

SUPPLEMENTAL MATERIAL

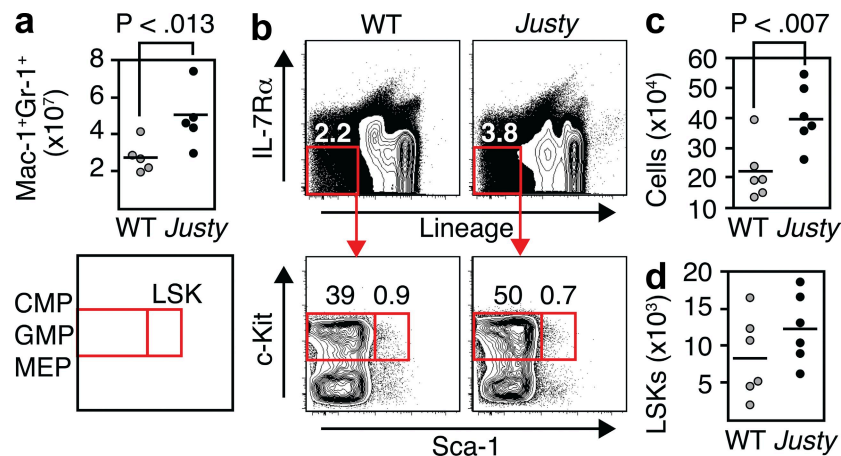
Lu et al., <http://www.jem.org/cgi/content/full/jem.20100147/DC1>

Figure S1. Analysis of myeloid and hematopoietic progenitors in bone marrow. (a) Yields of CD11b/Mac-1⁺Gr-1⁺ cells from bone marrow. (b) Flow cytometric analysis of bone marrow cells for expression of the indicated markers. Lineage refers to an antibody cocktail that recognizes Ter119, CD11b/Mac-1, Gr-1, CD49b, CD11c, CD3, and CD19. (c) Yields of myeloid/granulocytic/erythroid progenitors (CMP/GMP/MEP gate in b) from bone marrow. (d) Yields of hematopoietic progenitors (LSK gate in b) from bone marrow. Data in b are representative of six independent experiments. Horizontal bars in c and d indicate mean cell count.

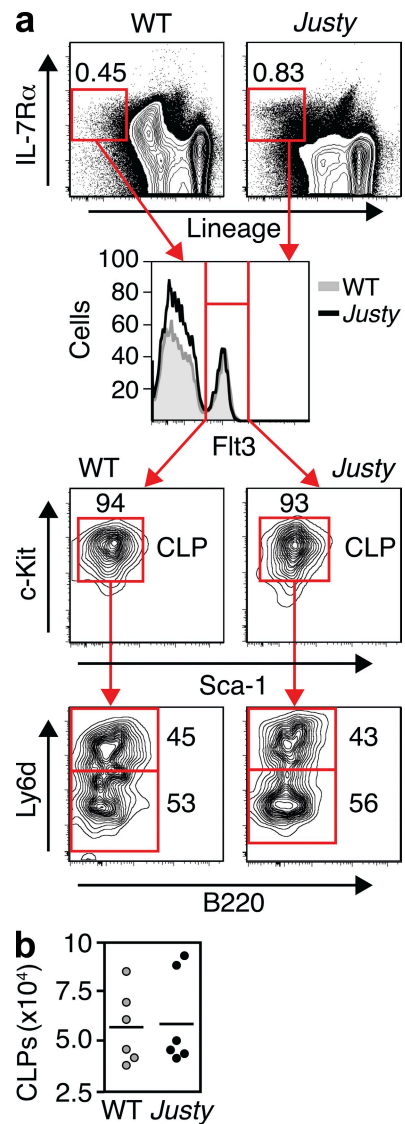


Figure S2. CLPs in *Justy* bone marrow appear normal. (a) Flow cytometric analysis of bone marrow cells for expression of the indicated markers. Lineage refers to an antibody cocktail that recognizes Ter119, CD11b/Mac-1, Gr-1, CD49b, CD11c, CD3, and CD19. The CLP gate denotes CLPs. (b) Yields of CLPs (CLP gate in a) from bone marrow. Data in a are representative of three independent experiments. Horizontal bars in b indicate mean cell count.

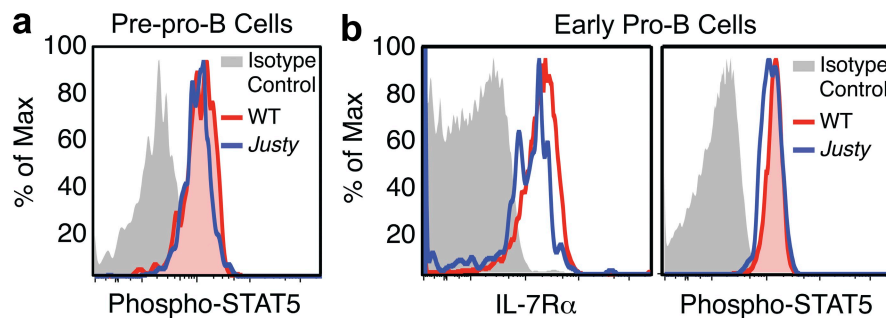


Figure S3. Similar levels of IL-7 receptor α expression and Stat5 phosphorylation in wild-type and *Justy* B cell progenitors. (a) Flow cytometric analysis of intracellular phospho-Stat5 levels in pre-pro-B cells. (b) Flow cytometric analysis of surface IL-7 receptor α expression and intracellular phospho-Stat5 levels in early pro-B cells. Data are representative of three independent experiments.

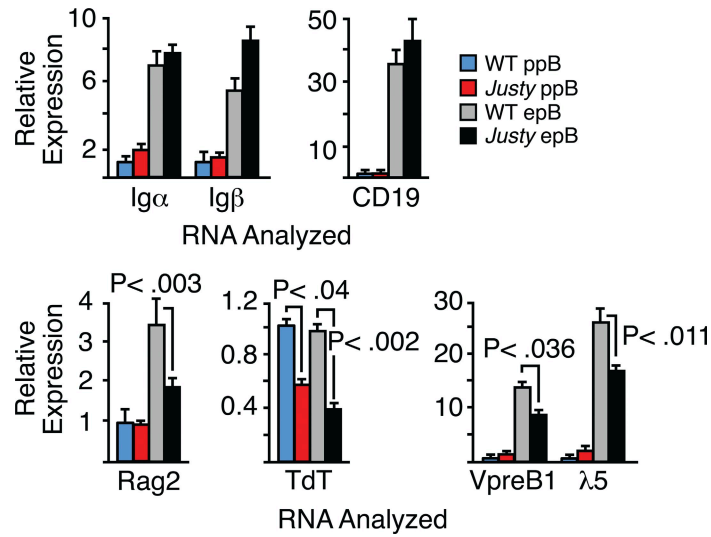


Figure S4. Expression of B-lineage genes is normal or modestly decreased in *Justy* cells. Q RT-PCR analysis of RNA encoding the indicated proteins in B cell progenitors. For all RNAs, values are plotted relative to the wild-type pre-pro-B cell value, which was set at 1. All bar graphs represent the mean and standard deviation of values obtained by Q RT-PCR analysis of three or four independent RNA samples, each generated from a separate sort purification of the indicated cells.

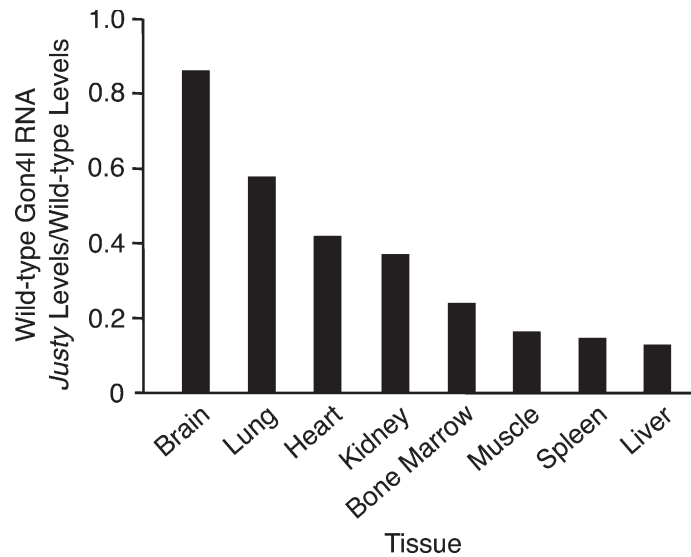


Figure S5. The impact of the *Justy* mutation on the expression of wild-type *Gon4l* RNA varies between tissues. Q RT-PCR analysis of wild-type *Gon4l* RNA levels in the indicated tissues from wild-type and *Justy* mice. A primer pair specific for normally spliced wild-type *Gon4l* RNA was used for PCR amplification (see Fig. 5 f). The *Gon4l* RNA level detected in each tissue sample was normalized to that for *Hprt*. Shown is the value obtained from each *Justy* sample divided by the corresponding wild-type sample value. Data are representative of two independent experiments.

Table S1. Genes within the interval on mouse chromosome 3 containing the *Justy* mutation

Gene	Location on chromosome 3	Expression pattern	Encoded protein	Function of protein
	<i>bp</i>			
<i>Arhgef2</i>	88,433,419–88,444,626	High in testis; low in other tissues	Guanine nucleotide exchange factor	Signal transduction
<i>Rxfp4</i>	88,455,820–88,457,064	Broad	Relaxin family peptide receptor 4	Signal transduction
2810403A07Rik	88,489,740–88,516,844	Unknown	Hypothetical RNA-binding protein	(Predicted) pre-mRNA splicing
<i>Rit1</i>	88,520,786–88,533,649	Broad; high in macrophages and mast cells	Ras-like GTP-binding protein	Regulation of signal transduction
<i>Syt11</i>	88,548,623–88,579,060	Restricted to brain and CNS	Synaptotagmin XI	Calcium binding and transport
5830417110Rik partial duplication of <i>Gon4l</i>	88,580,932–88,629,509	Broad	Hypothetical protein that contains PAH domain	Unknown
<i>Gon4l</i>	88,650,310–88,714,021	Broad	Nuclear protein; homology to transcriptional regulators	Transcriptional regulation
<i>Msto1</i>	88,713,733–88,714,732	Broad; high in testis	Mitochondrial protein	Mitochondrial morphology and distribution
<i>Dap3</i>	88,727,363–88,754,204	Broad; high in testis	Death-associated protein	Induction of apoptosis
<i>Ash1L</i>	88,769,734–88,883,297	Broad	Histone methyltransferase	Transcriptional activation
<i>Rusc1</i>	88,887,901–88,897,285	High in brain and CNS; low in other tissues	RUN and SH3 domain-containing	Signal transduction
<i>Fdps</i>	88,897,510–88,905,867	Broad; high in specific tissues (e.g., osteoclasts)	Farnesyl pyrophosphate synthetase	Isoprenoid synthesis
<i>Pklr</i>	88,940,064–88,950,516	Restricted to small intestine, liver and bone marrow	Pyruvate kinase, liver, and RBC isoform 1	Pyruvate kinase for glycolysis

Gene locations (in base pairs) were determined using the UCSC Genome Browser (July 2007 assembly). RNA expression pattern data were from the SymAtlas website (<http://biogps.gnf.org/>). We performed RT-PCR and Northern blot analysis to assess *Gon4l* RNA expression (unpublished data). Protein function was determined using the UCSC Genome Browser and National Center for Biotechnology Information Pubmed, OMIM, and BLAST databases.