

Description of Additional Supplementary Files

Supplementary Data 1

Nonsynonymous mutations identified by mWES in ZM alone-induced primary murine leukemia samples.

Supplementary Data 2

RNA-seq based transcriptome profiling revealed that ZM-transformed murine AML cells express a subset (15%) of LSK 'stemness'-related signature genes.

Supplementary Data 3

RNA-seq identified genes, including a LSK 'stemness' gene signature, significantly upregulated in the ZM- or MLL-AF9-transformed murine AML cells, relative to those transformed by co-expression of Hoxa9 plus Meis1 (A9M).

Supplementary Data 4

Integrated ChIP-seq and RNA-seq analyses revealed genes directly activated by ZM during leukemic transformation.

Supplementary Data 5

ZM-interacting proteins identified by BioID using murine HSPCs stably expressing ZM fused with a BirA domain at either its N- or C-terminus.

Supplementary Data 6

Primer sequences used in this study.