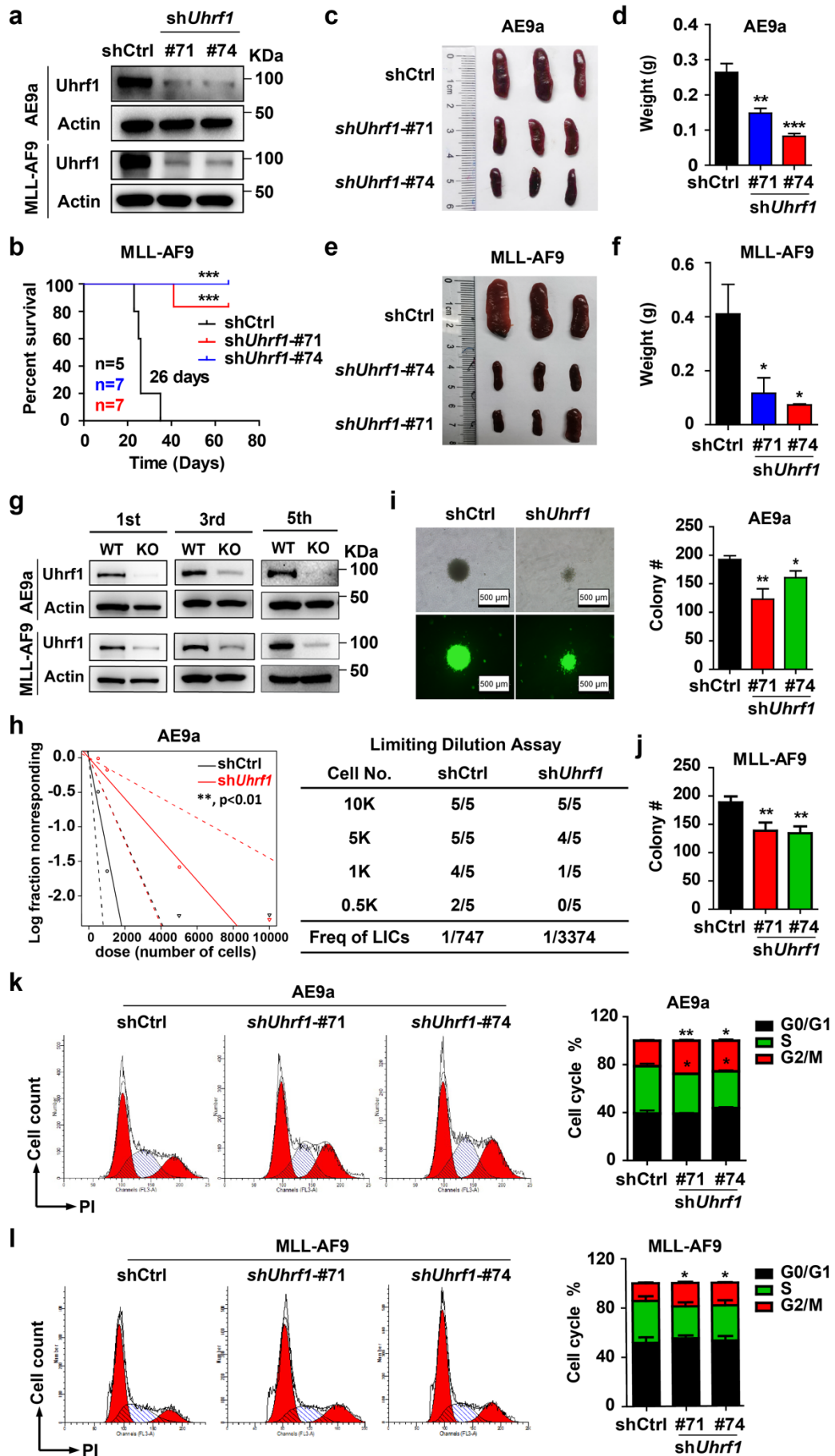




Supplementary information Fig. S3 The effects of Uhrf1 inhibition on AML cells and the progression of AML.

a The expression of Uhrf1 was examined by Western blotting analysis in AE9a or MLL-AF9 cells transduced with shRNA against *Uhrf1* or a control shRNA 48 hours after the puromycin selection. **b** The survival of mice that received MLL-AF9 cells expressing shRNA against *Uhrf1* or scrambled shRNA (n≥5). **c-d** The size (**c**) and weight (**d**) of the spleen in mice that received AE9a cells expressing the shRNA against *Uhrf1* or scrambled shRNA 2 weeks after transplantation (n=4). **e-f** The size (**e**) and weight (**f**) of the spleen in the mice that received MLL-AF9 cells expressing shRNA against *Uhrf1* or scrambled shRNA 3 weeks after transplantation (n=4). **g** The expression of Uhrf1 was examined by Western blotting analysis in cells from the colonies generated from AE9a*Uhrf1*^{fl/fl} CreER or MLL-AF9*Uhrf1*^{fl/fl} CreER LICs treated with 4-OHT or vehicle. **h** The inhibition of *Uhrf1* decreased the frequency of LICs in the limiting dilution assay. The log-fraction plots showed the result of the limiting dilution assay by using different dilutions of AE9a cells expressing shRNA against *Uhrf1* or scrambled shRNA in vivo. **i-j** The number of colonies generated from AE9a cells (**i**) or MLL-AF9 cells (**j**) transduced with shRNA against *Uhrf1* or scrambled shRNA (n≥3). **k-l** The cell cycle analysis of AE9a cells (**k**) or MLL-AF9 cells (**l**) transduced with shRNA against *Uhrf1* or scrambled shRNA 48 hours after the puromycin selection (n=3). Data are all presented as mean ± SD. Statistical analyses were performed using student's unpaired t-test for **d, f, i, j, k** and **l**, and log-rank test for **b**. EDLA software analysis was used for **h**. *p<0.05, **p<0.01, ***p<0.001.