

Figure S1. The treatment details of the patients with AE-AML. 63 patients received the '3+7' regimens consisting of daunorubicin (DNR) (n=23) and idarubicin (IDA) (n=36) and other anthracyclines (n=4) for 3 days and cytarabine (Ara-C) at 100-150 mg/m² per day for 7 days as induction chemotherapy for 1-2 cycles. A total of 59 cases achieved complete remission (CR) after induction therapy, and 3 without attaining CR received salvage chemotherapy. After CR (n=62), 31 patients were mainly treated with standard-dose Ara-C-based (SDAC-based) regimen; the other 31 cases were mainly treated with intermedium-dose Ara-C-based (IDAC-based) regimen. Allogeneic-hematopoietic stem cell transplantation (Allo-HSCT) was performed in 13 patients. AE-AML, *AML1-ETO*-positive acute myeloid leukemia.

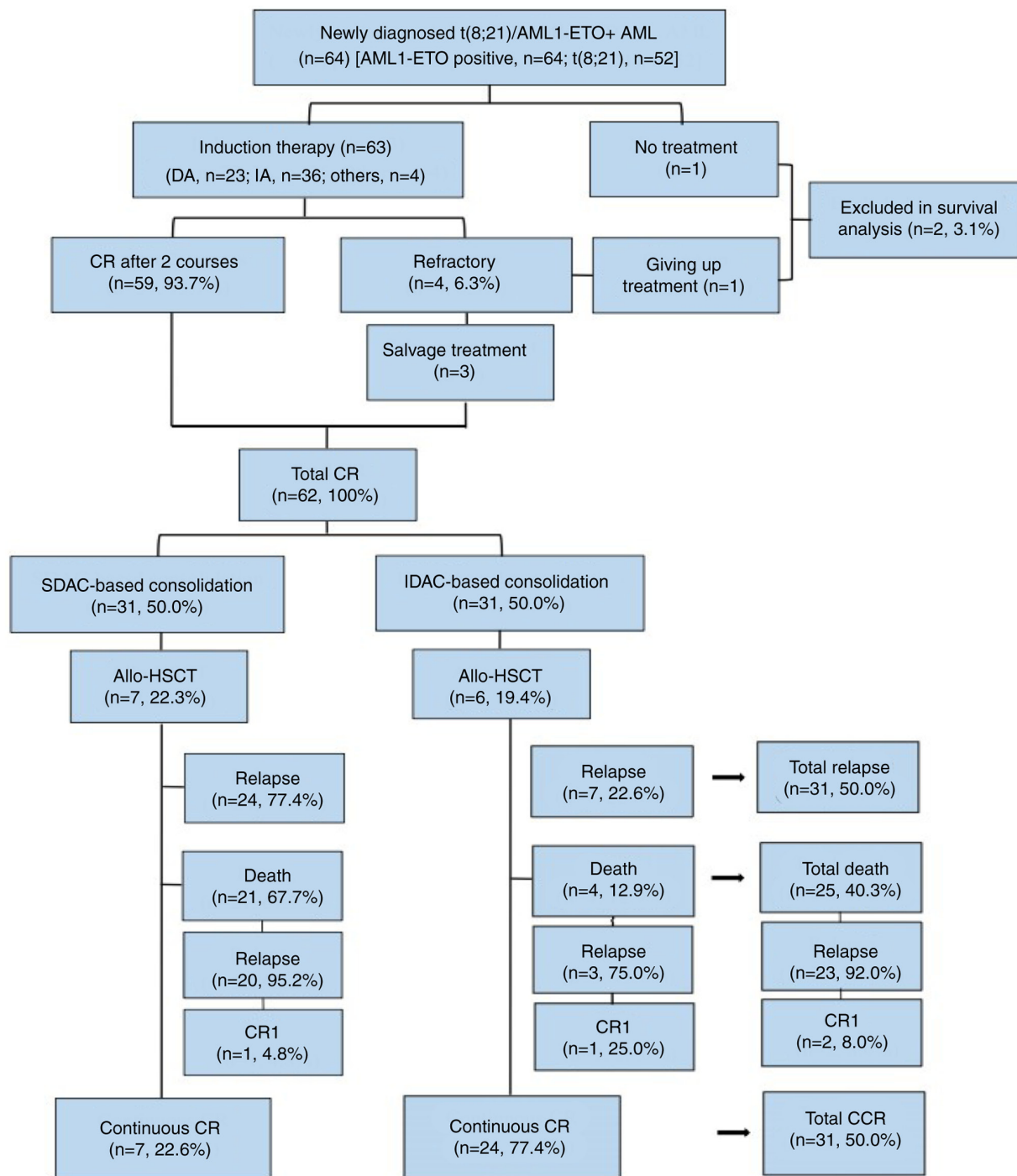


Figure S2. The consistency of gene sequencing with next generation sequencing (NGS) and Sanger sequencing. The positive and negative detection of *FLT3-ITD*, *c-KIT* (exon 8 and 17), *NPM1*, *JAK2* (*V617F*) and *DNMT3A* (*R882*) mutations showed 100% consistency between the NGS and Sanger sequencing. *FLT3*, Fms related tyrosine kinase 3; *c-KIT*, KIT proto-oncogene, receptor tyrosine kinase; *NPM1*, nucleophosmin 1; *JAK2*, Janus kinase 2; *DNMT3A*, DNA methyltransferase 3 α .

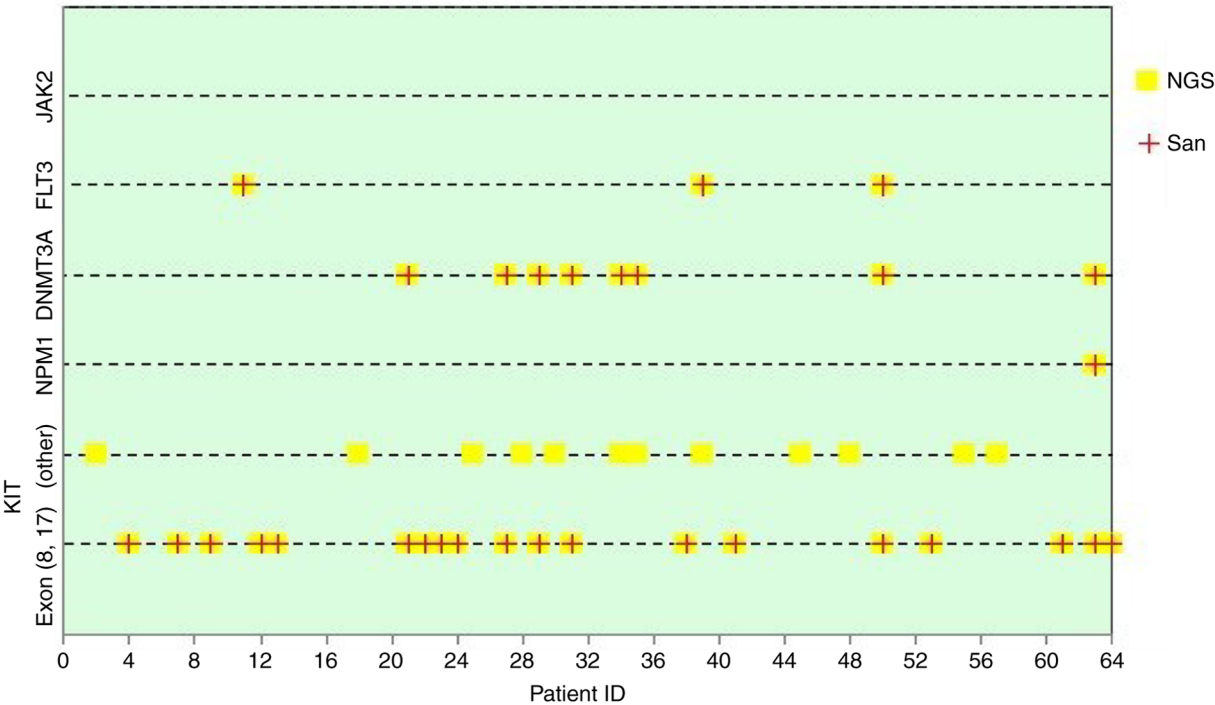


Figure S3. *c-KIT* (exon 8, 17) and *ASXL1* mutations were poor prognostic factors in the patients receiving either SDAC- or IDAC-based consolidation. Among the patients with SDAC-based consolidation: (A) *c-KIT* (exon 8, 17) vs. others: DFS: 22.4 ± 5.6 vs. $33.1 \pm 5.1\%$, $P=0.218$; OS: 24.4 ± 5.9 vs. $33.2 \pm 4.8\%$, $P=0.204$. (C) *ASXL1* mutation vs. *ASXL1*-WT: DFS: 13.3 ± 2.5 vs. $34.0 \pm 4.8\%$, $P=0.005$; OS: 13.3 ± 2.5 vs. $36.5 \pm 5.1\%$, $P=0.003$. (B) Among the patients with IDAC-based regimens as consolidation: *c-KIT* (exon 8, 17) vs. others: DFS: 41.5 ± 9.8 vs. $73.8 \pm 6.7\%$, $P=0.026$; OS: 49.0 ± 10.8 vs. $78.7 \pm 4.2\%$, $P=0.052$. There were only two patients with *ASXL1* mutation in the sub-group with IDAC-based regimens as consolidation; no further sub-group analysis of survival was considered. *c-KIT*, KIT proto-oncogene, receptor tyrosine kinase; *ASXL1*, ASXL transcriptional regulator 1; SDAC-based, standard-dose Ara-C-based regimen; IDAC-based, intermediate-dose cytarabine.

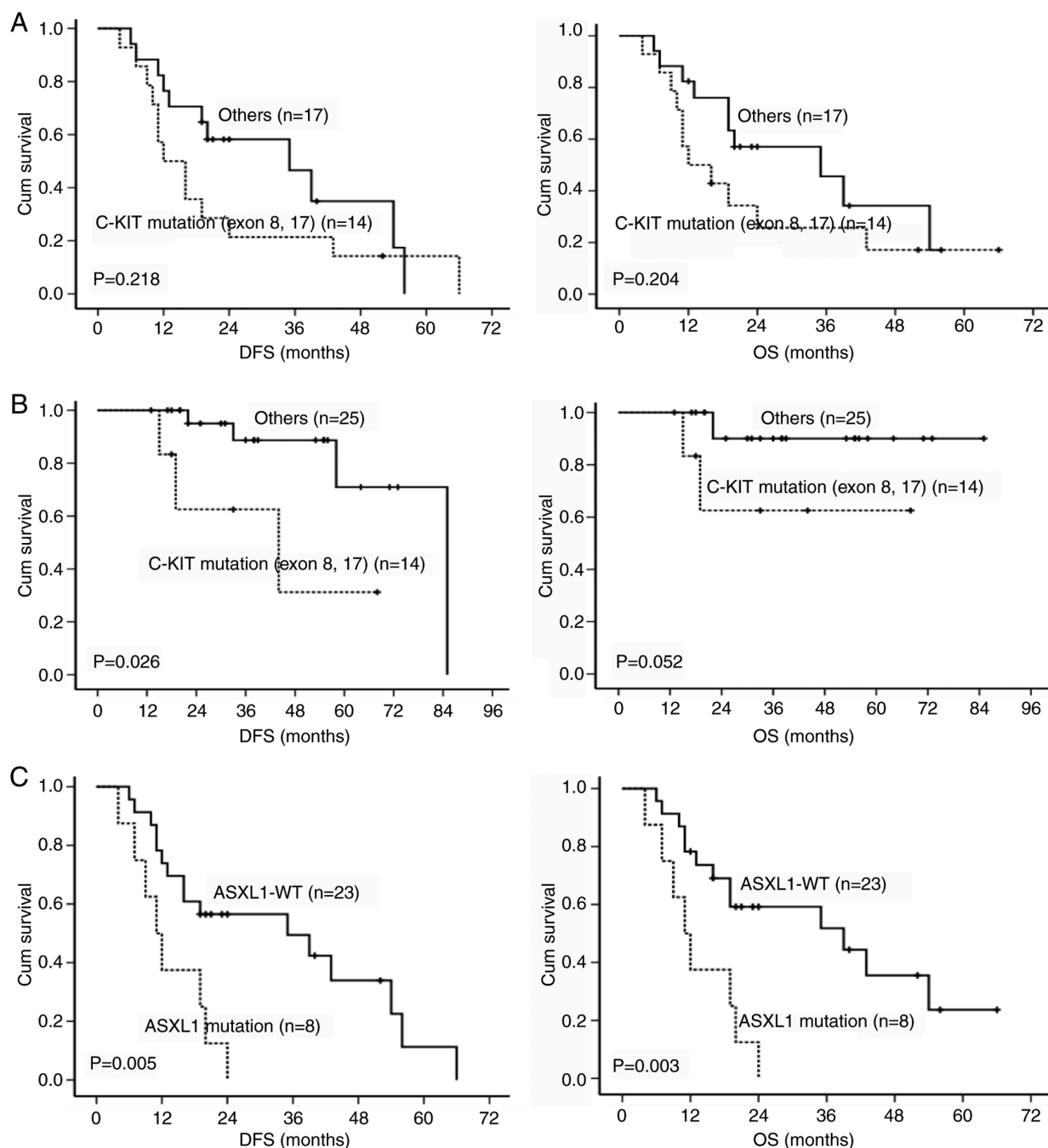


Table SI. Information regarding the 67 genes being targeted in the new panel.

Gene	Accession_number	Gene	Accession_number
<i>ABL1</i>	X16416	<i>AKT1</i>	NM_005163
<i>ALK</i>	NM_004304	<i>APC</i>	NM_000038
<i>ATM</i>	NM_000051	<i>BRAF</i>	NM_004333
<i>CDH1</i>	NM_004360	<i>CDKN2A</i>	NM_000077
<i>CSF1R</i>	NM_005211	<i>CTNNB1</i>	NM_001904
<i>EGFR</i>	NM_005228	<i>ERBB2</i>	NM_004448
<i>ERBB4</i>	NM_005235	<i>EZH2</i>	NM_004456
<i>FBXW7</i>	NM_033632	<i>FGFR1</i>	NM_000604
<i>FGFR2</i>	NM_000141	<i>FGFR3</i>	NM_000142
<i>FLT3</i>	Z26652	<i>GNAI1</i>	NM_002067
<i>GNAS</i>	NM_000516	<i>GNAQ</i>	NM_002072
<i>HNF1A</i>	NM_000545	<i>HRAS</i>	NM_005343
<i>IDH1</i>	NM_005896	<i>IDH2</i>	NM_002168
<i>JAK2</i>	ENST00000381652	<i>JAK3</i>	NM_000215
<i>KDR</i>	NM_002253	<i>KIT</i>	NM_000222
<i>KRAS</i>	NM_004985	<i>MET</i>	NM_000245
<i>MLH1</i>	NM_000249	<i>MPL</i>	NM_005373
<i>NOTCH1</i>	NM_017617	<i>NPM1</i>	NM_002520
<i>NRAS</i>	NM_002524	<i>PDGFRA</i>	NM_006206
<i>PIK3CA</i>	NM_006218	<i>PTEN</i>	NM_000314
<i>PTPN11</i>	NM_002834	<i>RB1</i>	NM_000321
<i>RET</i>	NM_020975	<i>SMAD4</i>	NM_005359
<i>SMARCB1</i>	NM_003073	<i>SMO</i>	NM_005631
<i>SRC</i>	NM_005417	<i>STK11</i>	NM_000455
<i>TP53</i>	NM_000546	<i>VHL</i>	NM_000551
<i>WT1</i>	NM_000378	<i>DNMT3A</i>	NM_022552
<i>CEBPA</i>	NM_004364	<i>RUNX1</i>	NM_001754
<i>PHF6</i>	NM_032458	<i>ASXL1</i>	NM_015338
<i>MLL</i>	NM_005933	<i>JAK1</i>	NM_002227
<i>PAX5</i>	NM_016734	<i>SF3B1</i>	NM_012433
<i>SH2B3</i>	NM_005475	<i>SRSF2</i>	NM_003016
<i>TET2</i>	NM_017628	<i>EBF1</i>	NM_024007
<i>DNMT1</i>	NM_001379	<i>DNMT3B</i>	NM_006892
<i>DNMT3L</i>	NM_013369		

The 50 genes (upper region of table) listed in the white cells come from the Ion AmpliSeq Cancer Hotspot Panel V2 kit (Thermo Fisher Scientific). The 17 genes listed in the gray cells (bottom region of table) are the common mutant genes being reported to occur in AML and newly added to our new panel.

Table SII. Detailed information of the 17 genes newly added to the panel.

Gene	Chr	Chr_start	Chr_end	Num_Amp	Total_bases	Covered_bases	Missed_bases	Cover age
<i>DNMT1</i>	chr19	10244337	10244382	1	46	46	0	1
<i>DNMT1</i>	chr19	10244887	10244988	1	102	102	0	1
<i>DNMT1</i>	chr19	10246406	10246533	1	128	128	0	1
<i>DNMT1</i>	chr19	10246791	10246968	1	178	178	0	1
<i>DNMT1</i>	chr19	10247755	10247961	2	207	207	0	1
<i>DNMT1</i>	chr19	10248502	10248690	1	189	189	0	1
<i>DNMT1</i>	chr19	10249109	10249286	2	178	178	0	1
<i>DNMT1</i>	chr19	10250346	10250498	2	153	153	0	1
<i>DNMT1</i>	chr19	10250716	10251009	3	294	294	0	1
<i>DNMT1</i>	chr19	10251451	10251590	1	140	140	0	1
<i>DNMT1</i>	chr19	10251775	10251870	1	96	96	0	1
<i>DNMT1</i>	chr19	10252698	10252901	1	204	204	0	1
<i>DNMT1</i>	chr19	10254436	10254668	2	233	233	0	1
<i>DNMT1</i>	chr19	10257021	10257205	2	185	185	0	1
<i>DNMT1</i>	chr19	10259554	10259698	2	145	145	0	1
<i>DNMT1</i>	chr19	10260123	10260338	2	216	216	0	1
<i>DNMT1</i>	chr19	10260523	10260649	1	127	127	0	1
<i>DNMT1</i>	chr19	10262068	10262226	1	159	159	0	1
<i>DNMT1</i>	chr19	10262420	10262528	2	109	109	0	1
<i>DNMT1</i>	chr19	10264963	10265160	2	198	198	0	1
<i>DNMT1</i>	chr19	10265256	10265454	1	199	199	0	1
<i>DNMT1</i>	chr19	10265575	10265737	1	163	163	0	1
<i>DNMT1</i>	chr19	10266523	10266626	1	104	104	0	1
<i>DNMT1</i>	chr19	10267061	10267190	1	130	130	0	1
<i>DNMT1</i>	chr19	10270328	10270448	2	121	121	0	1
<i>DNMT1</i>	chr19	10270512	10270603	2	92	92	0	1
<i>DNMT1</i>	chr19	10270688	10270744	1	57	57	0	1
<i>DNMT1</i>	chr19	10271054	10271099	1	46	46	0	1
<i>DNMT1</i>	chr19	10273337	10273429	1	93	75	18	0.806
<i>DNMT1</i>	chr19	10273996	10274041	1	46	46	0	1
<i>DNMT1</i>	chr19	10277268	10277366	2	99	99	0	1
<i>DNMT1</i>	chr19	10279000	10279045	1	46	46	0	1
<i>DNMT1</i>	chr19	10283760	10283855	1	96	96	0	1
<i>DNMT1</i>	chr19	10284541	10284586	1	46	46	0	1
<i>DNMT1</i>	chr19	10286210	10286299	1	90	90	0	1
<i>DNMT1</i>	chr19	10287962	10288048	1	87	87	0	1
<i>DNMT1</i>	chr19	10290857	10290915	0	59	0	59	0
<i>DNMT1</i>	chr19	10291020	10291250	2	231	107	124	0.463
<i>DNMT1</i>	chr19	10291448	10291566	1	119	119	0	1
<i>DNMT1</i>	chr19	10292711	10292758	1	48	48	0	1
<i>DNMT1</i>	chr19	10305490	10305580	1	91	91	0	1
<i>DNMT3A</i>	chr2	25457142	25457294	1	153	153	0	1
<i>DNMT3A</i>	chr2	25458570	25458699	2	130	130	0	1
<i>DNMT3A</i>	chr2	25459799	25459879	1	81	81	0	1
<i>DNMT3A</i>	chr2	25461993	25462089	1	97	97	0	1
<i>DNMT3A</i>	chr2	25463165	25463324	1	160	160	0	1
<i>DNMT3A</i>	chr2	25463503	25463604	1	102	102	0	1
<i>DNMT3A</i>	chr2	25464425	25464581	2	157	157	0	1
<i>DNMT3A</i>	chr2	25466761	25466856	2	96	96	0	1
<i>DNMT3A</i>	chr2	25467018	25467212	2	195	195	0	1
<i>DNMT3A</i>	chr2	25467403	25467526	2	124	124	0	1
<i>DNMT3A</i>	chr2	25468116	25468206	1	91	91	0	1
<i>DNMT3A</i>	chr2	25468883	25468938	1	56	56	0	1
<i>DNMT3A</i>	chr2	25469023	25469183	2	161	161	0	1
<i>DNMT3A</i>	chr2	25469483	25469650	1	168	168	0	1
<i>DNMT3A</i>	chr2	25469914	25470032	1	119	119	0	1
<i>DNMT3A</i>	chr2	25470454	25470623	1	170	170	0	1
<i>DNMT3A</i>	chr2	25470900	25471126	2	227	227	0	1
<i>DNMT3A</i>	chr2	25472520	25472598	1	79	79	0	1

Table SII. Continued.

Gene	Chr	Chr_start	Chr_end	Num_Amp	Total_bases	Covered_bases	Missed_bases	Cover age
<i>DNMT3A</i>	chr2	25475057	25475071	1	15	15	0	1
<i>DNMT3A</i>	chr2	25497804	25497961	1	158	158	0	1
<i>DNMT3A</i>	chr2	25498363	25498417	1	55	55	0	1
<i>DNMT3A</i>	chr2	25505251	25505585	2	335	335	0	1
<i>DNMT3A</i>	chr2	25505304	25505585	2	282	282	0	1
<i>DNMT3A</i>	chr2	25523002	25523117	1	116	116	0	1
<i>DNMT3A</i>	chr2	25536776	25536858	1	83	83	0	1
<i>ASXL1</i>	chr20	30946573	30946640	0	68	0	68	0
<i>ASXL1</i>	chr20	30954181	30954274	1	94	94	0	1
<i>ASXL1</i>	chr20	30956809	30956931	1	123	123	0	1
<i>ASXL1</i>	chr20	30959961	30959977	1	17	17	0	1
<i>ASXL1</i>	chr20	31015925	31016056	1	132	132	0	1
<i>ASXL1</i>	chr20	31016122	31016230	1	109	109	0	1
<i>ASXL1</i>	chr20	31017135	31017239	1	105	105	0	1
<i>ASXL1</i>	chr20	31017698	31017861	1	164	164	0	1
<i>ASXL1</i>	chr20	31019118	31019292	2	175	175	0	1
<i>ASXL1</i>	chr20	31019380	31019487	1	108	108	0	1
<i>ASXL1</i>	chr20	31020677	31020793	1	117	117	0	1
<i>ASXL1</i>	chr20	31021081	31021725	4	645	645	0	1
<i>ASXL1</i>	chr20	31022229	31025146	16	2,918	2,918	0	1
<i>DNMT3B</i>	chr20	31367916	31367956	1	41	41	0	1
<i>DNMT3B</i>	chr20	31368124	31368276	1	153	153	0	1
<i>DNMT3B</i>	chr20	31368118	31368276	1	159	159	0	1
<i>DNMT3B</i>	chr20	31369153	31369225	1	73	73	0	1
<i>DNMT3B</i>	chr20	31372558	31372670	1	113	113	0	1
<i>DNMT3B</i>	chr20	31374302	31374438	1	137	137	0	1
<i>DNMT3B</i>	chr20	31375030	31375262	2	233	233	0	1
<i>DNMT3B</i>	chr20	31376654	31376823	2	170	170	0	1
<i>DNMT3B</i>	chr20	31379401	31379519	1	119	119	0	1
<i>DNMT3B</i>	chr20	31380426	31380581	1	156	156	0	1
<i>DNMT3B</i>	chr20	31381336	31381406	0	71	0	71	0
<i>DNMT3B</i>	chr20	31383209	31383345	1	137	137	0	1
<i>DNMT3B</i>	chr20	31383450	31383505	1	56	56	0	1
<i>DNMT3B</i>	chr20	31384590	31384680	1	91	91	0	1
<i>DNMT3B</i>	chr20	31384987	31385110	2	124	124	0	1
<i>DNMT3B</i>	chr20	31386260	31386454	1	195	195	0	1
<i>DNMT3B</i>	chr20	31387044	31387139	1	96	96	0	1
<i>DNMT3B</i>	chr20	31387953	31388109	1	157	157	0	1
<i>DNMT3B</i>	chr20	31388635	31388736	1	102	102	0	1
<i>DNMT3B</i>	chr20	31389078	31389237	1	160	160	0	1
<i>DNMT3B</i>	chr20	31390185	31390281	1	97	97	0	1
<i>DNMT3B</i>	chr20	31393138	31393218	1	81	81	0	1
<i>DNMT3B</i>	chr20	31394009	31394138	1	130	130	0	1
<i>DNMT3B</i>	chr20	31395562	31395714	2	153	153	0	1
<i>WT1</i>	chr11	32410598	32410730	1	133	133	0	1
<i>WT1</i>	chr11	32413512	32413615	1	104	104	0	1
<i>WT1</i>	chr11	32413521	32413615	1	95	95	0	1
<i>WT1</i>	chr11	32414206	32414306	1	101	101	0	1
<i>WT1</i>	chr11	32417797	32417958	1	162	162	0	1
<i>WT1</i>	chr11	32421488	32421595	1	108	108	0	1
<i>WT1</i>	chr11	32438030	32438091	1	62	62	0	1
<i>WT1</i>	chr11	32439117	32439205	1	89	89	0	1
<i>WT1</i>	chr11	32449496	32449609	1	114	114	0	1
<i>WT1</i>	chr11	32450037	32450170	1	134	134	0	1
<i>WT1</i>	chr11	32452070	32452090	1	21	21	0	1
<i>WT1</i>	chr11	32456240	32456896	5	657	657	0	1
<i>CEBPA</i>	chr19	33792238	33793325	6	1,088	877	211	0.8061
<i>RUNX1</i>	chr21	36164426	36164912	4	487	487	0	1
<i>RUNX1</i>	chr21	36171592	36171764	1	173	173	0	1

Table SII. Continued.

Gene	Chr	Chr_start	Chr_end	Num_Amp	Total_bases	Covered_bases	Missed_bases	Cover age
<i>RUNX1</i>	chr21	36193959	36193998	1	40	40	0	1
<i>RUNX1</i>	chr21	36206701	36206903	3	203	203	0	1
<i>RUNX1</i>	chr21	36231765	36231880	1	116	116	0	1
<i>RUNX1</i>	chr21	36252848	36253015	1	168	168	0	1
<i>RUNX1</i>	chr21	36259134	36259398	2	265	265	0	1
<i>RUNX1</i>	chr21	36259134	36259414	2	281	281	0	1
<i>RUNX1</i>	chr21	36265216	36265265	1	50	50	0	1
<i>RUNX1</i>	chr21	36421133	36421201	1	69	69	0	1
<i>PAX5</i>	chr9	36840551	36840638	1	88	88	0	1
<i>PAX5</i>	chr9	36846834	36846931	1	98	98	0	1
<i>PAX5</i>	chr9	36881995	36882107	1	113	113	0	1
<i>PAX5</i>	chr9	36923346	36923486	1	141	141	0	1
<i>PAX5</i>	chr9	36966540	36966726	2	187	187	0	1
<i>PAX5</i>	chr9	37002639	37002778	2	140	140	0	1
<i>PAX5</i>	chr9	37006464	37006539	1	76	76	0	1
<i>PAX5</i>	chr9	37014988	37015196	2	209	209	0	1
<i>PAX5</i>	chr9	37020627	37020803	2	177	177	0	1
<i>PAX5</i>	chr9	37033977	37034033	1	57	57	0	1
<i>DNMT3L</i>	chr21	45666274	45666450	1	177	177	0	1
<i>DNMT3L</i>	chr21	45666274	45666453	1	180	180	0	1
<i>DNMT3L</i>	chr21	45668903	45668999	1	97	97	0	1
<i>DNMT3L</i>	chr21	45670687	45670837	2	151	151	0	1
<i>DNMT3L</i>	chr21	45671500	45671586	1	87	87	0	1
<i>DNMT3L</i>	chr21	45674494	45674593	1	100	100	0	1
<i>DNMT3L</i>	chr21	45675944	45676042	1	99	99	0	1
<i>DNMT3L</i>	chr21	45678400	45678582	1	183	183	0	1
<i>DNMT3L</i>	chr21	45679314	45679437	2	124	124	0	1
<i>DNMT3L</i>	chr21	45679509	45679599	0	91	0	91	0
<i>DNMT3L</i>	chr21	45680672	45680727	1	56	56	0	1
<i>DNMT3L</i>	chr21	45681031	45681147	1	117	117	0	1
<i>JAK1</i>	chr1	65300239	65300345	1	107	107	0	1
<i>JAK1</i>	chr1	65301073	65301194	2	122	122	0	1
<i>JAK1</i>	chr1	65301775	65301903	1	129	129	0	1
<i>JAK1</i>	chr1	65303609	65303792	1	184	184	0	1
<i>JAK1</i>	chr1	65304142	65304277	1	136	136	0	1
<i>JAK1</i>	chr1	65305280	65305483	2	204	204	0	1
<i>JAK1</i>	chr1	65306922	65307027	1	106	106	0	1
<i>JAK1</i>	chr1	65307128	65307289	1	162	162	0	1
<i>JAK1</i>	chr1	65309741	65309903	1	163	163	0	1
<i>JAK1</i>	chr1	65310431	65310577	1	147	147	0	1
<i>JAK1</i>	chr1	65311190	65311328	1	139	139	0	1
<i>JAK1</i>	chr1	65312326	65312424	1	99	99	0	1
<i>JAK1</i>	chr1	65313209	65313363	1	155	155	0	1
<i>JAK1</i>	chr1	65316481	65316598	1	118	118	0	1
<i>JAK1</i>	chr1	65321186	65321386	2	201	201	0	1
<i>JAK1</i>	chr1	65323333	65323467	1	135	135	0	1
<i>JAK1</i>	chr1	65325782	65325950	1	169	169	0	1
<i>JAK1</i>	chr1	65330464	65330660	2	197	197	0	1
<i>JAK1</i>	chr1	65332543	65332896	2	354	354	0	1
<i>JAK1</i>	chr1	65334988	65335162	1	175	175	0	1
<i>JAK1</i>	chr1	65339047	65339211	1	165	165	0	1
<i>JAK1</i>	chr1	65344702	65344836	1	135	135	0	1
<i>JAK1</i>	chr1	65348954	65349163	2	210	210	0	1
<i>JAK1</i>	chr1	65351936	65351952	1	17	17	0	1
<i>SRSF2</i>	chr17	74732237	74732551	2	315	315	0	1
<i>SRSF2</i>	chr17	74732875	74733247	3	373	373	0	1
<i>TET2</i>	chr4	1.06E+08	1.06E+08	18	3,420	3,420	0	1
<i>TET2</i>	chr4	1.06E+08	1.06E+08	18	3,509	3,509	0	1
<i>TET2</i>	chr4	1.06E+08	1.06E+08	1	102	102	0	1

Table SII. Continued.

Gene	Chr	Chr_start	Chr_end	Num_Amp	Total_bases	Covered_bases	Missed_bases	Cover age
<i>TET2</i>	chr4	1.06E+08	1.06E+08	1	105	105	0	1
<i>TET2</i>	chr4	1.06E+08	1.06E+08	2	220	220	0	1
<i>TET2</i>	chr4	1.06E+08	1.06E+08	2	162	162	0	1
<i>TET2</i>	chr4	1.06E+08	1.06E+08	1	101	101	0	1
<i>TET2</i>	chr4	1.06E+08	1.06E+08	2	149	104	45	0.698
<i>TET2</i>	chr4	1.06E+08	1.06E+08	2	366	366	0	1
<i>TET2</i>	chr4	1.06E+08	1.06E+08	7	1,483	1,483	0	1
<i>SH2B3</i>	chr12	1.12E+08	1.12E+08	4	743	725	18	0.976
<i>SH2B3</i>	chr12	1.12E+08	1.12E+08	1	113	113	0	1
<i>SH2B3</i>	chr12	1.12E+08	1.12E+08	1	103	103	0	1
<i>SH2B3</i>	chr12	1.12E+08	1.12E+08	1	106	106	0	1
<i>SH2B3</i>	chr12	1.12E+08	1.12E+08	2	226	226	0	1
<i>SH2B3</i>	chr12	1.12E+08	1.12E+08	2	183	183	0	1
<i>SH2B3</i>	chr12	1.12E+08	1.12E+08	2	331	331	0	1
<i>MLL</i>	chr11	1.18E+08	1.18E+08	3	443	185	258	0.418
<i>MLL</i>	chr11	1.18E+08	1.18E+08	1	81	81	0	1
<i>MLL</i>	chr11	1.18E+08	1.18E+08	14	2,665	2,665	0	1
<i>MLL</i>	chr11	1.18E+08	1.18E+08	1	189	189	0	1
<i>MLL</i>	chr11	1.18E+08	1.18E+08	2	246	246	0	1
<i>MLL</i>	chr11	1.18E+08	1.18E+08	1	76	76	0	1
<i>MLL</i>	chr11	1.18E+08	1.18E+08	2	389	389	0	1
<i>MLL</i>	chr11	1.18E+08	1.18E+08	1	85	85	0	1
<i>MLL</i>	chr11	1.18E+08	1.18E+08	1	143	143	0	1
<i>MLL</i>	chr11	1.18E+08	1.18E+08	2	125	125	0	1
<i>MLL</i>	chr11	1.18E+08	1.18E+08	1	158	158	0	1
<i>MLL</i>	chr11	1.18E+08	1.18E+08	1	107	107	0	1
<i>MLL</i>	chr11	1.18E+08	1.18E+08	2	132	132	0	1
<i>MLL</i>	chr11	1.18E+08	1.18E+08	1	125	125	0	1
<i>MLL</i>	chr11	1.18E+08	1.18E+08	1	134	134	0	1
<i>MLL</i>	chr11	1.18E+08	1.18E+08	1	196	196	0	1
<i>MLL</i>	chr11	1.18E+08	1.18E+08	1	185	185	0	1
<i>MLL</i>	chr11	1.18E+08	1.18E+08	2	122	122	0	1
<i>MLL</i>	chr11	1.18E+08	1.18E+08	1	85	85	0	1
<i>MLL</i>	chr11	1.18E+08	1.18E+08	2	205	205	0	1
<i>MLL</i>	chr11	1.18E+08	1.18E+08	1	118	118	0	1
<i>MLL</i>	chr11	1.18E+08	1.18E+08	1	149	149	0	1
<i>MLL</i>	chr11	1.18E+08	1.18E+08	2	170	161	9	0.947
<i>MLL</i>	chr11	1.18E+08	1.18E+08	1	129	129	0	1
<i>MLL</i>	chr11	1.18E+08	1.18E+08	1	90	90	0	1
<i>MLL</i>	chr11	1.18E+08	1.18E+08	1	172	172	0	1
<i>MLL</i>	chr11	1.18E+08	1.18E+08	2	197	197	0	1
<i>MLL</i>	chr11	1.18E+08	1.18E+08	22	4,260	4,260	0	1
<i>MLL</i>	chr11	1.18E+08	1.18E+08	1	92	92	0	1
<i>MLL</i>	chr11	1.18E+08	1.18E+08	2	76	76	0	1
<i>MLL</i>	chr11	1.18E+08	1.18E+08	2	182	182	0	1
<i>MLL</i>	chr11	1.18E+08	1.18E+08	1	86	86	0	1
<i>MLL</i>	chr11	1.18E+08	1.18E+08	1	186	186	0	1
<i>MLL</i>	chr11	1.18E+08	1.18E+08	1	119	119	0	1
<i>MLL</i>	chr11	1.18E+08	1.18E+08	1	95	95	0	1
<i>MLL</i>	chr11	1.18E+08	1.18E+08	1	141	141	0	1
<i>MLL</i>	chr11	1.18E+08	1.18E+08	2	287	287	0	1
<i>PHF6</i>	chrX	1.34E+08	1.34E+08	1	149	149	0	1
<i>PHF6</i>	chrX	1.34E+08	1.34E+08	2	113	113	0	1
<i>PHF6</i>	chrX	1.34E+08	1.34E+08	2	145	145	0	1
<i>PHF6</i>	chrX	1.34E+08	1.34E+08	1	55	55	0	1
<i>PHF6</i>	chrX	1.34E+08	1.34E+08	2	178	178	0	1
<i>PHF6</i>	chrX	1.34E+08	1.34E+08	2	181	181	0	1
<i>PHF6</i>	chrX	1.34E+08	1.34E+08	2	155	155	0	1
<i>PHF6</i>	chrX	1.34E+08	1.34E+08	2	116	116	0	1

Table SII. Continued.

Gene	Chr	Chr_start	Chr_end	Num_Amp	Total_bases	Covered_bases	Missed_bases	Cover age
<i>PHF6</i>	chrX	1.34E+08	1.34E+08	3	218	218	0	1
<i>PHF6</i>	chrX	1.34E+08	1.34E+08	1	145	145	0	1
<i>PHF6</i>	chrX	1.34E+08	1.34E+08	1	141	141	0	1
<i>EBF1</i>	chr5	1.58E+08	1.58E+08	1	43	43	0	1
<i>EBF1</i>	chr5	1.58E+08	1.58E+08	1	206	206	0	1
<i>EBF1</i>	chr5	1.58E+08	1.58E+08	1	191	191	0	1
<i>EBF1</i>	chr5	1.58E+08	1.58E+08	3	189	189	0	1
<i>EBF1</i>	chr5	1.58E+08	1.58E+08	1	77	77	0	1
<i>EBF1</i>	chr5	1.58E+08	1.58E+08	1	100	100	0	1
<i>EBF1</i>	chr5	1.58E+08	1.58E+08	1	138	138	0	1
<i>EBF1</i>	chr5	1.58E+08	1.58E+08	2	142	142	0	1
<i>EBF1</i>	chr5	1.58E+08	1.58E+08	1	153	153	0	1
<i>EBF1</i>	chr5	1.58E+08	1.58E+08	1	93	93	0	1
<i>EBF1</i>	chr5	1.59E+08	1.59E+08	1	80	80	0	1
<i>EBF1</i>	chr5	1.59E+08	1.59E+08	1	85	85	0	1
<i>EBF1</i>	chr5	1.59E+08	1.59E+08	1	67	67	0	1
<i>EBF1</i>	chr5	1.59E+08	1.59E+08	1	75	75	0	1
<i>EBF1</i>	chr5	1.59E+08	1.59E+08	2	168	168	0	1
<i>EBF1</i>	chr5	1.59E+08	1.59E+08	2	145	136	9	0.938
<i>SF3B1</i>	chr2	1.98E+08	1.98E+08	2	170	170	0	1
<i>SF3B1</i>	chr2	1.98E+08	1.98E+08	2	228	202	26	0.886
<i>SF3B1</i>	chr2	1.98E+08	1.98E+08	2	284	284	0	1
<i>SF3B1</i>	chr2	1.98E+08	1.98E+08	2	143	143	0	1
<i>SF3B1</i>	chr2	1.98E+08	1.98E+08	2	132	132	0	1
<i>SF3B1</i>	chr2	1.98E+08	1.98E+08	2	123	123	0	1
<i>SF3B1</i>	chr2	1.98E+08	1.98E+08	1	194	1	193	0.005
<i>SF3B1</i>	chr2	1.98E+08	1.98E+08	2	233	233	0	1
<i>SF3B1</i>	chr2	1.98E+08	1.98E+08	2	137	137	0	1
<i>SF3B1</i>	chr2	1.98E+08	1.98E+08	2	158	158	0	1
<i>SF3B1</i>	chr2	1.98E+08	1.98E+08	2	157	157	0	1
<i>SF3B1</i>	chr2	1.98E+08	1.98E+08	3	282	282	0	1
<i>SF3B1</i>	chr2	1.98E+08	1.98E+08	1	98	98	0	1
<i>SF3B1</i>	chr2	1.98E+08	1.98E+08	2	191	191	0	1
<i>SF3B1</i>	chr2	1.98E+08	1.98E+08	2	113	113	0	1
<i>SF3B1</i>	chr2	1.98E+08	1.98E+08	1	209	101	108	0.483
<i>SF3B1</i>	chr2	1.98E+08	1.98E+08	2	133	133	0	1
<i>SF3B1</i>	chr2	1.98E+08	1.98E+08	3	224	203	21	0.906
<i>SF3B1</i>	chr2	1.98E+08	1.98E+08	2	249	249	0	1
<i>SF3B1</i>	chr2	1.98E+08	1.98E+08	1	182	163	19	0.896
<i>SF3B1</i>	chr2	1.98E+08	1.98E+08	1	91	91	0	1
<i>SF3B1</i>	chr2	1.98E+08	1.98E+08	1	31	31	0	1
<i>SF3B1</i>	chr2	1.98E+08	1.98E+08	2	126	126	0	1
<i>SF3B1</i>	chr2	1.98E+08	1.98E+08	2	116	116	0	1
<i>SF3B1</i>	chr2	1.98E+08	1.98E+08	2	178	178	0	1
<i>SF3B1</i>	chr2	1.98E+08	1.98E+08	1	39	39	0	1

Table SIII. Characteristic of the gene mutations in the 65 patients with *AML1-ETO*-positive acute myeloid leukemia (AML).

Gene	Mutation exon	Mutation type	Mutation (CDS)	Mutation (amino acid)	Patient number	Exclusive mutation
<i>KIT</i>	17	Substitution-Missense	c.2446G>T	p.D816Y	2	c.1553C>T,
	17	Substitution-Missense	c.2446G>C	p.D816H	1	c.2201C>G,
	17	Substitution-Missense	c.2466T>G	p.N822K	1	c.251C>T,
	17	Substitution-Missense	c.2466T>A	p.N822K	5	c.1993C>G
	17	Substitution-Missense	c.2447A>T	p.D816V	8	
	17	Substitution-Missense	c.2447A>C	p.D816A	1	
	17	Insertion-In frame	c.2445_2446ins AGTGGT	p.R815_D816insVI	1	
<i>ASXL1</i>	8	Complex-deletion inframe	c.1253delA<G	p.Y418del	1	
	10	Substitution-Missense	c.1621A>C	p.M541L	8	
	12	Substitution-Missense	c.1954G>A	p.G652S	6	c.3692C>T,
	12	Substitution-Missense	c.2957A>G	p.N986S	3	c.3487G>A,
	12	Substitution-Nonsense	c.1773C>G	p.Y591*	1	c.3593G>T
<i>MET</i>	12	Substitution-Nonsense	c.2077C>T	p.R693*	1	
	2	Substitution-Missense	c.1124A>G	p.N375S	7	
<i>MHL1</i>	14	Substitution-Missense	c.3011C>T	p.A1004V	1	
	12	Substitution-Missense	c.1151T>A	p.V384D	6	
<i>TET2</i>	7	Substitution-Missense	c.3845G>C	p.G1282A	2	c.5162T>G,
	6	Substitution-Missense	c.3661T>C	p.C1221R	2	c.2440C>T,
	3	Substitution-Missense	c.3404G>A	p.C1135S	1	c.5284A>G,
	11	Substitution-Nonsense	c.4879C>T	p.Q1627*	1	c.2604T>G, c.652G>A
<i>FBXW7</i>	10	Substitution-Missense	c.1513C>T	p.R505C	1	
	11	Substitution-Missense	c.1694T>C	p.Val565Ala	4	
<i>TP53</i>	4	Deletion-Frameshift	c.215_215delC	p.V73fs*50	2	c.215C>G,
	4	Substitution-Missense	c.277C>A	p.L93M	2	c.98C>G
	4	Deletion-Frameshift	c.99_99delC	p.V163del	1	
<i>DNMT3A</i>	15	Substitution-Missense	c.1703G>T	p.G568V	3	
	8	Substitution-Missense	c.1010C>G	p.S337X	1	
	11	Substitution-Missense	c.1345G>A	p.A449T	1	
<i>PAX5</i>	2	Substitution-Missense	c.74G>T	p.G25V	3	
	2	Substitution-Missense	c.73G>C	p.G25R	1	
<i>CEBPA</i>	1	Substitution-Missense	c.568T>C	p.S190P	2	
	1	Deletion-In frame	c.878_880delACA	p.N293del	1	
	1	Substitution-Missense	c.41C>G	p.P14R	1	
<i>KMT2A</i>	3	Substitution-Missense	c.2625G>T	p.E875D	1	
	27	Substitution-Missense	c.7082C>T	p.S2361L	1	
	31	Substitution-Missense	c.11113T>A	p.S3705T	1	
<i>ATM</i>	63	Substitution-Missense	c.9104T>A	p.L3035H	1	
	34	Substitution-Missense	c.5063T>C	p.I1688T	1	
	26	Substitution-Missense	c.3963G>A	p.M1321I	1	
<i>FLT3</i>	20	Substitution-Missense	c.2523C>A	p.N841K	1	
	20	Substitution-Missense	c.2516A>G	p.D839G	1	
	20	Substitution-Missense	c.2453T>C	p.L818P	1	
<i>NRAS</i>	3	Substitution-Missense	c.182A>G	p.Q61R	3	
<i>DNMT3L</i>	11	Substitution-Missense	c.982C>A	p.P328T	1	c.139C>T
	2	Substitution-Missense	c.98C>A	p.G32R	1	
<i>PDGFRA</i>	12	Substitution-Missense	c.1681G>A	p.V561I	2	
	12	Substitution-Missense	c.1738C>G	p.L580V	1	
<i>APC</i>	16	Substitution-Missense	c.4027T>C	p.S1343P	1	
	16	Substitution-Missense	c.4681A>G	p.K1561E	1	
<i>HRAS</i>	2	Substitution-Missense	c.8A>G	p.GE3G	2	
<i>RUNX1</i>	8	Substitution-Missense	c.812G>A	p.R271K	1	
	9	Substitution-Missense	c.1396A>T	p.M466L	1	
<i>SH2B3</i>	8	Substitution-Missense	c.1703T>C	p.I568T	1	c.784T>C
<i>SMAD4</i>	11	Substitution-Nonsense	c.1348C>T	p.Q450*	1	
<i>KRAS</i>	2	Substitution-Missense	c.26T>G	p.V9D	1	
<i>NPM1</i>	11	Insertion-Frameshift	c.861_862insTGCA	p.W288fs*12	1	

Table SIV. Influence of single gene mutations on clinical characteristics of the *AML1-ETO*-positive acute myeloid leukemia (AML) patients.

Gene																								
KIT																								
Characteristics	Exon			ASXL1			MET			MLH1			TET2			FBXW7			TP53			DNMT3A		
	WT	8,17	Exon 10	P-value	WT	mut	P-value	WT	mut	P-value	WT	mut	WT	mut	WT	mut	WT	mut	WT	mut	WT	mut		
No.	37	20	7		54	10		58	6		59	5	59	5	59	5	59	5	59	5	59	5		
MAO	23	31	33	0.343	27	36	0.432	27.5	34		30	13	27	33	27	33	27	33	27	34	28	33		
Sex (M/F)	(2-58)	(5-65)	(20-46)		(2-60)	(5-65)		(2-65)	(8-60)		(2-65)	(5-36)	(2-60)	(13-65)	(2-65)	(13-54)	(2-65)	(13-54)	(2-65)	(13-54)	(2-58)	(5-65)		
Median WBC	23/14	11/9	5/2	0.725	32/22	7/3	0.523	37/21	2/4	0.923	35/24	4/1	37/22	2/3	37/22	2/3	37/22	2/3	37/22	2/3	36/23	3/2		
(x10 ⁹ /l)	18.0	23.2	22.5	0.637	20.3	20.5	0.839	21.3	11.4	0.598	19.3	23.8	21.2	10.7	21.4	10.7	21.4	10.7	21.4	10.7	19.3	22.4		
	(2.3-	(8.4-	(3.1-		(2.3-	(4.2-		(2.3-	(3.3-		(2.3-	(3.3-	(2.3-	(3.3-	(2.3-	(3.3-	(2.3-	(3.3-	(2.3-	(3.3-	(2.3-	(3.3-		
	70.3)	73.4)	41.0)		72.4)	37.6)		72.4)	40.2)		72.4)	70.3)	72.4)	29.1)	72.4)	33.3)	72.4)	29.1)	72.4)	33.3)	72.4)	37.6)		
EML (rate, %)	9	9	2	0.271	16	4	0.516	17	3	0.221	17	3	19	1	18	2	119	1	18	2	119	1		
	(24.3)	(45.0)	(28.6)		(29.6)	(40.0)		(29.3)	(50.0)		(28.8)	(60.0)	(32.2)	(20.0)	(30.5)	(40.0)	(32.2)	(20.0)	(30.5)	(40.0)	(32.2)	(20.0)		
Median	34.0	40.2	48.0	0.268	35.0	49.5	0.141	35.5	37.5	0.459	35.0	48.0	35.0	51.0	35.0	40.4	35.0	51.0	35.0	40.4	35.0	44.5		
BMB (%)	(3.0-	(15.0-	(16.0-		(4.0-	(3.0-		(3.0-	(15.0-		(3.0-	(31.0-	(3.0-	(23.0-	(3.0-	(27.0-	(3.0-	(23.0-	(3.0-	(27.0-	(3.0-	(31.0-		
	77.0)	94.0)	60.0)		93.0)	94.0)		94.0)	48.0)		94.0)	77.0)	94.0)	93.0)	93.0)	94.0)	94.0)	93.0)	93.0)	94.0)	94.0)	77.0)		
CD56 ⁺	23/36	14/20	4/7	0.807	32/53	9/10	0.071	38/57	3/6	0.155	37/58	4/5	36/58	5/5	37/58	4/5	36/58	5/5	37/58	4/5	36/58	5/5		
	(63.9)	(70.0)	(57.11)		(60.4)	(90.0)		(66.7)	(50.0)		(63.8)	(80.0)	(62.1)	(100)	(63.8)	(80.0)	(62.1)	(100)	(63.8)	(80.0)	(62.1)	(100)		
ACAs (%)	12/3	9/15	3/6	0.390	23/46	1/6	0.123	21/48	3/4	0.531	21/48	3/4	21/48	3/4	20/48	4/4	22/49	3/4	20/48	4/4	22/49	2/3		
	(38.7)	(60.0)	(50.0)		(50.0)	(16.7)		(43.8)	(75.0)		(43.8)	(75.0)	(43.5)	(75.0)	(41.7)	(100)	(44.9)	(75.0)	(41.7)	(100)	(44.9)	(66.7)		
x ² /y ² (rate, %)	12/31	6/15	1/6	0.559	18/46	1/6	0.282	18/48	1/4	0.224	16/48	3/4	16/48	3/4	16/48	3/4	17/49	3/4	16/48	3/4	17/49	2/3		
	(38.7)	(40.0)	(16.7)		(39.1)	(16.7)		(37.5)	(25.0)		(33.3)	(75.0)	(33.3)	(75.0)	(33.3)	(75.0)	(34.7)	(75.0)	(33.3)	(75.0)	(34.7)	(66.7)		
KIT (exon					15	5	0.164	17	3	0.221	17	3	16	4	17	3	17	4	16	3	17	3		
8,17) (%) ^a	4	5	1	0.369	(27.8)	(50.0)		(29.3)	(50.0)		(32.2)	(20.0)	(27.1)	0.014	(28.8)	(60.0)	(28.8)	0.014	(28.8)	(60.0)	(28.8)	(60.0)		
ASXL1 (%) ^b					8	2	0.435	10	0	0.435	10	0	9	1	9	1	8	1	9	1	8	2		
	(10.8)	(25.0)	(14.3)		(14.3)	(25.0)		(17.2)			(15.3)	(20.0)	(15.3)	(20.0)	(15.3)	(20.0)	(13.6)	(20.0)	(15.3)	(20.0)	(13.6)	(40.0)		
MET (%)	4	4	0	0.346	6	2	0.435	7	1		7	1	6	2	5	3	6	2	5	3	6	2		
	(10.8)	(20.0)			(11.1)	(20.0)		(12.1)	(16.7)		(11.9)	(20.0)	(10.2)	(40.0)	(8.5)	(60.0)	(10.2)	(40.0)	(8.5)	(60.0)	(10.2)	(40.0)		
MLH1 (%)	3	3	0	0.463	6	0	0.268			0.746	5	1	5	1	5	1	4	1	5	1	4	2		
	(8.1)	(15.0)			(11.1)						(8.5)	(20.0)	(8.5)	(20.0)	(8.5)	(20.0)	(6.8)	(20.0)	(8.5)	(20.0)	(6.8)	(40.0)		
TET2 (%)	4	1	0	0.529	4	1	0.779	4	1	0.597	4	1	4	1	4	1	3	1	4	1	3	2		
	(10.8)	(5.0)			(7.4)	(10.0)		(6.9)	(16.7)		(6.9)	(16.7)	(6.8)	(20.0)	(4.8)	(20.0)	(5.1)	(20.0)	(4.8)	(20.0)	(5.1)	(40.0)		
FBXW7 (%)	1	4	0	0.048	4	1	0.779	4	1	0.053	4	1	4	1	3	2	2	1	3	2	2	3		
	(2.7)	(20.0)			(7.4)	(10.0)		(6.9)	(16.7)		(6.8)	(20.0)			(5.1)	(40.0)	(3.4)		(5.1)	(40.0)	(3.4)	(60.0)		
																0.005						0.000		

Table SV. Influence of co-recurrent mutations on clinical features in the *AML1-ETO*-positive acute myeloid leukemia (AML) patients.

Gene	Tyrosine kinase pathway			Chromatin modifiers			Transcription factors			DNA methylation			Tumor suppressor			Miscellaneous		
	WT	mut	P-value	WT	mut	P-value	WT	mut	P-value	WT	mut	P-value	WT	mut	P-value	WT	mut	P-value
No.	30	34		48	16		52	12		55	9		55	9		59	5	
MAO	30.5 (2-58)	27.5 (5-65)	0.824	25.5 (2-58)	34 (5-65)	0.251	28.5 (2-65)	28 (3-47)	0.648	28 (2-58)	33 (5-65)	0.870	27 (2-60)	34 (5-65)	0.246	28 (2-60)	36 (5-65)	0.884
Sex (M/F)	19/11	20/14	0.712	30/18	9/7	0.657	31/21	8/4	0.652	33/22	6/3	0.704	35/20	4/5	0.274	35/24	4/1	0.363
Median WBC (x10 ⁹ /l)	15.0 (2.3-70.3)	22.5 (3.1-72.4)	0.077	21.3 (2.3-72.4)	17.1 (3.3-40.2)	0.540	21.3 (2.3-72.4)	15.5 (3.1-54.2)	0.582	19.3 (2.3-72.4)	22.4 (3.3-70.3)	0.977	21.2 (2.3-72.4)	14.7 (3.3-37.6)	0.493	19.3 (2.3-72.4)	22.4 (3.3-37.6)	1.000
EML (rate, %)	9 (30.0)	11 (32.4)	0.839	13 (27.1)	7 (43.8)	0.213	17 (32.7)	3 (25.0)	0.604	16 (29.1)	4 (44.4)	0.357	17 (30.9)	3 (33.3)	0.884	19 (32.2)	1 (20.0)	0.572
Median BMB (%)	35.0 (3.0-68.0)	40.0 (4.0-94.0)	0.397	34.5 (4.0-93.0)	42.3 (3.0-94.0)	0.373	34.5 (3.0-94.0)	54.5 (27.0-93.0)	0.007	34.0 (3.0-93.0)	48.0 (31.0-94.0)	0.023	35.0 (3.0-90.0)	40.4 (23.0-94.0)	0.145	35.0 (3.0-93.0)	54.0 (31.0-94.0)	0.033
CD56 ⁺	19/29 (65.5)	22/34 (64.7)	0.946	29/47 (61.7)	12/16 (75.0)	0.335	32/51 (62.7)	9/12 (75.0)	0.423	33/54 (61.1)	8/9 (88.9)	0.106	33/54 (61.1)	8/9 (88.9)	0.106	36/58 (62.1)	5 (100)	0.088
ACAs (%)	10/24 (41.7)	14/28 (50.0)	0.548	20/42 (47.6)	4/10 (40.0)	0.664	20/43 (46.5)	4/9 (44.4)	0.910	20/47 (42.6)	4/5 (80.0)	0.110	19/45 (42.2)	5/7 (71.4)	0.149	22/49 (44.9)	2/3 (66.7)	0.463
x/y (rate, %)	10/24 (41.7)	9/28 (32.1)	0.477	17/42 (40.5)	2/10 (20.01)	0.227	15/43 (34.9)	4/9 (44.4)	0.588	15/47 (31.9)	4/5 (80.0)	0.034	15/45 (33.3)	4/7 (57.1)	0.224	17/49 (34.7)	2/3 (66.7)	0.264
CR (%) ^a	29 (96.7)	30 (90.9)	0.349	44 (93.6)	15 (93.8)	0.985	48 (92.3)	11 (100)	0.342	51 (94.4)	8 (88.9)	0.527	50 (92.6)	9 (100)	0.399	55 (94.8)	4 (80.0)	0.192
MMR (%) ^b	10/25 (40.0)	8/30 (26.7)	0.294	17/43 (39.5)	1/12 (8.3)	0.042	16/47 (34.0)	2/8 (25.0)	0.614	17/47 (36.2)	1/8 (12.5)	0.187	17/47 (36.2)	1/8 (12.5)	0.187	18/50 (36.0)	0 (0)	0.102
CIR (%)	11/29 (37.9)	20/33 (6.06)	0.075	19/46 (41.3)	12/16 (75.0)	0.020	26/51 (51.0)	5/11 (45.5)	0.740	24/53 (45.3)	7/9 (77.8)	0.071	24/53 (45.3)	7/9 (77.8)	0.071	27/57 (47.4)	4/5 (80.0)	0.162
CID (%)	7/29 (24.1)	18/33 (54.5)	0.015	13/46 (28.3)	12/16 (75.0)	0.001	20/51 (39.2)	5/11 (45.5)	0.702	18/53 (34.0)	7/9 (77.8)	0.013	17/53 (32.1)	8/9 (88.9)	0.001	20/57 (35.1)	5/5 (100)	0.005

MAO, median age of onset; EML, extramedullary leukemia; BMB, bone marrow blast; ACA, additional chromosome abnormality; CR, complete remission; MMR, major molecular remission; CIR, cumulative incidence of relapse; CID, cumulative incidence of death. ^aCumulative CR rate after two course of induction therapy. ^bMMR was defined as a >3-log reduction in AML1-ETO mRNA transcript levels compared with those during pre-treatment and the checking time point was after two cycles of consolidation.