

## Supplementary figure legends.

### Supplementary Figure S1:

**A:** qPCR validation of array data. Results are shown as fold of enrichment of a peak region (57600-57825) over a control region (61800-61977). **B:** MA2C score of the peak (left) and control (right) regions used for qPCR. Open rectangles indicate the PCR product.

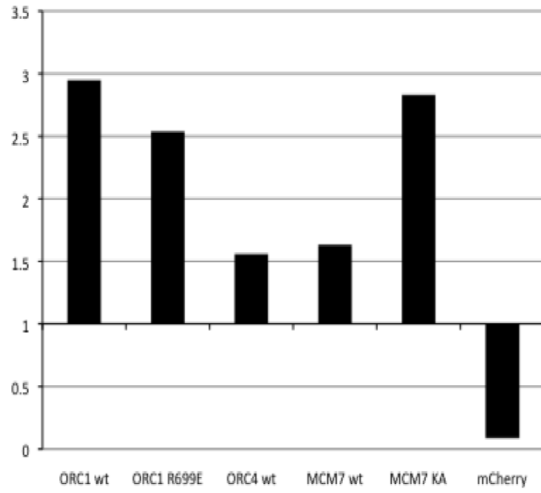
### Supplementary Figure S2:

**A:** Fibers from asynchronously growing cells. **B:** Fibers from aphidicolin synchronized cells. Cells were pulse labeled with IdU (blue) and then chased with CldU (red) for 20 minutes each. DNA fibers were prepared and aligned to each other and to the DHFR map using a combination of unevenly spaced FISH probes (green). FISH probes positions (from left to right) 89-7,870; 20,913-28401; 73,871-80,014; 104,339-110,685; 118,442-121,308.

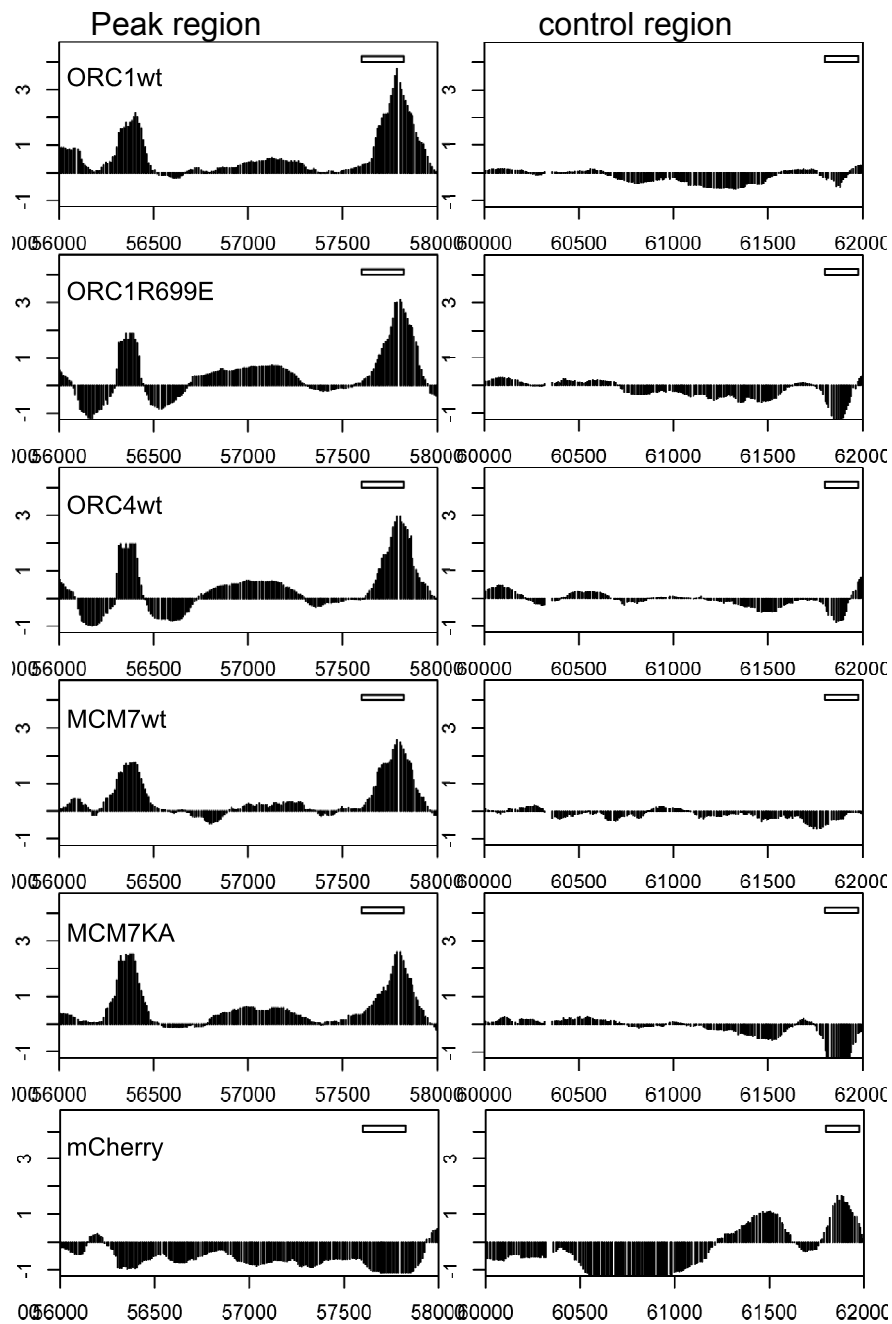
### Supplementary Figure S3:

Alignment of MNase nucleosome mapping from early (pre-ODP, black) and late (post-ODP, red) G1 cells over the entire DHFR region (top) as well as to representative regions at the DHFR/Msh3 promoter (middle) and ori $\beta$ / $\beta'$  (bottom).

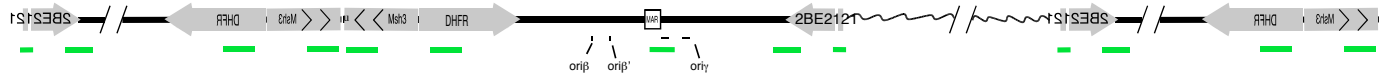
**A.**



**B.**



A.

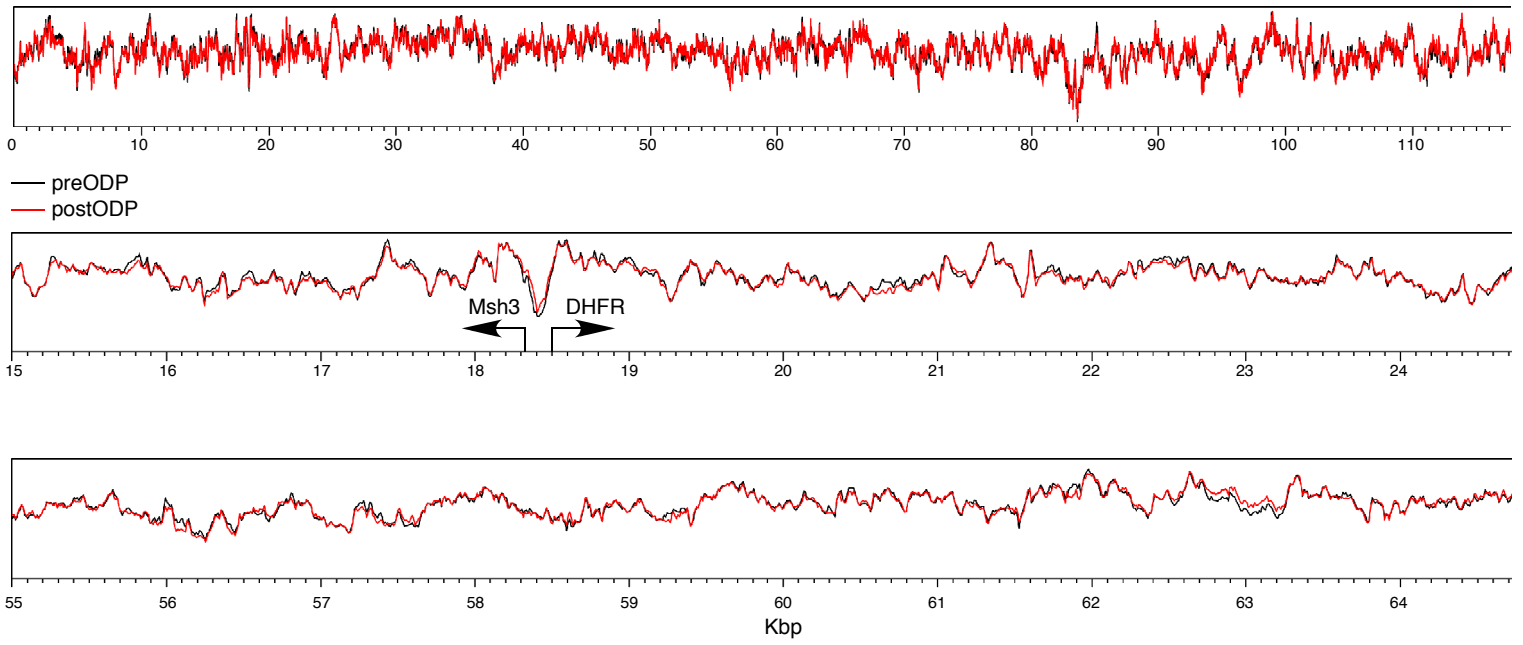


Asynchronous cells

supplementary Figure S2A







supplementary Figure S3