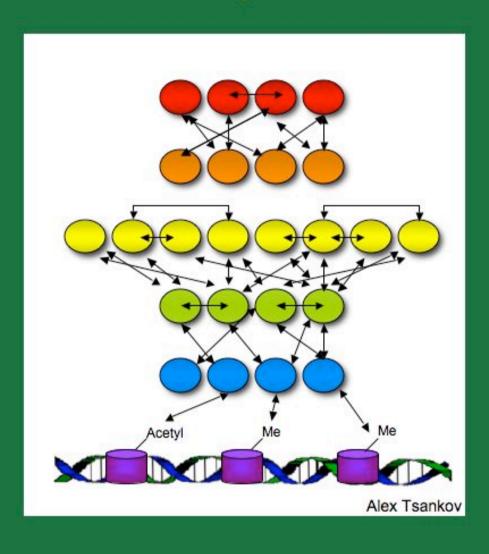


The Transcriptional Network is Complicated



Export factors

hnRNPs, splicing, etc.

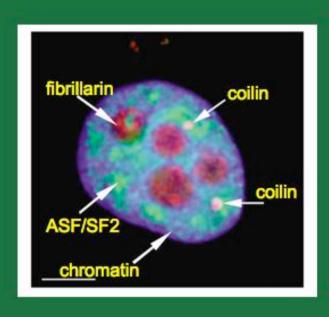
Transcription factors

Nucleosome remodelers

Histone modifiers

DNA, histones

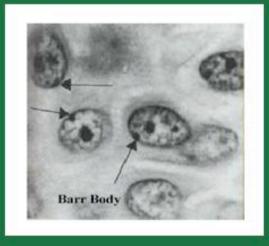
Nuclear Organization

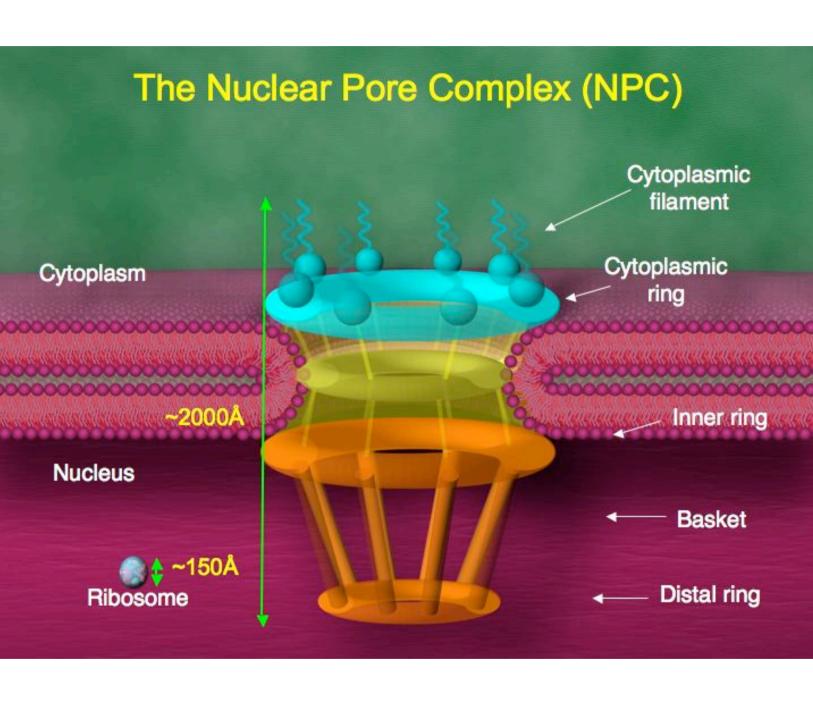


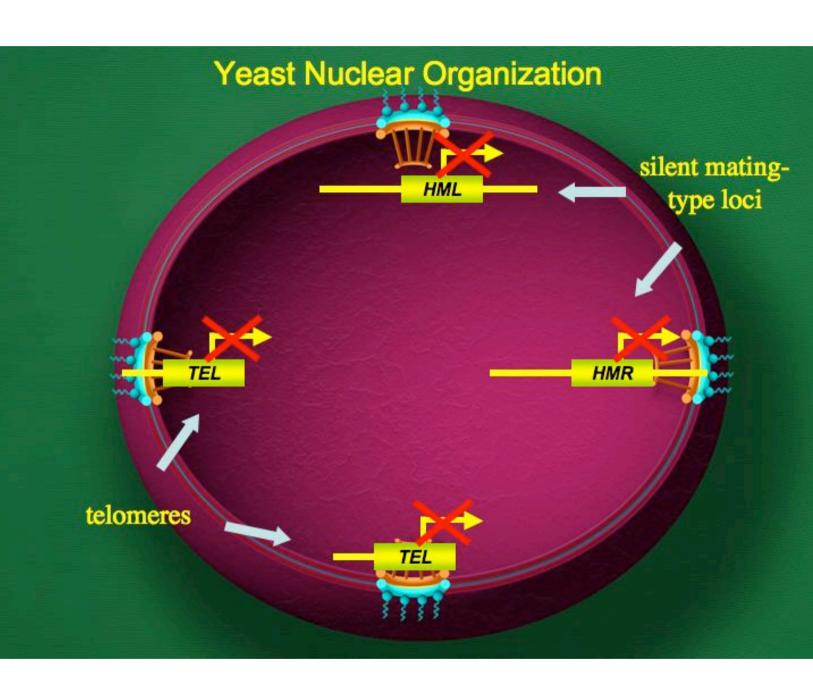
Subnuclear compartments

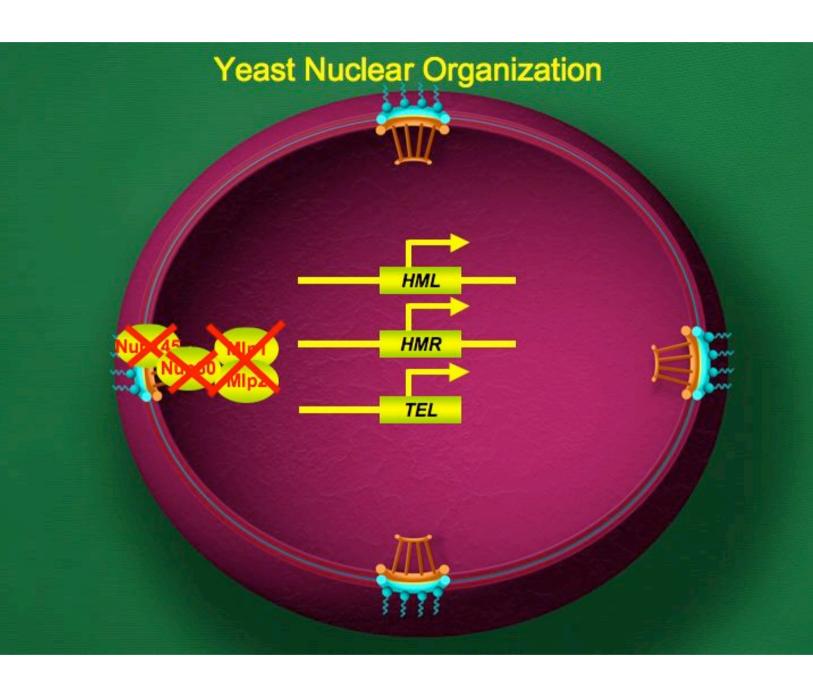
X-inactivation

Barr body at nuclear periphery

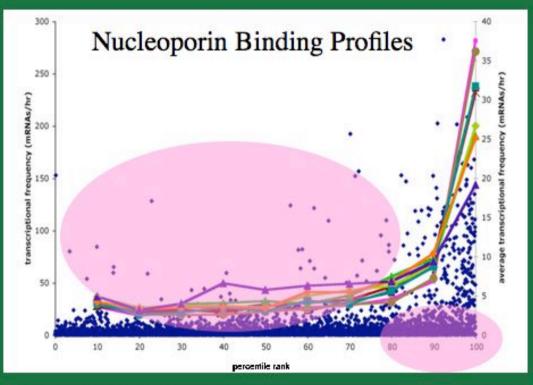


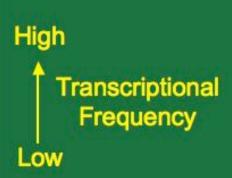






Transcriptional Correlation in Genomic Binding





- Positive binding correlation with transcription activity
- Not all highly expressed genes are bound

 Lowly expressed genes are bound as well

Clustering of Datasets

Mip2 Mip2

Nup60

Nic96 Xpo1 Nsp1

Nup2

Kap95 Nup145c

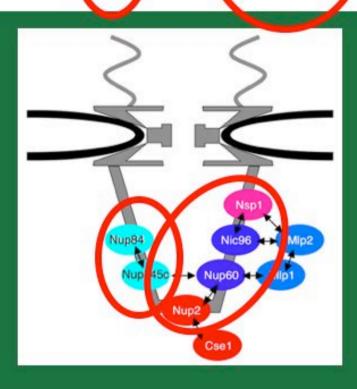
Nup84

Prp20 Nup100

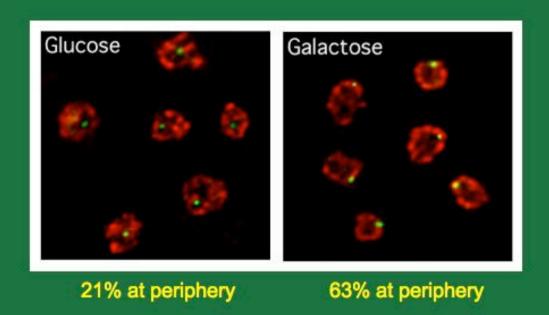
Nup116

PCA

Biochemical and functional subcomplexes



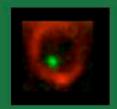
GAL Locus Peripheral Localization



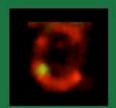
The GAL locus relocates to the nuclear periphery upon transcriptional induction

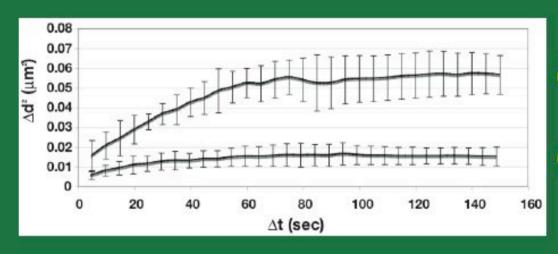
In Vivo Dynamics of the GAL Locus

Glucose



Galactose

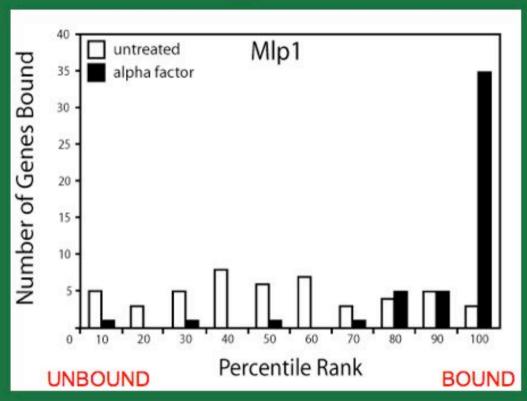




Glucose

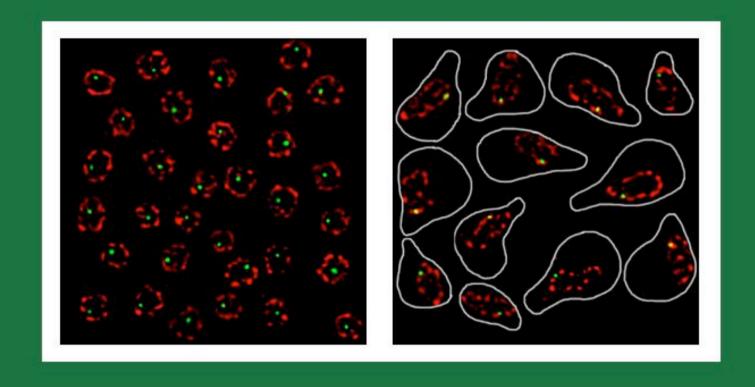
Galactose

Alpha Factor Induces Genome-Wide Reorganization



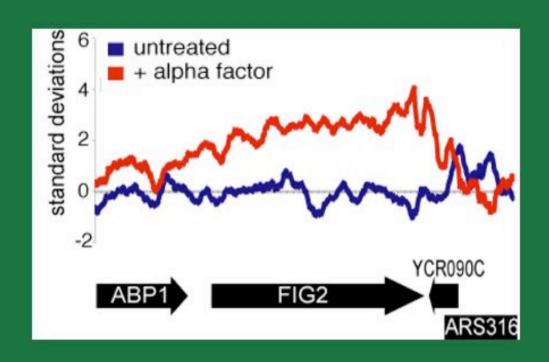
RNA levels of 49 genes are induced > 3-fold

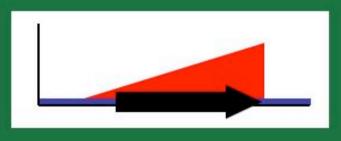
FIG2 Peripheral Localization



Genomic polarization?

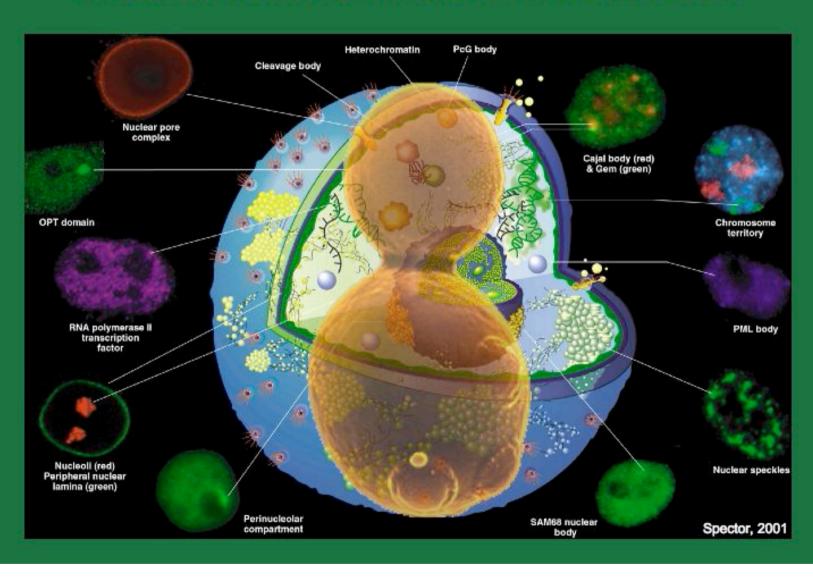
High-Resolution Mapping of NPC Components





3' Binding Bias

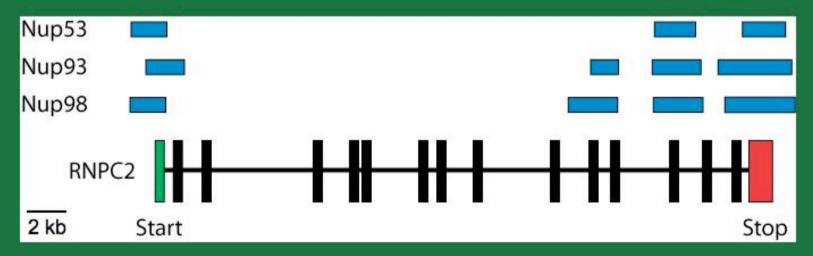
Genomic Association of the NPC in HeLa Cells



NPC-Bound Regions of RNPC2

RNPC2:

- Member of the SR family of alternative splicing factors
- Transcriptionally active in HeLa cells



Conclusions

- Transcriptionally active genes associate with the NPC
- Genomic polarity
- 3'-binding bias

Hypothesis

The nuclear pore complex plays a role in efficient mRNA export and subsequent localization in the cytoplasm.

Acknowledgments

Jason Casolari David Drubin

Oliver Rando Pamela Silver

