
3D organization of synthetic and scrambled chromosomes

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Abstract

While the design of the synthetic yeast genome Sc2.0 is highly conservative regarding gene content, the deletion of several classes of repeated sequences may affect genome organization and potentially alter cellular functions. We report here the 3D conformation of genomes containing Sc2.0 chromosomes using Hi-C. Overall, we found that the genomic organization is globally unaffected by the presence of one or several synthetic chromosomes, except for *synIII* lacking silent mating type cassettes, and *synXII* from which the rDNA has been removed and translocated to another chromosome. We conclude that dispersed repetitive DNA does not drive global average chromatin conformation in *S. cerevisiae*. Our approach also shows that the absence of repeats leads to a crisper and more precisely tractable chromosome conformation as assessed with Hi-C. We finally exploit the contact maps to detect rearrangements induced in SCRaMbLE strains as well as other chromosomal abnormalities that can occur during strain constructions.

Keywords: synthetic yeast, HiC, chromosome conformation

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