Impact of clinical, cytogenetic, and molecular profiles on long-term survival after transplantation in patients with chronic myelomonocytic leukemia

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SUPPLEMENTARY DATA for

Impact of clinical, cytogenetic, and molecular profiles on long-term survival after transplantation in patients with Chronic Myelomonocytic Leukemia

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Mutation analysis

Assays and analyses were developed and performed in conjunction with the Genomics & Bioinformatics Shared Resources at the Fred Hutchinson Cancer Research Center. After DNA extraction and NGS library construction, library size distributions were validated using an Agilent 2200 (Agilent Technologies, Santa Clara, CA, USA). Additional library quality control (QC), blending of pooled indexed libraries, and cluster optimization was performed using Life Technologies' Invitrogen Qubit 2.0 Fluorometer (Life Technologies-Invitrogen, Carlsbad, CA, USA). The Archer libraries were pooled (96-plex) and sequenced on an Illumina HiSeq 2500 in rapid-mode employing a paired-end, 150 base read length (PE150) sequencing strategy. We followed variant calling procedures as previously reported.\textsuperscript{1} Paired-end short reads were first aligned to the human genome reference assembly (GRCh37/hg19) using Burrows-Wheeler Aligner (BWA, v0.7.12).\textsuperscript{2} The resulting alignment data were further processed based on the best practice of Genome Analysis Toolkit (GATK, v3.5) (Broad Institute, Cambridge, Massachusetts, USA, \url{https://www.broadinstitute.org/gatk/}). The overview of sequence alignment statistics was computed for each sample using Samtools (v 1.0, http://samtools.sourceforge.net/). The sequence coverage was computed for each sample using GATK DepthOfCoverage, and the average of depth of coverage was 2556.5X. Variants were called using the standard variant caller GATK HaplotypeCaller, and annotated using Annovar (version 2015Mar22),\textsuperscript{3} and only variants covered by at least 2 independent high-quality reads (sequencing and mapping quality >20 and with no additional mismatches or indels in the same read) reporting a different base to the reference genome were analyzed for further evaluation. Mutations near polynucleotide tracks or with a clear read position or read orientation bias were removed. In parallel, the sequenced reads were analyzed through Archer analysis software (version 5.1.3) and common variants were entered for subsequent analysis. Variant calls supported by a variant allele frequency (VAF) of \( \geq 0.05 \) (5%) were cross-referenced against the Catalogue of Somatic Mutations in Cancer
(COSMIC) database (http://cancer.sanger.ac.uk/cosmic/). Missense, frameshift, or nonsense mutations at VAF > 0.05 and not present in COSMIC or within ±10 bases of a COSMIC mutation were reported only if they affected genes known to be targeted by somatic mutations at multiple sites throughout their length. Variants that were reported in dbSNP (www.ncbi.nlm.nih.gov/SNP), but not reported in the Catalogue of Somatic Mutations in Cancer (COSMIC, http://cancer.sanger.ac.uk/cancergenome/projects/cosmic/) and categorized tolerated or benign variants by SIFT (http://sift.jcvi.org/) or Polyphen (http://genetics.bwh.harvard.edu/pph2/), were excluded for variant calls. In addition, variants that are present in ExAC (http://exac.broadinstitute.org) at a population frequency > 0.1% were excluded unless they were a known somatic variant hotspot. All variants were visually inspected in Integrative Genomics Viewer (IGV, http://www.broadinstitute.org/igv/). In-house perl script was used to generate the final desired output. Mutational composites and ATRX and WT1 structural domains and associated mutations were generated by cBioPortal (http://www.cbioportal.org/tools.jsp).

References

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Supplementary Figures

Supplementary Figure S1. Clinical risk factors associated with relapse and overall mortality in patients with CMML following HCT. Relapse (A) by WHO classification and (B) by IPSS-R classification. Survival (C) by WHO classification, (D) by IPSS-R classification, (E) by CPSS and (F) by MDAPS, respectively. (G) Cumulative incidence of relapse and (H) survival by conditioning regimen.
Supplementary Figure S2. Molecular risk factors associated with HCT outcome (A) Mutation patterns in patients with CMML undergoing HCT. The plot represents the distribution and type of somatic lesions in genes mutated in ≥ 1% of patients. Each column represents an individual patient and each row a specific gene. Location of mutations and frequency (y axis) in ATRX (B), and in WT1 (C). The x axis represents position in the respective proteins.
Supplementary Figure S3. Molecular profiling and risk factors associated with HCT outcomes in patients with CMML. (A) Pairwise association of individual mutations and clinical features (blast count, cytogenetics, myeloproliferative type [MP], prognostic scoring systems MDAPS and CPSS). Associations are colored by odds ratio, corresponding to the scale bar. Mutations in signaling pathways frequently occurred with high blast counts in the MP-CMML category (Blue box). Mutations in epigenetic processes grouped separately and represent a distinct group, which was not associated with disease defined by unfavorable cytogenetics or elevated blast count (Black box, center). (B) Unsupervised clustering of individual patients depending upon high risk cytogenetics (Cytogenetics), functional groups of mutations (epigenetic regulators, signaling pathways and tumor suppressors [TP53/PPM1D]) and high mutation burden (total ≥10 mutations). Each row represents an individual patient. Prognostic scoring systems (MDAPS, CPSS and molecular CPSS) are depicted in separate columns, corresponding to the PS (prognostic score) risk scaling bar (group1). The status of variables (group 2; relapse, high risk cytogenetics (Cytogenetics), samples with ≥ 10 mutations) corresponds to the scaling bar of presence (light blue) or absence (dark blue). Number of mutations (group 3; Epigene = mutations in epigenetic regulators, Signaling = mutations in signaling pathways, TP53/PPM1D = mutations in TP53 or PPM1D) corresponds to the scaling bar of number of mutations. Diseases with high risk cytogenetics and higher mutation burden in epigenetic regulators as well as MDAPS and CPSS were significantly associated with relapse. Diseases with high mutation burden in epigenetic regulators were distinct from the high-risk group with complex cytogenetic abnormalities.
Supplementary Table S1. Genes in the mutation panel assay and their functional group

| Gene    | Function                  | Functional Group | Etc.         |
|---------|---------------------------|------------------|--------------|
| ABL1    | signaling pathway         | Signaling        |              |
| ANKRD26 | etc                       |                  | Mitochondria |
| ASXL1   | chromatin regulation      | Epigene          |              |
| ATRX    | chromatin regulation      | Epigene          |              |
| BCOR    | chromatin regulation      | Epigene          |              |
| BCORL1  | chromatin regulation      | Epigene          |              |
| BRAF    | signaling pathway         | Signaling        |              |
| BTK     | signaling pathway         | Signaling        |              |
| CALR    | signaling pathway         | Signaling        |              |
| CBL     | signaling pathway         | Signaling        |              |
| CBLB    | signaling pathway         | Signaling        |              |
| CBLC    | signaling pathway         | Signaling        |              |
| CCND2   | signaling pathway         | Signaling        |              |
| CDC25C  | signaling pathway         | Signaling        |              |
| CDKN2A  | signaling pathway         | Signaling        |              |
| CEBPA   | transcription factor       | TF               |              |
| CSF3R   | signaling pathway         | Signaling        |              |
| CUX1    | transcription factor       | TF               |              |
| CXCR4   | signaling pathway         | Signaling        |              |
| DCK     | signaling pathway         | Signaling        |              |
| DDX41   | chromatin regulation      | Epigene          |              |
| DHX15   | chromatin regulation      | Epigene          |              |
| DNMT3A  | methylation               | Epigene          |              |
| ETNK1   | etc                       |                  | Metabolic    |
| ETV6    | transcription factor       | TF               |              |
| EZH2    | chromatin regulation      | Epigene          |              |
| FBXW7   | transcription factor       | TF               |              |
| FLT3    | signaling pathway         | Signaling        |              |
| GATA1   | transcription factor       | TF               |              |
| GATA2   | transcription factor       | TF               |              |
| GNAS    | signaling pathway         | Signaling        |              |
| HRAS    | signaling pathway         | Signaling        |              |
| IDH1    | methylation               | Epigene          |              |
| IDH2    | methylation               | Epigene          |              |
| IKZF1   | transcription factor       | TF               |              |
**Supplementary Table S1.** Genes in the mutation panel assay and their functional group

| Gene   | Function                  | Functional Group | Etc.      |
|--------|---------------------------|------------------|----------|
| JAK2   | signaling pathway         | Signaling        |          |
| JAK3   | signaling pathway         | Signaling        |          |
| KDM6A  | chromatin regulation      | Epigene          |          |
| KIT    | signaling pathway         | Signaling        |          |
| KMT2A  | chromatin regulation      | Epigene          |          |
| KRAS   | signaling pathway         | Signaling        |          |
| LUC7L2 | splicing                 | Splicing         |          |
| MAP2K1 | signaling pathway         | Signaling        |          |
| MPL    | signaling pathway         | Signaling        |          |
| MYC    | signaling pathway         | Signaling        |          |
| MYD88  | signaling pathway         | Signaling        |          |
| NF1    | signaling pathway         | Signaling        |          |
| NOTCH1 | signaling pathway         | Signaling        |          |
| NPM1   | signaling pathway         | Signaling        |          |
| NRAS   | signaling pathway         | Signaling        |          |
| PDGFRA | signaling pathway         | Signaling        |          |
| PHF6   | transcription factor      | TF               |          |
| PPM1D  | tumor suppressor          | TS               |          |
| PTEN   | signaling pathway         | Signaling        |          |
| PTPN11 | signaling pathway         | Signaling        |          |
| RAD21  | cohesin                  | Cohesin          |          |
| RBBP6  | tumor suppressor          | TS               |          |
| RPS14  | etc                       | Ribosome         |          |
| RUNX1  | transcription factor      | TF               |          |
| SETBP1 | chromatin regulation      | Epigene          |          |
| SF3B1  | splicing                 | Splicing         |          |
| SH2B3  | signaling pathway         | Signaling        |          |
| SLC29A1| etc                       | Mitochondria     |          |
| SMC1A  | cohesin                  | Cohesin          |          |
| SMC3   | cohesin                  | Cohesin          |          |
| SRSF2  | splicing                 | Splicing         |          |
| STAG2  | cohesin                  | Cohesin          |          |
| STAT3  | transcription factor      | TF               |          |
| TET2   | methylation               | Epigene          |          |
| TP53   | tumor suppressor          | TS               |          |
### Supplementary Table S1. Genes in the mutation panel assay and their functional group

| Gene   | Function      | Functional Group | Etc. |
|--------|---------------|------------------|------|
| U2AF1  | splicing      | Splicing         |      |
| U2AF2  | splicing      | Splicing         |      |
| WT1    | chromatin regulation | Epigene        |      |
| XPO1   | signaling pathway | Signaling       |      |
| ZRSR2  | splicing      | Splicing         |      |

Seventy-five genes are listed and categorized by their function and functional group. The functional group was used in the analysis. Genes involved in DNA methylation and chromatin modification are grouped as epigenetic regulators (Epigene) in Functional Group column, and other functional groups remain the same as designated in Function column.
**Supplementary Table S2. Genetic Variants Identified in 52 patients with CMML Undergoing HCT**

| UPN  | Chr  | Start     | End       | Ref | Alt | Func. | Gen. | ExonicFunc. | AAChange.refGene | cytoBand |
|------|------|-----------|-----------|-----|-----|-------|------|-------------|------------------|----------|
| AC920| chr1 | 36932859  | 36932859  | C   | T   | exonic | CSF3R| nonsynonymous SNV | CSF3R:NM_000760:exon16:c.G2012A:p.G671D, CSF3R:NM_156039:exon16:c.G2012A:p.G671D, CSF3R:NM_173213:exon16:c.G2012A:p.G671D | 1p34.3 |
| AC920| chr11| 32456329  | 32456329  | G   | A   | exonic | WT1  | nonsynonymous SNV | WT1:NM_000378:exon1:c.G563T:p.A188V, | 11p13    |
| AC920| chr12| 1.13E+08  | 1.13E+08  | A   | T   | exonic | PTPN11| nonsynonymous SNV | PTPN11:NM_002834:exon11:c.A1342T:p.S448C | 12q24.13 |
| AC920| chr17| 74732959  | 74732959  | G   | T   | exonic | SRSF2| nonsynonymous SNV | SRSF2:NM_001195427:exon1:c.C563T:p.A188V, | 17q25.1 |
| AC920| chr17| 40475057  | 40475057  | C   | A   | exonic | STAT3 | nonsynonymous SNV | STAT3:NM_003150:exon20:c.G1853T:p.G618V, | 17q21.2 |
| AC920| chr20| 31022592  | 31022592  | C   | T   | exonic | ASXL1 | stopgain     | ASXL1:NM_005383:exon12:c.C2077T:p.R693X | 20q11.21 |
| AC920| chr4 | 1.06E+08  | 1.06E+08  | C   | T   | exonic | TET2  | nonsynonymous SNV | TET2:NM_001127208:exon11:c.G5977T:p.R1993W | 4q24    |
| AC920| chr4 | 1.06E+08  | 1.06E+08  | G   | A   | exonic | TET2  | nonsynonymous SNV | TET2:NM_001127208:exon11:c.G4918A:p.D1640N | 4q24    |
| AC920| chr8 | 1.18E+08  | 1.18E+08  | G   | A   | exonic | RAD21 | stopgain     | RAD21:NM_006265:exon11:c.C1444T:p.Q482X | 8q24.11 |
| AC920| chr9 | 1.34E+08  | 1.34E+08  | T   | A   | exonic | ABL1  | nonsynonymous SNV | ABL1:NM_005157:exon4:c.T557A:p.V186D, | 9q34.12 |
| AC920| chrX | 15822306  | 15822306  | A   | T   | exonic | ZRSR2 | stopgain     | ZRSR2:NM_005089:exon5:c.A385T:p.K129X | Xp22.2 |
| 93346| chr11| 1.19E+08  | 1.19E+08  | G   | A   | exonic | CBL   | nonsynonymous SNV | CBL:NM_005188:exon8:c.G1211A:p.C404Y | 11q23.3 |
| 93346| chr11| 1.19E+08  | 1.19E+08  | G   | T   | exonic | CBL   | nonsynonymous SNV | CBL:NM_005188:exon8:c.G1211T:p.C404F | 11q23.3 |
| 93346| chr17| 74732959  | 74732959  | G   | T   | exonic | SRSF2 | nonsynonymous SNV | SRSF2:NM_001195427:exon1:c.G563T:p.A188V, | 17q25.1 |
| 93346| chr17| 74732894  | 74732894  | G   | A   | exonic | SRSF2 | nonsynonymous SNV | SRSF2:NM_001195427:exon1:c.C349T:p.R117C, | 17q25.1 |
### Supplementary Table S2. Genetic Variants Identified in 52 patients with CMML Undergoing HCT

| UPN  | Chr   | Start  | End    | Ref | Alt | Func. refGene | Gene. refGene | ExonicFunc. refGene | AACchange.refGene | cytoBand |
|------|-------|--------|--------|-----|-----|---------------|---------------|--------------------|-------------------|----------|
| 93346| chr17 | 29560088 | 29560088 | C   | T   | exonic        | NF1           | stopgain           |                   | 17q11.2   |
| 93346| chr2  | 1.98E+08 | 1.98E+08 | C   | T   | exonic        | SF3B1         | nonsynonymous SNV  | SF3B1:NM_012433:exon15:c.G2128A:p.A710T | 2q33.1    |
| 91510| NA    | NA     | NA     | NA  | NA  | NA            | NA            | NA                 | NA                | NA       |
| 90541| chr1  | 1.15E+08 | 1.15E+08 | C   | T   | exonic        | NRAS          | nonsynonymous SNV  | NRAS:NM_002524:exon2:c.G38A:p.G13D       | 1p13.2    |
| 90541| chr9  | 1.39E+08 | 1.39E+08 | G   | A   | exonic        | NOTCH1        | nonsynonymous SNV  | NOTCH1:NM_017617:exon34:c.C6959T:p.L2320 | 9q34.3    |
| 88794| chr1  | 43818306 | 43818306 | T   | G   | exonic        | MPL           | nonsynonymous SNV  | MPL:NM_005373:exon12:c.T1771G:p.Y591D    | 1p34.2    |
| 88794| chr1  | 1.15E+08 | 1.15E+08 | C   | T   | exonic        | NRAS          | nonsynonymous SNV  | NRAS:NM_002524:exon3:c.G133A:p.V45I       | 1p13.2    |
| 88794| chr11 | 1.18E+08 | 1.18E+08 | C   | T   | exonic        | KMT2A         | nonsynonymous SNV  | KMT2A:NM_001195427:exon1:c.C284A:p.P95C,KMT2A:NM_001195427:exon1:c.C284A:p.P95C | 11q23.3   |
| 88794| chr17 | 74732959 | 74732959 | G   | T   | exonic        | SRSF2         | nonsynonymous SNV  | SRSF2:NM_001195427:exon1:c.C284A:p.P95C,SRSF2:NM_001195427:exon1:c.C284A:p.P95C | 17q25.1   |
| 88794| chr17 | 7573952  | 7573952  | G   | A   | exonic        | TP53          | nonsynonymous SNV  | TP53:NM_001126115:exon6:c.C679T:p.P227S,TP53:NM_001126115:exon6:c.C679T:p.P227S,TP53:NM_001126115:exon6:c.C679T:p.P227S,TP53:NM_001126115:exon6:c.C679T:p.P227S,TP53:NM_001126115:exon6:c.C679T:p.P227S,TP53:NM_001126115:exon6:c.C679T:p.P227S,TP53:NM_001126115:exon6:c.C679T:p.P227S,TP53:NM_001126115:exon6:c.C679T:p.P227S,TP53:NM_001126115:exon6:c.C679T:p.P227S,TP53:NM_001126115:exon6:c.C679T:p.P227S,TP53:NM_001126115:exon6:c.C679T:p.P227S,TP53:NM_001126115:exon6:c.C679T:p.P227S,TP53:NM_001126115:exon6:c.C679T:p.P227S,TP53:NM_001126115:exon6:c.C679T:p.P227S,TP53:NM_001126115:exon6:c.C679T:p.P227S,TP53:NM_001126115:exon6:c.C679T:p.P227S,TP53:NM_001126115:exon6:c.C679T:p.P227S,TP53:NM_001126115:exon6:c.C679T:p.P227S,TP53:NM_001126115:exon6:c.C679T:p.P227S,TP53:NM_001126115:exon6:c.C679T:p.P227S,TP53:NM_001126115:exon6:c.C679T:p.P227S,TP53:NM_001126115:exon6:c.C679T:p.P227S,TP53:NM_001126115:exon6:c.C679T:p.P227S,TP53:NM_001126115:exon6:c.C679T:p.P227S,TP53:NM_001126115:exon6:c.C679T:p.P227S,TP53:NM_001126115:exon6:c.C679T:p.P227S,TP53:NM_001126115:exon6:c.C679T:p.P227S,TP53:NM_001126115:exon6:c.C679T:p.P227S,TP53:NM_001126115:exon6:c.C679T:p.P227S,TP53:NM_001126115:exon6:c.C679T:p.P227S,TP53:NM_001126115:exon6:c.C679T:p.P227S | 17p13.1   |
| 88794| chr20 | 31022441 | 31022441 | -   | G   | exonic        | ASXL1         | frameshift insertion | ASXL1:NM_015338:exon12:c.1927dupG:p.G642fs | 20q11.21   |
| 88794| chr4  | 1.06E+08 | 1.06E+08 | GTC | AGG | exonic        | TET2          | frameshift deletion  | TET2:NM_001127208:exon11:c.5471_5480del:p.G1824fs | 4q24      |
| 84625| chr1  | 36932044 | 36932044 | C   | A   | exonic        | CSF3R         | nonsynonymous SNV   | CSF3R:NM_000760:exon17:c.G2425T:p.D809Y,CSF3R:NM_156039:exon17:c.G2506T:p.D836Y | 1p34.3    |
### Supplementary Table S2. Genetic Variants Identified in 52 patients with CMML Undergoing HCT

| UPN  | Chr  | Start  | End    | Ref | Alt | Func. refGene | Gene. refGene | Exonic Func. refGene | AAChange refGene | cytoBand |
|------|------|--------|--------|-----|-----|--------------|---------------|----------------------|-----------------|----------|
| 84625 | chr10 | 89711900 | 89711900 | G   | A   | exonic       | PTEN          | nonsynonymous SNV    | PTEN:NM_000314:exon6:c.G518A:p.R173H,PTEN:NM_001304717:exon7:c.G1037A:p.R346H | 10q23.31 |
| 84625 | chr2  | 2.09E+08 | 2.09E+08 | T   | A   | exonic       | IDH1          | nonsynonymous SNV    | IDH1:NM_001282386:exon3:c.A477T:p.D16V,IDH1:NM_005896:exon3:c.A477T:p.D16V | 2q34    |
| 84625 | chr20 | 31024354 | 31024354 | T   | A   | exonic       | ASXL1         | nonsynonymous SNV    | ASXL1:NM_015338:exon12:c.T3689A:p.R1232Q,ASXL1:NM_005896:exon12:c.T3689A:p.R1232Q | 20q11.21 |
| 84625 | chr4  | 1.06E+08 | 1.06E+08 | C   | T   | exonic       | TET2          | nonsynonymous SNV    | TET2:NM_001127208:exon11:c.C5977T:p.R1993W | 4q24    |
| 84625 | chr7  | 50467984 | 50467984 | C   | T   | exonic       | IKZF1         | stopgain             | IKZF1:NM_001282386:exon3:c.C529T:p.Q177X,IKZF1:NM_001282386:exon3:c.C529T:p.Q177X | 7p12.2  |
|       |      |         |         |     |     |              |               |                      | KZKF1:NM_001282386:exon4:c.C790T:p.Q264X,KZKF1:NM_001282386:exon4:c.C790T:p.Q264X |         |
|       |      |         |         |     |     |              |               |                      | KZKF1:NM_001282386:exon4:c.C664T:p.Q222X,KZKF1:NM_001282386:exon4:c.C664T:p.Q222X |         |
|       |      |         |         |     |     |              |               |                      | KZKF1:NM_001282386:exon4:c.C634T:p.Q212X,KZKF1:NM_001282386:exon4:c.C634T:p.Q212X |         |
|       |      |         |         |     |     |              |               |                      | KZKF1:NM_001282386:exon4:c.C958T:p.Q320X,KZKF1:NM_001282386:exon4:c.C958T:p.Q320X |         |
|       |      |         |         |     |     |              |               |                      | KZKF1:NM_001282386:exon5:c.C980T:p.Q268X,KZKF1:NM_001282386:exon5:c.C980T:p.Q268X |         |
|       |      |         |         |     |     |              |               |                      | KZKF1:NM_001282386:exon5:c.C790T:p.Q264X,KZKF1:NM_001282386:exon5:c.C790T:p.Q264X |         |
|       |      |         |         |     |     |              |               |                      | KZKF1:NM_001282386:exon5:c.C760T:p.Q254X,KZKF1:NM_001282386:exon5:c.C760T:p.Q254X |         |
|       |      |         |         |     |     |              |               |                      | KZKF1:NM_001282386:exon5:c.C928T:p.Q310X,KZKF1:NM_001282386:exon5:c.C928T:p.Q310X |         |
|       |      |         |         |     |     |              |               |                      | KZKF1:NM_001282386:exon6:c.C832T:p.Q278X,KZKF1:NM_001282386:exon6:c.C832T:p.Q278X |         |
|       |      |         |         |     |     |              |               |                      | KZKF1:NM_001282386:exon7:c.C1093T:p.Q365X,KZKF1:NM_001282386:exon7:c.C1093T:p.Q365X |         |
|       |      |         |         |     |     |              |               |                      | IKZF1:NM_001282386:exon7:c.C1093T:p.Q365X,IKZF1:NM_001282386:exon7:c.C1093T:p.Q365X |         |
|       |      |         |         |     |     |              |               |                      | IKZF1:NM_001282386:exon7:c.C1093T:p.Q365X,IKZF1:NM_001282386:exon7:c.C1093T:p.Q365X |         |
|       |      |         |         |     |     |              |               |                      | IKZF1:NM_001282386:exon7:c.C1093T:p.Q365X,IKZF1:NM_001282386:exon7:c.C1093T:p.Q365X |         |
|       |      |         |         |     |     |              | ASXL1         | nonsynonymous SNV    | ASXL1:NM_001282386:exon12:c.G3875A:p.G1292D,ASXL1:NM_001282386:exon12:c.G3875A:p.G1292D | 20q11.21 |
| 82825 | chr9  | 21994149 | 21994149 | G   | A   | exonic       | CDKN2A        | nonsynonymous SNV    | CDKN2A:NM_058195:exon1:c.C517T:p.R177X,CDKN2A:NM_058195:exon1:c.C517T:p.R177X | 9p12.13 |
| 82825 | chr10 | 89624271 | 89624271 | A   | T   | exonic       | PTEN          | nonsynonymous SNV    | PTEN:NM_000314:exon1:c.A45T:p.R151S,PTEN:NM_0019471:exon11:c.A564T:p.R188S | 10q23.31 |
| 82825 | chr11 | 32456329 | 32456329 | G   | A   | exonic       | WT1           | nonsynonymous SNV    | WT1:NM_000378:exon1:c.C563T:p.A188V,W1:NM_024424:exon1:c.C563T:p.A188V,W1:NM_024424:exon1:c.C563T:p.A188V | 11p13   |
| 82825 | chr12 | 1.12E+08 | 1.12E+08 | C   | T   | exonic       | SH2B3         | stopgain             | SH2B3:NM_005475:exon2:c.C130T:p.Q44X | 12q24.12 |
| 82825 | chr20 | 31024390 | 31024390 | G   | A   | exonic       | ASXL1         | nonsynonymous SNV    | ASXL1:NM_015338:exon12:c.G3875A:p.G1292D | 20q11.21 |
| UPN   | Chr | Start     | End       | Ref | Alt | Func. refGene | Gene. refGene | Exonic Func. refGene | AAChange refGene | cytoBand |
|-------|-----|-----------|-----------|-----|-----|---------------|---------------|---------------------|-------------------|-----------|
| 82825 | chr3| 1.28E+08  | 1.28E+08  | T   | A   | exonic        | GATA2         | nonsynonymous SNV   | GATA2:NM_001145662:exon3:c.A617T:p.E206V,GATA2:NM_032638:exon3:c.A617T:p.E206V,GATA2:NM_001145661:exon4:c.A617T:p.E206V | 3q21.3 |
| 82825 | chr8| 1.18E+08  | 1.18E+08  | G   | A   | exonic        | RAD21         | stopgain           | RAD21:NM_006265:exon10:c.C1303T:p.Q435X | 8q24.11 |
| 82825 | chr9| 1.34E+08  | 1.34E+08  | T   | A   | exonic        | ABL1          | nonsynonymous SNV   | ABL1:NM_005157:exon4:c.T557A:p.V186D,ABL1:NM_007313:exon4:c.T614A:p.V205D | 9q34.12 |
| 80621 | chr1| 36932044  | 36932044  | C   | A   | exonic        | CSF3R         | nonsynonymous SNV   | CSF3R:NM_000760:exon17:c.C1303T:p.Q435X | 1p34.3 |
| 80621 | chr11| 1.19E+08 | 1.19E+08  | C   | T   | exonic       | CBL           | nonsynonymous SNV   | CBL:NM_005188:exon4:c.C692T:p.T231I | 11q23.3 |
| 80621 | chr11| 533530   | 533530    | C   | T   | exonic       | HRAS          | nonsynonymous SNV   | HRAS:NM_001130442:exon4:c.G373A:p.V125M,HRAS:NM_005343:exon4:c.G373A:p.V125M,HRAS:NM_176795:exon4:c.G373A:p.V125M | 11p15.5 |
| 80621 | chr2| 25505324  | 25505324  | G   | A   | exonic        | DNMT3A        | nonsynonymous SNV   | DNMT3A:NM_022552:exon4:c.C434T:p.A145V,DNMT3A:NM_175629:exon4:c.C434T:p.A145V,DNMT3A:NM_175630:exon4:c.C434T:p.A145V | 2p23.3 |
| 80621 | chr20| 31024801 | 31024801  | C   | T   | exonic       | ASXL1         | nonsynonymous SNV   | ASXL1:NM_015338:exon12:c.1927dupG:p.G642fs | 20q11.21 |
| 80621 | chr21| 36164627  | 36164627  | -   | AACT| exonic       | RUNX1         | frameshift insertion | RUNX1:NM_001001890:exon6:c.1166_1167insAGTT:p.F389fs,RUNX1:NM_001754:exon9:c.1247_1248insAGTT:p.F416fs | 21q22.12 |
| 80621 | chr9| 21994149  | 21994149  | G   | A   | exonic        | CDKN2A        | nonsynonymous SNV   | CDKN2A:NM_058195:exon1:c.C182T:p.P61L | 9p21.3 |
| 80621 | chrX| 1.29E+08  | 1.29E+08  | A   | G   | exonic       | BCORL1        | nonsynonymous SNV   | BCORL1:NM_001184772:exon3:c.A2273G:p.E758G,BCORL1:NM_021946:exon3:c.A2273G:p.E758G | Xq26.1 |
| 79453 | chr19| 56173950  | 56173964  | AGA | -   | exonic       | U2AF2         | nonframeshift deletion | U2AF2:NM_001012478:exon6:c.569_583del:p.190_195del,U2AF2:NM_007279:exon6:c.569_583del:p.190_195del | 19q13.42 |
| 79453 | chr20| 31022441  | 31022441  | G   | exonic       | ASXL1         | frameshift insertion | ASXL1:NM_015338:exon12:c.1927dupG:p.G642fs | 20q11.21 |
## Supplementary Table S2. Genetic Variants Identified in 52 patients with CMML Undergoing HCT

| UPN   | Chr | Start     | End     | Ref | Alt | Func. refGene | Gene. refGene | ExonicFunc. refGene | AAChange.refGene | cytoBand |
|-------|-----|-----------|---------|-----|-----|---------------|---------------|---------------------|------------------|----------|
| 77347 | chr1| 36932859  | 36932859| C   | T   | exonic       | CSF3R         | nonsynonymous SNV   | CSF3R:NM_000760:exon16:c.G2012A:p.G671D, CSF3R:NM_156039:exon16:c.G2012A:p.G671D, CSF3R:NM_172313:exon16:c.G2012A:p.G671D | 1p34.3 |
| 77347 | chr10| 89720741  | 89720741| C   | T   | exonic       | PTEN          | stopgain            | PTEN:NM_000314:exon8:c.C892T:p.Q298X,PTEN:NM_001304718:exon8:c.C301T:p.Q101X,PTEN:NM_001304717:exon9:c.C1411T:p.Q471X | 10q23.31 |
| 77347 | chr12| 11992227  | 11992227| C   | T   | exonic       | ETV6          | nonsynonymous SNV   | ETV6:NM_001987:exon3:c.C317T:p.Q101X,ETV6:NM_001304718:exon8:c.C301T:p.Q101X,ETV6:NM_001304717:exon9:c.C1411T:p.Q471X | 12p13.2 |
| 77347 | chr19| 13054584  | 13054584| G   | T   | exonic       | CALR          | stopgain            | CALR:NM_004343:exon9:c.G1111T:p.E371X | 19p13.2 |
| 77347 | chr20| 31022441  | 31022441|     | G   | exonic       | ASXL1         | frameshift insertion | ASXL1:NM_015338:exon12:c.1927dupG:p.G642fs | 20q11.21 |
| 77347 | chr20| 57485133  | 57485133| G   | A   | exonic       | GNAS          | nonsynonymous SNV   | GNAS:NM_000314:exon7:c.C677A:p.S226Y,GNAS:NM_000314:exon7:c.C86A:p.S29Y,GNAS:NM_001304717:exon8:c.C1196A:p.S399Y | 20q13.32 |
| 77347 | chr4 | 1.06E+08  | 1.06E+08| C   | T   | exonic       | TET2          | nonsynonymous SNV   | TET2:NM_001127208:exon4:c.C3473T:p.A1158 | 4q24 |
| 77347 | chr4 | 1.06E+08  | 1.06E+08| C   | T   | exonic       | TET2          | nonsynonymous SNV   | TET2:NM_001127208:exon4:c.C3458T:p.A1153 | 4q24 |
| 77347 | chrX | 53442118  | 53442118| C   | T   | exonic       | SMC1A         | nonsynonymous SNV   | SMC1A:NM_001304718:exon8:c.C1196A:p.S399Y | Xp11.22 |
| 75750 | chr10| 89717652  | 89717652| C   | A   | exonic       | PTEN          | nonsynonymous SNV   | PTEN:NM_000314:exon7:c.C677A:p.S226Y,PTEN:NM_001304718:exon7:c.C86A:p.S29Y,PTEN:NM_001304717:exon8:c.C1196A:p.S399Y | 10q23.31 |
| 75750 | chr11| 1.18E+08  | 1.18E+08| C   | T   | exonic       | KMT2A         | nonsynonymous SNV   | KMT2A:NM_0011197104:exon26:c.C6451T:p.P2151S,KMT2A:NM_005933:exon26:c.C6442T:p.P2148S | 11q23.3 |
**Supplementary Table S2. Genetic Variants Identified in 52 patients with CMML Undergoing HCT**

| UPN  | Chr | Start    | End      | Ref | Alt | Func. refGene | Gene. refGene | ExonicFunc. refGene | AAChange.refGene | cytoBand |
|------|-----|----------|----------|-----|-----|---------------|---------------|--------------------|-------------------|-----------|
| 75750 | chr19 | 56173950 | 56173964 | AGA | TTA | exonic        | U2AF2         | nonframeshift deletion | U2AF2:NM_001012478:exon6:c.569_583del:p.190_195del, U2AF2:NM_007279:exon6:c.569_583del:p.190_195del | 19q13.42 |
| 75750 | chr2  | 1.37E+08 | 1.37E+08 | C   | A   | exonic        | CXCR4         | nonsynonymous SNV   | CXCR4:NM_0010008540:exon1:c.G704T:p.G235V,CXCR4:NM_003467:exon2:c.G692T:p.G231V | 2q22.1    |
| 75750 | chr20 | 31024101 | 31024101 | G   | A   | exonic        | ASXL1         | nonsynonymous SNV   | ASXL1:NM_015338:exon12:c.G704T:p.G235V,ASXL1:NM_007279:exon12:c.G692T:p.G231V | 20q11.21  |
| 75750 | chr21 | 36171607 | 36171607 | G   | A   | exonic        | RUNX1         | stopgain            | RUNX1:NM_001001890:exon5:c.G877T:p.R293X,RUNX1:NM_001001890:exon5:c.G877T:p.R293X | 21q22.12  |
| 75750 | chr3  | 1.28E+08 | 1.28E+08 | G   | T   | exonic        | GATA2         | nonsynonymous SNV   | GATA2:NM_001145662:exon3:c.G704T:p.G235V,GATA2:NM_001145662:exon3:c.G704T:p.G235V,GATA2:NM_001145662:exon3:c.G704T:p.G235V | 3q21.3    |
| 75750 | chr4  | 1.06E+08 | 1.06E+08 | C   | T   | exonic        | TET2          | stopgain            | TET2:NM_001127208:exon3:c.G877T:p.R293X,TET2:NM_001127208:exon3:c.G877T:p.R293X | 4q24      |
| 65041 | NA   | NA       | NA       | NA  | NA  | NA            | NA            | NA                 | NA                | NA        |
| 57547 | chr11 | 1.19E+08 | 1.19E+08 | C   | G   | exonic        | CBL           | nonsynonymous SNV   | CBL:NM_005188:exon9:c.G1250T:p.R417R,CBL:NM_005188:exon9:c.G1250T:p.R417R | 11q23.3   |
| 57547 | chr11 | 1.19E+08 | 1.19E+08 | G   | T   | exonic        | CBL           | stopgain            | CBL:NM_005188:exon10:c.C460T:p.R153X,CBL:NM_005188:exon10:c.C460T:p.R153X | 11q23.3   |
| 57547 | chr17 | 74732959 | 74732959 | G   | T   | exonic        | SRSF2         | nonsynonymous SNV   | SRSF2:NM_001195427:exon1:c.C284A:p.Q95H,SRSF2:NM_001195427:exon1:c.C284A:p.Q95H | 17q25.1   |
| 57547 | chr17 | 58740779 | 58740779 | C   | T   | exonic        | PPM1D         | stopgain            | PPM1D:NM_003620:exon6:c.C1684T:p.Q562X,PPM1D:NM_003620:exon6:c.C1684T:p.Q562X | 17q23.2   |
| 57547 | chr2  | 2.09E+08 | 2.09E+08 | T   | A   | exonic        | IDH1          | nonsynonymous SNV   | IDH1:NM_001282386:exon3:c.A477T:p.D167V,IDH1:NM_001282386:exon3:c.A477T:p.D167V | 2q34      |
| 57547 | chr20 | 31024801 | 31024801 | C   | T   | exonic        | ASXL1         | nonsynonymous SNV   | ASXL1:NM_015338:exon12:c.G704T:p.G235V,ASXL1:NM_007279:exon12:c.G692T:p.G231V | 20q11.21  |
| 57547 | chr21 | 36259140 | 36259160 | CTT | GGA | exonic        | RUNX1         | nonframeshift deletion | RUNX1:NM_001001890:exon1:c.G877T:p.R293X,RUNX1:NM_001001890:exon1:c.G877T:p.R293X | 21q22.12  |
| UPN  | Chr  | Start   | End   | Ref | Alt | Func.  | Gen. refGene | Exonic Func. refGene | AAClange.refGene | cytoBand |
|------|------|---------|-------|-----|-----|--------|--------------|-----------------------|------------------|-----------|
| 57547| chr21| 36171687| 36171687| G   | A   | exonic | RUNX1       | nonsynonymous SNV    | RUNX1:NM_001001890:exon5:c.C797T:p.S266F | 21q22.12 |
| 57547| chr4 | 1.06E+08| 1.06E+08| C   | T   | exonic | TET2       | stopgain             | TET2:NM_001127208:exon3:c.C3025T:p.Q1009 | 4q24 |
| 57547| chr4 | 1.06E+08| 1.06E+08| C   | T   | exonic | TET2       | stopgain             | TET2:NM_001127208:exon3:c.C3025T:p.Q1009 | 4q24 |
| 57547| chr5 | 1.77E+08| 1.77E+08| T   | A   | exonic | DDX41      | nonsynonymous SNV    | DDX41:NM_016222:exon14:c.A1537T:p.I513F | 5q35.3 |
| 57547| chr7 | 1.02E+08| 1.02E+08| C   | T   | exonic | CUX1       | stopgain             | CUX1:NM_001184772:exon3:c.A2273G:p.E758G, CUX1:NM_00117652:exon15:c.C1675T:p.Q559X | 7q22.1 |
| 57547| chr7 | 50435807| 50435807| T   | A   | exonic | IKZF1      | nonsynonymous SNV    | IKZF1:NM_001184772:exon3:c.A2273G:p.E758G | 7p12.2 |
| 57547| chrX | 44732933| 44732933| A   | T   | exonic | KDM6A      | nonsynonymous SNV    | KDM6A:NM_0011291415:exon1:c.A136T:p.R46W, KDM6A:NM_0011291416:exon1:c.A136T:p.R46W, KDM6A:NM_0011291417:exon1:c.A136T:p.R46W, KDM6A:NM_0011291418:exon1:c.A136T:p.R46W, KDM6A:NM_021140:exon1:c.A136T:p.R46W | Xp11.3 |
| 57547| chrX | 1.29E+08| 1.29E+08| A   | G   | exonic | BCORL1     | nonsynonymous SNV    | BCORL1:NM_001184772:exon3:c.A2273G:p.E758G | Xq26.1 |
| 42961| chr10| 89624302| 89624302| A   | G   | exonic | PTEN       | nonsynonymous SNV    | PTEN:NM_000314:exon1:c.A76G:p.T26A, PTEN:NM_001304717:exon2:c.A595G:p.T199A | 10q23.31 |
| 42961| chr11| 1.18E+08| 1.18E+08| C   | T   | exonic | KMT2A      | nonsynonymous SNV    | KMT2A:NM_001197104:exon26:c.C6442T:p.P2151S,KMT2A:NM_001197104:exon26:c.C6442T:p.P2148S | 11q23.3 |
| 42961| chr12| 12022873| 12022873| G   | A   | exonic | ETV6       | nonsynonymous SNV    | ETV6:NM_0011987:exon5:c.G979A:p.E327K | 12p13.2 |
| 42961| chr17| 40474369| 40474369| G   | A   | exonic | STAT3      | nonsynonymous SNV    | STAT3:NM_001350:exon21:c.C2032T:p.P678S, STAT3:NM_139276:exon21:c.C2032T:p.P678S, STAT3:NM_213662:exon21:c.C2032T:p.P678S | 17q21.2 |
| UPN   | Chr  | Start       | End       | Ref | Alt | Func. refGene | Gene. refGene | Exonic Func. refGene | AAChange refGene | cytoBand |
|-------|------|-------------|-----------|-----|-----|---------------|---------------|---------------------|------------------|-----------|
| 42961 | chr19| 56179891    | 56179891  | T   | C   | exonic        | U2AF2         | nonsynonymous SNV   | U2AF2:NM_001012478:exon8:c.T761C:p.V254A, U2AF2:NM_007279:exon8:c.T761C:p.V254A | 19q13.42 |
| 42961 | chr2 | 2.09E+08    | 2.09E+08  | C   | T   | exonic        | IDH1          | nonsynonymous SNV   | IDH1:NM_001282386:exon4:c.G395A:p.R132H, IDH1:NM_001282387:exon4:c.G395A:p.R132H, IDH1:NM_005896:exon4:c.G395A:p.R132H | 2q34     |
| 42961 | chr4 | 1.53E+08    | 1.53E+08  | G   | A   | exonic        | FBXW7         | nonsynonymous SNV   | FBXW7:NM_001013415:exon4:c.G395A:p.R132H, FBXW7:NM_001013415:exon4:c.G395A:p.R132H, FBXW7:NM_001013415:exon4:c.G395A:p.R132H | 4q31.3   |
| 42961 | chr4 | 55593648    | 55593648  | G   | A   | exonic        | KIT           | nonsynonymous SNV   | KIT:NM_002222:exon11:c.G1714A:p.D572N, KIT:NM_002222:exon11:c.G1714A:p.D572N, KIT:NM_002222:exon11:c.G1714A:p.D572N | 4q12     |
| 42961 | chrX | 39916426    | 39916426  | C   | T   | exonic        | BCOR          | nonsynonymous SNV   | BCOR:NM_001123384:exon10:c.G4412A:p.S147N, BCOR:NM_001123384:exon10:c.G4412A:p.S147N, BCOR:NM_001123384:exon10:c.G4412A:p.S147N | Xp11.4   |
| 42961 | chrX | 48649581    | 48649581  | C   | T   | exonic        | GATA1         | nonsynonymous SNV   | GATA1:NM_002049:exon2:c.G65T:p.A22V, GATA1:NM_002049:exon2:c.G65T:p.A22V, GATA1:NM_002049:exon2:c.G65T:p.A22V | Xp11.23  |
| 42961 | chrX | 1.34E+08    | 1.34E+08  | C   | T   | exonic        | PHF6          | nonsynonymous SNV   | PHF6:NM_001015877:exon5:c.C391T:p.H131Y, PHF6:NM_001015877:exon5:c.C391T:p.H131Y, PHF6:NM_001015877:exon5:c.C391T:p.H131Y | Xq26.2   |
| 42163 | chr20 | 31024101    | 31024101  | G   | A   | exonic        | ASXL1         | nonsynonymous SNV   | ASXL1:NM_015338:exon12:c.G3586A:p.A1196T, ASXL1:NM_015338:exon12:c.G3586A:p.A1196T, ASXL1:NM_015338:exon12:c.G3586A:p.A1196T | 20q11.21 |
| 42163 | chr4 | 1.06E+08    | 1.06E+08  | T   | C   | exonic        | TET2          | nonsynonymous SNV   | TET2:NM_017628:exon3:c.G3469C:p.S1157P, TET2:NM_017628:exon3:c.G3469C:p.S1157P, TET2:NM_017628:exon3:c.G3469C:p.S1157P | 4q24     |
| 41546 | chr17 | 40475057    | 40475057  | C   | A   | exonic        | STAT3         | nonsynonymous SNV   | STAT3:NM_003150:exon20:c.G1853T:p.G618V, STAT3:NM_003150:exon20:c.G1853T:p.G618V, STAT3:NM_003150:exon20:c.G1853T:p.G618V | 17q21.2  |
| 41546 | chr18 | 42531907    | 42531907  | G   | A   | exonic        | SETBP1        | nonsynonymous SNV   | SETBP1:NM_015559:exon4:c.G2602A:p.D868N, SETBP1:NM_015559:exon4:c.G2602A:p.D868N, SETBP1:NM_015559:exon4:c.G2602A:p.D868N | 18q12.3  |
| 41546 | chr2  | 25469107    | 25469107  | G   | A   | exonic        | DNMT3A       | nonsynonymous SNV   | DNMT3A:NM_153759:exon7:c.G784T:p.P262S,DNMT3A:NM_153759:exon7:c.G784T:p.P262S,DNMT3A:NM_153759:exon7:c.G784T:p.P262S | 2p23.3   |
| 41546 | chr2  | 1.98E+08    | 1.98E+08  | C   | T   | exonic        | SF3B1        | nonsynonymous SNV   | SF3B1:NM_012433:exon15:c.G2128A:p.A710T, SF3B1:NM_012433:exon15:c.G2128A:p.A710T, SF3B1:NM_012433:exon15:c.G2128A:p.A710T | 2q33.1   |
| UPN  | Chr | Start    | End     | Ref | Alt | Func. refGene | Gene. refGene | Exonic Func. refGene | AAChange refGene | cytoBand |
|------|-----|----------|---------|-----|-----|--------------|--------------|----------------------|-----------------|----------|
| 41546 | chr2 | 25505324 | 25505324 | G   | A   | exonic       | DNMT3A       | nonsynonymous SNV    | DNMT3A:NM_022552:exon4:c.C434T:p.A145V,DNMT3A:NM_175629:exon4:c.C434T:p.A145V,DNMT3A:NM_175630:exon4:c.C434T:p.A145V | 2p23.3 |
| 41546 | chr3 | 38181899 | 38181899 | G   | A   | exonic       | MYD88        | nonsynonymous SNV    | MYD88:NM_001172568:exon2:c.G388A:p.D130,NMYD88:NM_001172567:exon3:c.G523A:p.D175NMYD88:NM_002468:exon3:c.G523A:p.D175N | 3p22.2 |
| 41546 | chr4 | 55152018 | 55152018 | G   | A   | exonic       | PDGFRA       | nonsynonymous SNV    | PDGFRA:NM_006206:exon18:c.G2450A:p.R817H | 4q12    |
| 41546 | chr7 | 1.49E+08 | 1.49E+08 | C   | T   | exonic       | EZH2         | nonsynonymous SNV    | EZH2:NM_152998:exon9:c.G1075A:p.E359K,EZH2:NM_001203247:exon10:c.G1192A:p.E398K,EZH2:NM_001203248:exon10:c.G1165A:p.E389K,EZH2:NM_001203249:exon10:c.G1165A:p.E389K | 7q36.1 |
| 41546 | chrX | 15826380 | 15826380 | C   | T   | exonic       | ZRSR2        | stopgain             | ZRSR2:NM_005089:exon6:c.C424T:p.Q142X | Xp22.2 |
| 36470 | chr11 | 1.19E+08 | 1.19E+08 | C   | T   | exonic       | CBL          | stopgain             | CBL:NM_005188:exon2:c.C382T:p.Q128X | 11q23.3 |
| 36470 | chr11 | 32456507 | 32456507 | G   | A   | exonic       | WT1          | nonsynonymous SNV    | WT1:NM_000378:exon1:c.C385T:p.P129S,WT1:NM_004456:exon1:c.C385T:p.P129S | 11p13 |
| 36470 | chr12 | 1.13E+08 | 1.13E+08 | T   | G   | exonic       | PTPN11       | nonsynonymous SNV    | PTPN11:NM_002834:exon13:c.T1586G:p.I529S | 12q44.13 |
| 36470 | chr17 | 74732959 | 74732959 | G   | T   | exonic       | SRSF2        | nonsynonymous SNV    | SRSF2:NM_00195427:exon12:c.C284A:p.P95H | 17q25.1 |
| 36470 | chr20 | 31021700 | 31021700 | C   | T   | exonic       | ASXL1        | nonsynonymous SNV    | ASXL1:NM_015338:exon11:c.C1699T:p.P567S | 20q11.21 |
| 36470 | chr4  | 55141059 | 55141059 | G   | A   | exonic       | PDGFRA       | nonsynonymous SNV    | PDGFRA:NM_006206:exon12:c.G1705A:p.G569R | 4q12 |
| 36470 | chr5  | 1.77E+08 | 1.77E+08 | T   | A   | exonic       | DDX41        | nonsynonymous SNV    | DDX41:NM_016222:exon14:c.A1537T:p.I513F | 5q35.3 |
| 36470 | chr8  | 1.18E+08 | 1.18E+08 | G   | A   | exonic       | RAD21        | stopgain             | RAD21:NM_006265:exon10:c.C1303T:p.Q435X | 8q24.11 |
| 36470 | chr8  | 1.18E+08 | 1.18E+08 | G   | A   | exonic       | RAD21        | stopgain             | RAD21:NM_006265:exon10:c.C1444T:p.Q482X | 8q24.11 |
| 36470 | chr8  | 1.29E+08 | 1.29E+08 | A   | T   | exonic       | MYC          | nonsynonymous SNV    | MYC:NM_002467:exon2:c.A371T:p.D124V | 8q24.21 |
| 36470 | chrX  | 15826380 | 15826380 | C   | T   | exonic       | ZRSR2        | stopgain             | ZRSR2:NM_005089:exon6:c.C424T:p.Q142X | Xp22.2 |
### Supplementary Table S2. Genetic Variants Identified in 52 patients with CMML Undergoing HCT

| UPN   | Chr | Start   | End     | Ref | Alt | Func. refGene | Gene. refGene | ExonicFunc. refGene | AAChange.refGene | cytoBand |
|-------|-----|---------|---------|-----|-----|---------------|---------------|---------------------|------------------|-----------|
| 36470 | chrX| 39921487| 39921487| G   | A   | exonic        | BCOR          | stopgain            | BCOR:NM_001123384:exon9:c.C4177T:p.Q1393X,BCOR:NM_001123383:exon10:c.C4231T:p.Q1411X,BCOR:NM_001123385:exon10:c.C4333T:p.Q1445X,BCOR:NM_017745:exon10:c.C4231T:p.Q1411X | Xp11.4          |
| 36158 | chr1 | 36932859| 36932859| C   | T   | exonic        | CSF3R         | nonsynonymous SNV   | CSF3R:NM_000760:exon16:c.G2012A:p.G671D,CSF3R:NM_156039:exon16:c.G2012A:p.G671D,CSF3R:NM_172313:exon16:c.G2012A:p.G671D | 1p34.3          |
| 36158 | chr12| 1.12E+08| 1.12E+08| C   | T   | exonic        | SH2B3         | nonsynonymous SNV   | SH2B3:NM_001291424:exon7:c.C827T:p.P276L,SH2B3:NM_005475:exon8:c.C1433T:p.P478L | 12q24.12        |
| 36158 | chr18| 42531907| 42531907| G   | A   | exonic        | SETBP1        | nonsynonymous SNV   | SETBP1:NM_015559:exon4:c.C827T:p.P276L,SETBP1:NM_156039:exon4:c.C827T:p.P276L,SETBP1:NM_172313:exon4:c.C827T:p.P276L | 18q12.3         |
| 36158 | chr2 | 25471043| 25471043| C   | G   | exonic        | DNMT3A        | nonsynonymous SNV   | DNMT3A:NM_015373:exon3:c.G151C:p.E51N,DNMT3A:NM_022552:exon7:c.G718C:p.E240Q,DNMT3A:NM_175629:exon7:c.G718C:p.E240Q | 2p23.3          |
| 36158 | chr20| 31019255| 31019255| C   | T   | exonic        | ASXL1         | nonsynonymous SNV   | ASXL1:NM_015338:exon8:c.C850T:p.L284F | 20q11.21        |
| 36158 | chr4 | 1.06E+08| 1.06E+08| A   | G   | exonic        | TET2          | nonsynonymous SNV   | TET2:NM_001122708:exon6:c.A3644G:p.E1215G | 4q24            |
| 36158 | chr4 | 1.06E+08| 1.06E+08| C   | T   | exonic        | TET2          | nonsynonymous SNV   | TET2:NM_001122708:exon9:c.C4066T:p.P1356S | 4q24            |
| 36158 | chr5 | 1.77E+08| 1.77E+08| T   | A   | exonic        | DDX41         | nonsynonymous SNV   | DDX41:NM_016222:exon14:c.A1537T:p.I513F | 5q35.3          |
| 36158 | chrX | 48649535| 48649535| G   | A   | exonic        | GATA1         | nonsynonymous SNV   | GATA1:NM_002049:exon2:c.G19A:p.G7R | Xp11.23         |
| 36158 | chrX | 53442026| 53442026| C   | T   | exonic        | SMC1A         | nonsynonymous SNV   | SMC1A:NM_002049:exon2:c.G202A:p.A68T,SMC1A:NM_002049:exon2:c.G202A:p.A68T,SMC1A:NM_002049:exon2:c.G202A:p.A68T | Xp11.22         |
| 32015 | chr1 | 43818306| 43818306| T   | G   | exonic        | MPL           | nonsynonymous SNV   | MPL:NM_005373:exon12:c.T1771G:p.Y591D | 1p34.2          |
| 32015 | chr11| 32456348| 32456348| G   | T   | exonic        | WT1           | nonsynonymous SNV   | WT1:NM_002049:exon1:c.C544A:p.P182T,WT1:NM_002049:exon1:c.C544A:p.P182T,WT1:NM_002049:exon1:c.C544A:p.P182T | 11p13           |
| 32015 | chr12| 22811995| 22811995| A   | G   | exonic        | ETNK1         | nonsynonymous SNV   | ETNK1:NM_018638:exon3:c.A731G:p.N244S | 12p12.1         |
| 32015 | chr12| 1.13E+08| 1.13E+08| T   | G   | exonic        | PTPN11        | nonsynonymous SNV   | PTPN11:NM_002049:exon13:c.T1586G:p.I529S | 12q24.13        |
| 32015 | chr12| 22811995| 22811995| A   | G   | exonic        | ETNK1         | nonsynonymous SNV   | ETNK1:NM_018638:exon3:c.A731G:p.N244S | 12p12.1         |
Supplementary Table S2. Genetic Variants Identified in 52 patients with CMML Undergoing HCT

| UPN   | Chr   | Start   | End     | Ref | Alt | Func. refGene | Gene. refGene | ExonicFunc. refGene | AASrefGene | cytoBand |
|-------|-------|---------|---------|-----|-----|---------------|---------------|---------------------|------------|----------|
| 32015 | chr17 | 74732334| 74732334| G   | -   | exonic        | SRSF2         | frameshift deletion | SRSF2:NM_001195427:exon2:c.575delC:p.P192fs,SRSF2:NM_003016:exon2:c.575delC:p.P192fs | 17q25.1    |
| 32015 | chr20 | 31016167| 31016167| C   | T   | exonic        | ASXL1         | nonsynonymous SNV   | ASXL1:NM_015338:exon5:c.C413T:p.T138I | 20q11.21   |
| 32015 | chr21 | 36171600| 36171600| G   | C   | exonic        | RUNX1         | stopgain            | RUNX1:NM_001001890:exon5:c.C884G:p.S295X,RUNX1:NM_001754:exon8:c.C965G:p.S322X | 21q22.12   |
| 32015 | chr4  | 55152092| 55152092| G   | A   | exonic        | PDGFRA        | nonsynonymous SNV   | PDGFRA:NM_006206:exon18:c.G2524A:p.D842N | 4q12       |
| 32015 | chr4  | 1.06E+08| 1.06E+08| C   | T   | exonic        | TET2          | nonsynonymous SNV   | TET2:NM_001112708:exon3:c.C80T:p.T271I,TET2:NM_017628:exon3:c.C80T:p.T271I | 4q24       |
| 32015 | chr8  | 1.18E+08| 1.18E+08| G   | A   | exonic        | RAD21         | stopgain            | RAD21:NM_006265:exon11:c.C1432T:p.R478X | 8q24.11    |
| 32015 | chr8  | 1.18E+08| 1.18E+08| G   | A   | exonic        | RAD21         | stopgain            | RAD21:NM_006265:exon11:c.C1432T:p.R478X | 8q24.11    |
| 32015 | chr9  | 1.39E+08| 1.39E+08| G   | A   | exonic        | NOTCH1        | nonsynonymous SNV   | NOTCH1:NM_017617:exon34:c.C6959T:p.P2320L | 9q34.3     |
| 32015 | chrX  | 1.34E+08| 1.34E+08| C   | T   | exonic        | PHF6          | nonsynonymous SNV   | PHF6:NM_001015877:exon5:c.C391T:p.H131Y,PHF6:NM_032335:exon5:c.C391T:p.H131Y,PHF6:NM_032458:exon5:c.C391T:p.H131Y | Xq26.2     |
| 32015 | chrX  | 53441966| 53441966| C   | A   | exonic        | SMC1A         | nonsynonymous SNV   | SMC1A:NM_006306:exon2:c.G262T:p.G88CSMC1A:NM_01281463:exon3:c.G196T:p.G66C | Xp11.22    |
| 31517 | chr1  | 1.15E+08| 1.15E+08| C   | T   | exonic        | NRAS          | nonsynonymous SNV   | NRAS:NM_002524:exon2:c.G35A:p.G12D | 1p13.2     |
| 31517 | chr10 | 89720741| 89720741| C   | T   | exonic        | PTEN          | stopgain            | PTEN:NM_000314:exon8:c.G927T:p.Q298X,PTEN:NM_001304718:exon8:c.G301T:p.Q101X,PTEN:NM_001304717:exon9:c.C1411T:p.Q471X | 10q23.31   |
| 31517 | chr10 | 1.12E+08| 1.12E+08| C   | T   | exonic        | SMC3          | stopgain            | SMC3:NM_005445:exon25:c.C3088T:p.Q1030X | 10q25.2     |
| 31517 | chr11 | 1.19E+08| 1.19E+08| G   | T   | exonic        | CBL           | stopgain            | CBL:NM_005188:exon2:c.G406T:p.G136X | 11q23.3     |
| 31517 | chr11 | 32456329| 32456329| G   | A   | exonic        | WT1           | nonsynonymous SNV   | WT1:NM_000378:exon1:c.C563T:p.A188V,WT1:NM_024424:exon1:c.C563T:p.A188V,WT1:NM_024426:exon1:c.C563T:p.A188V | 11p13      |
| 31517 | chr11 | 1.18E+08| 1.18E+08| C   | A   | exonic        | KMT2A         | nonsynonymous SNV   | KMT2A:NM_001197104:exon27:c.A7923C:p.R2641S,KMT2A:NM_005933:exon27:c.A7914C:p.R26438S | 11q23.3     |
Supplementary Table S2. Genetic Variants Identified in 52 patients with CMML Undergoing HCT

| UPN  | Chr  | Start   | End     | Ref | Alt | Func. refGene | Gene. refGene | ExonicFunc. refGene | AAChange.refGene | cytoBand |
|------|------|---------|---------|-----|-----|---------------|---------------|--------------------|------------------|----------|
| 31517 | chr12 | 1.13E+08 | 1.13E+08 | C   | T   | exonic        | PTPN11        | non-synonymous SNV | PTPN11:NM_002834:exon11:c.C1285T:p.P429S | 12q24.13  |
| 31517 | chr15 | 66727405 | 66727405 | G   | A   | exonic        | MAP2K1        | non-synonymous SNV | MAP2K1:NM_002755:exon2:c.G121A:p.E41K | 15q22.31 |
| 31517 | chr18 | 42531907 | 42531907 | G   | A   | exonic        | SETBP1        | non-synonymous SNV | SETBP1:NM_015559:exon4:c.G2602A:p.D868N | 18q12.3 |
| 31517 | chr19 | 33792336 | 33792336 | C   | T   | exonic        | CEBPA         | non-synonymous SNV | CEBPA:NM_001285829:exon1:c.G628A:p.E210K,CEBPA:NM_001287424:exon1:c.G1090A:p.E364K,CEBPA:NM_001287435:exon1:c.G943A:p.E315K,CEBPA:NM_004364:exon1:c.G985A:p.E329K | 19q13.11 |
| 31517 | chr2  | 25464466 | 25464466 | A   | C   | exonic        | DNMT3A        | non-synonymous SNV | DNMT3A:NM_153759:exon13:c.T1480G:p.Y494D,DNMT3A:NM_022552:exon17:c.T2047G:p.Y683D,DNMT3A:NM_175629:exon17:c.T2047G:p.Y683D | 2p23.3 |
| 31517 | chr20 | 31022441 | 31022441 | -   | G   | exonic        | ASXL1         | frameshift insertion | ASXL1:NM_015338:exon12:c.1927dupG:p.G642fs | 20q11.21 |
| 31517 | chr21 | 36206722 | 36206722 | G   | A   | exonic        | RUNX1         | stopgain            | RUNX1:NM_001001890:exon4:c.C709T:p.Q237X,RUNX1:NM_001122607:exon4:c.C709T:p.Q237X,RUNX1:NM_001754:exon7:c.C790T:p.Q264X | 4q24 |
| 31517 | chr3  | 1.28E+08 | 1.28E+08 | G   | A   | exonic        | GATA2         | non-synonymous SNV | GATA2:NM_001145662:exon3:c.C688T:p.R230C,GATA2:NM_032638:exon3:c.C688T:p.R230C,GATA2:NM_001145661:exon4:c.C688T:p.R230C | 3q21.3 |
| 31517 | chr4  | 1.06E+08 | 1.06E+08 | T   | C   | exonic        | TET2          | non-synonymous SNV | TET2:NM_017628:exon3:c.T3469C:p.S1157P | 4q24 |
| 31517 | chr4  | 1.06E+08 | 1.06E+08 | C   | T   | exonic        | TET2          | stopgain            | TET2:NM_001127208:exon11:c.C5095T:p.Q169X | 4q24 |
| 31517 | chr4  | 55594043 | 55594043 | G   | A   | exonic        | KIT           | non-synonymous SNV | KIT:NM_000222:exon12:c.G1829A:p.G610D,KIT:NM_001093772:exon12:c.G1817A:p.G606D | 4q12 |
| 31517 | chr7  | 1.49E+08 | 1.49E+08 | C   | T   | exonic        | EZH2          | non-synonymous SNV | EZH2:NM_001203249:exon14:c.G1559A:p.C520Y,EZH2:NM_152998:exon14:c.G1595A:p.C532Y,EZH2:NM_001203247:exon15:c.G1712A:p.C571 | 7q36.1 |
### Supplementary Table S2. Genetic Variants Identified in 52 patients with CMML Undergoing HCT

| UPN  | Chr  | Start     | End       | Ref | Alt | Func. refGene | Gene. refGene | Exonic Func. refGene | AAChange.refGene | cytoBand |
|------|------|-----------|-----------|-----|-----|---------------|---------------|----------------------|------------------|----------|
| 31517 | chr9 | 1.34E+08  | 1.34E+08  | T   | A   | exonic        | ABL1          | nonsynonymous SNV   | Y,EZH2:NM_001203248:exon15:c.G1685A:p.C562Y,EZH2:NM_004456:exon15:c.G1727A:p.C576Y | 9q34.12 |
| 31517 | chrX | 76938974  | 76938974  | G   | A   | exonic        | ATRX          | nonsynonymous SNV   | ATRX:NM_138270:exon8:c.C1660T:p.P554S,ATRX:NM_000489:exon9:c.C1774T:p.P592S | Xq21.1 |
| 31517 | chrX | 53410031  | 53410031  | -   | A   | exonic        | SMC1A         | frameshift insertion | SMC1A:NM_006306:exon20:c.3116_3117insT:p.Q1039fs,SMC1A:NM_001281463:exon21:c.3050_3051insT:p.Q1017fs | Xp11.22 |
| 31071 | chr1 | 36937109  | 36937109  | G   | A   | exonic        | CSF3R         | stopgain            | CSF3R:NM_000760:exon10:c.C1210T:p.Q404X,CSF3R:NM_156039:exon10:c.C1210T:p.Q404X,CSF3R:NM_172313:exon10:c.C1210T:p.Q404X | 1p34.3 |
| 31071 | chr11 | 1.19E+08  | 1.19E+08  | C   | T   | exonic       | CBL           | stopgain            | CBL:NM_005188:exon2:c.C382T:p.Q128X | 11q23.3 |
| 31071 | chr11 | 32456507  | 32456507  | G   | A   | exonic       | WT1           | nonsynonymous SNV   | WT1:NM_000378:exon1:c.C385T:p.Q129S,WT1:NM_024424:exon1:c.C385T:p.P129S,WT1:NM_024426:exon1:c.C385T:p.P129S | 11p13 |
| 31071 | chr11 | 1.18E+08  | 1.18E+08  | A   | C   | exonic       | KMT2A         | nonsynonymous SNV   | KMT2A:NM_001197104:exon27:c.A7923C:p.R241S,KMT2A:NM_001281463:exon27:c.A7914C:p.R241S,KMT2A:NM_001281463:exon27:c.A7914C:p.R2638S | 11q23.3 |
| 31071 | chr17 | 74732959  | 74732959  | G   | T   | exonic       | SRSF2         | nonsynonymous SNV   | SRSF2:NM_001195427:exon1:c.C284A:p.Q95H,SRSF2:NM_003016:exon1:c.C284A:p.Q95H | 17q25.1 |
| 31071 | chr17 | 29560178  | 29560178  | G   | A   | exonic       | NF1           | nonsynonymous SNV   | NF1:NM_000267:exon27:c.G3655A:p.G1219R,NF1:NM_001042492:exon27:c.G3655A:p.G1219R | 17q11.2 |
| 31071 | chr2  | 25505324  | 25505324  | G   | A   | exonic       | DNMT3A        | nonsynonymous SNV   | DNMT3A:NM_0022552:exon4:c.C434T:p.A145V,DNMT3A:NM_175629:exon4:c.C434T:p.A145V,DNMT3A:NM_175630:exon4:c.C434T:p.A145V | 2p23.3 |
| 31071 | chr4  | 55602728  | 55602728  | G   | A   | exonic       | KIT           | nonsynonymous SNV   | KIT:NM_000222:exon18:c.G2549A:p.S850N,KIT:NM_001093772:exon18:c.G2537A:p.S846N | 4q12 |
| UPN  | Chr | Start       | End         | Ref | Alt | Func. refGene | Gene. refGene | ExonicFunc. refGene | AAChange.refGene | cytoBand |
|------|-----|-------------|-------------|-----|-----|---------------|---------------|---------------------|------------------|----------|
| 31071| chr4| 1.06E+08    | 1.06E+08    | C   | T   | exonic        | TET2          | nonsynonymous SNV   | TET2:NM_001122708:exon9:c.C4066T:p.P1356S | 4q24     |
| 31071| chr9| 21974768    | 21974768    | G   | A   | exonic        | CDKN2A        | nonsynonymous SNV   | CDKN2A:NM_000077:exon1:c.C597:p.A20V,CDKN2A:NM_001195132:exon1:c.C597:p.A20V,CDKN2A:NM_058197:exon1:c.C597:p.A20V | 9p21.3   |
| 31071| chrX| 48649581    | 48649581    | C   | T   | exonic        | GATA1         | nonsynonymous SNV   | GATA1:NM_002049:exon2:c.C657:p.A22V          | Xp11.23  |
| 31071| chrX| 53441966    | 53441966    | C   | A   | exonic        | SMC1A         | nonsynonymous SNV   | SMC1A:NM_0006306:exon2:c.G2627T:p.G88C,SMC1A:NM_001281463:exon3:c.G196T:p.G66C | Xp11.22  |
| 31071| chrX| 15822271    | 15822271    | -   | G   | exonic        | ZRSR2         | frameshift insertion| ZRSR2:NM_005089:exon5:c.350_351insG:p.K117fs | Xp22.2   |
| 30857| chr10| 89624271    | 89624271    | A   | T   | exonic        | PTEN          | nonsynonymous SNV   | PTEN:NM_000314:exon1:c.A457T:p.R155S,PTEN:NM_001304717:exon2:c.A564T:p.R188S | 10q23.3  |
| 30857| chr11| 1.19E+08    | 1.19E+08    | T   | C   | exonic        | CBL           | nonsynonymous SNV   | CBL:NM_0005188:exon3:c.T485C:p.L162P          | 11q23.3  |
| 30857| chr12| 12043942    | 12043942    | G   | A   | exonic        | ETV6          | nonsynonymous SNV   | ETV6:NM_0001987:exon8:c.G1321A:p.E441K          | 12p13.2  |
| 30857| chr12| 1.12E+08    | 1.12E+08    | C   | A   | exonic        | SH2B3         | nonsynonymous SNV   | SH2B3:NM_005475:exon2:c.C23A:p.P8H              | 12q24.12 |
| 30857| chr15| 90631934    | 90631934    | C   | T   | exonic        | IDH2          | nonsynonymous SNV   | IDH2:NM_001290114:exon2:c.G29A:p.R107Q,IDH2:NM_001289910:exon4:c.G263A:p.R88Q,IDH2:NM_002168:exon4:c.G419A:p.R140Q | 15q26.1  |
| 30857| chr17| 74732959    | 74732959    | G   | T   | exonic        | SRSF2         | nonsynonymous SNV   | SRSF2:NM_001195542:exon1:c.C284A:p.P95H          | 17q25.1  |
| 30857| chr17| 74732292    | 74732292    | G   | A   | exonic        | SRSF2         | nonsynonymous SNV   | SRSF2:NM_001195542:exon1:c.C284A:p.P95H          | 17q25.1  |
| 30857| chr17| 29560088    | 29560088    | C   | T   | exonic        | NF1           | stopgain        | NF1:NM_000267:exon27:c.C3565T:p.Q1189X,NF1:NM_001042492:exon27:c.C3565T:p.Q1189X | 17q11.2  |
| 30857| chr19| 33792759    | 33792759    | G   | A   | exonic        | CEBPA         | nonsynonymous SNV   | CEBPA:NM_001285829:exon1:c.C205T:p.P69S,CEBPA:NM_001287424:exon1:c.C667T:p.P223S,CEBPA:NM_001287435:exon1:c.C520T:p.P174,CEBPA:NM_004364:exon1:c.C562T:p.P188S | 19q13.11 |
| 30857| chr20| 31023523    | 31023523    | C   | T   | exonic        | ASXL1         | nonsynonymous SNV   | ASXL1:NM_015338:exon12:c.C3008T:p.S1003F        | 20q11.21 |
Supplementary Table S2. Genetic Variants Identified in 52 patients with CMML Undergoing HCT

| UPN   | Chr   | Start | End   | Ref | Alt | Func. refGene | Gene. refGene | ExonicFunc. refGene | AAGradient.refGene | cytoBand |
|-------|-------|-------|-------|-----|-----|---------------|---------------|---------------------|-------------------|----------|
| 30857 | chr21 | 36164627 | 36164627 | -   | AACT | exonic        | RUNX1          | frameshift insertion | RUNX1:NM_001001890:exon6:c.1166_1167insAGTT:p.F389fs,RUNX1:NM_001754:exon9:c.1247_1248insAGTT:p.F416fs | 21q22.12 |
| 30857 | chr3  | 1.06E+08 | 1.06E+08 | C   | T   | exonic        | CBLB          | nonsynonymous SNV   | CBLB:NM_170662:exon3:c.G277A:p.D93N | 3q13.11  |
| 30857 | chr4  | 1.06E+08 | 1.06E+08 | C   | T   | exonic        | TET2          | nonsynonymous SNV   | TET2:NM_001127208:exon7:c.C3809T:p.T1270I | 4q24     |
| 30857 | chr7  | 50450349 | 50450349 | G   | A   | exonic        | IKZF1         | nonsynonymous SNV   | IKZF1:NM_001220767:exon3:c.G272A:p.C91Y,IKZF1:NM_001220768:exon4:c.G533A:p.C178Y | 7p12.2   |
| 30857 | chrX  | 1.34E+08 | 1.34E+08 | G   | A   | exonic        | PHF6          | nonsynonymous SNV   | PHF6:NM_032335:exon8:c.G884A:p.C295Y | Xq26.2   |
| 30617 | chr11 | 1.19E+08 | 1.19E+08 | C   | T   | exonic        | CBL           | stopgain            | CBL:NM_005188:exon9:c.C1258T:p.R420X | 11q23.3  |
| 30617 | chr15 | 90631934 | 90631934 | G   | T   | exonic        | IDH2          | nonsynonymous SNV   | IDH2:NM_001195427:exon2:c.G29A:p.R10Q,IDH2:NM_002168:exon4:c.G419A:p.R140Q | 15q26.1  |
| 30617 | chr17 | 74732959 | 74732959 | G   | T   | exonic        | SRSF2         | nonsynonymous SNV   | SRSF2:NM_001195427:exon1:c.C284A:p.P95H | 17q25.1  |
| 30617 | chr20 | 31022441 | 31022441 | -   | G   | exonic        | ASXL1         | frameshift insertion | ASXL1:NM_015338:exon12:c.1927dupG:p.G642fs | 20q11.21 |
| 30617 | chr9  | 5073770  | 5073770  | G   | T   | exonic        | JAK2          | nonsynonymous SNV   | JAK2:NM_004972:exon14:c.G1849T:p.V617F | 9p24.1   |
| 30331 | chr11 | 32456348 | 32456348 | G   | T   | exonic        | WT1           | nonsynonymous SNV   | WT1:NM_000378:exon1:c.C544A:p.P182T,WT1:NM_0024424:exon1:c.C544A:p.P182T | 11p13    |
| 30331 | chr11 | 1.19E+08 | 1.19E+08 | G   | A   | exonic        | CBL           | nonsynonymous SNV   | CBL:NM_005188:exon8:c.G1211A:p.C404Y | 11q23.3  |
| 30331 | chr17 | 74732959 | 74732959 | G   | T   | exonic        | SRSF2         | nonsynonymous SNV   | SRSF2:NM_001195427:exon1:c.C284A:p.P95H | 17q25.1  |
### Supplementary Table S2. Genetic Variants Identified in 52 patients with CMML Undergoing HCT

| UPN  | Chr | Start   | End     | Ref | Alt | Func. refGene | Gen. refGene | Exonic Func. refGene | AAChange refGene | cytoband |
|------|-----|---------|---------|-----|-----|---------------|--------------|----------------------|------------------|----------|
| 30331 | chr17 | 74732959 | 74732959 | G   | T   | exonic       | SRSF2        | nonsynonymous SNV    | SRSF2:NM_001195427:exon1:c.C284A:p.P95H,SRSF2:NM_003016:exon1:c.C284A:p.P95H | 17q25.1 |
| 30331 | chr2  | 1.37E+08 | 1.37E+08 | C   | T   | exonic       | CXCR4        | nonsynonymous SNV    | CXCR4:NM_001008540:exon1:c.G949A:p.A317T,CXCR4:NM_003016:exon1:c.G937A:p.A313T | 2q22.1 |
| 30331 | chr20 | 31022592 | 31022592 | C   | T   | exonic       | ASXL1        | stopgain             | ASXL1:NM_015338:exon12:c.C2077T:p.R693X | 20q11.21 |
| 30331 | chr20 | 31022697 | 31022697 | G   | A   | exonic       | NOTCH1       | nonsynonymous SNV    | NOTCH1:NM_017617:exon34:c.C6310T:p.R2104C | 9q34.3 |
| 30331 | chr4  | 1.06E+08 | 1.06E+08 | TGA | -   | exonic       | TET2         | frameshift deletion  | TET2:NM_001127208:exon3:c.C80T:p.T271I | 4q24 |
| 30331 | chr4  | 1.06E+08 | 1.06E+08 | C   | T   | exonic       | TET2         | nonsynonymous SNV    | TET2:NM_001127208:exon6:c.A3644G:p.E1215G | 4q24 |
| 30331 | chr7  | 1.4E+08  | 1.4E+08  | C   | T   | exonic       | BRAF         | nonsynonymous SNV    | BRAF:NM_004333:exon13:c.C1567T:p.P523S | 7q34 |
| 30331 | chr9  | 1.39E+08 | 1.39E+08 | C   | A   | exonic       | NOTCH1       | nonsynonymous SNV    | NOTCH1:NM_017617:exon34:c.C6310T:p.R2104C | 9q34.3 |
| 30331 | chrX  | 76889140 | 76889140 | C   | T   | exonic       | ATRX         | nonsynonymous SNV    | ATRX:NM_138270:exon17:c.G4756A:p.V1586M,ATRX:NM_000489:exon18:c.G4870A:p.V1624M | Xq21.1 |
| 30331 | chrX  | 53432451 | 53432451 | C   | T   | exonic       | SMC1A        | nonsynonymous SNV    | SMC1A:NM_006306:exon11:c.G1858A:p.A629T,SMC1A:NM_001281463:exon12:c.G1819A:p.A607T | Xp11.22 |
| 30037 | chr1  | 1.15E+08 | 1.15E+08 | C   | T   | exonic       | NRAS         | nonsynonymous SNV    | NRAS:NM_002524:exon2:c.G35A:p.G12D | 1p13.2 |
| 30037 | chr19 | 33792759 | 33792759 | G   | A   | exonic       | CEBPA        | nonsynonymous SNV    | CEBPA:NM_001285829:exon1:c.C2057T:p.P695S,CEBPA:NM_001287424:exon1:c.C667T:p.P223S,CEBPA:NM_001287435:exon1:c.C520T:p.P174S,CEBPA:NM_004364:exon1:c.C562T:p.P188S | 19q13.11 |
| 30037 | chr7  | 1.49E+08 | 1.49E+08 | C   | T   | exonic       | EZH2         | nonsynonymous SNV    | EZH2:NM_152998:exon13:c.G1523A:p.C508Y,EZH2:NM_001203247:exon14:c.G1640A:p.C547Y,EZH2:NM_001203248:exon14:c.G1613A:p.C538Y,EZH2:NM_004456:exon14:c.G1655A:p.C552Y | 7q36.1 |
| 29524 | chr11 | 1.19E+08 | 1.19E+08 | T   | C   | exonic       | CBL          | nonsynonymous SNV    | CBL:NM_005188:exon3:c.T485C:p.L162P | 11q23.3 |
Supplementary Table S2. Genetic Variants Identified in 52 patients with CMML Undergoing HCT

| UPN  | Chr    | Start       | End       | Ref | Alt | Func. refGene | Gene. refGene | ExonicFunc. refGene | AAChange.refGene | cytoBand |
|------|--------|-------------|-----------|-----|-----|---------------|---------------|---------------------|------------------|----------|
| 29524| chr3   | 1.28E+08    | 1.28E+08  | T   | A   | exonic        | GATA2         | nonsynonymous SNV   | GATA2:NM_001145662:exon3:c.A617T:p.E206V,GATA2:NM_032638:exon3:c.A617T:p.E206V,GATA2:NM_001145661:exon4:c.A617T:p.E206V | 3q21.3 |
| 29524| chr4   | 1.06E+08    | 1.06E+08  | G   | A   | exonic        | TET2         | nonsynonymous SNV   | TET2:NM_001127208:exon3:c.G149A:p.G50E;TET2:NM_017628:exon3:c.G149A:p.G50E | 4q24   |
| 29524| chr4   | 1.06E+08    | 1.06E+08  | -   | A   | exonic        | TET2         | frameshift insertion| TET2:NM_001127208:exon3:c.1624dupA:p.L541fs;TET2:NM_017628:exon3:c.1624dupA:p.L541fs | 4q24   |
| 29524| chrX   | 76888836    | 76888836  | T   | A   | exonic        | ATRX         | stopgain            | ATRX:NM_138270:exon18:c.A4879T:p.R1627X,ATRX:NM_000489:exon19:c.A4993T:p.R1665X | Xq21.1 |
| 28845| chr1   | 1.15E+08    | 1.15E+08  | C   | T   | exonic        | NRAS         | nonsynonymous SNV   | NRAS:NM_002524:exon2:c.G35A:p.G12D | 1p13.2  |
| 28845| chr10  | 1.12E+08    | 1.12E+08  | C   | T   | exonic        | SMC3         | stopgain            | SMC3:NM_005445:exon25:c.C308T:p.Q103X | 10q25.2 |
| 28845| chr11  | 1.18E+08    | 1.18E+08  | C   | T   | exonic        | KMT2A        | nonsynonymous SNV   | KMT2A:NM_001197104:exon26:c.C6451T:p.P2151S,KMT2A:NM_005933:exon26:c.C6451T:p.P2148S | 11q23.3|
| 28845| chr19  | 33792336    | 33792336  | C   | T   | exonic        | CEBPA        | nonsynonymous SNV   | CEBPA:NM_001285829:exon1:c.G628A:p.E210K,CEBPA:NM_001287424:exon1:c.G7191A:p.R3014S,CEBPA:NM_001287435:exon1:c.G943A:p.R315K,CEBPA:NM_004364:exon1:c.G985A:p.E329K | 19q13.11|
| 28845| chr20  | 31021700    | 31021700  | C   | T   | exonic        | ASXL1        | nonsynonymous SNV   | ASXL1:NM_015338:exon11:c.C1699T:p.P567S | 20q11.21|
| 28845| chr4   | 1.06E+08    | 1.06E+08  | C   | T   | exonic        | TET2         | stopgain            | TET2:NM_001127208:exon3:c.C2887T:p.Q963X,TET2:NM_017628:exon3:c.C2887T:p.Q963X | 4q24   |
| 28845| chr4   | 1.53E+08    | 1.53E+08  | C   | T   | exonic        | FBXW7        | stopgain            | FBXW7:NM_001013415:exon8:c.G921A:p.W307X,FBXW7:NM_018315:exon8:c.G1035A:p.W345X,FBXW7:NM_033632:exon9:c.G1275A:p.W425X | 4q31.3  |
| 28845| chr5   | 1.77E+08    | 1.77E+08  | T   | A   | exonic        | DDX41        | nonsynonymous SNV   | DDX41:NM_016222:exon14:c.A1537T:p.I513F | 5q35.3  |
| 28845| chrX   | 76888836    | 76888836  | T   | A   | exonic        | ATRX         | stopgain            | ATRX:NM_138270:exon18:c.A4879T:p.R1627X,ATRX:NM_000489:exon19:c.A4993T:p.R1665X | Xq21.1  |
| UPN  | Chr | Start       | End         | Ref | Alt | Func. refGene | Gene. refGene | ExonicFunc. refGene | AAChange.refGene | cytoBand |
|------|-----|-------------|-------------|-----|-----|---------------|---------------|---------------------|-----------------|----------|
| 28258 | chr15 | 90631952    | 90631952    | C   | T   | exonic        | IDH2          | nonsynonymous SNV   | IDH2:NM_001290114:exon2:c.G11A:p.S4N,IDH2:NM_001289910:exon4:c.G245A:p.S82N,IDH2:NM_002168:exon4:c.G401A:p.S134N | 15q26.1          |
| 28258 | chr18 | 42532066    | 42532066    | C   | T   | exonic        | SETBP1        | nonsynonymous SNV   | SETBP1:NM_015559:exon4:c.C2761T:p.H921Y | 18q12.3         |
| 28258 | chr3  | 38181944    | 38181944    | G   | A   | exonic        | MYD88         | nonsynonymous SNV   | MYD88:NM_001172568:exon2:c.G433A:p.E145K,MYD88:NM_001172567:exon3:c.G568A:p.E190K,MYD88:NM_002168:exon3:c.G568A:p.E190K | 3p22.2          |
| 28258 | chr4  | 1.53E+08    | 1.53E+08    | C   | T   | exonic        | FBXW7         | stopgain            | FBXW7:NM_001013415:exon8:c.G921A:p.W307X,FBXW7:NM_018315:exon8:c.G1035A:p.W345X,FBXW7:NM_0033632:exon9:c.G1275A:p.W425X | 4q31.3          |
| 28258 | chr4  | 1.53E+08    | 1.53E+08    | C   | T   | exonic        | FBXW7         | nonsynonymous SNV   | FBXW7:NM_001013415:exon10:c.G1315A:p.G439R,FBXW7:NM_018315:exon10:c.G1429A:p.G477R,FBXW7:NM_0033632:exon11:c.G1669A:p.G557R | 4q31.3          |
| 28258 | chr4  | 55561718    | 55561718    | -   | T   | exonic        | KIT           | frameshift insertion| KIT:NM_000222:exon2:c.108_109insT:p.P36fs,KIT:NM_001093772:exon2:c.108_109insT:p.P36fs | 4q12            |
| 28258 | chr4  | 1.06E+08    | 1.06E+08    | C   | T   | exonic        | TET2          | nonsynonymous SNV   | TET2:NM_001127208:exon6:c.C3781T:p.R1261C | 4q24            |
| 28258 | chr4  | 1.06E+08    | 1.06E+08    | C   | T   | exonic        | TET2          | stopgain            | TET2:NM_001127208:exon3:c.C1771T:p.Q591X,TET2:NM_017628:exon3:c.C1771T:p.Q591X | 4q24            |
| 28258 | chrX  | 53442118    | 53442118    | C   | T   | exonic        | SMC1A         | nonsynonymous SNV   | SMC1A:NM_006306:exon2:c.G110A:p.G37D,SMC1A:NM_00281463:exon3:c.G44A:p.G15D | Xp11.22         |
| 26842 | NA   | NA          | NA          | NA  | NA  | NA            | NA            | NA                  | NA              | NA        |
| 26671 | chr12 | 1.12E+08    | 1.12E+08    | C   | T   | exonic        | SH2B3         | stopgain            | SH2B3:NM_005475:exon2:c.C130T:p.Q44X | 12q24.12        |
| 26671 | chr19 | 45303675    | 45303675    | G   | A   | exonic        | CBLC          | nonsynonymous SNV   | CBLC:NM_001130852:exon9:c.G1262A:p.G421E,CBLC:NM_00121116:exon10:c.G1400A:p.G467E | 19q13.32        |
| 26671 | chr19 | 56173950    | 56173964    | AGA | TTA | exonic        | U2AF2         | nonframeshift deletion| U2AF2:NM_001012478:exon6:c.569_583del:p.19_195del,U2AF2:NM_007279:exon6:c.569_583del:p.19_195del | 19q13.42        |
### Supplementary Table S2. Genetic Variants Identified in 52 patients with CMML Undergoing HCT

| UPN | Chr | Start | End | Ref | Alt | Func. refGene | Gene. refGene | ExonicFunc. refGene | AAClange.refGene | cytoBand |
|-----|-----|-------|-----|-----|-----|---------------|---------------|-------------------|-------------------|----------|
| 26671 | chr20 | 31022403 | 31022425 | AGG | ACA | CAC | CAC | TGC | CAT | AGA | GAG | GCG | GC | - | exonic | ASXL1 | frameshift deletion | ASXL1:NM_015338:exon12:c.1888_1910del:p.H630fs | 20q11.21 |
| 26671 | chr21 | 36171684 | 36171684 | G | A | exonic | RUNX1 | nonsynonymous SNV | RUNX1:NM_001001890:exon5:c.C800T:p.P267L,RUNX1:NM_001754:exon8:c.C881T:p.P294L | 21q22.12 |
| 26671 | chr4 | 55561704 | 55561704 | G | A | exonic | KIT | nonsynonymous SNV | KIT:NM_000222:exon2:c.G94A:p.G32R,KIT:NM_001093772:exon2:c.G94A:p.G32R | 4q12 |
| 26671 | chr4 | 1.06E+08 | 1.06E+08 | G | A | exonic | TET2 | nonsynonymous SNV | TET2:NM_001127208:exon3:c.G1696A:p.E566K,TET2:NM_017628:exon3:c.G1696A:p.E566K | 4q24 |
| 26671 | chr4 | 1.06E+08 | 1.06E+08 | C | T | exonic | TET2 | nonsynonymous SNV | TET2:NM_001127208:exon11:c.C4928T:p.S1643F | 4q24 |
| 26671 | chr7 | 1.49E+08 | 1.49E+08 | C | T | exonic | EZH2 | nonsynonymous SNV | EZH2:NM_152998:exon9:c.G1075A:p.E359K,EZH2:NM_001203247:exon10:c.G1192A:p.E398K,EZH2:NM_01203248:exon10:c.G1165A:p.E389K,EZH2:NM_001203249:exon10:c.G1165A:p.E389K,EZH2:NM_004456:exon10:c.G1207A:p.E403K | 7q36.1 |
| 26671 | chr8 | 1.29E+08 | 1.29E+08 | A | T | exonic | MYC | nonsynonymous SNV | MYC:NM_002467:exon2:c.A371T:p.D124V | 8q24.21 |
| 26671 | chr9 | 21971153 | 21971153 | C | T | exonic | CDKN2A | nonsynonymous SNV | CDKN2A:NM_000077:exon2:c.G205A:p.E69K,CDKN2A:NM_001195132:exon2:c.G205A:p.E69K,CDKN2A:NM_058195:exon2:c.G248A:p.G83E | 9p21.3 |
| 26671 | chr9 | 21974768 | 21974768 | G | A | exonic | CDKN2A | nonsynonymous SNV | CDKN2A:NM_000077:exon1:c.C59T:p.A20V,CDKN2A:NM_001195132:exon1:c.C59T:p.A20V,CDKN2A:NM_058197:exon1:c.C59T:p.A20V | 9p21.3 |
| UPN  | Chr    | Start   | End     | Ref  | Alt  | Func. refGene | Gene. refGene | ExonicFunc. refGene | AAChange.refGene | cytoBand |
|------|--------|---------|---------|------|------|---------------|---------------|---------------------|-----------------|----------|
| 26671| chrX   | 39922097| 39922097| C    | T    | exonic        | BCOR          | nonsynonymous SNV   | BCOR:NM_001123384:exon8:c.G3919A:p.G1307R,BCOR:NM_001123385:exon9:c.G3973A:p.G1359R,BCOR:NM_017745:exon9:c.G3973A:p.G1325R | Xp11.4          |
| 26671| chrX   | 1.29E+08| 1.29E+08| A    | G    | exonic        | BCORL1        | nonsynonymous SNV   | BCORL1:NM_001184772:exon3:c.A2273G:p.G13258G,BCORL1:NM_021946:exon3:c.A2273G:p.G13258G | Xq26.1          |
| 26181| chr20  | 31024840| 31024840| G    | A    | exonic        | ASXL1         | nonsynonymous SNV   | ASXL1:NM_015338:exon12:c.G4325A:p.G1442E | 20q11.21 |
| 26181| chr4   | 1.06E+08| 1.06E+08| G    | A    | exonic        | TET2          | nonsynonymous SNV   | TET2:NM_001127208:exon3:c.G901A:p.A301T,TET2:NM_017628:exon3:c.G901A:p.A301T | 4q24 |
| 26181| chr4   | 1.06E+08| 1.06E+08| G    | A    | exonic        | TET2          | nonsynonymous SNV   | TET2:NM_001127208:exon10:c.G4352A:p.R1451Q | 4q24 |
| 25661| chr11  | 32456685| 32456685| C    | T    | exonic        | WT1           | nonsynonymous SNV   | WT1:NM_000378:exon12:c.G207A:p.M69I,WT1:NM_024424:exon12:c.G207A:p.M69I,WT1:NM_024426:exon12:c.G207A:p.M69I | 11p13 |
| 25661| chr12  | 1.13E+08| 1.13E+08| C    | T    | exonic        | PTPN11        | nonsynonymous SNV   | PTPN11:NM_002834:exon11:c.C1285T:p.P429S,PTPN11:NM_080601:exon11:c.C1285T:p.P429S | 12q24.13 |
| 25661| chr12  | 1.13E+08| 1.13E+08| A    | T    | exonic        | PTPN11        | nonsynonymous SNV   | PTPN11:NM_002834:exon11:c.A1342T:p.S448C,PTPN11:NM_080601:exon11:c.A1342T:p.S448C | 12q24.13 |
| 25661| chr15  | 66727405| 66727405| G    | A    | exonic        | MAP2K1        | nonsynonymous SNV   | MAP2K1:NM_0002755:exon2:c.G121A:p.E41K | 15q22.31 |
| 25661| chr17  | 74732959| 74732959| G    | T    | exonic        | SRSF2         | nonsynonymous SNV   | SRSF2:NM_001195427:exon12:c.G284A:p.P95H,SRSF2:NM_003016:exon12:c.G284A:p.P95H | 17q25.1 |
| 25661| chr17  | 7577538| 7577538| C    | T    | exonic        | TP53          | nonsynonymous SNV   | TP53:NM_001126115:exon3:c.G347A:p.R116Q,TP53:NM_001126116:exon3:c.G347A:p.R116Q,TP53:NM_001126117:exon3:c.G347A:p.R116Q,TP53:NM_001276697:exon3:c.G266A:p.R89Q,TP53:NM_001276698:exon3:c.G266A:p.R89Q,TP53:NM_001276699:exon3:c.G266A:p.R89Q,TP53:NM_001276699:exon3:c.G266A:p.R89Q | 17p13.1 |
## Supplementary Table S2. Genetic Variants Identified in 52 patients with CMML Undergoing HCT

| UPN | Chr | Start | End | Ref | Alt | Func. refGene | Gene. refGene | ExonicFunc. refGene | AAChecke.refGene | cytoBand |
|-----|-----|-------|-----|-----|-----|--------------|--------------|---------------------|-----------------|----------|
| 25661 | chr17 | 74732959 | 74732959 | G | T | exonic | SRSF2 | nonsynonymous SNV | SRSF2:NM_001195427:exon1:c.C284A:p.P95H, SRSF2:NM_003016:exon1:c.C284A:p.P95H | 17q25.1 |
| 25661 | chr17 | 7577538 | 7577538 | C | T | exonic | TP53 | nonsynonymous SNV | TP53:NM_001126115:exon3:c.G347A:p.R116Q, TP53:NM_001126116:exon3:c.G347A:p.R116Q, TP53:NM_001126117:exon3:c.G347A:p.R116Q, TP53:NM_001276697:exon3:c.G266A:p.R89Q, TP53:NM_001276698:exon3:c.G266A:p.R89Q, TP53:NM_001276699:exon3:c.G266A:p.R89Q, TP53:NM_001126112:exon7:c.G743A:p.R248Q, TP53:NM_001126113:exon7:c.G743A:p.R248Q, TP53:NM_001126114:exon7:c.G743A:p.R248Q, TP53:NM_001276695:exon7:c.G626A:p.R209Q, TP53:NM_001276696:exon7:c.G626A:p.R209Q, TP53:NM_001276760:exon7:c.G626A:p.R209Q, TP53:NM_001276761:exon7:c.G626A:p.R209Q | 17p13.1 |
| 25661 | chr17 | 74732959 | 74732959 | G | T | exonic | SRSF2 | nonsynonymous SNV | SRSF2:NM_001195427:exon1:c.C284A:p.P95H, SRSF2:NM_003016:exon1:c.C284A:p.P95H | 17q25.1 |
Supplementary Table S2. Genetic Variants Identified in 52 patients with CMML Undergoing HCT

| UPN  | Chr   | Start   | End     | Ref | Alt | Func. refGene | Gene. refGene | ExonicFunc. refGene | AACHange.refGene | cytoBand |
|------|-------|---------|---------|-----|-----|---------------|---------------|---------------------|-------------------|----------|
| 25661 | chr2  | 25505442| 25505442| G   | A   | exonic        | DNMT3A        | nonsynonymous SNV   | DNMT3A:NM_022552:exon4:c.C316T:p.P106S,DNMT3A:NM_1575629:exon4:c.C316T:p.P106S,DNMT3A:NM_175630:exon4:c.C316T:p.P106S | 2p23.3 |
| 25661 | chr2  | 25464466| 25464466| A   | C   | exonic        | DNMT3A        | nonsynonymous SNV   | DNMT3A:NM_153759:exon13:c.T1480G:p.Y494D,DNMT3A:NM_022552:exon17:c.T2047G:p.Y683D,DNMT3A:NM_175629:exon17:c.T2047G:p.Y683D | 2p23.3 |
| 25661 | chr20 | 31021154| 31021154| G   | T   | exonic        | ASXL1         | nonsynonymous SNV   | ASXL1:NM_015338:exon11:c.G1153T:p.G385C | 20q11.21 |
| 25661 | chr4  | 1.06E+08| 1.06E+08| T   | A   | exonic        | TET2          | nonsynonymous SNV   | TET2:NM_001127208:exon11:c.T5724A:p.N1908K | 4q24    |
| 25661 | chr4  | 1.06E+08| 1.06E+08| -   | T   | exonic        | TET2          | frameshift insertion | TET2:NM_001127208:exon3:c.3358dupT:p.L1119fs,TET2:NM_0017628:exon3:c.3358dupT:p.L1119fs | 4q24    |
| 25661 | chr7  | 1.49E+08| 1.49E+08| C   | T   | exonic        | EZH2          | nonsynonymous SNV   | EZH2:NM_152998:exon13:c.G1523A:p.C508Y,EZH2:NM_001203247:exon14:c.G1640A:p.C547Y,EZH2:NM_001203248:exon14:c.G1613A:p.C538,Y,EZH2:NM_004456:exon14:c.G1655A:p.C552Y | 7q36.1  |
| 25661 | chr7  | 50450349| 50450349| G   | A   | exonic        | IKZF1         | nonsynonymous SNV   | IKZF1:NM_001220767:exon3:c.G272A:p.C91Y,IKZF1:NM_0011220770:exon3:c.G272A:p.C91Y,IKZF1:NM_001220768:exon4:c.G533A:p.C178Y,IKZF1:NM_001291838:exon4:c.G272A:p.C91Y,IKZF1:NM_001291839:exon4:c.G272A:p.C91Y,IKZF1:NM_001291837:exon5:c.G533A:p.C178Y,IKZF1:NM_006060:exon5:c.G533A:p.C178Y | 7p12.2  |
| 25661 | chrX  | 76937084| 76937084| C   | A   | exonic        | ATRX          | nonsynonymous SNV   | ATRX:NM_138270:exon8:c.G3550T:p.D1184Y,ATRX:NM_000489:exon9:c.G3664T:p.D1222Y | Xq21.1 |
| 25661 | chrX  | 44938498| 44938498| G   | A   | exonic        | KDM6A         | nonsynonymous SNV   | KDM6A:NM_001291418:exon18:c.G2809A:p.G937R,KDM6A:NM_001291421:exon18:c.G2158A:p.G720R,KDM6A:NM_001291417:exon19:c.G29 | Xp11.3 |
### Supplementary Table S2. Genetic Variants Identified in 52 patients with CMML Undergoing HCT

| UPN | Chr | Start   | End     | Ref | Alt | Func. refGene | Gen. refGene | ExonicFunc. refGene | AAChange.refGene | cytoBand |
|-----|-----|---------|---------|-----|-----|---------------|-------------|---------------------|------------------|----------|
| 25661 | chrX | 15822306 | 15822306 | A   | T   | exonic        | ZRSR2       | stopgain            | ZRSR2:NM_005089:exon5:c.A385T:p.K129X | Xp22.2   |
| 25597 | chr17 | 74732959 | 74732959 | G   | T   | exonic        | SRSF2       | nonsynonymous SNV  | SRSF2:NM_001195427:exon1:c.C284A:p.P95H, SRSF2:NM_003016:exon1:c.C284A:p.P95H | 17q25.1  |
| 25441 | chr17 | 7577097  | 7577097  | C   | T   | exonic        | TP53        | nonsynonymous SNV  | TP53:NM_001126115:exon4:c.G445A:p.D149N, TP53:NM_001126116:exon4:c.G445A:p.D149N, TP53:NM_001126117:exon4:c.G445A:p.D149N, TP53:NM_001276697:exon4:c.G364A:p.D122N, TP53:NM_001276698:exon4:c.G364A:p.D122N, TP53:NM_001276699:exon4:c.G364A:p.D122N, TP53:NM_001126118:exon7:c.G724A:p.D242N, TP53:NM_000546:exon8:c.G841A:p.D281N, TP53:NM_001126112:exon8:c.G841A:p.D281N, TP53:NM_001126113:exon8:c.G841A:p.D281N, TP53:NM_001126114:exon8:c.G841A:p.D281N, TP53:NM_001126115:exon8:c.G841A:p.D281N, TP53:NM_001126116:exon8:c.G841A:p.D281N, TP53:NM_001126117:exon8:c.G841A:p.D281N, TP53:NM_001276695:exon8:c.G724A:p.D242N, TP53:NM_001276696:exon8:c.G724A:p.D242N, TP53:NM_001276697:exon8:c.G724A:p.D242N, TP53:NM_001276698:exon8:c.G724A:p.D242N, TP53:NM_001276699:exon8:c.G724A:p.D242N, TP53:NM_001276760:exon8:c.G724A:p.D242N, TP53:NM_001276761:exon8:c.G724A:p.D242N | 17p13.1  |
| 24925 | chr1 | 1.15E+08  | 1.15E+08  | C   | T   | exonic        | NRAS        | nonsynonymous SNV  | NRAS:NM_002524:exon2:c.G35A:p.G12D | 1p13.2   |
| 24925 | chr19 | 56173950  | 56173964  | AGA |   | exonic        | U2AF2       | nonframeshift deletion | U2AF2:NM_001012478:exon6:c.569_583del:p.19_195del,U2AF2:NM_007279:exon6:c.569_583del:p.190_195del | 19q13.42 |
| 24925 | chr20 | 31022441  | 31022441  | -   | G   | exonic        | ASXL1       | frameshift insertion | ASXL1:NM_015338:exon12:c.1927dupG:p.G642fs | 20q11.21 |
Supplementary Table S2. Genetic Variants Identified in 52 patients with CMML Undergoing HCT

| UPN  | Chr  | Start   | End     | Ref | Alt | Func. refGene | Gene. refGene | ExonicFunc. refGene | AACHange.refGene | cytoBand |
|------|------|---------|---------|-----|-----|---------------|---------------|---------------------|------------------|----------|
| 24623| chr11| 1.19E+08| 1.19E+08| GG  | -   | exonic        | CBL           | frameshift deletion |                  | 11q23.3   |
| 24623| chr11| 32449539| 32449539| C   | T   | exonic        | WT1           | nonsynonymous SNV  |                  | 11p13     |
| 24623| chr12| 1.12E+08| 1.12E+08| G   | C   | exonic        | SH2B3         | nonsynonymous SNV  |                  | 12q24.12  |
| 24623| chr12| 25398281| 25398281| C   | T   | exonic        | KRAS          | nonsynonymous SNV  |                  | 12p12.1   |
| 24623| chr17| 74732959| 74732959| G   | T   | exonic        | SRSF2         | nonsynonymous SNV  |                  | 17q25.1   |
| 24623| chr21| 36259160| 36259160| CTT | GGA | exonic        | RUNX1         | nonframeshift deletion |                  | 21q22.12  |
| 24623| chr4  | 55593648| 55593648| G   | A   | exonic        | KIT           | nonsynonymous SNV  |                  | 4q12      |
| 24623| chr4  | 1.06E+08| 1.06E+08| G   | A   | exonic        | TET2          | nonsynonymous SNV  |                  | 4q24      |
| 24623| chr4  | 1.06E+08| 1.06E+08| G   | A   | exonic        | TET2          | nonsynonymous SNV  |                  | 4q24      |
| 24623| chr9  | 5073770 | 5073770 | G   | T   | exonic        | JAK2          | nonsynonymous SNV  |                  | 9p24.1    |
Supplementary Table S2. Genetic Variants Identified in 52 patients with CMML Undergoing HCT

| UPN   | Chr | Start | End   | Ref | Alt | Func. refGene | Gene. refGene | ExonicFunc. refGene | AAChange.refGene | cytoBand |
|-------|-----|-------|-------|-----|-----|---------------|---------------|--------------------|------------------|----------|
| 24623 | chrX| 76889140 | 76889140 | C   | T   | exonic        | ATRX          | nonsynonymous SNV  | ATRX:NM_138270:exon17:c.G4756A:p.V1586M, ATRX:NM_000489:exon18:c.G4870A:p.V1624M | Xq21.1 |
| 24623 | chrX| 44732933 | 44732933 | A   | T   | exonic        | KDM6A         | nonsynonymous SNV  | KDM6A:NM_001291415:exon1:c.A136T:p.R46W, KDM6A:NM_001291416:exon1:c.A136T:p.R46W, KDM6A:NM_001291417:exon1:c.A136T:p.R46W, KDM6A:NM_001291418:exon1:c.A136T:p.R46W | Xp11.3 |
| 24532 | chr12| 1.13E+08 | 1.13E+08 | G   | T   | exonic        | PTPN11        | nonsynonymous SNV  | PTPN11:NM_002834:exon13:c.G1508T:p.G503V | 12q24.13 |
| 24288 | NA  | NA    | NA    | NA  | NA  | NA            | NA            | NA                 | NA               | NA       |
| 24119 | chr12| 25398284 | 25398284 | C   | T   | exonic        | KRAS          | nonsynonymous SNV  | KRAS:NM_004985:exon2:c.G35A:p.G12D,KRAS:NM_001754:exon8:c.C958T:p.R320X | 12p12.1 |
| 21421 | chr11| 1.19E+08 | 1.19E+08 | CTG | -   | exonic        | CBL           | nonframeshift deletion | CBL:NM_005188:exon8:c.1113_1115del:p.371_372del | 11q23.3 |
| 21421 | chr2 | 25457242 | 25457242 | C   | T   | exonic        | DNMT3A        | nonsynonymous SNV  | DNMT3A:NM_153759:exon19:c.G2078A:p.R693H,DNMT3A:NM_022552:exon23:c.G2645A:p.R828H,DNMT3A:NM_175629:exon23:c.G2645A:p.R882H | 2p23.3 |
| 21421 | chr20| 31022441 | 31022441 | -   | G   | exonic        | ASXL1         | frameshift insertion | ASXL1:NM_015338:exon12:c.1927dupG:p.G642fs | 20q11.21 |
| 21421 | chr21| 36171607 | 36171607 | G   | A   | exonic        | RUNX1         | stopgain           | RUNX1:NM_001001890:exon5:c.C877T:p.R293X,RUNX1:NM_001754:exon8:c.C958T:p.R320X | 21q22.12 |
| 20950 | NA  | NA    | NA    | NA  | NA  | NA            | NA            | NA                 | NA               | NA       |
| 20948 | chr12| 25398281 | 25398281 | C   | T   | exonic        | KRAS          | nonsynonymous SNV  | KRAS:NM_004985:exon2:c.G38A:p.G13D,KRAS:NM_033360:exon2:c.G38A:p.G13D | 12p12.1 |
| 20948 | chr20| 31022403 | 31022425 | CAC | -   | exonic        | ASXL1         | frameshift deletion | ASXL1:NM_015338:exon12:c.1888_1910del:p.H630fs | 20q11.21 |
Supplementary Table S2. Genetic Variants Identified in 52 patients with CMML Undergoing HCT

| UPN  | Chr  | Start       | End       | Ref | Alt | Func. Gene | Gen. Gene | Exonic Func. Gene | AAClange.refGene | cytoBand |
|------|------|-------------|-----------|-----|-----|------------|-----------|-------------------|-----------------|----------|
| GCG  | GC   |             |           |     |     | PTEN       | PTEN     | nonsynonymous SNV | PTEN:NM_000314: | 10q23.31  |
| 20698| chr10| 89712007    | 89712007  | G   | A   | exonic     | PTEN     | PTEN:NM_000314: | ex4:c.G625A:p.G209R, |          |
|      |      |             |           |     |     |            |          | PTEN:NM_000314: | p.G209R, |          |
|      |      |             |           |     |     |            |          | PTEN:NM_000314: | ex6:c.G34A:p.G12R, |          |
|      |      |             |           |     |     |            |          | PTEN:NM_000314: | ex7:c.G1144A:p.G382R |          |
|      |      |             |           |     |     |            |          |                   |                 |          |
| 20698| chr11| 1.19E+08    | 1.19E+08  | C   | G   | exonic     | CBL      | nonsynonymous SNV| CBL:NM_005188: | 11q23.3   |
|      |      |             |           |     |     |            |          |                   | ex7:c.G835A:p.G279S,W |          |
|      |      |             |           |     |     |            |          |                   | WT1:NM_000378: |          |
|      |      |             |           |     |     |            |          |                   | ex3:c.G835A:p.G279S,WT1: |          |
|      |      |             |           |     |     |            |          |                   | NM_001198551: |          |
|      |      |             |           |     |     |            |          |                   | ex4:c.G199A:p.G67S,WT1:N |          |
|      |      |             |           |     |     |            |          |                   | M_001198552:exon3:c.G199A:p.G67S,WT1:NM_024424: |          |
|      |      |             |           |     |     |            |          |                   | exon3:c.G835A:p.G279S,WT1:NM_0244: |          |
|      |      |             |           |     |     |            |          |                   | 26:exon3:c.G835A:p.G279S |          |
| 20698| chr11| 1.19E+08    | 1.19E+08  | C   | G   | exonic     | CBL      | nonsynonymous SNV| CBL:NM_005188: | 11q23.3   |
|      |      |             |           |     |     |            |          |                   | ex7:c.G835A:p.G279S,WT1: |          |
|      |      |             |           |     |     |            |          |                   | NM_001198551: |          |
|      |      |             |           |     |     |            |          |                   | ex4:c.G199A:p.G67S,WT1:N |          |
|      |      |             |           |     |     |            |          |                   | M_001198552:exon3:c.G199A:p.G67S,WT1:NM_024424: |          |
|      |      |             |           |     |     |            |          |                   | exon3:c.G835A:p.G279S,WT1:NM_0244: |          |
|      |      |             |           |     |     |            |          |                   | 26:exon3:c.G835A:p.G279S |          |
| 20698| chr11| 32449539    | 32449539  | C   | T   | exonic     | WT1      | nonsynonymous SNV| WT1:NM_000378: | 11p13     |
|      |      |             |           |     |     |            |          |                   | ex3:c.G835A:p.G279S,WT1: |          |
|      |      |             |           |     |     |            |          |                   | NM_001198551: |          |
|      |      |             |           |     |     |            |          |                   | ex4:c.G199A:p.G67S,WT1:N |          |
|      |      |             |           |     |     |            |          |                   | M_001198552:exon3:c.G199A:p.G67S,WT1:NM_024424: |          |
|      |      |             |           |     |     |            |          |                   | exon3:c.G835A:p.G279S,WT1:NM_0244: |          |
|      |      |             |           |     |     |            |          |                   | 26:exon3:c.G835A:p.G279S |          |
| 20698| chr11| 1.19E+08    | 1.19E+08  | C   | G   | exonic     | CBL      | nonsynonymous SNV| CBL:NM_005188: | 11q23.3   |
|      |      |             |           |     |     |            |          |                   | ex7:c.G835A:p.G279S,WT1: |          |
|      |      |             |           |     |     |            |          |                   | NM_001198551: |          |
|      |      |             |           |     |     |            |          |                   | ex4:c.G199A:p.G67S,WT1:N |          |
|      |      |             |           |     |     |            |          |                   | M_001198552:exon3:c.G199A:p.G67S,WT1:NM_024424: |          |
|      |      |             |           |     |     |            |          |                   | exon3:c.G835A:p.G279S,WT1:NM_0244: |          |
|      |      |             |           |     |     |            |          |                   | 26:exon3:c.G835A:p.G279S |          |
| 20698| chr12| 12038861    | 12038861  | A   | T   | exonic     | ETV6     | nonsynonymous SNV| ETV6:NM_000378: | 12p13.2    |
|      |      |             |           |     |     |            |          |                   | ex3:c.G835A:p.G279S,WT1: |          |
|      |      |             |           |     |     |            |          |                   | NM_001198551: |          |
|      |      |             |           |     |     |            |          |                   | ex4:c.G199A:p.G67S,WT1:N |          |
|      |      |             |           |     |     |            |          |                   | M_001198552:exon3:c.G199A:p.G67S,WT1:NM_024424: |          |
|      |      |             |           |     |     |            |          |                   | exon3:c.G835A:p.G279S,WT1:NM_0244: |          |
|      |      |             |           |     |     |            |          |                   | 26:exon3:c.G835A:p.G279S |          |
| 20698| chr17| 7577078     | 7577078   | T   | A   | exonic     | TP53     | nonsynonymous SNV| TP53:NM_000378: | 17p13.1    |
|      |      |             |           |     |     |            |          |                   | ex3:c.G835A:p.G279S,WT1: |          |
|      |      |             |           |     |     |            |          |                   | NM_001198551: |          |
|      |      |             |           |     |     |            |          |                   | ex4:c.G199A:p.G67S,WT1:N |          |
|      |      |             |           |     |     |            |          |                   | M_001198552:exon3:c.G199A:p.G67S,WT1:NM_024424: |          |
|      |      |             |           |     |     |            |          |                   | exon3:c.G835A:p.G279S,WT1:NM_0244: |          |
|      |      |             |           |     |     |            |          |                   | 26:exon3:c.G835A:p.G279S |          |
| 20698| chr18| 42531907    | 42531907  | G   | A   | exonic     | SETBP1   | nonsynonymous SNV| SETBP1:NM_0015559: | 18q12.3    |
|      |      |             |           |     |     |            |          |                   | ex4:c.G2602A:p.D868N |          |

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**Supplementary Table S2. Genetic Variants Identified in 52 patients with CMML Undergoing HCT**

| UPN | Chr | Start | End   | Ref | Alt | Func. refGene | Gene. refGene | Exonic.Func. refGene | AAChange.refGene | cytoBand |
|-----|-----|-------|-------|-----|-----|---------------|---------------|---------------------|-------------------|-----------|
| 20698 | chr19 | 56179891 | 56179891 | T   | C   | exonic        | U2AF2         | nonsynonymous SNV   | U2AF2:NM_001012478:exon8:c.T761C:p.V254A, U2AF2:NM_007279:exon8:c.T761C:p.V254A | 19q13.42   |
| 20698 | chr2  | 25457242 | 25457242 | C   | T   | exonic        | DNMT3A       | nonsynonymous SNV   | DNMT3A:NM_153759:exon19:c.G2078A:p.R693H,DNMT3A:NM_022552:exon23:c.G2645A:p.R82H,DNMT3A:NM_175629:exon23:c.G2645A:p.R882H | 2p23.3     |
| 20698 | chr20 | 31016167 | 31016167 | C   | T   | exonic        | ASXL1        | nonsynonymous SNV   | ASXL1:NM_015338:exon5:c.C413T:p.T138I | 20q11.21   |
| 20698 | chr20 | 31022441 | 31022441 | -   | G   | exonic        | ASXL1        | frameshift insertion| ASXL1:NM_015338:exon12:c.1927dupG:p.G642fs | 20q11.21   |
| 20698 | chr4  | 1.06E+08 | 1.06E+08 | C   | T   | exonic        | TET2         | nonsynonymous SNV   | TET2:NM_001127208:exon3:c.C2104T:p.H702Y, TET2:NM_017628:exon3:c.C2104T:p.H702Y | 4q24       |
| 20698 | chr4  | 1.06E+08 | 1.06E+08 | C   | T   | exonic        | TET2         | nonsynonymous SNV   | TET2:NM_001127208:exon3:c.C2104T:p.H702Y, TET2:NM_017628:exon3:c.C2104T:p.H702Y | 4q24       |
| 20698 | chr7  | 1.02E+08 | 1.02E+08 | C   | T   | exonic        | CUX1         | nonsynonymous SNV   | CUX1:NM_001202544:exon18:c.C1684T:p.R562C,CUX1:NM_001202545:exon18:c.C1594T:p.R532C,CUX1:NM_001202546:exon18:c.C1615T:p.R539C,CUX1:NM_001913:exon19:c.C1732T:p.R578C,CUX1:NM_181500:exon19:c.C1726T:p.R576C | 7q22.1     |
| 20698 | chrX  | 1.34E+08 | 1.34E+08 | G   | A   | exonic        | PHF6         | nonsynonymous SNV   | PHF6:NM_001015877:exon9:c.G871A:p.G291R, PHF6:NM_032458:exon9:c.G871A:p.G291R | Xq26.2     |
| 20698 | chrX  | 53432451 | 53432451 | C   | T   | exonic        | SMC1A        | nonsynonymous SNV   | SMC1A:NM_006306:exon11:c.G1885A:p.A629T, SMC1A:NM_001281463:exon12:c.G1819A:p.A607T | Xp11.22    |
| 20698 | chrX  | 44938498 | 44938498 | G   | A   | exonic        | KDM6A        | nonsynonymous SNV   | KDM6A:NM_001291418:exon18:c.G2809A:p.G937R,KDM6A:NM_001291421:exon18:c.G2158A:p.G720R,KDM6A:NM_001291417:exon19:c.G2911A:p.G971R,KDM6A:NM_001291416:exon20:c.G3067A:p.G1023R,KDM6A:NM_021140:exon20 | Xp11.3     |
Supplementary Table S2. Genetic Variants Identified in 52 patients with CMML Undergoing HCT

| UPN  | Chr | Start   | End   | Ref | Alt | Func. | Gene. | ExonicFunc. | AAChange | cytoBand |
|------|-----|---------|-------|-----|-----|-------|-------|-------------|-----------|----------|
|      |     |         |       |     |     | refGene | refGene | refGene |           |          |          |
| 20698| chrX| 1.34E+08| 1.34E+08| G   | A   | exonic | PHF6   | nonsynonymous SNV | c.G3046A:p.G1016R,KDM6A:NM_001291415:exon21:c.G3202A:p.G1068R | Xq26.2 |
| 20480| chr21| 44524456| 44524456| G   | A   | exonic | U2AF1  | nonsynonymous SNV | U2AF1:NM_001025203:exon2:c.C101T:p.S34F, U2AF1:NM_006758:exon2:c.C101T:p.S34F | 21q22.3 |
| 18580| NA  | NA      | NA    | NA  | NA  | NA    | NA    | NA          | NA        | NA       |
| 18492| chrX| 1.01E+08| 1.01E+08| C   | G   | exonic | BTK    | nonsynonymous SNV | BTK:NM_001126117:exon6:c.C613T:p.R205X,T | Xq22.1 |
| 16252| chr17| 40475057| 40475057| C   | A   | exonic | STAT3  | nonsynonymous SNV | STAT3:NM_003150:exon20:c.G1853T:p.G618V, STAT3:NM_139276:exon20:c.G1853T:p.G618V, STAT3:NM_213662:exon20:c.G1853T:p.G618V | 17q21.2 |
| 16252| chr2 | 25469107| 25469107| G   | A   | exonic | DNMT3A | nonsynonymous SNV | DNMT3A:NM_001126117:exon6:c.C613T:p.R205X,T | 2p23.3 |
| 16252| chr20| 31022449| 31022449| G   | A   | exonic | ASXL1  | nonsynonymous SNV | ASXL1:NM_001126117:exon6:c.C613T:p.R205X,T | 20q11.21|
| 16252| chr4 | 55152018| 55152018| G   | A   | exonic | PDGFRA | nonsynonymous SNV | PDGFRA:NM_001126117:exon6:c.C613T:p.R205X,T | 4q12 |
| 16252| chr7 | 1.49E+08| 1.49E+08| C   | T   | exonic | EZH2   | nonsynonymous SNV | EZH2:NM_001126117:exon6:c.C613T:p.R205X,T | 7q36.1 |
| 15886| chr11| 1.18E+08| 1.18E+08| C   | T   | exonic | KMT2A  | nonsynonymous SNV | KMT2A:NM_001126117:exon6:c.C613T:p.R205X,T | 11q23.3 |
| 15886| chr17| 7576569 | 7576569 | G   | A   | exonic | TP53   | stopgain      | TP53:NM_001126117:exon6:c.C613T:p.R205X,T | 17p13.1 |
Supplementary Table S2. Genetic Variants Identified in 52 patients with CMML Undergoing HCT

| UPN   | Chr | Start   | End     | Ref | Alt | Func. refGene | Gene. refGene | ExonicFunc. refGene | AAChange.refGene | cytoBand |
|-------|-----|---------|---------|-----|-----|---------------|---------------|--------------------|-------------------|-----------|
| 15886 | chr7| 1.02E+08| 1.02E+08| C   | T   | exonic        | CUX1          | stopgain           | 53:NM_001126113:exon10:c.C1009T:p.R337X,T | 7q22.1    |
|       |     |         |         |     |     |               |               |                    | P53:NM_001276695:exon10:c.C892T:p.R298X |          |
|       |     |         |         |     |     |               |               |                    | CUX1:NM_001202543:exon15:c.C1708T:p.Q570 |          |
|       |     |         |         |     |     |               |               |                    | CUX1:NM_181552:exon15:c.C1675T:p.Q559X |          |
| 15886 | chr9| 1.34E+08| 1.34E+08| G   | A   | exonic        | ABL1          | nonsynonymous SNV | ABL1:NM_005157:exon10:c.G1519A:p.E507K,A | 9q34.12   |
|       |     |         |         |     |     |               |               |                    | ABL1:NM_007313:exon10:c.G1576A:p.E526K |          |
| 15886 | chrX| 39934019| 39934019| G   | A   | exonic        | BCOR          | nonsynonymous SNV | BCOR:NM_001123383:exon4:c.C580T:p.P194S, | Xp11.4    |
|       |     |         |         |     |     |               |               |                    | BCOR:NM_001123384:exon4:c.C580T:p.P194S, |          |
|       |     |         |         |     |     |               |               |                    | BCOR:NM_001123385:exon4:c.C580T:p.P194S, |          |
|       |     |         |         |     |     |               |               |                    | BCOR:NM_017745:exon4:c.C580T:p.P194S | Xp11.12   |
| 15886 | chrX| 53441966| 53441966| C   | A   | exonic        | SMC1A         | nonsynonymous SNV | SMC1A:NM_006306:exon2:c.G262T:p.G88C,SM | 12q22.3   |
|       |     |         |         |     |     |               |               |                    | SMC1A:NM_001281463:exon3:c.G196T:p.G66C |          |
| 13618 | NA  | NA      | NA      | NA  | NA  | NA            | U2AF1         | nonsynonymous SNV | U2AF1:NM_001025203:exon2:c.C101T:p.S34F, | 21q22.3   |
| 12817 | chr21| 44524456| 44524456| G   | A   | exonic        | U2AF1         | nonsynonymous SNV | U2AF1:NM_006758:exon2:c.C101T:p.S34F |          |
| 12238 | NA  | NA      | NA      | NA  | NA  | NA            | NA            | NA                 | NA                | NA       |
| 10087 | chr17| 58740779| 58740779| C   | T   | exonic        | PPM1D         | stopgain           | PPM1D:NM_0003620:exon6:c.C1684T:p.Q562X | 17q23.2   |
| 10087 | chr20| 31023780| 31023780| C   | T   | exonic        | ASXL1         | nonsynonymous SNV | ASXL1:NM_015338:exon12:c.C3265T:p.P1089S | 20q11.21  |
| 10087 | chr20| 31019271| 31019271| C   | T   | exonic        | ASXL1         | nonsynonymous SNV | ASXL1:NM_015338:exon8:c.C866T:p.P289L | 20q11.21  |
| 10087 | chr4 | 1.06E+08| 1.06E+08| C   | T   | exonic        | TET2          | nonsynonymous SNV | TET2:NM_001127208:exon3:c.C1790T:p.S597F, | 4q24      |
| 10087 | chr4 | 1.06E+08| 1.06E+08| C   | T   | exonic        | TET2          | stopgain           | TET2:NM_017628:exon3:c.C1790T:p.S597F, | 4q24      |
|       |     |         |         |     |     |               |               |                    | TET2:NM_017628:exon3:c.C1588T:p.Q530X, |          |
|       |     |         |         |     |     |               |               |                    | TET2:NM_017628:exon3:c.C1588T:p.Q530X |          |

UPN (unique patient number), genomic coordinates (hg19, chromosome, start and end), reference sequence (Ref), variant sequence (Alt), gene symbol, and consequence of variants (ExonicFunc, AA change) are included.
**Supplementary Table S3.** Odd ratios (OR) and adjusted p-values of pairwise association analysis in Figure 2D

| Row                  | Column            | OR       | adj p   |
|----------------------|-------------------|----------|---------|
| CPSS_high            | Blast_high        | 7.74138764 | 0.00124068 |
| Relapse              | epigene           | 8.80077042 | 0.00449015 |
| MDAPS_high           | Blast_high        | 2.17631615 | 0.00782631 |
| cytogenetics_high    | Blast_high        | 6.04333028 | 0.01645676 |
| MDAPS_high           | CPSS_high         | 5.72145091 | 0.02439858 |
| cytogenetics_high    | CPSS_high         | 10       | 0.02586088 |
| Relapse              | MDAPS_high        | 3.9899107 | 0.03110924 |
| Relapse              | cytogenetics_high | 3.21505872 | 0.04039357 |
| Relapse              | Blast_high        | 4.73815006 | 0.04127703 |
| TP53/PPM1D           | Blast_high        | 10       | 0.04276992 |
| Relapse              | CPSS_high         | 3.13725928 | 0.04383825 |
| cytogenetics_high    | MDAPS_high        | 3.23404124 | 0.11604774 |
| epigene              | TP53/PPM1D        | 3.72380577 | 0.13262011 |
| MDAPS_high           | signaling         | 4.85401514 | 0.19805198 |
| epigene              | Blast_high        | 2.36209065 | 0.25665650 |
| TP53/PPM1D           | CPSS_high         | 0.49092072 | 0.27009551 |
| Relapse              | TP53/PPM1D        | 1.90979153 | 0.3476631 |
| epigene              | signaling         | 6.26713804 | 0.35003297 |
| MDAPS_high           | epigene           | 7.65141998 | 0.36260122 |
| cytogenetics_high    | epigene           | 1.37529359 | 0.46054424 |
| epigene              | CPSS_high         | 1.46402833 | 0.49050244 |
| Relapse              | signaling         | 0.92789833 | 0.66631087 |
| signaling            | TP53/PPM1D        | 0.78949628 | 0.75633232 |
| cytogenetics_high    | TP53/PPM1D        | 0.75088483 | 0.76872561 |
| MDAPS_high           | TP53/PPM1D        | 0        | 0.79128673 |
| cytogenetics_high    | signaling         | 0.66436819 | 0.83927418 |
| signaling            | CPSS_high         | 0.71910087 | 0.90039113 |
| signaling            | Blast_high        | 0.36225494 | 0.9775384 |

Odds ratios (OR) and adjusted p-values in pairwise association analysis (see Figure 2D) with relapse, high blast count, groups of mutations (mutations in epigenetic regulators, signaling pathways and tumor suppressor genes) and risk stratification systems (cytogenetics, CPSS and MDAPS). OR and adjusted p-values in each pairwise association analysis from the heat map (Figure 2D) are listed.