

Supplemental Figure 1.

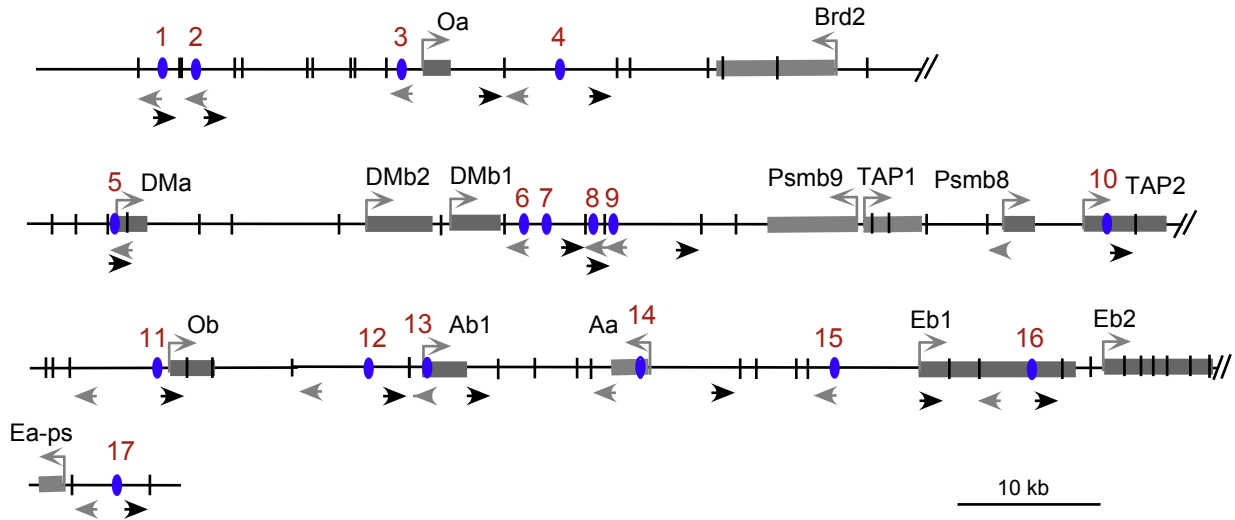
Sites	Strand	Sequences
1	+	ATACAACTGA CCTCTAGGGGGCTCTGGAGCT AAATCTACAG
2	+	GTTGTTTGTA CCACAAGAGGGCGCTCTAGGC CGGTTTATTA
3	+	TCGTGAGCAG CCTCTTAGGGGCGCTGTTTCC CAAACTCTGG
4	+	CAATAAATCC CCACCAGGGGGCGCTCGCGTG TGTAGCTCTA
5	+	GCCCGACCTT CCACCAGGGGGCGGAGGTCTC CAGAGAGGCC
6	-	GGAGCAATGG CCCAGAGGTGGC CCGCGTGC TTGCTGTGCA
7	-	TCCTCTCTAG CCTCCAGGGGGCACCAGGCAC AGCCATACAT
8	-	CAAGTTGTAG CCTGTAGGTGTCAGCAAAGAC TGACAATGGG
9	+	ACACATTTGT CCACTAGGTGGCGCCAAAGAC ATGTGCTCTC
10	+	CACCTACAGG CCAGAAGTGGCCACCATATCC CAGTATAGAT
11	-	TTTTACATGG CCACCAGATGGCACCAGACTC ACACTGCGCG
12	+	TGCTGTGTTA ACACTAGAGGGCGACTTTGAG CTTAGAAATC
13	-	AGGCCCTGAC CCCCTAGGGGGCACTCGTTCT CAGGAGAGCC
14	-	CAAACTGTA CCAGCAGGGGGCAGCGTGCAG TCCTCAGCAA
15	+	CCTACAGAAC TCAGTAGAGGGCATCAGATCC CTGGAACTGG
16	-	CAGTGGACAA ACAGCAGATGGCAGTGCTGAG CGAGGATCCT
17	-	CCACGAATGA <u>C CAGTAGATGGCGGAATTGAC</u> AAGACAAGAT

Core sequences

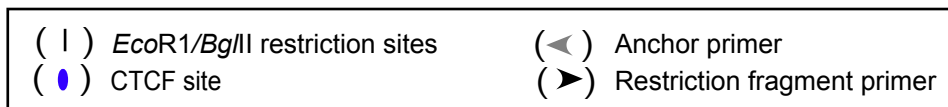
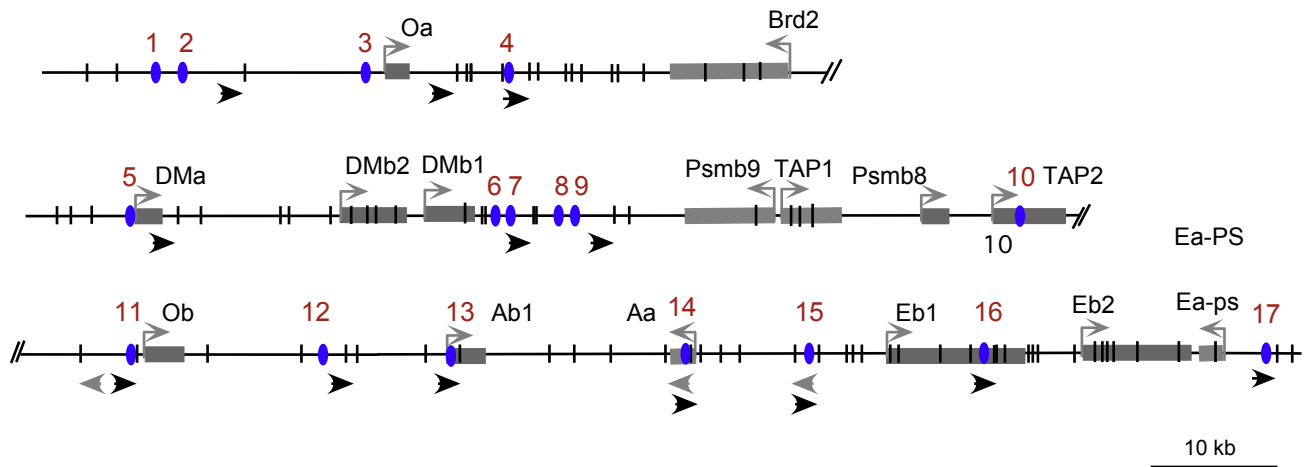
Supplemental Figure 1 – Alignment of CTCF sequences. The identified consensus sequence of CTCF binding sites from B cells and plasmablasts were aligned using MEME software (<http://meme.nbcr.net/meme/>). Core CTCF sequences are underlined in the middle of the sequences. A dash (-) indicates sequences in which the reverse complement of the sequence was used for the alignment.

**Supplemental Figure 2**  
**MHC-II Restriction Map and Location of 3C primers in the murine MHC-II locus**

*EcoR1* restriction sites



*BglII* restriction sites



Supplemental Figure 2 – MHC-II locus restriction maps and 3C primer and 3C anchor positions. *EcoRI* and *BglIII* restriction maps of the C57Bl/6 MHC-II locus are shown with the gene bodies, transcription start sites, and CTCF-binding sites identified in this study. 3C anchor primers used in this study are illustrated by gray arrowheads. 3C primers used are represented by black arrowheads.

**Supplemental Table 1:** ENCODE Data used in this study.

<b>Tissue</b>	<b>ENCODE Accession</b>	<b>Contributing Lab</b>	<b>Contributing Institution</b>	<b># of Peaks</b>
Bone Marrow	wgEncodeEM001687	Ren, Bing	LICR	15,611
Cerebellum	wgEncodeEM001689	Ren, Bing	LICR	23,680
Cortex	wgEncodeEM001690	Ren, Bing	LICR	37,080
Heart	wgEncodeEM001684	Ren, Bing	LICR	33,172
Kidney	wgEncodeEM001685	Ren, Bing	LICR	41,698
Limb	wgEncodeEM002589	Ren, Bing	LICR	31,566
Liver	wgEncodeEM001696	Ren, Bing	LICR	30,378
Lung	wgEncodeEM001697	Ren, Bing	LICR	24,582
Olfactory Bulb	wgEncodeEM002585	Ren, Bing	LICR	14,512
Small Intestine	wgEncodeEM002591	Ren, Bing	LICR	17,170
Testis	wgEncodeEM002593	Ren, Bing	LICR	20,968
Thymus	wgEncodeEM002587	Ren, Bing	LICR	53,124
Whole Brain	wgEncodeEM002595	Ren, Bing	LICR	42,042

## Supplemental table-2 – Oligonucleotide sequences used in this study

### RT-PCR primers

Primer	Forward Primer	Reverse Primer
<i>H2-Aa</i>	AGCCCAACACCCTCATCTGC	ACCGTCTGCGACTGACTTGC
<i>H2-Ab1</i>	GAGATCCTGGAGCGAACG	AGGGAGATGACGACATTGG
<i>H2-Eb1</i>	GCGGAGAGTTGAGCCTACG	ACCATCTGACTTCAATGTTGCC
<i>H2-Eb2</i>	ACACAGCCTCTGGAACACCATAACC	CAGTCTTCTCCTCCTCGCCATTCC
<i>RFX5</i>	CTCGGGATGAACTGGTAGAAG	CTGGACGATGGAAGTGAAGG
<i>mCIITA</i>	GATCCTTCCAGCCTTCTCTTC	CCTTGTCTCCGATCTTGTCTC
<i>hCIITA</i>	GTGGCGAAATCAAGGACAAG	CAGTTGTATAGGGCCTCTTC
<i>CTCF</i>	GAAGTCATGGAGGGTACAGTG	GTCACAGGAACAGGTACTTGG
<i>18S</i>	GTAACCCGTTGAACCCCAT	CCATCCAATCGGTAGTAGCG

### ChIP primers

	Forward	Reverse
C1	CTCCTTCTGAATTGTGATTTATGAATTA AGATGG	CGTGTGTATATCTCGCAGTATGTTCT AAGG
C2	ATCAGGCAAGCGAATCCGAAG	AAGCCTCCCTCGCCAAGC
C3	AGAGCAGCGTGGGATTTTAAGG	CAGCCAGTCTAGCCAAACAGG
C4	TGAACTTGACACAGCATAGAATC	GCCTCACAGCTCTCATATACAG
C5	GCAGGGTGAAGTTGATTCC	CCTCATGGCTCTCAGACC
C6	GGGATGCCTGCCTGGTTC	TCACTGAGACTGGAGCAATGG
C7	GTATGAGTGTGGCTGCCTGAATGC	GCTCACAACCATCTCTAACTCCAGTTC C
C8	CAGACAGACAGACAGACAGAC	TGACAATGGGCAGGAAACC
C9	GCTCTCCACACTTCCAAACC	TAATTGTGTCAGGCTGAGTCG
C10	ATGCGACTGGACAGGAAC	TGGCTCACCGTCATCTATAC
C11	GTAGGGAAGGCTGTCTTTGC	TGAGGCTCAATGCTGTTCTC
C12	ACAGTCTTCAAGGTTCTCATCC	TGCTCTGGTCCCTTAGTCTGG
C13	AGCAGGCAGTTCTCAGAGG	GGGGCACTCGTTCTCAGG
C14	CCACACCTCTCCATCAAAGC	GCAGTCCTCAGCAACACC
C15	CCCTTCCGTTCTCCTTCC	CTCACAGCCATCTGAAACC
C16	CGGAAATAACCAAAGAAAATGAAGG	ACAAGTCATAACAGCCATTAC
C17	AGCATCTTGTCTTGTCAATTCCG	CCCAGCCTTTGTATCCTTGAACC
N1	GTTCCCTTTCCTTGCTCTCTC	CATCCAACACAACACTGACTTTCC

### Quantitative 3C Primer Sets (CTCF/ CTCF)

Primer	Anchor Primer	Restriction Fragment Primer
C1	TCTTCATGTTGATAATCCGCATCC	AAGGAGCGATTATGGAGTTGG
C2	ACAGGGATTCAGTACATCTC	AAAGATTGTTCTAAAGTAGTTACC
C3	CTGGAACACTACTCTGTAGACC	GCGTATTAGCCAGGGTTC
C4	ATGGAGGGATGTAAGAACGG	CCAGGGCTATACAGAGAAACC
C5	AGAAAACAAGAAAGTGTCCCTTAGG	TAGCCTAGTGTCTCTTTCCC
C6.7	GGGCTCACGGGATTCTGG	TGACCTTGAACCAATGTAGCC
C8	TATAACATGATCCCCAATACACC	GCCATCTACTTATATTAGTTTCCAG
C9	ACACCCAGTCTCCAGCATTTAC	AATATAAGGAGAAACAATCTGAGCAC
C10	AGCAGTAAAGAGAAATGAGAGC	CTGCTGCTTTTCACTCTCTCC
C11	GTTCCCATATCTTTGAGG	CATCTGGTGGCCATGTAAA
C12	GTGTGCTGTGGGTGTTTATTGG	ATGAATGAAGCCTGAATTATGTCAAATG
C13	GCTGAGCCTCTTTCCAATCC	TCTCCCTCCTTACACTGCTTCC

C14	TTCTTTCTCTTCTTCAAGTGACC	TGTGTA CTGGAGCTTATTCTGACC
C15	AACAAAGGAAAGAGAAGATATTTATAGC	CCTGGAGACACGCCCTTACC
C16	TGAGGAGATCAGCAGTTAATGG	TGAAGTAACAAGGCTGAAGGAAGG
C17	CCTGCCTCTCCTCCCTATCC	CTTTAAGGGACTTCAAGTGGTAAATCTC

### Quantitative 3C Primer Sets (promoters/ CTCF)

Primer	Restriction Fragment Primer	Anchor Primer (Ab1)
Ab1	GTGGTCGGTTAGGCATCATATTC	AGCATTCCAGGGTCCACAC
C2	TGAAACTCTCGATGCAGACC	AGCATTCCAGGGTCCACAC
C3	TCGTGTGTCTCCTCCAGAAC	AGCATTCCAGGGTCCACAC
C4	AAGATATTTTCTATGCTTTTGGTATGG	AGCATTCCAGGGTCCACAC
C5	AGGTAGGTGTGCCGATCC	AGCATTCCAGGGTCCACAC
C6.7	GCCAAATCCCATTATTAGATCC	AGCATTCCAGGGTCCACAC
C9	AAGGAGGACCACCGATCATC	AGCATTCCAGGGTCCACAC
C11	GCAACCACATGGTGGCACAC	AGCATTCCAGGGTCCACAC
C12	GAGAAAGGGCTGAAAAGATGG	AGCATTCCAGGGTCCACAC
C13	GTGGTCGGTTAGGCATCATATTC	AGCATTCCAGGGTCCACAC
C14	TTCTAACAGCAGACCTCTACTCG	AGCATTCCAGGGTCCACAC
C15	GACGCCGAGA ACTGGAAC	AGCATTCCAGGGTCCACAC
C16	TCAGGGTGGTCATGTTTAAGG	AGCATTCCAGGGTCCACAC
C17	CTGGAAGTCACCTGGAAAGC	AGCATTCCAGGGTCCACAC
Primer		(Aa)
Aa	TCTGAGGAACATATAACTGAAGGG	TAAGTGAAGGGCTACATGAAAATATCC
C2	TGAAACTCTCGATGCAGACC	CTGCTCTTGCTGAGGACAC
C3	TCGTGTGTCTCCTCCAGAAC	CTGCTCTTGCTGAGGACAC
C4	AAGATATTTTCTATGCTTTTGGTATGG	CTGCTCTTGCTGAGGACAC
C5	AGGTAGGTGTGCCGATCC	CTGCTCTTGCTGAGGACAC
C6.7	GCCAAATCCCATTATTAGATCC	CTGCTCTTGCTGAGGACAC
C9	AAGGAGGACCACCGATCATC	CTGCTCTTGCTGAGGACAC
C11	GCAACCACATGGTGGCACAC	CTGCTCTTGCTGAGGACAC
C12	GAGAAAGGGCTGAAAAGATGG	CTGCTCTTGCTGAGGACAC
C13	GTGGTCGGTTAGGCATCATATTC	CTGCTCTTGCTGAGGACAC
C14	TTCTAACAGCAGACCTCTACTCG	CTGCTCTTGCTGAGGACAC
C15	GACGCCGAGA ACTGGAAC	CTGCTCTTGCTGAGGACAC
C16	TCAGGGTGGTCATGTTTAAGG	CTGCTCTTGCTGAGGACAC
C17	CTGGAAGTCACCTGGAAAGC	CTGCTCTTGCTGAGGACAC
Primer		(Eb1)
Eb1	GAAGCCTGGATGTTTGTGC	GGAGTGTGGAGAGCATGG
C2	TGAAACTCTCGATGCAGACC	TTAGCACACAGGCTGAGG
C3	TCGTGTGTCTCCTCCAGAAC	TTCATCTATCTTTTAGCACACAGG
C4	AAGATATTTTCTATGCTTTTGGTATGG	GCACAACAGGCTGAGGTC
C5	AGGTAGGTGTGCCGATCC	CACAACAGGCTGAGGTCAG
C6.7	GCCAAATCCCATTATTAGATCC	GGAGTGTGGAGAGCATGG
C9	AAGGAGGACCACCGATCATC	TTCATCTATCTTTTAGCACACAGG
C11	GCAACCACATGGTGGCACAC	GCACAACAGGCTGAGGTC
C12	GAGAAAGGGCTGAAAAGATGG	GCACAACAGGCTGAGGTC
C13	GTGGTCGGTTAGGCATCATATTC	GTGGAGAGCATGGCAGAGC
C14	TTCTAACAGCAGACCTCTACTCG	TCAGCAAGAGCAGCCAGTG
C15	GACGCCGAGA ACTGGAAC	GCACAACAGGCTGAGGTC
C16	TCAGGGTGGTCATGTTTAAGG	GCACAACAGGCTGAGGTC
C17	CTGGAAGTCACCTGGAAAGC	GCACAACAGGCTGAGGTC