SUPPLEMENTAL MATERIAL

Beisner et al., http://www.jem.org/cgi/content/full/jem.20121072/DC1

A

Mouse chromosome 2

mouse ID	908	209	257	507	510	327	208	196	197	878
phenotype	mut	mut	mut	mut	mut	mut	wt	wt	wt	wt
02.101.413	B	B	B	B	B	H	C	B	C	H
02.105.827	B	B	B	B	B	H	C		C	H
02.109.250	B	B	B	B	B	H	C		C	H
02.110.937	B	B	B	B	B		C	H	C	H
02.115.965	B	B	B	B	B		C	H	C	H
02.120.766	B	B	B	B	B	B	C	H	C	H
02.123.445	B	B	B	B	B	B	C	H	C	H
02.125.196	B	B	B	B	B	B	C	H	C	H
02.126.938	B	B	B	B	B	B	C	H	C	H
02.127.708	B	B	B	B	B	B	C	H	C	H
02.129.447	B	B	B	B	B	B	C	H	C	H
02.130.640	B	B	B	B	b	B	C	H	C	
02.132.605	B	B	B	B	B		C	H	C	C
02.140.157	B	H	B	B	B			H	C	C
02.146.634	B	H	B	B	B			H	C	C

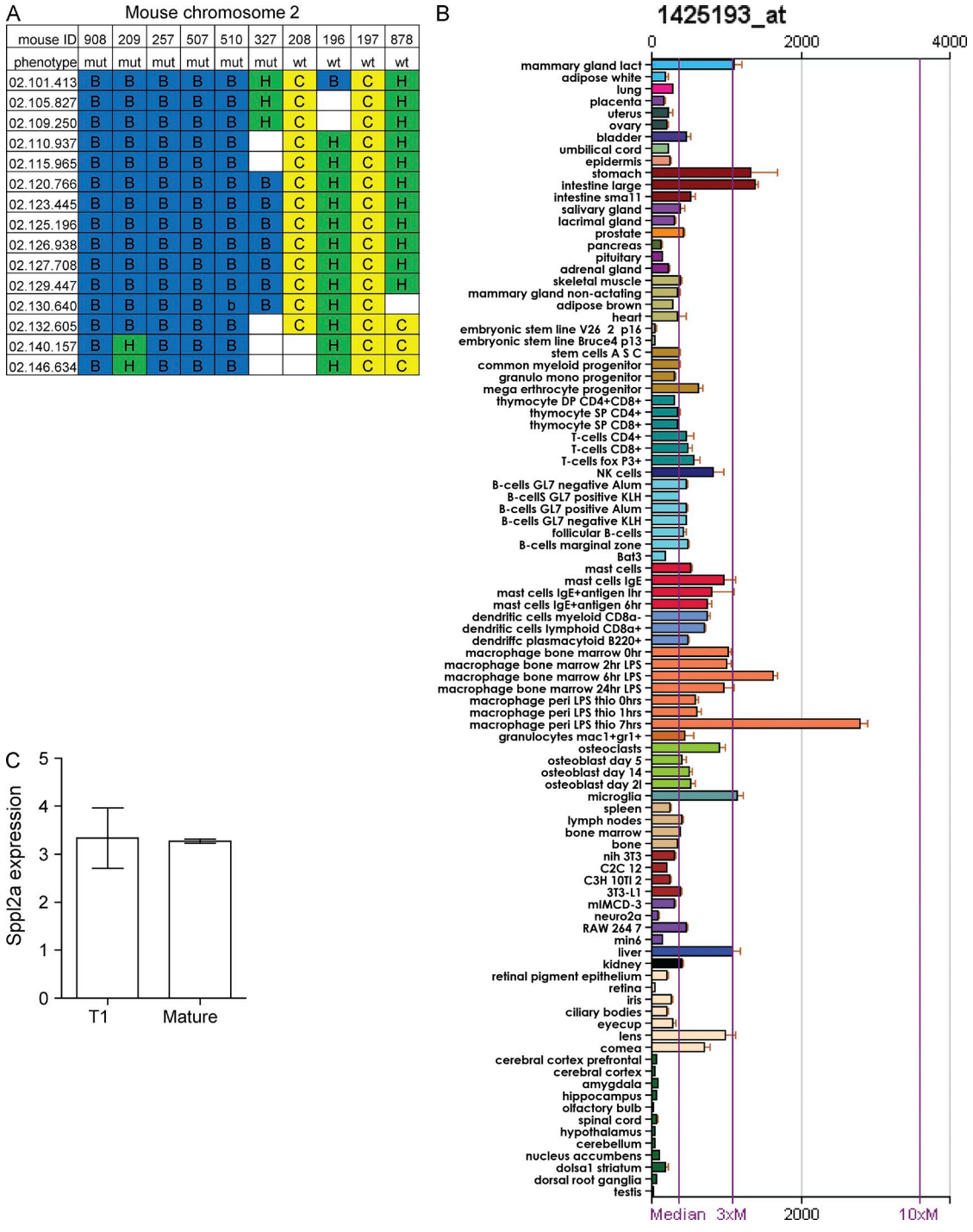

Figure S1. Identification of Sppl2a by ENU mutagenesis. (A) SNP analysis of B6 and BALB/c cross of mutants focusing in on chromosome 2. The far left column indicates chromosome number together with position in megabases. The genotype for each SNP is indicated as follows: B, homozygous C57BL/6J (blue); C, homozygous BALB/c (yellow); and H, heterozygous (green). This analysis maps the mutation to between 109.250Mb and 140.157Mb. (B) Sppl2a expression via microarray from a wide variety of mouse tissues. Data were downloaded from BioGPS (http://biogps.org/#goto=welcome). (C) Sppl2a mRNA expression was measured by quantitative PCR in FACS-sorted T1 ($CD24^{hi}CD21^{lo}$) and mature B cells ($CD24^{lo}CD21^{int}$; mean and average error, $n = 2$ from two independent experiments).