Supplementary Figure S1

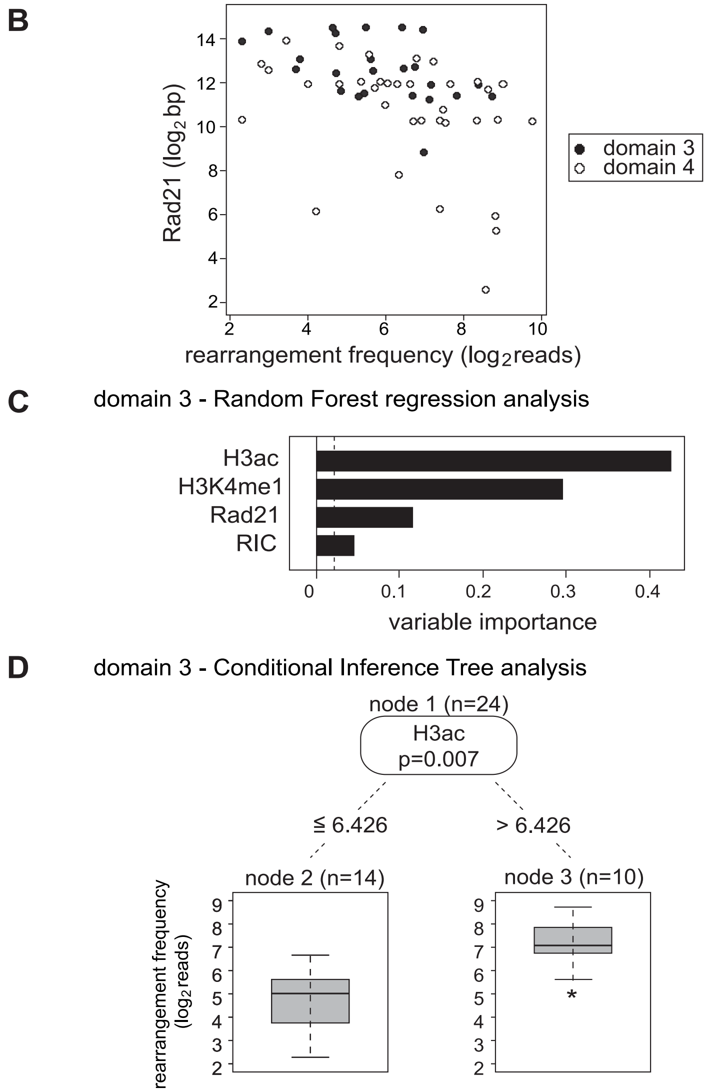
A

all parameters
(OOB error rate: 12.17%)

predicted \ observed	inactive	active	classification error
inactive	68	16	0.19
active	7	98	0.067

top 4 parameters
(OOB error rate: 11.11%)

predicted \ observed	inactive	active	classification error
inactive	70	14	0.17
active	7	98	0.067



Supplemental Fig. S1. Additional computational analysis results for accessibility elements (A) Tables show the number of active vs. inactive genes, prediced vs. observed, when either all 12 parameters were used for classification or only the top 4 significant parameters. (B) Scatter plot for distance to Rad21 vs. V_H gene rearrangement frequency (both in $\log_2$scale) in domains 3 and 4 for active genes only. (C) Random Forest regression analysis for active genes in domain 3 showing the elements with significant variable importance. The dotted line indicates P-value = 0.05. (D) Conditional Inference Tree for domain 3. Box and whisker plots show the median, the lower and upper quartiles (25% and 75%), and the minimum and maximum values of rearrangement frequency for genes that had a signal intensity greater than or less and equal values to 6.426 ($\log_2$) for H3ac.