Figure S1

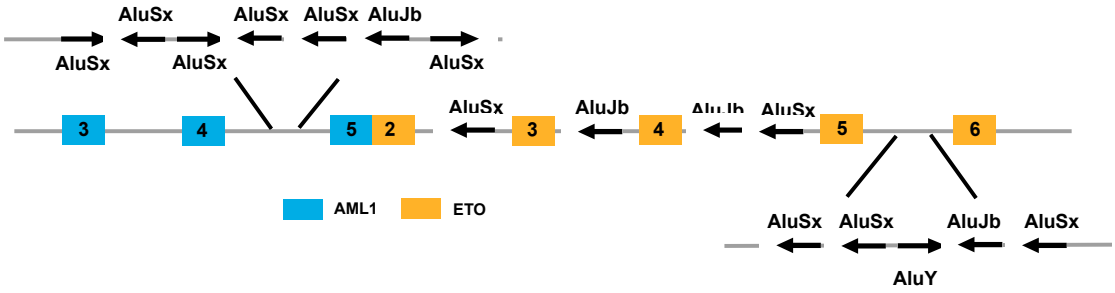

Figure S1 Alu repeats that existed in the intron sequence near the *AML1-ETO* breakpoint were recognized by RepeatMasker (http://www.repeatmasker.org).

Figure S2

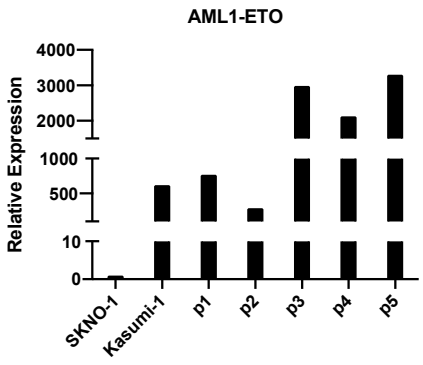

Figure S2 RT-PCR analysis of AML1-ETO expression in Kasumi-1, SKNO-1, and BMMNCs of AML patients.

Figure S3

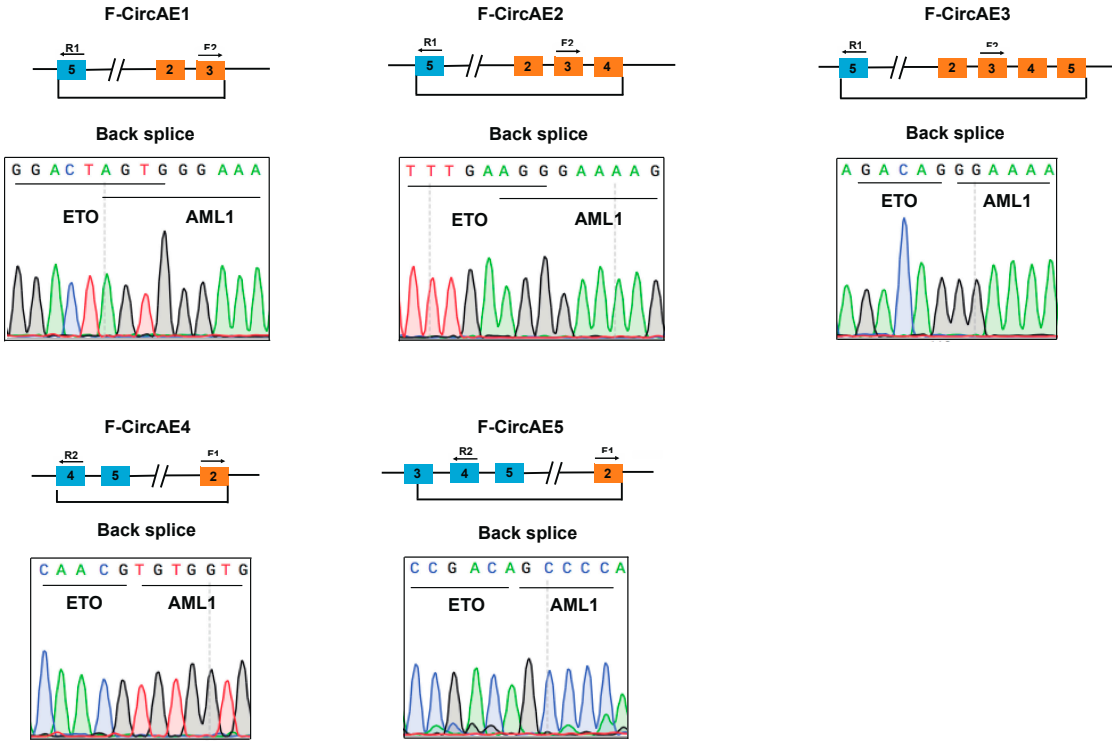

Figure S3 The composition and head-to-tail splicing sites of F-CircAEs were represented. The sequences of F-CircAE2 and F-CircAE3 have been submitted to the GenBank database (MG551955, MG551956).

Figure S4

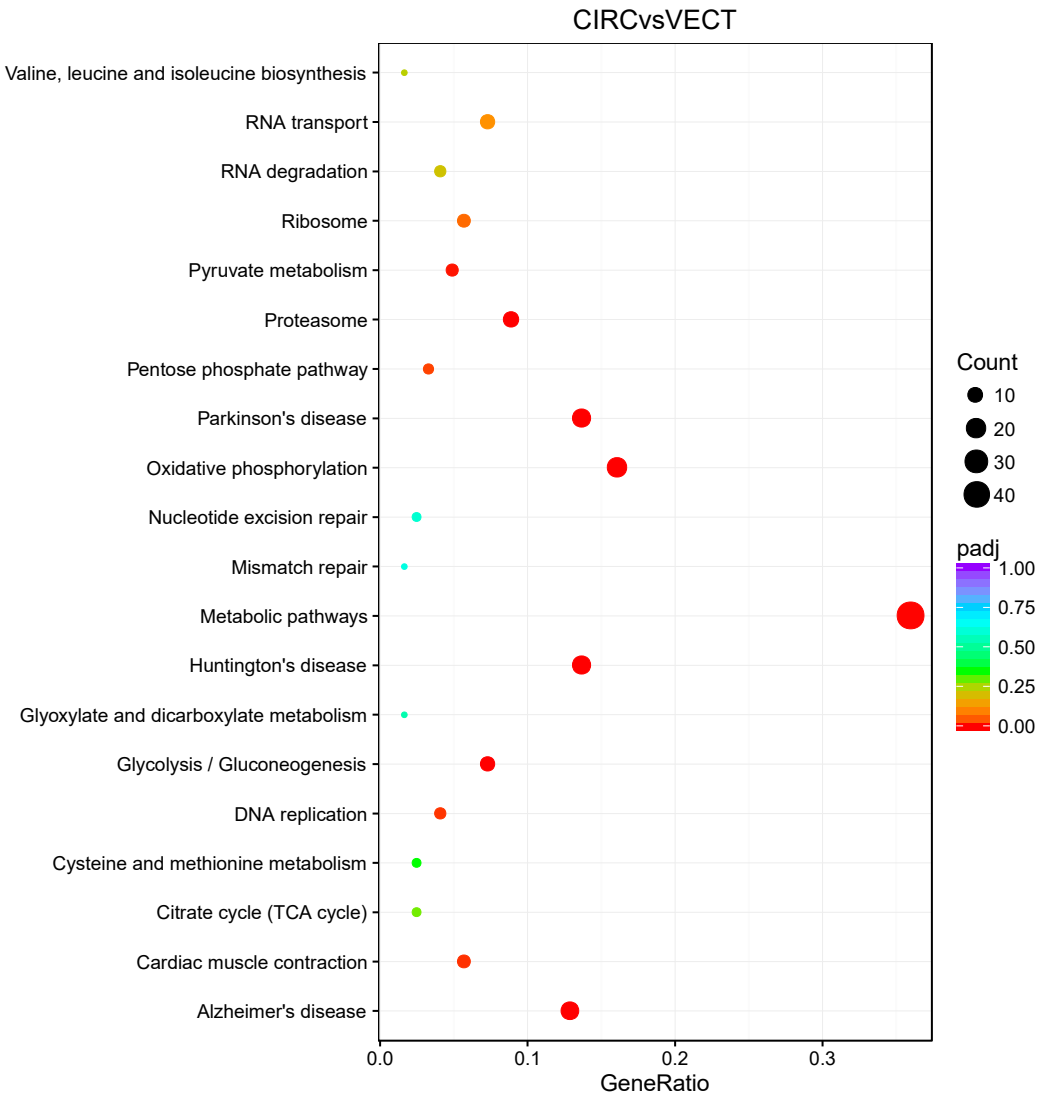

Figure S4 KEGG analysis was performed on the up-regulated DEGs between the F-CircAE2 and the VECT groups in NIH3T3 Cells. The vertical axis represents the top 20 enriched pathways according to the gene counts. The different colors represent the −log10 of adjusted *p* values. The horizontal axis represents the Gene ratio.

Figure S5

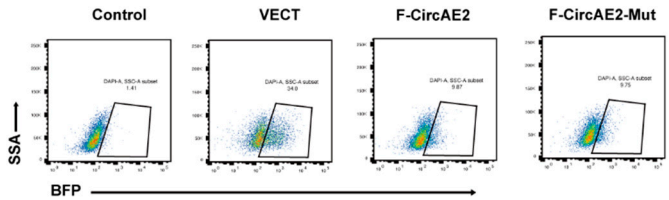

Figure S5 The BFP^{+} HSPCs were sorted through flow cytometry.

Figure S6

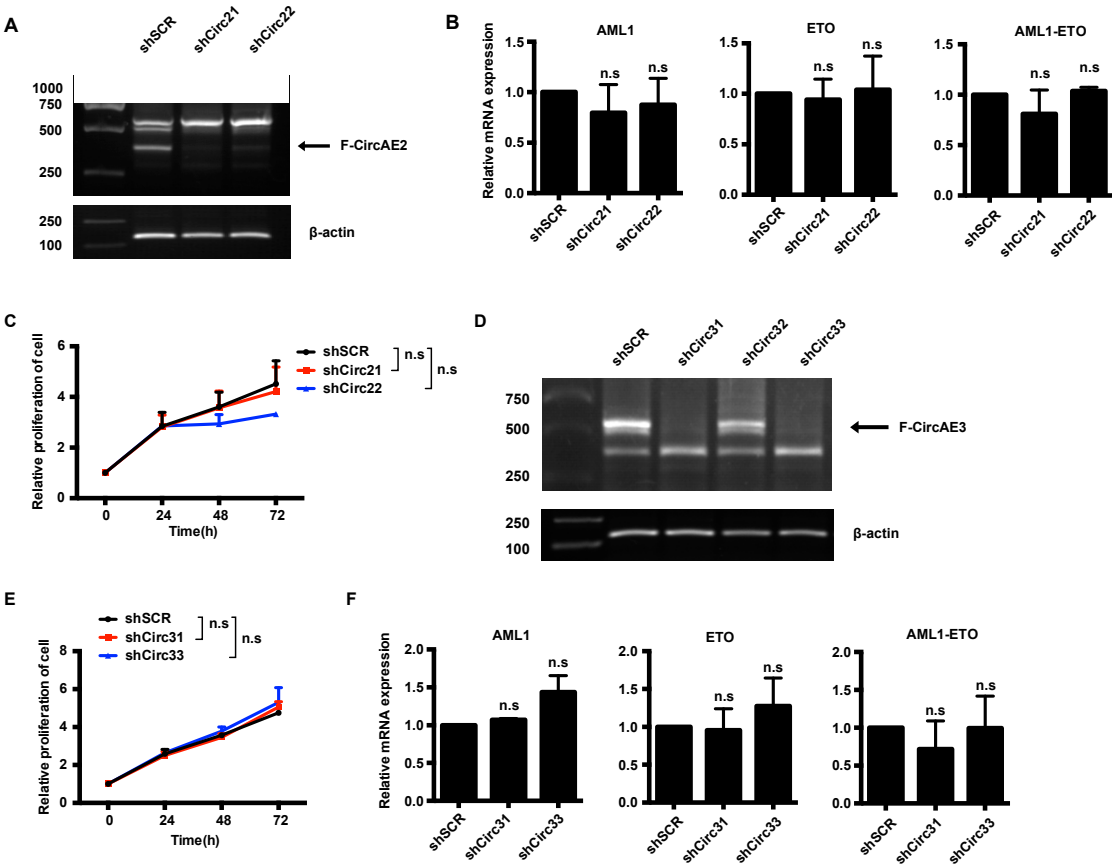

Figure S6

(A) shCirc21 and shCirc22 targeting the back-splice junction of F-CircAE2 efficiently knocked down the expression of F-CircAE2, β-actin was used as control.

(B) RT-PCR analysis of linear transcripts of *AML1*, *ETO,* and *AML1-ETO* using specific primers after F-CircAE2 knockdown.

(C) The proliferation of F-CircAE2 knockdown Kasumi-1 cells showed no significant difference compared with the scramble group.

(D) shCirc31, shCirc32, and shCirc33 were specific for F-CircAE3 knockdown. The knockdown efficiency was measured by PCR using outfacing primers, while β-actin was used as control.

(E) F-CircAE3 knockdown did not affect Kasumi-1 cells proliferation.

(F) RT-PCR analysis of linear transcripts of AML1, ETO, and AML1-ETO using specific primers.

Figure S7

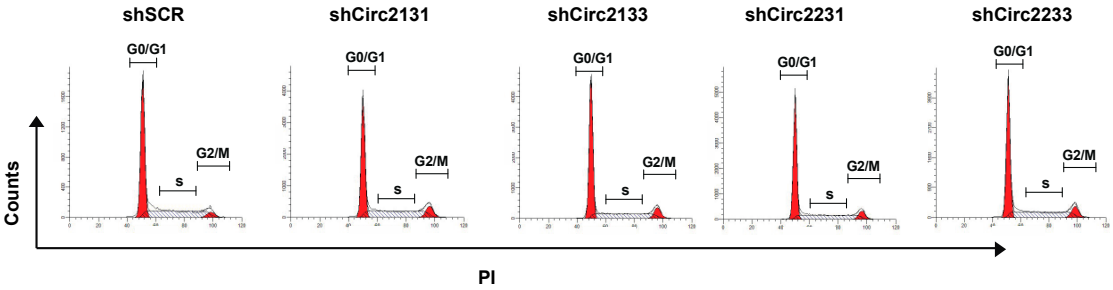

Figure S7 Cell cycle distribution was analyzed by flow cytometry using PI staining.

Figure S8

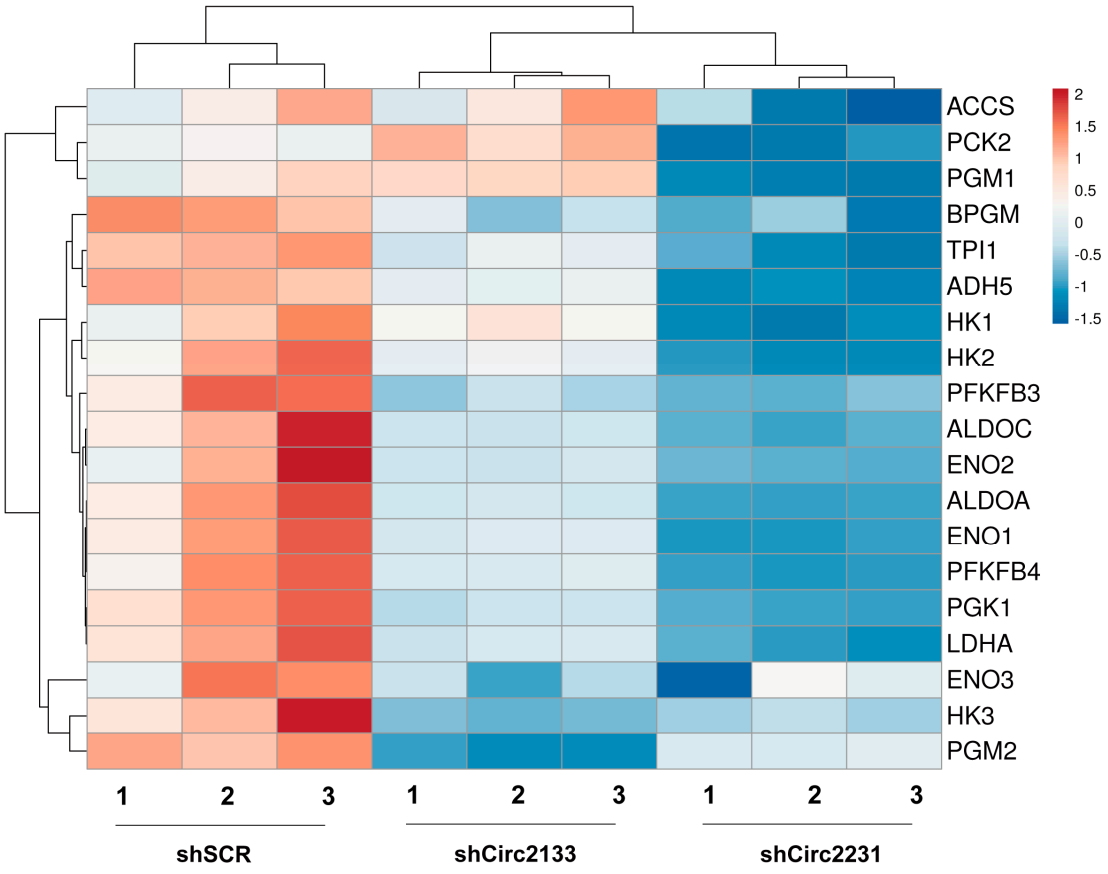

Figure S8 The heatmap of differentially expressed genes in the glycolysis pathway upon F-CircAEs knockdown in Kasumi-1 cells as identified by RNA-seq experiments. Heatmaps were generated using ClustVis (https://biit.cs.ut.ee/clustvis/). The different colors represent the row centered fold change values (blue = lower, white = intermediate, red = higher).