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Shared and distinct mechanisms of MAZ, CTCF, and cohesin in mediating the interplay between chromosomes and nuclear bodies

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The interplay between chromosomes and nuclear bodies is crucial in understanding the 3D genome organization, as higher-order 3D genome structure often shaped around nuclear bodies such as nuclear speckles and nucleoli. Previous studies verified that MYC Associated Zinc Finger Protein(MAZ) plays a significant role in chromosomal-speckles interaction. In addition CTCF and cohesin which forms topologically associated domains appear to collaborate with MAZ. Due to the potential influence of CTCF and cohesin on the chromosomal nuclear body interaction with MAZ, we decided to examine their shared and distinct functions. We investegated using Hi-C interchromosomal contact map analysis in combination with NMF (HiCAN), which systematically characterizes nuclear body-associated chromosomal contacts. Strikingly, CTCF and MAZ depletion demonstrates a more pronounced influence on chromosomal nuclear interactions compared to cohesin. In particular, CTCF affected 18.6% of the genome region, MAZ, 9.3%, while cohesion impacted only 0.2%. Interestingly, CTCF and MAZ regulated different chromosome regions, since only 21.7% were affected by both. However, these regulated regions exhibited patterns similar to those seen in CTCF and MAZ depleted models, showing an enrichment of active transcription histone markers such as H3K27ac and H3K4me3. Taken together, we deepen our understanding of how MAZ, CTCF, and cohesin function both jointly and independently, paving the way for a comprehensive grasp of chromatin and nuclear body interactions.