

Chromosomal scans of su-series

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Abstract

Using Fox/Zhao processing where we normalize per nucleotide coverages for sequencing differences (depth and breadth) before determining S/G1 ratios using strain-specific G1 denominator (suCTRL G1 for suCTRL S and suON G1 for suON S). To control for potential differences in S-phase harvests, we normalize the S/G1 ratio for each strain scaling with the median S/G1 ratio for that strain. After, we remove outliers as defined in Batrakou et al, 2020, and lastly we placed the S/G1 ratios on a “biological” scale by placing values between one and two. The steps mirror those published in Batrakou et al, 2020 with the exception of the S-phase normalization.

Scans

Confirmed origins were placed in three cohorts based on the Trep value measured in Yabuki et al, 2002. Origins with the lowest 1/3 of Trep values, consistent with the earliest replicating origins, are labeled “E.” Origins with the highest 1/3 of Trep values, consistent with latest replicating origins, are labeled “L.” Origins with values between the two are labeled “M” for middle.



