Supplemental Figures

Targeting NAT10 induces apoptosis associated with enhancing endoplasmic reticulum stress in acute myeloid leukemia cells Jie Zi^a, Qi Han^a, Siyu Gu^a, Mary McGrath^b, Shriya Kane^{b,c}, Zheng Ge^{a*} ^aDepartment of Hematology, Zhongda Hospital, Medical School of Southeast University, Institute of Hematology Southeast University, Nanjing 210009, China ; ^bDepartment of Pediatrics, Pennsylvania State University Medical College, Hershey, PA17033, USA. ^cGeorgetown University School of Medicine, Washington , DC 20007, USA

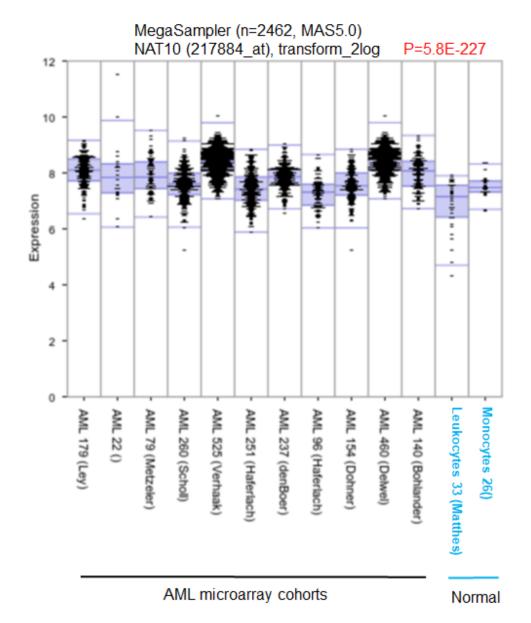
Running title: Targeting NAT10 inducing apoptosis in AML

*Corresponding authors:

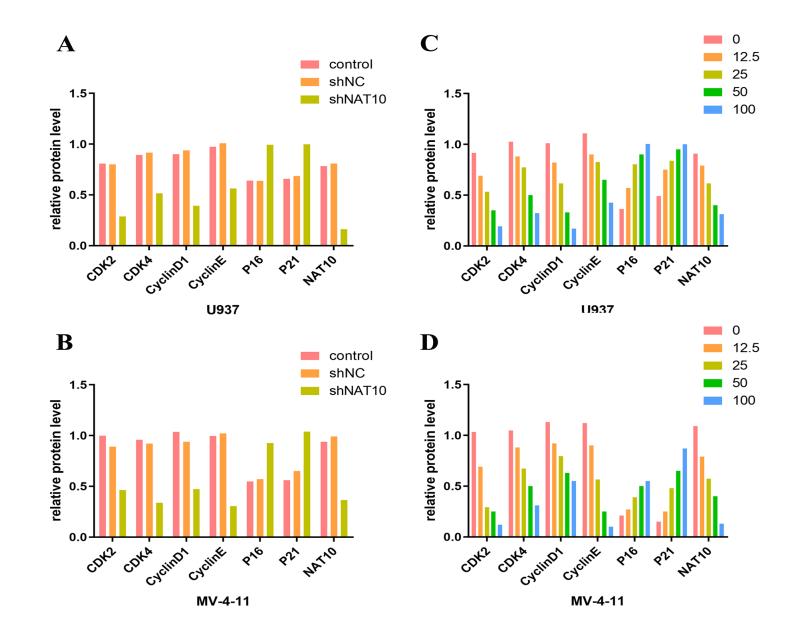
Zheng Ge, M.D., Ph.D. Department of Hematology, Zhongda Hospital, Medical School of Southeast University, Institute of Hematology Southeast University, No. 87, Dingjiaqiao, Nanjing 210009, Jiangsu, China.

Telephone: 86-25-83262468, FAX: 86-25-83262471, Email: Janege 879@hotmail.com

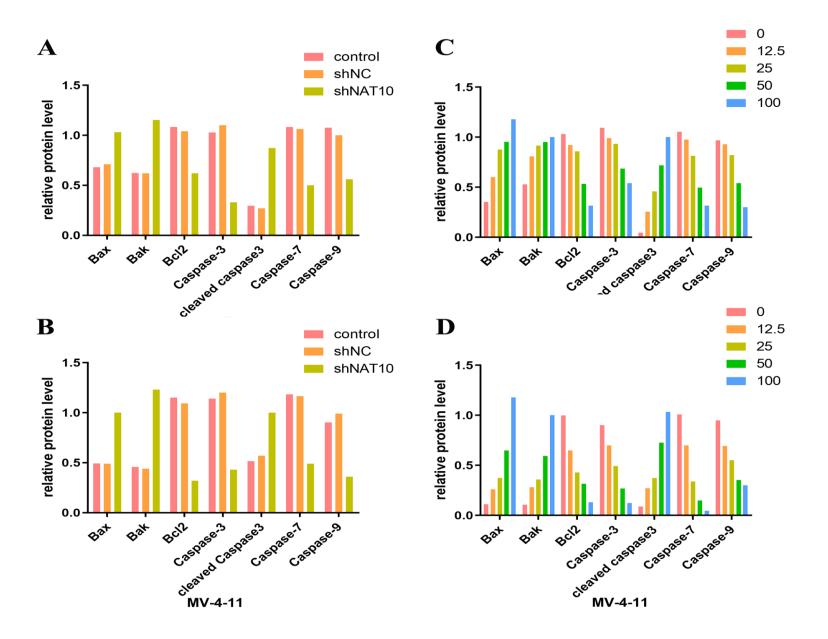
Total words: 3930 Number of figures: 7 Number of table: 1 Supplemental figures: 4



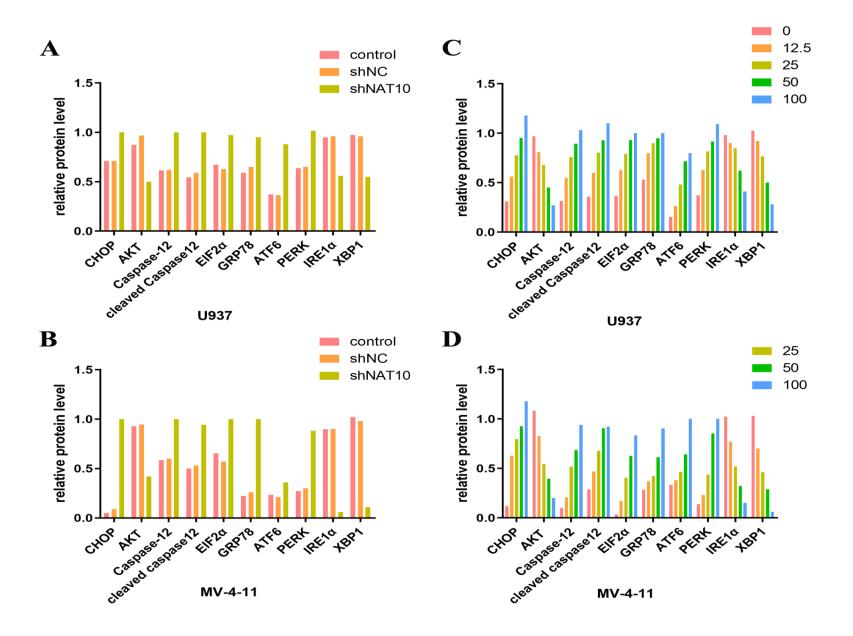
Supplemental Fig 1: NAT10 high expression in AML microarray cohorts studies compared to that of normal leukocytes cells and monocytes. The microarray data for NAT10 (217884_at) expression generated with MegaSampler (n=2462, MAS5.0) from human oncogenomics sever crossing all **microarray** database, which includes AMLand normal control (leukocytes and monocytes) cohort studies.



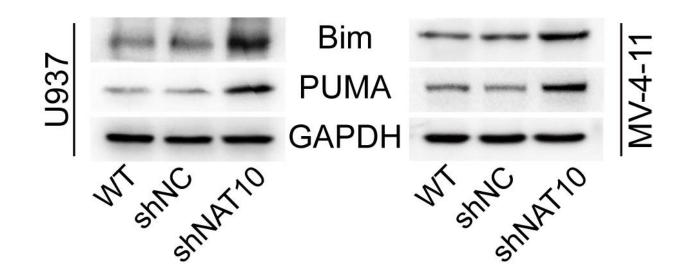
Supplemental Figure 2 Quantitative data for Western blot in NAT10 depletion and inhibition-mediated cell cycle-related proteins (A-D) Quantitative data of the western-blots were generated by NIH ImageJ in the NAT10 depletion cells (A, B) and NAT10 inhibitor treatment cells (C, D). For data in A-D, graphed are the representative of one of 3 independent experiments



Supplemental Figure 3 Quantitative data for Western blot in NAT10 depletion and inhibition-mediated apoptosis-related proteins (A-D) Quantitative data of the western-blots were generated by NIH ImageJ in the NAT10 depletion cells (A, B) and NAT10 inhibitor treatment cells (C, D). For data in A-D, graphed are the representative of one of 3 independent experiments



Supplemental Figure 3 Quantitative data for Western blot in NAT10 depletion and inhibition-mediated ER stress-related proteins (A-D) Quantitative data of the western-blots were generated by NIH ImageJ in the NAT10 depletion cells (A, B) and NAT10 inhibitor treatment cells (C, D). For data in A-D, graphed are the representative of one of 3 independent experiments



Supplemental Figure 4 Western-blotting analysis of the effect of NAT10 depletion by shRNA knockdown BH3-only proteins Bim and PUMA in U937 and MV4-11 cells.