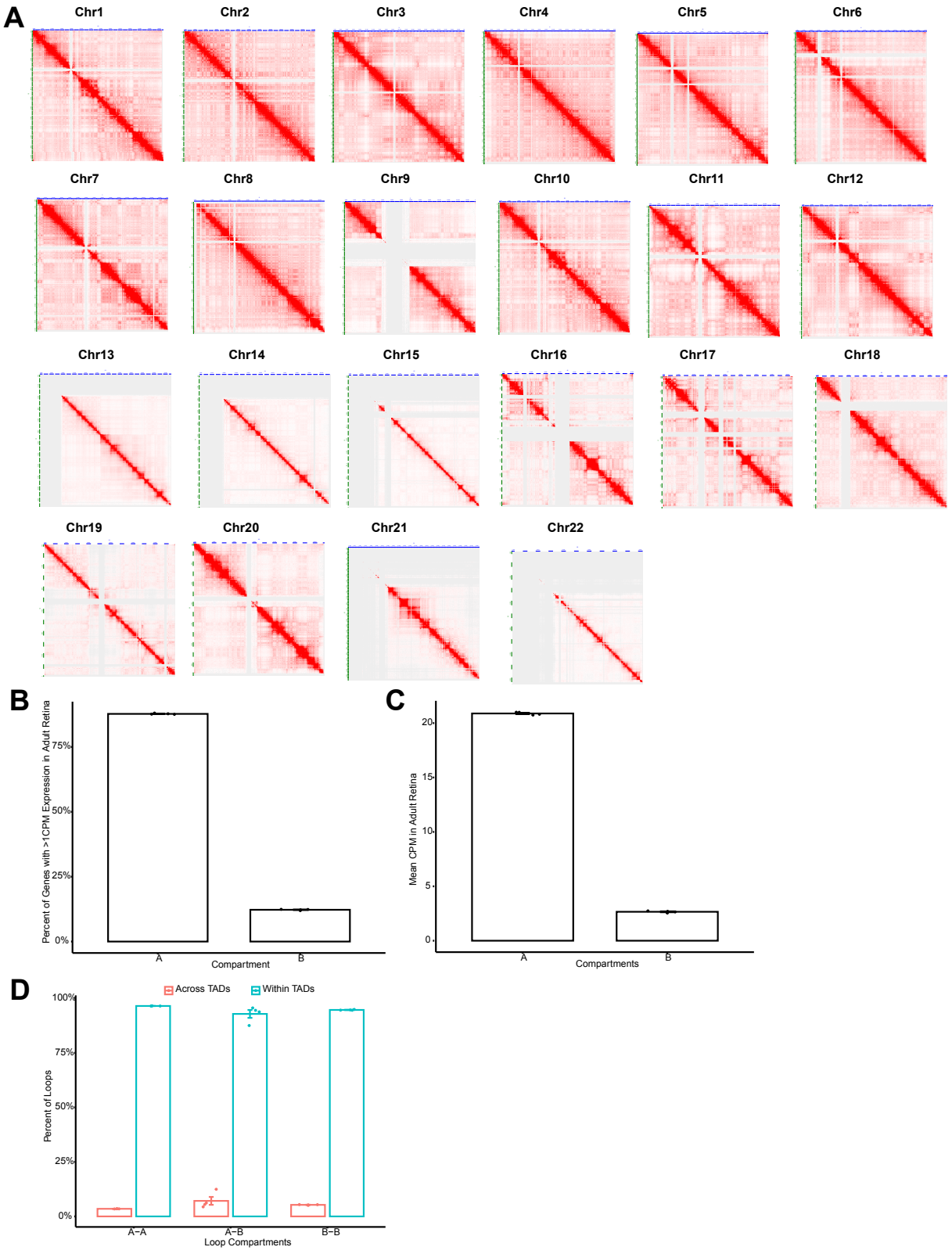
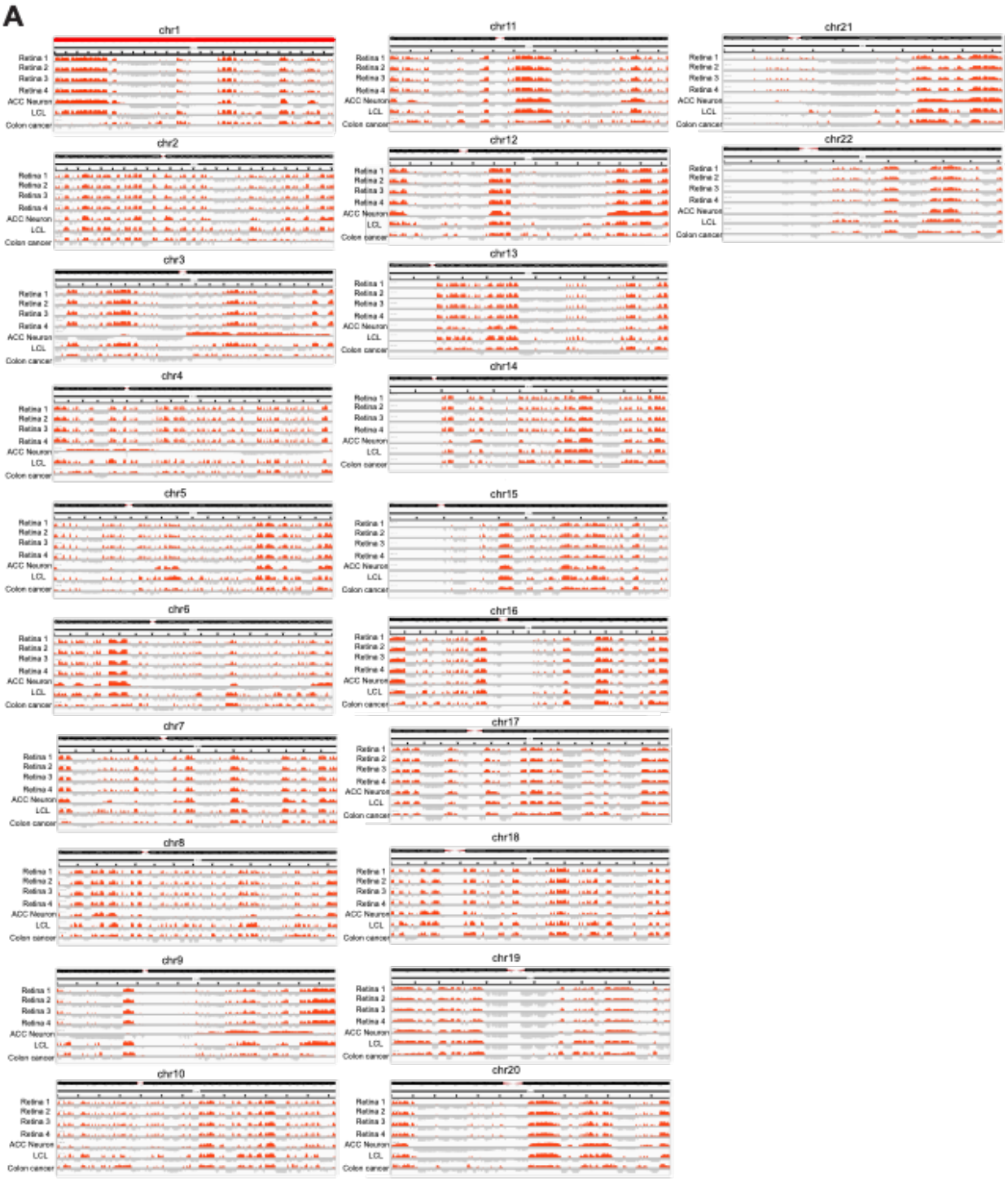
Supplementary Information



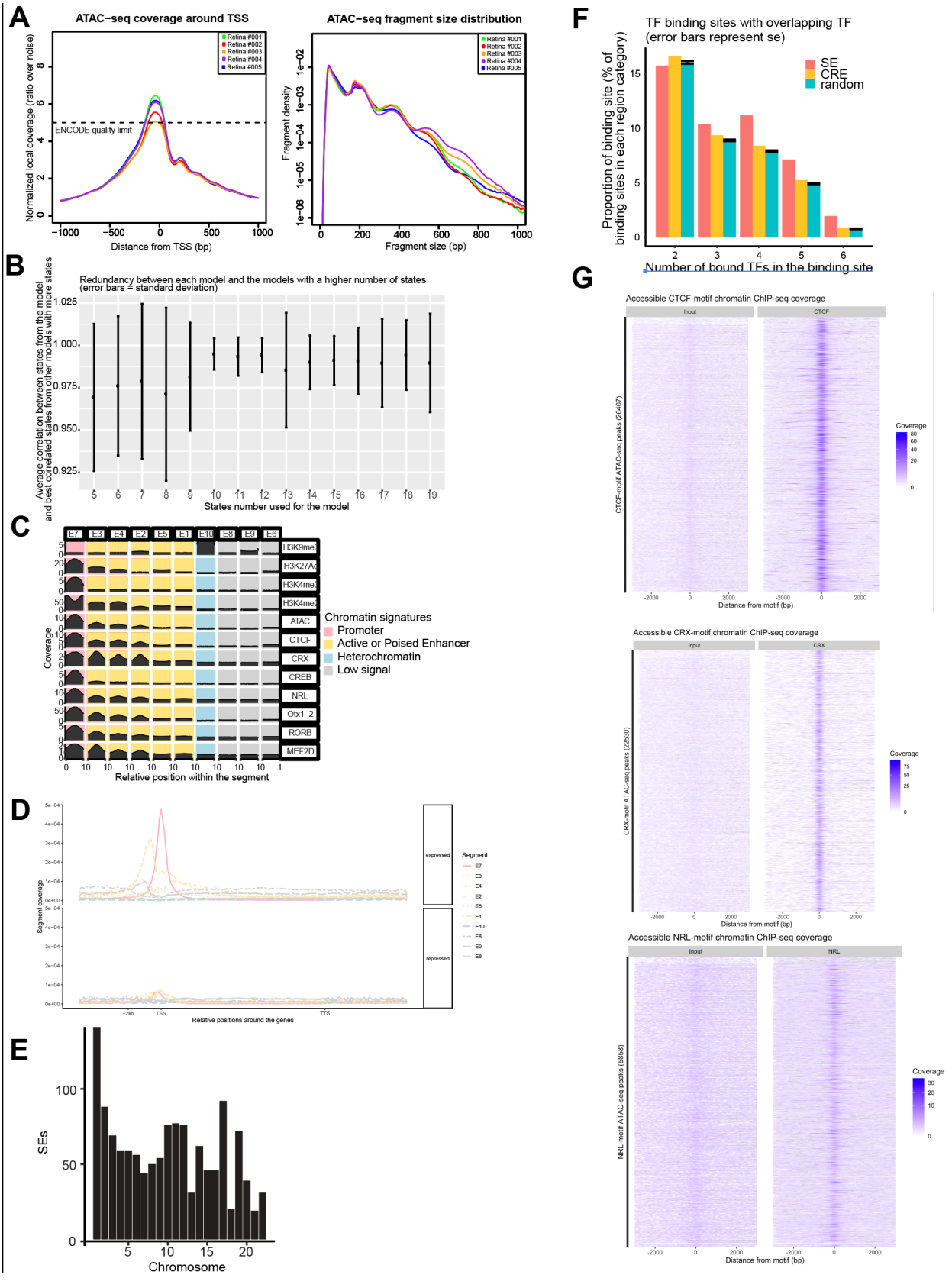
Supplementary Figure 1. Related to Figure 1.

[A] Hi-C contact maps of observed contacts across each autosome. [B] Proportion of expressed gene in A *versus* B retinal compartments. [C] Mean expression of genes in A *versus* B retinal compartments. [D] Proportion of intra-TAD versus inter-TAD loops within compartment A (A-A), between compartments A and B (A-B) and within compartment B (B-B).



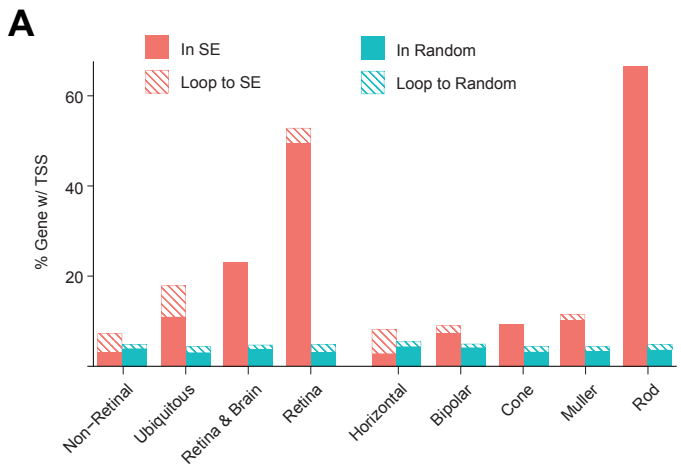
Supplementary Figure 2. Related to Figure 2.

[A] A (red) and B (grey) chromatin compartment represented by the PC1 value on all autosomes for the 4 human retina, the public ACC neurons, the public LCL and the colon cancer Hi-C.


A
ATAC−seq coverage around TSS
Normalized local coverage (ratio over noise)
ENCODE quality limit
Retina #001
Retina #002
Retina #003
Retina #004
Retina #005
Distance from TSS (bp)
ATAC−seq fragment size distribution
Fragment density
Fragment size (bp)
B
Redundancy between each model and the models with a higher number of states
(error bars = standard deviation)
Average correlation between states from the model and best correlated states from other models with more states
States number used for the model
C
Coverage
Relative position within the segment
Chromatin signatures
Promoter
Active or Poised Enhancer
Heterochromatin
Low signal
D
Segment coverage
expressed
repressed
Segment
Relative positions around the genes
TSS
TTS
E
SEs
Chromosome
F
TF binding sites with overlapping TF
(error bars represent se)
Proportion of binding site (% of binding sites in each region category)
SE
CRE
random
Number of bound TFs in the binding site
G
Accessible CTCF-motif chromatin ChIP-seq coverage
Input
CTCF
CTCF-motif ATAC-seq peaks (26407)
Distance from motif (bp)
Coverage
Accessible CRX-motif chromatin ChIP-seq coverage
CRX
CRX-motif ATAC-seq peaks (22530)
Accessible NRL-motif chromatin ChIP-seq coverage
NRL
NRL-motif ATAC-seq peaks (5858)

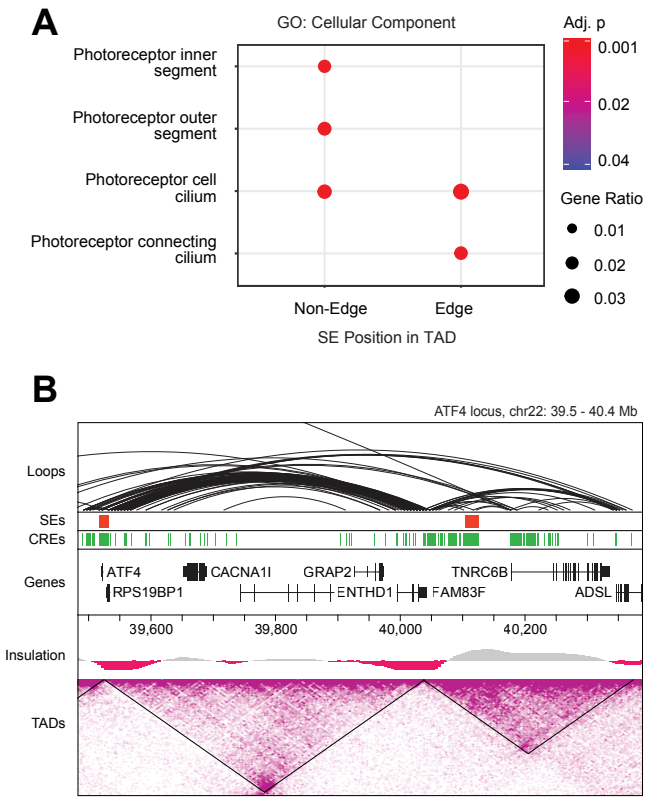
Supplementary Figure 3. Related to Figure 3.

[A] Quality control of the ATAC-seq experiments. Left panel: Normalized coverage around TSS (ratio over the coverage at + / – 800 to 1000 bp from the TSS), grey dotted line represents ENCODE quality threshold. Right panel: ATAC-seq fragments size distribution. [B] Assessment of the best number of chromatin states for the ChromHMM model. ChromHMM has be run using 5 to 20 states generating 16 models. Redundancy between models has been assessed by computing, for each model, the average correlation between each state from the model and the best correlated state from each model with more states. Models with > 10 chromatin states show a high redundancy, establishing that 10 states chromatin model is the best model to capture the different chromatin states from our data. [C] Plots of histone marks, chromatin accessibility and TF binding for each chromatin state identified by ChromHMM (named E1 to E10). Each cell indicates the mean coverage for each mark across the segments aligned and resized to a 0 to 1 scale. Color of each cell represents the manual annotation of the state. [D] Metaprofile showing the density of each chromatin state around expressed and non-expressed genes. Genomic regions of each gene are aligned and resized to overlap the TSS and TTS of the genes. [E] SEs distribution across each autosome. [F] Proportion of TF binding sites with 2, 3, 4, 5 or 6 TFs co-bound in SEs, CREs and random regions. [G] Heatmap of ChIP-seq coverage for Input and CTCF (top), CRX (central) and NRL (bottom). Each row represents a 5kb genomic region centered on a CTCF (top), CRX (central) or NRL (bottom) accessible motif, ordered by accessible motif score.



Supplementary Figure 4. Related to Figure 4.

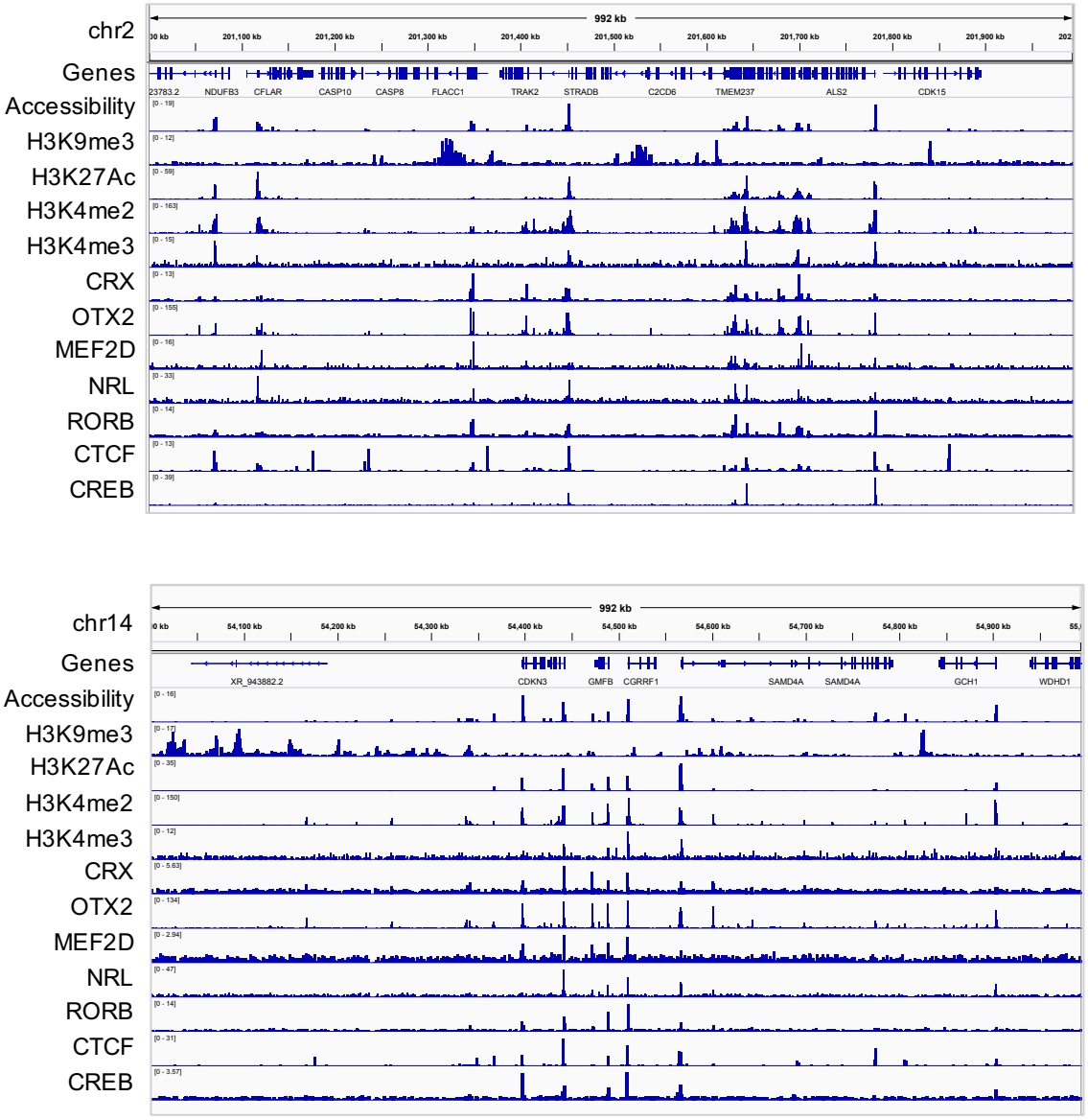
[A] Proportion of genes with the TSS overlapping (plain) or in contact with (hatched) a SE or a random region for different gene categories.



Supplementary Figure 5. Related to Figure 5.

[A] Enriched Cellular Component terms among genes with a TSS residing within or in contact via chromatin looping with a non-edge or edge SE. [B] Chromatin loops, Ses, CREs, $\log_2$ insulation score, TADs, and Hi-C contact maps for the *ATF4* locus.

A



Supplementary Figure 6. Related to Methods.

[A] Genomic coverages for the ATAC-seq, ChIP-seq and Cut&Run data on two representative genomic regions.

Supplementary Table 1

Hi-C statistics summary.

Sample	Read pairs sequenced	Mapped interactions	Valid interactions (% of mapped interactions)	Unique valid interactions	% trans interactions
Retina #1	290,246,313	195,675,050	187,878,052 (96.0%)	182,445,618	23.7
Retina #2	321,806,517	215,009,151	206,389,866 (96.0%)	200,569,059	25.3
Retina #3	283,092,274	190,013,243	180,233,826 (94.9%)	174,190,249	22.3
Retina #4	252,447,626	161,044,850	153,041,279 (95.0%)	147,055,055	23.4

Supplementary Table 2

List of genes overlapping a SE and their expression level in retina.

Supplementary Table 3

List of TF which motifs are enriched at CRX and NRL binding loci overlapping a SE.

Supplementary Table 4

List of retinal eQTL and their associated features (loops, CREs, SEs, close genes, genes in contact).

Supplementary Table 5

List of AMD and glaucoma-associated genomic variants and the target genes they are associated with.