Supplementary Legends

Supplementary Figure 1: Positional mapping relative to the NM of specific target DNA sequences by PCR. Naïve B lymphocyte nucleoids were treated with DNase-I (0.5 U/ml) for different times. The residual NM-bound DNA was directly used as template for PCR amplification of the target sequences (a-o). The specific amplicons were resolved in 2% agarose gels stained with ethidium bromide (0.5 µl/ml). C = control. Topological zones with respect to NM: D = distal, P = proximal, VC = very close, E = embedded within NM. (-) negative control (no template), (+) positive control (pure genomic DNA as template). The amplification patterns were consistently reproduced in separate experiments with samples from independent animals (n = 3).

Supplementary Figure 2: Comparison between the location of the experimentally determined NM-embedded regions and the location of potential MARs predicted by four different MAR-searching computer programs. A) The upper figure shows the experimentally determined structural DNA loop configuration of the 162 kbp genomic region in hepatocytes. The actual MARs (LARs) should be located within the regions embedded within the NM. B) The lower figure indicates the experimentally-inferred location of such LARs in hepatocytes as brown rectangles under the letter corresponding to the nearest target sequence mapped relative to the NM. The small coloured dashes, rectangles or squares indicate the predicted location of potential MARs by the respective MAR-searching computer program. The arrow indicates the location of the only MAR predicted by all four computer programs that happens to coincide with a possible LAR inferred from the mapping experiments. Notice that all programs inconsistently predict the presence of MARs in loop regions actually located far from the NM in hepatocytes.