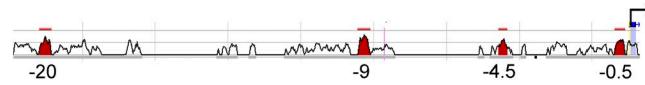


## SUPPLEMENTAL MATERIAL

Neumann et al., <http://www.jem.org/cgi/content/full/jem.20131548/DC1>STAT motif (Ehret et al., 2001): **TTCN<sub>(2-4)</sub>GAA**MAF response element (MARE) (Kataoka et al., 1994): **TGA<sup>9/c</sup>TCA**Blimp-1 motif (Kuo and Calame, 2004): **T<sub>c</sub>GAAAGT<sub>c</sub>*****II10* CNS-0.5 (identity: 80.7%)**

> mm10 chr1:131019438-131019696 259bps  
 GGAGGAAACAATTATTCCTAATCCTAATG**TTCTGGAA**TAGCCCATTATCCA  
 CGTCATTATGCCCTGGAGTGCCTGAATGGAATCCACAGATGAGGGCCTCTGTGA  
 CATAGAACAGCTGTC**TGCCCTCA**AGGAATACAACTTTAGTATTGAGAAGCTAAAA  
 AGAAAAAAAAAAATAAAAGAGAGGTAGGCCATACTAAAAATAGCTGTAATGCAGAA  
 GTTCATTCGACCAGTTCTTAGCGCTTACAATGCAAA

***II10* CNS-4.5 (identity: 80.0%)**

> mm10 chr1:131015400-131015593 194bps  
 CAAACTCTCATGTGAGAAGTTAGAGTAAGGTGTTGGTCT**TGAGTA**AAAGTCA  
 AATTGCTTATGTGGCACCACTGTTACACAAAGGGAAATCCACATTGGCTGTC  
 CAGCGATCAGCCCTTCGTTGCTTGCAACATCTGCTTGGCCACGA**TTCTCA**  
**GGA**CATTCAATCCGTTTGCTATAATCCCTGGCT

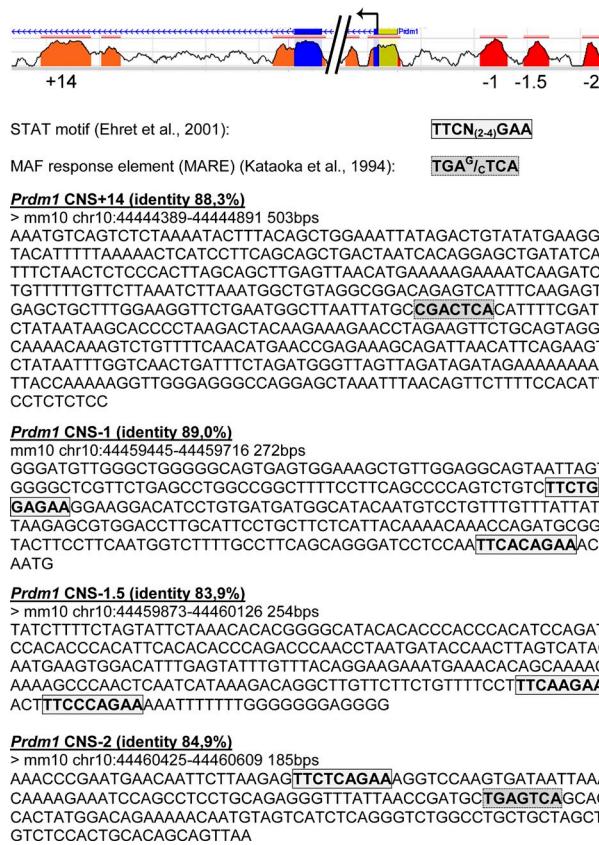
***II10* CNS-9 (identity: 83.9%)**

> mm10 chr1:131010529-131010907 379bps  
 TGTGGTGTCTCGAGGGTTTCCAGTAAATTCTCCCTGACACAGTCAA**TCCGAG**  
**AA**ACCCACACCTCCCTCCACACCTGGTGCACCCCTGGTCTGCT**TTGA**  
**GGAA**AAGCCACGATCATGTCTGCCACTCAATGAAGGCTCTCTGGTTCCGAT  
 GCTCTAGCAGGCT**TACTCACAA****CGAAACT**GCACCC**TCAAAGC**ACCGGGGG  
 CCAGGACGGCGAGAAGGAAACACAGGTGAACACCGCAAAAGCTGCCAGGA  
 AAAAGGTTGTTCTCTTACAGAATGGCACTCCAGAGCTGGCAGGAGCAG  
 ACTAGTAGAGACTGAAGGGGCTGCCCTGGTCTTGACCTGGGGTTTGTATG  
 GAAAAAA

***II10* CNS-20 (identity: 80.0%)**

> mm10 chr1:130999687-130999976 290bps  
 GTTAAAGAGATGGAGAACACTGGAAGGATTACAGCTTGACAAAACGCTAGGCTT  
 GATACAGGTCATGAAACATGG**TCCAGGGAA**ATCCCACAGAACGACCCCCAG  
 CTGGTTCCCCATCACTTTGGGTAACCTTCCATTGCCACACACATACACACAC  
 CCTGCCCTACCCCTCAGGTCTGCTCAAGAACCTAGCTGCTACTTGGCGGCCT  
 GGTAAAGGCATGGGAATCAAAAGAAGCAATGGACCCAGCTCCTGAACCTGAGAA  
 GCTACATTC**TCGTAGGGAA**

**Figure S1. Computational analysis of STAT, MARE, and Blimp-1 consensus sequences within CNSs upstream of *II10*.** Analysis of sequence homology and identification of putative regulatory sequences were performed using the ECR browser (<http://ecr.browser.dcode.org>) and rVista 2.0 software. Putative STAT, MARE, and Blimp-1 binding sites are highlighted within the respective CNS sequence (one mismatch within a presumed binding site compared with the published core sequence was tolerated).



**Figure S2.** Computational analysis of STAT and MARE consensus sequences within CNSs in the *Prdm1* locus. Analysis of sequence homology and identification of putative regulatory sequences were performed as in Fig. S1. Putative STAT and MARE binding sites are highlighted within the respective CNS-sequence (one mismatch within a presumed binding site compared with the published core sequence was tolerated).

**Table S1.** Sequences of primer used for qPCR analysis

Target	Forward primer (5'-3')	Reverse primer (5'-3')	MgCl <sub>2</sub> concentration	Annealing temperature
			<i>mM</i>	°C
Ubc	AGCCCAGTGTACCAAG	TCACACCAAGAACAGCAC	4	60°C
Il10	ATCGATTCTCCCCGTGAA	TTCGGAGAGAGGTACAAACGA	5	60°C
Maf	GCATGCTGGACATGTATGGT	ATGTACAACGGGAGGCTGAA	4	65°C
Prdm1	GACGGGGTACTCTGTTCA	GGCATTCTGGGAACGTGT	1	60°C

**Table S2.** Sequences of primer used for ChIP-qPCR

Target	Forward primer (5'-3')	Reverse primer (5'-3')	MgCl <sub>2</sub> concentration	Annealing temperature
			<i>mM</i>	°C
<i>I10</i> locus				
CNS-20	CTTCCATTGCCACACACAC	GGGTCATTGCTCTTTGA	2.5	65
CNS-9	CTTGAGGAAAAGCCAGCATC	TTTGCCTGTTCACCTGTGTT	2	65
CNS-4.5	GCCACGATTCTCAGGACATT	GTATCCAACCCCACCTGCAC	2	65
CNS-0.5	CTCTCCTGTACCAACTGCC	TGGGTTGAACGTCCGATATT	3	65
<i>Prdm1</i> locus				
CNS-2	CCCTGTCTCCAAAAACCAA	GCAGGAGGCTGGATITCTT	3	65
CNS-1.5	GCAAAACAAAAGCCCAACTC	TCTGTGATACTTCCACACACC	1.5	65
CNS-1	AGTGAGTGGAAAGCTGTTGGA	CAGGACATTGTATGCCATCATC	2.5	65
CNS+14 (intron 5; Ochiai et al., 2008)	GTAAATCTGCTTCTCGGTTTC	TCTTAATGGCTGTAGGCGGAC	3	65
Negative region; Stitrich et al., 2010)	GTGCATTCCCTGGTGTATCC	GATGTTGGGACGAGAGAAG	3	65

## REFERENCES

- Ehret, G.B., P. Reichenbach, U. Schindler, C.M. Horvath, S. Fritz, M. Nabholz, and P. Bucher. 2001. DNA binding specificity of different STAT proteins. Comparison of in vitro specificity with natural target sites. *J. Biol. Chem.* 276:6675–6688. <http://dx.doi.org/10.1074/jbc.M001748200>
- Kataoka, K., M. Noda, and M. Nishizawa. 1994. Maf nuclear oncoprotein recognizes sequences related to an AP-1 site and forms heterodimers with both Fos and Jun. *Mol. Cell. Biol.* 14:700–712.
- Kuo, T.C., and K.L. Calame. 2004. B lymphocyte-induced maturation protein (Blimp)-1, IFN regulatory factor (IRF)-1, and IRF-2 can bind to the same regulatory sites. *J. Immunol.* 173:5556–5563. <http://dx.doi.org/10.4049/jimmunol.173.9.5556>
- Ochiai, K., A. Muto, H. Tanaka, S. Takahashi, and K. Igarashi. 2008. Regulation of the plasma cell transcription factor Blimp-1 gene by Bach2 and Bcl6. *Int. Immunol.* 20:453–460. <http://dx.doi.org/10.1093/intimm/dxn005>
- Stitrich, A.-B., C. Haftmann, E. Sgouroudis, A.A. Kühl, A.N. Hegazy, I. Panse, R. Riedel, M. Flossdorf, J. Dong, F. Fuhrmann, et al. 2010. The microRNA miR-182 is induced by IL-2 and promotes clonal expansion of activated helper T lymphocytes. *Nat. Immunol.* 11:1057–1062. <http://dx.doi.org/10.1038/ni.1945>