

## *The Nucleus and its Functional Domains: How can I identify the functional regions of a nucleus?*

I mentioned in lecture that I would provide the legend to the nuclear domain summary figure that I used in class. Here's a smaller version of the figure to refer to:

Starting with the region labeled A, here is the figure legend:

A: Chromosomes occupy distinct territories within the nucleus, and extend regions of euchromatin out into the interchromosomal territories for transcription because that is where the transcriptional machinery is located. The red regions within the chromatin loop in the inset indicate transcriptionally active genes.

B: Not only does the chromosome occupy its own space, but the arms of the chromosome occupy their own territories and do not overlap each other. The green and red indicate chromosome arms, while the gold indicates the centromeric region of that chromosome.

C: The darker the color, the more compact the chromatin. So the lightest yellow indicates euchromatin, found predominantly at the periphery of the chromosomal territory where transcription and/or replication are occurring, while the deepest orange/red indicates heterochromatin, buried in the interior of the territory.

D: Foci of replication. Green color represents regions replicating early during S-phase, when the chromatin is already more unwound (and represents regions of high gene density). Red regions represent areas of low gene density, tightly bound into heterochromatin, which will not be replicated until late in S-phase.

E: Regions of chromatin with transcriptionally active genes (white dots) will be on the periphery of a chromosomal territory, while transcriptionally inactive (or silent) genes (black circles) will be in the interior of a territory. Gold circles represent "Speckles" or clusters of transcription, replication, or repair machinery.

F: Speckles are recruited to regions of activity from much larger collections of machinery.

N: The nucleolus.

*Unique solution ID: #1177*

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*Last update: 2007-09-04 14:50*