3 H3K9me2					
H3K9me					
H3K4me2		<u>ki. dirita di</u>		ili ya Alati ya Mudala	
H3K4me3	and the second of the second of the second	Ant. Alban and an a	LAGE DEC MAR AND	ic di Alian Carlo and	
H3K18ac	a. dia	i. inclus a	kail in a mar senta	i i di di suer i da i un solli di	
H3K23ac	004-00 5.04-00 5.04-07	1.0±+08	. A	- 11. 11. 11. 11. 11. 11. 11. 11. 200-08	2.5e+08

Figure S1. Distribution of histone modifications measured with ChIP-seq experiments on human CD4+ T cells for chromosome 2.

H3K9me2 35 20 5			an sheed ye the	ىرىلى سەركىرىكى بىلىرىكى ئىلىرىكى بىلىرىكى سەركى سەركىرىكى بىلىرىكى بىلىرىكى بىلىرىكى	ang dia ^a ng dia pa ^{ng}
<9me3 60 20		en frank Santa (se politik di tan di tanan tan bahar) na panangana an tan			
H3K4me2				and the last of the state of the	
H3K4me3		un ministrati di sectori	. The least states	Lange and An a Market and	A A A A A A A A A A A A A A A A A A A
H3K18ac H	i Billio 11	nd. 1991. de anticipation de la companya de la comp	<u>. 188 . 11. 201</u>	<u>Lander de lindra di</u>	10 10 10 IS
H3K23ac	0.00-00	5.0+07	1.0e+08	1.5+00	2.00+08

Figure S2. Distribution of histone modifications measured with ChIP-seq experiments on human CD4+ T cells for chromosome 3.

H3K9me2 16 10 6				
H3K9me3 80 40				
H3K4me2 00 100 2	and the last of the set	<u> 1. Martin and 1. Martin a</u>	i. The issues of the state of the	
c H3K4me3 500 200 4		an a	n he here entities a web .	<u>e estál a lata de taxados</u>
c H3K18ac H	land and college , the instates de s		a land arth i handar a tha a sh	Americanic estatus
H3K23ac	0e-00 2e-07		6+07	80-07

Figure S3. Distribution of histone modifications measured with ChIP-seq experiments on human CD4+ T cells for chromosome 17.

H3K9me2		
H3K9me3	an an an an an an an an Anna an	
H3K4me2	lania ini taida a izati izati	AND A DESCRIPTION OF AN AND AND AND
H3K4me3	LIN LEW LANK ALLERTHIC STAFF FRAN	

Figure S4. Distribution of histone modifications measured with ChIP-seq experiments on human HeLa cells for chromosome 1.

1e2 20	
H3K9me	
49me3 10 5 6 1 1 5 6	المراز المحيد فيتحدث والمحتجز والمحتجز والمحتجز والمحتج والمتحافظ والمحتجز المحتجز والمحتجز والمحتجز والمحتجز والمحتجز
15 H3	
K4me2 200	
Ê .	al a characterization was the terms of the terms of the second second second second second second second second
4me3 250	The second second states of the second se
H3K4 0 100	

Figure S5. Distribution of histone modifications measured with ChIP-seq experiments on human HeLa cells for chromosome 2.

H3K9me2 30 20 10	a na haran ang ang manya pang tang ang ang ang ang ang ang ang ang ang
H3K9me3	
H3K4me2	
H3K4me3	ed sid middle her herhold

Figure S6. Distribution of histone modifications measured with ChIP-seq experiments on human HeLa cells for chromosome 3.

(9me2	
163 H3P	an a
15 10	an new sense water and the sense of the sense I also need to be a sense of the s
H3K4me2	
H3K4me3	AND CONCEPTED OF CONTRACTOR OF CARLES INCOME

Figure S7. Distribution of histone modifications measured with ChIP-seq experiments on human HeLa cells for chromosome 17.

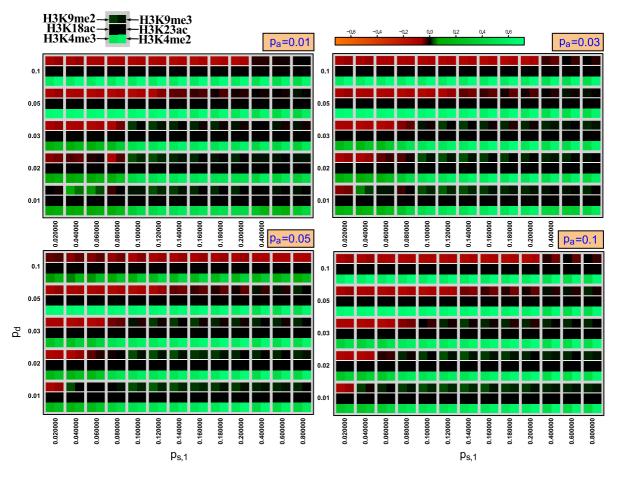


Figure S8. Pearson's correlation between simulations and experiments on chromosome 1 on HeLa cells for different values of the parameters $p_{s,1}$, p_d and p_a . No data was available for the marks H3K18ac and H3K23ac (fields remain black). The results are almost identical to the ones for CD4+ cells.

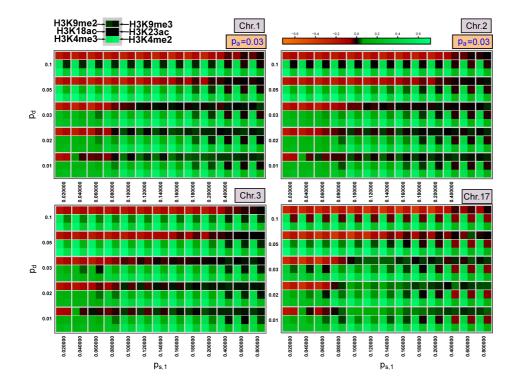


Figure S9. Pearson's correlation between simulations and experiments on chromosomes 1-3 ad 17 on CD4+ cells for different values of the parameters $p_{s,1}$, p_d and $p_a = 0.03$. The results are very similar between the different chromosomes.

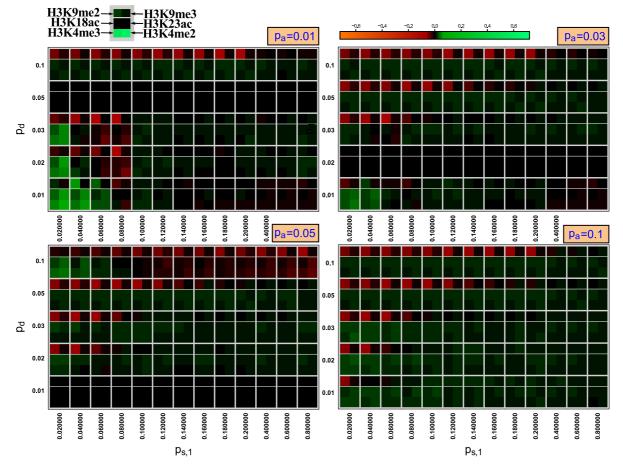


Figure S10. Pearson's correlation between simulations and experiments on chromosome 1 on CD4+ T cells for different values of the parameters $p_{s,1}$, p_d and p_a . We used wrong coordinates for the nucleation sites based on human genome hg19 instead of hg18. Resulting correlation values are much lower than for correct nucleation site positions. Hence, these slightly differently positioned sites impede accurate reproduction of the chromatin domains for all parameter values.

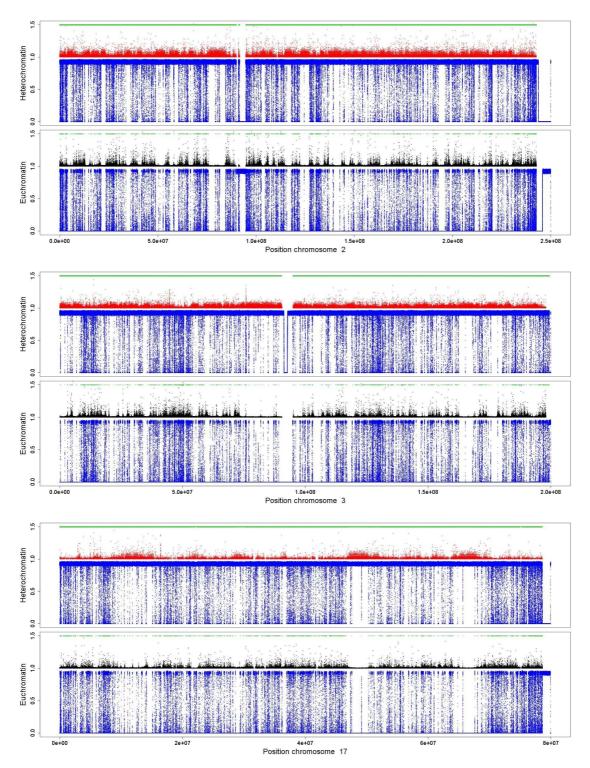


Figure S11. Comparing the simulation results for chromosomes 2,3 and 17 to the CD4+ T cells data set. Parameters are the same as in Fig. 5.

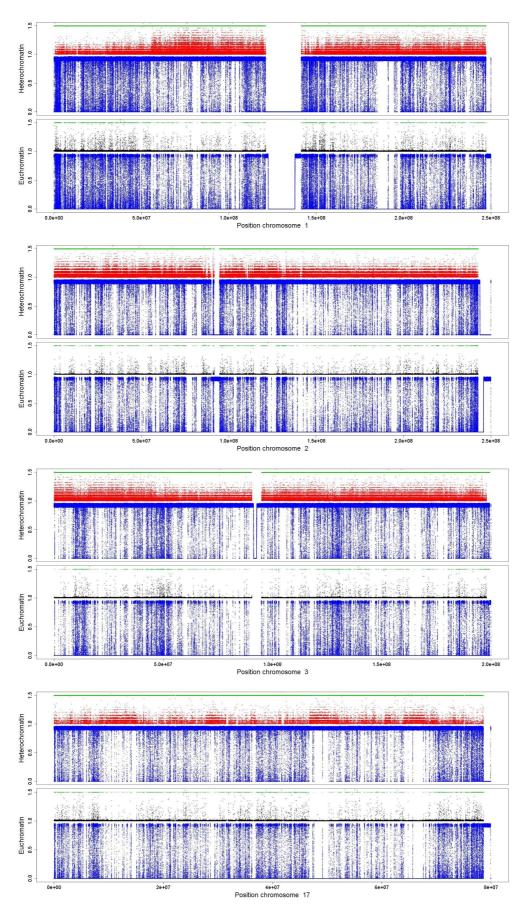


Figure S12. Comparing the simulation results for chromosomes 1-3 and 17 to the HeLa cells data set. Parameters are the same as in Fig. 5.

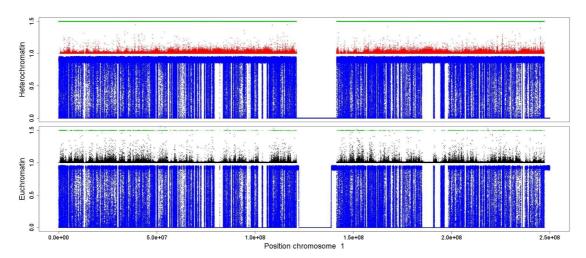


Figure S13. Comparing the simulation results for chromosome 3 to the CD4+ ChIP-seq data set. Parameters are the same as in Fig. 5 except of a smaller propagation rate for heterochromatin, $p_{s,1} = 0.08$ leading to an aberrant state of chromatin domain distribution.

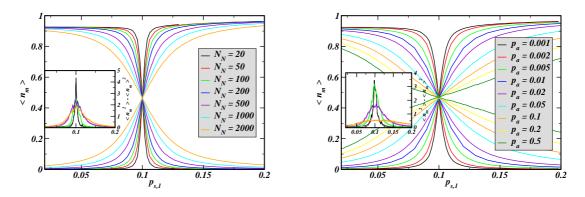


Figure S14. General model behavior. Comparing the average frequency of modifications versus the propagation rate $p_{s,1}$ for different numbers of nucleation sites N_N (left) and for different values of the association rate p_a (right). The inner panels exhibit the temporal fluctuations $\langle n_m^2 \rangle - \langle n_m \rangle^2$ in the system for each mark. The system exhibits a behavior similar to a phase transition when changing the propagation constant leading to a drastic increase of the fluctuations at the transition point at $p_{s,1} = p_{s,2}$. At this point, the domains actively compete against each other by changing their size and temporally occupying regions that have been previously occupied by the competing mark. The fluctuations become larger for sharper transitions. The transition becomes smoother for smaller numbers of nucleation sites and/or for larger nucleation rates. The other parameters were $p_{s,2} = 0.1$, $p_d = p_a = 0.01$.

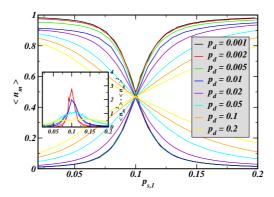


Figure S15. General model behavior. Comparing the average frequency of modifications versus the dissociation rate $p_{s,1}$ for different dissociation rates p_d . The other parameters were $p_s = 0.1, p_a = 0.01, N_N = 1000.$

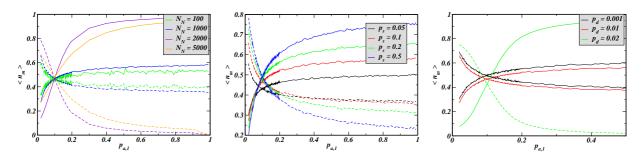


Figure S16. Model behavior for different nucleation rates. We compare the average frequency of modifications versus the association rate $p_{a,1}$ for different numbers of nucleation sites (left), for different values of the propagation rate (center) and for different values of the deletion rate (right). There is no sensitive reaction to a change of the association rate.