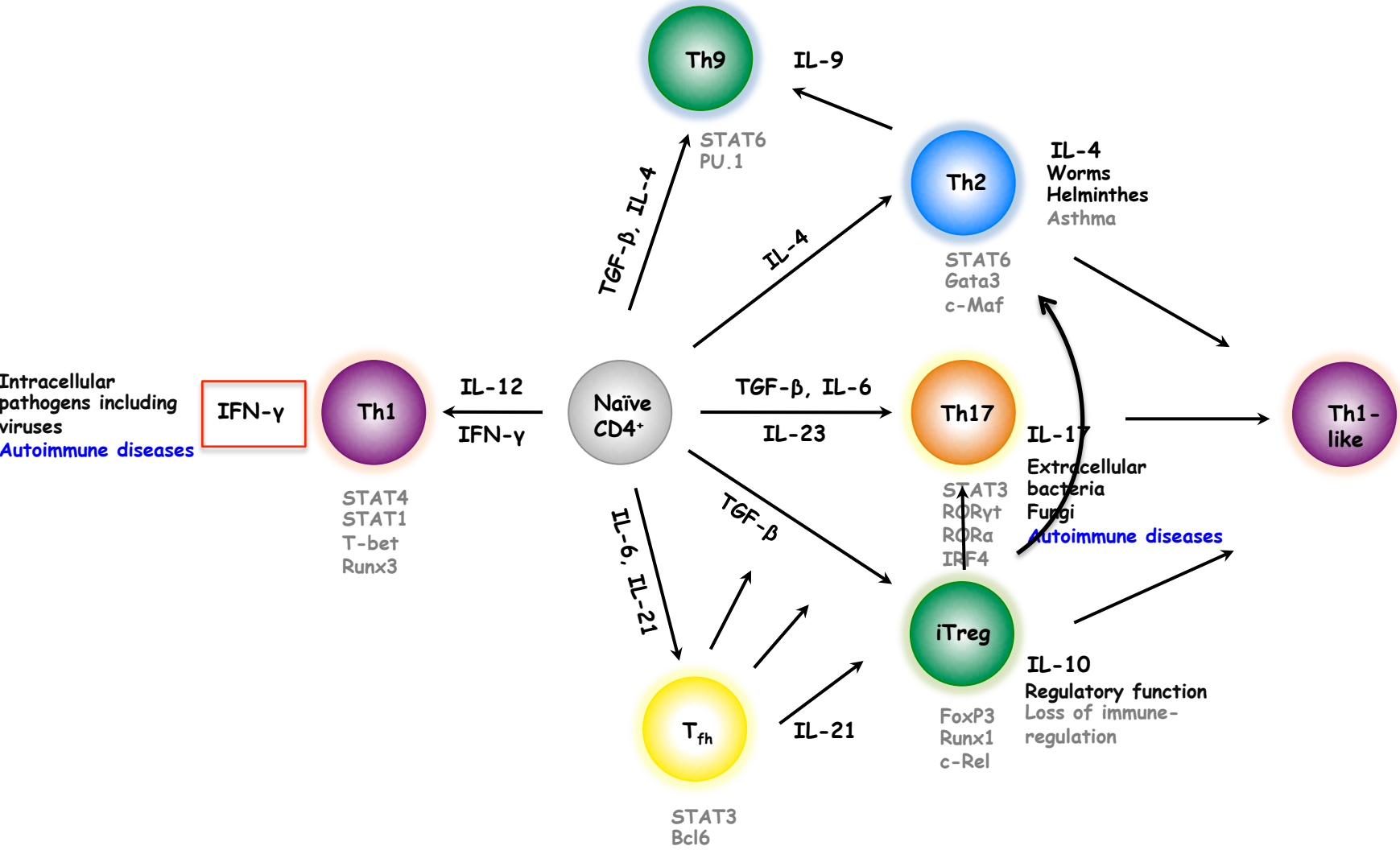


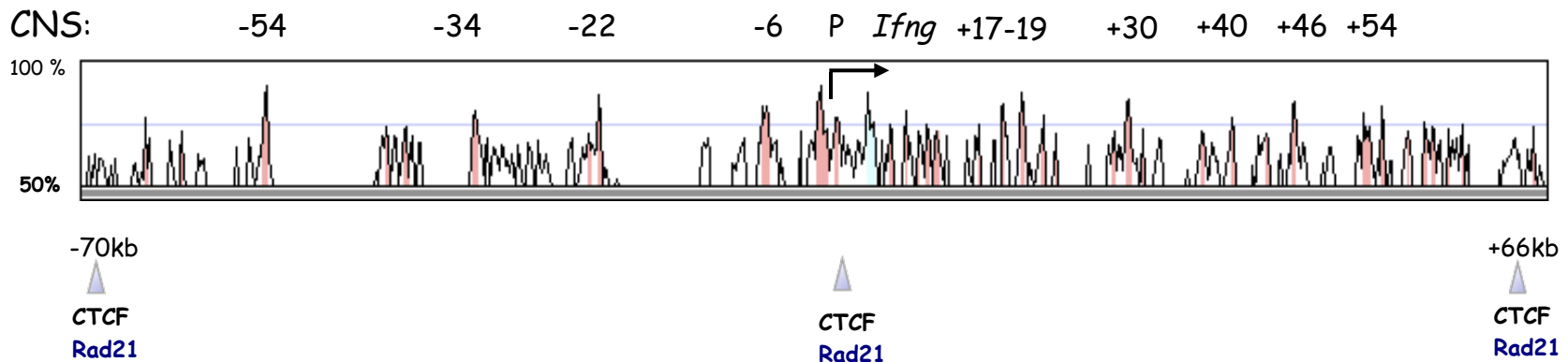
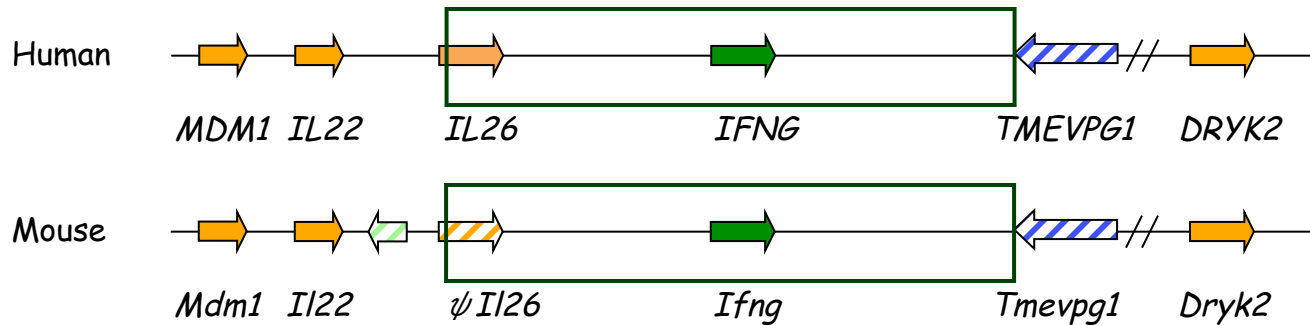
Epigenetic Control of Effector T cell Development

Robin D. Hatton, PhD
University of Alabama at
Birmingham

Diversity of T Helper Cell (Th) Responses

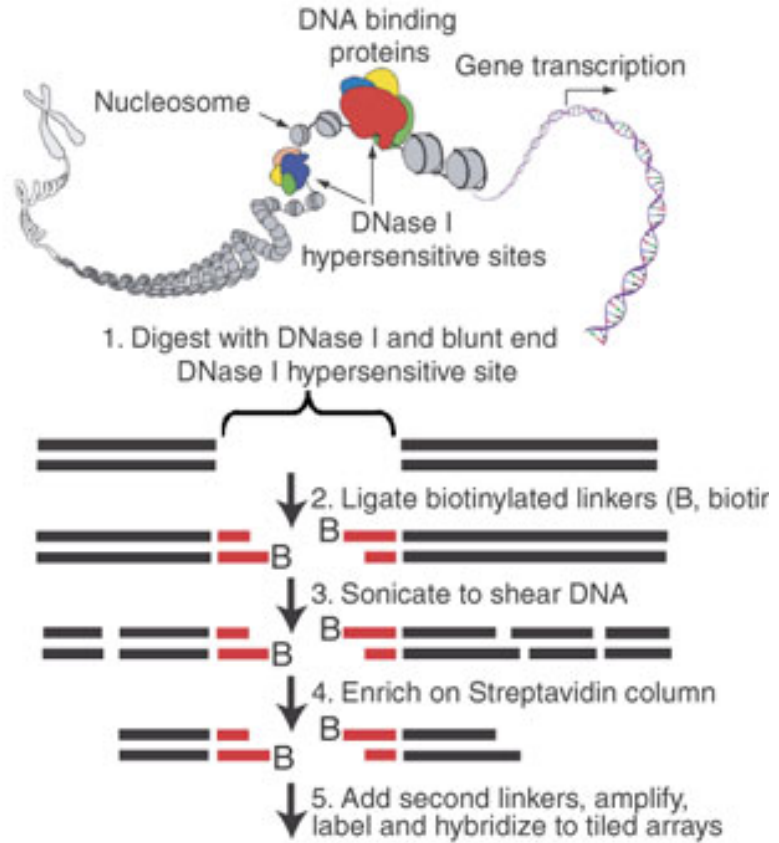
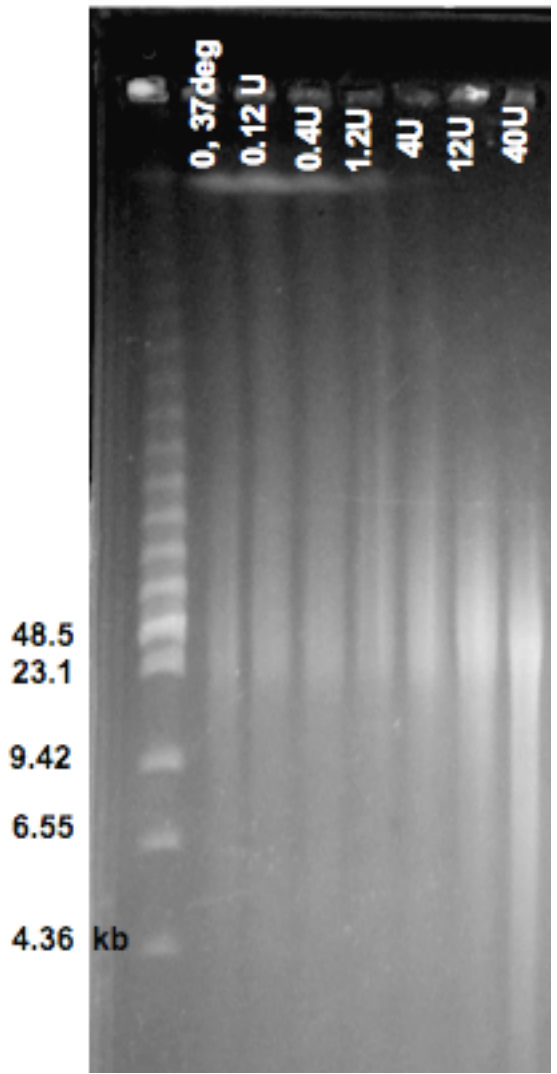


Homology-based Prediction of Regulatory Functions

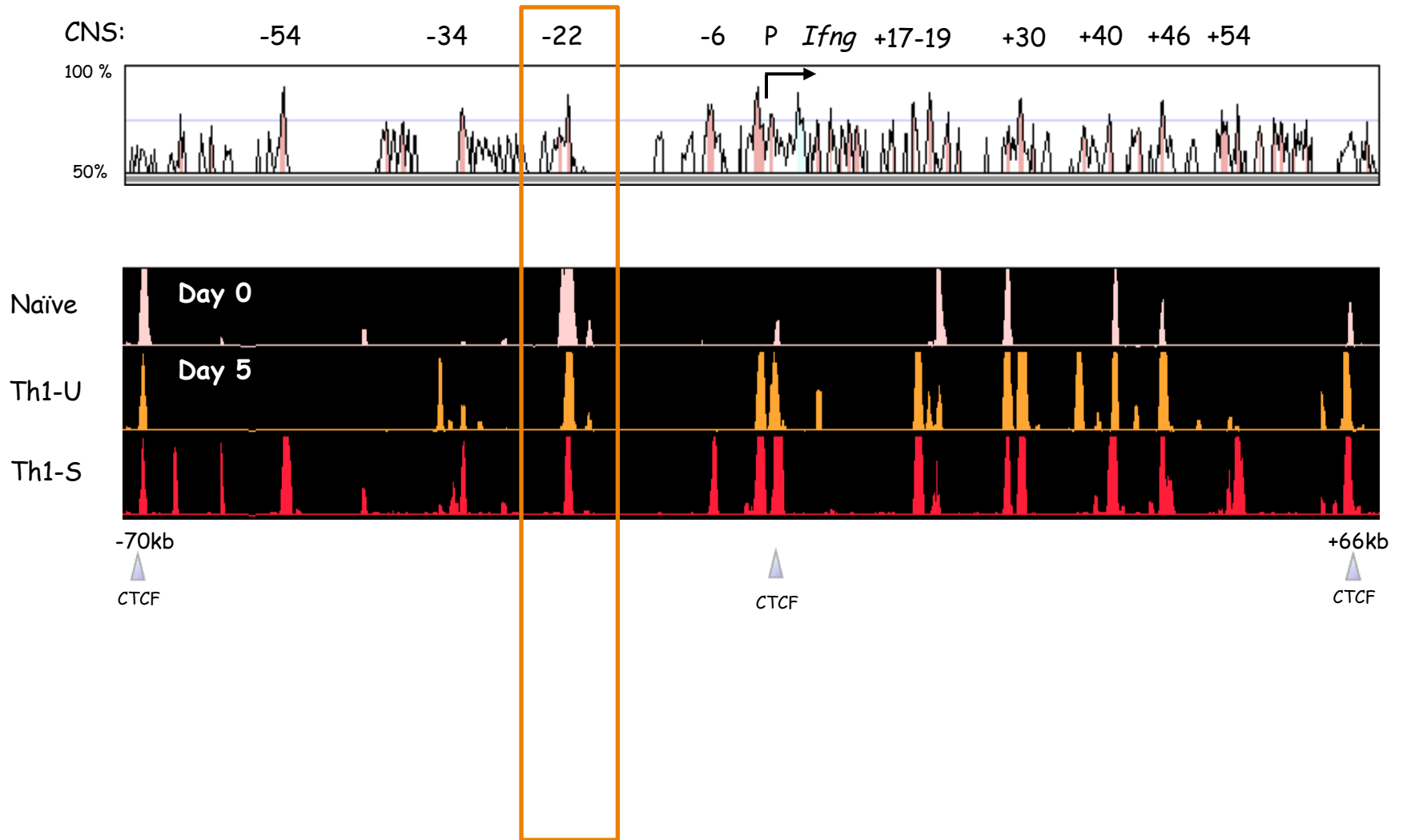


- ~ 140 kb encompasses the *Ifng* locus
- **All *Ifng* CNSs interact with the promoter** although functions of individual CNSs yet to be established

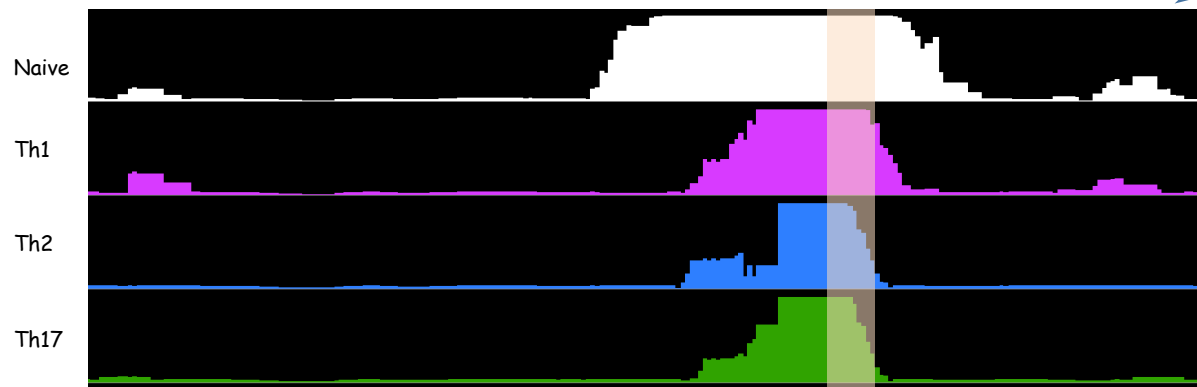
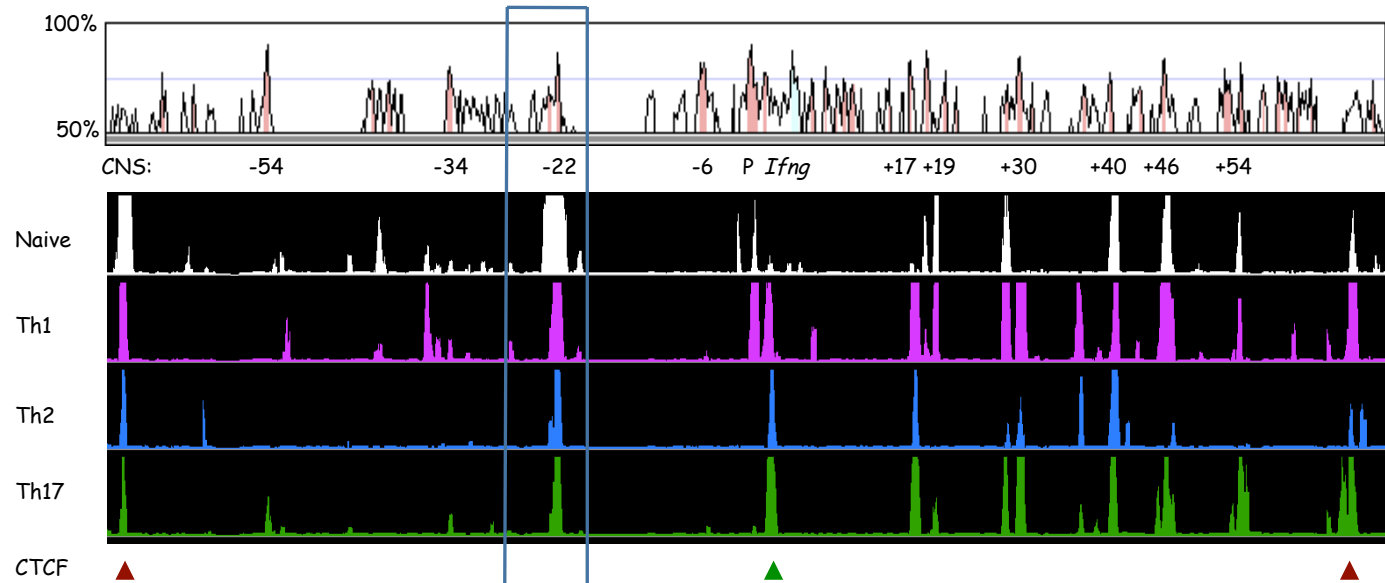
High-throughput Analyses: ChIP-chip and DNase-chip



The Extended *Ifng* Locus : Th1 Specific Accessibility

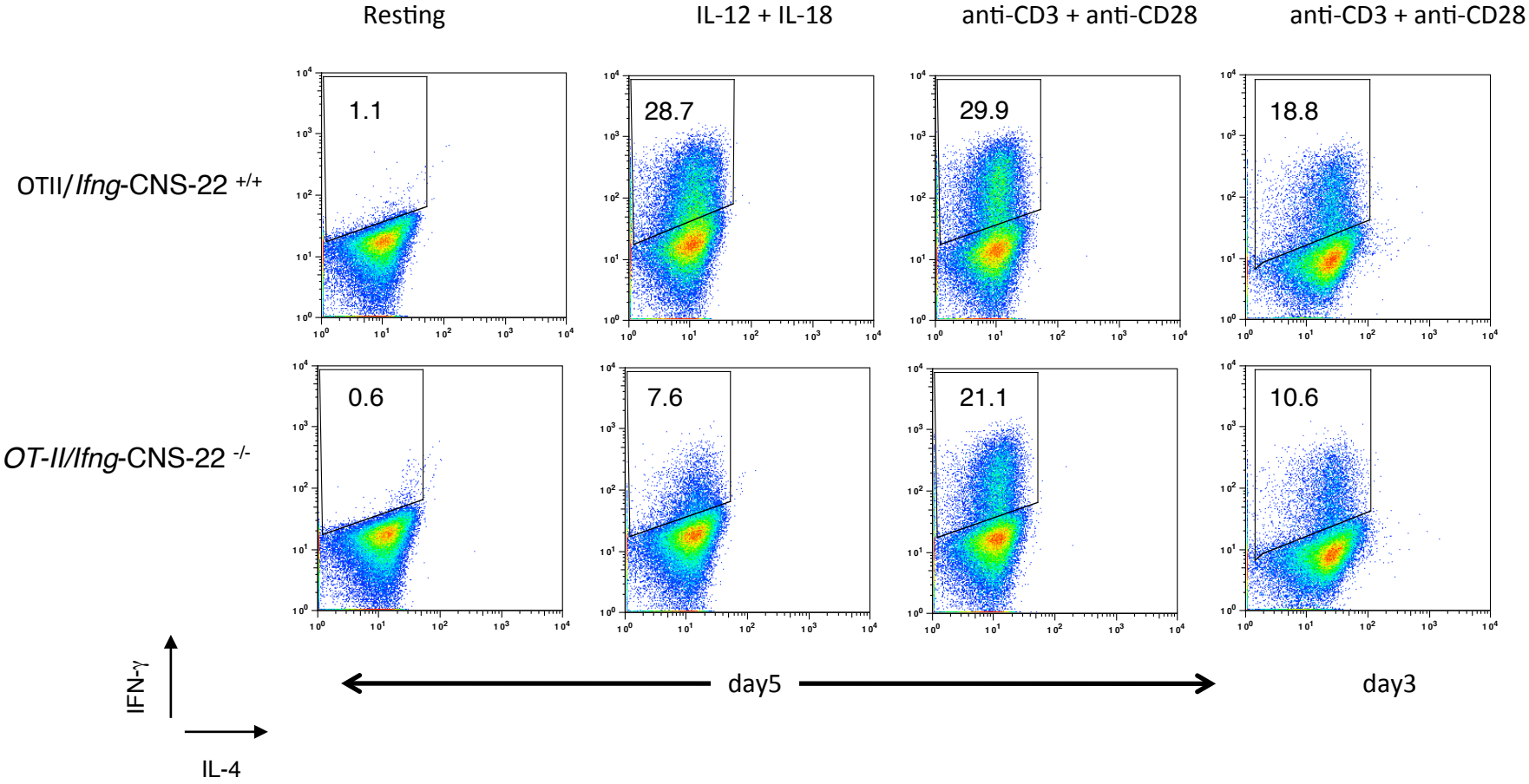


Ifng CNS-22 Deletion

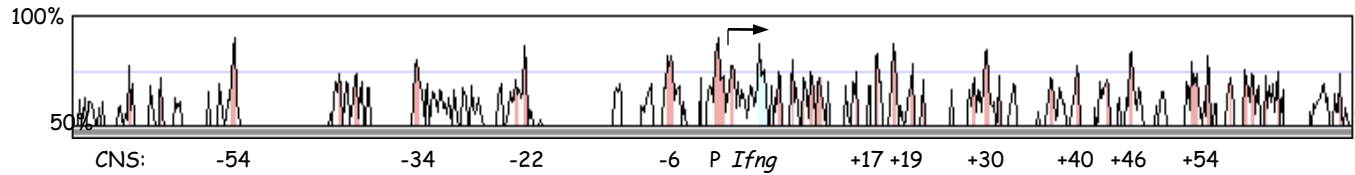


391bp
CNS-22 deletion

Impairment in Cytokine Driven *Ifng* Gene Transcription in CD4⁺ T Cells



CNS-22 Partially Controls *Ifng* Locus Remodeling



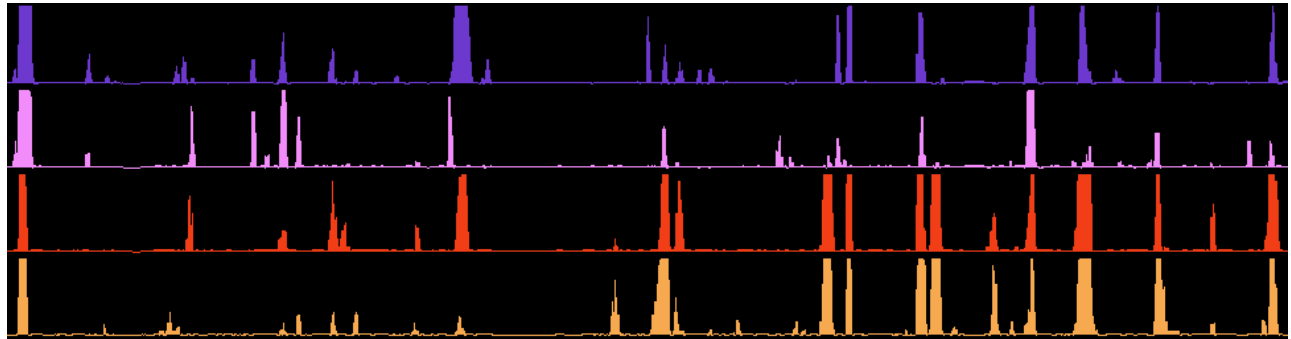
DNase I

Naïve CNS-22 wt

Naïve -CNS-22 KO

Th1 CNS-22 wt

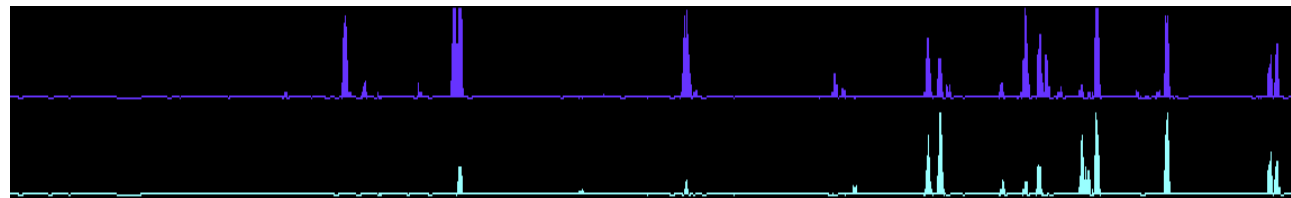
Th1 CNS-22 KO



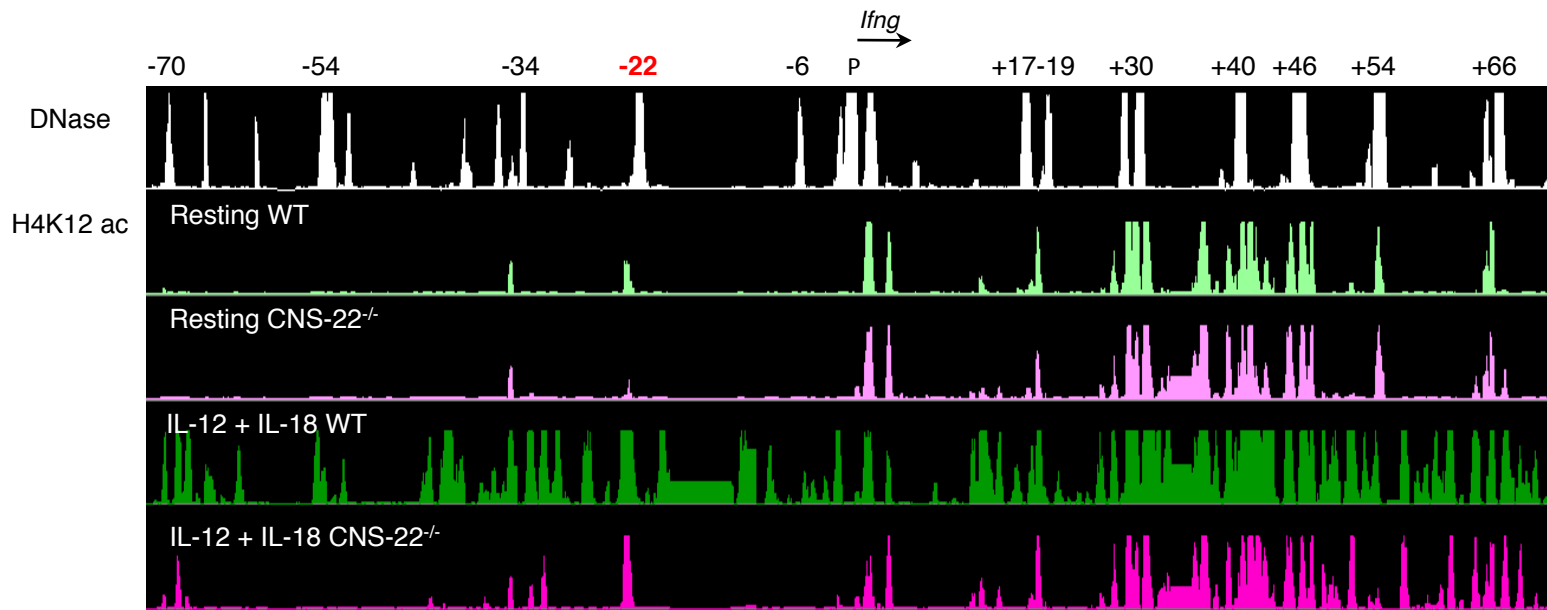
H3K4me1

Th1 CNS-22 wt

Th1 CNS-22 KO



Diminished Hyperacetylation in the Absence of CNS-22



Summary

- CNS-22 resides in an area of open chromatin early in T cell development and in all T cell lineages analyzed
- CNS-22 recruits factors involved in the optimal expression of IFN γ
- Deletion of CNS-22
 - Impacts IL-12 and IL-18 driven induction of *Ifng* in both T cells and NK cells
 - Impacts local chromatin structure

Acknowledgements

Casey Weaver

Weaver Lab

Anand Balasubramani

Henrietta Turner

Karen Janowski

James Oliver

Craig Maynard

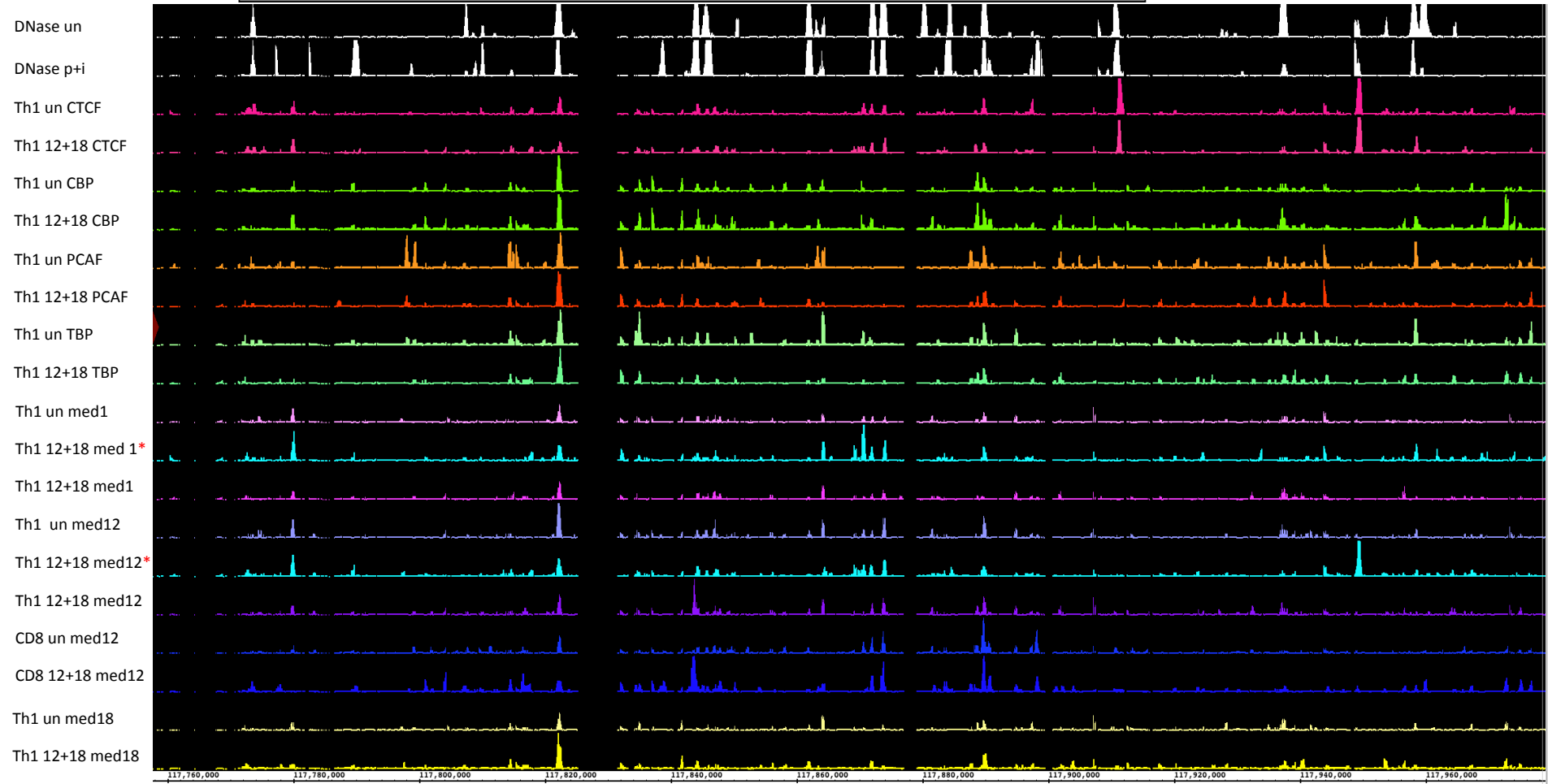
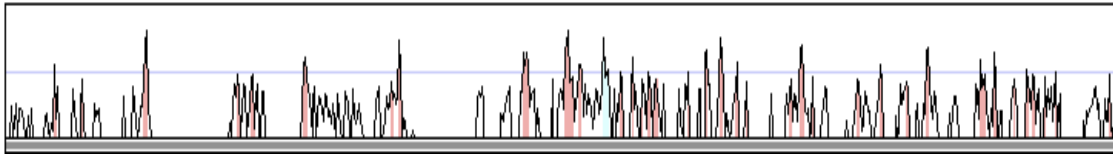
Benjamin Weaver

Rita Luther

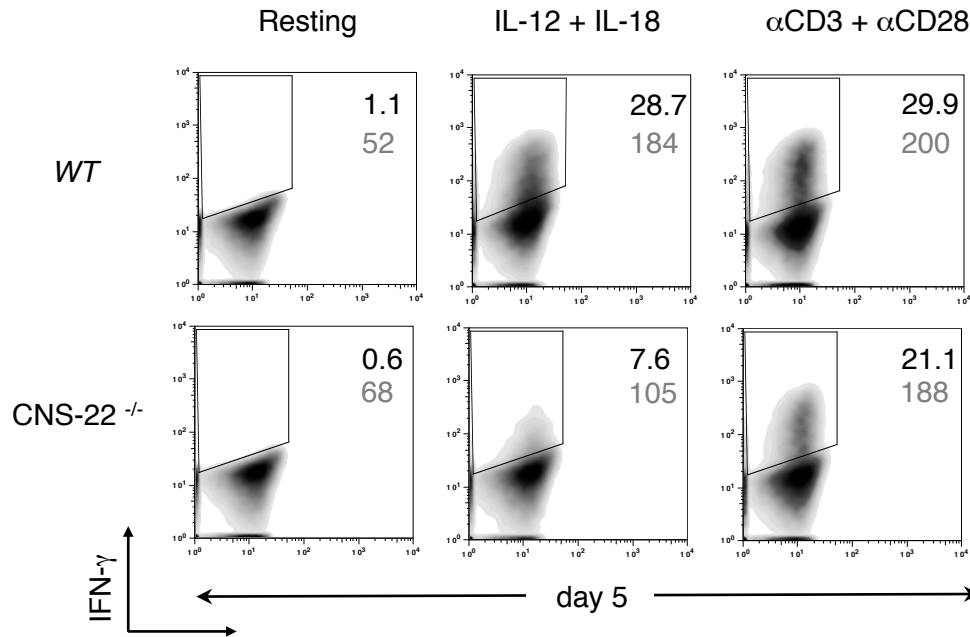
Collaborators

Greg Crawford (Duke)

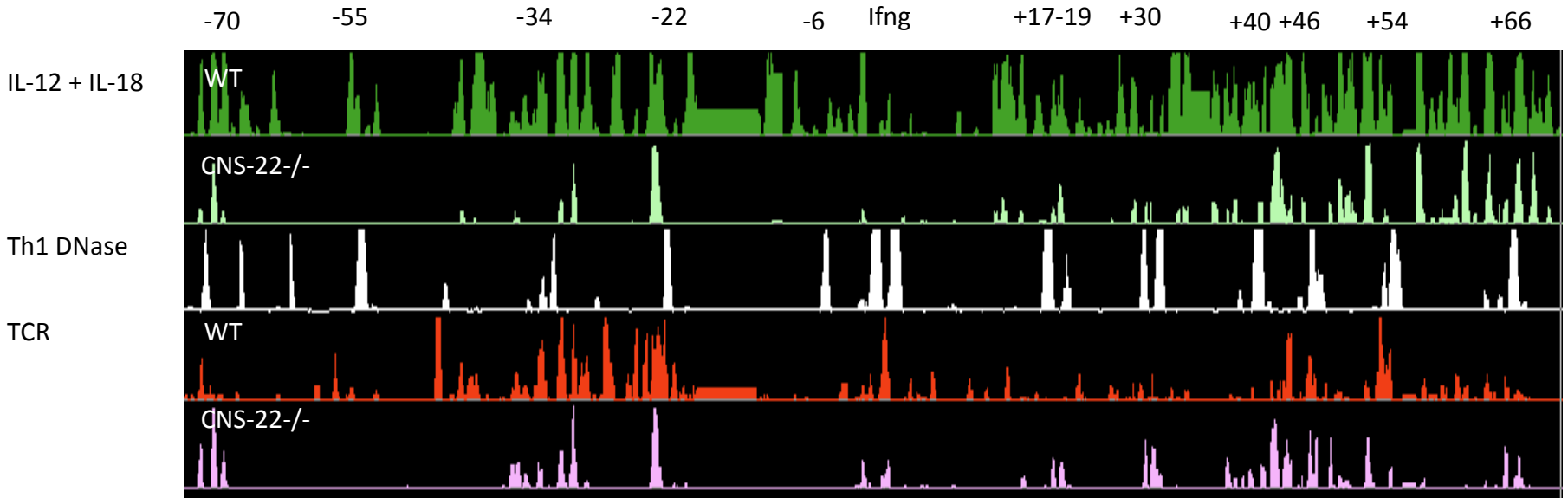
Yoichiro Shibata (Duke)

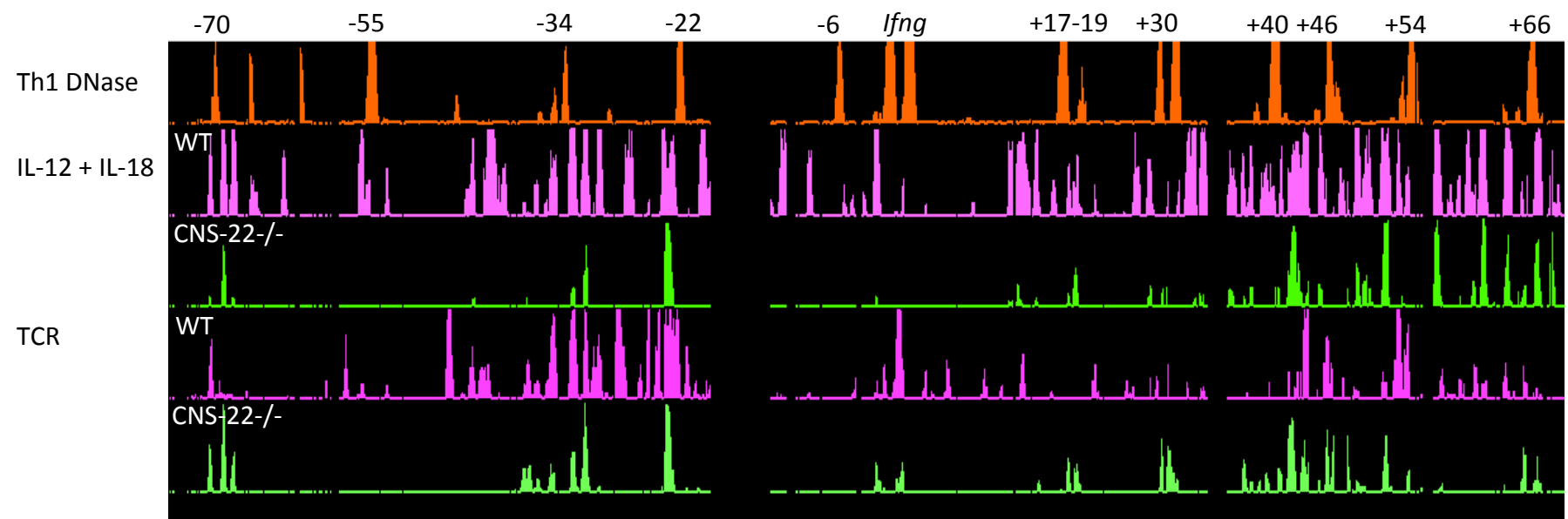


* From the first set of data for med1 and med12

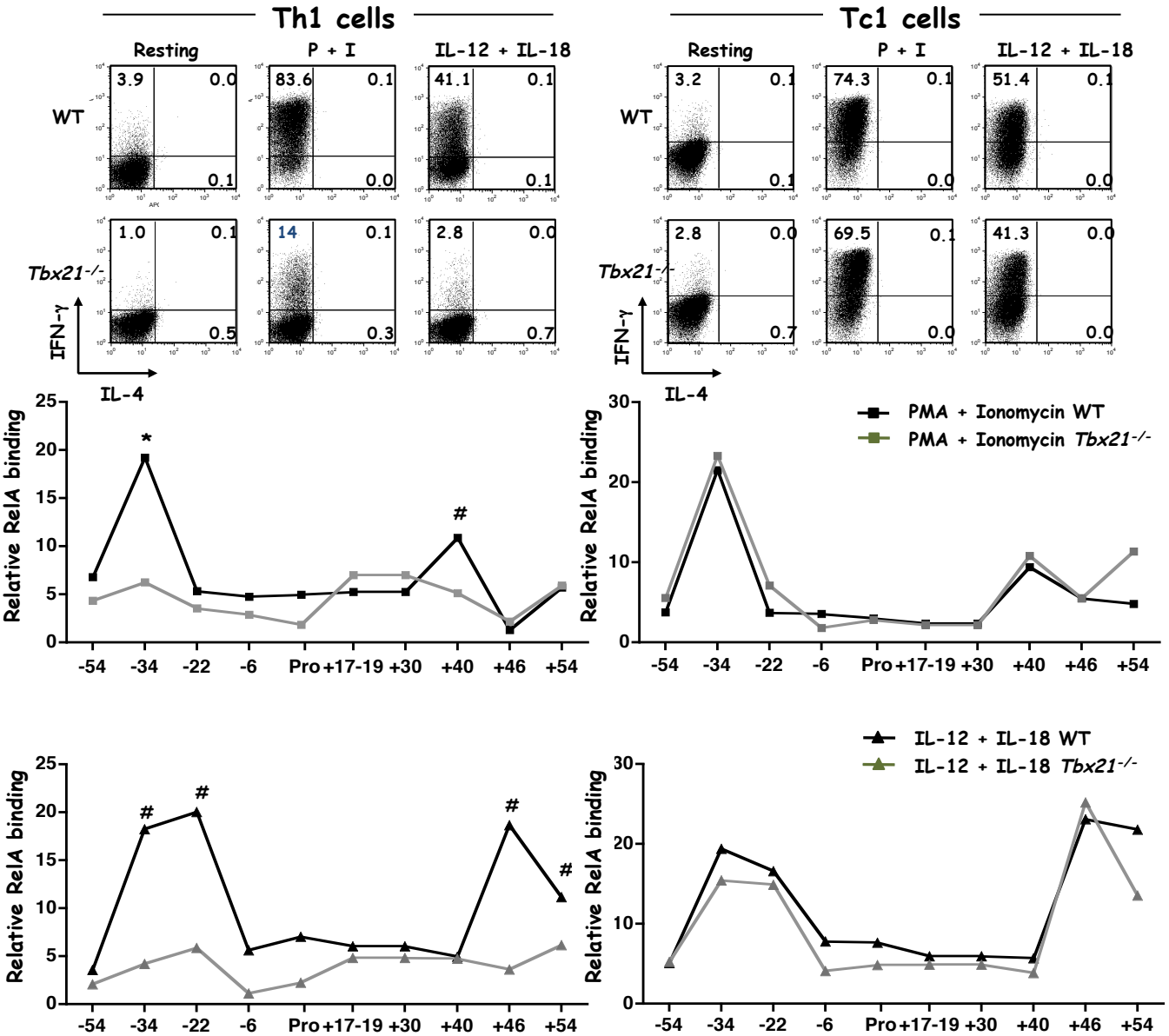


ChIP-chip datasets normalized against respective resting H4K12ac levels..

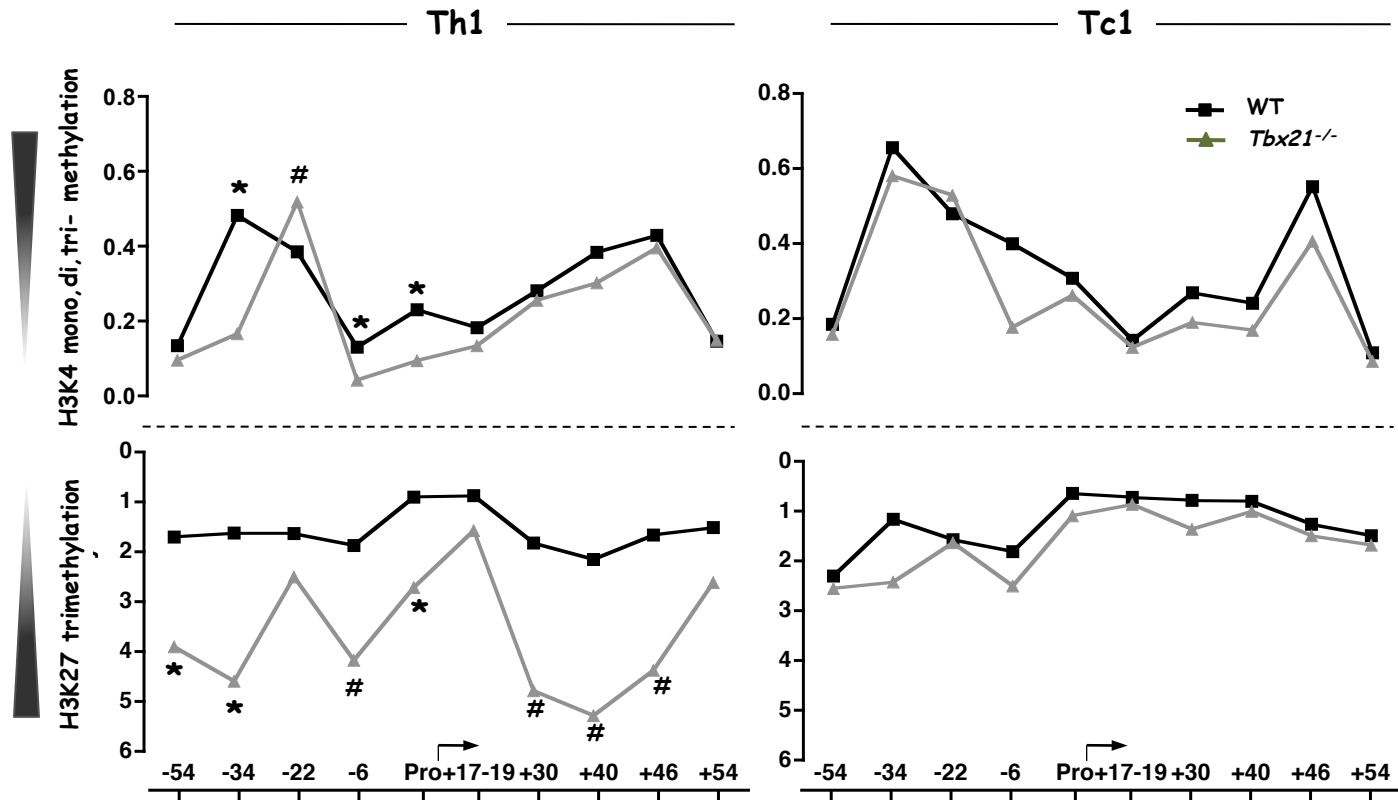




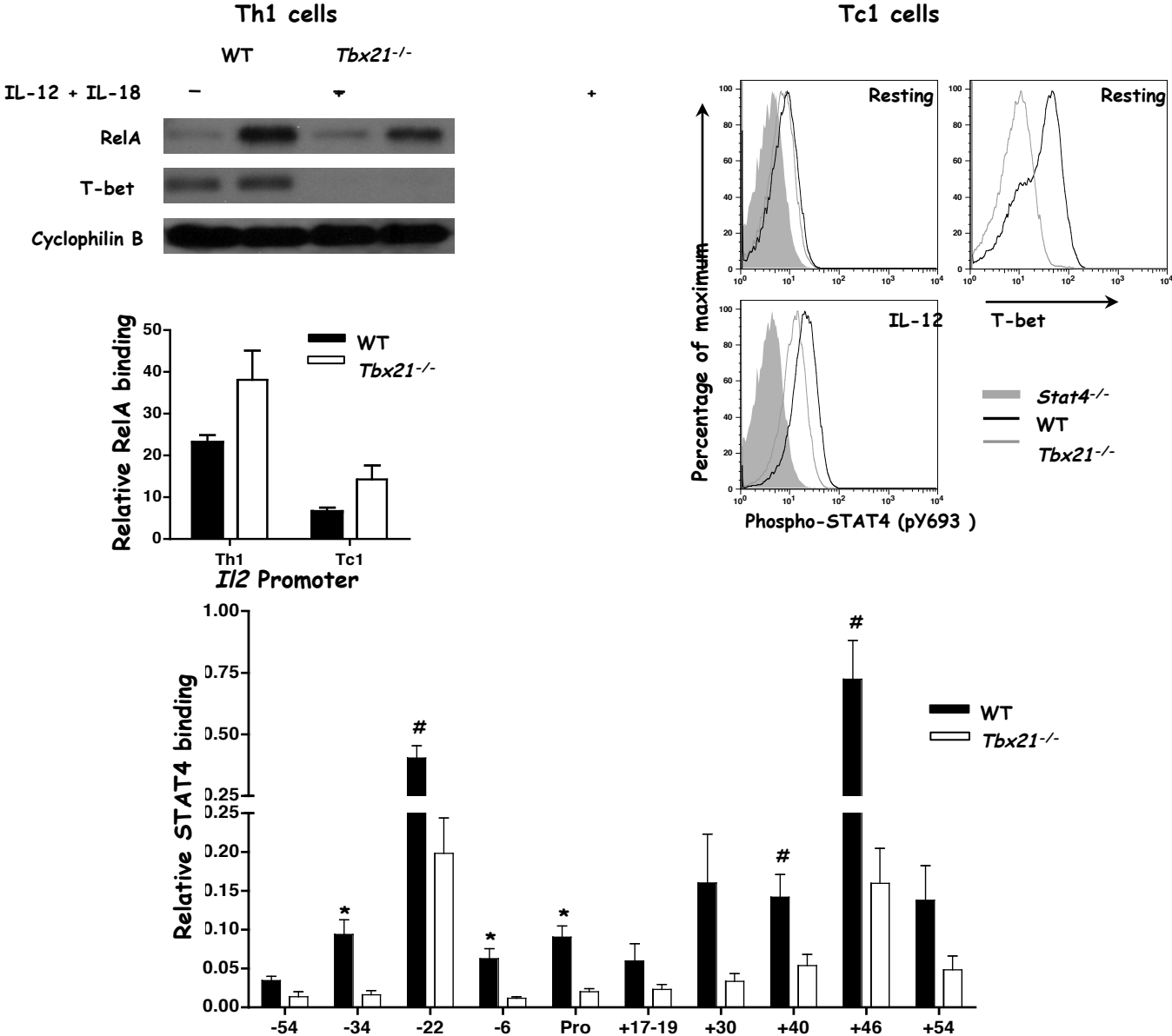
T-bet-Dependent Rel A Recruitment to *Ifng* Locus in Th1 Cells



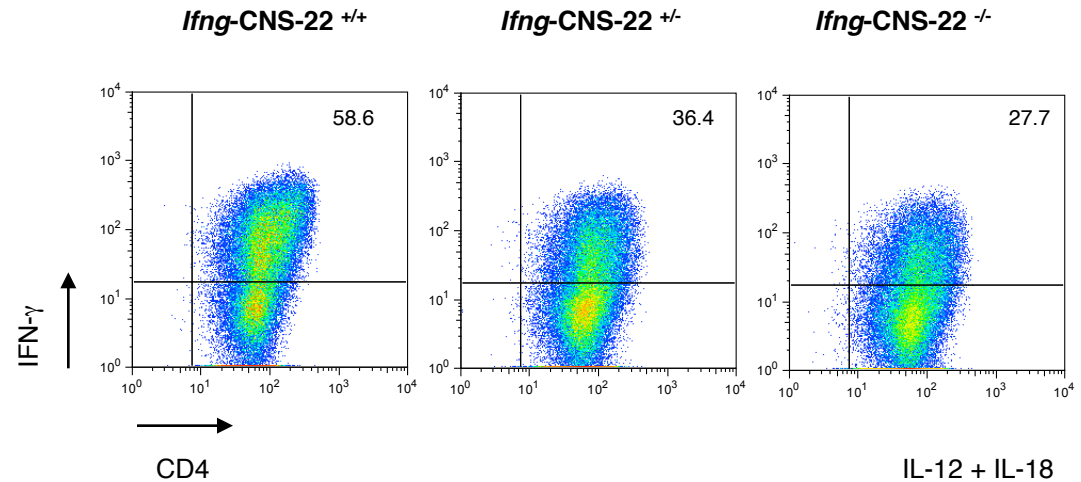
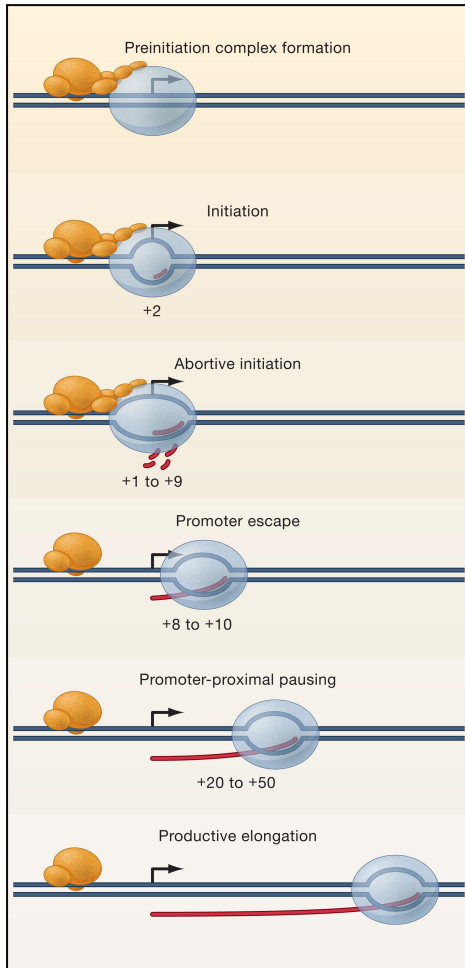
T-bet Dependent Remodeling of the *Ifng* Locus



Diminished STAT4 Recruitment to *Ifng* Locus in the Absence of T-bet

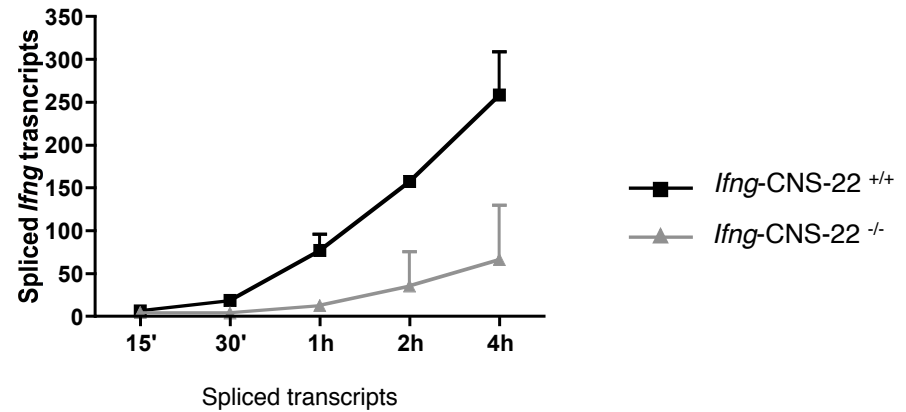
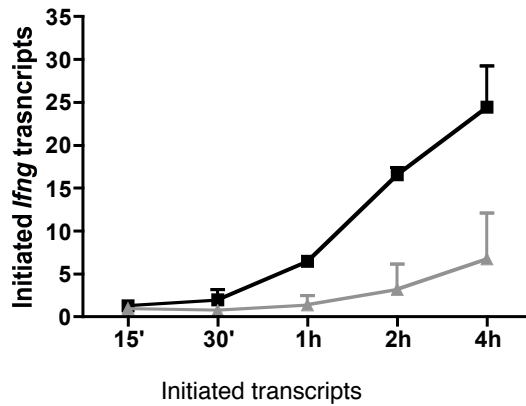
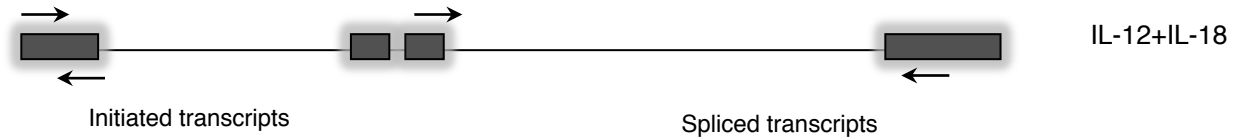


Enhancers: How Do They Drive RNA Pol II Dependent Transcription

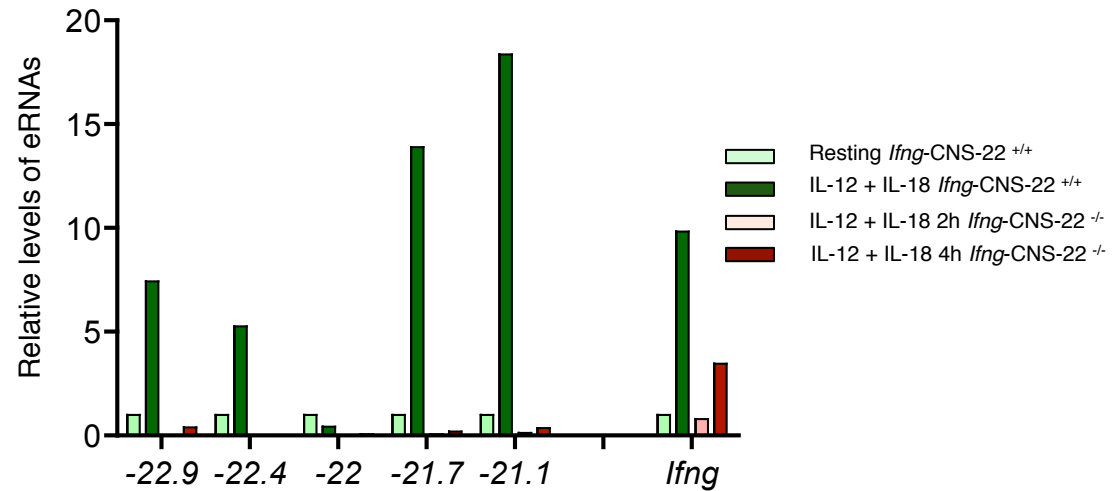
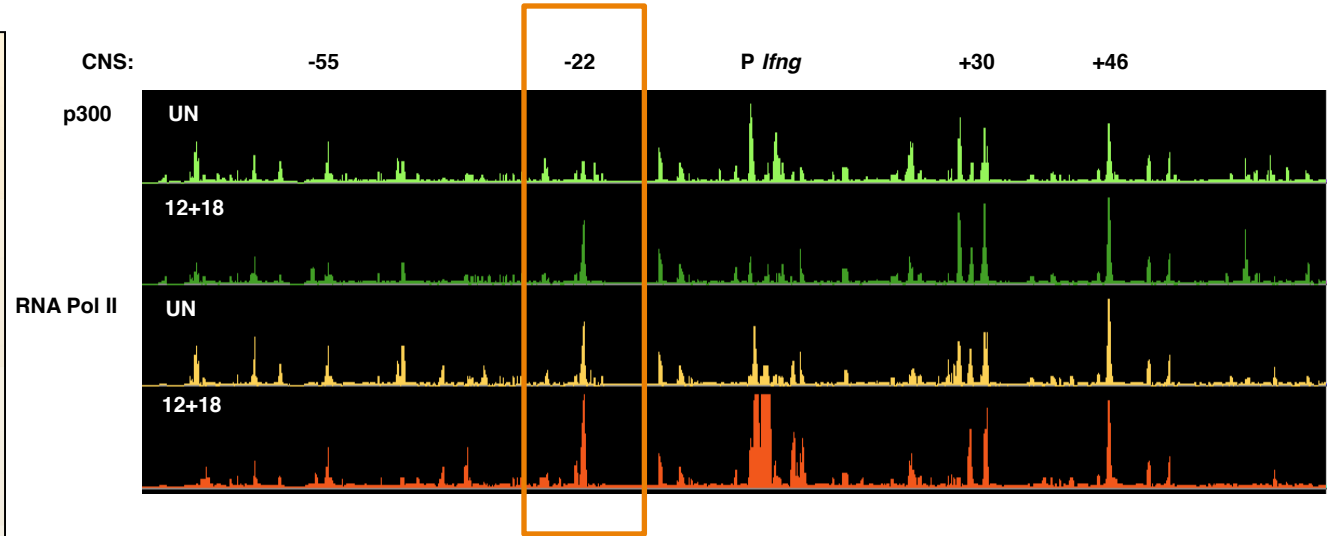
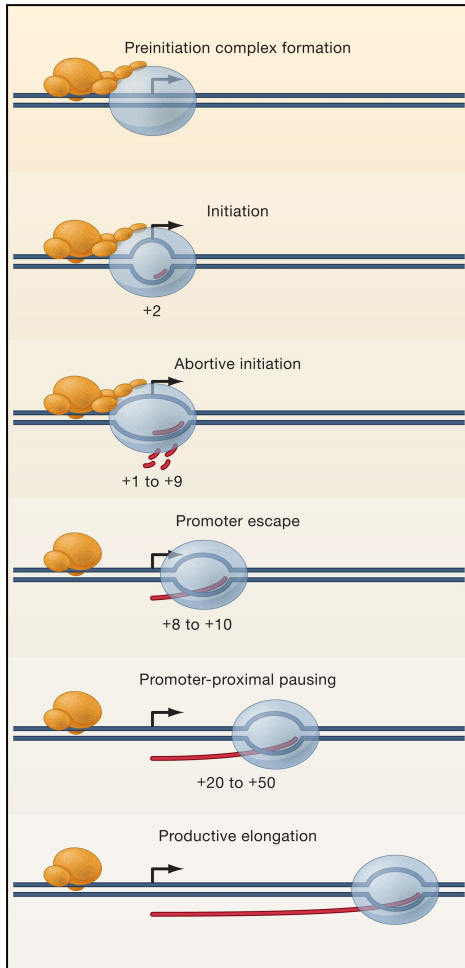


- **Pol II dynamics**
 - Abortive transcription
 - Productive elongation
- **Enhancers**
 - Permissive epigenetic remodeling
 - Push Pol II past the promoter i.e. facilitate transition from initiation to elongation: Thought to impact elongation, but dispensable for Pol II recruitment and initiation
 - Pol II has been shown to be recruited to other enhancers: even involved in generation of enhancer associated transcripts (eRNAs)

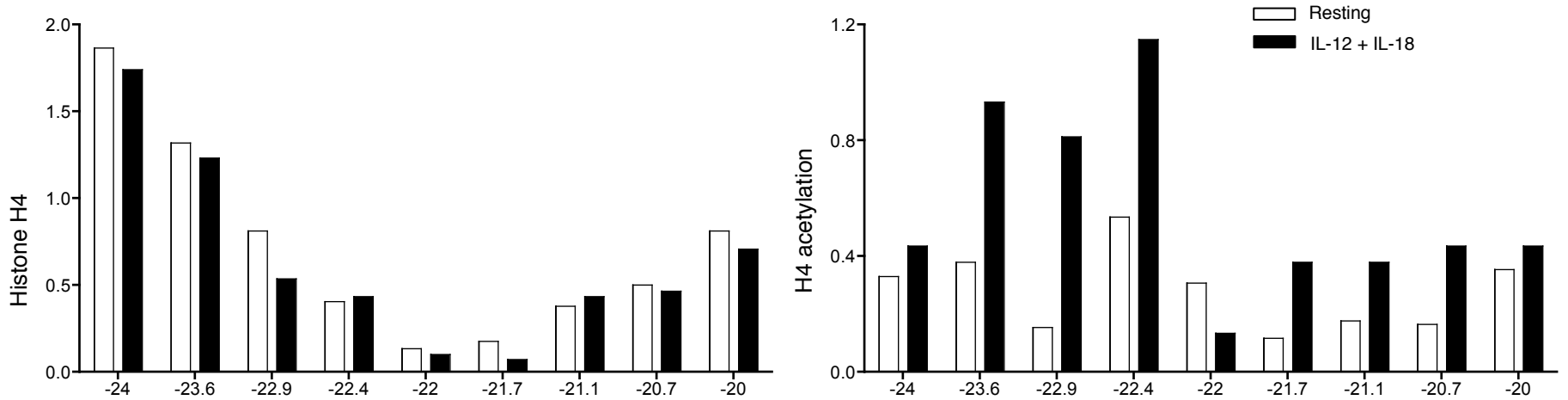
CNS-22: Transcript Initiation or Elongation



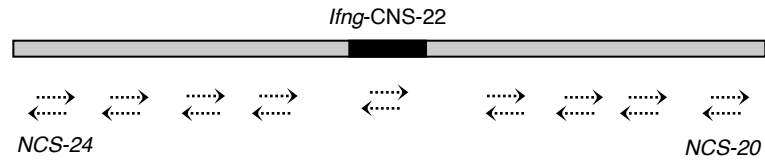
Recruitment of p300 and RNA Pol II to Distal Enhancers



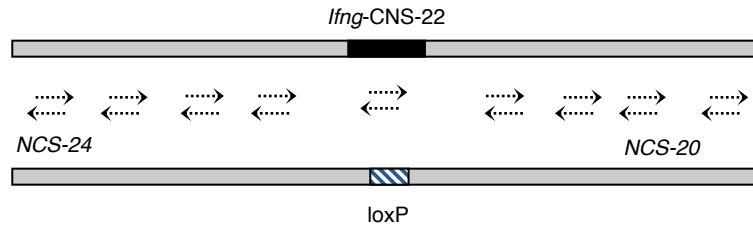
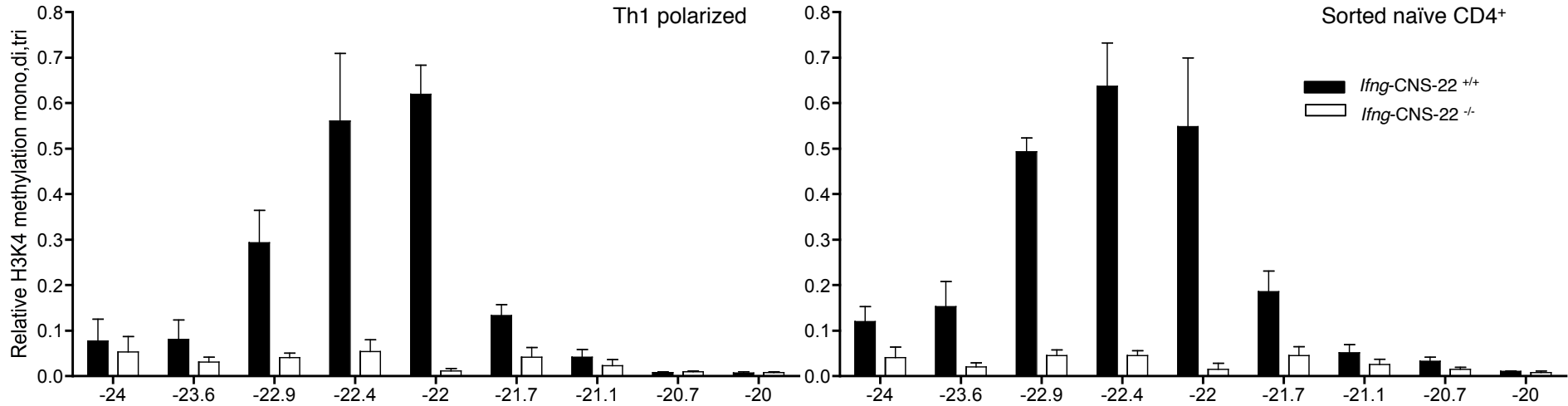
H4 Association Remains Unperturbed



Th1 cells



CNS-22 Dependent Local Permissive Remodeling



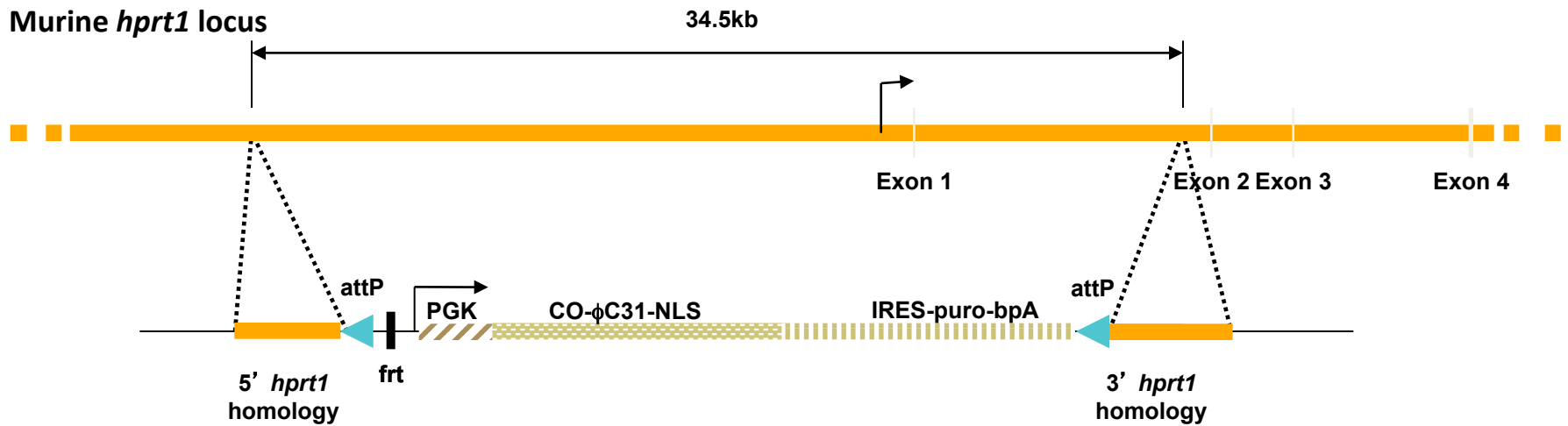
Development of a Novel System for Site-Specific, Single-Copy, Directional Targeting of BAC Transgenes; The HAT-BAC System

- ES cell based
- Targeting to *hprt1* locus;
 - X-linked (single copy in ES cells)
 - ubiquitously expressed, provides a favorable chromatin environment for transgene expression
 - prior success in targeting and expressing BAC transgenes
 - mice derived from independent ES cell clones containing transgene expressed from the same promoter exhibit comparable levels of expression
 - reconstitution of *hprt1* expression permits HAT selection of correctly targeted clones
- Implementation of a novel DNA recombinase for efficient targeting via exchange reaction

Cre and Flp vs ϕ C31 Integrase

- Cre or Flp
 - insertion of a circular DNA into the genome (*trans* event), two *cis*-positioned recognition sites are created
 - intramolecular interactions are kinetically favored over intermolecular interactions; these recombinases favor deletion rather than integration of DNA
 - transgene integration occurs at low efficiency because the reaction equilibrium is shifted in favor of excision
- ϕ C31 integrase
 - can be optimized to work well in mammalian cells (NLS, codon usage); no other phage or bacterially-encoded proteins or factors required
 - catalyzes only the attB x attP reaction and not the reverse reaction (lack of excisionase)
 - better suited for cassette exchange reactions due to its unidirectionality

Targeting of *hprt1* Locus in ES Cells



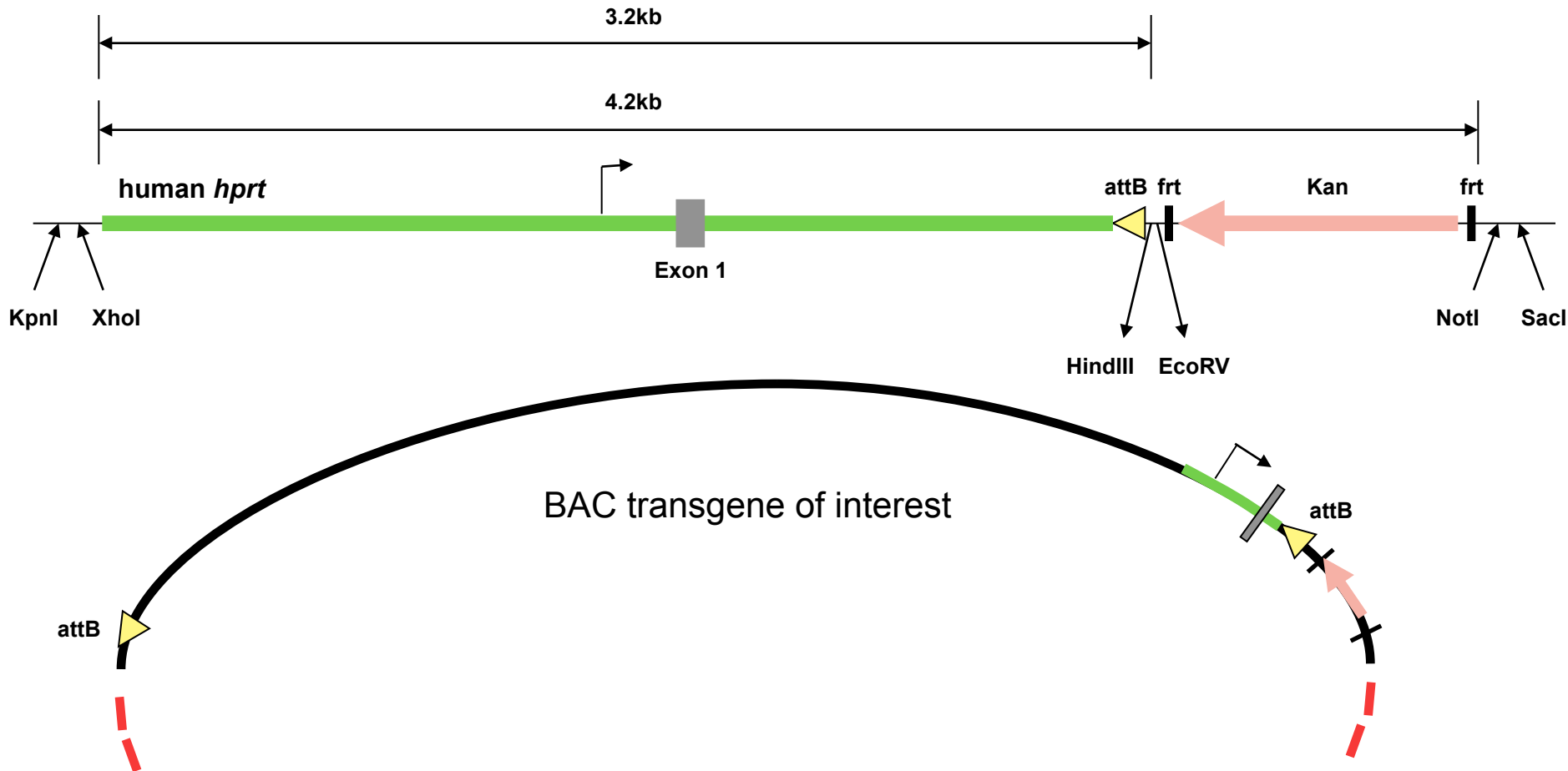
Select with puromycin

Murine *hprt1* locus with ϕ C31 Integrase docking site



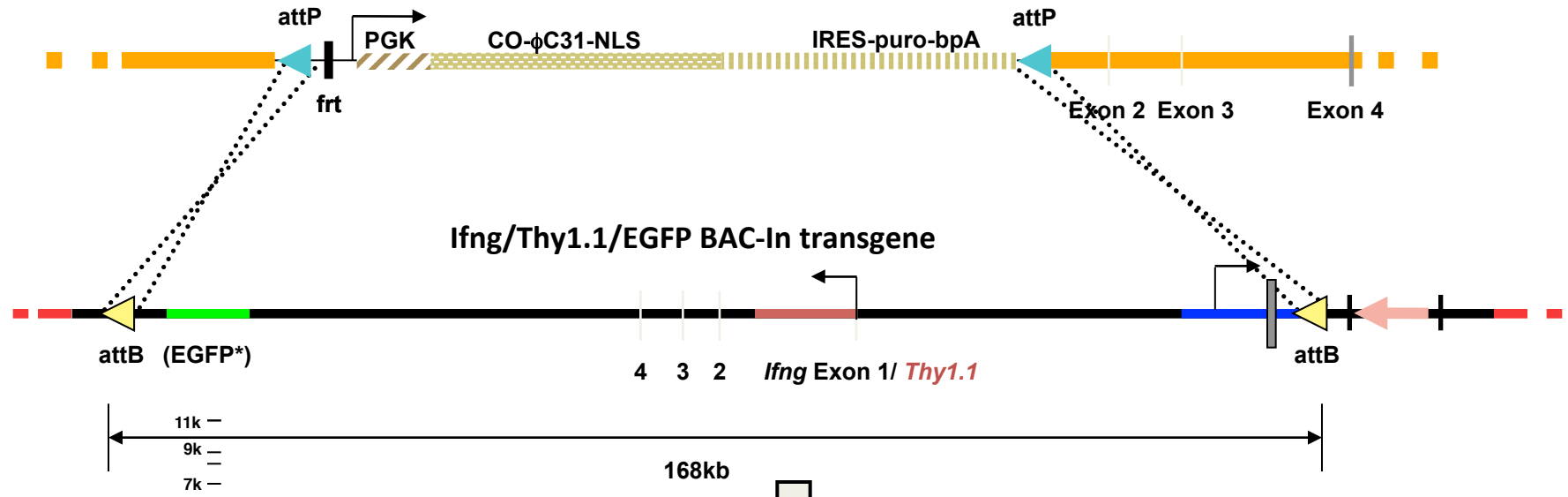
Engineering BACs for Site-Specific Recombination

- Insert 5' attB site
- Insert the cassette: [human *hpert* promoter/exon 1+ second attB site]



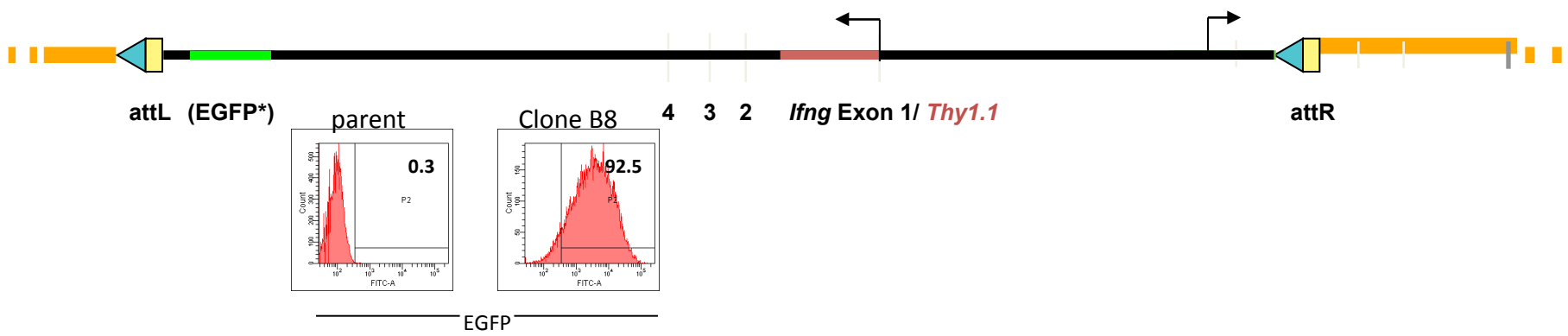
Targeting of BAC Transgene to the Docking Site in HAT-BAC ES Cells

HAT-BAC ES *hprt1* locus containing docking site



Select with HAT

Restored *hprt1* locus containing BAC transgene



- - Acetylation
- - Deacetylation
- - Methylation
- - Demethylation
- - Isomeration
- - Phosphorylation
- - Ubiquitination

Histone Modifying Enzymes

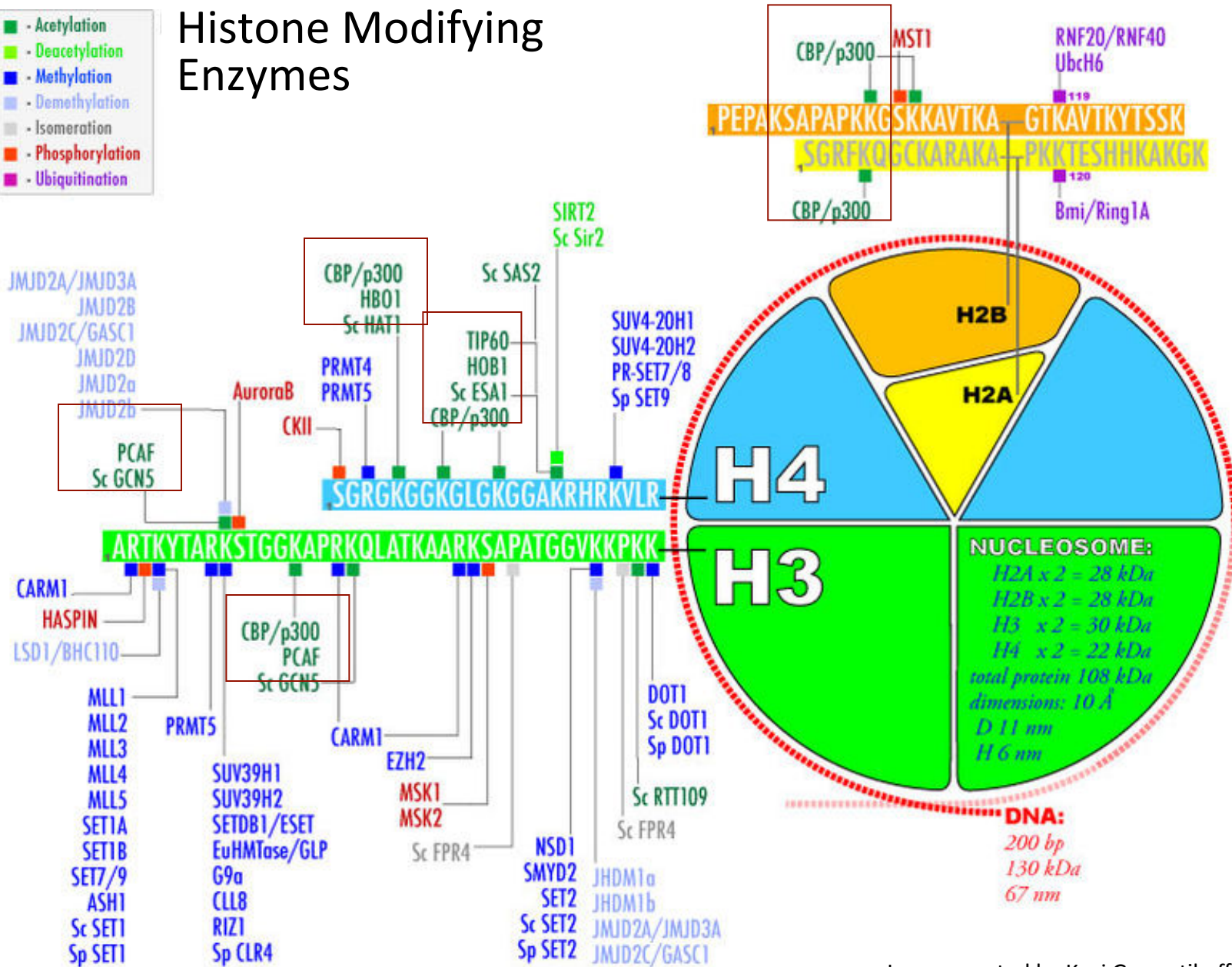
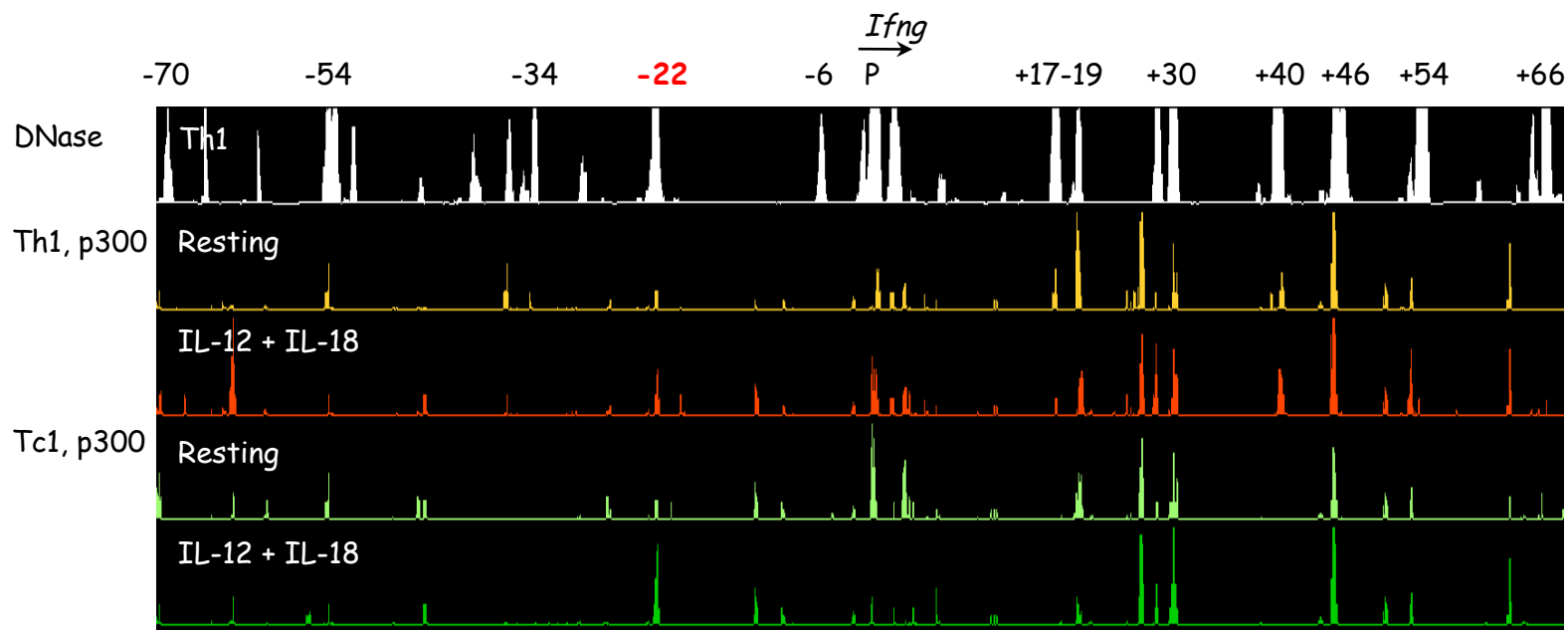


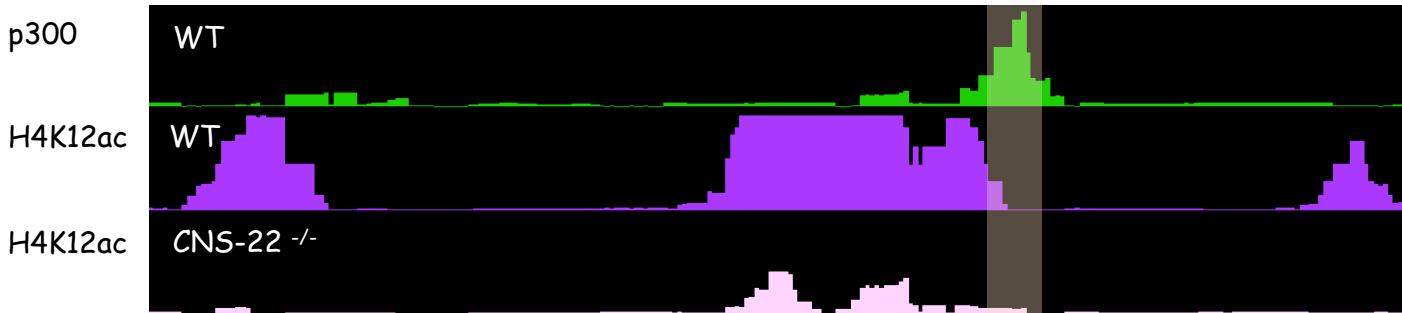
Image created by Kosi Gramatikoff

p300 Binding Maps to CNS Elements Across *Ifng* Locus



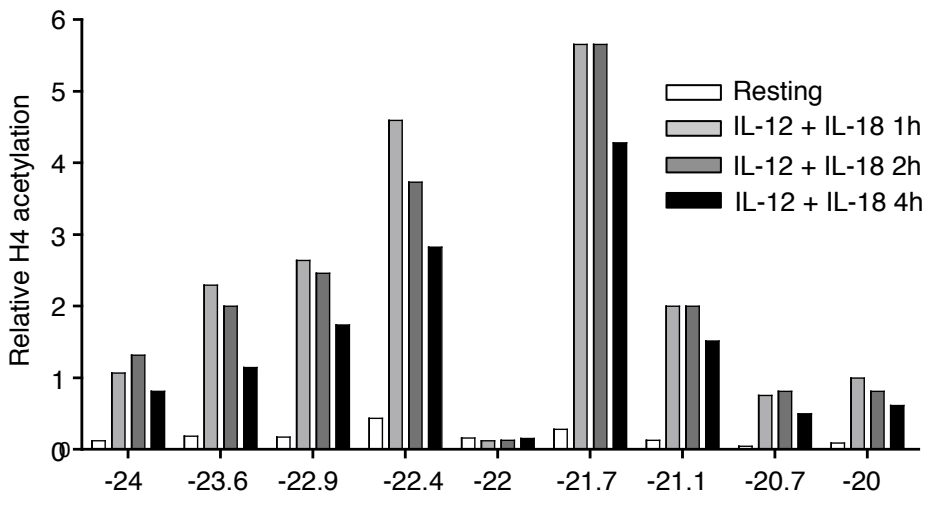
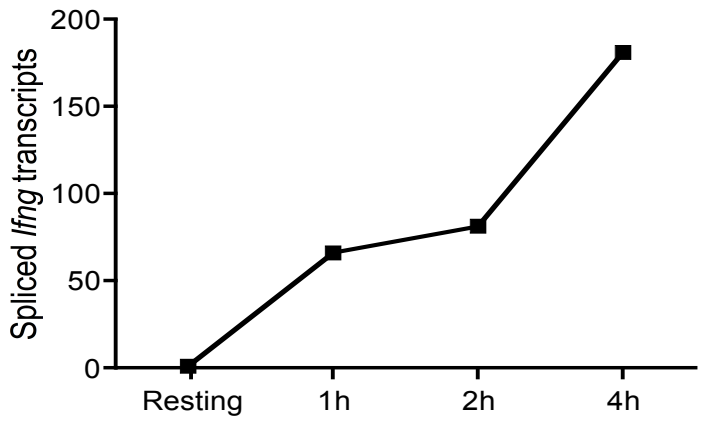
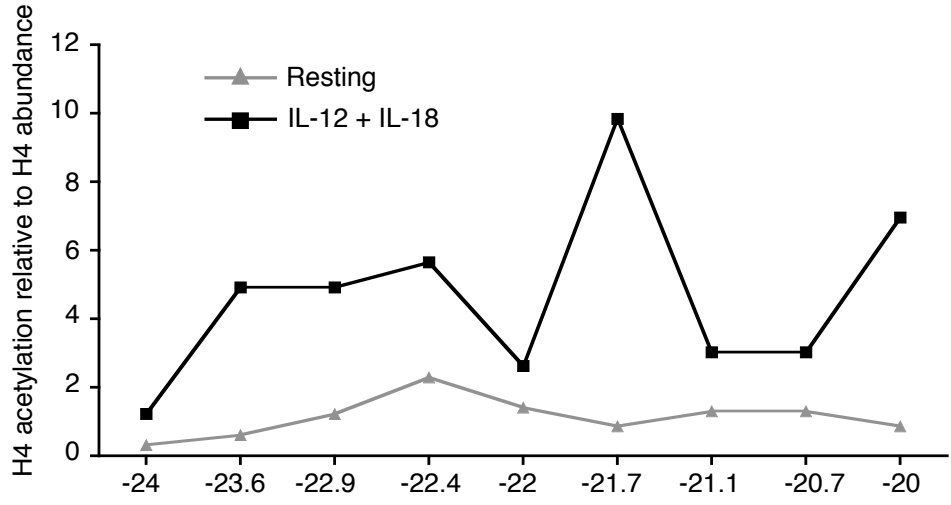
Tc1 : IL-12 + IL-18

9126bp

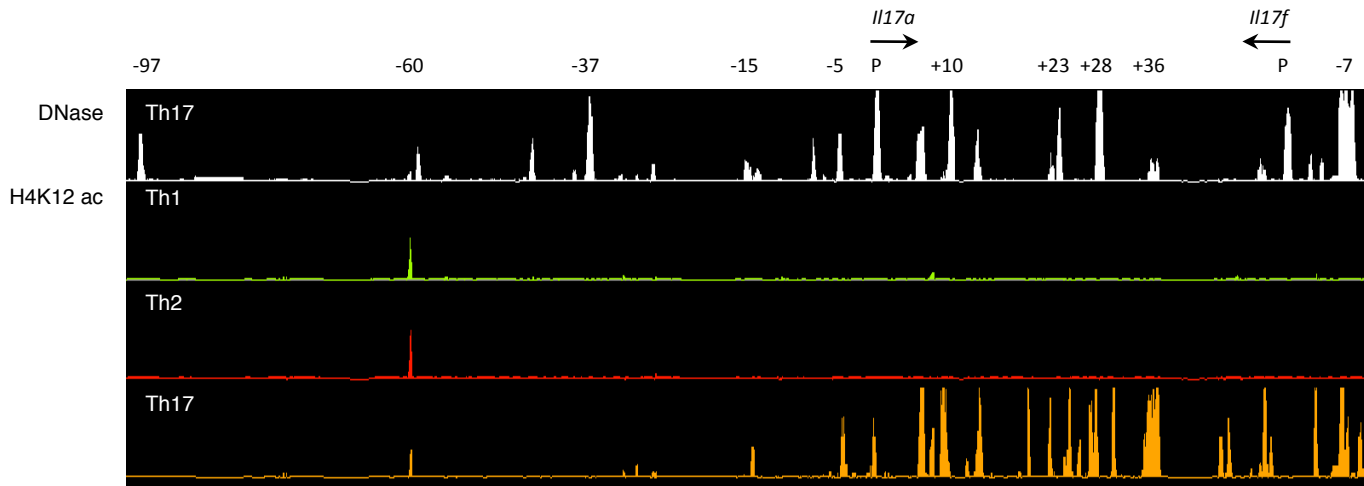
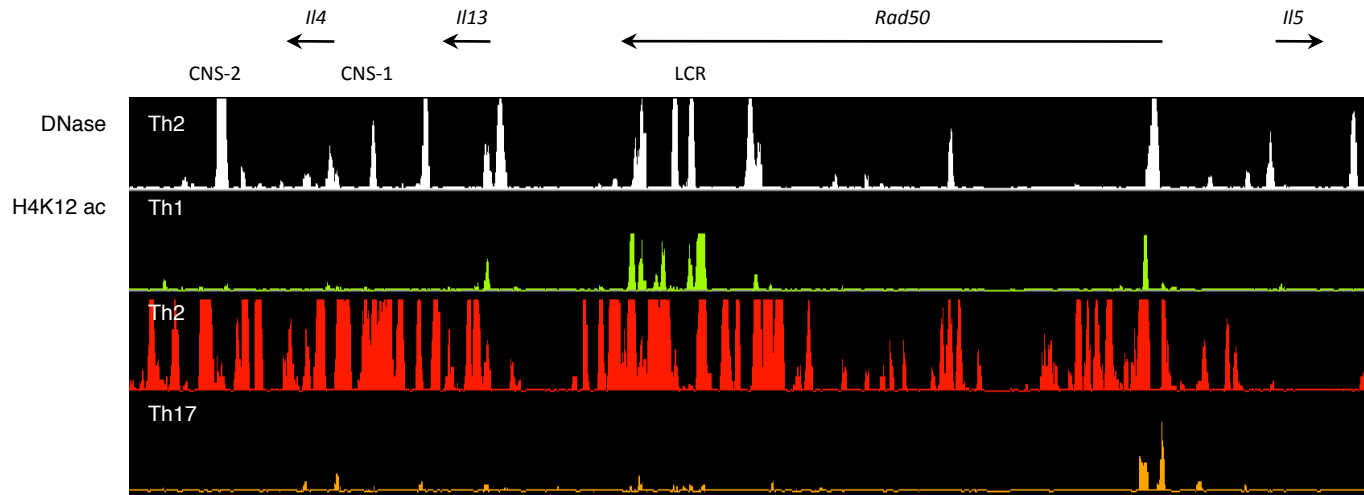


391bp
CNS-22

Activation-induced Hyperacetylation of CNS-22 Precedes *Ifng* Transcript Induction



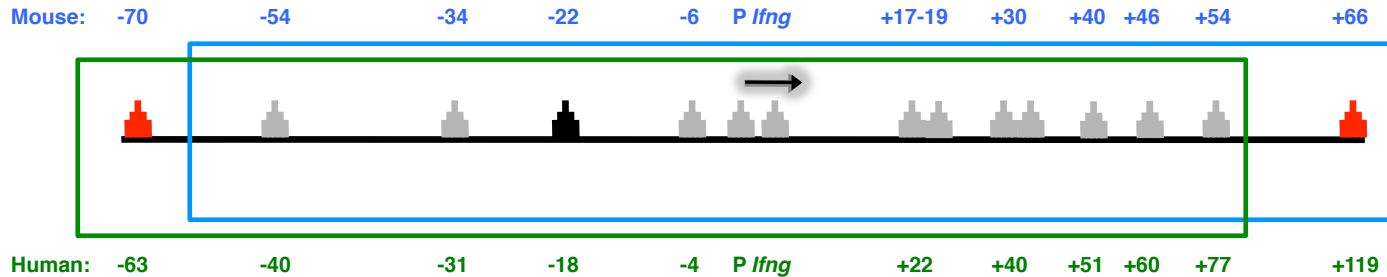
Histone Acetylation as a Measure of Transcriptional Activity



Acetylation of Lineage-specifying Genes

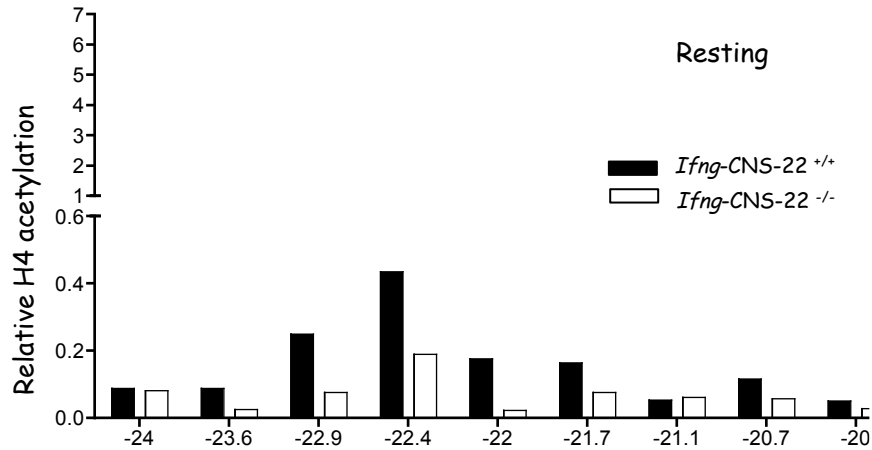
Gene	Expression pattern	Levels of H4K12 acetylation		
		Th1	Th2	Th17
<i>Tbx21</i>	Th1	+++++	+	-
<i>Gata3</i>	Th2	+	+++++	-
<i>Rora</i>	Th17	-	-	+++++
<i>Rorc</i>	Th17	-	-	+++++
<i>Il21</i>	Th17 > Th1/Th2	++	+++	+++++
<i>Il10</i>	Th2 > Th1/Th17	++	+++++	-
<i>Ccr6</i>	Th17	-	-	+++++
<i>Fasl</i>	Th1	+++++	-	-

Summary II

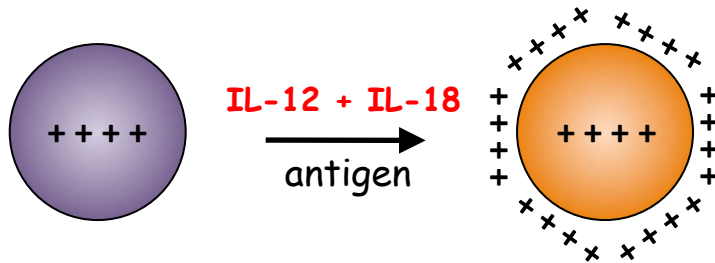
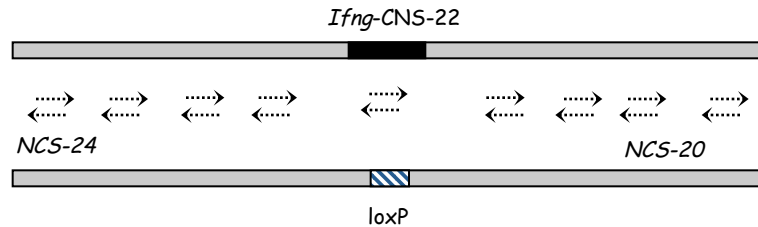


- **Deletion of CNS-22 impacts *Ifng* gene transcription**
 - 391 bp deletion in a locus that is approximately 140 kb in length.
 - First element in the *Ifng* locus whose function has been directly examined *in vivo*
- **Original Hypothesis: CNS-22 plays an essential role in long-range remodeling of the *Ifng* locus**
 - Several differences between the BAC-transgenic and endogenous deletion of CNS-22
 - So what is the function of CNS-22?

CNS-22 Initiates Local Changes in Remodeling



Th1 cells



Th1 day 5 (Resting)

Activated : IFN- γ secreting cell