AAML1531			
NCT02521493			
D1			
34320162			
Blanks represent missing data or not applicable for analyses.  Data can be used to approximate published study findings, but exact reproduction of previous manuscripts may not be possible in some cases (e.g., when data must be modified for deidentification purposes or have undergone further data cleaning).  One of the five sample IDs in Supplemental Table 3 appears differently in variable <i>USI</i> .  The data in variables <i>p1_neutro</i> , <i>p2_neutro</i> , <i>p3_neutro</i> , <i>p4_neutro</i> , and <i>p5_neutro</i> are further cleaned/QCed since the analyses performed in the corresponding publication (34320162) and they represent the most accurate values.			
Variable Name	Variable Type	Label	Notes
USI	Char	Universal Specimen Identifier	
study	Char	Study category	
consort_cat	Char	Consort diagram categories	
SR_elig	Char	Standard risk patient eligible for analysis	
ageyr_ons	Num	Age at study entry in years	
sex	Num	Sex	1=Male 2=Female
race_cat	Num	Race	1=American Indian or Alaska Native 2=Asian 4=Black or African American 5=White 6=Multiple Races 9=Unknown
ethnic_cat	Num	Ethnicity	1=Hispanic or Latino 2=Not Hispanic or Latino 3=Unknown
pthtmd	Char	History of transient myeloproliferative disorder (TAM)	
chemintv	Char	Prior treatment for TAM	
cnsstat	Char	Central nervous system (CNS) Status	
extmedis	Char	Was the patient diagnosed with non-CNS extramedullary disease at study entry?	
hgb	Num	Hemoglobin (g/dL)	
pb_wbc	Num	Peripheral WBC Count (x1000/μL)	
	D1  34320162  Blanks represent missing data or modata can be used to approximate possible in identification purposes or have uncome of the five sample IDs in Suppose The data in variables p1_neutro, p.cleaned/QCed since the analyses prepresent the most accurate values. Variable Name  USI  study  consort_cat  SR_elig  ageyr_ons  sex  race_cat  ethnic_cat  pthtmd  chemintv  cnsstat  extmedis	NCT02521493  D1  34320162  Blanks represent missing data or not applicated Data can be used to approximate published signanuscripts may not be possible in some casidentification purposes or have undergone furone of the five sample IDs in Supplemental The data in variables p1_neutro, p2_neutro, p2_leaned/QCed since the analyses performed in represent the most accurate values.  Variable Name  Variable Name  Variable Type  USI  Char  study  Char  consort_cat  SR_elig  Char  ageyr_ons  Num  race_cat  Num  pthtmd  Char  chemintv  chemintv  chemintv  char  extmedis  Num  Num  Num  Num  Num  Char  Char	D1  34320162  Blanks represent missing data or not applicable for analyses. Data can be used to approximate published study findings, but exact reparameteristication purposes or have undergone further data cleaning). One of the five sample IDs in Supplemental Table 3 appears differently The data in variables pl_neutro, p2_neutro, p3_neutro, p4_neutro, and cleaned/QCed since the analyses performed in the corresponding public represent the most accurate values.  Variable Name  Variable Type  USI  Char Universal Specimen Identifier  study  Char Study category  consort_cat  Char Consort diagram categories  SR_elig  Char Standard risk patient eligible for analysis ageyr_ons  Num Age at study entry in years  sex  Num Sex  race_cat  Num Ethnicity  pthtmd  Char History of transient myeloproliferative disorder (TAM)  cheminty  Char Central nervous system  (CNS) Status  extmedis  Char Was the patient diagnosed with non-CNS extramedullary disease at study entry?  hgb Num Hemoglobin (g/dL)  Perpheral WBC Count

15	pb_plt	Num	Peripheral platelet Count (x1000/μL)	
16	perblsts	Num	Peripheral blasts (%)	
17	bmblast	Num	Bone marrow blast percentage	
18	cyto_avail	Char	Cytogenetics available?	
19	normal_cyto	Char	Normal (constitutional	
			trisomy 21 only)	
20	trans_inv	Char	Translocations and inversions recurrent in de novo acute myeloid leukemia (AML)	
21	_1qG	Char	Cytogenetic finding, 1q gain	
22	_3qL	Char	Cytogenetic finding, 3q loss	
23	_5pL	Char	Cytogenetic finding, 5p loss	
24	mono5	Char	Cytogenetic finding, Monosomy 5	
25	_7pL	Char	Cytogenetic finding, 7p loss	
26	mono7	Char	Cytogenetic finding, Monosomy 7	
27	_8G	Char	Cytogenetic finding, +8	
28	_11qG_11G	Char	Cytogenetic finding, +11 or 11q gain	
29	_13qL	Char	Cytogenetic finding, 13q loss	
30	_14G	Char	Cytogenetic finding, +14	
31	_21G	Char	Cytogenetic finding, +21	
32	complex_k	Char	Complex karyotype	
33	mrpghdx	Char	Morphological diagnosis	
34	yrs_folup	Num	Years follow-up for patients alive at last contact	
35	yrsefs1	Num	Years to event-free survival (EFS) from EOI1	
36	efs1i	Num	EFS from EOI1 indicator	0=No EFS event, 1=EFS event
37	yrsos1	Num	Years to overall survival (OS) from EOI1	
38	osli	Num	OS from EOI1 begin indicator	0=Alive, 1=Dead
39	yrsrr1	Num	Years to cumulative incidence of relapse from end of induction I (EOI1)	
40	mli	Num	Cumulative incidence of relapse (from EOI1) indicator	0=No EFS event, 1=relapse, 2=competing event

41	dysrel_ons	Num	Days since study entry to	
42	txphase_rel	Char	relapse event  Treatment phase of relapse	
			event	
43	relapse_site	Char	Relapse site	
44	salvage_tx	Char	Salvage therapy after relapse event	
45	dysosr	Num	Days to OS from relapse event	
46	oslr	Num	OS from relapse event begin indicator	0=Alive, 1=Dead
47	p1data	Char	Induction I data available?	
48	p2data	Char	Induction II data available?	
49	p3data	Char	Induction III data available?	
50	p4data	Char	Intensification I data available?	
51	p5data	Char	Intensification II data available?	
52	plancevl	Char	Did patient have an absolute neutrophil count (ANC) recovery during this reporting period? (Induction I)	
53	p2ancevl	Char	Did patient have an ANC recovery during this reporting period? (Induction II)	
54	p3ancevl	Char	Did patient have an ANC recovery during this reporting period? (Induction III)	
55	p4ancevl	Char	Did patient have an ANC recovery during this reporting period? (Intensification I)	
56	p5ancevl	Char	Did patient have an ANC recovery during this reporting period? (Intensification II)	
57	p1dys_ancrev	Num	Days to ANC recovery (Induction I)	
58	p2dys_ancrev	Num	Days to ANC recovery (Induction II)	
59	p3dys_ancrev	Num	Days to ANC recovery (Induction III)	
60	p4dys_ancrev	Num	Days to ANC recovery (Intensification I)	
61	p5dys_ancrev	Num	Days to ANC recovery (Intensification II)	

62	plicuadm	Char	Intensive care unit (ICU) admission (Induction I)
63	p2icuadm	Char	ICU admission (Induction II)
64	p3icuadm	Char	ICU admission (Induction III)
65	p4icuadm	Char	ICU admission (Intensification I)
66	p5icuadm	Char	ICU admission (Intensification II)
67	p1_neutro	Char	Febrile neutropenia, grade 3 and higher (Induction I)
68	p2_neutro	Char	Febrile neutropenia, grade 3 and higher (Induction II)
69	p3_neutro	Char	Febrile neutropenia, grade 3 and higher (Induction III)
70	p4_neutro	Char	Febrile neutropenia, grade 3 and higher (Intensification I)
71	p5_neutro	Char	Febrile neutropenia, grade 3 and higher (Intensification II)
72	p1_bac_infc	Char	Sterile site bacterial infection, grade 3 and higher (Induction I)
73	p2_bac_infc	Char	Sterile site bacterial infection, grade 3 and higher (Induction II)
74	p3_bac_infc	Char	Sterile site bacterial infection, grade 3 and higher (Induction III)
75	p4_bac_infc	Char	Sterile site bacterial infection, grade 3 and higher (Intensification I)
76	p5_bac_infc	Char	Sterile site bacterial infection, grade 3 and higher (Intensification II)
77	p1agntad	Char	Dexrazoxane administrated (Induction I)
78	p2agntad	Char	Dexrazoxane administrated (Induction II)
79	p3agntad	Char	Dexrazoxane administrated (Induction III)
80	p4agntad	Char	Dexrazoxane administrated (Intensification I)
81	p5agntad	Char	Dexrazoxane administrated (Intensification II)
82	tox_detail_id	Char	Specific toxicity details of identified patients

83	mdata01	Char	Targeted sequencing: Chromosome
84	mdata02	Num	Targeted sequencing: Start identification
85	mdata03	Char	Targeted sequencing: reference (Ref)
86	mdata04	Char	Targeted sequencing: alternative (Alt)
87	mdata05	Char	Targeted sequencing: Gene
88	mdata06	Char	Targeted sequencing: Type
89	mdata07	Char	Targeted sequencing: AA change
90	mdata08	Char	Catalogue Of Somatic Mutations In Cancer (COSMIC)
91	mdata09	Num	Variant allele fraction (VAF) Replicate 1
92	mdata10	Num	VAF Replicate 2
93	TK_mutation	Char	Tyrosine kinase family gene mutation status