Figure S1. Mouse lncRNA Dleu2 transcript map. Location of mDleu2 which can encode 15 different transcripts; the spliced-in exons are shown by vertical bars, and the spliced-out introns are shown by horizontal lines. Promoter regions are shown in red at the bottom. Introns coding for miR-15/16 denoted by yellow star. Figure obtained from ENSEMBL (uswest.ensembl.org/Mus_musculus/Gene/Summary?db=core;g=ENSMUSG00000097589;r=14:61602839-61682373). lncRNA, long non-coding RNA; miRNA/miR, microRNA; misc, miscellaneous; lincRNA, long intervening noncoding RNA; Dleu2, deleted in leukemia 2 gene.

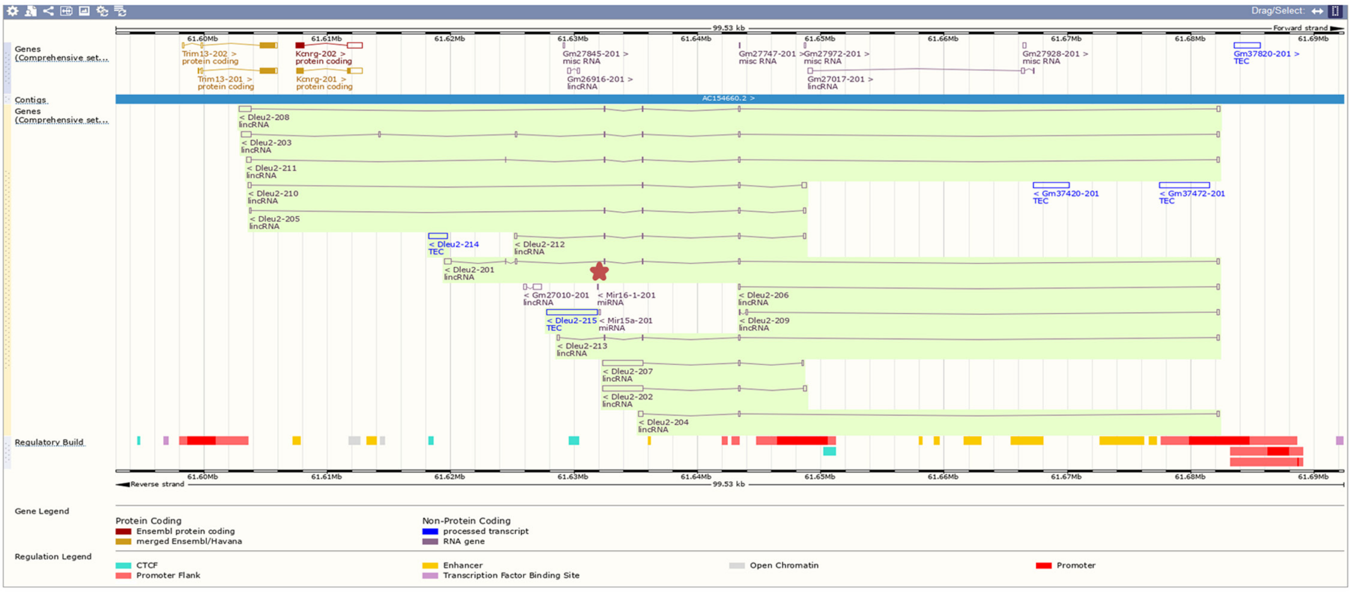

Figure S2. Expression of genes associated with proliferation. (A) PCNA, (B) TGF-β and (C) EGFR expression in the negative control and Dleu2-silenced AML-12 cells. n=6. Data are presented as the mean ± the standard error of the mean of at least 6 independent experiments. siRNA, small interfering RNA; Dleu2, deleted in leukemia 2 gene; PCNA, proliferating cell nuclear antique; TGF-β, transforming growth factor-β; EGFR, epidermal growth factor receptor.

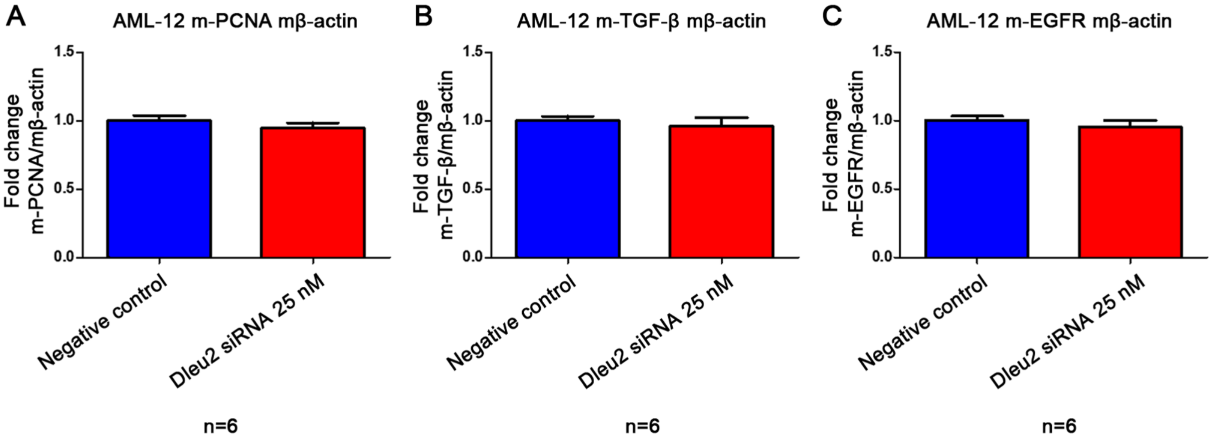

Figure S3. Differences between the mouse Dleu2 splicing organization compared with Human DLEU2 splicing organization. (A) Mouse Dleu2 transcripts are more nested compared with (B) human DLEU2, which have a longer range away from the miR15a/16 loci and are more spread out across different promoter sites. Figures obtained from ENSEMBL (uswest.ensembl.org/Mus_musculus/Gene/Summary?db=core;g=ENSMUSG00000097589;r=14:61602839-61682373 and uswest.ensembl.org/Homo_sapiens/Gene/Summary?db=core;g=ENSG00000231607;r=13:49956670-50125720). Dleu2/ DLEU2, deleted in leukemia 2 gene; lncRNA, long non-coding RNA; miRNA/miR, microRNA; misc, miscellaneous; lincRNA, long intervening noncoding RNA.

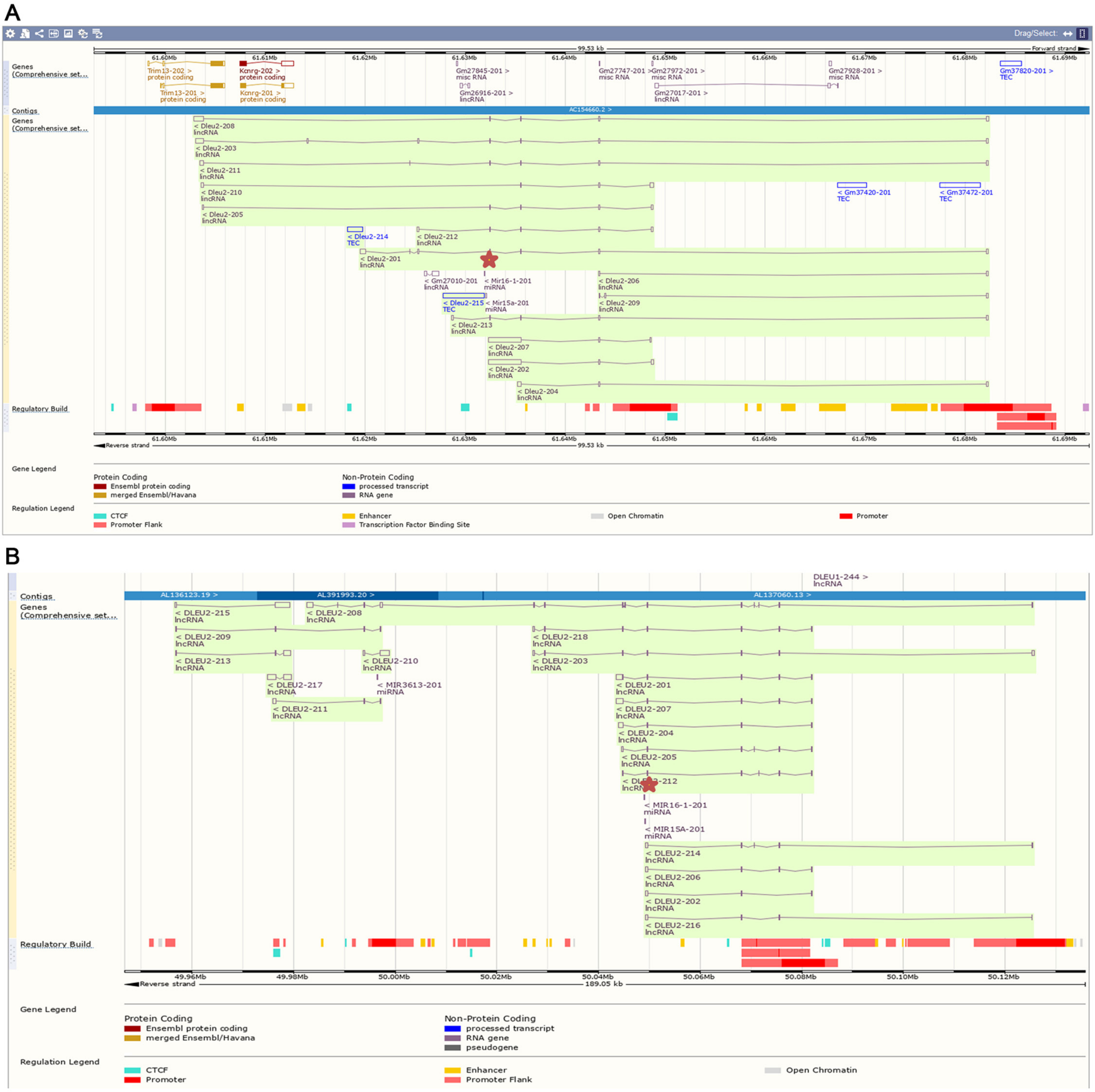

Table SI. Primer sets used for identifying mDleu2 transcripts and genes associated with proliferation[a].

Target	Sequence, 5'-3'	Length, bp
mDleu2-Alt1	GCGCTACACCGACTGACATT	125
mDleu2-Alt1	ACTGATTGGGTAGTGGCACAG	125
mDleu2-208	ATGTGAGGGTTATTGGGGAATT	117
mDleu2-208	GCCACACTCCAACCCTTTCT	117
mDleu2-203	TGACTTGAGTATGAAAGCTGTGA	51
mDleu2-203	ATCCATTCTGTCTGCCTGGC	51
mDleu2-210	AAGCGGGTCTCGAGAGGT	118
mDleu2-210	TAGCAACCGGATCCCCTGG	118
mDleu2-201	AGCAAGGAAGTTGGACGTGA	119
mDleu2-201	ATGGCTAGGATACACGCAGG	119
mDleu2-Gm27010-201	AGTGCTTTGTTGGCTCTCAA	102
mDleu2-Gm27010-201	GCCGCTGACAAACATGAACA	102
mDleu2-204	ACCCATCACCACTGCAATGA	113
mDleu2-204	ACATGAATAGAGTGTTAATGGGCA	113
mDleu2-215 TEC	TGTGTAGTGCAGTGGGATGT	145
mDleu2-215 TEC	GACCCAGGCTCAAAAGACCA	145
mDleu2-213	AGAACCTCAGAGGGCTCTACT	149
mDleu2-213	GGGGAGGAGAGGGTACTTCA	149
mDleu2-207+202	TGGCTATGGTTCAGAAGCGT	137
mDleu2-207+202	GTCCGAACCCTGACACTGTC	137
mDleu2-207+202	AGAAGCGTCCTACAAAGGCT	122
mDleu2-207+202	CGAACCCTGACACTGTCCTT	122
mDleu2-209 71	TGTTAAGTCATTAAGAACCAGAAAGGG	71
mDleu2-209 71	TCGAGGTGAAAATGCAACGTTAT	71
mPCNA		-
Forward	TTTGAGGCACGCCTGATCC	
Reverse	GGAGACGTGAGACGAGTCCAT	
mTGF-b		-
Forward	TCCAACCGCAGCTACTCTG	
Reverse	CCCGTACAGGAAGCAGTTATTTT	
mEGFR		-
Forward	GCCATCTGGGCCAAAGATACC	
Reverse	GTCTTCGCATGAATAGGCCAAT	

[a] Primers targeting specific Dleu2 transcripts are shown outlined in various colors on ENSEMBL map in Fig. 1B.