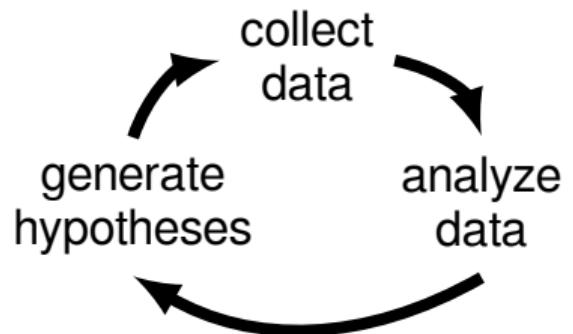
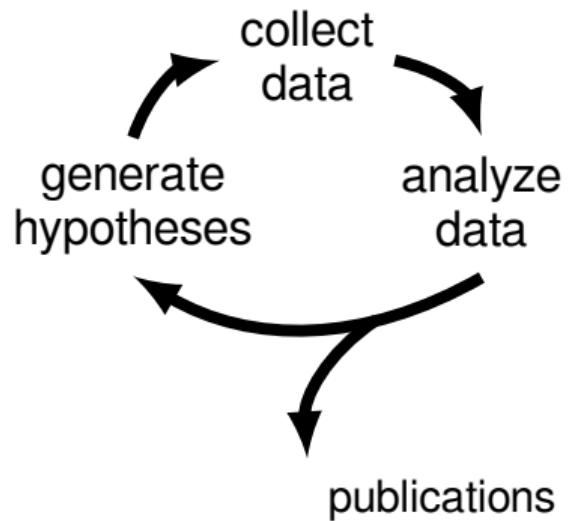


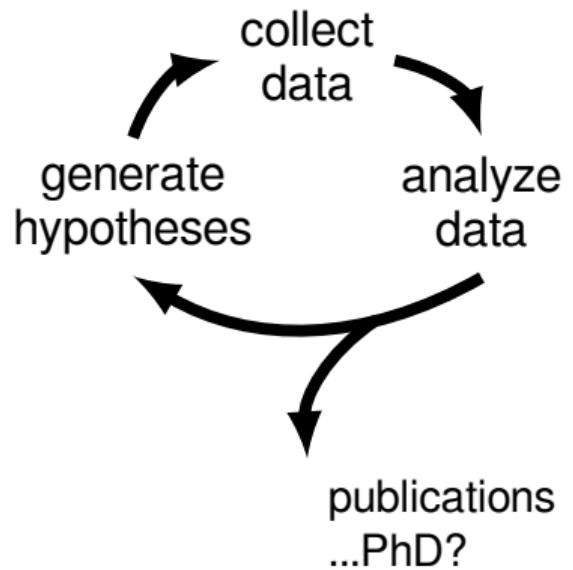
Genomic analyses of transcription elongation factors and intragenic transcription

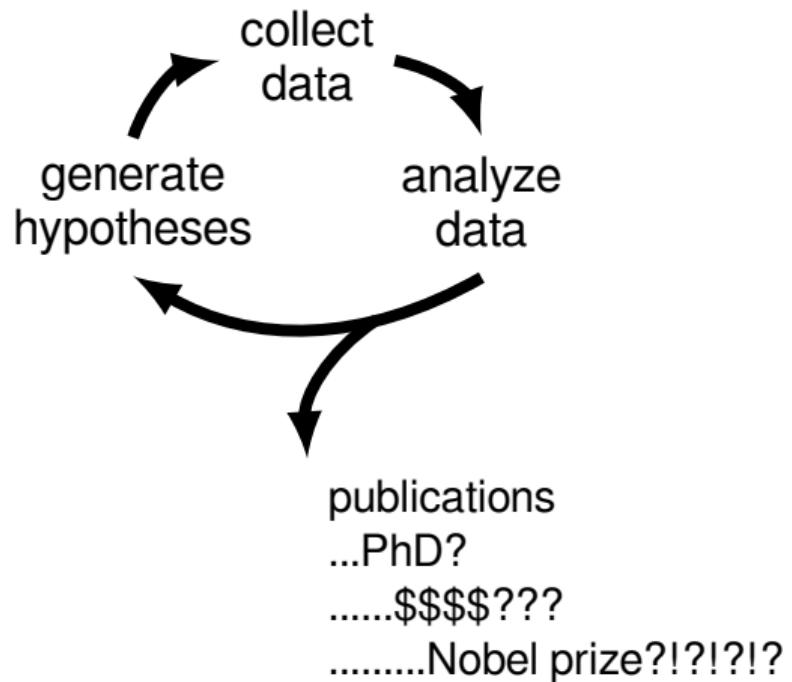
James Chuang

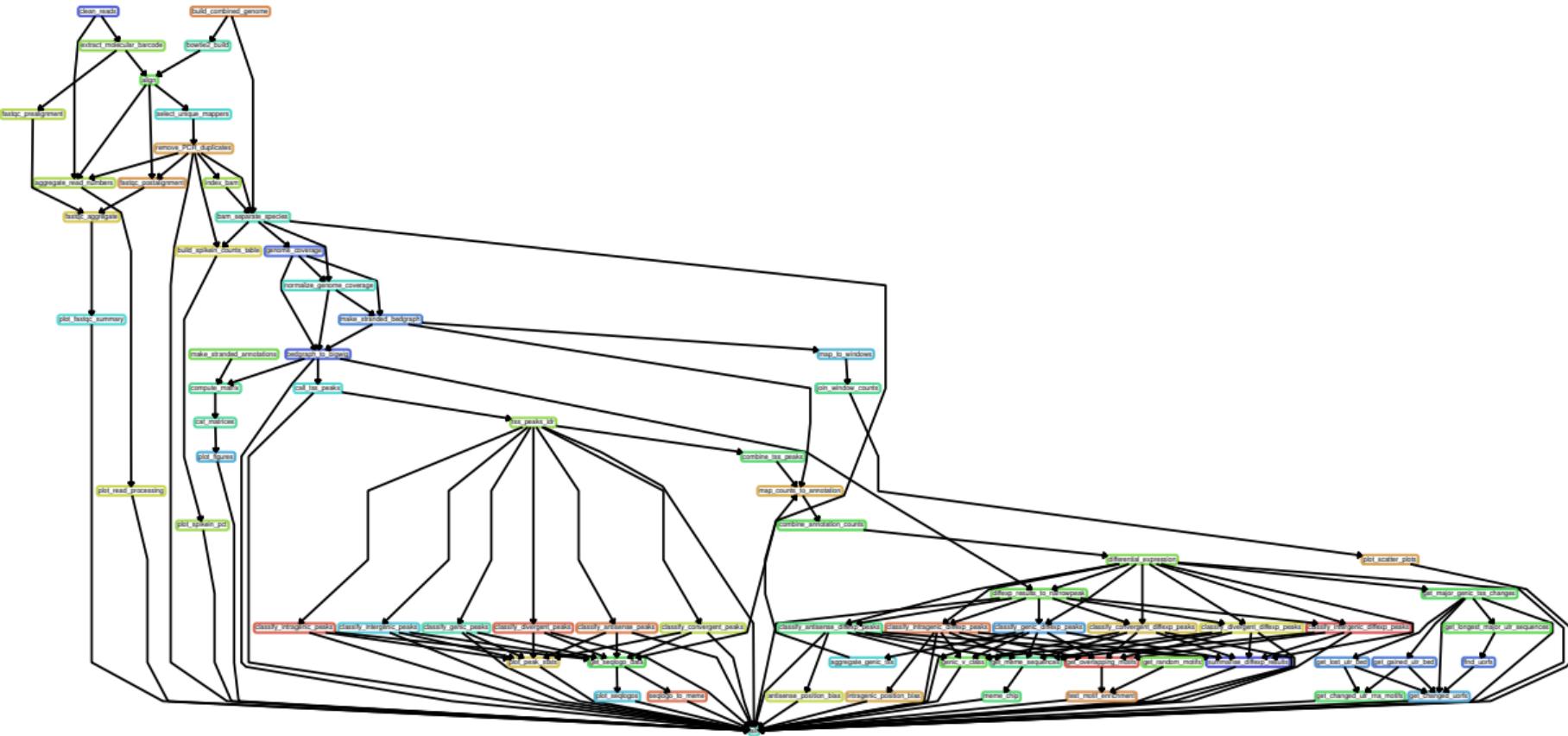
June 19, 2019

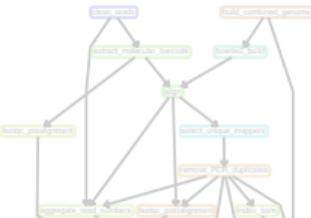






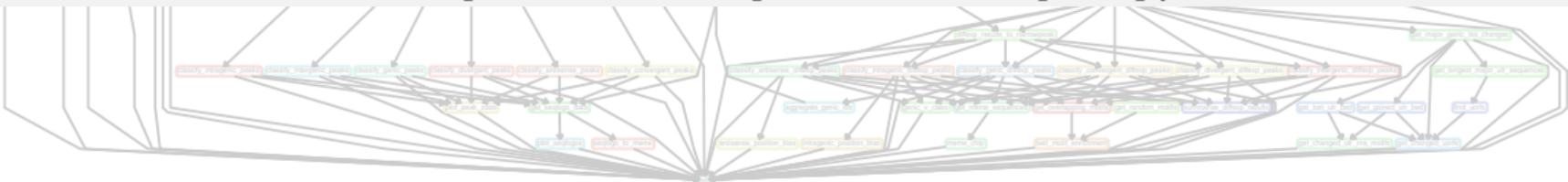


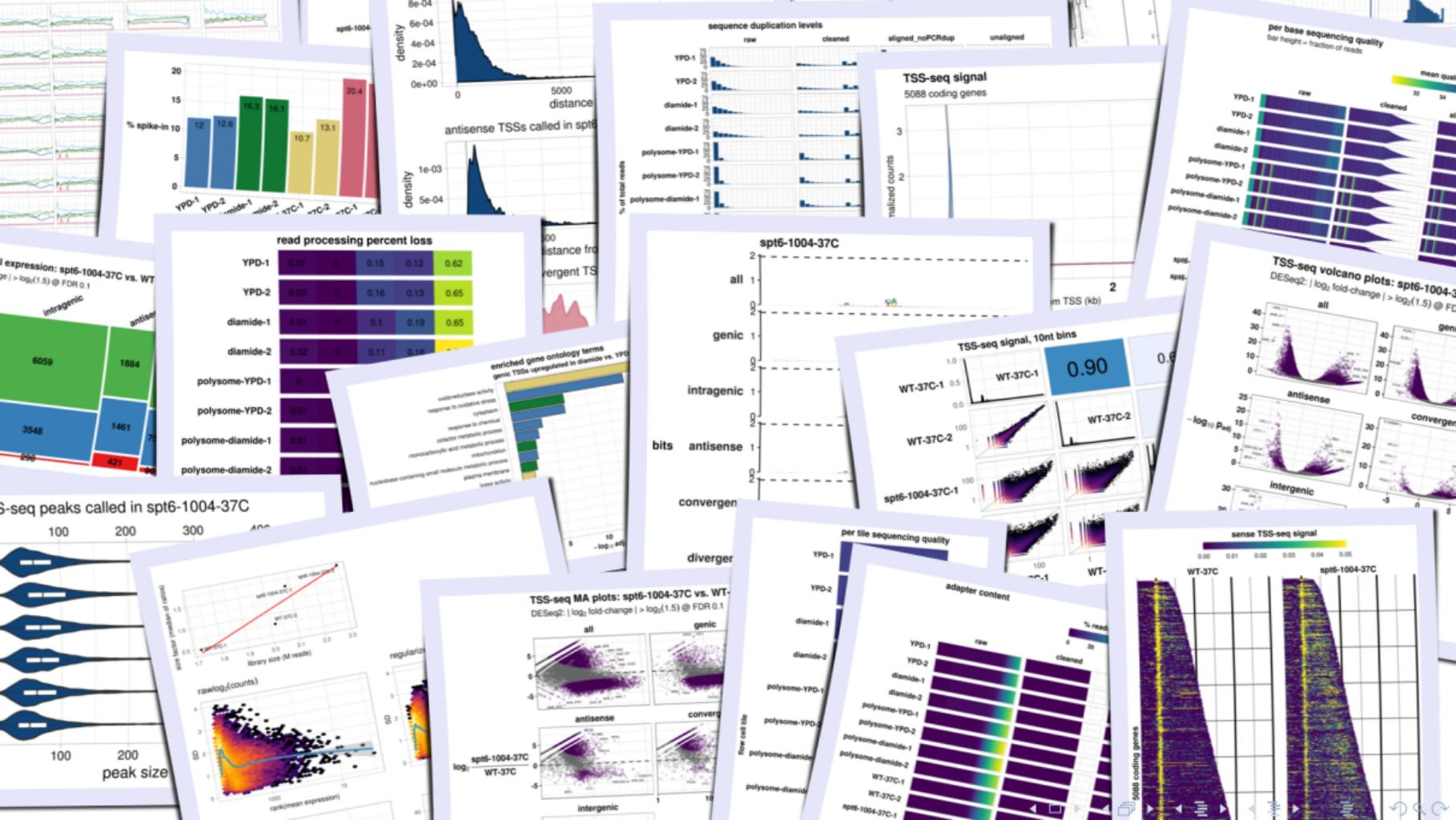




an example Snakemake rule:

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

Contact person(s)

Winston, Fred

Data collector(s)

Spatt, Dan

Data manager(s)

Chuang, James

Other(s)

Churchman, L. Stirling

Researcher(s)

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

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](#).

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Keyword(s):

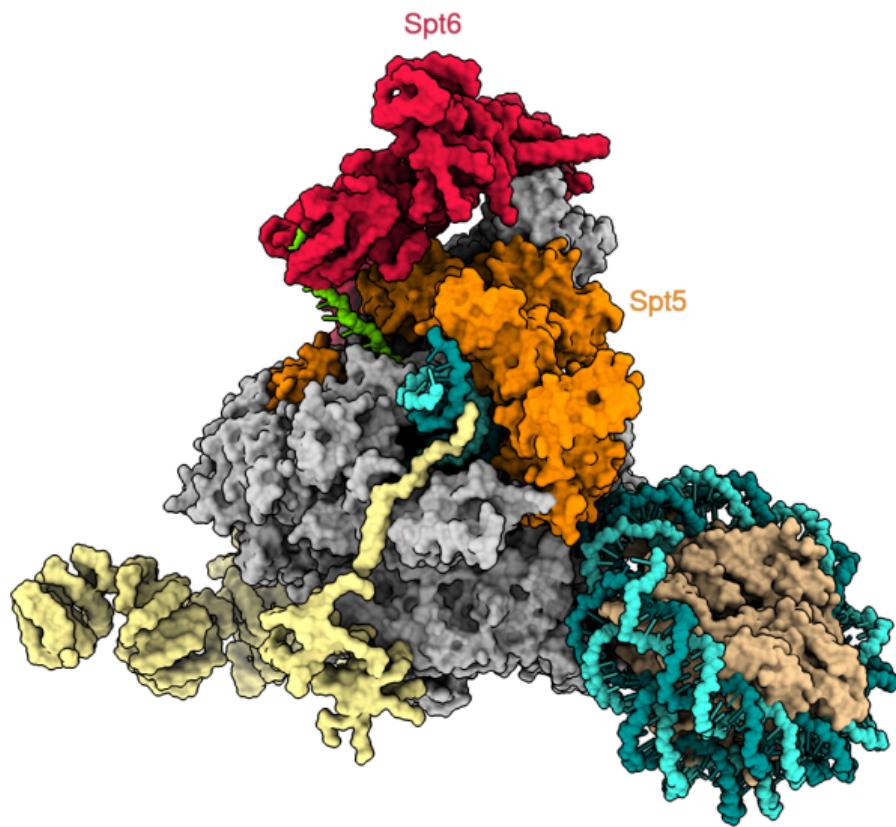
Spt6 transcription chromatin genomics
intragenic transcription TSS-seq ChIP-nexus NET-seq
MNase-seq

Published in:



transcription





Spt6 project collaborators

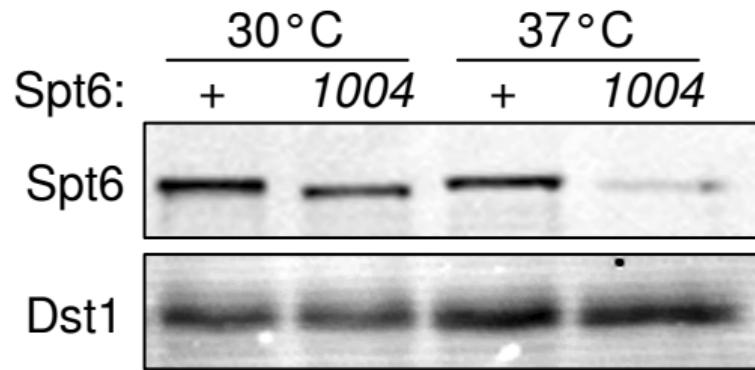
Steve Doris optimized TSS-seq and ChIP-nexus protocols
generated TSS-seq and ChIP-nexus libraries

Olga Viktorovskaya generated MNase-seq libraries

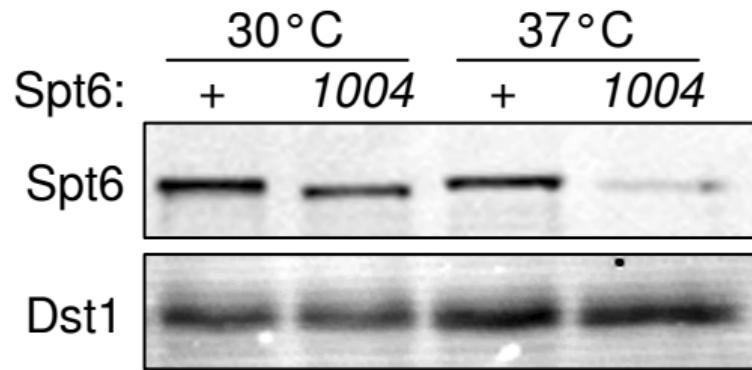
Magdalena Murawska generated NET-seq libraries

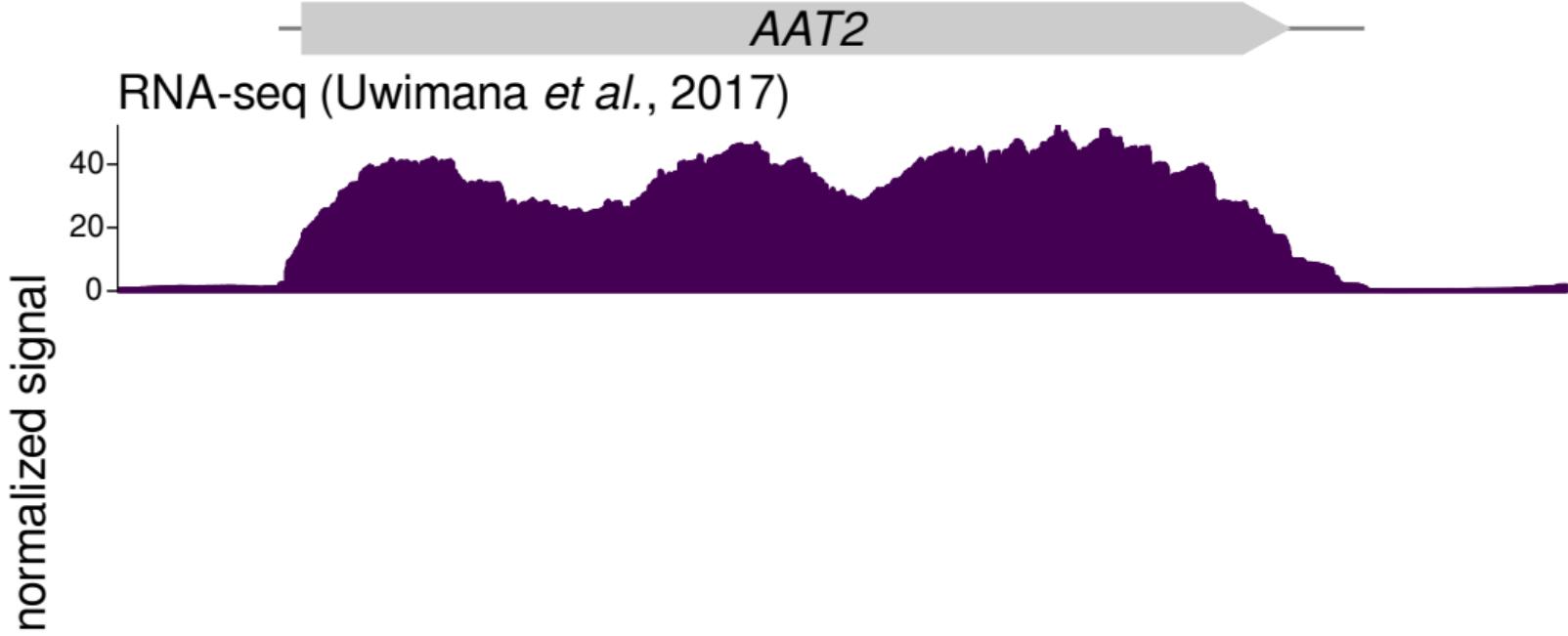
Dan Spatt Northern, Western, and ChIP experiments

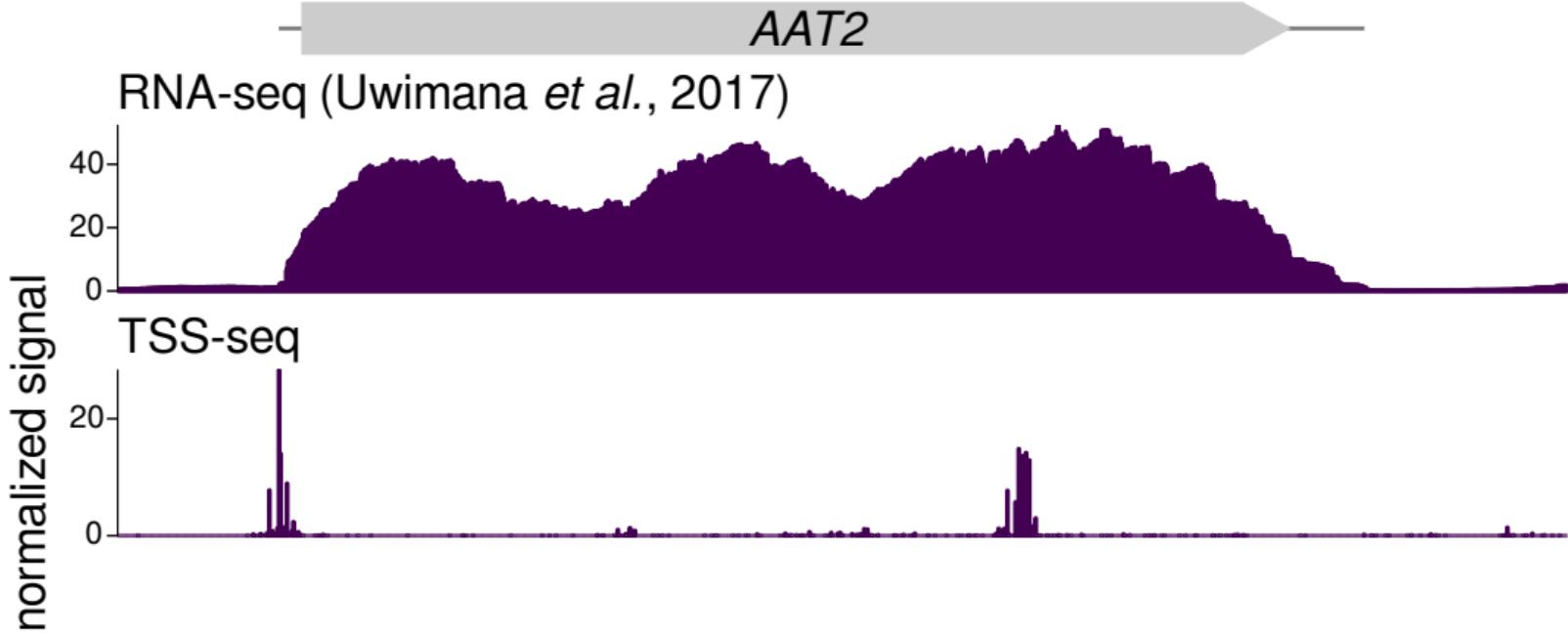
The *spt6-1004* mutant expresses intragenic transcripts

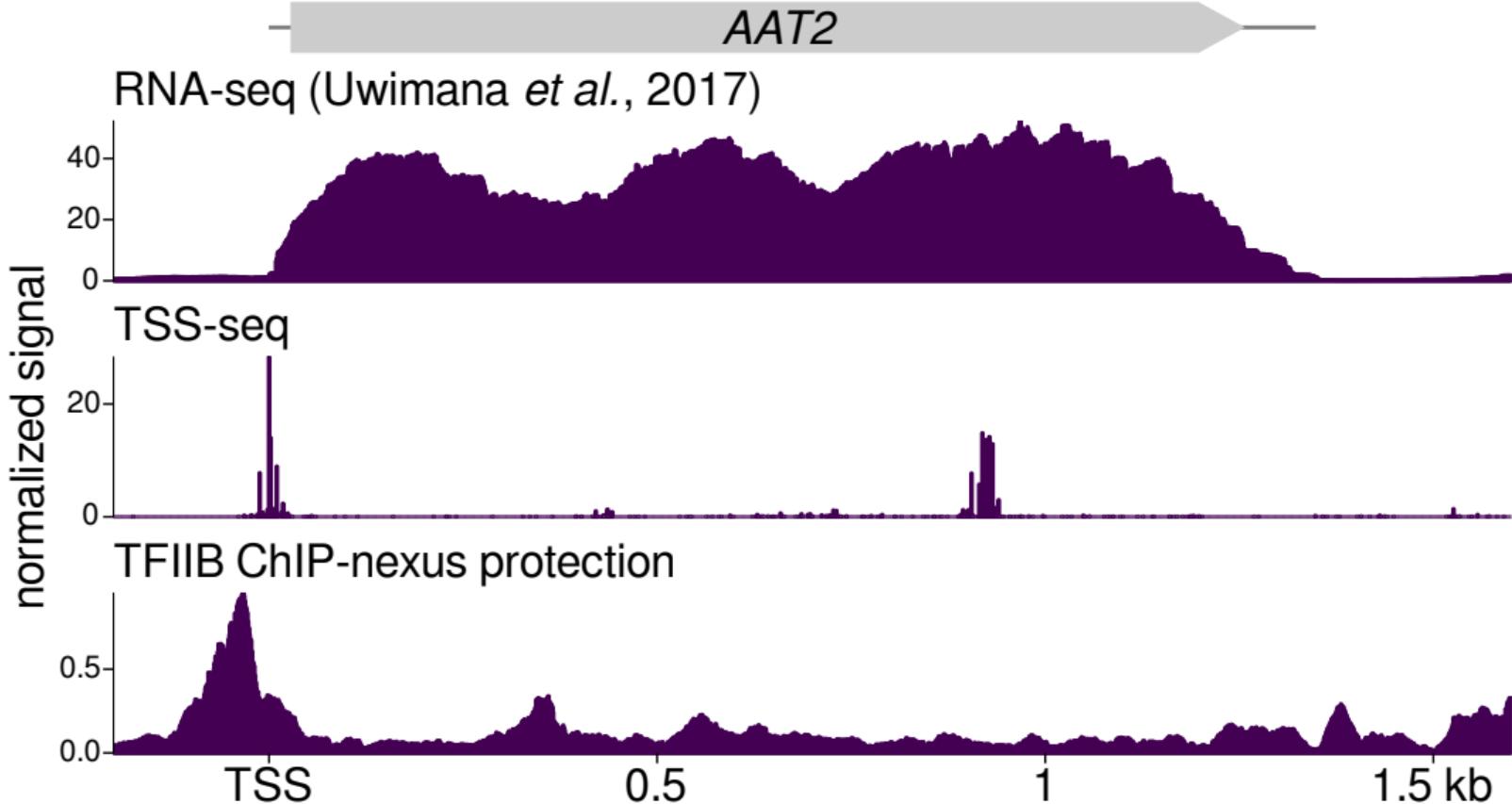


The *spt6-1004* mutant expresses intragenic transcripts

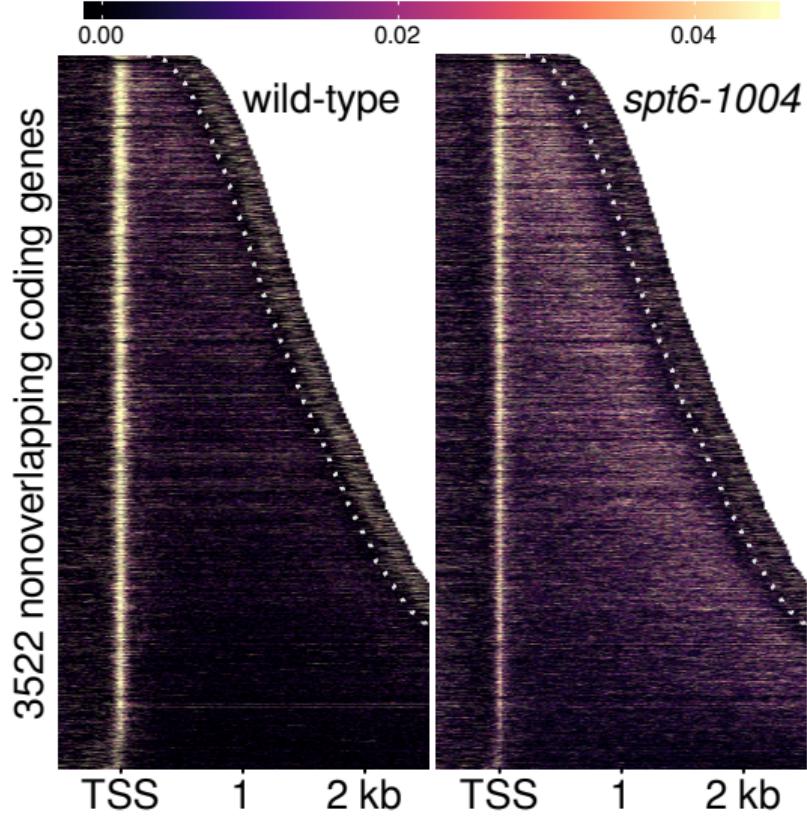


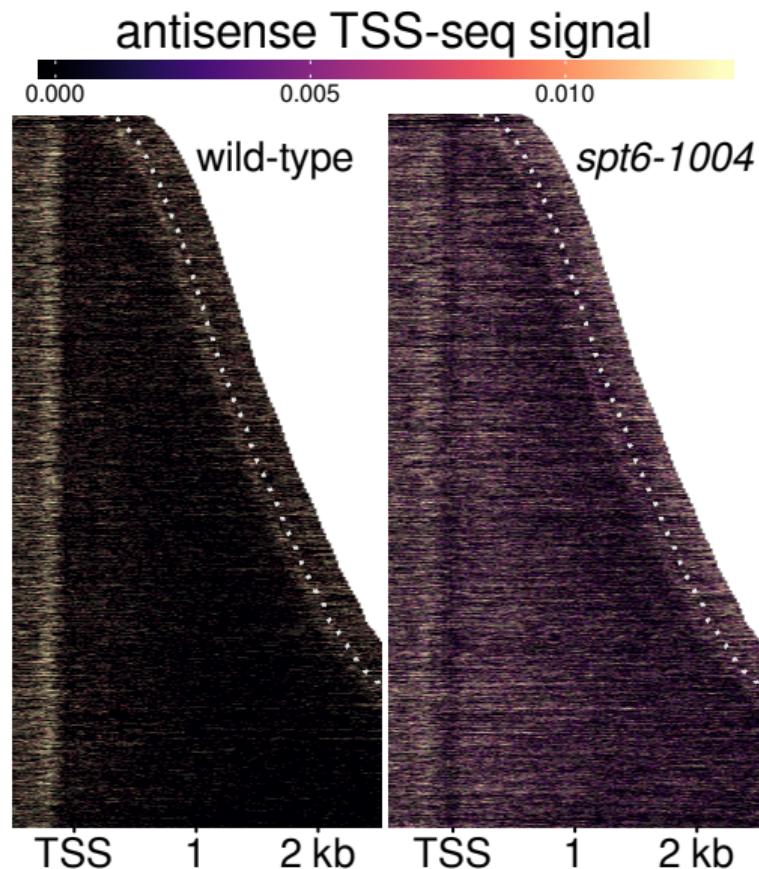
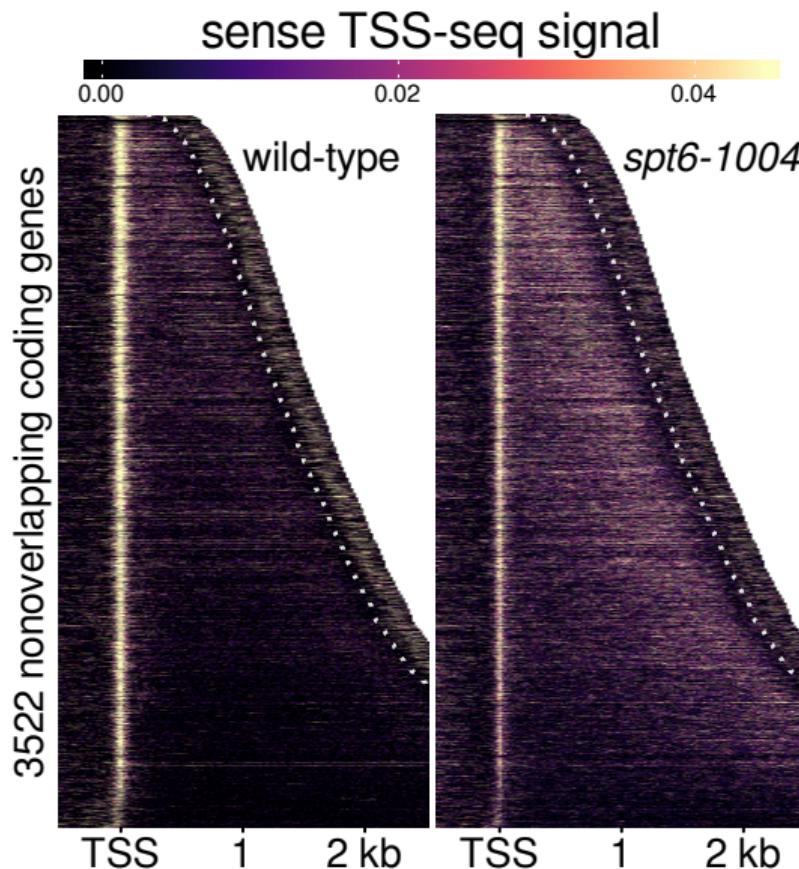




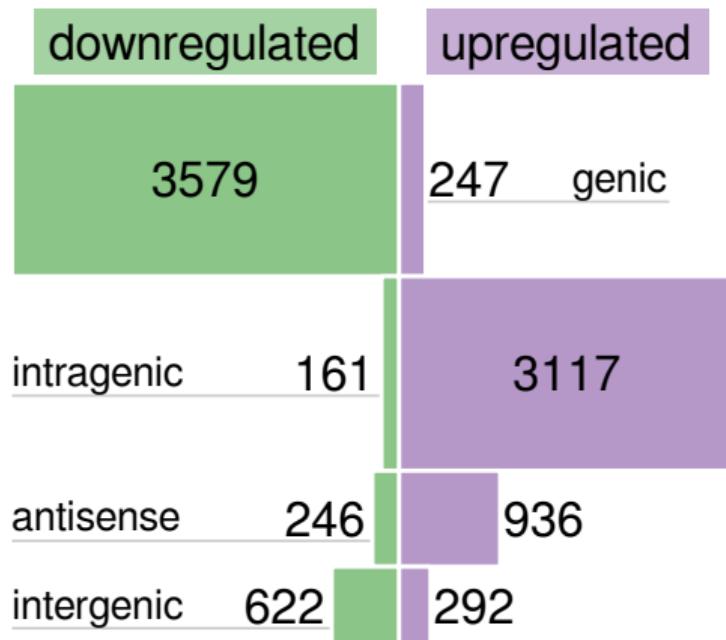


sense TSS-seq signal

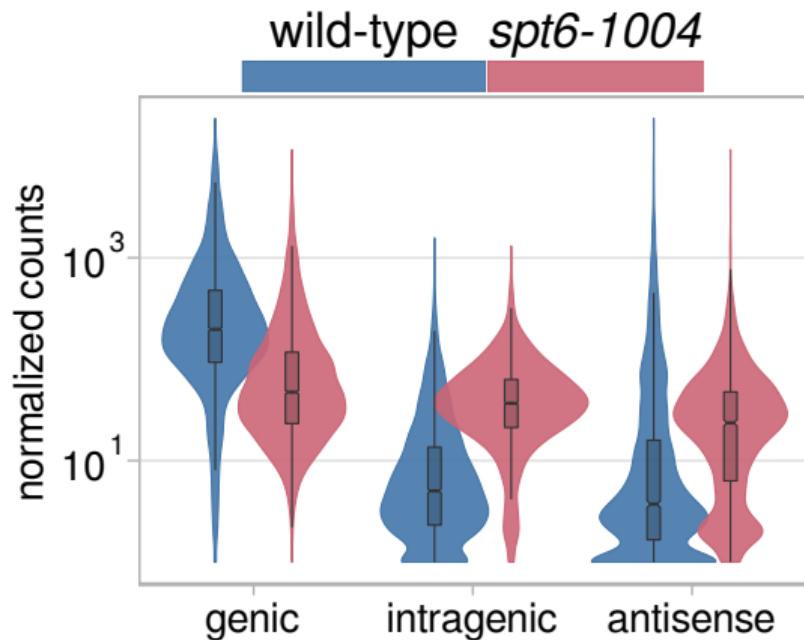
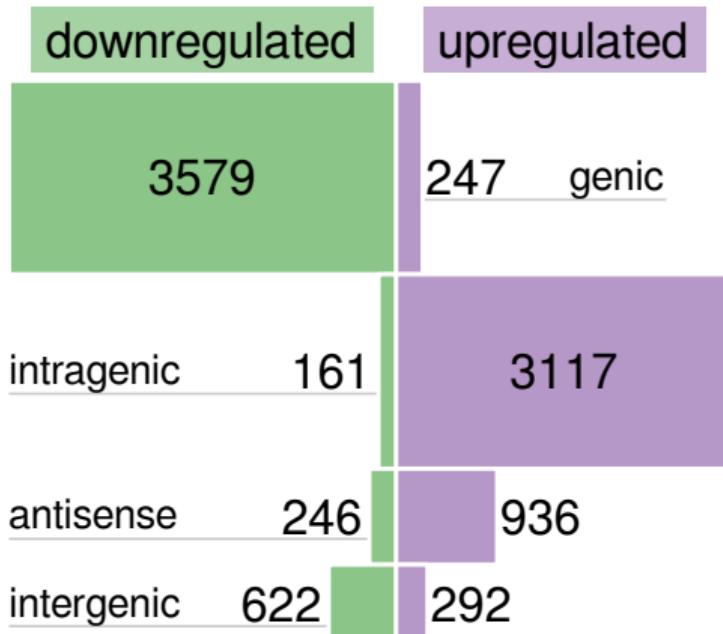




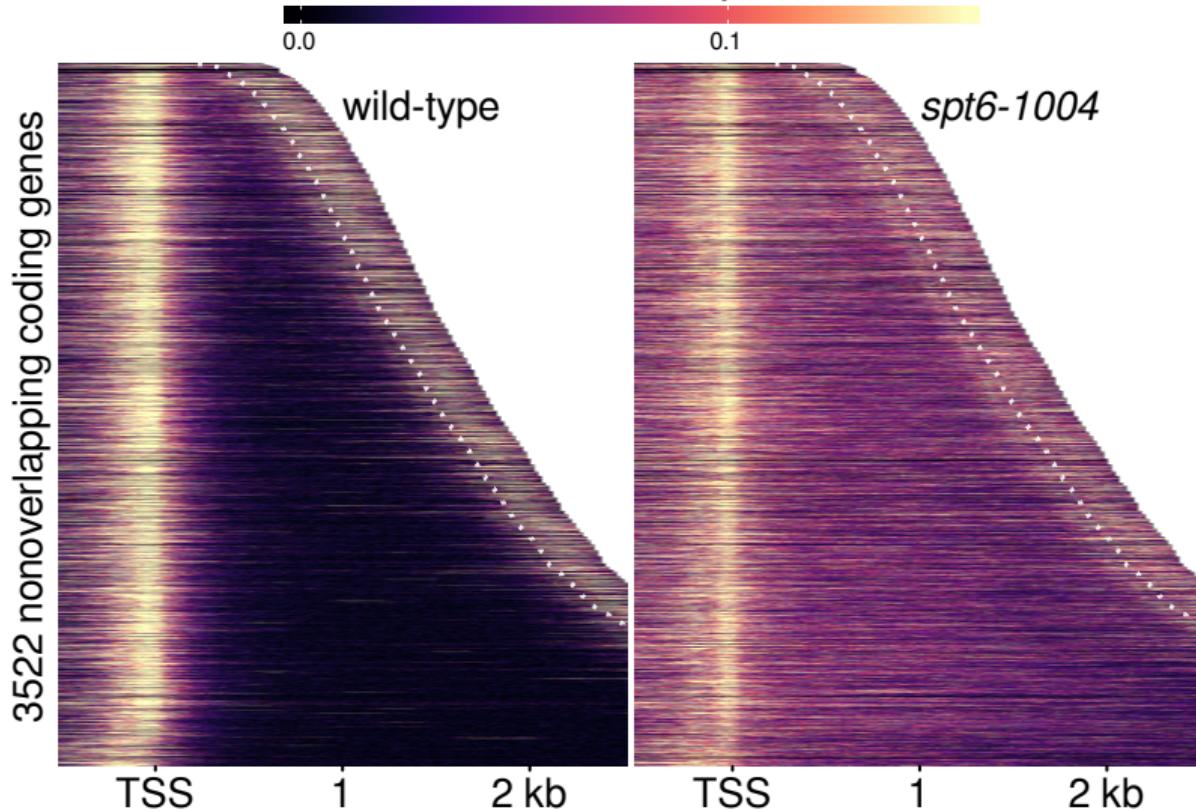
Downregulation of genic TSSs in *spt6-1004*:



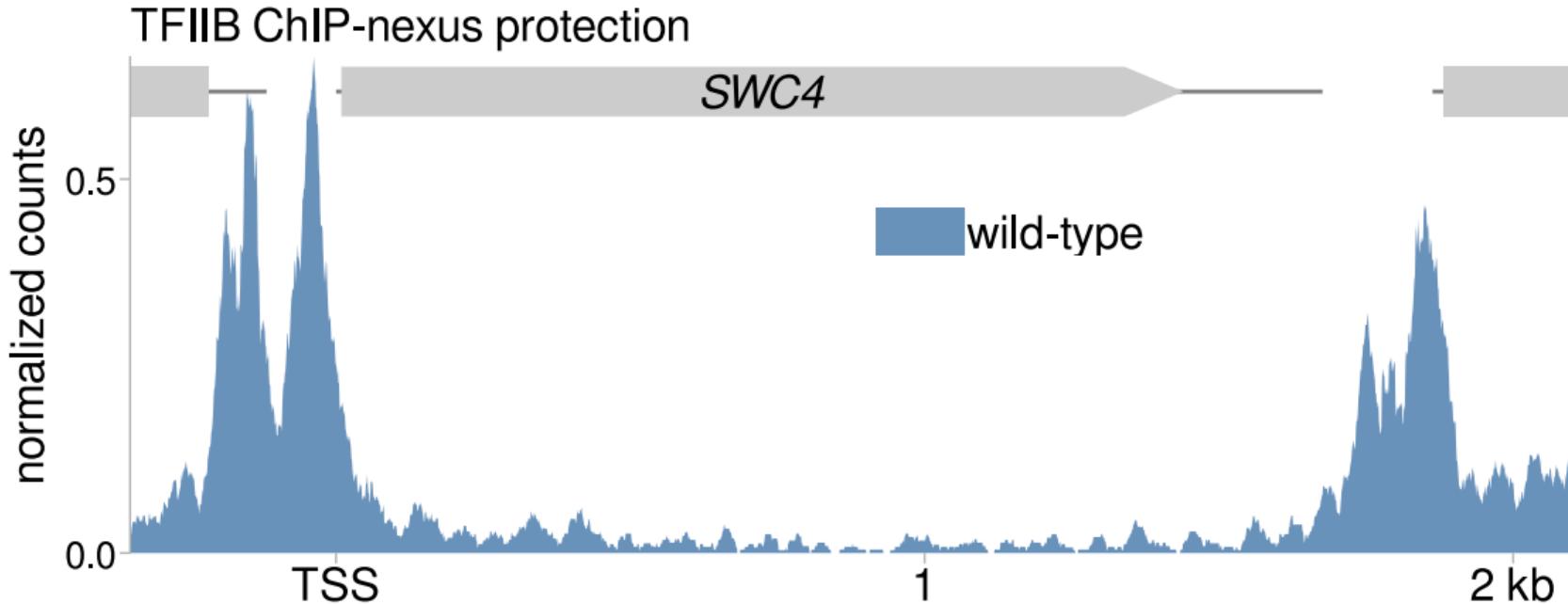
Downregulation of genic TSSs in *spt6-1004*:



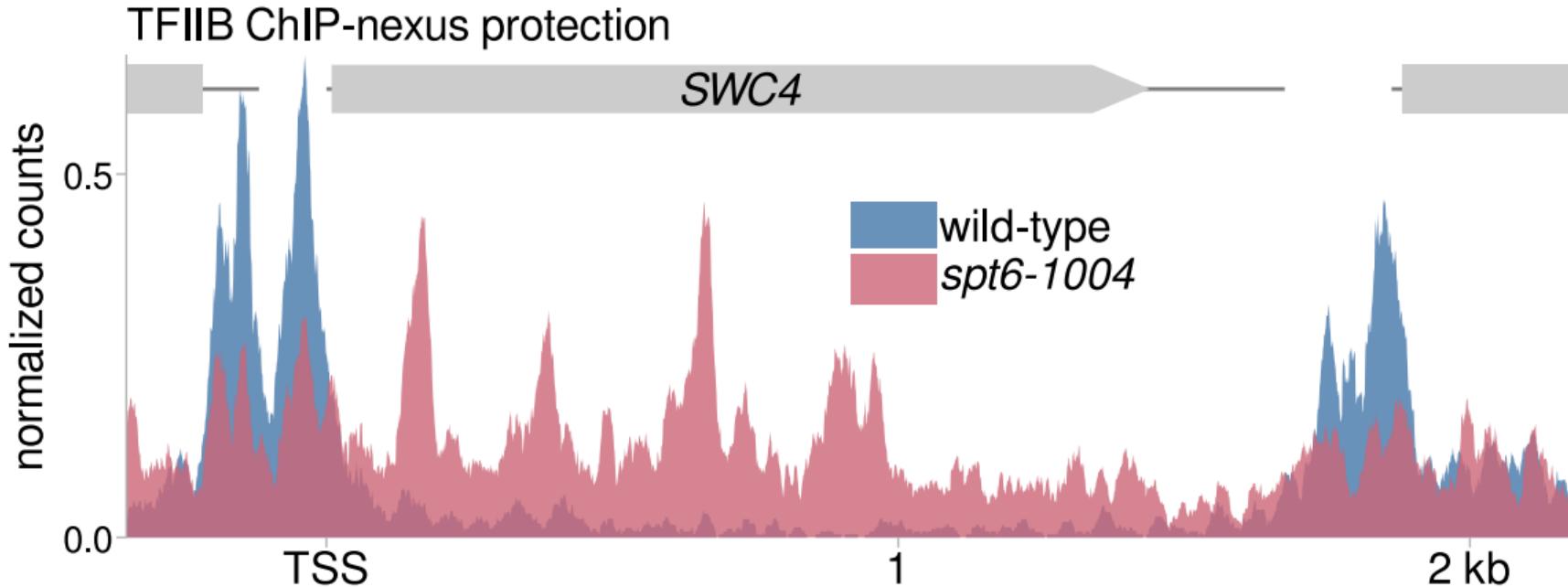
TFIIB ChIP-nexus protection



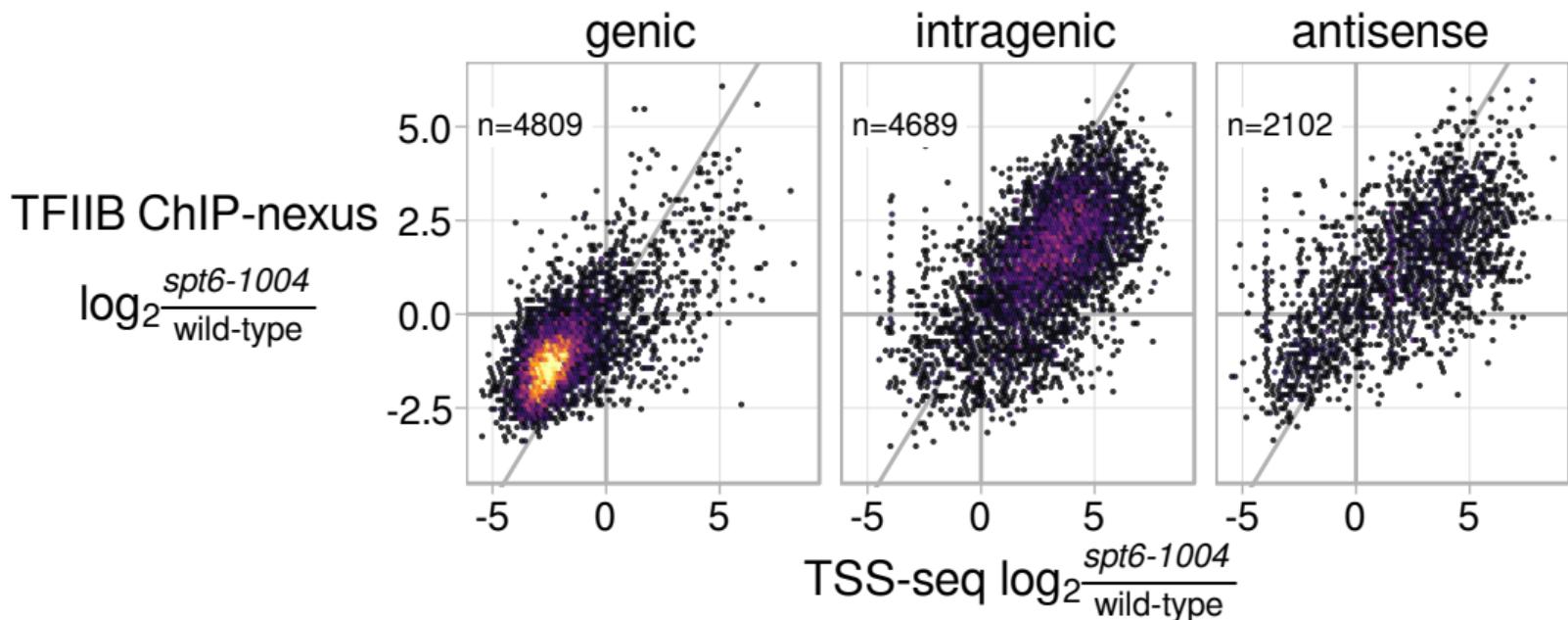
TFIIB binding changes dramatically in *spt6-1004*:



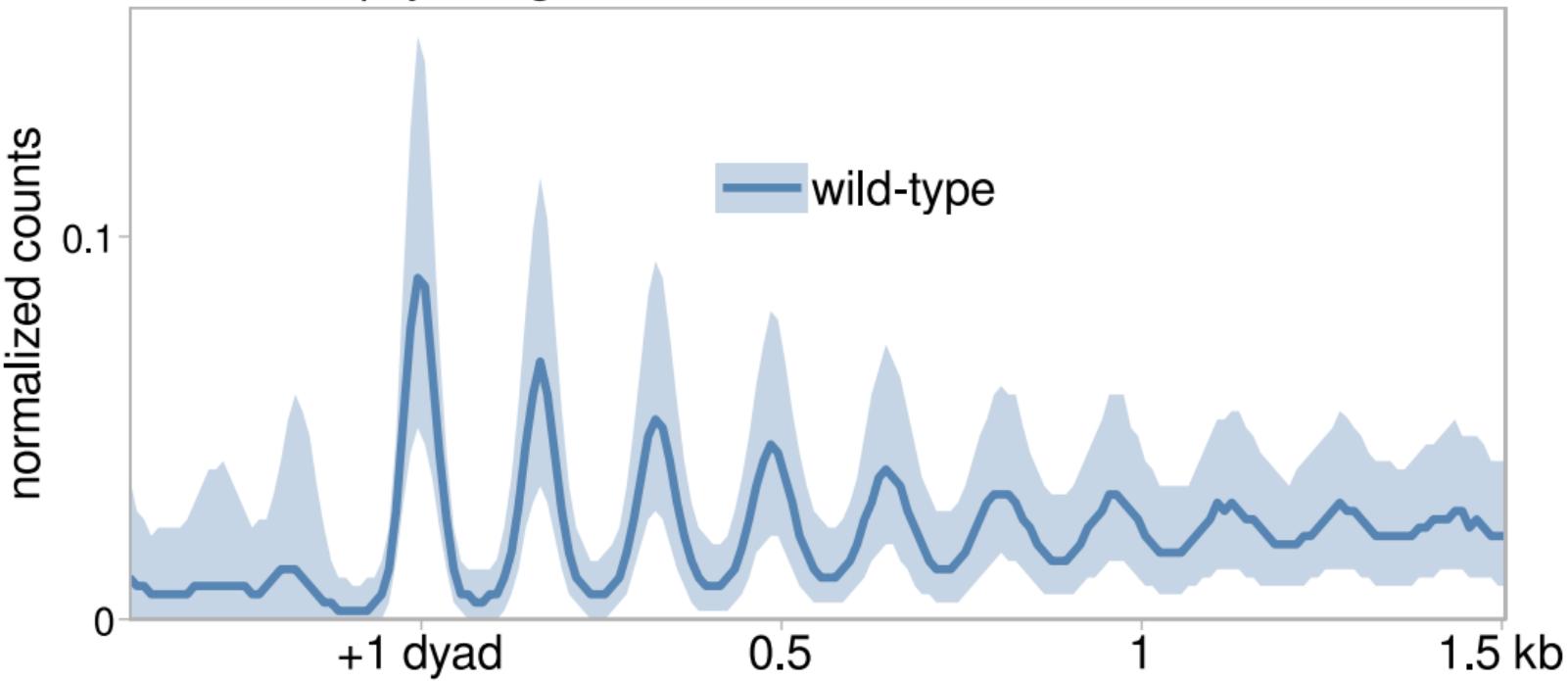
TFIIB binding changes dramatically in *spt6-1004*:



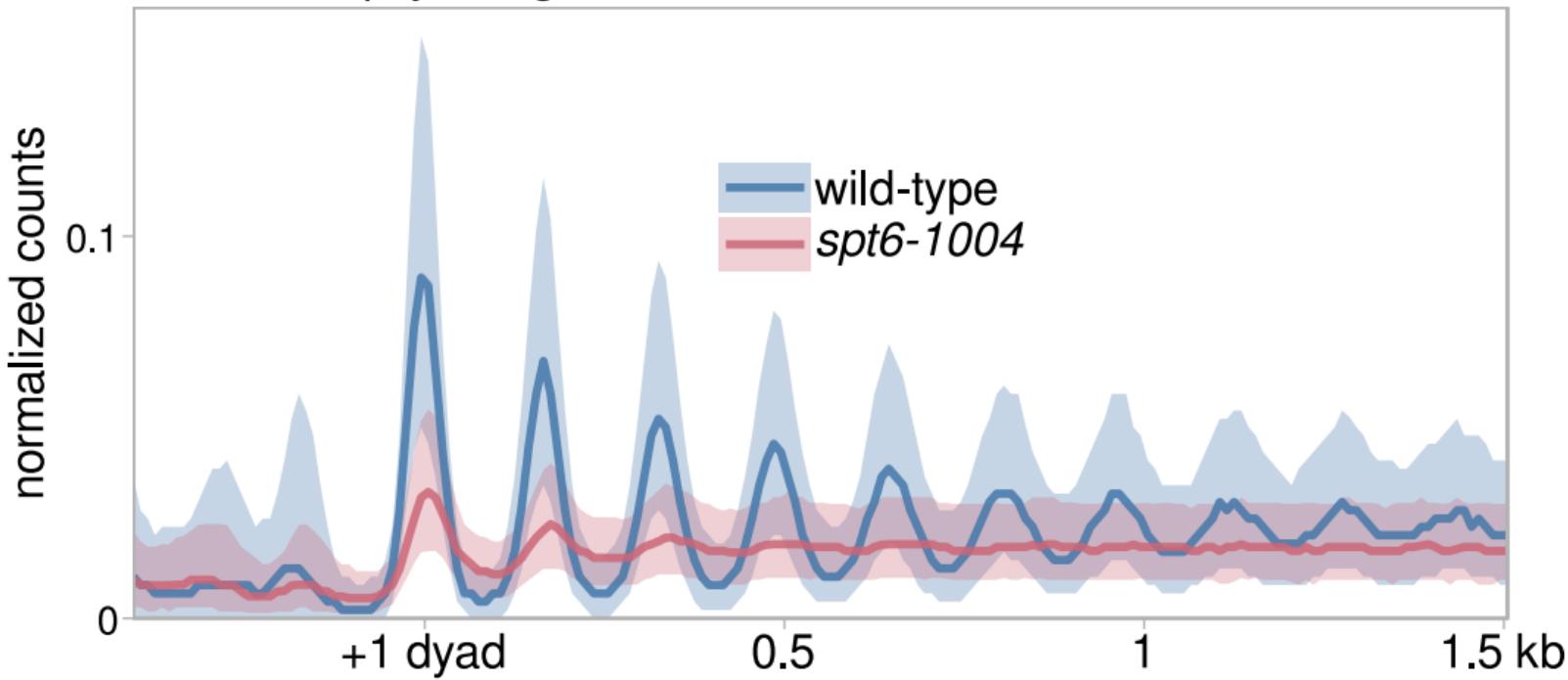
new intragenic initiation explains most intragenic transcripts



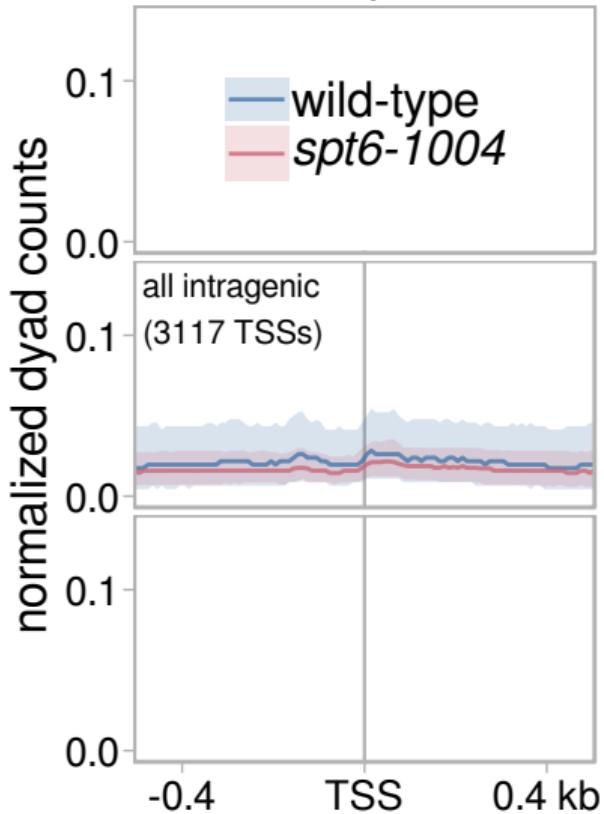
MNase-seq dyad signal



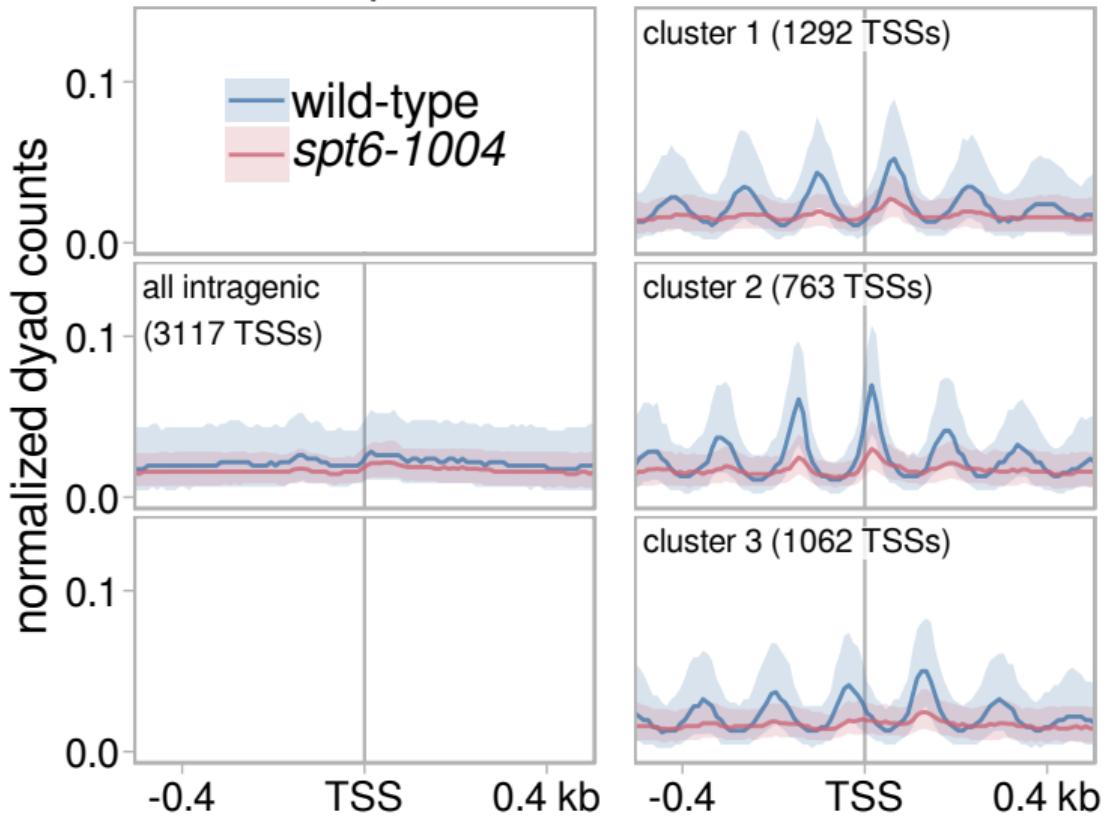
MNase-seq dyad signal



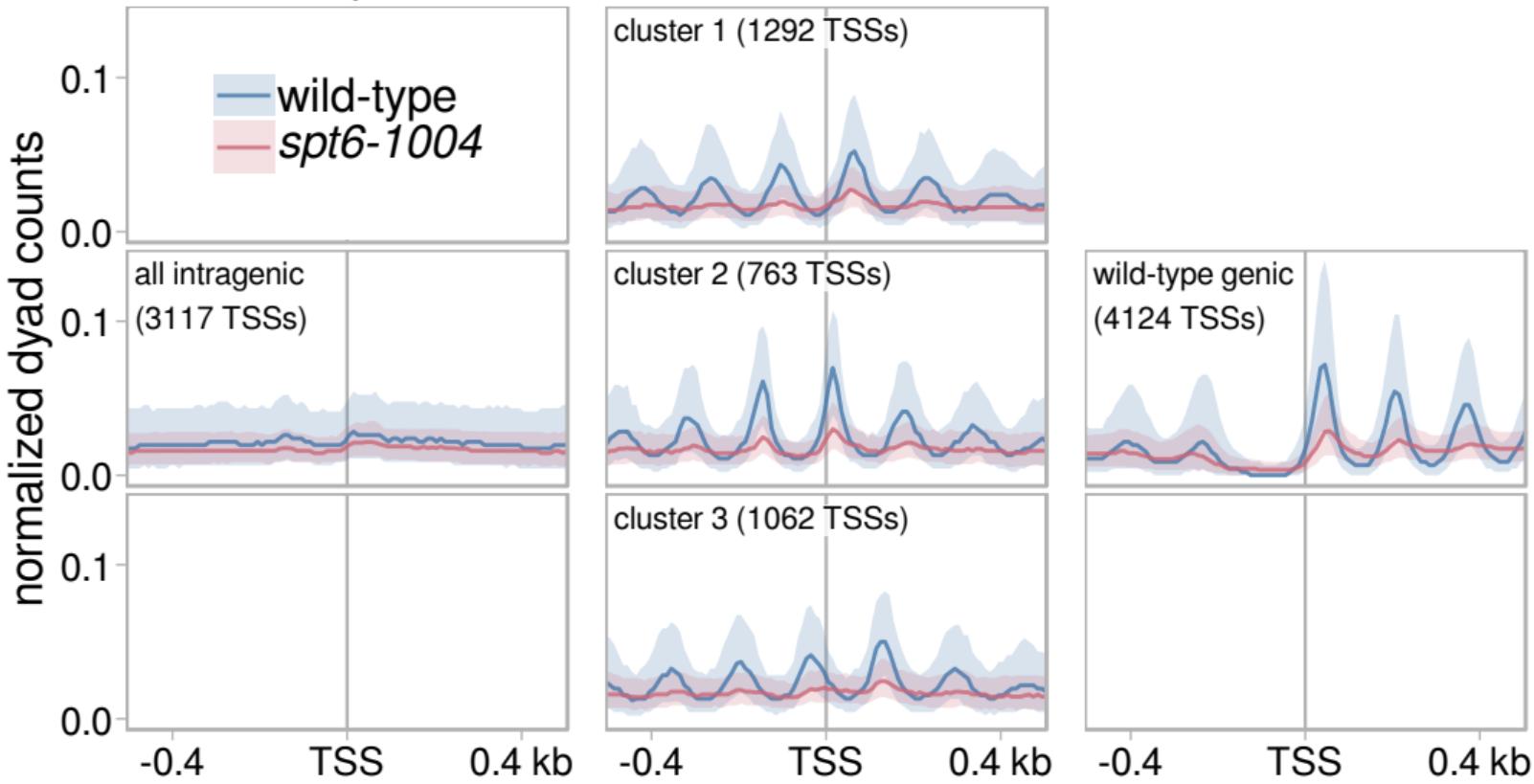
MNase-seq



MNase-seq

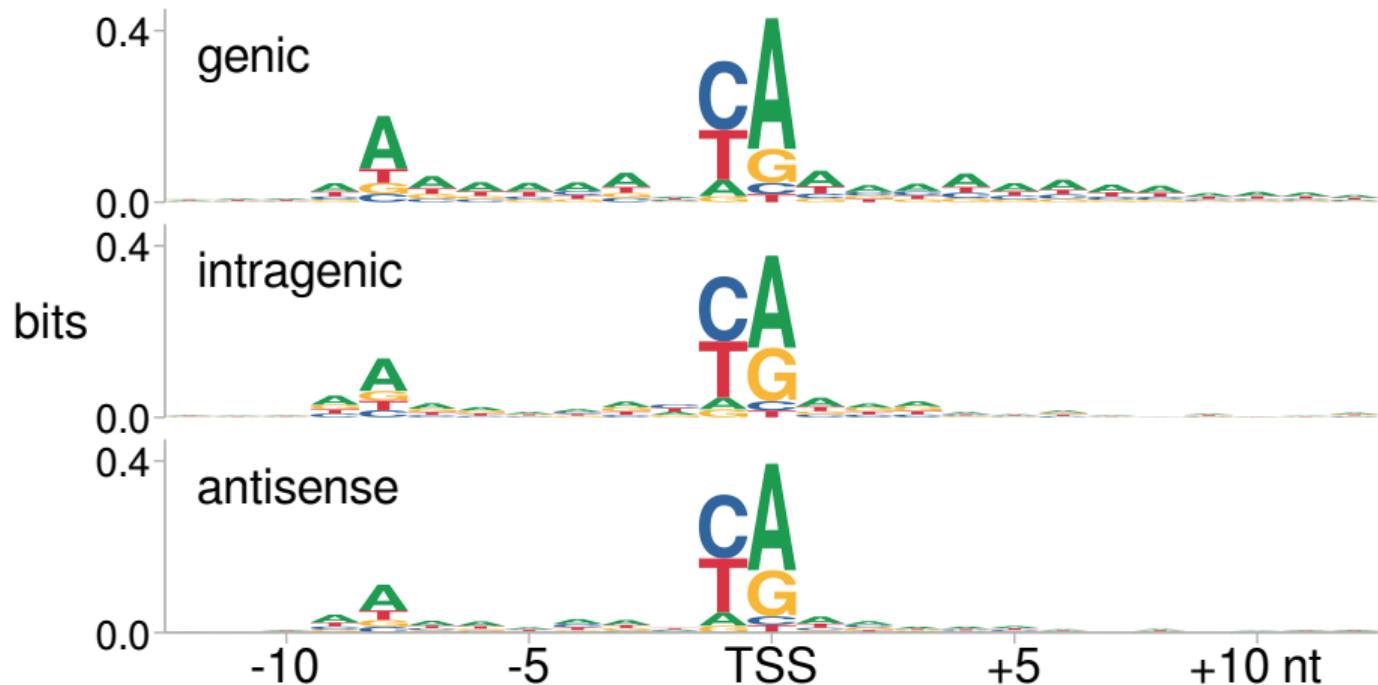


MNase-seq

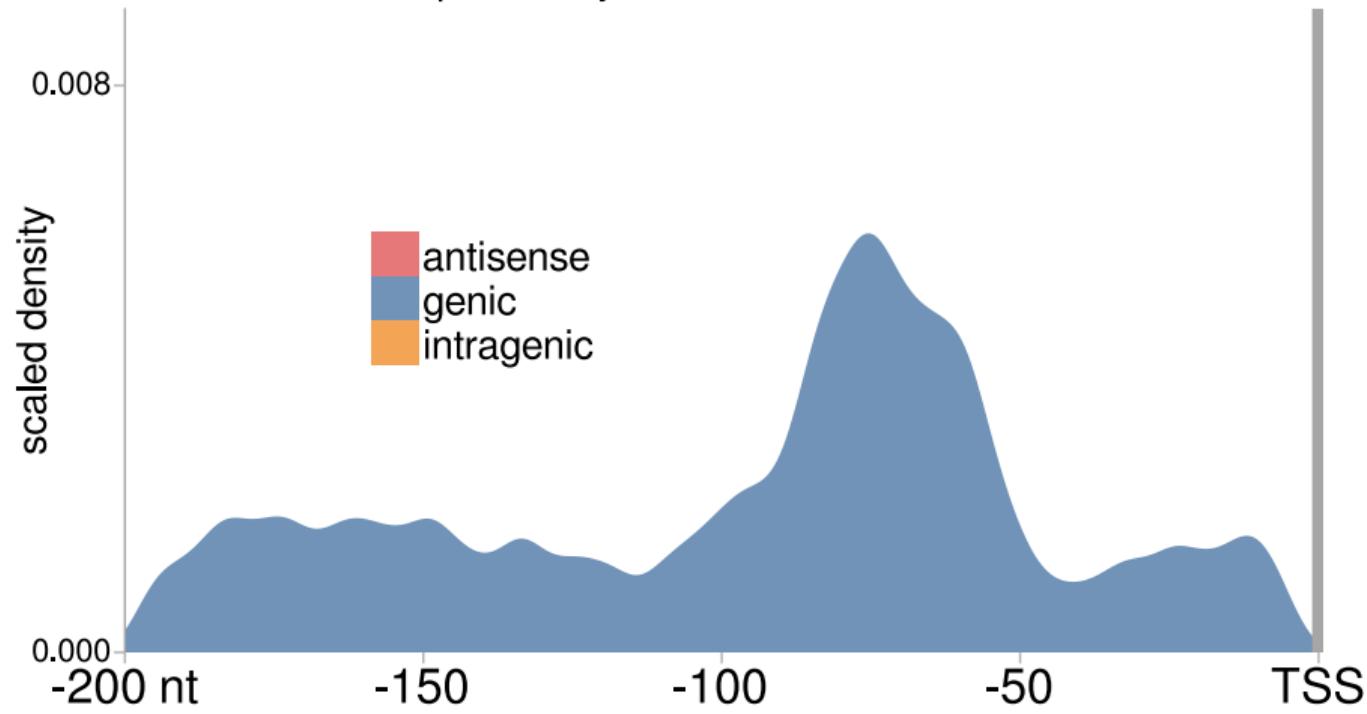


GC content

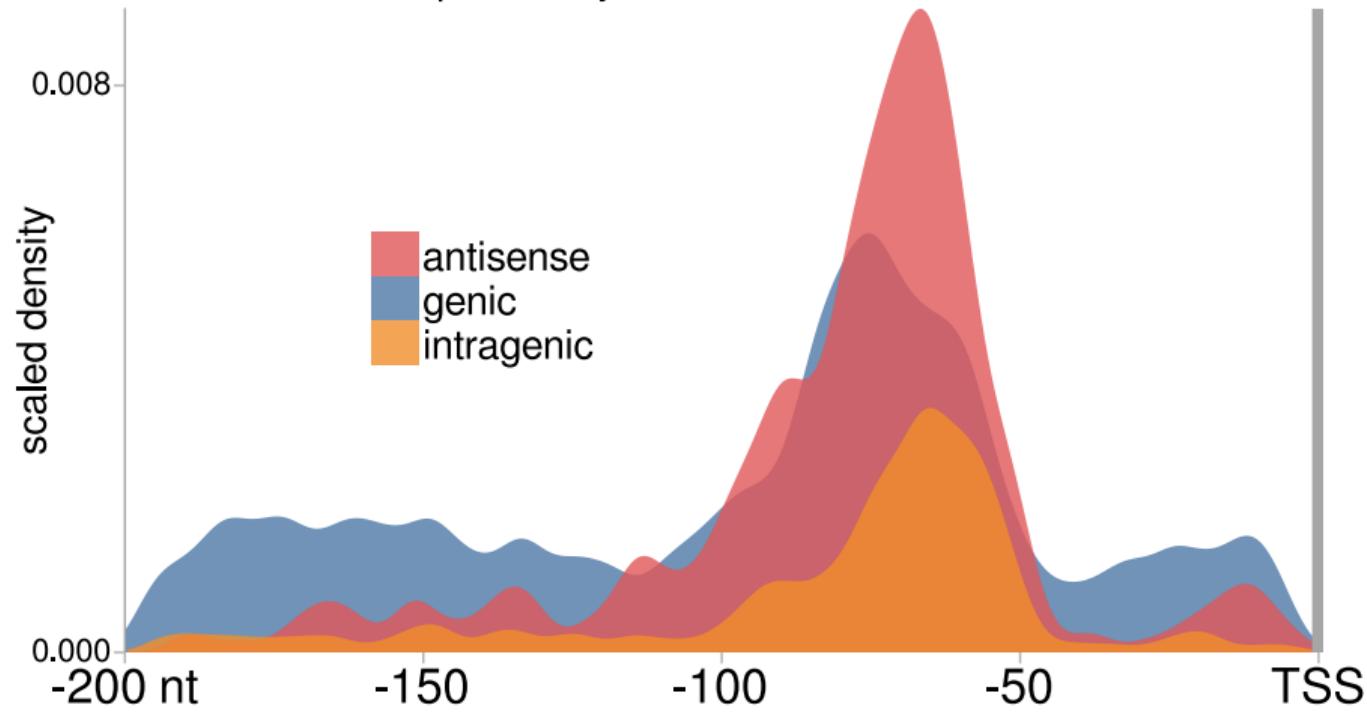
spt6-1004 TSSs



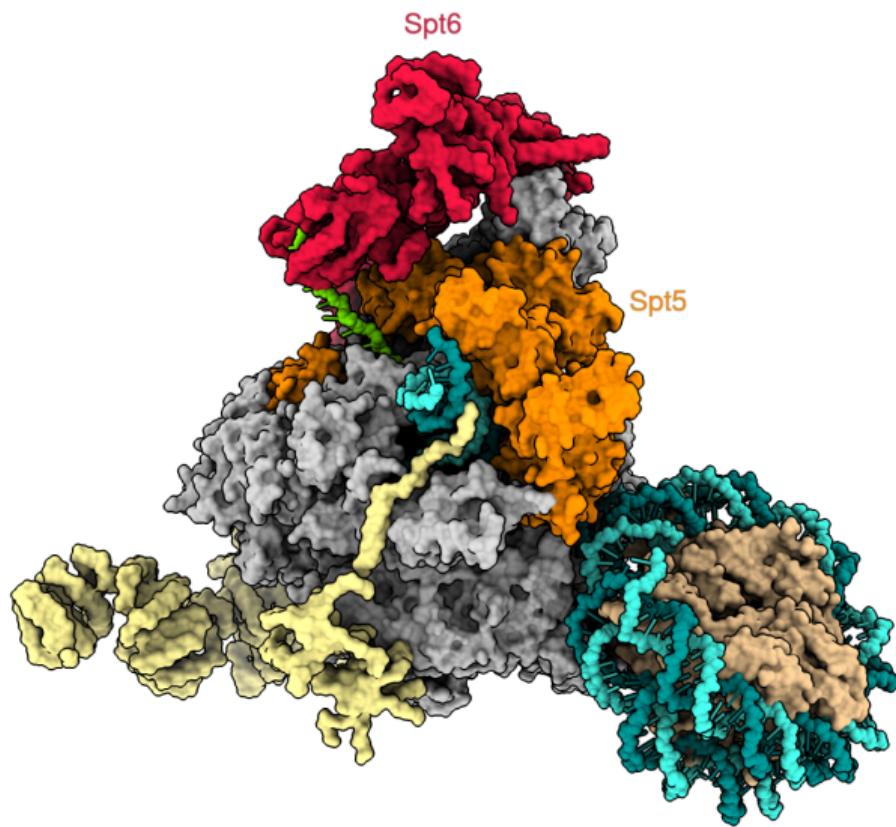
TATA consensus probability



TATA consensus probability



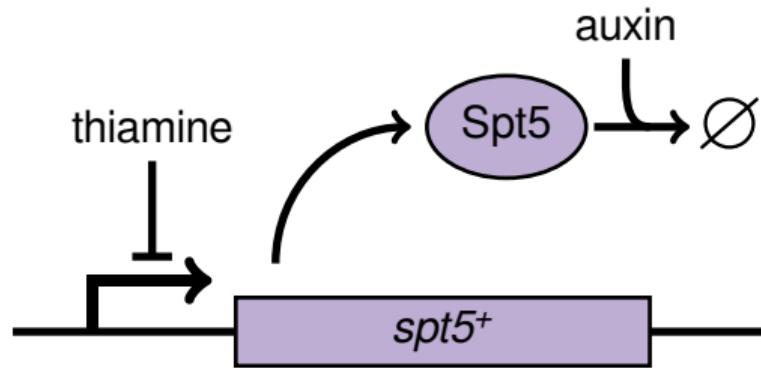
Spt6 summary and model



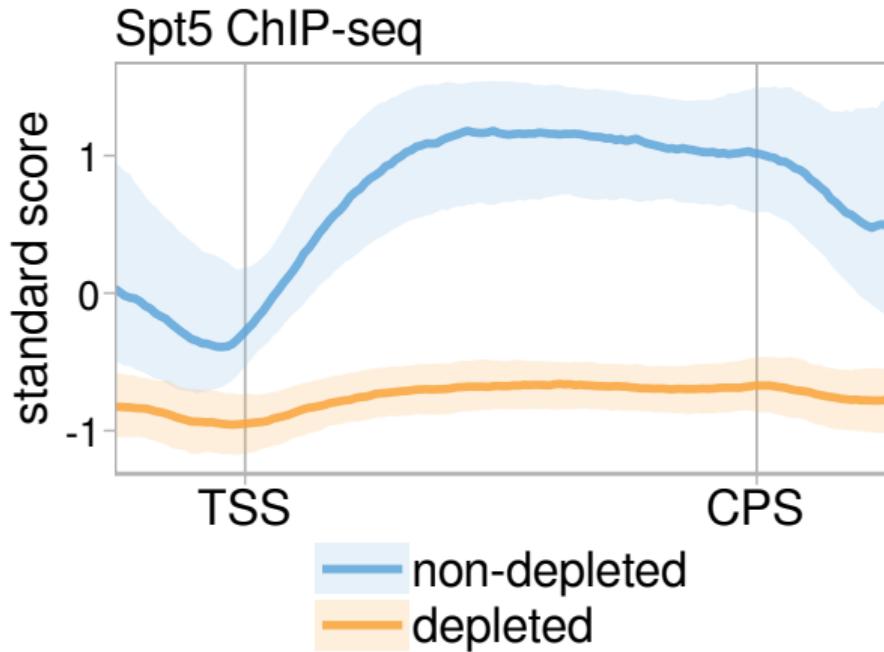
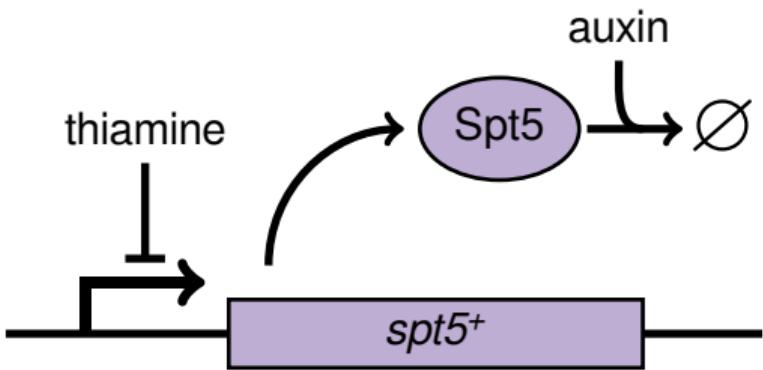
Spt5 project collaborators

Ameet Shetty generated NET-seq, ChIP-seq, RNA-seq, TSS-seq, and MNase-seq libraries

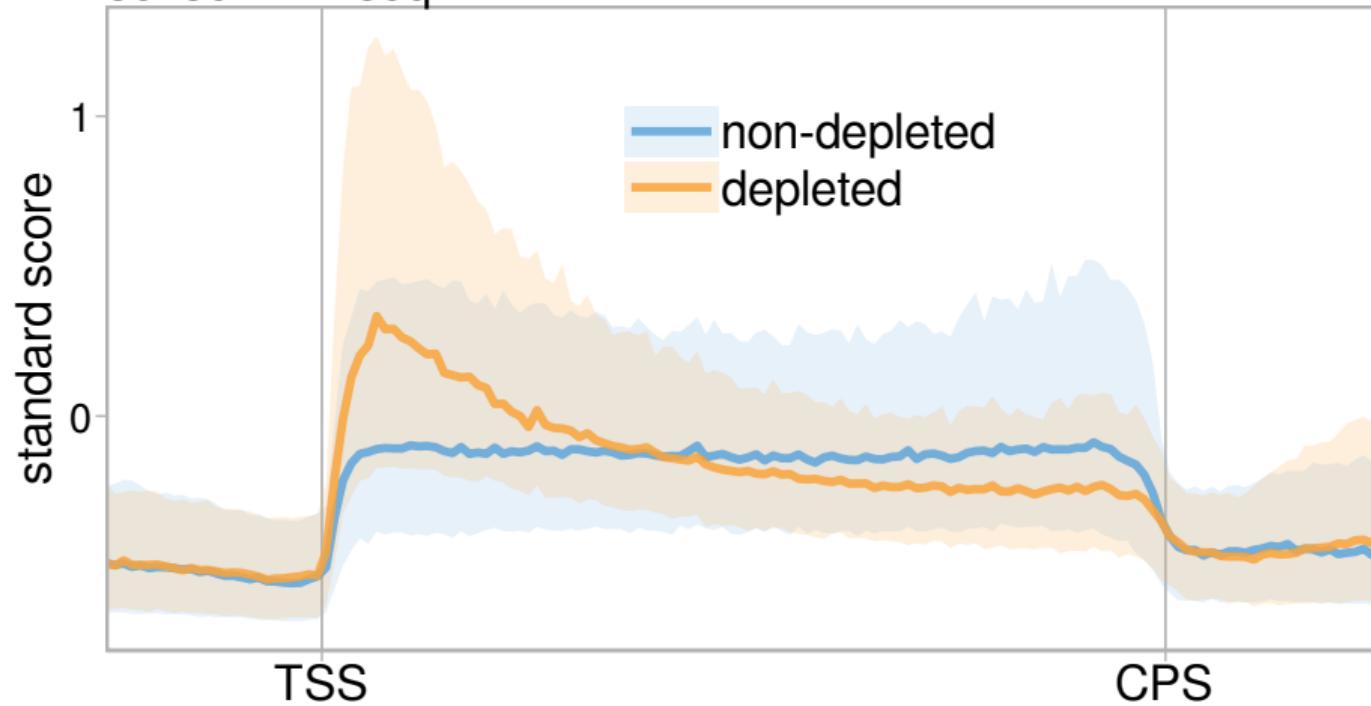
Spt5 depletion system



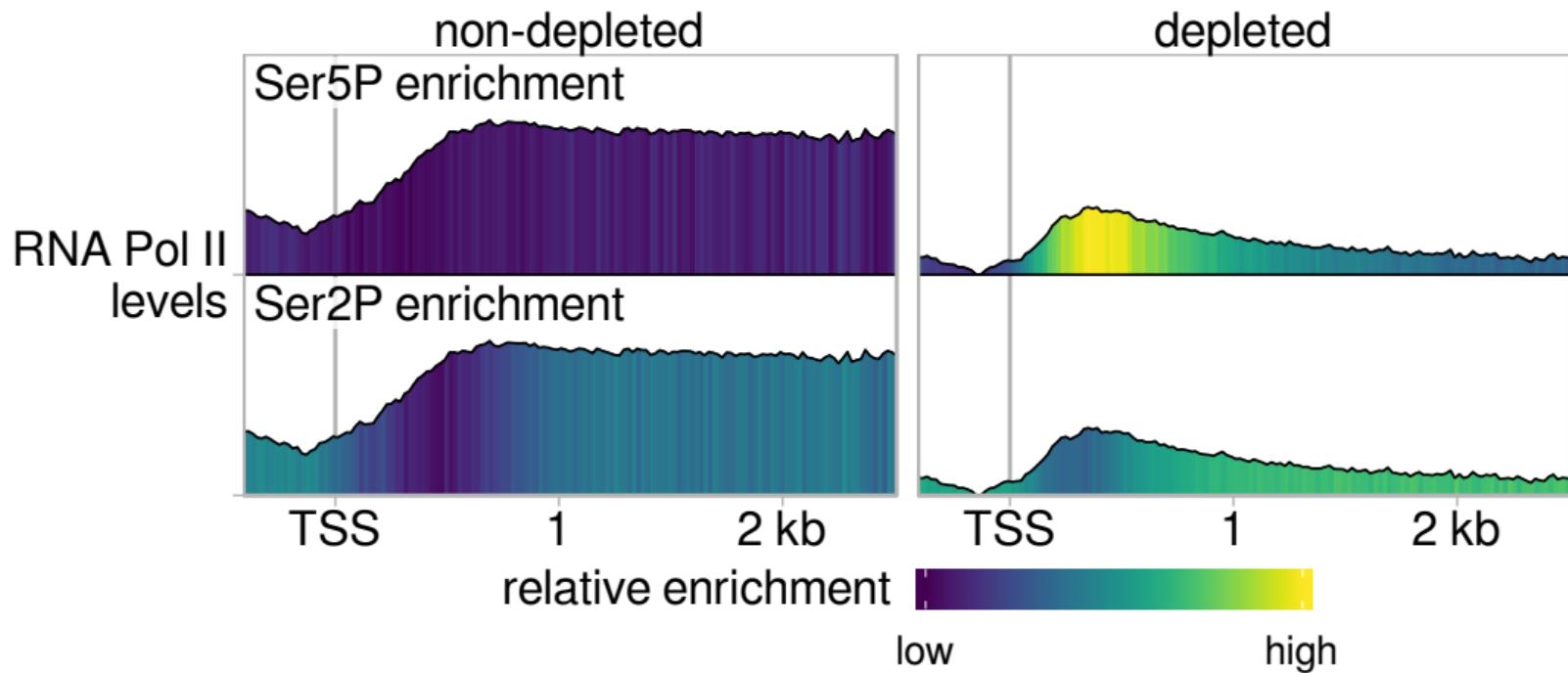
Spt5 depletion system



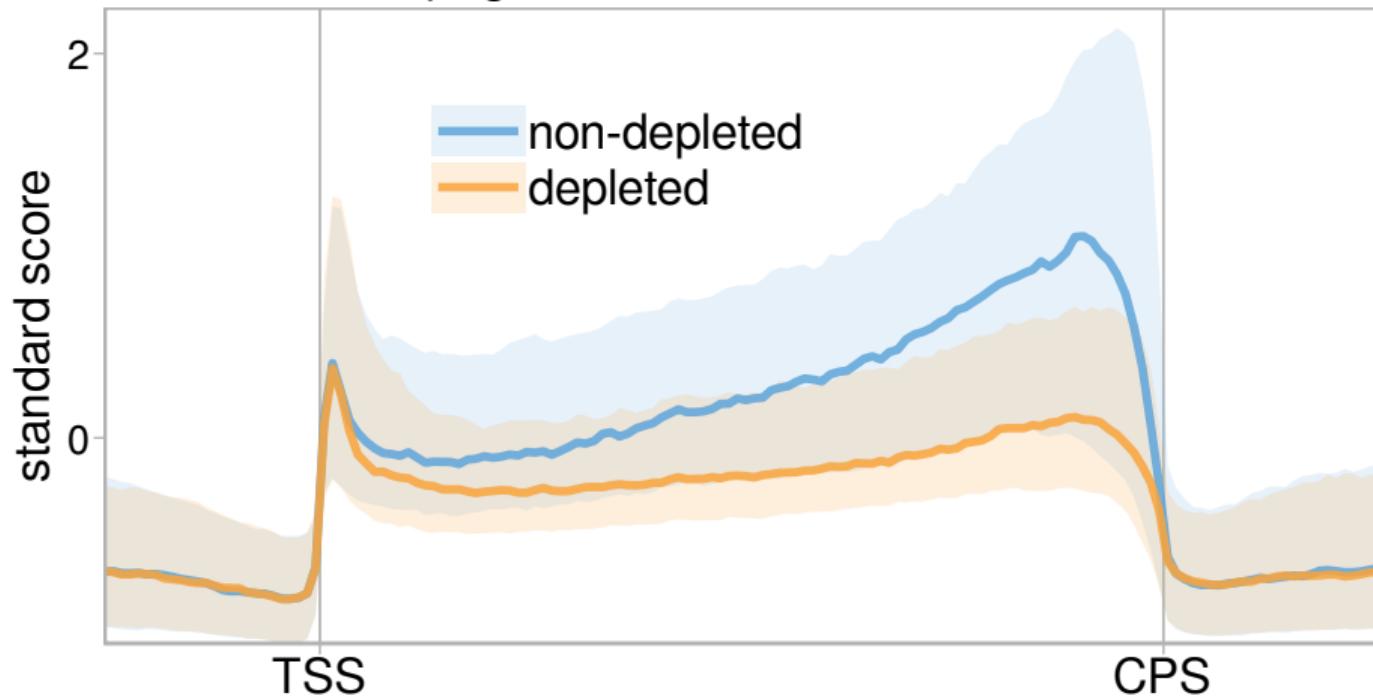
sense NET-seq



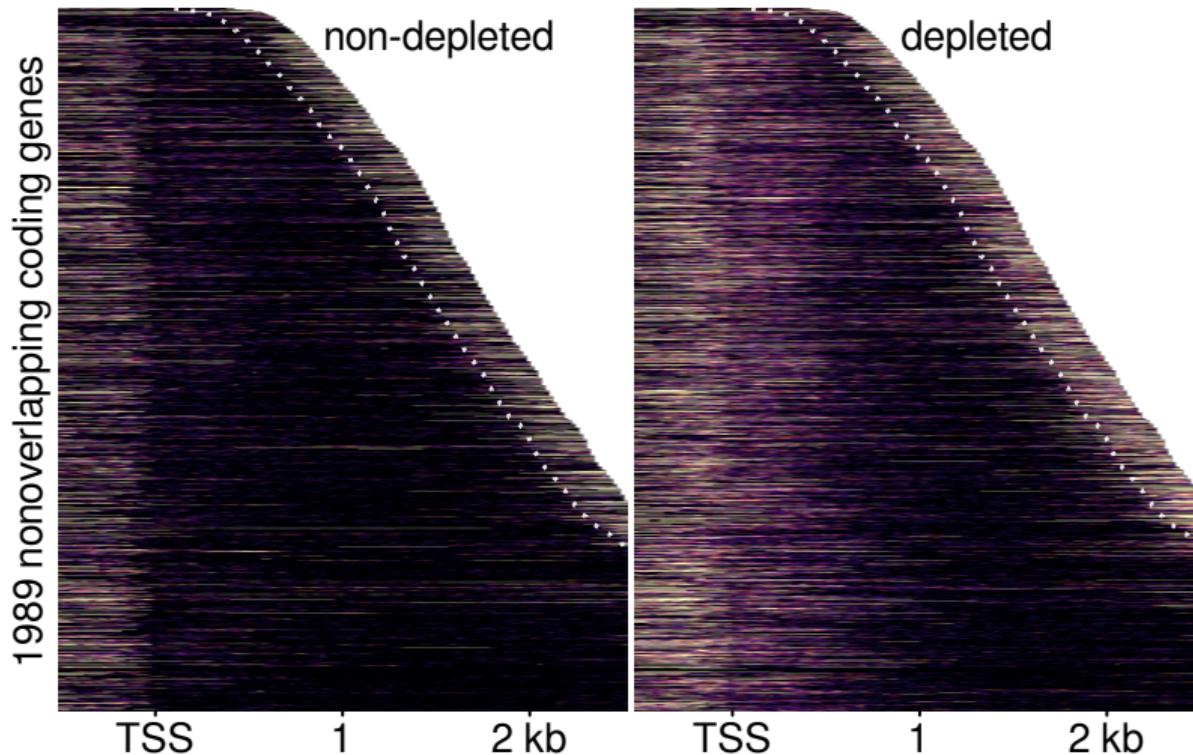
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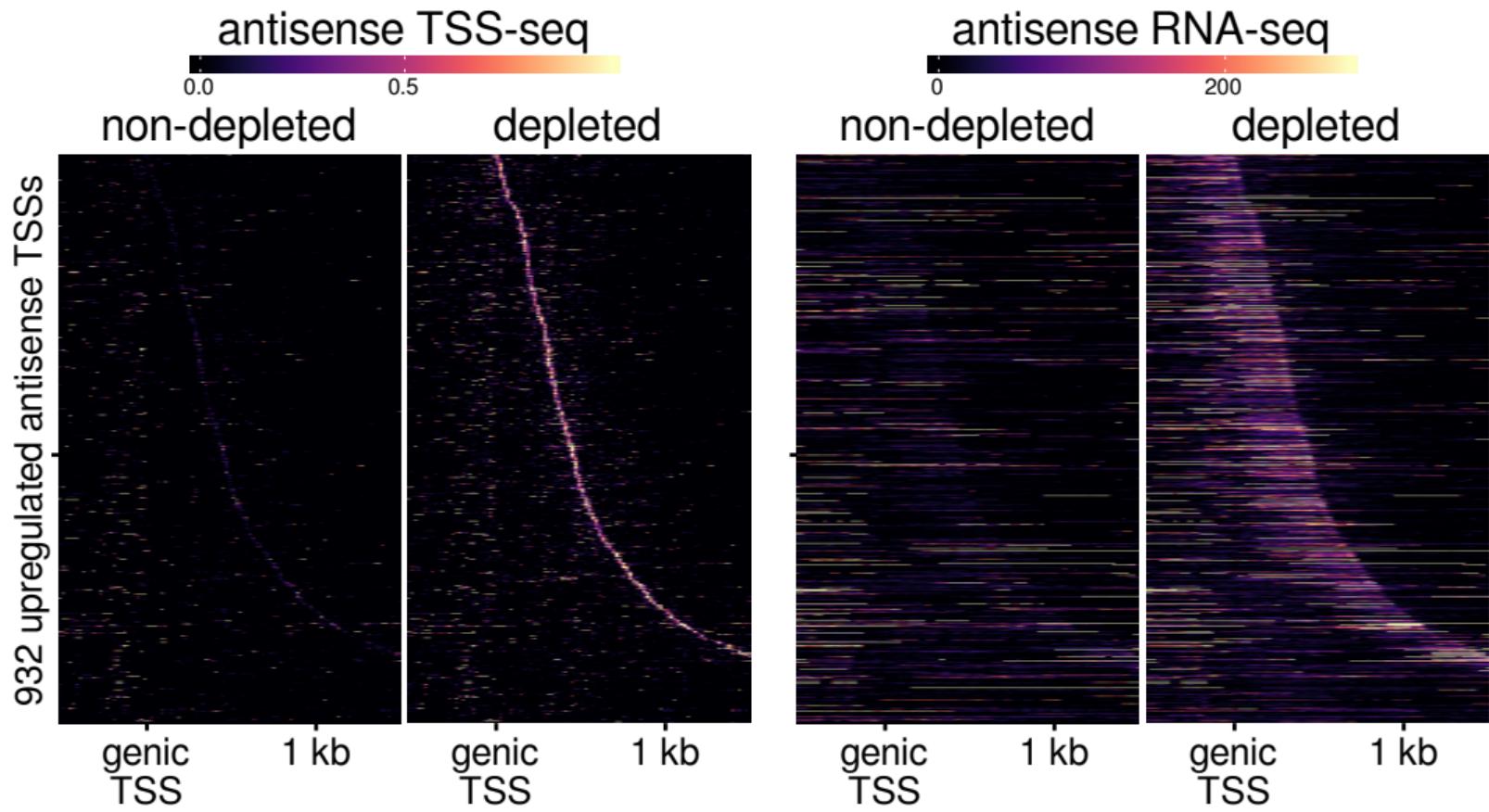


sense RNA-seq signal

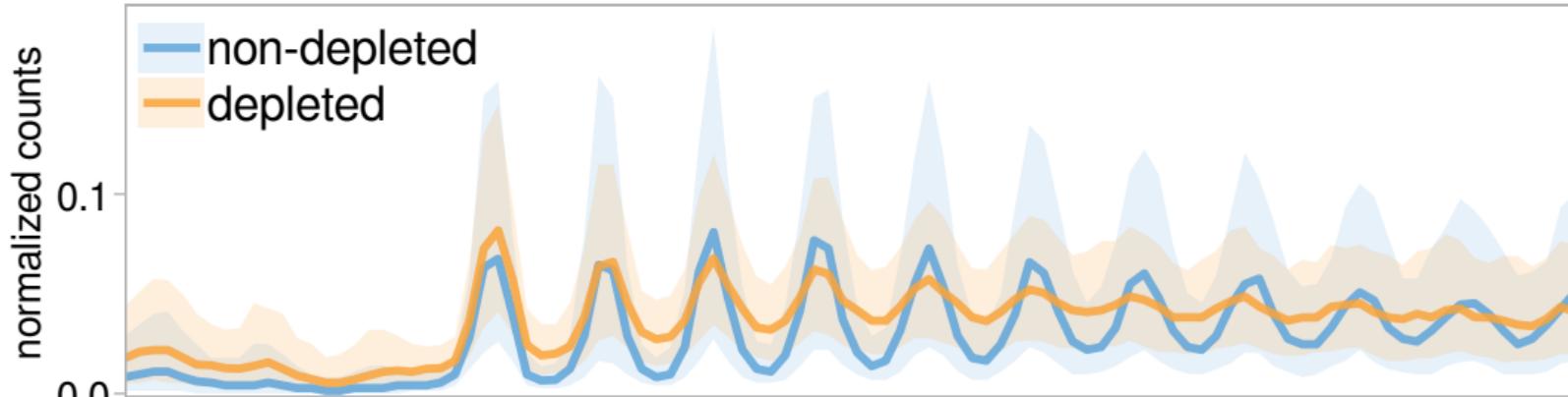


antisense RNA-seq signal

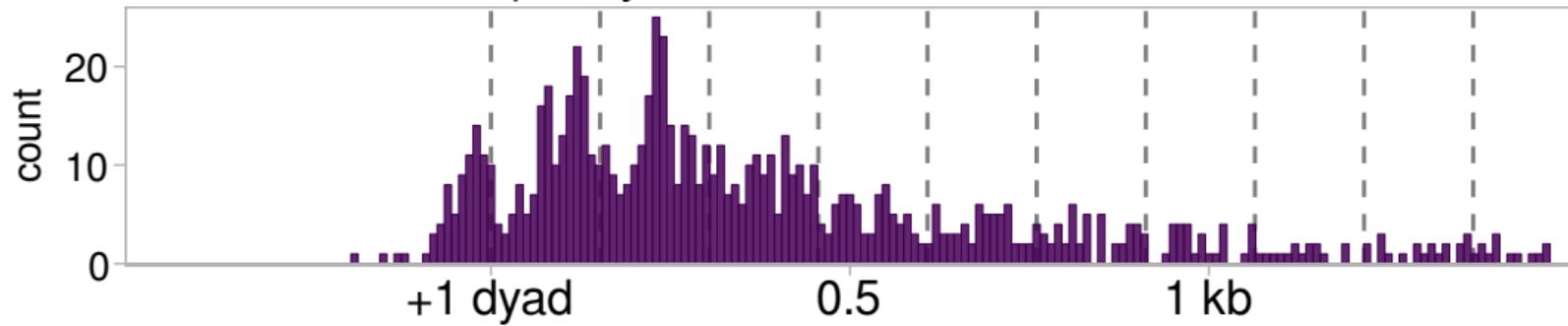




MNase-seq dyad signal



antisense TSS frequency



Spt5 summary and model

WT intragenic transcription

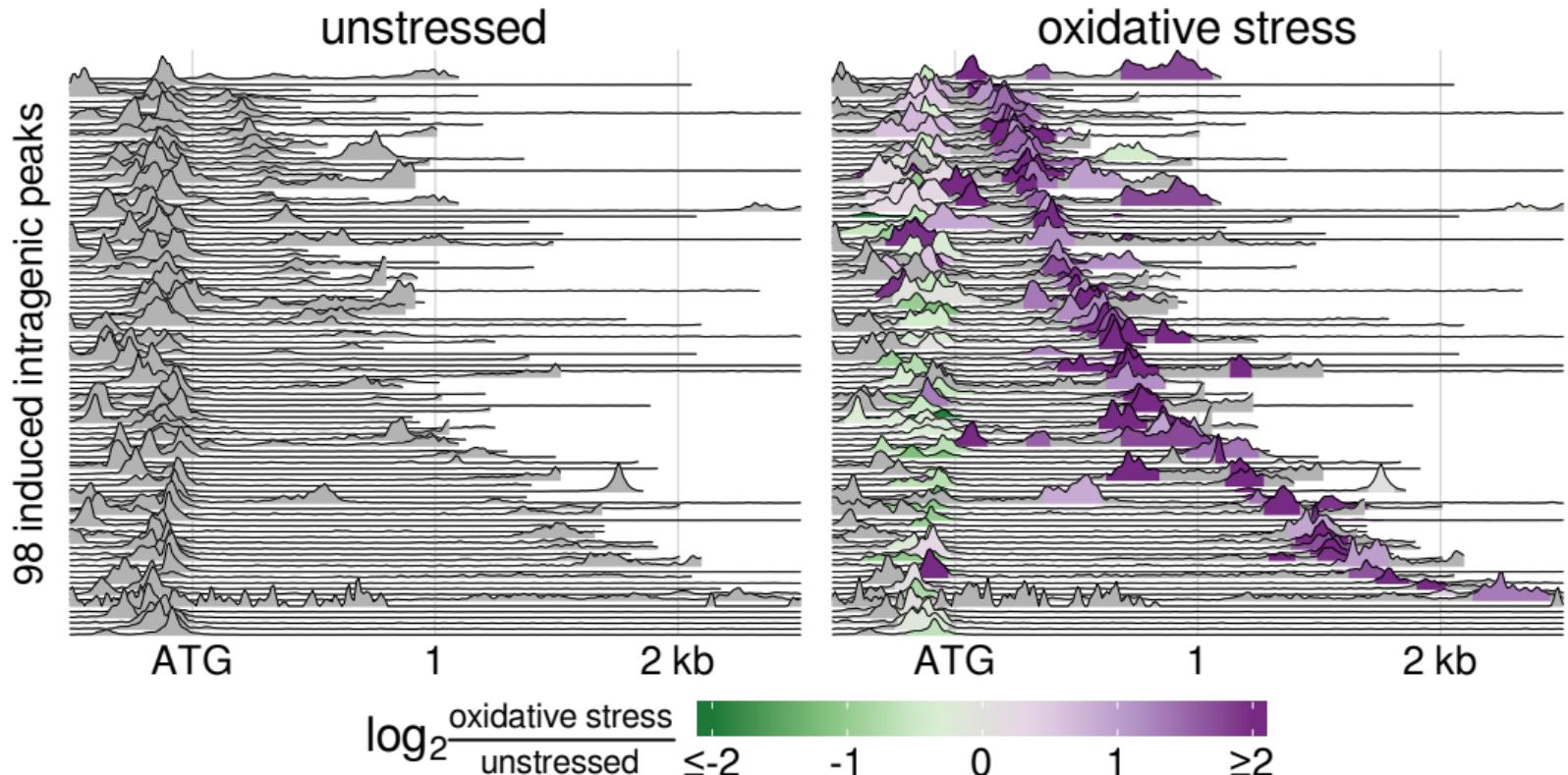
project collaborators

Steve Doris generated TSS-seq and ChIP-nexus libraries

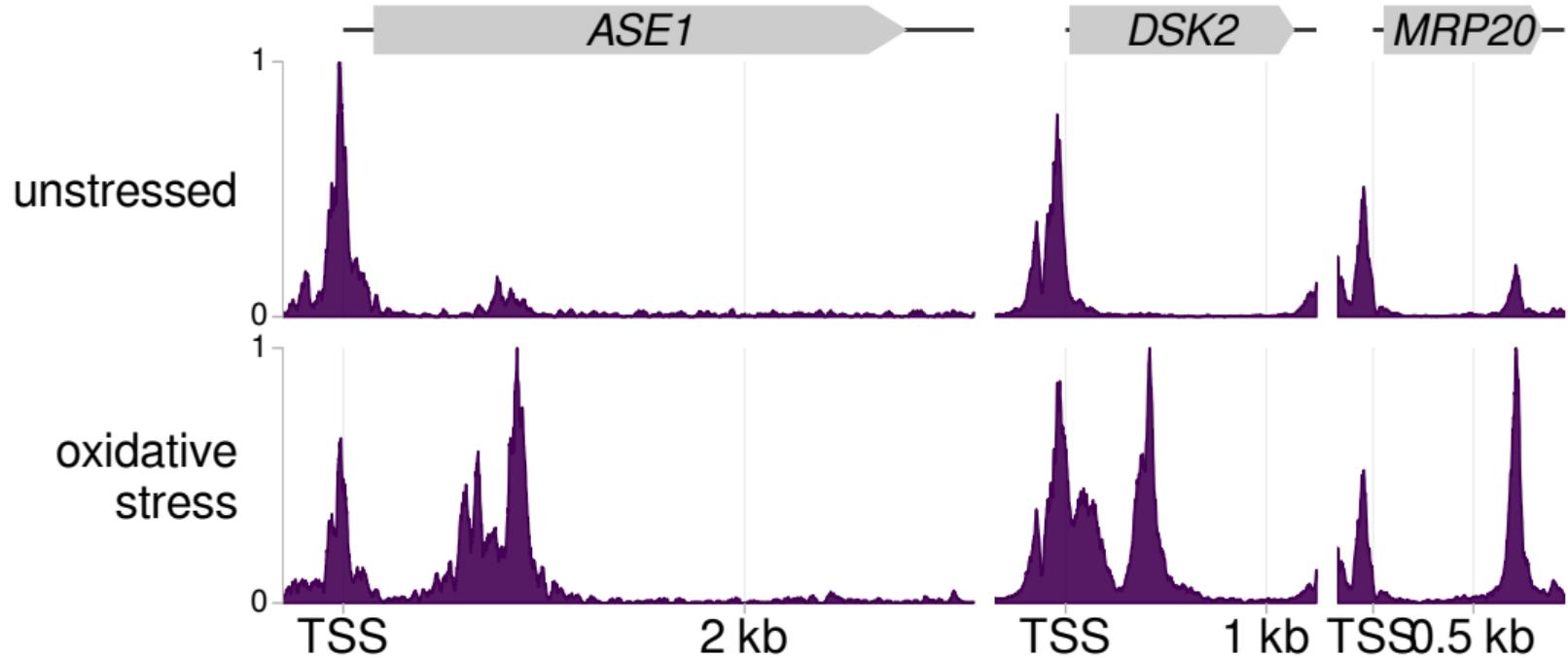
Dan Spatt polyribosome fractionation, competitive growth assays, and Northern blots

James Warner Northern blots

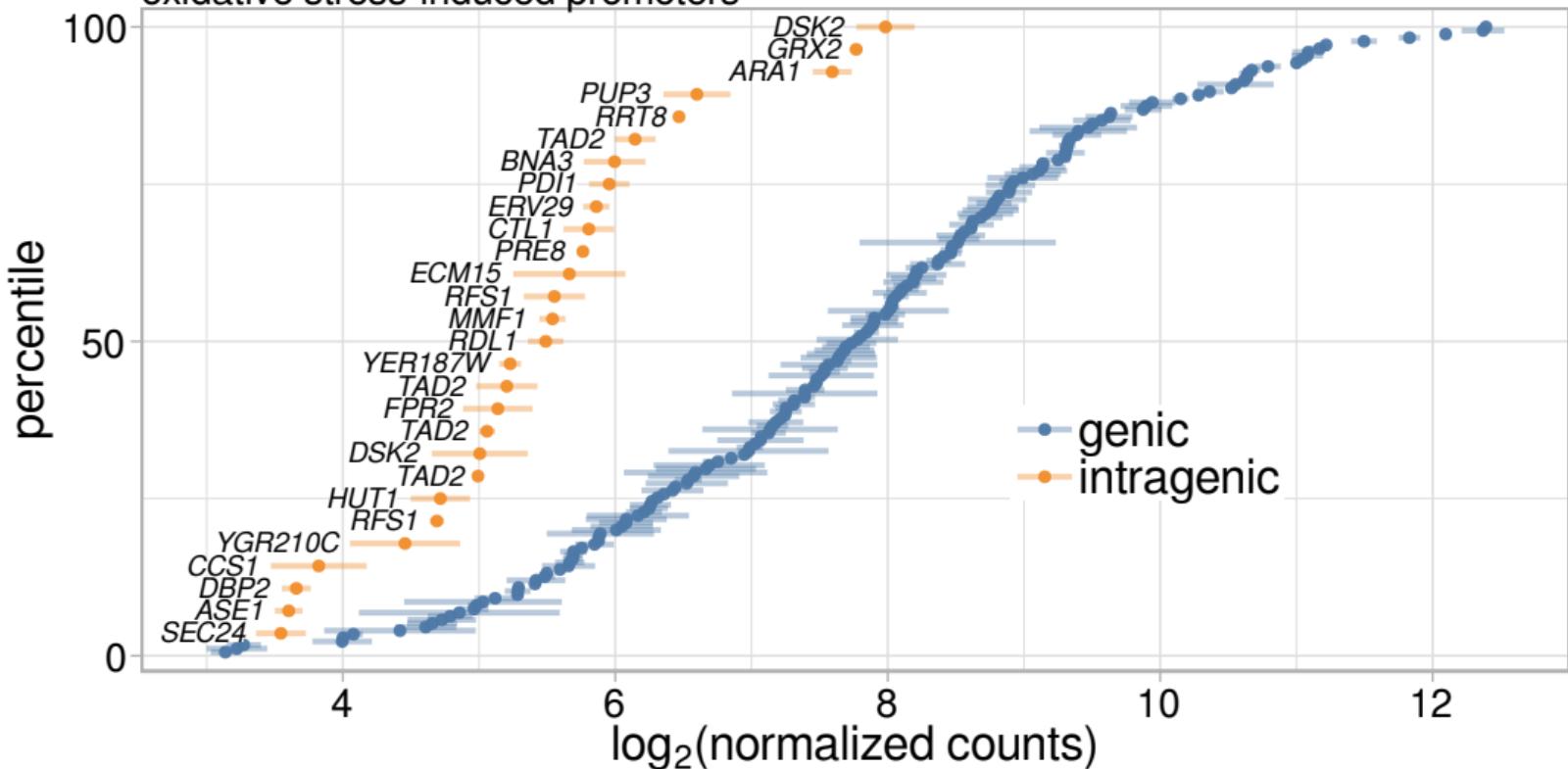
relative TFIIB ChIP-nexus protection



relative TFIIB ChIP-nexus protection

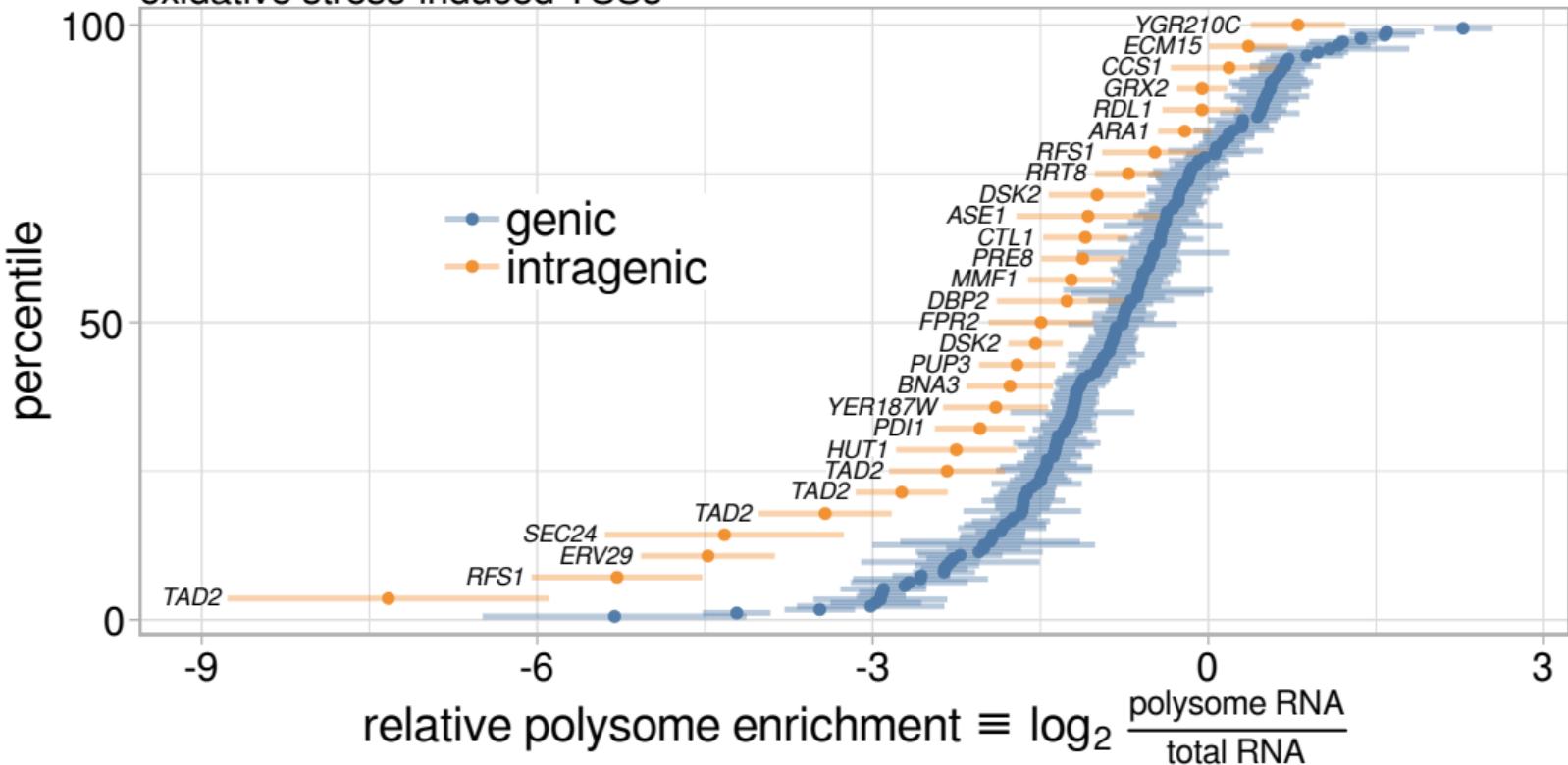


TSS expression levels in oxidative stress oxidative stress-induced promoters

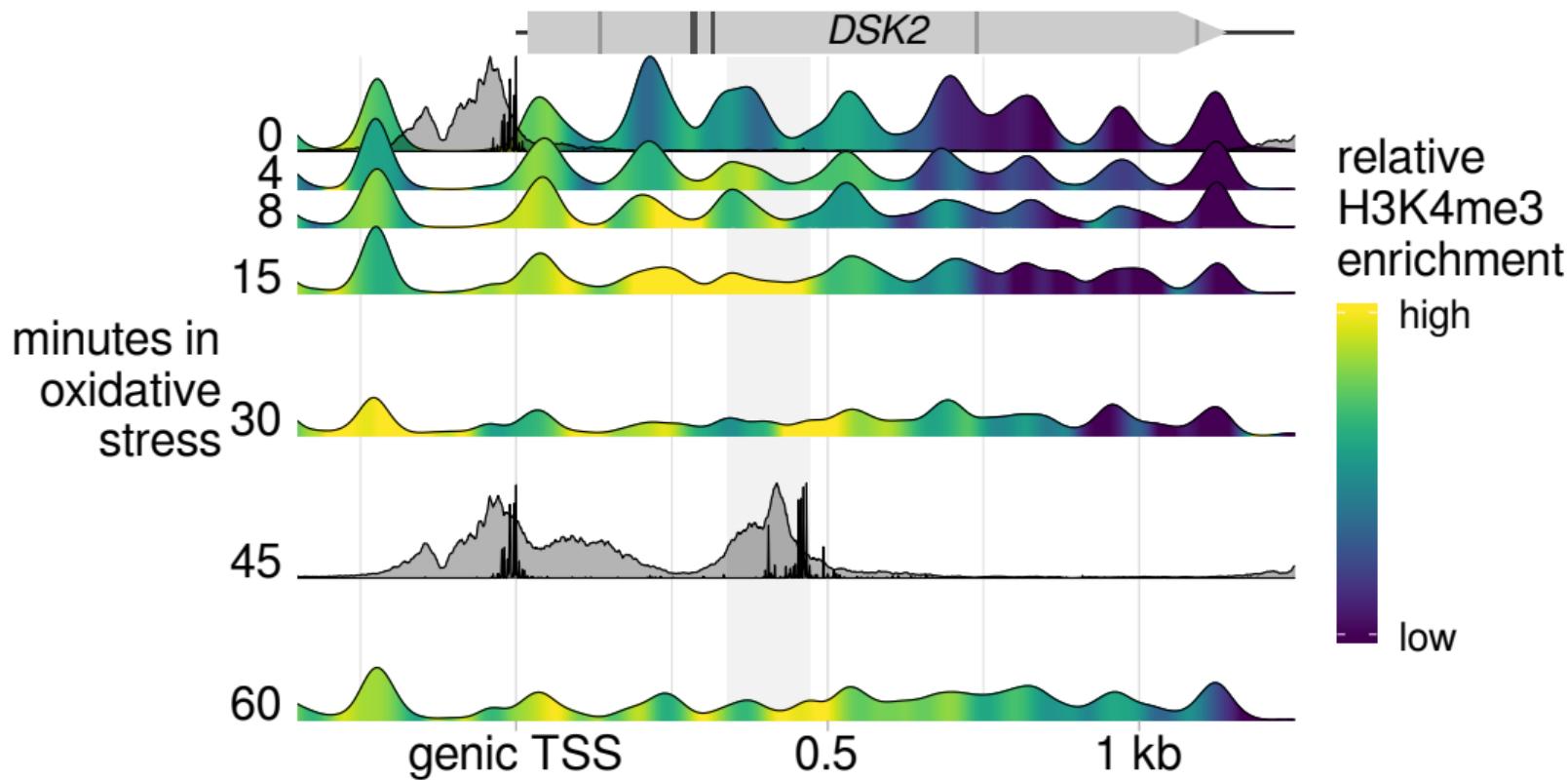


polysome enrichment in oxidative stress

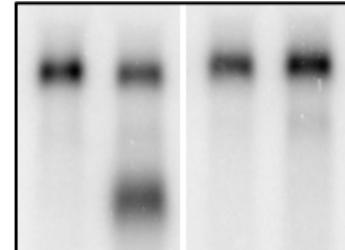
oxidative stress-induced TSSs



MNase dyads, TFIIB protection, and sense TSSs



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



DSK2 full-length

DSK2 intragenic

SNR190

