

# **Identification of ubiquitination-related hub genes in chronic myeloid leukemia cell by bioinformatics analysis**

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### **Supplementary figure 1**

(A) The KEGG enrichment analysis of DEGs in GSE47927 NetworkAnalyst.

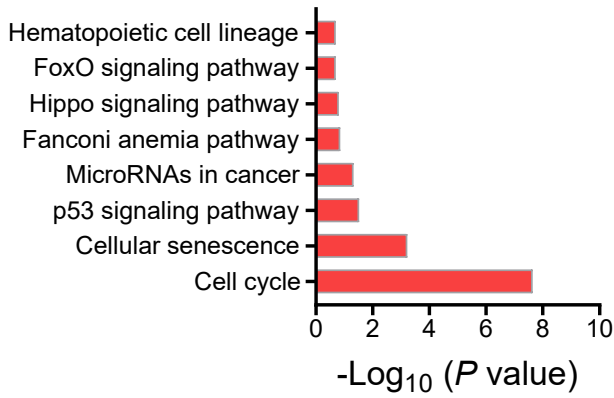
(B) The scree plots of DEGs in GSE47927.

(C) The PCA of normal and CML samples.

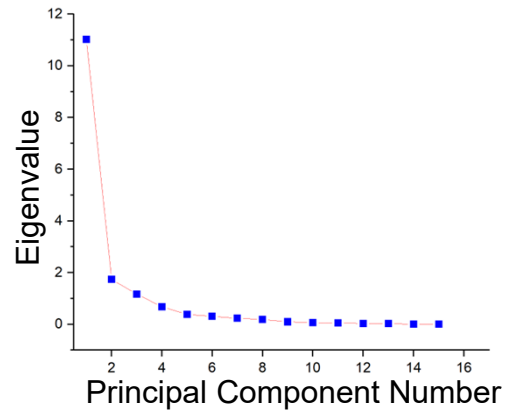
(D-E) The GO and KEGG enrichment pathway analysis of UUC-related DEGs using the DAVID database.

# Supp Fig1

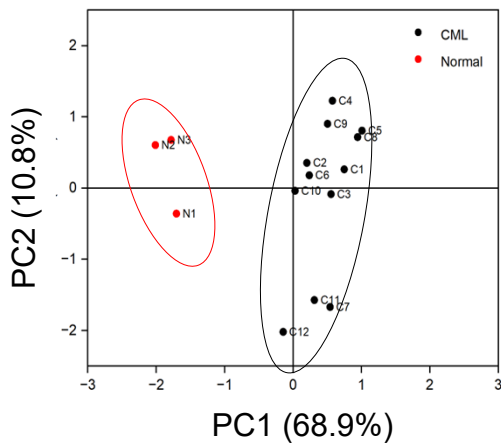
**A**



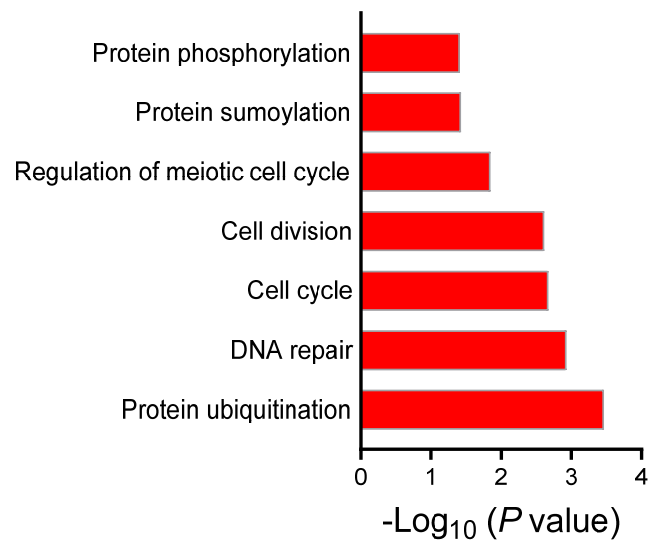
**B**



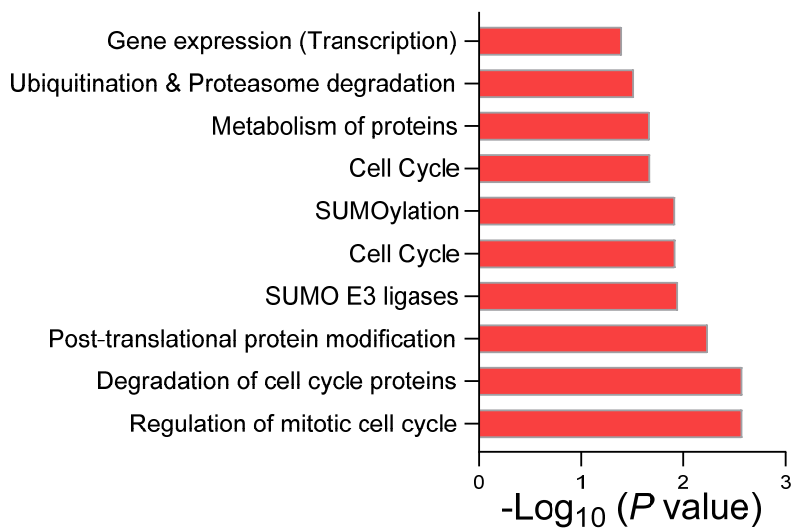
**C**



**D**



**E**



**Table S2: Primers**

Gene	Species	Sequence
FANCD2-F	mouse	CAAATCAGCTAGGTGTGGATCA
FANCD2-R	mouse	CCAGGCCATTAACAAACTCTTCT
UHRF1-F	mouse	CCACACCGTGA ACTCTCTGTC
UHRF1-R	mouse	GGCGCACATCATAATCGAAGA
CDC20-F	mouse	TTCGTGTTTCGAGAGCGATTG
CDC20-R	mouse	ACCTTGGA ACTAGATTTGCCAG
AURKA-F	mouse	CTGGATGCTGCAAACGGATAG
AURKA-R	mouse	CGAAGGGAACAGTGGTCTTAACA
18S-F	Mouse/ human	GGAATATGCACC ACTTGGAAACA
18S-R	mouse/human	TAAGACAGGGC ATTTGCCAAT
FANCD2-shRNA	human	CGTCTATTAGATTGGAGGATT
UHRF1-shRNA	human	ATGTGGGATGAGACGGAATTG
CDC20-shRNA	human	AGACCAACCCATCACCTCAGT

**Table S5: Hub-UUB-DEGs/TFs/ miRNA network genes**

<b>Hub-UUB-DEGs</b>	FANCD2; AURKA; UHRF1; CDC20
<b>TFs</b>	VDR; YY1; POU2F1; TBP; MAZ; SRF; AR; ATF3
<b>miRNA</b>	hsa-miR-106a-5p; hsa-miR-1182; hsa-miR-12118; hsa-miR-363-3p; hsa-miR-370-3p; hsa-miR-4251; hsa-miR-6788-5p; hsa-miR-6829-3p; hsa-miR-6876-5p; hsa-miR-140-5p; hsa-miR-153-3p; hsa-miR-29b-2-5p; hsa-miR-4728-5p; hsa-miR-4739; hsa-miR-506-3p; hsa-miR-4728-6p; hsa-miR-8077; hsa-miR-5787; hsa-miR-1226-5p; hsa-miR-510-5p; hsa-miR-3173-3p; hsa-miR-6891-5p; hsa-miR-4505