

Table S5. Patient characteristic of the TCGA cohort evaluated for clinical significance of complex karyotype.

	Total (n=133)	CK (n=23)	Non-CK (n=110)	P
Sex (%)				0.307
Male	65 (48.9)	9 (69.2)	56 (50.9)	
Female	58 (51.1)	4 (30.8)	54 (49.1)	
Age (years)				0.152
Median (range)	60.0 (18.0-88.0)	65.0 (18.0-81.0)	59.0 (21.0-88.0)	
WBC count (× 10 ⁹ /L)				0.009
Median (range)	16.0 (0.6-297.4)	9.9 (0.7-47.6)	24.5 (0.6-297.4)	
BM blasts (%)				0.009
Median (range)	72.0 (30.0-100.0)	58.0 (30.0-97.0)	75.0 (30.0-100.0)	
Risk stratification by 2022 ELN				0.000
Favorable	37 (27.8)	0 (0.0)	37 (33.6)	
Intermediate	39 (29.3)	0 (0.0)	39 (35.5)	
Adverse	48 (36.1)	23 (100.0)	25 (22.7)	
Not assessed	9 (6.7)	0 (0.0)	9 (8.2)	
Risk stratification by genetics				
<i>FLT3-ITD</i>				0.098
<i>without</i>	108 (81.2)	22 (95.7)	86 (78.2)	
<i>with</i>	25 (18.8)	1 (4.3)	24 (21.8)	
<i>NA</i>	0 (0.0)	0 (0.0)	0 (0.0)	
mutated <i>RUNX1</i>				0.171
<i>without</i>	118 (88.7)	23 (100.0)	95 (86.4)	
<i>with</i>	15 (11.3)	0 (0.0)	15 (13.6)	
<i>NA</i>	0 (0.0)	0 (0.0)	0 (0.0)	
Overall survival (months)				0.021
Median (range)	13.8 (0.0-118.1)	7.2 (0.0-95.5)	16.4 (0.1-118.1)	

TCGA The Cancer Genome Atlas, WBC White blood cell, BM Bone marrow, ITD Internal tandem duplication, NA Not applicable.