



Figure S8 Assigning High density regions (HDRs). Using a cut-off of the top 3% of Yan-bound peaks the genome was divided into Yan bound and Yan unbound regions. For each unbound region, starting with the largest (1), Yan chromatin occupancy (length of Yan bound region/total region length) was calculated from the 3' end of the unbound region to the 3' end of the chromosome and the 5' end of the bound region to the 5' end of the chromosome. If Yan chromatin occupancy was less than 40%, the boundaries for querying were reset to the edges of the unbound region and the ends of the chromosome. Yan chromatin occupancy was then calculated from the second largest unbound region (2) to the end of the reset boundary. If Yan chromatin occupancy was greater than or equal to 40% and $>2\text{kb}$ then this region would be assigned as an HDR as depicted above. Yan chromatin occupancy was calculated for the third largest unbound region (3) to end of the reset boundary. Although here Yan chromatin occupancy is $>40\%$ since the region length is $<2\text{kb}$ then this region is not assigned as an HDR.