

Fig. S3. Comprehensive search for IKZF2 downstream genes and pathways by transcriptomics analysis. (a) Volcano plot of up-regulated (red) and down-regulated (green) differential genes (DEGs) (|log2 Fold Change| > 0.6 and p-value < 0.05) between Hut78-shIKZF2 cells and sh0. (b) Enriched pathways of up-regulated DEGs in Hut78-shIKZF2 compared with sh0 via DAVID platform. (c) Gene set enrichment analysis (GSEA) enrichment plot for apoptosis gene signatures in control (sh0) and IKZF2-suppressed (shIKZF2) Hut78 cells. (d) mRNA expression of apoptosis-related genes overlapped from differential expressed genes and leader genes of enriched apoptosis gene signatures in IKZF2-suppressed (shIKZF2) Hut78 cells compared with control (sh0). Data are represented as means±standard deviation (SD). Unpaired Student's t-test. *p < 0.01; ***p < 0.01; ***p < 0.01. (e) Pearson correlation between IKZF2 and BTG3 or LMNA mRNA expression in the 49 MF cohort. (f) GSEA enrichment plot for MHC protein complex gene signatures in IKZF2-suppressed (shIKZF2) and control (sh0). (g) mRNA expression level of MHC II molecules overlapped from differential expressed genes and leader genes of enriched MHC protein complex gene signatures in Hut78-shIKZF2 and sh0. (h) Overall survival (OS) (left panel) and progression-free survival (PFS) (right panel) of patients with MF stratified by HLA-DRA mRNA expression from the 49 MF cohort. Log rank (Mantel-Cox) test. (i-k) GSEA enrichment plot for IFN-a response, IFN-a response, inflammatory response gene signatures in IKZF2-suppressed (shIKZF2) and control(sh0). (l-m) mRNA (l) and represented as means±standard deviation (SD). unpaired Student's t-test. (n) OS (left panel) and PFS (right panel) of patients with MF stratified by IL-10 mRNA expression from the 49 MF cohort. Log rank (Mantel-Cox) test. *p<0.05; **p<0.01; ***p<0.001; ****p<0.001. ns: no significance.