

Transcriptional features of acute leukemia with promyelocytic differentiation lacking retinoic acid receptor rearrangements

Zhan Su,^{1,2*} Xin Liu,^{3*} Yuanfeng Zhang,⁴ Wei Wang,² Xuerong Li,⁵ Jie Yu,⁶ Xinru Wang⁷ and Jun Peng¹

¹Department of Hematology, Qilu Hospital, Cheeloo College of Medicine, Shandong University, Jinan; ²Department of Hematology, Affiliated Hospital of Qingdao University, Qingdao; ³Department of Stem Cell Transplantation, Blood Diseases Hospital & Institute of Hematology, Chinese Academy of Medical Sciences & Peking Union Medical College, Tianjin; ⁴Department of Hematology, Affiliated Yantai Yuhuangding Hospital of Qingdao University, Yantai; ⁵Department of Pediatric Hematology, Affiliated Hospital of Qingdao University, Qingdao; ⁶Department of Hematology, Weihai Municipal Hospital, Cheeloo College of Medicine, Shandong University, Weihai and ⁷Department of Hematology, Liaocheng People's Hospital, Liaocheng, China

**ZS and XL contributed equally as first authors.*

Correspondence:

J. PENG - junpeng88@sina.com

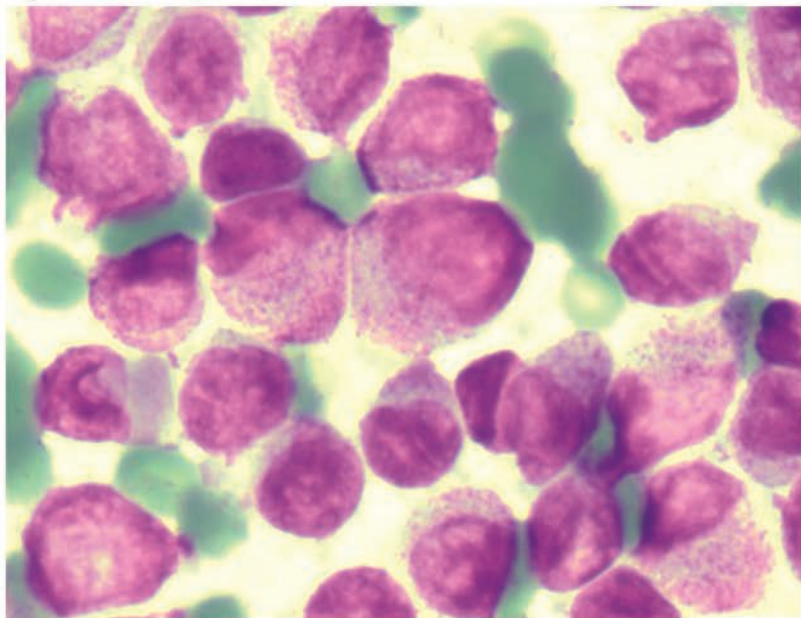
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Supplementary Table S1. Characteristics of cases in the experimental group

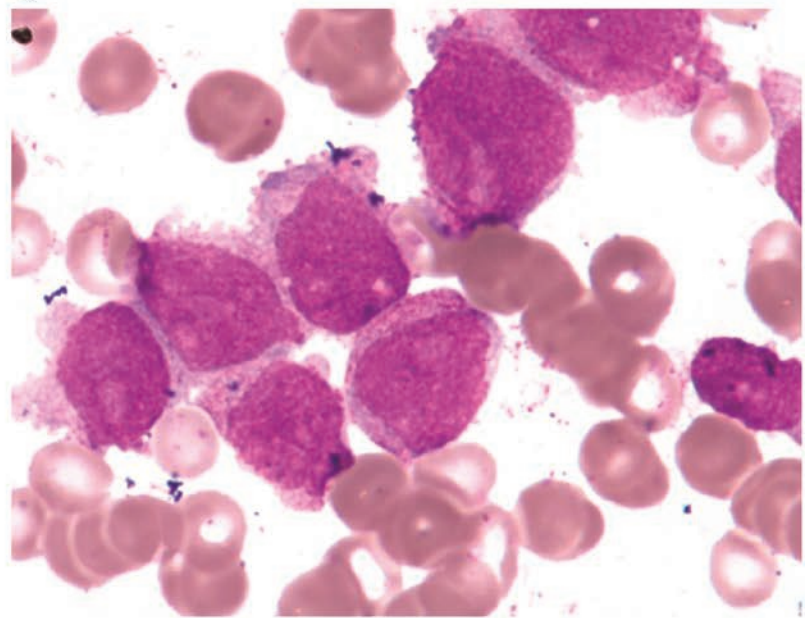
No.	Age	Gender	WBC ($\times 10^9/L$)	HgB (g/L)	PLT ($\times 10^9/L$)	coagulation profiles	Bone Marrow	Cytogenetics	Mutations	Immunophenotyping	Treatments	Outcome
1	8	F	3.72	99	134	normal	9% myeloblasts, 66.5% promyelocytes	46, XX, i(17)(q10)	KMT2D, UNC13D, TP53, ASXL; FISH: TP53 deletion	positive: CD117, CD38, CD13, CD123, MPO; weak: HLA-DR, CD64, CD9	ATRA+ATO(16 days), IAE followed; ATRA+ATO(12 days)+I, ATRA+ATO(33 days)+I, BM CR; then ATRA+ATO(27 days)+I, ATO(20 days), ATO(14 days); 3 cycles of FA, after extramedullary relapse	multiple abnormal signals of vertebral body and skull on magnetic resonance images onset, suggests possibility of leukemia infiltration(lacking pathologic examination); the same to the left acetabulum and bilateral femurs deemed extramedullary relapse. OS 20 months, died
2	19	M	0.94	114	62	normal	53.5% myeloblasts, 32% promyelocytes	43, X,-Y, add(8)(q24),add(10)(p13),del(11)(q13),der(12;13)(q10;q10),-14,- 16,del(17)(q23),+mar,1dmin(3)/44 ,idem,+der(12;13)(q10;q10)(1)	NA	positive: CD33, CD38, CD36, CD9, CD13, MPO; partially positive: CD7, CD15, CD123, CD4; weak: CD34, CD117, CD64, CD11b, CD56, CD19, CD14	ATRA for 12 days, then IA for 3 days;	5 weeks, died; NR
3	53	M	9.36	81	50	hypofibrinogenemia (1.2g/L)	32% myeloblasts, 38.5% promyelocytes	46, XY, t(2;11)	NA	positive: CD117, CD33, CD13, CD123, CD38, MPO; partially positive: CD15, CD64; weak: CD11b	DA, CR; then DA, HD-Ara-C, HD-Ara-C, DA, HA; IA + UCBI when relapsed	CR for 44 months; lost after 1 cycle of reinduction when relapsed
4	71	F	13.4	132	40	normal	21.5% myeloblasts, 68% promyelocytes	46, XX	NPM1, KIT, TET2, ETV6	positive: CD117, CD33, MPO; weak : CD13	IA, decitabine+CAG, decitabine+CAG, decitabine+MAG, Ara-C, NR	NR for 10 months, died

No., number; M, male; F, female; WBC, white blood cell; HgB, hemoglobin; PLT, platelet; FISH: fluorescence in situ hybridization; NA, not analysed; ATRA, all-trans retinoic acid; ATO, arsenic trioxide; IAE, idarubicin, cytarabine, and etoposide; I, idarubicin; BM, bone marrow; CR, complete response; FA, fludarabine and high dose cytarabine; NR, no response; HD-Ara-C, high dose cytarabine; Ara-C, cytarabine; IA, idarubicin and cytarabine; DA, daunorubicin and cytarabine; HA, homoharringtonine and cytarabine; UCBI, umbilical cord blood infusion; CAG, acylamycin, cytarabine, and granulocyte-colony stimulating factor(G-CSF); MAG, mitoxantrone, cytarabine, and granulocyte-colony stimulating factor; OS, overall survival.

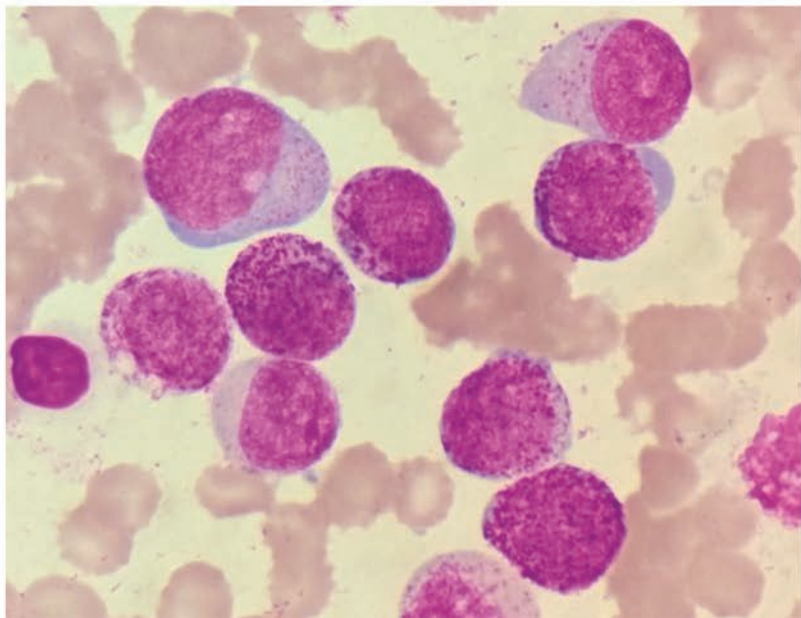
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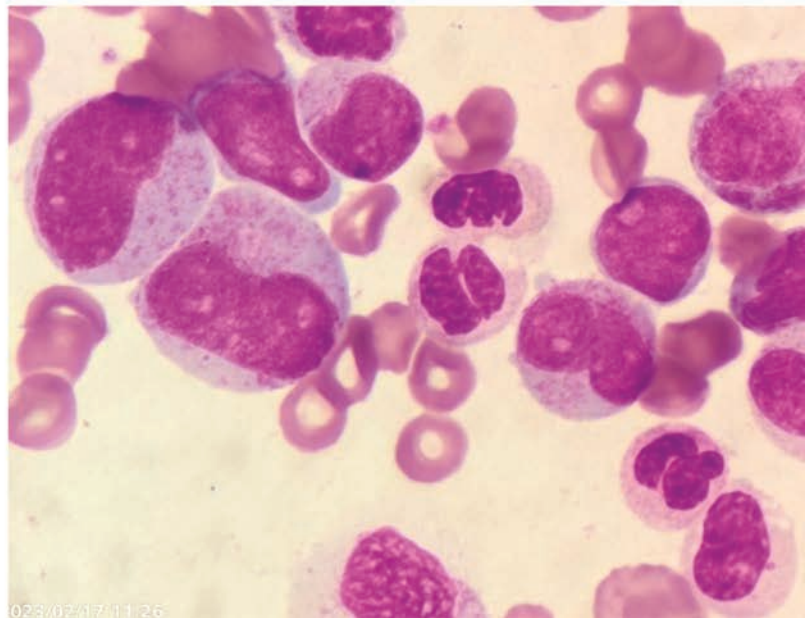
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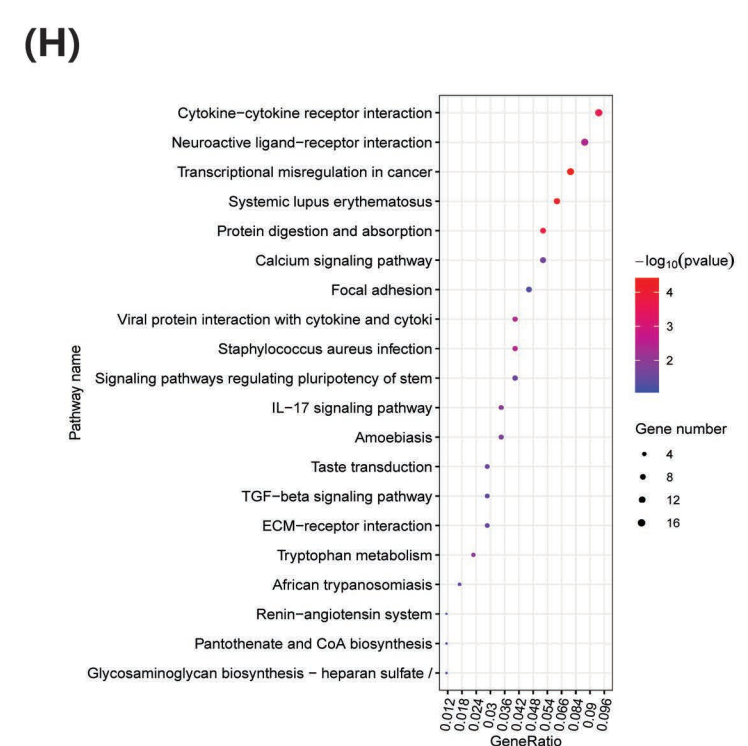
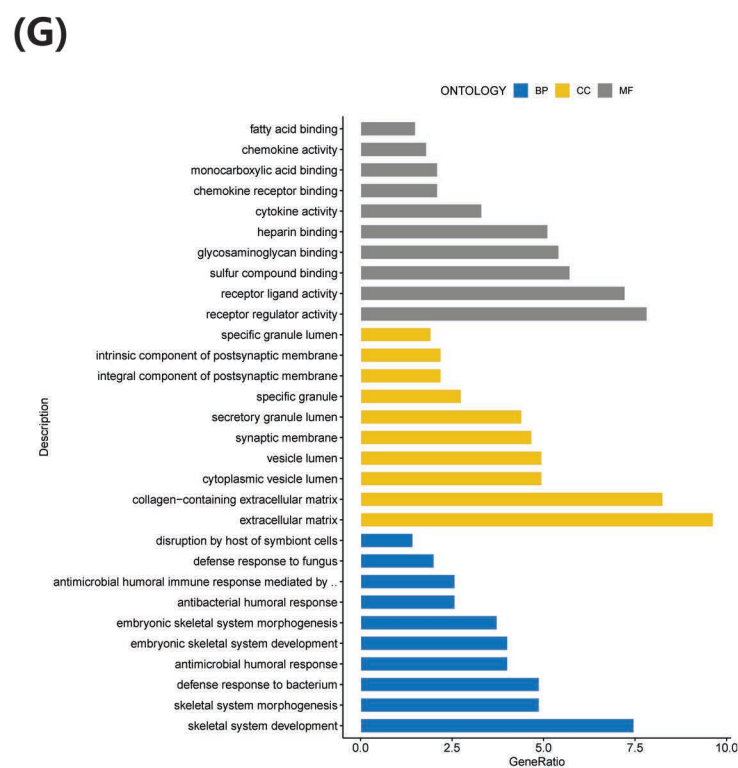
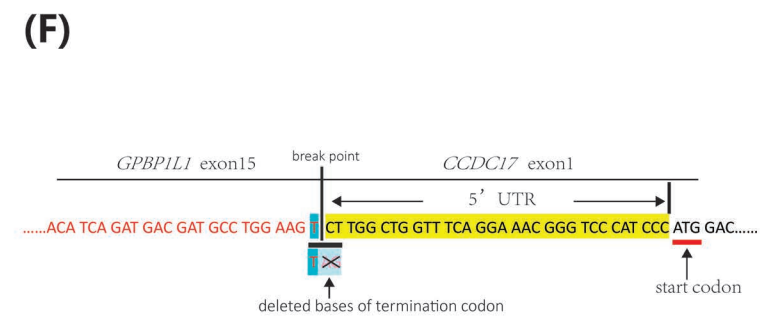
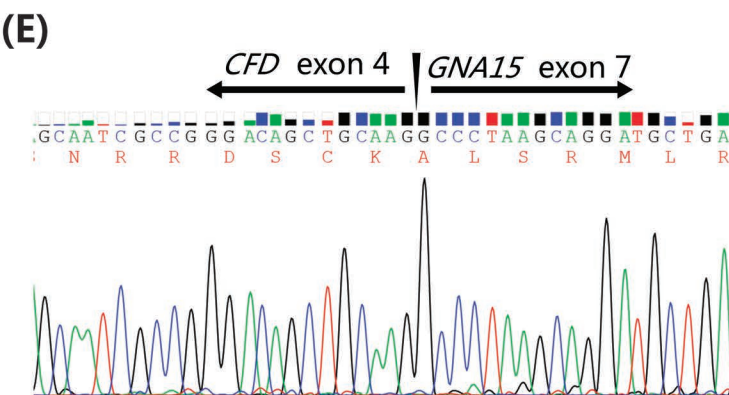
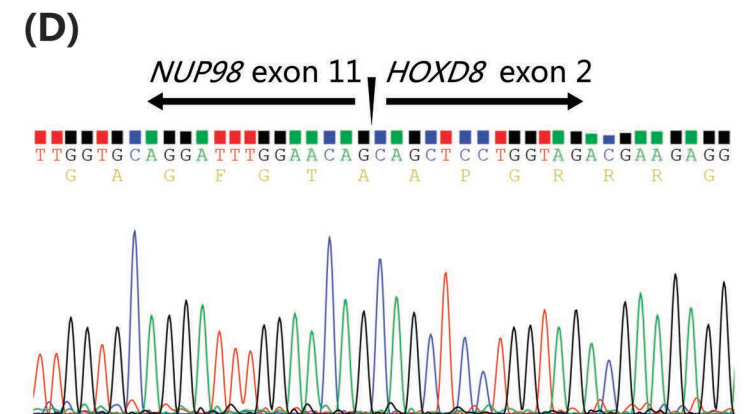
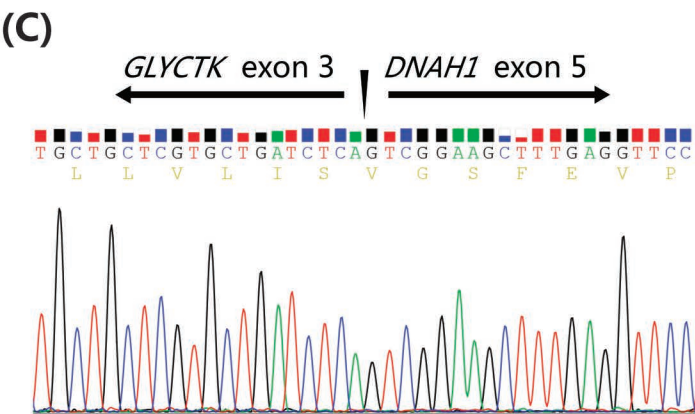
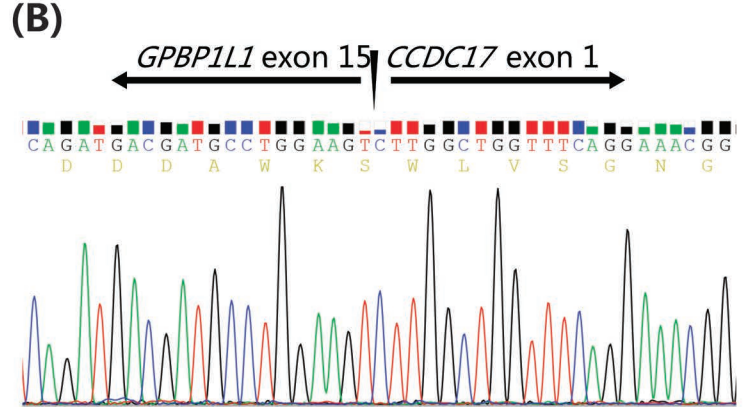
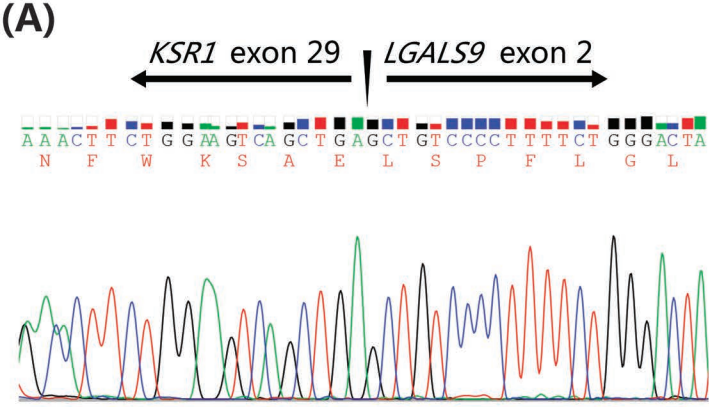


(C)



(D)





Supplementary Figure legends

Supplementary Figure S1.

Bone marrow smear of the four cases (Wright-Giemsa staining, $\times 1000$). The numbers of cases are indicated from A to D.

Supplementary Figure S2.

Figures from (A) to (E) are results of Sanger sequencing of novel fusion genes. (F) Junction region of *GPBP1L1-CCDC17* fusion gene. The breakpoint of *GPBP1L1* is located in the termination codon (TAG, missing AG bases), which destroys the termination codon. The breaking point of *CCDC17* is in the 5'UTR region, up-stream closing to the start codon. (G) & (H) GO and KEGG analysis. Obviously down-regulated genes were selected for GO and KEGG analysis. From the GO enrichment analysis results, the most significant 30 terms (the top 10 of each classification) were selected to draw a histogram. Among the KEGG enrichment results, the most significant 20 KEGG pathways were selected to draw the bubble map. BP, biological process; CC, cellular component; MF, molecular function.

Supplementary Document A

Sequences of novel transcripts of *RXRA*, *RARB*, and *RARA*

>Case 1. novel RXRA transcript

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>Case 3 & 4. novel RARB transcript

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>Case 4. novel RARA transcript

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