

Outcomes and genetic dynamics of acute myeloid leukemia at first relapse

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Supplementary material

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Table S1. 81-gene NGS panel

Gene	Exons (codons) tested
<i>ANKRD26</i> (NM_014915)	1 (1-6)
<i>ASXL1</i> (NM_015338)	11-12 (362-1542)
<i>ASXL2</i> (NM_018263)	11-12 (381-1436)
<i>BCOR</i> (NM_017745)	2-4 (1-512), 4-6 (514-1080), 7 (1122-1124), 7 (1091-1099), 7-15 (1124-1722)
<i>BCORL1</i> (NM_021946)	1-6 (1-1261), 6 (1264-1323), 6-11 (1326-1600), 11-12 (1614-1699), 12 (1706-1712)
<i>BRAF</i> (NM_004333)	11 (439-478), 15 (581-620)
<i>BRINP3</i> (NM_199051)	2-8 (1-471), 8 (475-767)
<i>CALR</i> (NM_004343)	9 (352-418)
<i>CBL</i> (NM_005188)	7-9 (336-477)
<i>CBLB</i> (NM_170662)	7-10 (282-469)
<i>CBLC</i> (NM_012116)	7-9 (336-454), 10 (464-475)
<i>CEBPA</i> (NM_004364)	1 (1-56), 1 (59-91), 1 (96), 1 (128-143), 1 (146-175), 1 (178-201), 1 (249-358)
<i>CREBBP</i> (NM_004380)	2-8 (29-608), 9-10 (615-705), 12-16 (724-1084), 17-31 (1094-1943), 31 (1950-2235), 31 (2238-2443)
<i>CSF3R</i> (NM_156039)	14 (575-622), 17 (681-864)
<i>CUX1</i> (NM_181552)	2-6 (11-172), 6-9 (174-241), 10-12 (248-359), 13-14 (367-408)
<i>DDX41</i> (NM_016222)	1-10 (1-366), 11 (369-410), 12-17 (420-623)
<i>DNMT3A</i> (NM_022552)	8-22 (286-862), 23 (866-913)
<i>EED</i> (NM_003797)	1-2 (1-69), 2-8 (71-287), 9-12 (289-442)
<i>ELANE</i> (NM_001972)	1-2 (5-46), 2 (69-75), 4-5 (123-268)
<i>ETNK1</i> (NM_018638)	3 (228-275)
<i>ETV6</i> (NM_001987)	1-6 (1-378), 7-8 (385-453)
<i>EZH2</i> (NM_004456)	2-5 (1-158), 6 (162-205), 7 (209-217), 8-13 (243-512), 14 (516-538), 14-19 (547-732), 20 (752)
<i>FBXW7</i> (NM_033632)	9-12 (413-708)
<i>FLT3</i> (NM_004119)	11-17 (437-709), 18-20 (736-847)
<i>GATA1</i> (NM_002049)	2-3 (1-84)
<i>GATA2</i> (NM_032638)	2-5 (1-377), 5-6 (379-481)
<i>GFI1</i> (NM_005263)	2 (2-39)
<i>GNAS</i> (NM_000516)	8 (200-202), 11 (315-324)
<i>HNRNPK</i> (NM_002140)	3-7 (1-96), 7 (101-106), 8-17 (111-465)
<i>HRAS</i> (NM_005343)	2-3 (1-60), 3-4 (87-150)
<i>IDH1</i> (NM_005896)	4 (132-133)
<i>IDH2</i> (NM_002168)	4 (125-178)
<i>IKZF1</i> (NM_006060)	2-8 (1-443), 8 (445-518)
<i>IL2RG</i> (NM_000206)	1-2 (1-45), 2-8 (51-340), 8 (360-370)
<i>IL7R</i> (NM_002185)	5-7 (180-292)
<i>JAK1</i> (NM_002227)	3-9 (3-445), 10 (453-465), 10-22 (470-1023), 22-24 (1026-1123)
<i>JAK2</i> (NM_004972)	10 (405-442), 12-14 (505-622), 16 (665-711), 18 (762-802)

<i>JAK3</i> (NM_000215)	2-23 (1-1069)
<i>KDM6A</i> (NM_021140)	1-19 (1-971), 19-21 (976-1070), 22-29 (1080-1402)
<i>KIT</i> (NM_000222)	8-9 (411-514), 11 (550-592), 17 (788-828)
<i>KMT2A</i> (NM_005933)	2-4 (145-1075), 4-13 (1081-1561), 14-15 (1566-1665), 27 (2178-2195), 27 (2201-2362), 27 (2365-2715), 27 (2721-3216), 27 (3219-3327), 27 (3336-3505), 27 (3521-3582)
<i>KRAS</i> (NM_004985)	2-4 (1-150)
<i>MAP2K1</i> (NM_002755)	2 (27-90), 3 (98-146)
<i>MPL</i> (NM_005373)	10 (490-522), 12 (552-636)
<i>NF1</i> (NM_001042492)	2-4 (21-160), 5 (165-190), 6 (201-218), 8-13 (244-468), 13-14 (478-547), 15-17 (568-667), 18 (674-728), 18-22 (746-992), 23-26 (997-1146), 26-30 (1160-1330), 30-31 (1353-1378), 31-34 (1382-1493), 34-35 (1512-1550), 35 (1563-1575), 36-38 (1601-1868), 39 (1870-1884), 39-40 (1886-1947), 40-47 (1952-2322), 47-49 (2325-2438), 50-51 (2441-2491), 51-52 (2494-2555), 53-58 (2580-2840)
<i>NOTCH1</i> (NM_017617)	26 (1529-1600), 26-28 (1604-1795), 34 (2061-2228), 34 (2234-2274), 34 (2290-2309), 34 (2290-2556), 34 (2061-2228), 34 (2234-2274), 34 (2309-2556)
<i>NPM1</i> (NM_002520)	11 (283-295)
<i>NRAS</i> (NM_002524)	2-4 (1-150)
<i>PAX5</i> (NM_016734)	1-10 (1-392)
<i>PHF6</i> (NM_032458)	2-3 (1-79), 4-10 (81-366)
<i>PIGA</i> (NM_002641)	2 (1-6), 2-5 (15-396), 6 (399-485)
<i>PML</i> (NM_033238)	3 (201-255)
<i>PRPF40B</i> (NM_001031698)	2-19 (2-609), 19-20 (611-658), 20-24 (661-807), 25-26 (815-893)
<i>PTEN</i> (NM_000314)	7-8 (212-340)
<i>PTPN11</i> (NM_002834)	3-4 (46-125), 7 (253-285), 12 (460-462), 12-13 (465-533)
<i>RAD21</i> (NM_006265)	2-12 (1-540), 13 (544-560), 14 (569-632)
<i>RARA</i> (NM_000964)	6-7 (211-338)
<i>RUNX1</i> (NM_001754)	2-9 (1-419), 9 (426-437), 9 (456-474)
<i>SETBP1</i> (NM_015559)	4 (838-885)
<i>SF1</i> (NM_004630)	1-2 (1-31), 2 (39-54), 3-12 (57-524), 13 (544-578), 13 (596-600), 13 (605-640)
<i>SF3A1</i> (NM_005877)	2-7 (22-322), 7-9 (355-424), 9-12 (427-646), 13-16 (651-794)
<i>SF3B1</i> (NM_012433)	13-16 (574-790)
<i>SH2B3</i> (NM_005475)	2 (1-40), 2 (43-119), 2 (132-164), 2-6 (233-374), 6-8 (380-576)
<i>SMC1A</i> (NM_006306)	1-25 (1-1234)
<i>SMC3</i> (NM_005445)	1 (1-5), 2-6 (19-110), 6-11 (113-299), 11-15 (308-477), 15-16 (498-504), 16-17 (507-580), 17-19 (591-706), 20-25 (708-975), 25 (979-1035), 26-29 (1038-1217)
<i>SRSF2</i> (NM_003016)	1 (1-38), 1 (45-121)
<i>STAG1</i> (NM_005862)	2 (1-5), 3-5 (10-101), 5-12 (121-392), 13-20 (402-703), 21-22 (724-738), 22-27 (740-953), 27 (955-979), 28 (985-1008), 29-34 (1022-1259)
<i>STAG2</i> (NM_006603)	2-8 (1-273), 9-16 (287-518), 16 (521-539), 17-22 (547-751), 23-33 (756-1232)
<i>STAT3</i> (NM_139276)	17 (489-509), 17-22 (521-715)
<i>STAT5A</i> (NM_003152)	3-6 (1-177), 6-7 (181-189), 8-20 (261-795)
<i>STAT5B</i> (NM_012448)	16 (636-673)

<i>SUZ12</i> (NM_015355)	1 (20-44), 1 (46-84), 2 (92-97), 4-5 (129-169), 7-11 (198-431), 12-16 (468-740)
<i>TERC</i> (NR_001566)	1 (1-36)
<i>TERT</i> (NM_198253)	1-2 (1-172), 2 (258-342), 2 (349-474), 2-4 (477-630), 4-5 (633-692), 6 (711-749), 6-12 (753-954), 12-16 (957-1133)
<i>TET2</i> (NM_001127208)	3 (1-77), 3 (91-92), 3 (98-815), 3 (829-853), 3-10 (867-1453), 10-11 (1465-2003)
<i>TP53</i> (NM_000546)	2 (1-25), 4-11 (80-394)
<i>U2AF1</i> (NM_006758)	2 (15-44), 6 (117-161)
<i>U2AF2</i> (NM_007279)	1-5 (1-161), 6-12 (163-437), 12 (441-476)
<i>WT1</i> (NM_024426)	1 (1-5), 1 (7-63), 1-10 (127-518)
<i>ZRSR2</i> (NM_005089)	1-4 (1-90), 5 (105-130), 6-8 (134-257), 9-11 (260-419), 11 (465-483)

Table S2. Baseline characteristics of all AML patients

	All patients (n = 875)
Age, years	65 (18-94)
Male sex, n (%)	468 (53.5)
Race/ethnicity, n (%)	
White	654 (74.7)
Black	73 (8.3)
Asian	42 (4.8)
Other	72 (8.2)
Unknown/NA	34 (3.9)
WBC	3.4 (0.1-336)
Hgb	8.7 (3.5-14.3)
Platelets	36 (1-1625)
BM blasts	45 (1-97)
Cytogenetics	
Diploid	291 (35.5)
-5/-5q	151 (18.4)
-7/-7q	112 (13.7)
+8	80 (9.8)
inv16/t(16;16)	45 (5.5)
t(8:21)	27 (3.3)
KMT2Ar	47 (5.7)
MECOMr	11 (1.2)
Complex/Monosomal	208 (25.4)
ELN 2022	
Favorable	175 (20.7)
Intermediate	199 (23.6)
Adverse	470 (55.7)
Mutations	
ASXL1	108 (12.8)
BCOR	40 (4.8)
BCORL1	26 (3.1)
DNMT3A	198 (23.5)
EZH2	28 (3.3)
FLT3-ITD	140 (16.6)
IDH1	71 (8.4)
IDH2	119 (14.1)
NPM1	183 (21.8)
PTPN11	82 (9.8)
RUNX1	108 (12.8)
SRSF2	122 (14.5)
TET2	132 (15.7)
TP53	190 (22.6)
U2AF1	62 (7.4)
WT1	61 (7.3)
ZRSR2	17 (2.0)
Treatment	
IT	348 (39.8)
IT + Ven	144 (41.4)*
LIT	527 (60.2)
LIT + Ven	379 (71.9)*

* Percentages calculated by treatment subgroup (IT or LIT).

Table S3. Emergence and clearance rates of mutations and cytogenetic findings

Emergence rate = n of patients with acquired mutation at relapse / n of patients without mutation at diagnosis

Clearance rate = n of patients with acquired mutation at relapse / n of patients without mutation at diagnosis

Gene mutation	All patients		Intensive chemotherapy		Low intensity chemotherapy	
	Emergence rate	Clearance rate	Emergence rate	Clearance rate	Emergence rate	Clearance rate
ASXL1	6/137 (4.4%)	1/19 (5.3%)	2/48 (4.2%)	0/5	4/89 (4.5%)	1/14 (7.1%)
ASXL2	1/156 (0.6%)	0/0	0/53	0/0	1/103 (1%)	0/0
BCOR	3/148 (2%)	2/8 (25%)	0/50	1/3 (33.3%)	3/98 (3.1%)	1/5 (20%)
BCORL1	4/153 (2.6%)	2/3 (66.7%)	0/53	0/0	4/100 (4%)	2/3 (66.7%)
BRAF	0/154	1/2 (50%)	0/53	0/0	0/101	1/2 (50%)
BRINP3	1/155 (0.6%)	0/1	0/53	0/0	1/102 (1%)	0/1
CALR	1/155 (0.6%)	0/1	1/53 (1.9%)	0/0	0/102	0/1
CBL	2/150 (1.3%)	2/6 (33.3%)	1/52 (1.9%)	0/1	1/98 (1%)	2/5 (40%)
CBLC	0/155	1/1 (100%)	0/52	1/1 (100%)	0/103	0/0
CEBPA	1/149 (0.7%)	3/7 (42.9%)	1/50 (2%)	2/3 (66.7%)	0/99	1/4 (25%)
CREBBP	1/156 (0.6%)	0/0	0/53	0/0	1/103 (1%)	0/0
CSF3R	2/154 (1.3%)	0/2	1/52 (1.9%)	0/1	1/102 (1%)	0/1
DDX41	1/150 (0.7%)	1/6 (16.7%)	1/50 (2%)	0/3	0/100	1/3 (33.3%)
DNMT3A	9/106 (8.5%)	4/50 (8%)	3/34 (8.8%)	1/19 (5.3%)	6/72 (8.3%)	3/31 (9.7%)
ETV6	2/155 (1.3%)	0/1	2/53 (3.8%)	0/0	0/102	0/1
EZH2	5/152 (3.3%)	2/4 (50%)	2/52 (3.8%)	1/1 (100%)	3/100 (3%)	1/3 (33.3%)
FBXW7	0/155	1/1 (100%)	0/53	0/0	0/102	1/1 (100%)
FLT3_TKD	3/141 (2.1%)	11/15 (73.3%)	1/44 (2.3%)	6/9 (66.7%)	2/97 (2.1%)	5/6 (83.3%)
FLT3_ITD	6/132 (4.5%)	14/24 (58.3%)	1/41 (2.4%)	5/12 (41.7%)	5/91 (5.5%)	9/12 (75%)
GATA2	4/153 (2.6%)	0/3	1/52 (1.9%)	0/1	3/101 (3%)	0/2
GNAS	1/155 (0.6%)	1/1 (100%)	1/53 (1.9%)	0/0	0/102	1/1 (100%)
IDH1	4/144 (2.8%)	4/12 (33.3%)	1/47 (2.1%)	2/6 (33.3%)	3/97 (3.1%)	2/6 (33.3%)
IDH2	3/137 (2.2%)	2/19 (10.5%)	1/48 (2.1%)	1/5 (20%)	2/89 (2.2%)	1/14 (7.1%)
IKZF1	4/151 (2.6%)	2/5 (40%)	1/51 (2%)	0/2	3/100 (3%)	2/3 (66.7%)
JAK1	1/156 (0.6%)	0/0	0/53	0/0	1/103 (1%)	0/0
JAK2	1/153 (0.7%)	2/3 (66.7%)	0/53	0/0	1/100 (1%)	2/3 (66.7%)
JAK3	1/156 (0.6%)	0/0	0/53	0/0	1/103 (1%)	0/0
KDM6A	2/155 (1.3%)	0/1	2/53 (3.8%)	0/0	0/102	0/1
KIT	0/152	3/4 (75%)	0/49	3/4 (75%)	0/103	0/0
KMT2A	1/155 (0.6%)	0/1	0/53	0/0	1/102 (1%)	0/1
KRAS	3/145 (2.1%)	5/11 (45.5%)	1/49 (2%)	2/4 (50%)	2/96 (2.1%)	3/7 (42.9%)
MPL	1/156 (0.6%)	0/0	0/53	0/0	1/103 (1%)	0/0
NF1	2/146 (1.4%)	6/10 (60%)	0/49	2/4 (50%)	2/97 (2.1%)	4/6 (66.7%)
NOTCH1	0/155	1/1 (100%)	0/53	0/0	0/102	1/1 (100%)
NPM1	0/129	4/27 (14.8%)	0/40	2/13 (15.4%)	0/89	2/14 (14.3%)
NRAS	5/130 (3.8%)	8/26 (30.8%)	1/44 (2.3%)	5/9 (55.6%)	4/86 (4.7%)	3/17 (17.6%)
PHF6	3/150 (2%)	3/6 (50%)	2/51 (3.9%)	0/2	1/99 (1%)	3/4 (75%)
PIGA	0/155	0/1	0/53	0/0	0/102	0/1
PRPF40B	2/155 (1.3%)	0/1	0/53	0/0	2/102 (2%)	0/1
PTPN11	1/149 (0.7%)	3/7 (42.9%)	1/49 (2%)	2/4 (50%)	0/100	1/3 (33.3%)

RAD21	2/154 (1.3%)	0/2	1/51 (2%)	0/2	1/103 (1%)	0/0
RUNX1	5/126 (4%)	4/30 (13.3%)	0/46	2/7 (28.6%)	5/80 (6.2%)	2/23 (8.7%)
SETBP1	0/152	2/4 (50%)	0/53	0/0	0/99	2/4 (50%)
SF3B1	1/150 (0.7%)	0/6	0/51	0/2	1/99 (1%)	0/4
SH2B3	1/155 (0.6%)	0/1	0/52	0/1	1/103 (1%)	0/0
SMC1A	3/155 (1.9%)	0/1	2/53 (3.8%)	0/0	1/102 (1%)	0/1
SMC3	1/155 (0.6%)	0/1	1/52 (1.9%)	0/1	0/103	0/0
SRSF2	1/129 (0.8%)	1/27 (3.7%)	1/49 (2%)	1/4 (25%)	0/80	0/23
STAG1	0/155	1/1 (100%)	0/53	0/0	0/102	1/1 (100%)
STAG2	2/150 (1.3%)	1/6 (16.7%)	2/51 (3.9%)	1/2 (50%)	0/99	0/4
STAT5A	1/155 (0.6%)	0/1	0/53	0/0	1/102 (1%)	0/1
STAT5B	0/155	1/1 (100%)	0/52	1/1 (100%)	0/103	0/0
SUZ12	0/155	1/1 (100%)	0/52	1/1 (100%)	0/103	0/0
TERT	0/155	1/1 (100%)	0/53	0/0	0/102	1/1 (100%)
TET2	10/128 (7.8%)	1/28 (3.6%)	5/44 (11.4%)	0/9	5/84 (6%)	1/19 (5.3%)
TP53	8/107 (7.5%)	2/49 (4.1%)	7/45 (15.6%)	1/8 (12.5%)	1/62 (1.6%)	1/41 (2.4%)
U2AF1	0/145	1/11 (9.1%)	0/51	0/2	0/94	1/9 (11.1%)
U2AF2	0/155	0/1	0/53	0/0	0/102	0/1
WT1	7/149 (4.7%)	2/7 (28.6%)	3/49 (6.1%)	1/4 (25%)	4/100 (4%)	1/3 (33.3%)
ZRSR2	2/154 (1.3%)	2/2 (100%)	1/52 (1.9%)	1/1 (100%)	1/102 (1%)	1/1 (100%)
	All patients		Intensive chemotherapy		Low intensity chemotherapy	
CG finding	Emergence rate	Clearance rate	Emergence rate	Clearance rate	Emergence rate	Clearance rate
Normal CG	5/100 (5%)	14/49 (28.6%)	4/29 (13.8%)	9/21 (42.9%)	1/71 (1.4%)	5/28 (17.9%)
Complex	6/100 (6%)	2/45 (4.4%)	2/43 (4.7%)	0/7	4/57 (7%)	1/42 (2.4%)
Chr 5 abn	3/104 (2.9%)	2/45 (4.4%)	0/43	0/7	3/61 (4.9%)	2/38 (5.3%)
Chr 7 abn	11/110 (10%)	3/39 (7.7%)	6/46 (13%)	0/4	5/64 (7.8%)	3/35 (8.6%)
Chr 17 abn	6/120 (5%)	2/29 (6.9%)	2/46 (4.3%)	0/4	4/74 (5.4%)	2/25 (8)
t(8;21)	0/147	0/5	0/48	0/2	0/0	0/0
inv(16)	0/143	0/6	0/44	0/6	0/0	0/0
KMT2Ar	0/144	0/144	0/48	0/2	0/96	0/3
MECOMr	0/142	1/7 (14.3%)	0/47	1/3 (33.3%)	0/95	0/4
t(6;9)	0/147	0/2	0/49	0/1	0/98	0/1

Table S4. Salvage treatments for rAML

Therapy intensity	therapy type	FLT3i	IDHi	Immunotherapy	Other	Treatment
IT	Chemotherapy IT (n = 23)	Gilteritinib (n = 2)	Ivosidenib (n = 1)	GO (CD33 ADC) (n = 2)	LY2606368 (CHEK1 inh) (n = 1)	HDAC: 1 (4.3%) Ara-C + VP16: 1 (4.3%) CLIA: 2 (8.7%) CLIA + GO: 3 (13%) CLIA + decitabine: 1 (4.3%) CPX-351 + GO: 4 (17.3%) CPX-351 + ivosidenib: 1 (4.3%) FA + LY2606368: 1 (4.3%) FAI: 1 (4.3%) FAI + gilteritinib: 2 (4.3%) FAI + GO: 1 (4.3%) FA BID: 1 (4.3%) FLAG: 1 (4.3%) FLAG + Ida: 1 (4.3%) FLAG + Ida + GO: 1 (4.3%) Direct HSCT: 1 (4.3%)
	Chemo IT + Ven (n = 9)	-	-	-	-	FLAG+Ida+Ven: 1 (11.1%) CPX-351+Ven: 6 (55.5%) BID FA+Ven: 1 (11.1%) FAI+Ven: 1 (11.1%)
LIT	LIT (n = 35)	Gilteritinib (n = 1) Quizartinib (n = 5) Sorafenib (n = 2)	Enasidenib (n = 6) Ivosidenib (n = 1)	GO (CD33 ADC) (n = 1) Avelumab (PD-L1) (n = 1) Magrolimab (CD47) (n = 3) Nivolumab (PD1) (n = 6) Ipilimumab (CTLA-4) (n = 5)	BGB324 (AXL1 inh) (n = 1) DS-3032B (MDM2 inh) (n = 1) Imatinib (n = 1) Palbociclib (CDK4/6 inh) (n = 1) PLX51107 (BET inh) (n = 1)	Aza + quizartinib: 1 (%) Aza + nivolumab + ipilimumab: 5 (16.1%) Aza + nivolumab: 1 (3.2%) Aza + sorafenib + enasidenib: 1 (3.2%) Aza + sorafenib: 1 (3.2%) Aza + enasidenib: 5 (16.1%) Aza + DS-3032B: 1 (3.2%) Aza + ivosidenib + imatinib: 1 (3.2%) Aza + PLX51107: 1 (3.2%) Aza + avelumab + GO: 1 (3.2%) Aza + magrolimab: 3 (9.7%) Dec: 4 (%) Dec + palbociclib: 1 (3.2%) Dec + quizartinib: 3 (9.7%) SGI + Ida: 1 (3.2%) LDAC + Quizartinib: 1 (%) LDAC + BGB324: 1 (%) Clad + LDAC + gilteritinib: 1 (20%) Clad + LDAC: 1 (%) Aspacytarabine: 1 (%)

	<p>LIT + Ven (n = 64)</p>	<p>Gilteritinib (n = 5) Midostaurin (n = 1) Sorafenib (n = 1)</p>	<p>Enasidenib (n = 4) Ivosidenib (n = 1)</p>	<p>GO (CD33 ADC) (n = 2) Avelumab (PD-L1) (n = 2) Magrolimab (CD47) (n = 1) IMGN632 (CD123 ADC) (n = 1)</p>	<p>Trametinib (MEK inh) (n = 1) DS-3032B (MDM2 inh) (n = 1)</p>	<p>Aza + Ven: 7 (%) Aza + Ven + avelumab: 2 (%) Aza + Ven + GO: 1 (2.1%) Aza + Ven + enasidenib: 3 (4.7%) Aza + Ven + magrolimab: 1 (2.1%) Aza + Ven + trametinib: 1 (2.1%) Aza + Ven + IMGN632: 1 (2.1%) Aza + Ven + gilteritinib: 2 (4.2%) Aza + Ven + ivosidenib: 1 (2.1%) Dec + Ven: 18 (%) Dec 10d + Ven: 3 (6.2%) Dec + Ven + Enasid: 1 (2.1%) Dec + Ven + GO: 1 (2.1%) Dec + Ven + gilteritinib: 3 (%) Dec + Ven + sorafenib: 1 (2.1%) Dec + Ven + midostaurin: 1 (2.1%) Clad LDAC + Dec Ven: 1 (6.2%) LDAC + Ven: 3 (%) LDAC + Ven + DS3032b: 1 (6.2%) Clad LDAC + Ven: 10 (62.5%) HHT + Ven: 1 (6.2%) Sapacitabine + Ven: 1 (2.1%)</p>
	<p>Ven (n = 4)</p>	<p>Quizartinib (n = 1)</p>	<p>Ivosidenib (n = 1)</p>	<p>-</p>	<p>APR-246 (TP53mut) (n = 1) CYC065 (CDK inh) (n = 1)</p>	<p>Ivosidenib + Ven: 1 (25%) APR-246 + Ven: 1 (25%) CYC065 + Ven: 1 (25%) Quizartinib + Ven: 1 (25%)</p>

	Other (n = 29)	-	Enasidenib (n = 2) Ivosidenib (n = 2)	AGS62P1 (FLT3 ADC) (n = 1) AMG330 (CD33-CD3) (n = 2) AMV564 (CD33-CD3) (n = 2) MGD006 (CD123-CD3) (n = 1) HU8F4 (PR1) (n = 1) IMGN632 (CD123 ADC) (n = 6) MCLA-117 (CLL1-CD3) (n = 1) Nivolumab (PD1) (n = 2) Ipilimumab (CTLA-4) (n = 2) NKX101 (NK therapy) (n = 1) FT538 (NK therapy) (n = 2)	APTO-253 (cMyc inh) (n = 1) BTX-A51 (CK1a inh) (n = 1) CA4948 (IRAK4 inh) (n = 2) CB-5339 (VCP inh) (n = 1) DS-1594b (Menin inh) (n = 1)	Enasidenib: 2 (6.9%) Ivosidenib: 2 (6.9%) Nivolumab + Ipilimumab: 2 (3.4%) IMGN632: 6 (20.7%) AGS62P1: 1 (3.4%) AMG330: 2 (6.9%) AMV564: 2 (6.9%) APTO-253: 1 (3.4%) BTX-A51: 1 (3.4%) CA-4948: 2 (6.9%) CB-5339: 1 (3.4%) DS-1594b: 1 (3.4%) NKX101: 1 (3.4%) FT538: 2 (6.9%) HU8F4: 1 (3.4%) MCLA-117: 1 (3.4%) MGD006: 1 (3.4%)
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Figures

Figure S1

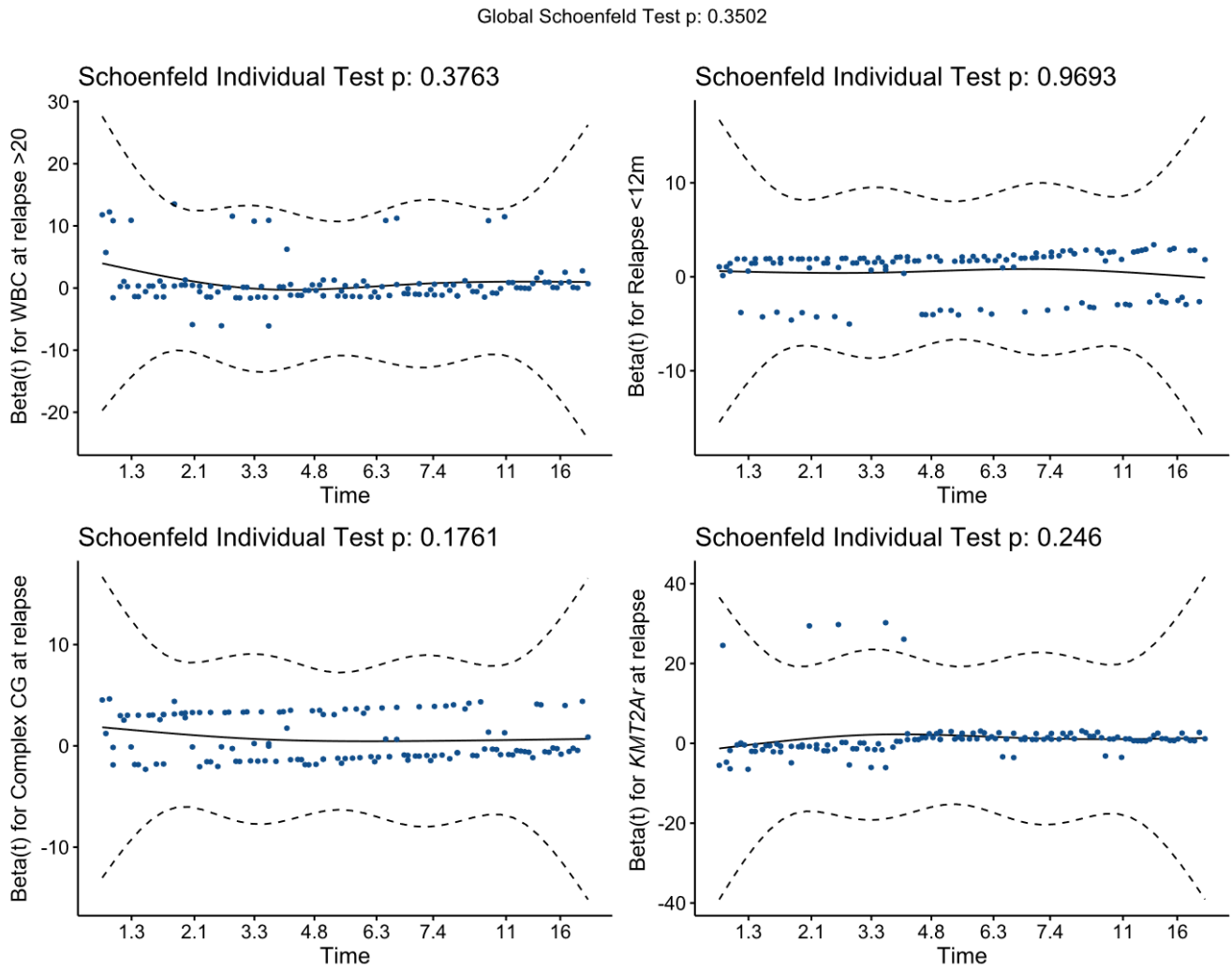


Figure S1. Schoenfeld residuals for variables included in the multivariate analysis for all patients.

Figure S2

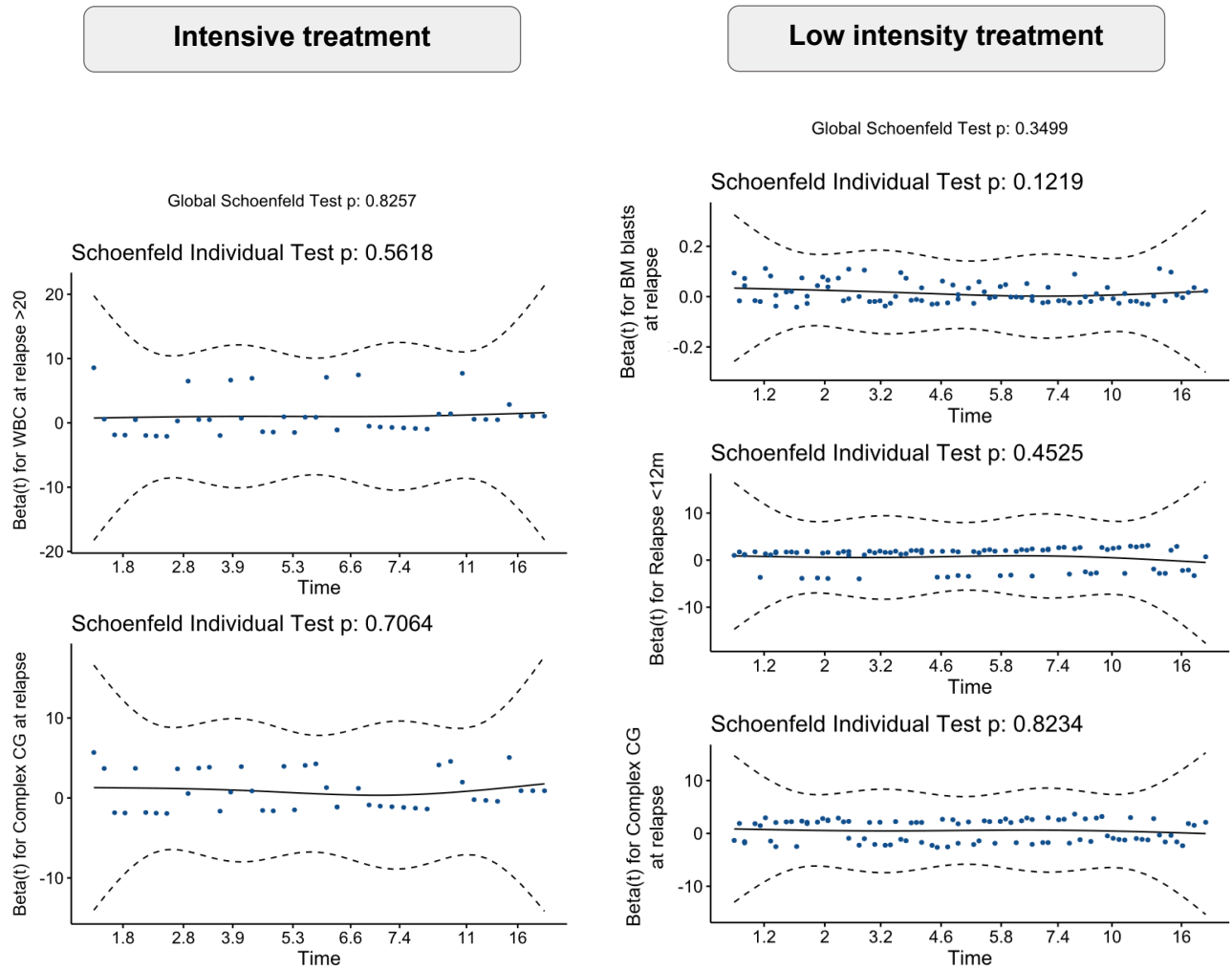


Figure S2. Schoenfeld residuals for variables included in the multivariate analysis for patients treated with intensive and low intensity treatment.

Figure S3

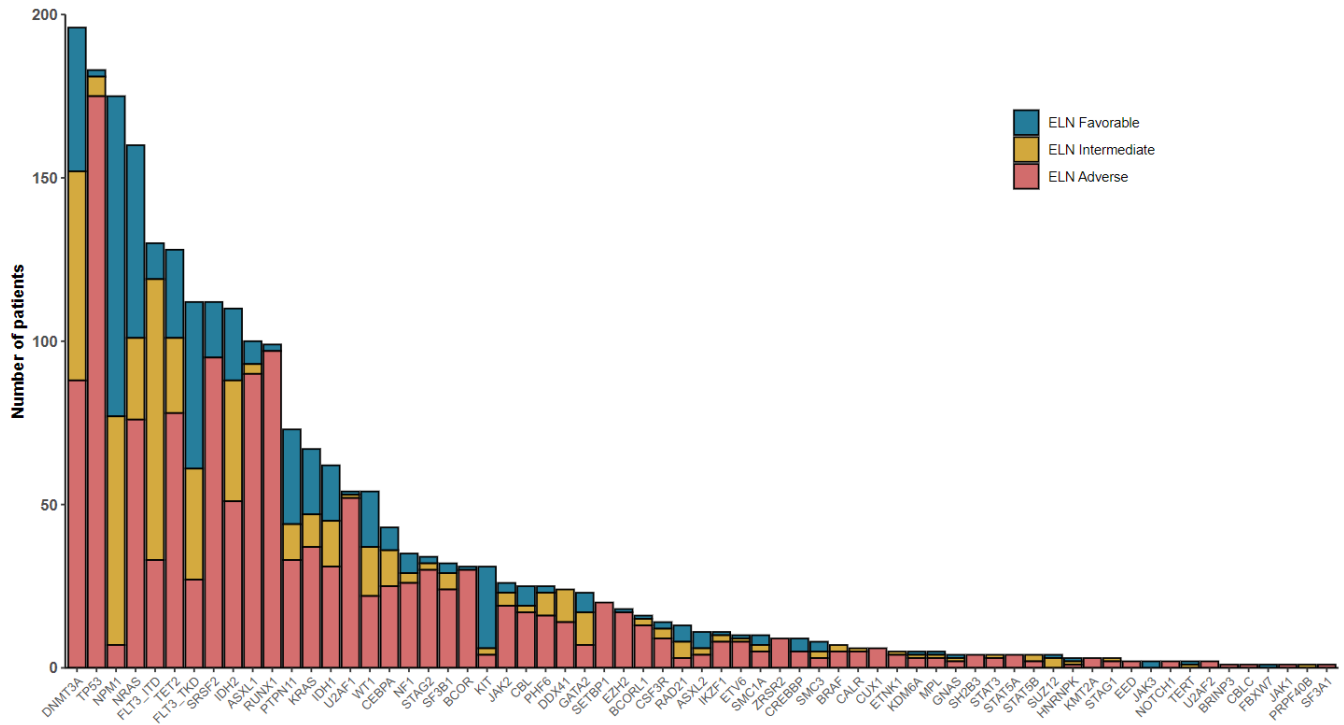


Figure S3. Bar plot describing all mutations detected in all patients at diagnosis, stratified by ELN 2022 risk.

Figure S4

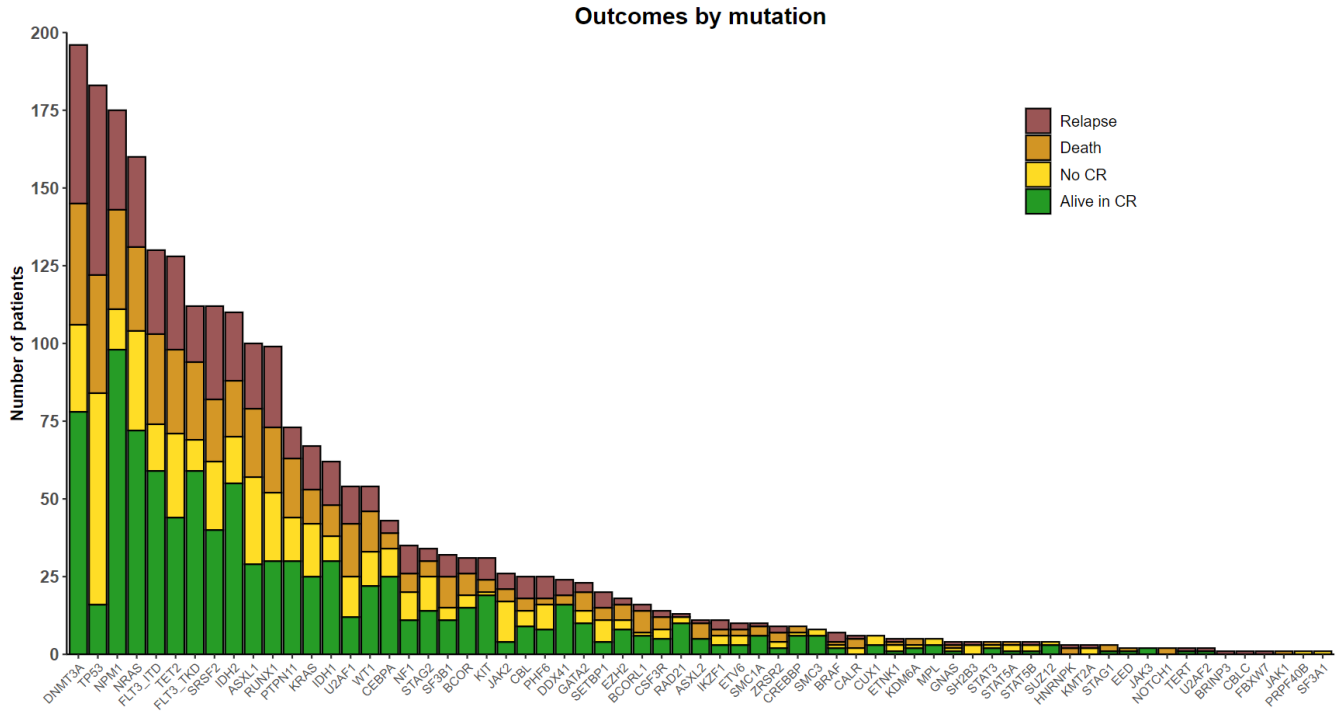


Figure S4. Bar plot describing all mutations detected in all patients at diagnosis, by the outcome of each patient.

Figure S5

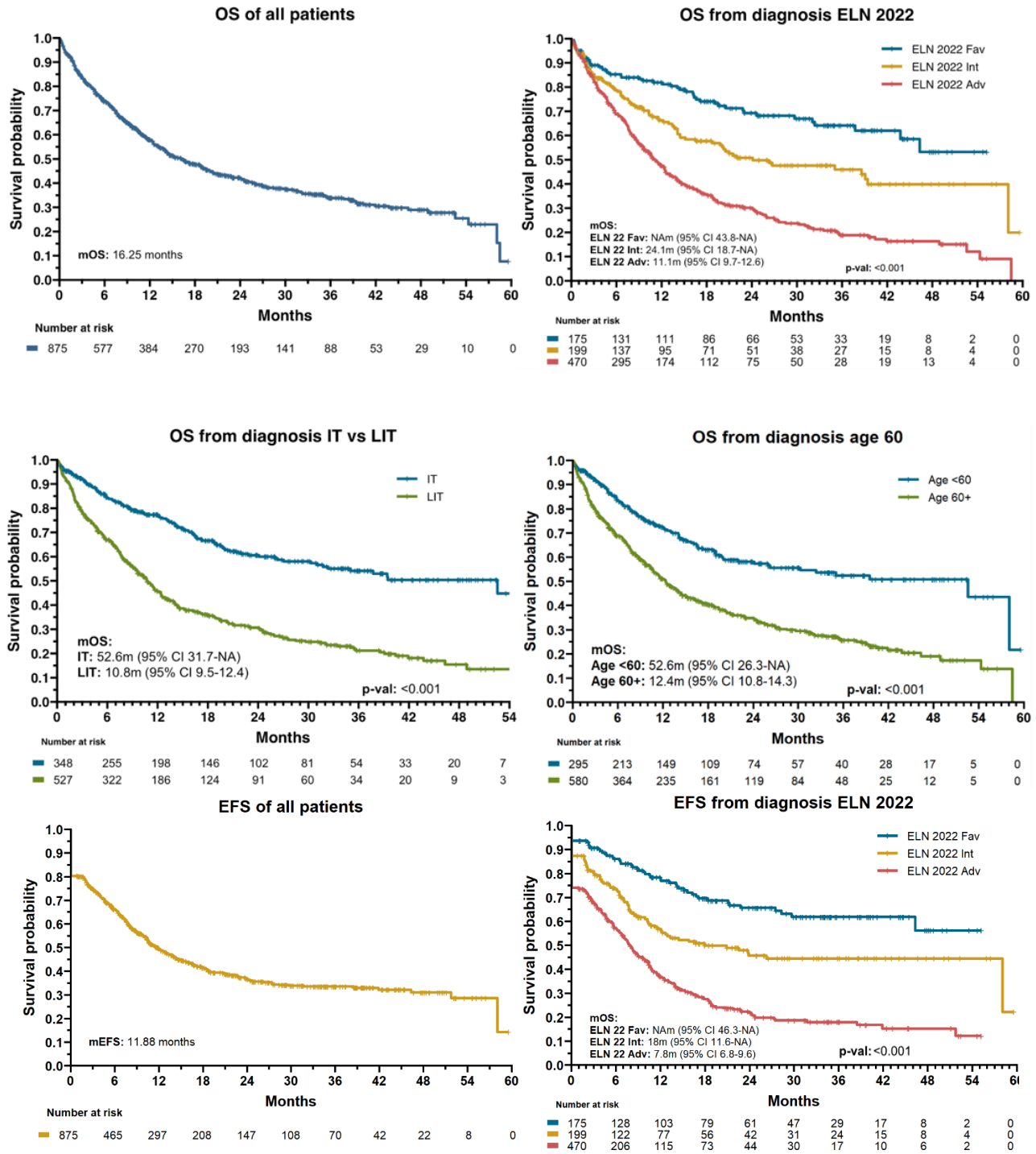


Figure S5. (A) OS of the entire cohort. (B) OS of the entire cohort stratified by the ELN 2022 risk classification. (D) OS of the entire cohort stratified by frontline treatment received. (E) OS of the entire cohort by age. Event-free survival (EFS) of all patients (left) and according to the ELN 2022 classification (right).

Figure S6

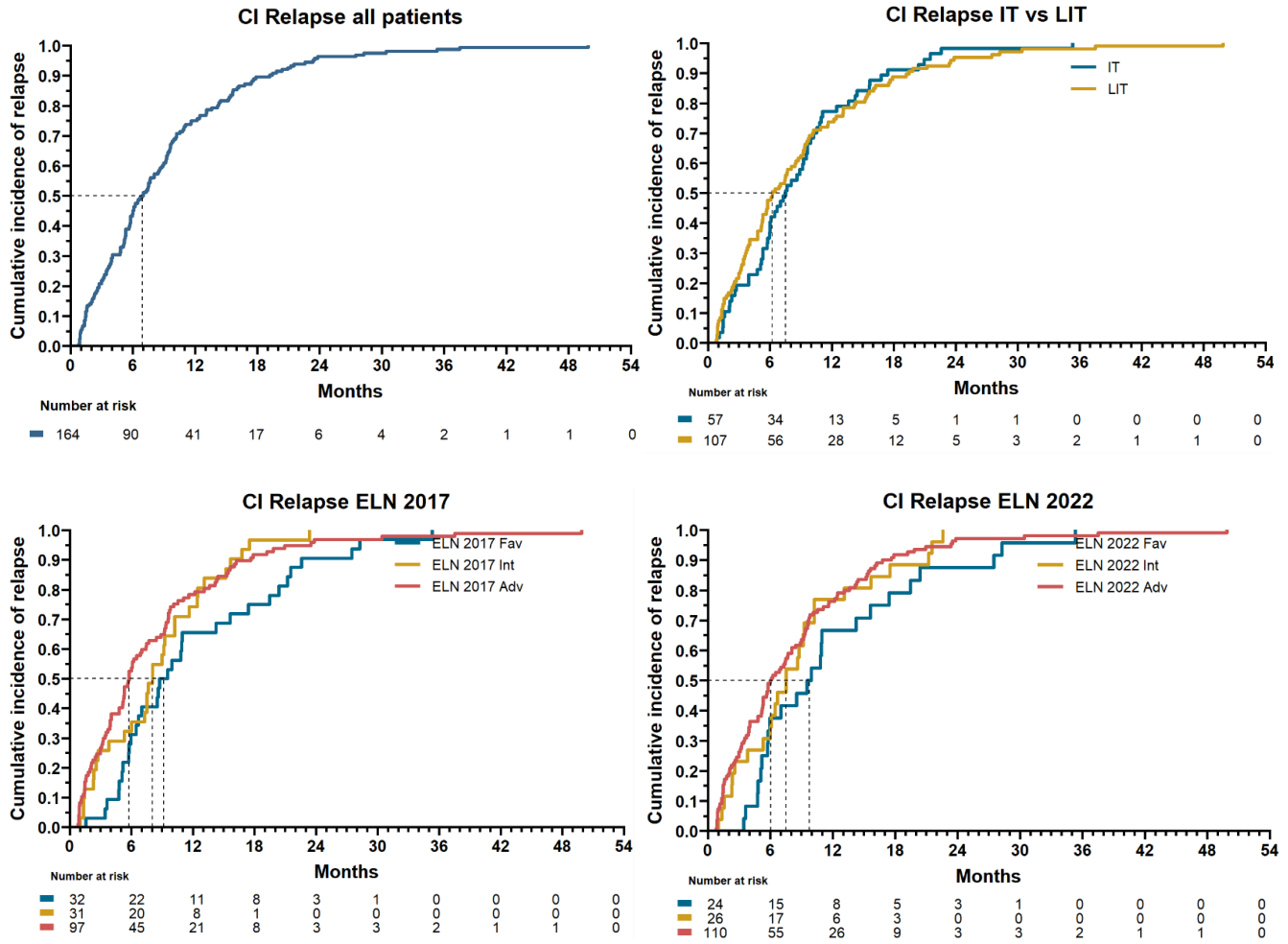


Figure S6. Cumulative incidence of relapse of all rAML patients (upper left), according to therapy received (upper right), according to ELN 2017 (lower left), and according to ELN 2022 (lower right).

Figure S7

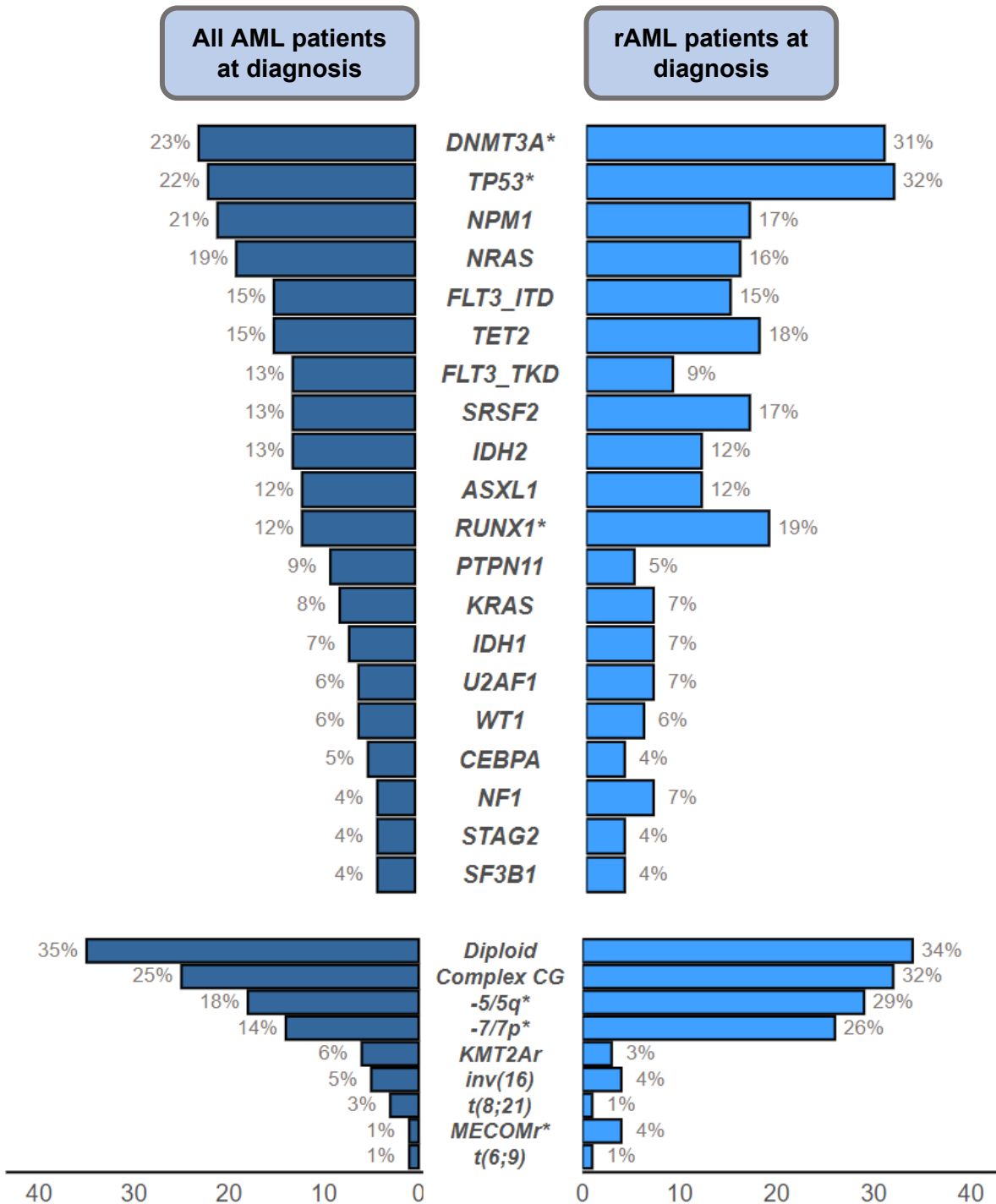


Figure S7. Frequency of mutations and cytogenetic findings in all patients at diagnosis vs rAML patients at diagnosis. An asterisk specifies genes/cytogenetic findings with significant proportion changes.

Figure S8

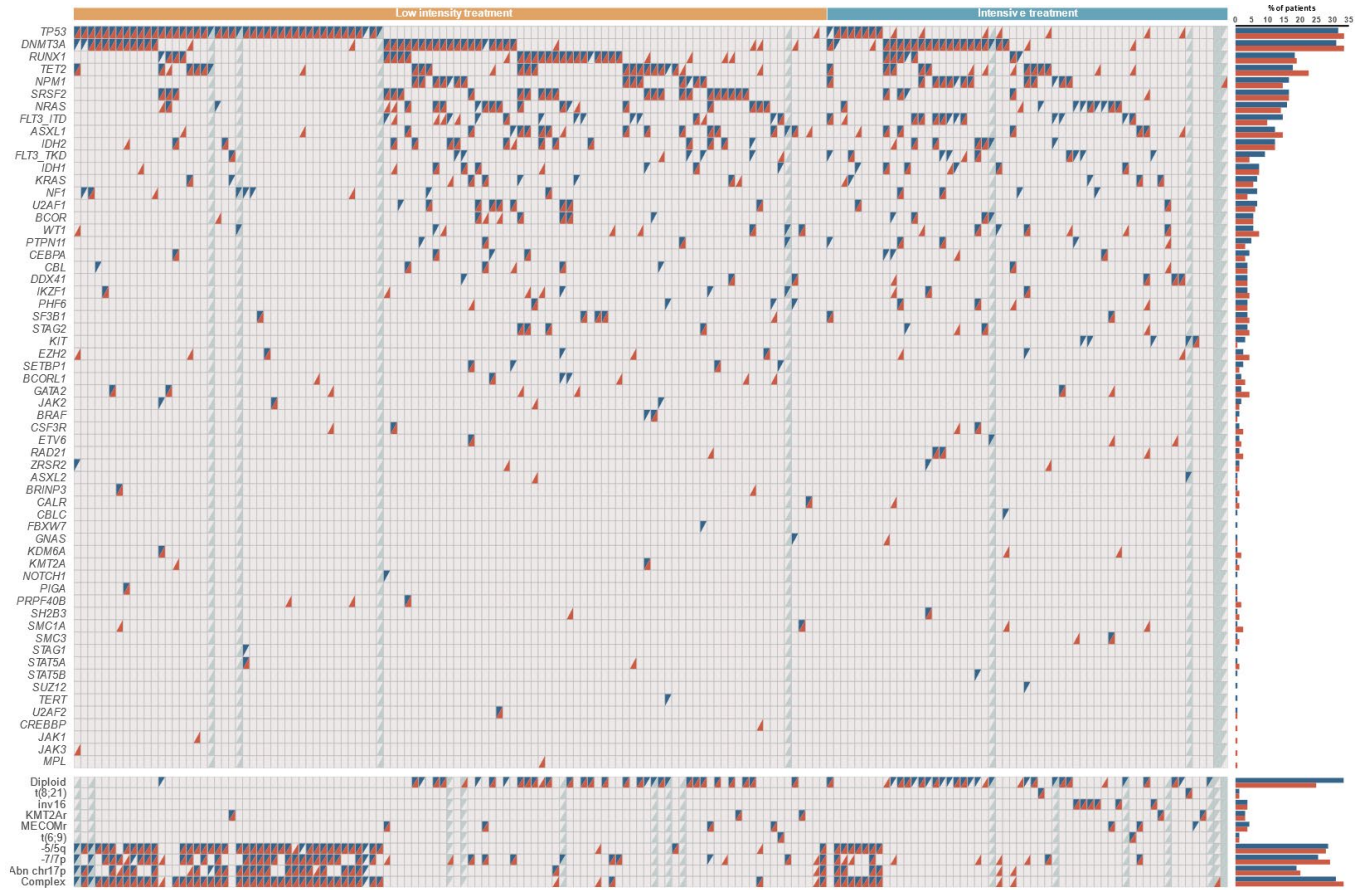


Figure S8. Oncoplot describing mutations at cytogenetic abnormalities at diagnosis (blue) and relapse (red). Patients with no data available are highlighted in grey.

Figure S9

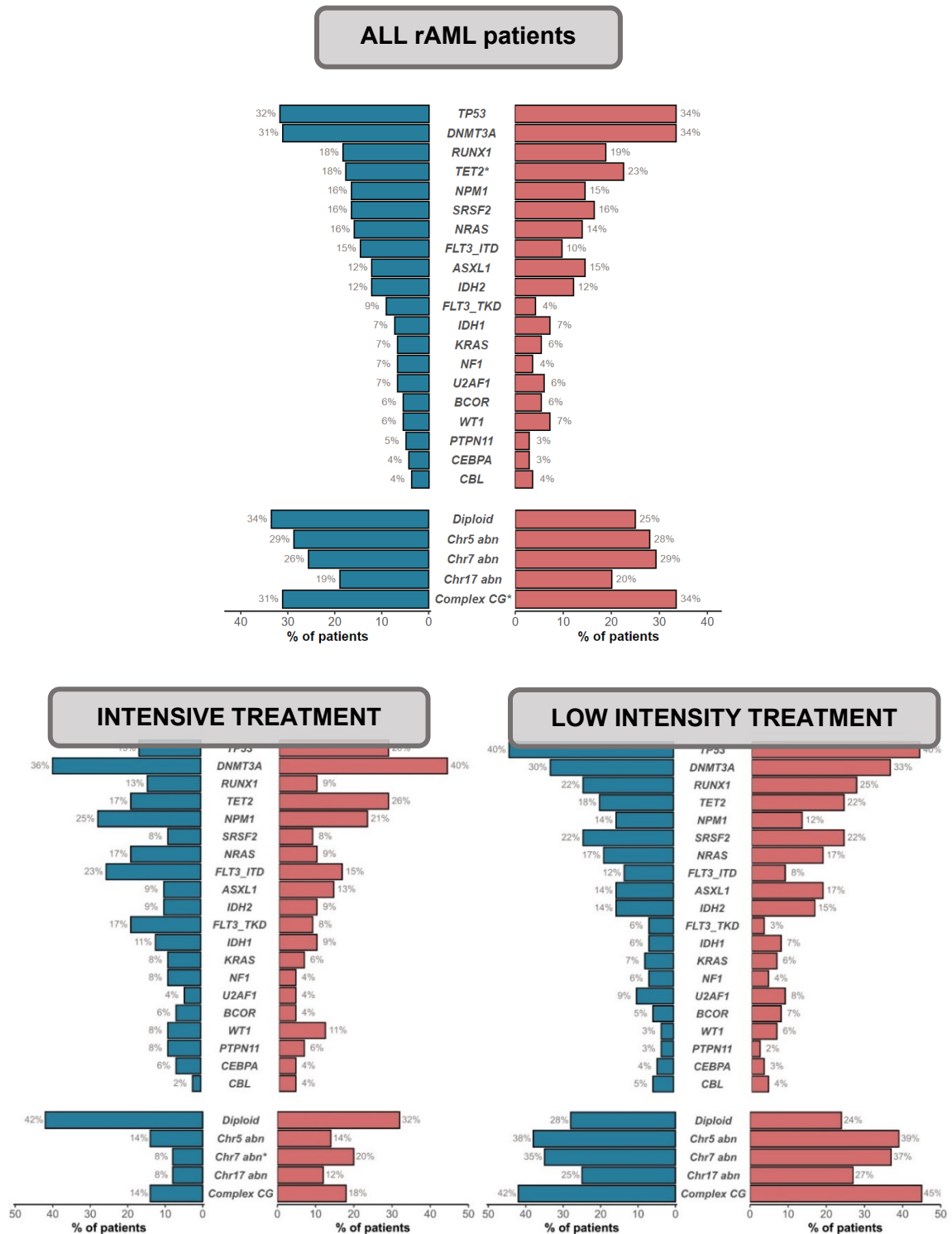


Figure S9. Frequency of mutations and cytogenetic findings at diagnosis and relapse in rAML patients with paired samples. An asterisk specifies genes/cytogenetic findings with significant proportion changes using a paired-sample approach with the McNemar test.

Figure S10

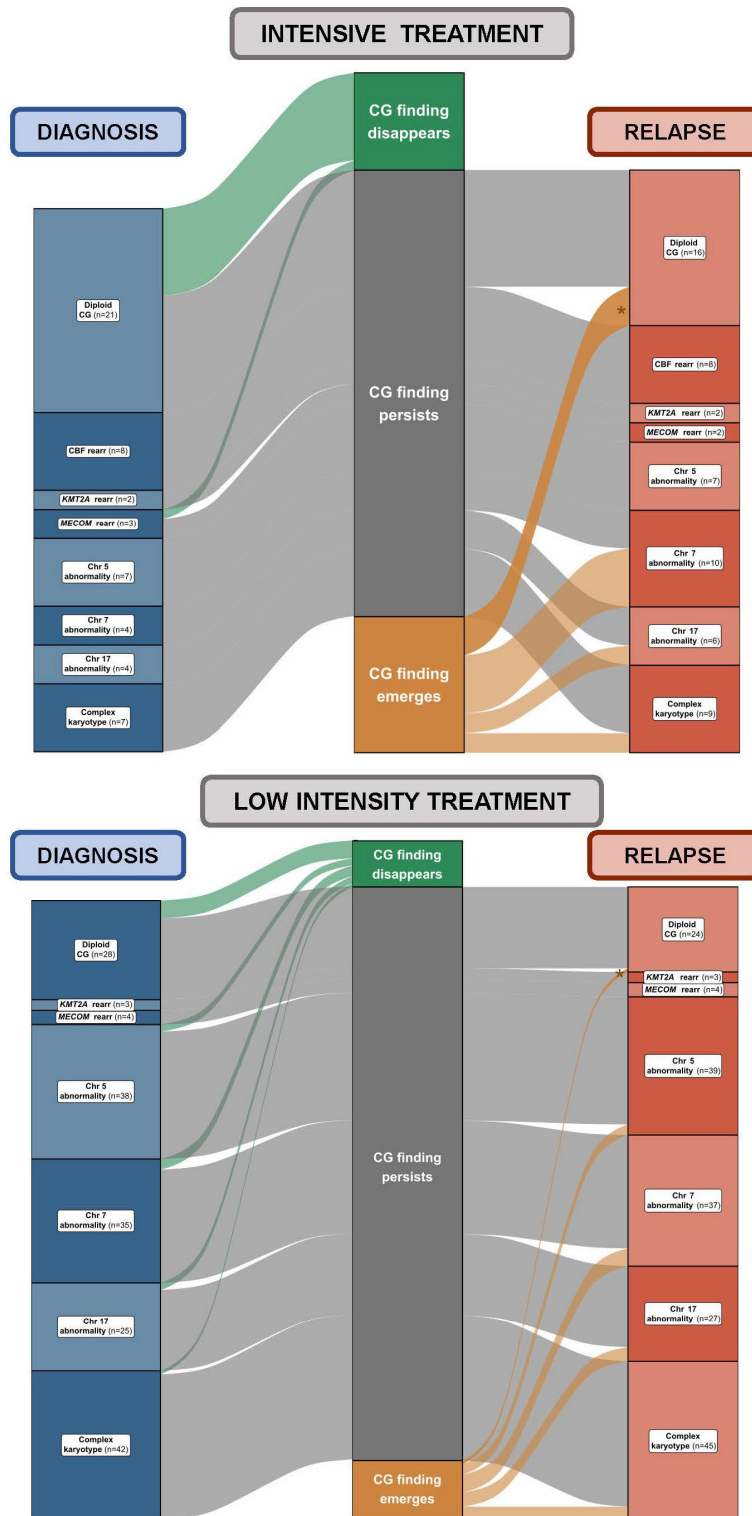


Figure S10. Cyto-genetic dynamics from diagnosis to relapse of patients treated with IT (top) or treated with LIT (bottom).

Figure S11

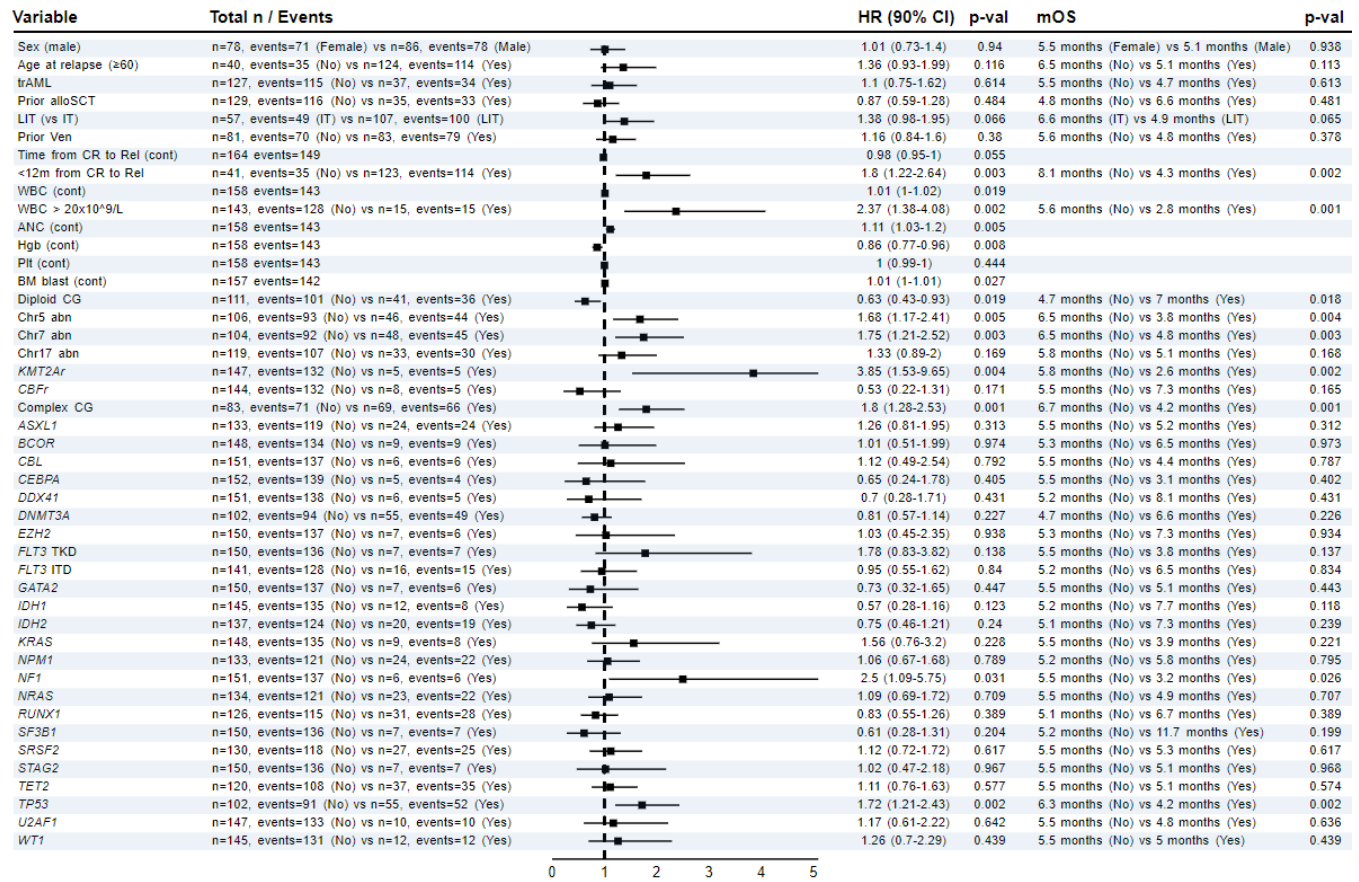


Figure S11. Univariate analysis for OS in all patients.

Figure S12

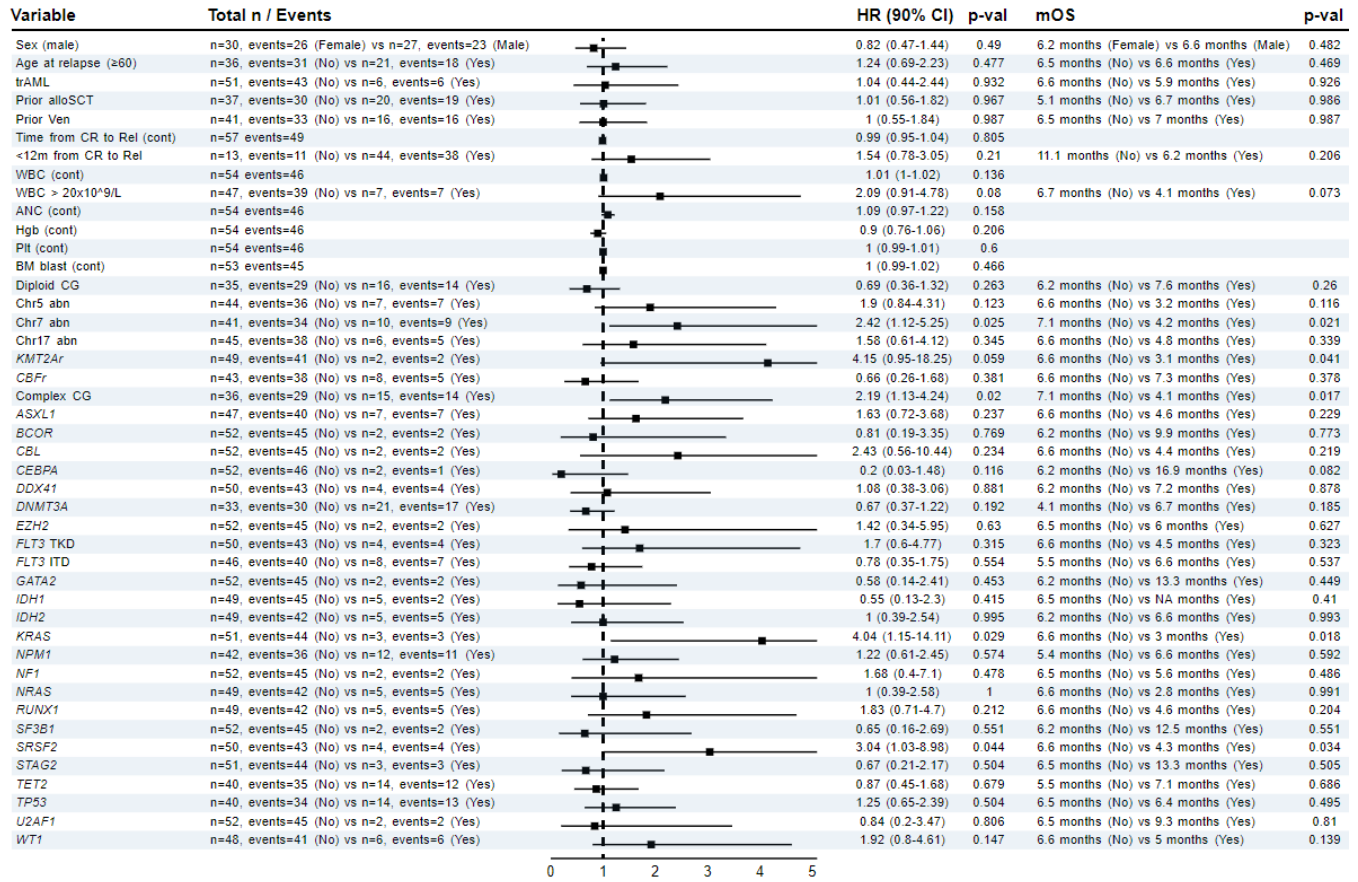


Figure S12. Univariate analysis for OS in patients receiving IT at diagnosis.

Figure S13

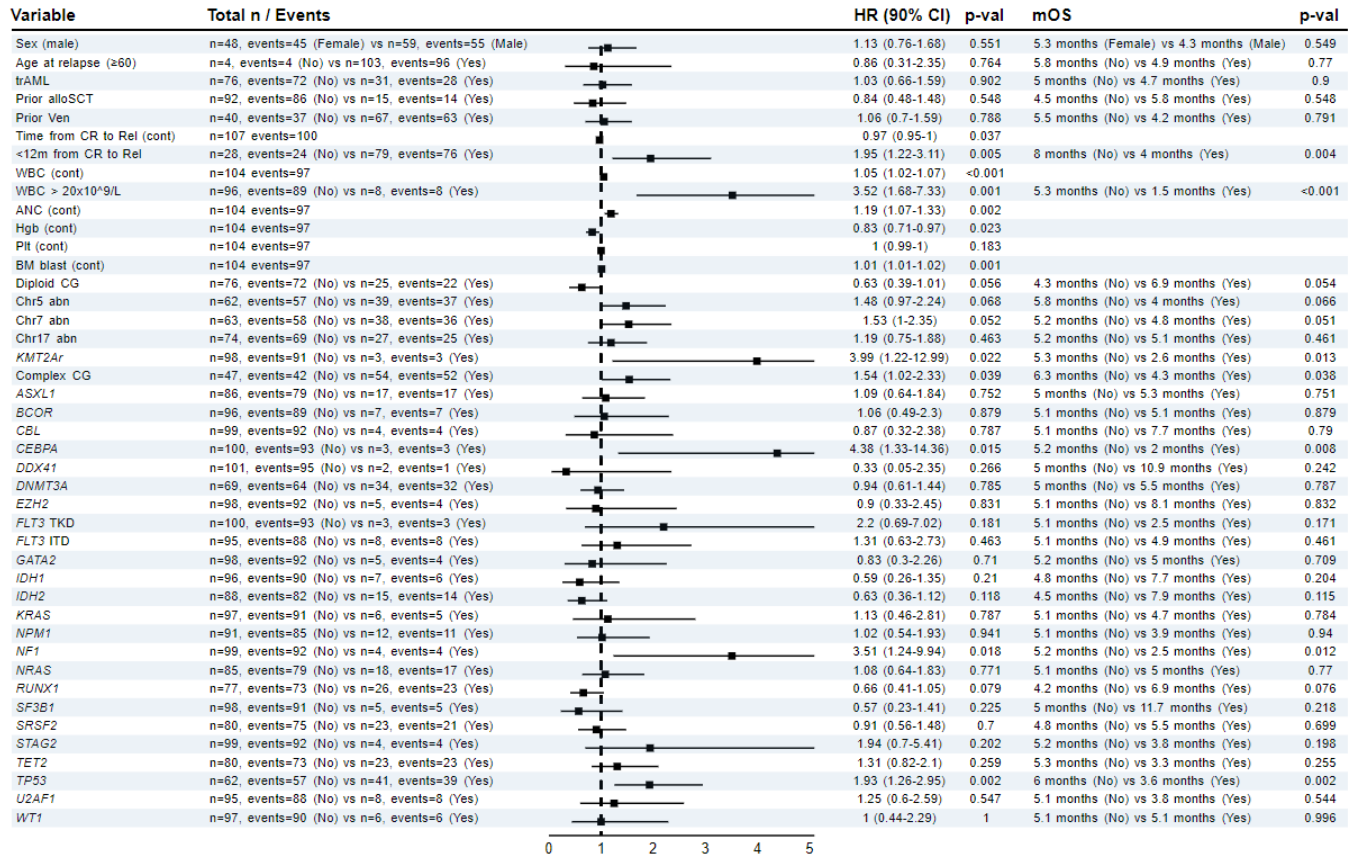


Figure S13. Univariate analysis for OS in patients receiving LIT at diagnosis.

Figure S14

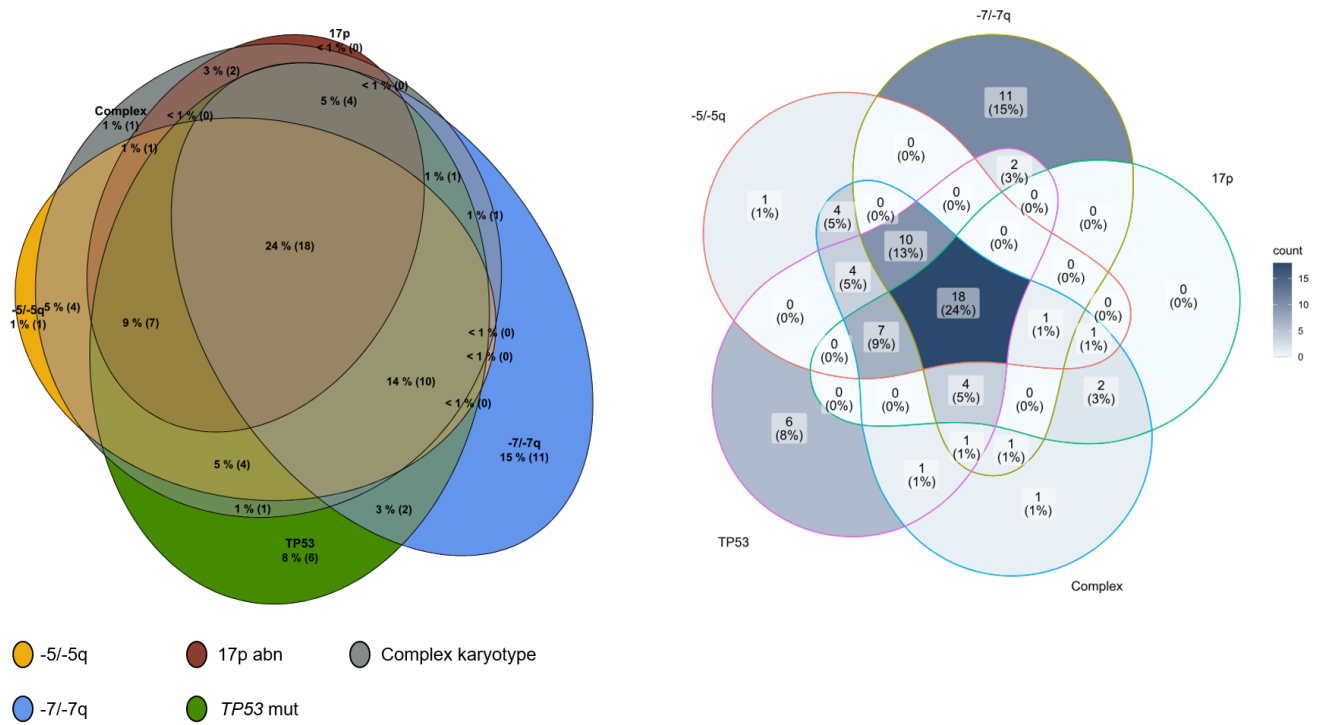


Figure S14. Venn diagram (left) and Euler plot (right) describing cooccurrence of cytogenetic and molecular abnormalities (Chr5, Chr7 and Chr17 abnormalities, complex karyotype, and TP53 mutation). In the Venn diagram, area of interaction is proportional to the number of patients.

Supplementary analysis 1 (SA1)

Patients receiving FLT3 inhibitors

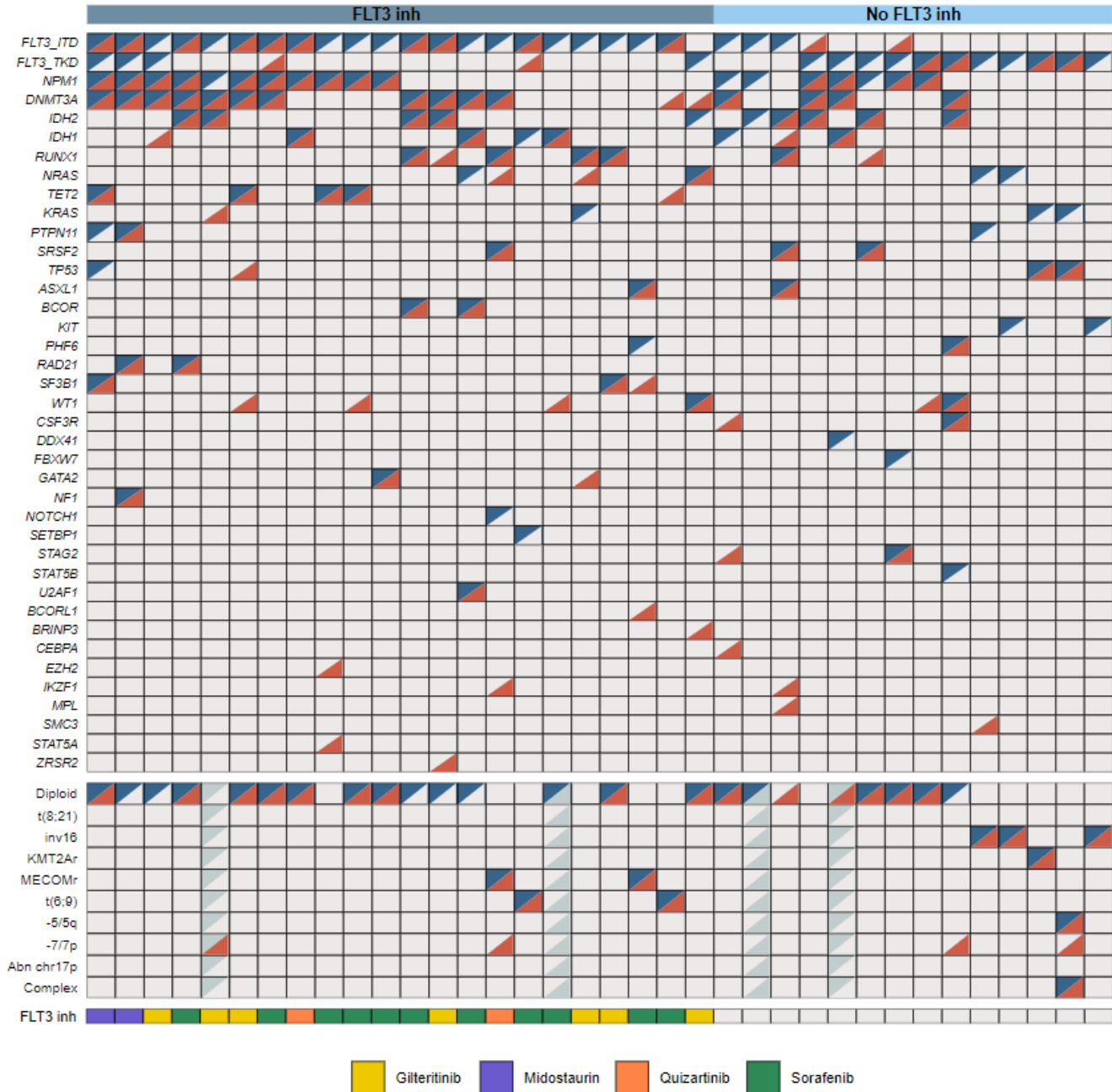


Figure S15. Mutations and cytogenetics at diagnosis and relapse in patients with *FLT3* (ITD and TKD mutations), stratified by therapy (FLT3 inhibitor).

Gene	FLT3 inhibitor (n=22)		No FLT3 inhibitor (n=134)	
	Emergence rate	Clearance rate	Emergence rate	Clearance rate
<i>ASXL1</i>	0/21 (0%)	0/1 (0%)	6/116 (5.2%)	1/18 (5.6%)
<i>BCOR</i>	0/20 (0%)	0/2	3/128 (2.3%)	2/6 (33.3%)
<i>BCORL1</i>	1/22 (4.5%)	0/0	3/131 (2.3%)	2/3 (66.7%)
<i>BRINP3</i>	1/22 (4.5%)	0/0	0/133	0/1
<i>DNMT3A</i>	2/11 (18.2%)	0/11	7/95 (7.4%)	4/39 (10.3%)
<i>EZH2</i>	1/22 (4.5%)	0/0	4/130 (3.1%)	2/4 (50%)
<i>FLT3_TKD</i>	2/18 (11.1%)	4/4 (100%)	1/123 (0.8%)	7/11 (63.6%)
<i>FLT3_ITD</i>	0/1	11/21 (52.4%)	6/131 (4.6%)	3/3 (100%)
<i>GATA2</i>	1/21 (4.8%)	0/1	3/132 (2.3%)	0/2
<i>IDH1</i>	1/18 (5.6%)	1/4 (25%)	3/126 (2.4%)	3/8 (37.5%)
<i>IDH2</i>	0/17	1/5 (20%)	3/120 (2.5%)	1/14 (7.1%)
<i>IKZF1</i>	1/22 (4.5%)	0/0	3/129 (2.3%)	2/5 (40%)
<i>KRAS</i>	1/21 (4.8%)	1/1 (100%)	2/124 (1.6%)	4/10 (40%)
<i>NF1</i>	0/21	0/1	2/125 (1.6%)	6/9 (66.7%)
<i>NOTCH1</i>	0/21	1/1 (100%)	0/134	0/0
<i>NPM1</i>	0/11	1/11 (9.1%)	0/118	3/16 (18.8%)
<i>NRAS</i>	2/20 (10%)	1/2 (50%)	3/110 (2.7%)	7/24 (29.2%)
<i>PHF6</i>	0/21	1/1 (100%)	3/129 (2.3%)	2/5 (40%)
<i>PTPN11</i>	0/20	1/2 (50%)	1/129 (0.8%)	2/5 (40%)
<i>RAD21</i>	0/20	0/2	2/134 (1.5%)	0/0
<i>RUNX1</i>	1/18 (5.6%)	0/4	4/108 (3.7%)	4/26 (15.4%)
<i>SETBP1</i>	0/21	1/1 (100%)	0/131	1/3 (33.3%)
<i>SF3B1</i>	1/20 (5%)	0/2	0/130	0/4
<i>SRSF2</i>	0/21	0/1	1/108 (0.9%)	1/26 (3.8%)
<i>STAG1</i>	0/22	0/0	0/133	1/1 (100%)
<i>TET2</i>	1/18 (5.6%)	0/4	9/110 (8.2%)	1/24 (4.2%)
<i>TP53</i>	1/21 (4.8%)	1/1 (100%)	7/86 (8.1%)	1/48 (2.1%)
<i>U2AF1</i>	0/21	0/1	0/124	1/10 (10%)
<i>WT1</i>	3/21 (14.3%)	0/1	4/128 (3.1%)	2/6 (33.3%)
<i>ZRSR2</i>	1/22 (4.5%)	0/0	1/132 (0.8%)	2/2 (100%)

Table S5 Mutations and cytogenetic abnormalities at diagnosis and relapse in patients with *FLT3* (ITD and TKD mutations), stratified by therapy (FLT3 inhibitor).

Supplementary analysis 2 (SA2)

Patients with normal karyotype

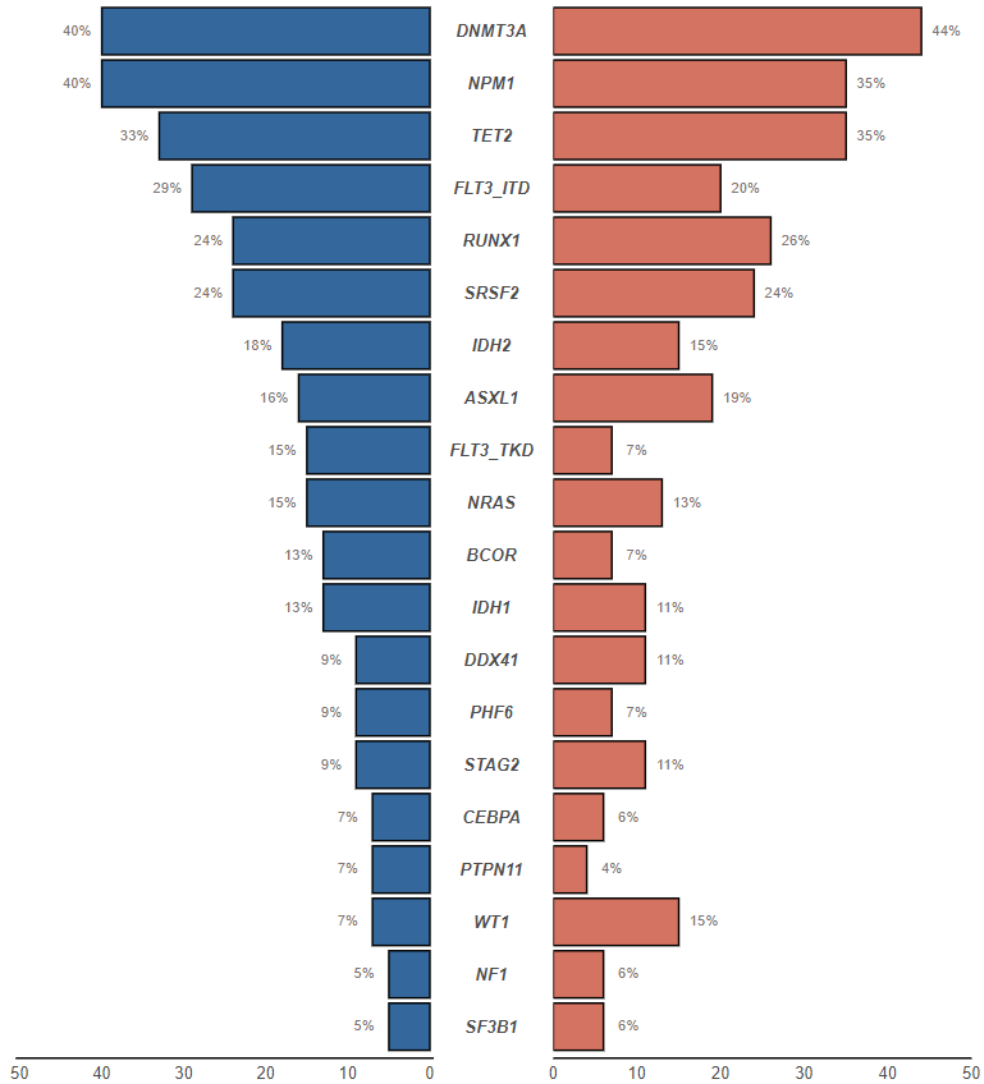


Figure S16. Mutations and cytogenetics at diagnosis (blue) and relapse (red) in rAML patients with normal karyotype at the moment of diagnosis.

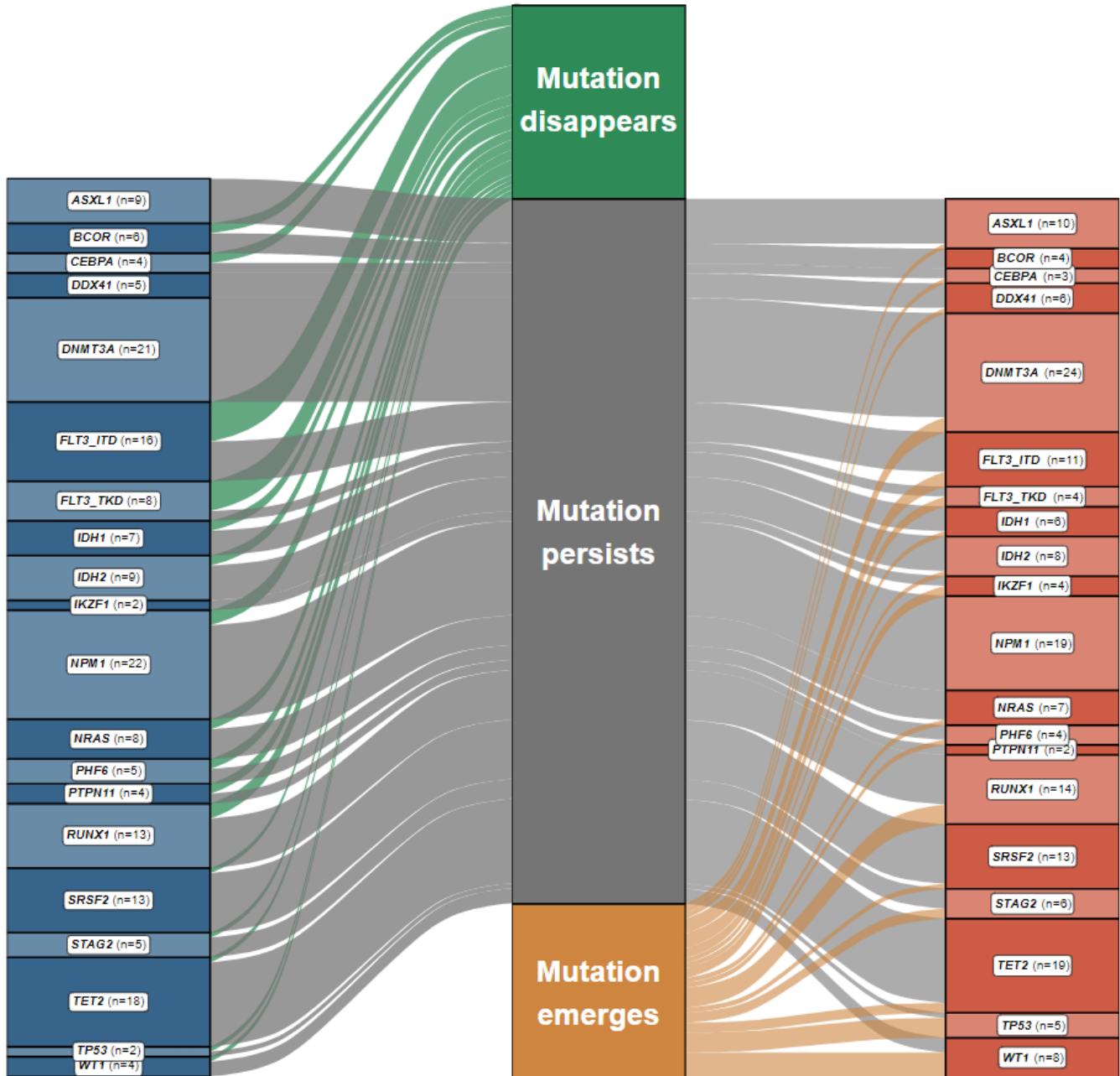


Figure S17. Mutation dynamics between diagnosis and relapse in patients with normal karyotype.

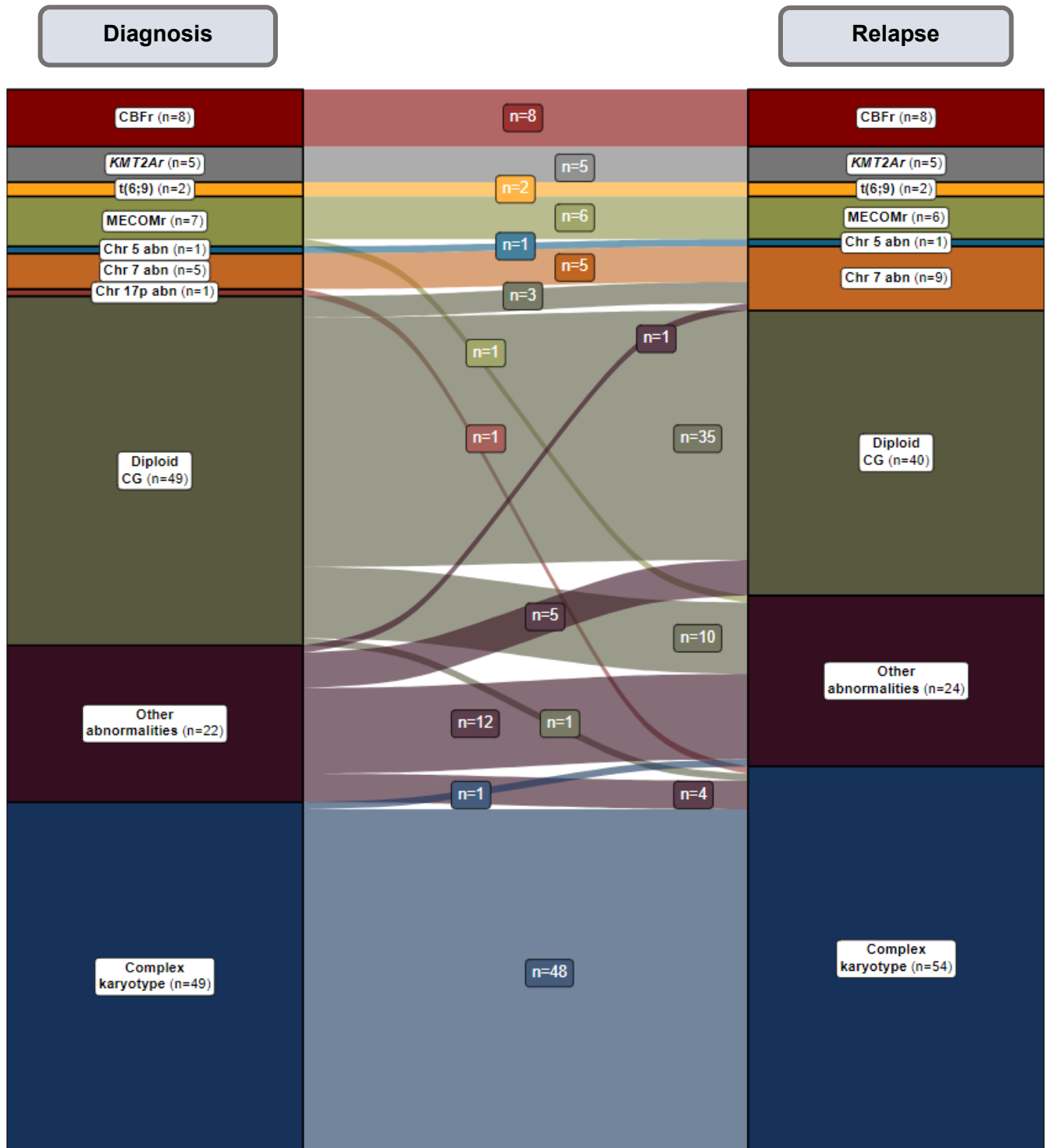


Figure S18. Flow of all patients according to their cytogenetic classification at diagnosis and at relapse. Numbers in the labels represent the number of patients.

ID	CG diagnosis	CG Relapse
9	46,XY[20]	46,XY[18]
20	46,XY[20]	46,XY[20]
24	46,XY,t(4;15)(q21;q21)[1]/46,XY[19]	46,XY[20]
26	46,XY[20]	45,XY,der(5;17)(p10;q10),add(7)(q22),del(12)(p12)[6]/ 44,XY,der(5;17)(p10;q10),-7[14]
34	46,XX[20]	46,XX[20]
35	46,XY[20]	46,XY[20]
37	46,XX[18]	46,XX[20]
38	46,XX[20]	46,XX[20]
43	47,XX,+mar[1]/46,XX[19]	NA
48	46,XX[20]	46,XX[20]
49	46,XY[20]	47,XY,+6[3]/48,idem,+8[2]/46~50,idem,+8,+13[cp3]/ 46,XY[12]
51	46,XY[20]	46,XY[20]
52	46,XY[20]	46,XY[20]
57	46,XY[20]	46,XY[20]
61	46,XX[20]	41,X,-X,-4,add(11)(q24),add(16)(q24)[1]/46,XX[19]
63	46,XX[20]	46,XX[20]
65	46,XY[20]	46,XY[20]
67	46,XY[20]	46,XY[20]
75	46,XX[20]	46,XY[20]
77	46,XX[19]	47,XX,+8[1]/46,XX[19]
78	46,XX,del(7)(p15)[1]/46,XX[19]	46,XX,inv(1)(p13q44)[1]/46,XX,t(1;18)(q22;p11.3)[1]/ 46,XX,-13,+mar[1]/46,XX[15]/46,XY[2]
80	46,XY[20]	46,XY,dup(1)(q21q32)[13]/46,XY,der(6)t(1;6)(q21;p23)[1]/ 46,XY[6]
83	46,XY[20]	46,XY[11]
89	46,XX,add(2)(q21),add(19)(p13.3)[1]/ 46,XX[19]	46,XX[19]/46,XY[1]
90	46,XY[20]	46,XX[20]
92	46,XX[20]	46,XX,t(9;20)(p22;p13)[2]/46,XX,add(9)(p24),- 18[1]/46,XX[5]/46,XY[12]
93	46,XX[20]	50,XX,+6,+8,+8,+8[17]/46,XX[3]
94	46,XY[20]	46,XY[20]
95	46,XY[20]	46,XY[20]
97	46,XX[3]	46,XX[20]
98	46,XY[20]	46,XY,del(1)(q21q22)[5]/46,Y,del(X)(q24q26)[1]/ 46,XY[14]
101	46,XX[20]	46,XX,t(4;17)(q12;q25)[15]/46,XX[5]
104	46,XY[20]	46,XY[20]
109	46,XX[20]	46,XX[20]
110	46,XY[20]	47,XY,+8,add(17)(p13)[12]/46,XY[8]
111	46,XY[20]	46,XY,t(6;22)(q25;q11.2)[20]
112	47,XY,+mar[2]/46,XX[18]	46,XY[20]
113	47,XY,+mar[1]/46,XY[19]	46,XY[20]
115	46,XX[20]	45,XX,-7[14]/45,XX,der(7;17)(q10;q10)[2]/ 46,XY,inv(9)(p12q13)[6]
117	46,XY[20]	46,XY[20]
123	46,XY[20]	47,XY,+1[1]/46,XY[19]
125	47,XY,+11[1]/46,XY[19]	46,XY[20]
126	46,XY[20]	NA

129	48,XY,+12,+14[1]/46,XY[19]	NA
133	46,XX[20]	46,XX[20]
134	46,XY[20]	48,XY,+8,+21[3]/49,idem,+13[1]/46,XY[16]
136	46,XX[20]	47,XX,+4[17]/46,XX,del(7)(q22)[2]/46,XX[1]
137	46,XY[20]	46,XY[20]
140	46,XX[20]	46,XX[20]
141	46,XX[20]	NA
144	42,XY,-6,-7,-7,+8,add(15)(q24), add(19)(q13.3),-21,-21[1]/46,XY[19]	NA
145	47,XX,+mar[1]/46,XX[19]	47,XX,+11[9]/46,XX,del(7)(q22)[8]/46,XX[3]
150	47,XY,del(2)(p12),-3,+2mar[1]/ 45,XY,der(14;21)(q10;q10)[1]/46,XY[18]	46,XY[20]
161	46,XX[20]	46,XX,del(12)(p13p12)[9]/46,XX[11]
162	46,XY[20]	NA

Table S6. Karyotypes at diagnosis and relapse in patients with normal karyotype. Non-class defining abnormalities found in only one metaphase were not considered clonal.

Supplementary analysis 3 (SA3)

Prognostic scores for rAML

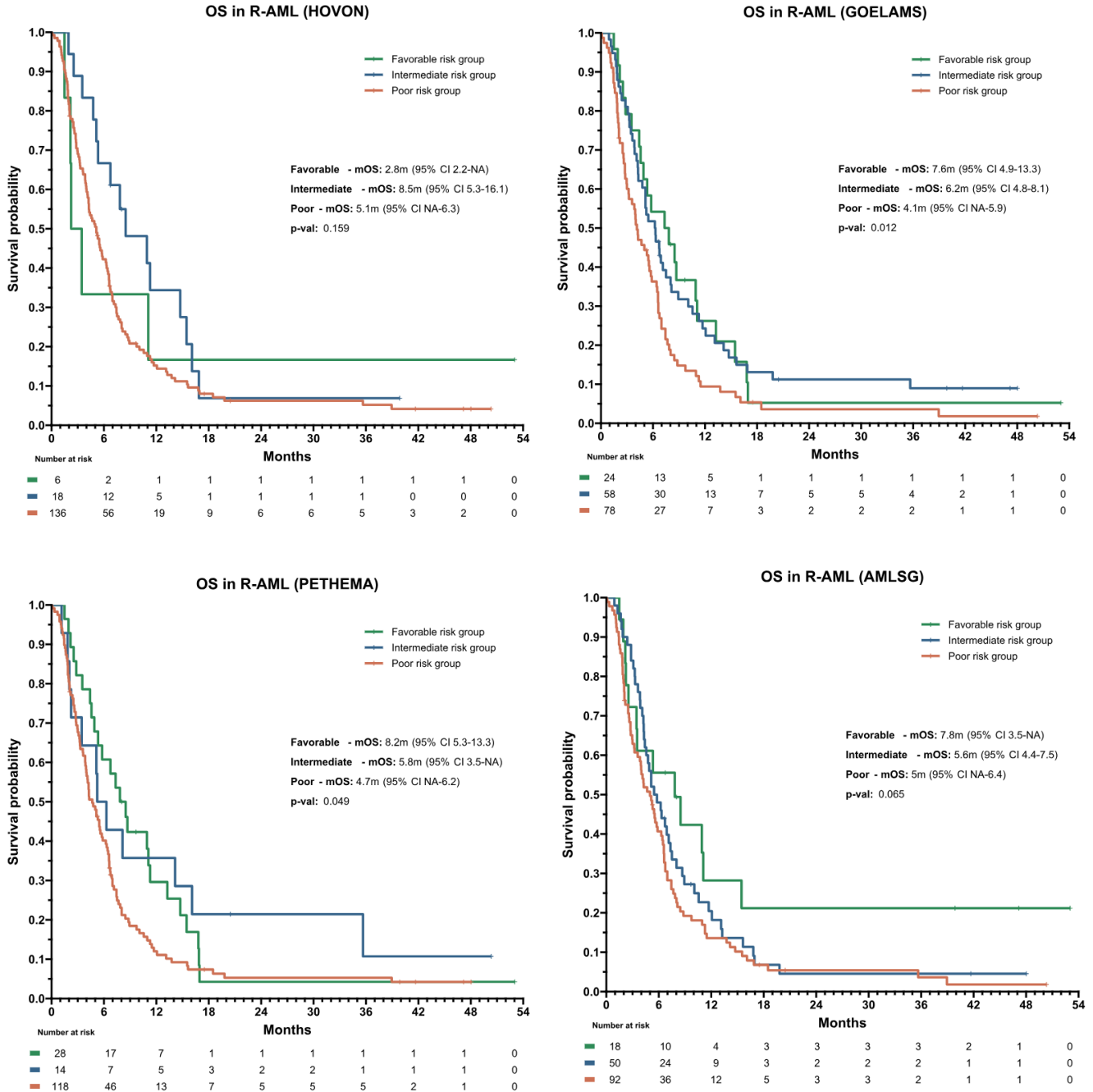


Figure S19. OS according to different prognostic scores. Upper left: HOVON (Breems et al, J Clin Oncol 2005). Upper right: GOELAMS (Chevallier et al, Leukemia 2011). Lower left: PETHEMA (Bergua et al, Br J Haematol 2016). Lower right: AMLSG (Schlenk et al, Leukemia 2017).

	Breems et al J Clin Oncol 2005	Chevallier et al Leukemia 2011	Bergua et al Br J Haematol 2016	Schlenk et al Leukemia 2017	Van der Maas NG et al ASH 2023
Relapse-free interval	Yes (6 - 18m)	Yes (12m)	Yes (12m)	Yes (6 - 18m)	Yes (12m)
Cytogenetics	CBF vs other	Adverse vs non-adverse	Inv16 vs Int vs High risk + t(8;21)	CBF (fav)	MLL, Complex karyotype (unfav)
Age	Yes (35 - 45yo)	No	Yes (60yo)	Yes	Yes (60yo)
Previous SCT	Yes (unfav)	No	Yes (AutoSCT unfav, alloSCT no effect)	Yes (unfav)	Yes (unfav)
WBC at diagnosis	No	No	No	No	Yes (>10K)
FLT3-ITD	NA	Yes (unfav)	Yes (unfav)	Yes (unfav)	Yes (unfav)
TP53 mut	NA	NA	NA	No	Yes
CEBPA mut	NA	NA	NA	Yes (fav)	No

Table S7. Summary of the different prognostic scores for rAML with the variables included in each classification.

	HOVON			GOLEAMS			PETHEMA			AMLSG		
	n	mOS (months)	1-yr OS	n	mOS (months)	1-yr OS	n	mOS (months)	1-yr OS	n	mOS (months)	1-yr OS
Low risk	6	2.8	17%	24	7.6	26%	28	8.2	30%	18	7.8	28%
Intermediate risk	18	8.5	34%	58	6.2	24%	14	5.8	36%	50	5.6	20%
High risk	136	5.1	15%	78	4.1	9%	118	4.7	12%	92	5	13%
<i>P</i> value (log-rank)	0.159			0.012			0.049			0.065		
Harrell's C-index	0.535			0.575			0.554			0.553		

Table S8. Overall survival, log-rank test and Harrell's C-index for each prognostic score evaluated.

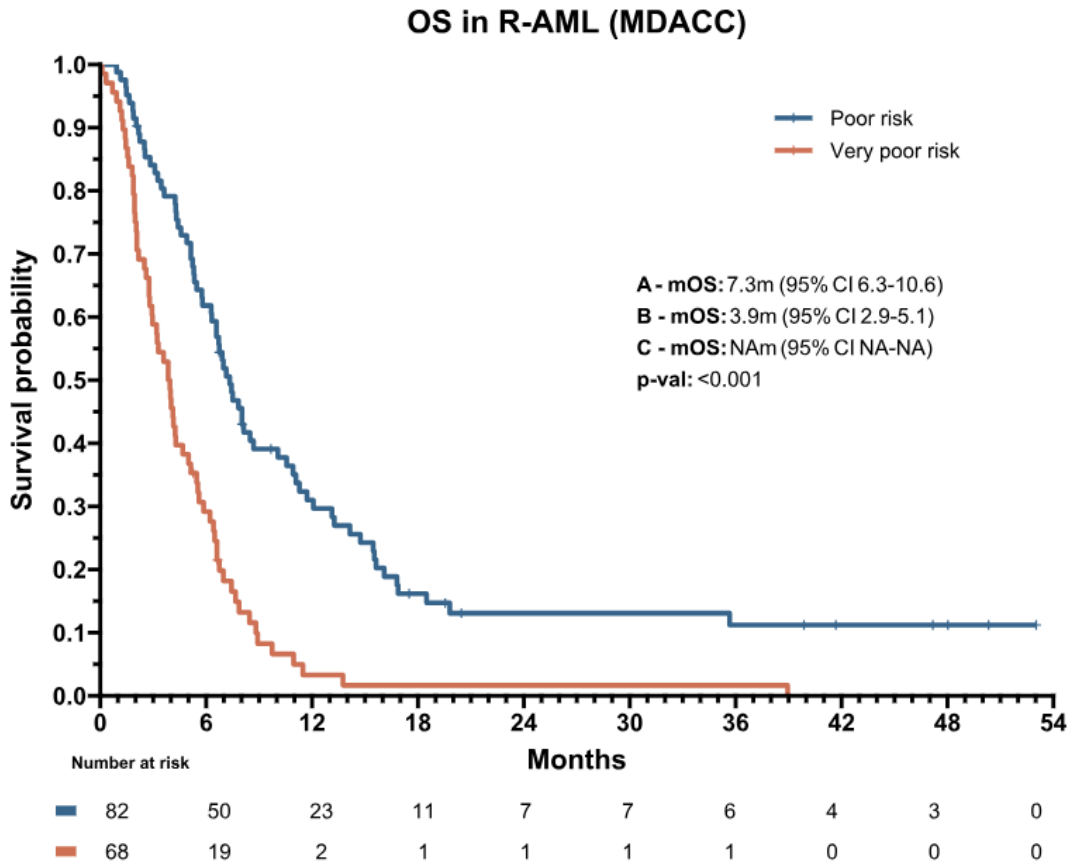


Figure S20. OS according to an exploratory analysis looking at risk groups defined the multivariate analysis. Patients with no or one risk factor (poor risk) vs patients with two or more risk factors (very poor risk). Risk factors are defined by time in remission < 12 months, adverse cytogenetics or *KMT2A* rearrangement at relapse, and a WBC > 20 x 10⁹/L at relapse