

## **Table S1**

### **Bone marrow flow cytometry**

Cell suspensions were depleted of RBC, blocked with anti-Fc $\gamma$ II/III receptor mAb, and surface-stained with PE- or FITC-conjugated Abs. Data was collected on a FACS Calibur (BD Pharmingen). Data were analyzed using FCS EXPRESS (De Novo Software, Thornhill, ON, Canada). Primary Abs used include anti-B220-PE, anti-IgMa-FITC, anti-IgMb-FITC, and anti-CD21-FITC (BD Pharmingen).

## **Table S3**

### **Determining *MYC* mutations in TCL1-tg B cell lymphomas**

The *MYC* gene was amplified by genomic PCR using the following primers: 5'-CG-CTTTTTTCTGACTCGCTGTAG-3' and 5'-GCGGGGGTCAGGCTAAATTTTACT-3'. Thirty amplification cycles were performed with Advantage2 polymerase (Clontech). PCR products were subcloned into pCR2.1TOPO (Invitrogen), sequenced, and analyzed for mutations, as previously described.<sup>1-3</sup>

## **Figure S1**

### **Proliferation analyses**

Purified B cells were labeled with carboxyfluorescein diacetate, succinimidyl ester (CFSE) according to the manufacturer's instructions (Molecular Probes, Eugene, OR) for 10m at 37°C, washed twice, and resuspended in RPMI with 10% FBS at  $3 \times 10^6$  cells/ml. Proliferation of GC and non-GC B cells was determined by flow cytometry at 72h post-

stimulation with anti-IgM (20 $\mu$ g/ml, Jackson ImmunoResearch Laboratories West Grove, PA) plus IL-4 (50u/ml, Biosource International, Camarillo, CA).

## **Figure S2**

### **Immunohistochemical staining**

Standard ABC methods were employed. Briefly, slides were de-paraffinized in xylenes and re-hydrated through a series of different percentages of ethanol to water. To block the endogenous peroxidase activity, slides were treated in 3% H<sub>2</sub>O<sub>2</sub> in methanol for 30m. Slides were then heated a pressure cooker for 3m after reaching full pressure in 10 mmol/L citrate buffer solution (pH 6.0) for antigen retrieval. After that, sections were incubated for 1h with M.O.M<sup>TM</sup> mouse Ig blocking reagent and then incubated with PAX-5 mouse monoclonal antibody (clone 24, BD Transduction Laboratories, Lexington, KY) for 30m diluted 1:25 in working M.O.M<sup>TM</sup> diluent. The slides were rinsed in PBS and incubated for 10m in biotinylated anti-mouse IgG diluted 1:250 in working M.O.M<sup>TM</sup> diluent, and subsequently incubated for 5m in VECTORSTAIN *ELITE* ABC reagent. 3,3'-diaminobenzidine (Vector laboratories) was used for chromogen. Slides were counterstained for 2-3m with hematoxylin (Fisher Scientific, Pittsburgh, PA) and mounted with Permount (Fisher Scientific).

## **Figure S3.**

### **Clonality determination**

Genomic DNA isolated from WT spleen or TCL1-tg tumors was digested with *EcoRI* or *StuI*, followed by Southern blot with a <sup>32</sup>P-labeled J<sub>H</sub> probe corresponding to the *JH4*

region of the *IgH*.<sup>4</sup> The DNA fragment used to make the probe was amplified by PCR using the following primers: 5'–TGTGGTGACATTAGAACTGAAGTA–3' and 5'–CAAGATTAGTCTGCAATGCTCAGA–3'. The probe was prepared using the Prime-It II Random Primer Labeling Kit (Stratagene).

## **Figure S5.**

### **SKY analyses of TCL1-tg B cell lymphomas**

Primary tumors from TCL1-tg mice ( $5 \times 10^6$  cells each) were cultured in RPMI medium supplemented with 10% FBS under standard conditions. After 18h, colcemid (GIBCO/BRL; KaryoMAX Colcemid solution) was added to a final concentration of 25  $\mu\text{g/ml}$ , followed by an additional 75m incubation. Metaphase-frozen cells were then treated with 0.075M KCl for 10m at 37°C to prevent aggregation. Following treatment with methanol: acetic acid fixative, nuclei were dropped onto glass slides and dispersed chromosomes were dried overnight. Spectral karyotyping probes were employed according to the manufacturer's protocol (Applied Spectral Imaging, Carlsbad, CA). Karyotypes were captured with a Nikon Eclipse microscope equipped with an Applied Spectral Imaging interferometer and 40 $\times$  and 63 $\times$  objectives.

## **Figure S6.**

### **Analysis of *Aicda* expression in TCL1-tg B cell lymphomas**

qPCR (SYBRgreen) was performed on an Applied Biosystems 7700 sequence detector. Expression was normalized to a *36B4* control sequence.<sup>5</sup> The qPCR primers used for

*Aicda* were FWD: 5'-GATGGAACCCTAACCTCAGCC-3' and REV: 5'-GCCTTGCG-GTCTTCACAGAA-3'.

## References:

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