

Supplemental_Figure_S4. Positioning of mHOR, hHOR and HAC segments in nuclei of retinal and cultured cells.

A1-A5, Proportion of signals from gene-poor (yellow), gene desert (red) and gene-dense (green) segments in different nuclear compartments scored in cultured mouse cells (A1, A2) and human cultured cells (A3) and mouse inner retinal neurons (*INL*, A4, A5) after FISH with probes for mHOR (A1, A4) and for hHOR (A2, A3, A5). For comparison, locations of the L-HAC segments in rods are shown in **A6**. Numbers of scored alleles indicated in brackets above the histograms. In conventional nuclei (A1-A5), the nuclear periphery, surface of chromocenters and nucleolar periphery are considered as heterochromatin compartment (HC, shaded with dark-grey); the nuclear interior as euchromatin compartment (EC, shaded with light-grey). In rods (A6), the single chromocenter surface and L1-rich shell around the chromocenter are classified as HC; the outmost peripheral layer of B1-rich chromatin constitutes the EC compartment.

B, Different arrangement of the three segments within an allele observed for orthologous regions. **B1**, examples of A9 cell nuclei after FISH with BAC probes for mHOR. Images are projections of three consecutive confocal sections over ca. 500 nm. Nuclei are counterstained with DAPI (blue); the color code of signals is the same as on B4; scale bar: 5 μ m. **B2**, zoomed FISH signals outlined in B1. **B3**, Grey scale DAPI images of the selected regions. The nuclear periphery and the chromocenter surface are marked by arrows; arrowheads point to internally located signals. **B4**, schematics of the locus arrangement with gene-poor (yellow), gene desert (red) and gene-dense (green) segments corresponding to the observed spatial arrangements detected by FISH and shown in B2. Segments are depicted as circles; HC and EC marked with dark-and light-grey, respectively. Five different arrangements of the segments are shown: all three segments are adjacent to the nuclear periphery (1a) or to the chromocenter (1b); gene desert and gene-poor segments (2) or only gene-desert segment (3) are attached to the nuclear periphery; all three segments are in the nuclear interior (4).

C, Distribution of allele spatial arrangements (1-4) is shown for the same loci and cell types as in A. Note, that the most common arrangement of the orthologous loci was the one with gene-rich segment in the nuclear interior and gene-poor and gene desert segments towards the nuclear periphery, the periphery of the chromocenters or nucleoli (2).

