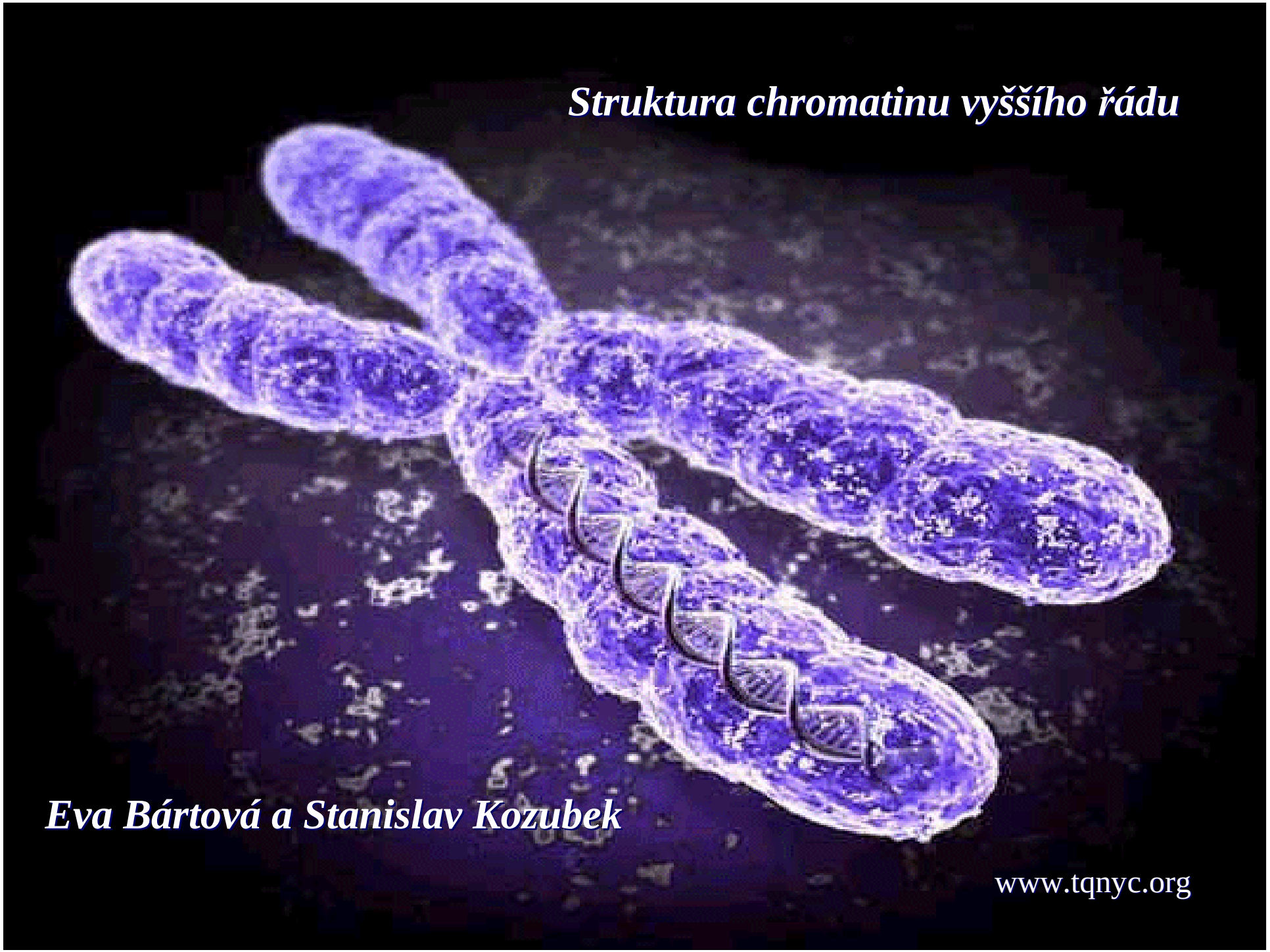
- Kompartmentalizace interfazních jader
- Morfologické a jaderně-topografické aspekty buněčné diferenciace.
- Apoptóza a struktura chromatinu.
- Cytoskelet a jaderná matrix - studium cytoskeletu pomocí mikroskopie s vysokým rozlišením.
- BAC/PAC knihovny a jejich využití pro FISH techniku
- Epigenetické procesy probíhající v buněčných jádrech.
- Cytogenetické a jaderně-topografické změny u vybraných typů nádorů.
- Patofyziologie, cytogenetika a jaderná topografie mnohočetného myelomu.

Struktura chromatinu vyššího řádu



Eva Bártová a Stanislav Kozubek

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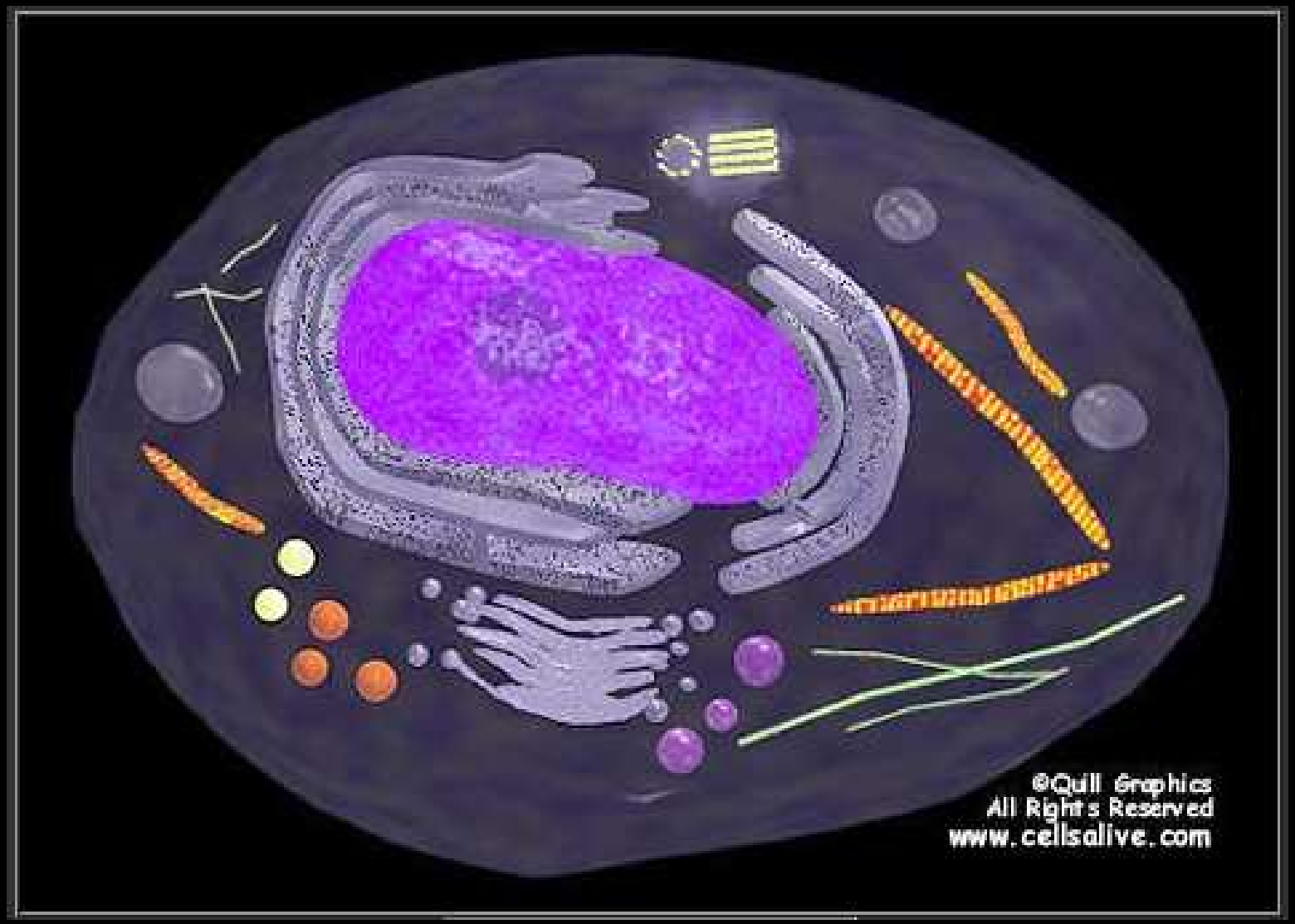
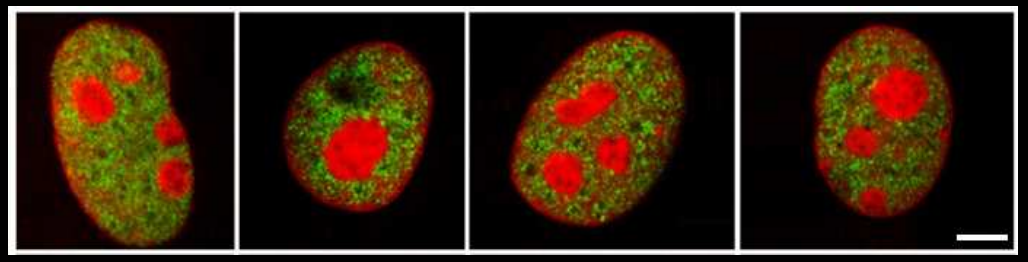
Buněčné jádro

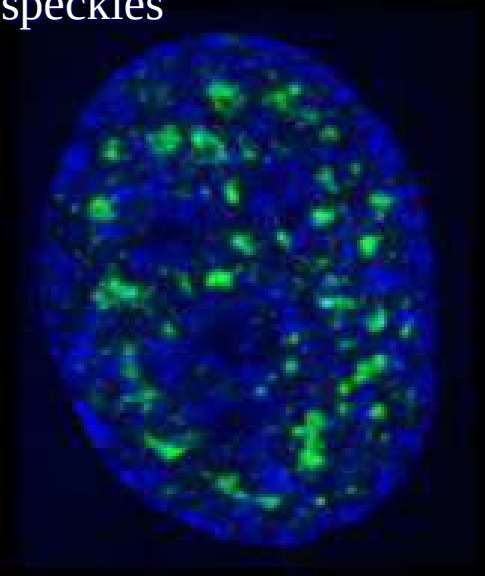


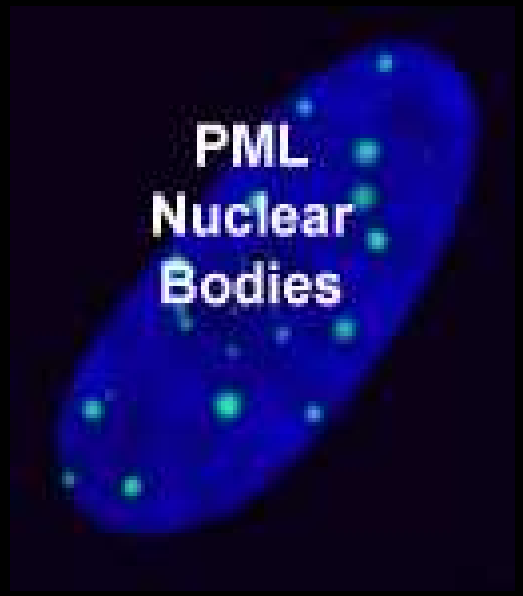
Nuclear compartments:

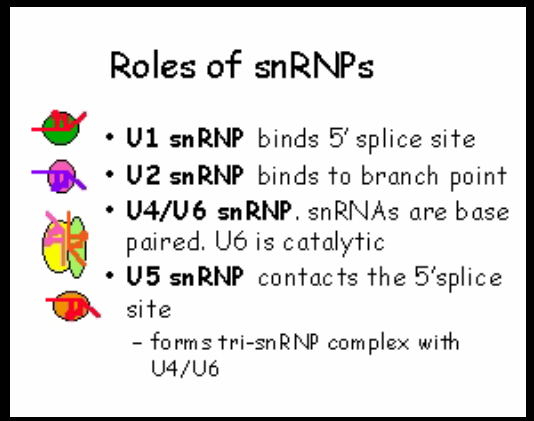
1. **Nucleolus**
2. **Splicing speckles**
3. **Cajal bodies**
4. **PML bodies**
5. **snRNP**
6. **Clustery interchromatinový granulí (IGCs)**



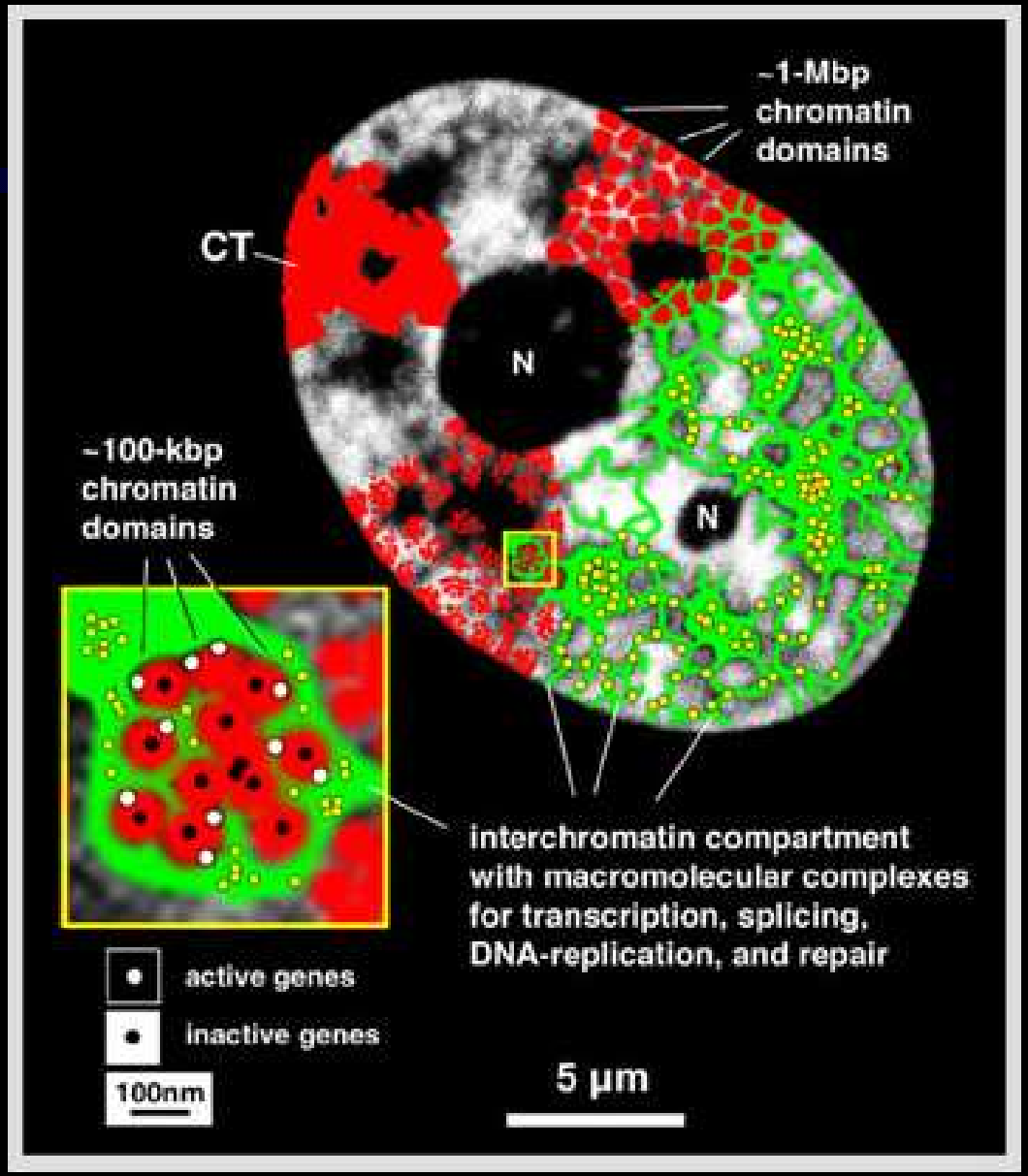
speckles



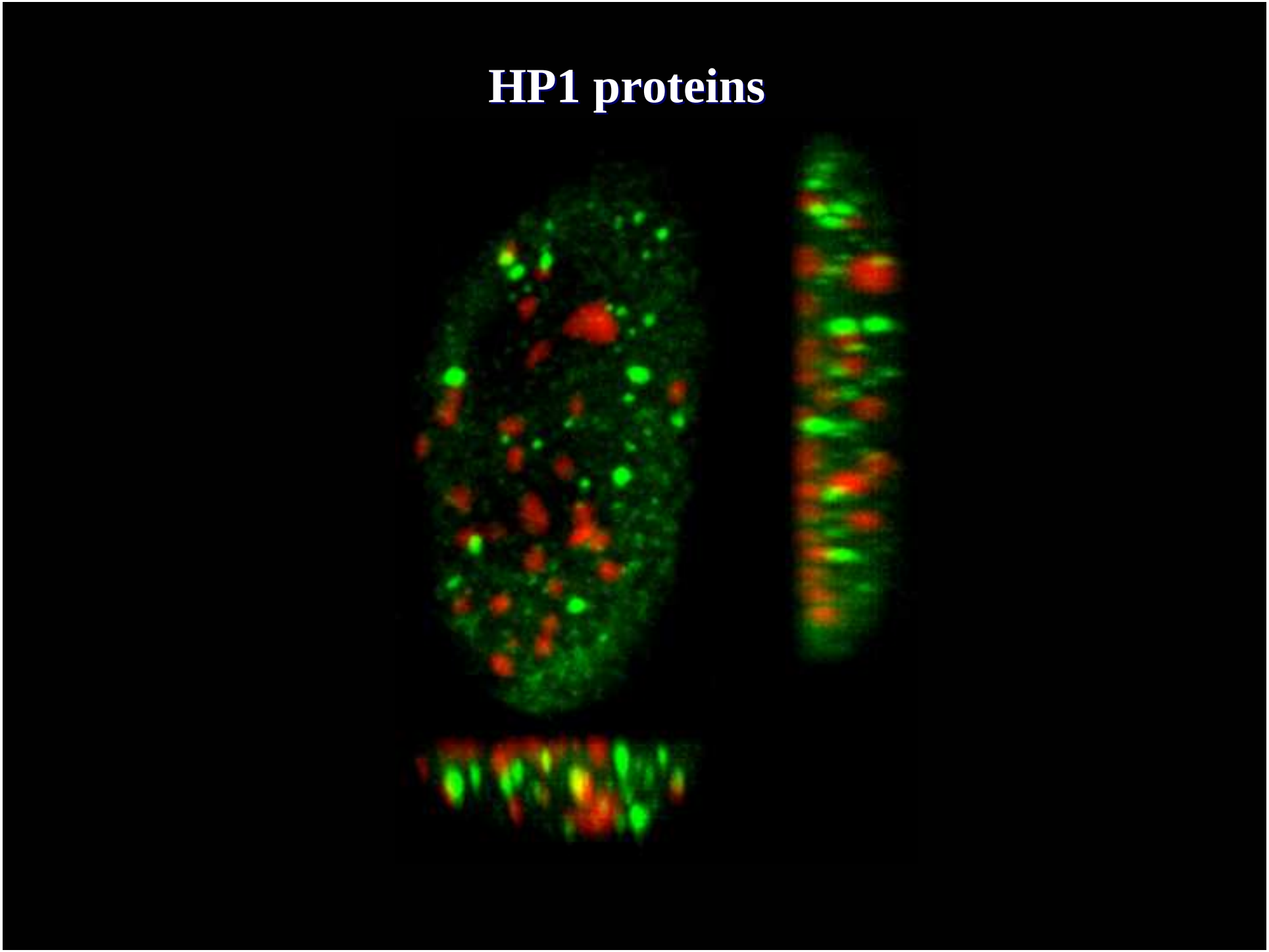


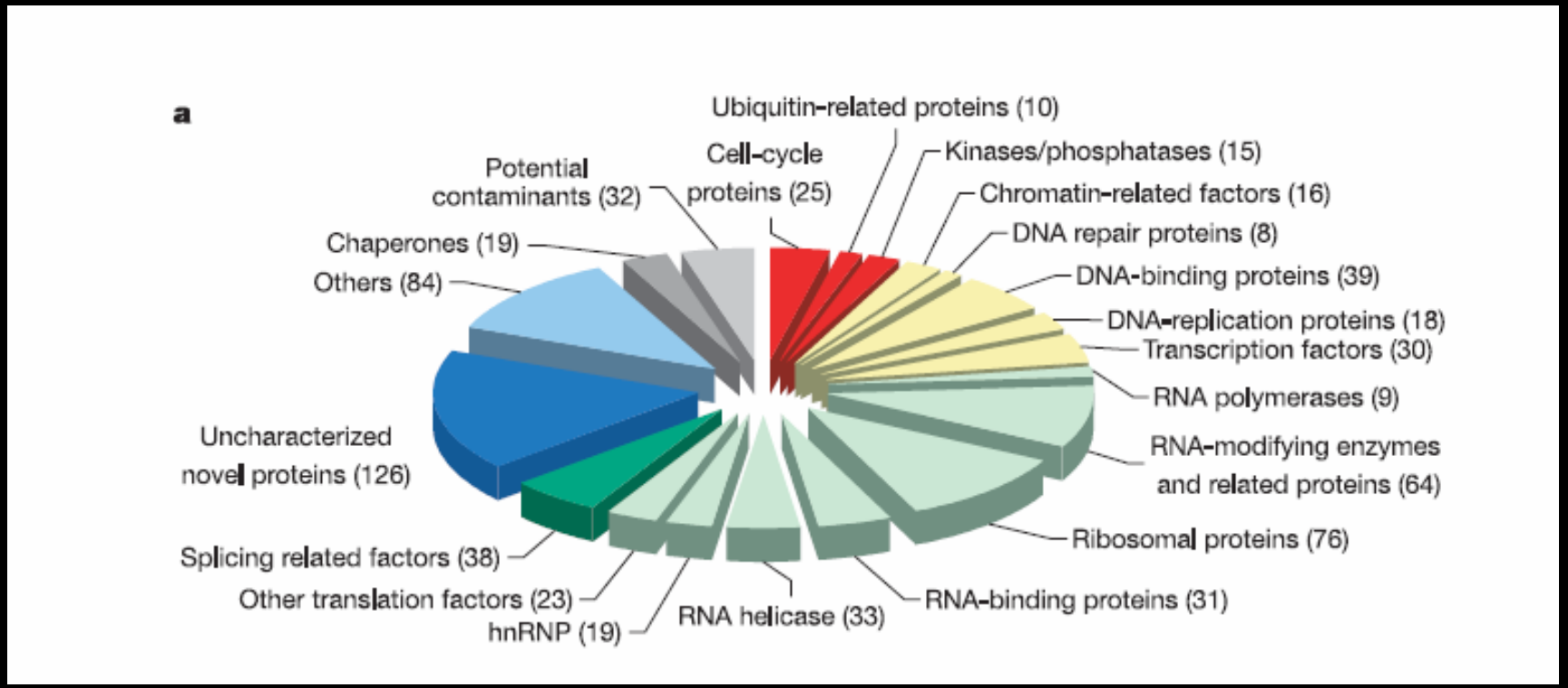


CT-IC MODEL (T. Cremer)



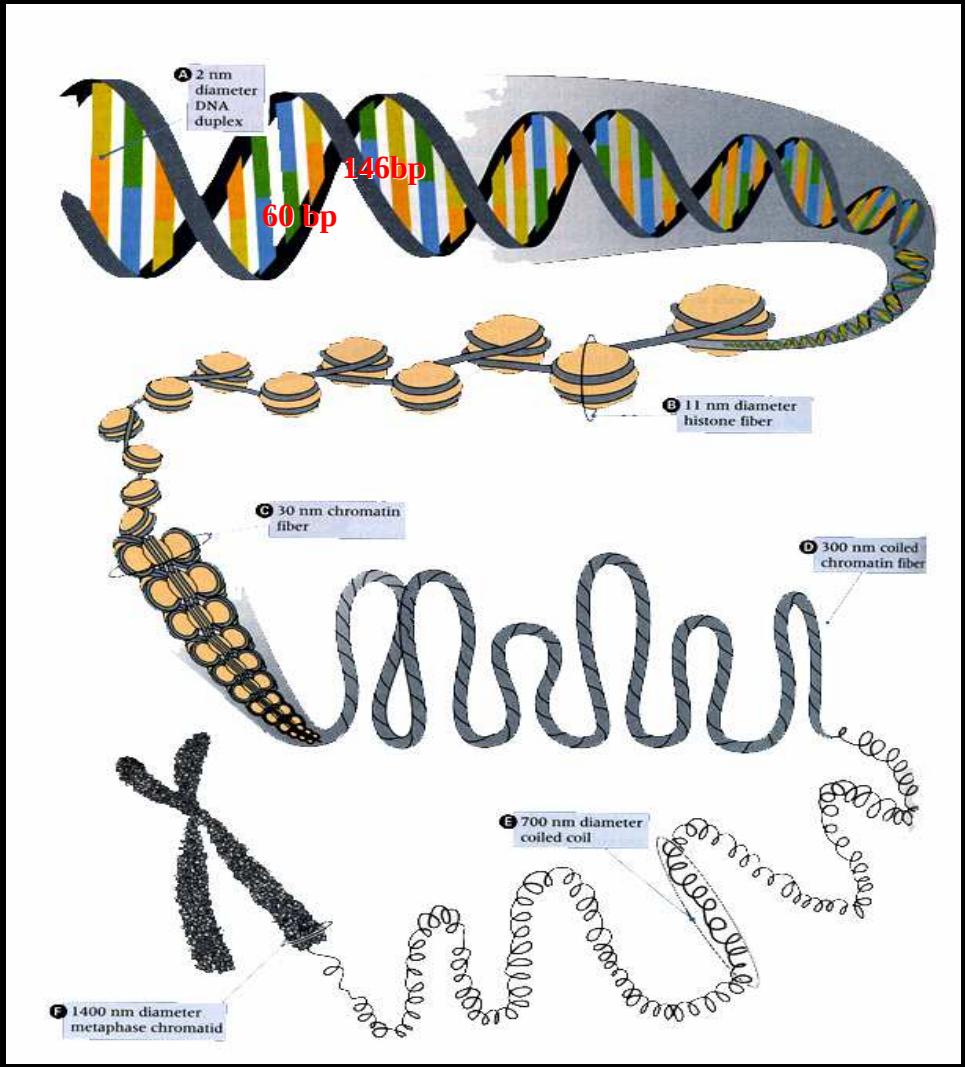
HP1 proteins



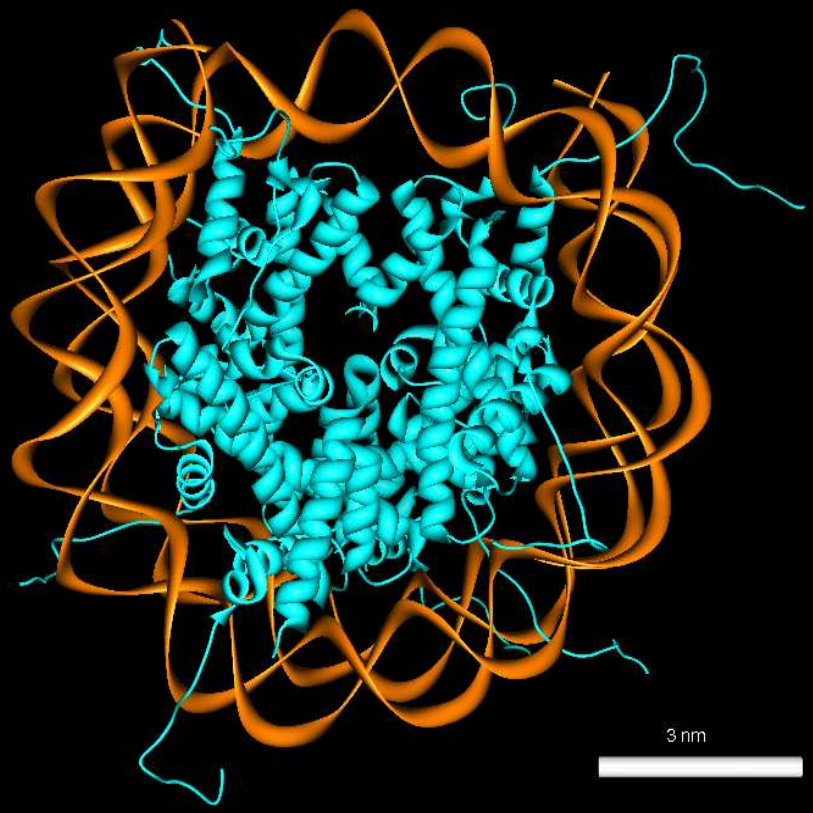


Andersen et al., Nature, 2005

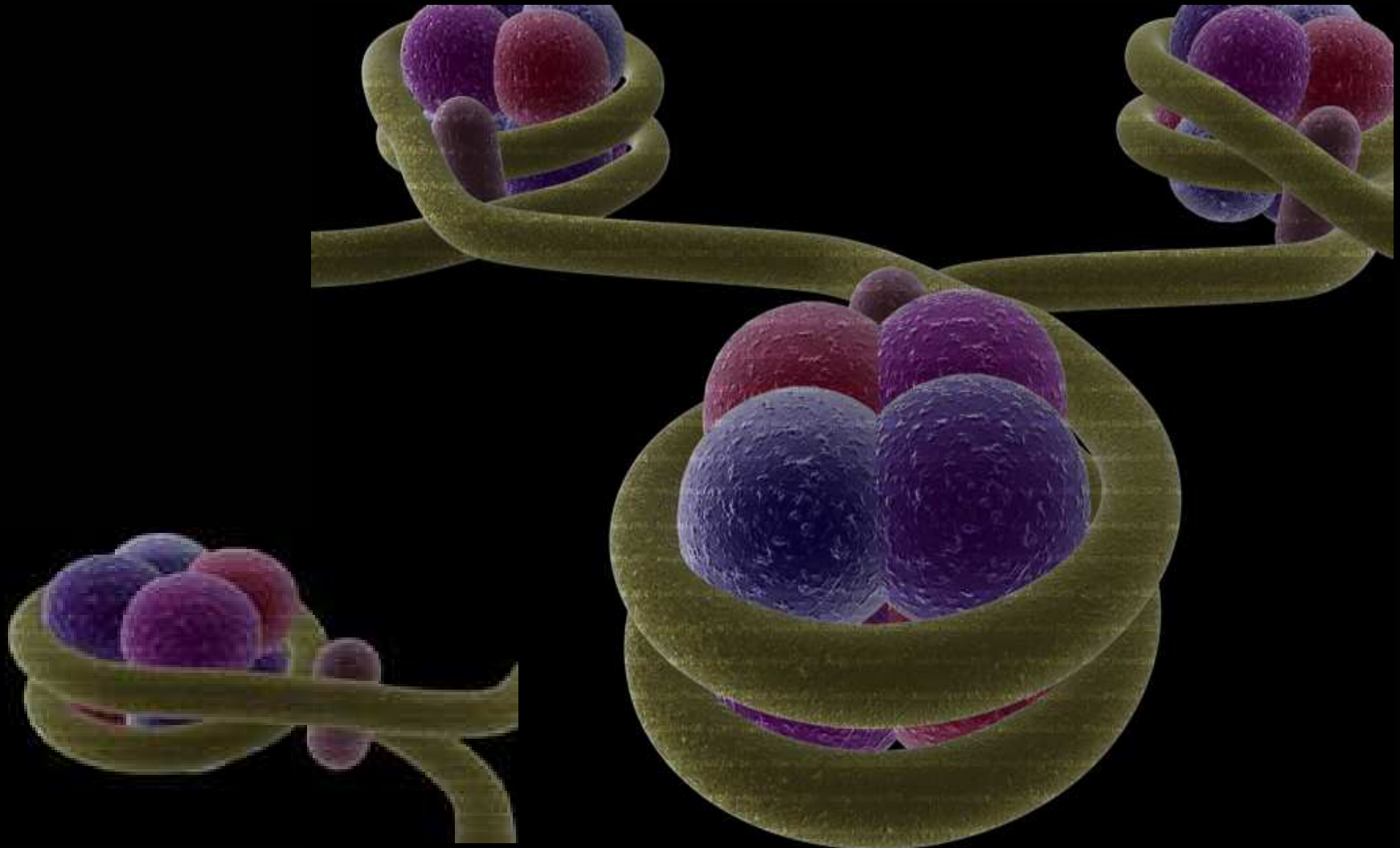
CHROMATIN: materiál jader eukaryotních buněk; nukleoproteinový komplex tvořený DNA vázanou na histony a další bílkoviny. V nedělícím se jádru lze rozlišit euchromatin, kde probíhá transkripce, a heterochromatin, který je transkripčně inaktivní.



HISTONY: skupina basických bílkovin v jádře eukaryotních buněk, kde vytvářejí reversibilní komplexy s DNA. Rozlišuje se pět typů histonů: H1, H2A, H2B, H3 a H4. Histony H2A, H2B, H3 a H4 tvoří vždy ve dvou kopiích oktamery, kolem nichž se obtáčí dvojšroubovicová DNA; tento útvar se nazývá nukleosom. Histon H1 je přítomen v menším množství než ostatní histony, a ačkoli je též vázán na DNA, není součástí nukleosomů. Histony se tak podílejí na uspořádání DNA v eukaryontním chromosomu do vlákna vyššího řádu.

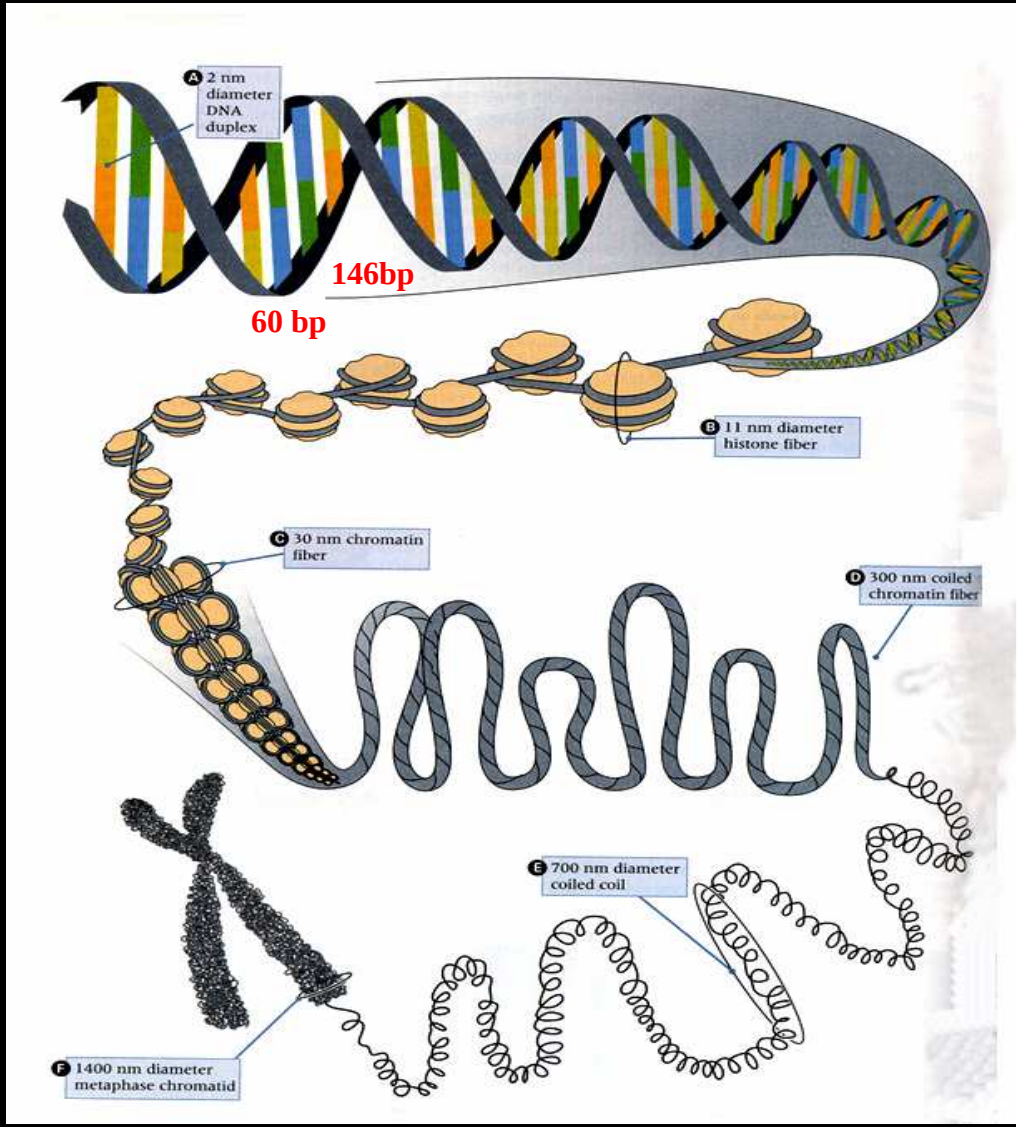


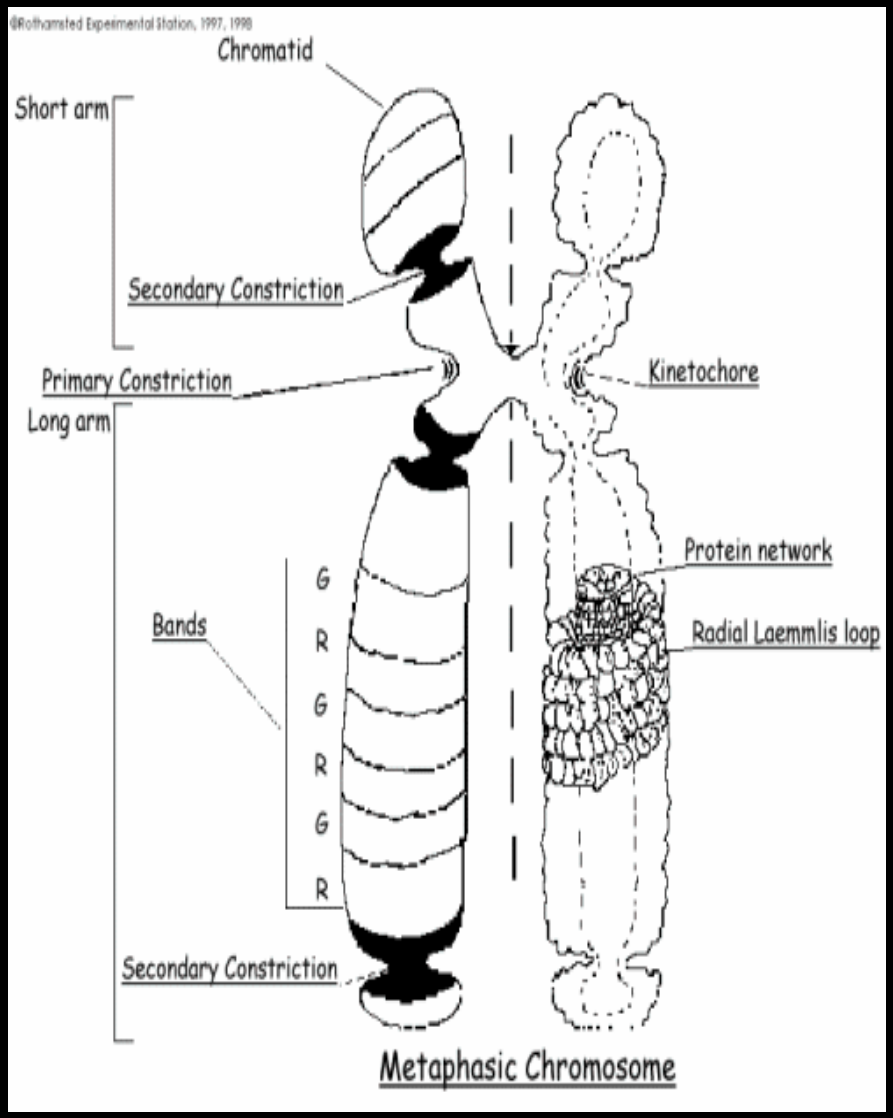
NUKLEOSOM



Joseph Roland 2003

CHROMATIN: materiál jader eukaryotních buněk; nukleoproteinový komplex tvořený DNA vázanou na histony a další bílkoviny. V nedělícím se jádru lze rozlišit euchromatin, kde probíhá transkripce, a heterochromatin, který je transkripčně inaktivní.





Kondenzace chromatinu

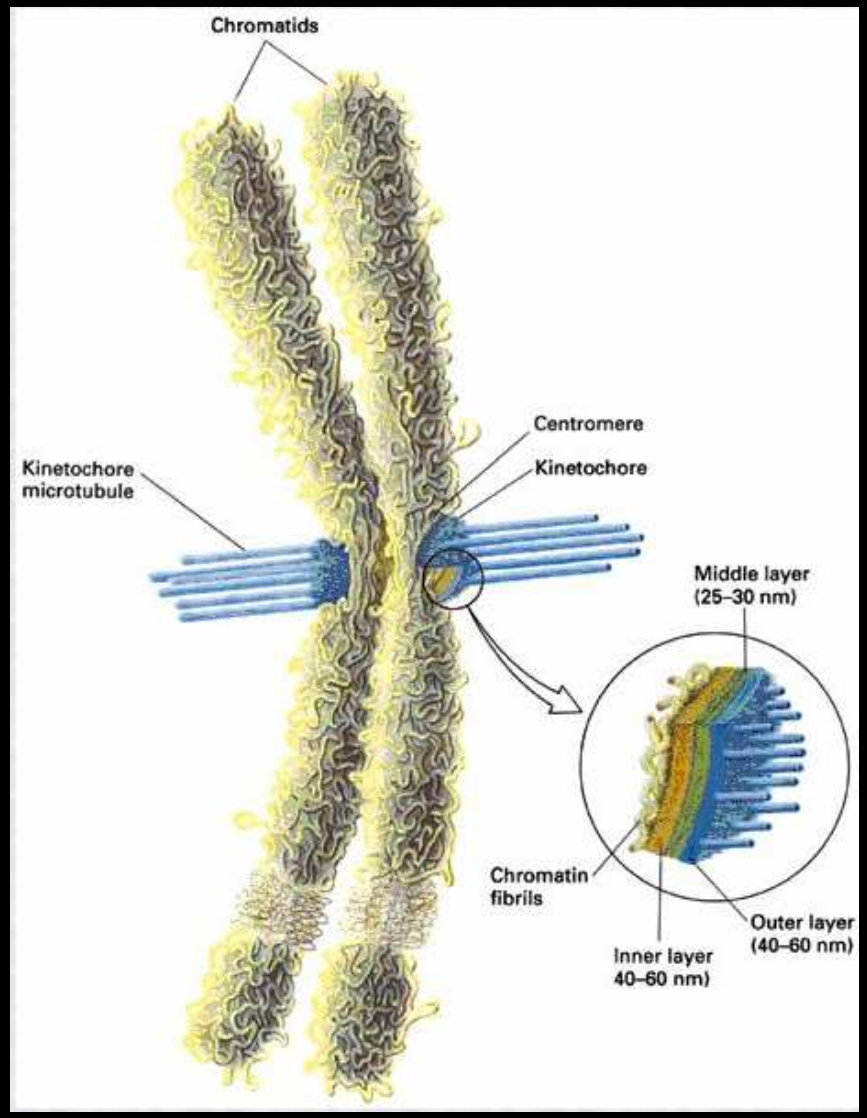


Figure 23-38, p. 1094, Molecular Cell Biology, 3rd ed., Lodish, et al., copyright 1995,

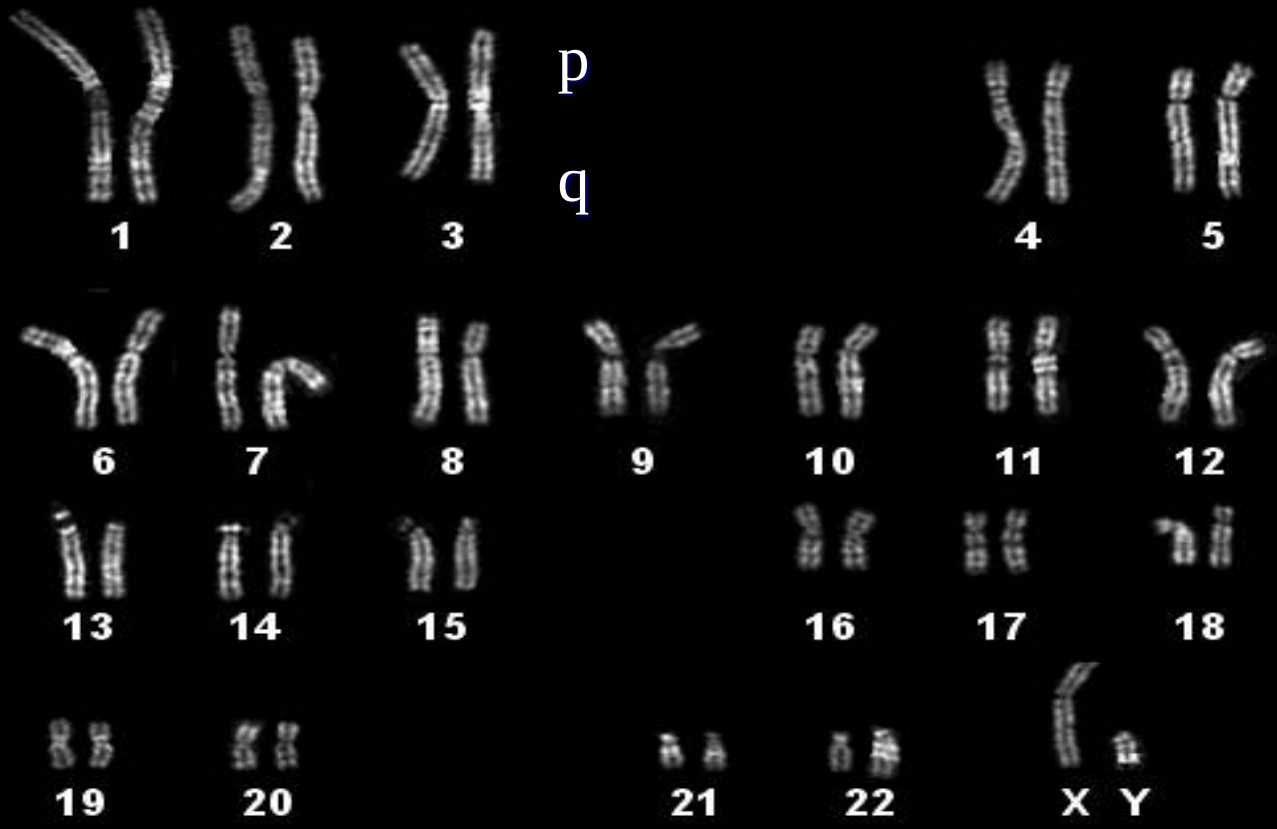
The centromere is together with telomeres and origin of replications one of the essential parts of any eukaryotic chromosomes. The centromere is usually defined by specific DNA (AT-rich) sequences which are in higher eukaryotes typical tandem repetitive sequences, often called "satellite DNA". SAT1,2,3, alpha satellites, beta satellites.
CENP A, B, C, G, H.

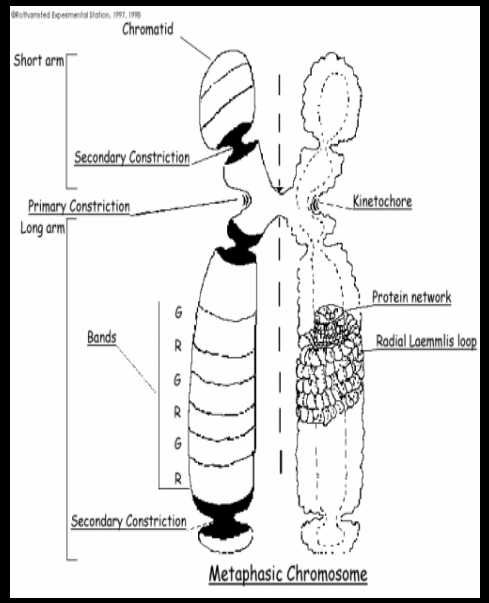
The kinetochores are the sites where the spindle fibers attach. Kinetochores and the spindle apparatus are responsible for the movement of the two sister chromatids to opposite poles of dividing cell nucleus during anaphase.

A centromere functions in sister chromatid adhesion, kinetochore formation, and pairing of homologous chromosomes.

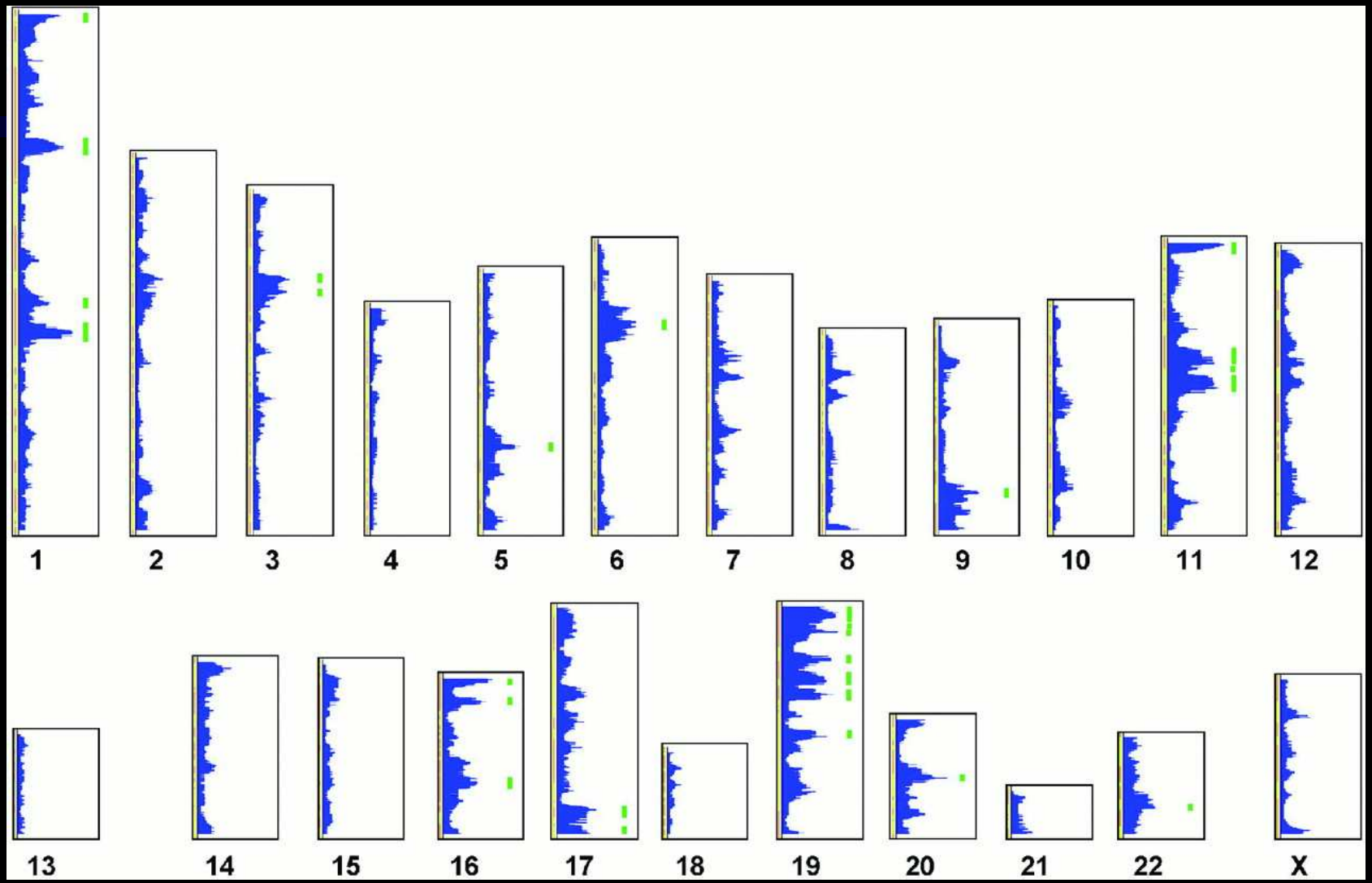
When the centromere doesn't function properly, the chromosomes don't align and separate properly, resulting in the wrong number of chromosomes in the daughter cells (aneuploidy), and conditions such as Down syndrome, if the cells survive at all.

Typy chromozomů: meta-submeta-, akrocentrické

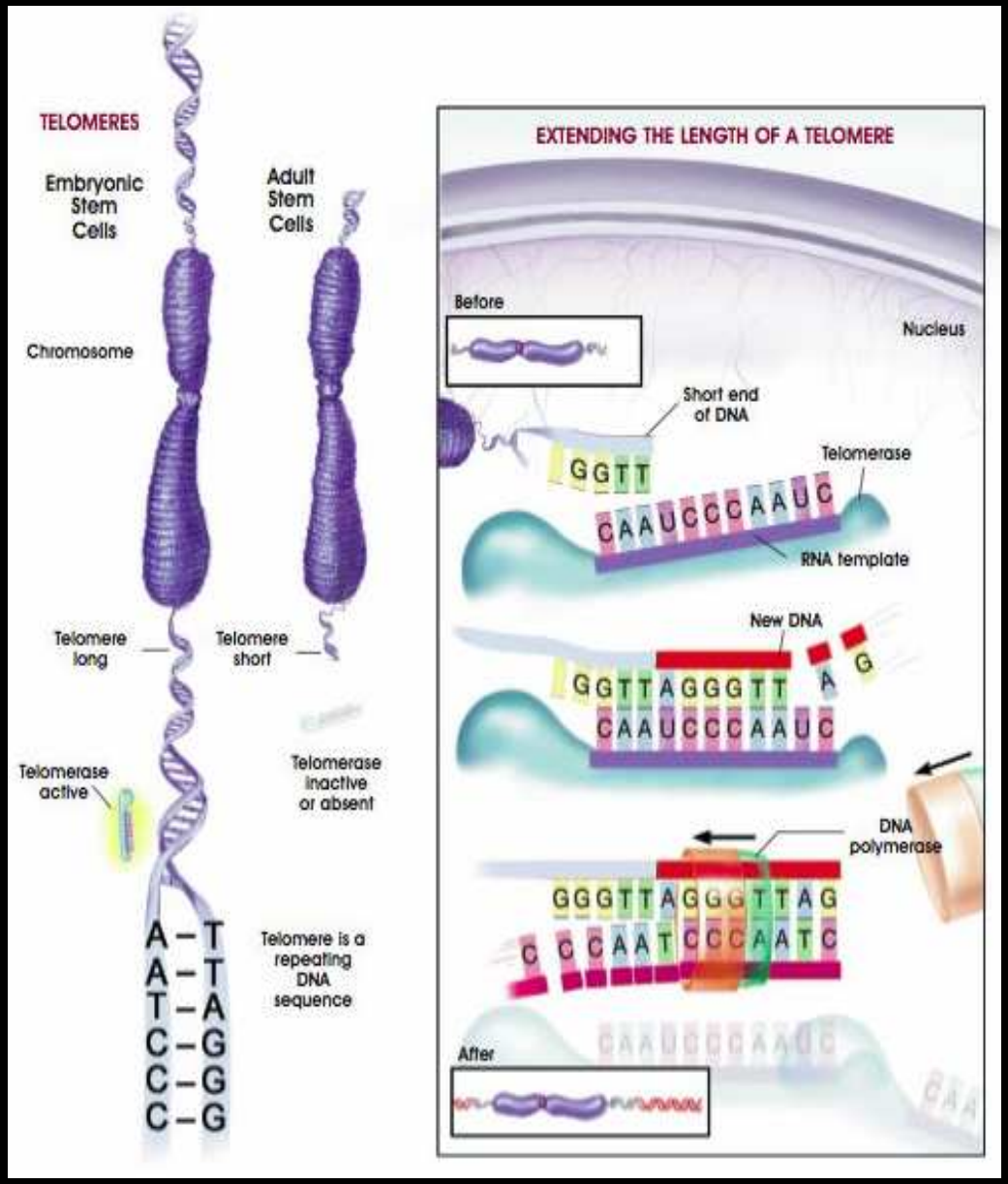




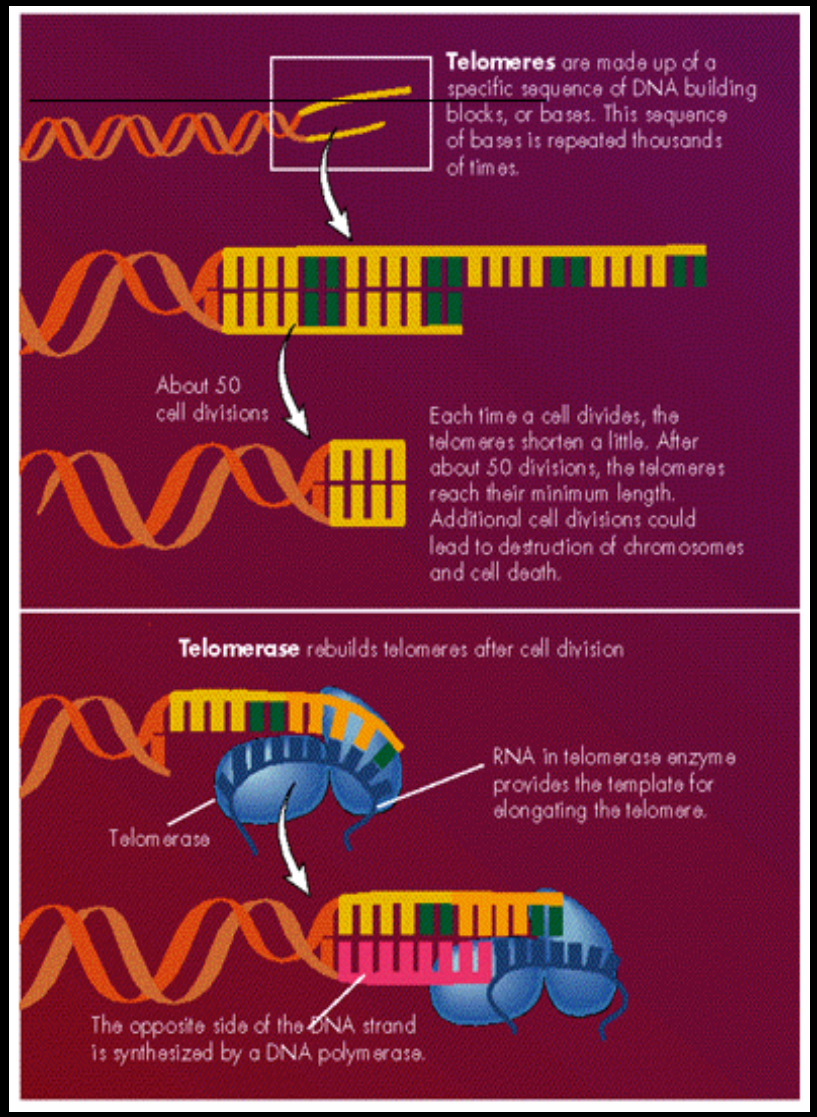
Transcriptome map (Caron et al., 2001)



Telomeres (TTAGGG sequence and different proteins)

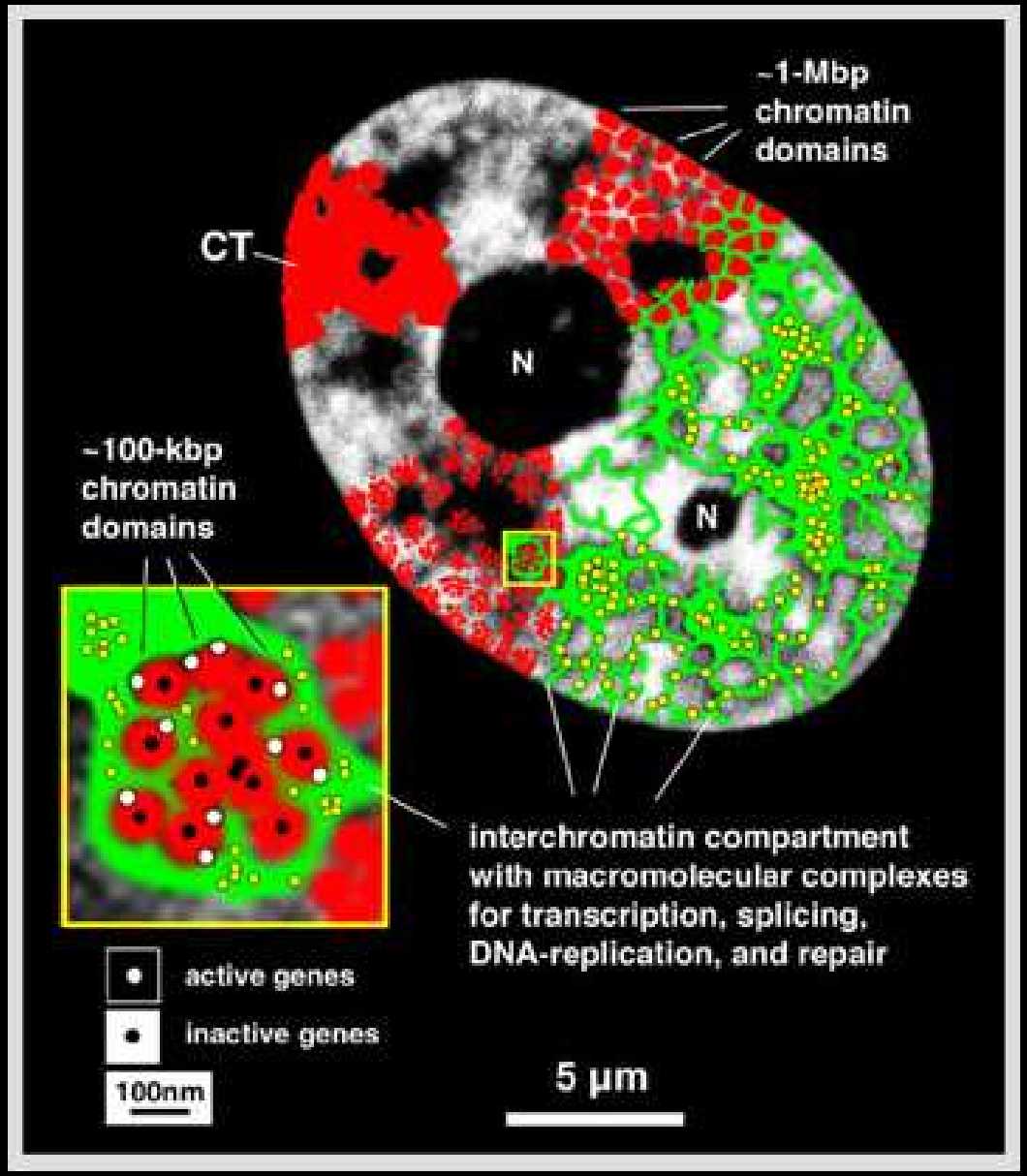


Telomerase is composed of two subunits, Telomerase Reverse Transcriptase (hTERT, the 'h' is for human) and hTR (Telomerase RNA). These two subunits are coded for by two different genes in the genome. Using hTR template, hTERT can add a six nucleotide repeating sequence, 5'-TTAGGG to the 3' strand of chromosomes. This repeating TTAGGG sequence is called the telomere. The template region of hTR is 3'-CCCAAUCCC -5'.

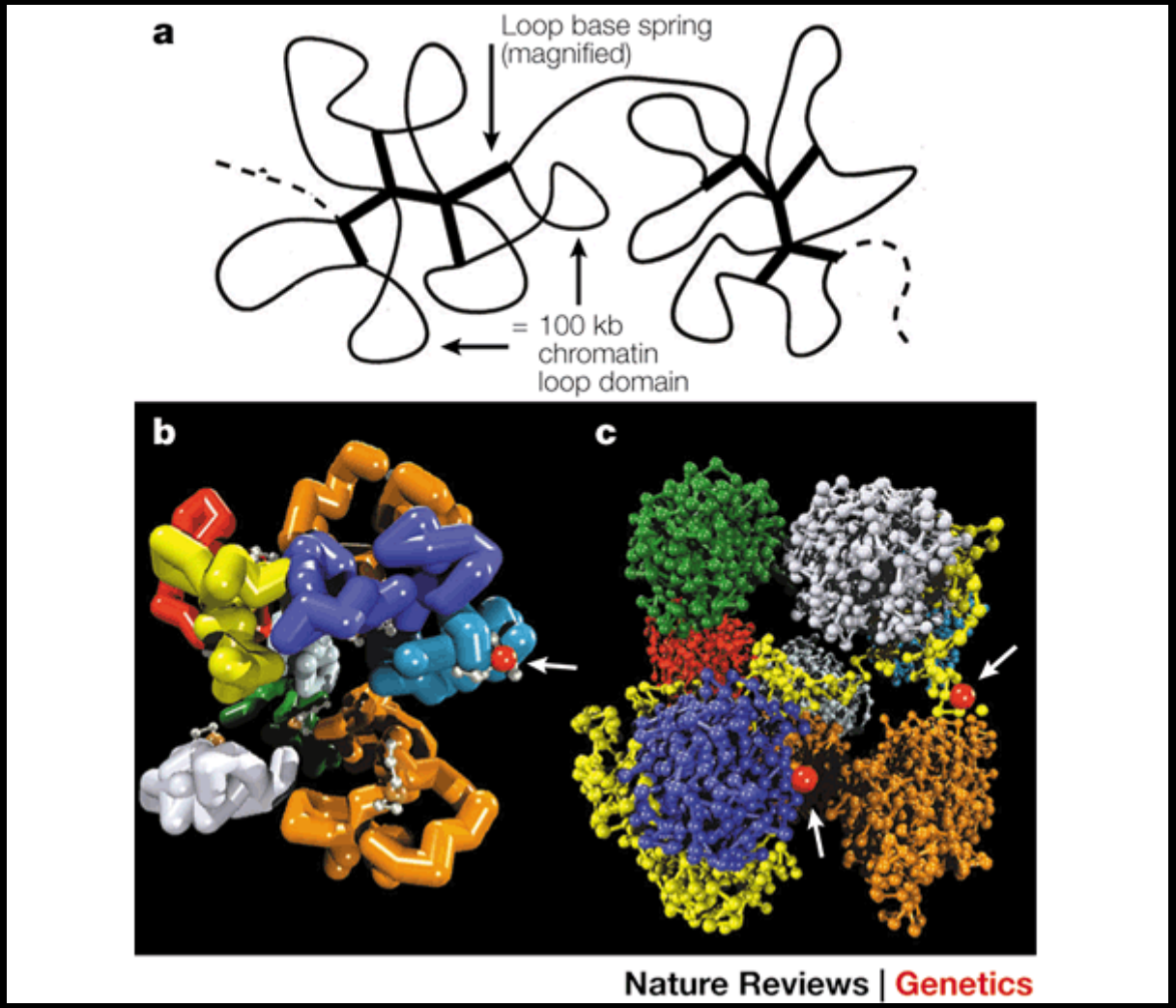


Telomerase is an enzyme that lengthens telomeres by adding on repeating sequences of DNA. Telomerase binds to the ends of the telomere via an RNA template that is used for the attachment of a new strand of DNA. Telomerase adds several repeated DNA sequences then releases and a second enzyme, DNA Polymerase, attaches the opposite or complementary strand of DNA completing the double stranded extension of the chromosome ends. High levels of telomerase activity are detected in embryonic stem cells and cancer cells, whereas little or no telomerase activity is present in most mature, differentiated cell types.

CT-IC MODEL (T. Cremer)

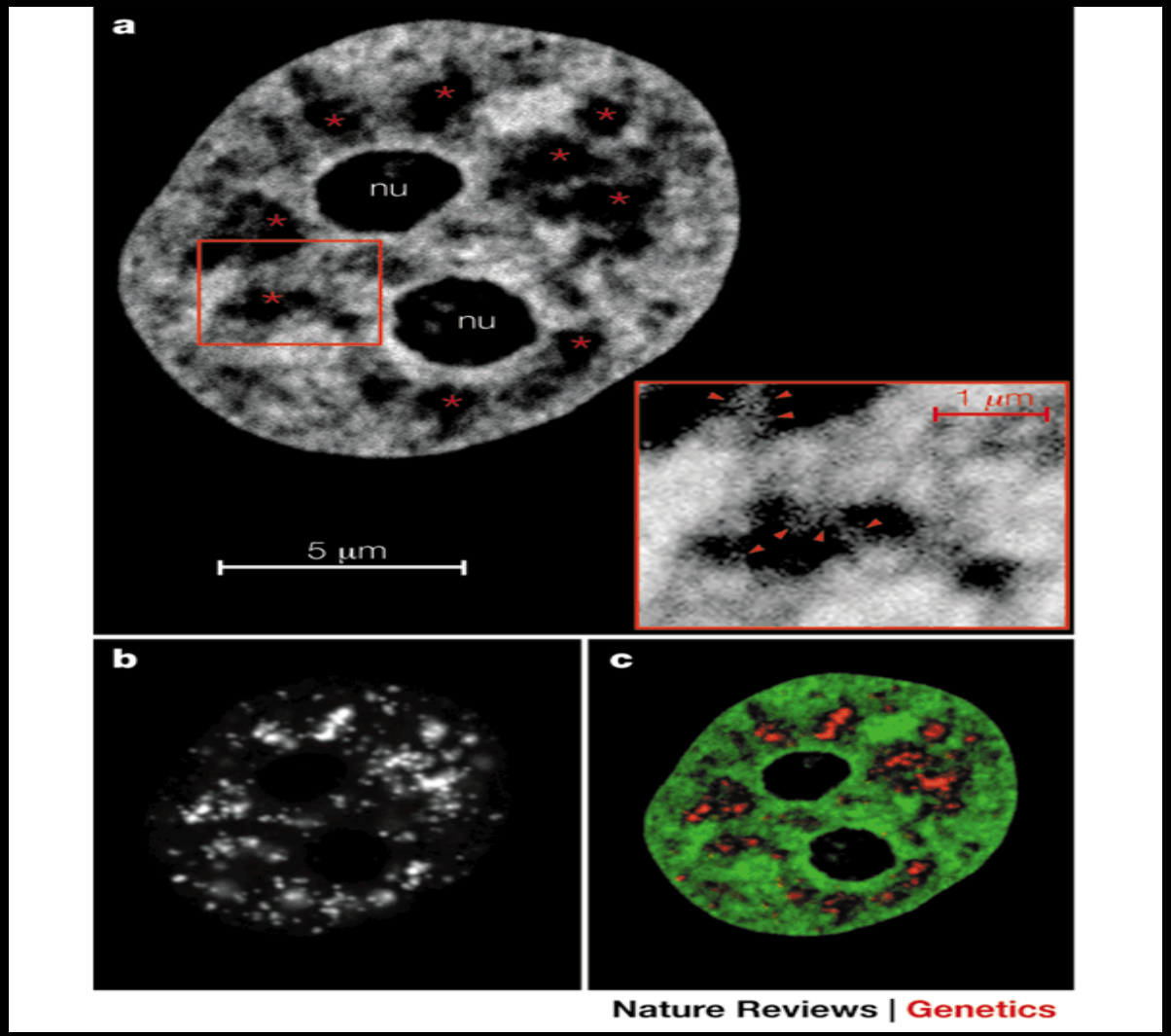


Chromatin loops



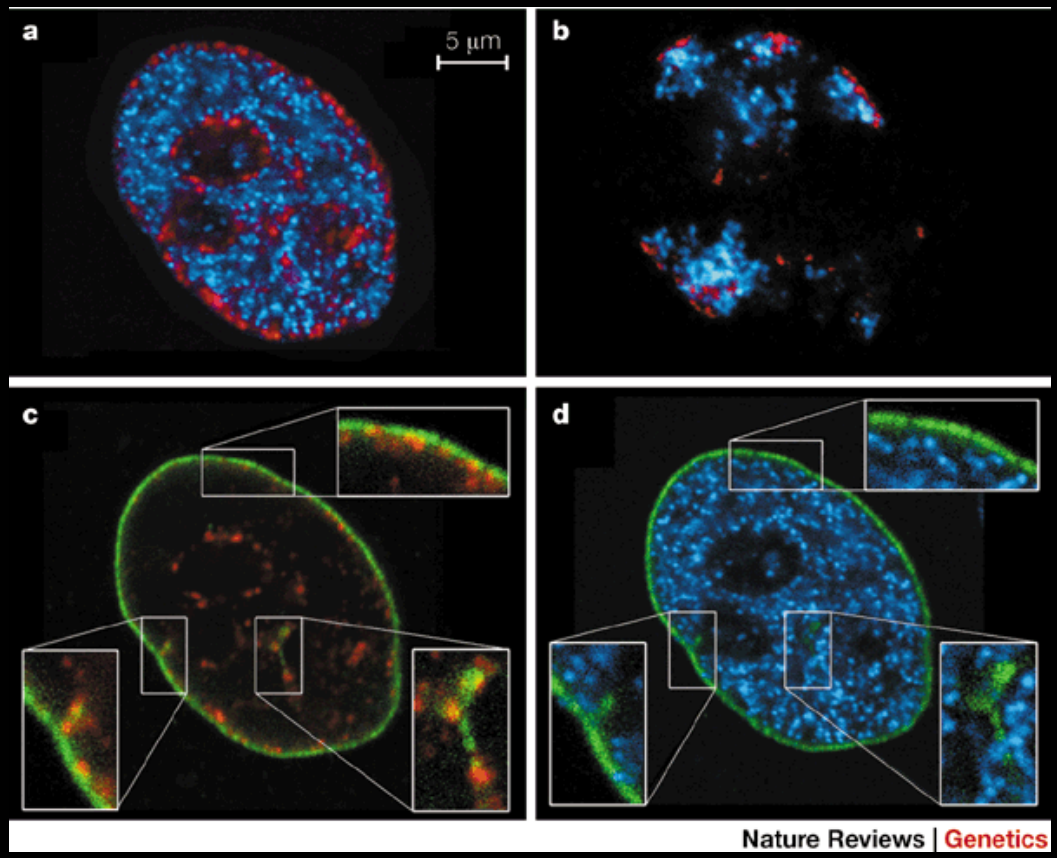
T. Cremer group, Munich

Chromatinové meziprostory

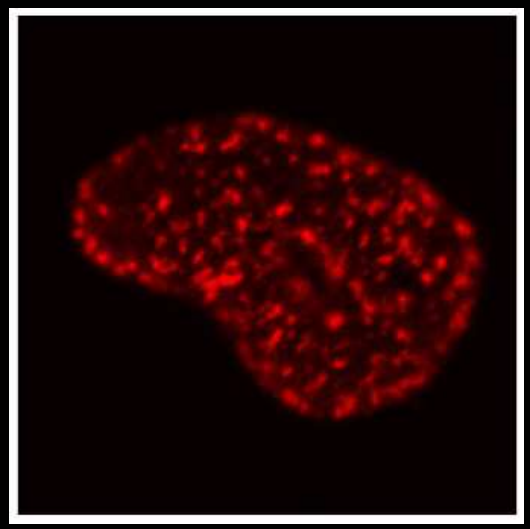


T. Cremer group, Munich

Pozdně a časně se replikující chromatin

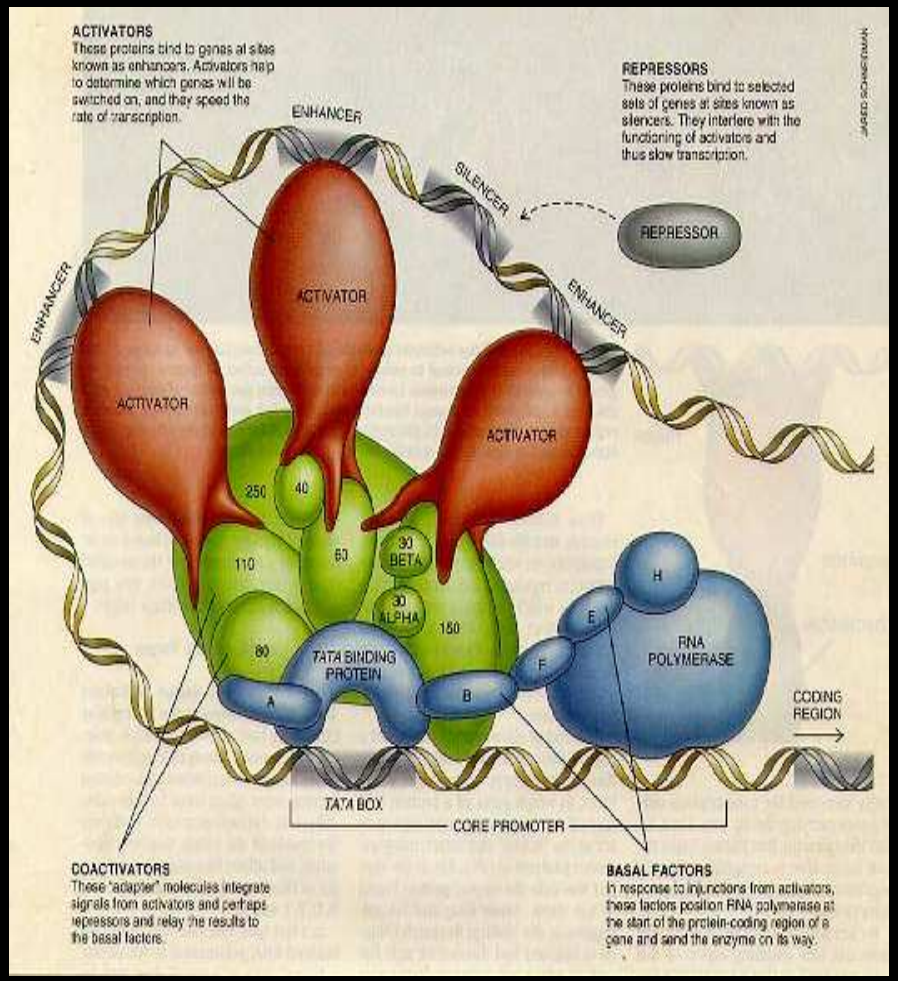


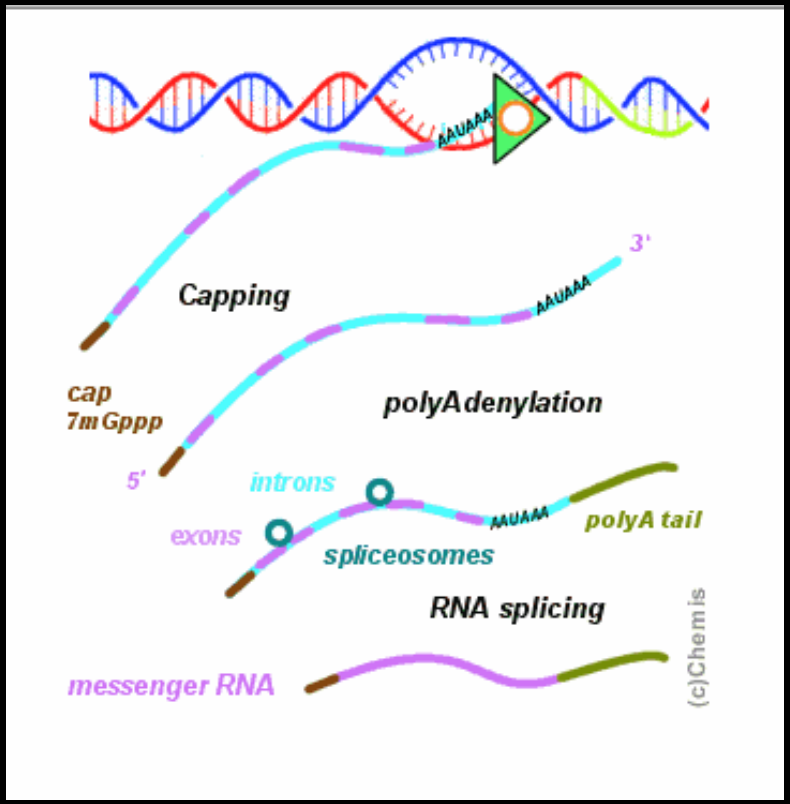
Replikační ohniska

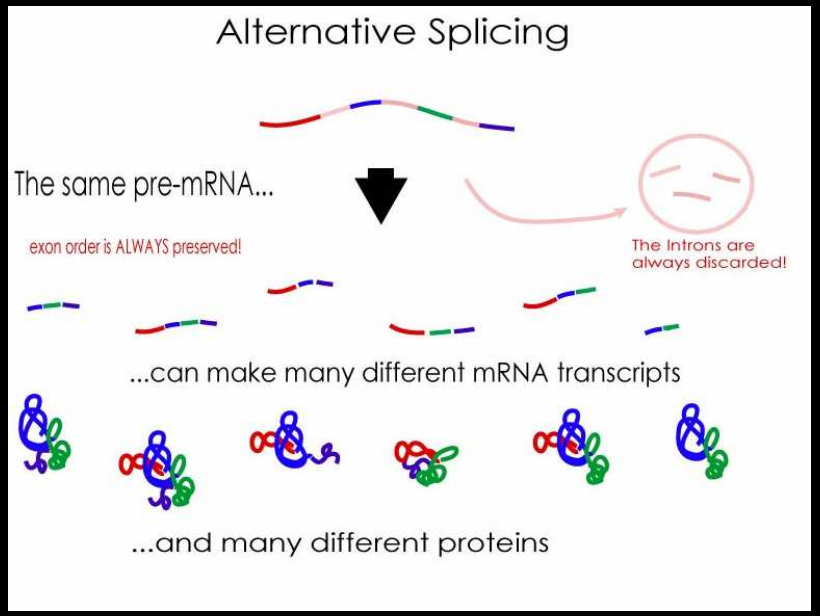


T. Cremer group, Munich

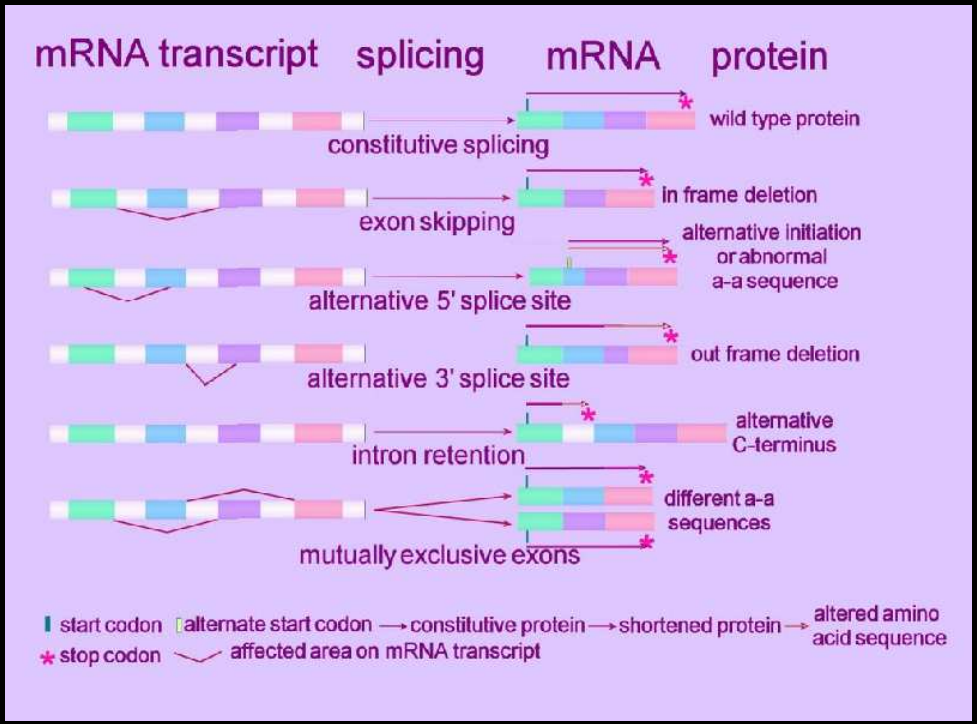
TRANSKRIPCE: přepis, biosynthesa řetězce **RNA** podle **templátového** řetězce **DNA**, přičemž jednotlivé **nukleotidy** jsou připojovány na základě **komplementarity** (viz **base nukleových kyselin**). Klíčovým enzymem této synthesy je **RNA-polymerasa**. Transkripce probíhá ve třech stupních: **a)** iniciace (zahájení), kdy se RNA-polymarasa váže na specifickou sekvenci DNA (viz **promotor**) a přesunuje se k místu, kde začíná vlastní synthesa; **b)** elongace, kdy se RNA-polymerasa posunuje podél řetězce DNA, uvolňuje kódující řetězec a podle templátového řetězce postupně synthetisuje novou RNA tím, že na volnou 3´-OH skupinu **ribosy** připojuje komplementární nukleotidy, jejichž donorem jsou nukleosidtrifosfáty; vznikající RNA se postupně uvolňuje od komplexu s DNA a dvojitý helix DNA se samovolně obnovuje; **c)** terminace (ukončení synthesy a úplné uvolnění RNA) je signalisováno zvláštními sekvencemi ve struktuře DNA, které jsou rozpoznávány bílkovinami, tzv. terminačními neboli ρ (ro) faktory. Řízení transkripce jednotlivých genů patří k nejdůležitějším mechanismům regulace enzymové aktivity a diferenciace buněk.


ACTIVATORS
These proteins bind to genes at sites known as enhancers. Activators help to determine which genes will be switched on, and they speed the rate of transcription.
REPRESSORS
These proteins bind to selected sets of genes at sites known as silencers. They interfere with the functioning of activators and thus slow transcription.
ENHANCER
SILENCER
REPRESSOR
ENHANCER
ENHANCER
ACTIVATOR
ACTIVATOR
ACTIVATOR
250
40
110
60
30 BETA
30 ALPHA
150
80
TATA BINDING PROTEIN
RNA POLYMERASE
H
E
F
A
B
CODING REGION
TATA BOX
CORE PROMOTER
COACTIVATORS
These "adapter" molecules integrate signals from activators and perhaps repressors and relay the results to the basal factors.
BASAL FACTORS
In response to injunctions from activators, these factors position RNA polymerase at the start of the protein-coding region of a gene and send the enzyme on its way.

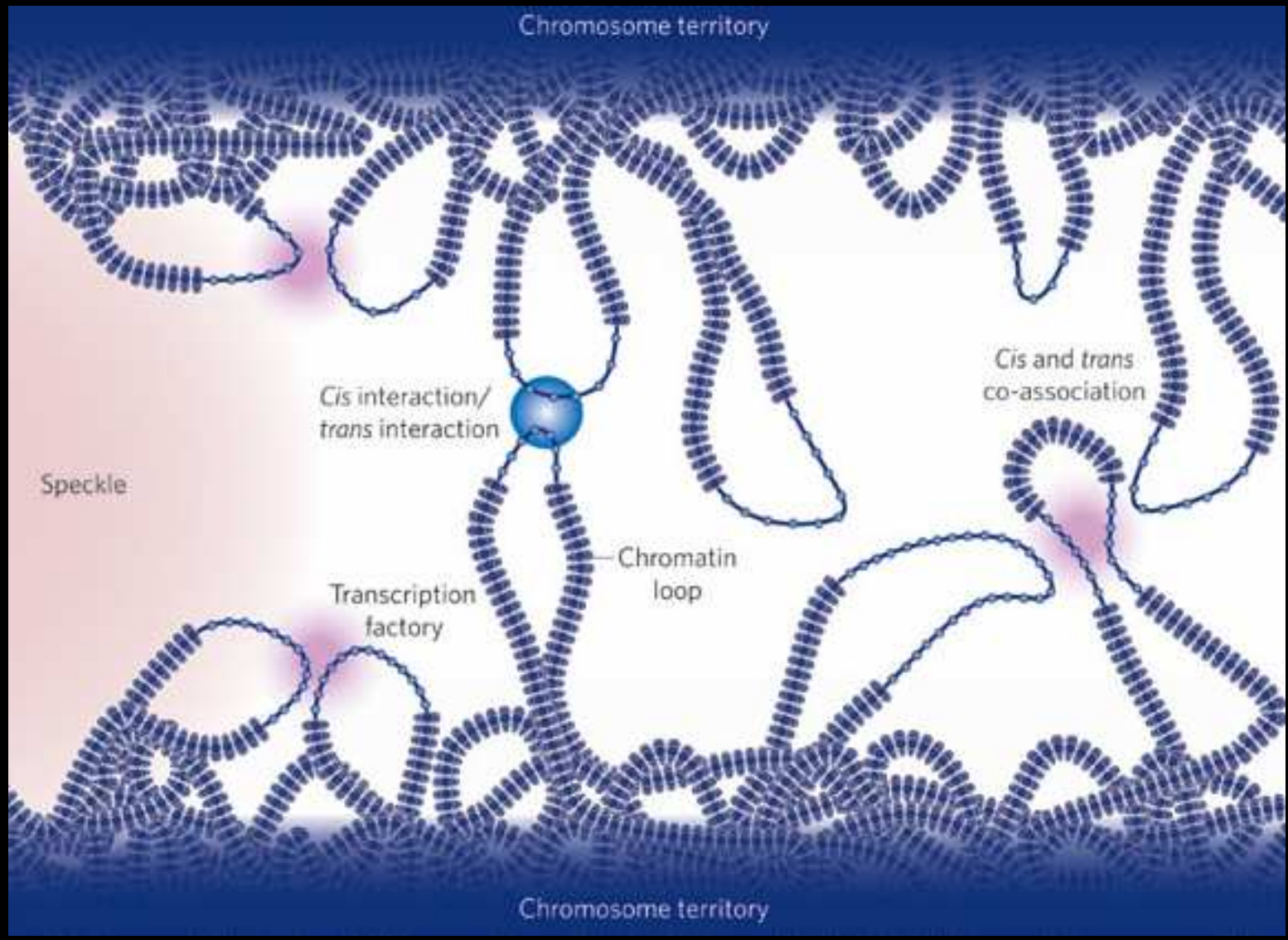

AAUAAA
3'
Capping
AAUAAA
cap
7m Gppp
polyAdenylation
5'
introns
exons
AAUAAA
polyA tail
spliceosomes
RNA splicing
messenger RNA
(c)Chemis



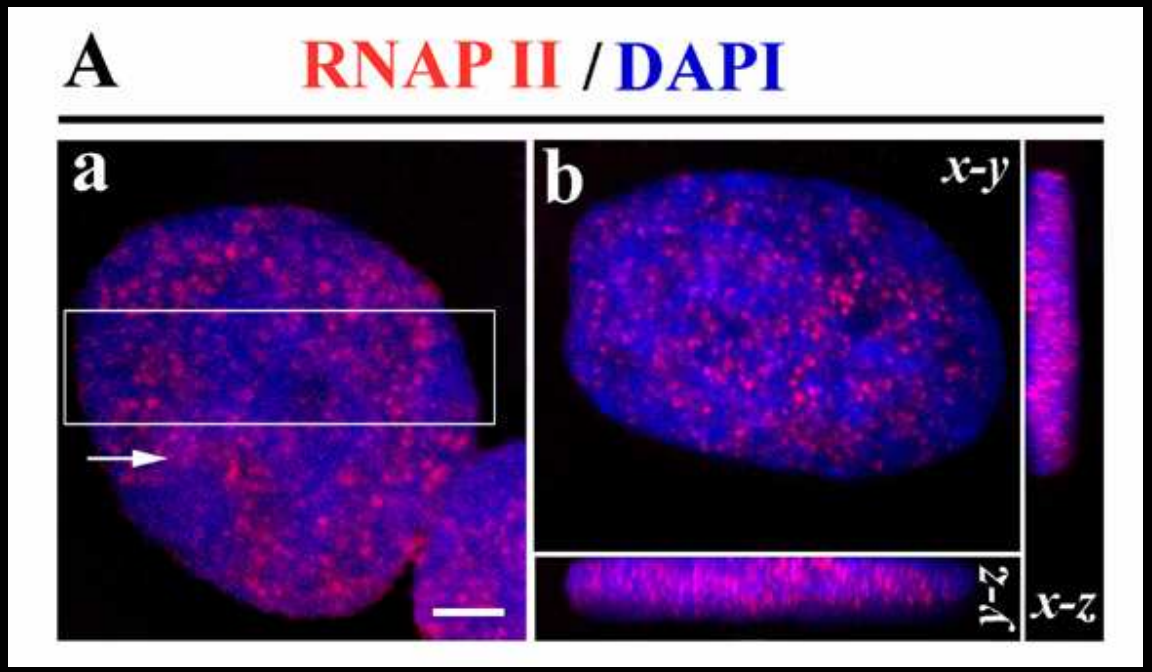
Alternative splicing is a form of epigenetic mechanism that enables a single gene to give rise to multiple, differentially spliced versions of a protein, increasing complexity without a change in the genome.



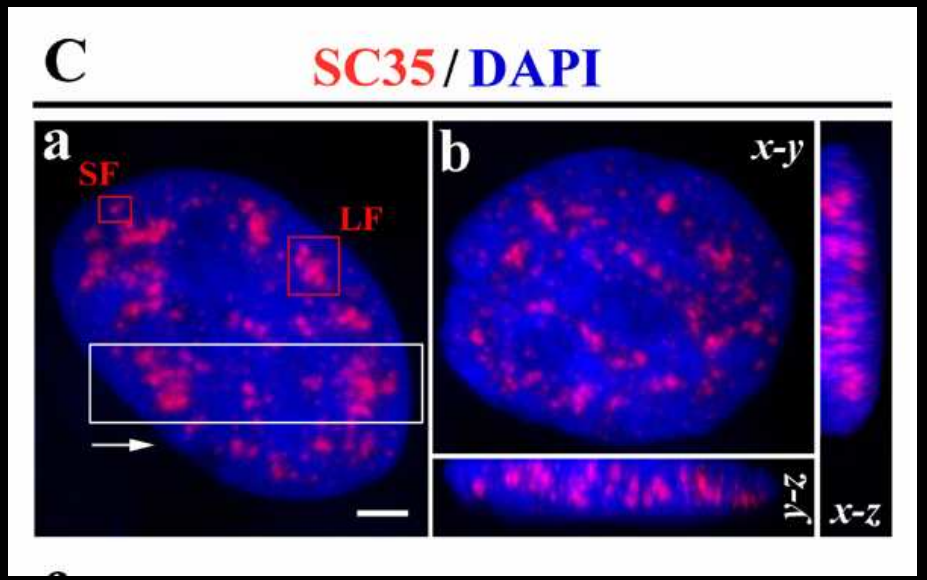
Transcription factories

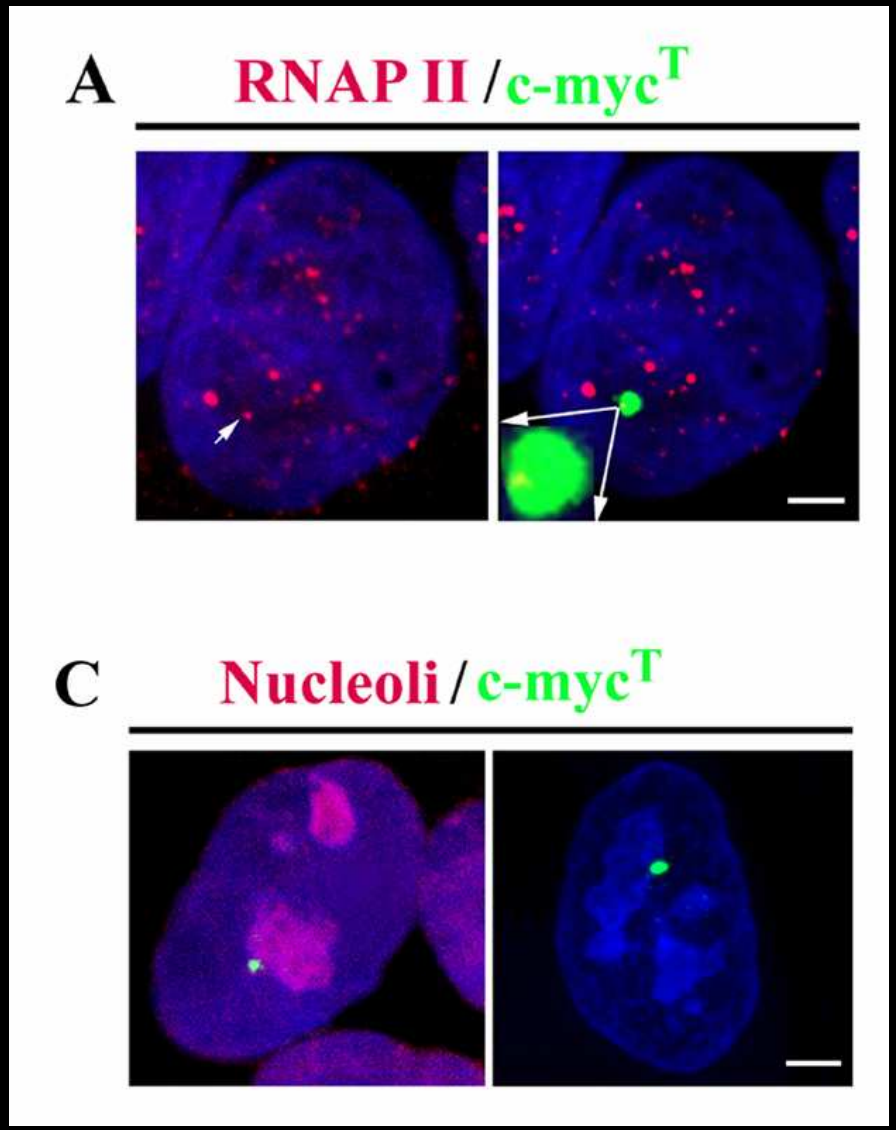


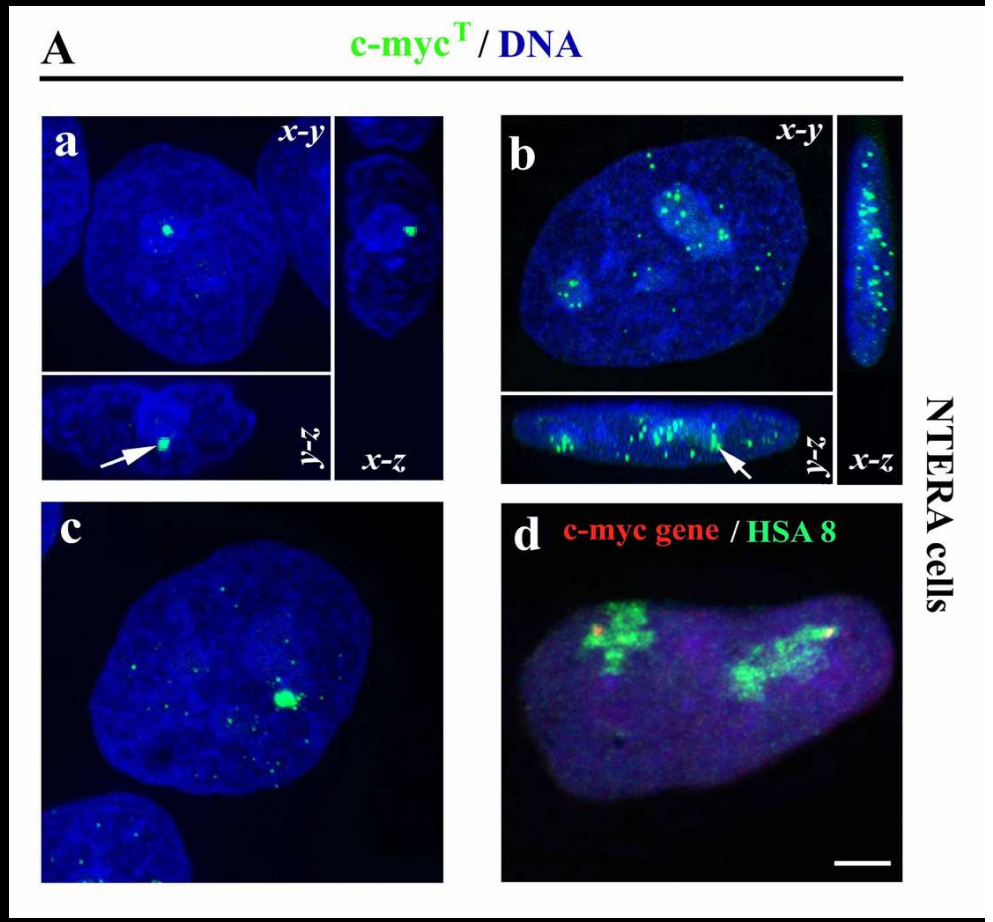
Cis acting elements: Enhancers, LCR
Trans acting elements: proteins, Ikoros, Helios, HP1 proteins



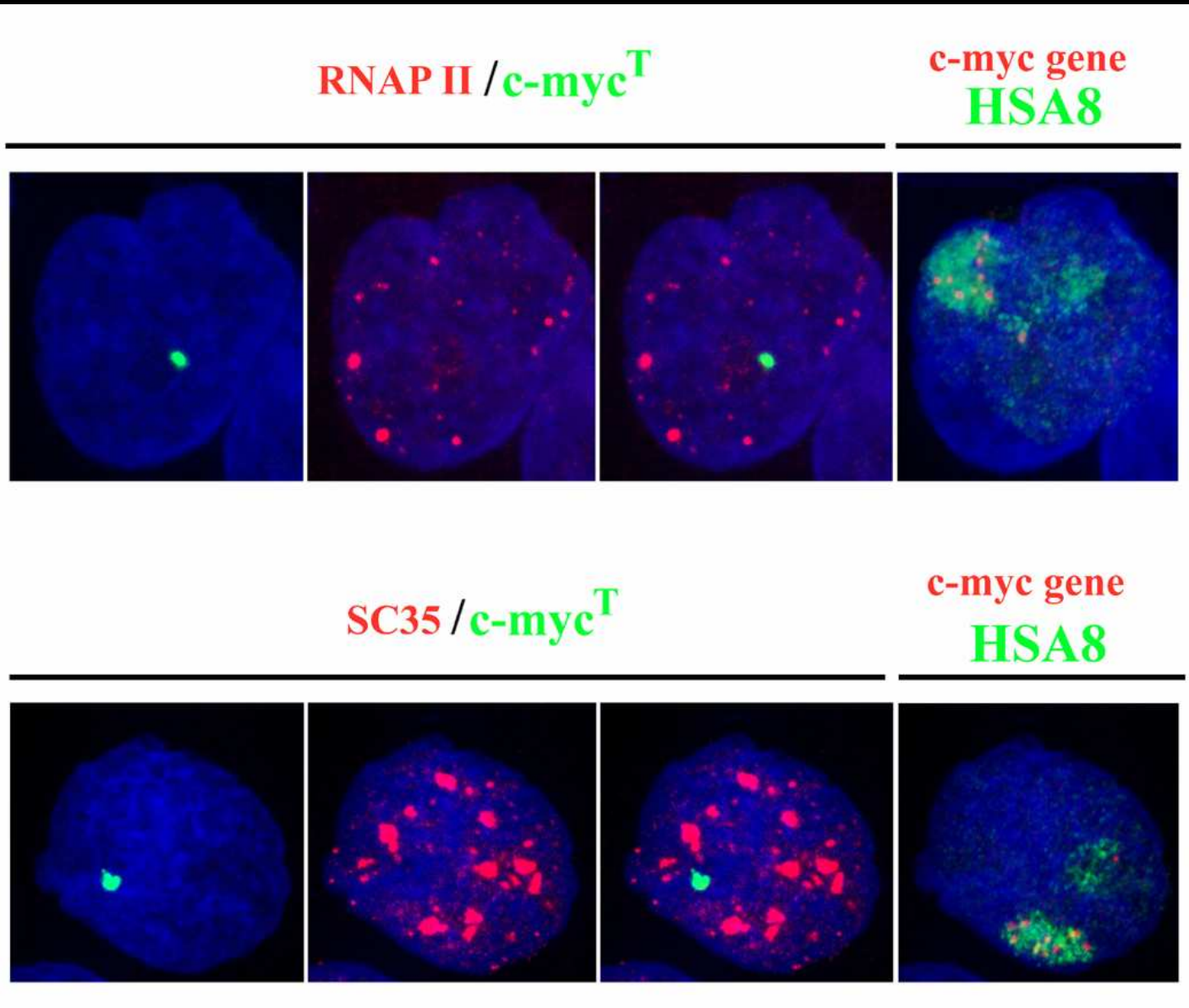
Faktory sestřihu jsou v SC-35 doménách, dále snRNP U1-U6 jsou součástí faktoru sestřihu SF2/ASF

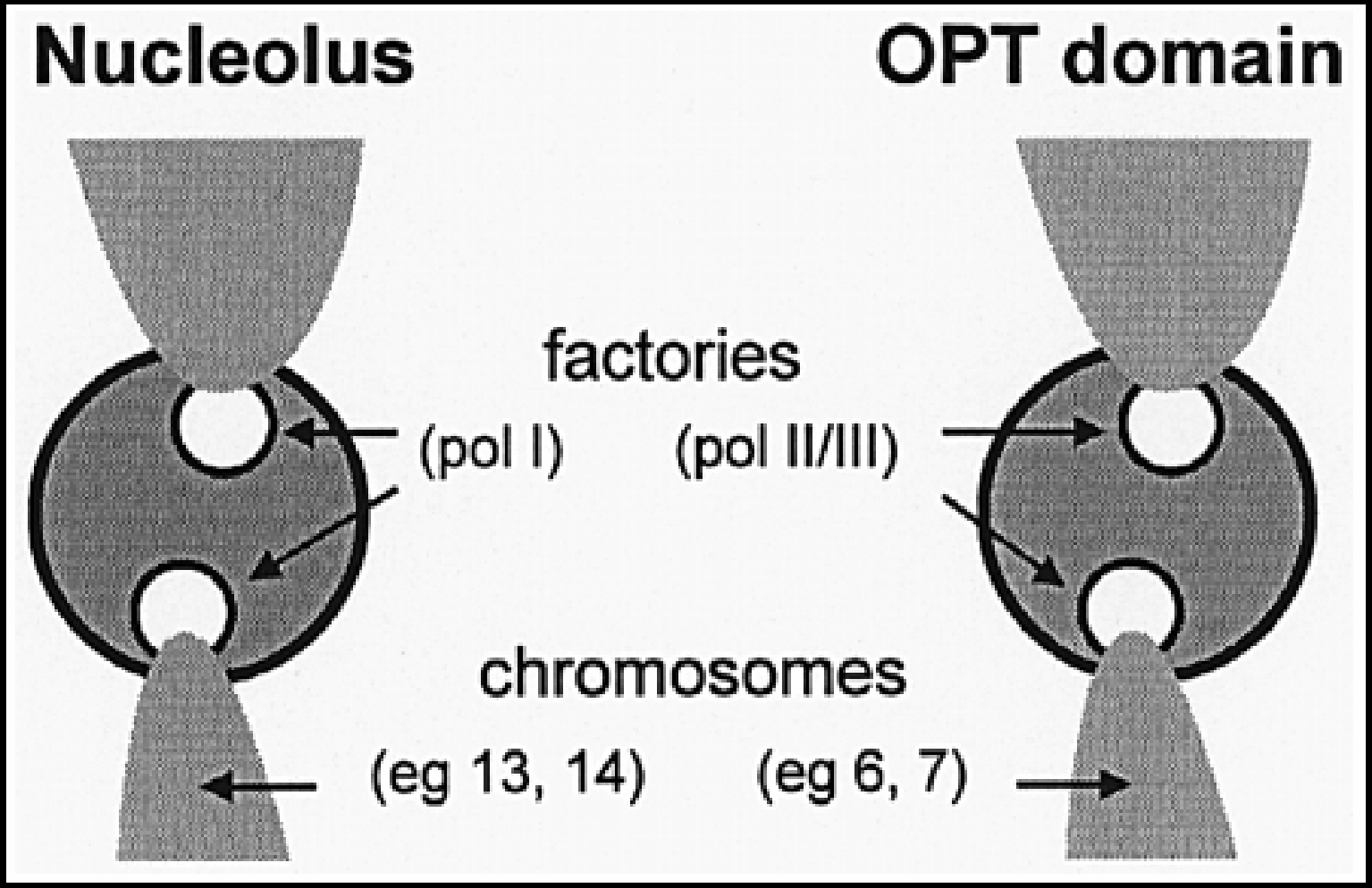




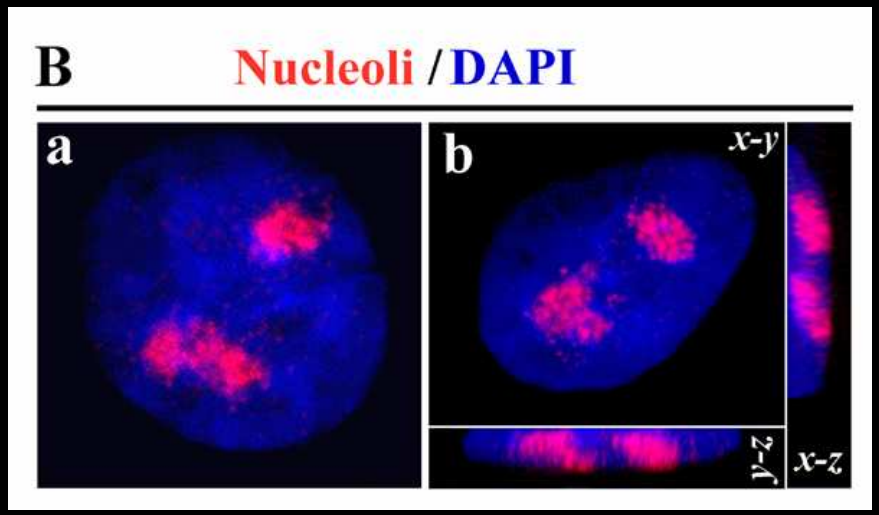


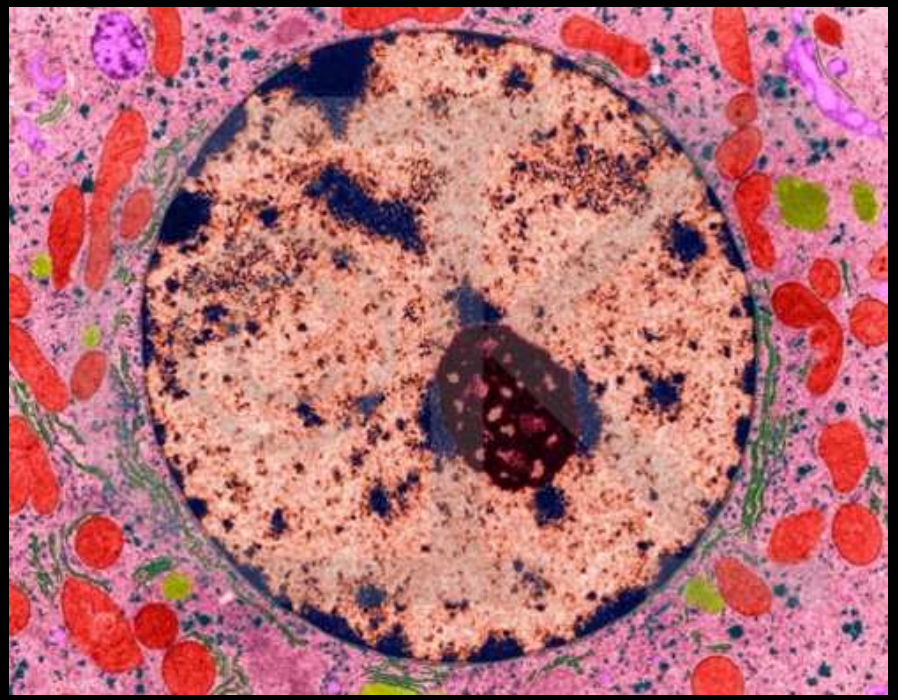
Note: Interleukin-1beta pre-mRNA splicing proceeds in cytoplasm of enucleated platelets (Denis M. et al., 2005).

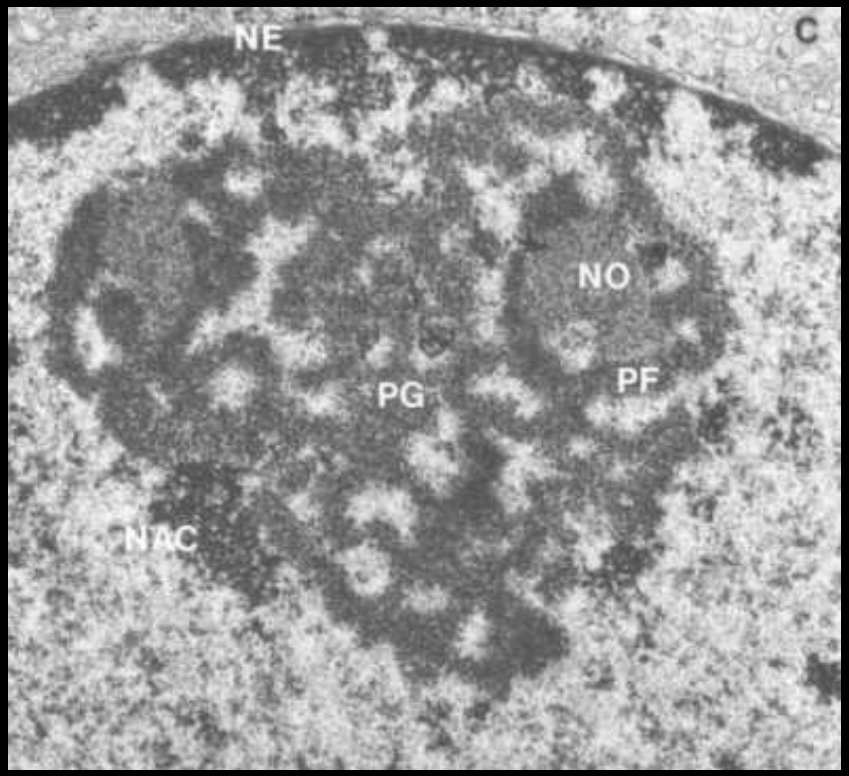

RNAP II / c-myc^T
c-myc gene
HSA8
SC35 / c-myc^T
c-myc gene
HSA8

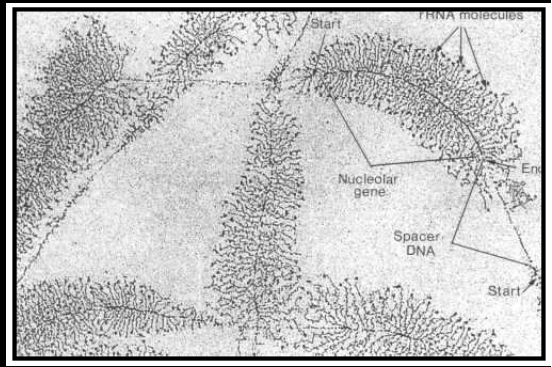

Nucleolus
OPT domain
factories
(pol I)
(pol II/III)
chromosomes
(eg 13, 14)
(eg 6, 7)

Nucleolus









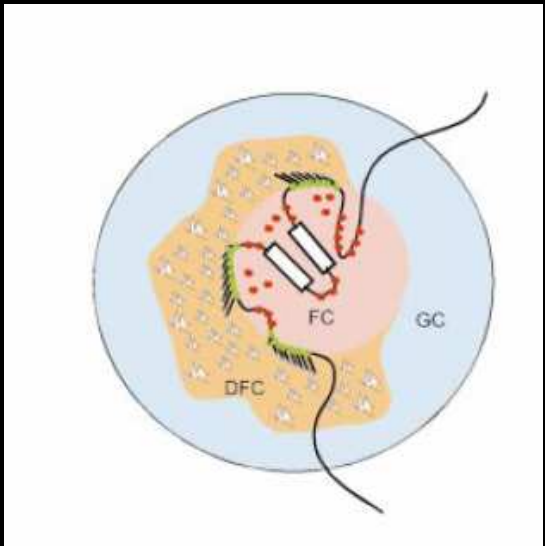
NOR

400 (540) rDNA genů

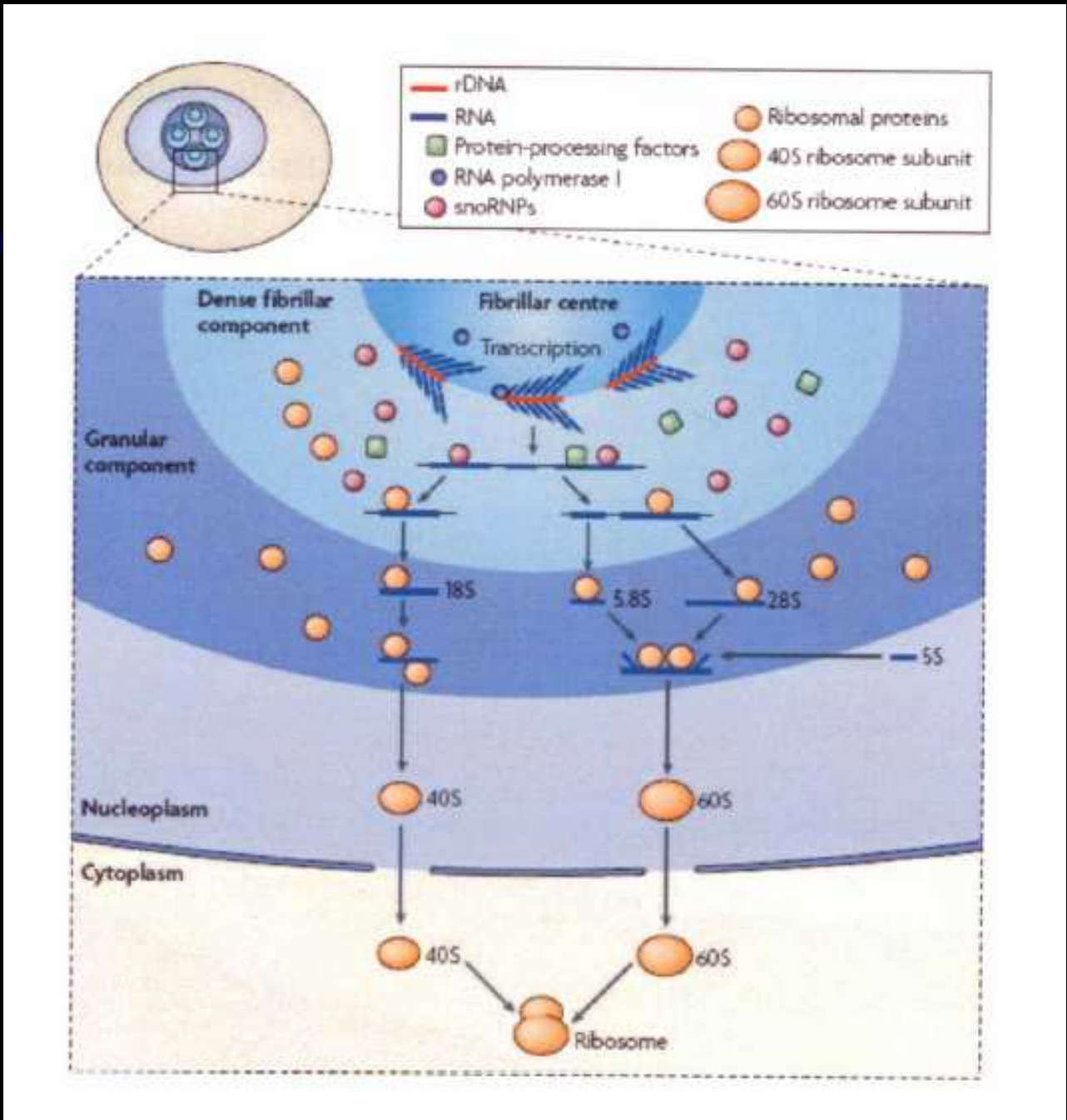
FIBRILÁRNÍ CENTRUM (FC):
zodpovídá za změny v buněčné aktivitě

DENSE FIBRILAR COMPONENT (DFC):
místo syntézy ribozomálních podjednotek

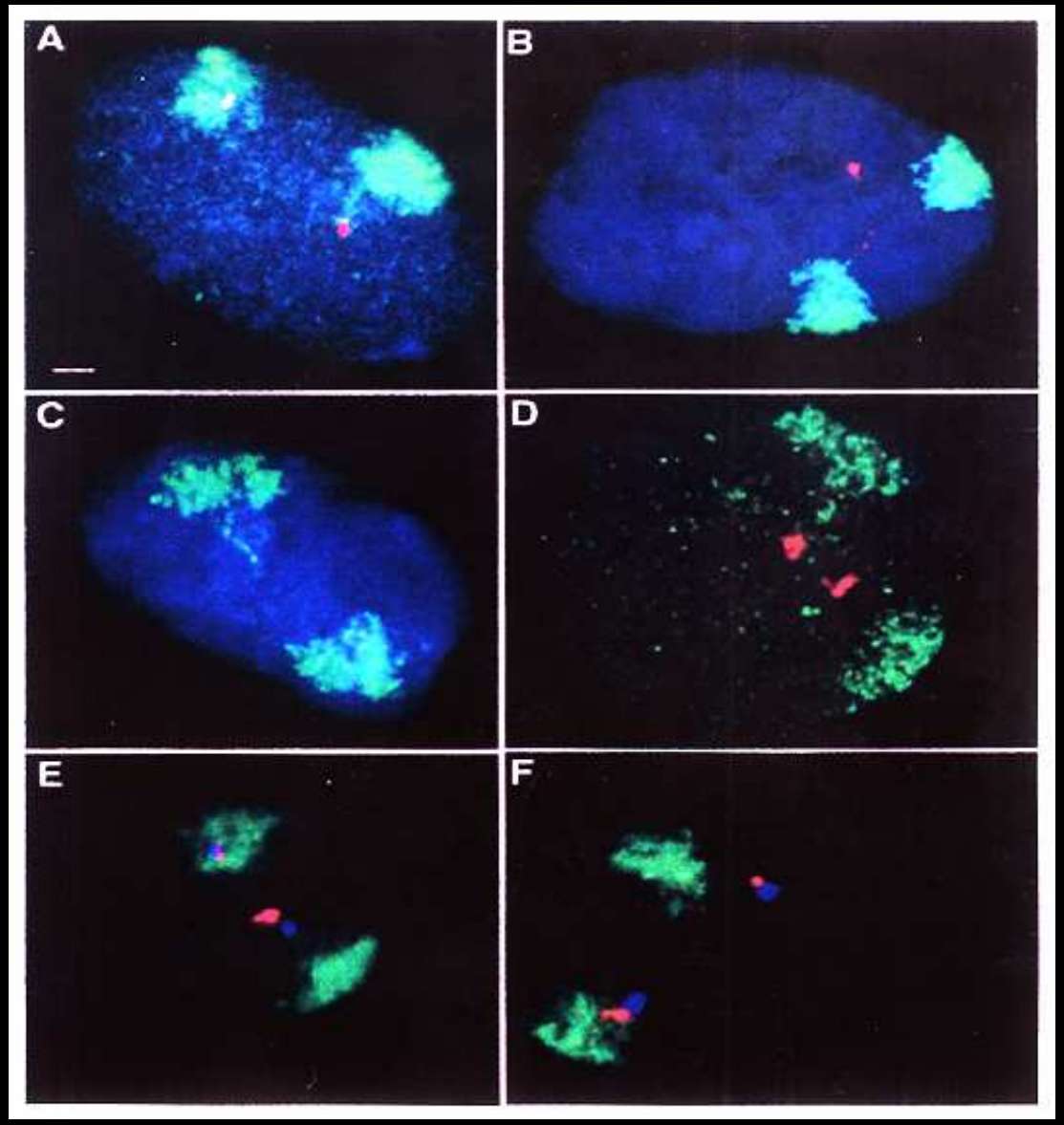
GRANULAR COMPONENTS:
ukotvuje DFC a FC



Tvorba ribozomů je komplexní proces zahrnující transkripci 45S prekurzorické rRNA, její vyzrávání, modifikaci a asociaci s ribozomálními proteiny a 5S rRNA, která se syntetizuje mimo jadérko. Vyzrávání rRNA probíhá v procesomu, který obsahuje mnoho komplexů a snRNA

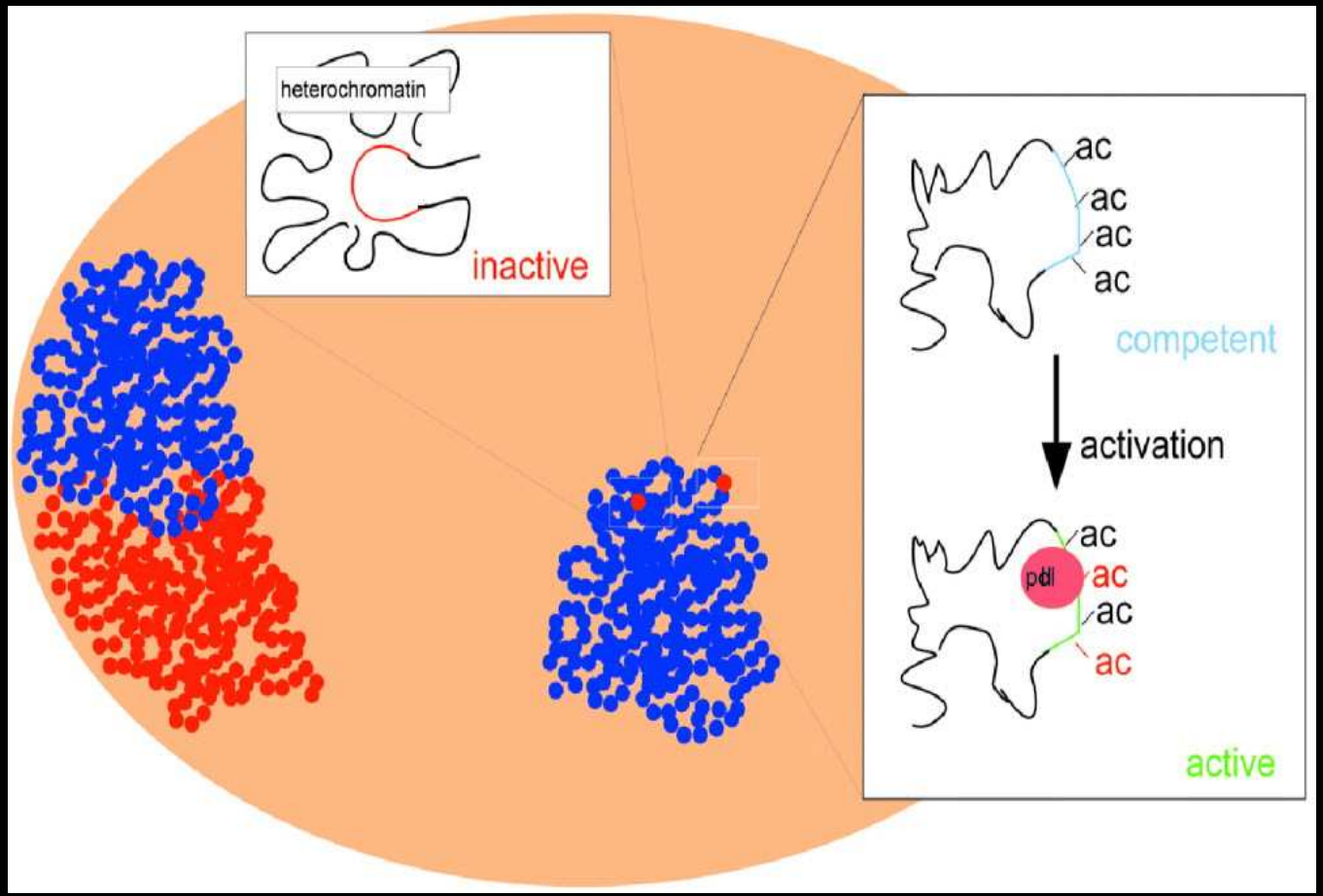

rDNA
RNA
Protein-processing factors
RNA polymerase I
snoRNPs
Ribosomal proteins
40S ribosome subunit
60S ribosome subunit
Dense fibrillar component
Fibrillar centre
Transcription
Granular component
18S
5.8S
28S
5S
Nucleoplasm
40S
60S
Cytoplasm
40S
60S
Ribosome

MHC on HSA 6



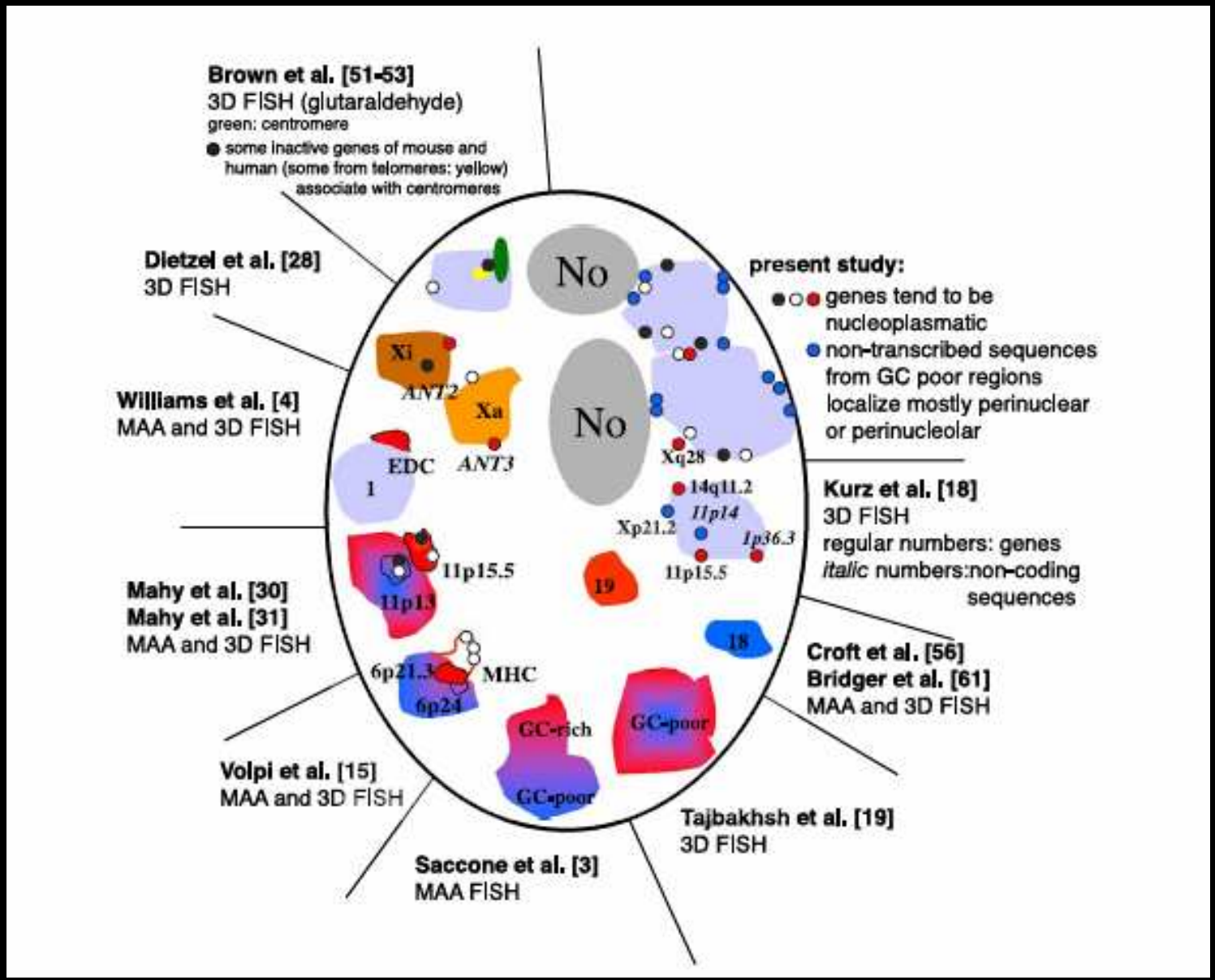
Volpi et al., 2000

Active / inactive chromatin

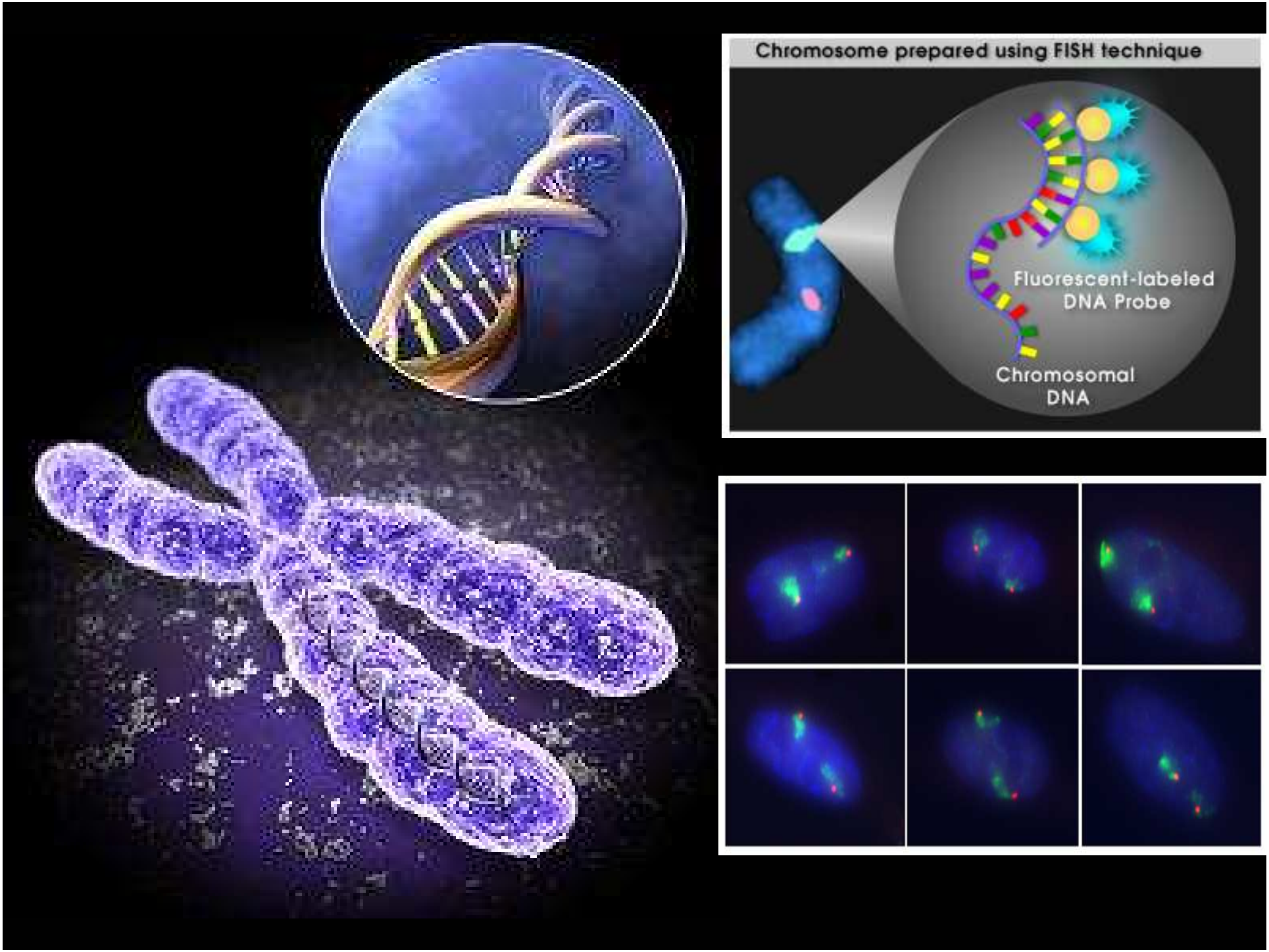


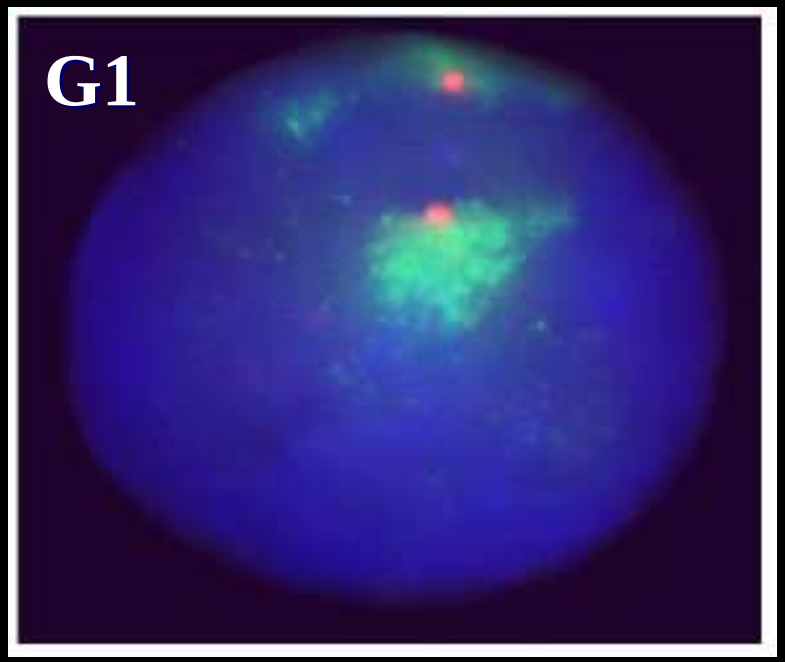
T. Cremer group, Munich

IMTERMINGLING

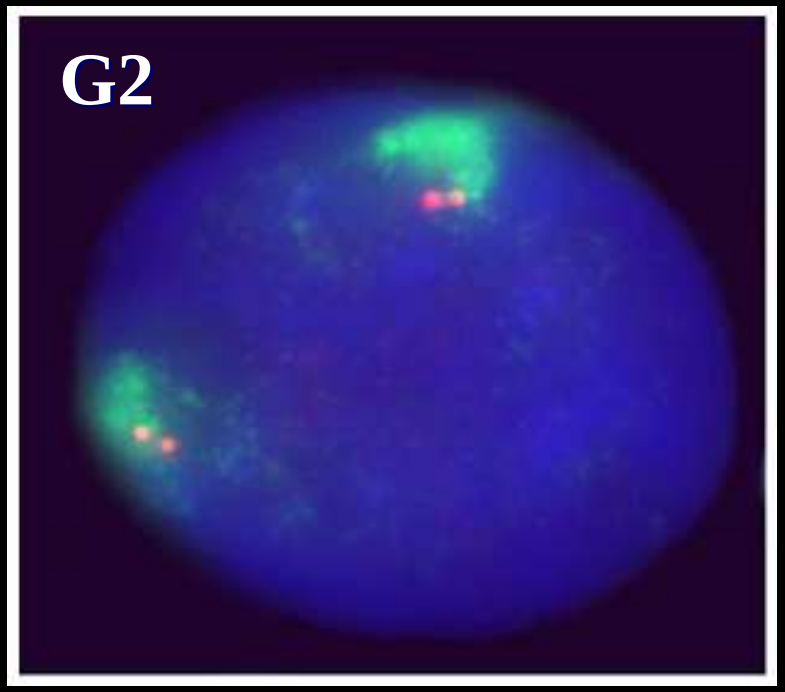


Scheuermann et al., Exp. Cell Res. (2004)


Chromosome prepared using FISH technique
Fluorescent-labeled DNA Probe
Chromosomal DNA

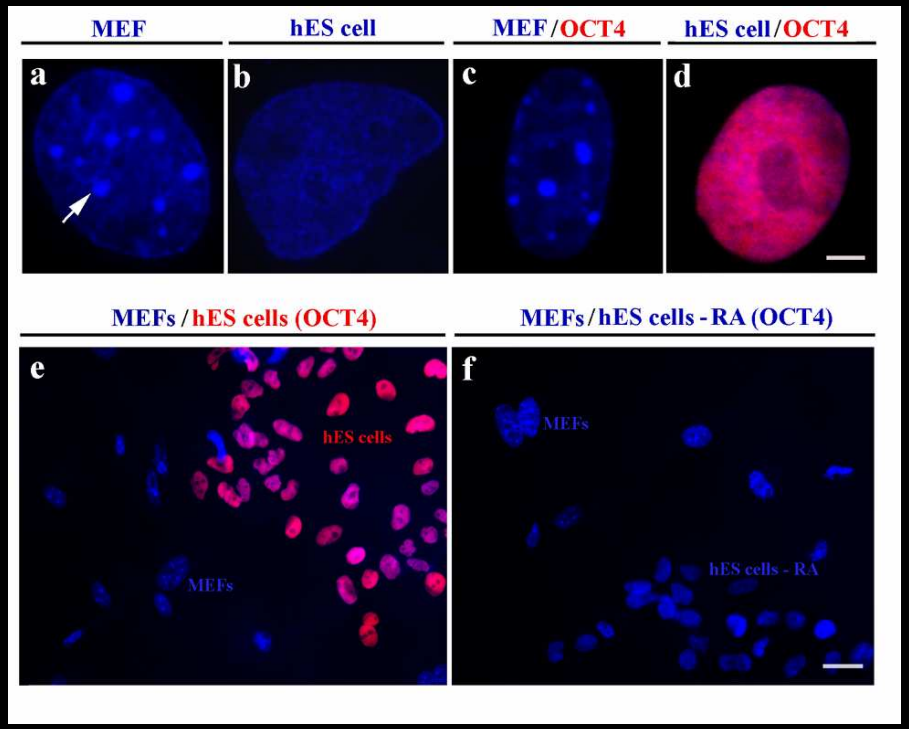


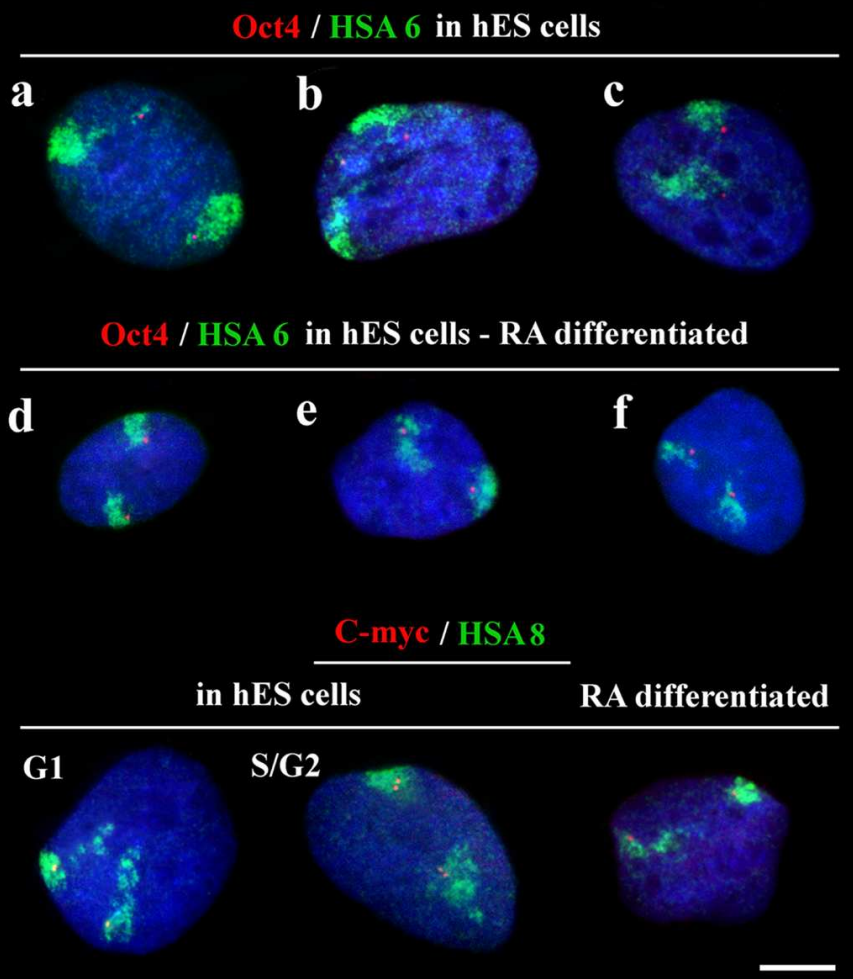
Rb1 gene



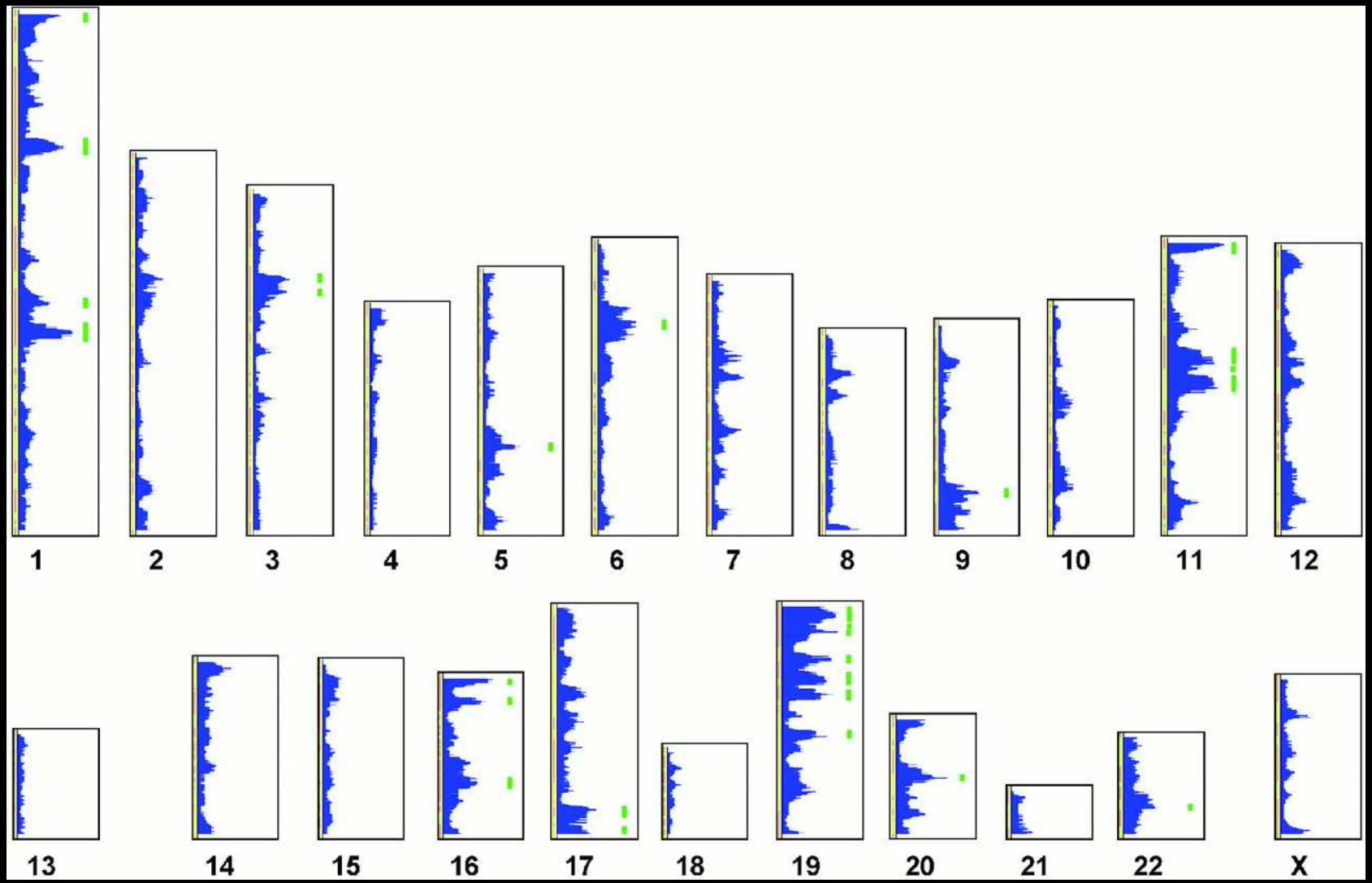
Bártová et al., 2002

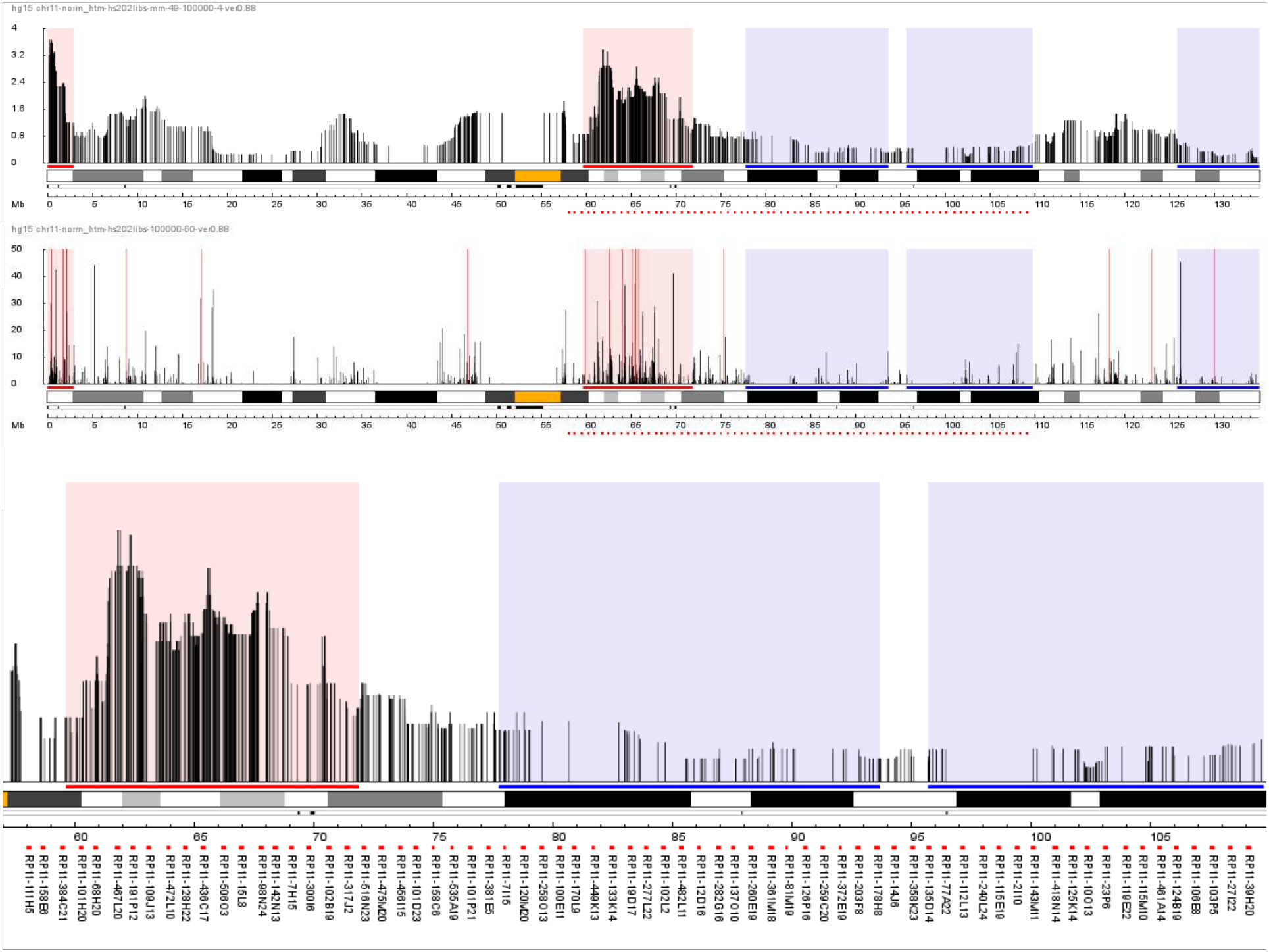
Genes in human embryonic stem cells



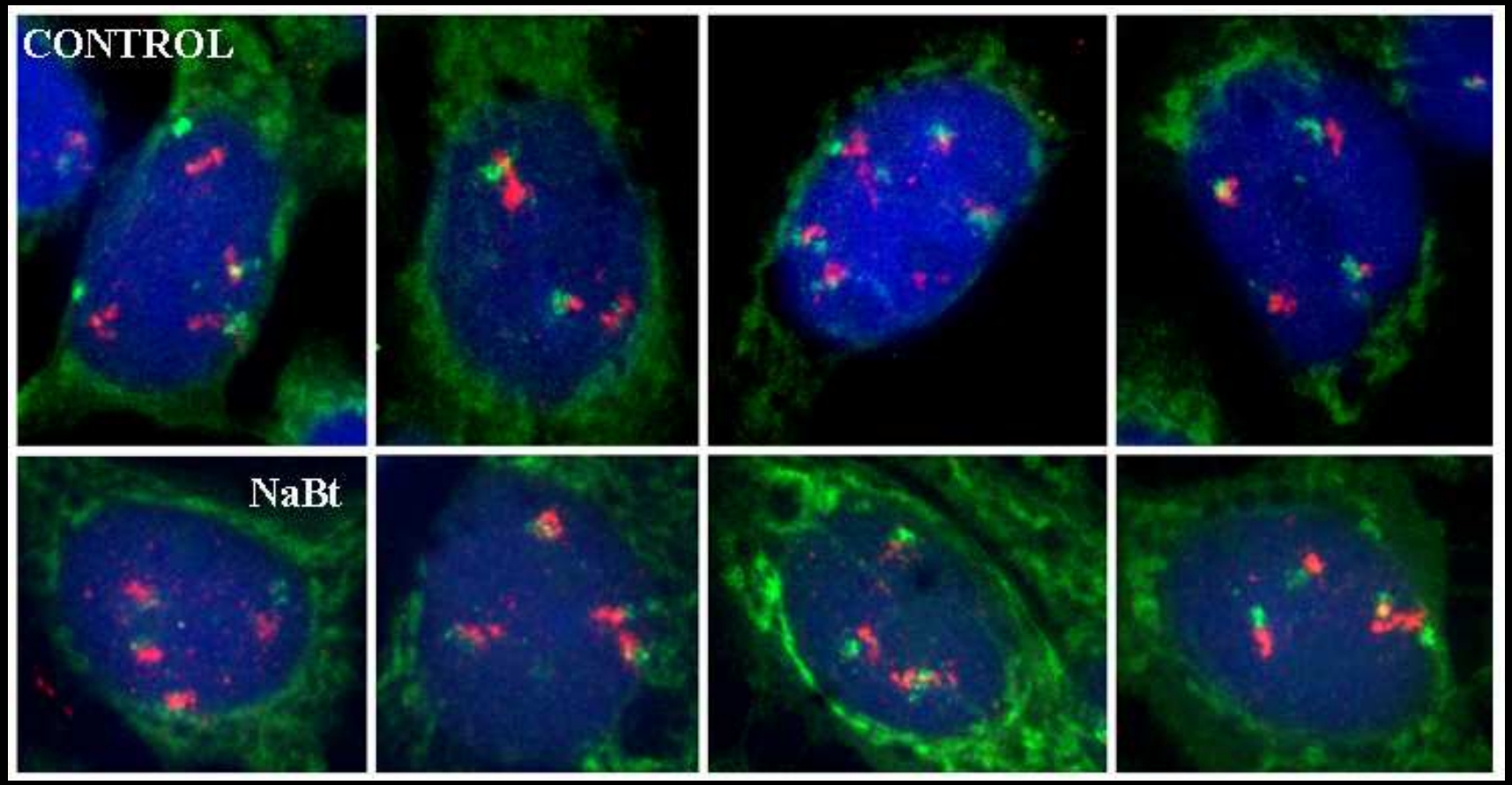


Transcriptome map (Caron et al., 2001)

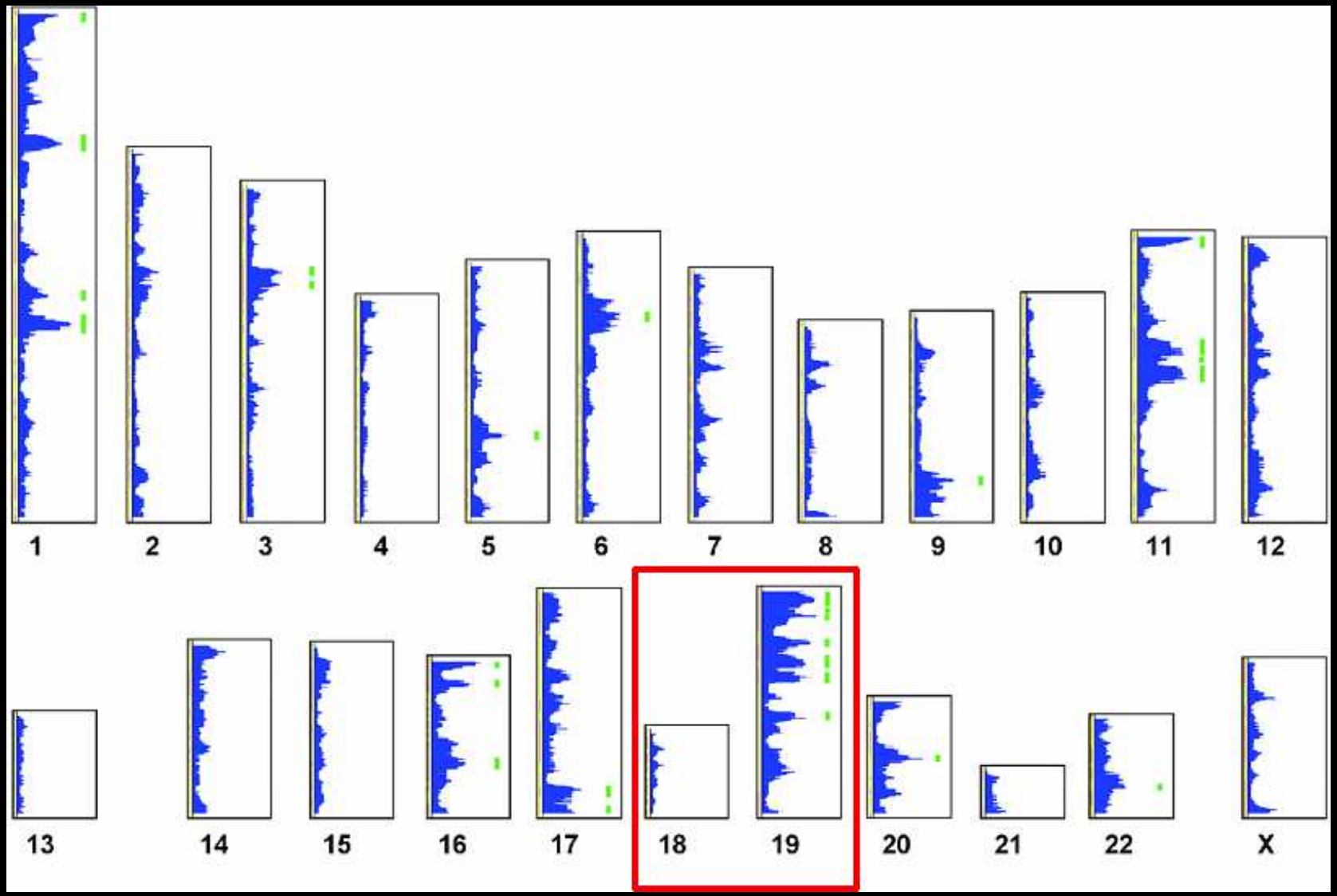



hg15 chr11-norm_htm-hs202libs-mm-49-100000-4-ver0.88
4
3.2
2.4
1.6
0.8
0
Mb
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130
hg15 chr11-norm_htm-hs202libs-100000-50-ver0.88
50
40
30
20
10
0
Mb
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130
60 65 70 75 80 85 90 95 100 105
RP11-111H5
RP11-158E8
RP11-384C21
RP11-101H20
RP11-88H20
RP11-467L20
RP11-191P12
RP11-109J13
RP11-472L10
RP11-128H22
RP11-436C17
RP11-506O3
RP11-15L8
RP11-98N24
RP11-142N13
RP11-7H15
RP11-300I6
RP11-102B19
RP11-317J2
RP11-516N23
RP11-475M20
RP11-466I15
RP11-1010D23
RP11-158C8
RP11-535A19
RP11-101P21
RP11-381E5
RP11-7I15
RP11-120M20
RP11-258O13
RP11-100E11
RP11-170L9
RP11-448K13
RP11-133K14
RP11-19D17
RP11-277L22
RP11-102L2
RP11-482L11
RP11-12D16
RP11-282G16
RP11-137O10
RP11-260E19
RP11-381M18
RP11-81M19
RP11-128P16
RP11-259C20
RP11-372E19
RP11-203F8
RP11-178H8
RP11-14J6
RP11-358K23
RP11-135D14
RP11-77A22
RP11-112L13
RP11-240L24
RP11-115E19
RP11-2I10
RP11-143M11
RP11-418N14
RP11-125K14
RP11-10O13
RP11-23P6
RP11-119E22
RP11-115M10
RP11-461A14
RP11-124B19
RP11-106E8
RP11-103P5
RP11-27I22
RP11-39H20

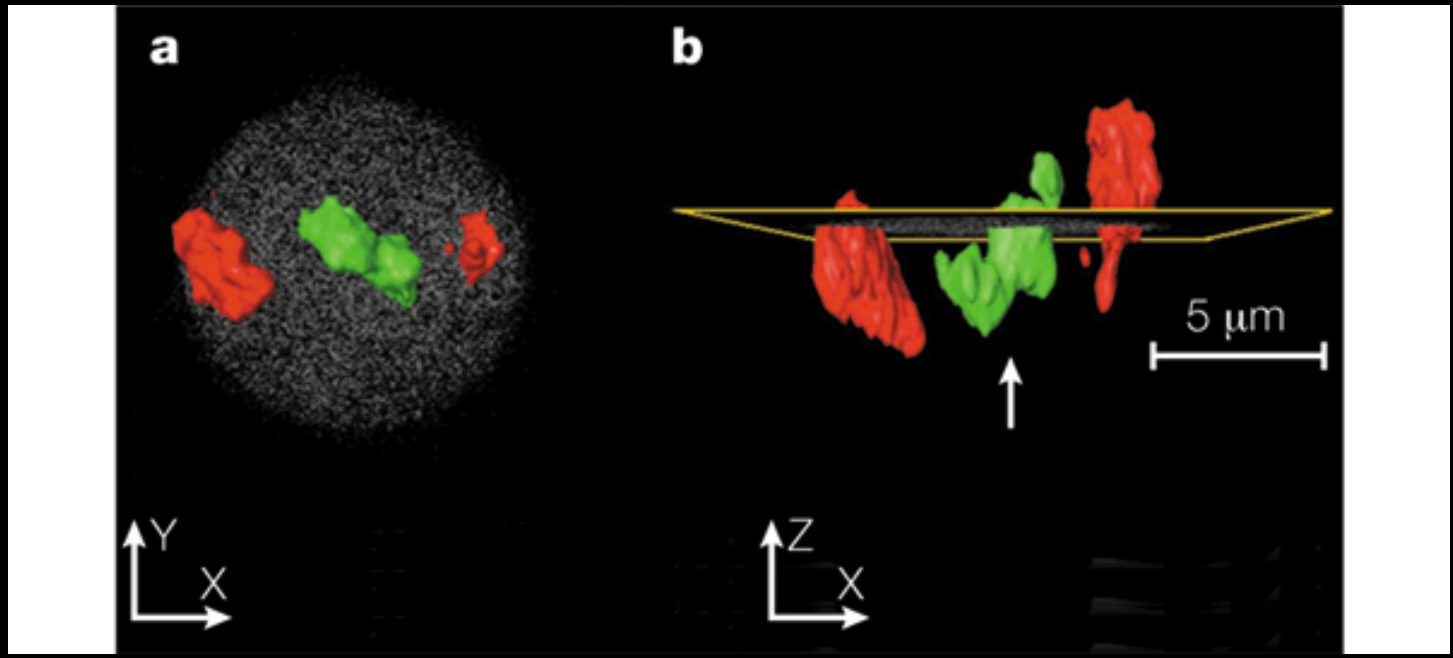
Enterocytic cell differentiation and RIDGE/ANTI-RIDGE



Transcriptome map (Caron et al., 2001)



HSA 18 and 19 (positioning x gene density)



T. Cremer group, Munich

Center of nucleus-to-gene distances

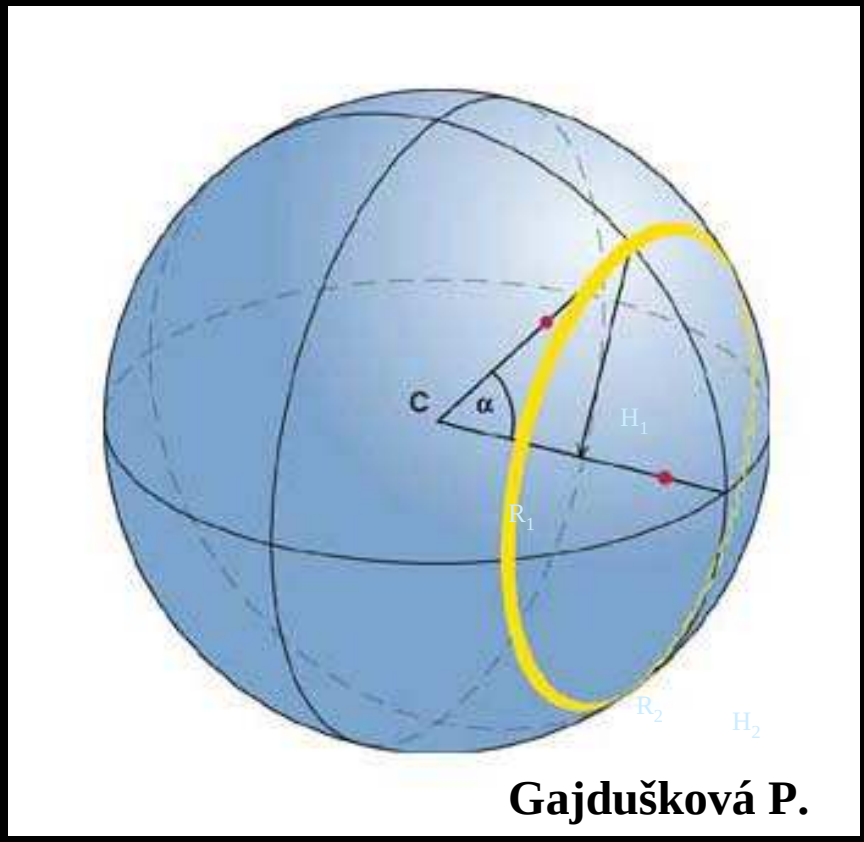
$$CS = \frac{\overline{CR_i}}{\overline{CH_i}} * 100$$

Gene-to-gene distances

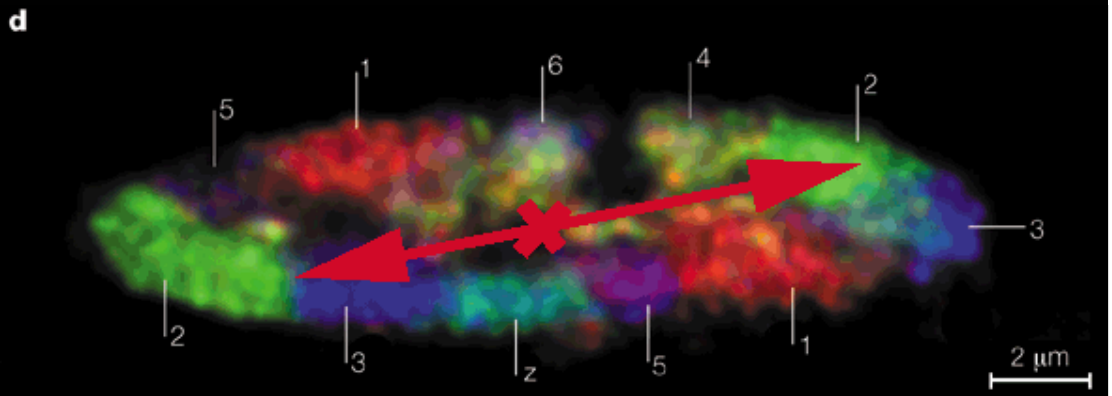
$$SS = \frac{\overline{R_1R_2}}{(\overline{CH_1} + \overline{CH_2})/2} * 100$$

Gene-center of nucleus-gene angles

$$\cos(\alpha) = \frac{\overline{CR_1} * \overline{CR_2}}{|\overline{CR_1}| * |\overline{CR_2}|}$$



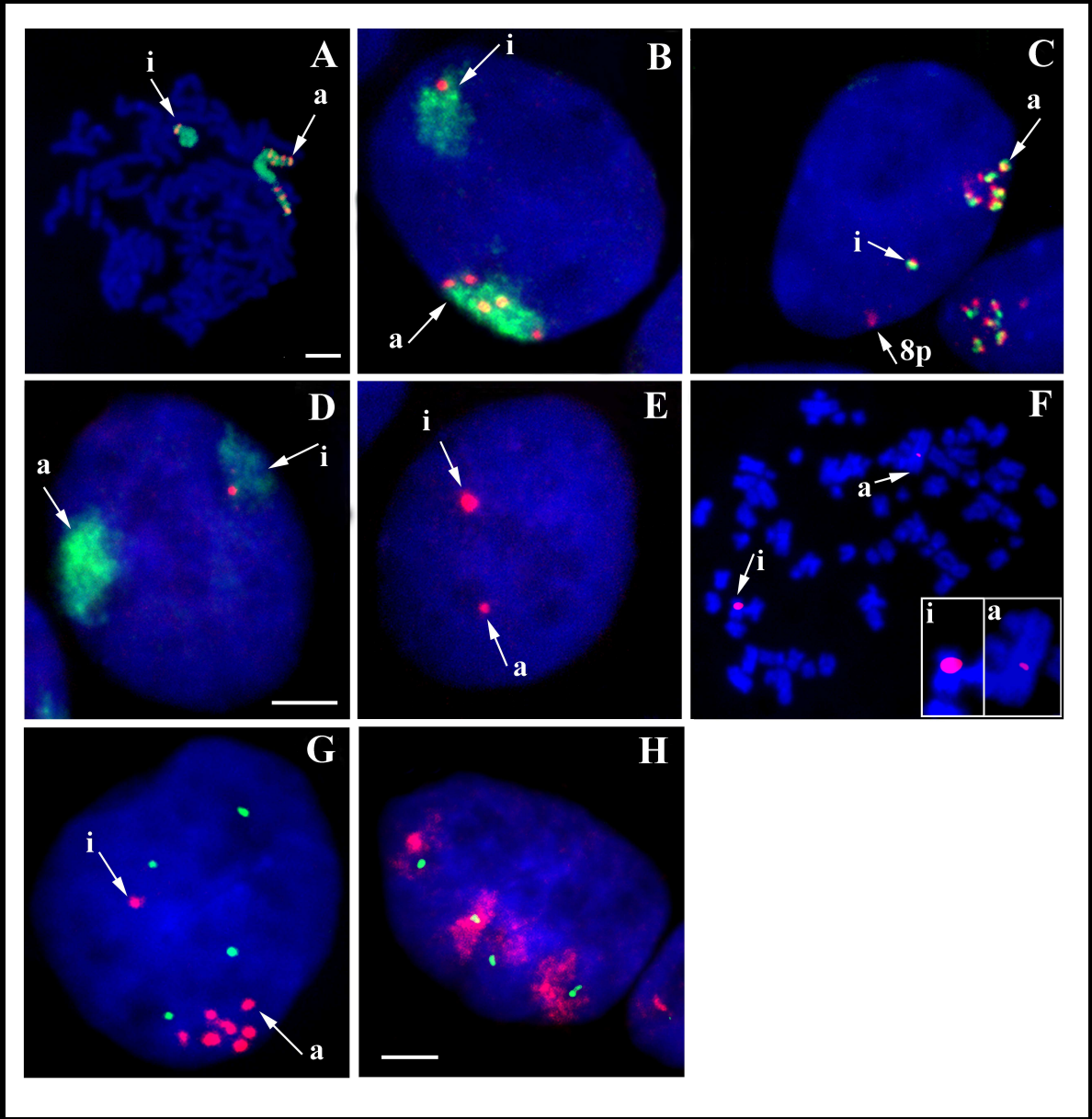
Gajdušková P.

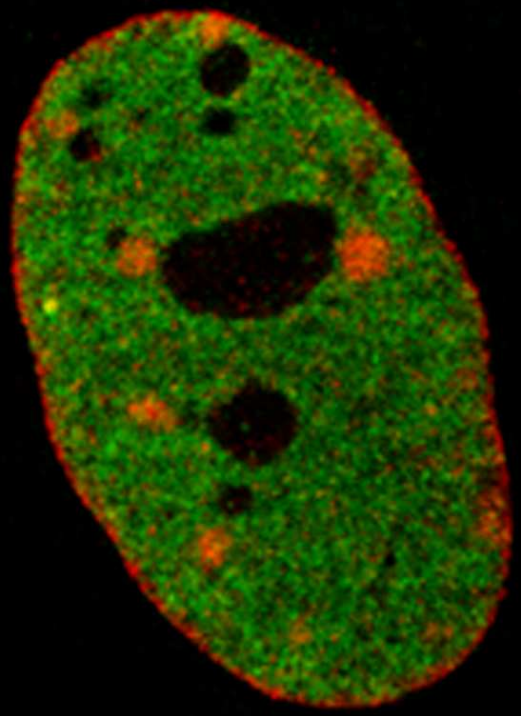


T. Cremer group

HSA 8 and related structures

Harničarová et al., 2005





ZÁVĚR

Struktura chromatinu hraje
důležitou úlohu v regulaci
jaderných procesů jako je replikace,
transkripce, sestřih
a DNA reparace.