

# Gene expression profiling of acute myeloid leukemia samples from adult patients with AML-M1 and -M2 through boutique microarrays, real-time PCR and droplet digital PCR

LUIZA HANDSCHUH<sup>1,2</sup>, MACIEJ KAŻMIERCZAK<sup>2</sup>, MAREK C. MILEWSKI<sup>1</sup>, MICHAŁ GÓRALSKI<sup>1</sup>, MAGDALENA ŁUCZAK<sup>1,3</sup>, MARZENA WOJTASZEWSKA<sup>2</sup>, BARBARA USZCZYŃSKA-RATAJCZAK<sup>1</sup>, KRZYSZTOF LEWANDOWSKI<sup>2</sup>, MIECZYŚLAW KOMARNICKI<sup>2</sup> and MAREK FIGLEROWICZ<sup>1,4</sup>

<sup>1</sup>European Center for Bioinformatics and Genomics, Institute of Bioorganic Chemistry, Polish Academy of Sciences, 61-704 Poznan; <sup>2</sup>Department of Hematology and Bone Marrow Transplantation, Poznan University of Medical Sciences, 60-569 Poznan; <sup>3</sup>Institute of Technology and Chemical Engineering, Poznan University of Technology, 61-131 Poznan; <sup>4</sup>Institute of Computing Science, Poznan University of Technology, 61-138 Poznan, Poland

Received September 21, 2017; Accepted December 12, 2017

DOI: 10.3892/ijo.2017.4233

**Abstract.** Acute myeloid leukemia (AML) is the most common and severe form of acute leukemia diagnosed in adults. Owing to its heterogeneity, AML is divided into classes associated with different treatment outcomes and specific gene expression profiles. Based on previous studies on AML, in this study, we designed and generated an AML-array containing 900 oligonucleotide probes complementary to human genes implicated in hematopoietic cell differentiation and maturation, proliferation, apoptosis and leukemic transformation. The AML-array was used to hybridize 118 samples from 33 patients with AML of the M1 and M2 subtypes of the French-American-British (FAB) classification and 15 healthy volunteers (HV). Rigorous analysis of the microarray data revealed that 83 genes were differentially expressed between the patients with AML and the HV, including genes not yet discussed in the context of AML pathogenesis. The most overexpressed genes in AML were *STMN1*, *KITLG*, *CDK6*, *MCM5*, *KRAS*, *CEBPA*, *MYC*, *ANGPT1*, *SRGN*, *RPLP0*, *ENO1* and *SET*, whereas the most underexpressed genes were *IFITM1*,

*LTB*, *FCN1*, *BIRC3*, *LYZ*, *ADD3*, *S100A9*, *FCER1G*, *PTRPE*, *CD74* and *TMSB4X*. The overexpression of the *CPA3* gene was specific for AML with mutated *NPM1* and *FLT3*. Although the microarray-based method was insufficient to differentiate between any other AML subgroups, quantitative PCR approaches enabled us to identify 3 genes (*ANXA3*, *S100A9* and *WT1*) whose expression can be used to discriminate between the 2 studied AML FAB subtypes. The expression levels of the *ANXA3* and *S100A9* genes were increased, whereas those of *WT1* were decreased in the AML-M2 compared to the AML-M1 group. We also examined the association between the *STMN1*, *CAT* and *ABL1* genes, and the *FLT3* and *NPM1* mutation status. *FLT3*<sup>+</sup>/*NPM1* AML was associated with the highest expression of *STMN1*, and *ABL1* was upregulated in *FLT3*<sup>+</sup> AML and *CAT* in *FLT3*<sup>-</sup> AML, irrespectively of the *NPM1* mutation status. Moreover, our results indicated that *CAT* and *WT1* gene expression levels correlated with the response to therapy. *CAT* expression was highest in patients who remained longer under complete remission, whereas *WT1* expression increased with treatment resistance. On the whole, this study demonstrates that the AML-array can potentially serve as a first-line screening tool, and may be helpful for the diagnosis of AML, whereas the differentiation between AML subgroups can be more successfully performed with PCR-based analysis of a few marker genes.

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*Correspondence to:* Dr Luiza Handschuh, European Center for Bioinformatics and Genomics, Institute of Bioorganic Chemistry, Polish Academy of Sciences, Noskowskiego 12/14, 61-704 Poznan, Poland  
E-mail: luizahan@ibch.poznan.pl

*Abbreviations:* AML, acute myeloid leukemia; CN-AML, cytogenetically normal AML; ddPCR, droplet digital PCR; FAB, French-American-British (classification of leukemia); PCR, polymerase chain reaction

*Key words:* acute myeloid leukemia, French-American-British2, M1, M2, gene expression profiling, DNA microarrays, boutique arrays, RT-qPCR, real-time PCR, droplet digital PCR

## Introduction

Acute myeloid leukemia (AML), the most common and severe form of acute leukemia in adults, is responsible for the highest mortality from leukemia in general (1). The origin of AML is multifactorial and has not yet been entirely elucidated. The disease begins in a bone marrow stem cell exposed to a complex interplay of hereditary and environmental factors. Disturbances in myeloid progenitor cell growth, differentiation and proliferation lead to the clonal expansion of bone marrow myeloblasts and their infiltration into the peripheral blood (1,2).

Therefore, the number of immature, non-functional leukocytes is increased, and normal blood cell production is impaired.

AML is a heterogeneous type of cancer in which subsets of molecularly different types can be distinguished. According to the first classification of hematological disorders, the French-American-British (FAB) system (3), there are 8 types of AML (M0-M7), with specific morphological characteristics and differentiation stages. The more recent World Health Organization (WHO) classification (4) is based on a combination of clinical symptoms, cell morphology, immunophenotype and genetic abnormalities. In ~55% of patients with AML, clonal chromosome rearrangements are present (5); e.g., translocations t(8;21), t(15;17) and t(16;16), which result in the fusion genes, *RUNX1/RUNX1T1*, *PML-RAR $\alpha$*  and *CBFB-MYH11*, respectively. In a large group of patients with AML (40-49%) with normal karyotypes (NK-AML or CN-AML, from cytogenetically normal AML) (5,6), recurrent small mutations have been identified. They usually occur in genes encoding signaling proteins, transcription factors and chromatin modifiers, which affect cell signaling or general gene expression. The most frequent are mutations in *NPM1* (7), *FLT3* (8), *CEBPA* (9), *KIT* (10), *NRAS/KRAS* (11), *TET2* (12), *DNMT3A* (13) and *IDH1/2* (14). Some of these mutations are clinically relevant as diagnostic or prognostic markers and potential therapeutic targets (15).

The development of high-throughput technologies, such as microarrays and next generation sequencing has contributed to progress in leukemia research (16-18). Since 1999, when the first applications of DNA microarrays in leukemia classification and outcome prediction were demonstrated (19,20), many publications based on gene expression profiling in hematological malignancies have appeared. Among these, several hundred have focused on AML [such as for example (21-23)]. Some have shown that certain genetic alterations correspond with specific gene expression signatures (24,25). Gene expression profiles have also been correlated with prognosis and treatment outcomes (26,27). However, in clinical practice, age, white blood cell (WBC) counts in the blood and karyotype abnormalities are still the key outcome determinants (6). Diagnostic tests based on single gene mutations [including one recently published by our group (28)], are being increasingly applied; however, the number of mutations and their detection methods are not standardized among laboratories. A reasonable compromise between a single gene test and a genome-wide tool, irrespective of the purpose (mutation detection or gene expression measurements), is a small dedicated microarray, also known as a boutique array (29,30). Based on our experience in boutique microarray design, production and data normalization (30-32), we decided to create a small microarray dedicated to gene expression profiling in AML (AML-array). The main aims of this study were to test the utility of this array, verify the selected results with 2 quantitative polymerase chain reaction (PCR) approaches, standard real-time PCR and droplet-digital PCR (ddPCR), and to examine gene expression in a new group of patients with AML. Into the analysis, we included Polish adult patients with *de novo* AML, prior to therapy, classified as M1 and M2, 2 FAB subtypes in which myeloid differentiation is arrested in the first stages of granulopoiesis. In the same group of patients, we have previously performed

a comparative proteomics analysis of AML with and without maturation (33,34). The additional aim of the study was to compare presented here transcriptomic results with our earlier proteomic results and with other AML transcriptomic data. We hoped to find the novel factors, such as gene groups, gene expression patterns or gene associations with molecular or clinical characteristics, which can be correlated with AML pathogenesis. Such analyses are valuable as it was shown that AML pathogenesis can differ among individual patients (35) and our understanding of AML genomics is still incomplete.

## Materials and methods

**Samples.** Peripheral blood (PB) and bone marrow (BM) samples were collected from 41 adult patients with AML-M1/M2 and from 20 adult healthy volunteers (HV). Each individual provided signed informed consent for treatment and for their participation in this study. Appropriate approval was also obtained from the Bioethical Commission of the Karol Marcinkowski Poznan University of Medical Sciences, Poznan, Poland. The patients were diagnosed and treated at the Department of Hematology and Bone Marrow Transplantation at the Poznan University Hospital of the Lord's Transfiguration of the University of Medical Sciences in Poznan, Poland. Standard AML therapy using cytosine arabinoside plus daunorubicin (3'+7') was administered to all patients to induce complete remission (CR), which was defined according to the European Leukemia Net guidelines (2). When available, the samples were collected at the 3 following time-points: when AML was diagnosed, prior to first therapy (T0), when CR was established [between day +21 and +28 after the start of induction therapy (T1)], and when the disease relapsed (T2). However, from the T1 samples, the number of cells was much lower than that of cells from the T0 and T2 samples, and often, there was not sufficient material to perform replicate experiments. Moreover, not all microarray images met the required quality criteria and had to be filtered out. The material from the T1 time-point was the most heterogeneous, and preliminary microarray analysis revealed that the T1 samples did not cluster together and did not exhibit clear common characteristics. The T2 samples were generally similar to the T0 samples and we were not able to distinguish them by unsupervised hierarchical clustering. Therefore, we decided to limit our analyses to the samples collected at the T0 time-point, with the use of available information about the history of treatment. The advantage of this selection was that the T0 samples were the most homogenous (the fractions of blood and bone marrow-derived mononuclear cells isolated from patients with AML-M1 contained ~90% leukemic cells, whereas from those from the patients with AML-M2 contained ~70% myeloblasts). Table I presents the summarized information on the patient and HV samples.

**Cell separation.** Mononuclear cells from the peripheral blood (termed PBMCs) and bone marrow (termed BMMCs) were separated through density gradient centrifugation (Gradisol L; Aqua-Medica, Bogucin, Poland) and washed 3 times with 1X phosphate-buffered saline (PBS; Ca and Mg-free; IBSS Biomed S.A., Warsaw, Poland). The cell pellet was suspended in lysis buffer from a mirVana miRNA Isolation kit

Table I. Sample summary.

A, General information							
	Total no. of samples	Age range (median)	Sex, F/M/unknown	WBC count [ $\times 10^9/l$ ] range (median)	No. of microarray hybridizations (individual samples)	No. of samples in real-time PCR experiment	No. of samples in ddPCR experiment
HV	20	23-60 (36.4)	10/07/03	5.1-25.3 (6.2)	15 (15)	14	16
AML	41	19-78 (48.8)	17/24	0.5-345 (13.7)	103 (33)	21	37

B, FAB classification and mutation status of AML samples							
	FAB M1	FAB M2	<i>RUNX1/RUNX1T1</i> [t(8;21)]	<i>NPM1/FLT3</i> <sup>+</sup>	<i>NPM1</i> <sup>+</sup> / <i>FLT3</i> <sup>-</sup>	<i>NPM1</i> <sup>+</sup> / <i>FLT3</i> <sup>+</sup>	
Patients (micr. <sup>a</sup> )	15 (11/31)	26 (22/72)	5 (5/15)	3 (2/11)	8 (6/23)	2 (2/8)	

C, Classification of AML samples in respect to treatment response					
	RES	CR	CR-short	CR-long	X
Patients (micr. <sup>a</sup> )	10 (9/26)	20 (15/49)	14 (12/40)	6 (3/9)	11 (9/28)

<sup>a</sup>The number of patients/samples included into the microarray experiment; WBC, white blood cell count; HV, healthy volunteers (controls); AML, acute myeloid leukemia; RES, resistance to therapy; CR, complete remission (CR-short, lasting up to 1 year; CR-long, -lasting >1 year); X, death during therapy; *FLT3*<sup>+</sup>-*FLT3*-ITD (internal tandem duplication in the *FLT3* gene); RT-qPCR -reverse transcription-quantitative PCR; ddPCR, droplet digital PCR.

(Ambion/Thermo Fisher Scientific, Waltham, MA, USA) and immediately frozen at -80°C.

**RNA isolation.** Total RNA was extracted from the PBMCs and BMMCs using a mirVana miRNA Isolation kit and the DNase-treated (TURBO DNA-free kit) (both from Ambion/Thermo Fisher Scientific). RNA integrity was evaluated with the use of a Bioanalyzer 2100 and Total RNA Nano assay (Agilent Technologies, Santa Clara, CA, USA). Only RNAs with an RNA integrity number (RIN)  $\geq 7.5$  were used for the gene expression analyses.

**Microarray construction.** Screening of the literature enabled us to identify the following groups of genes: i) Proven and postulated acute leukemia biomarkers; ii) general oncogenes; and iii) predicted to be specifically involved in leukemic transformation. In addition, we selected a set of control genes. Human housekeeping genes, not associated with oncogenesis, were used as the positive controls, whereas plant- and bacterial-specific genes served as the negative controls. We ordered 903 chemically synthesized, amino-modified microarray probes from 2 companies: Ocimum Biosolutions Ltd. (Hyderabad, India; 783 probes 50-nt-long) and Operon Biotechnologies GmbH (Cologne, Germany; 120 probes 70-nt-long). As an additional control, we used 4 short DNA probes (24-28-nt-long; Institute of Biochemistry and Biophysics, Warsaw, Poland), 8 probes complementary to external spike RNAs (AM1781; Ambion/Thermo Fisher Scientific) and one random oligo probe (Operon

Biotechnologies GmbH). In total, the microarray contained 916 unique probes: 896 probes complementary to 838 human genes, 8 probes specific for 5 bacterial genes, 3 probes specific for 3 plant genes and 9 artificial control probes. The probes were diluted in Pronto Epoxide Spotting Solution to a 20  $\mu$ M concentration and spotted in triplicates onto Epoxide-Coated Slides (both from Corning Inc., New York, NY, USA) with a SpotArray 24 instrument (Perkin-Elmer, Waltham, MA, USA). The design of our AML-array has been deposited in the ArrayExpress database (<http://www.ebi.ac.uk/arrayexpress>) under the accession no. A-MEXP-2220.

**Labeling and microarray hybridization.** A quantity of 10  $\mu$ g of each total RNA sample was reverse transcribed using anchored-oligo(dT)<sub>20</sub>, aminoallyl-modified dNTPs and SuperScript III reverse transcriptase from a SuperScript Plus Indirect cDNA Labeling System (Invitrogen, Carlsbad, CA, USA). Amino-modified cDNAs from the patients with AML and HV were labeled with Alexa Fluor 647 and the reference cDNA from the HL60 cell line sample (obtained from Dr Marcin Schmidt from Poznan University of Life Sciences) with AlexaFluor 555. The labeled cDNA was purified (MinElute Reaction Cleanup kit; Qiagen, Hilden, Germany), dissolved in hybridization buffer (5X SSC, 0.1% SDS and 0.1 mg BSA/ml) and kept up to 30 min at 50°C prior to hybridization in Corning microarray hybridization chambers in a HybArray12 (Perkin-Elmer) or a water bath by using a step-down hybridization protocol (5 h/50°C, 5 h/45°C and 5 h/40°C). Three subsequent wash steps were applied: i) 2X SSC and 0.1% SDS at 40°C for 5 min;

ii) 2X SSC at room temperature for 5 min; and iii) 0.2X SSC at room temperature for 5 min. The slides were dried through centrifugation with the Microarray High-Speed Centrifuge (Arrayit Corp., Sunnyvale, CA, USA; 5 sec, 2,000 x g, room temperature) and scanned with a ScanArrayExpress system (Perkin-Elmer) at 5- $\mu$ m resolution.

**Microarray data analysis.** The microarray images were processed using GenePix Pro version 6.0 software (Molecular Devices, LLC, Sunnyvale, CA, USA). Spots that did not meet a set of criteria (SNR >5; Dia., 110-250 nm; F CV  $\leq$ 100; SD  $\geq$ 1000; satur.  $\leq$ 1%) were filtered out. The raw data files (deposited in the ArrayExpress database under the accession no. E-MTAB-5434) were loaded into R Bioconductor version 3.2.0 (R Development Core Team 2009) and processed and analyzed with the limma package (36). Briefly, the foreground and background median signal values (excluding those with weights of 0) were background-corrected with the subtraction method and normalized with the global loess method. Probed replicates were averaged, and the replicate arrays from the same patient were merged. Differential gene expression was tested using a linear model suitable for experiments with common reference design. The final p-values were adjusted with FDR correction (37). Data clustering was conducted and visualized with the Heatplus R package.

**Real-time PCR analysis.** DNA-free RNA (3  $\mu$ g per sample) was reverse transcribed using SuperScript III RT and oligo(dT) (Invitrogen). The reaction mixtures (20  $\mu$ l vol) were incubated for 2 h at 50°C, and additional enzyme (1  $\mu$ l) was added after the first hour. Following reverse transcription, the samples were incubated for 20 min at 70°C with 10  $\mu$ l of 1 M NaOH. Subsequently, 10  $\mu$ l of HCl 1 M were added for neutralization, and the cDNA was precipitated overnight at -20°C with 100  $\mu$ l (2.5 vol) of 96% ethanol and 4  $\mu$ l (1/10 vol) of 3 M sodium acetate, pH 5.2. The centrifuged pellet was washed twice with 70% ethanol and dissolved in with 60  $\mu$ l of DEPC-H<sub>2</sub>O. A total of 1  $\mu$ l of each cDNA, diluted 3-fold, served as a template for real-time PCR in reactions, including MESA Green qRT-PCR MasterMix Plus (Eurogentec, Seraing, Belgium) and primers specific for the *STMN1*, *NPM1*, *S100A8* and *S100A9* transcripts. From 4 reference genes [*ACTB*, glyceraldehyde 3-phosphate dehydrogenase (*GAPDH*), *PGKI* and *PPIA*], the last 2 were selected as the most stable using geNorm (<https://genorm.cmgg.be>). The sequences of all the primers are presented in Table II. Each gene analysis was performed in duplicate. The standards were generated by PCR amplification of the HeLa cDNA template, obtained as a result of reverse transcription of control HeLa RNA with a SuperScript Plus Indirect cDNA Labeling system (Invitrogen). Real-time analysis was performed in a Rotor-Gene Q thermocycler (Qiagen), using the following program: initial denaturation (94°C, 2 min), 40 cycles of denaturation (94°C, 1 min), annealing (60°C, 1 min) and elongation (72°C, 30 sec), final elongation (72°C, 10 min) and a final hold (4°C). The melting curve was generated in the range of 60-95°C. The reaction volume was 20  $\mu$ l. Each reaction was performed in triplicate. The real-time PCR products were verified by melting curve analysis. The product quantities were estimated using the two standard curves' method. The values obtained for the triplicates were averaged. Subsequently, the

results obtained for the 2 biological replicates (separate reverse transcription reactions and separate real-time analyses) were averaged and divided by the average of the replicates of the 2 reference genes.

**Droplet digital PCR analysis.** DNA-free RNA (2.5  $\mu$ g per sample) was reverse transcribed and purified, as described above for real-time PCR, with the exception that the RT reaction lasted 1.5 h and only 1  $\mu$ l of enzyme was used. The precipitated cDNA, dissolved in 50  $\mu$ l of DEPC-H<sub>2</sub>O, served as a template for quantitative PCR with the use of a QX200 ddPCR system, QX200 EvaGreen ddPCR Supermix (Bio-Rad, Hercules, CA, USA), and primers specific for 4 candidate genes (*ABLI*, *ANXA3*, *CAT* and *WT1*) and one reference gene (*PGKI*). The reaction volume was 20  $\mu$ l, with a primer concentration of 250 nM, and the volume of cDNA (1-3  $\mu$ l) was optimized for each candidate gene and sample. The PCR conditions were as follows: initial denaturation (95°C, 5 min), 40 cycles of denaturation (95°C, 30 sec), annealing (60°C, 30 sec) and elongation (72°C, 45 sec), cooling (4°C, 5 min), final denaturation (90°C, 5 min) and final hold (12°C). The temperature ramping rate was 2°C/sec. Following PCR, the plates were directly analyzed with a QX200 Droplet Reader. The data were processed using Quanta Soft version 1.5.38.1118 software (Bio-Rad). The number of droplets for each candidate gene was divided by the number of droplets obtained for the reference gene analyzed in the same run (for *ABLI*, *ANXA3* and *WT1*) or in the same multiplex reaction (*CAT*). Each reaction was performed in duplicate. The sequences of all the primers are presented in Table II.

**Statistical analysis of RT-qPCR data.** Statistical analyses and bar plots were made in R version 3.2.0 R and R Studio version 0.98.1102. Welch two sample t-tests (unpaired) were applied for pairwise comparisons and ANOVA was applied for comparisons across 2 or more groups. For two- or more-way ANOVA, Tukey honestly significant difference (HSD) tests based on multiple comparisons of means were applied to determine which pairwise comparisons were statistically significant. To test the correlations between the expression values of 2 genes or between a particular gene's expression and clinical data (WBC, age), Pearson's correlations were calculated. The threshold p-value was always set as 0.05.

**Database screening.** The following open-source software tools and databases were explored: NCBI databases ([www.ncbi.nlm.nih.gov/](http://www.ncbi.nlm.nih.gov/)), including PubMed, Gene and Gene Expression Omnibus (GEO) and GDSbrowser, Expression Atlas ([www.ebi.ac.uk/gxa/](http://www.ebi.ac.uk/gxa/)) and DAVID ([david.abcc.ncifcrf.gov/](http://david.abcc.ncifcrf.gov/)).

## Results

**Microarray analysis.** To study gene expression in AML, we designed a small boutique AML-array, as deposited in the ArrayExpress database (A-MEXP-2220). The array contained >900 long oligonucleotide probes that are complementary to human genes implicated, *inter alia*, in hematopoietic cell differentiation and maturation, proliferation, apoptosis and leukemic transformation. Gene functional analysis with DAVID (38) revealed that our microarray was significantly

Table II. PCR primers.

Gene	Gene ID	Description	NCBI nucleotide reference	Primer sequences (forward and reverse)	T <sub>m</sub>	PCR product length name (bp)
<i>ABL1</i>	25	ABL proto-oncogene 1	NM_005157.5	5'-TCATATCAACCCGAGTGTCT-3' 5'-AACTTGTTCCTCATTGCTG-3'	56°C 54°C	229
<i>ANXA3</i>	306	Annexin A3	NM_005139.2	5'-CGCAATCAGGTGGAGTCGAG-3' 5'-TCACTAGGGCCACCATGAGA-3'	61°C 60°C	467
<i>ACTB</i>	60	Actin beta	NM_001101.4	5'-TCCCTGGAGAAGAGCTACGA-3' 5'-AGGAAGGAAGGCTGGAAGAG-3'	59°C 59°C	98
<i>CAT</i>	847	Catalase	NM_001752.3	5'-CTCCGGAACAACAGCCTTCT-3' 5'-GATGAGCGGGTTACACGGAT-3'	60°C 60°C	412
<i>GAPDH</i>	2597	Glyceraldehyde-3-phosphate dehydrogenase	NM_002046.5	5'-CCGTCTAGAAAAACCTGCC-3' 5'-AGCCAAATTCGTTGTCATACC-3'	56°C 57°C	218
<i>NPM1</i>	4869	Nucleophosmin 1	NM_001037738.2	5'-GCGCATTGAACAGTCCTGGG-3' 5'-CCAGCCTGAAGAGGCATGGGT-3'	62°C 64°C	172
<i>PGK1</i>	5230	Phosphoglycerate kinase 1	NM_000291.3	5'-GGGAAAAGATGCTTCTGGGAA-3' 5'-TTGAAAAGTGAAGCTCGGAAA-3'	58°C 58°C	72
<i>PPIA</i>	5478	Peptidylprolyl isomerase A	NM_021130.4	5'-CTGGACCCAACACAAATGGT-3' 5'-GCCTTCTTTCACCTTTCGCAAAAC-3'	58°C 59°C	98
<i>S100A8</i>	6279	S100 calcium binding protein A8	NM_001319196.1	5'-TGAAGAAATTGCTAGAGAC-3' 5'-CTTTATCACCAGAATGAGGA-3'	50°C 52°C	131
<i>S100A9</i>	6280	S100 calcium binding protein A9	NM_002965.3	5'-CCTGGACACAAATGCAGACAA-3' 5'-CGTCACCCTCGTGCATCTT-3'	59°C 60°C	101
<i>STMN1</i>	3925	Stathmin 1	NM_203401.1	5'-GCCCTCGGTCAAAGAATCTG-3' 5'-TGCTTCAAGACCTCAGCTTCA-3'	59°C 60°C	139
<i>WT1</i>	7490	Wilms tumor 1	NM_000378.4	5'-ACAGGGTACGAGAGCGATAACCA-3' 5'-CACACGTCGCACATCCTGAAT-3'	63°C 61°C	105

The primer sequences of 3 reference genes (*ACTB*, *PGK1* and *PPIA*) were from the study by Lossos *et al* (69). The *STMN1* primers were from the study by Hussein *et al* (70). The *WT1* primers were from the study by Kreuzer *et al* (71). The design of the remaining primers and melting temperature (T<sub>m</sub>) calculation was supported by NCBI Primer Blast ([www.ncbi.nlm.nih.gov/tools/primer-blast/](http://www.ncbi.nlm.nih.gov/tools/primer-blast/)).

enriched in genes linked with immune, infection and cancer classes of disease. Out of OMIM diseases, only AML was found to be statistically significant. The genes covered by the AML-array encode proteins from the following KEGG pathways: Cancer (111 genes), cytokine-cytokine receptor interaction (102 genes), Jak-STAT signaling (64 genes), chemokine signaling (59 genes), MAPK signaling (54 genes), focal adhesion (49 genes), hematopoietic cell lineage (42 genes) and regulation of actin cytoskeleton (41 genes).

The AML-array was used to estimate relative gene expression in PBMCs and/or BMMCs obtained from 33 *de novo* AML patients, prior to therapy, and 15 HV (Table I). The AML samples were classified as M1 or M2 FAB subtypes, which were characterized on the basis of the early blast cell differentiation arrest and either no myeloid cell maturation (M1) or partial maturation (M2). The microarray experiment was based on two-color hybridization, wherein each studied sample was matched with a common reference (HL60 cell line). Data from 118 hybridizations, as deposited in the ArrayExpress database under the accession no. E-MTAB-5434, were background-corrected and normalized, and technical replicates (of

probes and arrays) were then merged and analyzed using the R Bioconductor limma package.

First, we assessed whether there were any differences between the transcriptomes of the BMMCs and PBMCs. Similar to the proteomics analysis results of our previous study (33), there were no statistically significant differences between the AML-PBMCs and AML-BMMCs (differential expression analysis with a limma linear model, adjusted p-value > 0.11) (Table III). Therefore, in the following transcriptome analyses, we did not divide the samples into BMMC- and PBMC-derived groups.

Our next aim was to identify the differences between the AML and HV samples. Assuming a significance level  $\alpha$  0.05 as the threshold, we selected 163 differentially expressed genes (DEGs), of which 78 were underexpressed and 85 were overexpressed in AML (Table III). However, after sample clustering with these DEGs, 2 samples were still misclassified (one AML sample was included in the HV cluster, and one HV was in the AML cluster). The application of a more restrictive threshold ( $\alpha$  0.01) limited the list of DEGs to 83 (42 underexpressed and 41 overexpressed) (Table IV). In total, 36 genes

Table III. The summary of microarray data analysis results.

Comparison	The smallest adjusted p-value (top gene)	The no. of DEGs (over-/underexpressed)	Overexpressed genes	Underexpressed genes
AML-PBMC vs. AML-BMMC	0.11 ( <i>FAS</i> )	0	<i>FAS, DUSP2</i>	<i>PRG1, THY1, STAT4, CTSG, CCL7, PRG2, SRGN, SRP9</i>
AML vs. HV	1.67x10 <sup>-10</sup> ( <i>STMN1</i> )	163 (85/78)	Genes from Table IV, and <i>ABL1, BCR, CBL, CCL24, CCND1, CCND2, CCNDBP1, CCR10, CD34, CD38, CDKN1A, CFL1, CLU, CTSG, DNAJB4, DNMT3B, GAB1, GSTP1, HOXB5, HOXC8, HPH, HSPA4L, IFNGR2, INPP5D, IRS2, JUNB, METTL3, MME, MT1H, NUP98, PHB2, PPIF, PRG2, RAF1, RHOH, SLC25A1, SLC7A5, SLITRK6, SMAD3, TLE1, TRAF4, ZEB2</i>	Genes from Table IV, and <i>AIF1, CBF, CRIP2, CSF3, CYBB, DRAP1, E2F1, FAS, FOSB, GDII, HIF1A, HLA-DPA1, HLA-DRB1, IGHM, IL12B, KDR, LGALS3, MLLT10, MTMR11, MYLPF, NFKB2, PAK1, PHB2, PROCR, RHAG, S100A8, SHC1, SLC29A1, SULT1E1, TNFRSF10A, XCL1, XCR1, ZFP36</i>
AML-M1 vs. AML-M2	0.35 ( <i>IL5B</i> )	0	<i>IL5B, CASP2, LCP1, FLT3, BIRC2</i>	<i>PRG1, CST7, MAPK6, SRGN, CTSG</i>
AML-M1 vs. AML-M2 <sup>a</sup>	0.11 ( <i>CASP2</i> )	0	<i>CASP2, IL5B, BIRC2, FLT3, TPM1</i>	<i>PRG1, CST7, MAPK6, CTSG, SRGN</i>
AML-M1 vs. HV	2.84x10 <sup>-08</sup> ( <i>STMN1</i> )	53 (28/25)	Set 1, and <i>ARHGEF12, ERCC2, HSP90AB1, HSPA8, HSPA9, IGFBP7, ANGTP1, INPP5D, ITGB4, KIT, KITLG, MN1, MYB, RHOH</i>	Set 3, and <i>BIRC3, BTG1, CCL5, FCER1G, HCK, IFNA1, LYZ, NFKBIA, PGK1, S100A9, ACTB, CST7, LBD1</i>
AML-M2 vs. HV	2.09x10 <sup>-09</sup> ( <i>STMN1</i> )	146 (74/72)	Set 2, and <i>ABCF1, ABL1, ANGTP1, ARF1, ATP6V0C, BCR, CBL, CCL24, CCND2, CCR10, CD34, CDKN1A, CFL1, CTSD, CTSG, DNAJB4, DNMT3B, ETV6, GAB1, GAL, GAPDH, HIGD1A, HPH, HSPA4L, HSPD1, IFNGR2, ITGB4, KIT, KITLG, MAP7, METTL3, MME, MN1, MPO, MYB, MYH9, NPM1, PHB2, PPIF, PRG1, PRG2, RAF1, SLC7A5, SMAD3, TUBB, ZEB2</i>	Set 4, and <i>BTG1, FCER1G, HCK, HLA-DPB1, PGK1, PLBD1, CBF, CD44, CD52, CD74, CRIP2, CX3CR1, CYP2E1, DRAP1, FAS, HIF1A, HLA-DRB1, IGHM, JUN, KDR, LCP1, LGALS3, MLLT10, MYLPF, NFKB2, PAK1, PROCR, PTPRE, PXN, RARA, RHAG, RHOB, SLC29A1, SPTBN1, STAT5B, STAU2, SULT1E1, TNFRSF10B, TNFSF10, XCR1, ZFP36</i>
<i>RUNX1/RUNXIT1</i> <sup>+</sup>	1.75x10 <sup>-06</sup> ( <i>STMN1</i> )	13 (7/6)	<i>STMN1, CDK6, MYC, RPLP0, MPO, HSPA8, ATP6V0C</i>	<i>TMSB4X, LT, IFITM1, PF4, FCN1, CD44</i>
AML vs. HV <i>FLT3</i> <sup>+</sup>	3.32x10 <sup>-07</sup> ( <i>CDK6</i> )	17 (10/7)	<i>CDK6, STMN1, RPLP0, ANGTP1, SET, MCM5, ENO1, RASSF5, DNNT, MYL9</i>	<i>TRADD, TMSB4X, CAPN10, LT, PDGFRB, XBP1, SPTBN1</i>
<i>NPM1</i> <sup>+</sup> AML vs. HV	7.35x10 <sup>-07</sup> ( <i>STMN1</i> )	97 (50/47)	Set 2, and <i>ABCF1, AK2, ANGTP1, ARHGAP4, BCR, DAD1, GAB1, GAL, GAPDH, HSPA1A, HSPD1, IFNGR2, ITGB4, MAP7, MN1, NPM1, NUP98, PRG1, RHOH, SLC25A1, TRAF2, TUBB</i>	Set 4, and <i>HCK, HLA-DPB1, PGK1, PLBD1, CD52, CEBPB, CYBB, FOSB, GJB1, IL12B, IL9, PAK1, PRODH, PTPRE, SPTBN1, SWAP70</i>
CR AML vs. HV	4.44x10 <sup>-09</sup> ( <i>STMN1</i> )	74 (31/43)	Set 1, and <i>ADRA2C, HSP90AB1, HSPA8, HSPA9, IGFBP7, ANGTP1, ATP6V0C, GAL, GAPDH, HOXB5, HPH, ITGB4, KIT, MT1H, MYB, PRTN3, TUBB</i>	Set 3, and <i>ADD3, BTG1, CCL3, CCL5, CSF3R, FCER1G, HCK, HLA-DPB1, IFNA1, LYZ, NFKBIA, PLBD1, S100A9, XBP1, AGPAT1, AIF1, BIRC3, CBF, CD74, CX3CR1, CYP2E1, HIF1A, PTPRE, RARA, RHOB, S100A8, SPTBN1, STAT5B, SULT1E1, TNFSF10</i>
RES AML vs. HV	7.98x10 <sup>-07</sup> ( <i>STMN1</i> )	84 (41/43)	Set 2, and <i>ABL1, ARF1, CBL, CD38, CDKN1A, DNAJB4, KIT, MYH9, PRG1, SMAD3, TBLIX, TLE1, TRAP1</i>	Set 3, and <i>ADD3, BIRC3, CSF3, DUSP2, FCER1G, HLA-DPB1, IGF1, PGK1, PIM1, PLBD1, STK4, XBP1, CRIP2, CYP2E1, DRAP1, GDII, HLA-DRB1, HOXA3, IGHM, IL8, KDR, MLLT10, NFKB2, PAK1, PXN, RARA, SLC29A1, STAU2, SWAP70, TNFSF10, XCR1</i>

Table III. Continued.

Comparison	The smallest adjusted p-value (top gene)	The no. of DEGs (over-/underexpressed)	Overexpressed genes	Underexpressed genes
X AML vs. HV	5.57x10 <sup>-07</sup> ( <i>STMN1</i> )	79 (37/42)	Set 1, and <i>ARHGEF12, ERCC2, HOXA10, HSPA8, IGFBP7, MYH11, PDE3B, PRKAR1B, ZNF22, ANGTP1, CD81, FUS, GAB1, HSPD1, IFNGR2, KIT, KITLG, MAP7, MNI, MYB, NPM1, RHOH, TUBB</i>	Set 4, and <i>BTG1, FCER1G, CD74, FOSB, IGHM, IL12B, PRAME, PXN, TIPARP, TNFRSF10A, ZFP36</i>
<i>RUNX1/RUNX1T1</i> <sup>+</sup> AML vs. remaining AML	0.99 ( <i>TERT</i> )	0	<i>TERT, MPO, OGFR, STK32B, CST7, IL5RA, SPI1, PLXNC1</i>	<i>HPRT1, PML</i>
<i>RUNX1/RUNX1T1</i> <sup>+</sup> AML vs. remaining AML <sup>a</sup>	0.96 ( <i>HPRT1</i> )	0	<i>MPO, CXCL2, IL5RA, OGFR, STK32B, CST7, TERT, PLXNC1, SWAP70</i>	<i>HPRT1</i>
<i>FLT3</i> <sup>+</sup> AML vs. remaining AML	0.48 ( <i>VIM</i> )	0	<i>VIM, DNNT, CDK6, CEACAM6</i>	<i>IL4, G6PD, PSMA6, PMAIP1, TRADD, TUBB4</i>
<i>FLT3</i> <sup>+</sup> AML vs. remaining AML <sup>a</sup>	0.088 ( <i>CDK6</i> )	0	<i>CDK6, VIM, CEACAM6, DNNT, CASP3</i>	<i>PMAIP1, IL4, G6PD, MKI67, CDKN2A</i>
<i>NPM1</i> <sup>+</sup> AML vs. remaining AML	0.99 ( <i>FOSB</i> )	0	<i>ANXA8, TRAF2, NAP1L1</i>	<i>FOSB, HLA-DPA1, STOM, KLF4, MLLT1, PRODH, EBF1</i>
<i>NPM1</i> <sup>+</sup> AML vs. remaining AML <sup>a</sup>	0.9 ( <i>FOSB</i> )	0	<i>TRAF2, ANXA8, RHOH, PGK2, HSPA1A</i>	<i>FOSB, KLF4, HLA-DPA1, EBF1, MLLT1</i>
<i>NPM1</i> <sup>+</sup> / <i>FLT3</i> <sup>+</sup> AML vs. remaining AML	0.26 ( <i>CPA3</i> )	0	<i>CPA3, CCL17, HOXA5, PLCG1, ANXA1, CLEC2B, TUBA1A, CCNG2, VIM</i>	<i>RTN2</i>
<i>NPM1</i> <sup>+</sup> / <i>FLT3</i> <sup>+</sup> AML vs. remaining AML <sup>a</sup>	0.043 ( <i>CPA3</i> )	1	<i>CPA3, (CASP3, PKN2, CCL17, CLEC2B, PBX3, RB1)</i>	<i>PMAIP1, RTN2, LTA</i>
<i>NPM1</i> <sup>+</sup> / <i>FLT3</i> <sup>-</sup> AML vs. remaining AML	0.79 ( <i>TRAF2</i> )	0	<i>TRAF2, ANXA8, ITGB4, HSPA9, BCR, MYL9, RHOH</i>	<i>PRODH, GTF2E2, STOM</i>
<i>NPM1</i> <sup>+</sup> / <i>FLT3</i> <sup>-</sup> AML vs. remaining AML <sup>a</sup>	0.28 ( <i>TRAF2</i> )	0	<i>TRAF2, RHOH, SLC25A1, ANXA8, NONO, ITGB4, ABCF1, BCR, MYL9</i>	<i>PRODH</i>
<i>NPM1</i> <sup>-</sup> / <i>FLT3</i> <sup>+</sup> AML vs. remaining AML	0.63 ( <i>PSMA6</i> )	0	<i>PTK7, SRP9, DNAJB5, CD247</i>	<i>PSMA6, NUP88, CANX, NUBPL, BUD31, CASP2</i>
<i>NPM1</i> <sup>-</sup> / <i>FLT3</i> <sup>+</sup> AML vs. remaining AML <sup>a</sup>	0.36 ( <i>CASP2</i> )	0	<i>PTK7, CDK6, CEACAM6, FGF13</i>	<i>CASP2, APOC1, PSMA6, NUP88, NUBPL, CANX</i>
<i>NPM1</i> <sup>+</sup> / <i>FLT3</i> <sup>-</sup> AML vs. <i>NPM1</i> <sup>-</sup> / <i>FLT3</i> <sup>+</sup> AML	0.77 ( <i>CANX</i> )	0	<i>CANX, PSMA6, NUP88, ITGB4, G6PD, TRAF2</i>	<i>DNAJB5, CEACAM6, PTK7, CEBPB</i>
<i>NPM1</i> <sup>+</sup> / <i>FLT3</i> <sup>-</sup> AML vs. <i>NPM1</i> <sup>-</sup> / <i>FLT3</i> <sup>+</sup> AML <sup>a</sup>	0.42 ( <i>CDK6</i> )	0	<i>CASP2, CANX, APOC1, TRAF2, HSPA8, PSMA6</i>	<i>CDK6, CEACAM6, PTK7, DNAJB5</i>
<i>NPM1</i> <sup>+</sup> / <i>FLT3</i> <sup>-</sup> AML vs. <i>NPM1</i> <sup>+</sup> / <i>FLT3</i> <sup>+</sup> AML	0.56 ( <i>RTN2</i> )	0	<i>RTN2, IL4, PKLR</i>	<i>CPA3, CCL17, PLCG1, GTF2E2, ITGA4, CCL1, RNHI</i>
<i>NPM1</i> <sup>+</sup> / <i>FLT3</i> <sup>-</sup> AML vs. <i>NPM1</i> <sup>+</sup> / <i>FLT3</i> <sup>+</sup> AML <sup>a</sup>	0.17 ( <i>PMAIP1</i> )	0	<i>PMAIP1, RTN2, IL4</i>	<i>CPA3, PRKCQ, CCL17, CCL1, PKN2, CASP3, PLCG1</i>
<i>NPM1</i> <sup>-</sup> / <i>FLT3</i> <sup>+</sup> AML vs. <i>NPM1</i> <sup>+</sup> / <i>FLT3</i> <sup>+</sup> AML	0.83 ( <i>DNAJB5</i> )	0	<i>DNAJB5, FGF13, CD247</i>	<i>APOC1, NUBPL, PKN2, NAP1L1, FOXP1, CCL17, BUD31</i>
<i>NPM1</i> <sup>-</sup> / <i>FLT3</i> <sup>+</sup> AML vs. <i>NPM1</i> <sup>+</sup> / <i>FLT3</i> <sup>+</sup> AML <sup>a</sup>	0.09 ( <i>PKN2</i> )	0	<i>DNAJB5, FGF13, ABR</i>	<i>PKN2, APOC1, CPA3, CASP2, NUBPL, JUN, CCL1</i>
CR AML vs. RES AML	0.52 ( <i>TRAP1</i> )	0	<i>GAPDH, HOP, TERT, PXN, MT1H</i>	<i>TRAP1, NFKBIA, ABL1, AGPAT1, NUBPL</i>
CR AML vs. RES	0.46 ( <i>GAPDH</i> )	0	<i>GAPDH, MT1H, TERT, TUBA1</i>	<i>NFKBIA, NUBPL, TRAP1, TBLIX, CFLAR, PRDX2</i>
CR AML vs. X AML	0.72 ( <i>ARHGEF12</i> )	0	<i>PRAME, ROBO1, RBPMS, TERT</i>	<i>ARHGEF12, MEIS1, PTPN6, EPHB2, ANXA8, AVEN</i>
CR AML vs. X AML <sup>a</sup>	0.71 ( <i>MEIS1</i> )	0	<i>PRAME, ROBO1, IGHM, IL6</i>	<i>MEIS1, ARHGEF12, ERCC2, PTPN6, CFLAR, HIF1A</i>
RES AML vs. X AML	0.98 ( <i>AZU1</i> )	0	<i>AZU1, LYZ, SIRPA, STOM, GP1BB, TOP2B, HPH</i>	<i>MAFB, MLLT10, CACNA2D2</i>

Table III. Continued.

Comparison	The smallest adjusted p-value (top gene)	The no. of DEGs (over-/underexpressed)	Overexpressed genes	Underexpressed genes
RES AML vs. X AML <sup>a</sup>	0.95 ( <i>AZU1</i> )	0	<i>AZU1, HPH, TOP2B, SIRPA, CD7</i>	<i>CD81, CACNA2D2, MLLT10, MAFB, BIRC2</i>
CR_long AML vs. CR_short AML	0.98 ( <i>CAST</i> )	0	<i>CAST, BIRC5, MAF, FBXL10, PTPRC, SHQ1, MYH11, NPM1</i>	<i>CRIP2, CREBBP</i>
CR_long AML vs. CR_short AML <sup>a</sup>	0.98 ( <i>CRIP2</i> )	0	<i>CAST, BIRC5, MAF, HMGA2, MCM3, SHQ1, PTPRC</i>	<i>CRIP2, ID1, SQSTM1</i>

<sup>a</sup>The analysis repeated with AML samples only (without HV). All analyses were performed with the use of Bioconductor limma package and linear models. Differentially expressed genes (DEGs) were identified with a significance level of  $\alpha$  0.05. p-values were corrected for multiple testing. When no statistically significant genes were identified in a comparison, the table includes the top 10 genes ranked according to p-value (in parentheses). The sets of genes common for multiple comparisons - set 1: *CDK6, CEBPA, EEF1G, ENO1, GSN, HOXB6, KRAS, MCM5, MYC, PKM2, RASSF5, RPLP0, SET, STMN1* (14 overexpressed genes common for 7 comparisons); set 2: set 1 and *ADRA2C, ARHGGEF12, ERCC2, HOXA10, HSP90AB1, HSPA8, HSPA9, IGFBP7, JUNB, MYH11, PDE3B, PRKAR1B, SRGN, ZNF22* (28 overexpressed genes common for 4 comparisons); set 3: *B2M, CAPN10, CCL19, FCN1, HOXA9, IFITM1, LTB, MAP4K2, PDGFRB, PF4, TMSB4X, TRADD* (12 underexpressed genes common for 7 comparisons); set 4: set 3 and *ADD3, BIRC3, CCL3, CCL5, CSF3, CSF3R, DUSP2, E2F1, HLA-DPA1, IFNA1, IGF1, LYZ, NFKBIA, PIMI, RALGDS, S100A9, SHC1, STK4, XBP1* (31 underexpressed genes common for 4 comparisons).

from the list (43%, up- and downregulated in equal proportions) encoded proteins involved in signal transduction and transcriptional regulation, affecting processes, such as cell growth, proliferation, adhesion and apoptosis. Of note, 10 genes (12%, 4 up- and 6 downregulated) were associated with cytoskeletal organization and functioning, and 12 genes (14,5%, exclusively underexpressed in AML) were engaged in immune and inflammatory response. With the use of these 83 DEGs, we were able to perfectly distinguish the AML from the HV samples (Fig. 1A); the entire set of arrays was clearly divided into 2 clusters: 15 control HV samples constituted a separate cluster, whereas all 33 AML samples belonged to a second cluster.

Considering another criterion, the level of expression, we selected from the list of 83 DEGs, 23 genes with the greatest change in expression ( $\log_2FC$  values  $>1.0$  or  $<-1.0$ , equivalent to a  $>2$ -fold change in expression in both directions): 12 up- and 11 downregulated (Fig. 1B). The most significantly overexpressed gene in AML ( $\log_2FC$  close to 3, equal to an 8-fold enrichment) was *STMN1*, which encodes a protein involved in the regulation of the microtubule filament system, stathmin 1. *STMN1* was also the top statistically significant gene in the comparison between the AML and HV samples (adjusted p-value  $1.67 \times 10^{-10}$ ) (Tables III and IV). Other upregulated genes encoded proteins associated with myeloid leukemia and cancer development: Oncogenes, cell cycle and apoptosis regulators [CCAAT/enhancer binding protein  $\alpha$  (*CEBPA*), Kirsten rat sarcoma viral oncogene homolog (*KRAS*), v-myc myelocytomatosis viral oncogene homolog, avian (*MYC*), cyclin-dependent kinase 6 (*CDK6*), minichromosome maintenance complex component 5 (*MCM5*), SET nuclear proto-oncogene (*SET*), proto-oncogene c-Kit ligand (*KITLG*) and serglycin (*SRGN*)], proteins involved in angiogenesis [angiopoietin 1 (*ANGPT1*)], cell growth, glucose metabolism and the transcriptional regulator, enolase 1 (*ENO1*) and ribosomal protein *RPLP0*.

Among the downregulated genes, predominantly those encoding defense/immunity proteins, were the following: Cell

surface receptors *CD74* and Fc fragment of IgE (*FCER1G*), ficolin 1 (*FCN1*) typically expressed in the peripheral blood leukocytes, antimicrobial agent lysozyme (*LYZ*), tumor necrosis factor (*TNF*) family member lymphotoxin  $\beta$  (*LTB*), interferon induced transmembrane protein 1 (*IFITM1*) and calcium binding protein *S100A9*. Moreover, decreased gene expression in AML was observed for the cell cycle regulator protein tyrosine phosphatase (*PTPRE*), apoptosis suppressor baculoviral IAP repeat-containing 3 (*BIRC3*), regulator of actin polymerization, cell proliferation, migration and differentiation thymosin  $\beta$ 4 (*TMSB4X*) and membrane skeletal protein adducin 3 (*ADD3*).

To determine whether AML FAB subtypes could be distinguished by using our boutique array, we compared the gene expression profiles obtained for 11 patients diagnosed as AML-M1 and for 22 patients classified as AML-M2. However, we did not detect any statistically significant differences (adjusted p-value  $>0.35$ ) (Table III). A separate analysis of AML-M1 vs. HV and AML-M2 vs. HV revealed 54 and 149 DEGs, respectively ( $\alpha=0.05$ ). Among the 54 DEGs from the comparison between AML-M1 and HV, 50 were shared with the list of 149 DEGs obtained from the comparison between AML-M2 and HV, thus suggesting that the AML-M1 subtype is a subset of AML-M2 and the latter shows some unique features. The list of genes shared between the M1 and M2 FAB subtypes included all the genes shown in Fig. 1B apart from *SRGN, CD74, PTPRE* and *ADD3*, which were unique for the comparison between AML-M2 and HV. Other genes shared between M1 and M2 were *ERCC2, ITGB4, HSPA8, EEF1G, HOXB6, IGFBP7, KIT, PKM2, RASSF5, MNI, ARHGGEF12, HSP90AB1, MYB, HSPA9* and *GSN* (overexpressed), and *CCL19, MAP4K2, PF4, CCL5, B2M, HCK, CAPN10, HOXA9, TRADD, PGK1, PLBD1, IFNA1, BTG1, NFKBIA* and *PDGFRB* (underexpressed). To 4 genes unique for AML-M1 belonged 2 underexpressed (*ACTB* and *CST7*) and 2 overexpressed (*INPP5D* and *RHOH*) genes. The list of overexpressed genes unique for AML-M2 included *inter alia*



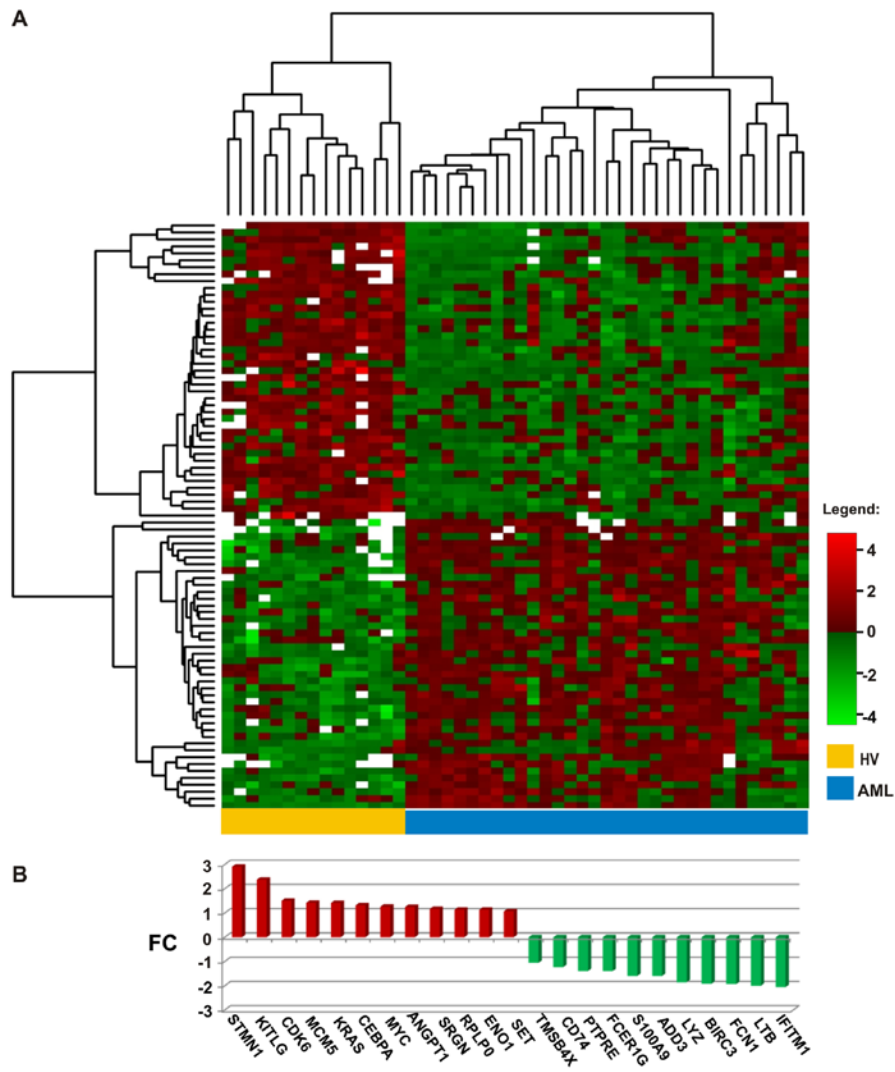


Figure 1. (A) Heatmap presenting the normalized log<sub>2</sub> expression values of 83 genes (horizontally) selected as being over- or underexpressed in acute myeloid leukemia (AML) when compared with healthy volunteers (HV) samples (vertically) with the adjusted p-value threshold of 0.01. Two dendrograms represent the results of clustering: Genes (left side of the heatmap) and samples (above the heatmap). White points mean missing values, referring to the probes with weight 0 that were excluded from the analysis because of poor quality. (B) Changes in the expression (log<sub>2</sub>FC values) of 23 genes selected as the most overexpressed (red) or underexpressed (green) in AML compared with the HV samples. The genes are ranked according to the log<sub>2</sub>FC value.

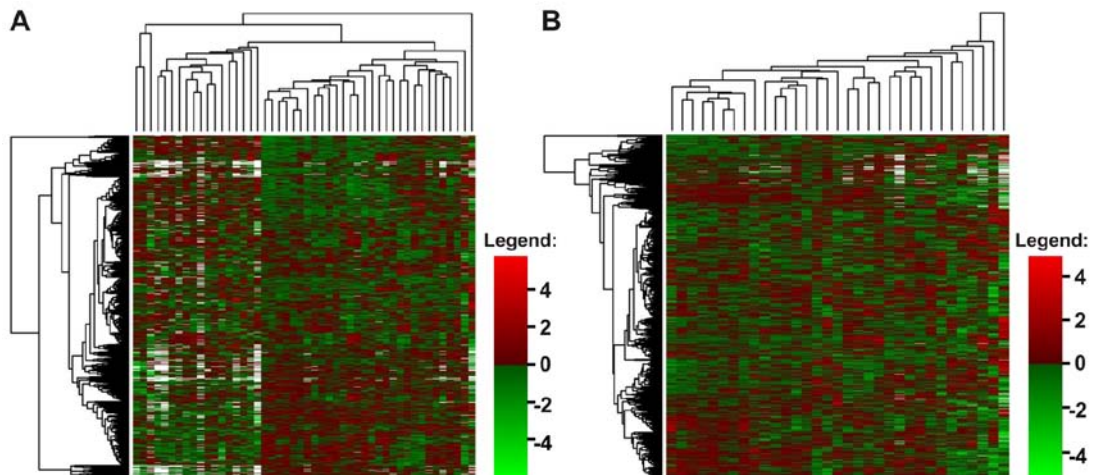


Figure 2. Heatmaps presenting the normalized log<sub>2</sub> expression values of all acute myeloid leukemia (AML)-array genes (horizontally) in all studied samples, (A) AML and healthy volunteers (HV), and (B) only in AML samples, excluding HV. Dendrograms represent the results of clustering: Genes (left side of the heatmap) and samples (above the heatmap). White points indicate missing values, referring to the probes with weight 0 that were excluded from the analysis because of poor quality. (A) Reveals the existence of outlier samples (first sample from the right and three samples from the left) and two major clusters (in the middle), with all HV samples collected at the left side of a heatmap. (B) Shows general homogeneity of AML samples. No clear sample clusters cannot be distinguished.

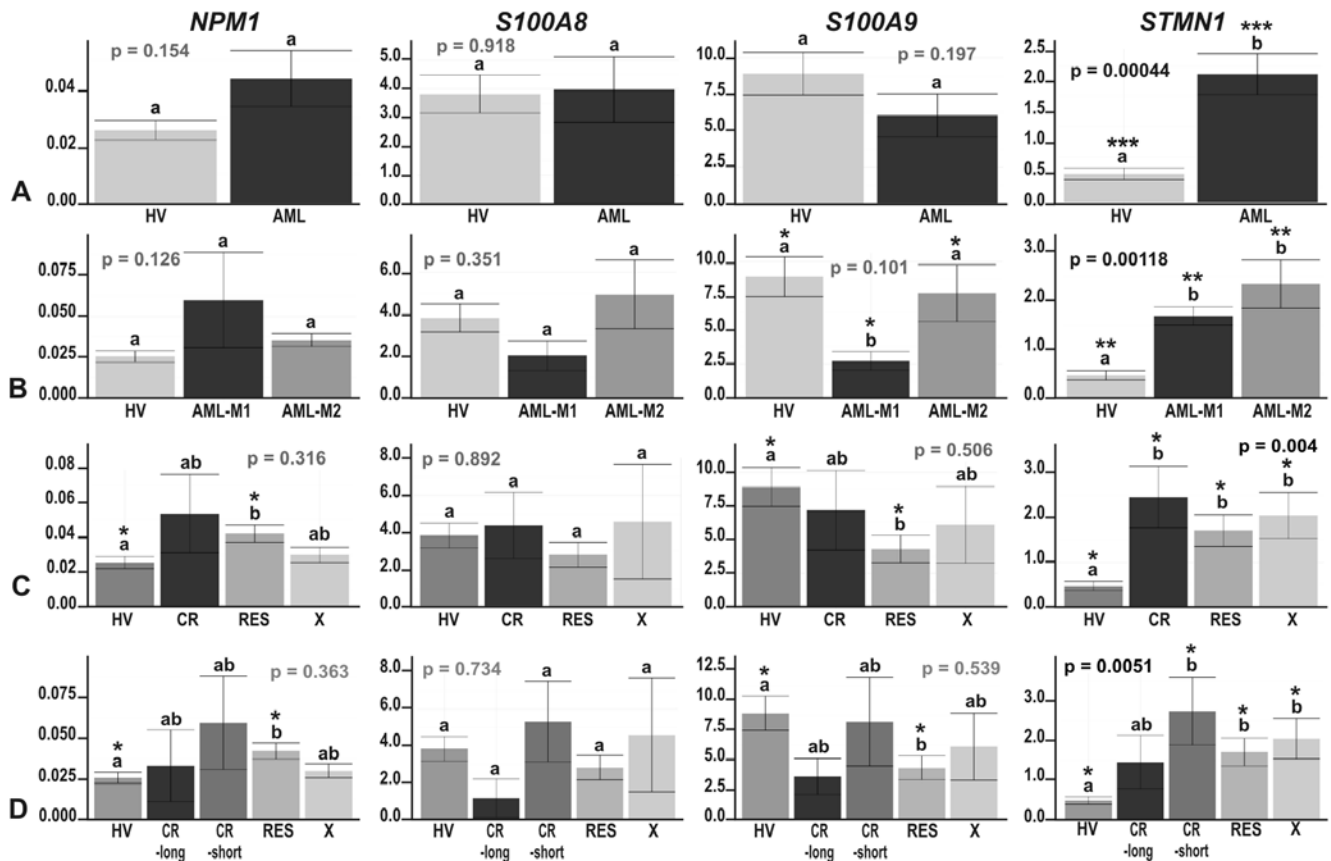


Figure 3. The results of real-time PCR-based expression analysis of 4 genes (*NPM1*, *S100A8*, *S100A9* and *STMN1*) in (A) acute myeloid leukemia (AML) compared with healthy volunteers (HV) samples; (B) in the context of the AML French-American-British (FAB) subtypes, M1 and M2; and in the context of the response to therapy, with the AML divided into (C) 3 (CR, RES, X) subgroups or (D) 4 subgroups (CR\_long, CR\_short, RES, X). The y-axes show relative expression values of a studied gene compared to the reference genes. Each plot contains the ANOVA p-value obtained for a whole test. Pair-wise comparisons with statistically significant differences, verified with a t-test and HSD Tukey test, are indicated by letters and asterisk symbols above each bar. Bars showing the same letter indicate no significant difference ( $p > 0.05$ ). The numbers of asterisks denote the level of statistical significance: \* $p < 0.05$ , \*\* $p < 0.01$  and \*\*\* $p < 0.001$ .

*CTSG*, *CTSD*, *GAL*, *MYH11*, *GAPDH*, *ADRA2C*, *ATP6V0C*, *MAP7*, *ARF1*, *METTL3*, *BCR*, *TUBB*, *ABL1*, *NPM1*, *CD34*, *JUNB* and *MPO*, encoding myeloperoxidase, marker protein of AML with maturation.

As regards the effects of mutations, we analyzed the gene expression profiles from the following AML subgroups: *RUNX1/RUNX1T1*<sup>+</sup> [5 patients with translocation t(8;21), typical of the AML-M2 FAB subtype], *NPM1*<sup>+</sup> (8 patients with an *NPM1* mutation) and *FLT3*<sup>+</sup> (4 patients with *FLT3*-ITD). Owing to the co-existence of the *FLT3*-ITD and *NPM1* mutation in some patients, we were also able to distinguish 3 additional subgroups: *NPM1*<sup>+</sup>/*FLT3*<sup>+</sup> (2 patients), *NPM1*<sup>+</sup>/*FLT3*<sup>-</sup> (6 patients) and *NPM1*<sup>-</sup>/*FLT3*<sup>+</sup> (2 patients). However, we were not able to identify any distinct clusters or detect significant differences in any of the comparisons (Table III).

The last result worth mentioning regarding the AML analysis using the AML-array is the classification of the patients according to their response to therapy. The association of gene expression with the prognosis and treatment outcome is a clinically important aspect of leukemia studies. Although all the studied samples were collected at the time of diagnosis, further monitoring of patients enabled to divide them into 3 general subgroups corresponding to their responses to therapy: Patients who reached complete remission (CR, 15 patients), patients who resisted to therapy (RES, 9 patients)

and patients who succumbed to the disease during therapy (X, 9 patients). The CR subgroup was further divided into 2 smaller subgroups: Patients with complete remission lasting up to 1 year (CR-short, 12 patients) and patients with complete remission lasting >1 year (CR-long, 3 patients). We did not detect any statistically significant differences in gene expression between any of the above subgroups (Table III).

In all analyses performed with the AML-array, significant differences were detected only when an AML subgroup was compared with HV. Notably, the obtained lists of DEGs, despite being of variable length, consisted a high number of shared genes, and *STMN1* was always at the top of the ranking (Table III). To eliminate the HV impact, we repeated all the analyses, focusing solely on the AML samples. The result was the same: No statistically significant differences were detected between AML subgroups apart from one: The overexpression of the *CPA3* gene, encoding a carboxypeptidase, in *NPM1*<sup>+</sup>/*FLT3*<sup>+</sup> AML vs. remaining AML samples ( $p = 0.043$ ) (Table III). Unsupervised hierarchical clustering of the data also indicated that the patients with AML were generally a homogenous group, despite individual variations (Fig. 2).

**Real-time PCR analysis.** To verify the results of the microarray analysis, we selected 4 genes, *STMN1*, *NPM1*, *S100A9* and *S100A8*, and quantified their expression with the use of real-time

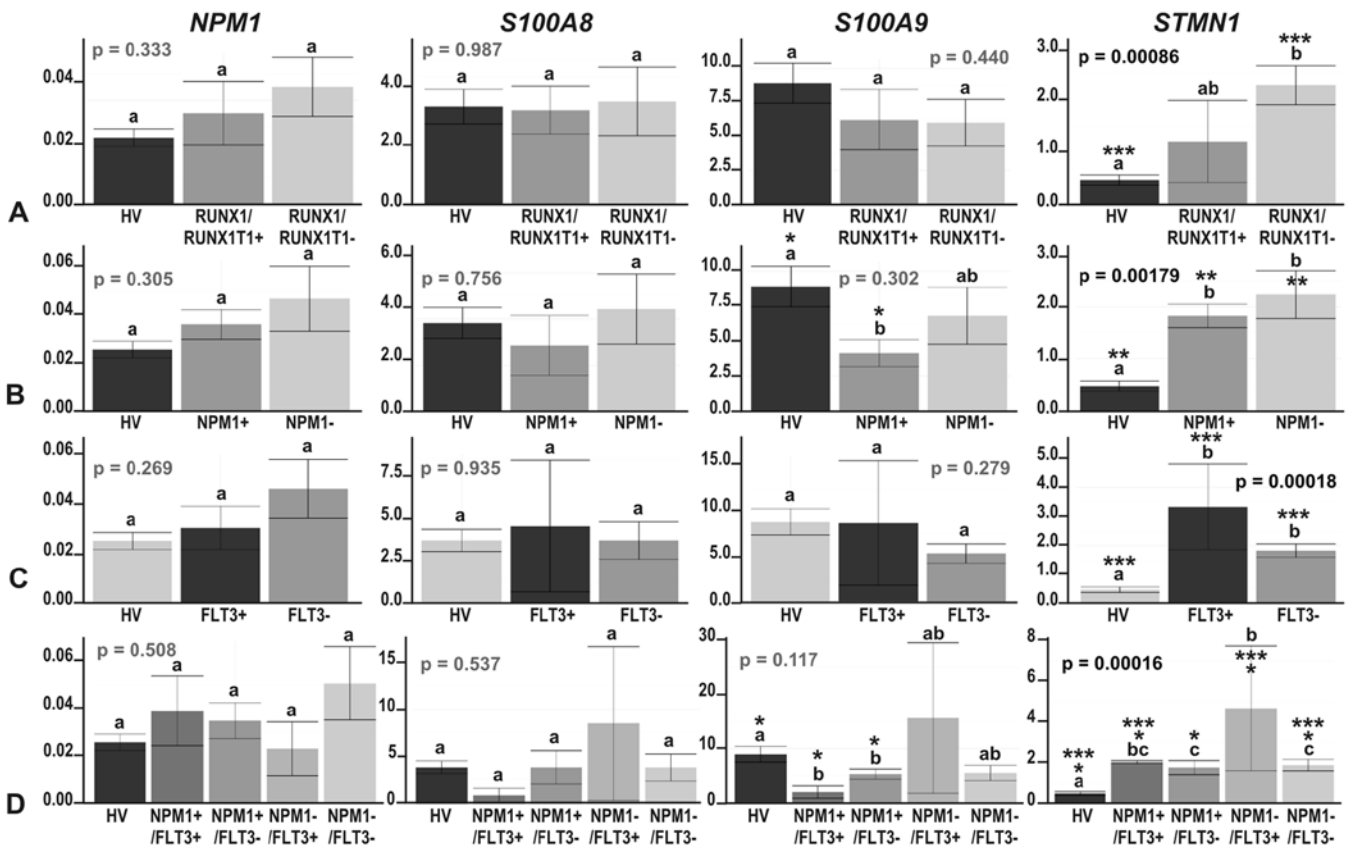


Figure 4. The results of real-time PCR-based expression analysis of 4 genes (*NPM1*, *S100A8*, *S100A9* and *STMN1*) in acute myeloid leukemia (AML) compared with healthy volunteers (HV) samples, with the AML divided according to the mutation status of (A) *RUNX1/RUNX1T1*; (B) *NPM1*; (C) *FLT3*; and (D) *NPM1* and *FLT3* together. The y-axes show relative expression values of a studied gene compared to the reference genes. Each plot contains the ANOVA p-value obtained for a whole test. Pair-wise comparisons with statistically significant differences, verified with a t-test and HSD Tukey test, are indicated by letters and asterisk symbols above each bar. Bars showing the same letter indicate no significant difference ( $p > 0.05$ ). The numbers of asterisks denote the level of statistical significance: \* $p \leq 0.05$ , \*\* $p \leq 0.01$  and \*\*\* $p \leq 0.001$ .

PCR and a Rotor-Gene Q instrument. In this case, our sample set contained 14 HV and 21 AML samples. The *STMN1* gene was selected as the most upregulated gene in AML compared with HV and *NPM1* was selected as upregulated only in some AML subgroups (AML-M2, AML-*NPM1*<sup>+</sup> and AML X), whereas *S100A9* was selected as one of the most downregulated genes in AML and different AML subgroups compared with HV (Table III). *S100A8* was underexpressed with statistical significance only in AML and in the AML-CR subgroup (Table III); however, we were interested whether 2 genes belonging to the same gene family present similar expression patterns.

First, owing to the variable expression of many so-called 'housekeeping genes', we tested 4 commonly used reference genes: *ACTB*, *GAPDH*, *PGK1* and *PPIA*. The expression stability of each gene across the samples was estimated with geNorm. *PGK1* and *PPIA* were indicated as the most stable, whereas *GAPDH* was the most variable, showing a trend toward upregulation in the AML samples (data not shown). This finding was consistent with the results of microarray analysis, in which *GAPDH* was in the list of DEGs between the AML and HV samples. Finally, 2 reference genes, *PGK1* and *PPIA*, were used as normalization factors. Gene expression was analyzed in the context of AML subtypes, mutation status and response to therapy (Figs. 3 and 4).

The most consistent results between the microarray and real-time PCR experiments were obtained for the *STMN1*

gene, which was significantly induced in AML compared with HV ( $p = 0.00044$ ), although the fold change was somewhat lower (~4.5-fold compared with an almost 8-fold change in the microarray data analysis) (Fig. 3A). Similar to the microarray data analysis results, *STMN1* upregulation was visible in each AML subgroup compared with HV (t-test  $p = 0.038$ - $0.000019$ ) (Figs. 3 and 4). There were no significant differences in *STMN1* expression between particular AML subgroups with the following two exceptions: *NPM1*/*FLT3*<sup>+</sup> vs. *NPM1*/*FLT3*<sup>-</sup> ( $p = 0.015$ ) and *NPM1*/*FLT3*<sup>+</sup> vs. *NPM1*<sup>+</sup>/*FLT3*<sup>-</sup> ( $p = 0.029$ ). The highest *STMN1* expression was observed in the *NPM1*/*FLT3*<sup>+</sup> subgroup (Fig. 4D).

As regards *NPM1* gene expression, we observed a trend toward an upregulation in AML (Fig. 3A); however, the increase in *NPM1* expression was statistically significant in only one comparison (RES vs. HV; t-test  $p = 0.021$ ) (Fig. 3C and D).

Real-time PCR-based analysis of *S100A8* and *S100A9* genes confirmed their general suppression trend in AML or at least some AML subgroups compared to HV. The expression levels of these 2 relative genes, coding for calcium-binding proteins, highly correlated (Pearson's correlation, 1;  $p$ -value  $< 2.2 \times 10^{-16}$ ); however, a statistically significant decrease was observed only for *S100A9*: In the AML-M1 subtype compared with HV (t-test  $p = 0.0012$ ), as well as with AML-M2 (t-test  $p = 0.038$ ) (Fig. 3B), in *NPM1*-mutated AML vs. HV (t-test  $p = 0.013$ ) (Fig. 4B), irrespective of the *FLT3* mutation status

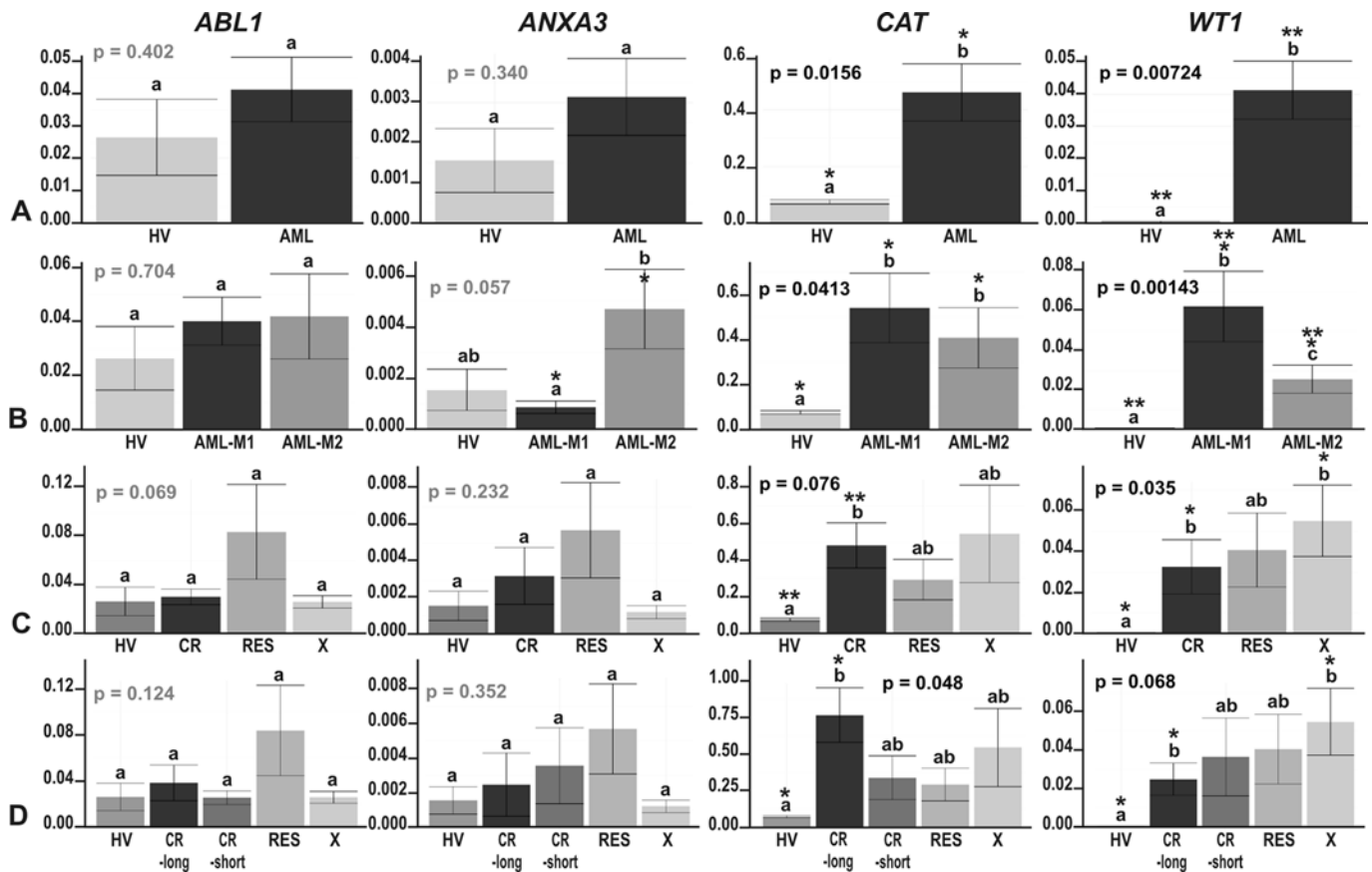


Figure 5. The results of ddPCR-based expression analysis of 4 genes (*ABL1*, *ANXA3*, *CAT* and *WT1*) in (A) acute myeloid leukemia (AML) compared with healthy volunteers (HV) samples; (B) in the context of the AML French-American-British (FAB) subtypes, M1 and M2; and in the context of the response to therapy, with the AML divided into (C) 3 (CR, RES, X) subgroups or (D) 4 subgroups (CR\_long, CR\_short, RES, X). The y-axes show relative expression values of a studied gene compared to a reference gene. Each plot contains the ANOVA p-value obtained for a whole test. Pair-wise comparisons with statistically significant differences, verified with a t-test and HSD Tukey test, are indicated by letters and asterisk symbols above each bar. Bars showing the same letter indicate no significant difference ( $p > 0.05$ ). The numbers of asterisks denote the level of statistical significance: \* $p \leq 0.05$  and \*\* $p \leq 0.01$ .

(t-test  $p = 0.048$  for HV vs. *NPM1*<sup>+</sup>/*FLT3*<sup>-</sup> and t-test  $p = 0.01$  for HV vs. *NPM1*<sup>+</sup>/*FLT3*<sup>+</sup>) (Fig. 4D), and in the RES subgroup vs. HV (t-test  $p = 0.018$ ) (Fig. 3C and D).

*Comparisons of the results from the transcriptomic and proteomic studies.* As the same group of AML samples was also previously analyzed in a proteomic analysis in our laboratory (33,34), in this study, we attempted to compare the results of the AML transcriptome and proteome analyses. However, owing to the limitations of both approaches, the comparison could be made for only a small subset of genes/proteins. The AML-array consisted of probes that were complementary for >900 genes, representing ~4% of all human genes. However, the 2-DE-MS analysis of AML proteomes enabled the detection of <200 proteins (33), representing much <1% of all the human proteins. In detail, from the 184 unique proteins detected in the proteomic study, only 52 (28%) had corresponding gene-specific probes on the AML-array. From the 184 identified proteins, 40 were determined to be differentially accumulated in the studied samples, of which 20 were represented on the AML-array: 13 by gene-specific probes and 7 by the probes complementary to the related genes (from the same gene family). Half of the results of the proteomics and transcriptomic analyses were concordant or partially concordant, but the other half was discordant (Table V).

*Droplet digital PCR analysis.* To verify some of the discrepancies between the transcriptomic and proteomic results, we applied another quantitative PCR method, ddPCR, which is one of the most precise, sensitive and accurate PCR types. We expanded our research group to 20 HV samples and 41 AML samples. For the analysis, performed with a QX200 Droplet Digital PCR system (Bio-Rad), we selected 4 genes. Two of these, *ANXA3*, encoding Annexin 3, and *CAT*, encoding catalase, were determined as being differentially accumulated in the proteomics analyses. None of these genes were identified with the AML-array as being differentially expressed, and the expression trend was concordant for *CAT*, but was discordant for *ANXA3*. As a type of positive control, we used the *ABL1* oncogene, which was slightly, but significantly, increased in AML-M2 and AML-RES compared with HV in the microarray experiment. Additionally, we analyzed Wilms tumor 1 gene (*WT1*), which has recently been described as overexpressed and prognostically relevant in most acute leukemias (39,40), but was not included in our AML-array probe set. As a reference gene, we selected *PGK1*, on the basis of our previous real-time PCR analysis. As regards the *CAT* gene, we were able to multiplex reactions with a reference gene, due to the differences in PCR product sizes (Table II). For the *ABL1*, *ANXA3* and *WT1* genes, a reference gene was analyzed in a separate reaction, but always within the same run. The

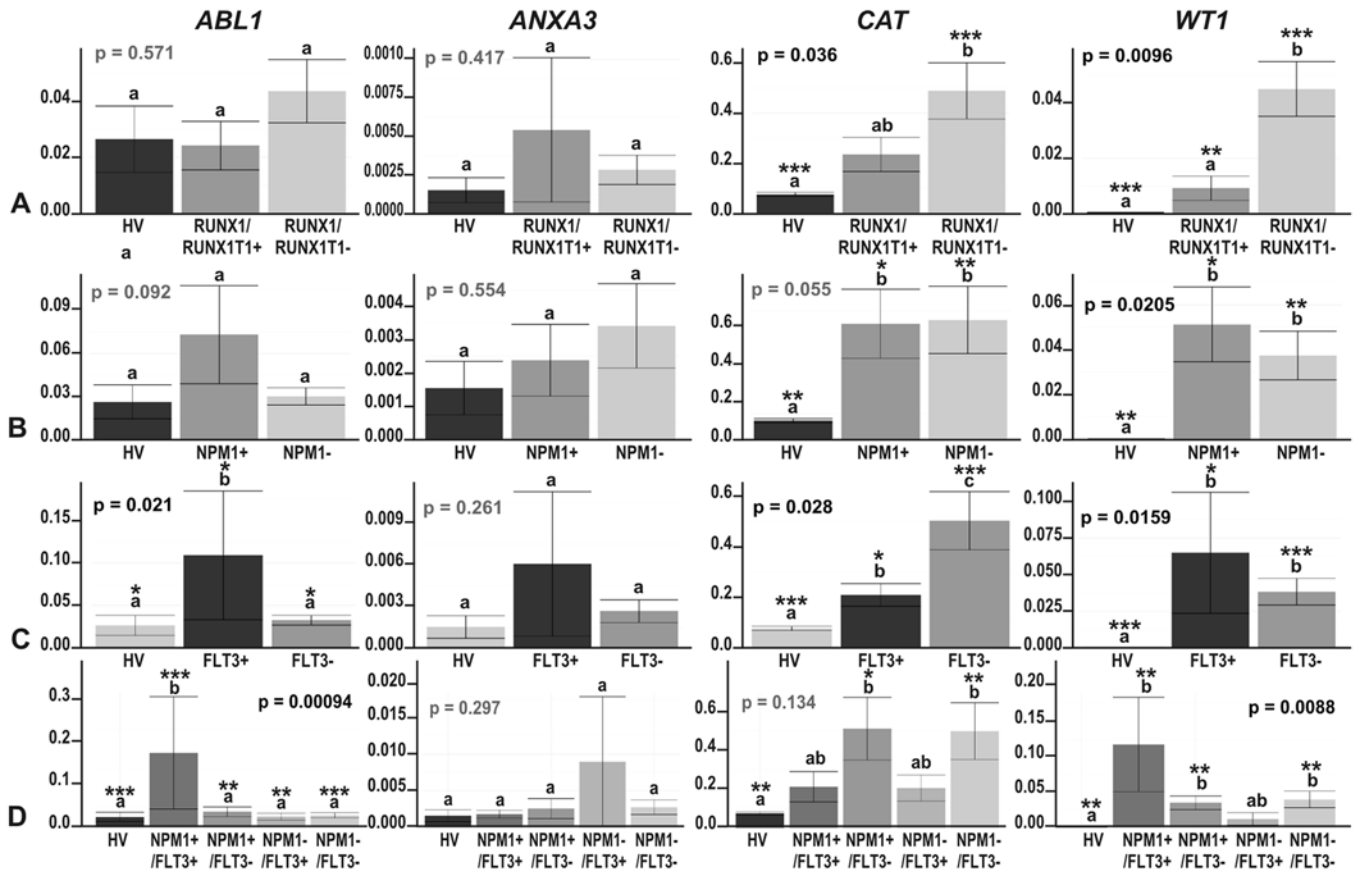


Figure 6. The results of ddPCR-based expression analysis of 4 genes (*ABL1*, *ANXA3*, *CAT* and *WT1*) in acute myeloid leukemia (AML) compared with healthy volunteers (HV) samples, with the AML divided according to the mutation status of (A) *RUNX1/RUNX1T1*; (B) *NPM1*; (C) *FLT3*; and (D) *NPM1* and *FLT3* together. The y-axes show relative expression values of a studied gene compared to a reference gene. Each plot contains the ANOVA p-value obtained for a whole test. Pair-wise comparisons with statistically significant differences, verified with a t-test and HSD Tukey test, are indicated by letters and asterisk symbols above each bar. Bars showing the same letter indicate no significant difference ( $p > 0.05$ ). The numbers of asterisks denote the level of statistical significance: \* $p \leq 0.05$ , \*\* $p \leq 0.01$  and \*\*\* $p \leq 0.001$ .

data from duplicate experiments were separately processed in Quanta Soft version 1.5.38.1118 software (Bio-Rad). The relative expression value of each gene was calculated as the ratio of droplet numbers for the studied gene vs. the reference gene. The results of the statistical analysis, performed in R Bioconductor, are presented in Figs. 5 and 6.

Our positive control gene, *ABL1*, revealed a trend towards an upregulation in AML, statistically significant in *FLT3*<sup>-</sup> and *NPM1*-mutated AML vs. HV (HSD Tukey test  $p = 0.02$  for HV vs. *FLT3*<sup>+</sup>; HSD Tukey test  $p = 0.0003$  for HV vs. *NPM1*/*FLT3*<sup>+</sup>) (Fig. 6C and D). *ABL1* gene expression was also significantly upregulated in the *FLT3*<sup>+</sup> samples when compared with the *FLT3*<sup>-</sup> samples (HSD Tukey test  $p = 0.02$ ) (Fig. 6C) and significantly different in the following comparisons: *NPM1*/*FLT3*<sup>-</sup> vs. *NPM1*/*FLT3*<sup>+</sup> (HSD Tukey test  $p = 0.0003$ ), *NPM1*/*FLT3*<sup>+</sup> vs. *NPM1*/*FLT3*<sup>-</sup> (HSD Tukey test  $p = 0.002$ ) and *NPM1*/*FLT3*<sup>+</sup> vs. *NPM1*/*FLT3*<sup>+</sup> (HSD Tukey test  $p = 0.0097$ ). The *ANXA3* gene was generally expressed at a very low level, with a trend towards overexpression in the AML vs. HV; however, the greatest increase in *ANXA3* expression was observed in AML-M2 (Fig. 5B). The only statistically significant difference in the expression of this gene was observed between AML-M1 and AML-M2 (t-test  $p = 0.023$ ) (Fig. 5B), what definitively confirmed the proteomics results. Partially concordant results were obtained for the *CAT*

gene. In agreement with the proteomics results, we observed a significant increase in *CAT* expression in AML and some AML subgroups compared with HV (Figs. 5 and 6, t-test  $p = 0.0096$  for HV vs. AML-M1; t-test  $p = 0.022$  for HV vs. AML-M2; t-test  $p = 0.00085$  for HV vs. *RUNX1/RUNX1T1*;  $p = 0.006$  for HV vs. *NPM1*;  $p = 0.02$  for HV vs. *NPM1*<sup>+</sup>;  $p = 0.00085$  for HV vs. *FLT3*<sup>+</sup>; t-test  $p = 0.04$  for HV vs. *FLT3*<sup>+</sup>; t-test  $p = 0.008$  for HV vs. *NPM1*/*FLT3*<sup>+</sup>; t-test  $p = 0.03$  for HV vs. *NPM1*/*FLT3*<sup>+</sup>). We also detected a significant increase in *CAT* expression in the *FLT3*<sup>-</sup> compared to the *FLT3*<sup>+</sup> samples (t-test  $p = 0.023$ ). However, the differences in the *CAT* gene expression levels between the M1 and M2 AML subtypes were subtle and not significant (t-test  $p = 0.52$ ), in contrast to the proteomics findings (Fig. 5B). As regards the response to therapy, the only statistically significant difference, and the most elevated *CAT* expression was observed in the CR and CR-long AML subgroups (t-test  $p = 0.0044$  for HV vs. CR and t-test  $p = 0.013$  for HV vs. CR-long) (Fig. 5C and D). As regards the *WT1* gene, the ddPCR experiment revealed an evident and statistically significant upregulation of this gene in all AML subgroups, whereas in the HV samples, its expression was scarcely detectable (t-test  $p = 0.046$ - $0.000066$ ) (Figs. 5 and 6). An interesting observation was the increasing trend in *WT1* expression in the therapy-related AML subgroups: The higher the *WT1* level, the less responsive was AML to therapy (Fig. 5C and D). High

Table IV. The list of 83 differentially expressed genes between AML and HV samples.

Gene name (ID)	Gene description	Gene function	Log <sub>2</sub> FC	Adjusted p-value
<b>A. Genes overexpressed in AML</b>				
<i>STMN1</i> (3925)	Stathmin 1	Regulation of the microtubule filament system by destabilizing microtubules	2.91	1.67x10 <sup>-10</sup>
<i>KITLG</i> (4254)	KIT ligand	The ligand of the tyrosine-kinase receptor, required in hematopoiesis	2.38	0.0088481
<i>CDK6</i> (1021)	Cyclin-dependent kinase 6	Cell cycle regulation, G1 phase progression and G1/S transition; altered expression in multiple human cancers	1.51	1.88x10 <sup>-9</sup>
<i>MCM5</i> (4174)	Minichromosome maintenance complex component 5	DNA replication, cell cycle regulation; upregulated in the transition from the G0 to G1/S phase	1.42	0.0001986
<i>KRAS</i> (3845)	KRAS proto-oncogene, GTPase	Oncogene, member of the small GTPase superfamily; mutated in various malignancies	1.42	0.0005584
<i>CEBPA</i> (1050)	CCAAT/enhancer binding protein $\alpha$	Transcription factor, modulator of the expression of genes involved in cell cycle regulation and body weight homeostasis; mutated in AML	1.32	0.0006135
<i>MYC</i> (4609)	MYC proto-oncogene, bHLH transcription factor	Regulation of cell cycle progression, apoptosis and cellular transformation; amplified in numerous human cancers, translocated in Burkitt's lymphoma and multiple myeloma	1.26	4.32x10 <sup>-7</sup>
<i>ANGPT1</i> (284)	Angiotensinogen 1	Role in vascular development and angiogenesis, interactions between the endothelium and surrounding matrix, blood vessel maturation and stability	1.25	0.0022923
<i>SRGN</i> (5552)	Serglycin	Hematopoietic cell granule proteoglycan, associated with complex of granzymes and perforin, and granule-mediated apoptosis	1.17	0.0064793
<i>RPLP0</i> (6175)	Ribosomal protein lateral stalk subunit P0	Ribosomal protein, component of the 60S subunit, protein synthesis	1.14	0.0000199
<i>ENO1</i> (2023)	Enolase 1	Glycolytic enzyme, structural lens protein (tau-crystallin)	1.14	0.0000584
<i>SET</i> (6418)	SET nuclear proto-oncogene	Inhibitor of histone acetylases (HAT), nucleosome acetylation and transcription	1.07	0.0000584
<i>MYB</i> (4602)	MYB proto-oncogene, transcription factor	Transcription regulator, regulation of hematopoiesis, aberrantly expressed, rearranged or translocated in leukemias and lymphomas	0.88	0.0058191
<i>GAL</i> (51083)	Galanin and GMAP prepropeptide	Nociception, feeding and energy homeostasis, osmotic regulation and water balance	0.87	0.0015198
<i>HSPA8</i> (3312)	Heat shock protein family A (Hsp70) member 8	Chaperone, correct folding of nascent polypeptides, disassembly of clathrin-coated vesicles in transport of cell membrane components (ATPase)	0.72	0.0014811
<i>ADRA2C</i> (152)	Adrenoceptor $\alpha$ 2C	G protein-coupled receptor, regulation of neurotransmitter release at lower levels of nerve activity	0.70	0.0017407
<i>HSPD1</i> (3329)	Heat shock protein family D (Hsp60) member 1	Chaperone, folding and assembly of newly imported proteins in the mitochondria, signalling molecule in the innate immune system	0.61	0.0058191
<i>IGFBP7</i> (3490)	Insulin like growth factor (IGF) binding protein 7	Regulation of IGF availability in body fluids and tissues and modulation of IGF binding to its receptors, stimulation of prostacyclin production and cell adhesion	0.59	0.0014913
<i>RASSF5</i> (83593)	Ras association domain family member 5	Tumor suppressor, inactivated in a variety of cancers, regulation of lymphocyte adhesion, cell growth suppression	0.58	0.0016728
<i>EEF1G</i> (1937)	Eukaryotic translation elongation factor 1 g	Subunit of the elongation factor-1 complex, enzymatic delivery of aminoacyl tRNAs to the ribosome	0.56	0.0002401
<i>GSN</i> (2934)	Gelsolin	Calcium-regulated protein, assembly and disassembly of actin filaments	0.55	0.0005526

Table IV. Continued.

Gene name (ID)	Gene description	Gene function	Log <sub>2</sub> FC	Adjusted p-value
<i>ZNF22</i> (7570)	Zinc finger protein 22	DNA binding, transcription regulation	0.51	0.0054429
<i>GAPDH</i> (2597)	Glyceraldehyde-3-phosphate dehydrogenase	Carbohydrate metabolism, phosphorylation of glyceraldehyde-3-phosphate in the presence of inorganic phosphate and nicotinamide adenine dinucleotide (NAD)	0.49	0.0015715
<i>KIT</i> (3815)	KIT proto-oncogene receptor tyrosine kinase	Transmembrane receptor for MGF (mast cell growth factor, stem cell factor), mutated in gastrointestinal tumors, mast cell disease, AML and piebaldism	0.46	0.0017591
<i>HOXA10</i> (3206)	Homeobox A10	Transcription factor, regulation of gene expression, morphogenesis, differentiation, fertility, embryo viability, and hematopoietic lineage commitment	0.43	0.0047731
<i>ERCC2</i> (2068)	ERCC excision repair 2, TFIIH core complex helicase subunit	DNA damage repair, transcription-coupled nucleotide excision repair, member of the basal transcription factor BTF2/TFIIH complex	0.43	0.0005584
<i>ATP6V0C</i> (527)	ATPase H <sup>+</sup> transporting V0 subunit c	Component of vacuolar multisubunit enzyme ATPase (V-ATPase), acidification of eukaryotic intracellular organelles, necessary for protein sorting, zymogen activation, receptor-mediated endocytosis, synaptic vesicle proton gradient generation	0.43	0.0080978
<i>HSPA9</i> (3313)	Heat shock protein family A (Hsp70) member 9	Role in cell proliferation, stress response and maintenance of the mitochondria	0.42	0.0026984
<i>ARHGEF12</i> (23365)	Rho guanine nucleotide exchange factor 12	Numerous cellular processes initiated by extracellular stimuli through G protein-coupled receptors, fusion partner in AML	0.42	0.0014811
<i>PDE3B</i> (5140)	Phosphodiesterase 3B	Regulation of energy metabolism, energy homeostasis and energy intake	0.42	0.0046975
<i>HOXB6</i> (3216)	Homeobox B6	DNA binding, sequence-specific transcription factor, regulation of e.g. lung and skin development	0.40	0.0000475
<i>HSP90AB1</i> (3326)	Heat shock protein 90α family class B member 1	Signal transduction, protein folding and degradation, morphological evolution, role in gastric apoptosis and inflammation	0.39	0.0006700
<i>ARF1</i> (375)	ADP ribosylation factor 1	Phospholipase D activator, a role in vesicular trafficking, intra-Golgi transport	0.38	0.0080978
<i>CTSD</i> (1509)	Cathepsin D	Pepsin-like activity, role in protein turnover and proteolytic activation of hormones and growth factors	0.37	0.0086744
<i>MAP7</i> (9053)	Microtubule associated protein 7	Microtubule stabilization, essential for cell polarization, differentiation and spermatogenesis	0.37	0.0058191
<i>ITGB4</i> (3691)	Integrin subunit β4	Mediation in cell-matrix or cell-cell adhesion, gene expression and cell growth, receptor for the laminins, pivotal role in the biology of invasive carcinoma	0.36	0.0058191
<i>MYH11</i> (4629)	Myosin heavy chain 11	Major contractile protein, rearranged in AML of the M4Eo subtype	0.35	0.0020442
<i>PRKAR1B</i> (5575)	Protein kinase cAMP-dependent type I regulatory subunit β	Signaling pathway of the second messenger cAMP, regulation of ion transport, metabolism, and transcription	0.32	0.0080978
<i>PKM</i> (5315)	Pyruvate kinase M1/2	Glycolysis, mediation of cellular metabolic effects induced by thyroid hormones, role in bacterial pathogenesis	0.31	0.0006463
<i>TUBB</i> (203068)	Tubulin β class I	Structural component of microtubules	0.29	0.0081504
<i>MNI</i> (4330)	MNI proto-oncogene, transcriptional regulator	Translocated in meningioma, myeloproliferation stimulation, leukemogenesis	0.25	0.0070082

Table IV. Continued.

Gene name (ID)	Gene description	Gene function	Log <sub>2</sub> FC	Adjusted p-value
<b>B, Genes underexpressed in AML</b>				
<i>IFITM1</i> (8519)	Interferon induced transmembrane protein 1	Regulation of angiogenesis, tumorigenesis	-2.05	0.0000584
<i>LTB</i> (4050)	Lymphotoxin β	Induction of the inflammatory response system, role in normal development of lymphoid tissue	-2.00	1.29x10 <sup>-7</sup>
<i>FCN1</i> (2219)	Ficolin 1	Plasma protein with elastin-binding activity, expressed in the peripheral blood leukocytes	-1.93	0.0000173
<i>BIRC3</i> (330)	Bleuloviral IAP repeat containing 3	Inhibition of apoptosis by binding to tumor TRAF1 and TRAF2 necrosis factor receptor-associated factors	-1.90	0.0014913
<i>LYZ</i> (4069)	Lysozyme	Antimicrobial agent, cleavage of bacterial cell wall peptidoglycan	-1.85	0.0005526
<i>ADD3</i> (120)	Adducin 3	Membrane skeletal protein, assembly of spectrin-actin network; expression restricted to brain and hematopoietic tissues	-1.60	0.0014913
<i>S100A9</i> (6280)	S100 calcium binding protein A9	Regulation of cell cycle progression and differentiation, inhibition of casein kinase, antifungal and antibacterial activity	-1.59	0.0014811
<i>FCER1G</i> (2207)	Fc fragment of IgE receptor Ig	Key molecule involved in allergic reactions	-1.39	0.0006135
<i>PTPRE</i> (5791)	Protein tyrosine phosphatase, receptor type E	Signaling molecule, regulation of cell growth, differentiation, mitotic cycle and oncogenic transformation	-1.39	0.0024662
<i>CD74</i> (972)	CD74 molecule	Associates with class II major histocompatibility complex (MHC), chaperone regulating antigen presentation for immune response, mediation in survival pathways and cell proliferation	-1.23	0.0058191
<i>TMSB4X</i> (7114)	Thymosin β4, X-linked	Actin sequestering protein, regulation of actin polymerization, cell proliferation, migration, and differentiation	-1.05	1.32x10 <sup>-8</sup>
<i>PF4</i> (5196)	Platelet factor 4	Member of the CXC chemokine family, involved in platelet aggregation, inhibitor of hematopoiesis, angiogenesis and T-cell function	-0.97	0.0002201
<i>B2M</i> (567)	β-2-microglobulin	Serum protein associating with the MHC class I heavy chain on the surface of nucleated cells, antibacterial activity	-0.95	0.0006700
<i>HLA-DPBI</i> (3115)	Major histocompatibility complex, class II, DP β1	Central role in the immune system by presenting peptides derived from extracellular proteins, expressed in B lymphocytes, dendritic cells and macrophages	-0.77	0.0025915
<i>CSF3R</i> (1441)	Colony stimulating factor 3 receptor	Cytokine controlling production, differentiation, and function of granulocytes, involvement in cell surface adhesion and recognition processes	-0.71	0.0025443
<i>HOXA9</i> (3205)	Homeobox A9	DNA-binding transcription factor, regulation of gene expression, morphogenesis, and differentiation, translocated in myeloid leukemias	-0.70	0.0006135
<i>CCL5</i> (6352)	C-C motif chemokine ligand 5	Chemokine involved in immunoregulatory and inflammatory processes, chemoattractant for blood monocytes, memory T helper cells and eosinophils	-0.53	0.0033854
<i>CCL3</i> (6348)	C-C motif chemokine ligand 3	Small inducible cytokine, macrophage inflammatory protein 1 α, role in inflammatory responses	-0.51	0.0034134
<i>RARA</i> (5914)	Retinoic acid receptor α	Nuclear retinoic acid receptor, transcription regulation in a ligand-dependent manner, regulation of development, differentiation, apoptosis,	-0.49	0.0053657
<i>CCL19</i> (6363)	C-C motif Chemokine ligand 19	granulopoiesis, and clock genes, translocated in acute promyelocytic leukemia	-0.46	0.0000612
<i>NFKBIA</i> (4792)	NFKB inhibitor α	Cytokine involved in immunoregulatory and inflammatory processes, antimicrobial, role in normal lymphocyte recirculation and homing	-0.46	0.0054429
		Interactions with REL dimers to inhibit NF-κB/REL complexes involved in inflammatory responses		



Table IV. Continued.

Gene name (ID)	Gene description	Gene function	Log <sub>2</sub> FC	Adjusted p-value
<i>TNFSF10</i> (8743)	TNF superfamily member 10	Cytokine from the tumor necrosis factor (TNF) ligand family, preferential induction of apoptosis in transformed and tumor cells	-0.46	0.0033432
<i>CD52</i> (1043)	CD52 molecule	Lymphocyte surface antigen, involved in fertilisation and response to therapy in large granular lymphocytic leukemia, AML and MDS	-0.45	0.0095319
<i>PLBD1</i> (79887)	Phospholipase B domain containing 1	Role in the defence against microorganisms; generation of lipid mediators of inflammation	-0.43	0.0058191
<i>CAPN10</i> (11132)	Calpain 10	Calcium-dependent cysteine protease, associated with type 2 or non-insulin-dependent diabetes	-0.38	0.0005178
<i>STAT5B</i> (6777)	Signal transducer and activator of transcription 5B	Transcription factor, signal transduction triggered by IL2, IL4, CSF1, and growth hormones, involved in apoptosis, adult mammary gland development, and sexual dimorphism of liver gene expression	-0.36	0.0026984
<i>PGKI</i> (5230)	Phosphoglycerate kinase 1	Glycolytic enzyme, conversion of 1,3-diphosphoglycerate to 3-phosphoglycerate, involved in angiogenesis of tumor cells	-0.35	0.0064868
<i>RALGDS</i> (5900)	Ral guanine nucleotide dissociation stimulator	Effector of Ras-related GTPase, signaling for a variety of cellular processes	-0.35	0.0070755
<i>SPTBN1</i> (6711)	Spectrin $\beta$ , non-erythrocytic 1	Actin crosslinking and molecular scaffold protein, cytoskeleton functioning, determination of cell shape, arrangement of transmembrane proteins, and organization of organelles	-0.35	0.0056936
<i>BTG1</i> (694)	BTG anti-proliferation factor 1	Anti-proliferative activity, co-activator of cell differentiation, regulation of cell growth	-0.34	0.0079167
<i>TRADD</i> (8717)	TNFRSF1A associated via death domain	Programmed cell death signaling and NF- $\kappa$ B activation, suppression of TRAF2-mediated apoptosis	-0.34	0.0005526
<i>CYP2E1</i> (1571)	Cytochrome P450 family 2 subfamily E member 1	Involved in drug metabolism, synthesis of cholesterol, steroids and other lipids, induced by ethanol, the diabetic state, and starvation	-0.33	0.0052990
<i>MAP4K2</i> (5871)	Mitogen-activated protein kinase kinase kinase 2	Involved in B-cell differentiation, activated by TNF- $\alpha$ , interacting with TNF receptor-associated factor 2 (TRAF2)	-0.32	0.0001674
<i>IGF1</i> (3479)	Insulin like growth factor 1	Involved in mediating growth and development	-0.32	0.0032632
<i>STK4</i> (6789)	Serine/threonine kinase 4	Acting upstream of the stress-induced mitogen-activated protein kinase cascade, involved in apoptosis and chromatin condensation induction	-0.31	0.0022923
<i>HCK</i> (3055)	HCK proto-oncogene, Src family tyrosine kinase	Hemopoietic protein, present myeloid and B-lymphoid cell lineages, role in activation of the respiratory burst, neutrophil migration and degranulation of neutrophils	-0.29	0.0059276
<i>PDGFRB</i> (5159)	Platelet-derived growth factor receptor $\beta$	Cell surface tyrosine kinase receptor for growth factors, development of the cardiovascular system, rearrangement of the actin cytoskeleton	-0.28	0.0001623
<i>RHOB</i> (388)	Ras homolog family member B	Tumor suppressor, regulation of cytoskeletal dynamics and vesicle trafficking, control of endothelial barrier function	-0.28	0.0048010
<i>XBPI</i> (7494)	X-box binding protein 1	Transcription factor regulating MHC class II genes, increase of viral protein expression	-0.27	0.0014913
<i>IFNA1</i> (3439)	Interferon $\alpha 1$	Antiviral activity, pathogen clearance and tissue inflammation	-0.26	0.0024163
<i>PIMI1</i> (5292)	Pim-1 proto-oncogene, serine/threonine kinase	Signal transduction in blood cells, propagation of cell proliferation and survival, tumorigenesis, overexpressed in hematopoietic malignancies and prostate cancer	-0.24	0.0013396
<i>PXN</i> (5829)	Paxillin	Cytoskeletal protein involved in actin-membrane attachment at sites of cell adhesion to the extracellular matrix (focal adhesion)	-0.24	0.0086744

The genes were identified with a significance level of  $\alpha$  0.01 and ranked according to the normalized expression fold change (Log<sub>2</sub>FC). p-values were corrected for multiple testing. Gene descriptions and functions come from the NCBI gene database.

Table V. Comparisons of the results from the transcriptomic and proteomic studies.

Protein identified in the proteomic study (33)	Corresponding gene	Microarray probe	Protein accumulation	Gene expression	Concordant
Actin $\gamma$ 1	<i>ACTG1</i>	Target-specific	In HV present only in BM, in AML higher in CR-short	In HV higher in PB, in AML higher in CR-short	Partially
$\alpha$ -actinin	<i>ACTN4</i>	For <i>ACTN1</i>	Higher in AML	Slightly lower in AML	No
Fructose-bisphosphate aldolase A	<i>ALDOA</i>	For <i>ALDOC</i>	In HV present only in BM	In HV higher in PB	No
Annexin I	<i>ANXA1</i>	Target-specific	In HV higher in BM, higher in AML vs. HV and in CR vs. RES AML	In HV higher in BM, no difference between AML and HV, lower in CR vs. RES AML	No
Annexin III	<i>ANXA3</i>	Target-specific	In HV higher in PB, in AML present only in M2	In HV higher in BM, higher in AML vs. HV, higher in AML M1 vs. M2	No
Rho GDP-dissociation inhibitor 2	<i>ARHGDIB</i>	For <i>ARHGAP4</i> , <i>ARHGEF1</i> , <i>ARHGEF12</i>	In HV higher in BM, higher in AML vs. HV	In HV higher in PB, ARHGEF12 and ARHGAP4 - higher in AML, ARHGEF1 - slightly lower in AML	Partially
Catalase	<i>CAT</i>	Target-specific	In HV higher in PB, higher in AML and in AML M2 vs. M1	In HV higher in PB, slightly higher in AML vs. HV, higher in AML M2 vs. M1	Yes
Cofilin-1	<i>CFL1</i>	Target-specific	In HV higher in PB	In HV slightly higher in PB	Yes
$\alpha$ -enolase (ENO1 protein)	<i>ENO1</i>	Target-specific	In HV higher in BM	In HV higher in PB, significantly higher in AML vs. HV	No
Glutathione transferase $\omega$	<i>GSTO</i> (1,2)	For <i>GSTP1</i>	Present only in AML CR	Significantly higher in AML, slightly lower in CR	No
Tumor rejection antigen (Gp96)	<i>HSP90B1</i>	Target-specific	In HV higher in PB, lower in AML vs. HV	In HV higher in PB, higher in AML vs. HV	Partially
L-Plastin (lymphocyte cytosolic protein 1)	<i>LCPI</i>	Target-specific	Present only in AML M2	Significantly lower in AML vs. HV, higher in AML M1	No
Pyruvate kinase	<i>PKM</i>	Target-specific	Much higher in AML vs. HV	Significantly higher in AML vs. HV	Yes
Purine nucleoside phosphorylase	<i>PNP</i>	Target-specific	In HV higher in BM, lower in AML	In HV higher in PB, higher in AML	No
Acetyl-cypa:cyclosporine complex [peptidylprolyl isomerase A (cyclophilin A)]	<i>PPIA</i>	For <i>PPIF</i>	In HV higher in PB	In HV no difference between PB and BM, higher in AML vs. HV	No
Peroxiredoxin-2	<i>PRDX2</i>	Target-specific	In HV higher in BM, higher in AML vs. HV PB, lower in AML vs. HV BM	In HV higher in BM, slightly lower in AML vs. HV	Partially
Histone-binding protein RBBP4 (retinoblastoma binding protein)	<i>RBBP4</i>	Target-specific	Higher in AML, in HV merely detectable	Slightly lower in AML vs. HV	No
Tropomyosin $\alpha$	<i>TPM1</i>	Target-specific	In HV present only in PB, much lower in AML vs. HV	In HV higher in BM, lower in AML vs. HV	Partially
Tubulin $\beta$	<i>TUBB</i>	Target-specific	In HV higher in BM, lower in AML vs. HV	In HV higher in BM, higher in AML vs. HV	Partially
14-3-3 protein $\zeta/\delta$	<i>YWHAZ</i>	For <i>YWHAQ</i>	In HV higher in PB, lower in AML vs. HV	In HV higher in PB, slightly lower in AML vs. HV	Yes

levels of *WT1* were also detected in the AML-M1 (Fig. 5B) and AML samples without the *RUNX1/RUNX1T1* mutation (Fig. 6A), but harboring *NPM1*, *FLT3* or both of these mutations (Fig. 6B-D). The differences across the particular AML subgroups were not significant, apart from 2 compari-

sons: AML-M1 vs. AML-M2, where *WT1* was upregulated in AML-M1 (HSD Tukey's test  $p=0.039$ ) (Fig. 5B) and *RUNX1/RUNX1T1*<sup>+</sup> vs. *RUNX1/RUNX1T1*<sup>-</sup>, where *WT1* was upregulated in AML without translocation t(8;21) (t-test  $p=0.0023$ ) (Fig. 6A).

Table VI. The results of comparative analysis of our data and 3 GEO datasets.

Dataset	Our data	GDS3057	GDS1059	GDS2251
Our data		47.8 (51.8)	51.9 (59.8)	47.8 (78.3)
GDS3057	<i>15.5</i>		43.3 (47.4)	39.3 (58.1)
GDS1059	<i>31.3</i>	<i>20.9</i>		35.3 (64.2)
GDS2251	<i>21.7</i>	<i>10.0</i>	<i>27.1</i>	

Only 238 genes identified as differentially expressed in our data (using AML-array, RT-qPCR and proteomics) were considered. The numbers refer to the percentage of concordant genes (the same trend in expression; regular font; the numbers in parentheses include also partially concordant genes) or discordant genes (the opposite trend; italics). Each percentage value was calculated based on the number of genes represented in both compared data sets (214-229).

**Correlations among the molecular and clinical features of AML.** In order to identify links between gene expression measured by RT-qPCR, the mutation status and the clinical characteristics of the patients with AML (WBC, age and sex), we performed a series of statistical tests (t-test, one- and two-way ANOVA, Tukey multiple comparison of means and Pearson's correlation). The strongest correlations were observed between the WBC counts and the AML FAB subtypes (one-way ANOVA,  $p=0.0101$ , WBC counts were higher in AML-M1), WBC counts and *NPM1* mutation status (one-way ANOVA,  $p=0.0229$ ), WBC counts and *FLT3* mutation status (one-way ANOVA,  $p=0.0308$ ), and WBC counts and both *FLT3* and *NPM1* mutation status (two-way ANOVA,  $p=0.0160$ ), and the highest WBC count was observed in mutated AML samples.

As regards the effects of age, we observed a moderately positive correlation between patient age and *NPM1* gene expression (Pearson's correlation, 0.348;  $p=0.1222$ ), a moderately negative correlation between age and the expression of the 2 genes, *S100A9* (Pearson's correlation, -0.380;  $p=0.0899$ ) and *ANXA3* (Pearson's correlation, -0.33;  $p=0.046$ ) and a correlation between age and the mutation status of *NPM1* (one-way ANOVA,  $p=0.0411$ ) or *NPM1* and *FLT3* together (two-way ANOVA,  $p=0.0446$ ). There were no correlations between the RT-qPCR-determined expression of any other gene and age (Pearson's correlations equal to -0.23, 0.019, 0.15, 0.07 and 0.2 for *S100A8*, *STMN1*, *ABL1*, *CAT* and *WT1*, respectively). We also did not find any correlations between the gene expression levels and sex (one-way ANOVA,  $p$ -values equal to 0.45, 0.659, 0.286, 0.555, 0.633, 0.302, 0.628 and 0.263 for *NPM1*, *S100A8*, *S100A9*, *STMN1*, *ABL1*, *ANXA3*, *CAT* and *WT1*, respectively) or WBC count (Pearson's correlations equal to -0.02, -0.25, -0.27, -0.02, 0.07, -0.19, -0.18 and 0.28 for *NPM1*, *S100A8*, *S100A9*, *STMN1*, *ABL1*, *ANXA3*, *CAT* and *WT1*, respectively).

Of note, there was no correlation between *NPM1* gene expression and the *NPM1* mutation status (one-way ANOVA;  $p=0.634$ ). The presence of the translocation t(8;21) and fusion gene *RUNX1/RUNX1T1* did not correlate with any molecular or clinical characteristic.

**Gene expression database exploration.** To compare our results with other AML gene expression profiling results, we explored the Gene Expression Omnibus (GEO) database ([www.ncbi.nlm.nih.gov/sites/GDSbrowser](http://www.ncbi.nlm.nih.gov/sites/GDSbrowser)) to identify the most relevant datasets. We selected 7 datasets, including 6 derived from Affymetrix Gene Chips, the most commonly used microarray platform, and one from Agilent microarrays. Among these datasets, only 3 (GDS3057, GDS1059 and GDS2251) contained healthy control samples. These 3 datasets were screened with 238 names of genes, which we had identified as differentially expressed between AML (or particular AML subgroups) and HV by using the AML-array, RT-qPCR and proteomics. Table VI shows the results of comparative analysis. The percentage of genes with an expression trend concordant in our data and any GEO dataset, was in the range 47.8-51.9% (mean, 49.2%) or in the range 51.8-78.3% (mean, 65.3%), when including partially concordant genes, for which expression trends were concordant for some (but not all) conditions/cell lines/microarray probes. Interestingly, the level of coincidence between GEO datasets was much lower: The percentage of concordant genes remained in the range 35.3-43.4% (mean, 39.3%) or in the range 47.4-64.2% (mean, 56.6%), when including partially concordant genes. In reference to discordant genes, an opposite effect could be observed, although the difference was smaller: The percentage of discordant genes in comparative analysis between our data and any GEO data set was in the range 15.5-31.3% (mean, 22.8%) while within GEO datasets in the range 10.0-27.1% (mean, 19.3%). Analyzing 238 gene expression trends, we were able to select 45 strong candidate genes with expression trends concordant in our dataset and all 3 GEO datasets. In total, 26 genes (*ABCF1*, *ABL1*, *AK2*, *ANGPT1*, *BCR*, *CD34*, *CDK6*, *CEBPA*, *HOXA10*, *HSP90AB1*, *HSPA8*, *HSPA9*, *IGFBP7*, *MAP7*, *MCM5*, *MT1H*, *MYB*, *NPM1*, *RBBP4*, *RPLP0*, *SET*, *SLC25A1*, *SMAD3*, *STMN1*, *TRAF4* and *WT1*) were consequently increased in AML when compared to the normal control, whereas 19 were decreased in AML (*BTG1*, *CEBPB*, *CSF3R*, *CX3CR1*, *CYBB*, *FCER1G*, *FCN1*, *HCK*, *IGHM*, *LCPI*, *LGALS3*, *LYZ*, *PF4*, *S100A8*, *S100A9*, *STAT5B*, *STK4*, *TMSB4X* and *TRADD*). The above-mentioned list contained 14 (10 increased and 4 decreased) from the 23 genes presented in Fig. 1B, identified as the genes with the highest expression fold change in AML-array-based analysis, and one gene (*RBBP4*) identified in our data only by proteomic approach. Not all of these genes were up-to-date described as AML biomarkers. It is also worth mentioning that 2 members of the CCAAT/enhancer binding protein family of transcription factors, *CEBPA* and *CEBPB*, exhibited opposite expression trends in all studied datasets.

As regards FAB subtypes, we analyzed the expression trends of 6 genes, including 5 genes encoding proteins determined as differentially accumulated between AML-M1 and AML-M2 by proteomic approach (*ANXA3*, *CAT*, *LCPI*, *PGD* and *PRDX6*) (33) and one gene identified with ddPCR (*WT1*). In comparison to the GDS1064 dataset, referring to AML in different stages of maturation, we observed concordant results for only 2 genes (33%), *WT1* and *ANXA3*, the only 1 gene out of 5 selected by proteomic approach.

**Discussion**

Taking advantage of genomic tools, tremendous progress in the molecular studies of AML has been achieved (16,41). Although many studies have already been published in this

area, to the best of our knowledge, our research is the first transcriptomics analysis of the Polish adult AML population. Moreover, for the same group of patients, a proteomics analysis has also been performed (33). The number of samples was not high; however, the advantage was the preselection of the M1 and M2 FAB subtypes and a significant enrichment in CN-AML samples. Previous microarray-based AML analyses have often included more subtypes, but fewer patients. The present study is also one of the few reports of custom-made array applications in AML studies.

The majority of AML research has been conducted with the use of Affymetrix Gene Chips (19,22,42-44), and some studies have been conducted with large cDNA microarrays (21,45,46). Both platforms utilize arrays constructed from probes corresponding to at least several thousand genes. The advantages of boutique arrays are their lower price, higher flexibility and smaller laboratory infrastructure requirements. Comparative analysis of our results with the results of 3 other gene expression studies based on Affymetrix Gene Chips, proved the utility and reliability of the AML-array. The level of concordance was even higher for our results and any GEO dataset than between GEO datasets. However, we still observed discordant results for ~20% of genes, irrespectively of the datasets compared. There are 3 main reasons for this discrepancy: Different patients, different laboratories, and varying numbers of samples, all of which contribute to technical and biological bias.

The application of the boutique array presented herein enabled us to identify a set of genes differentiating AML and HV. However, we were not able to detect statistically significant differences between AML subgroups. The lack of success can be explained by a few factors: The method was not effective enough, the studied samples were not an accurate representation of the population, or the sample size was not sufficient. The limitation of the method is a pre-selected set of genes, which could be not adequate to distinguish between particular AML subgroups. Home-made microarray production could also contribute to more technical bias comparing to commercial gene chips. Based on our experience with microarray design, production, hybridization and data normalization, we performed many technical replicates, carefully inspected microarray images and filtered out all slides which did not respect quality criteria. As regards patients with AML, we did not apply additional selection criteria; we included all AML patients classified as M1 or M2 FAB subtypes at the time of our project. Unsupervised clustering revealed that the AML subpopulation was generally homogenous. In addition, some of the studied AML subgroups were represented by only a few samples, and thus statistical significance was more difficult to achieve. Probably, a substantial increase in the sample size could overcome this problem. Taking into account the above-mentioned limitations, we consider that microarray-based analysis should be always treated as a first-line screening tool. When precise gene expression measurements are needed, RT-qPCR, in particular its more sophisticated version, ddPCR, is more reliable.

Among the genes overexpressed in AML in the presented AML-array-based study, there were already-established AML markers, e.g., *KIT*, *MYH11*, *MNI*, *MPO*, *SET* and *HOXA10* (44,47,48), genes associated with AML or potential biomarkers, such as *STMNI*, *CDK6* and *ANGPT1*, or genes not

yet discussed in the context of AML, such as *RPLP0* or *ENO1*, reported in neoplasms other than leukemia (49,50). As these genes often play fundamental roles in cell metabolism and function, their upregulation may be explained by the needs of the highly proliferating cancer cells. The *STMNI* gene, which encodes stathmin 1, formerly known as oncoprotein 18 (Op18), was the most significantly overexpressed gene that we observed in AML. The upregulation of this gene, confirmed by real-time PCR, is consistent with the results of other gene expression studies. *STMNI*, highly expressed in acute leukemias, lymphomas and intensively proliferating cells (51,52) and decreased after the induction of cell differentiation (53), is a good AML biomarker candidate and potential therapeutic target. Other possible candidates are *CDK6*, which encodes one of the cyclin dependent kinase and cell cycle regulators and prevents differentiation and apoptosis (54), and *ANGPT1*, which encodes a proangiogenic protein abundant in AML (55) and early myeloblast cell lines (56).

Similarly, the suppression of numerous genes in the AML samples detected with the AML-microarray was consistent with data in the literature. The examples are *PF4*, which is among the 10 hematopoietic-specific genes found to be significantly downregulated in *CD34<sup>+</sup>* cells obtained from patients with therapy-related AML (57), or *TMSB4X*, which encodes thymosin  $\beta$ 4 and is a regulator of actin polymerization, cell proliferation, migration and differentiation. As *TMSB4X* expression was higher in the lymphoid than the granulocytic lineage, and its transcript levels increased during granulocyte maturation, it has been proposed to be a marker of differentiation in hematopoietic cells (58). For some genes, such as *FCN1*, which encodes ficolin 1 and was the second most downregulated gene in AML in our microarray experiment, we did not find any reports associating its gene function with AML. The role of this gene may therefore be the subject of further studies.

From a diagnostic point of view, it is important to correlate gene expression with the classes and types of a disease. For example, the distinction between M1 and M2, the two most frequent and closely related AML FAB subtypes, is challenging. Microarray analyses of AML usually result in the clear separation of AML M3 (APL) and AML with the most frequent cytogenetic aberrations (42,21,22). The M4 subtype has additionally been distinguished by (43) and (21), whereas the M0-M2 subtypes are usually indistinguishable (43). By analyzing the AML-M1 and M2 proteomes, we succeeded in determining five proteins with higher accumulation levels in AML M2 (33). For three of those proteins (catalase, Annexin 3 and L-plastin) we had gene-specific probes on the AML-array, but none of the genes were differentially expressed between the M1 and M2 FAB subtypes. However, with the use of ddPCR, one of the most sensitive types of quantitative PCR, we demonstrated that *ANXA3* expression, despite being generally low and not detectable in all samples, was definitely higher in M2 compared with M1 as well as HV. These results prove the usefulness of Annexin 3 as a potential biomarker at both the protein and transcript levels. In the case of 4 other proteins, inconsistent results were found both in our data and GEO data, what implicates utility of these markers only at the protein level. This inconsistency may be explained by the following: Gene expression is not exclusively regulated by transcription; instead, the abundance of proteins is predominantly controlled

at the translational level (59). The lifetimes of the proteins and corresponding transcripts vary due to different synthesis and degradation rates, moreover, from one transcript more than one protein isoform can be synthesized through alternative splicing and posttranslational modifications. Vogel and Marcotte (60) claimed that only ~40% of the protein concentration variation is determined by mRNA abundance. Weak correlation or a lack of correlation between gene expression in the same cells or tissues has also been demonstrated by (61,62).

The presented RT-qPCR-based analyses enabled the identification of 2 other genes with statistically significant differential expression between the M1 and M2 FAB subtypes: *S100A9* and *WT1*, which were decreased and increased in AML-M1, respectively. *WT1* overexpression in AML-M1 compared with -M2 is consistent with the observation that the expression of Wilms' tumor gene is limited to immature leukemias and inversely correlates with cell differentiation (63). As regards the *S100A* genes, which encode calcium binding proteins implicated in cell cycle regulation, cell differentiation, growth, inflammation and progression of cancer, the data in the literature are contradictory. The upregulation of *S100A8* and *S100A9* has been reported in many solid tumor types (64,65) and in the late myeloblast and monoblast leukemic cell lines (56); their downregulation has been reported in childhood AML (E-GEOD-2191). Our data indicated a high variance of *S100A* gene expression within the AML samples. Similar conclusions can be drawn from the results obtained by (21), in which NK-AML samples clustered into 2 major subgroups; one associated with very high expression of the *S100A9* gene and the second associated with very low expression. In agreement with our results, the majority of the AML-M1 samples had low expression levels of *S100A9*.

Whole-genome analyses of AML have enabled the determination of gene expression signatures specific for AML subgroups harboring the most frequent mutations (24,21). With the use of AML-array, we were able to identify only one gene that exhibited a statistically significant difference in the expression level between AML samples, which was *CPA3*, encoding mast cell carboxypeptidase A3. This gene, whose expression was 16-fold higher in the *FLT3*<sup>+</sup>/*NPM1*<sup>+</sup> samples compared with the remaining AML, has also been identified by (66) as the fourth most upregulated gene in the comparison between *FLT3*-ITD and *FLT3*-wt in older AML patients. Our RT-qPCR analyses of the AML samples also revealed significantly increased levels of 4 other genes: *STMN1* in *FLT3*<sup>+</sup>/*NPM1*<sup>-</sup> samples, *ABL1* in *FLT3*<sup>+</sup> and *FLT3*<sup>+</sup>/*NPM1*<sup>+</sup> AML samples, *CAT* in *FLT3*<sup>-</sup> AML samples and the *WT1* gene in *FLT3*<sup>+</sup>/*NPM1*<sup>+</sup> AML. The *WT1* expression pattern is consistent with the results of the study by Whitman *et al* (66), who reported *WT1* as one of the most upregulated genes in AML with *FLT3*-ITD compared with wild-type AML. In contrast to the upregulation of *CAT* in *FLT3*<sup>-</sup> AML described herein, other authors have linked the elevated expression of this gene to the presence of *FLT3*-ITD (22,66). The association of the *STMN1* and *ABL1* genes with the *FLT3* and *NPM1* mutations has not yet been discussed.

While analyzing therapy-related AML subgroups, we observed differential expression in only two genes by using ddPCR: *CAT* and *WT1*. *CAT* exhibited the highest expression in the CR-long group, whereas *WT1* was gradually increased with the resistance to AML treatment. The results obtained for

catalase remain consistent with the described catalase down-regulation in the doxorubicin-resistant AML subline (67). High expression of the *WT1* gene, the postulated tumor suppressor, has been described in lymphomas and leukemias (68). The correlation of *WT1* expression and AML prognosis has also been reported (39,40).

In conclusion, the present study demonstrates that a small AML-dedicated array, designed and generated in our laboratory, despite some limitations, is suitable for preliminary gene expression studies of AML. Although many of the genes identified with the use of AML-array, are confirmed in the literature, we show that some genes encoding basic metabolism proteins (e.g., *RPLP0*, *ENO1*, *GAPDH*, *PDE3B*, *PKM* and *FCNI*), may also contribute to leukemogenesis, though were not yet discussed in this context. The raw data were deposited in publically available repository and can be downloaded and re-analyzed by any researcher. Despite the lack of success in distinguishing between particular AML subgroups, AML-array can be potentially applied at the stage of first diagnosis of AML based on gene expression profile. It can also be modified to elaborate an improved array version with better rate of diagnostic and prognostic success. However, for more accurate transcript measurement, quantitative PCR approaches, in particular ddPCR, are more appropriate. Application of this strategy enabled us to obtain results valuable from the diagnostic and prognostic point of view. We identified three genes (*S100A9*, *ANXA3* and *WT1*), whose expression levels can be used for discrimination between two AML FAB subtypes, M1 and M2, which are usually difficult to distinguish. We showed for the first time relationship of the *STMN1* and *ABL1* genes with the *FLT3* and *NPM1* mutation status, and correlation of high *CAT* expression with positive response to AML treatment.

### Acknowledgements

This study was financially supported by the Polish Ministry of Science and Higher Education (grant no. PBZ\_MniI-2/1/2005). This study was also supported by the Polish Ministry of Science and Higher Education under the SPUB (no. 5536/E-63/SPUB/2015) and KNOW programs. We are grateful to Dr Marcin Schmidt from the Poznan University of Life Sciences for providing the HL60 cells. We would also like to thank Dr Joanna Zyprych-Walczak, Dr Alicja Szabelska-Beręsewicz and Professor Idzi Siatkowski from Poznan University of Life Sciences for their assistance with microarray data normalization.

### Competing interests

The authors declare that they have no competing interests.

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