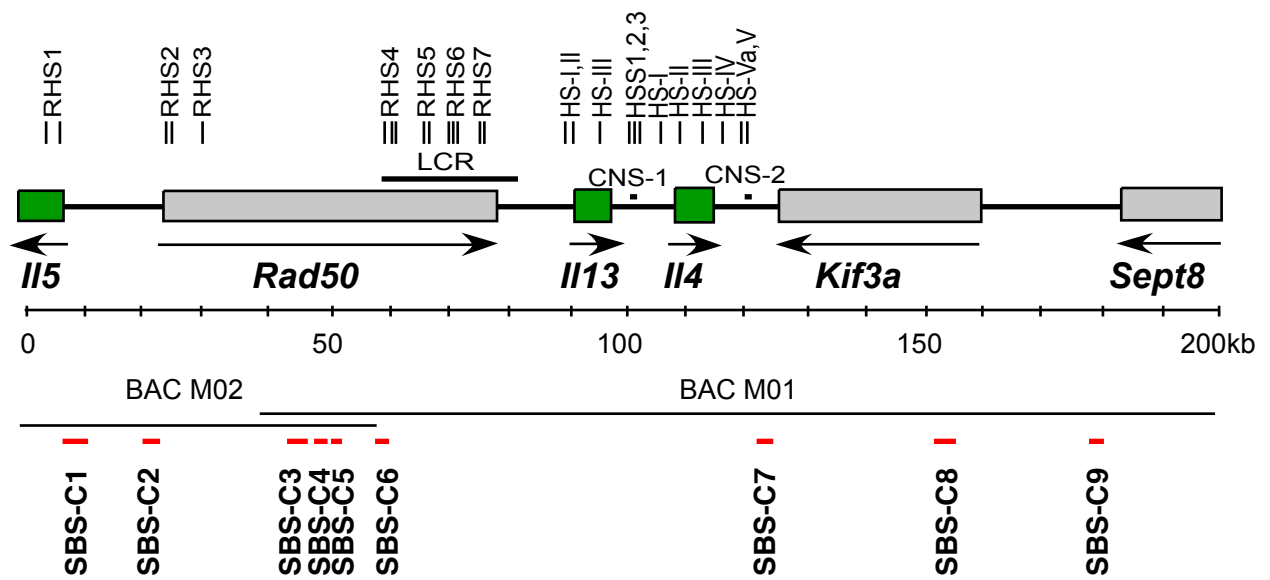
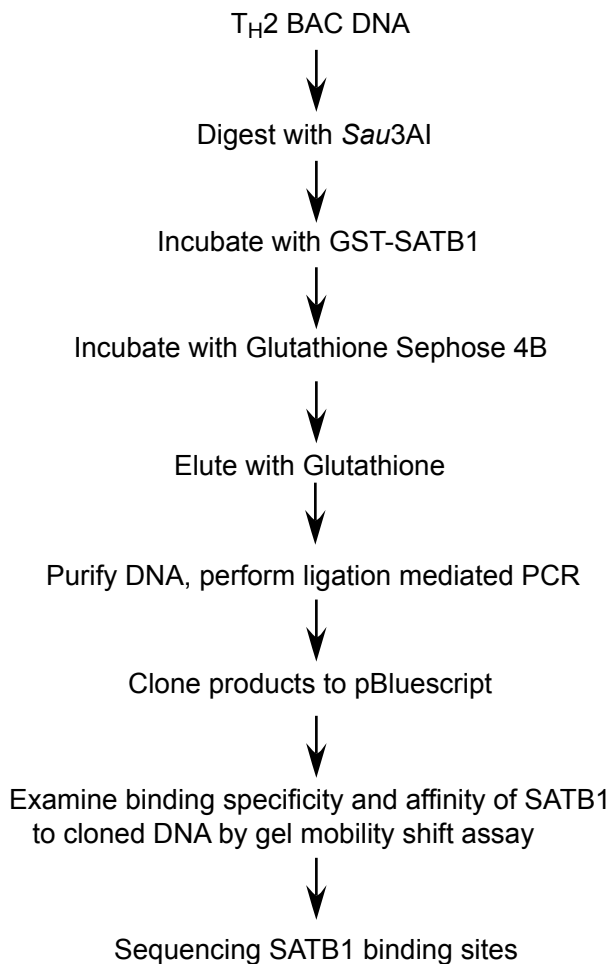


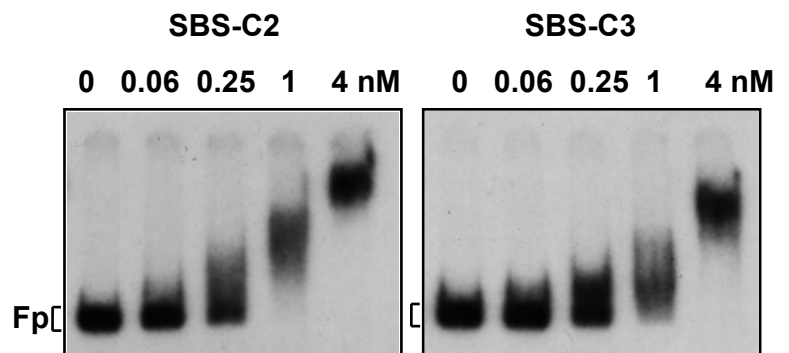
# Supplementary Figure 1



**a**



**b**



**c**

SBS	Size (bp)	Kd (nM)	Position*
C1	2210	0.25	chr11:53,559,750-53,561,957
C2	1842	0.25	chr11:53,547,379-53,549,220
C3	1696	0.25	chr11:53,525,340-53,527,035
C4	968	0.25-1	chr11:53,522,065-53,523,032
C5	1133	0.25-1	chr11:53,519,697-53,520,829
C6	908	0.25-1	chr11:53,511,507-53,512,414
C7	859	2-4	chr11:53,445,830-53,446,688
C8	1552	0.25-1	chr11:53,416,073-53,417,624
C9	815	0.25	chr11:53,390,647-53,391,461

\*UCSC Genome Browser on Mouse Feb 2006 Assembly

**Supplementary Fig. 1 Cloning of genomic sequences which bind to SATB1 *in vitro*.**

**a,** We used two overlapping BAC clones (MO1 and MO2) derived from the 200-kb T<sub>H</sub>2 cytokine locus and followed the scheme illustrated to obtain a series of pBluescript plasmid DNA containing SATB1-binding sequences (see Methods). After sequencing, the cloned fragments were digested, end-labeled with {<sup>32</sup>P}dATP and Klenow polymerase. Gel mobility shift assay was performed using Glutathione *S*-transferase (GST)-fused SATB1 (amino acid 346-763) (Dickinson, L.A., Dickinson, C.D., Kohwi-Shigematsu, T., *J. Biol. Chem.* **272**:11463-11470, 1997). **b,** Representative gel-mobility data are shown for SBS-C2 and SBS-C3. Under conditions of protein excess, the dissociation constant (K<sub>d</sub>) was estimated at the concentration of protein that results in a 50% shift. **c,** Size of fragment, K<sub>d</sub>, and genomic positions are shown.