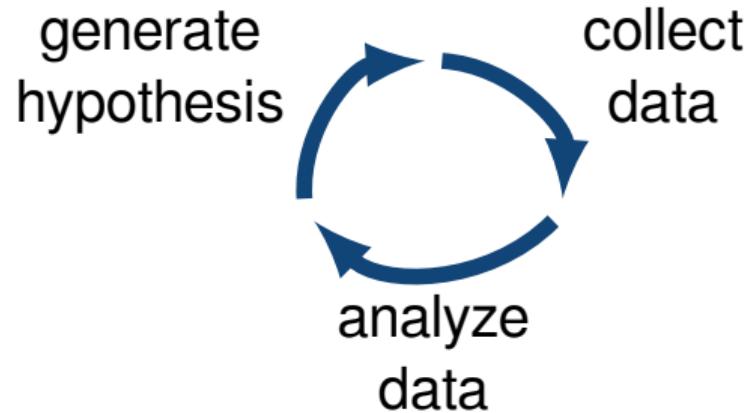


Genomic analyses of transcription elongation factors and intragenic transcription

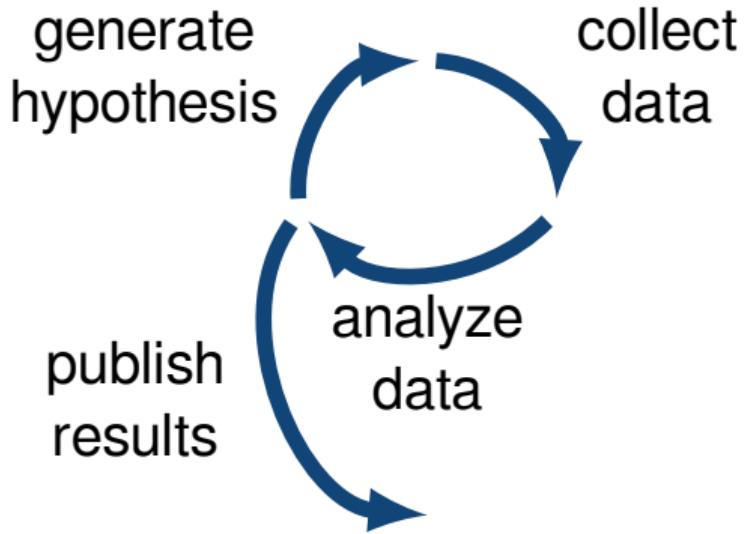
James Chuang

June 19, 2019

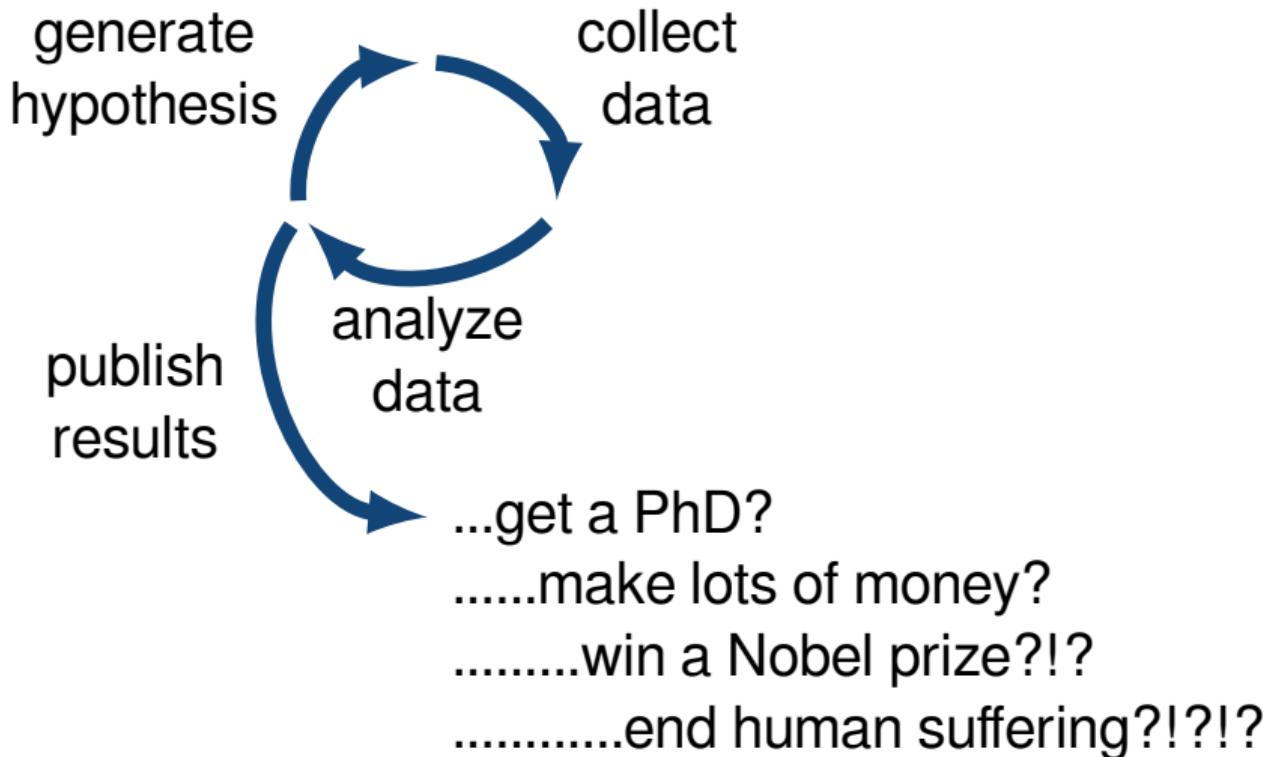
The scientific process

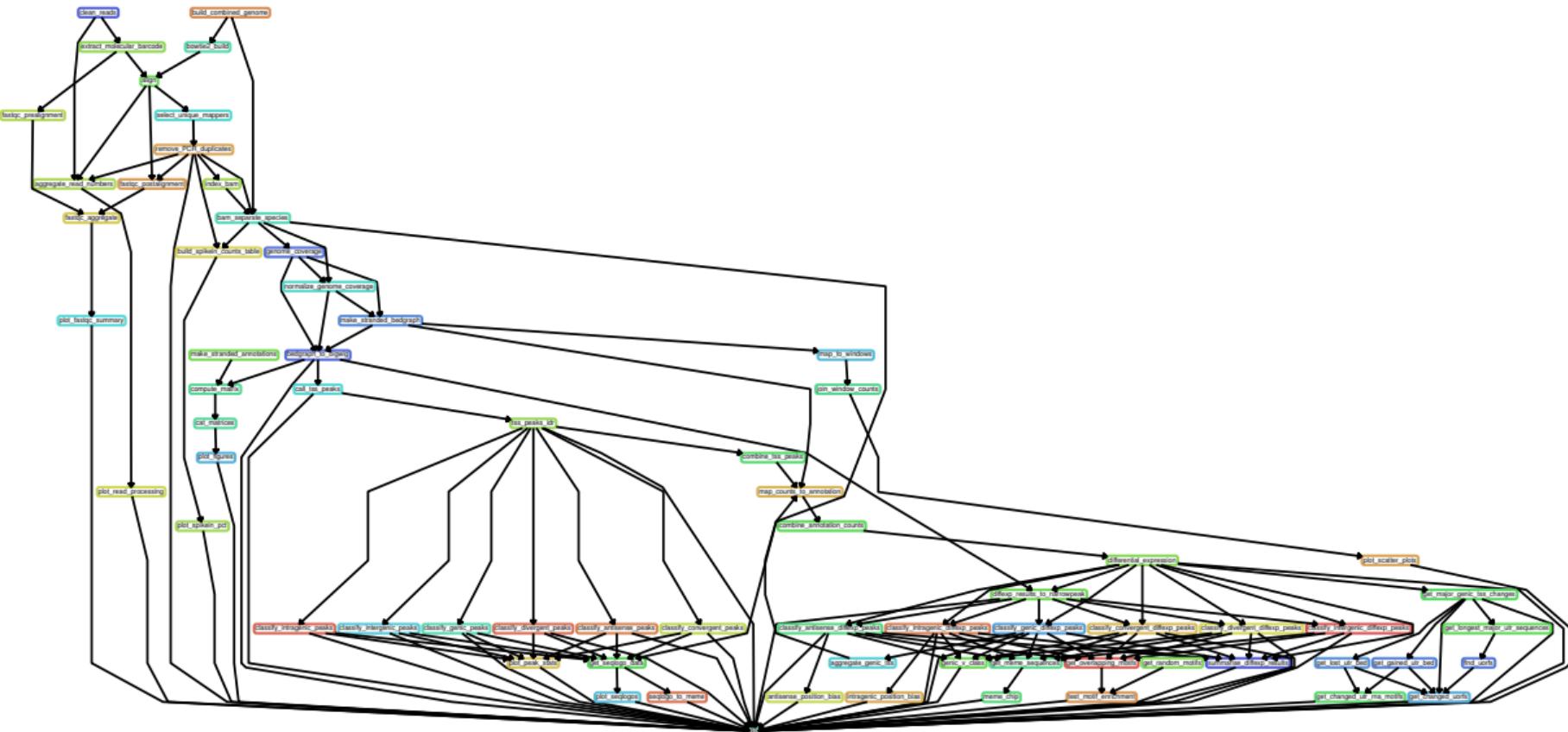


The scientific process



The scientific process







an example Snakemake rule:

```
rule foobar:
    input: 'input.txt'
    output: 'output.txt'
    params: species='cerevisiae'
    conda: 'environment.yaml'
    script: 'make_output_from_input.py'
```





September 7, 2018

Journal article

Open Access

Spt6 is required for the fidelity of promoter selection

Doris, Stephen M.; Chuang, James; Viktorovskaya, Olga; Murawska, Magdalena; Spatt, Dan; Churchman, L.; Stirling; Winston, Fred

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 Winston, Fred

Data collector(s)

Spatt, Dan

Data manager(s)

IP Chuang James

Other(s)

Churchman, L. Stirling

Researcher(s)

Doris, Stephen M.; Viktorovskaya, Olga; Murawska, Małgorzata

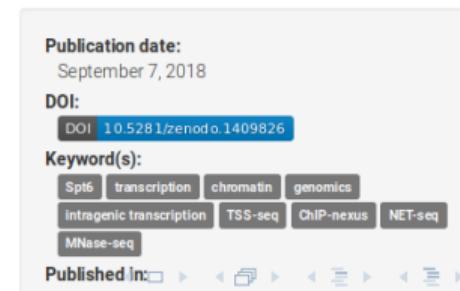
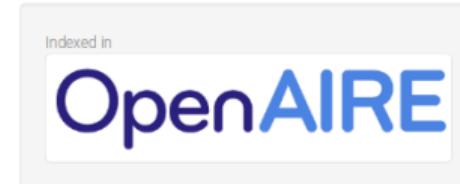
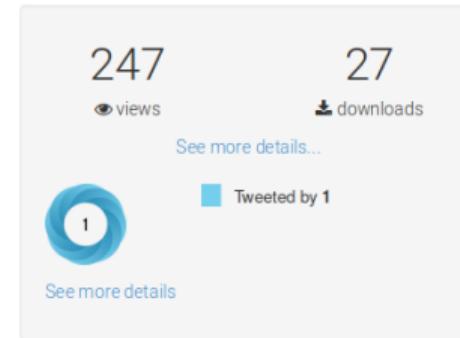
All data analyses supporting our publication "Spt6 is required for the fidelity of promoter selection". Reproduce the figures of the paper starting from raw data, as well as thousands of figures and analyses that aren't shown.

See README.md for instructions.

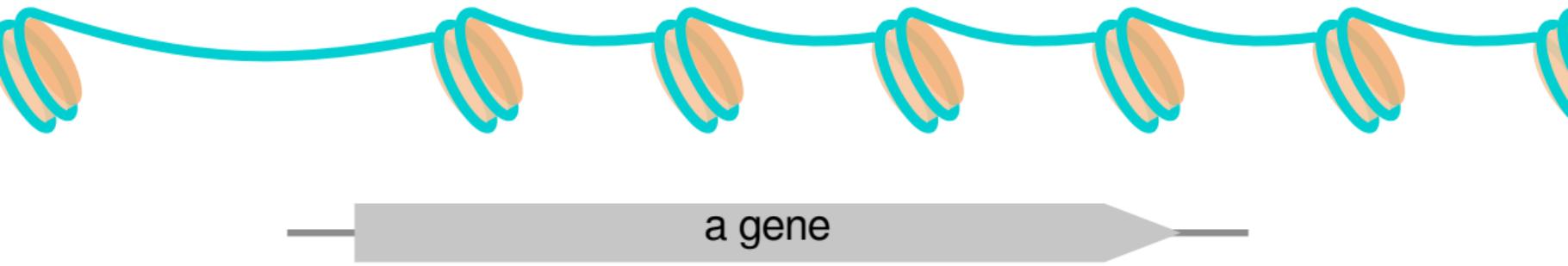
For updated versions of the pipelines used, see our [github page](#)

Files (47.2 GB)

Name	Size	
spt6_2018.tar.gz	47.2 GB	 Download

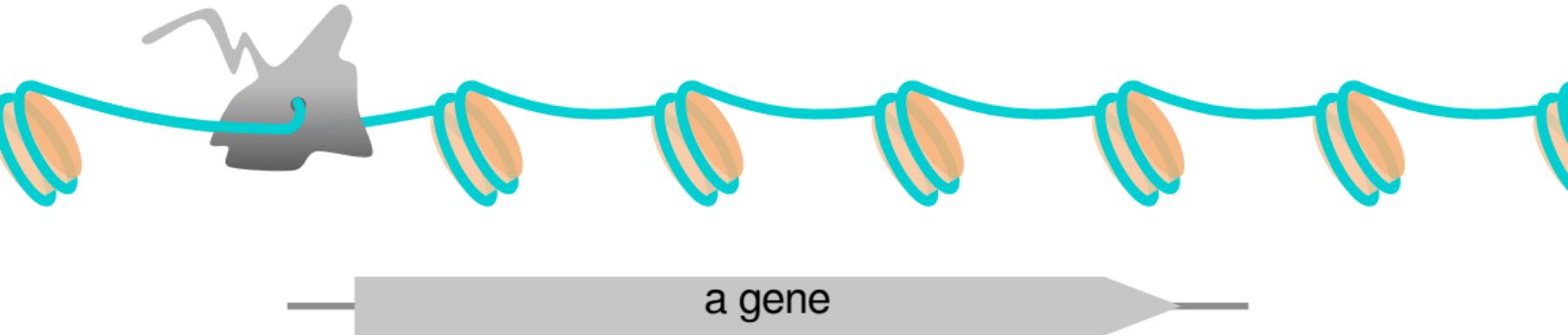


Transcription

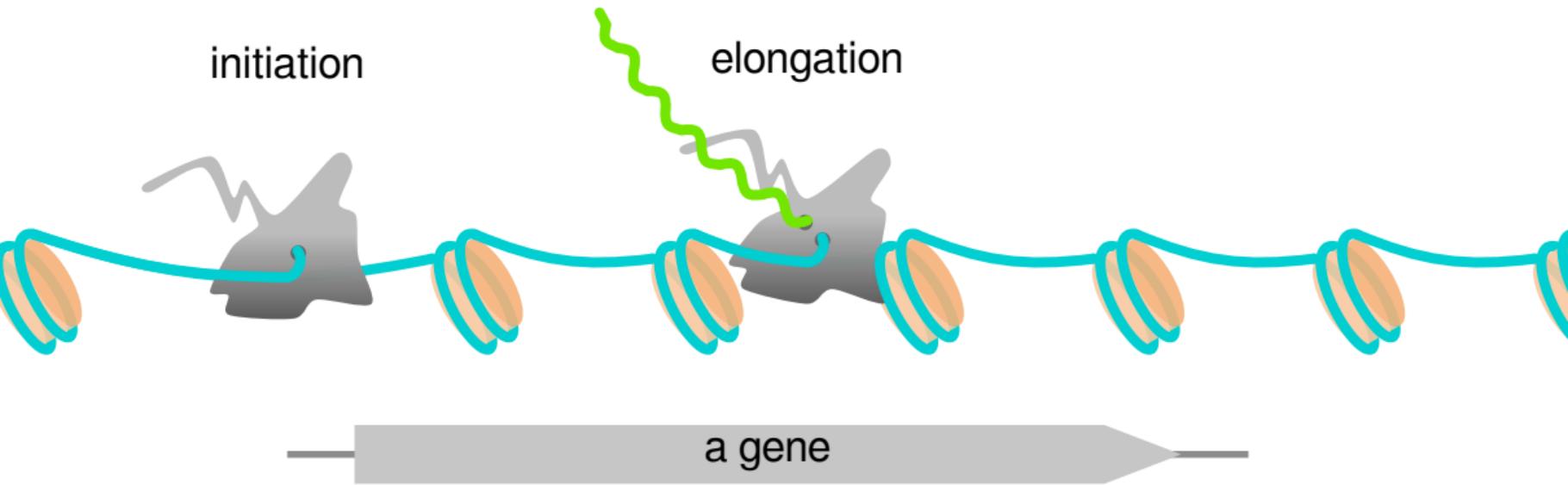


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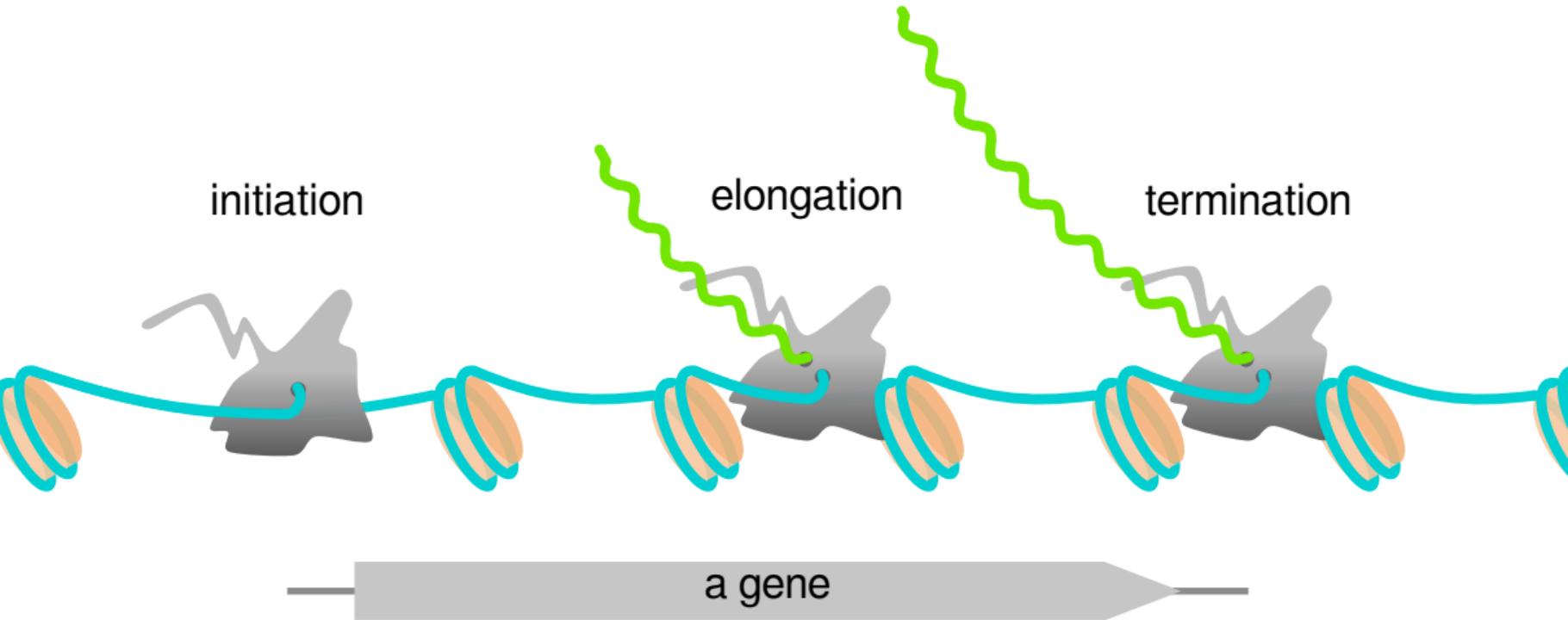
initiation



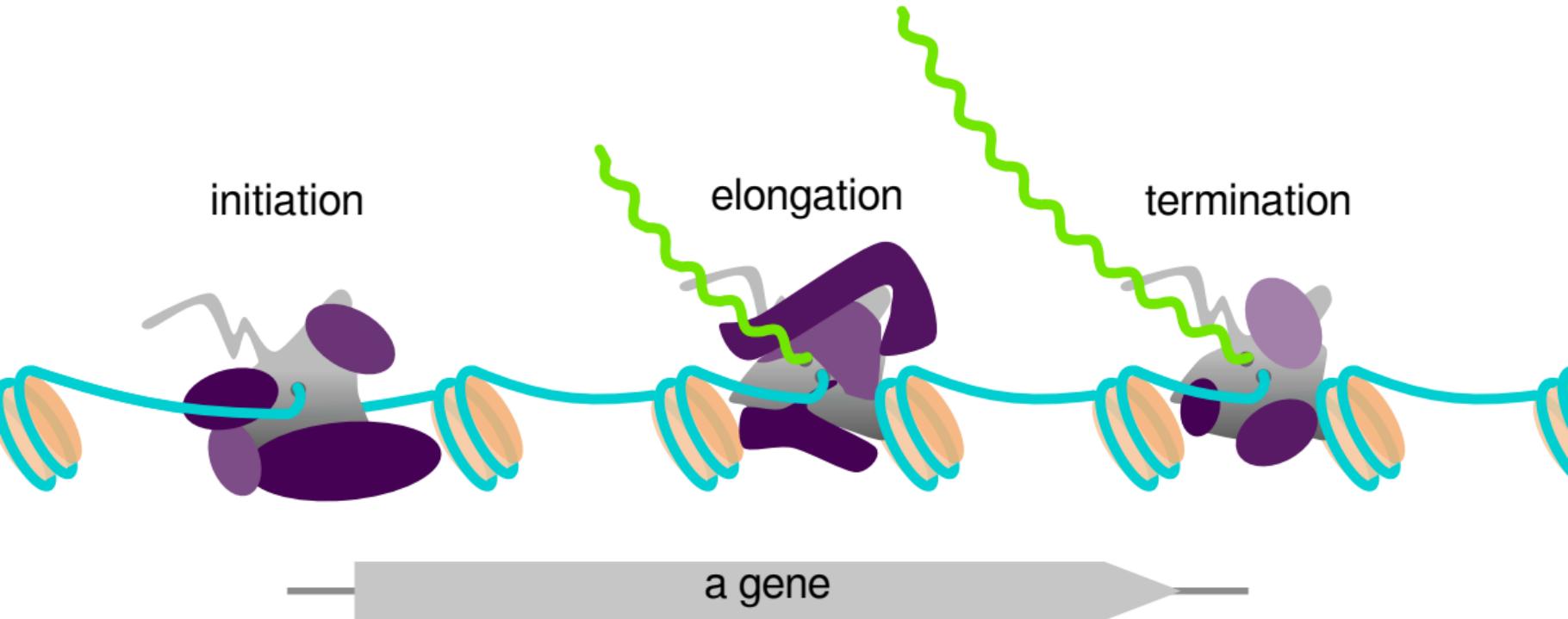
Transcription

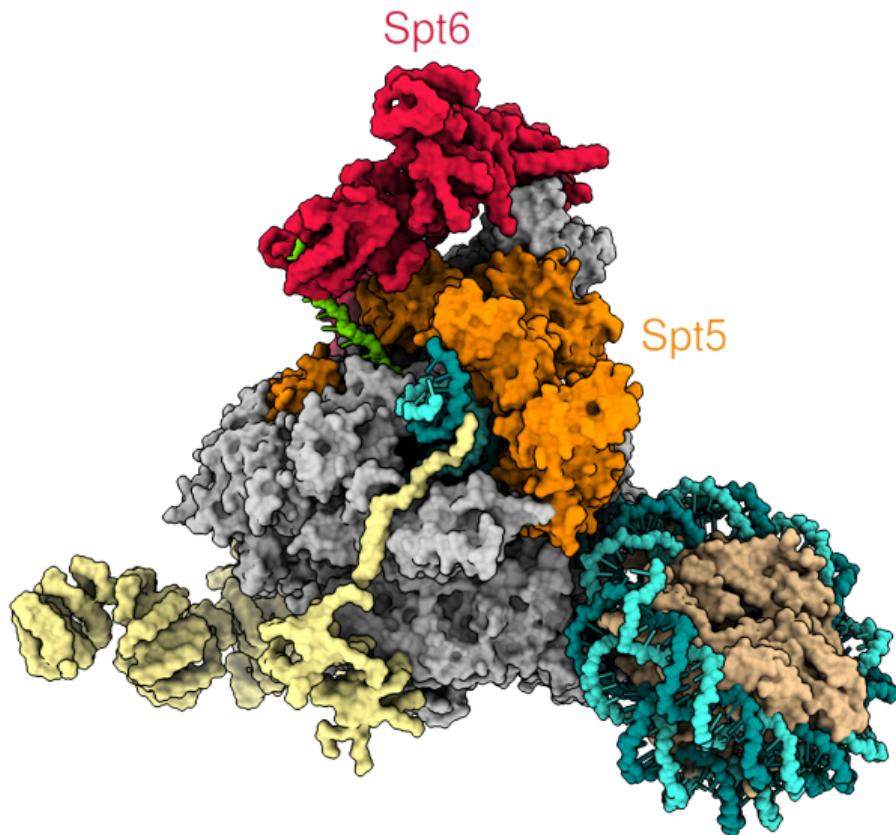


Transcription



Transcription





Vos *et al.* (2018). *Nature*
Farnung *et al.* (2018). *Nat. Commun.*

Spt6 project collaborators

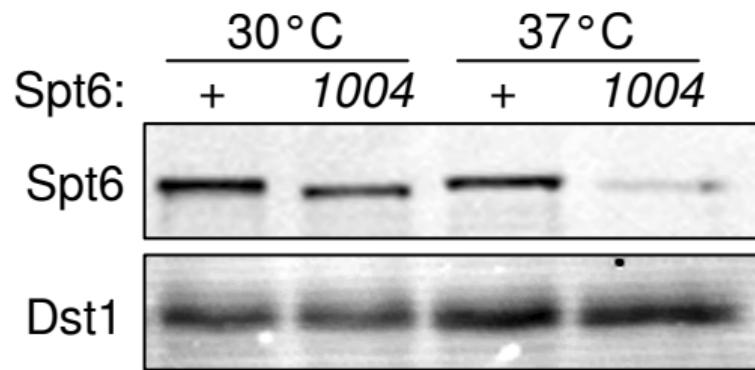
Steve Doris TSS-seq and ChIP-nexus

Olga Viktorovskaya MNase-seq

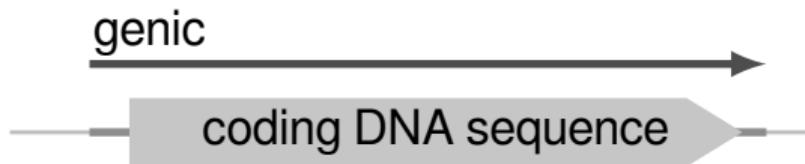
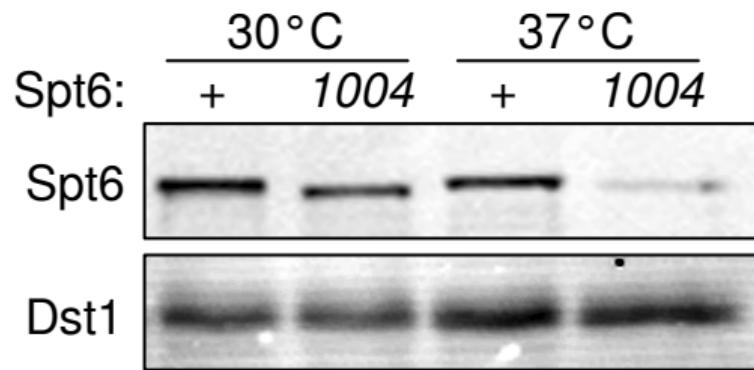
Magdalena Murawska NET-seq

Dan Spatt Northern, Western, and ChIP experiments

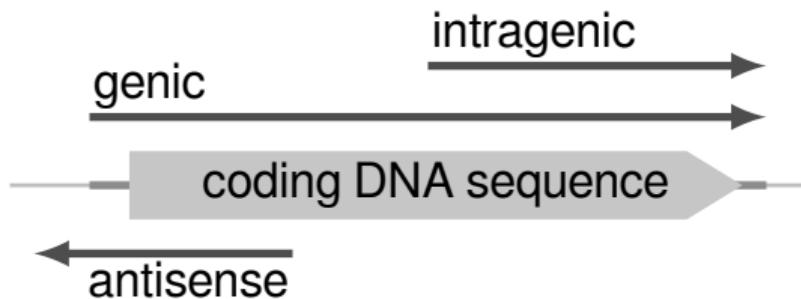
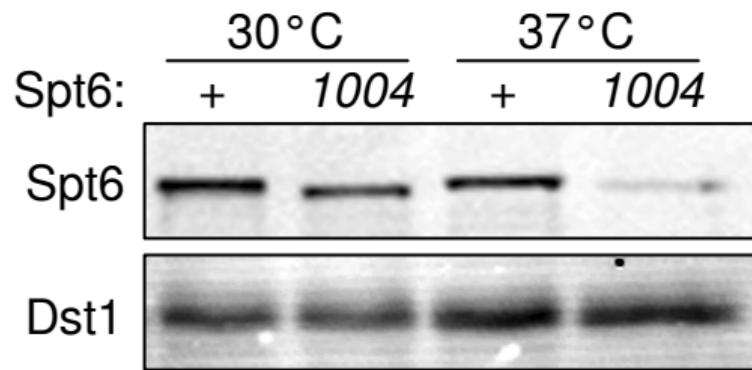
The *spt6-1004* mutant expresses intragenic transcripts

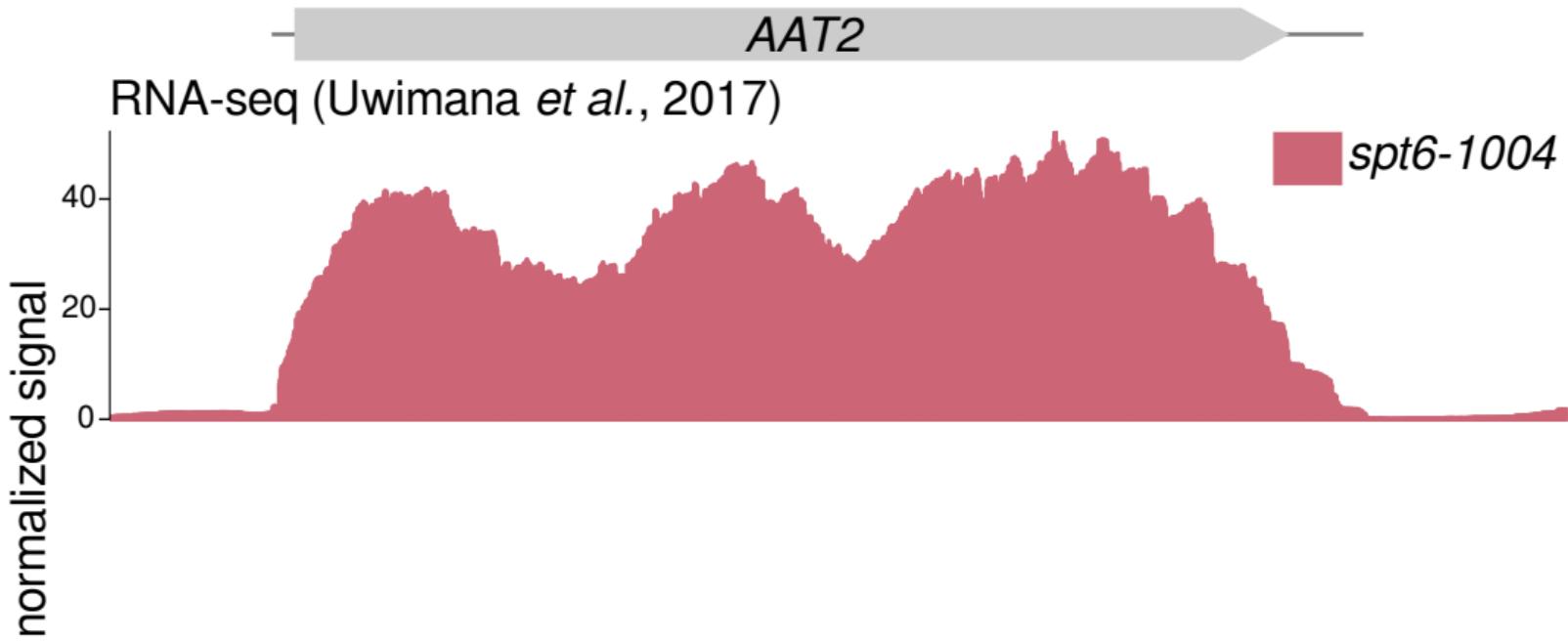


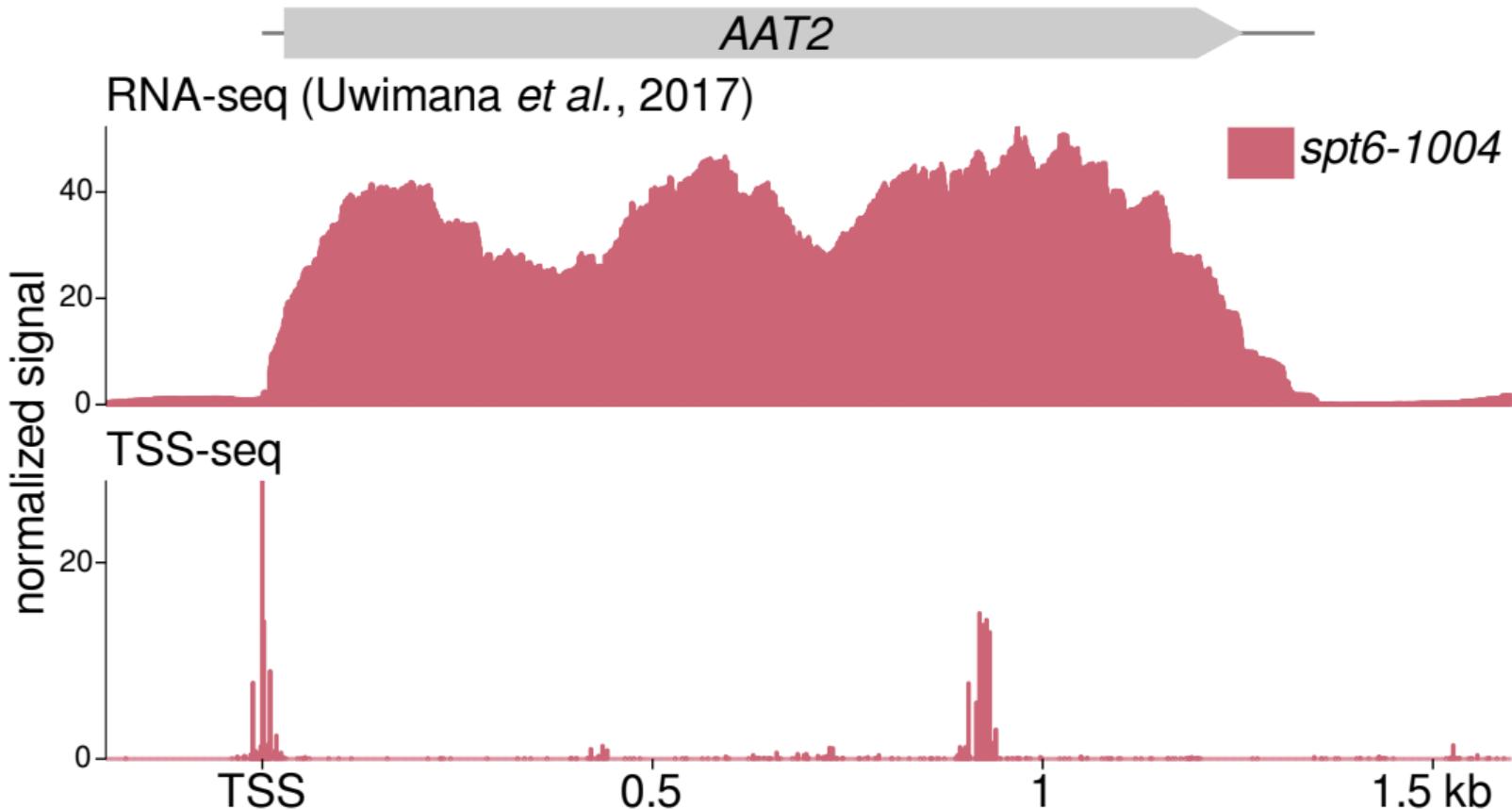
The *spt6-1004* mutant expresses intragenic transcripts



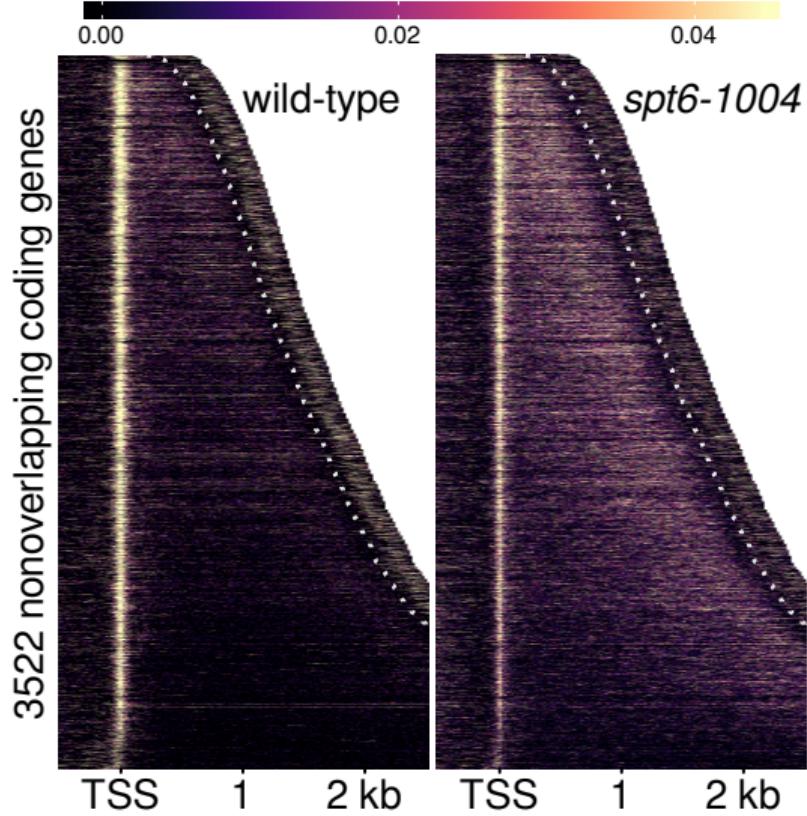
The *spt6-1004* mutant expresses intragenic transcripts

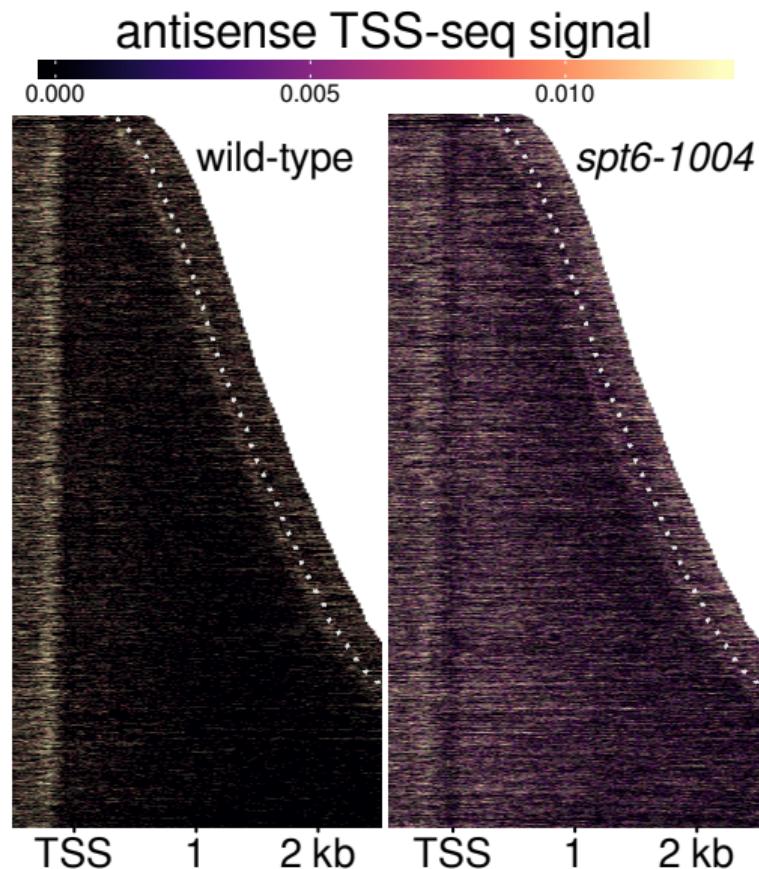
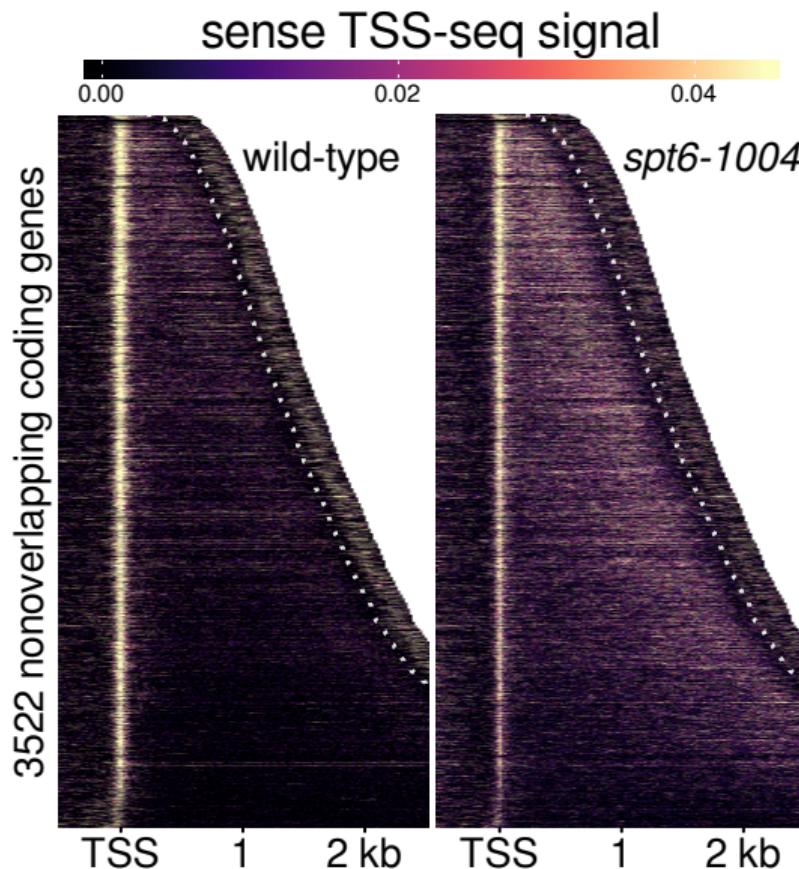




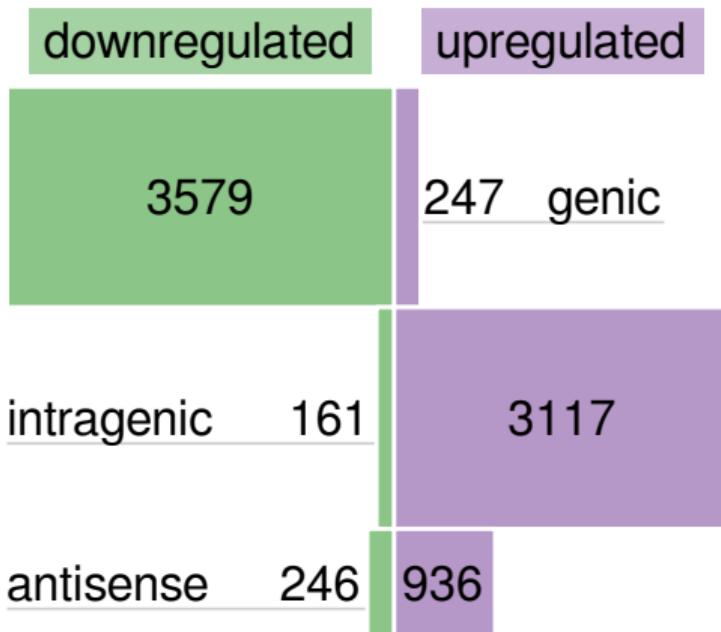


sense TSS-seq signal

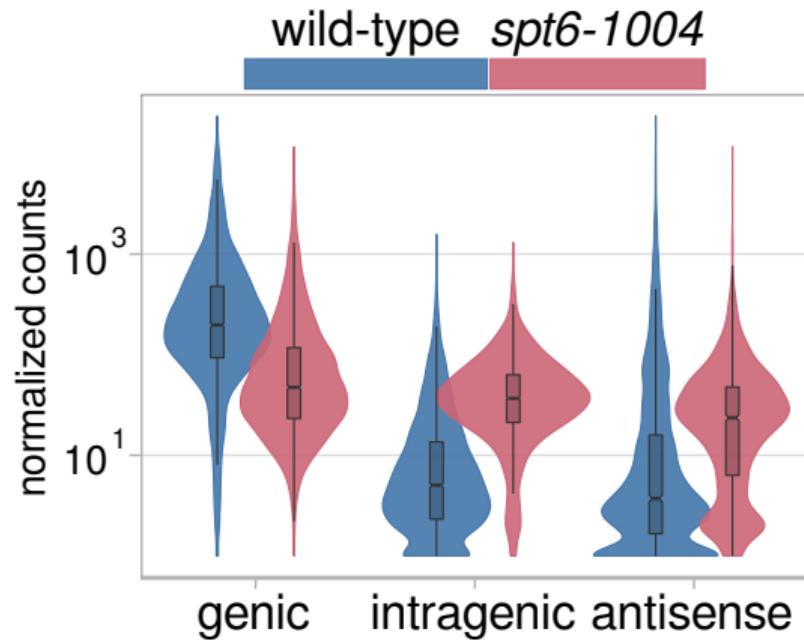
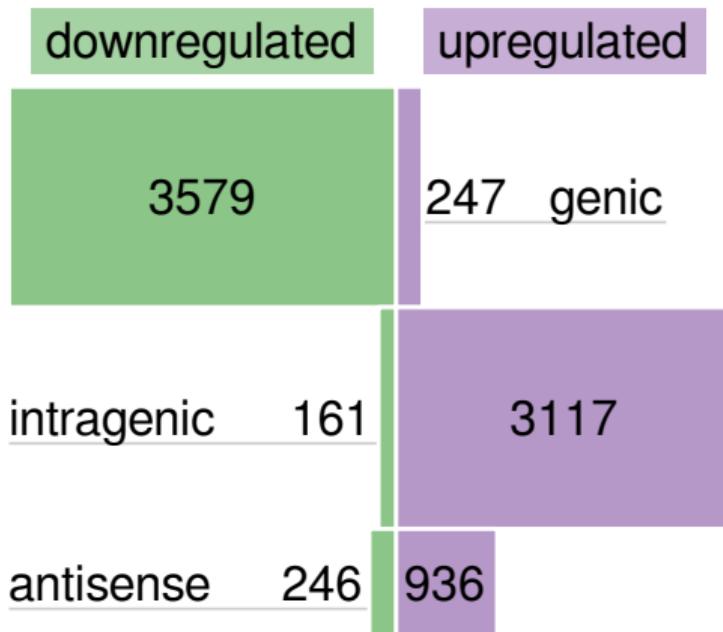




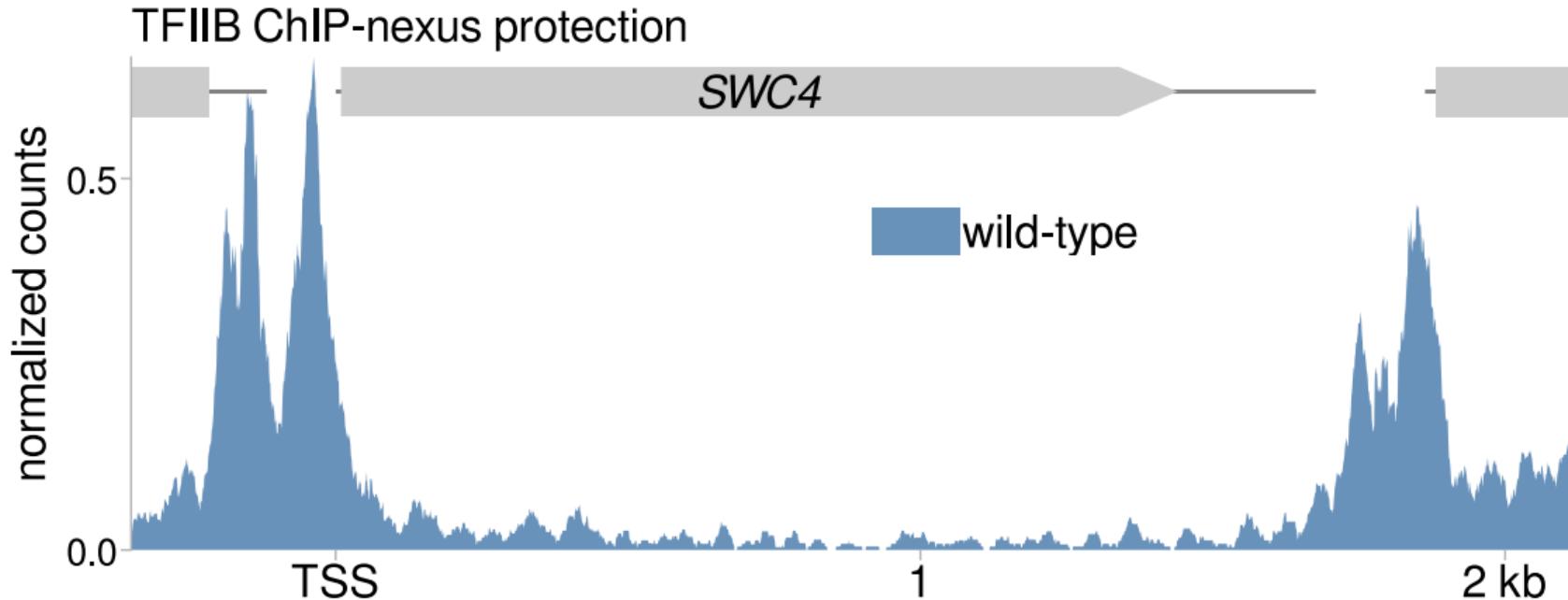
Downregulation of genic TSSs in *spt6-1004*:



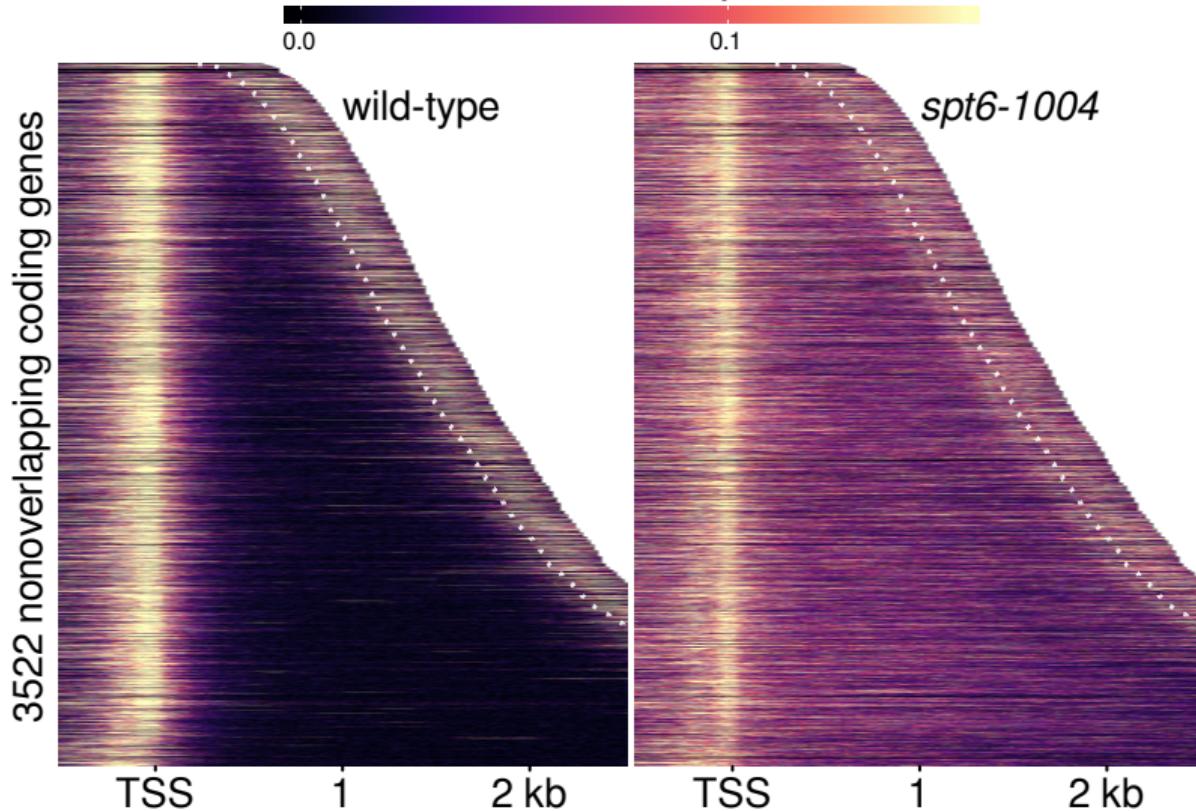
Downregulation of genic TSSs in *spt6-1004*:



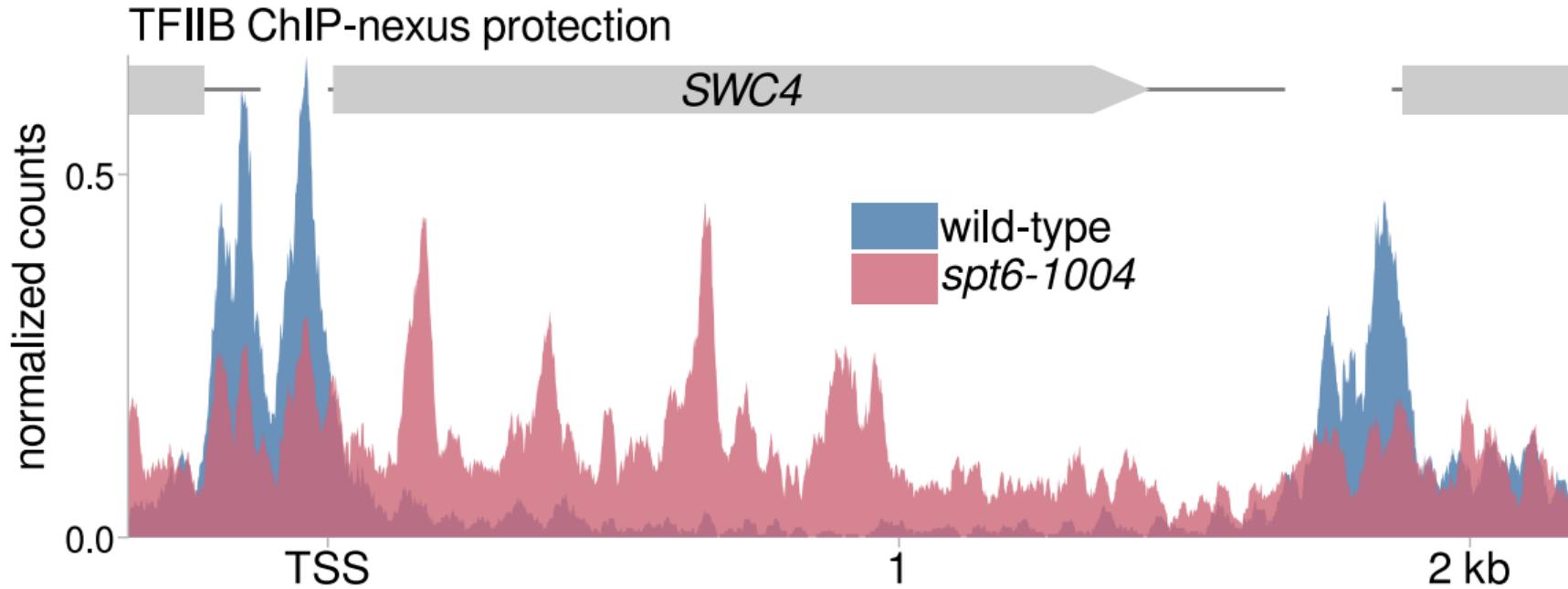
Measuring transcription initiation with TFIIB ChIP-nexus



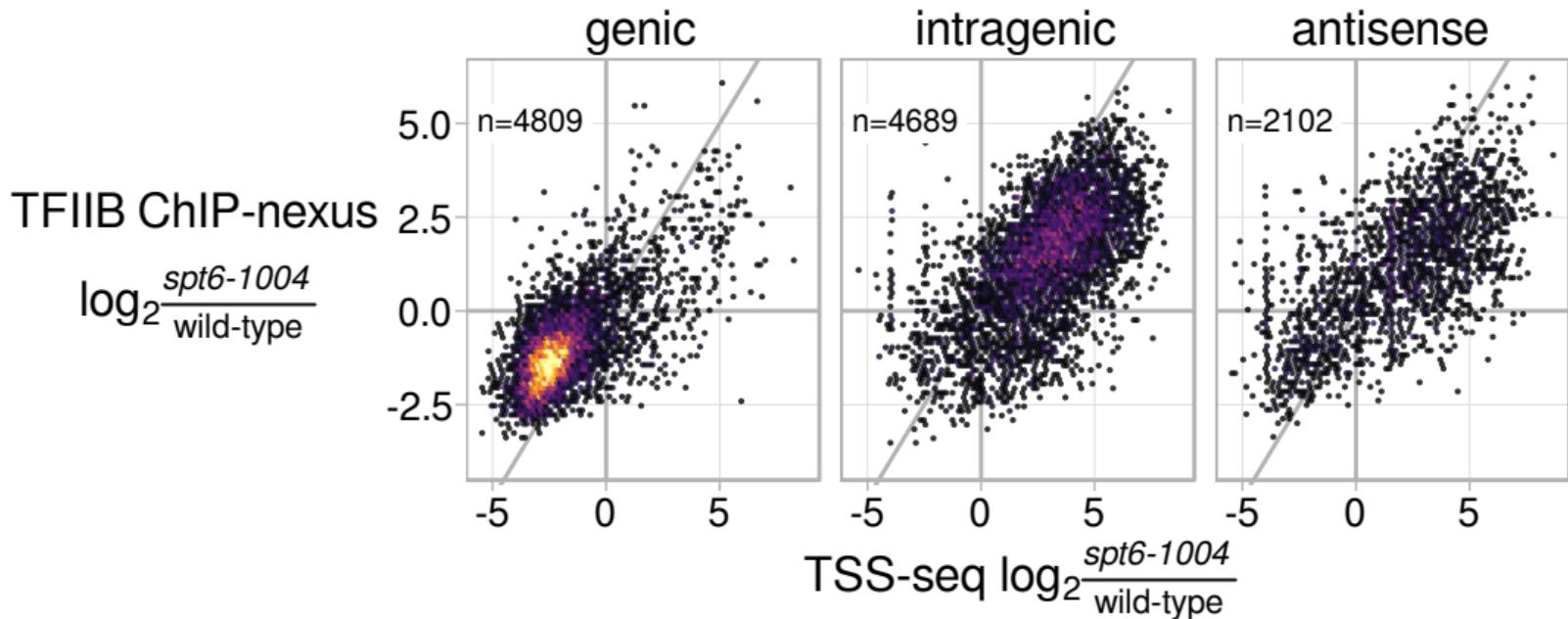
TFIIB ChIP-nexus protection



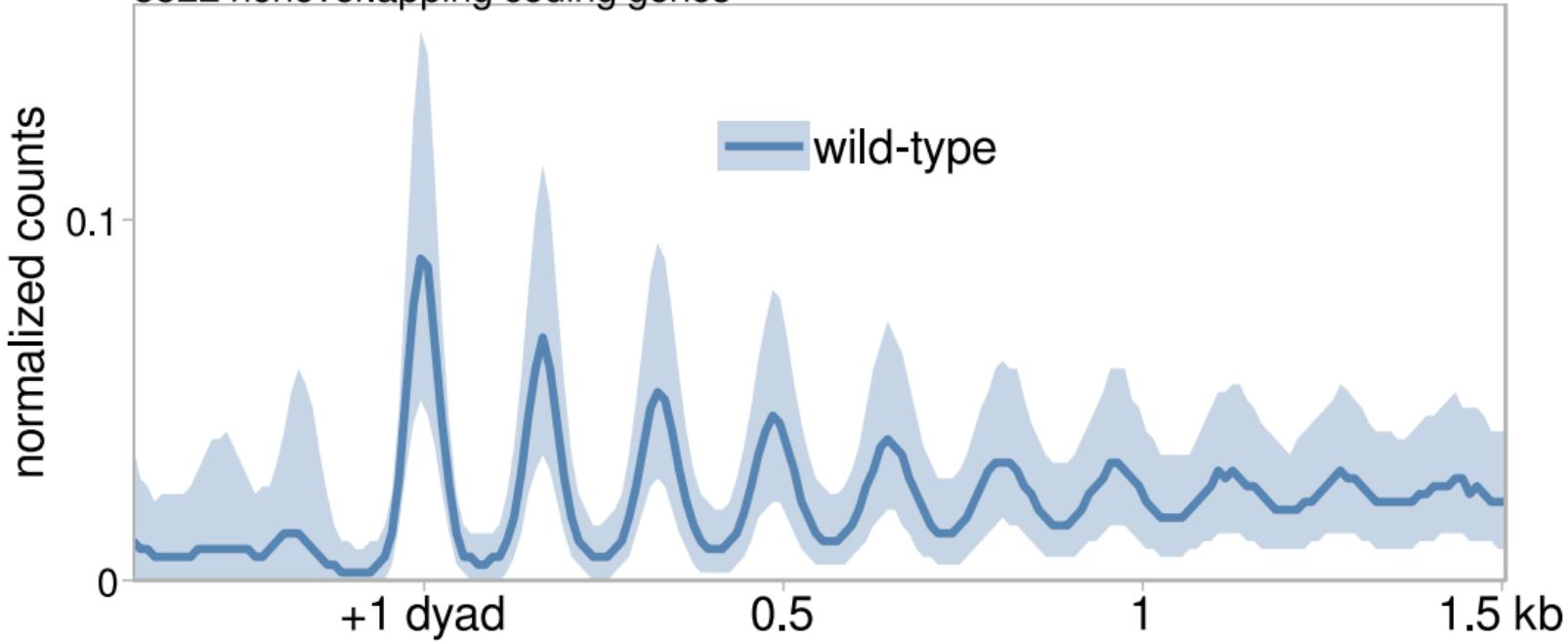
TFIIB binding changes dramatically in *spt6-1004*:



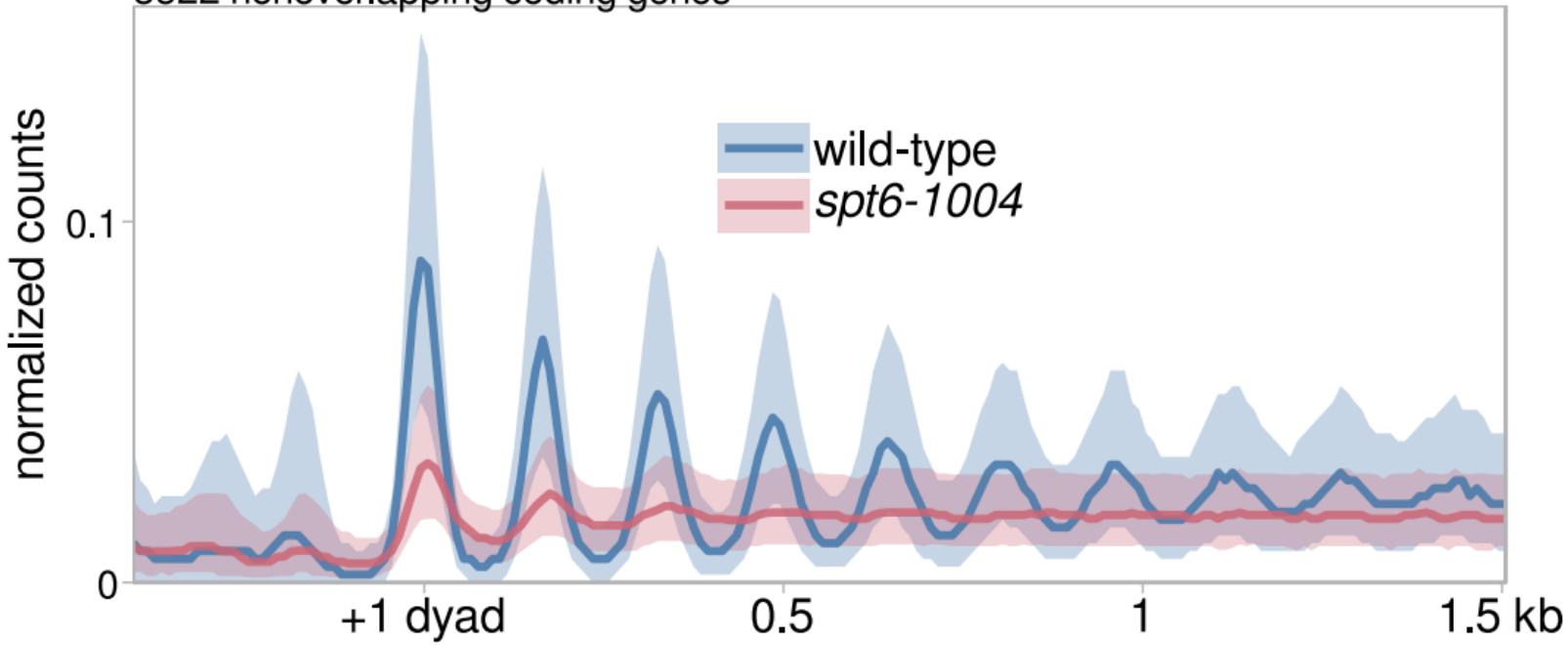
new intragenic initiation explains most intragenic transcripts



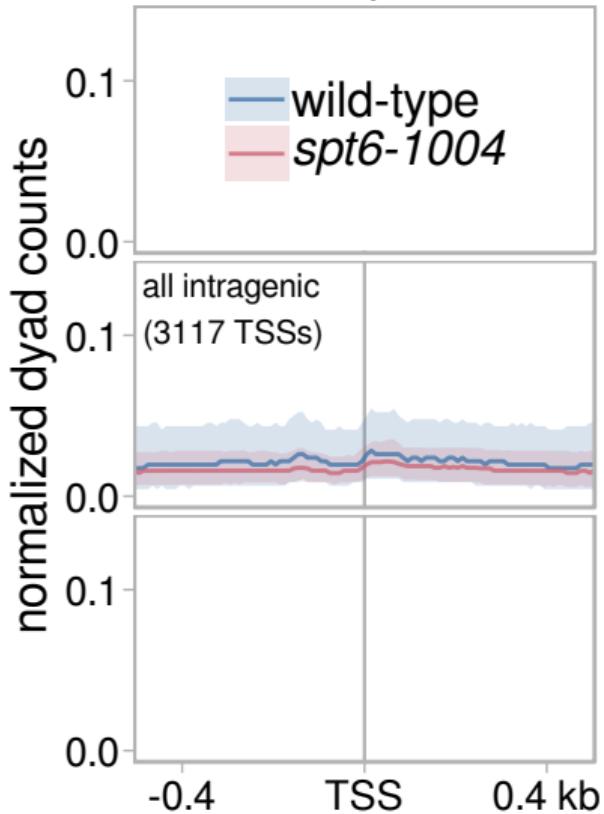
MNase-seq dyad signal
3522 nonoverlapping coding genes



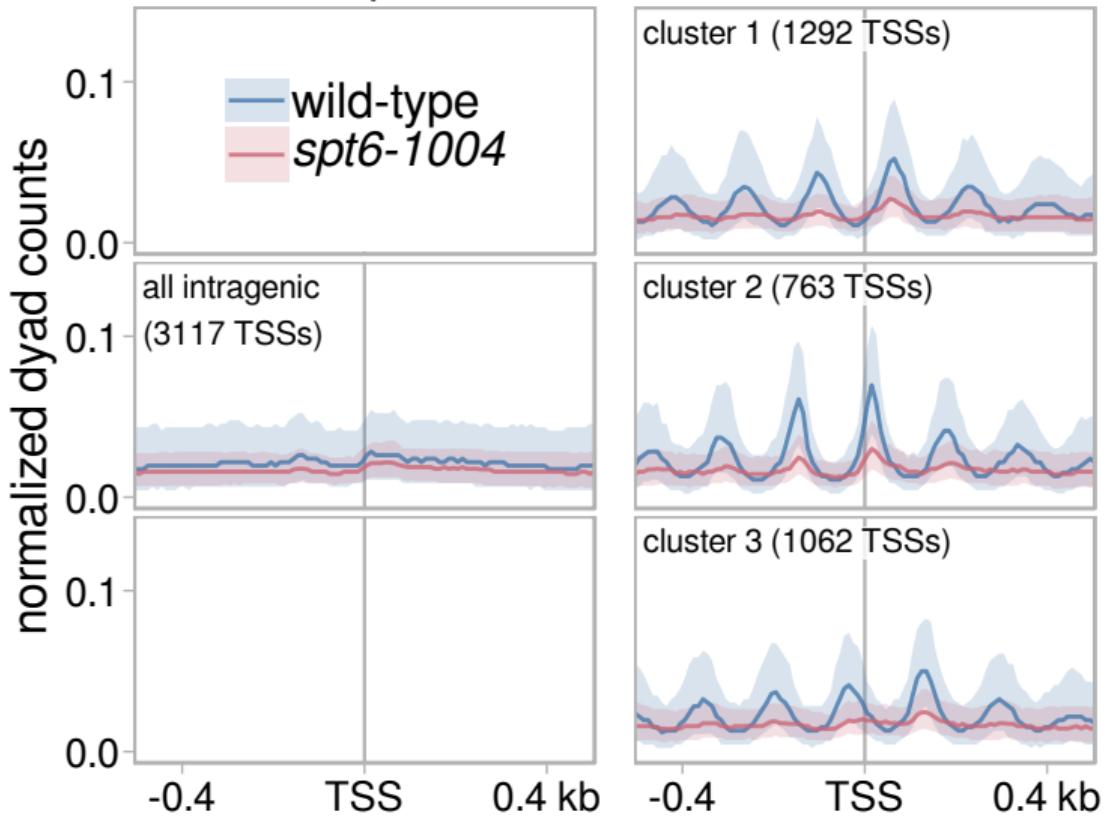
MNase-seq dyad signal
3522 nonoverlapping coding genes



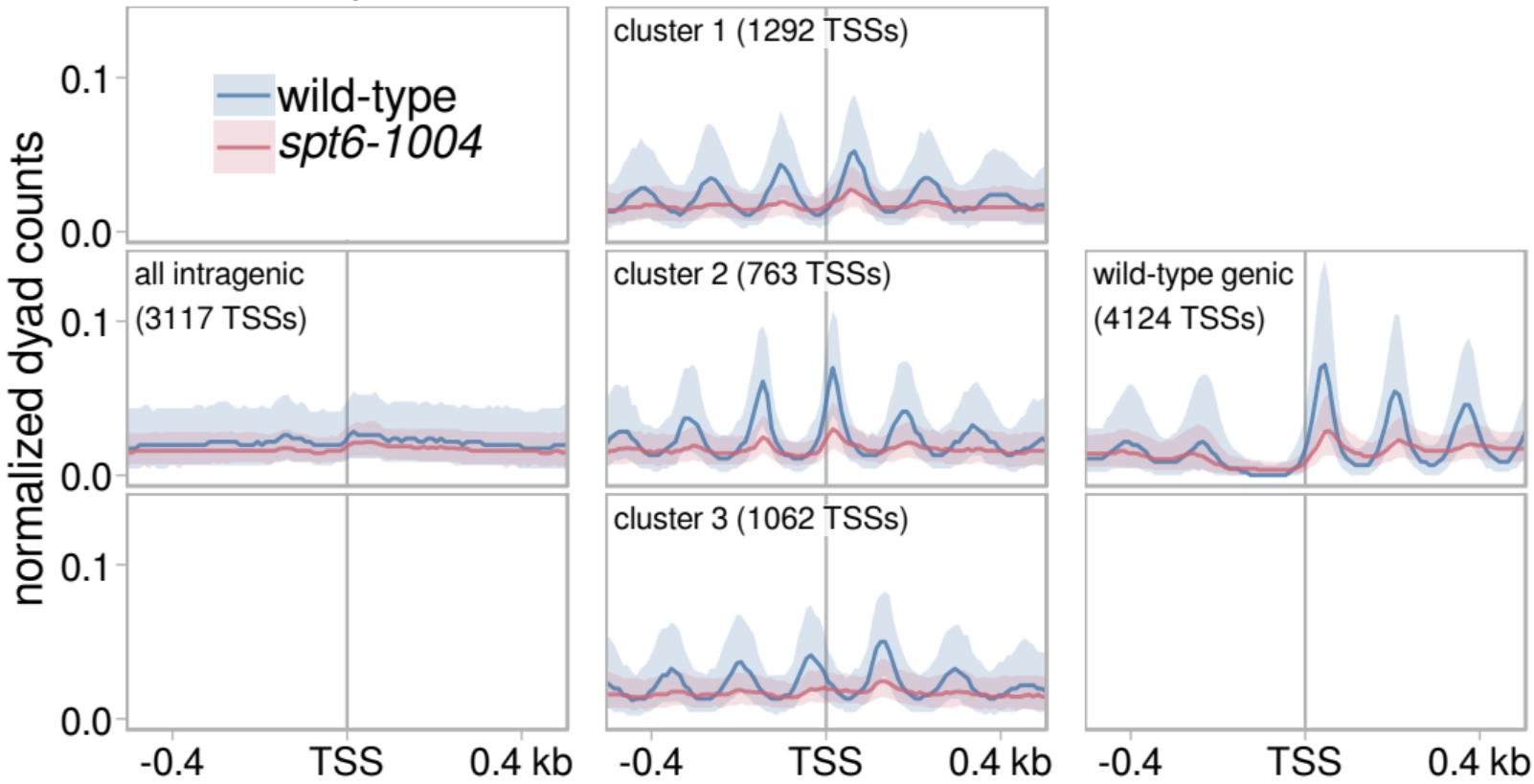
MNase-seq



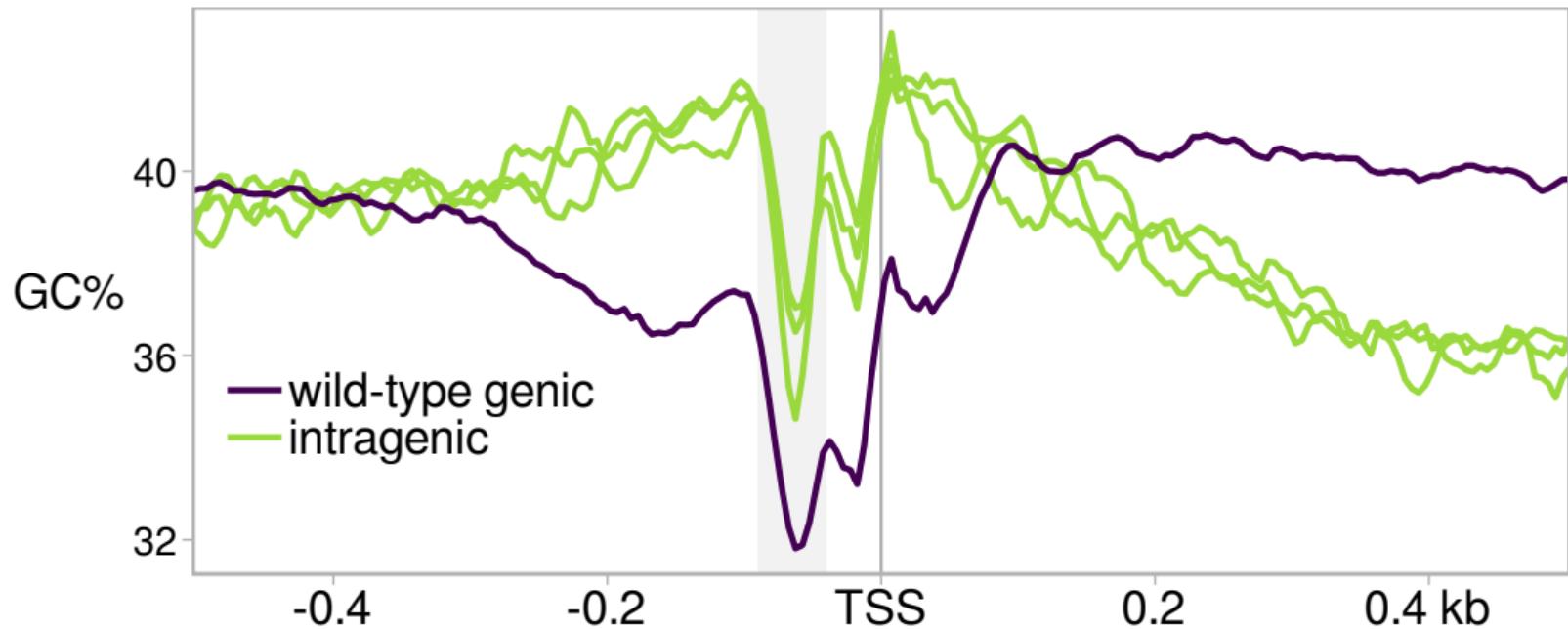
MNase-seq



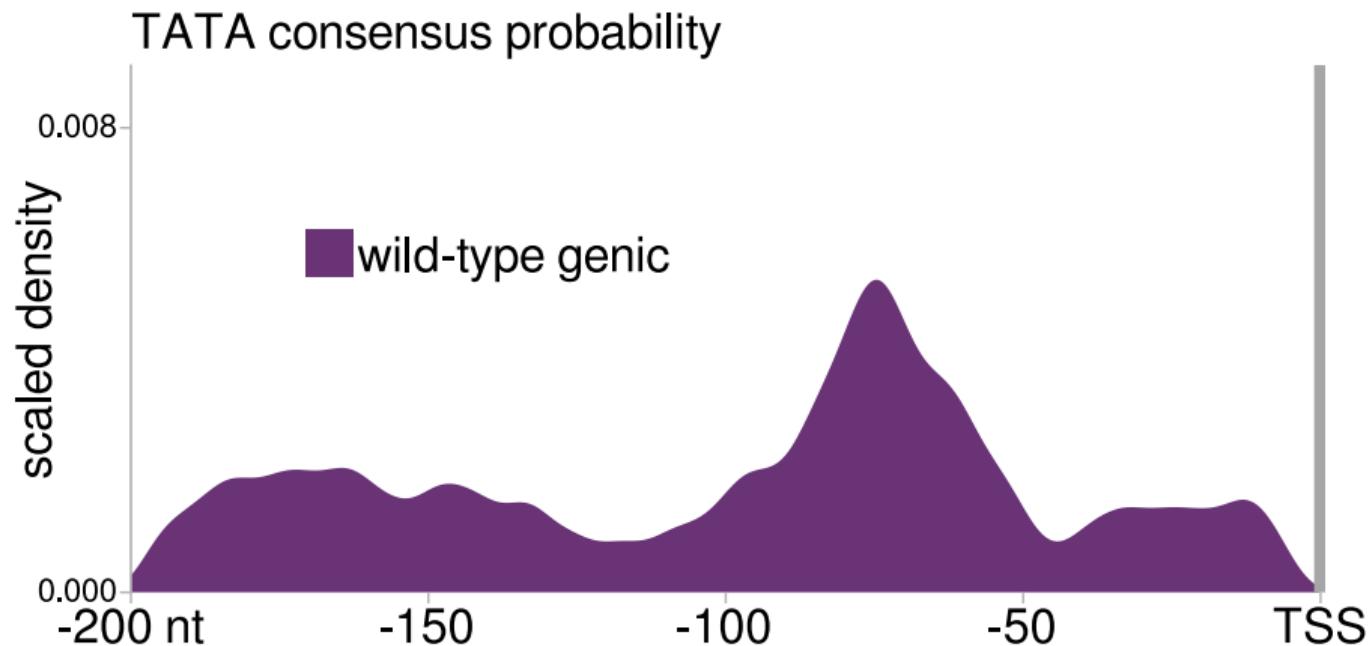
MNase-seq



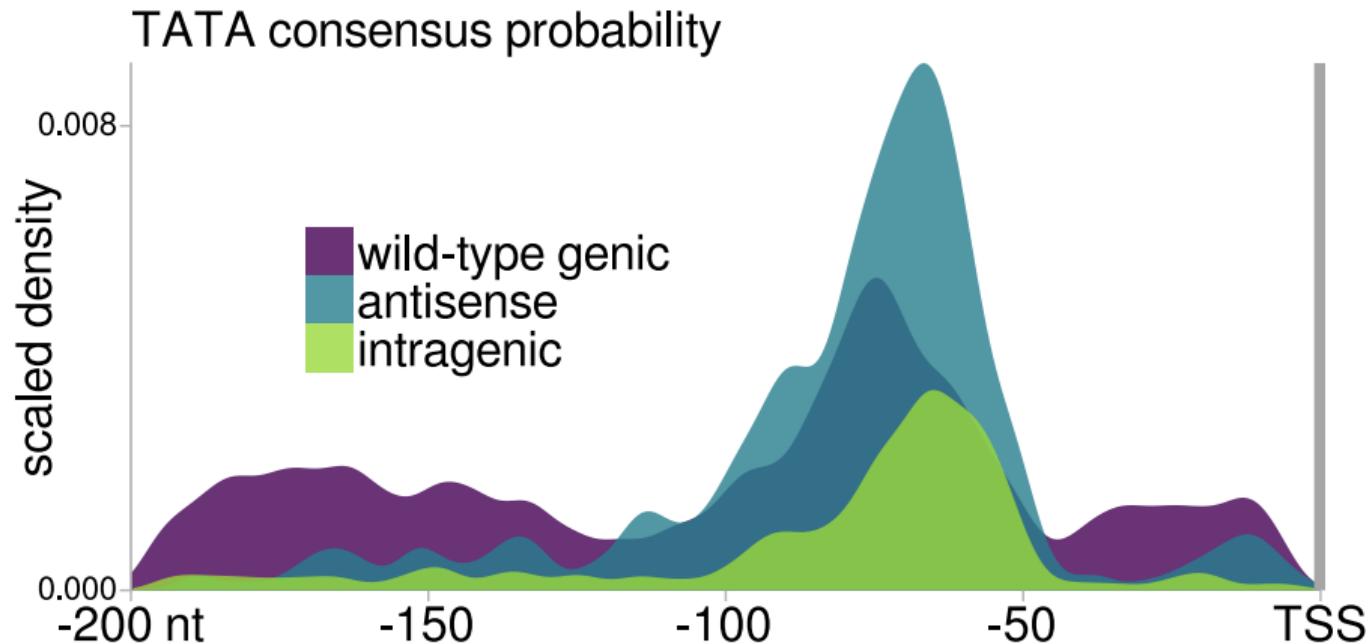
Features of intragenic promoters



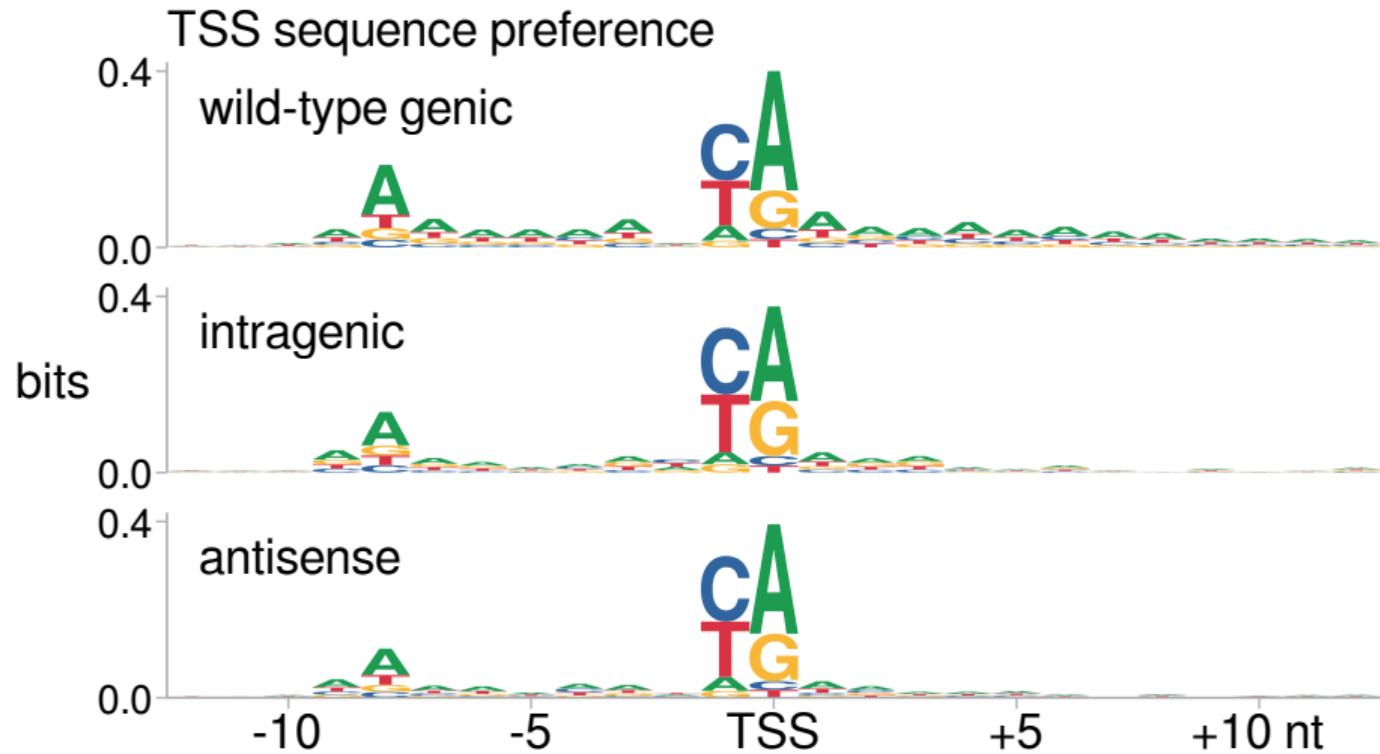
Features of intragenic promoters



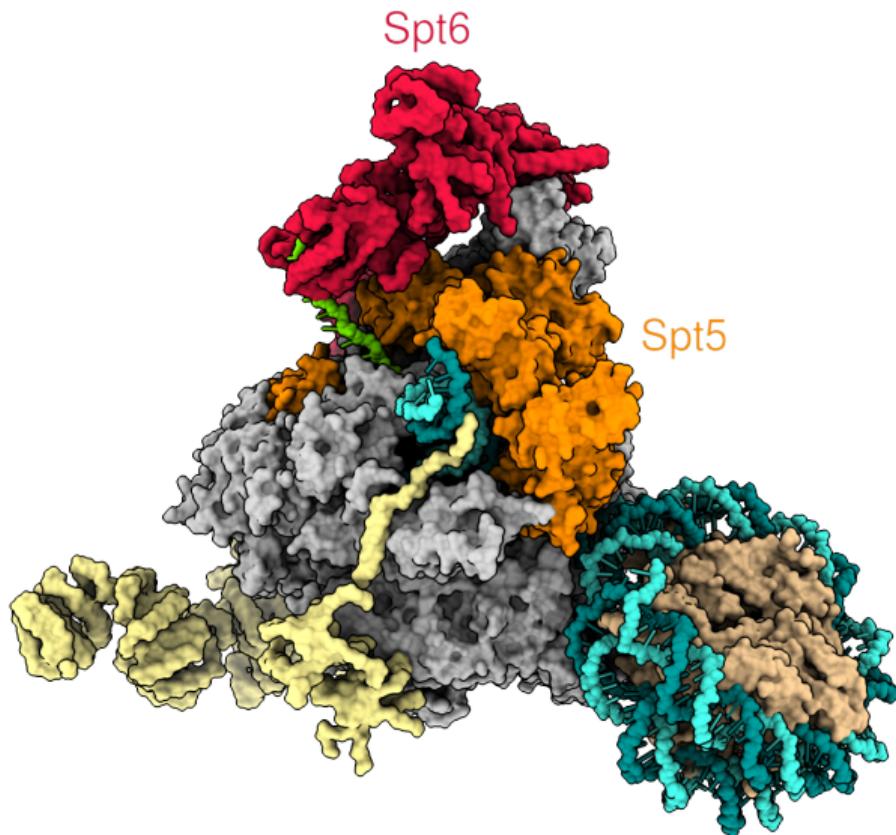
Features of intragenic promoters



Features of intragenic promoters



Spt6 summary and model

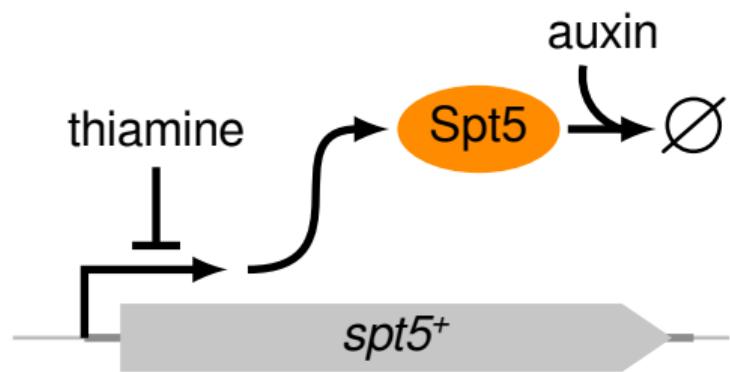


Vos *et al.* (2018). *Nature*
Farnung *et al.* (2018). *Nat. Commun.*

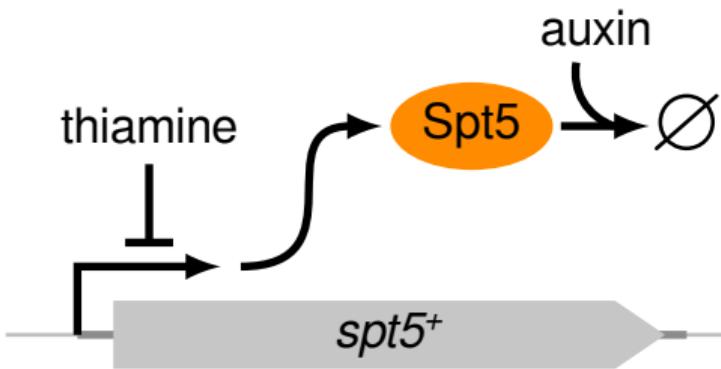
Spt5 project collaborators

Ameet Shetty NET-seq,
ChIP-seq,
RNA-seq,
TSS-seq,
MNase-seq,
etc.

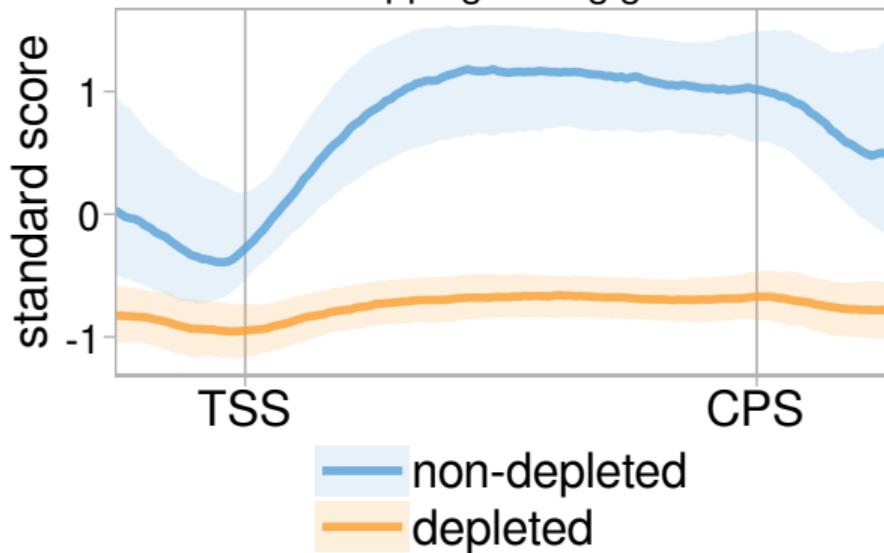
Spt5 depletion system



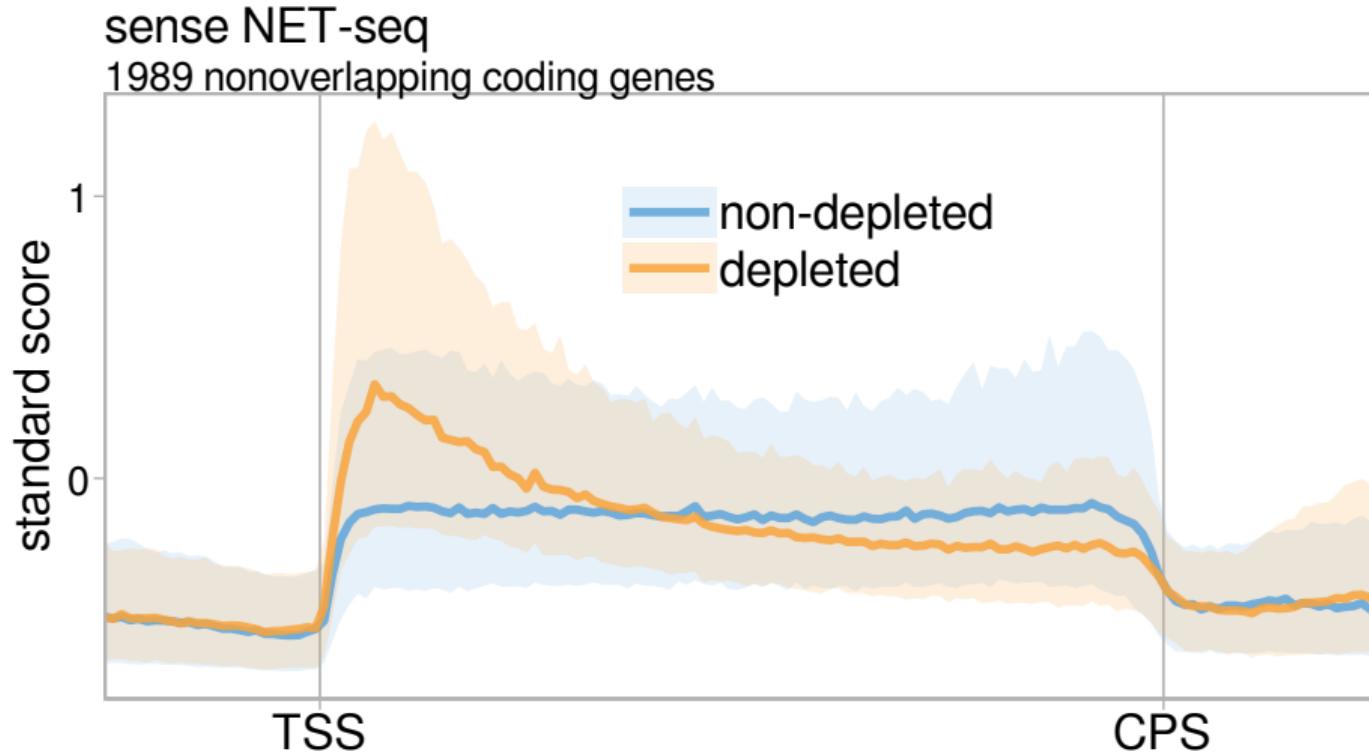
Spt5 depletion system



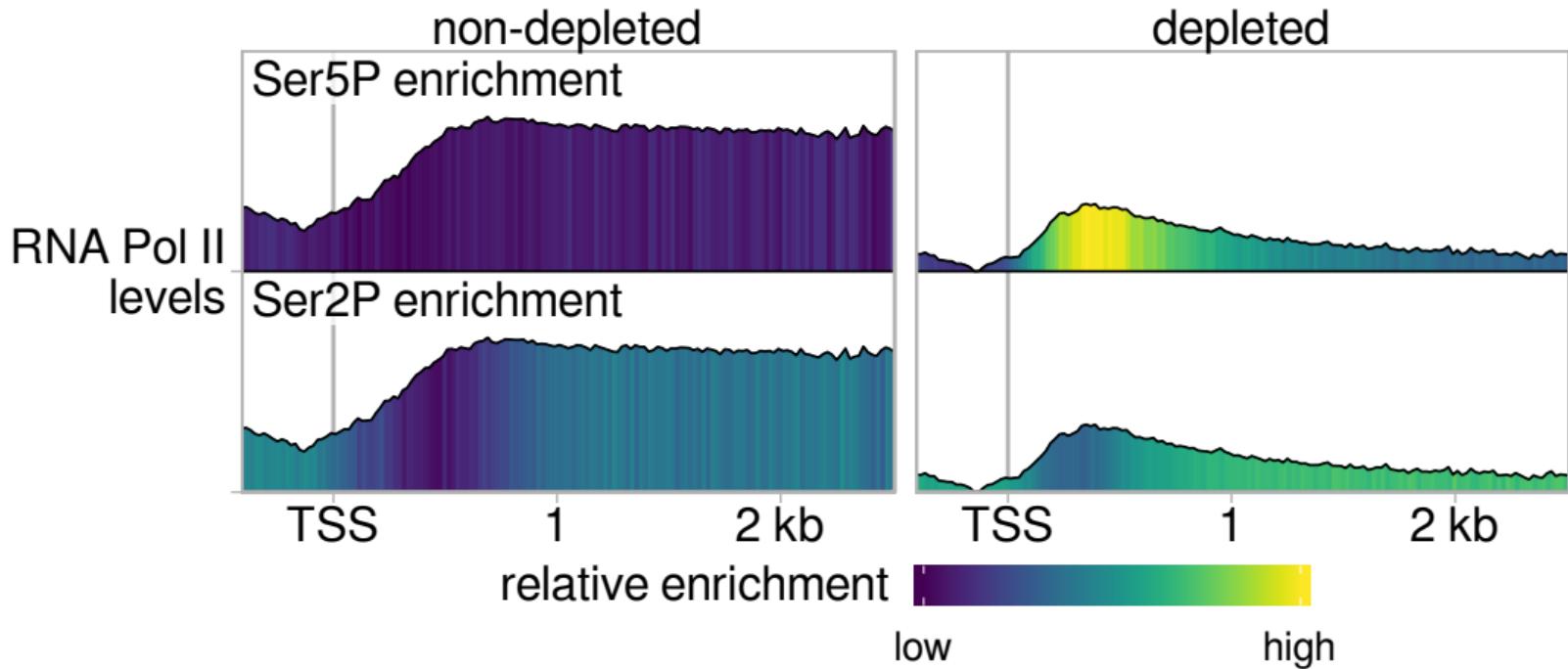
Spt5 ChIP-seq
1989 nonoverlapping coding genes



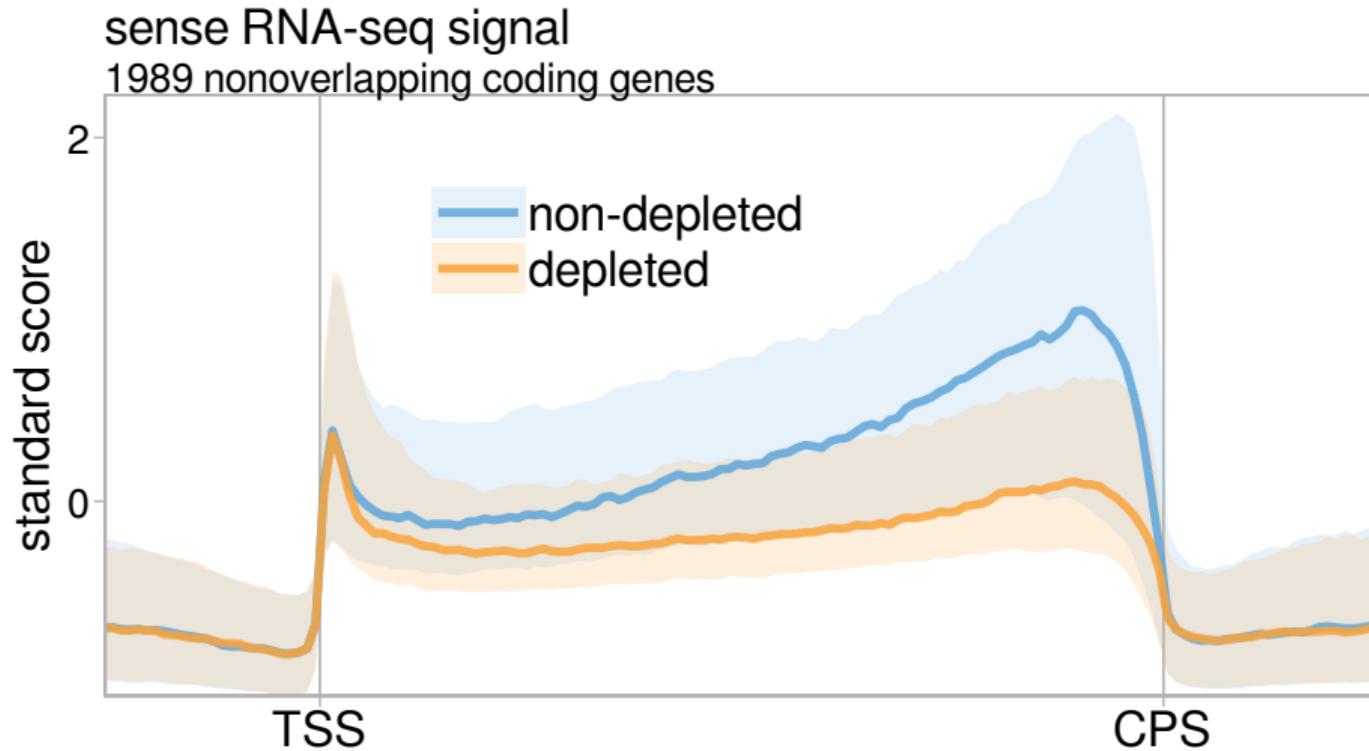
Elongation defects upon Spt5 depletion



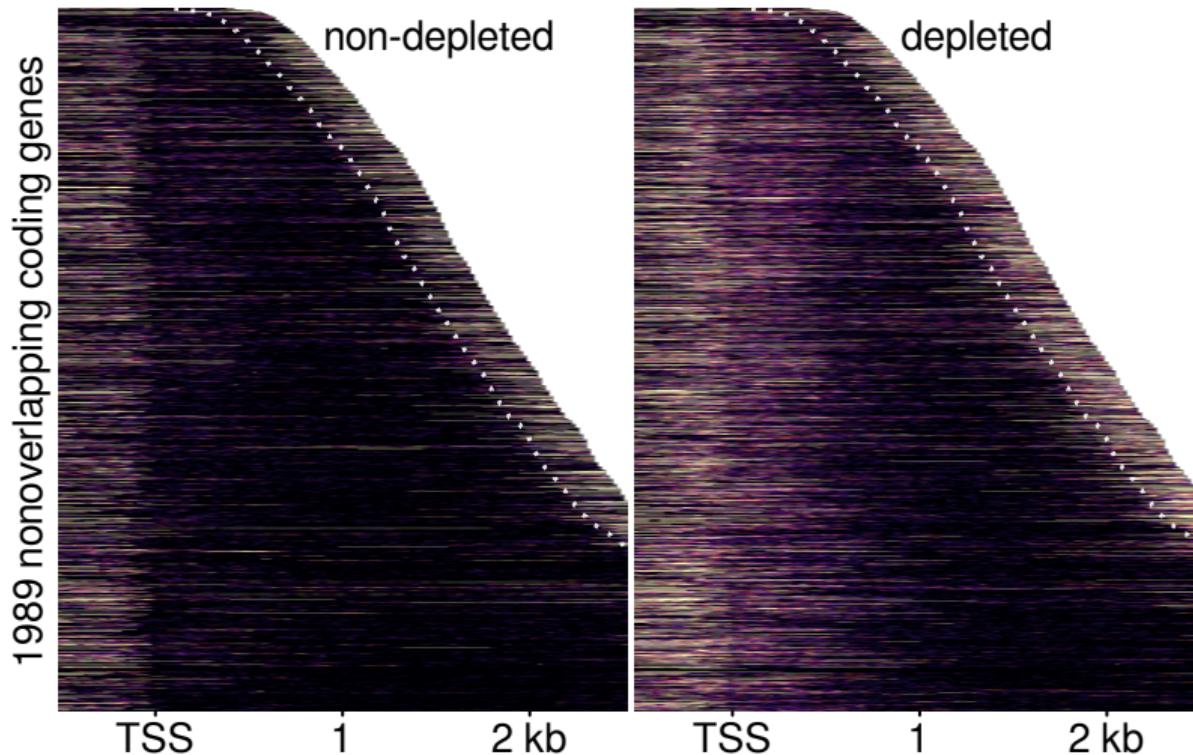
Trapped Pol II is enriched for CTD serine 5 phosphorylation

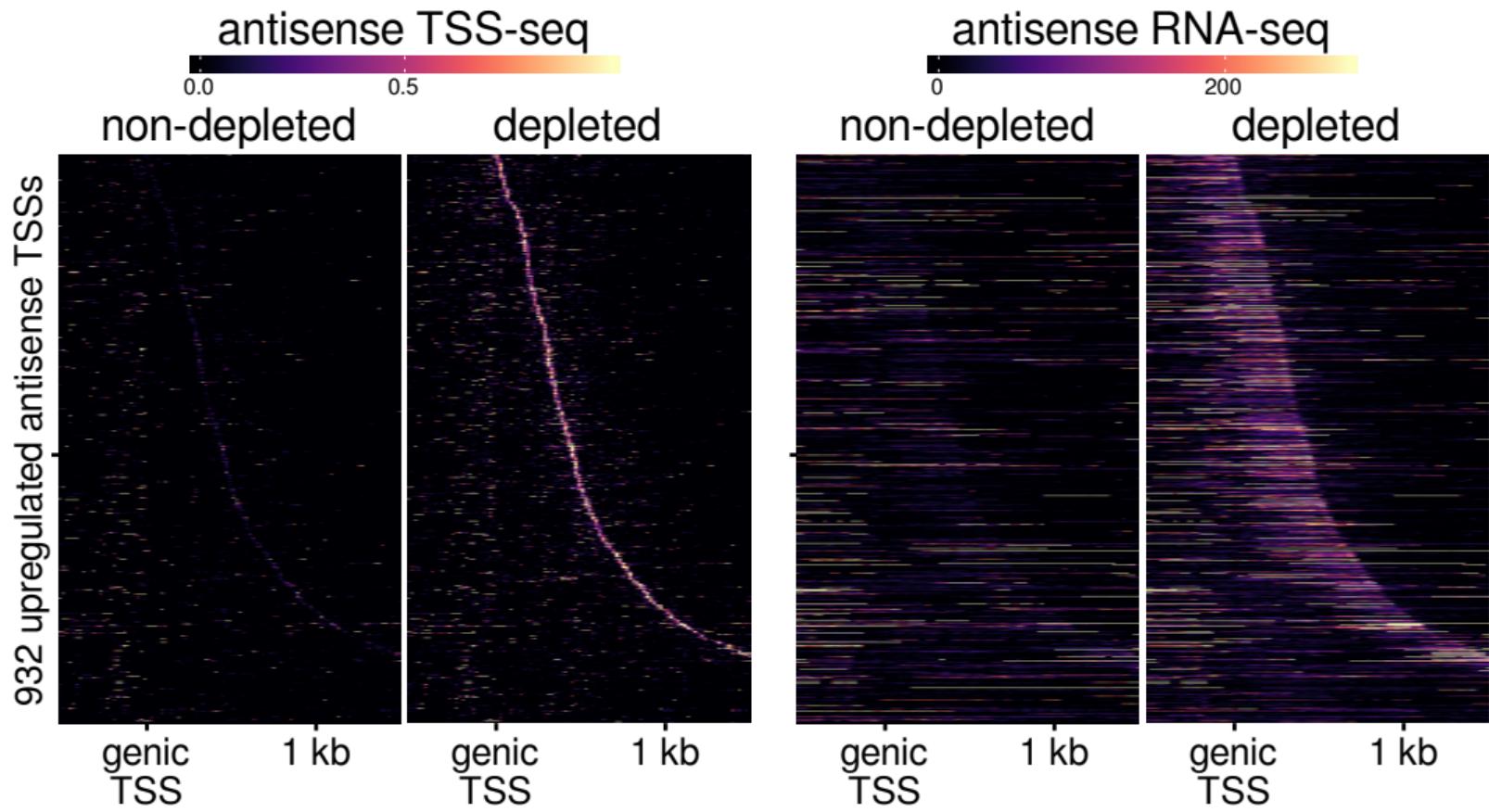


Evidence for premature termination upon Spt5 depletion

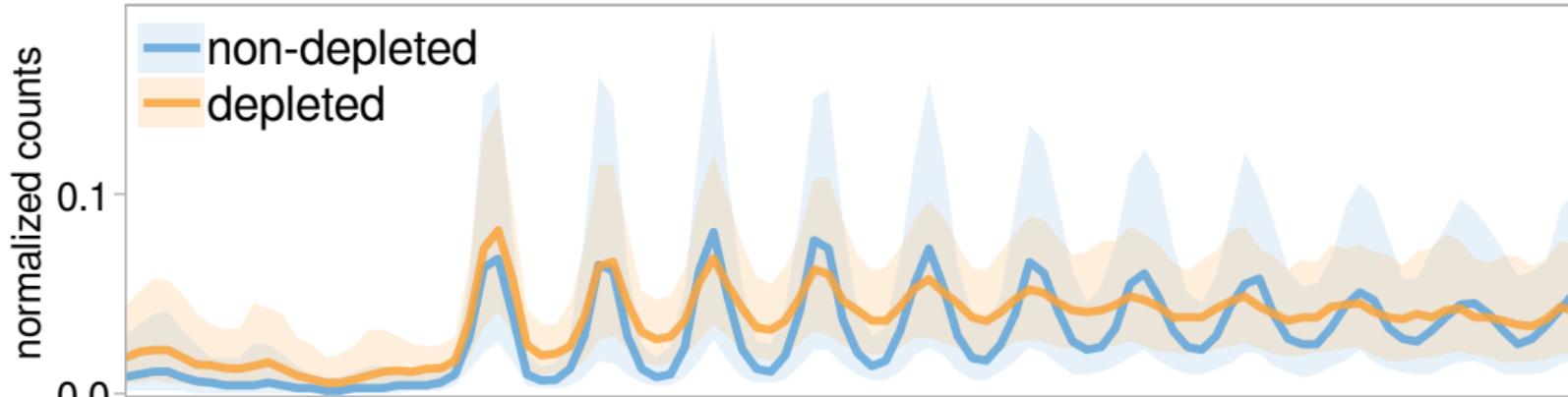


antisense RNA-seq signal

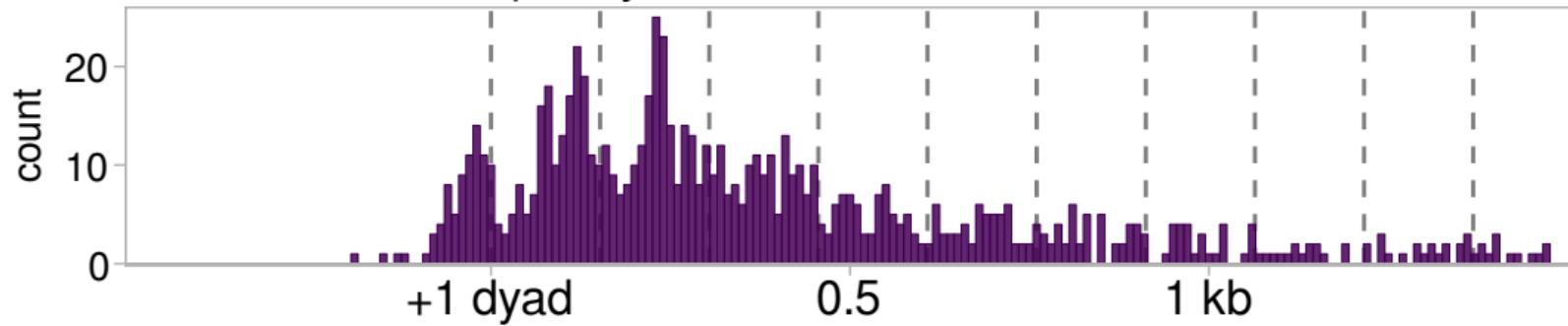




MNase-seq dyad signal



antisense TSS frequency



Spt5 summary and model

WT intragenic transcription

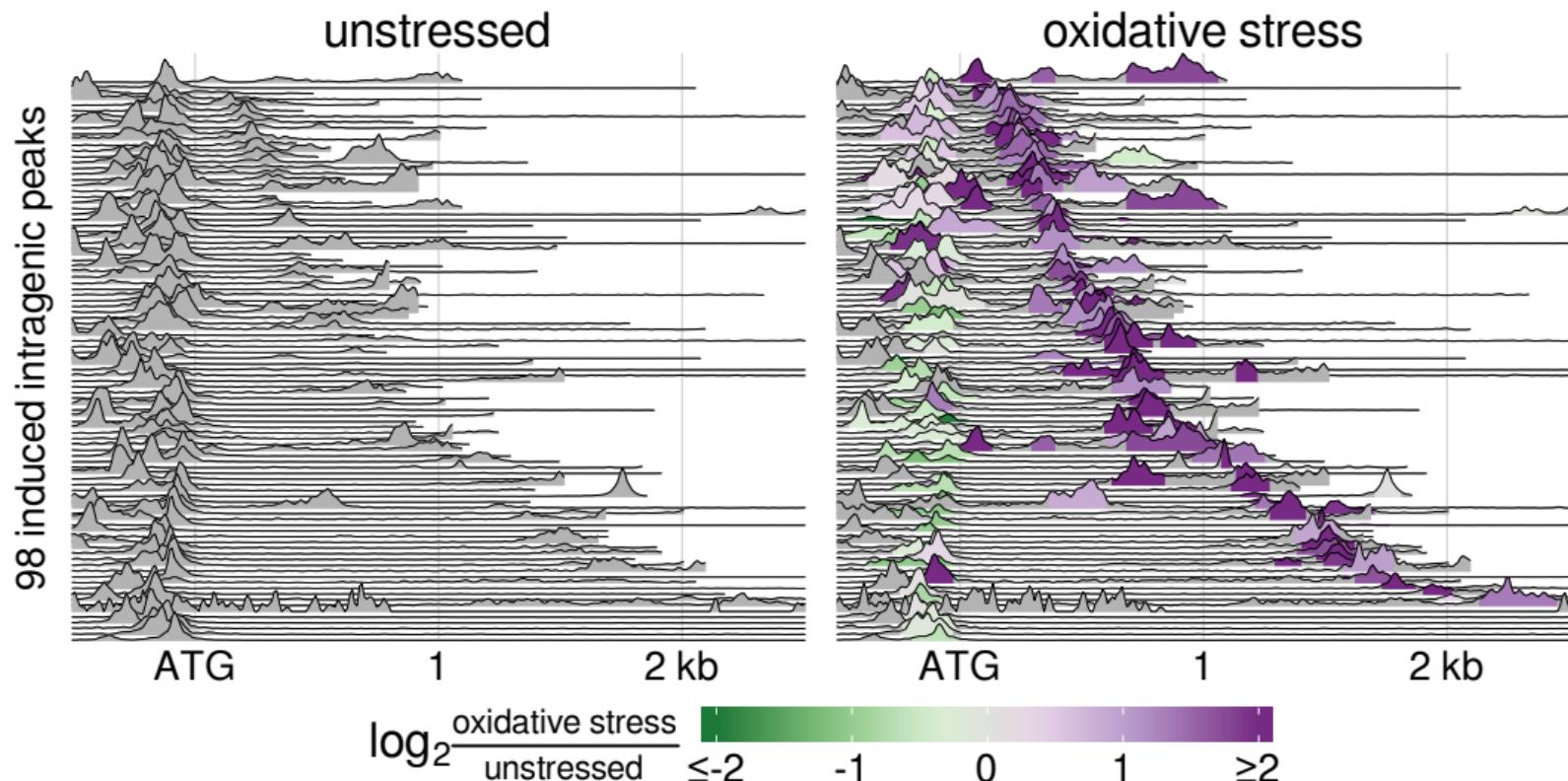
project collaborators

Steve Doris TSS-seq and ChIP-nexus

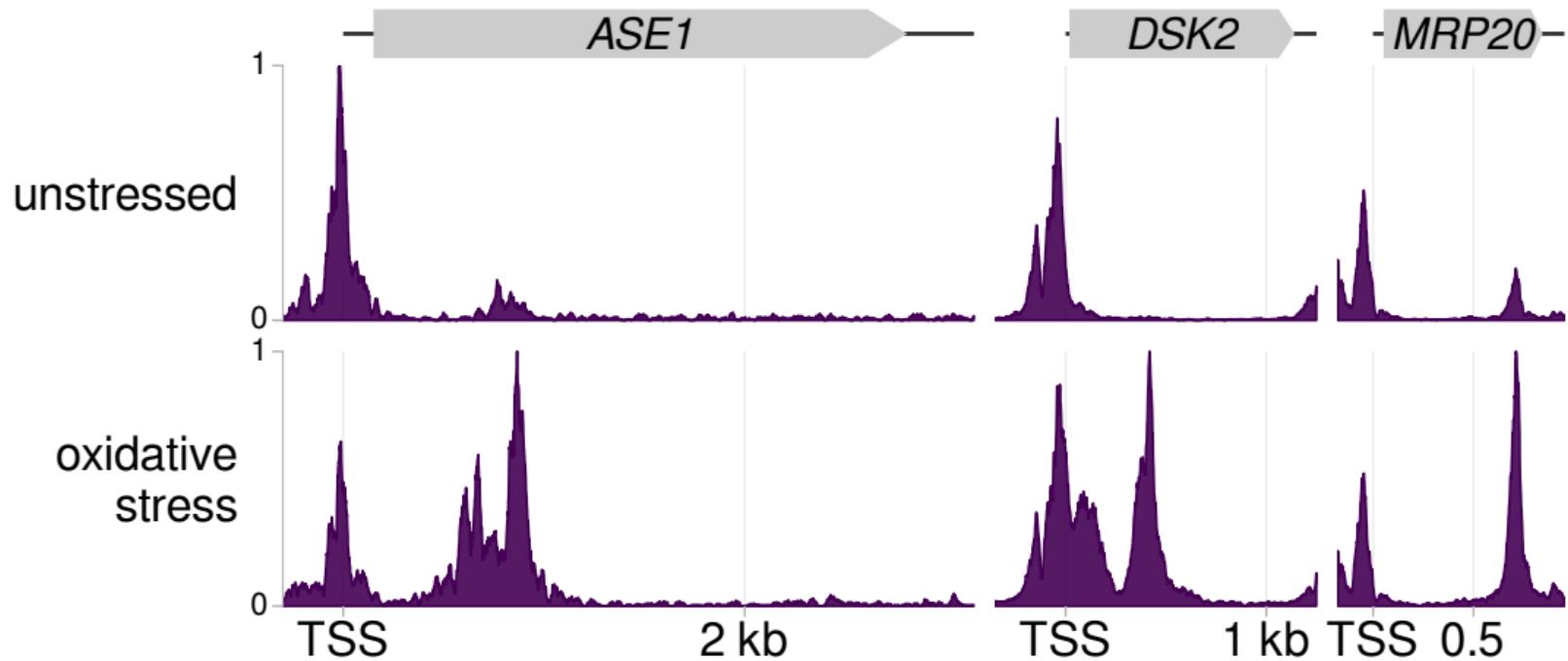
Dan Spatt polyribosome fractionation,
competitive growth assays,
and Northern blots

James Warner Northern blots

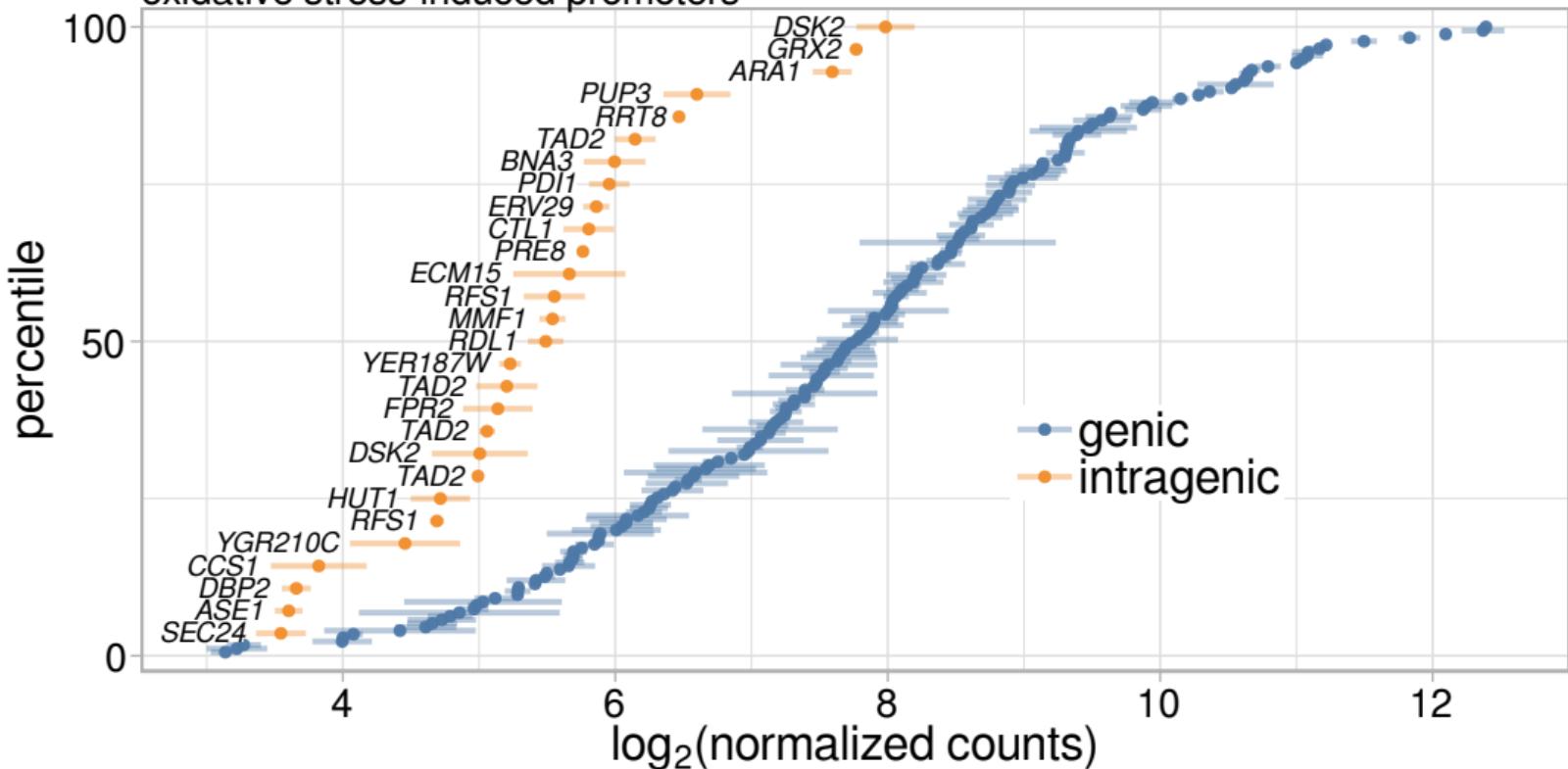
relative TFIIB ChIP-nexus protection



relative TFIIB ChIP-nexus protection

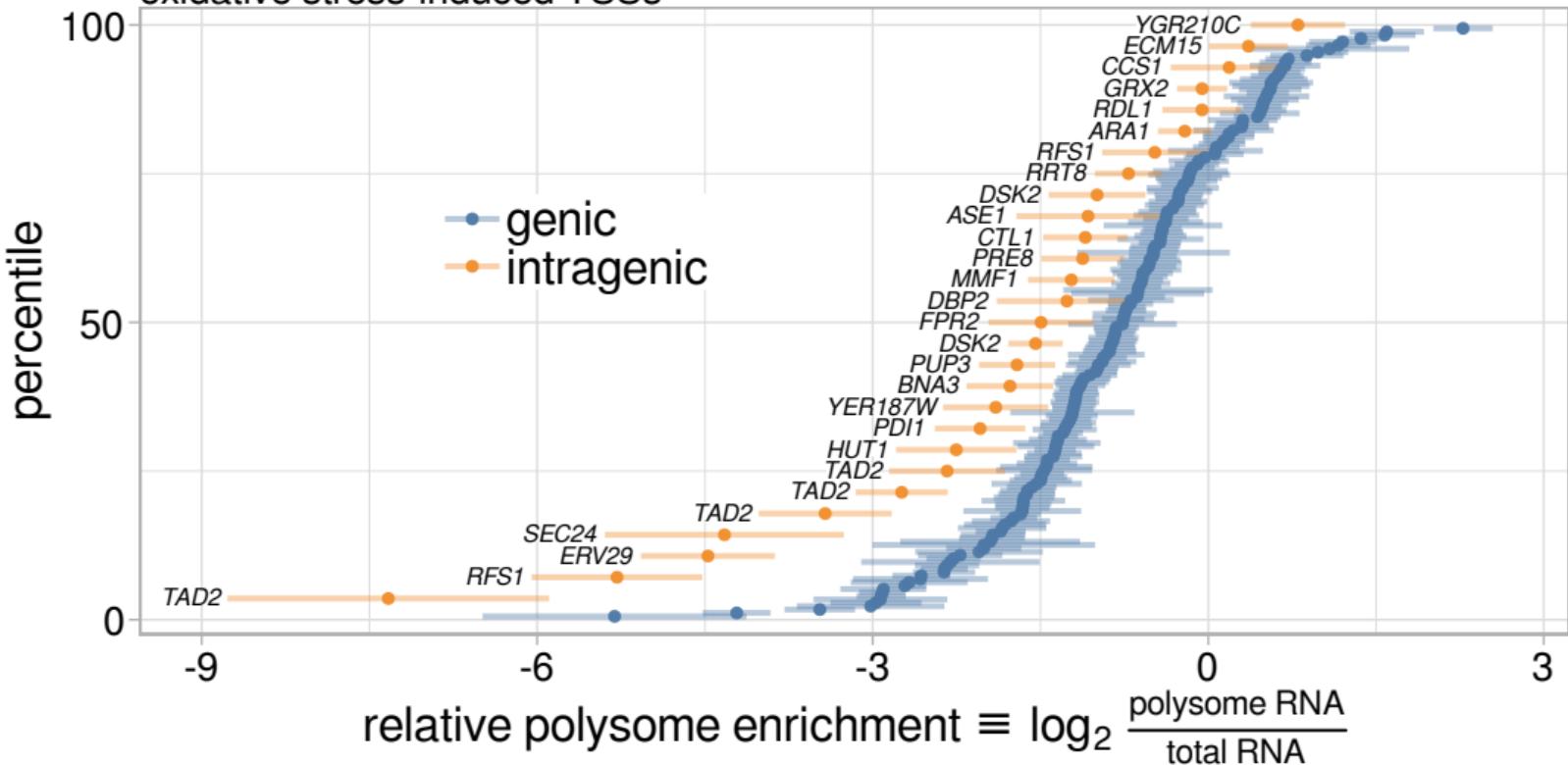


TSS expression levels in oxidative stress oxidative stress-induced promoters

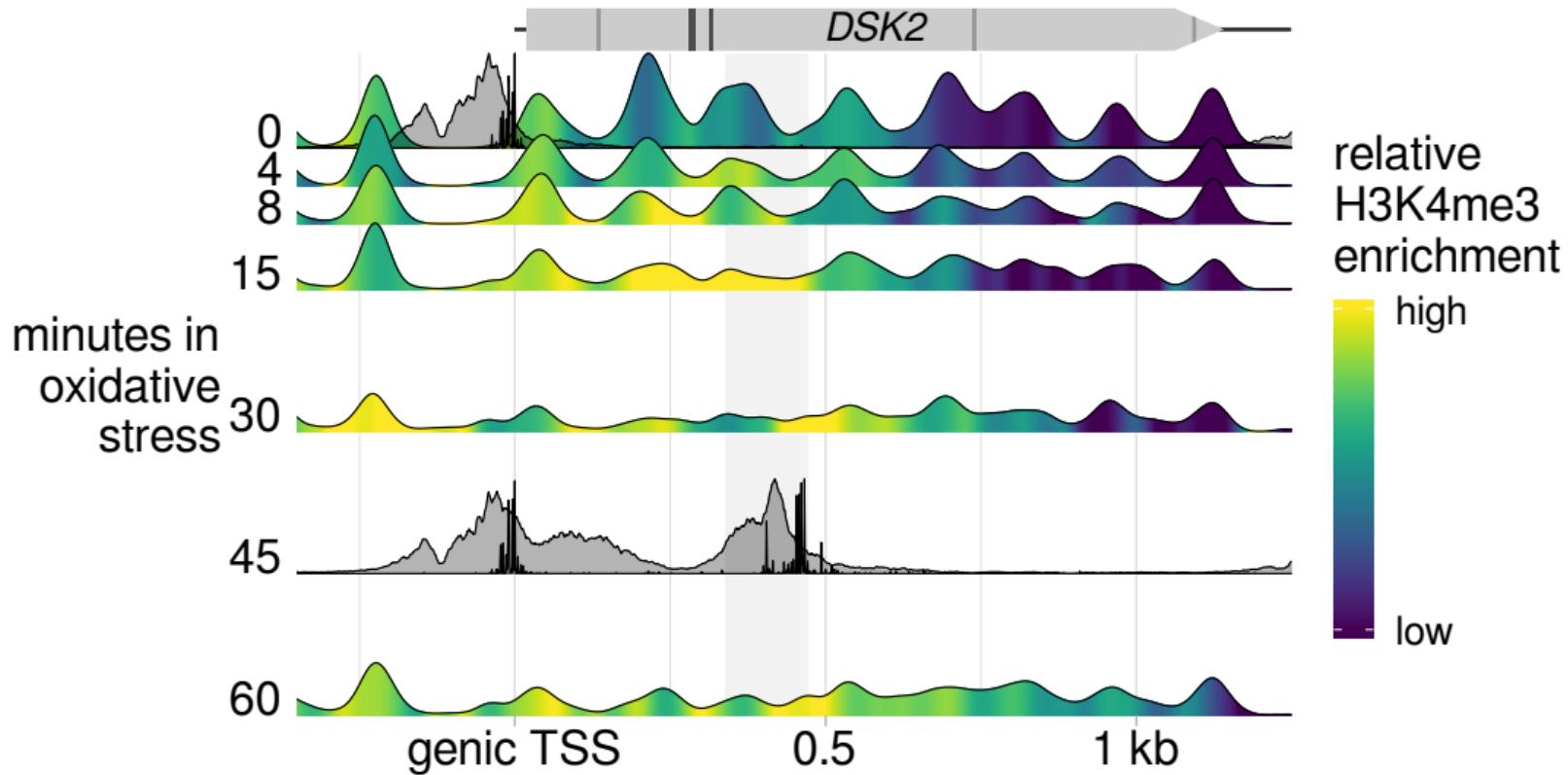


polysome enrichment in oxidative stress

oxidative stress-induced TSSs

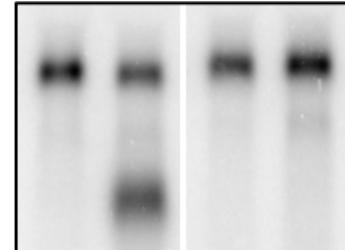


MNase dyads, TFIIB protection, and sense TSSs



MNase-ChIP-seq: Weiner *et al.* (2015). Mol. Cell

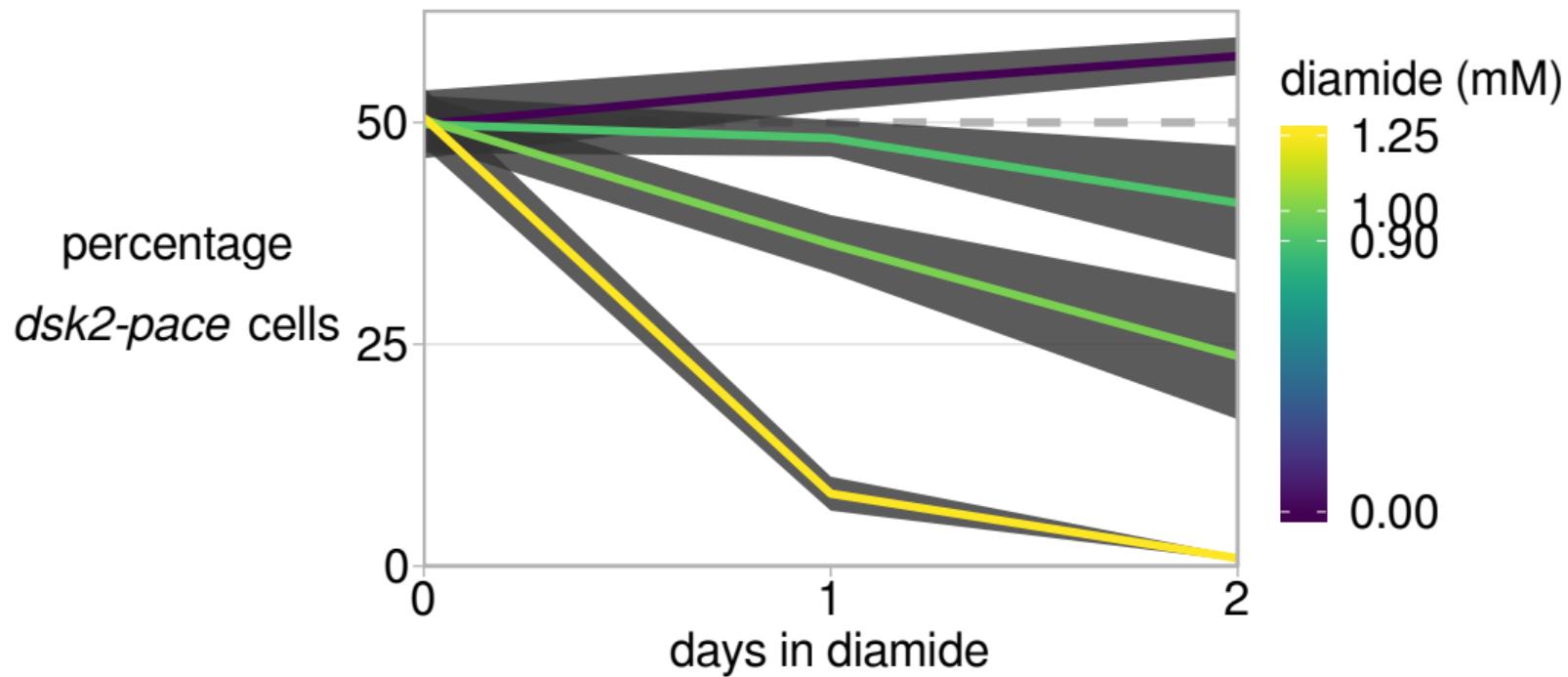
diamide: $\frac{DSK2}{- +}$ $\frac{dsk2\text{-pace}}{- +}$



DSK2 full-length

DSK2 intragenic

SNR190



Summary

Acknowledgements