

SUPPLEMENTARY FIGURES

Figure S1

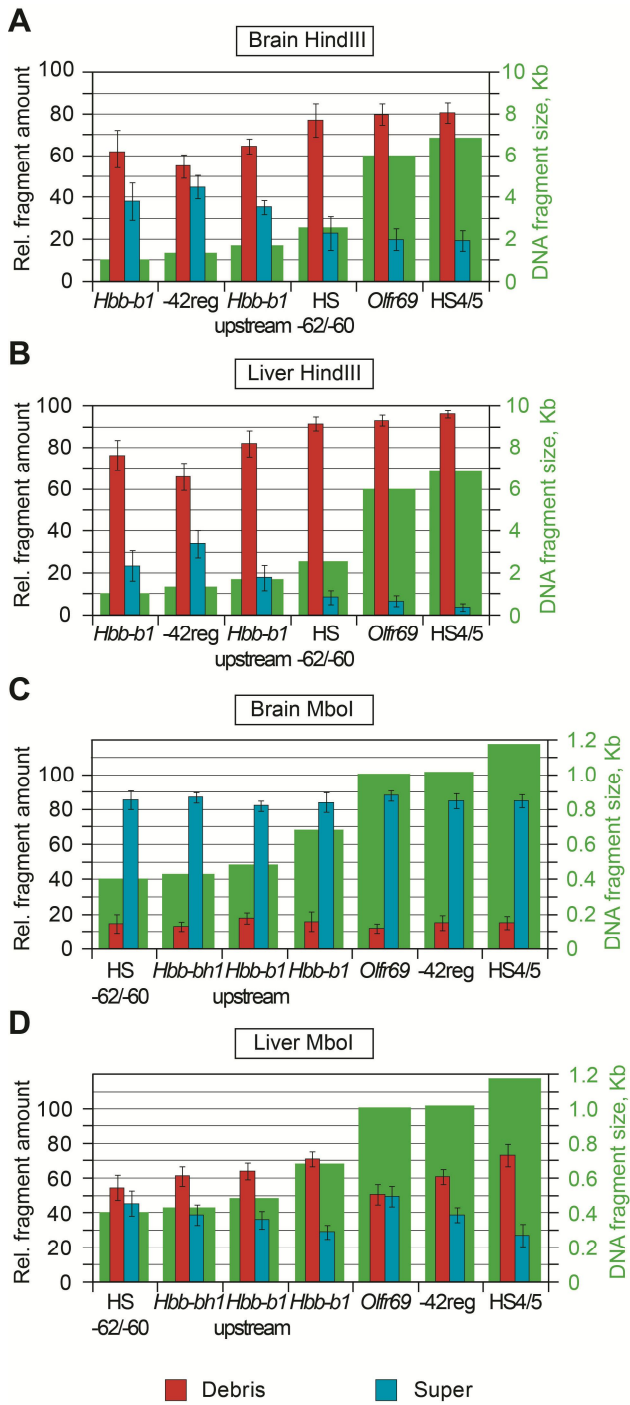


Figure S2

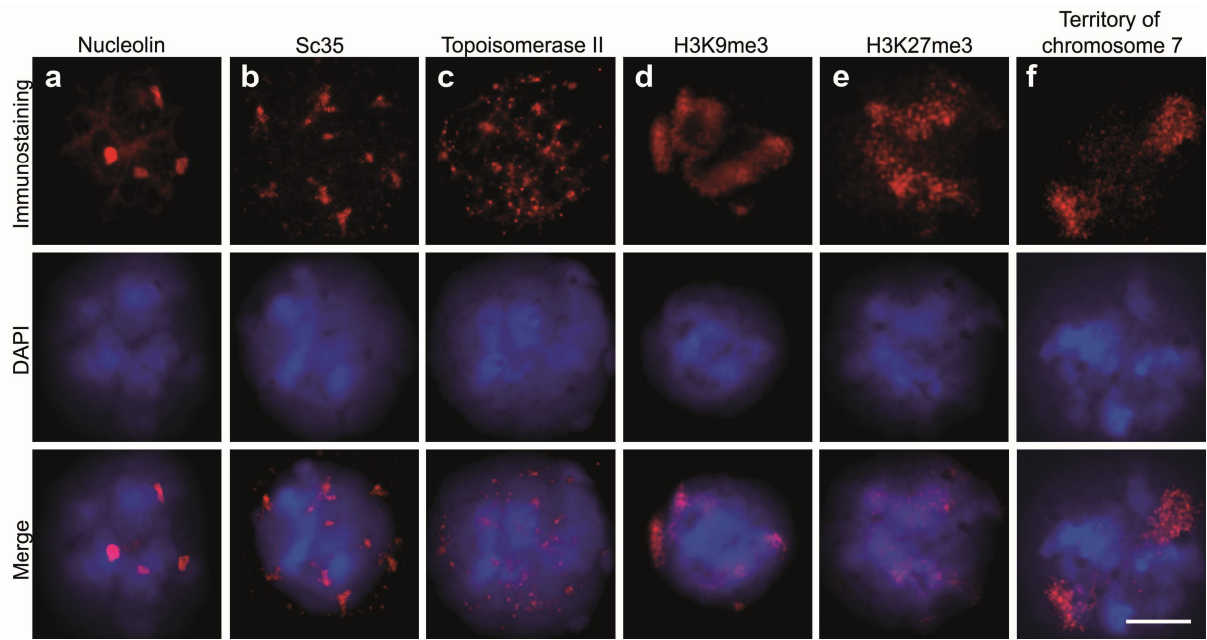


Figure S3

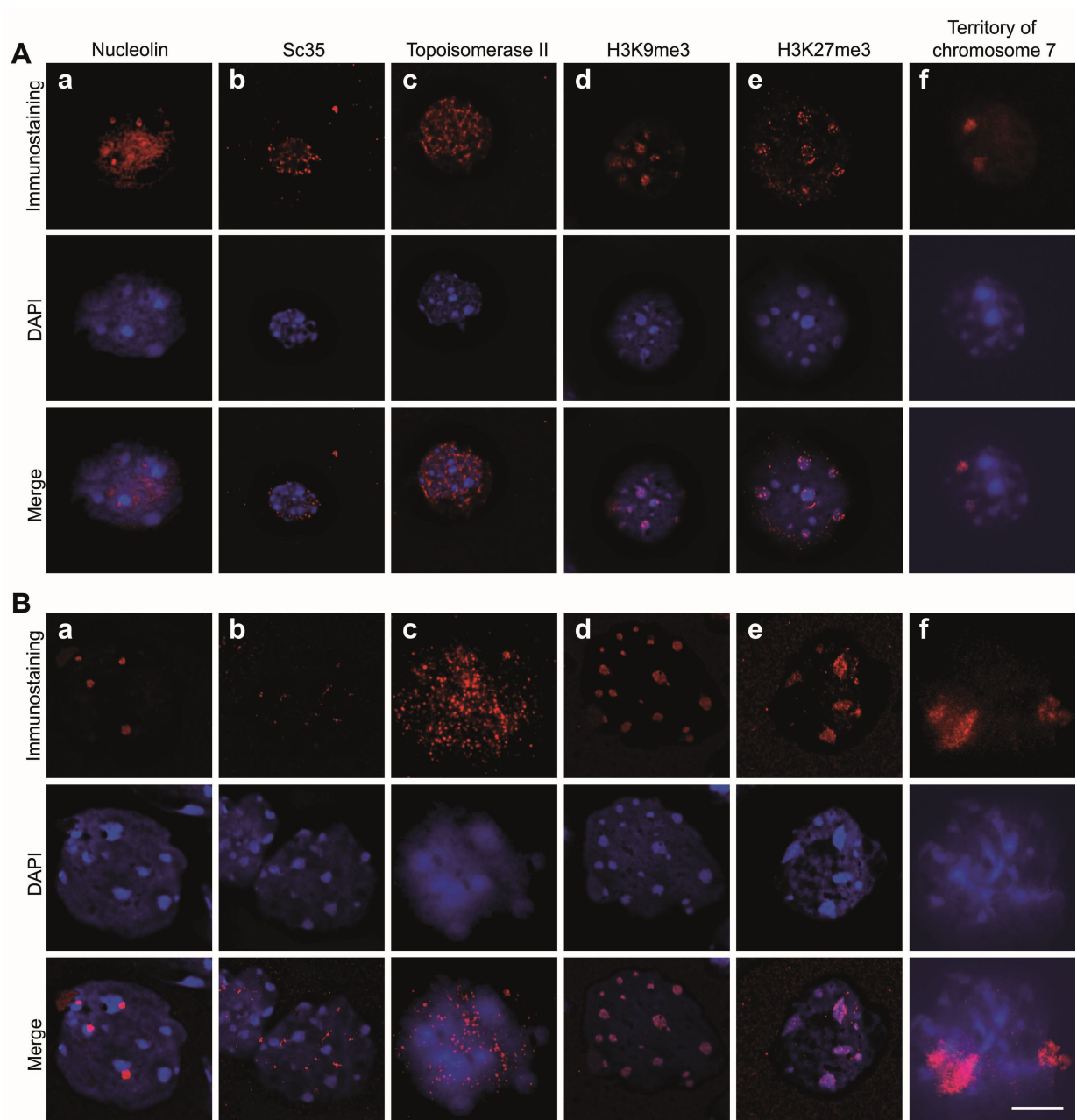
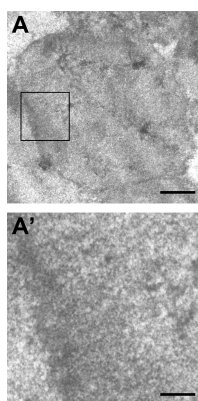


Figure S4



SUPPLEMENTARY FIGURE LEGENDS

Figure S1. Partitioning of the analyzed beta-globin gene domain restriction fragments between the soluble and the insoluble portions of the 3C material. Shown are relative amounts of indicated fragments in the soluble (super) and insoluble (debris) fractions in experiments with brain cells and HindIII digestion (A), liver cells and HindIII digestion (B), brain cells and MboI digestion (C), and liver cells and MboI digestion (D), as determined by qPCR analysis using primers to inner regions of the restriction fragments (the sequences of the primers and TaqMan probes are presented in Supplementary Table S2). The total amount of each fragment in two fractions is set as 100. Green columns in the background of each graph show the size of the corresponding restriction fragments according to the scale shown at the right of the graph. The error bars represent SEM for two independent experiments.

Figure S2. Visualization of nuclear compartments and chromatin domains in the insoluble 3C material obtained from liver cells using MboI digestion. All designations are as in Figure 3.

Figure S3. Visualization of nuclear compartments and chromatin domains in non-treated brain cells (A) and the same cells treated according to the 3C protocol up to the ligation step (B). The insoluble fraction was collected after HindIII digestion and 1.6% SDS extraction. All designations are as in Figure 3.

Figure S4. Electron microscopic analysis of the insoluble 3C material obtained from liver cells using MboI digestion. All designations are as in Figure 4.

SUPPLEMENTARY TABLES

Table S1. Sequences of primers and TaqMan probes used for 3C analysis. s, sense primers, a/s, antisense primers (with respect to the direction of transcription of beta-globin genes; for ERCC3 primers – transcription of *Ercc3* gene), TM, TaqMan probes.

HindIII

Test fragment	Primer/TaqMan set (5'-3')
HS-62/-60	a/s GGGTGTGGGTATTTGTAAGAG
-42 region	a/s ATGAACAAGTTTCATGGGG
HS4/5	a/s TTCAAGTTCTCATCCTTCACTG
upstream of <i>Hbb-b1</i> promoter	s AGAAGGAGATTCATCCATGCACT
<i>Hbb-b1</i> promoter (anchor)	s AATCGCTGCTCCCCCTCACT TM FAM-ACCAAAGAAAGAGGAAA(T-BHQ1)GACAACACAGAACA-PO ₄
<i>Olf1r69</i>	s ACTGCACTGTCTTCCAAATCACT
<i>Ercc3</i> (anchor)	s CAGACAGTTTGCAGAGATGGC TM FAM-AGCTTTATGAAG(T-BHQ1)GAACTCAAGGCAGAGG-PO ₄
<i>Ercc3</i> (test)	s CCCTTCTTGATAGTGATGTGACAGT

MboI

Test fragment	Primer/TaqMan set (5'-3')
HS-62/-60	s TGTAGTTCTCTAGTGTAGCCACCAG
-42 region	a/s TAGATGCATGGTCTTAATGGTCC
HS4/5	a/s TACTAATAAAAGCAAGCCATCTCG
<i>Hbb-bh1</i>	a/s AGATGCTTGTGATAGCTGCCTT
upstream of <i>Hbb-b1</i> promoter	s TGAGGACTTGGTTCAGTAAATAA
<i>Hbb-b1</i> promoter (anchor)	s CTGATTCCGTAGAGCCACACC TM FAM-CCTACCTCACC(T-BHQ1)TATATGCTCTGCCCTG-PO ₄
<i>Olf1r69</i>	s AAAACAAGATGAGAATCGCCTG
<i>Ercc3</i> (anchor)	s CTGTCTCGTCCTGGGCAACT TM FAM FAM-ATGGTTGACCACA(T-BHQ1)CTTAAACTGGGCTT-PO ₄
<i>Ercc3</i> (test)	s C ATTCCTAGAGATTTACAACCCTCAC

Table S2. Sequences of primers and TaqMan probes used to estimate the quantities of restriction fragments. s, sense primers, a/s, antisense primers (with respect to the direction of transcription of beta-globin genes), TM, TaqMan probes.

Test fragment	Primer/TaqMan set (5'-3')
HS-62/-60 (HindIII)	s GGTATGGTGAAGTCCAGAGGG TM FAM-TCCAGCAGTA(T-BHQ1)CATTCCAGCCTTAAAGAC-PO ₄ a/s GTGTGCAGGGCAATAGAGGAT
HS-62/-60 (MboI)	s ATACCCATGCTGGTTGAATCA TM FAM-TGAAACC(T-BHQ1)GACGCTCCTTCCAAACTG-PO ₄ a/s CCTGGTGGCTACACTAGAGAAGT
-42 region	s TATCCCGTGACTATACCTTAATGAA TM FAM-CTTGTGGAGAA(T-BHQ1)GTCATAGACTATACGAGTGAA-PO ₄ a/s GCCAATGTGATGAGTGCAGAG
HS4/5	s TACAAGTCTCCTCATGTTCCCAA TM FAM-TAGCCTCAGT(T-BHQ1)ACCCGACATTAGTTCTTAGT-PO ₄ a/s TTTTCAGACATACTCCTCTATCCAG
<i>Hbb-bhl</i>	s CTATGTCTTAGGCTCCTGATTGTT TM FAM-CCAAAGTGTG(T-BHQ1)CAAAGAATCTCTGAGTCCAT-PO ₄ a/s GCCAGGGCAGAAGAGAGGTT
upstream of <i>Hbb-b1</i> promoter	s AAAATTGAATAGAATCACTACTGCAC TM FAM-AATAAGGTACA(T-BHQ1)TTGAATTGAGCATACCCTG-PO ₄ a/s TGCCTCTCTATTTGTATGTGAAGT
<i>Hbb-b1</i> promoter	s TCAGTAGTTGATTGAGCAAATGTGT TM FAM-TCCCTCTGAA(T-BHQ1)AATGTTTGTCTTATCTGTG-PO ₄ a/s TCGGTGATGACAAGCATATTTCT
<i>Olf69</i>	s GGCAAAGCACATTTACCTGAT TM 5' FAM-TCCACCCTCA(T-BHQ1)AGCATCCTCATAGCAT-PO ₄ a/s ACACTTGTTCCCTGAGATGGTT