Figure S1. Southern blot for IgH rearrangement
Southern blot of EcoR1 digested DNA from CALM-AF10 leukemic spleens hybridized to an IgH probe. Mouse identification numbers are indicated; C is germline control tissue; asterisk denotes germline band; size standards are in kilobases.
**Figure S2. Mn1-pol fusion**

(A) RTPCR analysis of leukemic spleens with Mn1 integrations demonstrates a fusion transcript between Mn1 exon 1 and the retroviral pol gene. Samples 38, 39, and 46, all had integrations within the first intron; samples 25 and 80 had integrations that occurred in the opposite orientation as Mn1 transcription and occurred 3’ of exon 2. (B) Samples 38, 39, and 46 were sequenced and shown to form an Mn1-pol fusion as indicated. Uppercase nucleotides and amino acids refer to Mn1 sequences, lower case refer to retroviral pol sequences.
Figure S3. Southern blot of 15 WT mice infected with the MOL4070LTR virus, hybridized to either the upstream or downstream Zeb2 probes (probes “A” and “B” of Fig. 3). Control DNA (C) is from non-infected spleen. A minor clone with Zeb2 integration is indicted with an asterisk.
Figure S4. Two additional transcribed RNAs near Zeb2 integration sites

(A) Mouse chromosome 2. Insertions identified by LM-PCR are indicated by black arrows. Insertion events reported in the RTCGD are indicated by red arrows. The vertical red arrow represents an insertion event for which the integration orientation was not reported in the RTCGD. Black circles indicate insertion events identified by Southern blot. Zeb2 exons are indicated in blue. The location of a spliced EST (BB633916) and a non-coding RNA (MMU56439) are shown, and their transcriptional orientation is indicated with a black arrow.

(B) Expression of MMU56439 analyzed by RQ-PCR. The assay was performed with SYBR green according to the manufacturers protocol (Applied Biosystems). PCR cycling conditions were: 50°C for 2 minutes, 95°C for 10 minutes, followed by 40 cycles of 95°C for 15 seconds and 60°C for 1 minute. Primer sequences for MMU56439 were as follows- F1 5’-ATGAGCATCATTAAGCAGTGAGCAGC-3’ and R1 5’-TGTTTACTGAAAGTCAAGCTGC-3’.
Figure S5. *Ptpn11* spontaneous point mutation
Chromatograph of DNA sequence of *Ptpn11* codons 68-76 with mouse and human genomic sequence and the amino shared acid sequence. Mouse number 5 has one normal allele and one C to T mutation at codon 72 resulting in a Ala to Val amino acid change.