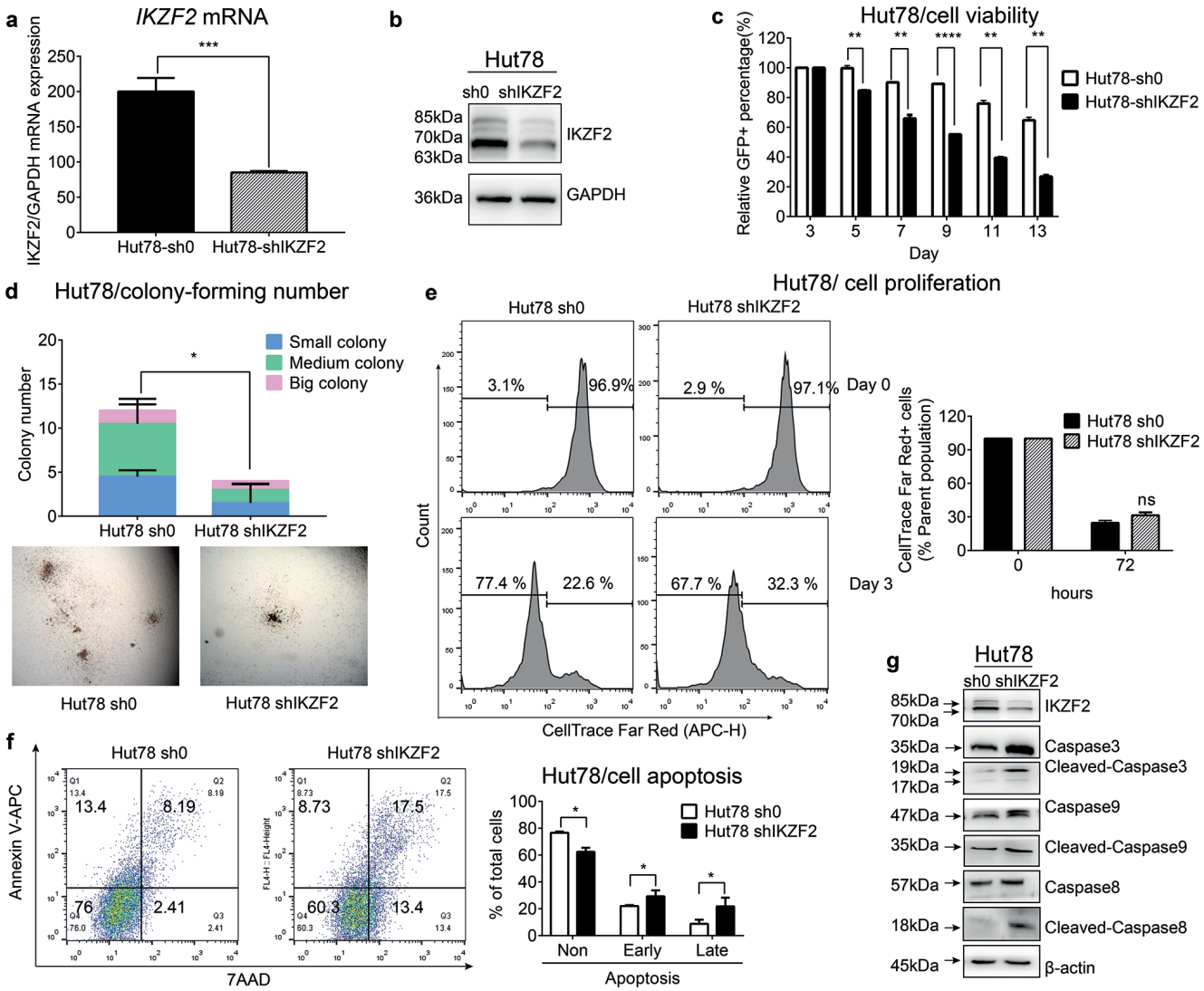

Fig. S1. IKZF2 suppression causes growth inhibition to cutaneous T cell lymphoma (CTCL) cells through promoting cell apoptosis. (a–b) Suppression of (a) IKZF2 RNA and (b) protein expression in Hut78 by lentiviral transduction with a shRNA sequence (shIKZF2); cells transduced with scrambled shRNA (sh0) serve as control. (c) Cell competition-based viability assay for Hut78 cells expressing the GFP-shRNA targeting endogenous IKZF2. The percentages of the GFP+ cells were tracked and normalized to the percentages at day 3. (d) The number of colonies formed in the colony-forming cell assay among IKZF2-suppressed (shIKZF2) Hut78 cells and control cells (sh0). (e) Cell Trace Far Red-based cell viability assay of IKZF2-suppressed (shIKZF2) Hut78 cells and control cells (sh0). Representative flow cytometry profiles of cell viability among control (sh0) and IKZF2-suppressed (shIKZF2) Hut78 cells. (f) 7AAD+ and Annexin V+ -based apoptosis assay of IKZF2-suppressed (shIKZF2) and control (sh0) Hut78 cells in flow cytometry. Representative flow cytometry profiles of cell viability among control (sh0) and IKZF2-suppressed (shIKZF2) Hut78 cells. (g) Cleavage of caspase-3 and cleavage of caspase-8 were detected in Hut78 cells with IKZF2 silencing (shIKZF2) and control cells (sh0) via western blot analysis. Data are represented as means ± standard deviation (SD). Unpaired Student's *t*-test. * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$; **** $p < 0.0001$. ns: no significance.