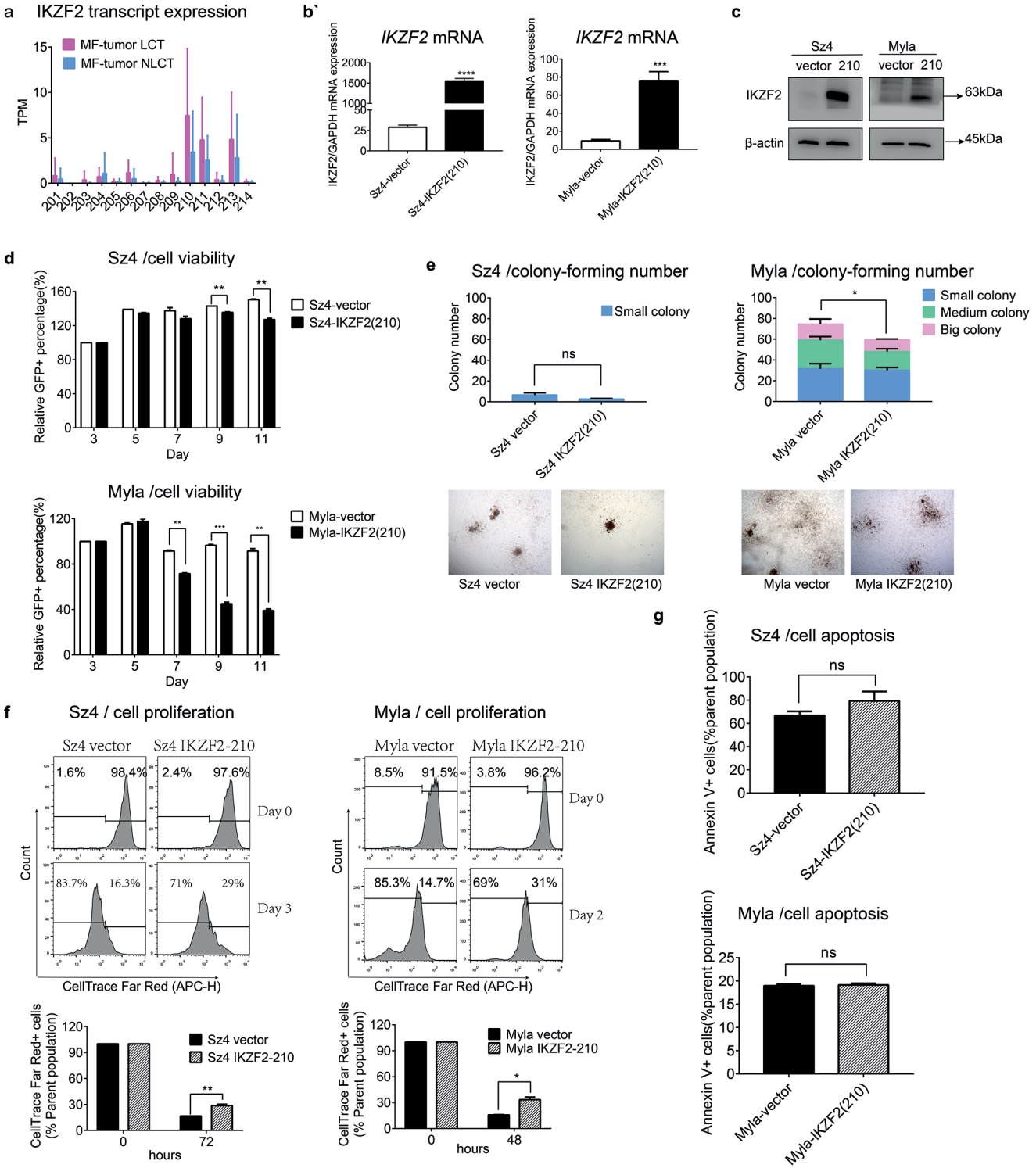

Fig. S2. (a) Over-expression of IKZF2 confers cell growth disadvantage through inhibiting the cell proliferation of cutaneous T cell lymphoma (CTCL) cells. The transcript expression of IKZF2 isoforms in the 49 RNA-seq cohort. Overexpression of (b) IKZF2 RNA and (c) protein level in Sz4, Myla by lentiviral transduction with IKZF2-210 transcript sequence; cells transduced with vector serve as control. (d) Cell competition-based viability assay for Sz4, Myla cells expressing the GFP-lentivirus targeting exogenous IKZF2. The percentages of the GFP+ cells were tracked and normalized to the percentages at day 3. (e) The number of colonies formed in the colony-forming cell assay among IKZF2-overexpressed (IKZF2-210) Sz4, Myla cells and control cells (vector). (f) Cell trace far red-based cell viability assay of IKZF2-overexpressed (IKZF2-210) Sz4, Myla cells and control cells (vector). Representative flow cytometry profiles of cell viability among vector and IKZF2-210 Sz4 and Myla cells. (g) Annexin V^+ -based apoptosis assay of IKZF2-overexpressed (IKZF2-210) Sz4, Myla cells and control cells (vector) in flow cytometry. Unpaired Student's *t*-test. $*p<0.05$; $**p<0.01$; $***p<0.001$; $****p<0.0001$. ns: no significance.