

Supplementary figures

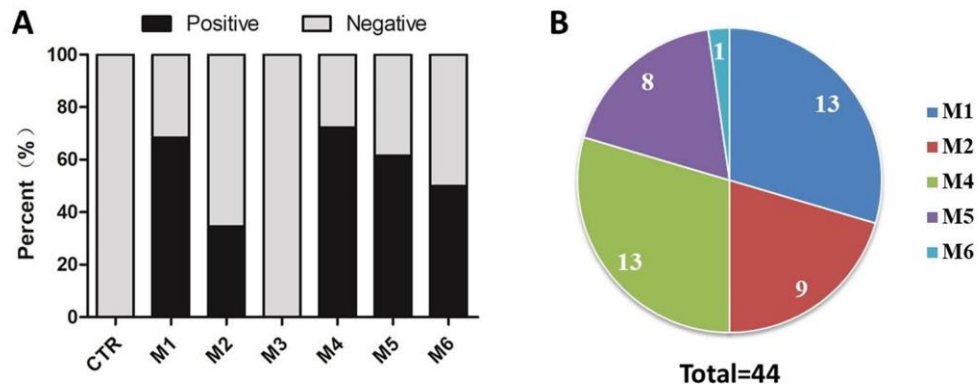


Fig. S1 The distribution of METTL3 and METTL14 in different FAB AML subtypes. **A.** METTL3/14 expression in mononuclear cell of normal and AML patients. **B.** Case distribution of positive METTL3/14 patients according to the AML subtypes.

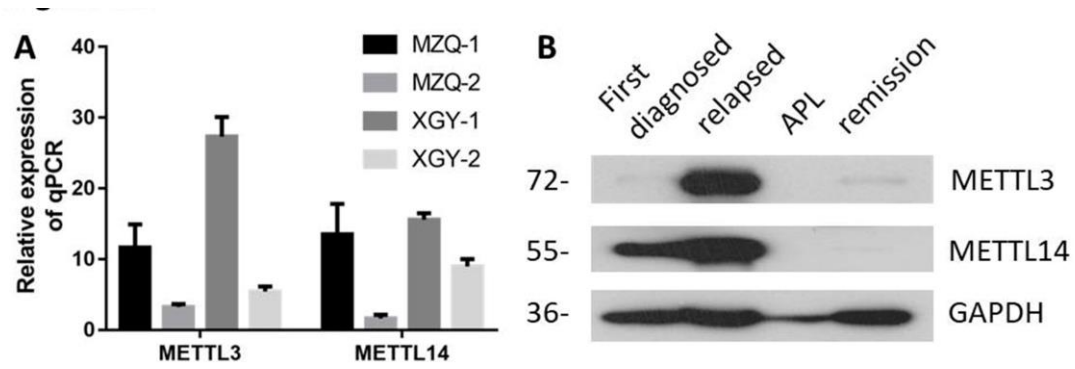


Fig. S2 The differences in METTL3 and METTL14 during remission and relapsed AML. A. qPCR analysis of *METTL3* and *METTL14* expression in MZQ-1, MZQ-2, XGY-1, XGY-2 (MZQ-1, XGY-1: Pre-treatment; MZQ-2, XGY-2: Post-treatment); B. Western Bolt assays showed the expression of METTL3, METTL14 and GAPDH (loading control) in some clinical samples (lane 1: first diagnosed AML, lane 2: relapsed AML, lane 3: APL; lane 4: remission AML).

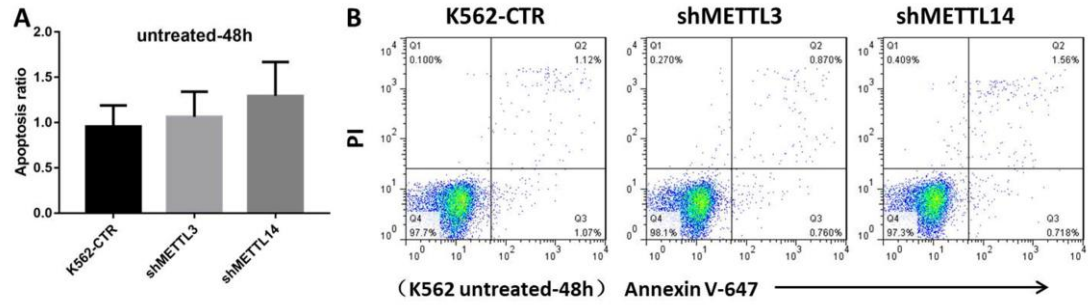


Fig. S3 The apoptosis of *METTL3* and/or *METTL14* knockdown cells slightly increased. A and B. Apoptosis were examined by flow cytometry in untreated control (K562-CTR) K562 cells, *METTL3* knockdown (shMETTL3) and *METTL14* knockdown (shMETTL14) cells for 48h, and the data are expressed as the mean ± SD. Experiments were performed in triplicate. * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$, with the Student's *t*-test

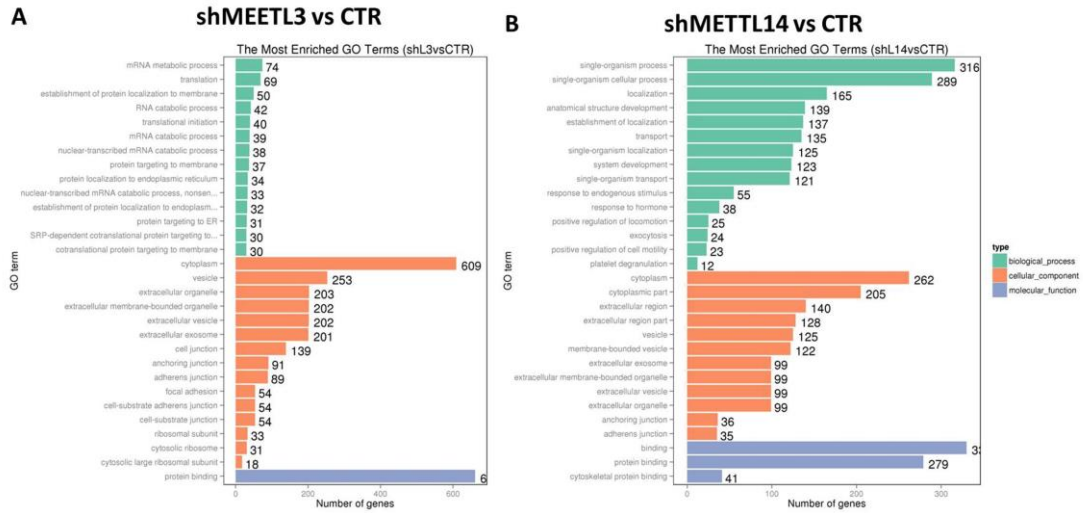


Fig. S4 GO analysis in *METTL3*/*METTL14* knockdown cells. A and B. The GO analysis upon *METTL3*(A) or *METTL14*(B) knockdown; green represents biological process, red represents cellular component, blue represents molecular function.