SUPPLEMENTAL DATA

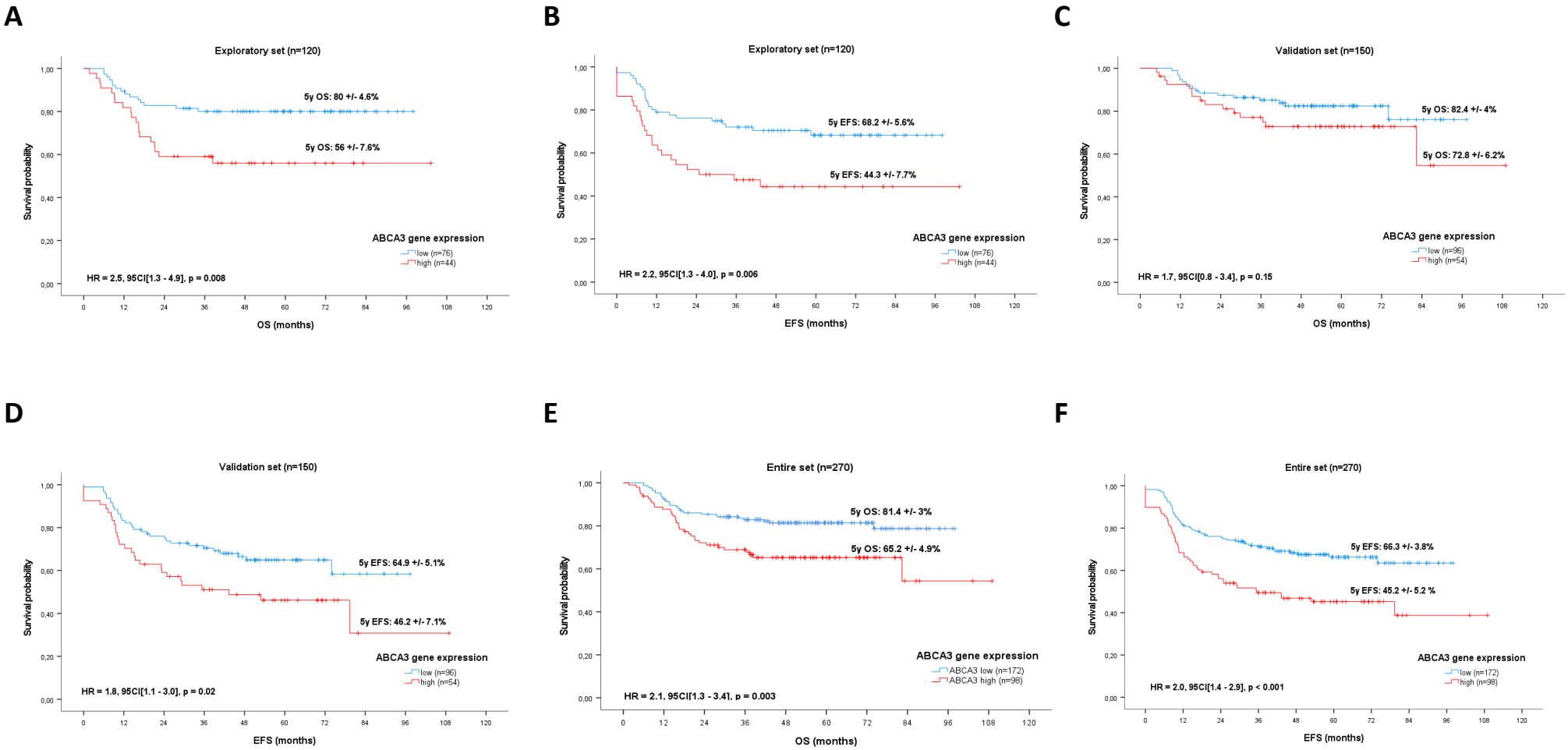
	Exploratory set (N=120)	Validation set (N=150)	p-value
Clinical features			
Median age (years), range	9.4 [0.2 - 17.2]	10 [0.4 - 17.9]	0.97
M/F ratio	1.26	1.27	1.00
Median WBC (G/L), range	19.3 [1.2 - 575]	13.6 [1.3 - 514]	0.10
Median medullar blast percentage	73.5% [1 - 98]	65% [1 - 99]	0.23
CNS involvement	22 (18%)	22 (15%)	0.51
Cytogenetics			
Normal karyotype	39 (32%)	37 (25%)	0.18
CBF-AML	20 (16.7%)	54 (36%)	**0.0005**
KMT2A rearranged-AML	20 (16.7%)	33 (22%)	0.29
Anomalies moléculaires			
FLT3-ITD	12 (10%)	18 (12%)	0.70
NPM1 muté	14 (12%)	8 (5%)	0.07
CEBPA double-mutation	2 (2%)	4 (3%)	0.70
Risk stratification			**0.001**
Standard risk	20 (17%)	55 (36%)	**0.0003**
Intermediate risk	77 (64%)	67 (45%)	**0.002**
High risk	23 (19%)	28 (19%)	1.0
Results			
CR	108 (90%)	145 (97%)	**0.04**
Relapse	33/108 (31%)	54/145 (37%)	0.29
HSCT	38 (32%)	41 (27%)	0.50
5-years OS ± SE	70.8% ± 5.1%	77.2% ± 4.1%	0.33
5-years LFS ± SE	62.0% ± 5.9%	56.7% ± 5.1%	0.44

Supplementary Table 1. Main clinical and biological features of the exploratory (N=120) and the validation (N=150) sets. Fisher's exact tests were used for comparing categorical variables, Mann-Whitney's tests for numerical variables and log-rank tests for survival variables. *M (male), F (female), WBC (white blood cells), Min (minimum), Max (maximum), CNS (central nervous system), AML (acute myeloid leukemia), CBF (core-binding factor), ITD (internal-tandem duplication), CR (complete remission rate), HSCT (hematopoietic stem cell transplant), OS (overall survival), LFS (leukemia-free survival), SE (standard-error).*

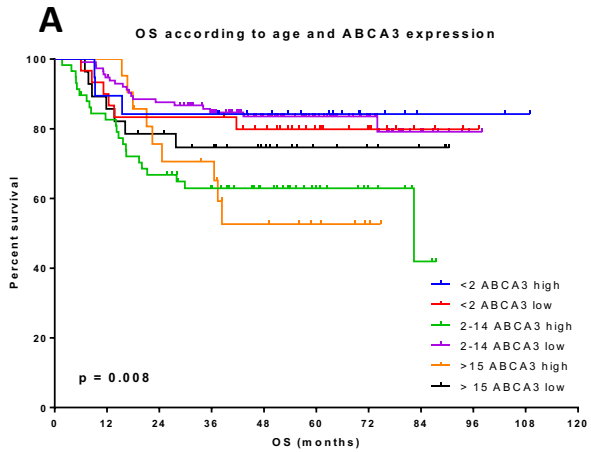
ELAM02	High *ABCA3* expression (N=98)	Low *ABCA3* expression (N=172)	p-value
Clinical features			
Median age (years), range	10 [0.16 - 17.2]	9.65 [0.24 - 17.9]	0.56
M/F ratio	1.33	1.23	0.80
Median WBC (G/L), range	15 [1.8 - 514]	17 [1.2 - 575]	0.90
Median medullar blast percentage	74% [1 - 99]	65% [9 - 98]	0.20
CNS involvement	15 (15%)	29 (17%)	0.86
Cytogenetics			
Normal karyotype	28 (29%)	48 (28%)	1.00
CBF-AML	21 (21%)	53 (31%)	0.12
KMT2A rearranged-AML	23 (23%)	30 (17%)	0.27
Anomalies moléculaires			
FLT3-ITD	11 (11%)	19 (11%)	1.00
NPM1 muté	6 (6%)	16 (9%)	0.49
CEBPA double-mutation	1 (1%)	5 (3%)	0.42
Risk stratification			0.10
Standard risk	23 (24%)	55 (32%)	0.05
Intermediate risk	55 (56%)	88 (51%)	0.45
High risk	20 (20%)	29 (17%)	0.20
Results			
CR	85 (87%)	168 (98%)	**0.001**
Relapse	42/85 (49%)	50/168 (30%)	**0.004**
HSCT	27 (28%)	52 (30%)	0.68
5-years OS ± SE	65.2% ± 4.9%	84.3% ± 3%	**0.003**
5-years LFS ± SE	50.3% ± 5.6%	67.4% ± 3.8%	**0.005**

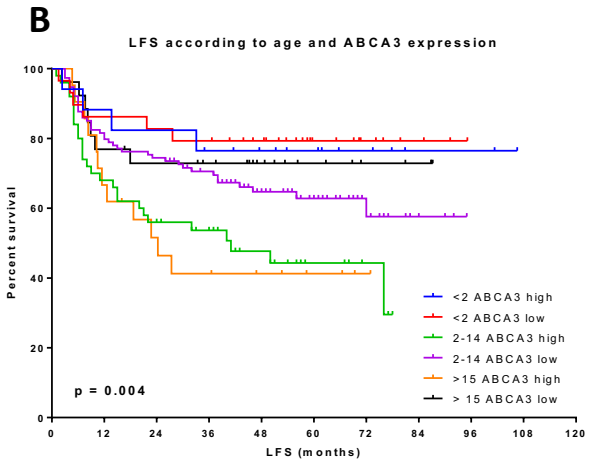
Supplementary Table 2. Main clinical and biological features of the high and low *ABCA3* expressers in the entire pediatric dataset (N=270). Fisher's exact tests were used for comparing categorical variables, Mann-Whitney's tests for numerical variables and log-rank tests for survival variables. *M (male), F (female), WBC (white blood cells), Min (minimum), Max (maximum), CNS (central nervous system), AML (acute myeloid leukemia), CBF (core-binding factor), ITD (internal-tandem duplication), CR (complete remission), HSCT (hematopoietic stem cell transplant), OS (overall survival), LFS (leukemia-free survival), SE (standard-error).*

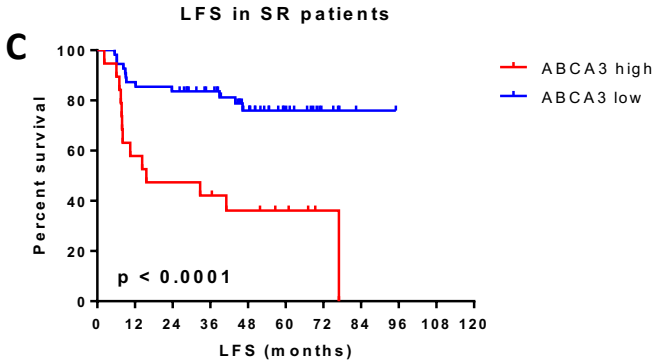
Sup Fig 1

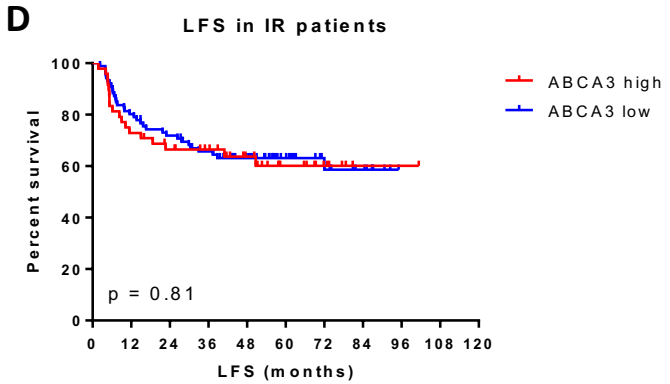

A
Exploratory set (n=120)
5y OS: 80 +/- 4.6%
5y OS: 56 +/- 7.6%
ABCA3 gene expression
low (n=76)
high (n=44)
HR = 2.5, 95CI[1.3 - 4.9], p = 0.008
Survival probability
OS (months)
B
Exploratory set (n=120)
5y EFS: 68.2 +/- 5.6%
5y EFS: 44.3 +/- 7.7%
ABCA3 gene expression
low (n=76)
high (n=44)
HR = 2.2, 95CI[1.3 - 4.0], p = 0.006
Survival probability
EFS (months)
C
Validation set (n=150)
5y OS: 82.4 +/- 4%
5y OS: 72.8 +/- 6.2%
ABCA3 gene expression
low (n=96)
high (n=54)
HR = 1.7, 95CI[0.8 - 3.4], p = 0.15
Survival probability
OS (months)
D
Validation set (n=150)
5y EFS: 64.9 +/- 5.1%
5y EFS: 46.2 +/- 7.1%
ABCA3 gene expression
low (n=96)
high (n=54)
HR = 1.8, 95CI[1.1 - 3.0], p = 0.02
Survival probability
EFS (months)
E
Entire set (n=270)
5y OS: 81.4 +/- 3%
5y OS: 65.2 +/- 4.9%
ABCA3 gene expression
ABCA3 low (n=172)
ABCA3 high (n=98)
HR = 2.1, 95CI[1.3 - 3.4], p = 0.003
Survival probability
OS (months)
F
Entire set (n=270)
5y EFS: 66.3 +/- 3.8%
5y EFS: 45.2 +/- 5.2 %
ABCA3 gene expression
low (n=172)
high (n=98)
HR = 2.0, 95CI[1.4 - 2.9], p < 0.001
Survival probability
EFS (months)

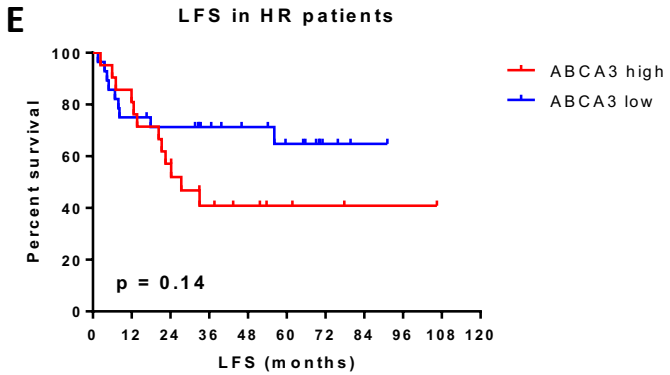
Sup Fig 2

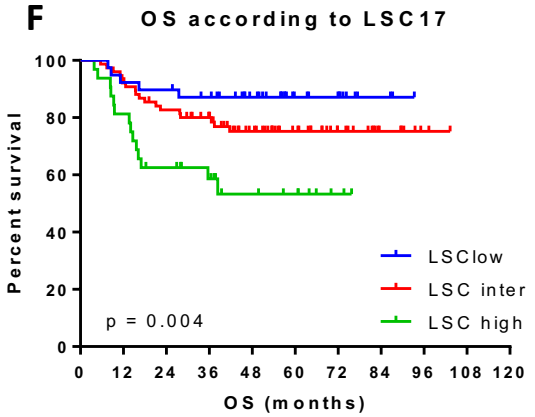

A
OS according to age and ABCA3 expression
Percent survival
OS (months)
p = 0.008
<2 ABCA3 high
<2 ABCA3 low
2-14 ABCA3 high
2-14 ABCA3 low
>15 ABCA3 high
> 15 ABCA3 low

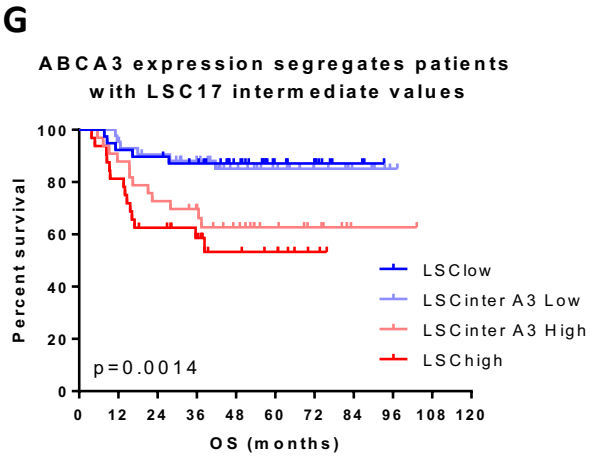

B
LFS according to age and ABCA3 expression
Percent survival
LFS (months)
p = 0.004
<2 ABCA3 high
<2 ABCA3 low
2-14 ABCA3 high
2-14 ABCA3 low
>15 ABCA3 high
> 15 ABCA3 low


C
LFS in SR patients
Percent survival
LFS (months)
p < 0.0001
ABCA3 high
ABCA3 low

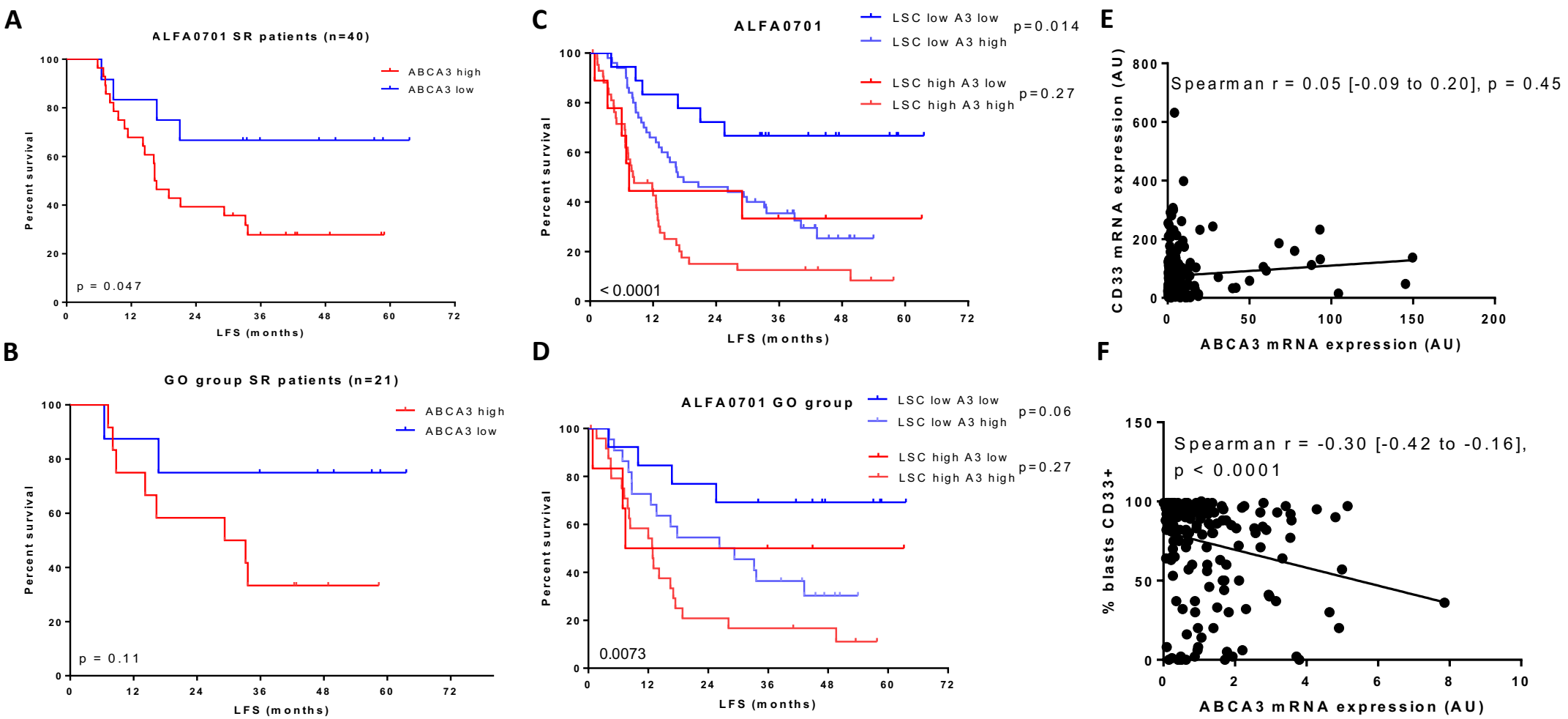

D
LFS in IR patients
Percent survival
LFS (months)
p = 0.81
ABCA3 high
ABCA3 low


E
LFS in HR patients
Percent survival
LFS (months)
p = 0.14
ABCA3 high
ABCA3 low


F
OS according to LSC17
Percent survival
OS (months)
p = 0.004
LSClow
LSC inter
LSC high


G
ABCA3 expression segregates patients with LSC17 intermediate values
Percent survival
OS (months)
p=0.0014
LSClow
LSCinter A3 Low
LSCinter A3 High
LSChigh

Sup Fig 3


A
ALFA0701 SR patients (n=40)
ABCA3 high
ABCA3 low
Percent survival
p = 0.047
LFS (months)
B
GO group SR patients (n=21)
ABCA3 high
ABCA3 low
Percent survival
p = 0.11
LFS (months)
C
ALFA0701
LSC low A3 low
LSC low A3 high
LSC high A3 low
LSC high A3 high
p=0.014
p=0.27
Percent survival
< 0.0001
LFS (months)
D
ALFA0701 GO group
LSC low A3 low
LSC low A3 high
LSC high A3 low
LSC high A3 high
p=0.06
p=0.27
Percent survival
0.0073
LFS (months)
E
Spearman r = 0.05 [-0.09 to 0.20], p = 0.45
CD33 mRNA expression (AU)
ABCA3 mRNA expression (AU)
F
Spearman r = -0.30 [-0.42 to -0.16],
p < 0.0001
% blasts CD33+
ABCA3 mRNA expression (AU)

Supplemental figures:

Supplementary Figure 1. OS (overall survival) and EFS (event-free survival) in pediatric AML patients. (A-B) Survival analyses in the pediatric exploratory set, (C-D) the validation set, and (E-F) the entire ELAM02 cohort. Kaplan-Meier curves and p-values of the log-ranks are shown. Statistical analyses and plots were performed using SPSS for Windows version 27.0 (IBM Corp.).

Supplementary Figure 2. Subgroup analyses in pediatric AML. Kaplan-Meier curves (A) OS and (B) LFS according to age (<2, 2-14, and >15 years old) and *ABCA3* expression levels. LFS in SR (standard-risk) (C), IR (intermediate risk) (D), and HR (high risk) pediatric AML patients (E) according to *ABCA3* expression levels. **(**F) OS in the entire pediatric cohort stratified according to LSC17 values.(G) *ABCA3* expression as a prognostic factor in patients with LSC17 intermediate values (log-rank p=0.026), Kaplan-Meier curves of respective OS. Statistical analyses and plots were performed using GraphPad Prism for Windows version 6.00 (GraphPad Software).

Supplementary Figure 3. Subgroup analyses in adult AML. LFS in adult SR (A) and SR GO-treated (B) AML patients according to *ABCA3* expression levels. LFS according to LSC17 values and *ABCA3* expression in (C) the ALFA0701 cohort and (D) the GO-treated group. Kaplan-Meier curves and p-values of the log-ranks are shown. Spearman rank correlation between gene expression levels of *ABCA3* and CD33 (E) and percent blast positive for CD33 expression at the cell surface (F). Statistical analyses and plots were performed using GraphPad Prism for Windows version 6.00 (GraphPad Software).