Figure S1

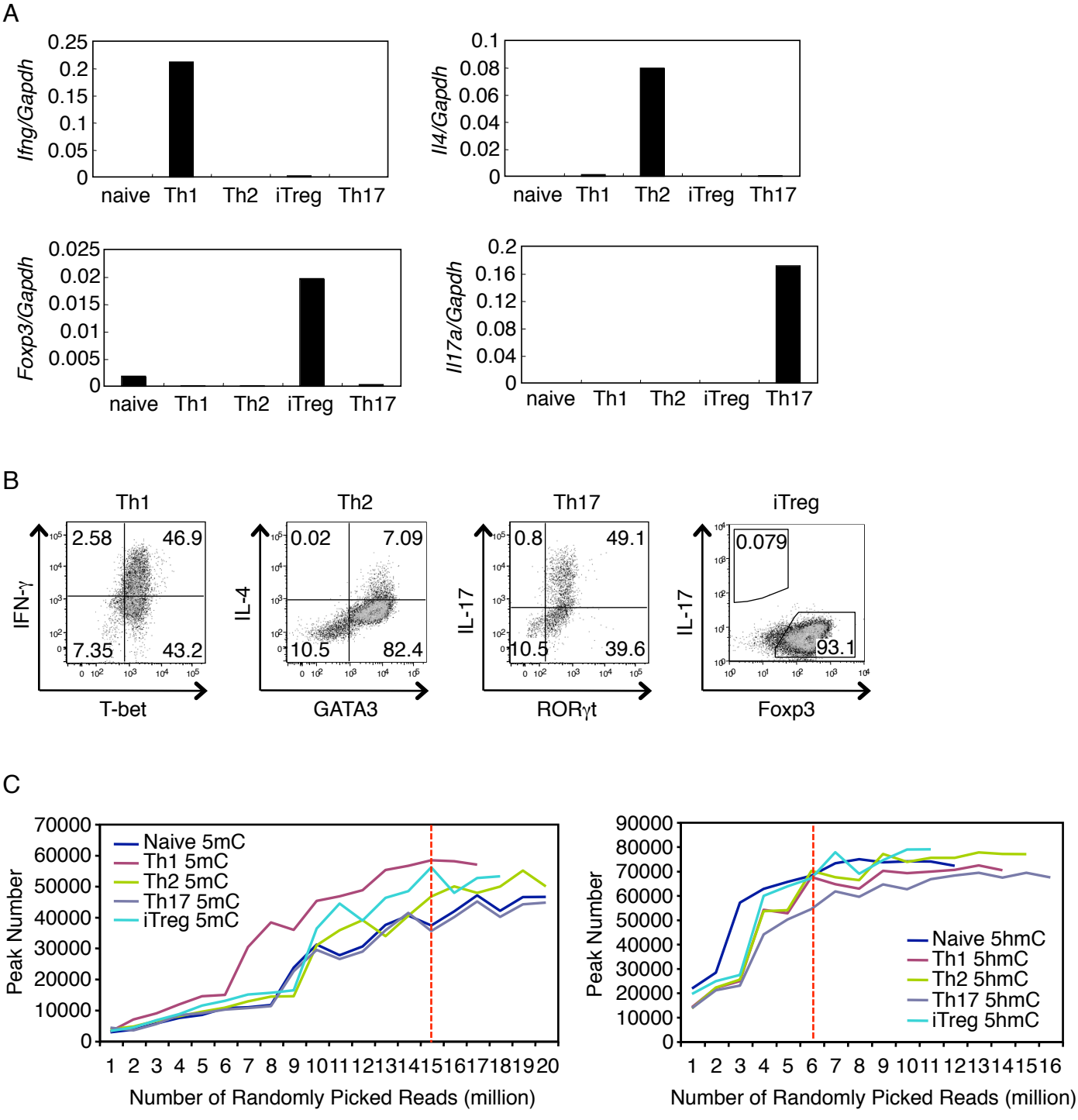

A
Ifng/Gapdh
0.25
0.2
0.15
0.1
0.05
0
naive Th1 Th2 iTreg Th17
Il4/Gapdh
0.1
0.08
0.06
0.04
0.02
0
naive Th1 Th2 iTreg Th17
Foxp3/Gapdh
0.025
0.02
0.015
0.01
0.005
0
naive Th1 Th2 iTreg Th17
Il17a/Gapdh
0.2
0.16
0.12
0.08
0.04
0
naive Th1 Th2 iTreg Th17
B
Th1
IFN-γ
T-bet
2.58
46.9
7.35
43.2
Th2
IL-4
GATA3
0.02
7.09
10.5
82.4
Th17
IL-17
RORγt
0.8
49.1
10.5
39.6
iTreg
IL-17
Foxp3
0.079
93.1
C
Peak Number
Number of Randomly Picked Reads (million)
Naive 5mC
Th1 5mC
Th2 5mC
Th17 5mC
iTreg 5mC
Naive 5hmC
Th1 5hmC
Th2 5hmC
Th17 5hmC
iTreg 5hmC

Figure S2

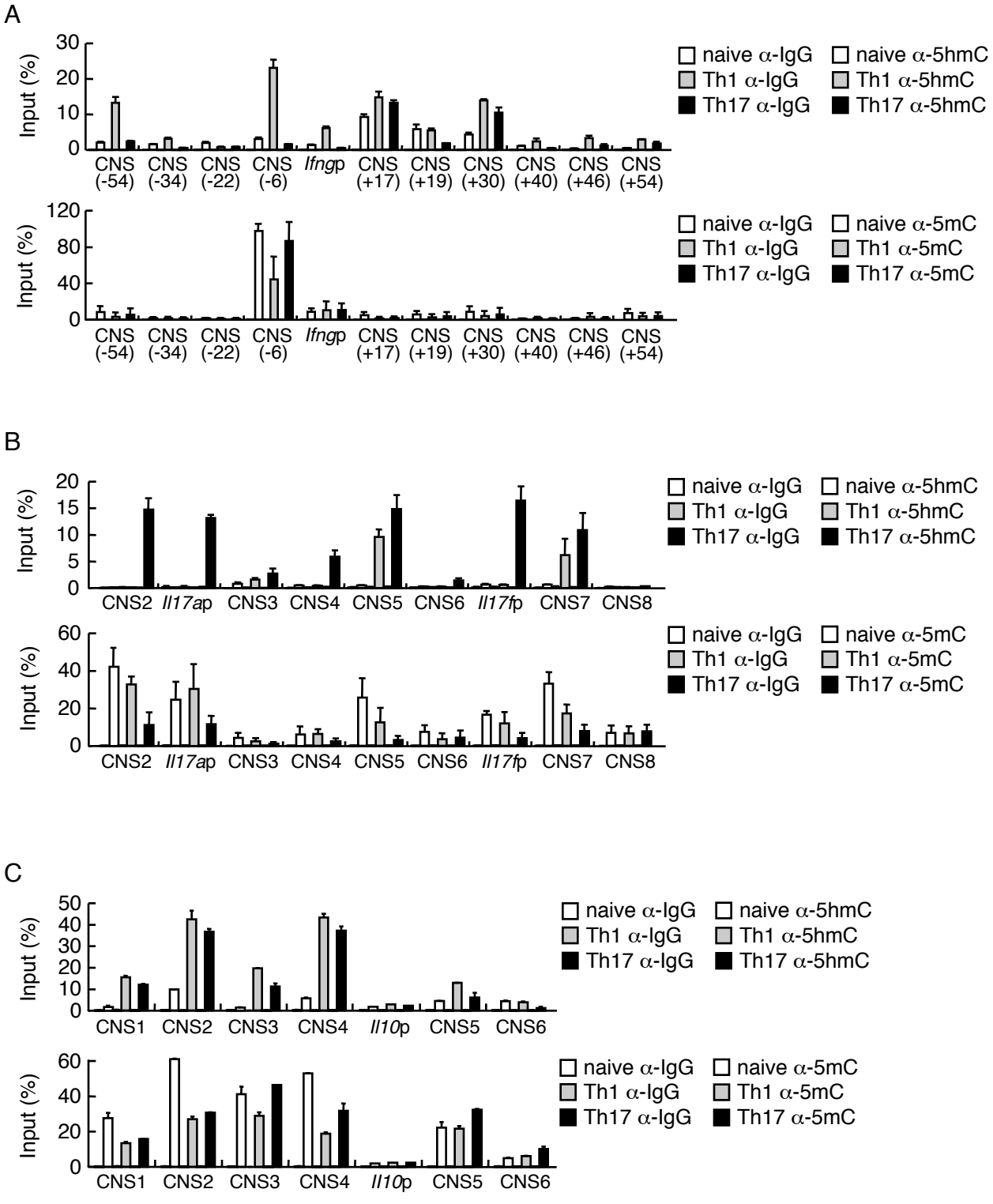

A
Input (%)
naive α-IgG
naive α-5hmC
Th1 α-IgG
Th1 α-5hmC
Th17 α-IgG
Th17 α-5hmC
CNS (-54)
CNS (-34)
CNS (-22)
CNS (-6)
Ifngp
CNS (+17)
CNS (+19)
CNS (+30)
CNS (+40)
CNS (+46)
CNS (+54)
naive α-5mC
Th1 α-5mC
Th17 α-5mC
B
CNS2
Il17ap
CNS3
CNS4
CNS5
CNS6
Il17fp
CNS7
CNS8
C
CNS1
Il10p

Figure S3

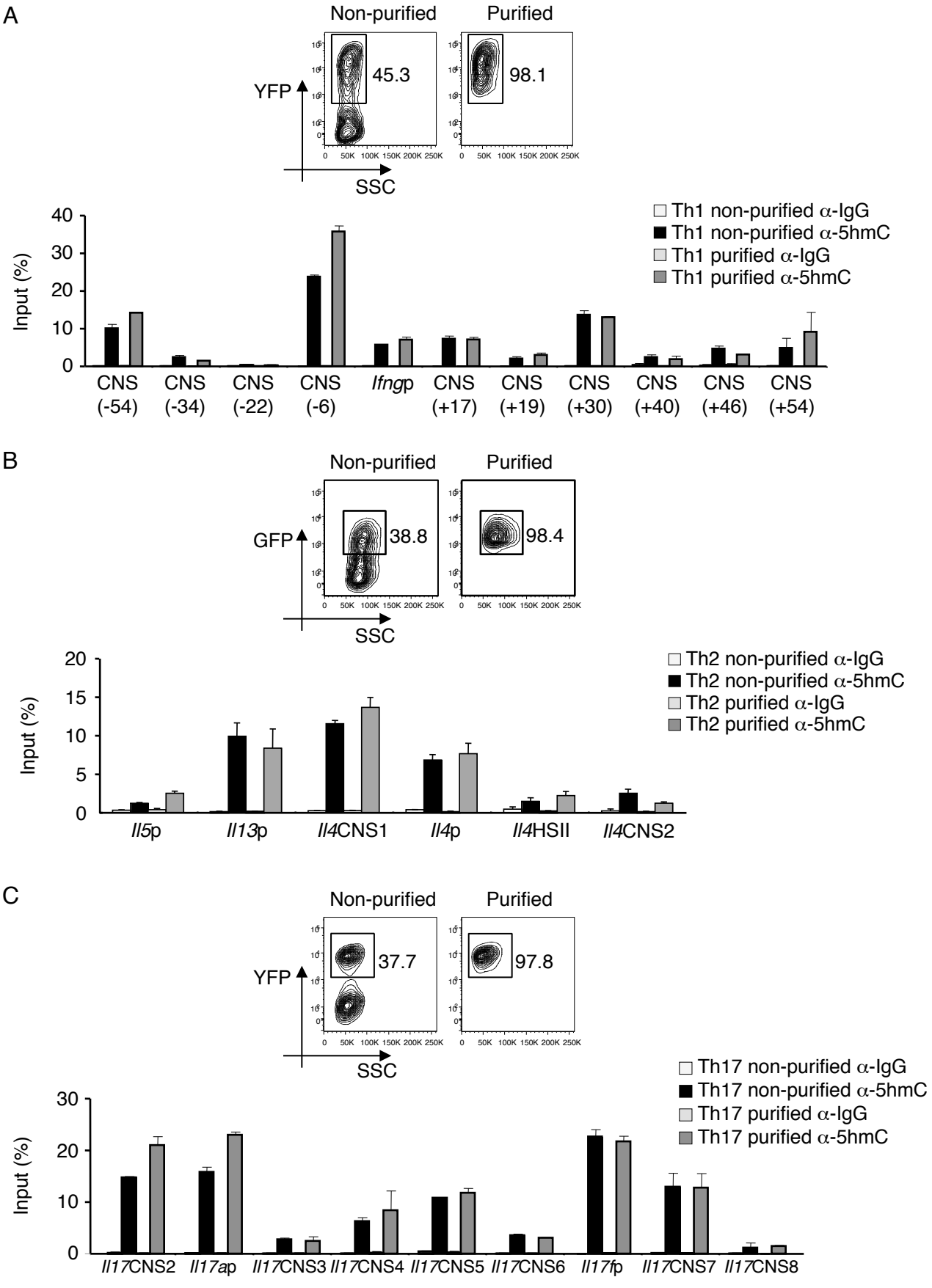

A
Non-purified
Purified
YFP
SSC
45.3
98.1
Input (%)
Th1 non-purified α-IgG
Th1 non-purified α-5hmC
Th1 purified α-IgG
Th1 purified α-5hmC
CNS (-54)
CNS (-34)
CNS (-22)
CNS (-6)
Ifngp
CNS (+17)
CNS (+19)
CNS (+30)
CNS (+40)
CNS (+46)
CNS (+54)
B
Non-purified
Purified
GFP
SSC
38.8
98.4
Input (%)
Th2 non-purified α-IgG
Th2 non-purified α-5hmC
Th2 purified α-IgG
Th2 purified α-5hmC
Il5p
Il13p
Il4CNS1
Il4p
Il4HSII
Il4CNS2
C
Non-purified
Purified
YFP
SSC
37.7
97.8
Input (%)
Th17 non-purified α-IgG
Th17 non-purified α-5hmC
Th17 purified α-IgG
Th17 purified α-5hmC
Il17CNS2
Il17ap
Il17CNS3
Il17CNS4
Il17CNS5
Il17CNS6
Il17fp
Il17CNS7
Il17CNS8

Figure S4

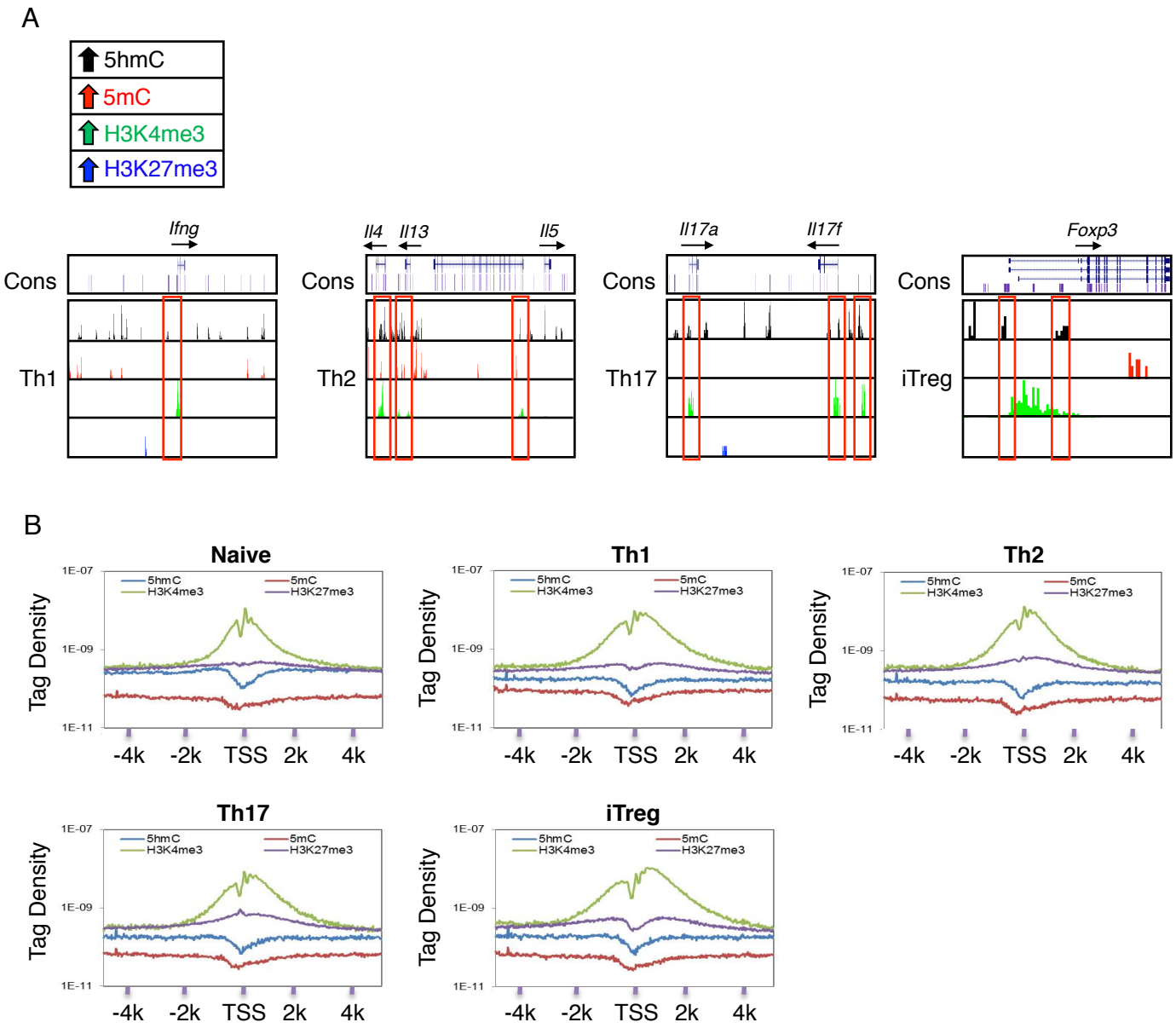

A
5hmC
5mC
H3K4me3
H3K27me3
Ifng
Il4
Il13
Il5
Il17a
Il17f
Foxp3
Cons
Th1
Th2
Th17
iTreg
B
Naive
Th1
Th2
Th17
iTreg
Tag Density
1E-07
1E-09
1E-11
-4k
-2k
TSS
2k
4k
C
naive
Th1
Th17
5hmC
62223
14615
6091
1175
33617
320
12313
5mC
H3K4me3
52996
14967
2729
560
41951
395
13139
62036
13210
1874
245
30878
196
13763

Figure S5

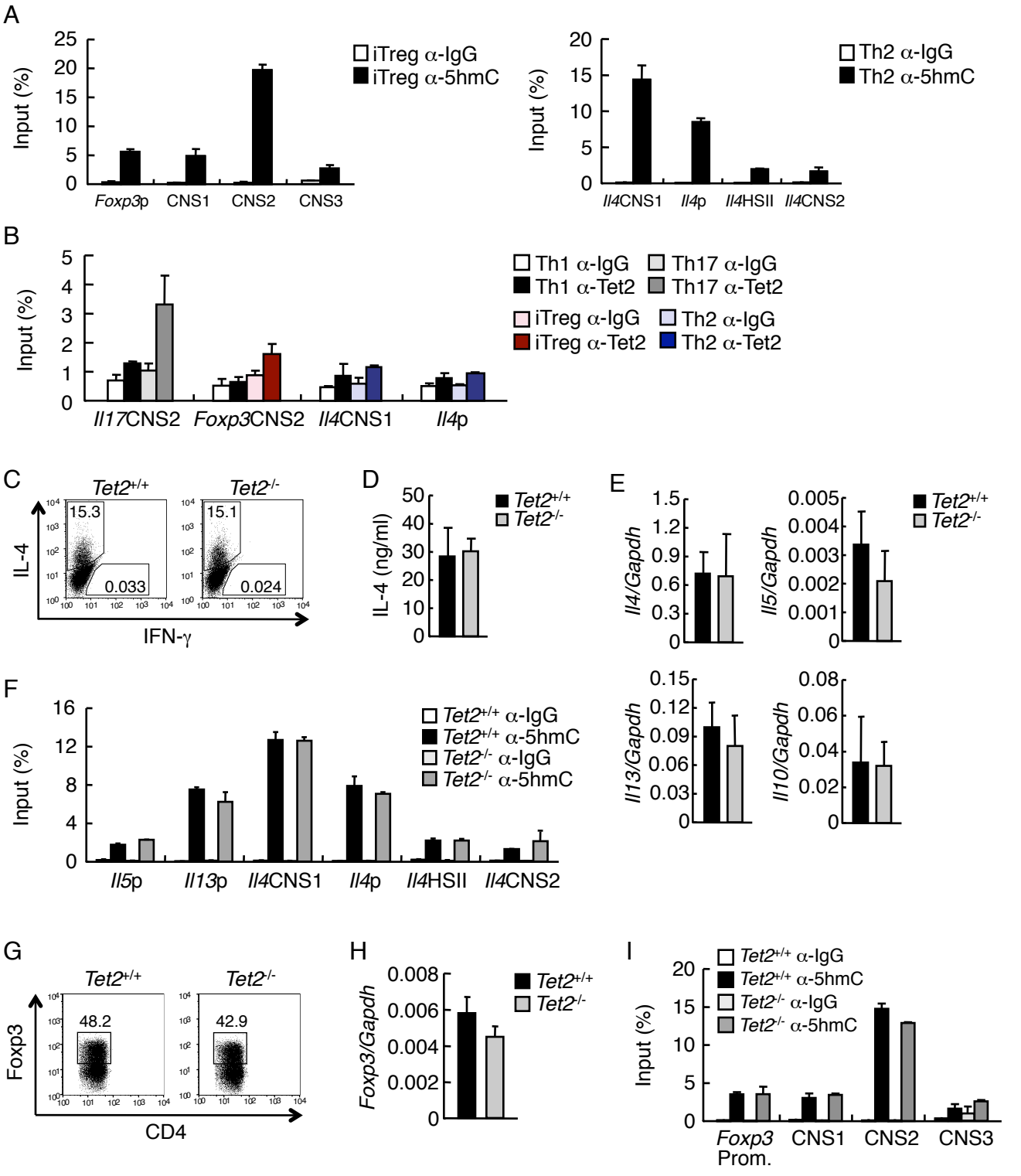
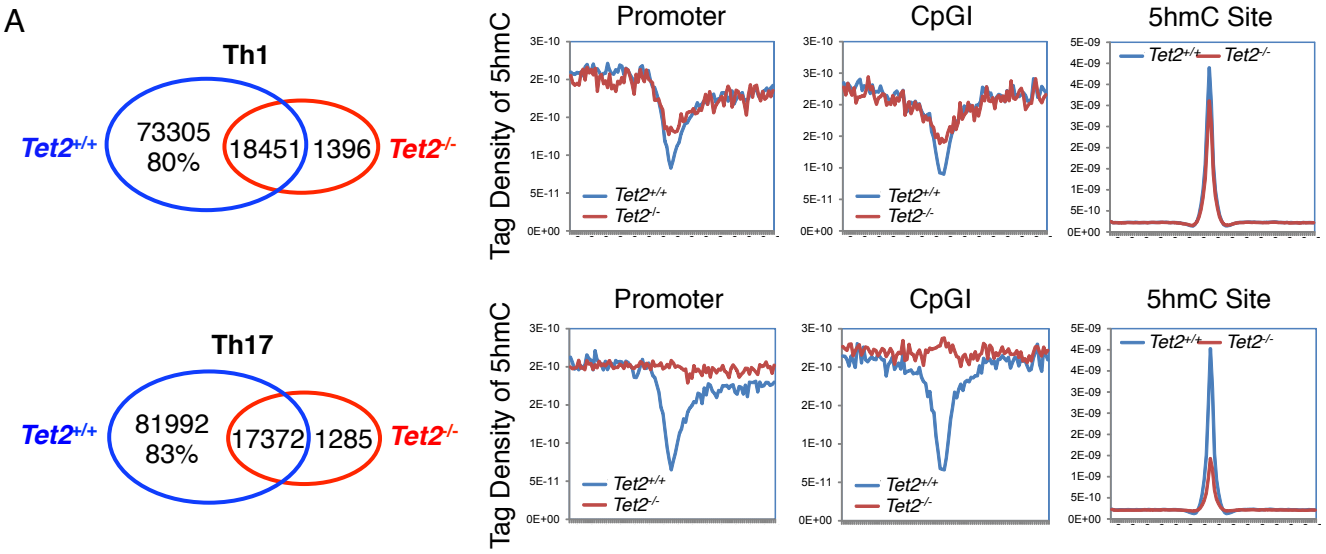

A
Input (%)
iTreg α-IgG
iTreg α-5hmC
Foxp3p
CNS1
CNS2
CNS3
Th2 α-IgG
Th2 α-5hmC
Il4CNS1
Il4p
Il4HSII
Il4CNS2
B
Th1 α-IgG
Th1 α-Tet2
Th17 α-IgG
Th17 α-Tet2
iTreg α-IgG
iTreg α-Tet2
Th2 α-IgG
Th2 α-Tet2
Il17CNS2
Foxp3CNS2
Il4CNS1
Il4p
C
Tet2+/+
Tet2-/-
15.3
0.033
15.1
0.024
IL-4
IFN-γ
D
IL-4 (ng/ml)
E
Il4/Gapdh
Il5/Gapdh
Il13/Gapdh
Il10/Gapdh
F
Input (%)
Il5p
Il13p
Il4CNS1
Il4p
Il4HSII
Il4CNS2
G
48.2
42.9
Foxp3
CD4
H
Foxp3/Gapdh
I
Input (%)
Foxp3 Prom.
CNS1
CNS2
CNS3

Figure S6



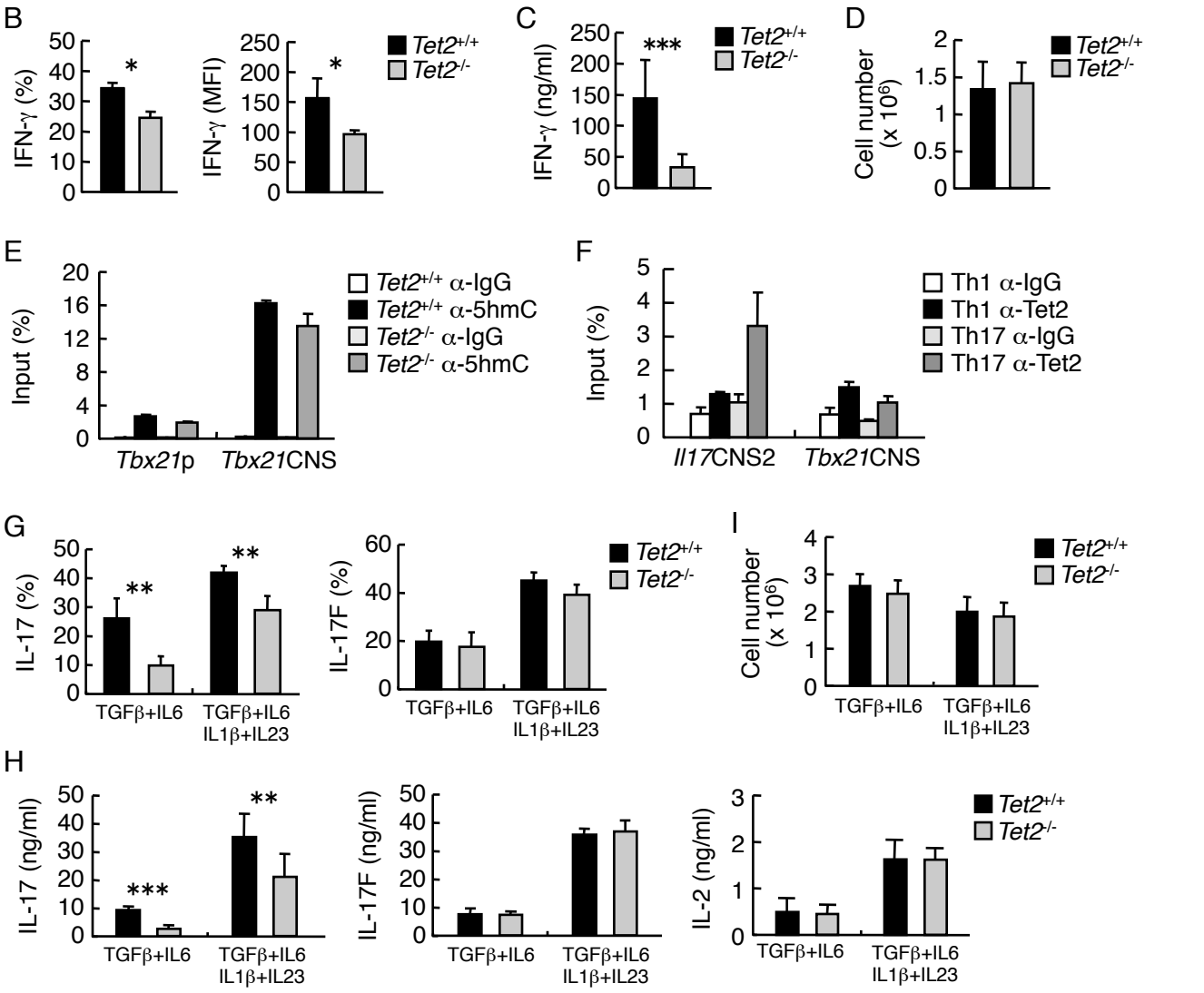


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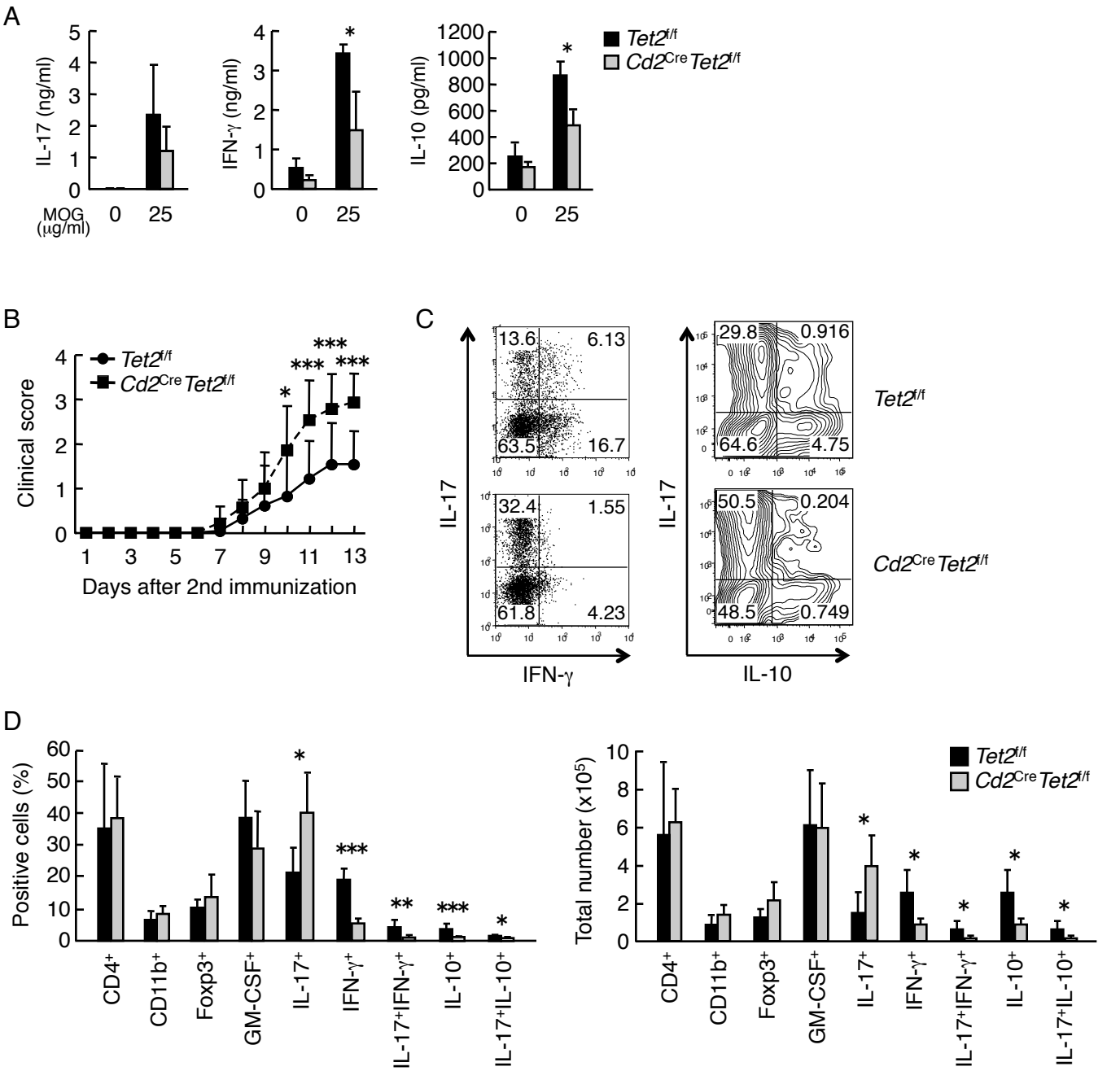
Figure S7


A
IL-17 (ng/ml)
IFN-γ (ng/ml)
IL-10 (pg/ml)
MOG (μg/ml)
0
25
Tet2f/f
Cd2Cre Tet2f/f
B
Clinical score
Days after 2nd immunization
C
IL-17
IFN-γ
IL-10
13.6
6.13
63.5
16.7
32.4
1.55
61.8
4.23
29.8
0.916
64.6
4.75
50.5
0.204
48.5
0.749
D
Positive cells (%)
Total number (x10^5)
CD4+
CD11b+
Foxp3+
GM-CSF+
IL-17+
IFN-γ+
IL-17+IFN-γ+
IL-10+
IL-17+IL-10+

Supplemental Figure Legends

Figure S1, Related to Figure 1: Quality verification of DIP-sequencing samples and reads. (A) Naive T cells were cultured under iTreg, Th1, Th2 and Th17 conditions. Expression of signature genes in differentiated Th cells was measured by real-time RT-PCR. (B) Proportions of transcription factor positive cells as well as and cytokine-producing cells in cell cultures were determined by intracellular staining. (C) Randomly sampled fractions of reads from each sample were subjected to peak identification using SICER. A red line was drawn at the number of reads with which the number of peaks identified would be saturated for 5hmC and 5mC libraries.

Figure S2, Related to Figure 2: Confirmation of 5mC and 5hmC distribution in the *Ifng*, *Il17a, Il17f* and *Il10* loci by qPCR. The DIP-PCR assay on the *Ifng* (A), *Il17a, Il17f* (B) and *Il10* (C) loci was performed in naïve, Th1 and Th17 cells. Cell lysates were immunoprecipitated with α-5mC, α-5hmC or control IgG. The results were normalized to the input control. Data are a representative of at least three individual experiments and shown as mean ± SD.

Figure S3, **Related to Figure 2: Comparison of 5hmC distribution between purified and non-purified cells.** Naive T cells were from *Ifng*^{yfp} (A), *Il4*^{gfp} (B) and *Il17f*^{Cre}*Rosa26*^{yfp} (C) mice cultured under Th1, Th2 and Th17 conditions for 4-6 days, respectively. Reporter positive cells were purified by a FACSAria. 5hmC modification in the purified and non-purified cells was analyzed by hMeDIP-PCR.

Data are a representative of two individual experiments and shown as mean ± SD.

Figure S4, Related to Figure 3: Comparison of genome-wide DNA modifications with histone modifications. (A) Distribution of 5hmC, 5mC, H3K4me3 and H3K27me3 islands along the *Ifng*, *Il4, Il13, Il5*, *Il17a, Il17f* and *Foxp3* genomic regions in naïve and appropriate Th subsets is shown. The regions of overlapping peaks are highlighted by red squares. (B) Compiled tag density profiles for 5hmC, 5mC, H3K4me3 and H3K27me3 in each T cell subset are shown. The diagrams represent all genes that showed positive signals for the respective marks, and show tag density profiles across promoter ±5 kb flanking regions with 25 bp resolution. (C) The concordance between 5hmC/5mC modifications and H3K4me3 modifications in naïve, Th1 and Th17 cells are shown.

Figure S5, Related to Figure 5 and 6: The role of Tet2-mediated active DNA demethylation in Th2 and iTreg development. (A) A MeDIP-PCR analysis on the *Foxp3* and *Il4* loci was performed in iTreg and Th2 cells, respectively. Cell lysates were immunoprecipitated with α-5hmC or control IgG. (B) A ChIP-PCR analysis on the *Foxp3*, *Il4* and *Il17* loci were performed in Th1, Th2, iTreg and Th17 cells. Cell lysates were immunoprecipitated with α-Tet2 or control IgG. The results were normalized to the input control. Data are a representative of two

individual experiments and shown as mean ± SD. (C, D) Naïve T cells from *Tet2*$^{f/f}$ and *Cd2*^{Cre}*Tet2*$^{f/f}$ mice were cultured under Th2 condition for 7 days. IL-4 expression was analyzed by flow cytometry (C) and by ELISA (D). (E) The expression of *Il4*, *Il5*, *Il13* and *Il10* mRNA were analyzed by real-time RT-PCR. (F) A hMeDIP assay of the *Il4* gene was performed in Th2 cells from *Tet2*$^{f/f}$ and *Cd2*^{Cre}*Tet2*$^{f/f}$ mice. Cell lysates were immunoprecipitated with α-5hmC or control IgG. The results were normalized to the input control. (G, H) Naïve T cells from *Tet2*$^{f/f}$ and *Cd2*^{Cre}*Tet2*$^{f/f}$ mice were cultured under iTreg condition for 4 days. Foxp3 expression was analyzed by flow cytometry (G) and by real-time RT-PCR (H). (I) A hMeDIP assay of the *Foxp3* gene was performed in iTreg cells from *Tet2*$^{f/f}$ and *Cd2*^{Cre}*Tet2*$^{f/f}$ mice. Cell lysates were immunoprecipitated with α-5hmC or control IgG. The results were normalized to the input control. Data are a representative of at least two individual experiments and shown as mean ± SD.

Figure S6, Related to Figure 5 and 6: The role of Tet2-mediated active DNA demethylation in Th1 and Th17 development. (A) The venn diagram showing the numbers of 5hmC peaks that appear in only Tet2$^{+/+}$ or Tet2$^{-/-}$ cells or in both cells. The normalized tag density profiles for 5hmC around ±5 kb regions flanking TSS (Promoter), CpG island centers (CpGI), and 5hmC peak center (5hmC Site) with 200 bp resolution are shown. Th1 cells (upper), Th17 cells (lower). (B) The statistics of intracellular staining in Figure 5A. (C) Naïve T cells from *Tet2*$^{f/f}$ and *Cd2*^{Cre}*Tet2*$^{f/f}$ mice were cultured under Th1 condition for 5 days and restimulated

with α-CD3 for overnight. The amount of IFNγ in supernatants was measured by ELISA. All groups are analyzed in triplicates. (D) The number of viable cells in Figure S6B. (E) A MeDIP assay of the *Tbx21* gene was performed in Th1 cells from *Tet2*$^{f/f}$ and *Cd2*^{Cre}*Tet2*$^{f/f}$ mice. Cell lysates were immunoprecipitated with α-5hmC or control IgG. (F) A ChIP-PCR analysis on the *Tbx21* and *Il17* loci were performed in Th1 and Th17 cells. Cell lysates were immunoprecipitated with α-Tet2 or control IgG. The results were normalized to the input control. Data are a representative of two individual experiments and shown as mean ± SD. (G) The statistics of intracellular staining in Figure 6A. (H) Naïve T cells from *Tet2*$^{f/f}$ and *Cd2*^{Cre}*Tet2*$^{f/f}$ mice were cultured under Th17 condition for 4 days and restimulated with α-CD3 for overnight. The amount of IL17, IL17F and IL-2 in supernatants was measured by ELISA. All groups are analyzed in triplicates. (I) The number of viable cells in Figure S6G. (B-D, G-I) All data represent the average of at least three independent experiments and are shown as mean ± SD.

Figure S7, Related to Figure 7: Tet2 regulates *in vivo* immune responses. (A) *Tet2*$^{f/f}$ and *Cd2*^{Cre}*Tet2*$^{f/f}$ mice (n = 4) were immunized with MOG_{35-55} peptide on day 0 and then analyzed on day 7 for IL17, IFNγ and IL10 production. (B) Age-matched *Tet2*$^{f/f}$ and *Cd2*^{Cre}*Tet2*$^{f/f}$ mice were immunized twice with MOG_{35-55}. Mean clinical scores are shown versus days after second MOG immunization. Shown here is the combinational result of three EAE experiments (the total number of mice used: WT = 16, KO = 16). (C) The IL17, IFNγ and IL10 levels

were determined in the infiltrates of CNS of MOG_{35-55}-immunized mice. (D) Statistics of the cell frequencies and absolute numbers. All the data are shown as mean ± SD.

Table S1, Related to Figure 1: Distribution of 5mC and 5hmC. The mouse genome was divided into four kinds of regions: proximal promoter (1 kb upstream and downstream of transcription start site), exon, intron, and intergenic regions. The number of islands for each sample was listed as the total identified islands (Total Peak), followed by the islands among genomic regions with the percentage listed in the parenthesis. Normal distribution of promoter, exon, intron, and intergenic regions in mouse genome was calculated based on RefSeq Genes downloaded from UCSC Genome Browser on Sep 17, 2014.

Table S2, Related to Figure 1: Colocalization of both 5hmC and 5mC. The numbers of peaks uniquely associated with 5hmC, 5mC, or both modifications are shown.

Table S3, Related to Figure 2: Distribution of lineage specific 5hmC. All 5hmC peaks that only appeared in one of naïve, Th1, Th2, Th17, or iTreg lineages were identified as the lineage-specific 5hmC modification.

Table S4, Related to Figure 5 and 6: The list of genes regulated by Tet2 in Th1 and Th17 cells. The genes with at least 1.5 fold differences in their expression between wild-type and Tet2-deficient Th1 and Th17 cells are shown, respectively. 5hmC peaks that were present on their promoter plus gene body regions (-3K to TTS) are shown.

Supplemental Experimental Procedures

Flow Cytometry

For intracellular cytokine staining, cells were stimulated for 4-6 hr in complete medium with phorbol 12-myristate 13-acetate (50 ng/ml) and ionomycin (500 ng/ml; both from Sigma-Aldrich) in the presence of brefeldin A (eBioscience). Intracellular staining was performed with the Fixation and Permiabilization kit (BD Biosciences and eBioscience) according to the manufacturer's instructions. Data were acquired through a BD FACSAria or BD FACSCalibur and were analyzed with FlowJo software (Tree Star, Ashland, OR).

ELISA and Quantitative Real-Time RT-PCR

Supernatants were collected after the indicated periods of cell culture and were analyzed with an ELISA kit (BD Biosciences and R&D Systems) according to the manufacturer's instructions.

The cells were lysed in Trizol reagent (Invitrogen), which allowed RNA extraction. cDNAs were synthesized with Superscript reverse transcriptase and oligo(dT)

primers (Invitrogen) and analyzed with an iCycler Optical System and an iQ SYBR green real-time PCR kit (Bio-Rad). The data were normalized to a *Gapdh* control. The following genes were amplified with primers as described: *Gapdh* (Ichiyama et al., 2008); *Il10*, *Il4*, *Il5* and *Il13* (Angkasekwinai et al., 2010); *Il17a, Il17f, Rorc, Ifng, Tbx21 and Foxp3* (Yang et al., 2008).

Chromatin immunoprecipitation (ChIP) Assay

The chromatin immunoprecipitation (ChIP) assay was performed as previously described (Ichiyama et al., 2011) using a ChIP assay kit (Millipore, Cat# 17-295). Briefly, cells were fixed with 1% formaldehyde at 37°C for 10 min and then suspended in an SDS lysis buffer. After sonication, samples were incubated with antibodies against p300 (SantaCruz), acetylated histone H3 (H3Ac) (Millipore), trimethylated histone H3K4 (H3K4me3) (Millipore), trimethylated histone H3K27 (H3K27me3) (Millipore), Tet2 (SantaCruz), RORc (SantaCruz), T-bet (SantaCruz) or control IgG overnight at 4°C. Antibody-DNA complexes were captured by protein A agarose/Salmon sperm DNA. The immunoprecipitated DNA was purified and quantified by real-time PCR. The results were normalized relative to the input control.

DNA Immunoprecipitation (DIP) Assay

The DNA immunoprecipitation (DIP) assay was performed as previously described (Vucic et al., 2009). In brief, the genomic DNA was purified and

sonicated. DNA fragments (4 μg) were denatured and incubated with antibodies against 5mC (Eurogentec), 5hmC (Active Motif) or control IgG at 4°C overnight. Antibody-DNA complexes were captured by protein A agarose/Salmon sperm DNA. The immunoprecipitated DNA was purified and quantified by real-time PCR. The results were normalized relative to the input control.

MOG Immunization and Induction of EAE

Both MOG immunization and EAE induction were performed by immunizing mice with 300 μg MOG_{35-55} peptide (amino acids 35-55; MEVGWYRSPFS ROVHLYRNGK) emulsified in CFA and analyzed as previously described (Wang et al., 2012). For neutralization of IL10, α-IL10R (1B1.3A; BioXCell) or α-Rat IgG1 (HRPN; BioXCell) as control was intraperitoneally injected at every 4 days after MOG/CFA immunization. The disease scores were assigned on a scale of 0–5 as follows: 0, none; 1, limp tail or waddling gait with tail tonicity; 2, wobbly gait; 3, hindlimb paralysis; 4, hindlimb and forelimb paralysis; 5, death.

$CD4^+$ T Cell Transfer

Total $CD4^+$ T cell populations were isolated from the spleens and lymph nodes of *Tet2*$^{f/f}$ and *Cd2*^{Cre}*Tet2*$^{f/f}$ mice. $CD4^+$ T cells were further purified using CD4 microbeads and autoMACS (Miltenyi). Cells were counted and washed 3X in PBS and then injected intravenously into tail veins of *Rag1*$^{-/-}$ mice at 8 x 10^6 cells per mouse. EAE was induced the day following $CD4^+$ transfer.

Microarray

Two independent sets of microarray assays were performed. Total cellular RNA was extracted from Th1 and Th17 cells with Trizol reagent (Invitrogen) in *Tet2*$^{f/f}$ and *Cd2*^{Cre}*Tet2*$^{f/f}$ mice. DNA microarray labeling and analysis were performed in the microarray core at the Institute for Systems Biology. Approximately 10 μg RNA was labeled and hybridized to GeneChip Mouse Genome 430 2.0 arrays (Affymetrix) according to the manufacturer's protocols. Expression values were defined with GeneChip Operating Software (GCOS; Affymetrix).

Primers

The primers used for real-time RT-PCR, ChIP-PCR, DIP-PCR and genotyping are listed below.

Primer name (forward)	Sequence (5' → 3')	Primer name (reverse)	Sequence (5' → 3')
*Cd2*Cre	AGATGCCAGGACATCAGGAACCTG	*Cd2*Cre	ATCAGCCACACCAGACACAGAGATC
*Tet2*flox	AAGAATTGCTACAGGCCTGC	*Tet2*flox	TTCTTTAGCCCTTGCTGAGC
Tet1	GAAGGAACAGGAAGCTGCAC	*Tet1*	CTGGCCAAACCTAGTCTCCA
Tet2	GATCCAGGAGGAGCAGTGAG	*Tet2*	TGGGAGAAGGTGGTGCTATC
Tet3	CCGGATTGAGAAGGTCATCTAC	*Tet3*	AAGATAACAATCACGGCGTTCT
H19	GCATGGTCCTCAAATTCTGCA	*H19*	GCATCTGAACGCCCCAATTA
*Ifng*CNS(-54)	CACACTCGAAGCTTTCCACA	*Ifng*CNS(-54)	CTAAGCCGGACCAGAATGAG
*Ifng*CNS(-34)	CCCAGGCACTTTCCTACTGA	*Ifng*CNS(-34)	TGGTTGACACTCTGGGCTTT

*Ifng*CNS(-22)	CACAGGAAGGAGATGGGAAG	*Ifng*CNS(-22)	ACCTGCCTCCTGTCTTTTGA
*Ifng*CNS(-6)	ATCTGTCTGAACGGGTGGAG	*Ifng*CNS(-6)	AGCAGGTCGGTCCTCTGTAA
*Ifng*p	GGGGGAGACGTAAAAGCAAT	*Ifng*p	GGGCTCTCTGACGATGAGAC
*Ifng*CNS(+17)	AGCAAGAGCAAAGAGGATGC	*Ifng*CNS(+17)	CACCAAGTCTCAGGCATTGA
*Ifng*CNS(+19)	AGCCAAACCACAGACTGGAT	*Ifng*CNS(+19)	AGTTTGGGAAGTTGGGTGTG
*Ifng*CNS(+30)	AAGCCTTGTACTTCCGACGA	*Ifng*CNS(+30)	CCAGTTTTACCACCCACACC
*Ifng*CNS(+40)	CAGCATTGTCTGACGACCAC	*Ifng*CNS(+40)	ATGTGAGCAAGCCATCTTCC
*Ifng*CNS(+46)	CATGTGGAACCCACAACAAG	*Ifng*CNS(+46)	GTGCTCCTAGCGACTCTTGC
*Ifng*CNS(+54)	TGGGCTGCTCTTCCAGTATT	*Ifng*CNS(+54)	GACAGTTTCAGTGCCACCAA
*Tbx21*p	CCCAATCTGGGAAAGAGTCA	*Tbx21*p	AGGCGTGAGAATGCTCAGAT
*Tbx21*CNS	CCACTTATCACCCCAGATGC	*Tbx21*CNS	TACACACTGGGTCGCTGAGA
*Il17*CNS2	TGTGGTTGTCTAAGCCATGC	*Il17*CNS2	CAGCAACTGACTGGGTTTCA
*Il17a*p	CAGCTCCCAAGAAGTCATGC	*Il17a*p	TGAGGTCAGCACAGAACCAC
*Il17*CNS3	TTAGTGAGGTCGGGGAAGTG	*Il17*CNS3	TTTGATGGCAGCACATTCAT
*Il17*CNS4	TCGCCTCTTGACAAACAGTG	*Il17*CNS4	TTCGTCCCTGTGATTTCCTC
*Il17*CNS5	AGGCCCACAATGTAGGTCAG	*Il17*CNS5	CAGGCTGGGAAGTCTCTCTG
*Il17*CNS6	TGCCTAGGGCTTGAGTGTCT	*Il17*CNS6	CAGGTCCGCTTTGGTATGTT
*Il17f*p	TCCCTGTTTCCACTGACCTC	*Il17f*p	TTAGGGTCCCCCTTTGATTC
*Il17*CNS7	CTGAGTTGGGGGCTGTGTAT	*Il17*CNS7	CATATCGAGGGTGTCGGACT
*Il17*CNS8	CAGCAGACACACATGCAAGA	*Il17*CNS8	CCTCAGGGGAGGGAATTAAG
*Il10*CNS1	AACCCTGGCTAGAAGGGAAG	*Il10*CNS1	GGAGGGAGGAACAGAAAAGG
*Il10*CNS2	GGTGTTGGTGTGTGCAAGTC	*Il10*CNS2	GTCGGAACCTTGATTGAGGA

*Il10*CNS3	CACACCCTCCCCTCTAACAA	*Il10*CNS3	CTACTGTGGCTGGGCTTCTC
*Il10*CNS4	CTTGAGGAAAAGCCAGCATC	*Il10*CNS4	GGTGCTTTGAGGTTGCAGTT
*Il10*p	AGGGAGGAGGAGCCTGAATA	*Il10*p	TGTGGCTTTGGTAGTGCAAG
*Il10*CNS5	CAGTCGGGGCATCTATGTCT	*Il10*CNS5	CCAGAACCGTTGCACAAGTA
*Il10*CNS6	CCAAAGGATGCAACCACTCT	*Il10*CNS6	CCCCTTATCCTCAAAGTCACG
*Il5*p	GGGTGGGGGTCAAGATGTTA	*Il5*p	AAGGCGAGTCCTGAAACTCA
*Il13*p	GTGGCCTTAGCCTGTTGAAG	*Il13*p	CTGTCCCAGACCCTTCTCAA
*Il4*CNS1	GGGGAGGAAGAGAGAGCAAC	*Il4*CNS1	CATTCATTTCTCGGCTCCAC
*Il4*p	TCCTGCAGAGAAGGAAGAGG	*Il4*p	CCAGAGTCAGCTTTCCCAAG
*Il4*HSII	GAAAAGCAGGCAGTCTGGAG	*Il4*HSII	TTTGTAGTGGGAGGGGACAG
*Il4*CNS2	CCAAACACCGTTATGGCTCT	*Il4*CNS2	TCGGCTGTAAAGTCCCAGTT
*Foxp3*p	CCTCCAACGTCTCACAAACA	*Foxp3*p	CCCCTCACCACAGAGGTAAA
*Foxp3*CNS1	CTTTTCTTGTGGGGCTTCTG	*Foxp3*CNS1	GACAGTCTGGCTCCCATACC
*Foxp3*CNS2	ATCTGGCCAAGTTCAGGTTG	*Foxp3*CNS2	GGCGTTCCTGTTTGACTGTT
*Foxp3*CNS3	TAAGCAGGGTGGGGTACTTG	*Foxp3*CNS3	CTCTGAAGCCTGGAGAGTGG

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