# Appendix.

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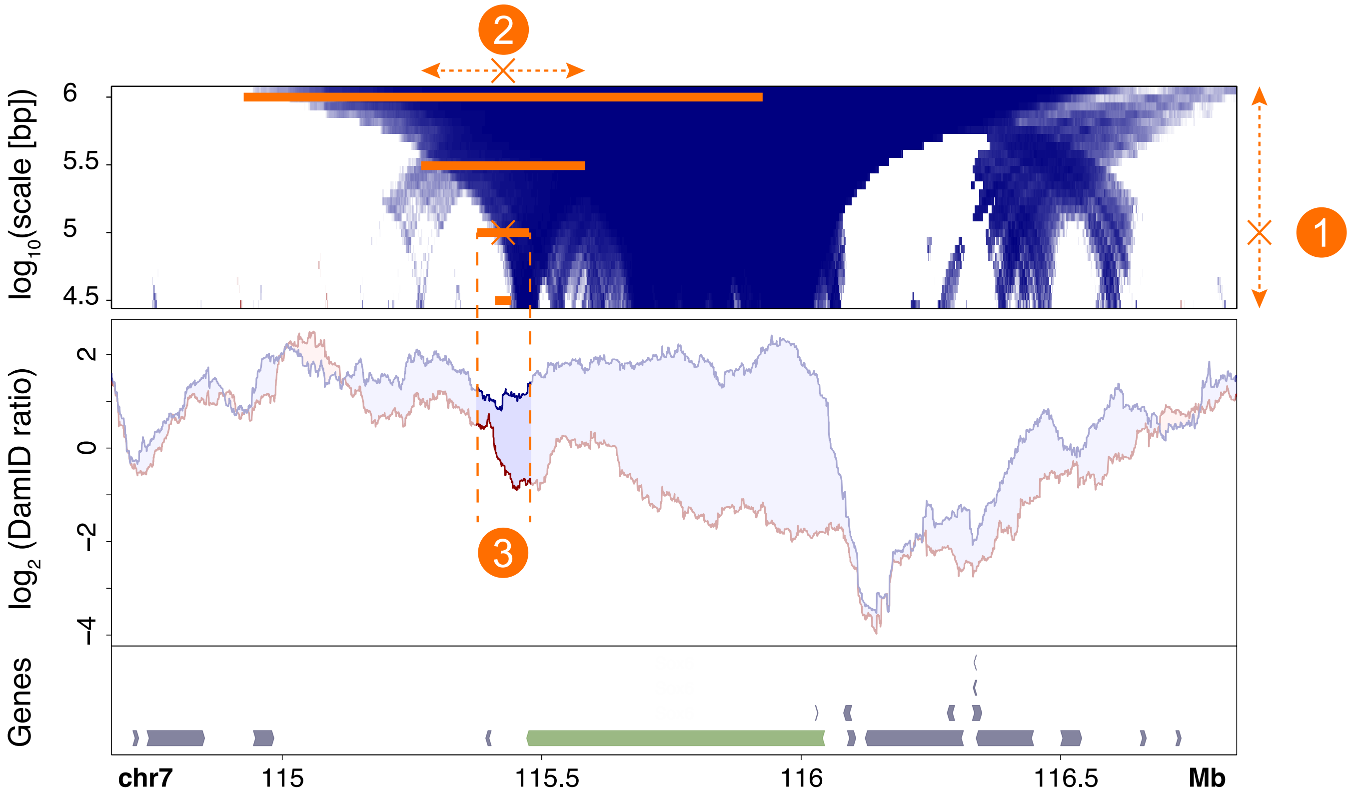
Figure S1



① Choose window size (vertical axis)

② Choose window position (horizontal axis)

③ Calculate change in DamID average logratio within this window

④ Compare this change to that of all other windows of same size genome-wide:
color pixel in domainogram at center of window (x):
blue if in top-5%
red if in bottom-5%

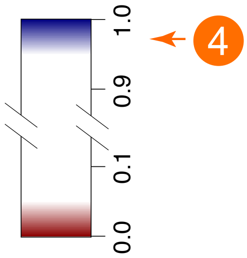


**Figure S1. Explanation of domaingram principle.**
Text box at the bottom describes the major steps followed to calculate and plot a domainogram.

# Figure S2

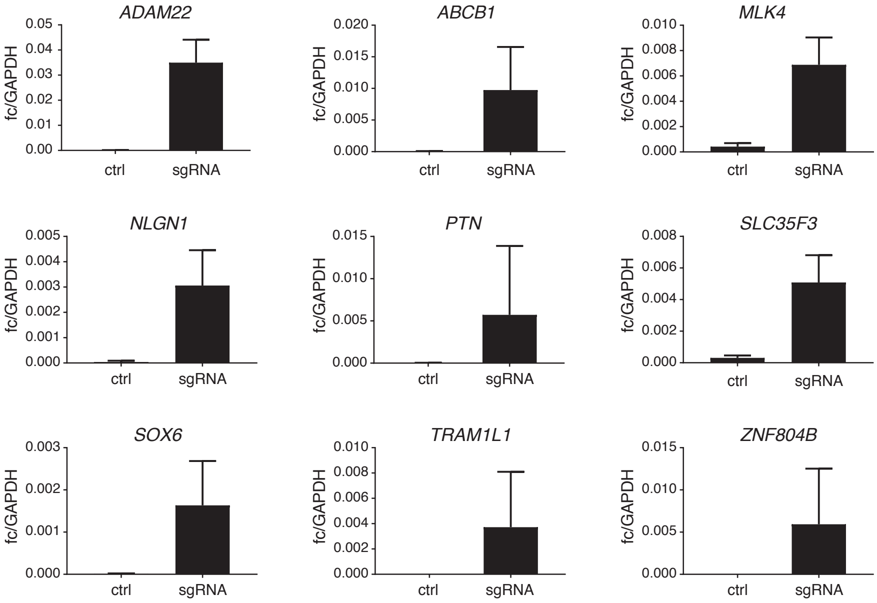


**Figure S2. Expression of genes in RPE-1 cells targeted by CRISPRa.** Expression levels were determined by RT-qPCR. Average of three technical replicates, error bar indicates standard deviation. fc/GAPDH: expression level normalized to GAPDH gene. sgRNA: transfection with sgRNA targeting the indicated gene; ctrl: untransfected control.

Figure S3

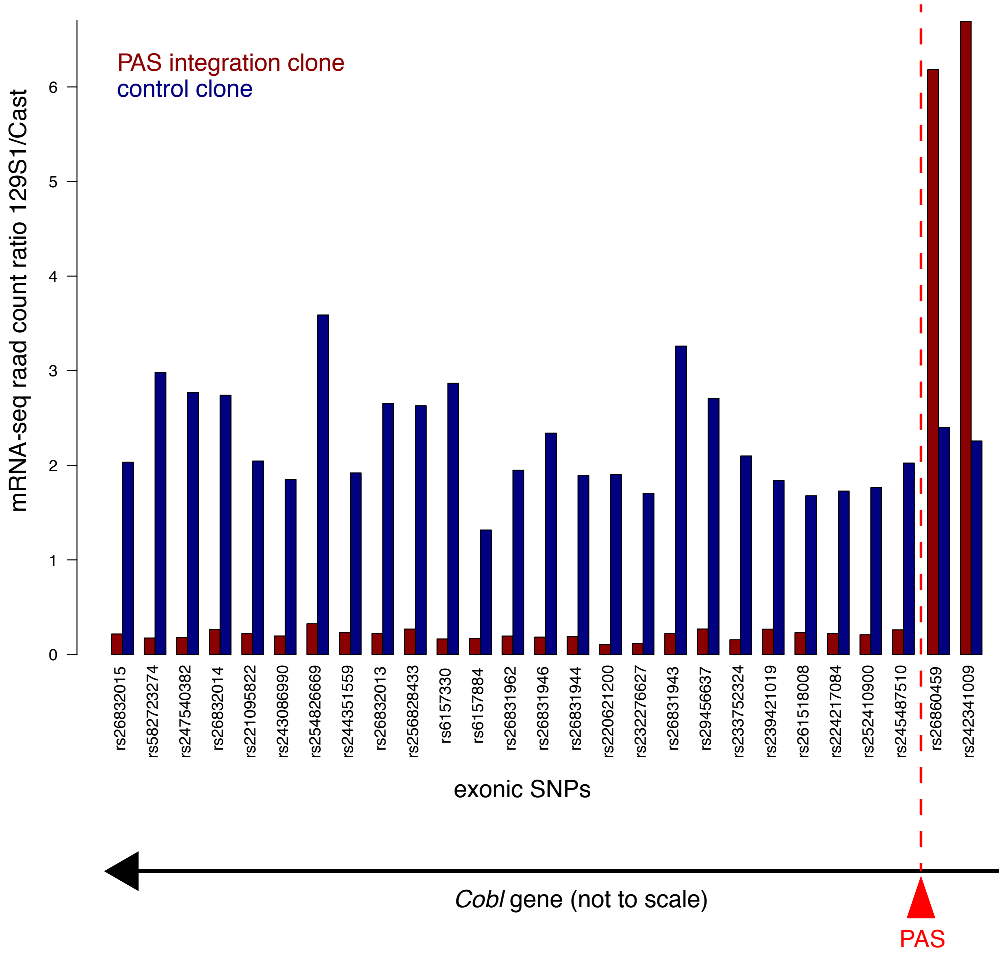


**Figure S3. Effect of PAS integration on Cobl gene transcription.** Ratio of allele-specific mRNA-seq read counts of 129Sv and Cast SNP variants located in the Cobl gene. Two SNPs are located upstream of the PAS integration site; all other SNPs are downstream. Note that the 5’ to 3’ orientation of the gene is from right to left. In a control clone without the PAS, the Sv129 allele is consistently expressed ~2-fold higher than the Cast allele. In the clone with the PAS integration in the 129Sv allele, expression of the 129Sv variants downstream of the PAS is strongly reduced. The increased level of the 129Sv variants upstream may be due to greater stability of the mRNA due to its altered 3’ end. Data are average of two independent biological replicates.