTCTAATTTTTCTCTTGGAAACTCCCATTTGAGATCT	INDEL	FLT3	0.071	0.165229	p.Glu598_Tyr599insTer	Y	Y
731757	chr10	110596398	G	A	SNV	SMC3	0.455	0.447479	p.Gly655Asp	Y	Y
731757	chr2	25241590	C	A	SNV	DNMT3A	0.456	0.514398	p.Gly685Val	Y	Y
731757	chr5	171410539	C	CTCTG	INDEL	NPM1	0.282	0.40767	p.Trp288CysfsTer12	Y	Y
335141	chr2	25234373	C	T	SNV	DNMT3A	0.521	0.448179	p.Arg882His	Y	Y
335141	chr13	28034113	T	TTTGAGATCATATTCATATTCTCTGAAATCAACGTAG	INDEL	FLT3	0.216	0.188447	p.Leu601_Lys602insAsnTyrValAspPheArgGluTyrGluTyrAspLeu	Y	Y
335141	chr2	197402110	T	C	SNV	SF3B1	0.394	0.443825	p.Lys700Glu	Y	Y
155912	chr5	171410539	C	CTCTG	INDEL	NPM1	0.371	0.384372	p.Trp288CysfsTer12	Y	Y
155912	chr2	25244337	A	G	SNV	DNMT3A	0.369	0.421749	p.Cys557Arg	Y	Y
155912	chr13	28034103	G	GAAACTCCCATTTGAGATCATATTCATGTCT	INDEL	FLT3	0.179	0.128768	p.Phe605_Pro606insArgHisGluTyrAspLeuLysTrpGluPhe	Y	Y
155912	chr11	32396401	G	GCC	INDEL	WT1	0.421	0.432269	p.Arg369GlyfsTer7	Y	Y
155912	chr12	112502202	C	T	SNV	PTPN11	0.476	0.457831	p.Thr553Met	Y	Y
103744	chr17	7675212	A	C	SNV	TP53	0.5	0.295972	p.Phe134Val	Y	Y
956161	chr2	197402636	T	G	SNV	SF3B1	0.491	0.449367	p.Lys666Thr	Y	Y
956161	chr13	28034125	T	TTCATATTATCTGAAATCATCGTAGTAGTACTCATTATCTGAGGAGCCGGTCACCTGTACCTCC	INDEL	FLT3	0.271	0.0524246	p.Glu598_Tyr599insGluValGlnValThrGlySerSerAspAsnGluTyrTyrTyrAspAspPheArgTerTyrGlu	Y	Y
673325	chr1	114716126	C	T	SNV	NRAS	0.075	0.100521	p.Gly12Asp	Y	Y
673325	chr21	43104346	G	A	SNV	U2AF1	0.406	0.4625	p.Ser34Phe	Y	Y
673325	chrX	124076340	CA	C	INDEL	STAG2	0.611	0.949219	p.Glu849ArgfsTer23	Y	Y
673325	chr1	114716123	C	T	SNV	NRAS	0.087	0.112836	p.Gly13Asp	Y	Y
673325	chrX	40072420	G	A	SNV	BCOR	0.95	0.961319	p.Arg976Ter	Y	Y
451688	chr9	5073770	G	T	SNV	JAK2	0.048			Y	N
451688	chr20	32434638	A	AG	INDEL	ASXL1	0.302	0.306122	p.Gly646TrpfsTer12	Y	Y
451688	chr7	148818035	CCTCTT	C	INDEL	EZH2	0.167	0.207852	p.Arg360ThrfsTer5	Y	Y
451688	chrX	15818643	G	A	SNV	ZRSR2	0.68	0.594937		Y	Y
891309	chr20	32434599	TCACCACTGCCATAGAGAGGCGGC	T	INDEL	ASXL1	0.082	0.188329	p.Glu635ArgfsTer15	Y	Y
891309	chr20	32435095	TC	T	INDEL	ASXL1	0.048	0.0591982	p.Trp796GlyfsTer22	Y	Y

891309	chr17	7673704	G	A	SNV	TP53	0.195	0.224138	p.Arg306Ter	Y	Y
572410	chr17	7674894	G	A	SNV	TP53		0.127092	p.Arg213Ter	N	Y
395906	chr17	31261733	C	T	SNV	NF1	0.545	0.525622	p.Arg1534Ter	Y	Y
395906	chr20	32435474	C	T	SNV	ASXL1	0.586	0.482759	p.Ser921Phe	Y	Y
395906	chr21	34886904	A	G	SNV	RUNX1	0.352	0.431412	p.Phe97Ser	Y	Y
395906	chr21	43104346	G	A	SNV	U2AF1	0.568	0.434457	p.Ser34Phe	Y	Y
395906	chr2	25234373	C	T	SNV	DNMT3A	0.509	0.44625	p.Arg882His	Y	Y
395906	chr17	60663185	T	G	SNV	PPM1D	0.472	0.450064	p.Leu484Ter	Y	Y
830563	chr17	7674872	T	C	SNV	TP53	0.63	0.418228	p.Tyr220Cys	Y	Y
830563	chr17	7675112	T	TGTGA	INDEL	TP53	0.478	0.424208	p.Gln167LeufsTer15	Y	Y
467399	chr13	28018485	G	T	SNV	FLT3	0.236	0.159091	p.Asn841Lys	Y	Y
467399	chr4	105243605	G	GTGTT	INDEL	TET2	0.434	0.402878	p.Val1213PhefsTer11	Y	Y
467399	chr4	105259626	T	TG	INDEL	TET2	0.205	0.240192	p.Cys1271TrpfsTer29	Y	Y
467399	chr2	25234373	C	T	SNV	DNMT3A	0.532	0.453649	p.Arg882His	Y	Y
467399	chr5	171410539	C	CTCTG	INDEL	NPM1	0.432	0.416667	p.Trp288CysfsTer12	Y	Y
764488	chr4	105269703	C	T	SNV	TET2	0.462	0.489555	p.His1380Tyr	Y	Y
764488	chr19	33302240	C	CGG	INDEL	CEBPA	0.346	0.251295	p.Glu59ProfsTer102	Y	Y
764488	chr5	171410539	C	CTCTG	INDEL	NPM1	0.333	0.304025	p.Trp288CysfsTer12	Y	Y
764488	chr2	25241710	G	C	SNV	DNMT3A	0.524	0.468603		Y	Y
764488	chr13	28034192	A	T	SNV	FLT3	0.173	0.139981	p.Leu576Gln	Y	Y
764488	chr4	105276262	GA	G	INDEL	TET2	0.361	0.453328	p.Ala1919ProfsTer31	Y	Y
809382	chr5	171410540	T	TCTGC	INDEL	NPM1	0.446	0.365055	p.Trp288CysfsTer12	Y	Y
809382	chr17	76736877	G	C	SNV	SRSF2	0.534	0.257143	p.Pro95Arg	Y	Y
809382	chr4	105236826	C	T	SNV	TET2	0.461	0.432432	p.Gln962Ter	Y	Y
809382	chr4	105236412	A	T	SNV	TET2	0.476	0.390805	p.Lys824Ter	Y	Y
809382	chr2	25244163	G	A	SNV	DNMT3A	0.49	0.42976	p.Gln615Ter	Y	Y
211740	chr2	197402637	T	C	SNV	SF3B1	0.391	0.555556	p.Lys666Glu	Y	Y
211740	chr21	34859492	C	T	SNV	RUNX1	0.353	0.285714	p.Gly199Arg	Y	Y
211740	chr11	32392020	G	A	SNV	WT1	0.172			Y	N
462268	chr10	110580903	G	C	SNV	SMC3	0.373	0.439402		Y	Y
267935	chr4	54723599	TGAC	T	INDEL	KIT		0.113437	p.Thr417del	N	Y
267935	chr4	54723604	TACG	T	INDEL	KIT		0.122227	p.Asp419del	N	Y
491972	chr5	171410541	C	CTGCT	INDEL	NPM1	0.491	0.272581	p.Trp288CysfsTer12	Y	Y
491972	chr2	25234362	G	C	SNV	DNMT3A	0.481	0.341866	p.Gln886Glu	Y	Y
491972	chr4	105236679	C	T	SNV	TET2	0.465	0.289855	p.Gln913Ter	Y	Y
872523	chr17	7674858	C	T	SNV	TP53	0.429	0.443163		Y	Y
872523	chr21	34834517	C	A	SNV	RUNX1	0.607	0.490385	p.Arg233Leu	Y	Y
872523	chr17	7675237	C	T	SNV	TP53	0.465	0.436013		Y	Y

188798	chr17	7674221	G	A	SNV	TP53	0.277	0.20453	p.Arg248Trp	Y	Y
188798	chr17	7675178	A	G	SNV	TP53	0.274	0.312127	p.Leu145Pro	Y	Y
739025	chr17	7673796	C	T	SNV	TP53	0.759	0.752982	p.Cys275Tyr	Y	Y
506517	chrX	130013757	G	C	SNV	BCORL1	0.485	0.495667	p.Val329Leu	Y	Y
506517	chr5	171410539	C	CTCTG	INDEL	NPM1	0.422	0.482097	p.Trp288CysfsTer12	Y	Y
506517	chr11	32396357	A	AGATGCCGACCGTACAAGAGTCG	INDEL	WT1	0.514	0.388773	p.Glu384AspfsTer8	Y	Y
506517	chrX	40073314	G	A	SNV	BCOR	0.526	0.459042	p.Pro678Ser	Y	Y
506517	chr13	28033964	C	CCAAAAGCACCTGATCCTAGTACCTTCCCTGCAAAGACAAATGGTGAGTACGTGCATTTTAAAGATTTTCCAATGGAAAAGAAATGCTGCAGAAACATTTGGCACATTCCATTCTTACCAAACTCTAAATTTTCTCTTGGAAACTCCCATTTGAGATCATATTCATATT	INDEL	FLT3	0.214	0.1	p.Phe594_Asp600dup	Y	Y
985517	chr17	7674872	T	C	SNV	TP53		0.0852149	p.Tyr220Cys	N	Y
985517	chr10	110602879	G	T	SNV	SMC3		0.0625	p.Gly1118Ter	N	Y
537017	chr17	7675109	T	C	SNV	TP53	0.432	0.331058	p.His168Arg	Y	Y
666013	chr2	25247160	T	G	SNV	DNMT3A	0.542	0.30184		Y	Y
666013	chrX	134415110	GA	G	INDEL	PHF6	0.321	0.108225	p.Arg277GlufsTer2	Y	Y
666013	chrX	40074977	CT	C	INDEL	BCOR	0.227	0.0941176	p.Gln123ArgfsTer38	Y	Y
666013	chr2	208248389	G	A	SNV	IDH1	0.238	0.115979	p.Arg132Cys	Y	Y
887041	chr21	34880580	C	T	SNV	RUNX1	0.963	0.954333	p.Arg162Lys	Y	Y
887041	chr2	208248388	C	A	SNV	IDH1	0.553	0.444444	p.Arg132Leu	Y	Y
887041	chr1	114716124	C	G	SNV	NRAS		0.0694444	p.Gly13Arg	N	Y
887041	chr13	28018503	A	T	SNV	FLT3	0.174	0.216931	p.Asp835Glu	Y	Y
887041	chr17	76736877	G	T	SNV	SRSF2	0.431	0.464758	p.Pro95His	Y	Y
887041	chr20	32434638	A	AG	INDEL	ASXL1	0.508	0.387805	p.Gly646TrpfsTer12	Y	Y
887041	chr2	25244214	G	A	SNV	DNMT3A	0.507	0.466172	p.Arg598Ter	Y	Y
887041	chr2	25282695	G	T	SNV	DNMT3A	0.516	0.494454	p.Thr65Lys	Y	Y
681540	chr20	32434599	TCACCACTGCCATAGAGAGGCGGC	T	INDEL	ASXL1	0.099	0.105932	p.Glu635ArgfsTer15	Y	Y
681540	chr21	34886941	G	GGT	INDEL	RUNX1	0.505	0.443262	p.His85ThrfsTer38	Y	Y
681540	chr4	105276142	C	T	SNV	TET2		0.0654326	p.Arg1878Cys	N	Y
681540	chr4	105275394	T	G	SNV	TET2		0.0576565	p.Tyr1628Ter	N	Y
681540	chrX	15818643	G	A	SNV	ZRSR2		0.247059		N	Y
748511	chrX	130025362	G	A	SNV	BCORL1	1	1	p.Arg1354Gln	Y	Y
748511	chr17	7673567	T	A	SNV	TP53	0.239	0.284669	p.Lys321Ter	Y	Y
748511	chr17	7670700	G	A	SNV	TP53	0.271	0.354723	p.Arg337Cys	Y	Y
416413	chr11	119278568	T	A	SNV	CBL	0.409	0.43937	p.Ile429Asn	Y	Y
416413	chr20	32434638	A	AG	INDEL	ASXL1	0.359	0.414966	p.Gly646TrpfsTer12	Y	Y
416413	chr4	105236832	C	T	SNV	TET2		0.452273	p.Gln964Ter	N	Y
416413	chr1	114716126	C	T	SNV	NRAS	0.273	0.273469	p.Gly12Asp	Y	Y
416413	chr4	105235633	G	A	SNV	TET2		0.50289	p.Trp564Ter	N	Y

416413	chrX	124081379	G	A	SNV	STAG2		0.9375		N	Y
416413	chr17	7673773	G	A	SNV	TP53	0.545	0.466263	p.Arg283Cys	Y	Y
416413	chr19	33301429	T	TC	INDEL	CEBPA		0.141844	p.Glu329GlyfsTer74	N	Y
853337	chr19	33302347	GGGGGGCTCTGCAGGTGGCTGCTCATC	G	INDEL	CEBPA	0.373			Y	N
853337	chr2	25244640	C	A	SNV	DNMT3A	0.433	0.444315	p.Glu523Ter	Y	Y
853337	chr10	110578707	G	A	SNV	SMC3	0.48	0.372549		Y	Y
853337	chr12	112450362	A	G	SNV	PTPN11	0.456	0.385787	p.Asp61Gly	Y	Y
853337	chr2	208248388	C	T	SNV	IDH1		0.0573248	p.Arg132His	N	Y
853337	chr5	171410539	C	CTCTG	INDEL	NPM1	0.383	0.426966	p.Trp288CysfsTer12	Y	Y
800962	chr21	43094667	T	G	SNV	U2AF1	0.365	0.102083	p.Gln157Pro	Y	Y
800962	chr20	32434638	A	AG	INDEL	ASXL1	0.413	0.110988	p.Gly646TrpfsTer12	Y	Y
787399	chr21	43104346	G	T	SNV	U2AF1	0.3	0.213693	p.Ser34Tyr	Y	Y
293825	chr12	112450359	G	C	SNV	PTPN11		0.137595	p.Gly60Ala	N	Y
293825	chr5	171410540	T	TCTGC	INDEL	NPM1	0.385	0.304487	p.Trp288CysfsTer12	Y	Y
293825	chr15	90088702	C	A	SNV	IDH2	0.302	0.295045	p.Arg140Leu	Y	Y
293825	chr2	25234374	G	A	SNV	DNMT3A	0.333	0.292651	p.Arg882Cys	Y	Y
541728	chr2	25240720	C	T	SNV	DNMT3A	0.459	0.477824	p.Trp698Ter	Y	Y
541728	chr1	114713909	G	T	SNV	NRAS	0.433	0.428473	p.Gln61Lys	Y	Y
541728	chr5	171410539	C	CTCTG	INDEL	NPM1	0.407	0.444976	p.Trp288CysfsTer12	Y	Y
632997	chr20	32434599	TCACCACTGCCATAGAGAGGCGGC	T	INDEL	ASXL1	0.433	0.453125	p.Glu635ArgfsTer15	Y	Y
632997	chr17	76736877	G	T	SNV	SRSF2	0.722	0.59153	p.Pro95His	Y	Y
632997	chr12	112489106	G	T	SNV	PTPN11		0.283298	p.Gln510His	N	Y
632997	chr12	11884558	G	A	SNV	ETV6	0.615	0.445295	p.Gly375Arg	Y	Y
187885	chr5	171410547	G	GAGGA	INDEL	NPM1	0.509	0.461326	p.Trp290ArgfsTer10	Y	Y
187885	chr13	28018504	T	G	SNV	FLT3		0.0743551	p.Asp835Ala	N	Y
187885	chr13	28034144	A	G	SNV	FLT3	0.196	0.131746	p.Val592Ala	Y	Y
187885	chr2	25234374	G	A	SNV	DNMT3A	0.5	0.485876	p.Arg882Cys	Y	Y
187885	chr2	208248388	C	T	SNV	IDH1	0.432	0.368295	p.Arg132His	Y	Y
191374	chr20	32369060	T	A	SNV	ASXL1	0.5	0.459397	p.Asn63Lys	Y	Y
191374	chr4	105236370	C	T	SNV	TET2	0.413	0.456621	p.Gln810Ter	Y	Y
191374	chr7	102195540	G	T	SNV	CUX1	0.528	0.505155	p.Glu398Ter	Y	Y
191374	chr8	116851977	C	T	SNV	RAD21	0.477	0.449458	p.Gly481Arg	Y	Y
191374	chrX	134417275	T	C	SNV	PHF6	0.96	0.924528	p.Ile314Thr	Y	Y
191374	chr11	119278165	G	T	SNV	CBL	0.562	0.415294		Y	Y
191374	chr4	105236672	AG	A	INDEL	TET2	0.286	0.476404	p.Ala911LeufsTer10	Y	Y
314322	chr17	31227294	A	T	SNV	NF1	0.686			Y	N
314322	chr17	31227278	CAGGAAACACT	C	INDEL	NF1	0.758	0.6464	p.Gly772ArgfsTer16	Y	Y
314322	chr21	43104346	G	A	SNV	U2AF1	0.469	0.433566	p.Ser34Phe	Y	Y

480059	chr17	76736877	G	A	SNV	SRSF2	0.491	0.532544	p.Pro95Leu	Y	Y
480059	chr17	60663168	C	A	SNV	PPM1D	0.4	0.278061	p.Cys478Ter	Y	Y
480059	chr17	31236022	G	A	SNV	NF1	0.349	0.285182		Y	Y
480059	chr5	171410539	C	CTCTG	INDEL	NPM1	0.278	0.284821	p.Trp288CysfsTer12	Y	Y
480059	chr20	32434638	A	AG	INDEL	ASXL1	0.464	0.416667	p.Gly646TrpfsTer12	Y	Y
905861	chr3	128481877	C	T	SNV	GATA2	0.879	0.924138	p.Arg362Gln	Y	Y
905861	chr17	7676051	G	C	SNV	TP53	0.953	0.955598	p.Ser106Arg	Y	Y
654925	chr2	208248389	G	C	SNV	IDH1	0.421	0.408559	p.Arg132Gly	Y	Y
654925	chr5	171410539	C	CTCTG	INDEL	NPM1	0.351	0.406682	p.Trp288CysfsTer12	Y	Y
654925	chr2	25234377	TC	T	INDEL	DNMT3A	0.441	0.340381	p.Met880IlefsTer26	Y	Y
654925	chr13	28034144	A	G	SNV	FLT3		0.161203	p.Val592Ala	N	Y
654925	chr13	28018483	T	C	SNV	FLT3	0.186	0.0766269	p.Tyr842Cys	Y	Y
653268	chr5	171410539	C	CTCTG	INDEL	NPM1	0.393	0.421652	p.Trp288CysfsTer12	Y	Y
653268	chr13	28018504	T	A	SNV	FLT3	0.147	0.118372	p.Asp835Val	Y	Y
653268	chr1	114716123	C	T	SNV	NRAS	0.079	0.065833	p.Gly13Asp	Y	Y
653268	chr12	112489080	T	C	SNV	PTPN11	0.159	0.124005	p.Ser502Pro	Y	Y
653268	chr2	25240423	AACT	A	INDEL	DNMT3A	0.364	0.464334	p.Glu733_Phe734delinsVal	Y	Y
946179	chr5	171410542	T	TGCCA	INDEL	NPM1	0.569	0.445455	p.Trp288CysfsTer12	Y	Y
946179	chr1	114716126	C	T	SNV	NRAS	0.511	0.470024	p.Gly12Asp	Y	Y
717042	chr13	28034113	T	TTTGAGATCATATTCATATTCTCTGAAATCAACGTAGAAGTACTCATTATCTGAGGAGCCGGTCACCTGTACCCCC	INDEL	FLT3	0.222	0.126066	p.Lys602_Trp603insGlyValGlnValThrGlySerSerAspAsnGluTyrPheTyrValAspPheArgGluTyrGluTyrAspLeuLys	Y	Y
717042	chr5	171410539	C	CTCTG	INDEL	NPM1	0.417	0.402138	p.Trp288CysfsTer12	Y	Y
717042	chr2	25234373	C	T	SNV	DNMT3A	0.538	0.455	p.Arg882His	Y	Y
262878	chr12	25245347	C	T	SNV	KRAS		0.0517711	p.Gly13Asp	N	Y
262878	chr12	25245350	C	T	SNV	KRAS	0.117	0.0574866	p.Gly12Asp	Y	Y
262878	chr13	28018505	C	G	SNV	FLT3		0.131068	p.Asp835His	N	Y
262878	chr8	116849009	GC	G	INDEL	RAD21	0.339	0.362069	p.Gly547AlafsTer65	Y	Y
262878	chr5	171410539	C	CTCTG	INDEL	NPM1	0.352	0.379061	p.Trp288CysfsTer12	Y	Y
262878	chr17	31221870	G	T	SNV	NF1	0.511	0.420455	p.Gln554His	Y	Y
516070	chr7	102197245	C	T	SNV	CUX1	0.087	0.0434478	p.Gln623Ter	Y	Y
869318	chr12	25245347	C	T	SNV	KRAS	0.387	0.268056	p.Gly13Asp	Y	Y
736399	chr4	105275734	C	T	SNV	TET2	0.579	0.466248	p.Pro1742Ser	Y	Y
736399	chr17	60663160	G	T	SNV	PPM1D	0.657	0.459295	p.Glu476Ter	Y	Y
736399	chr5	171410539	C	CTCTG	INDEL	NPM1	0.392	0.465184	p.Trp288CysfsTer12	Y	Y
736399	chr4	105275730	ACC	A	INDEL	TET2	0.419	0.479167	p.Pro1741ThrfsTer11	Y	Y
736399	chr4	105269665	C	A	SNV	TET2	0.5	0.285057	p.Pro1367Gln	Y	Y
183114	chr20	32434638	A	AG	INDEL	ASXL1	0.524	0.40051	p.Gly646TrpfsTer12	Y	Y
924089	chr17	7675140	G	C	SNV	TP53		0.178506	p.Arg158Gly	N	Y
924089	chr12	112489081	C	T	SNV	PTPN11	0.151	0.198807	p.Ser502Leu	Y	Y

924089	chr11	119278299	T	C	SNV	CBL	0.262	0.25594		Y	Y
924089	chr13	28034142	CAACGTAGA AGTA	C	INDEL	FLT3	0.15	0.188322	p.Tyr589_Val592del	Y	Y
924089	chr11	119278165	G	T	SNV	CBL	0.26	0.16895		Y	Y
525644	chr12	112450352	A	T	SNV	PTPN11		0.0551446	p.Asn58Tyr	N	Y

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Table S7. WGS results for 117 prospective AML/MDS patients.

UPN	Diagnosis	Specimen	Cytogenetics ISCN.Line	Gene.mutations	IPSSR.risk.group	Conventional ELN.Risk	WGS.CNAs	WGS Recurrent.SVs	WGS.Gene.mutations	WGS.ELN.Risk	WGS IPSSR.risk.group	New.information	New.ELN.Risk.vs.Cyto.and.FISH	New.IPSSR
780327	AML	BM	46,XY[5]	NPM1:p.Trp288CysfsTer12[36.5%],CUX1:p.Leu173Phe[50.3%],CUX1:p.Gly709Val[45.5%],IDH2:p.Arg140Gln[42.9%]	NA	NA	0	0	CUX1:p.L173F[46.0%],CUX1:p.G709V[48.0%],IDH2:p.R140Q[41.2%],NPM1:p.W288Cfs*12[51.9%]	Favorable	NA	NK	Y	NA
776603	MDS	BM	46,XY[20]	ASXL1:p.Gly646TrpfsTer12[24.5%],RUNX1:p.Ile342HisfsTer258[14.9%],RUNX1:p.Val238GlyfsTer23[5.7%],RUNX1:p.Arg162Lys[17.2%],U2AF1:p.Ser34Phe[32.7%]	Good	NA	0	0	ASXL1:p.G646Wfs*12[38.5%],RUNX1:p.I342Hfs*258[14.0%],RUNX1:p.R162K[24.4%],U2AF1:p.S34F[52.2%]	NA	Good	N	NA	N
474383	AML	BM	unsuccessful	NA	NA	APL	0	t(15;17)(q24.1;q21.2)[15.2%],t(15;17)(q24.1;q21.2)[27.6%]	ETV6:p.P223L[44.8%],FLT3:p.D835Y[43.3%],WT1:p.Y402Ffs*2[25.8%]	APL	NA	N	N	NA
994357	AML	BM	46,XX[20]	None detected	NA	Intermediate	0	t(11;19)(q23.3;p13.11)[23.6%],t(11;19)(q23.3;p13.11)[28.5%]	0	Adverse	NA	t(11;19)(q23.3;p13.11)[23.6%],t(11;19)(q23.3;p13.11)[28.5%]	Y	NA
586748	AML	BM	46,XY[20]	ETV6:p.Ser131PhefsTer23[35.7%]	NA	Intermediate	0	t(7;21)(p22.1;q22.12)[23.1%]	ETV6:p.S131Ffs*23[46.3%]	Intermediate	NA	t(7;21)(p22.1;q22.12)[23.1%]	N	NA
651844	MDS	BM	45,X,-Y[8]/46,XY[12]	NA	Very good	NA	-Y[11.8%]	0	DNMT3A:NA[17.2%],NF1:p.V1909Afs*16[8.8%],GATA2:p.K390del[2.8%]	NA	Very good	N	NA	N
553306	MDS	BM	46,XX,del(X)(p11.2),?t(2;4)(q33;q31),t(3;10)(p21;p15),del(5)(q13q33),del(6)(q13q23),del(7)(p11.2p13),del(10)(q22),-11,add(12)(p11.1),+15,add(15)(p11.1),-16,add(17)(p11.2),add(21)(q22)[20]	TP53:p.Arg273His[83.5%]	Very poor	NA	del(2)(q33.3q34)[85.0%],del(2)(q36.1q37.1)[85.2%],del(3)(p21.31p22.1)[82.6%],del(4)(q13.1q13.2)[85.8%],del(4)(q31.3q32.2)[83.3%],del(5)(q14.3q34)[86.0%],del(11)(q13.4q22.1)[76.7%],gain(11)(q24.2qter)[303.4%],del(11)(q25qter)[78.4%],del(12)(p12.2p13.2)[85.3%],gain(15)(q15.3qter)[70.7%],-16[87.1%],del(17)(p13.1p13.2)[82.4%]	0	TP53:p.R273H[80.0%]	NA	Very poor	N	NA	N
677322	AML	BM	46,XY[20]	DNMT3A:p.Met548Thr[43.7%],IDH1:p.Arg132His[42.5%],EZH2:p.Glu392Lys[49.2%],CEBPA:p.Pro196TrpfsTer117[76.6%],CEBPA:p.Arg35ProfsTer126[34.5%],SMC1A:p.Arg586Trp[89.4%],PHF6:p.His43ProfsTer2[8.0%],PHF6:p.Glu293Ter[5.7%]	NA	Favorable	0	0	DNMT3A:p.M548T[42.5%],IDH1:p.R132H[28.9%],EZH2:p.E392K[56.5%],SMC1A:p.R586W[89.7%],CEBPA:p.P196Wfs*117[33.3%],CEBPA:p.R35Pfs*126[49.0%]	Favorable	NA	N	N	NA
120644	MDS	BM	unsuccessful	None detected	NA	NA	0	0	0	NA	Good	NK	NA	Y
281935	PNH	BM	46,XY[20]	PIGA:p.Tyr43ThrfsTer18[3.9%]	NA	NA	0	0	0	NA	NA	N	NA	Y
902503	AML	BM	46,XY[20]	IDH2, SRSF2, TET2, RUNX1	NA	Adverse	0	0	IDH2:p.R140Q[54.1%],SRSF2:p.P95H[50.7%],RUNX1:p.R232W[59.5%]	Adverse	NA	N	N	NA
504451	MDS	BM	46,XY,add(5)(q11.2),-13,der(15)t(13;15)(q14;p11.2),-20[10]/46,XY,add(7)q11.2[5]/46,XY[5]	TP53:p.Arg273His[81.2%]	Very poor	NA	del(5)(q11.2qter)[43.3%],del(7)(q11.22qter)[36.7%],del(13)(q12.13q14.3)[42.3%],del(20)(q11.22q13.31)[39.9%],gain(21)(q11.2q21.2)[67.1%],gain(21)(q22.13qter)[67.5%]	0	TP53:p.R273H[84.4%]	NA	Very poor	N	NA	N
410110	AML	BM	48,XX,+13,+13[7]/50,idem,+X,-13,+15,+19[2]/46,XX[7]	DNMT3A:p.Arg882Cys[45.6%],SRSF2:p.Pro95His[48.4%],RUNX1:p.Arg166Ter[44.9%],RUNX1:p.Asp123GlyfsTer15[39.0%],FLT3:p.Phe612_Gly613insValTyrAspLeuLysTr	NA	Adverse	gain(13)(q12.11qter)[87.1%],gain(15)(q11.2qter)[38.2%],+19[38.3%],+X[32.8%]	0	DNMT3A:p.R882C[54.3%],SRSF2:p.P95H[37.0%],RUNX1:p.R166*[49.3%],RUNX1:p.D123Gfs*15[55.3%],FLT3:p.F612_G613ins	Adverse	NA	N	N	NA

				pGluPheProArgGluAsnLeuGluPhe[0.1%]					VYDLKWEFPRENLEF[6.5%]					
296442	AML	BM	46~52,XY,-3,?add(5)(q3?3),del(7)(q22q34),-10,-13,-22,+2~9mar[cp20]	TP53:[47.0%],TP53:p.Cys238Tyr[43.1%]	NA	Adverse	del(3)(p11.2pter)[94.2%],del(3)(q12.2q13.12)[89.9%],del(3)(q13.32q23)[93.7%],del(3)(q25.33q26.2)[93.8%],del(3)(q27.3qter)[94.1%],del(7)(q21.11qter)[94.3%],gain(13)(q12.11q14.11)[443.9%],del(13)(q14.11q21.33)[87.9%],gain(13)(q21.33q31.3)[476.9%],del(13)(q31.3qter)[93.4%]	0	TP53:NA[46.7%],TP53:p.C238Y[45.7%]	Adverse	NA	N	N	NA
889663	AML	BM	46,XX,del(5)(q22q35)[10]/46,XX[10]	WT1:p.Arg380ThrfsTer5[9.4%],RUNX1:p.Arg107Cys[8.3%],BCOR:[14.0%],BCORL1:p.Ser1143TrpfsTer82[5.9%]	NA	Adverse	del(5)(q21.1q33.3)[36.8%]	0	0	Adverse	NA	N	N	NA
508617	MDS	BM	46,XX[20]	TET2:p.Asp162ArgfsTer9[36.1%],TET2:p.Asn1118LysfsTer12[4.9%],IDH2:p.Arg140Gln[2.3%],SRSF2:p.Pro95His[45.7%],RUNX1:p.Gly165Ser[25.2%]	Good	NA	0	0	TET2:p.D162Rfs*9[51.8%],TET2:p.Q866*[28.6%],SRSF2:p.P95H[42.2%],RUNX1:p.G165S[27.3%]	NA	Good	N	NA	N
437892	MDS	BM	46,XX,add(1)(p13),der(6)t(1;6)(p32;q12),del(11)(q21)[8]/46,XX[12]	CBL:p.Ile383Leu[22.0%],NF1:p.Arg897Gln[44.4%]	Poor	NA	del(1)(p12p32.3)[53.8%],del(6)(q12q23.3)[53.9%],del(11)(q14.1q23.3)[53.3%]	0	CBL:p.I383L[32.8%],NF1:p.R897Q[59.7%]	NA	Poor	N	NA	N
343604	AML	BM	unsuccessful	EZH2:[91.0%],KRAS:p.Gly13Asp[35.0%],ASXL1:p.Gly646TrpfsTer12[43.4%]	NA	NA	+8[65.5%],del(12)(p12.1p13.2)[94.8%]	0	EZH2:NA[95.5%],KRAS:p.G13D[35.0%],ASXL1:p.G646Wfs*12[39.3%]	Adverse	NA	Not Complex	Y	NA
726806	AML	BM	46,XX[20]	CSF3R:p.Gly366Arg[51.6%],TET2:p.Asn439ThrfsTer8[52.3%],NPM1:p.Trp288CysfsTer12[46.4%],FLT3:p.Trp603_Glu604insAspArgGluTyrGluTyrAspLeuLysTrp[23.4%],ASXL1:p.Gly219Val[44.0%]	NA	Adverse	0	0	CSF3R:p.G366R[63.3%],TET2:p.N439Tfs*8[37.7%],FLT3:p.W603_E604insDREYEYDLKW[41.0%],ASXL1:p.G219V[50.0%],NPM1:p.W288Cfs*12[48.1%]	Adverse	NA	N	N	NA
375074	AML	BM	45,XY,del(1)(p36.2),-7[18]/46,XY[2]	TET2:p.Val1180Asp[78.0%],NPM1:p.Trp288CysfsTer12[30.9%],IDH2:p.Arg140Gln[48.7%],SRSF2:p.Pro95Arg[44.8%]	NA	Adverse	del(1)(p35.1p36.32)[56.8%],-7[63.2%]	0	TET2:p.V1180D[83.7%],IDH2:p.R140Q[39.0%],SRSF2:p.P95R[52.2%],NPM1:p.W288Cfs*12[20.3%]	Adverse	NA	N	N	NA
557196	AML	BM	46,XY[20]	NRAS:p.Gly12Asp[3.8%],NRAS:p.Gly12Ser[23.6%],DNMT3A:p.Glu733Ter[37.7%],DNMT3A:p.Cys710Tyr[40.9%],TET2:[37.2%],KRAS:p.Ala18Asp[5.8%],FLT3:p.Lys602_Phe612dup[0.4%],FLT3:p.Tyr589_Glu604dup[0.8%],FLT3:p.Phe594_Glu598dup[0.5%],FLT3:p.Val581_Arg595dup[1.0%],ZRSR2:p.Glu133GlyfsTer11[74.6%],BCORL1:p.Cys908Ter[79.1%]	NA	Adverse	0	0	NRAS:p.G12S[16.3%],DNMT3A:p.E733*[44.4%],DNMT3A:p.C710Y[32.5%],TET2:NA[45.5%],ZRSR2:p.E133Gfs*11[37.9%],BCORL1:p.C908*[77.8%],FLT3:p.Y589_E604dup[6.3%]	Adverse	NA	N	N	NA
271002	MDS	BM	45,XY,-7[14]/46,XY[6]	DNMT3A:p.Arg882Cys[41.1%],EZH2:p.Gln612Ter[9.5%],ETV6:p.Val158ProfsTer10[11.6%],IDH2:p.Arg140Gln[38.9%],BCORL1:p.Asn1481Ser[99.5%],PHF6:p.Ser246Thr[13.6%],PHF6:p.Ser247Tyr[13.6%],PHF6:p.Arg342Ter[5.7%]	Poor	NA	-7[76.5%]	0	DNMT3A:p.R882C[42.5%],IDH2:p.R140Q[44.7%],BCORL1:p.N1481S[100.0%],ETV6:p.V158Pfs*10[12.2%]	NA	Poor	N	NA	N
259112	AML	BM	46,XY[20]	DNMT3A:p.Arg882His[89.7%],IDH2:p.Arg140Gln[44.3%],SRSF2:p.Pro95His[49.5%]	NA	Intermediate	0	0	DNMT3A:p.R882H[94.8%],IDH2:p.R140Q[51.7%],SRSF2:p.P95H[43.8%]	Intermediate	NA	N	N	NA
819978	AML	BM	60~65<3n>,XXYY,+1,-2,-4,+6,add(6)(p22),-7,-8,-11,-12,add(12)(p11.2),-13x3,-14,-15,-17,-18,-19,+20,+21,-22,-22,+1~4mar[cp13]/86<4n>,XXXXYYY,-2,-3,-4x2,+6,add(6)(p22),-7x2,-8,-10x2,-11,-13x2,-14,-15,+16,+3mar[1]/46,XY[6]	NRAS:p.Gly13Asp[9.0%],KRAS:p.Gly13Asp[10.6%],IDH2:p.Arg140Gln[41.0%],TP53:p.Lys132Arg[77.8%],NF1:p.Gln985Ter[4.8%],SRSF2:p.Pro95Leu[51.0%]	NA	Adverse	+1[55.9%],-2[27.8%],-4[30.9%],+6[57.3%],-7[27.7%],-8[16.7%],-11[28.5%],-12[25.0%],del(13)(q12.11qter)[35.3%],del(15)(q11.2qter)[30.4%],gain(21)(q11.2qter)[36.7%],del(22)(q11.21qter)[18.5%],+Y[27.2%]	0	NRAS:p.G13D[9.0%],IDH2:p.R140Q[36.2%],TP53:p.K132R[72.2%],SRSF2:p.P95L[54.7%]	Adverse	NA	N	N	NA

895870	AML	BM	46,XX[20]	NPM1:p.Leu287IlefsTer13[27.5%],NPM1:p.Trp288CysfsTer12[28.0%],NPM1:p.Trp288CysfsTer12[28.1%],FLT3:p.Val592Gly[27.1%],IDH2:p.Arg140Gln[48.9%],SRSF2:p.Arg94dup[45.9%],ASXL1:p.Gly646TrpfsTer12[11.1%],STAG2:p.Ala956PhefsTer4[9.0%]	NA	Favorable	0	0	FLT3:p.V592G[38.6%],IDH2:p.R140Q[37.5%],SRSF2:p.R94dup[48.9%],NPM1:p.W288Cfs*12[30.0%]	Favorable	NA	N	N	NA
992091	AML	BM	44,XY,add(2)(p?14),add(3)(q21),add(5)(q31),-6,-7,i(8)(q10)x2,add(12)(q13),add(15)(p11.2),-16,-17,-18,add(22)(q13),+1~4mar[cp13]/46,XY[7]	DNMT3A:p.Gly532Ser[2.4%],TP53:p.Arg342Ter[67.1%],ASXL1:p.Leu1413Ser[34.8%]	NA	Adverse	del(2)(p23.3pter)[78.3%],del(3)(q13.11q13.31)[83.5%],del(4)(q26q28.3)[80.3%],del(5)(q23.3qter)[77.0%],-6[83.1%],del(7)(q11.23qter)[82.6%],del(8)(p11.22pter)[81.1%],+8[212.1%],del(12)(q13.2q14.2)[82.3%],del(12)(q21.32q22)[82.2%],-16[77.6%],-17[74.2%],del(18)(q11.2qter)[83.2%]	0	TP53:p.R342*[71.9%],NF1:p.I679Dfs*21[71.7%],ASXL1:p.L1413S[44.9%]	Adverse	NA	N	N	NA
150377	MDS	BM	46,XX[20]	None detected	Good	NA	0	0	0	NA	Good	N	NA	N
438506	MDS	BM	46,XY[20]	NA	Good	NA	0	0	DNMT3A:p.M406Dfs*2[24.8%],EZH2:p.P132L[39.5%],ASXL1:p.Y591*[44.8%],ASXL1:p.L1304V[46.7%],U2AF1:p.Q157P[33.3%]	NA	Good	N	NA	N
333171	MDS	BM	46,XY[10]	TET2:p.Tyr1964His[47.9%],ETV6:p.Arg353Gln[49.7%],KRAS:p.Gly12Ala[37.0%],SMC1A:p.Arg96His[28.6%]	NA	NA	0	0	TET2:p.Y1964H[40.4%],ETV6:p.R353Q[50.8%],KRAS:p.G12A[40.5%],SMC1A:p.R96H[21.2%]	NA	Good	NK	NA	Y
606753	MDS	BM	46,XY[20]	ZRSR2:p.R442dup[100%]	Good	NA	0	0	ZRSR2:p.R442dup[68.0%]	NA	Good	N	NA	N
704854	AML	BM	46,XY[20]	DNMT3A:p.Arg899Cys[42.0%],DNMT3A:p.Arg598Ter[45.9%],GATA2:p.Thr387_Lys389del[30.2%],EZH2:p.Ile744Thr[5.3%],PTPN11:p.Gly503Val[25.8%],ASXL1:p.Ala640GlyfsTer60[4.3%],ASXL1:p.Pro808LeufsTer10[41.1%]	NA	Adverse	0	0	DNMT3A:p.R899C[40.6%],DNMT3A:p.R598*[36.8%],PTPN11:p.G507V[31.2%],ASXL1:p.P808Lfs*10[20.8%],GATA2:p.T387_K389del[29.8%]	Adverse	NA	N	N	NA
952492	MDS	BM	46,XY[20]	DNMT3A:p.Thr44Met[48.3%],ASXL1:p.Gln428ThrfsTer10[21.9%],BCOR:p.Val11Ala[100.0%]	Good	NA	0	0	DNMT3A:p.T44M[52.5%],ASXL1:p.Q428Tfs*10[32.9%],BCOR:p.V11A[100.0%]	NA	Good	N	NA	N
312088	AML	BM	47,XY,+21[17]/46,XY[3]	NRAS:p.Gly13Asp[7.7%],NRAS:p.Gly12Ser[2.4%],DNMT3A:p.Arg882Cys[44.7%],NPM1:p.Trp288CysfsTer12[38.4%],NPM1:p.Trp288CysfsTer12[38.4%],RAD21:p.Met362SerfsTer8[42.6%],WT1:p.Ala5Val[47.6%],WT1:p.Ala5Thr[47.7%],KRAS:p.Gln61Leu[8.8%],PTPN11:p.Gly60Val[18.8%]	NA	Favorable	gain(21)(q11.2qter)[88.6%]	0	NRAS:p.G13D[7.7%],DNMT3A:p.R882C[53.1%],WT1:p.A5V[33.3%],WT1:p.A5T[39.1%],NPM1:p.W288Cfs*12[24.2%],RAD21:p.M362Sfs*8[32.3%]	Favorable	NA	N	N	NA
430826	AML	BM	46,XY,t(15;17)(q24;q21)[5]/46,XY[1]	NA	NA	APL	gain(2)(q14.1qter)[23.6%],gain(7)(p12.3p14.1)[23.6%],-7[21.5%],del(9)(p21.1pter)[17.4%],gain(9)(q22.33qter)[21.4%],del(10)(p11.21pter)[23.8%],gain(10)(q11.21qter)[22.1%],del(13)(q12.11qter)[20.7%],del(16)(q23.1qter)[21.7%],del(18)(p11.21pter)[15.2%],gain(19)(p12pter)[21.7%],gain(20)(q11.21qter)[35.8%]	t(15;17)(q24.1;q21.2)[3.3%],t(15;17)(q24.1;q21.2)[4.1%]	0	APL	NA	Complex	N	NA
570496	MDS	BM	46,XY[20]	SF3B1:p.Glu592Lys[41.2%],IDH2:p.Arg140Gln[49.4%],CEBPA:p.Glu284Ter[2.7%],ASXL1:p.Gly646TrpfsTer12[46.3%],STAG2:p.Arg216Ter[40.4%],STAG2:p.Arg614Ter[35.4%]	Good	NA	0	0	SF3B1:p.E592K[46.6%],IDH2:p.R140Q[43.5%],ASXL1:p.G646Wfs*12[36.3%],STAG2:p.R216*[52.0%],STAG2:p.R614*[32.1%]	NA	Good	N	NA	N

994807	None	BM	46,XY[20]	None detected	NA	NA	0	0	0	NA	NA	N	NA	Y
229201	AML	BM	46,XY[5]	NPM1:p.Trp288CysfsTer12[26.2%],FLT3:p.Leu601_Lys602insGlySerAspAsnGluTyrPheTyrValAspPheArgGluTyrGluTyrAspLeu[7.3%],FLT3:p.Leu601_Lys602insGlySerAspAsnGluTyrPheTyrValAspPheArgGluTyrGluTyrAspLeu[7.0%],FLT3:p.Arg595_Glu596insTer[12.3%],FLT3:p.Asp593_Phe594insLeuArgAspPheGluTyrAspLeuValSerAspAsnGluTyrPheTyrPheAsp[8.9%],IDH2:p.Arg140Gln[37.0%]	NA	NA	0	0	IDH2:p.R140Q[37.7%],NPM1:p.W288Cfs*12[15.5%],FLT3:p.S585_L601dup[14.0%]	Favorable	NA	NK	Y	NA
983349	AML	BM	42~43,XY,add(3)(q10),add(5)(q13),-7,-9,add(11)(p10),der(11)hsr(11)(q23),-12,add(16)(p11.2),add(16)(q12),-17,-18,+mar[cp20]	TP53:p.Tyr126Cys[53.5%],SMC1A:p.Ile1062Met[100.0%]	NA	Adverse	del(3)(q11.2q24)[41.7%],gain(3)(q26.1qter)[34.1%],+5[30.3%],del(5)(q11.2q12.3)[79.7%],del(5)(q31.1qter)[74.3%],-7[41.3%],gain(9)(p13.3pter)[102.6%],del(11)(p11.2pter)[36.4%],gain(11)(q23.2qter)[110.4%],del(12)(q23.1q24.13)[77.2%],del(16)(q23.3qter)[75.1%],del(17)(p13.1pter)[75.3%],del(17)(q11.2q21.33)[29.8%],-18[46.0%],+19[36.6%],gain(21)(q11.2qter)[61.4%]	0	TP53:p.Y126C[71.8%],SMC1A:p.I1062M[100.0%]	Adverse	NA	N	N	NA
534164	MDS	BM	45,XY,-7[20]	DNMT3A:p.Arg326Cys[44.2%],RAD21:p.Gly273Cys[13.2%],ETV6:p.Ala377Val[40.4%]	Poor	NA	-7[83.9%],del(13)(q14.2q14.3)[85.3%]	0	DNMT3A:p.R326C[50.9%],ETV6:p.A377V[37.9%]	NA	Poor	del(13)(q14.2q14.3)[85.3%]	NA	N
931622	MDS	BM	46,XY,del(10)(p1?3)[2]/46,XY,t(1;3)(p36.3;q21)[1]/46,XY[17]	NA	Good	NA	0	0	SF3B1:p.K700E[34.2%],RUNX1:p.G170Rfs*43[23.2%]	NA	Good	N	NA	N
925086	AML	BM	46,XX[20]	DNMT3A:p.Arg882His[40.1%],NPM1:p.Trp288CysfsTer12[40.6%],ASXL1:p.Thr1498Met[50.6%],BCOR:p.Asn790Ser[49.6%]	NA	Favorable	0	0	DNMT3A:p.R882H[42.9%],ASXL1:p.T1498M[46.6%],BCOR:p.N790S[52.7%],NPM1:p.W288Cfs*12[40.3%]	Favorable	NA	N	N	NA
875579	AML	BM	47,XX,t(3;21)(q26;q22),del(7)(q32),+14[19]/46,XX[1]	CSF3R:p.Gln770Ter[28.6%],U2AF1:p.Gln157Pro[28.2%]	NA	Adverse	del(7)(q33q36.2)[46.7%],gain(14)(q11.2qter)[46.2%]	t(3;21)(q26.2;q22.12)[6.5%],t(3;21)(q26.2;q22.12)[11.4%]	CSF3R:p.Q770*[15.7%],U2AF1:p.Q157P[14.8%]	Adverse	NA	N	N	NA
679540	AML	BM	46,XX,inv(3)(q21q26.1)[3]/45,sl,der(16;17)(p10;q10)[4]/46,sdl,+13[5]/46,XX[8]	SF3B1:p.His662Asp[24.4%],TP53:p.Met160_Ala161del[38.7%],NF1:p.Arg816Ter[11.5%]	NA	Adverse	del(16)(q11.2qter)[81.4%],-17[78.9%]	inv(3)(q21.3q26.2)[29.2%],inv(3)(q21.3q26.2)[30.6%]	SF3B1:p.H662D[39.7%],TP53:p.M160_A161del[67.2%],NF1:p.R816*[43.3%]	Adverse	NA	N	N	NA
477377	AML	BM	46,XY[20]	NRAS:p.Gly12Asp[4.6%],NRAS:p.Gly12Ser[6.5%],IDH2:p.Arg140Gln[44.5%],SRSF2:p.Pro95_Arg102del[44.3%],SMC1A:p.Arg790Gln[81.4%]	NA	Intermediate	0	0	IDH2:p.R140Q[50.8%],SRSF2:p.P95_R102del[45.2%],SMC1A:p.R790Q[80.6%]	Intermediate	NA	N	N	NA
493436	AML	BM	46,XX,t(2;15)(q23;q15)[11]/46,XX[9]	NRAS:p.Gly12Cys[36.9%],RUNX1:p.Pro294GlnfsTer12[36.8%],RUNX1:p.Ser141_Ala142insGlyPro[37.7%]	NA	Adverse	0	0	NRAS:p.G12C[45.8%],RUNX1:p.P294Qfs*12[22.4%],RUNX1:p.S141_A142insGP[21.3%]	Adverse	NA	N	N	NA
429293	AML	BM	47,XX,+8[7]/46,XX[13]	RAD21:p.Arg65Ter[20.9%],PTPN11:p.Gln79Arg[21.9%],IDH2:p.Arg140Gln[24.5%],RUNX1:[26.7%],RUNX1:p.Ala149Pro[22.8%],BCOR:[31.3%]	NA	Adverse	+8[50.3%]	0	RAD21:p.R65*[22.8%],PTPN11:p.Q79R[30.4%],IDH2:p.R140Q[19.6%],RUNX1:NA[25.9%],BCOR:NA[36.9%]	Adverse	NA	N	N	NA
802619	MDS	BM	42~49,XX,add(1)(p13),add(1)(q12),del(1)(q32q44)x1~2,-2,der(14;15)(q10;q10),der(15;22)(q10;q10),-19,-20,-21,-22,+2~6mar[cp10]/46,XX[10]	RAD21:[18.3%],TP53:p.Ile232Thr[24.9%],TP53:p.Ala86CysfsTer63[24.7%]	Very poor	NA	gain(1)(q31.1q41)[13.1%],gain(1)(q43qter)[14.7%],gain(19)(p12pter)[34.9%],gain(21)(q21.1q22.2)[18.0%]	0	TP53:p.A86Cfs*63[27.5%]	NA	Very poor	N	NA	N
294891	MDS	BM	46,XX[20]	TET2:p.Thr1554AspfsTer24[18.8%],NPM1:p.Trp288CysfsTer12[26.7%],SRSF2:p.Pro95His[36.7%],STAG2:p.Ala520Asp[3.1%]	Good	NA	0	0	TET2:p.Q530Lfs*4[37.5%],TET2:p.T1554Dfs*24[49.2%],SRSF2:p.P95H[42.2%],NPM1:p.W288Cfs*12[7.3%]	NA	Good	N	NA	N

731757	AML	BM	46,XY[20]	DNMT3A:p.Gly685Val[51.4%],NPM1:p.Trp288CysfsTer12[40.8%],NPM1:p.Trp288CysfsTer12[40.8%],SMC3:p.Gly655Asp[44.7%],FLT3:[10.8%],FLT3:[15.6%],FLT3:p.Lys602delinsAsnProProGluGlyGlyGlyIleTerIleTerSerGlnMetGlyValSerLysArgLysPheArgValTer[9.2%],FLT3:p.Leu601_Lys602insProProGluGlyGlyGlyIleTerIleTerSerGlnMetGlyValSerLysArgLysPheArgValCys[8.0%],FLT3:p.Leu601delinsProProArgLysValGlyGluTyrGluTyrAspLeuLysTrpGluPheProArgGluAsnLeuGluPheVal[9.7%],FLT3:p.Asp600_Leu601insProProGlyArgTrpGlyAsnMetAsnMetIleSerAsnGlySerPheGlnGluLysIleTerSerLeu[9.7%],FLT3:p.Asp600_Leu601insProLysValGlnLeuThrGlySerSerAspTyrGluTerPheTerValAspPheArgGluTyrGluTyrAsp[10.1%],FLT3:p.Glu598_Tyr599insTer[16.5%],FLT3:p.Tyr597_Glu598insThrPheAspPheArgGluTyr[12.0%]	NA	Favorable	0	0	DNMT3A:p.G685V[45.6%],SMC3:p.G655D[45.5%],NPM1:p.W288Cfs*12[28.2%],FLT3:NA[7.1%]	Favorable	NA	N	N	NA
335141	AML	BM	46,XY, add(2)(q37)[6]	DNMT3A:p.Arg882His[44.8%],SF3B1:p.Lys700Glu[44.4%],FLT3:p.Leu601_Lys602insAsnTyrValAspPheArgGluTyrGluTyrAspLeu[18.8%],FLT3:p.Phe594_Asp600dup[27.6%],FLT3:p.Arg595_Glu596insAspHisValAspPheArg[30.7%],FLT3:p.Val581_Phe594dup[31.8%],FLT3:p.Val592_Asp593insValPheValThrGlySerSerAspAsnGluTyrPheTyrVal[33.7%]	NA	Adverse	del(2)(q36.3qter)[89.1%],gain(11)(q13.4qter)[90.2%]	0	DNMT3A:p.R882H[52.1%],SF3B1:p.K700E[39.4%],FLT3:p.L601_K602insNYVDFREYEYDL[21.6%],FLT3:p.V581_F594dup[22.5%]	Adverse	NA	Not Complex	N	NA
155912	AML	BM	46,XX,der(3)t(3;6)(q25;q13),der(6)t(3;6)(q25;q13)t(6;8)(p23;q13)[19]/46,XX[1]	DNMT3A:p.Cys557Arg[42.2%],NPM1:p.Trp288CysfsTer12[38.4%],WT1:p.Arg369GlyfsTer7[43.2%],PTPN11:p.Thr553Met[45.8%],FLT3:p.Phe605_Pro606insArgHisGluTyrAspLeuLysTrpGluPhe[12.9%],FLT3:p.Tyr597_Glu598insAspProAlaAspPheArgGluTyr[19.9%],NF1:p.Ile679AspfsTer21[2.4%]	NA	Intermediate	del(3)(p12.2p14.1)[76.6%],del(6)(p24.1pter)[75.1%],del(6)(q14.1q14.3)[77.6%],gain(8)(q12.1qter)[72.8%]	0	DNMT3A:p.C557R[36.9%],PTPN11:p.T557M[47.6%],NPM1:p.W288Cfs*12[37.1%],WT1:p.R369Gfs*7[42.1%],FLT3:p.F605_P606insRHEYDLKWEF[17.9%]	Adverse	NA	Complex	Y	NA
677982	AML	BM	47,XY,+i(21)(q10)[14]/47,XY,+21[2]/46,XY[4]	None detected	NA	Intermediate	gain(21)(q11.2qter)[173.8%]	t(6;11)(q27;q23.3)[28.8%]	0	Adverse	NA	t(6;11)(q27;q23.3)[28.8%]	Y	NA
103744	AML	BM	46,XX[3]	TP53:p.Phe134Val[29.6%],NF1:p.Gln756Ter[4.3%]	NA	Adverse	del(3)(p11.2pter)[61.8%],+5[76.7%],del(5)(q11.2qter)[60.6%],-7[57.2%],+8[57.6%],+9[52.3%],gain(15)(q11.2qter)[43.2%],del(16)(q21qter)[58.5%],del(17)(p13.1pter)[53.0%],+18[43.5%],gain(22)(q11.21q12.3)[64.0%]	0	TP53:p.F134V[50.0%]	Adverse	NA	Complex	N	NA
956161	AML	BM	45,X,-Y[22]	SF3B1:p.Lys666Thr[44.9%],FLT3:p.Glu598_Tyr599insGluValGlnValThrGlySerSerAspAsnGluTyrTyrTyrAspAspPheArgTerTyrGlu[5.2%],FLT3:p.Val581_Glu596dup[6.8%],FLT3:p.Arg595_Glu596insAspGluValGlnLeuThrGlySerThrAspAsnGluTyrIleTyrValAspPheArgGluTyr[6.9%],FLT3:p.Tyr589_Phe590insLeuValGlnValThrGlySerSerAspAsnGluTyr[3.9%],FLT3:p.Glu588_Tyr589insPhePheTyrValAspPheArgAspTyrTerLeuValGlnValThrGlySerSerAspIleGlu[7.6%],FLT3:p.Asp586_Asn587insIleGluPhePheTyrValAspLeuArgGluTyrGluGluValGlnValThrGlySerSerAsp[7.6%],FLT3:p.Ser584_Ser585insTer[7.6%],STAG2:p.Ile790Phe[3.9%],STAG2:p.Ile794Phe[3.3%]	NA	Adverse	-Y[96.7%]	0	SF3B1:p.K666T[49.1%],FLT3:p.E598_Y599insEVQVTGSSDNEYFYVDFREYE[27.1%]	Adverse	NA	N	N	NA
673325	MDS	BM	46,XY[20]	NRAS:p.Gly13Asp[11.3%],NRAS:p.Gly12Asp[10.1%],FLT3:p.Arg595_Asp600dup[0.3%],FLT3:p.L	Good	NA	0	0	NRAS:p.G13D[8.7%],NRAS:p.G12D[7.5%],U2AF1:p.S34F[40.6	NA	Good	N	NA	N

				eu576_Tyr589dup[0.2%],U2AF1:p.Ser34Phe[46.2%],BCOR:p.Arg976Ter[96.1%],STAG2:p.Glu849ArgfsTer23[94.9%]					%],BCOR:p.R976*[95.0%],STAG2:p.E849Rfs*23[61.1%]					
451688	MDS	BM	46,XY[3]	EZH2:p.Arg360ThrfsTer5[20.8%],ASXL1:p.Gly646TrpfsTer12[30.6%],ZRSR2:[59.5%]	NA	NA	del(4)(q21.1q25)[53.3%],-Y[27.1%]	0	ASXL1:p.G646Wfs*12[30.2%],ZRSR2:NA[68.0%],EZH2:p.R360Tfs*5[16.7%],JAK2:p.V617F[4.8%]	NA	Intermediate	Independent clones	NA	Y
905177	ALL	BM	46,XY,t(9;22)(q34;q11.2)[20]	NA	NA	NA	gain(9)(q34.12qter)[58.2%],del(19)(p13.3pter)[53.8%],gain(22)(q11.21q11.23)[54.9%]	t(9;22)(q34.12;q11.23)[32.6%],t(9;22)(q34.12;q11.23)[43.8%]	0	NA	NA	gain(9)(q34.12qter)[58.2%],del(19)(p13.3pter)[53.8%],gain(22)(q11.21q11.23)[54.9%]	NA	Y
891309	MDS	BM	46,XY[5]	TP53:p.Arg306Ter[22.4%],TP53:p.Met237Ile[2.4%],ASXL1:p.Glu635ArgfsTer15[18.8%],ASXL1:p.Trp796GlyfsTer22[5.9%]	NA	NA	0	0	TP53:p.R306*[19.5%],ASXL1:p.E635Rfs*15[8.2%]	NA	Good	NK	NA	Y
869692	MDS	BM	46,XY[21]	NA	Good	NA	0	0	SF3B1:p.E622D[37.0%]	NA	Good	N	NA	N
572410	MDS	BM	41~47,X,add(X)(p11.2),+3,add(3)(q11.2),?add(5)(q11.2),-17,der(17)t(11;17)(q13;p12),-20,add(20)(q11.2),+21,i(21)(q10),+1~2mar[cp4]/46,XX[16]	TP53:p.Arg213Ter[12%]	Very poor	NA	gain(1)(p21.2p36.32)[18.8%],del(5)(q13.1q34)[18.5%],gain(11)(q13.4qter)[17.3%],del(16)(q23.1qter)[16.8%],del(17)(p13.1pter)[16.6%],del(18)(q12.1qter)[16.7%],gain(22)(q11.21qter)[52.5%],gain(X)(p21.1pter)[11.7%]	0	0	NA	Very poor	N	NA	N
395906	MDS	BM	46,XY,del(3)(q12q25),+8[20]	DNMT3A:p.Arg882His[44.6%],NF1:p.Arg1534Ter[52.6%],PPM1D:p.Leu484Ter[45.0%],ASXL1:p.Ser921Phe[48.3%],RUNX1:p.Phe97Ser[43.1%],U2AF1:p.Ser34Phe[43.4%]	Poor	NA	del(3)(q21.2q24)[83.4%],del(4)(q28.3q31.1)[65.6%],+8[82.7%]	0	DNMT3A:p.R882H[50.9%],NF1:p.R1534*[54.5%],PPM1D:p.L484*[47.2%],ASXL1:p.S921F[58.6%],RUNX1:p.F97S[35.2%],U2AF1:p.S34F[56.8%]	NA	Poor	Complex	NA	N
830563	ALL	BM	45~48,XX,+1,-4,-5,del(5)(q13q31),der(7)del(p?14)add(q32),+8,del(9)(p22),-13,?del(13)(q22),+15,add(15)(p11.2),-16,-19,-20,+21,-22,+1~4mar[cp20].	TP53:p.Tyr220Cys[41.8%],TP53:p.Gln167LeufsTer15[42.4%]	NA	NA	del(4)(q23q24)[93.3%],del(5)(q14.2q34)[93.6%],del(7)(q32.3q36.1)[93.0%],gain(9)(p21.3pter)[227.4%],del(9)(p21.1p21.3)[88.0%],gain(9)(p13.1p21.1)[227.5%],-16[86.3%],del(20)(q11.21q13.13)[90.1%],gain(21)(q11.2qter)[45.3%]	0	TP53:p.Y220C[63.0%],TP53:p.Q167Lfs*15[47.8%]	NA	NA	NA	NA	Y
467399	AML	BM	46,XY[20]	DNMT3A:p.Arg882His[45.4%],TET2:p.Val1213PhefsTer11[40.3%],TET2:p.Cys1271TrpfsTer29[24.0%],NPM1:p.Trp288CysfsTer12[41.7%],FLT3:p.Asn841Lys[15.9%]	NA	Favorable	0	0	DNMT3A:p.R882H[53.2%],TET2:p.V1213Ffs*11[43.4%],TET2:p.C1271Wfs*29[20.5%],FLT3:p.N841K[23.6%],NPM1:p.W288Cfs*12[43.2%]	Favorable	NA	N	N	NA
205587	AML	BM	46,XY,t(15;17)(q24;q21)[1]/47,sl,+8[1]/48,sdl,+21[18]/46,XY[2]	NA	NA	APL	+8[47.6%],gain(21)(q11.2qter)[47.7%]	t(15;17)(q24.1;q21.2)[21.9%],t(15;17)(q24.1;q21.2)[12.9%]	FLT3:p.S584_D593dup[17.2%]	APL	NA	N	N	NA
764488	AML	PB	46,XY[10]	NRAS:p.Gly12Asp[3.5%],DNMT3A:[46.9%],TET2:p.His1380Tyr[49.0%],TET2:p.Ala1919ProfsTer31[45.3%],NPM1:p.Trp288CysfsTer12[30.4%],FLT3:p.Leu576Gln[14.0%],FLT3:p.Tyr572Cys[4.1%],CEBPA:p.Glu59ProfsTer102[25.1%]	NA	NA	+4[7.7%],gain(21)(q22.2qter)[10.7%]	0	DNMT3A:NA[52.4%],TET2:p.H1380Y[46.2%],TET2:p.A1919Pfs*31[36.1%],FLT3:p.L576Q[17.3%],CEBPA:p.E59Pfs*102[34.6%],NPM1:p.W288Cfs*12[33.3%]	Favorable	NA	Not Complex	Y	NA
809382	AML	BM	46,XX[20]	DNMT3A:p.Gln615Ter[43.0%],TET2:p.Lys824Ter[39.1%],TET2:p.Gln962Ter[43.2%],NPM1:p.Trp288CysfsTer12[36.5%],SRSF2:p.Pro95Arg[25.7%]	NA	Favorable	0	0	DNMT3A:p.Q615*[49.0%],TET2:p.K824*[47.6%],TET2:p.Q962*[46.1%],SRSF2:p.P95R[53.4%],NPM1:p.W288Cfs*12[44.6%]	Favorable	NA	N	N	NA
917922	AML	BM	46,XY,t(15;17)(q24;q21)[20]	NA	NA	APL	0	t(15;17)(q24.1;q21.2)[26.9%],t(15;17)(q24.1;q21.2)[27.4%]	FLT3:p.W603_N609dup[50.5%]	APL	NA	N	N	NA
211740	AML	BM	46,XX,t(3;3)(q21;q26.2)[20]	SF3B1:p.Lys666Glu[55.6%],WT1:p.Arg380ProfsT	NA	Adverse	0	gain(3)(q21.3q26.2)[23.1%	SF3B1:p.K666E[39.1%],WT1:p.	Adverse	NA	N	N	NA

				er2[2.7%],RUNX1:p.Gly199Arg[28.6%]				],del(3)(q21.3q26.2)[26.5%]	R462W[17.2%],RUNX1:p.G199R[35.3%]					
462268	AML	BM	46,XY,t(8;21)(q22;q22)[4]/46,idem,inv(18)(p11.2q21.3)[13]	SMC3:[43.9%]	NA	Favorable	0	t(8;21)(q21.3;q22.12)[26.3%],t(8;21)(q21.3;q22.12)[28.6%]	SMC3:NA[37.3%]	Favorable	NA	N	N	NA
267935	AML	BM	46,XY,inv(16)(p13.1q22)[6]/46,XY[4]	NRAS:p.Gly13Arg[2.5%],KIT:p.Thr417del[11.3%],KIT:p.Asp419del[12.2%],KIT:p.Trp557Arg[3.8%],KIT:p.Asn655Lys[3.1%],WT1:p.Val371CysfsTer14[2.8%]	NA	Favorable	0	inv(16)(q22.1p13.11)[38.8%],inv(16)(q22.1p13.11)[25.3%]	0	Favorable	NA	N	N	NA
491972	AML	BM	46,XY[20]	DNMT3A:p.Gln886Glu[34.2%],TET2:p.Gln913Ter[29.0%],NPM1:p.Trp288CysfsTer12[27.3%]	NA	Favorable	0	0	DNMT3A:p.Q886E[48.1%],TET2:p.Q913*[46.5%],NPM1:p.W288Cfs*12[49.1%]	Favorable	NA	N	N	NA
783803	MDS	BM	46,XX[20]	NA	Good	NA	0	0	NRAS:p.G13V[47.8%],TET2:p.H1868Y[52.6%],TET2:p.H1881R[36.7%],EZH2:p.Y153D[92.0%],STAG2:p.R259*[46.5%]	NA	Good	N	NA	N
872523	MDS	BM	44~45,XY,add(5)(p13),del(7)(q32),-12,-16,add(17)(p11.2),-20,+21,+1~2mar[cp19]/46,XY[1]	TP53:[44.3%],TP53:[43.6%],RUNX1:p.Arg233Leu[49.0%]	Very poor	NA	del(12)(p11.21pter)[89.0%],del(12)(q21.32qter)[85.8%],del(16)(q11.2qter)[85.6%],del(17)(p13.2pter)[65.9%],-17[83.5%]	0	TP53:NA[42.9%],TP53:NA[46.5%],RUNX1:p.R233L[60.7%]	NA	Very poor	N	NA	N
188798	AML	BM	47,XX,der(1)t(1;7)(q32;p13),del(5)(q22q35),-7,+8,del(12)(p11.2),der(13)del(13)(q14q14)inv(13)(p13q13),add(18)(p11.2),+19[4].	TP53:p.Arg248Trp[20.5%],TP53:p.Leu145Pro[31.2%]	NA	Adverse	del(5)(q21.3q33.3)[47.1%],del(7)(q11.23q36.1)[47.5%],+8[41.3%],del(12)(p11.21p13.2)[42.2%],del(18)(p11.23pter)[38.7%],+19[37.5%]	0	TP53:p.R248W[27.7%],TP53:p.L145P[27.4%]	Adverse	NA	N	N	NA
739025	MDS	BM	46~47,XY,-5,del(7)(q22q34),+8,t(11;15)?(p15;q22),+mar[cp14]/46,XY[6]	TP53:p.Cys275Tyr[75.3%]	Poor	NA	del(5)(q11.2qter)[63.2%],del(7)(q21.2qter)[63.2%],+8[43.1%]	0	TP53:p.C275Y[75.9%]	NA	Poor	Complex	NA	N
506517	AML	BM	46,XX[20]	NPM1:p.Trp288CysfsTer12[48.2%],WT1:p.Glu384AspfsTer8[38.9%],BCOR:p.Pro678Ser[45.9%],BCORL1:p.Val329Leu[49.6%]	NA	Intermediate	0	0	WT1:p.E384Dfs*8[51.4%],BCOR:p.P678S[52.6%],BCORL1:p.V329L[48.5%],NPM1:p.W288Cfs*12[42.2%],FLT3:p.F621_G622insEYEYDLKWEFPRENLEFGKNGMCQMFLQHFFSIGKSLKCTYSPFVFAGKVLGSGAF[21.4%]	Intermediate	NA	N	N	NA
985517	MDS	BM	47,XY,+11[3]	SMC3:p.Gly1118Ter[6.2%],TP53:p.Tyr220Cys[8.5%]	Intermediate	NA	+11[8.1%]	0	0	NA	Intermediate	N	NA	N
553902	AML	BM	49,XY,+1,del(5)(q13q33),+8,-16,add(17)(p13),der(17)del(17)(p12)del(17)(q11.1q12),+21,+21[18]/50,idem,+mar[2]	None detected	NA	Adverse	gain(1)(p31.1p36.32)[82.9%],+1[67.1%],del(5)(q11.2q34)[82.9%],+8[80.5%],del(16)(q23.1qter)[83.1%],del(17)(p13.1pter)[78.8%],gain(21)(q11.2qter)[116.7%]	0	0	Adverse	NA	N	N	NA
538465	AML	BM	46,XY,t(15;17)(q24;q21)[17]/46,XY[3]	NA	NA	APL	+8[27.6%],+10[29.3%]	t(15;17)(q24.1;q21.2)[34.2%],t(15;17)(q24.1;q21.2)[28.8%]	0	APL	NA	Not Complex	N	NA
537017	AML	BM	74<3N>,XXY,+1,?add(1)(p22),+2,+3,+6,-19,+21,+22[1]/82<4N>,XXYY,-1,?add(1)(p22),-2,-3,-4,-5,-7,-11,add(11)(q13),-12,-13,-14,-15,-16,-17,-18,-18,-19,add(19)(q13.3),-21,-22,+8mar[1]/46,XY[18].	TP53:p.His168Arg[33.1%]	NA	Adverse	gain(1)(p32.1p35.2)[26.1%],-4[14.5%],-5[30.4%],+6[32.3%],-7[13.3%],gain(8)(q21.11qter)[18.8%],-11[21.3%],-12[11.3%],gain(13)(q12.11qter)[28.5%],-16[29.2%],del(17)(p12pter)[28.7%],+19[32.2%],gain(21)(q11.2qter)[17.8%]	0	TP53:p.H168R[43.2%]	Adverse	NA	N	N	NA
666013	AML	BM	46,XX,del(3)(?p24)[10]/46,XX[10]	DNMT3A:p.Asn797Ser[2.2%],DNMT3A:[30.2%],IDH1:p.Arg132Cys[11.6%],TET2:p.Ser1239Cys[2.	NA	Adverse	del(5)(q31.2q31.2)[10.1%]	0	DNMT3A:NA[54.2%],IDH1:p.R132C[23.8%],BCOR:p.Q123Rfs*	Adverse	NA	N	N	NA

				1%],BCOR:p.Gln123ArgfsTer38[9.4%],PHF6:p.Arg277GlufsTer2[10.8%]					38[22.7%],PHF6:p.R277Efs*2[32.1%]					
967740	MDS	BM	46,XX[18]	TP53:p.Tyr126His[2.7%]	NA	NA	0	0	0	NA	Good	NK	NA	Y
887041	AML	BM	46,XY[20]	NRAS:p.Gly13Asp[2.9%],NRAS:p.Gly13Arg[6.9%],DNMT3A:p.Arg598Ter[46.6%],DNMT3A:p.Thr65Lys[49.4%],IDH1:p.Arg132Leu[44.4%],FLT3:p.Asp835Glu[21.7%],SRSF2:p.Pro95His[46.5%],ASXL1:p.Gly646TrpfsTer12[38.8%],RUNX1:p.Arg162Lys[95.4%]	NA	Adverse	0	0	DNMT3A:p.R598*[50.7%],DNMT3A:p.T65K[51.6%],IDH1:p.R132L[55.3%],FLT3:p.D835E[17.4%],SRSF2:p.P95H[43.1%],ASXL1:p.G646Wfs*12[50.8%],RUNX1:p.R162K[96.3%]	Adverse	NA	N	N	NA
681540	MDS	BM	unsuccessful	TET2:p.Tyr1628Ter[5.8%],TET2:p.Arg1878Cys[6.5%],CBL:p.Cys404Ser[3.4%],ASXL1:p.Glu635ArgfsTer15[10.6%],RUNX1:p.His85ThrfsTer38[44.3%],ZRSR2:[24.7%]	NA	NA	del(11q)[12.8%]	0	ASXL1:p.E635Rfs*15[9.9%],RUNX1:p.H85Tfs*38[50.5%]	NA	Very good	del(11q)	NA	Y
748511	MDS	BM	unsuccessful	TP53:p.Arg337Cys[35.5%],TP53:p.Lys321Ter[28.5%],BCORL1:p.Arg1354Gln[100.0%]	NA	NA	gain(1)(p32.2p36.32)[7.6%],+8[7.1%],+19[12.8%]	0	TP53:p.R337C[27.1%],TP53:p.K321*[23.9%],BCORL1:p.R1354Q[100.0%]	NA	Poor	Complex	NA	Y
416413	MDS	BM	46,XY[20]	NRAS:p.Gly12Asp[27.3%],TET2:p.Trp564Ter[50.3%],TET2:p.Gln964Ter[45.2%],EZH2:p.Val626Met[3.3%],CBL:p.Ile429Asn[43.9%],FLT3:p.Asn841Ile[2.3%],TP53:p.Arg283Cys[46.6%],CEBPA:p.Glu329GlyfsTer74[14.2%],ASXL1:p.Gly646TrpfsTer12[41.5%],STAG2:[93.8%]	Good	NA	0	0	NRAS:p.G12D[27.3%],CBL:p.I429N[40.9%],TP53:p.R283C[54.5%],ASXL1:p.G646Wfs*12[35.9%]	NA	Good	N	NA	N
218281	MDS	BM	46,XY,del(5)(q22q35)[20]	NA	Good	NA	del(5)(q21.3q34)[95.9%]	0	DNMT3A:p.R882C[33.3%],TET2:p.S1284F[54.2%],TET2:p.K1468*[53.8%],PTPN11:p.E76K[72.0%],TP53:p.K132N[56.0%]	NA	Good	N	NA	N
228950	MDS	BM	46,XY[20]	None detected	Good	NA	0	0	0	NA	Good	N	NA	N
853337	AML	BM	46,XX[14]	DNMT3A:p.Glu523Ter[44.4%],IDH1:p.Arg132His[5.7%],NPM1:p.Leu287IlefsTer13[40.5%],NPM1:p.Trp288CysfsTer12[42.7%],NPM1:p.Trp288CysfsTer12[42.7%],SMC3:[37.3%],ETV6:p.Leu117AsnfsTer7[4.1%],PTPN11:p.Asp61Gly[38.6%],NF1:p.Arg1306Ter[3.8%]	NA	NA	0	0	DNMT3A:p.E523*[43.3%],SMC3:NA[48.0%],PTPN11:p.D61G[45.6%],NPM1:p.W288Cfs*12[38.3%],CEBPA:p.M15Afs*84[37.3%]	Favorable	NA	NK	Y	NA
800962	MDS	BM	47,XY,+19[19]/46,XY[1]	ASXL1:p.Gly646TrpfsTer12[11.1%],U2AF1:p.Gln157Pro[10.2%]	Intermediate	NA	+19[74.9%]	0	U2AF1:p.Q157P[36.5%],ASXL1:p.G646Wfs*12[41.3%]	NA	Intermediate	N	NA	N
787399	MDS	BM	46,XY[3]	TET2:p.Gln232Ter[5.0%],TET2:p.Asn535LysfsTer6[2.7%],U2AF1:p.Gln157Arg[20.6%],U2AF1:p.Ser34Tyr[21.4%]	NA	NA	0	0	U2AF1:p.Q157R[24.1%],U2AF1:p.S34Y[30.0%]	NA	Good	NK	NA	Y
293825	AML	BM	46,XX[21]	DNMT3A:p.Arg882Cys[29.3%],NPM1:p.Trp288CysfsTer12[30.4%],PTPN11:p.Gly60Ala[13.8%],IDH2:p.Arg140Leu[29.5%]	NA	Favorable	0	0	DNMT3A:p.R882C[33.3%],IDH2:p.R140L[30.2%],NPM1:p.W288Cfs*12[38.5%]	Favorable	NA	N	N	NA
541728	MDS	BM	46,XX[20]	NRAS:p.Gln61Lys[42.8%],DNMT3A:p.Trp698Ter[47.8%],NPM1:p.Trp288CysfsTer12[44.5%]	Good	NA	0	0	NRAS:p.Q61K[43.3%],DNMT3A:p.W698*[45.9%],NPM1:p.W288Cfs*12[40.7%]	NA	Good	N	NA	N
632997	MDS	BM	46,XY,i(17)(q10)[15]/46,XY[5]	ETV6:p.Gly375Arg[44.5%],PTPN11:p.Gln510His[28.3%],SRSF2:p.Pro95His[59.2%],ASXL1:p.Glu635ArgfsTer15[45.3%]	Intermediate	NA	del(17)(p11.2pter)[73.4%],+17[77.9%]	0	ETV6:p.G375R[61.5%],SRSF2:p.P95H[72.2%],ASXL1:p.E635Rfs*15[43.3%]	NA	Intermediate	N	NA	N
207247	MDS	BM	unsuccessful	DNMT3A:p.Val563Met[4.0%]	NA	NA	0	0	0	NA	Good	NK	NA	Y
187885	AML	BM	46,XY[20]	DNMT3A:p.Arg882Cys[48.6%],IDH1:p.Arg132His[36.8%],NPM1:p.Trp290ArgfsTer10[46.1%],FLT3:p.Asp835Ala[7.4%],FLT3:p.Val592Ala[13.2%]	NA	Favorable	0	0	DNMT3A:p.R882C[50.0%],IDH1:p.R132H[43.2%],FLT3:p.V592A[19.6%],NPM1:p.W290Rfs*10[50.9%]	Favorable	NA	N	N	NA
191374	MDS	BM	45,X,-Y[20]	TET2:p.Gln810Ter[45.7%],TET2:p.Ala911LeufsTer10[47.6%],CUX1:p.Glu398Ter[50.5%],RAD21:p.Gly481Arg[44.9%],CBL:[41.5%],ASXL1:p.Asn63Lys[45.9%],PHF6:p.Ile314Thr[92.5%]	Very good	NA	-Y[96.0%]	0	TET2:p.Q810*[41.3%],TET2:p.A911Lfs*10[28.6%],CUX1:p.E398*[52.8%],RAD21:p.G481R[47.7%],CBL:NA[56.2%],ASXL1:p.N63K[50.0%],PHF6:p.I314T[96.0%]	NA	Very good	N	NA	N
314322	MDS	BM	46,XY,del(20)(q11.2)[19]/46,XY[1]	NF1:p.Gly772ArgfsTer16[64.6%],U2AF1:p.Ser34Phe[43.4%]	Good	NA	del(20)(q11.21qter)[81.8%]	0	NF1:p.G772Rfs*16[75.8%],NF1:NA[68.6%],U2AF1:p.S34F[46.9%]	NA	Good	N	NA	N

480059	AML	BM	46,XX,t(4;7)(q25;q22)?c[20]	NPM1:p.Trp288CysfsTer12[28.5%],CBL:[3.1%],NF1:[28.5%],PPM1D:p.Cys478Ter[27.8%],SRSF2:p.Pro95Leu[53.3%],ASXL1:p.Gly646TrpfsTer12[41.7%]	NA	Favorable	del(7)(q22.1q22.1)[90.7%]	0	NF1:NA[34.9%],PPM1D:p.C478*[40.0%],SRSF2:p.P95L[49.1%],ASXL1:p.G646Wfs*12[46.4%],NPM1:p.W288Cfs*12[27.8%]	Favorable	NA	N	N	NA
905861	AML	BM	44,XY,-3,del(5)(q23),add(7)(q11.2),-9 ,-10,-14,-15,del(16)(q21),der(19)t(4;19)(q11.2;q13.3),+1~3mar[cp17]/44,idem,+1,add(2)(p21),-del(16)(q21),+2~7mar[cp8]	NRAS:p.Gly10dup[3.6%],GATA2:p.Arg362Gln[92.4%],TP53:p.Ser106Arg[95.6%]	NA	Adverse	-3[92.1%],del(5)(q11.2qter)[92.1%],del(7)(q11.23qter)[92.8%],del(15)(q21.2q22.32)[93.4%],gain(19)(q13.33qter)[90.2%]	0	GATA2:p.R362Q[87.9%],TP53:p.S106R[95.3%]	Adverse	NA	N	N	NA
654925	AML	BM	46,XY[20]	NRAS:p.Gly12Asp[2.7%],DNMT3A:p.Met880IlefsTer26[34.0%],IDH1:p.Arg132Gly[40.9%],NPM1:p.Trp288CysfsTer12[40.7%],FLT3:p.Tyr842Cys[7.7%],FLT3:p.Val592Ala[16.1%]	NA	Favorable	0	0	DNMT3A:p.M880Ifs*26[44.1%],IDH1:p.R132G[42.1%],FLT3:p.Y842C[18.6%],NPM1:p.W288Cfs*12[35.1%]	Favorable	NA	N	N	NA
653268	AML	BM	46,XY[20]	NRAS:p.Gly13Asp[6.6%],DNMT3A:p.Glu733_Phe734delinsVal[46.4%],NPM1:p.Trp288CysfsTer12[42.2%],KRAS:p.Gln61Pro[3.9%],PTPN11:p.Ser502Pro[12.4%],FLT3:p.Asp835Val[11.8%],FLT3:p.Val592_Tyr599dup[0.9%],FLT3:p.Asn587_Phe594dup[1.0%],NF1:p.Ile679AspfsTer21[2.0%]	NA	Favorable	0	0	NRAS:p.G13D[7.9%],DNMT3A:p.E733_F734delinsV[36.4%],PTPN11:p.S506P[15.9%],FLT3:p.D835V[14.7%],NPM1:p.W288Cfs*12[39.3%]	Favorable	NA	N	N	NA
888204	MDS	BM	43,XX,dic(3;8)(p11;p11.2),del(5)(q13),der(6)t(1;6)(p32;p22),inv(7)(p21q22),add(9)(q34),add(11)(p11.1),-12,-16,-17,add(17)(p11.2),del(20)(q11.2q13.1),add(22)(q13),+mar[21]	NA	Very poor	NA	gain(1)(p32.3p36.32)[91.9%],del(3)(p12.3p14.1)[93.4%],del(5)(q14.2qter)[93.1%],del(7)(p12.2p15.3)[90.8%],del(8)(p11.23pter)[96.4%],del(11)(p14.1p15.4)[92.5%],-12[92.9%],del(12)(q14.1q24.11)[93.3%],-16[94.2%],del(17)(p13.1pter)[92.5%],del(17)(q11.2q12)[90.9%],del(20)(q11.21q13.32)[92.5%],gain(22)(q11.21qter)[91.5%]	0	TP53:p.R175H[92.5%]	NA	Very poor	N	NA	N
946179	AML	BM	46,XX[20]	NRAS:p.Gly12Asp[47.0%],NPM1:p.Trp288CysfsTer12[44.5%]	NA	Favorable	0	0	NRAS:p.G12D[51.1%],NPM1:p.W288Cfs*12[56.9%]	Favorable	NA	N	N	NA
717042	AML	BM	46,XY[20]	DNMT3A:p.Arg882His[45.5%],NPM1:p.Trp288CysfsTer12[40.2%],FLT3:p.Val579_Trp603dup[12.8%],FLT3:p.Trp603_Glu604insValGlnValThrGlySerSerAspAsnGluTyrPheTyrValAspPheArgGluTyrGluTyrAspLeuLysSer[12.3%],FLT3:p.Lys602_Trp603insGlyValGlnValThrGlySerSerAspAsnGluTyrPheTyrValAspPheArgGluTyrGluTyrAspLeuLys[12.6%],FLT3:p.Leu601_Lys602insGlnTrpValGlnValThrGlySerSerAspAsnGluTyrPheTyrValAspPheArgGluTyrGluTyrAspLeu[12.1%],FLT3:p.Lys602_Trp603insGlyValGlnValThrGlySerSerAspAsnGluTyrPheTyrValAspPheArgGluTyrGluTyrAspLeuLys[12.1%],FLT3:p.Asp600_Leu601insGlyValGlnLeuThrGlySerSerAspAsnAlaAsnIleTyrValTyrIleIleTerAspGluTyrAspLeuAsn[4.5%],FLT3:p.Glu598delinsGlyGlyTyrArgTerGlnAlaProGlnIleMetIleThrSerThrPheIleSerGluAsnMetAsnMetIleSerLys[4.3%],FLT3:p.Tyr597delinsTrpAlaLeuAsn[4.2%],FLT3:p.Val592_Asp593insMetAsnMetIleSerArgGlyTyrArgArgGlnHisProGlnIleLysSerThrSerThrLeuIleSerGluAsn[4.2%],FLT3:p.Phe590_Tyr591insTer[12.2%],FL	NA	Intermediate	0	0	DNMT3A:p.R882H[53.8%],NPM1:p.W288Cfs*12[41.7%],FLT3:p.V579_K602dup[22.2%]	Intermediate	NA	N	N	NA

				T3:p.Val581_Phe590dup[1.0%]										
262878	AML	BM	46,XX[20]	NPM1:p.Trp288CysfsTer12[37.9%],RAD21:p.Gly547AlafsTer65[36.2%],KRAS:p.Gly13Asp[5.2%],KRAS:p.Gly12Asp[5.7%],PTPN11:p.Asp61Val[2.5%],FLT3:p.Asp835His[13.1%],FLT3:p.Val592_Asp593insGluThrGlySerSerAspAsnGluTyrPheTyrVal[0.8%],NF1:p.Gln554His[42.0%]	NA	Favorable	0	0	KRAS:p.G12D[11.7%],NF1:p.Q554H[51.1%],NPM1:p.W288Cfs*12[35.2%],RAD21:p.G547Afs*65[33.9%]	Favorable	NA	N	N	NA
880398	ALL	BM	47,XX,+3[1]/48,idem,+X,t(9;22)(q34;q11.2)[1]/46,XX[1]	NA	NA	NA	+3[26.4%],del(7)(p11.2pter)[29.8%],+8[26.2%],del(13)(q12.3q33.1)[28.8%],gain(14)(q11.2qter)[27.3%],+X[29.3%]	t(9;22)(q34.12;q11.23)[8.1%],t(9;22)(q34.12;q11.23)[10.3%]	ASXL1:p.G646Wfs*12[11.0%]	NA	NA	Complex	NA	Y
332282	AML	BM	47,XX,+8[20]	None detected	NA	Intermediate	+8[77.9%]	t(9;11)(p21.3;q23.3)[34.5%],t(9;11)(p21.3;q23.3)[26.2%]	0	Intermediate	NA	t(9;11)(p21.3;q23.3)[34.5%],t(9;11)(p21.3;q23.3)[26.2%]	N	NA
516070	AML	BM	46,XY[13]	CUX1:p.Gln623Ter[4.3%],EZH2:p.Val626Met[4.9%],SRSF2:p.Phe62Val[4.6%],ASXL1:p.Gly646TrpfsTer12[5.8%]	NA	NA	0	0	CUX1:p.Q623*[8.7%],ASXL1:p.G646Wfs*12[4.8%]	Adverse	NA	NK	Y	NA
869318	AML	BM	46,XX,?t(12;16)(q24.3;q22)[4]/46,XX[4]	KRAS:p.Gly13Asp[26.8%],KRAS:p.Gly12Asp[4.4%]	NA	Favorable	0	inv(16)(q22.1p13.11)[32.5%]	KRAS:p.G13D[38.7%]	Favorable	NA	N	N	NA
736399	AML	BM	46,XX[20]	TET2:p.Pro1367Gln[28.5%],TET2:p.Pro1741ThrfsTer11[47.9%],TET2:p.Pro1742Ser[46.6%],NPM1:p.Trp288CysfsTer12[46.5%],PPM1D:p.Glu476Ter[45.9%]	NA	Favorable	0	0	TET2:p.P1367Q[50.0%],TET2:p.P1741Tfs*11[41.9%],TET2:p.P1742S[57.9%],PPM1D:p.E476*[65.7%],NPM1:p.W288Cfs*12[39.2%]	Favorable	NA	N	N	NA
324214	ALL	BM	46,XX[20](hyperdiploid)	NA	NA	NA	+1[44.6%],-2[21.4%],-3[21.6%],-4[22.0%],del(5)(q21.2qter)[20.7%],+6[42.6%],-7[21.7%],+8[42.3%],-9[20.8%],-12[21.3%],del(13)(q12.11qter)[21.5%],del(15)(q11.2qter)[20.7%],-16[19.7%],-17[19.2%],+18[42.1%],+19[47.4%],-20[19.1%],gain(21)(q11.2qter)[43.2%],-X[24.2%]	0	TP53:p.R248W[31.2%]	NA	NA	N	NA	Y
183114	AML	BM	unsuccessful	ASXL1:p.Gly646TrpfsTer12[40.1%]	NA	NA	0	t(9;11)(p21.3;q23.3)[50.0%]	ASXL1:p.G646Wfs*12[52.4%]	Intermediate	NA	t(9;11)(p21.3;q23.3)[50.0%]	Y	NA
924089	AML	BM	46,XX,t(9;11)(p22;q23)[20]	CBL:[16.9%],CBL:[25.6%],PTPN11:p.Ser502Leu[19.9%],FLT3:p.Tyr589_Val592del[18.8%]	NA	Intermediate	0	t(9;11)(p21.3;q23.3)[27.3%],t(9;11)(p21.3;q23.3)[23.2%]	CBL:NA[26.0%],CBL:NA[26.2%],PTPN11:p.S506L[15.1%],FLT3:p.Y589_V592del[15.0%]	Intermediate	NA	N	N	NA
663125	AML	BM	no growth	DNMT3A:p.Ala410Ser[2.57%],SF3B1:p.Asp907His[0.85%],TP53:p.His179Tyr[1.97%],TP53:p.Arg158Gly[17.85%],STAG2:[3.86%]	NA	Adverse	del(5)(q14.3q33.2)[22.0%],del(11)(p15.4pter)[19.5%],del(12)(p12.1pter)[21.0%],del(17)(p12pter)[14.7%],del(17)(q11.2q21.32)[14.9%],+18[23.4%],del(18)(q21.1qter)[14.0%],gain(19)(q13.12qter)[42.1%],gain(21)(q11.2q21.1)[32.5%],del(21)(q21.1q22.11)[16.7%],gain(21)(q22.11qter)[36.4%]	0	0	Adverse	NA	Complex	N	NA
525644	AML	BM	46,Y,t(X;15)(q25;q22),der(3;21)(q10;q10),del(5)(q22q33),der(6)add(6)(p23)t(3;6)(q25;p21),del(12)(p13),+21[cp20]	NRAS:p.Gly12Val[2.3%],PTPN11:p.Asn58Tyr[5.5%]	NA	Adverse	del(5)(q23.2q31.3)[80.6%],del(6)(p22.3p25.1)[82.1%],del(6)(q23.2q23.3)[82.9%],del(12)(p13.1p13.32)[80.7%],del(12)(q21.33q22)[81.3%]	0	0	Adverse	NA	N	N	NA

869658	ALL	BM	43~44,XY,add(4)(p16),-7,-9,t(9;22)(q34;q11.2),der(10)t(9;10)(q22;p11.2),?add(17p),add(19)(p13),-20,+1~2mar[cp20]. ish der(10)(ABL1+)[3/3]	None detected	NA	NA	del(4)(p16.1pter)[93.4%],-7[97.5%],-9[79.6%],del(20)(q12qter)[92.8%]	t(9;22)(q34.12;q11.23)[39.9%],t(9;22)(q34.12;q11.23)[36.0%]	0	NA	NA	NA	NA	Y

Blank cells, ‘0’, or ‘NA’ indicate no data.
Downloadable version with more information can be found here: https://wustl.box.com/v/rapidclinicalwgs-tables7

Table S8. Results prospective AML/MDS patients with new findings by WGS.

UPN	Diagnosis	Specimen	Cytogenetics ISCN.Line	Gene.mutations	IPSSR.risk.group	Conventional ELN.Risk	WGS.CNAs	WGS Recurrent.SVs	WGS Gene.mutations	WGS.ELN.Risk	WGS IPSSR.risk.group	New.information	New.ELN.Risk.vs. Cyto.and.FISH	New.IPSSR
780327	AML	BM	46,XY[5]	NPM1:p.Trp288CysfsTer12[36.5%],CUX1:p.Leu173Phe[50.3%],CUX1:p.Gly709Val[45.5%],IDH2:p.Arg140Gln[42.9%]	NA	NA	0	0	CUX1:p.L173F[46.0%],CUX1:p.G709V[48.0%],IDH2:p.R140Q[41.2%],NPM1:p.W288Cfs*12[51.9%]	Favorable	NA	NK	Y	NA
994357	AML	BM	46,XX[20]	None detected	NA	Intermediate	0	t(11;19)(q23.3;p13.11)[23.6%],t(11;19)(q23.3;p13.11)[28.5%]	0	Adverse	NA	t(11;19)(q23.3;p13.11)[23.6%],t(11;19)(q23.3;p13.11)[28.5%]	Y	NA
586748	AML	BM	46,XY[20]	ETV6:p.Ser131PhefsTer23[35.7%]	NA	Intermediate	0	t(7;21)(p22.1;q22.12)[23.1%]	ETV6:p.S131Ffs*23[46.3%]	Intermediate	NA	t(7;21)(p22.1;q22.12)[23.1%]	N	NA
120644	MDS	BM	unsuccessful	None detected	NA	NA	0	0	0	NA	Good	NK	NA	Y
343604	AML	BM	unsuccessful	EZH2:[91.0%],KRAS:p.Gly13Asp[35.0%],ASXL1:p.Gly646TrpfsTer12[43.4%]	NA	NA	+8[65.5%],del(12)(p12.1p13.2)[94.8%]	0	EZH2:NA[95.5%],KRAS:p.G13D[35.0%],ASXL1:p.G646Wfs*12[39.3%]	Adverse	NA	Not Complex	Y	NA
333171	MDS	BM	46,XY[10]	TET2:p.Tyr1964His[47.9%],ETV6:p.Arg353Gln[49.7%],KRAS:p.Gly12Ala[37.0%],SMC1A:p.Arg96His[28.6%]	NA	NA	0	0	TET2:p.Y1964H[40.4%],ETV6:p.R353Q[50.8%],KRAS:p.G12A[40.5%],SMC1A:p.R96H[21.2%]	NA	Good	NK	NA	Y
430826	AML	BM	46,XY,t(15;17)(q24;q21)[5]/46,XY[1]	NA	NA	APL	gain(2)(q14.1qter)[23.6%], gain(7)(p12.3p14.1)[23.6%],-7[21.5%],del(9)(p21.1pter)[17.4%],gain(9)(q22.33qter)[21.4%],del(10)(p11.21pter)[23.8%],gain(10)(q11.21qter)[22.1%],del(13)(q12.11qter)[20.7%],del(16)(q23.1qter)[21.7%],del(18)(p11.21pter)[15.2%],gain(19)(p12pter)[21.7%],gain(20)(q11.21qter)[35.8%]	t(15;17)(q24.1;q21.2)[3.3%],t(15;17)(q24.1;q21.2)[4.1%]	0	APL	NA	Complex	N	NA
229201	AML	BM	46,XY[5]	NPM1:p.Trp288CysfsTer12[26.2%],FLT3:p.Leu601_Lys602insGlySerAspAsnGluTyrPheTyrValAspPheArgGluTyrGluTyrAspLeu[7.3%],FLT3:p.Leu601_Lys602insGlySerAspAsnGluTyrPheTyrValAspPheArgGluTyrGluTyrAspLeu[7.0%],FLT3:p.Arg595_Glu596insTer[12.3%],FLT3:p.Asp593_Phe594insLeuArgAspPheGluTyrAspLeuValSerAspAsnGluTyrPheTyrPheAsp[8.9%],IDH2:p.Arg140Gln[37.0%]	NA	NA	0	0	IDH2:p.R140Q[37.7%],NPM1:p.W288Cfs*12[15.5%],FLT3:p.S585_L601dup[14.0%]	Favorable	NA	NK	Y	NA
534164	MDS	BM	45,XY,-7[20]	DNMT3A:p.Arg326Cys[44.2%],RAD21:p.Gly273Cys[13.2%],ETV6:p.Ala377Val[40.4%]	Poor	NA	-7[83.9%],del(13)(q14.2q14.3)[85.3%]	0	DNMT3A:p.R326C[50.9%],ETV6:p.A377V[37.9%]	NA	Poor	del(13)(q14.2q14.3)[85.3%]	NA	N
335141	AML	BM	46,XY, add(2)(q37)[6]	DNMT3A:p.Arg882His[44.8%],SF3B1:p.Lys700Glu[44.4%],FLT3:p.Leu601_Lys602insAsnTyrValAspPheArgGluTyrGluTyrAspLeu[18.8%],FLT3:p.Phe594_Asp600dup[27.6%],FLT3:p.Arg595_Glu596insAspHisValAspPheArg[30.7%],FLT3:p.Val581_Phe594dup[31.8%],FLT3:p.Val592_Asp593insValPheValThrGlySerSerAspAsnGluTyrPheTyrVal[33.7%]	NA	Adverse	del(2)(q36.3qter)[89.1%],gain(11)(q13.4qter)[90.2%]	0	DNMT3A:p.R882H[52.1%],SF3B1:p.K700E[39.4%],FLT3:p.L601_K602insNYVDFREYEYDL[21.6%],FLT3:p.V581_F594dup[22.5%]	Adverse	NA	Not Complex	N	NA

155912	AML	BM	46,XX,der(3)t(3;6)(q25;q13),der(6)t(3;6)(q25;q13)t(6;8)(p23;q13)[19]/46,XX[1]	DNMT3A:p.Cys557Arg[42.2%],NPM1:p.Trp288CysfsTer12[38.4%],WT1:p.Arg369GlyfsTer7[43.2%],PTPN11:p.Thr553Met[45.8%],FLT3:p.Phe605_Pro606insArgHisGluTyrAspLeuLysTrpGluPhe[12.9%],FLT3:p.Tyr597_Glu598insAspProAlaAspPheArgGluTyr[19.9%],NF1:p.Ile679AspfsTer21[2.4%]	NA	Intermediate	del(3)(p12.2p14.1)[76.6%],del(6)(p24.1pter)[75.1%],del(6)(q14.1q14.3)[77.6%],gain(8)(q12.1qter)[72.8%]	0	DNMT3A:p.C557R[36.9%],PTPN11:p.T557M[47.6%],NPM1:p.W288Cfs*12[37.1%],WT1:p.R369Gfs*7[42.1%],FLT3:p.F605_P606insRHEYDLKWEF[17.9%]	Adverse	NA	Complex	Y	NA
677982	AML	BM	47,XY,+i(21)(q10)[14]/47,XY,+21[2]/46,XY[4]	None detected	NA	Intermediate	gain(21)(q11.2qter)[173.8%]	t(6;11)(q27;q23.3)[28.8%]	0	Adverse	NA	t(6;11)(q27;q23.3)[28.8%]	Y	NA
103744	AML	BM	46,XX[3]	TP53:p.Phe134Val[29.6%],NF1:p.Gln756Ter[4.3%]	NA	Adverse	del(3)(p11.2pter)[61.8%],+5[76.7%],del(5)(q11.2qter)[60.6%],-7[57.2%],+8[57.6%],+9[52.3%],gain(15)(q11.2qter)[43.2%],del(16)(q21qter)[58.5%],del(17)(p13.1pter)[53.0%],+18[43.5%],gain(22)(q11.21q12.3)[64.0%]	0	TP53:p.F134V[50.0%]	Adverse	NA	Complex	N	NA
451688	MDS	BM	46,XY[3]	EZH2:p.Arg360ThrfsTer5[20.8%],ASXL1:p.Gly646TrpfsTer12[30.6%],ZRSR2:[59.5%]	NA	NA	del(4)(q21.1q25)[53.3%],-Y[27.1%]	0	ASXL1:p.G646Wfs*12[30.2%],ZRSR2:NA[68.0%],EZH2:p.R360Tfs*5[16.7%],JAK2:p.V617F[4.8%]	NA	Intermediate	Independent clones	NA	Y
891309	MDS	BM	46,XY[5]	TP53:p.Arg306Ter[22.4%],TP53:p.Met237Ile[2.4%],ASXL1:p.Glu635ArgfsTer15[18.8%],ASXL1:p.Trp796GlyfsTer22[5.9%]	NA	NA	0	0	TP53:p.R306*[19.5%],ASXL1:p.E635Rfs*15[8.2%]	NA	Good	NK	NA	Y
395906	MDS	BM	46,XY,del(3)(q12q25),+8[20]	DNMT3A:p.Arg882His[44.6%],NF1:p.Arg1534Ter[52.6%],PPM1D:p.Leu484Ter[45.0%],ASXL1:p.Ser921Phe[48.3%],RUNX1:p.Phe97Ser[43.1%],U2AF1:p.Ser34Phe[43.4%]	Poor	NA	del(3)(q21.2q24)[83.4%],del(4)(q28.3q31.1)[65.6%],+8[82.7%]	0	DNMT3A:p.R882H[50.9%],NF1:p.R1534*[54.5%],PPM1D:p.L484*[47.2%],ASXL1:p.S921F[58.6%],RUNX1:p.F97S[35.2%],U2AF1:p.S34F[56.8%]	NA	Poor	Complex	NA	N
764488	AML	PB	46,XY[10]	NRAS:p.Gly12Asp[3.5%],DNMT3A:[46.9%],TET2:p.His1380Tyr[49.0%],TET2:p.Ala1919ProfsTer31[45.3%],NPM1:p.Trp288CysfsTer12[30.4%],FLT3:p.Leu576Gln[14.0%],FLT3:p.Tyr572Cys[4.1%],CEBPA:p.Glu59ProfsTer102[25.1%]	NA	NA	+4[7.7%],gain(21)(q22.2qter)[10.7%]	0	DNMT3A:NA[52.4%],TET2:p.H1380Y[46.2%],TET2:p.A1919Pfs*31[36.1%],FLT3:p.L576Q[17.3%],CEBPA:p.E59Pfs*102[34.6%],NPM1:p.W288Cfs*12[33.3%]	Favorable	NA	Not Complex	Y	NA
739025	MDS	BM	46~47,XY,-5,del(7)(q22q34),+8,t(11;15)?(p15;q22),+mar[cp14]/46,XY[6]	TP53:p.Cys275Tyr[75.3%]	Poor	NA	del(5)(q11.2qter)[63.2%],del(7)(q21.2qter)[63.2%],+8[43.1%]	0	TP53:p.C275Y[75.9%]	NA	Poor	Complex	NA	N
538465	AML	BM	46,XY,t(15;17)(q24;q21)[17]/46,XY[3]	NA	NA	APL	+8[27.6%],+10[29.3%]	t(15;17)(q24.1;q21.2)[34.2%],t(15;17)(q24.1;q21.2)[28.8%]	0	APL	NA	Not Complex	N	NA
967740	MDS	BM	46,XX[18]	TP53:p.Tyr126His[2.7%]	NA	NA	0	0	0	NA	Good	NK	NA	Y
681540	MDS	BM	unsuccessful	TET2:p.Tyr1628Ter[5.8%],TET2:p.Arg1878Cys[6.5%],CBL:p.Cys404Ser[3.4%],ASXL1:p.Glu635ArgfsTer15[10.6%],RUNX1:p.His85ThrfsTer38[44.3%],ZRSR2:[24.7%]	NA	NA	del(11q)[12.8%]	0	ASXL1:p.E635Rfs*15[9.9%],RUNX1:p.H85Tfs*38[50.5%]	NA	Very good	del(11q)	NA	Y
748511	MDS	BM	unsuccessful	TP53:p.Arg337Cys[35.5%],TP53:p.Lys321Ter[28.5%],BCORL1:p.Arg1354Gln[100.0%]	NA	NA	gain(1)(p32.2p36.32)[7.6%],+8[7.1%],+19[12.8%]	0	TP53:p.R337C[27.1%],TP53:p.K321*[23.9%],BCORL1:p.R1354Q[100.0%]	NA	Poor	Complex	NA	Y
853337	AML	BM	46,XX[14]	DNMT3A:p.Glu523Ter[44.4%],IDH1:p.Arg132His[5.7%],NPM1:p.Leu287IlefsTer13[40.5%],NPM1:p.Trp288CysfsTer12[42.7%],NPM1:p.Trp288CysfsTer12[42.7%],SMC3:[37.3%],ETV6:p.Leu117AsnfsTer7[	NA	NA	0	0	DNMT3A:p.E523*[43.3%],SMC3:NA[48.0%],PTPN11:p.D61G[45.6%],NPM1:p.W288Cfs*12[38.3%],CEBPA:p.M15Afs*84[37.3%]	Favorable	NA	NK	Y	NA

				4.1%],PTPN11:p.Asp61Gly[38.6%],NF1:p.Arg1306Ter[3.8%]										
787399	MDS	BM	46,XY[3]	TET2:p.Gln232Ter[5.0%],TET2:p.Asn535LysfsTer6[2.7%],U2AF1:p.Gln157Arg[20.6%],U2AF1:p.Ser34Tyr[21.4%]	NA	NA	0	0	U2AF1:p.Q157R[24.1%],U2AF1:p.S34Y[30.0%]	NA	Good	NK	NA	Y
207247	MDS	BM	unsuccessful	DNMT3A:p.Val563Met[4.0%]	NA	NA	0	0	0	NA	Good	NK	NA	Y
332282	AML	BM	47,XX,+8[20]	None detected	NA	Intermediate	+8[77.9%]	t(9;11)(p21.3;q23.3)[34.5%],t(9;11)(p21.3;q23.3)[26.2%]	0	Intermediate	NA	t(9;11)(p21.3;q23.3)[34.5%],t(9;11)(p21.3;q23.3)[26.2%]	N	NA
516070	AML	BM	46,XY[13]	CUX1:p.Gln623Ter[4.3%],EZH2:p.Val626Met[4.9%],SRSF2:p.Phe62Val[4.6%],ASXL1:p.Gly646TrpfsTer12[5.8%]	NA	NA	0	0	CUX1:p.Q623*[8.7%],ASXL1:p.G646Wfs*12[4.8%]	Adverse	NA	NK	Y	NA
183114	AML	BM	unsuccessful	ASXL1:p.Gly646TrpfsTer12[40.1%]	NA	NA	0	t(9;11)(p21.3;q23.3)[50.0%]	ASXL1:p.G646Wfs*12[52.4%]	Intermediate	NA	t(9;11)(p21.3;q23.3)[50.0%]	Y	NA
663125	AML	BM	no growth	DNMT3A:p.Ala410Ser[2.57%],SF3B1:p.Asp907His[0.85%],TP53:p.His179Tyr[1.97%],TP53:p.Arg158Gly[17.85%],STAG2:[3.86%]	NA	Adverse	del(5)(q14.3q33.2)[22.0%],del(11)(p15.4pter)[19.5%],del(12)(p12.1pter)[21.0%],del(17)(p12pter)[14.7%],del(17)(q11.2q21.32)[14.9%],+18[23.4%],del(18)(q21.1qter)[14.0%],gain(19)(q13.12qter)[42.1%],gain(21)(q11.2q21.1)[32.5%],del(21)(q21.1q22.11)[16.7%],gain(21)(q22.11qter)[36.4%]	0	0	Adverse	NA	Complex	N	NA

Blank cells, ‘0’, or ‘NA’ indicate no data.
Downloadable version with more information can be found here: https://wustl.box.com/v/rapidclinicalwgs-tables8

Table S9. Results and clinical outcomes for 101 AML patients with determined risk

UPN	Age	Gender	Ethnic	Race	FAB	%BM.Blast	WBC	%PB.Blast	Treatment	Cytogenetics ISCN.Line	Conventional ELN.Risk	WGS.CNAs	WGS Recurrent.SVs	WGS.ELN.Risk	Time.to.relapse.or.last.follow.up	Time.to.transplant	Time.to.expire.or.last.follow.up	Relapsed	Transplanted	Expired
103744	67	F	NH	C	M0	62	0.9	6	7+3, uproleselan on A041701	46,XX[3]	Adverse	del(3)(p11.2pter)[61.8%],+5[76.7%],del(5)(q11.2qter)[60.6%],-7[57.2%],+8[57.6%],+9[52.3%],gain(15)(q11.2qter)[43.2%],del(16)(q21qter)[58.5%],del(17)(p13.1pter)[53.0%],+18[43.5%],gain(22)(q11.21q12.3)[64.0%]	0	Adverse	16		16	0	0	1
104895	60	F	NH	AA	M2	32	2	24.3	7+3	46,XX,del(3)(q12)[16]/46,XX[4]	Intermediate	del(3)(q13.11q26.33)[23.6%]	0	Intermediate	398	77	398	1	1	1
142083	50	F	NH	C	M2	27	2.5	3	7+3	unknown	Adverse	del(5)(q13.3qter)[88.6%],del(7)(q11.22qter)[87.6%],del(11)(q14.1q14.2)[89.5%],del(12)(p12.1pter)[88.7%],gain(13)(q12.11q12.3)[57.9%],del(13)(q12.3q22.3)[88.3%],gain(13)(q31.1q33.1)[100.6%],del(16)(q23.1qter)[87.4%],del(17)(p13.1pter)[84.6%],del(18)(q21.31qter)[87.8%],del(19)(q12q13.41)[84.5%],gain(21)(q11.2qter)[88.0%],del(X)(p22.12pter)[89.4%]	0	Adverse			18	0	0	1
142194	20	M	NH	C	M4	52	18.6	0	7+3+Mylotarg	46,XY,inv(16)(p13.1q22)[13]/46,XY[7]	Favorable	0	inv(16)(q22.1p13.11)[29.8%],inv(16)(q22.1p13.11)[19.7%]	Favorable	733		733	0	0	0
142639	45	F	NH	C	M5	96	18.7	13.5	7+3	46,XX[19]/46,XX,+mar[1]	Intermediate	del(7)(q22.1qter)[60.0%],del(10)(q22.2q22.3)[58.6%],gain(13)(q21.32qter)[56.6%]	0	Adverse	40		102	1	0	1
155912	56	F	NH	C	M2	38	32.4	29.5	7+3	46,XX,der(3)t(3;6)(q25;q13),der(6)t(3;6)(q25;q13)t(6;8)(p23;q13)[19]/46,XX[1]	Intermediate	del(3)(p12.2p14.1)[76.6%],del(6)(p24.1pter)[75.1%],del(6)(q14.1q14.3)[77.6%],gain(8)(q12.1qter)[72.8%]	0	Adverse	34		34	1	0	0
187885	66	M	NH	AA	M1	78	39.4	66.7	7+3, midostaurin	46,XY[20]	Favorable	0	0	Favorable	148		148	0	0	0
188798	66	F	NH	C	nc	23	3.3	17	7+3, SOC on A0401701	47,XX,der(1)t(1;7)(q32;p13),del(5)(q22q35),-7,+8,del(12)(p11.2),der(13)del(13)(q14q14)inv(13)(p13q13),add(18)(p11.2),+19[4].	Adverse	del(5)(q21.3q33.3)[47.1%],del(7)(q11.23q36.1)[47.5%],+8[41.3%],del(12)(p11.21p13.2)[42.2%],del(18)(p11.23pter)[38.7%],+19[37.5%]	0	Adverse	182	90	182	0	1	0
192545	47	F	NH	C	M4	71	59.2	11	idarubicin, cytarabine, vorinostat	no growth	Favorable	0	inv(16)(q22.1p13.11)[25.6%]	Favorable	342		591	1	0	1
200915	53	M	NH	C	M0	23	2.9	0	7+3	46,XY[20]	Intermediate	0	0	Intermediate	1125		1125	0	0	0
206801	60	F	NH	C	M2	24	24	1.5	7+3	46,XX[20]	Adverse	0	0	Adverse	989	87	989	0	1	0
211740	73	F	NH	C	2ndary	28	3.8	0	Hypomethylating agents	46,XX,t(3;3)(q21;q26.2)[20]	Adverse	0	gain(3)(q21.3q26.2)[23.1%],del(3)(q21.3q26.2)[26.5%]	Adverse	209		209	0	0	0
242129	51	F	NH	AA	M4	39	50.3	39	7+3	44~46,XX,del(11)(q23),der(19)?t(11;19)(q23;p13.1)[cp11]/44~45,XX,-19[cp4]/46,XX[5]	Adverse	0	t(11;19)(q23.3;p13.11)[29.8%]	Adverse	112	230	112	0	1	0
250911	59	M	NH	C	M1	89	36.1	97.7	7+3	46,XY[20]	Intermediate	0	0	Intermediate	1253		1253	0	0	0
258135	22	F	NH	C	M2	55	51.8	70	7+3	46,XX,inv(16)(p13q22)[5]/46,idem,t(3;3)(p13;q?28)[5]/46,XX[6]	Favorable	gain(11)(q23.3qter)[15.0%]	inv(16)(q22.1p13.11)[36.5%]	Favorable	2995		2995	0	0	1
259112	75	M	NH	C	N/A	73	4.8	34	Hypomethylating agent (decitabine), Venetoclax	46,XY[20]	Intermediate	0	0	Intermediate	83		83	0	0	1
262878	55	F	NH	C	M5	46	26.9	12.7	7+3	46,XX[20]	Favorable	0	0	Favorable	112		112	0	0	0
267935	33	M	NH	C	M2	68	3.4	18.6	7+3, mylotarg	46,XY,inv(16)(p13.1q22)[6]/46,XY[4]	Favorable	0	inv(16)(q22.1p13.11)[38.8%],inv(16)(q22.1p13.11)[25.3%]	Favorable	194		194	0	0	0
275291	54	M	NH	C	M4	87	119.7	0	idarubicin, cytarabine, vorinostat	no growth	Favorable	0	inv(16)(q22.1p13.11)[22.5%],inv(16)(q22.1p13.11)[31.6%]	Favorable	273	344	526	1	1	1
275786	43	M	NH	C	M2	40	4.3	39	7+3+3	45,X,-Y,t(8;21)(q22;q22)[19]/46,XY[1]	Favorable	-Y[38.7%]	t(8;21)(q21.3;q22.12)[26.6%],t(8;21)(q2	Favorable	3624		3624	0	0	1

													1.3;q22.12)[19.5%]							
285982	49	M	NH	C	M4	29	62.8	39	7+3	46,XY,t(16;22)(q22;q13)[10]	Favorable	0	inv(16)(q22.1p13.11)[33.3%]	Favorable			3081	0	0	0
293825	71	F	NH	C	M5	47	32.7	0	7+3, midostaurin	46,XX[21]	Favorable	0	0	Favorable	158	115	158	0	1	0
296442	59	M	NH	C	M0	76	30.8	81	liposomal daunorubicin/cytarabine	46~52,XY,-3,?add(5)(q3?3),del(7)(q22q34),-10,-13,-22,+2~9mar[cp20]	Adverse	del(3)(p11.2pter)[94.2%],del(3)(q12.2q13.12)[89.9%],del(3)(q13.32q23)[93.7%],del(3)(q25.33q26.2)[93.8%],del(3)(q27.3qter)[94.1%],del(7)(q21.11qter)[94.3%],gain(13)(q12.11q14.11)[443.9%],del(13)(q14.11q21.33)[87.9%],gain(13)(q21.33q31.3)[476.9%],del(13)(q31.3qter)[93.4%]	0	Adverse	138		212	1	0	1
312088	57	M	NH	C	M2	68	28.4	30.2	7+3	47,XY,+21[17]/46,XY[3]	Favorable	gain(21)(q11.2qter)[88.6%]	0	Favorable	98		98	1	0	1
319590	26	F	NH	C	M2	36	3.2	0	7+3	87,<4n>,XXXX,-2,-5,-8,-11,-12,-14,-16,+2mar[1]/46,XX[19] FISH:tetrasomy9q(41.5%),tetrasomy22q(41.5%),tetrasomy15q(45%),trisomy16q(46%),tetrasomy17q(45%)	Adverse	gain(1)(p12p34.3)[24.2%],gain(1)(q25.2qter)[25.7%],del(2)(q34qter)[50.8%],del(5)(q31.3q33.2)[53.2%],gain(5)(q33.2q34)[48.6%],del(5)(q35.1qter)[44.3%],gain(6)(q22.33qter)[50.7%],del(9)(p13.1pter)[52.2%],del(11)(q12.2qter)[50.2%],del(12)(q23.1q24.21)[49.4%],del(13)(q12.11q31.1)[28.0%],gain(13)(q31.1qter)[23.5%],del(14)(q12q21.3)[51.9%]	0	Adverse	476	145	476	1	1	0
325191	44	F	NH	C	M2	35	44	32.4	7+3(Ida)	46,XX,t(11;20)(p15;q11.2)[20]	Favorable	0	t(11;20)(p15.4;q12)[31.2%],t(11;20)(p15.4;q12)[25.5%]	Favorable	1184	142	1184	0	1	0
327472	24	F	NH	C	M0	80	4.8	49.1	7+3	46,XX,t(9;11)(p21;q23)[10]/47,idem,+21[7]/46,XX[3]	Intermediate	gain(21)(q11.2qter)[33.8%]	t(9;11)(p21.3;q23.3)[22.8%],t(9;11)(p21.3;q23.3)[28.2%]	Intermediate	268	117	268	0	1	1
335141	72	M	NH	Oth	M1	89	14.1	59.3	7+3	46,XY, add(2)(q37)[6]	Adverse	del(2)(q36.3qter)[89.1%],gain(11)(q13.4qter)[90.2%]	0	Adverse	265		265	0	0	0
347494	36	M	NH	C	M5	60	29.7	49.1	7+3	47,XY,+8[5]/47,idem,inv(16)(p13.1q22)[15]	Favorable	+8[86.8%]	inv(16)(q22.1p13.11)[26.2%],inv(16)(q22.1p13.11)[26.5%]	Favorable	669		669	0	0	0
375074	70	M	NH	C	M5	78	67.4	21.9	7+3, uproleselan on A041701	45,XY,del(1)(p36.2),-7[18]/46,XY[2]	Adverse	del(1)(p35.1p36.32)[56.8%],-7[63.2%]	0	Adverse	333		333	0	0	0
380949	59	F	NH	C	M5	95	12.1	0	7+3+3	45,X,-X[21]/46,XX[9]	Intermediate	-X[88.4%]	t(10;11)(p12.31;q23.3)[32.1%]	Adverse	346		359	1	0	1
391518	52	M	NH	C	M4	90	11.8	0	7+3	46,XY[21]	Favorable	0	0	Favorable	575		575	0	0	0
410110	87	F	H	C	M0	86	7.7	51.3	Hypomethylating agents	48,XX,+13,+13[7]/50,idem,+X,-13,+15,+19[2]/46,XX[7]	Adverse	gain(13)(q12.11qter)[87.1%],gain(15)(q11.2qter)[38.2%],+19[38.3%],+X[32.8%]	0	Adverse	107		107	0	0	1
410324	60	M	NH	C	M5	94	6.7	30	7+3	52~54,XY,+2,+4,+6,+8,del(11)(q23),+19,+19,+21[17]/46,XY[3]	Adverse	+2[59.0%],+4[56.4%],+6[57.7%],+8[59.0%],gain(11)(q23.3qter)[71.0%],+19[146.2%],gain(21)(q11.2qter)[60.6%]	t(6;11)(q27;q23.3)[37.9%],t(6;11)(q27;q23.3)[32.7%]	Adverse	4299	116	4299	0	1	0
429293	35	F	NH	C	M0	48	0.8	11.5	7+3	47,XX,+8[7]/46,XX[13]	Adverse	+8[50.3%]	0	Adverse	275		275	0	0	0
462268	23	M	NH	C	M2	54	3	31	7+3, mylotarg	46,XY,t(8;21)(q22;q22)[4]/46,idem,inv(18)(p11.2q21.3)[13]	Favorable	0	t(8;21)(q21.3;q22.12)[26.3%],t(8;21)(q21.3;q22.12)[28.6%]	Favorable	202		202	0	0	0
463352	25	M	NH	C	M2	72	11	50	7+3+3	45,X,-Y,t(8;21)(q22;q22)[13]/45,idem,del(9)(q22q32)[7]	Favorable	del(9)(q21.11q31.1)[70.5%],-X[99.5%]	t(8;21)(q21.3;q22.12)[23.1%],t(8;21)(q21.3;q22.12)[19.7%]	Favorable	3777		3777	0	0	0
465146	39	M	NH	C	M5	60	35.4	44.3	7+3	47,XY,+8[19]/46,XY[1]	Favorable	+8[67.3%]	0	Favorable	21		58	1	0	1
467399	34	M	NH	AA	M5	65	88.7	49.6	7+3	46,XY[20]	Favorable	0	0	Favorable	225		225	0	0	0
467825	27	F	NH	C	M2	43	9.8	0	7+3(Ida)	47,XX,del(7)(q22),+8[20]	Adverse	del(7)(q21.3q36.1)[92.7%],+8[66.1%]	0	Adverse	966	170	966	0	1	0
477377	50	M	NH	C	M2	64	1.8	50.4	7+3	46,XY[20]	Intermediate	0	0	Intermediate	278		278	0	0	0
480059	86	F	NH	C	2ndary	75	212	56	Hypomethylating agent (decitabine), Venetoclax	46,XX,t(4;7)(q25;q22)?c[20]	Favorable	del(7)(q22.1q22.1)[90.7%]	0	Favorable	4		4	0	0	1
491972	50	M	NH	C	M5	24	3.7	14.3	7+3	46,XY[20]	Favorable	0	0	Favorable	214		214	0	0	0
493436	45	F	NH	C	N/A	73	25.9	5.3	7+3	46,XX,t(2;15)(q23;q15)[11]/46,XX[9]	Adverse	0	0	Adverse	298	76	298	0	1	0
499829	59	M	NH	C	M5	49	91	5.2	7+3	47,XY,+8[2]/46,XY[18]	Favorable	gain(3)(q13.33qter)[8.1%],+8[8.4%]	0	Adverse	7		819	1	0	0

504394	64	M	NH	C	M2	22	96	18	7+3	47,XY,+8[8]	Intermediate	+8[85.8%]	0	Adverse	33		84	1	0	1
506517	64	F	NH	C	M1	88	84.4	84.3	7+3, midostaurin	46,XX[20]	Intermediate	0	0	Intermediate	180		180	0	0	0
509179	38	M	NH	C	M5	79	154.5	14.2	7+3	46,XY[20]	Favorable	0	0	Favorable	1023		1023	0	0	0
525644	77	M	NH	C	wMDS	39	9.7	34	Vyxeos	46,Y,t(X;15)(q25;q22),der(3;21)(q10;q10),del(5)(q22q33),der(6)add(6)(p23)t(3;6)(q25;p21),del(12)(p13),+21[cp20]	Adverse	del(5)(q23.2q31.3)[80.6%],del(6)(p22.3p25.1)[82.1%],del(6)(q23.2q23.3)[82.9%],del(12)(p13.1p13.32)[80.7%],del(12)(q21.33q22)[81.3%]	0	Adverse	55		55	0	0	0
537017	69	M	NH	C	M6	68	3.5	0	Hypomethylating agents	74<3N>,XXY,+1,?add(1)(p22),+2,+3,+6,-19,+21,+22[1]/82<4N>,XXYY,-1,?add(1)(p22),-2,-3,-4,-5,-7,-11,add(11)(q13),-12,-13,-14,-15,-16,-17,-18,-18,-19,add(19)(q13.3),-21,-22,+8mar[1]/46,XY[18].	Adverse	gain(1)(p32.1p35.2)[26.1%],-4[14.5%],-5[30.4%],+6[32.3%],-7[13.3%],gain(8)(q21.11qter)[18.8%],-11[21.3%],-12[11.3%],gain(13)(q12.11qter)[28.5%],-16[29.2%],del(17)(p12pter)[28.7%],+19[32.2%],gain(21)(q11.2qter)[17.8%]	0	Adverse	83		83	0	0	1
553902	63	M	NH	C	wMDS	12 flo-36%	20.6	6.1	Vyxeos and then hypomethylating agent (decitabine), Venetoclax	49,XY,+1,del(5)(q13q33),+8,-16,add(17)(p13),der(17)del(17)(p12)del(17)(q11.1q12),+21,+21[18]/50,idem,+mar[2]	Adverse	gain(1)(p31.1p36.32)[82.9%],+1[67.1%],del(5)(q11.2q34)[82.9%],+8[80.5%],del(16)(q23.1qter)[83.1%],del(17)(p13.1pter)[78.8%],gain(21)(q11.2qter)[116.7%]	0	Adverse	173		173	0	0	0
557196	54	M	NH	C	M5	78	67.4	21.9	7+3	46,XY[20]	Adverse	0	0	Adverse	332		332	0	0	0
578200	38	M	NH	C	M1	69	9.3	52.7	7+3	46,XY[20]	Favorable	del(9)(p13.3p21.3)[11.6%]	0	Favorable	275	374	275	1	1	0
586748	58	M	NH	C	M0	73	2.6	37.2	7+3	46,XY[20]	Intermediate	0	t(7;21)(p22.1;q22.12)[23.1%]	Intermediate	360	112	360	0	1	0
595704	67	F	NH	C	M4	69	37	61	7+3	46,XX,inv(16)(p13q22)[19]/46,XX[1]	Favorable	0	inv(16)(q22.1p13.11)[31.5%],inv(16)(q22.1p13.11)[38.3%]	Favorable	4244		4244	0	0	0
607160	49	F	NH	C	M2	61	7.6	42.7	7+3	46,XX[20]	Intermediate	0	0	Intermediate	1074		1074	0	0	0
616274	36	F	NH	C	M5	87	2.9	17	7+3	47,XX,+8[7]/46,XX[13]	Intermediate	+8[23.6%]	t(9;11)(p21.3;q23.3)[19.7%],t(9;11)(p21.3;q23.3)[20.8%]	Intermediate	178		274	1	0	1
618671	56	F	NH	C	M1	66	7.7	48.7	7+3(Ida) soc	46,XX[20]	Favorable	0	0	Favorable	1383		1383	0	0	0
623930	56	F	NH	C	M2	68	23.6	43	7+3	46,XX[20]	Favorable	0	0	Favorable	929		929	0	0	0
653268	44	M	NH	C	M5	66	76.3	8	7+3	46,XY[20]	Favorable	0	0	Favorable	149		149	0	0	0
654925	48	M	NH	C	M1	80	22.9	89.7	7+3	46,XY[20]	Favorable	0	0	Favorable	138		138	0	0	0
662555	50	M	NH	C	M1	67	80.9	54.203	7+3	46,XY[20]	Intermediate	0	0	Intermediate	193		760	1	0	0
666013	80	F	NH	C	M1	45	1.9	24.5	Hypomethylating agent (azacitidine), Venetoclax	46,XX,del(3)(?p24)[10]/46,XX[10]	Adverse	del(5)(q31.2q31.2)[10.1%]	0	Adverse	18		18	0	0	1
668971	56	M	NH	C	M5	81	2	2	7+3	45~47,XY,+8[cp10]	Intermediate	0	0	Intermediate			4817	0	0	0
672014	60	M	NH	C	M5	77	28.3	0	7+3	46,XY[20]	Favorable	0	0	Favorable	988	88	988	1	1	1
675128	51	M	NH	C	nc	13 dilute	1.3	10.5	7+3(Ida), fail then 5+2	46~49,XY,add(5)(q13),del(5)(q33),+6,add(6)(q13),-7,+8,+9,+10,-17,+19,+1~2mar[cp19]/46/XY[1]	Adverse	del(7)(q21.11qter)[82.3%],-17[78.2%],gain(17)(q22qter)[51.8%],+20[42.5%],del(20)(q11.21q13.32)[79.2%]	0	Adverse	422		422	0	0	1
677322	55	M	NH	C	M2	50	3.6	32.8	7+3	46,XY[20]	Favorable	0	0	Favorable	358	161	358	0	1	0
677982	68	M	NH	C	M5	88	60.4	84.2	7+3, uproleselan on A041701	47,XY,+i(21)(q10)[14]/47,XY,+21[2]/46,XY[4]	Intermediate	gain(21)(q11.2qter)[173.8%]	t(6;11)(q27;q23.3)[28.8%]	Adverse	37		37	0	0	1
679540	75	F	NH	C	M0	74	2.8	2	Hypomethylating agent (decitabine), Venetoclax	46,XX,inv(3)(q21q26.1)[3]/45,sl,der(16;17)(p10;q10)[4]/46,sdl,+13[5]/46,XX[8]	Adverse	del(16)(q11.2qter)[81.4%],-17[78.9%]	inv(3)(q21.3q26.2)[29.2%],inv(3)(q21.3q26.2)[30.6%]	Adverse	278		278	0	0	0
692900	39	M	NH	C	M0	83	5	53	7+3+3	47,XY,del(5)(q22q33),+5,t(10;11)(p13~p15;q22~23),i(17)(q10)[3]/46,XY[17]	Adverse	+4[72.1%],del(5)(q31.1q33.1)[77.6%],del(17)(p11.2pter)[72.2%],gain(17)(q11.2qter)[89.0%]	t(10;11)(p12.31;q14.2)[18.0%],t(10;11)(p12.31;q14.2)[17.1%]	Adverse	5772	189	5772	0	1	0
704854	55	M	NH	C	M4	32	8.3	0	7+3	46,XY[20]	Adverse	0	0	Adverse	58		281	1	0	0
706350	41	F	NH	C	M1	37	1.6	0	7+3	46,XX[20]	Intermediate	0	0	Intermediate	964	94	964	0	1	0
717042	48	M	NH	C	M0	50	25.5	64.9	CLAG + midostaurin	46,XY[20]	Intermediate	0	0	Intermediate	132		132	0	0	0

726806	75	F	NH	C	M1	88	49.6	87.4	Hypomethylating agent (decitabine), Venetoclax	46,XX[20]	Adverse	0	0	Adverse	181		181	1	0	0
736399	82	F	NH	C	M1	93	87.9	85.5	Hypomethylating agent (azacitidine), Venetoclax	46,XX[20]	Favorable	0	0	Favorable	79		79	0	0	0
791810	47	M	NH	C	M4/5	34	32.6	24.8	7+3(Ida)	46,XY,inv(16)(p13.1q22)[7]/47,idem,+22[9]/46,XY[4]	Favorable	gain(22)(q11.21qter)[41.2%]	inv(16)(q22.1p13.11)[18.9%],inv(16)(q22.1p13.11)[25.8%]	Favorable	1191		1191	0	0	0
809382	63	F	NH	C	M2	79	39.3	73.5	7+3, uproleselan on A041701	46,XX[20]	Favorable	0	0	Favorable	214	222	214	0	1	0
819978	75	M	NH	C	N/A	35	2.6	15.5	Hypomethylating agent (azacitidine), cytarabine	60~65<3n>,XXYY,+1,-2,-4,+6,add(6)(p22),-7,-8,-11,-12,add(12)(p11.2),-13x3,-14,-15,-17,-18,-19,+20,+21,-22,-22,+1~4mar[cp13]/86<4n>,XXXXYYY,-2,-3,-4x2,+6,add(6)(p22),-7x2,-8,-10x2,-11,-13x2,-14,-15,+16,+3mar[1]/46,XY[6]	Adverse	+1[55.9%],-2[27.8%],-4[30.9%],+6[57.3%],-7[27.7%],-8[16.7%],-11[28.5%],-12[25.0%],del(13)(q12.11qter)[35.3%],del(15)(q11.2qter)[30.4%],gain(21)(q11.2qter)[36.7%],del(22)(q11.21qter)[18.5%],+Y[27.2%]	0	Adverse	21		21	0	0	1
847670	58	M	NH	C	M2	34	9.1	40.4	7+3(Ida) +Mylotarg +Midostaurin	46,XY,der(X)t(8;21)(q22;q22)t(X;21)(q28;?q22),der(8)t(8;21)(q22;q22),der(21)t(8;21)(q22;q22)t(X;21)(q28;?q22)[18]/46,XY[2]	Favorable	del(9)(q21.11q31.1)[13.2%],-Y[15.4%]	t(8;21)(q21.3;q22.12)[26.5%],t(8;21)(q21.3;q22.12)[27.9%]	Favorable	706	627	706	0	1	0
856681	56	F	NH	C	M0	91	130.7	89	7+3	46,XX,del(7)(q32)[4]	Intermediate	+7[92.3%],del(7)(q11.21qter)[93.8%]	0	Intermediate		125	1676	0	1	0
869318	68	F	NH	C	M4	23	12.8	4.5	7+3, uproleselan on A041701	46,XX,?t(12;16)(q24.3;q22)[4]/46,XX[4]	Favorable	0	inv(16)(q22.1p13.11)[32.5%]	Favorable	79		79	0	0	0
875579	71	F	NH	C	2ndary	20	1.2	6.3	Hypomethylating agent (decitabine), Venetoclax	47,XX,t(3;21)(q26;q22),del(7)(q32),+14[19]/46,XX[1]	Adverse	del(7)(q33q36.2)[46.7%],gain(14)(q11.2qter)[46.2%]	t(3;21)(q26.2;q22.12)[6.5%],t(3;21)(q26.2;q22.12)[11.4%]	Adverse	17		17	0	0	1
879308	39	M	NH	C	N/A	15	21	3.5	7+3	46,XY[20]	Intermediate	0	0	Intermediate	460	165	460	0	1	0
887041	64	M	NH	C	M0	71	18.2	33.9	7+3	46,XY[20]	Adverse	0	0	Adverse	168	159	168	0	1	0
895870	63	F	NH	C	M2	62	49	86.4	7+3, SOC on A0401701	46,XX[20]	Favorable	0	0	Favorable	318		318	0	0	0
902503	70	M	NH	C	wMDS	22	5.8	51	Vyxeos	46,XY[20]	Adverse	0	0	Adverse	353	158	353	0	1	0
905861	58	M	NH	C	wMDS	16	1.9	20	7+3	44,XY,-3,del(5)(q23),add(7)(q11.2),-9 ,-10,-14,-15,del(16)(q21),der(19)t(4;19)(q11.2;q13.3),+1~3mar[cp17]/44,idem,+1,add(2)(p21),-del(16)(q21),+2~7mar[cp8]	Adverse	-3[92.1%],del(5)(q11.2qter)[92.1%],del(7)(q11.23qter)[92.8%],del(15)(q21.2q22.32)[93.4%],gain(19)(q13.33qter)[90.2%]	0	Adverse	139	74	139	0	1	0
907523	53	M	NH	C	M1	94	212.5	78.2	7+3(Ida)	46,XY[20]	Intermediate	0	0	Intermediate	82	167	82	1	1	0
907716	54	M	NH	C	M5	91	0.7	0	7+3	47,XY+8[17]/46,XY[3]	Intermediate	+8[74.5%]	t(9;11)(p21.3;q23.3)[32.7%],t(9;11)(p21.3;q23.3)[34.0%]	Intermediate	1151		1151	0	0	0
922771	20	M	NH	C	M2	21	13.8	26.8	7+3, 5+2	46,XY,der(8)t(8;21}(q22;q22),der(12)t(8;12)(q22;p13)[6]	Favorable	0	t(8;21)(q21.3;q22.12)[32.6%]	Favorable	1134	194	1134	0	1	0
924089	28	F	NH	AA	M5	73	71.4	82.2	FLAG-IDA	46,XX,t(9;11)(p22;q23)[20]	Intermediate	0	t(9;11)(p21.3;q23.3)[27.3%],t(9;11)(p21.3;q23.3)[23.2%]	Intermediate	105		105	0	0	0
925086	37	F	NH	C	M5	57-flo mono	69.9	2.5	7+3	46,XX[20]	Favorable	0	0	Favorable	279		279	0	0	0
938927	53	F	NH	C	M0	73	34.8	76.5	7+3	46,XX[20]	Favorable	0	0	Favorable	923	85	923	0	1	0
946179	26	F	NH	C	M4	23 + mon 30	19	8.1	7+3	46,XX[20]	Favorable	0	0	Favorable	133		133	0	0	0
950919	51	M	NH	C	M2	65	211.1	77.4	7+3	47,XY,+4[20]	Intermediate	+4[88.0%]	0	Intermediate	896	207	896	1	1	0
956161	76	M	NH	C	wMDS	40	49.3	20	Hypomethylating agent (decitabine), Venetoclax	45,X,-Y[22]	Adverse	-Y[96.7%]	0	Adverse	250		250	0	0	0
976116	59	M	NH	C	nc	45	2.1	5.6	7+3	41~43,XY,der(1)t(1;17)(q12;q11.2),add(3)(p?13),add(5)(q11.2),add(5)(q11.2),-7,t(14;17)q(11.2;p13),-17,-18,add(19)(p13.3)add(21)(p11.2)[cp20]	Adverse	del(1)(p13.2p13.3)[71.6%],del(3)(p21.1pter)[71.6%],del(5)(q13.3q33.3)[72.8%],-7[71.6%],del(17)(p13.2pter)[68.2%],-18[71.5%],del(19)(p13.12p13.2)[66.6%],gain(19)(p13.11p13.12)[149.2%]	0	Adverse	647		647	0	0	0

978141	56	F	H	C	N/A	32	18.8	0	7+3	46,XX[20]	Favorable	0	0	Favorable	95		101	1	0	1
983349	47	M	NH	C	nc	48	2.5	15.2	7+3	42~43,XY,add(3)(q10),add(5)(q13),-7,-9,add(11)(p10),der(11)hsr(11)(q23),-12,add(16)(p11.2),add(16)(q12),-17,-18,+mar[cp20]	Adverse	del(3)(q11.2q24)[41.7%],gain(3)(q26.1qter)[34.1%],+5[30.3%],del(5)(q11.2q12.3)[79.7%],del(5)(q31.1qter)[74.3%],-7[41.3%],gain(9)(p13.3pter)[102.6%],del(11)(p11.2pter)[36.4%],gain(11)(q23.2qter)[110.4%],del(12)(q23.1q24.13)[77.2%],del(16)(q23.3qter)[75.1%],del(17)(p13.1pter)[75.3%],del(17)(q11.2q21.33)[29.8%],-18[46.0%],+19[36.6%],gain(21)(q11.2qter)[61.4%]	0	Adverse	24	118	24	1	1	0
991679	19	M	NH	C	M2	59	5.2	11	7+3	45,X,-Y[2]/45,idem,del(9)(q21q22)[3]	Intermediate	del(9)(q21.11q21.33)[23.2%],-X[95.9%]	0	Favorable			3532	0	0	0
994357	77	F	NH	C	2ndary	22	11	0	Hypomethylating agent (decitabine), Venetoclax	46,XX[20]	Intermediate	0	t(11;19)(q23.3;p13.11)[23.6%],t(11;19)(q23.3;p13.11)[28.5%]	Adverse	289		289	0	0	1

Blank cells, ‘0’, or ‘NA’ indicate no data.
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Table S10. Results and outcomes AML patients undetermined cytogenetic risk.

UPN	Age	Gender	Ethnic	Race	FAB	%BM.Blast	WBC	%PB.Blast	Treatment	Cytogenetics ISCN.Line	WGS.CNAs	WGS Recurrent.SVs	WGS Gene.mutations	WGS.ELN.Risk	Time.to.relapse.or.last.follow.up	Time.to.transplant	Time.to.expire.or.last.follow.up	Relapsed	Transplanted	Expired
143628	44	F	NH	C	M1	not done	77.6	90	7+3+3	unknown	0	0	IDH2:p.R140Q[48.1%],NPM1:p.W288Cfs*12[44.9%],FLT3:p.F594_N609dup[41.5%],FLT3:p.E598_Y599insFDFREYE[43.2%]	Intermediate			5648	0	0	0
167999	48	M	NH	C	M5	93	40.2	0	7+3	46,XY[12]	del(13)(q21.2q21.31)[96.6%]	0	DNMT3A:p.R882H[39.3%],KRAS:p.Q61L[41.7%],NPM1:p.W288Cfs*12[27.9%]	Intermediate	370		623	1	0	1
168973	65	F	NH	C	M4	84	19.6	3	7+3	46,XX[11]	0	0	DNMT3A:p.R882H[42.9%],TET2:p.E1874Sfs*13[10.0%],TET2:p.Y1998Sfs*25[34.4%],KRAS:p.G13D[15.9%],NPM1:p.W288Cfs*12[41.7%],FLT3:p.D593_L610dup[21.8%]	Intermediate	1147	84	1401	1	1	1
171485	66	M	NH	C	M5	40	78	17	7+3	unsuccessful	del(9)(q21.11q22.31)[85.8%]	0	DNMT3A:p.R882H[47.9%],KIT:p.D816V[12.7%],PTPN11:p.A72T[19.2%],PTPN11:p.P495S[31.9%],NPM1:p.W288Cfs*12[40.7%]	Favorable		175	719	0	1	0
183114	28	F	NH	C	M5	90	96.3	73.7	7+3	unsuccessful	0	t(9;11)(p21.3;q23.3)[50.0%]	ASXL1:p.G646Wfs*12[52.4%]	Intermediate	64		64	0	0	0
196785	59	M	NH	C	N/A	not done	33.2	22	7+3	unknown	0	0	DNMT3A:NA[39.5%],PTPN11:p.A72D[38.8%],NPM1:p.W288Cfs*12[41.1%],IDH2:p.R140Q[5.5%]	Favorable			965	0	0	1
220882	71	F	NH	C	M2	82	60	59	7+3	unsuccessful	0	0	NRAS:p.G12D[33.3%],DNMT3A:p.R882H[56.1%],IDH2:p.R140Q[56.6%],NPM1:p.W288Cfs*12[31.8%]	Favorable	242		314	1	0	1
229201	77	M	NH	C	M1	60	4.7	34.5	Hypomethylating agent (decitabine), Venetoclax	46,XY[5]	0	0	IDH2:p.R140Q[37.7%],NPM1:p.W288Cfs*12[15.5%],FLT3:p.S585_L601dup[14.0%]	Favorable	286		286	0	0	0
277960	76	F	NH	C	M1	79	25.5	91.9	7+3 + midostaurin	46,XX[11]	0	0	TET2:p.L615Sfs*24[36.4%],TET2:p.L1244Qfs*25[38.9%],TET2:p.R1572W[39.6%],BCOR:p.R763Q[50.0%],NPM1:p.W288Cfs*12[55.4%],FLT3:p.R595_F612dup[16.4%]	Intermediate			519	0	0	0
295	76	F	NH	AA	M2	48	61.6	88	no treatment	unknown	-X[6.6%]	0	ETV6:p.A28T[46.2%],IDH2:p.R140Q[36.4%],SRSF2:p.P95H[23.9%],NPM1:p.W288Cfs*12[37.3%]	Favorable			37	0	0	1
301733	76	M	NH	C	M2	68	3.9	3	7+3	unknown	0	0	NRAS:p.G12D[41.8%],TET2:p.D162Rfs*9[28.3%],JAK2:p.V617F[36.1%],ETV6:p.L277Sfs*23[43.1%],BCOR:p.Y393Lfs*47[71.1%],BCORL1:p.R1332*[63.2%],RUNX1:p.L98Sfs*24[30.9%]	Adverse			576	0	0	1
320036	60	F	NH	C	M2	dry tap	54.1	97	7+3	46,XX[3]	0	0	IDH1:p.R132S[38.6%],FLT3:NA[23.1%],FLT3:p.D600_L601insNEYFYVDFREYEYDLKWEFPRENLEFGD[8.3%],NPM1:p.W288Cfs*12[46.4%]	Intermediate			1179	0	0	1
332923	54	F	NH	C	nc	not done	46.1	4	7+3	46,XY[8]	0	0	NRAS:p.Q61K[25.0%],DNMT3A:p.R729W[34.4%],DNMT3A:p.A357Pfs*50[36.9%],NPM1:p.W288Cfs*12[25.5%]	Favorable			341	0	0	1
343604	66	F	NH	AA	M5	68	44	28.9	7+3	unsuccessful	+8[65.5%],del(12)(p12.1p13.2)[94.8%]	0	EZH2:NA[95.5%],KRAS:p.G13D[35.0%],ASXL1:p.G646Wfs*12[39.3%]	Adverse	337	116	337	0	1	0
433677	33	M	NH	AA	M2	4	3	3	7+3	unknown	gain(15)(q11.2q15.1)[82.4%],del(15)(q15.1q21.1)[77.1%],gain(15)(q21.1qter)[85.3%]	t(8;21)(q21.3;q22.12)[21.9%],t(8;21)(q21.3;q22.12)[30.2%]	0	Favorable	341		678	1	0	1
459785	24	F	NH	C	M0	84	32	90	7+3	46,XX[11]	0	0	FLT3:p.D835V[36.5%],STAG2:NA[57.7%]	Intermediate		114	3543	0	1	0
461513	39	F	NH	C	M5	91	33	75.9	7+3(Ida)	47,XX,+8[1]/46,XX[4]	+8[84.9%]	t(10;11)(p12.31;q23.3)[37.0%]	NRAS:p.G12D[25.0%],ASXL1:p.G646Wfs*12[25.5%],ASXL1:p.E1370G[49.2%]	Adverse	55	219	281	0	1	1
516070	51	M	NH	C	M0	25	2.7	0	7+3	46,XY[13]	0	0	CUX1:p.Q623*[8.7%],ASXL1:p.G646Wfs*12[4.8%]	Adverse	87		87	0	0	0
529324	68	F	NH	AA	M1	88	102.2	89	7+3(Ida)	unsuccessful	0	0	DNMT3A:p.R882H[50.8%],TET2:p.N338Kfs*2[47.5%],TET2:p.N752Rfs*59[45.8%],SRSF2:p.P95H[68.2%],CEBPA:p.S277*[46.2%],NPM1:p.W288Cfs*12[32.8%],FLT3:p.L601_K602insGLIDFREYEYDL[17.3%]	Intermediate			206	0	0	1
544583	26	F	NH	C	M5	dry tap	42.6	50	7+3	46,XX[11]	0	t(11;19)(q23.3;pter)[18.0%]	NF1:p.R1509H[54.0%]	Adverse	265	295	300	1	1	1
562600	60	M	NH	C	wMDS	dilute 20-flo	30.4	27.2	7+3	46,XY[9]	0	0	DNMT3A:p.R882C[39.7%],IDH2:p.R140W[11.3%],CEBPA:p.Q41*[17.0%],CEBPA:p.H24Afs*84[10.2%],NPM1:p.W288Cfs*12[51.5%],FLT3:p.R595_E596insDYVDFR[15.5%]	Intermediate	345		345	0	0	0

578613	70	M	NH	C	M1	80	9	41.7	azacitidine	46,XY[8]	0	0	TET2:p.S794*[38.9%],TET2:p.D1425*[42.6%],SUZ12:p.I525V[53.7%],NPM1:p.W288Cfs*12[42.4%]	Favorable	59		157	1	0	1
588094	57	M	NH	AA	M4	dry tap	70.2	24	7+3	unsuccessful	0	0	TET2:p.D527Efs*6[44.3%],TET2:p.T1047Lfs*9[50.0%],SUZ12:p.R439S[56.9%],SRSF2:p.P95L[37.5%]	Intermediate			2648	0	0	0
611521	64	M	NH	C	M5	85	89.5	46	7+3	49,XY,+3mar[2]/46,XY[2]	0	0	SMC3:p.G1118V[41.5%],FLT3:p.D835Y[55.8%],CEBPA:p.Q83Pfs*25[11.9%],NPM1:p.W288Cfs*12[41.7%]	Favorable		201	1123	0	1	0
622631	63	M	NH	C	N/A	dry tap	19.6	0	7+3	unknown	0	0	DNMT3A:p.R882H[40.5%],IDH2:p.R140Q[33.9%],SRSF2:p.P95L[51.0%],NPM1:p.W288Cfs*12[32.3%]	Favorable		161	173	0	1	1
652725	71	M	Unk	AA	M0	94	13.8	75	decitabine	unknown	gain(13)(q12.11qter)[7.3%]	0	DNMT3A:p.R882C[41.3%],TET2:p.M207Sfs*43[41.9%],RUNX1:p.R166*[35.1%],RUNX1:p.G165R[57.1%],U2AF1:p.Q157P[43.6%]	Adverse			58	0	0	1
721214	41	F	NH	C	M1	92	134.4	90	7+3	unsuccessful	0	0	DNMT3A:p.R882H[45.7%],GATA2:p.R361C[20.5%],FLT3:NA[26.4%],FLT3:p.F612_G613insEYDLKWEFPRENLEL[33.3%],FLT3:p.F612L[39.0%],NPM1:p.W288Cfs*12[48.6%]	Intermediate			170	0	0	1
723101	65	M	NH	C	M1	79	67.9	84	7+3	46,XY[15]	0	0	DNMT3A:p.R736H[51.9%],DNMT3A:p.G646V[39.2%],IDH2:p.R140Q[39.7%],FLT3:p.D600Gfs*30[8.8%]	Adverse		137	199	0	1	1
724606	72	F	NH	AA	M2	45	3	0	7+3	unknown	0	0	0	Intermediate			57	0	0	1
735764	76	M	NH	AA	M5	52	31.4	21	CLAG	46,XY[12]	0	0	DNMT3A:p.R882H[50.0%],FLT3:p.Y597_W603dup[44.9%],FLT3:p.V592_D593insGEVGAGSSDNEYFYV[60.9%],NPM1:p.W288Cfs*12[52.4%]	Intermediate	149		173	1	0	1
780327	58	M	NH	C	nc	65	31.6	81.2	7+3	46,XY[5]	0	0	CUX1:p.L173F[46.0%],CUX1:p.G709V[48.0%],IDH2:p.R140Q[41.2%],NPM1:p.W288Cfs*12[51.9%]	Favorable	372	163	372	0	1	0
816895	63	F	NH	C	nc	dry tap	170.6	91.9	7+3(Ida)	46,XX[5]	0	0	IDH2:p.R140Q[53.8%],NPM1:p.W288Cfs*12[45.3%],CEBPA:p.D80Gfs*28[50.0%],FLT3:p.V592_L610dup[10.5%],FLT3:p.F594_D600dup[9.8%]	Intermediate			1305	0	0	0
853337	70	F	NH	C	M2	67	12.4	48.2	7+3, uproleselan on A041701	46,XX[14]	0	0	DNMT3A:p.E523*[43.3%],SMC3:NA[48.0%],PTPN11:p.D61G[45.6%],NPM1:p.W288Cfs*12[38.3%],CEBPA:p.M15Afs*84[37.3%]	Favorable	160		160	0	0	0
875663	68	F	NH	C	M4	59	57.7	0	7+3 + sorafenib	unsuccessful	0	0	NRAS:p.G12D[26.0%],DNMT3A:p.A884V[39.7%],DNMT3A:p.L344R[35.5%],SF3B1:p.K700E[46.0%],TET2:p.Q659*[40.0%],TET2:NA[63.0%],FLT3:p.D835E[14.6%],BCOR:p.P326L[66.7%],NPM1:p.W288Cfs*12[28.3%]	Favorable	350	499	667	1	1	1
895959	80	M	NH	C	M7	29	0.8	0	lenalidomide	unknown	del(5)(q21.2q34)[20.8%],-7[20.8%],+8[15.1%],del(12)(p11.21pter)[21.8%],del(15)(q11.2q21.2)[19.7%],-18[18.1%],del(20)(q11.23qter)[19.4%]	0	TP53:NA[8.4%],TP53:p.H179Q[8.9%]	Adverse			100	0	0	1
898627	26	F	NH	C	M4	89	99.8	81	7+3(Ida)	46,XX[5]	-7[80.9%],+8[83.2%],del(12)(p12.2pter)[78.2%]	t(9;11)(p21.3;q23.3)[19.3%],t(9;11)(p21.3;q23.3)[18.4%]	CBL:p.D459_D460del[46.9%],TP53:p.P152Rfs*18[70.1%]	Adverse	62		154	1	0	1
960821	74	M	NH	C	M4	52	19.1	30	7+3	46,XY[10]	0	0	DNMT3A:p.R736H[54.7%],TET2:p.D162Vfs*9[45.3%],RAD21:p.Q613R[47.4%],U2AF1:p.S34F[42.4%],FLT3:p.W603_E604insDYVDFREYEYDLKW[22.2%]	Adverse			52	0	0	1
988026	61	M	NH	C	M5	90	87.1	32.8	CLAM	unsuccessful	0	0	DNMT3A:p.R882H[43.7%],NPM1:p.W288Cfs*12[38.9%],FLT3:NA[36.0%],FLT3:p.E598delinsVREYEYDLKWEFPRENLEFGK[11.8%]	Intermediate	39		84	1	0	1

Blank cells, ‘0’, or ‘NA’ indicate no data.

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