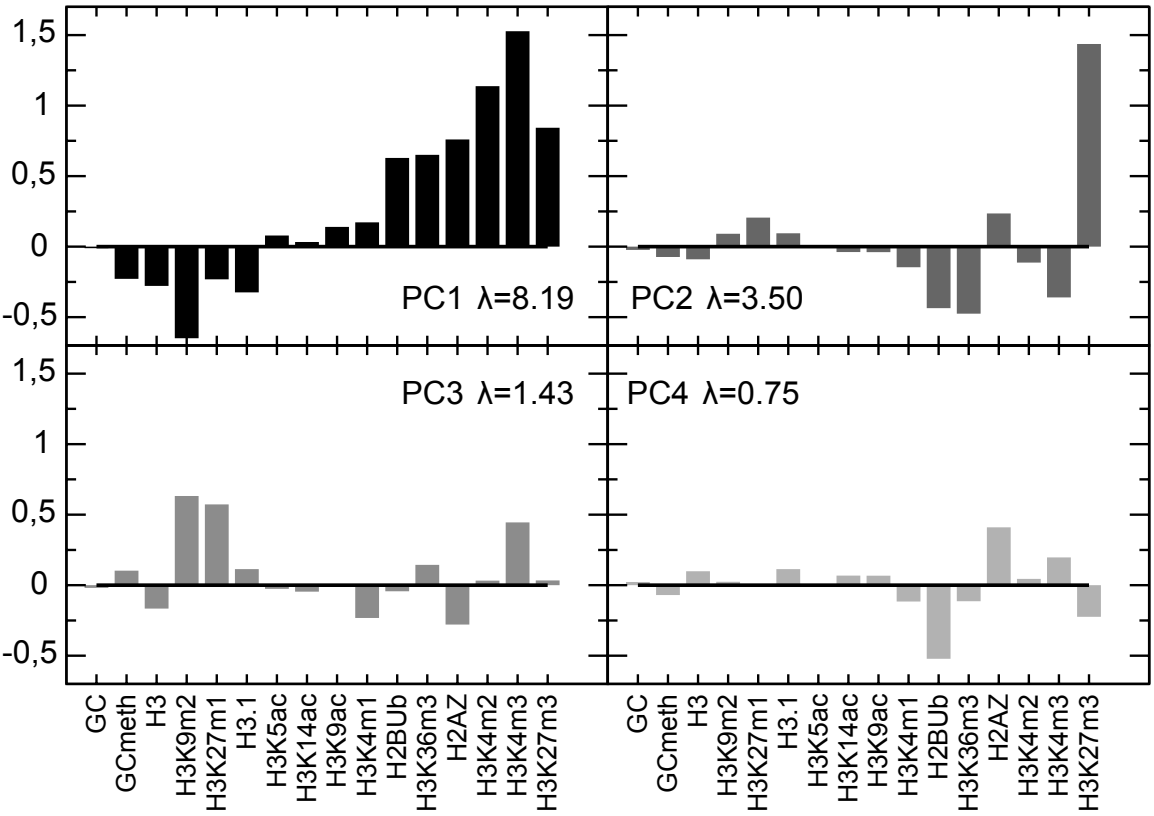
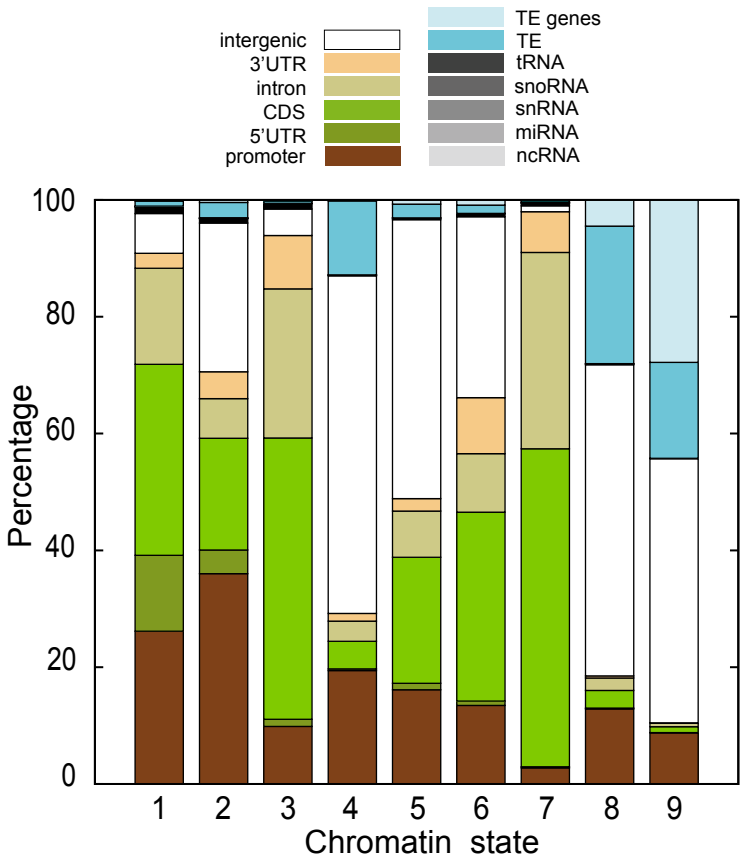
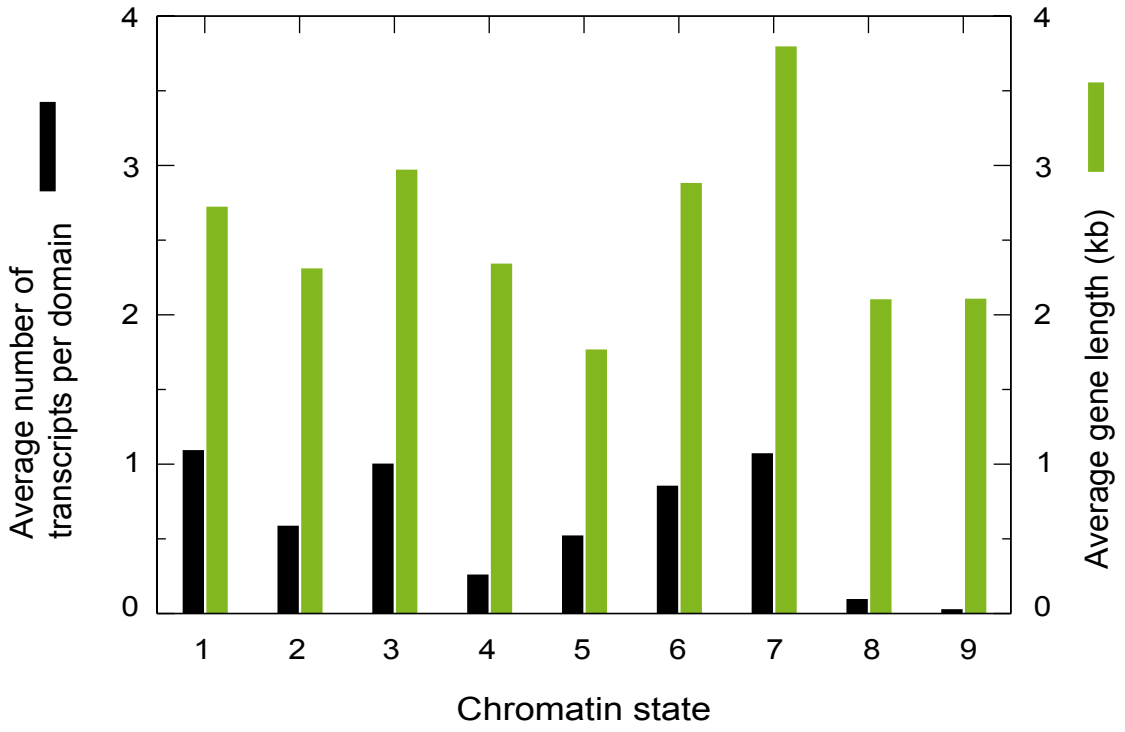


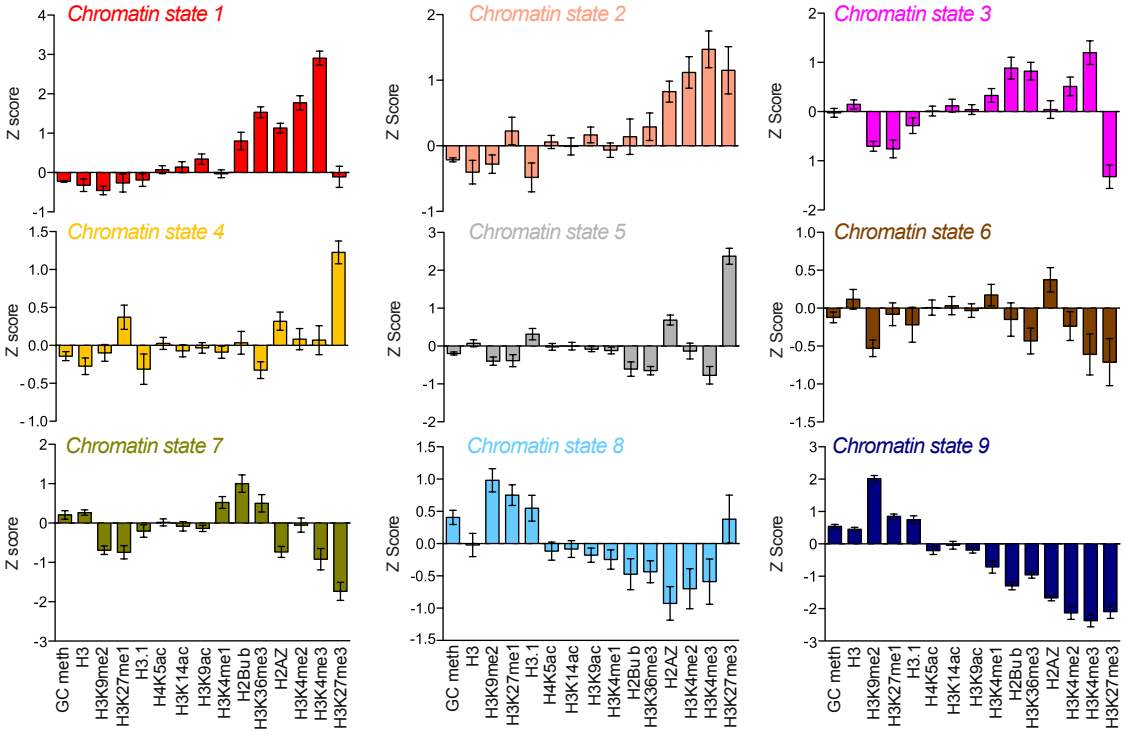
Supplemental Figure 1. Relative values of each of the genomic features used in this study for each of the principal components considerd. See Methods for details.



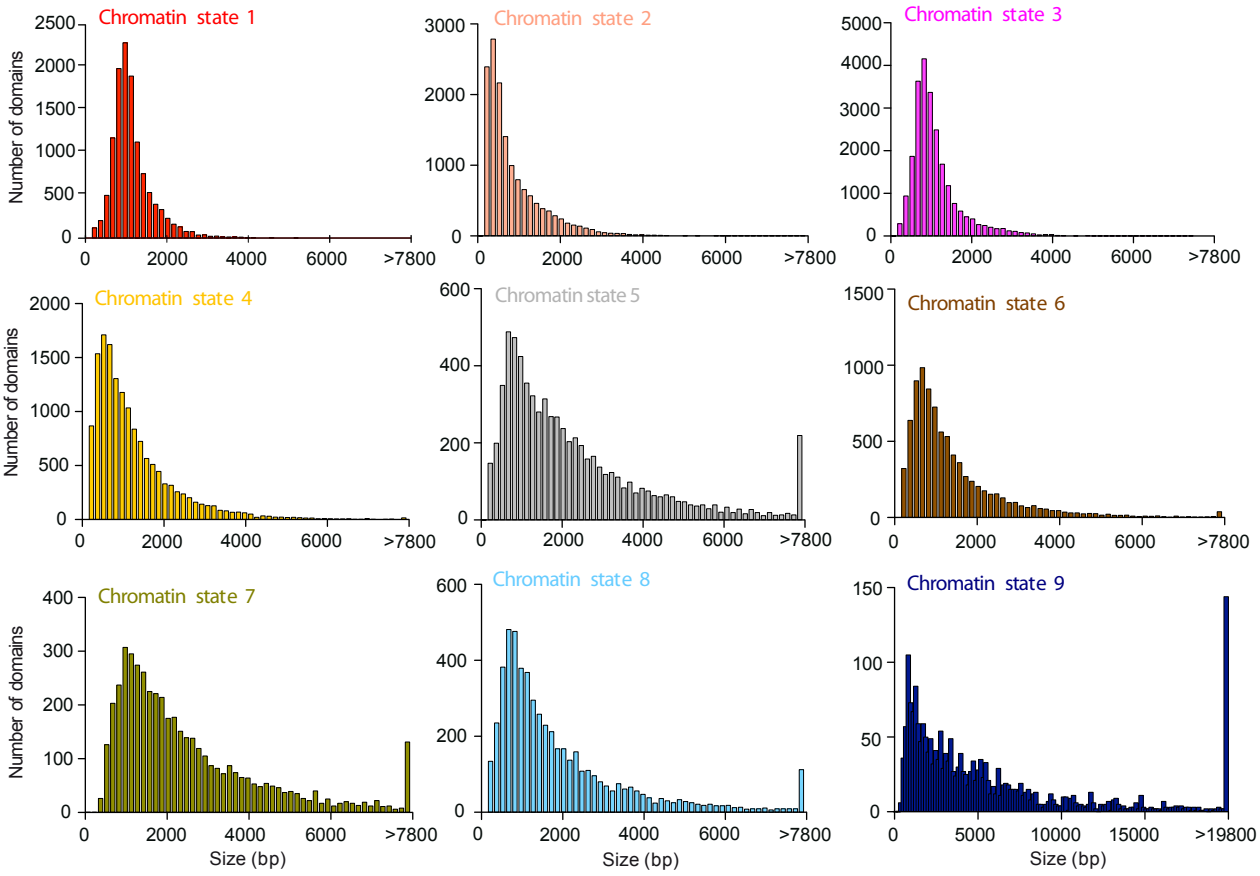
Supplemental Figure 2. Relationship between genomic elements and chromatin states. The overlap (in bp) between the indicated genomic elements and each chromatin state was computed and expressed as a percentage. A promoter region of 1 kb was considered.



Supplemental Figure 3. Calculation of the number of transcripts per domain (black bars and the average size of genes (in kb; green bars) associated with each chromatin state. See Methods for details and Supplemental Figure 5 for domain size summary.

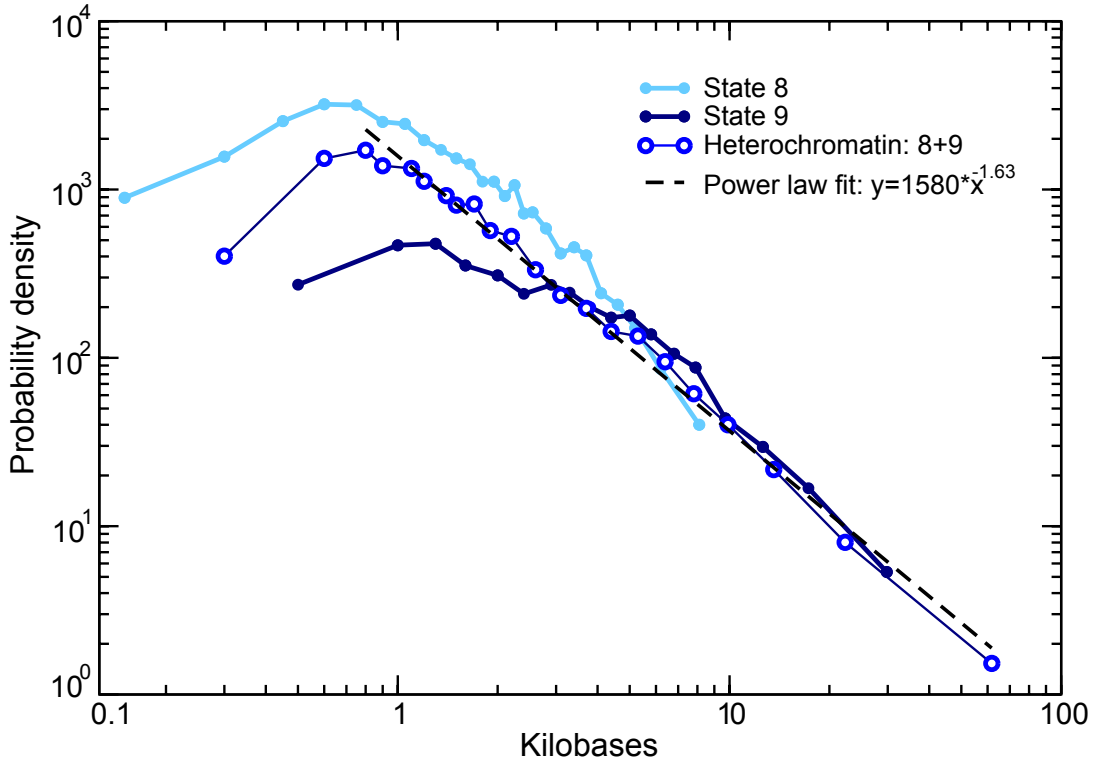


Supplemental Figure 4. Evaluation of PCA without considering the GC content. The robustness of the nine chromatin states obtained if the GC content is not used for the clustering is evaluated here by plotting the average values for each epigenetic property. The parameters w=150, s=0.10, n=4 were used. Error bars represent the standard error of the mean. This number is estimated as the total number of windows divided by the correlation length of the mark considered.

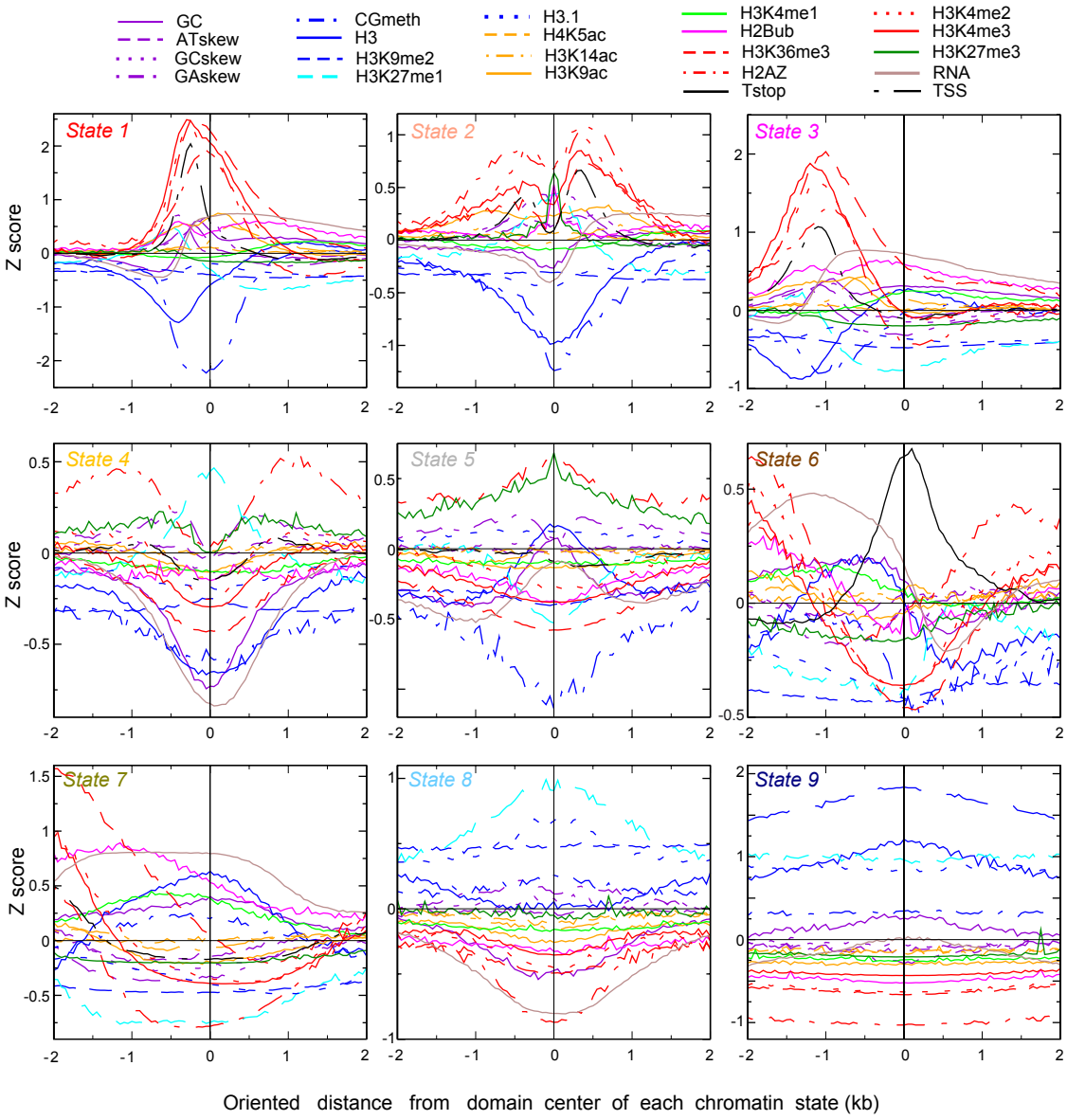


States	n	Mean Size (kb)	Median Size (kb)	Typical Size (kb)
1	12220	1.079	0.90	0.687
2	14502	0.785	0.45	0.725
3	11751	1.023	0.90	0.721
4	14950	1.179	0.90	1.060
5	6943	2.299	1.65	2.196
6	8603	1.368	0.90	1.279
7	4715	2.497	1.80	2.039
8	5470	1.965	1.20	1.845
9	2191	6.702	3.60	4.185

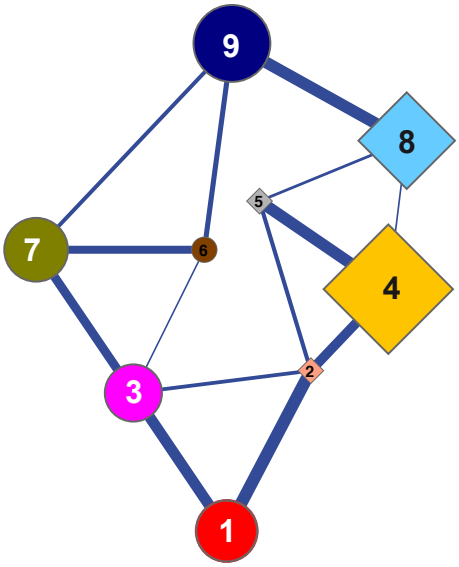
Supplemental Figure 5. Domain size distributions for the different chromatin states. Information of number of domains, mean, median and typical size (i.e. the parameter l of the exponential distribution of domain size, $e^{-s/\lambda}/l$) (in kb) is given at the bottom.



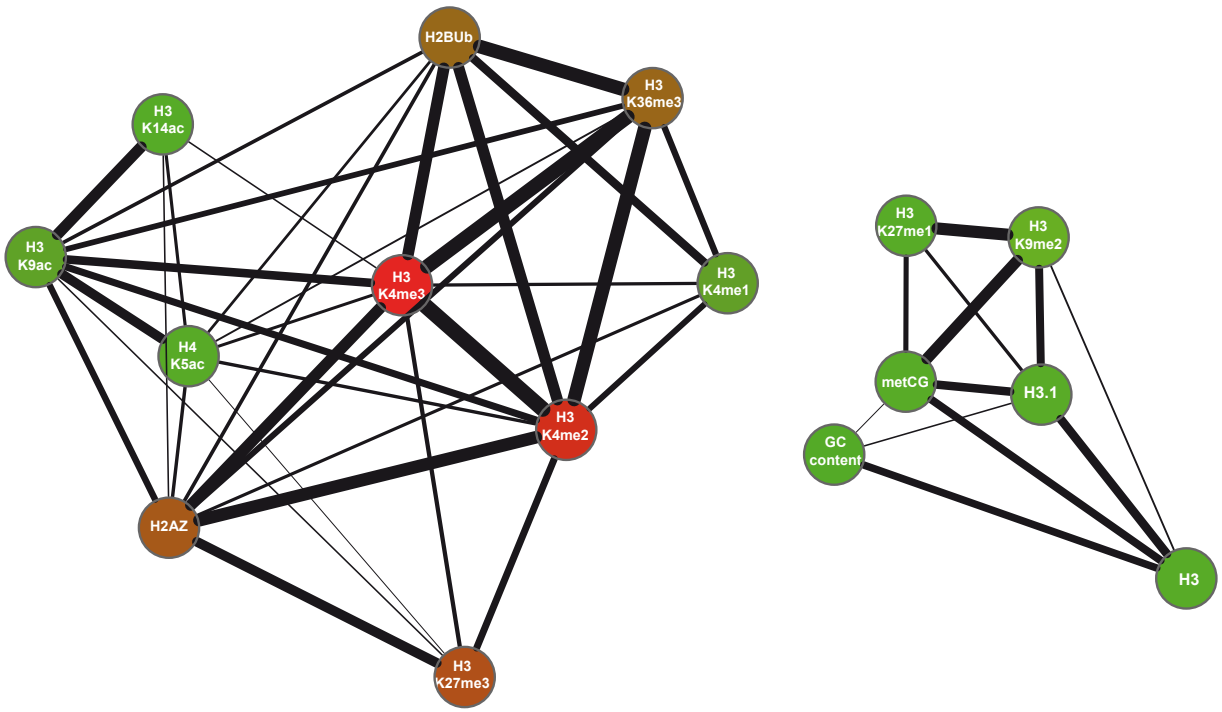
Supplemental Figure 6. Distribution of the domain size of the heterochromatin states 8 and 9 considered individually or combined. While state 8 domains (AT-rich heterochromatin) show an exponential distribution, and state 9 domains are depleted of short domains, the heterochromatin state obtained by joining states 8 and 9 presents a power law distribution with exponent -1.63 over one and half decade (from 2 to 70 kbp), which suggests that heterochromatin is approximately scale-free.



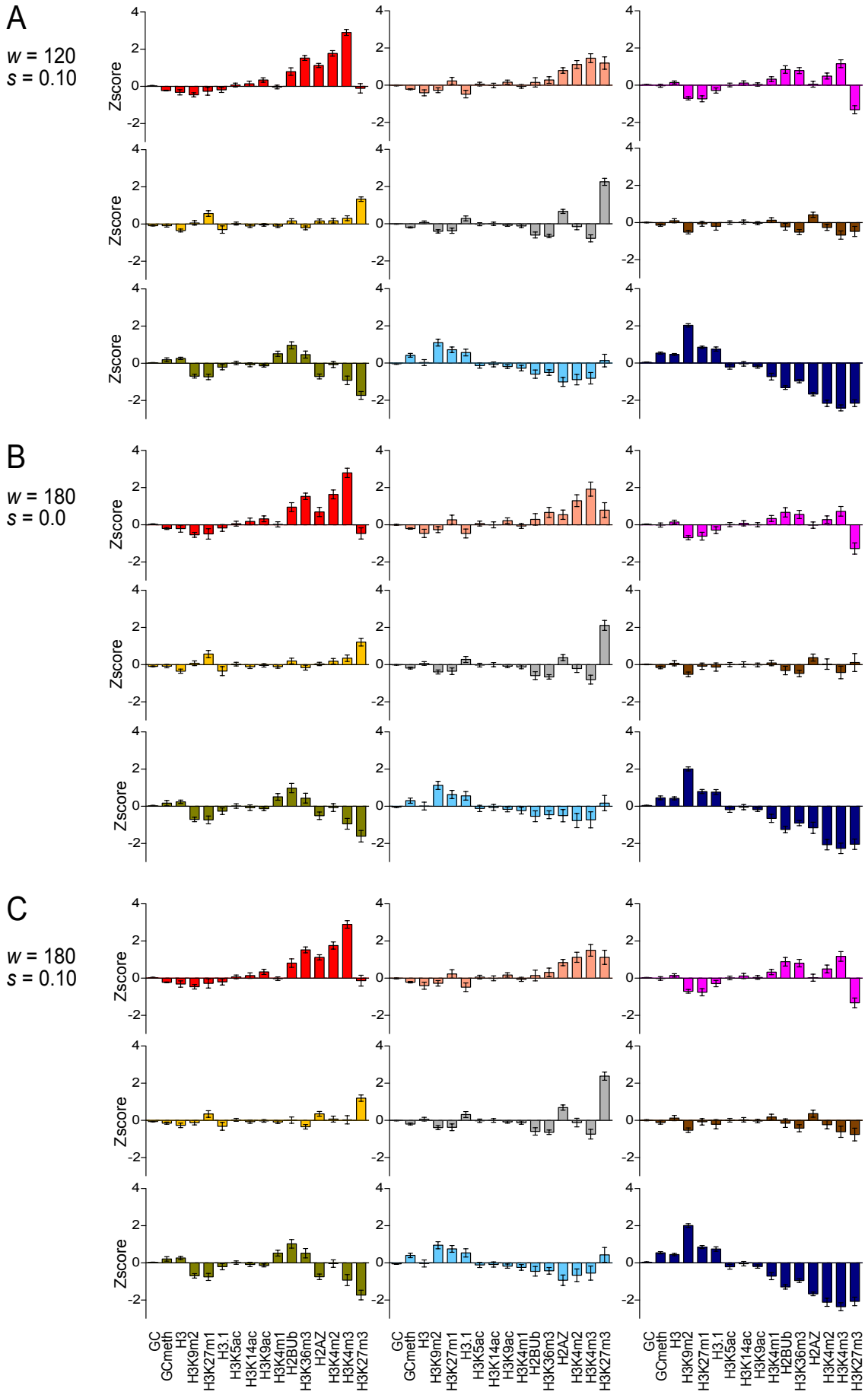
Supplemental Figure 7. Estimation of the relative enrichment of histone marks and DNA sequence features in the 9 chromatin states. The distribution of each chromatin and DNA feature was determined around the center of the domain taking into account the orientation of transcription.



Supplemental Figure 8. Network similarity diagram of the frequency of transition between the 9 chromatin states. Diamonds and circles represent AT-rich and GC-rich states, respectively. Symbol size represents the deviation in GC content with respect to the average genomic content. Circles are states with GC content larger than average, and diamonds are states with low GC content. The thickness of the lines connecting chromatin states is proportional to the similarity degree between two given states.



Supplemental Figure 9. Network correlation diagram of the frequency of transition between different chromatin features (histone marks and GC content) used in this study. Chromatin features are connected by lines, the thickness of which is proportional to the positive correlation between them. Colors of marks depend on their contribution to PC1 (red, high contribution; brown, mid contribution; green, low contribution). Note that chromatin features separate into two groups largely corresponding to euchromatin and heterochromatin.



Supplemental Figure 10. Robustness of the nine chromatin states obtained with different parameters.
The average values of the genomic and epigenomic marks of each of the nine states are shown for parameters w=120, s=0.10 (A), w=180, s=0.0 (B), w=180, s=0.10 (C). Similarity with the optimized parameters w=150, s=0.10 shows that the results are robust even to large variations in parameters.

Supplemental Table 1. Oligonucleotides used in the sequential ChIP (Re-ChIP)-qPCR

Region a (Chr1-16,578 kb)		
	1F	ccggctctaaaacaccaaaa
	1R	gggtcgggtaagaaagaagc
Region b (Chr1-11,630 kb)		
	1F	tcttctctgccatgtcgatg
	1R	catctgtggaaaccgactga
Region c (Chr1-27,397 kb)		
	1F	tctcgaagcaaaggtggatt
	1R	cccttggctgagatgagaag
Region d (Chr5- kb)		
	1F	caacggttcttcatccgatt
	1R	ctgctcgaaatggctctacc
Region control (Chr1-9,039 kb)		
	1F	tgctcgtcccatttcctatc
	1R	ggcatagtgattttgccaca