

The genome-wide nucleosome positions in procyclic and bloodstream form *Trypanosoma brucei*.

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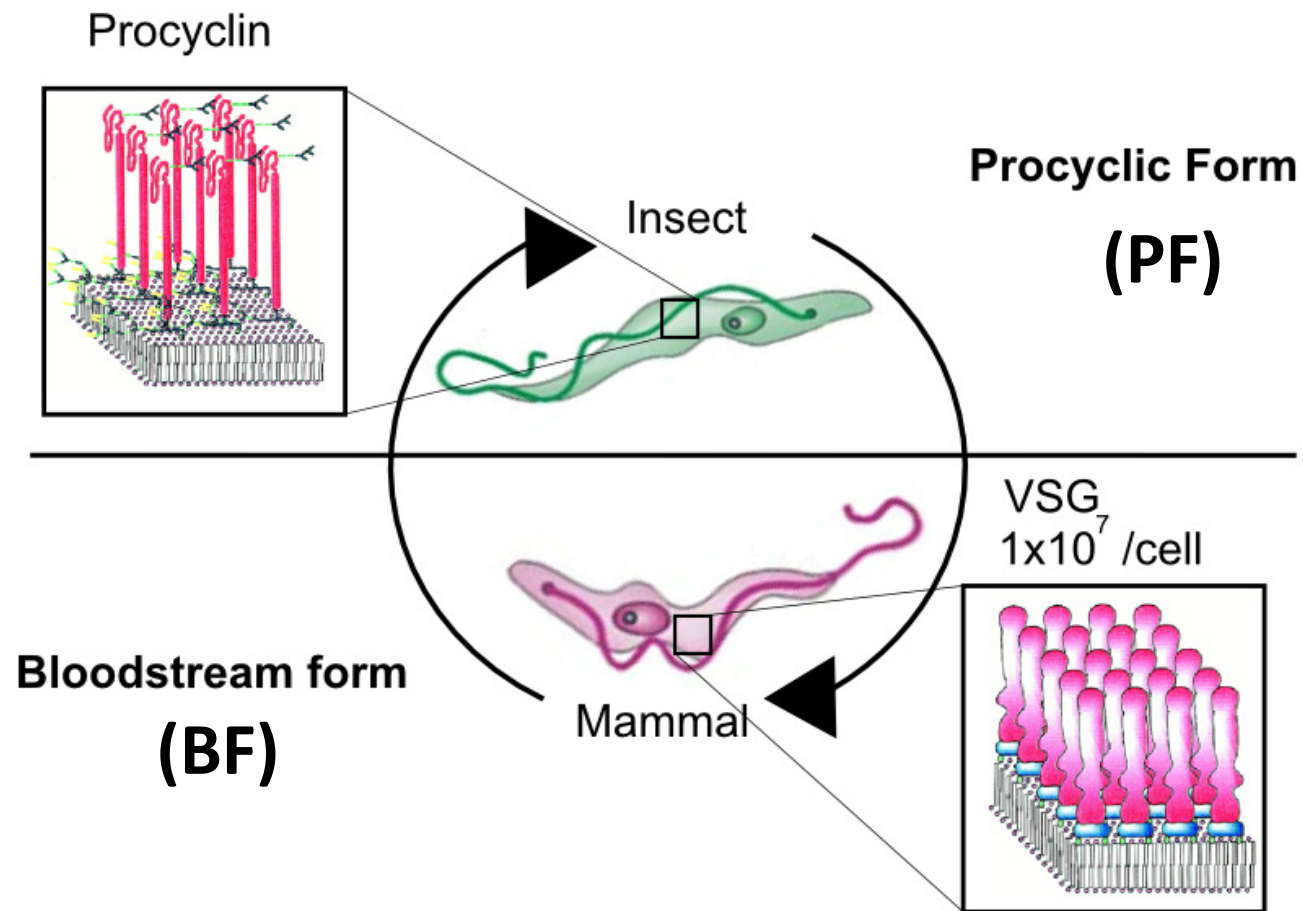
The disease with the highest mortality rate in Africa, untreated, is African trypanosomiasis or sleeping sickness. It kills 100% of those infected. [SIC]

- *Trypanosoma brucei* transmitted by *Glossina spp.*
- 500, 000 people infected
- 70 mil. people at risk, increase to 100 – 140 mil by 2050
- Hemolymphatic phase followed by Neurological phase

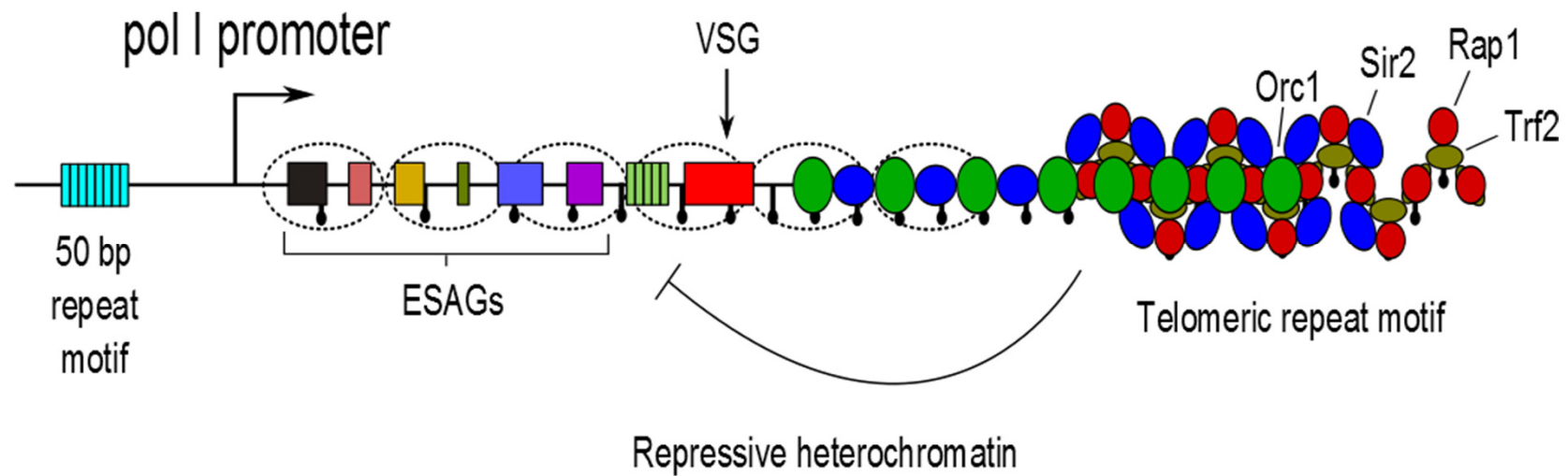


Rodgers *et al.*, 2011, Moore *et al.*, 2011, WHO 2012, Seattle biomed 2014

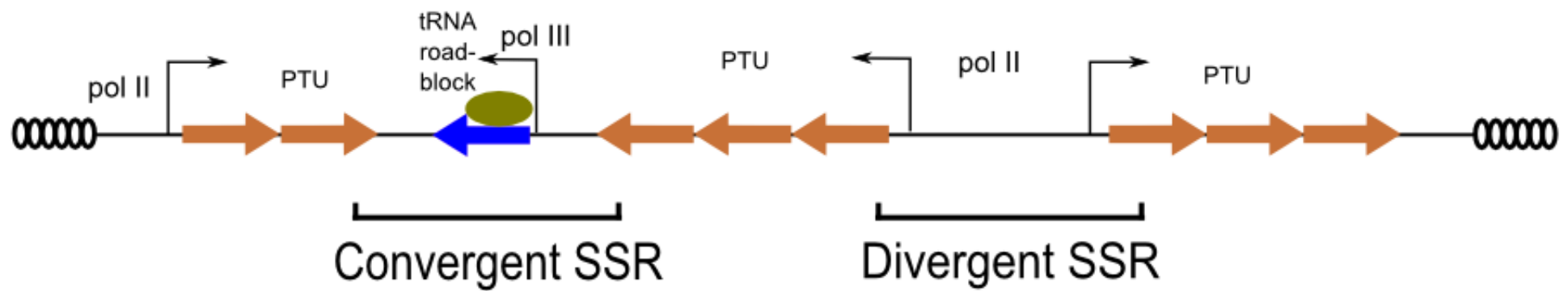
Parasitic life cycle



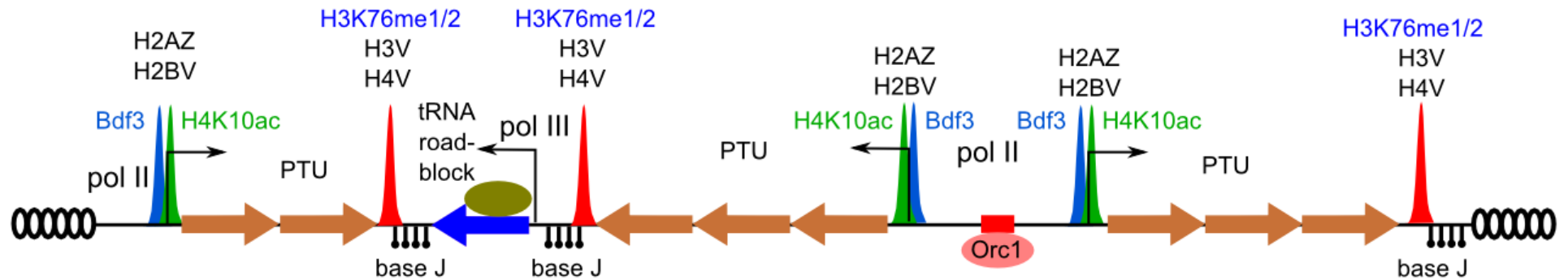
Bloodstream Expression Site



The epigenome of *Trypanosoma brucei*

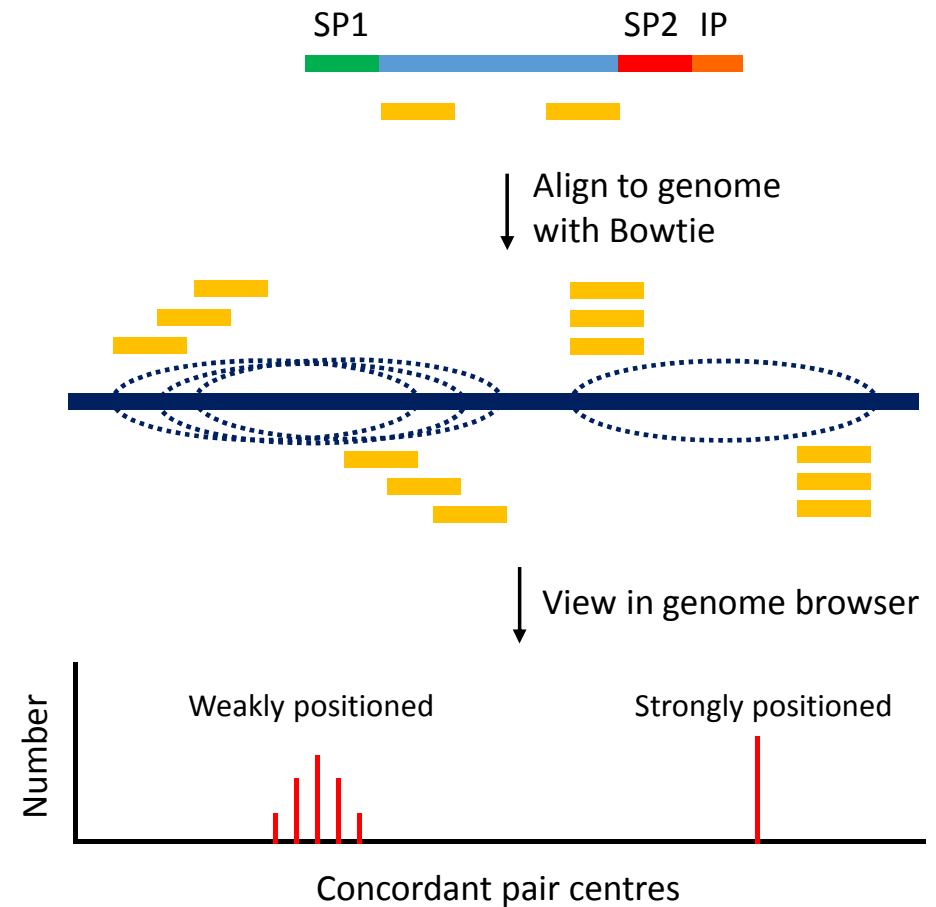
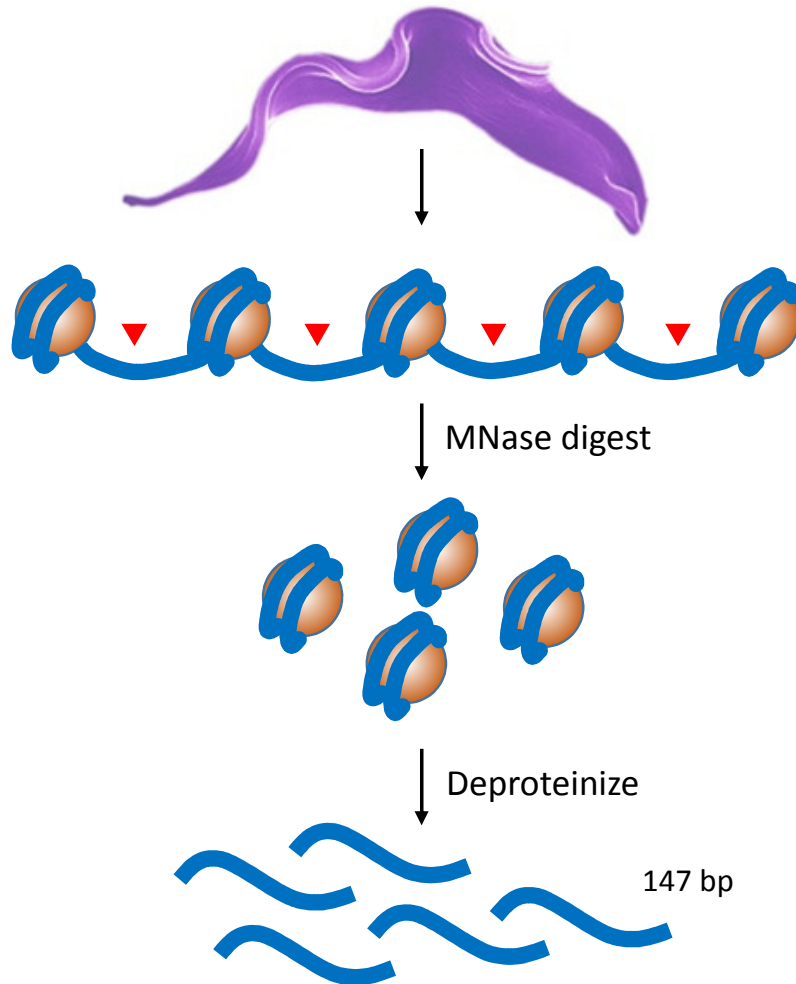


The epigenome of *Trypanosoma brucei*

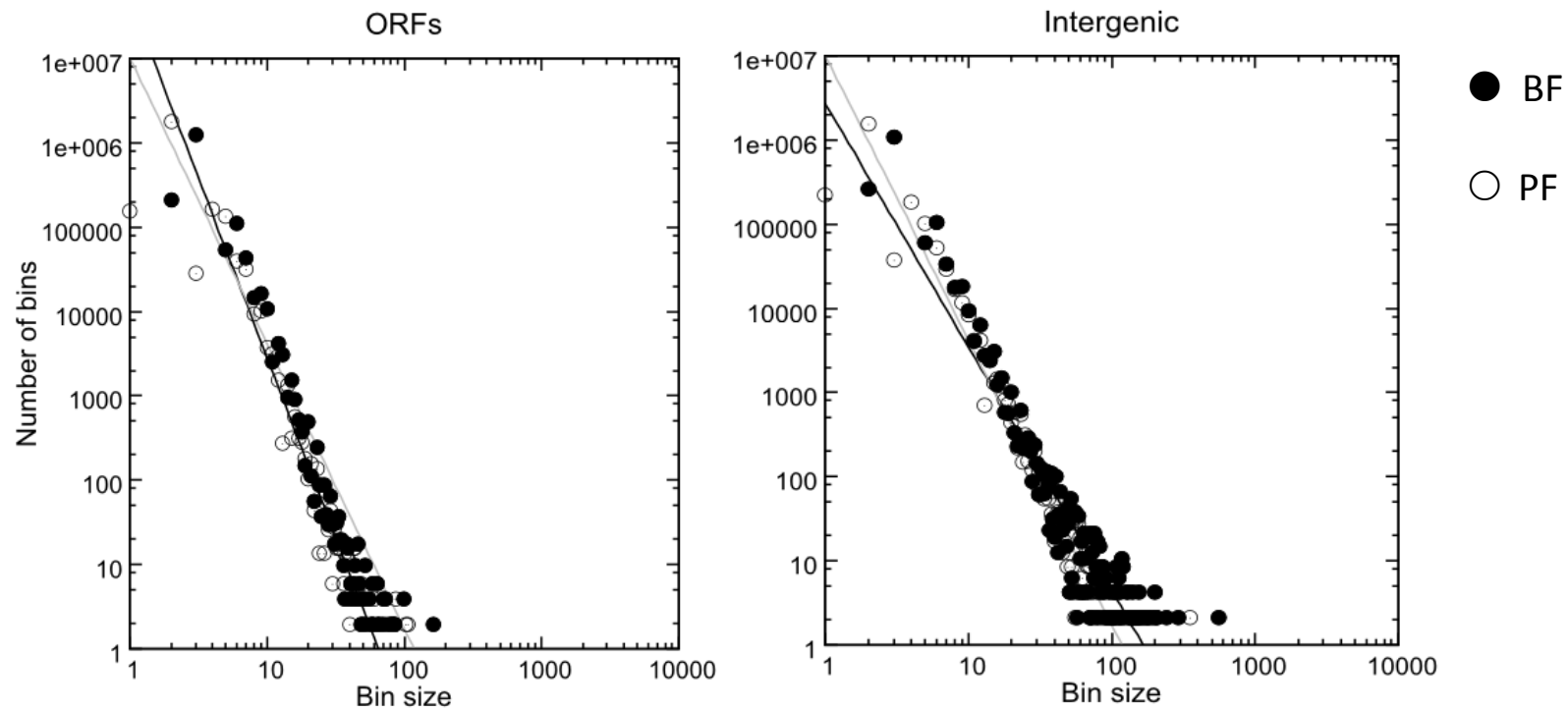


Maree and Patterton, 2014.

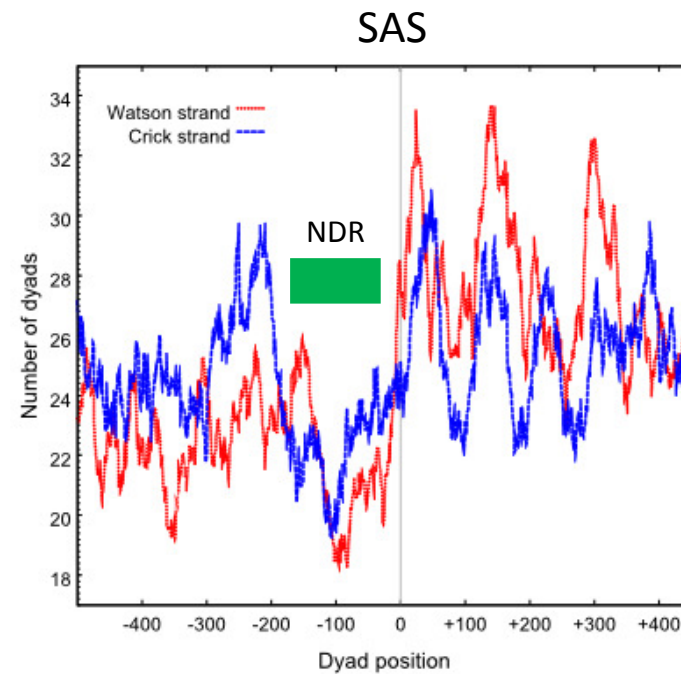
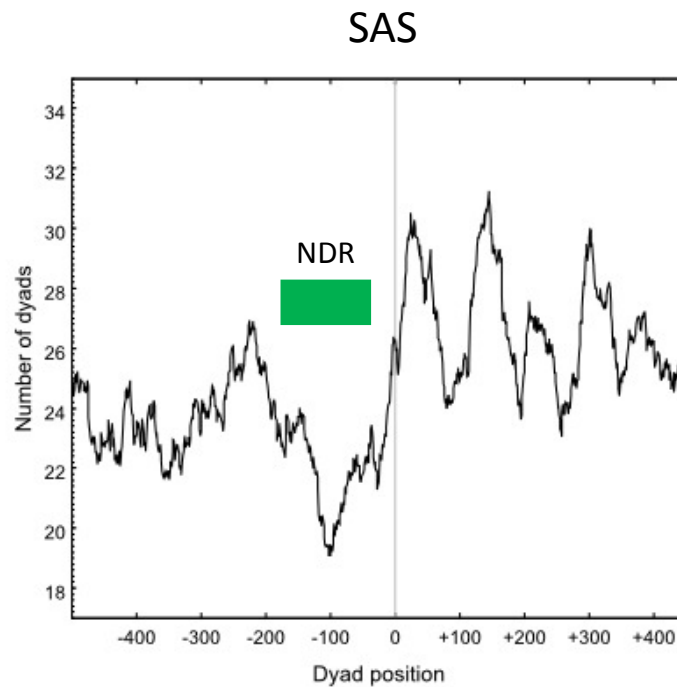
Determining nucleosome positions by paired ends sequencing



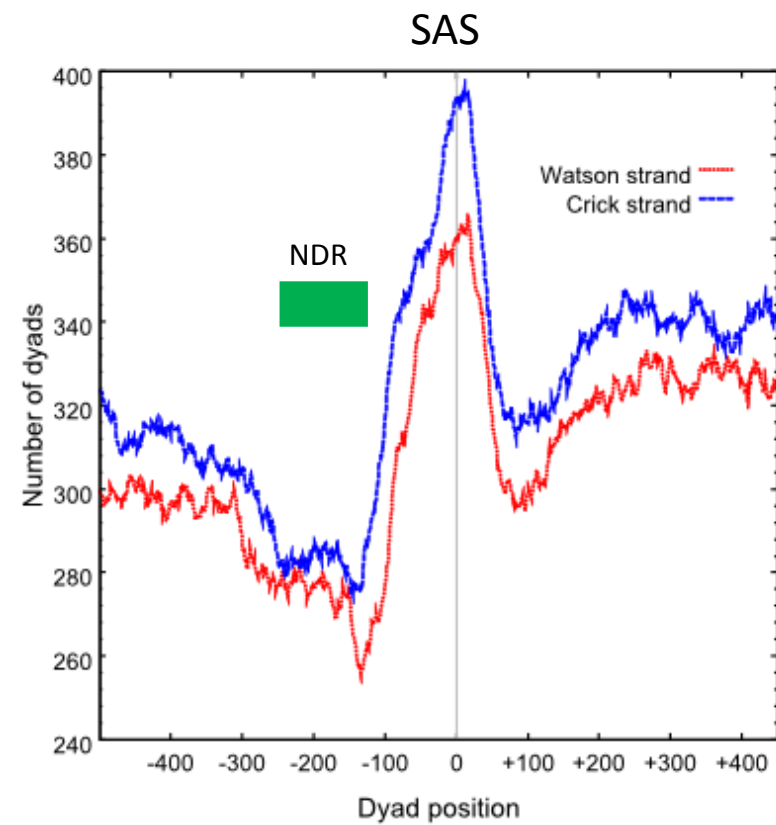
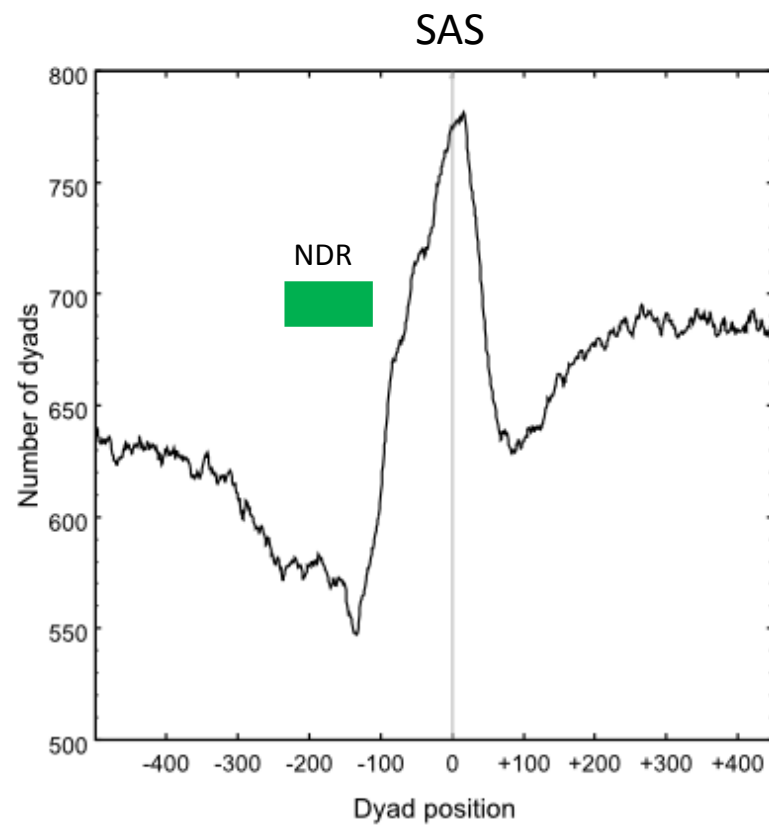
Bin analysis reveal differential nucleosomal densities



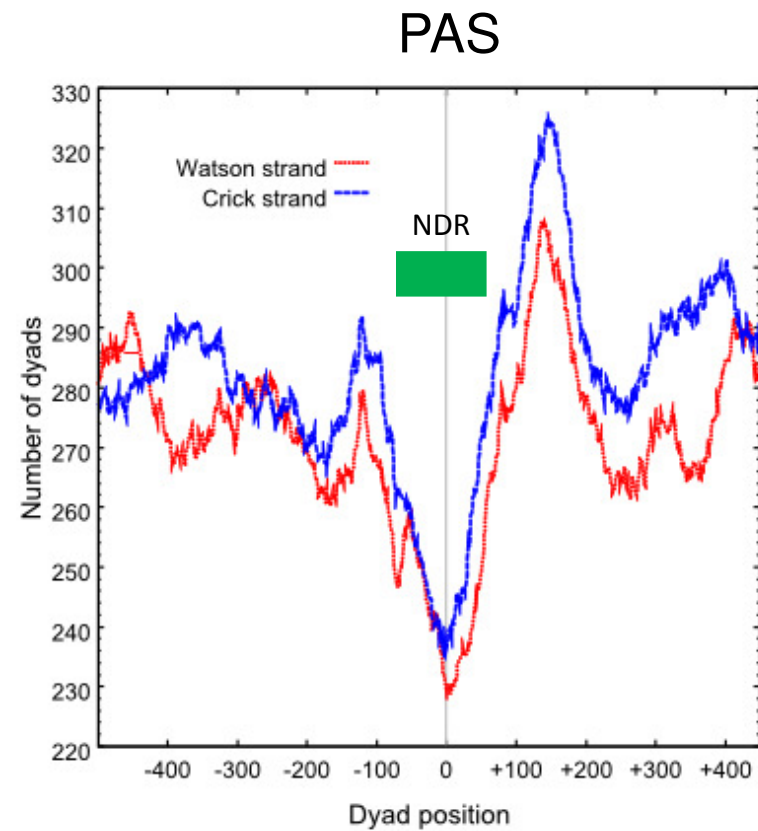
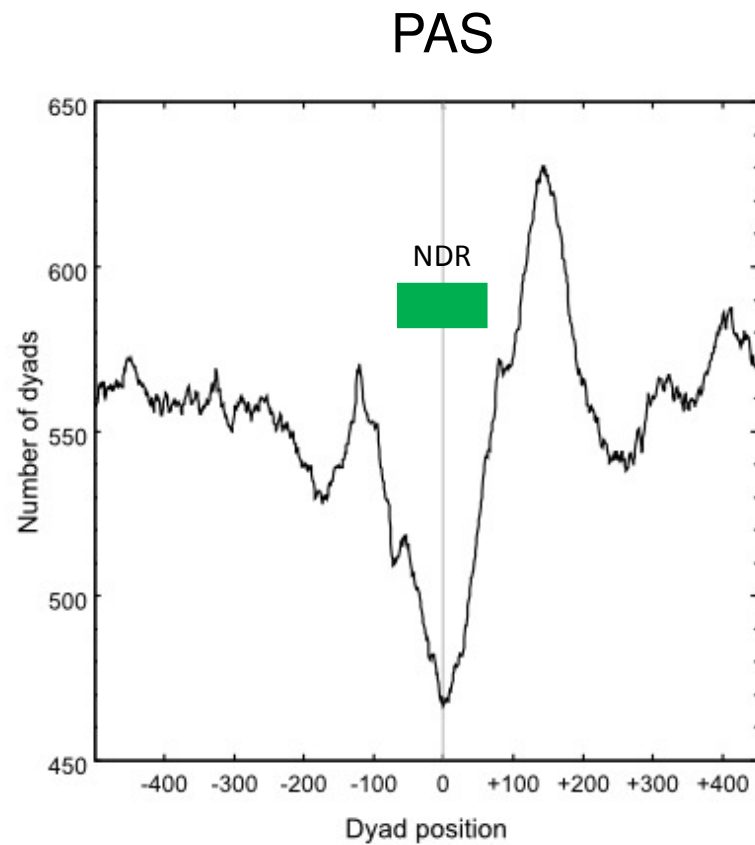
Nucleosomal organization of pol II PTU transcription initiation regions



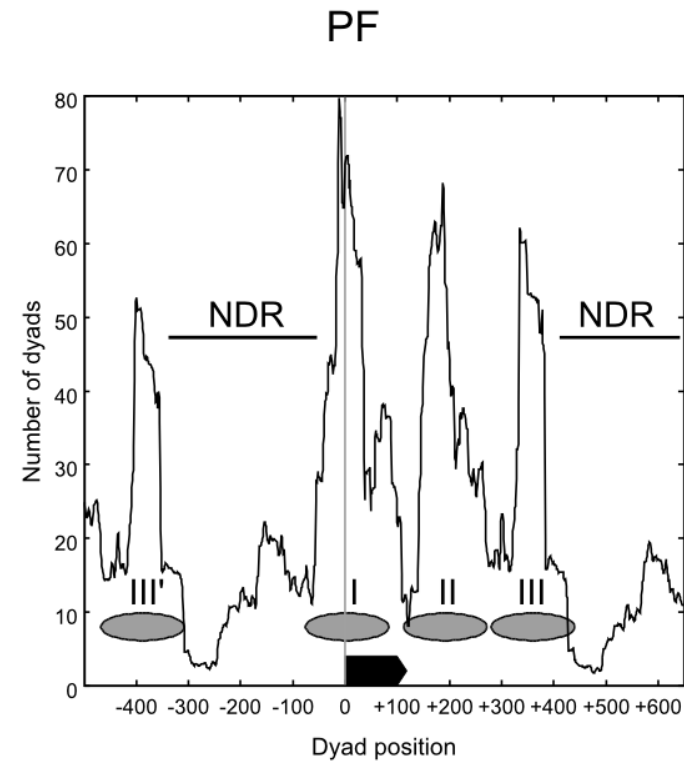
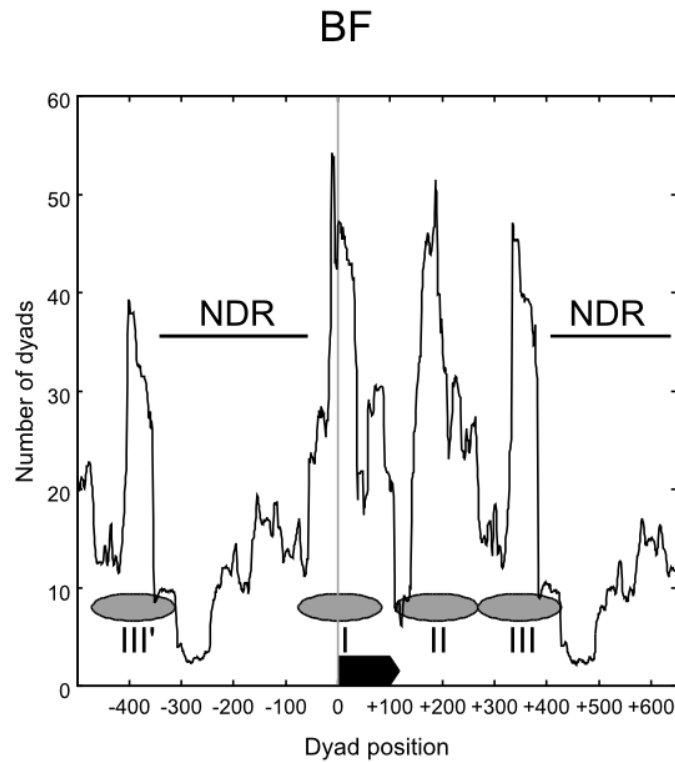
The NDR is not a feature of all SAS regions



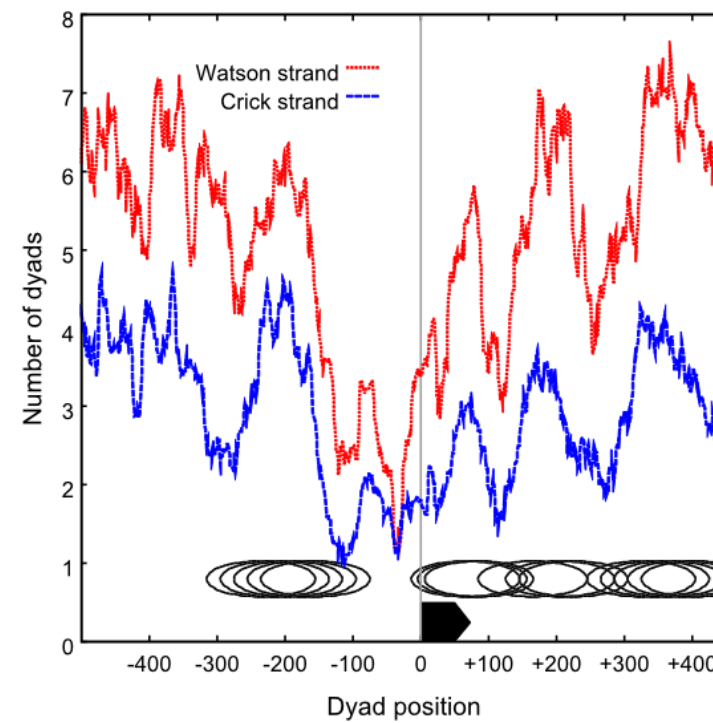
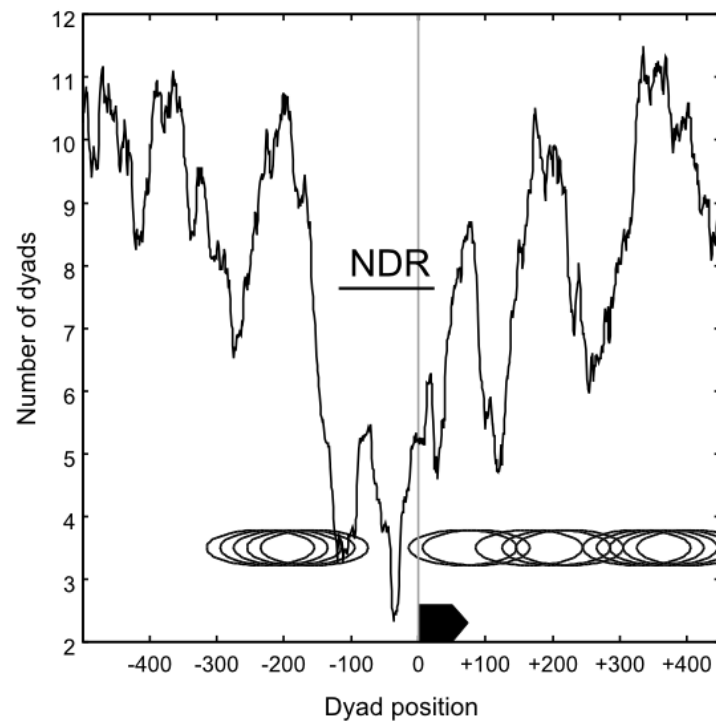
Nucleosomal organization at pol II termination regions



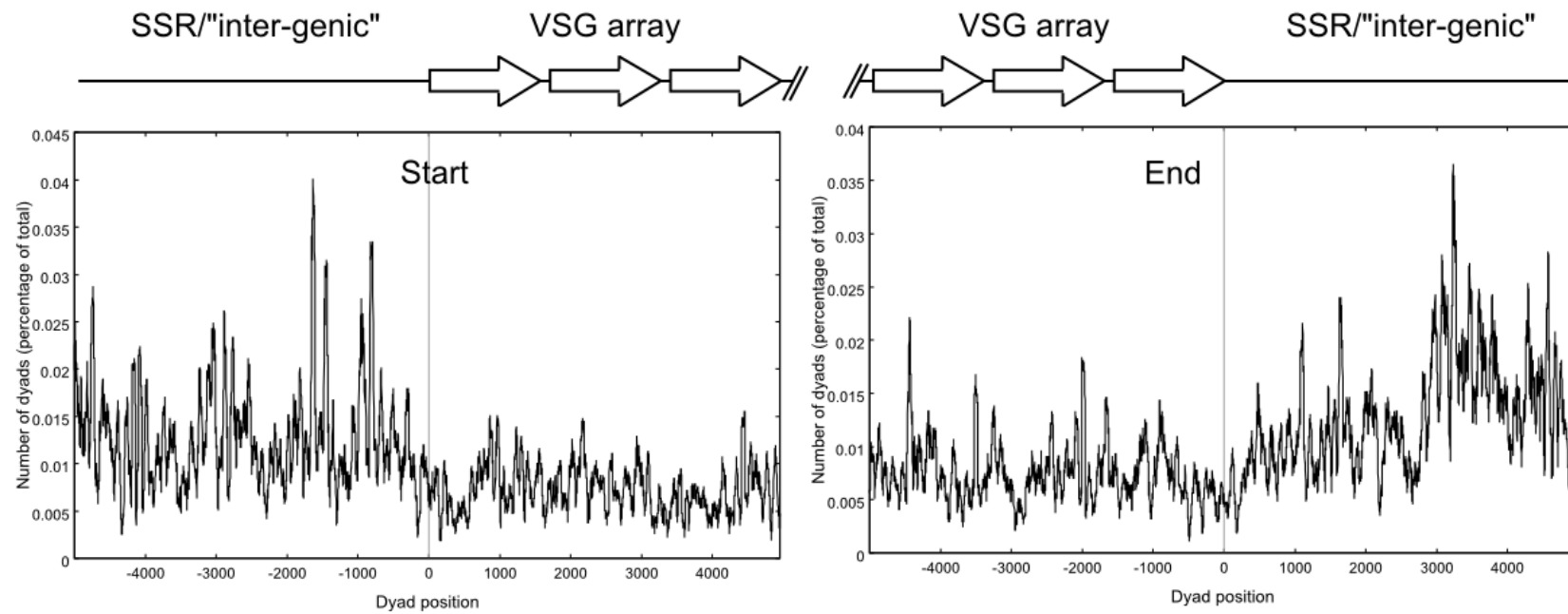
Nucleosomal organization of pol I transcribed 5S rDNA



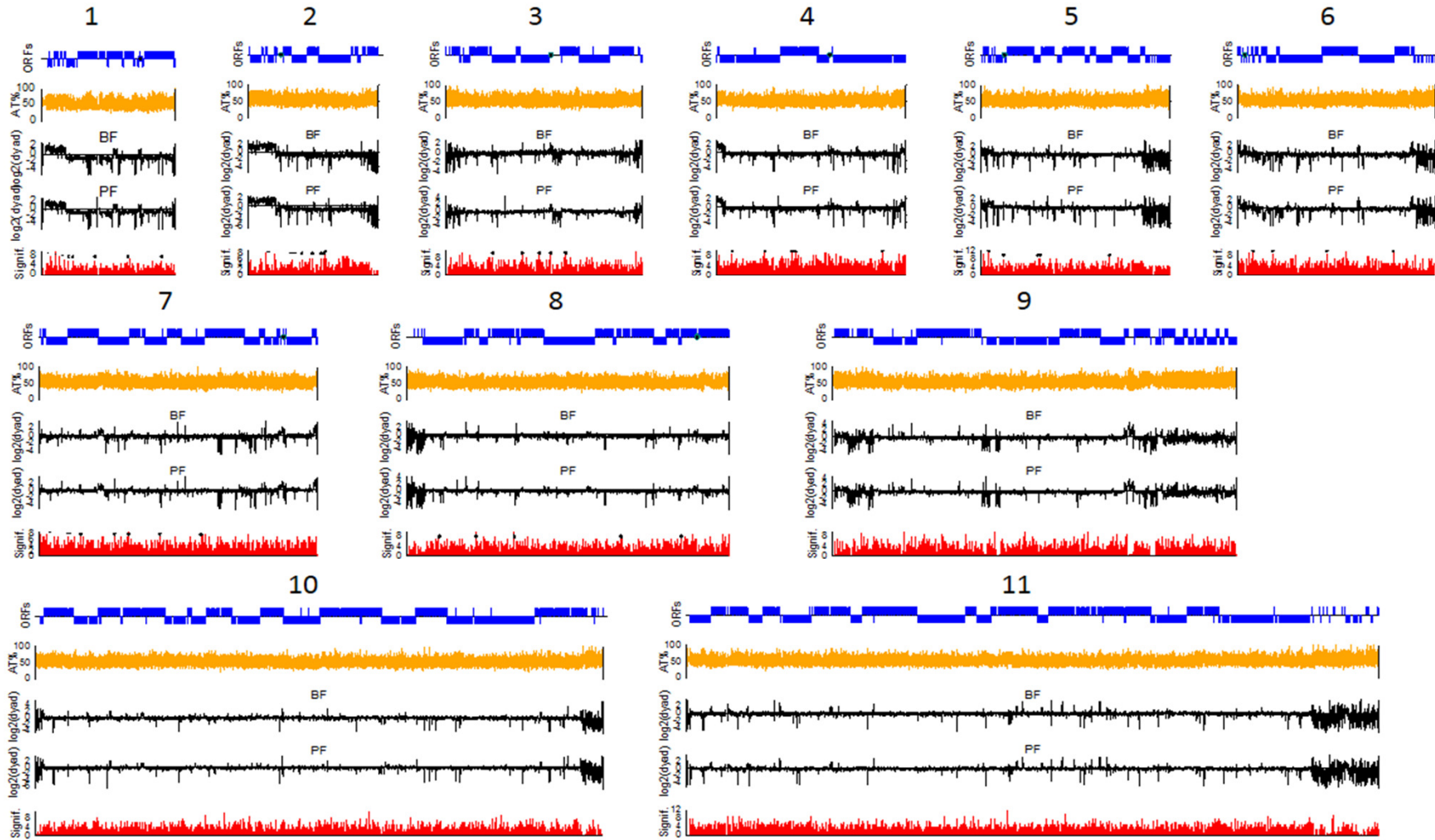
Nucleosomal organization of pol III transcribed tRNA



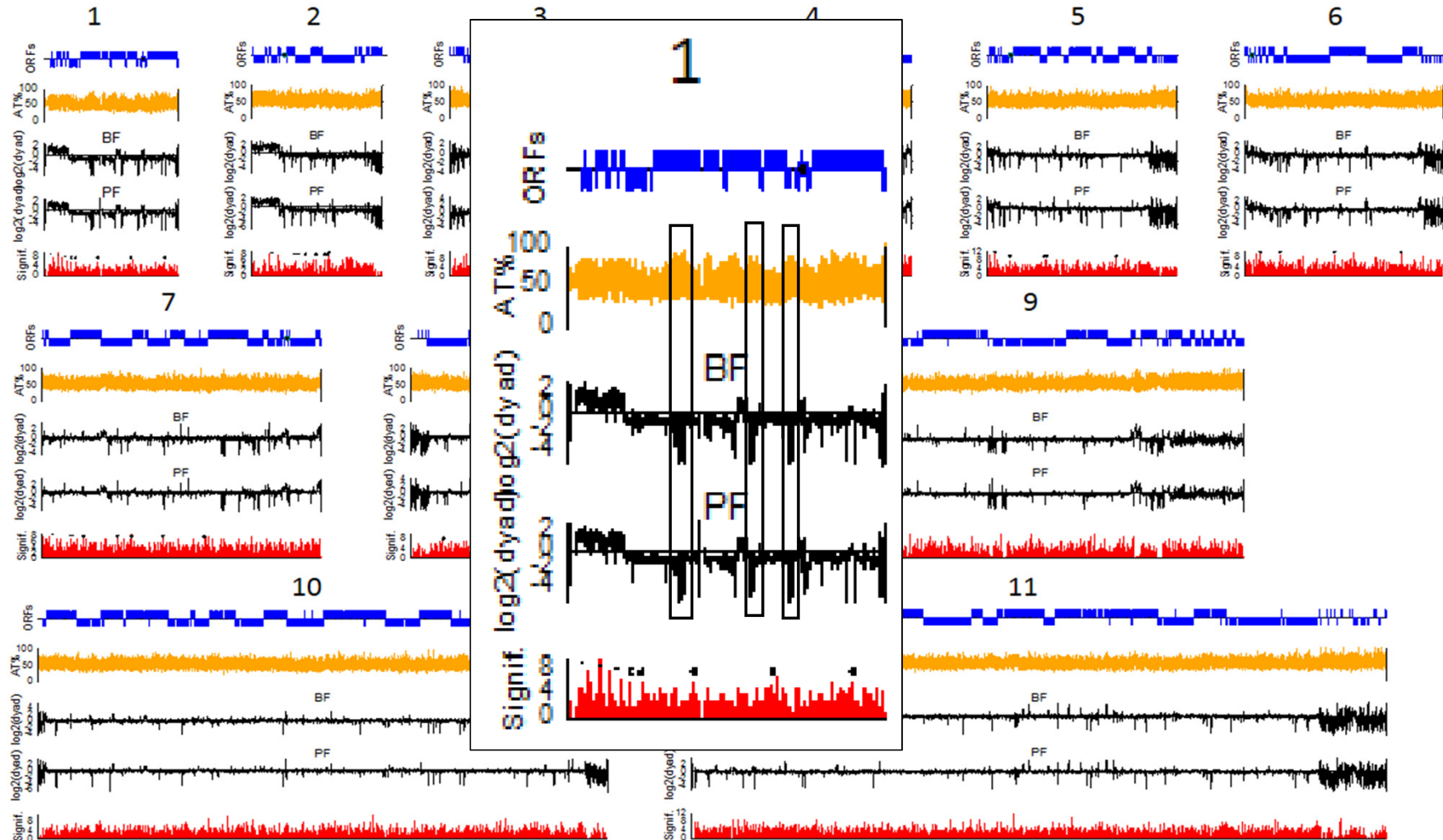
Nucleosomal organization of silent VSG arrays



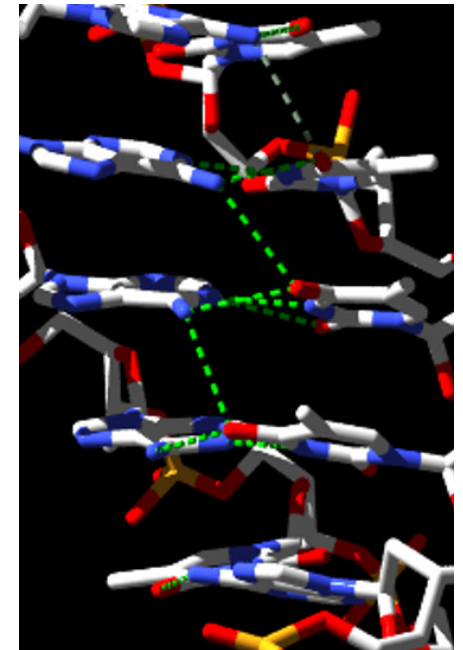
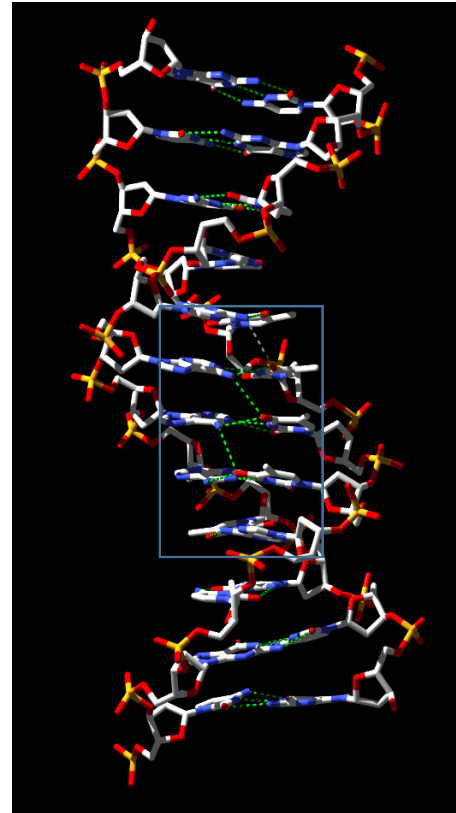
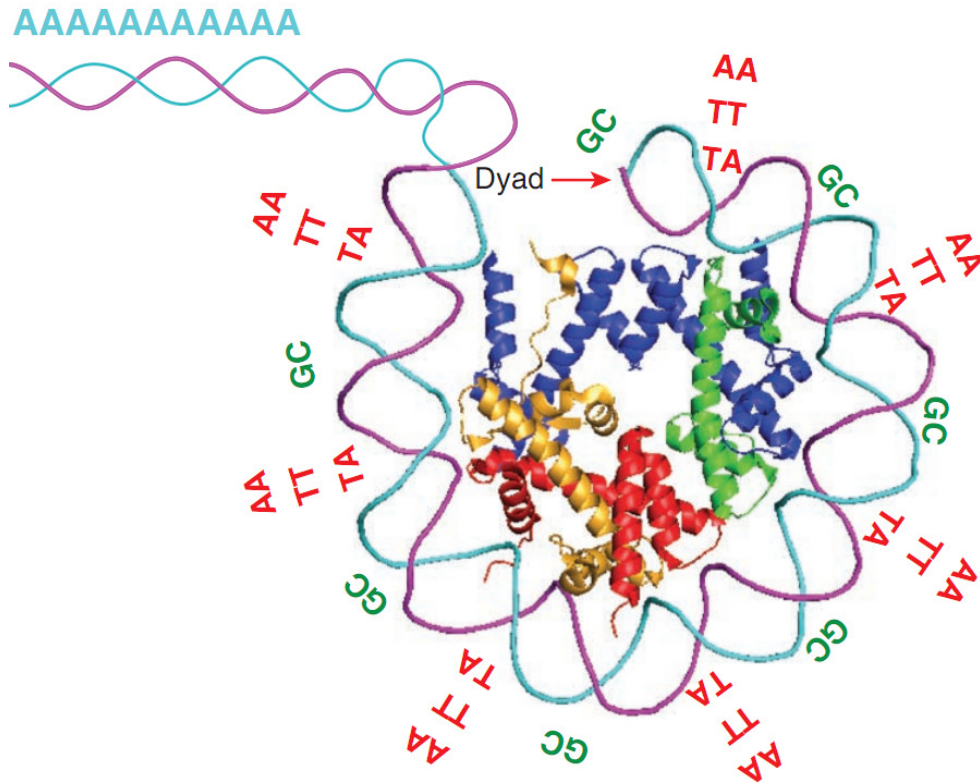
Differences between BF and PF



Differences between BF and PF

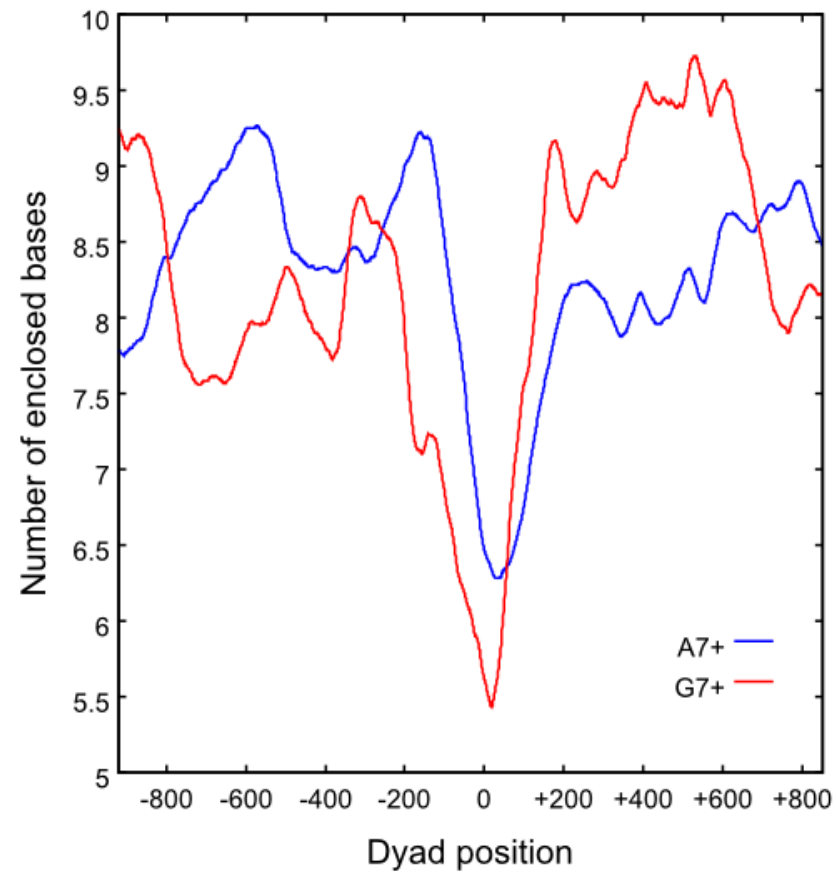


Sequence directed nucleosomal positioning



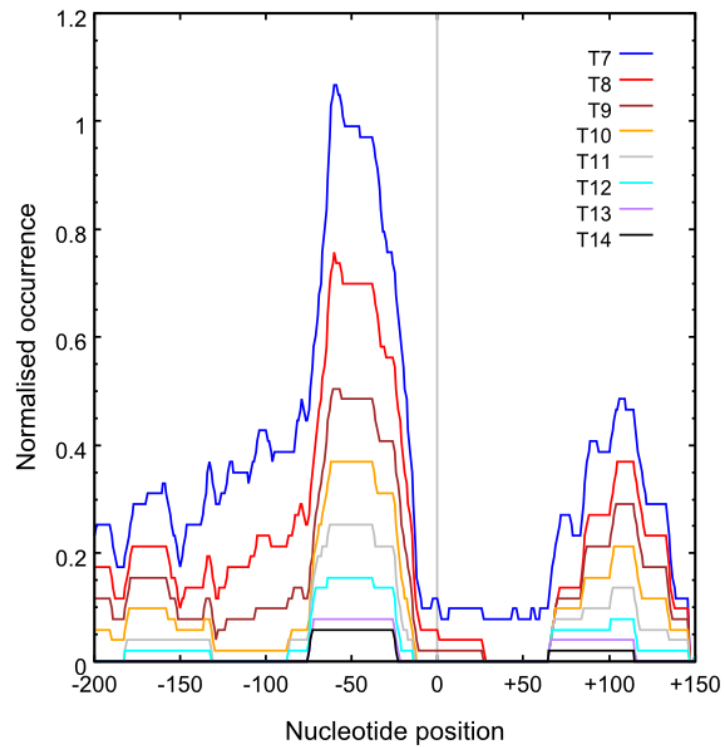
Struhl and Segal, 2013.

Oligo-dA and -dG runs are depleted in nucleosomes

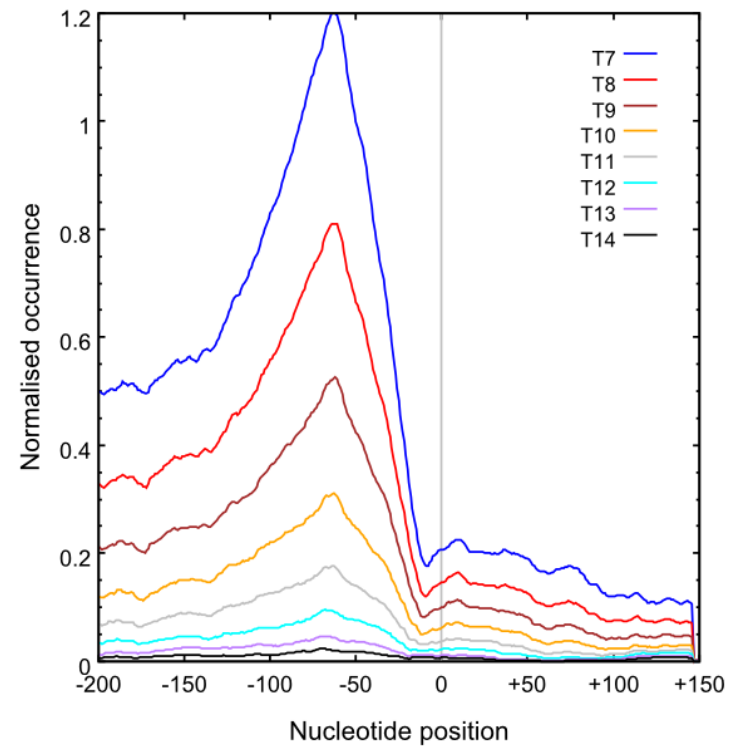


Sequence directed nucleosomal positioning

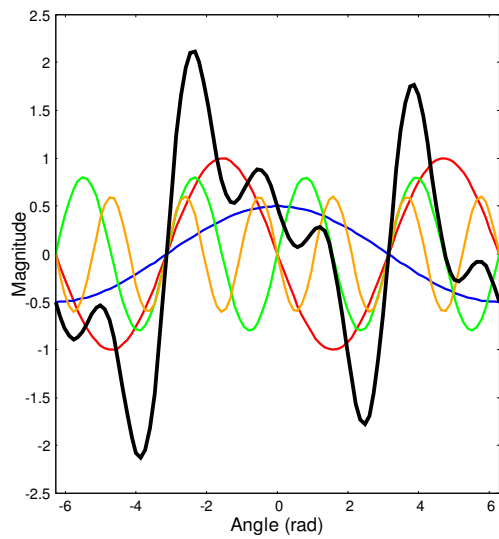
1st SAS of PTU



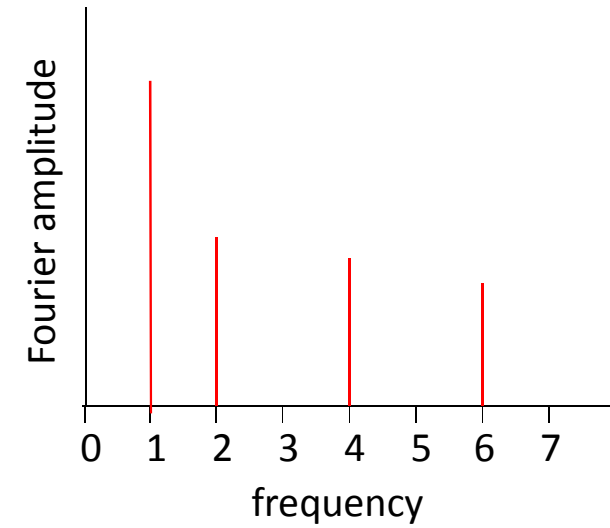
All SASs of PTU



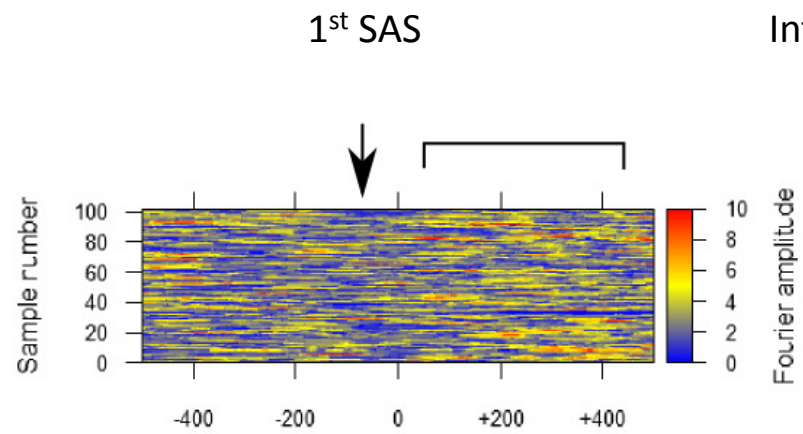
Periodicity in a complex signal



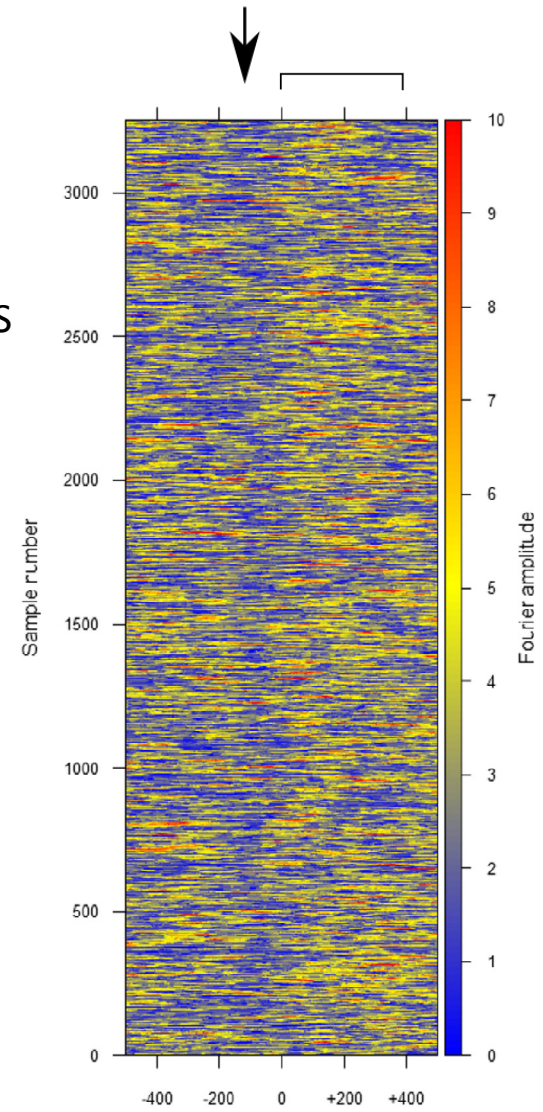
Fourier transform



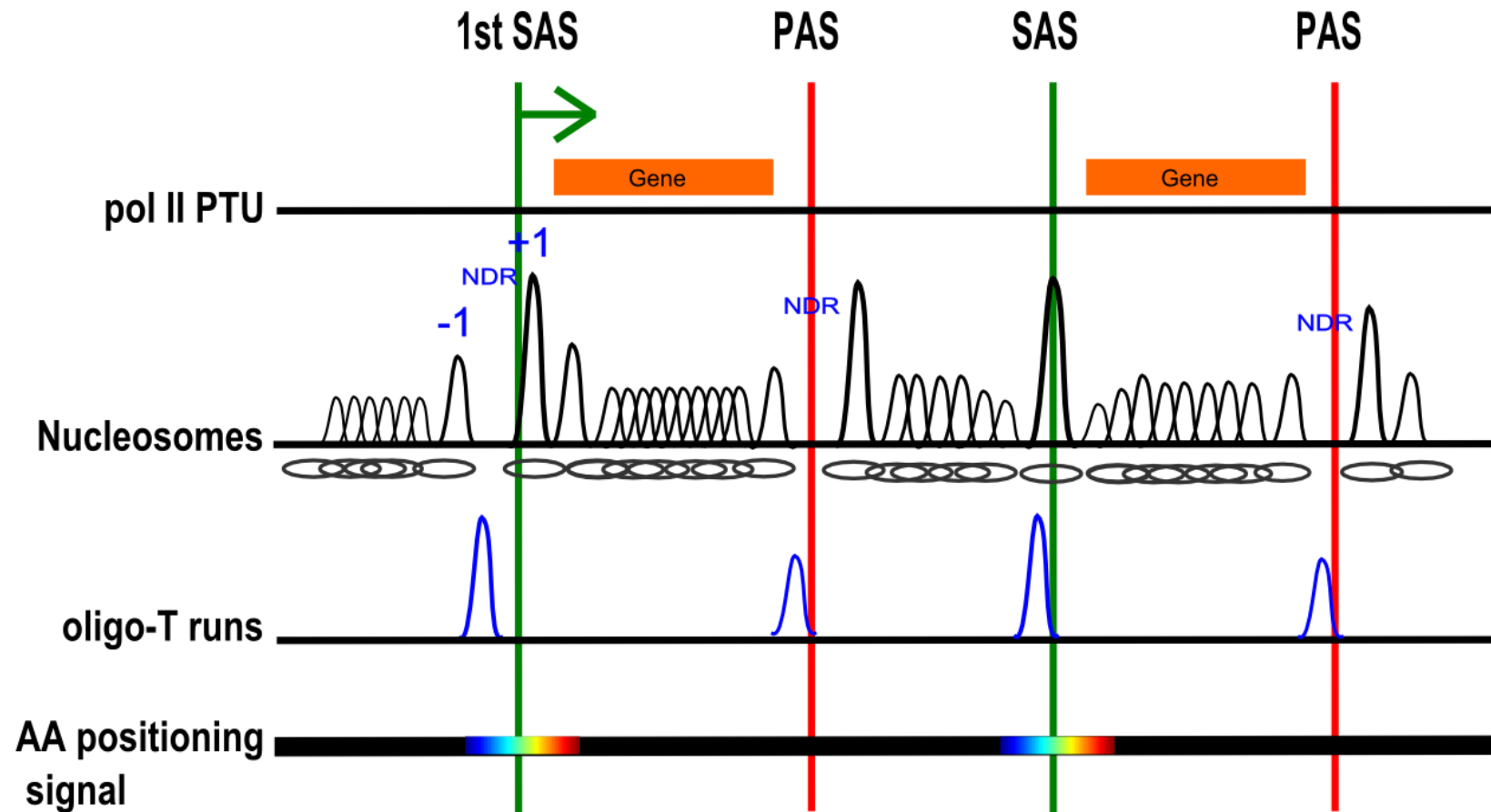
FFT of AA dinucleotides at SAS



Internal SAS



Conclusion



- 1. Summary of initial goals, sampling framework, data collection, analysis plan and power for discovery**
 - Genome-wide map of nucleosomes in BF and PF *T. brucei*
 - Analysis of PTM's of Histone H3 N-terminal tail
 - Genome-wide distribution of select PTM's
- 2. Progress to date, including benchmarks achieved**
 - Genome-wide nucleosome map completed, manuscript nearing completion
 - Isolation and MS analysis of H3 ongoing
- 3. Progress in patient recruitment and data collection in the context of the proposed sampling framework**
 - Not applicable
- 4. Any changes in goals or expected timeline**
 - None foreseen
- 5. Challenges experienced to date, including any ethical issues**
 - None

Acknowledgements

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