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

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List of Supplementary Items:

Supplementary Methods

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.[1] Paired-end short reads were first aligned to the human genome reference assembly (GRCh37/hg19) using Burrows-Wheeler Aligner (BWA, v0.7.12).[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, 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),[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 ≥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)[4] 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) [5]

References

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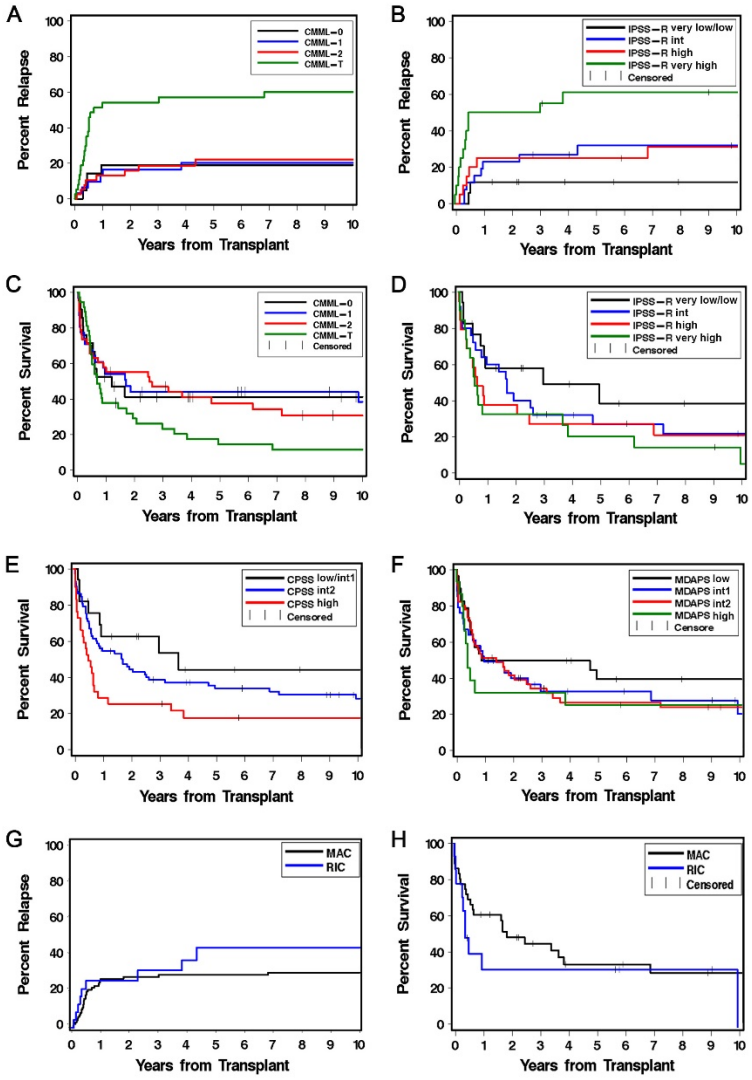
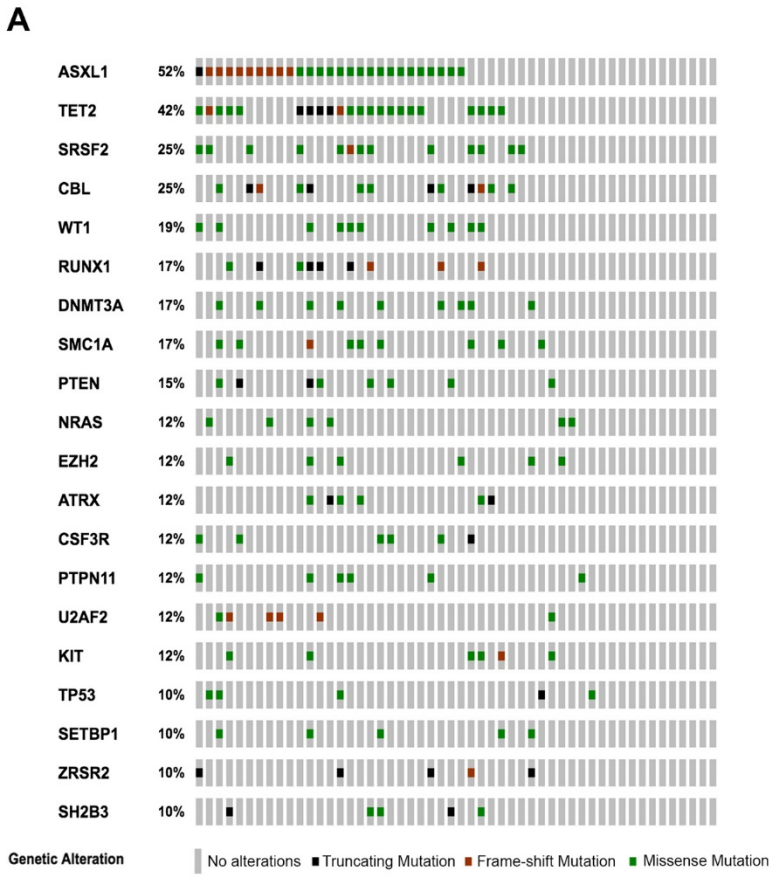
Supplemental Figure 1

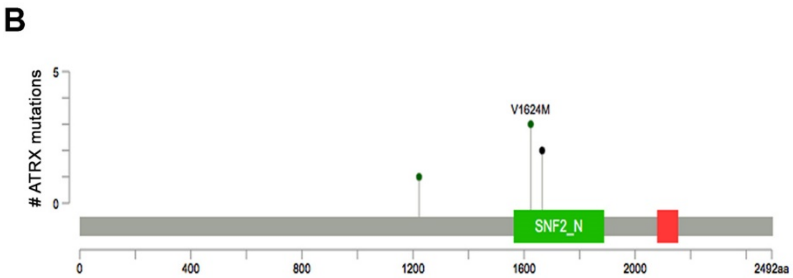


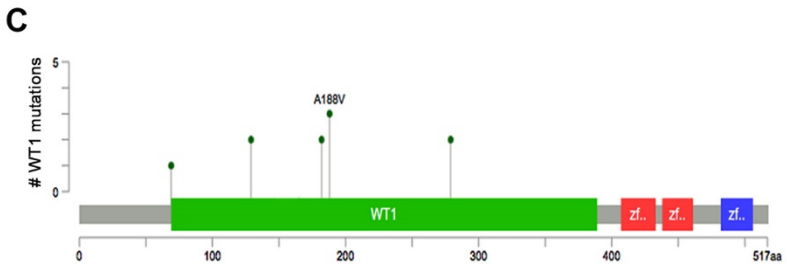
Supplementary Figures

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, (**D**) by CPSS and (**F**) by MDAPS, respectively. (**G**) Cumulative incidence of relapse and (**H**) survival by conditioning regimen.

Supplemental Figure 2

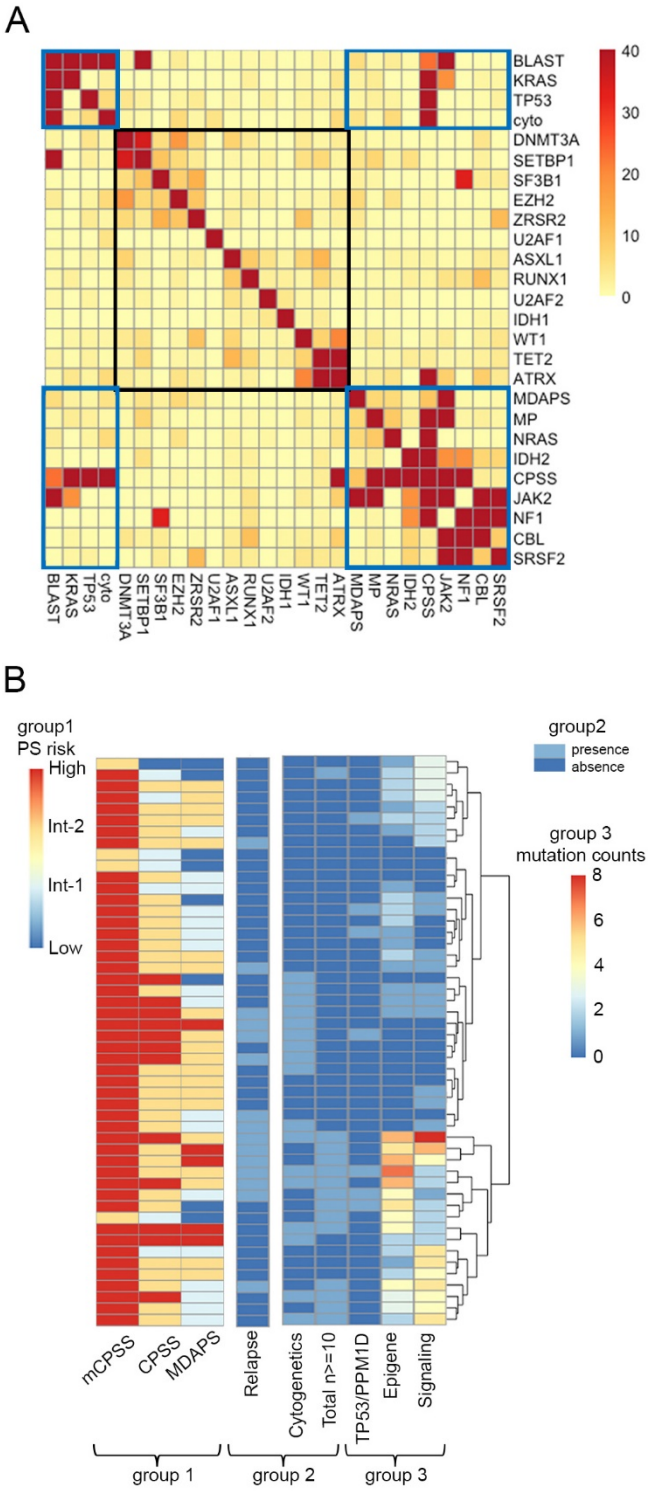






Supplementary Figure S2. Molecular risk factors associated with HCT outcome (**A**) Mutation patterns in patients with CMML undergoing HCT. The plot represents the distribution and type of somatic lesions in genes mutated in ≥ 1% of patients. Each column represents an individual patient and each row 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.

Supplemental Figure 3



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		Miitochondria
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. refGene	Gene. refGene	ExonicFunc. refGene	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_172313:exon16:c.G2012A:p.G671D	1p34.3
AC920	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
AC920	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
AC920	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
AC920	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
AC920	chr20	31022592	31022592	C	T	exonic	ASXL1	stopgain	ASXL1:NM_015338: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.C5977T: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,ABL1:NM_007313:exon4:c.T614A:p.V205D	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.C284A:p.P95H, SRSF2:NM_003016:exon1:c.C284A:p.P95H	17q25.1
93346	chr17	74732894	74732894	G	A	exonic	SRSF2	nonsynonymous SNV	SRSF2:NM_001195427:exon1:c.C349T:p.R117C,SRSF2:NM_003016:exon1:c.C349T:p.R117C	17q25.1

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UPN	Chr	Start	End	Ref	Alt	Func. refGene	Gene. refGene	ExonicFunc. refGene	AAChange.refGene	cytoBand
93346	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
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.P2320L	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_001197104:exon11:c.C4432T:p.R1478C,KMT2A:NM_005933:exon11:c.C4432T:p.R1478C	11q23.3
88794	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
88794	chr17	7573952	7573952	G	A	exonic	TP53	nonsynonymous SNV	TP53:NM_001126115:exon6:c.C679T:p.P227S,TP53:NM_001276697:exon6:c.C598T:p.P200S,TP53:NM_001126118:exon9:c.C958T:p.P320S,TP53:NM_000546:exon10:c.C1075T:p.P359S,TP53:NM_001126112:exon10:c.C1075T:p.P359S,TP53:NM_001276760:exon10:c.C958T:p.P320S,TP53:NM_001276761:exon10:c.C958T:p.P320S	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	GTCAGGAAAA	-	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	ExonicFunc. 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.A47T:p.D16V,IDH1:NM_001282387:exon3:c.A47T:p.D16V,IDH1:NM_005896:exon3:c.A47T:p.D16V	2q34
84625	chr20	31024354	31024354	T	A	exonic	ASXL1	nonsynonymous SNV	ASXL1:NM_015338:exon12:c.T3839A:p.I1280N	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_001291840:exon3:c.C529T:p.Q177X,IKZF1:NM_001220771:exon4:c.C790T:p.Q264X,IKZF1:NM_001291843:exon4:c.C664T:p.Q222X,IKZF1:NM_001291844:exon4:c.C634T:p.Q212X,IKZF1:NM_001220768:exon5:c.C958T:p.Q320X,IKZF1:NM_001220770:exon5:c.C802T:p.Q268X,IKZF1:NM_001291841:exon5:c.C790T:p.Q264X,IKZF1:NM_001291842:exon5:c.C760T:p.Q254X,IKZF1:NM_001220767:exon6:c.C928T:p.Q310X,IKZF1:NM_001291839:exon6:c.C832T:p.Q278X,IKZF1:NM_001220765:exon7:c.C1093T:p.Q365X,IKZF1:NM_001291837:exon7:c.C1093T:p.Q365X,IKZF1:NM_001291838:exon7:c.C958T:p.Q320X,IKZF1:NM_006060:exon8:c.C1219T:p.Q407X	7p12.2
84625	chr9	21994149	21994149	G	A	exonic	CDKN2A	nonsynonymous SNV	CDKN2A:NM_058195:exon1:c.C182T:p.P61L	9p21.3
82825	chr10	89624271	89624271	A	T	exonic	PTEN	nonsynonymous SNV	PTEN:NM_000314:exon1:c.A45T:p.R15S,PTEN:NM_001304717:exon2:c.A564T:p.R188S	10q23.31
82825	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
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

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
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.G2425T:p.D809Y,CSF3R:NM_156039:exon17:c.G2506T:p.D836Y	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.C4286T:p.S1429F	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	AGATTAACCAGGACA	-	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.S106F	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_001077489:exon10:c.G922A:p.D308N,GNAS:NM_080426:exon10:c.G925A:p.D309N, GNAS:NM_000516:exon11:c.G967A:p.D323N,GNAS:NM_001077488:exon11:c.G970A:p.D324N, GNAS:NM_001309840:exon11:c.G790A:p.D264N,GNAS:NM_001309861:exon11:c.G790A:p.D264N,GNAS:NM_080425:exon11:c.G2896A:p.D966N	20q13.32
77347	chr4	1.06E+08	1.06E+08	C	T	exonic	TET2	nonsynonymous SNV	TET2:NM_001127208:exon4:c.C3473T:p.A1158V	4q24
77347	chr4	1.06E+08	1.06E+08	C	T	exonic	TET2	nonsynonymous SNV	TET2:NM_001127208:exon4:c.C3458T:p.A1153V	4q24
77347	chrX	53442118	53442118	C	T	exonic	SMC1A	nonsynonymous SNV	SMC1A:NM_006306:exon2:c.G110A:p.G37D,SMC1A:NM_001281463:exon3:c.G44A:p.G15D	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_001197104: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	AGATTACCAGGACA	-	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_001008540: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.G3586A:p.A1196T	20q11.21
75750	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
75750	chr3	1.28E+08	1.28E+08	G	T	exonic	GATA2	nonsynonymous SNV	GATA2:NM_001145662:exon3:c.C389A:p.A130D,GATA2:NM_032638:exon3:c.C389A:p.A130D,GATA2:NM_001145661:exon4:c.C389A:p.A130D	3q21.3
75750	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
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.C1250G:p.P417R	11q23.3
57547	chr11	1.19E+08	1.19E+08	G	T	exonic	CBL	stopgain	CBL:NM_005188:exon2:c.G406T:p.G136X	11q23.3
57547	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
57547	chr17	58740779	58740779	C	T	exonic	PPM1D	stopgain	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.A47T:p.D16V,IDH1:NM_001282387:exon3:c.A47T:p.D16V,IDH1:NM_005896:exon3:c.A47T:p.D16V	2q34
57547	chr20	31024801	31024801	C	T	exonic	ASXL1	nonsynonymous SNV	ASXL1:NM_015338:exon12:c.C4286T:p.S1429F	20q11.21
57547	chr21	36259140	36259160	CTTGAAAGCGATGGG	-	exonic	RUNX1	nonframeshift deletion	RUNX1:NM_001001890:exon1:c.250_270del:p.84_90del,RUNX1:NM_001122607:exon1:c.250_270del:p.84_90del,RUNX1:NM_001754:exon4:c.331_351del:p.111_117del	21q22.12

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
				CAG GGT						
57547	chr21	36171687	36171687	G	A	exonic	RUNX1	nonsynonymous SNV	RUNX1:NM_001001890:exon5:c.C797T:p.S266F,RUNX1:NM_001754:exon8:c.C878T:p.S293F	21q22.12
57547	chr4	1.06E+08	1.06E+08	C	T	exonic	TET2	stopgain	TET2:NM_001127208:exon3:c.C3025T:p.Q1009X,TET2:NM_017628:exon3:c.C3025T:p.Q1009X	4q24
57547	chr4	1.06E+08	1.06E+08	C	T	exonic	TET2	stopgain	TET2:NM_001127208:exon3:c.C3025T:p.Q1009X,TET2:NM_017628:exon3:c.C3025T:p.Q1009X	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_001202543:exon15:c.C1708T:p.Q570X,CUX1:NM_181552:exon15:c.C1675T:p.Q559X	7q22.1
57547	chr7	50435807	50435807	T	A	exonic	IKZF1	nonsynonymous SNV	IKZF1:NM_001291845:exon4:c.T264A:p.H88Q	7p12.2
57547	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,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,BCORL1:NM_021946: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.C6451T:p.P2151S,KMT2A:NM_005933:exon26:c.C6442T:p.P2148S	11q23.3
42961	chr12	12022873	12022873	G	A	exonic	ETV6	nonsynonymous SNV	ETV6:NM_001987:exon5:c.G979A:p.E327K	12p13.2
42961	chr17	40474369	40474369	G	A	exonic	STAT3	nonsynonymous SNV	STAT3:NM_003150:exon21:c.C2032T:p.P678S,STAT3:NM_139276:exon21:c.C2032T:p.P678S,STAT3:NM_213662:exon21:c.C2032T:p.P678S	17q21.2

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
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:exon8:c.C1034T:p.T345I,FBXW7:NM_018315:exon8:c.C1148T:p.T383I,FBXW7:NM_033632:exon9:c.C1388T:p.T463I	4q31.3
42961	chr4	55593648	55593648	G	A	exonic	KIT	nonsynonymous SNV	KIT:NM_000222:exon11:c.G1714A:p.D572N,KIT:NM_001093772:exon11:c.G1702A:p.D568N	4q12
42961	chrX	39916426	39916426	C	T	exonic	BCOR	nonsynonymous SNV	BCOR:NM_001123384:exon10:c.G4421A:p.S1474N,BCOR:NM_001123383:exon11:c.G4475A:p.S1492N,BCOR:NM_001123385:exon11:c.G4577A:p.S1526N,BCOR:NM_017745:exon11:c.G4475A:p.S1492N	Xp11.4
42961	chrX	48649581	48649581	C	T	exonic	GATA1	nonsynonymous SNV	GATA1:NM_002049:exon2:c.C65T: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_032335:exon5:c.C391T:p.H131Y,PHF6:NM_032458: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	20q11.21
42163	chr4	1.06E+08	1.06E+08	T	C	exonic	TET2	nonsynonymous SNV	TET2:NM_017628:exon3:c.T3469C:p.S1157P	4q24
41546	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
41546	chr18	42531907	42531907	G	A	exonic	SETBP1	nonsynonymous SNV	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.C784T:p.P262S,DNMT3A:NM_022552:exon11:c.C1351T:p.P451S, DNMT3A:NM_175629:exon11:c.C1351T:p.P451S	2p23.3
41546	chr2	1.98E+08	1.98E+08	C	T	exonic	SF3B1	nonsynonymous SNV	SF3B1:NM_012433:exon15:c.G2128A:p.A710T	2q33.1

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
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.D130N,MYD88:NM_001172567:exon3:c.G523A:p.D175N,MYD88: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,EZH2:NM_004456:exon10:c.G1207A:p.E403K	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_024424:exon1:c.C385T:p.P129S,WT1:NM_024426: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	12q24.13
36470	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
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:exon11: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.G2602A:p.D868N	18q12.3
36158	chr2	25471043	25471043	C	G	exonic	DNMT3A	nonsynonymous SNV	DNMT3A:NM_153759:exon3:c.G151C:p.E51Q,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_001127208:exon6:c.A3644G:p.E1215G	4q24
36158	chr4	1.06E+08	1.06E+08	C	T	exonic	TET2	nonsynonymous SNV	TET2:NM_001127208: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_006306:exon2:c.G202A:p.A68T,SMC1A:NM_001281463:exon3:c.G136A:p.A46T	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_000378:exon1:c.C544A:p.P182T,WT1:NM_024424:exon1:c.C544A:p.P182T,WT1:NM_024426: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_002834: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	AAChange.refGene	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_001127208:exon3:c.C80T:p.T27I,TET2:NM_017628:exon3:c.C80T:p.T27I	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.G88C,SMC1A:NM_001281463: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.C892T:p.Q298X,PTEN:NM_001304718:exon8:c.C301T: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	A	C	exonic	KMT2A	nonsynonymous SNV	KMT2A:NM_001197104:exon27:c.A7923C:p.R2641S,KMT2A:NM_005933:exon27:c.A7914C:p.R2638S	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	nonsynonymous SNV	PTPN11:NM_002834:exon11:c.C1285T:p.P429S,PTPN11:NM_080601:exon11:c.C1285T:p.P429S	12q24.13
31517	chr15	66727405	66727405	G	A	exonic	MAP2K1	nonsynonymous SNV	MAP2K1:NM_002755:exon2:c.G121A:p.E41K	15q22.31
31517	chr18	42531907	42531907	G	A	exonic	SETBP1	nonsynonymous SNV	SETBP1:NM_015559:exon4:c.G2602A:p.D868N	18q12.3
31517	chr19	33792336	33792336	C	T	exonic	CEBPA	nonsynonymous 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	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
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	21q22.12
31517	chr3	1.28E+08	1.28E+08	G	A	exonic	GATA2	nonsynonymous 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	nonsynonymous 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.Q1699X	4q24
31517	chr4	55594043	55594043	G	A	exonic	KIT	nonsynonymous 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	nonsynonymous 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	ExonicFunc. refGene	AAChange.refGene	cytoBand
									Y,EZH2:NM_001203248:exon15:c.G1685A:p.C562Y,EZH2:NM_004456:exon15:c.G1727A:p.C576Y	
31517	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
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.P129S,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.R2641S,KMT2A:NM_005933:exon27:c.A7914C:p.R2638S	11q23.3
31071	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
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_022552: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

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
31071	chr4	1.06E+08	1.06E+08	C	T	exonic	TET2	nonsynonymous SNV	TET2:NM_001127208:exon9:c.C4066T:p.P1356S	4q24
31071	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
31071	chrX	48649581	48649581	C	T	exonic	GATA1	nonsynonymous SNV	GATA1:NM_002049:exon2:c.C65T:p.A22V	Xp11.23
31071	chrX	53441966	53441966	C	A	exonic	SMC1A	nonsynonymous SNV	SMC1A:NM_006306:exon2:c.G262T: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.A45T:p.R15S,PTEN:NM_001304717:exon2:c.A564T:p.R188S	10q23.31
30857	chr11	1.19E+08	1.19E+08	T	C	exonic	CBL	nonsynonymous SNV	CBL:NM_005188:exon3:c.T485C:p.L162P	11q23.3
30857	chr12	12043942	12043942	G	A	exonic	ETV6	nonsynonymous SNV	ETV6:NM_001987: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.R10Q,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_001195427:exon1:c.C284A:p.P95H,SRSF2:NM_003016:exon1:c.C284A:p.P95H	17q25.1
30857	chr17	74732292	74732292	G	A	exonic	SRSF2	nonsynonymous SNV	SRSF2:NM_001195427:exon2:c.C617T:p.S206L,SRSF2:NM_003016:exon2:c.C617T:p.S206L	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.P174S,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

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UPN	Chr	Start	End	Ref	Alt	Func. refGene	Gene. refGene	ExonicFunc. refGene	AAChange.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_001220770: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_001220765:exon5:c.G533A:p.C178Y,IKZF1:NM_001291837:exon5:c.G533A:p.C178Y,IKZF1:NM_006060:exon5: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	C	T	exonic	IDH2	nonsynonymous SNV	IDH2:NM_001290114:exon2:c.G29A:p.R10Q,IDH2:NM_001289910:exon4:c.G263A:p.R88Q,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,SRSF2:NM_003016: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_024424:exon1:c.C544A:p.P182T,WT1:NM_024426: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,SRSF2:NM_003016:exon1:c.C284A:p.P95H	17q25.1

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UPN	Chr	Start	End	Ref	Alt	Func. refGene	Gene. refGene	ExonicFunc. 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_003467:exon2: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	ASXL1	nonsynonymous SNV	ASXL1:NM_015338:exon12:c.G2182A:p.E728K	20q11.21
30331	chr4	1.06E+08	1.06E+08	C	T	exonic	TET2	nonsynonymous SNV	TET2:NM_001127208:exon3:c.C80T:p.T27I,TET 2:NM_017628:exon3:c.C80T:p.T27I	4q24
30331	chr4	1.06E+08	1.06E+08	A	G	exonic	TET2	nonsynonymous SNV	TET2:NM_001127208:exon6:c.A3644G:p.E1215 G	4q24
30331	chr4	1.06E+08	1.06E+08	TGA G	-	exonic	TET2	frameshift deletion	TET2:NM_001127208:exon11:c.5619_5622del:p. I1873fs	4q24
30331	chr7	1.4E+08	1.4E+08	G	A	exonic	BRAF	nonsynonymous SNV	BRAF:NM_004333:exon13:c.C1567T:p.P523S	7q34
30331	chr9	1.39E+08	1.39E+08	G	A	exonic	NOTCH1	nonsynonymous SNV	NOTCH1:NM_017617:exon34:c.C6310T:p.R210 4C	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.G1885A:p.A629T, SMC1A:NM_001281463:exon12:c.G1819A:p.A60 7T	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.C205T:p.P69S, CEBPA:NM_001287424:exon1:c.C667T:p.P223S ,CEBPA:NM_001287435:exon1:c.C520T:p.P174 S,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,E ZH2: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
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.C3088T:p.Q1030X	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.C6442T: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.G1090A:p.E364K,CEBPA:NM_001287435:exon1:c.G943A:p.E315K,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

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
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_002468: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_033632: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_033632: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_001281463: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_012116:exon10:c.G1400A:p.G467E	19q13.32
26671	chr19	56173950	56173964	AGATTAACC	-	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

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UPN	Chr	Start	End	Ref	Alt	Func. refGene	Gene. refGene	ExonicFunc. refGene	AAChange.refGene	cytoBand
				AGG ACA						
26671	chr20	31022403	31022425	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_001203248: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

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
26671	chrX	39922097	39922097	C	T	exonic	BCOR	nonsynonymous SNV	BCOR:NM_001123384:exon8:c.G3919A:p.G1307R,BCOR:NM_001123383:exon9:c.G3973A:p.G1325R,BCOR:NM_001123385:exon9:c.G4075A: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.E758G,BCORL1:NM_021946:exon3:c.A2273G:p.E758G	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:exon1:c.G207A:p.M69I,WT1:NM_024424:exon1:c.G207A:p.M69I,WT1:NM_024426:exon1: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_002755:exon2:c.G121A:p.E41K	15q22.31
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,TP	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
									53:NM_001276699:exon3:c.G266A:p.R89Q,TP5 3:NM_001126118:exon6:c.G626A:p.R209Q,TP5 3:NM_000546:exon7:c.G743A:p.R248Q,TP53:N M_001126112:exon7:c.G743A:p.R248Q,TP53:N M_001126113:exon7:c.G743A:p.R248Q,TP53:N M_001126114:exon7:c.G743A:p.R248Q,TP53:N M_001276695:exon7:c.G626A:p.R209Q,TP53:N M_001276696:exon7:c.G626A:p.R209Q,TP53:N M_001276760:exon7:c.G626A:p.R209Q,TP53:N M_001276761:exon7:c.G626A:p.R209Q	
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,T P53:NM_001276698:exon3:c.G266A:p.R89Q,TP 53:NM_001276699:exon3:c.G266A:p.R89Q,TP5 3:NM_001126118:exon6:c.G626A:p.R209Q,TP5 3:NM_000546:exon7:c.G743A:p.R248Q,TP53:N M_001126112:exon7:c.G743A:p.R248Q,TP53:N M_001126113:exon7:c.G743A:p.R248Q,TP53:N M_001126114:exon7:c.G743A:p.R248Q,TP53:N M_001276695:exon7:c.G626A:p.R209Q,TP53:N M_001276696:exon7:c.G626A:p.R209Q,TP53:N M_001276760:exon7:c.G626A:p.R209Q,TP53:N M_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_175629: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_017628: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.C538Y,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_001220770: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_001220765:exon5:c.G533A:p.C178Y,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

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UPN	Chr	Start	End	Ref	Alt	Func. refGene	Gene. refGene	ExonicFunc. refGene	AAChange.refGene	cytoBand
									11A:p.G971R,KDM6A:NM_001291416:exon20:c.G3067A:p.G1023R,KDM6A:NM_021140:exon20:c.G3046A:p.G1016R,KDM6A:NM_001291415:exon21:c.G3202A:p.G1068R	
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_001276695:exon8:c.G724A:p.D242N,TP53:NM_001276696: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	AGATTAACCAGGACA	-	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
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	CBL:NM_005188:exon8:c.1096_1096del:p.E366fs	11q23.3
24623	chr11	32449539	32449539	C	T	exonic	WT1	nonsynonymous SNV	WT1:NM_000378:exon3:c.G835A:p.G279S,WT1:NM_001198551:exon3:c.G199A:p.G67S,WT1:NM_001198552:exon3:c.G199A:p.G67S,WT1:NM_024424:exon3:c.G835A:p.G279S,WT1:NM_024426:exon3:c.G835A:p.G279S	11p13
24623	chr11	1.19E+08	1.19E+08	GG	-	exonic	CBL	frameshift deletion	CBL:NM_005188:exon8:c.1096_1096del:p.E366fs	11q23.3
24623	chr12	1.12E+08	1.12E+08	G	C	exonic	SH2B3	nonsynonymous SNV	SH2B3:NM_001291424:exon5:c.G514C:p.A172P,SH2B3:NM_005475:exon6:c.G1120C:p.A374P	12q24.12
24623	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
24623	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
24623	chr21	36259140	36259160	CTTGAAAGCGATGGGCAGGGT	-	exonic	RUNX1	nonframeshift deletion	RUNX1:NM_001001890:exon1:c.250_270del:p.84_90del,RUNX1:NM_001122607:exon1:c.250_270del:p.84_90del,RUNX1:NM_001754:exon4:c.331_351del:p.111_117del	21q22.12
24623	chr4	55593648	55593648	G	A	exonic	KIT	nonsynonymous SNV	KIT:NM_000222:exon11:c.G1714A:p.D572N,KIT:NM_001093772:exon11:c.G1702A:p.D568N	4q12
24623	chr4	1.06E+08	1.06E+08	G	A	exonic	TET2	nonsynonymous SNV	TET2:NM_001127208:exon3:c.G484A:p.D162N,TET2:NM_017628:exon3:c.G484A:p.D162N	4q24
24623	chr4	1.06E+08	1.06E+08	G	A	exonic	TET2	nonsynonymous SNV	TET2:NM_001127208:exon6:c.G3602A:p.R1201H	4q24
24623	chr9	5073770	5073770	G	T	exonic	JAK2	nonsynonymous SNV	JAK2:NM_004972:exon14:c.G1849T:p.V617F	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, KDM6A:NM_021140: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_033360:exon2:c.G35A:p.G12D	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.R882H,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	CACCACTGCCATAGAGAG	-	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. refGene	Gene. refGene	ExonicFunc. refGene	AAChange.refGene	cytoBand
				GCG GC						
20698	chr10	89712007	89712007	G	A	exonic	PTEN	nonsynonymous SNV	PTEN:NM_000314:exon6:c.G625A:p.G209R,PTEN:NM_001304718:exon6:c.G34A:p.G12R,PTEN:NM_001304717:exon7:c.G1144A:p.G382R	10q23.31
20698	chr11	1.19E+08	1.19E+08	C	G	exonic	CBL	nonsynonymous SNV	CBL:NM_005188:exon9:c.C1250G:p.P417R	11q23.3
20698	chr11	32449539	32449539	C	T	exonic	WT1	nonsynonymous SNV	WT1:NM_000378:exon3:c.G835A:p.G279S,WT1:NM_001198551:exon3:c.G199A:p.G67S,WT1:NM_001198552:exon3:c.G199A:p.G67S,WT1:NM_024424:exon3:c.G835A:p.G279S,WT1:NM_024426:exon3:c.G835A:p.G279S	11p13
20698	chr11	1.19E+08	1.19E+08	C	G	exonic	CBL	nonsynonymous SNV	CBL:NM_005188:exon9:c.C1250G:p.P417R	11q23.3
20698	chr12	12038861	12038861	A	T	exonic	ETV6	nonsynonymous SNV	ETV6:NM_001987:exon7:c.A1154T:p.N385I	12p13.2
20698	chr17	7577078	7577078	T	A	exonic	TP53	nonsynonymous SNV	TP53:NM_001126115:exon4:c.A464T:p.E155V,TP53:NM_001126116:exon4:c.A464T:p.E155V,TP53:NM_001126117:exon4:c.A464T:p.E155V,TP53:NM_001276697:exon4:c.A383T:p.E128V,TP53:NM_001276698:exon4:c.A383T:p.E128V,TP53:NM_001276699:exon4:c.A383T:p.E128V,TP53:NM_001126118:exon7:c.A743T:p.E248V,TP53:NM_000546:exon8:c.A860T:p.E287V,TP53:NM_001126112:exon8:c.A860T:p.E287V,TP53:NM_001126113:exon8:c.A860T:p.E287V,TP53:NM_001126114:exon8:c.A860T:p.E287V,TP53:NM_001276695:exon8:c.A743T:p.E248V,TP53:NM_001276696:exon8:c.A743T:p.E248V,TP53:NM_001276760:exon8:c.A743T:p.E248V,TP53:NM_001276761:exon8:c.A743T:p.E248V	17p13.1
20698	chr18	42531907	42531907	G	A	exonic	SETBP1	nonsynonymous SNV	SETBP1:NM_015559:exon4:c.G2602A:p.D868N	18q12.3

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
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.R882H,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. refGene	Gene. refGene	ExonicFunc. refGene	AAChange.refGene	cytoBand
									c.G3046A:p.G1016R,KDM6A:NM_001291415:exon21:c.G3202A:p.G1068R	
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
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_000061:exon15:c.G1372C:p.V458L,BTK:NM_001287344:exon15:c.G1474C:p.V492L	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_153759:exon7:c.C784T:p.P262S,DNMT3A:NM_022552:exon11:c.C1351T:p.P451S, DNMT3A:NM_175629:exon11:c.C1351T:p.P451S	2p23.3
16252	chr20	31022449	31022449	G	A	exonic	ASXL1	nonsynonymous SNV	ASXL1:NM_015338:exon12:c.G1934A:p.G645D	20q11.21
16252	chr4	55152018	55152018	G	A	exonic	PDGFRA	nonsynonymous SNV	PDGFRA:NM_006206:exon18:c.G2450A:p.R817H	4q12
16252	chr7	1.49E+08	1.49E+08	C	T	exonic	EZH2	nonsynonymous SNV	EZH2:NM_001203249:exon14:c.G1559A:p.C520Y,EZH2:NM_152998:exon14:c.G1595A:p.C532Y, EZH2:NM_001203247:exon15:c.G1712A:p.C571Y,EZH2:NM_001203248:exon15:c.G1685A:p.C562Y,EZH2:NM_004456:exon15:c.G1727A:p.C576Y	7q36.1
15886	chr11	1.18E+08	1.18E+08	C	T	exonic	KMT2A	nonsynonymous SNV	KMT2A:NM_001197104:exon11:c.C4432T:p.R1478C,KMT2A:NM_005933:exon11:c.C4432T:p.R1478C	11q23.3
15886	chr17	7576569	7576569	G	A	exonic	TP53	stopgain	TP53:NM_001126117:exon6:c.C613T:p.R205X,TP53:NM_001276699:exon6:c.C532T:p.R178X,TP	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
									53:NM_001126113:exon10:c.C1009T:p.R337X,TP53:NM_001276695:exon10:c.C892T:p.R298X	
15886	chr7	1.02E+08	1.02E+08	C	T	exonic	CUX1	stopgain	CUX1:NM_001202543:exon15:c.C1708T:p.Q570X,CUX1:NM_181552:exon15:c.C1675T:p.Q559X	7q22.1
15886	chr9	1.34E+08	1.34E+08	G	A	exonic	ABL1	nonsynonymous SNV	ABL1:NM_005157:exon10:c.G1519A:p.E507K,ABL1:NM_007313:exon10:c.G1576A:p.E526K	9q34.12
15886	chrX	39934019	39934019	G	A	exonic	BCOR	nonsynonymous SNV	BCOR:NM_001123383:exon4:c.C580T:p.P194S, BCOR:NM_001123384:exon4:c.C580T:p.P194S, BCOR:NM_001123385:exon4:c.C580T:p.P194S, BCOR:NM_017745:exon4:c.C580T:p.P194S	Xp11.4
15886	chrX	53441966	53441966	C	A	exonic	SMC1A	nonsynonymous SNV	SMC1A:NM_006306:exon2:c.G262T:p.G88C,SMC1A:NM_001281463:exon3:c.G196T:p.G66C	Xp11.22
13618	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
12817	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
12238	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
10087	chr17	58740779	58740779	C	T	exonic	PPM1D	stopgain	PPM1D:NM_003620: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, TET2:NM_017628:exon3:c.C1790T:p.S597F	4q24
10087	chr4	1.06E+08	1.06E+08	C	T	exonic	TET2	stopgain	TET2:NM_001127208:exon3:c.C1588T:p.Q530X, TET2:NM_017628:exon3:c.C1588T:p.Q530X	4q24

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	0.2566565
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	0.97758384

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.