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POSTER ABSTRACTS

617.ACUTE MYELOID LEUKEMIAS: BIOMARKERS, MOLECULAR MARKERS AND MINIMAL RESIDUAL DISEASE IN DIAGNOSIS AND PROGNOSIS

A 46 Long Non-Coding RNAs Expression Signature Accurately Predicts Relapse and Acts As an Independent Prognostic Factor in Pediatric Acute Myeloid Leukemia

Zhiyao Ren, MD [1,2,3], Jolien Vanhooren [2,3,1], Charlotte Derpoorter [2,1,3], Barbara De Moerloose [4,2,3], Tim Lammens, PhD [1,2,3]

[1] Department of Pediatric Hematology-Oncology and Stem Cell Transplantation, Ghent University Hospital, Ghent, Belgium
[2] Cancer Research Institute Ghent (CRIG), Ghent, Belgium
[3] Department of Internal Medicine and Pediatrics, Ghent University, Ghent, Belgium
[4] Ghent University Hospital, Ghent, Belgium

Risk stratification using cytogenetics, mutations and minimal residual disease (MRD) has allowed to increase the cure rates of pediatric acute myeloid leukemia (AML), reaching now up to 70% in contemporary protocols. Nevertheless, approximately 30% of patients still experience relapse, indicating that there is a need to optimize stratification strategies. Recently, long non-coding RNA (lncRNA) expression has been shown to hold prognostic power in multiple cancer types. Here, we built a 46 relapse-related lncRNAs prognostic signature, named AML ^{lnc46}, using 790 pediatric acute myeloid leukemia transcriptomes obtained from the Therapeutically Applicable Research To Generate Effective Treatments (TARGET) repository. Bootstrap validation (bootstrap resampling times = 1000) was used for internal validation and showed that the signature performed good in predicting the 1-, 2-, and 3-year relapse-free survival (RFS), with an area under the curve of 0.825, 0.824, and 0.822, respectively. Moreover, external validation using the TARGET repository validated the efficiency of the signature. Most importantly, we demonstrate that AML ^{lnc46} not only is an independent predictor of RFS, but also identifies patients who were assigned a different risk-group by currently-used classification methods. In conclusion, the identified AML ^{lnc46} might, after further prospective validation, provide additional information to guide management of pediatric AML patients.

Figure 1. (A) Kaplan-Meier survival curve of relapse-free survival of high-and-low risk AML ^{lnc46} pediatric AML patients, (B) Univariate and multivariate independent Cox regression analyses of known clinical and molecular characteristics and the AML ^{lnc46} signature.

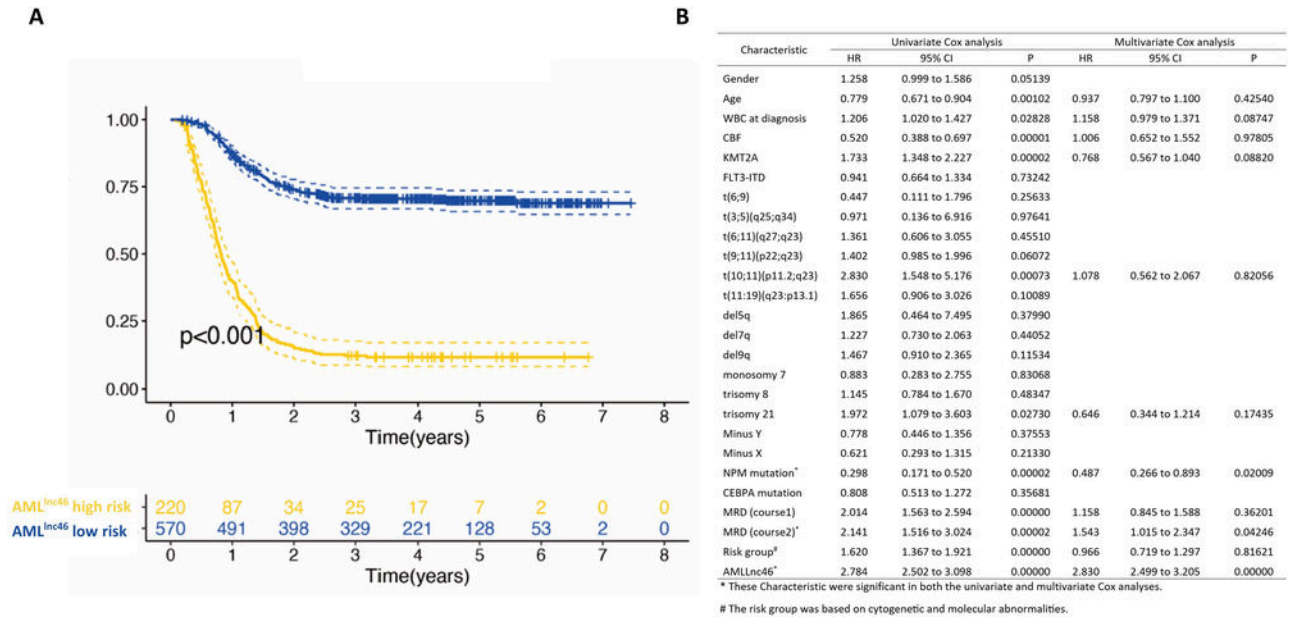**Disclosures** No relevant conflicts of interest to declare.

A

B

Characteristic	Univariate Cox analysis			Multivariate Cox analysis		
	HR	95% CI	P	HR	95% CI	P
Gender	1.258	0.999 to 1.586	0.05139			
Age	0.779	0.671 to 0.904	0.00102	0.937	0.797 to 1.100	0.42540
WBC at diagnosis	1.206	1.020 to 1.427	0.02828	1.158	0.979 to 1.371	0.08747
CBF	0.520	0.388 to 0.697	0.00001	1.006	0.652 to 1.552	0.97805
KMT2A	1.733	1.348 to 2.227	0.00002	0.768	0.567 to 1.040	0.08820
FLT3-ITD	0.941	0.664 to 1.334	0.73242			
t(6;9)	0.447	0.111 to 1.796	0.25633			
t(3;5)(q25;q34)	0.971	0.136 to 6.916	0.97641			
t(6;11)(q27;q23)	1.361	0.606 to 3.055	0.45510			
t(9;11)(p22;q23)	1.402	0.985 to 1.996	0.06072			
t(10;11)(p11.2;q23)	2.830	1.548 to 5.176	0.00073	1.078	0.562 to 2.067	0.82056
t(11;19)(q23:p13.1)	1.656	0.906 to 3.026	0.10089			
del5q	1.865	0.464 to 7.495	0.37990			
del7q	1.227	0.730 to 2.063	0.44052			
del9q	1.467	0.910 to 2.365	0.11534			
monosomy 7	0.883	0.283 to 2.755	0.83068			
trisomy 8	1.145	0.784 to 1.670	0.48347			
trisomy 21	1.972	1.079 to 3.603	0.02730	0.646	0.344 to 1.214	0.17435
Minus Y	0.778	0.446 to 1.356	0.37553			
Minus X	0.621	0.293 to 1.315	0.21330			
NPM mutation[*]	0.298	0.171 to 0.520	0.00002	0.487	0.266 to 0.893	0.02009
CEBPA mutation	0.808	0.513 to 1.272	0.35681			
MRD (course1)	2.014	1.563 to 2.594	0.00000	1.158	0.845 to 1.588	0.36201
MRD (course2)[*]	2.141	1.516 to 3.024	0.00002	1.543	1.015 to 2.347	0.04246
Risk group[#]	1.620	1.367 to 1.921	0.00000	0.966	0.719 to 1.297	0.81621
AMLLnc46[*]	2.784	2.502 to 3.098	0.00000	2.830	2.499 to 3.205	0.00000

* These Characteristic were significant in both the univariate and multivariate Cox analyses.

The risk group was based on cytogenetic and molecular abnormalities.

Figure 1