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COLLEGE OF ENGINEERING

Dissertation

**THE TITLE IS WASDA**

by

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M.S., Boston University, 2018

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Doctor of Philosophy

2019

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## Acknowledgments

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James Chuang

# **THE TITLE IS WASDA**

**JAMES CHUANG**

Boston University, College of Engineering, 2019

Major Professors: Fred Winston, PhD  
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## **ABSTRACT**

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## **Introduction**

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## **Chapter 1**

### **Genomics of transcription elongation factor Spt6**

#### **1.1 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** wetlab experiments for publication

#### **1.2 Introduction to Spt6 and intragenic transcription**

The work described in this chapter relates to understanding how a eukaryotic cell specifies which sites in its genome are permitted to become sites of transcription initiation. To get a rough idea of the specificity of transcription initiation, it is useful to start with a simple back-of-the-envelope calculation of the proportion of the human genome at which transcription initiation occurs. The human genome is approximately three billion base pairs in length, and each base pair can potentially be transcribed from each of its two strands. Each gene in the genome can have multiple transcription start sites (TSSs), which I assume to be five in number for the average gene. At last count, the human genome contains about twenty thousand protein-coding genes. To

be conservative in our estimate with regards to specificity, we assume that all twenty thousand genes are expressed, which leads to the following proportion:

$$\frac{(2 \times 10^4 \text{ genes}) \left( 5 \frac{\text{TSS}}{\text{gene}} \right)}{(3 \times 10^9 \text{ base pairs}) \left( 2 \frac{\text{TSS}}{\text{base pair}} \right)}.$$

However, this expression underestimates the extent of transcription initiation by only considering protein-coding genes, neglecting the many classes of noncoding genes present in the genome. If we assume that there are five noncoding genes for each coding gene, the updated expression,

$$\frac{(1.2 \times 10^5 \text{ genes}) \left( 5 \frac{\text{TSS}}{\text{gene}} \right)}{(3 \times 10^9 \text{ base pairs}) \left( 2 \frac{\text{TSS}}{\text{base pair}} \right)} = 0.0001,$$

says that when presented with a thousand positions to choose from, RNA polymerase chooses just one to start transcribing from!

Where transcription initiates is determined in large part by DNA sequence: the presence of certain sequence motifs increases the probability that RNA polymerase binds to DNA along with numerous co-factors required for initiation. However, DNA sequence alone does not entirely account for the specificity of transcription initiation. Genetic studies in yeast first showed that some transcription *elongation* factors, including histone chaperones and histone modification enzymes, play a role in restricting where transcription is allowed to initiate (Cheung et al., 2008, Hennig and Fischer, 2013, Kaplan et al., 2003). In this project, we study the role of a particular transcription elongation factor called **Spt6** in this process. Many years of research on Spt6 is summarised as follows (Doris et al., 2018):

- Spt6 interacts directly with:

- RNA polymerase II (RNAPII) (Close et al., 2011, Diebold et al., 2010b, Liu et al., 2011, Sdano et al., 2017, Sun et al., 2010, Yoh et al., 2007)
  - histones (Bortvin and Winston, 1996, McCullough et al., 2015)
  - the essential factor Spn1 (IWS1) (Diebold et al., 2010a, Li et al., 2018, McDonald et al., 2010)
- Spt6 is believed to function primarily as an elongation factor based on:
  - association with elongating RNAPII (Andrulis et al., 2000, Ivanovska et al., 2011, Kaplan et al., 2000, Mayer et al., 2010)
  - ability to enhance elongation in vitro (Endoh et al., 2004) and in vivo (Ardehali et al., 2009)
- Spt6 has been shown to regulate initiation in some cases (Adkins and Tyler, 2006, Ivanovska et al., 2011)
- Spt6 regulates:
  - chromatin structure (Bortvin and Winston, 1996, DeGennaro et al., 2013, Ivanovska et al., 2011, Jeronimo et al., 2015, Kaplan et al., 2003, Perales et al., 2013, van Bakel et al., 2013)
  - histone modifications, including:
    - \* H3K36 methylation (Carrozza et al., 2005, Chu et al., 2006, Yoh et al., 2008, Youdell et al., 2008)
    - \* in some organisms, H3K4 and H3K27 methylation (Begum et al., 2012, Chen et al., 2012, DeGennaro et al., 2013, Wang et al., 2017, 2013)
- Spt6 is likely a histone chaperone required to reassemble nucleosomes in the wake of transcription (Duina, 2011).

Previous studies in the yeasts *Saccharomyces cerevisiae* and *Schizosaccharomyces pombe* have examined the requirement for Spt6 in normal transcription (Cheung et al., 2008, DeGennaro et al., 2013, Kaplan et al., 2003, Pathak et al., 2018, Uwimana et al., 2017, van Bakel et al., 2013). Many of these studies make use of the same temperature-sensitive *S. cerevisiae* *spt6*-1004 mutant used in this project, ***spt6-1004***, in which Spt6 protein is depleted at the non-permissive temperature of 37°C (Kaplan et al., 2003). The most notable phenotype of the *spt6-1004* mutant is the expression of **intragenic transcripts**, transcripts which appear to start within protein-coding genes, both in the same orientation and in the antisense orientation relative to the coding gene (Figure 1.1) (Cheung et al., 2008, DeGennaro et al., 2013, Kaplan et al., 2003, Uwimana et al., 2017).

Previous genome-wide measurements of transcript levels in *spt6-1004* relied on tiled microarrays (Cheung et al., 2008) and RNA sequencing (Uwimana et al., 2017). These methods assay steady-state RNA levels, making them unable to determine whether the intragenic transcripts

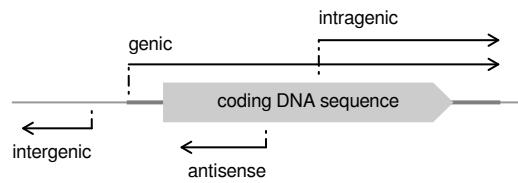


Figure 1.1: Diagram of transcript orientation with respect to coding DNA sequences, for the categories of transcripts referred to in this document.

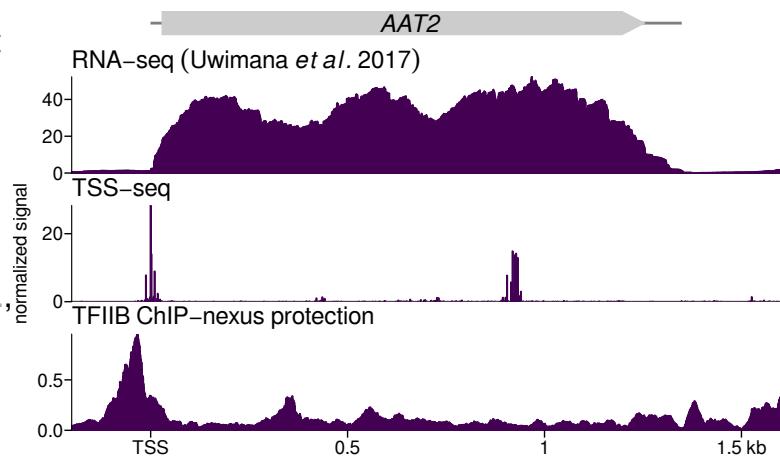


Figure 1.2: Sense strand RNA-seq signal, sense strand TSS-seq signal, and TFIIB ChIP-nexus protection at the *AAT2* gene, in *spt6-1004* after 80 minutes at 37°C.

observed in *spt6-1004* result from: A) new intragenic transcription initiation in the mutant, B) reduced decay of intragenic transcripts which are rapidly turned over in wild-type, or C) processing of full-length protein-coding RNAs. Additionally, these methods are suboptimal for identifying where intragenic transcription occurs, since the signal for an intragenic transcript in the same orientation as the gene it overlaps is convoluted with the signal from the full-length ‘genic’ transcript (Figure 1.2) (Cheung et al., 2008, Lickwar et al., 2009).

To overcome these issues, one of my collaborators applied two assays to study transcription in *spt6-1004*: transcription start-site sequencing (**TSS-seq**), and **ChIP-nexus of TFIIB**, a component of the RNA polymerase II pre-initiation complex (PIC). The TSS-seq technique sequences the 5' end of capped and polyadenylated RNAs (Arribere and Gilbert, 2013, Malabat et al., 2015), allowing separation of intragenic from genic RNA signals and identification of intragenic transcript starts with single-nucleotide resolution. The ChIP-nexus technique used is a high-resolution chromatin immunoprecipitation technique in which the ChIPed DNA is exonuclease digested up to the bases crosslinked with the factor of interest before sequencing (He et al., 2015). When applied to the PIC component TFIIB, ChIP-nexus provides a way to determine whether intragenic transcripts result from new intragenic transcription initiation.

### 1.3 pipeline development for TSS-seq and ChIP-nexus

In order to use TSS-seq and ChIP-nexus to answer questions about Spt6 and intragenic transcription, I developed analysis pipelines for TSS-seq and ChIP-nexus data. The pipelines are written using the Python-based Snakemake workflow specification language (Köster and Rahmann, 2012), and perform steps including read cleaning (Martin, 2011), various quality controls (Andrews, 2012), read alignment (Kim et al.,

2013, Langmead and Salzberg, 2012), data normalization, coverage track generation (Quinlan and Hall, 2010), peak calling (Zhang et al., 2008), differential expression/binding analyses (Love et al., 2014), data visualization with clustering, motif enrichment analyses (Bailey et al., 2015), and gene ontology analyses (Young et al., 2010). The Snakemake framework allows these data analyses to be reproducible and scalable from workstations up to computing clusters. Updated versions of these pipelines with more details on their capabilities are available at [github.com/winston-lab](https://github.com/winston-lab). In the following subsections I will describe the thought behind only a few of the more novel pipeline steps before moving on to results relating to Spt6 and intragenic transcription.

### 1.3.1 TSS-seq peak calling

TSS-seq data from a single region of transcription initiation tends to occur as a cluster of signal distributed over a range of positions, rather than a single nucleotide (Figure ??) (Arribere and Gilbert, 2013, Malabat et al., 2015). It is reasonable to consider such a cluster of TSS-seq signal as a single entity, because the signals within the cluster are usually highly correlated to one another across different conditions. Therefore, to identify TSSs from TSS-seq data and quantify them for downstream analyses such as differential expression, it is necessary to annotate these groups of signal by using the data to perform peak-calling.

In its current state, the TSS-seq pipeline calls peaks using 1-D [watershed segmentation](#), followed by filtering for reproducibility by the Irreproducible Discovery Rate (IDR) method (Li et al., 2011). First, a smoothed version of the TSS-seq coverage is generated for each sample using a discretized Gaussian kernel. Next, an initial set of peaks is generated by: 1) assigning all nonzero signal in the original, unsmoothed

coverage to the nearest local maximum of the smoothed coverage in the direction of positive derivative, and 2) taking the minimum and maximum genomic coordinates of the original coverage assigned to each local maximum as the peak boundaries. The peaks are then trimmed to the smallest genomic window that includes 95% of the original coverage, and the probability of the peak being generated by noise is estimated by a Poisson model where  $\lambda$ , the expected coverage, is the maximum of the expected coverage over the chromosome and the expected coverage in a window upstream of the peak (as for the ChIP-seq peak caller MACS2 (Zhang et al., 2008)). The influence of local read density on  $\lambda$  is intended to reduce false positive peaks within gene bodies, especially for highly expressed genes: Since there are more fragments of RNA present for highly expressed genes, more fragments within the gene body will make it into the final library, even if they are not true 5' ends. To generate the final set of peaks, the peaks are ranked by significance under the Poisson model, and filtered by IDR. In brief, IDR attempts to separate true peaks from experimental noise based on the intuition that, when peaks in each replicate are independently ranked by a metric such as significance, true peaks will have more similar ranks between replicates than peaks representing noise (Li et al., 2011).

The IDR algorithm currently only works for two replicates. Future improvements could include expanding the IDR implementation to handle more replicates and improve the accuracy of peak calling with more data.

### 1.3.2 ChIP-nexus peak calling

A number of tools have been created specifically for peak-calling using data from high-resolution ChIP techniques such as ChIP-nexus and ChIP-exo (Hansen et al., 2016, Wang et al., 2014). When applied to our TFIIB ChIP-nexus data, these tools

tended to split what appeared to be a single TFIIB binding event into multiple peaks. This may be because TFIIB has been observed to crosslink to DNA at multiple points (Figure ??) (Rhee and Pugh, 2012), which suggests that while these tools may work well for factors that bind symmetrically with a single crosslinking point on either side, there is still room for improvement when it comes to factors with more complex binding patterns. For the purposes of this project, the standard ChIP-seq peak caller MACS2 was used (Zhang et al., 2008).

ChIP-seq peaks lack strand information, as DNA binding factors usually do not bind DNA in a strand-specific manner. Because of this, we could not separate intragenic TFIIB peaks into peaks associated with sense or antisense transcription. The distinctive shape of the aggregate TFIIB ChIP-nexus signal (Figure ??) suggests that information about the strand of transcription may be present in the ChIP-nexus binding profile. Future work could include learning the direction of transcription from labeled ChIP-nexus training data.

#### 1.4 TSS-seq and TFIIB ChIP-nexus results from *spt6-1004*

To assay transcription start sites and transcription initiation in *spt6-1004*, one of my collaborators performed TSS-seq and ChIP-nexus of TFIIB. In wild-type cells, TSS-seq and TFIIB ChIP-nexus signal has the expected distribution over the genome, with most TSS-seq signal at annotated genic TSSs and most TFIIB signal just upstream (Figures 1.3, 1.4). In *spt6-1004*, the signal for both assays infiltrates gene bodies, consistent with a role for intragenic initiation in the intragenic transcription phenotype. Notably, sense strand TSS-seq signal in *spt6-1004* tends to occur towards the 3' end of genes, while antisense strand TSS-seq signal tends to occur towards the 5' ends of genes.

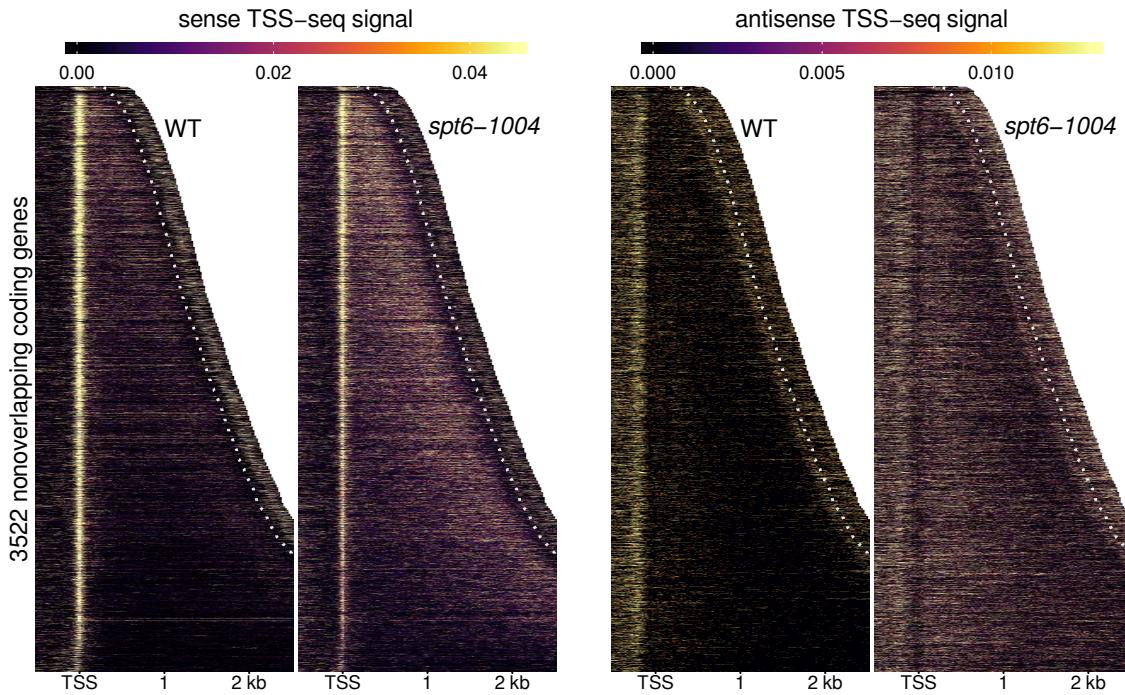


Figure 1.3: Heatmaps of sense and antisense TSS-seq signal from wild-type and *spt6-1004* cells, over 3522 non-overlapping genes aligned by wild-type genic TSS and sorted by annotated transcript length. Data are shown for each gene up to 300 nucleotides 3' of the cleavage and polyadenylation site (CPS), indicated by the white dotted line. Values are the mean of spike-in normalized coverage in non-overlapping 20 nucleotide bins, averaged over two replicates. Values above the 92nd percentile are set to the 92nd percentile for visualization.

The TSS-seq data were quantified by peak calling and differential expression analysis, and classified into genomic categories based on their position relative to coding genes (Figure 1.5). The results from this analysis support the pattern observed in the heatmap visualization (Figure 1.3), with most genic TSSs downregulated and almost 8000 TSSs upregulated intragenic or antisense to genes. The overall effect of this on expression levels is to equalize expression levels between the different classes of transcripts (Figure ??).

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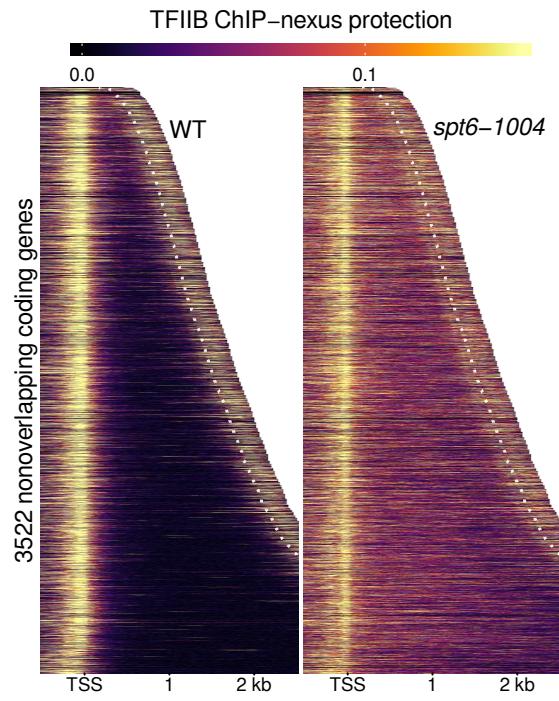


Figure 1.4: Heatmaps of TFIIB binding measured by ChIP-nexus, over the same regions shown in Figure 1.3. Values are the mean of library-size normalized coverage in non-overlapping 20 bp bins, averaged over two replicates. Values above the 85th percentile are set to the 85th percentile for visualization.

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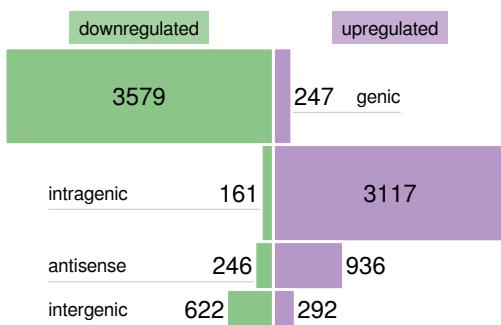


Figure 1.5: Bar plots of the number of TSS-seq peaks differentially expressed in *spt6-1004* after 80 minutes at 37°C versus wild-type after 80 minutes at 37°C. The height of each bar is proportional to the total number of peaks in the category, including those not found to be significantly differentially expressed.

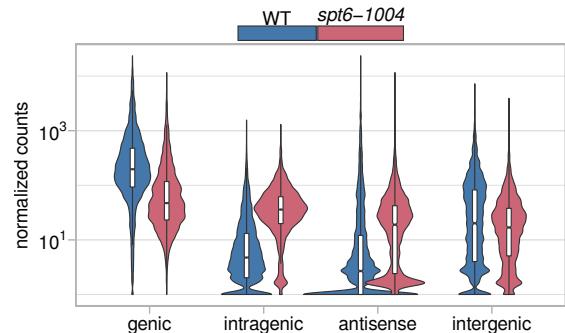


Figure 1.6: Violin plots of expression level distributions for genomic classes of TSS-seq peaks in wild-type and *spt6-1004*, both after 80 minutes at 37°C. Normalized counts are the mean of spike-in size factor normalized counts from two replicates.

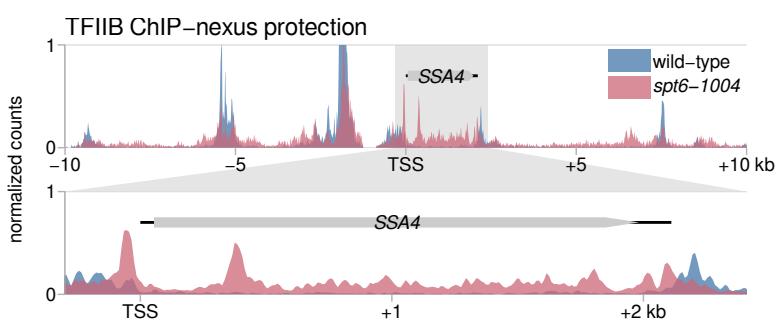
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Figure 1.7:

top) TFIIB ChIP-nexus protection in wild-type and *spt6-1004* strains over 20 kb of chromosome II flanking the *SSA4* gene.

bottom) Expanded view of TFIIB protection over the *SSA4* gene.



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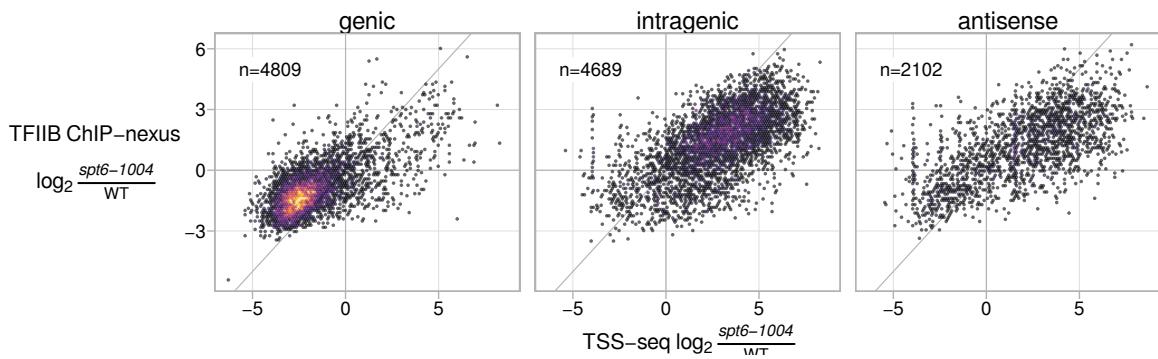


Figure 1.8: Scatterplots of fold-change in *spt6-1004* over wild-type, comparing TSS-seq and TFIIB ChIP-nexus. Each dot represents a TSS-seq peak paired with the window extending 200 bp upstream of the TSS-seq peak summit for quantification of TFIIB ChIP-nexus signal. Fold-changes are regularized fold-change estimates from DESeq2, with size factors determined from the *S. pombe* spike-in (TSS-seq), or *S. cerevisiae* counts (ChIP-nexus).

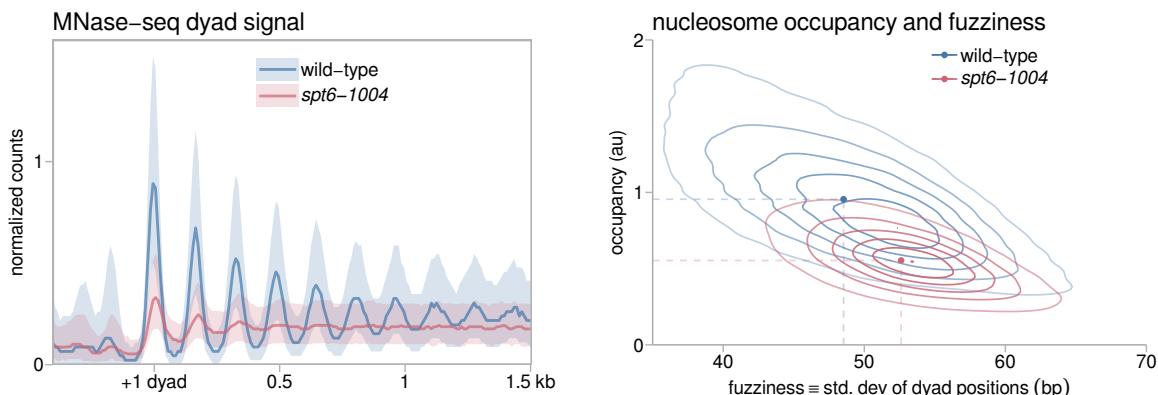


Figure 1.9: Average MNase-seq dyad signal in wild-type and *spt6-1004*, over 3522 non-overlapping genes aligned by wild-type +1 nucleosome dyad. Values are the mean of spike-in normalized coverage in non-overlapping 20 bp bins, averaged over two replicates (*spt6-1004*) or one experiment (wild-type). The solid line and shading are the median and the inter-quartile range.

Figure 1.10: Contour plot of the global distributions of nucleosome occupancy and fuzziness in wild-type and *spt6-1004*. Dashed lines indicate median values.

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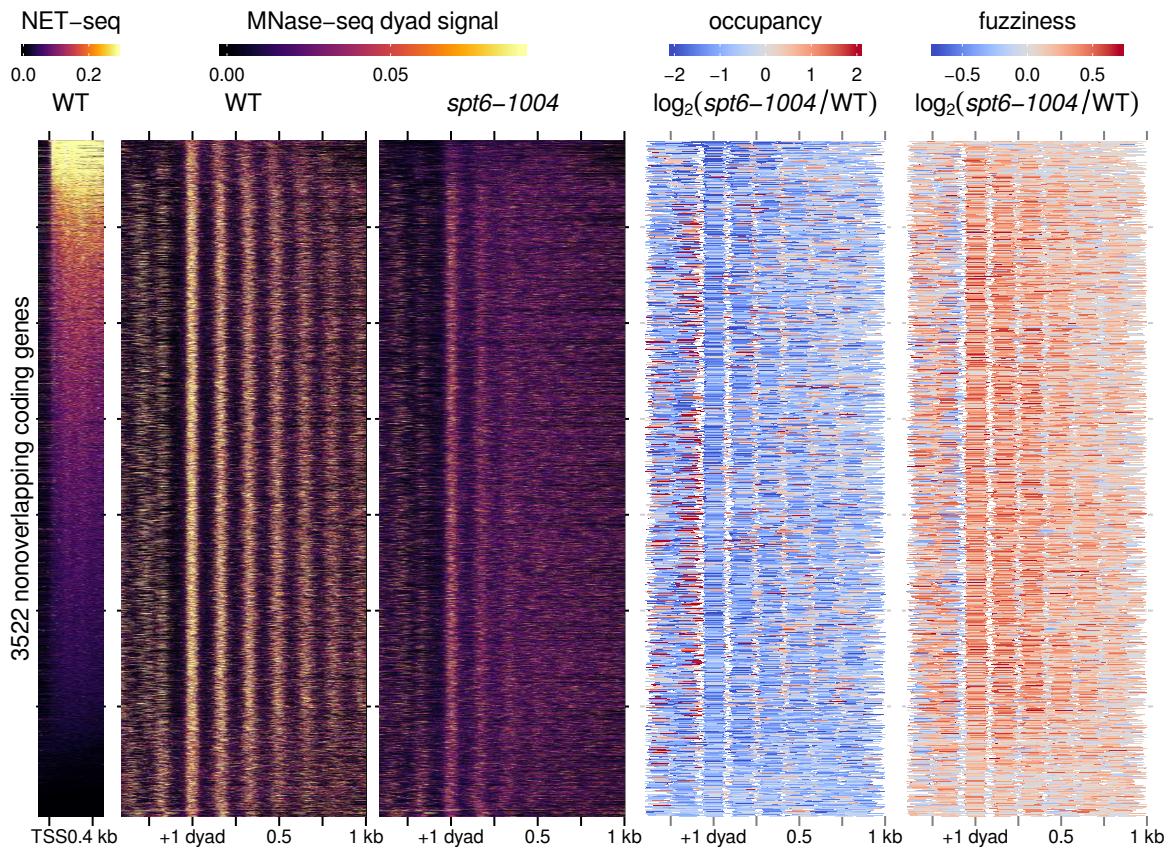


Figure 1.11:

- left) Heatmap of sense strand NET-seq signal for 3522 non-overlapping genes, aligned by genic TSS and sorted by total sense strand NET-seq signal in the window extending 500 nucleotides downstream from the genic TSS. Values are the mean of library-size normalized coverage in non-overlapping 20 nt bins, averaged over two replicates.
- middle) Heatmaps of MNase-seq dyad signal in wild-type and *spt6-1004* for the same genes, aligned by wild-type +1 nucleosome dyad and arranged by sense NET-seq signal as in the leftmost panel. Values are the mean of spike-in normalized coverage in non-overlapping 20 bp bins, averaged over two replicates (*spt6-1004*) or one experiment (wild-type).
- right) Heatmaps of fold-change in nucleosome occupancy and fuzziness for the same genes, aligned by wild-type +1 nucleosome dyad and arranged by sense NET-seq signal as in the leftmost panel.

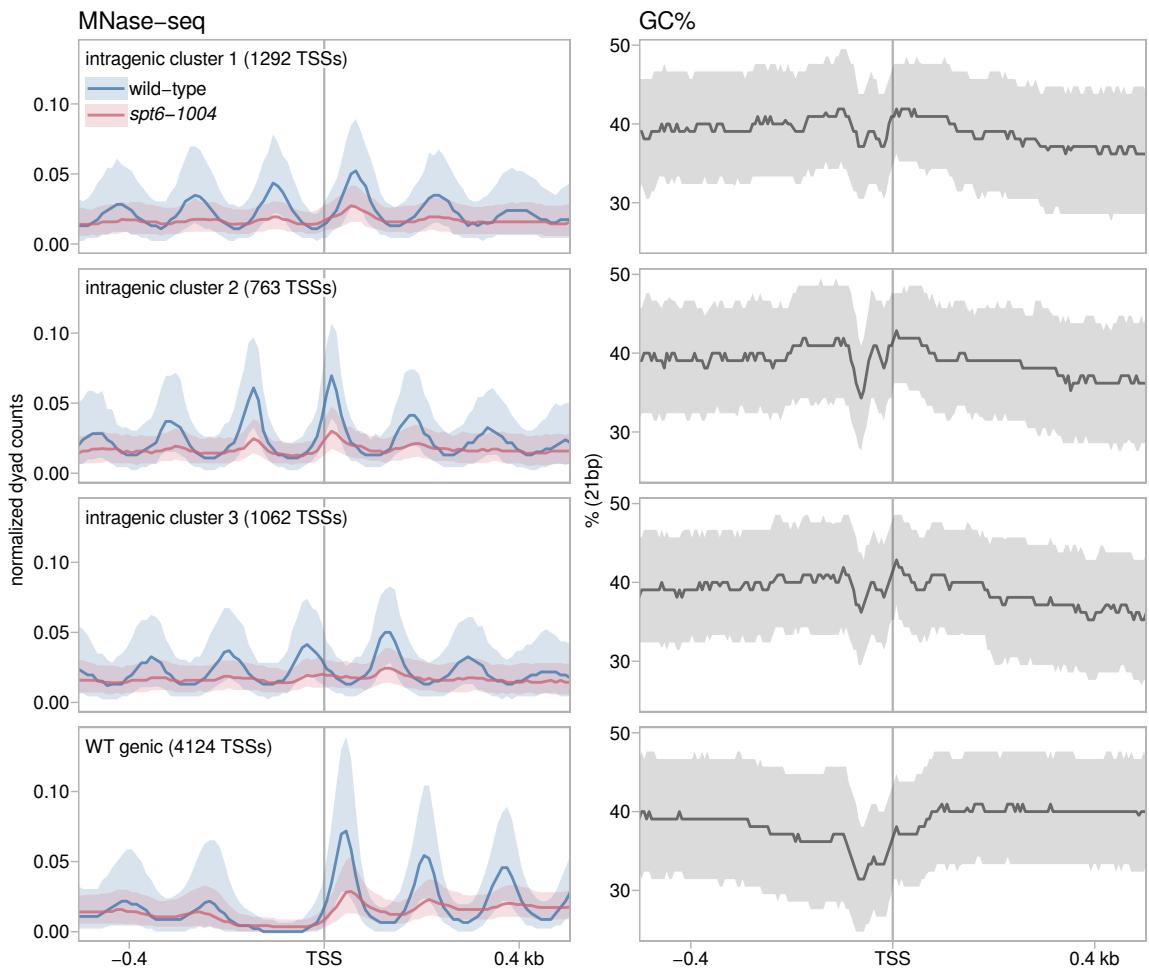


Figure 1.13:

- top row) Average MNase-seq dyad signal for two clusters of *spt6-1004* intragenic TSSs (clustered by wild-type and *spt6-1004* MNase-seq dyad signal flanking the TSS), as well as all genic TSSs detected in wild-type and *spt6-1004*. Values are the mean of spike-in normalized dyad coverage in non-overlapping 10 bp bins, averaged over two replicates (*spt6-1004*) or one experiment (wild-type). The solid line and shading are the median and inter-quartile range.
- bottom row) Average GC content of the DNA sequence, as above.

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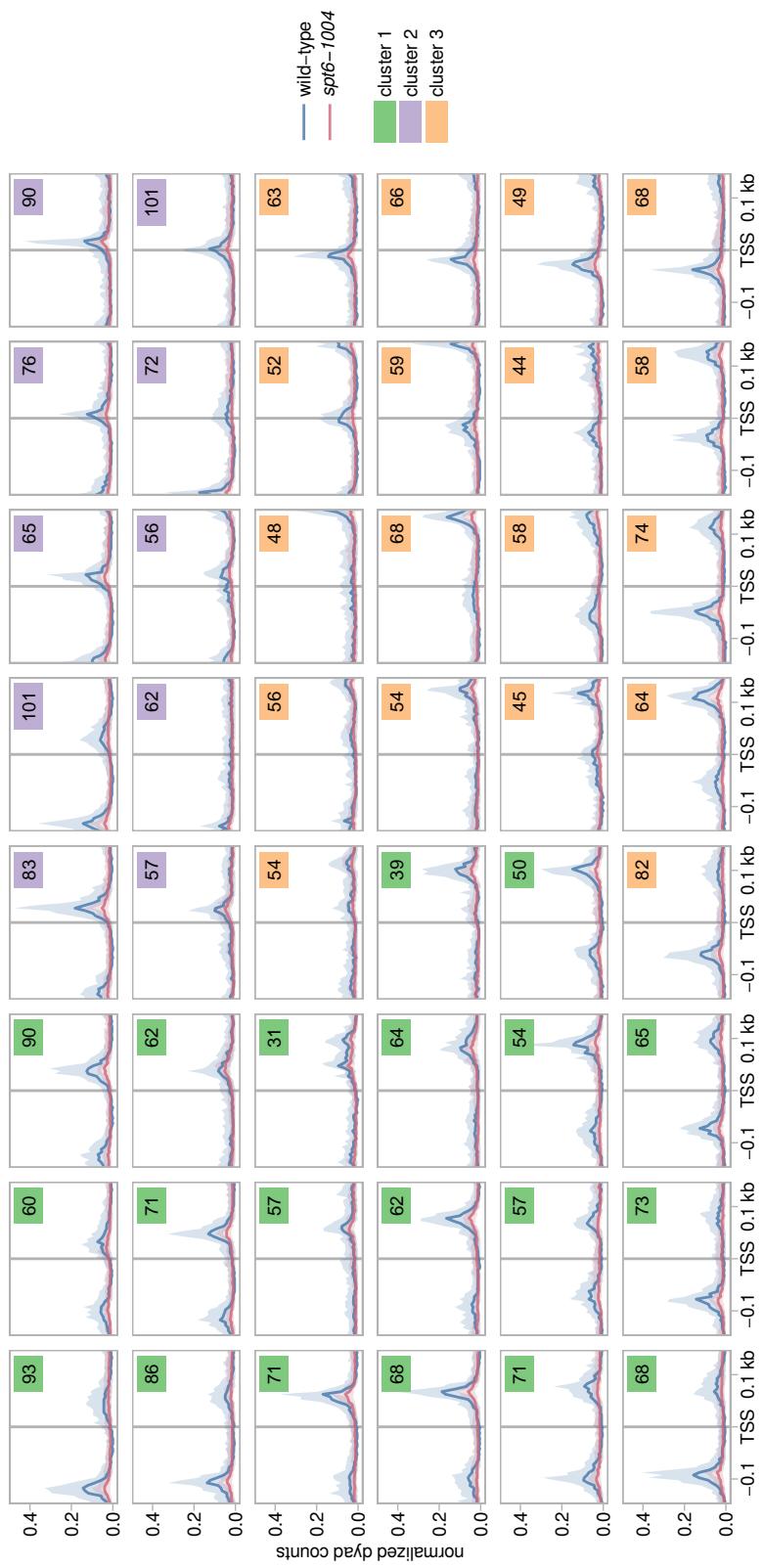


Figure 1.12: bar

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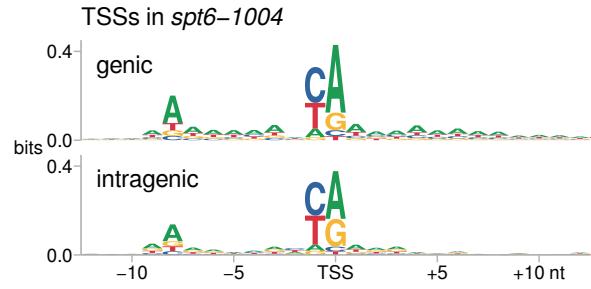


Figure 1.14: Sequence logos of the information content of TSS-seq reads overlapping genic and intragenic TSS-seq peaks in *spt6-1004*.

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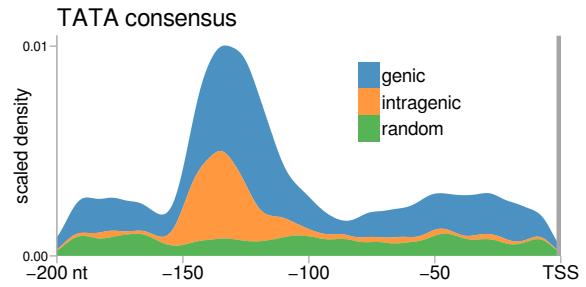


Figure 1.15: Scaled density of occurrences of exact matches to the motif TATAAWWR upstream of TSSs. For each category, a Gaussian kernel density estimate of the positions of motif occurrences is multiplied by the number of motif occurrences in the genomic category and divided by the number of regions in the category.

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## **Chapter 2**

### **Genomics of transcription elongation factor Spt5**

#### **2.1 Collaborators**

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

## **2.2 Bibliography**

## **Chapter 3**

### **Searching for stress-responsive intragenic transcription**

#### **3.1 Collaborators**

**Steve Doris** generated TSS-seq and ChIP-nexus libraries

**Dan Spatt** polyribosome fractionation

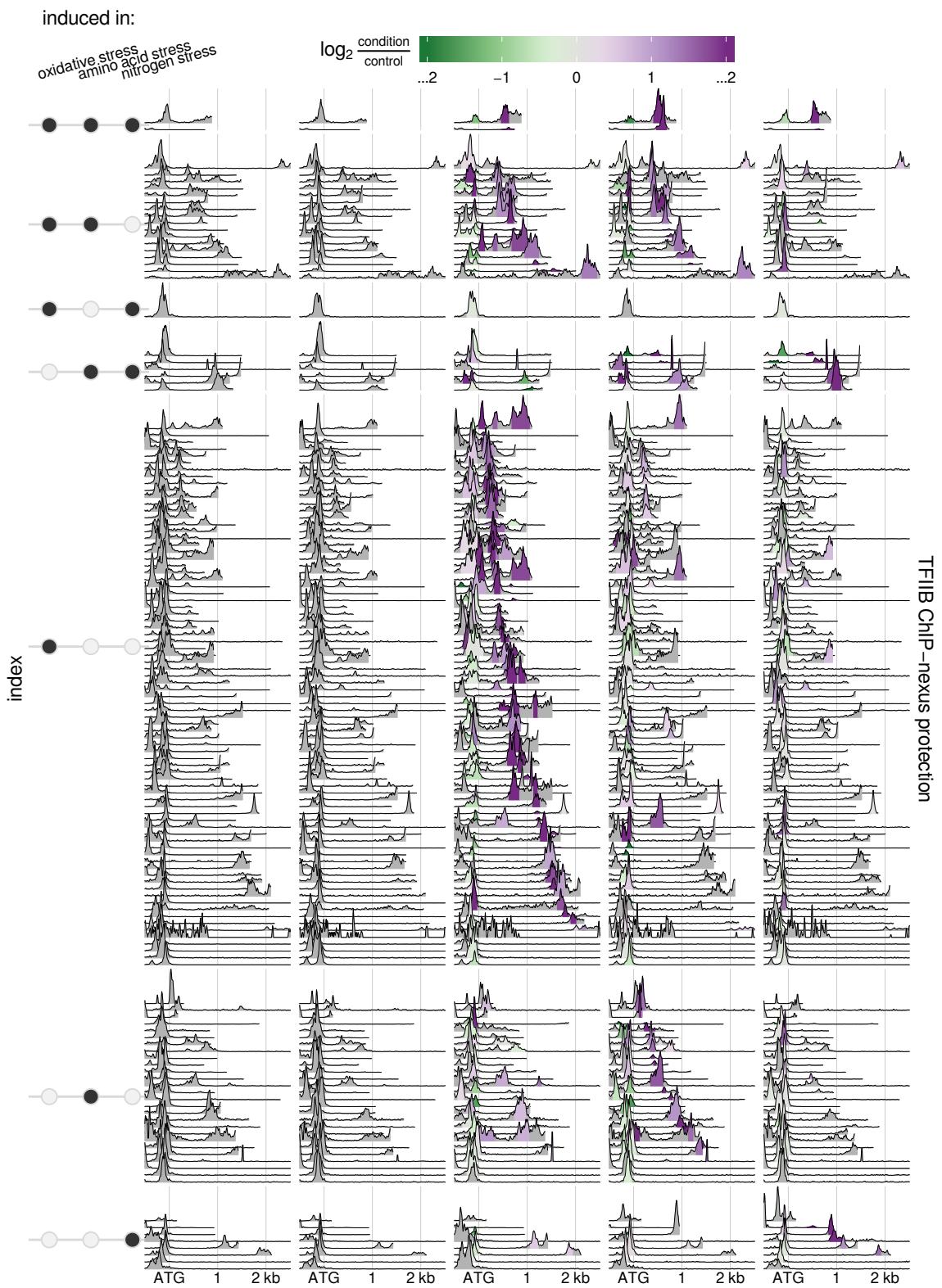


Figure 3.1: Wasldfkjlk asldkfj.

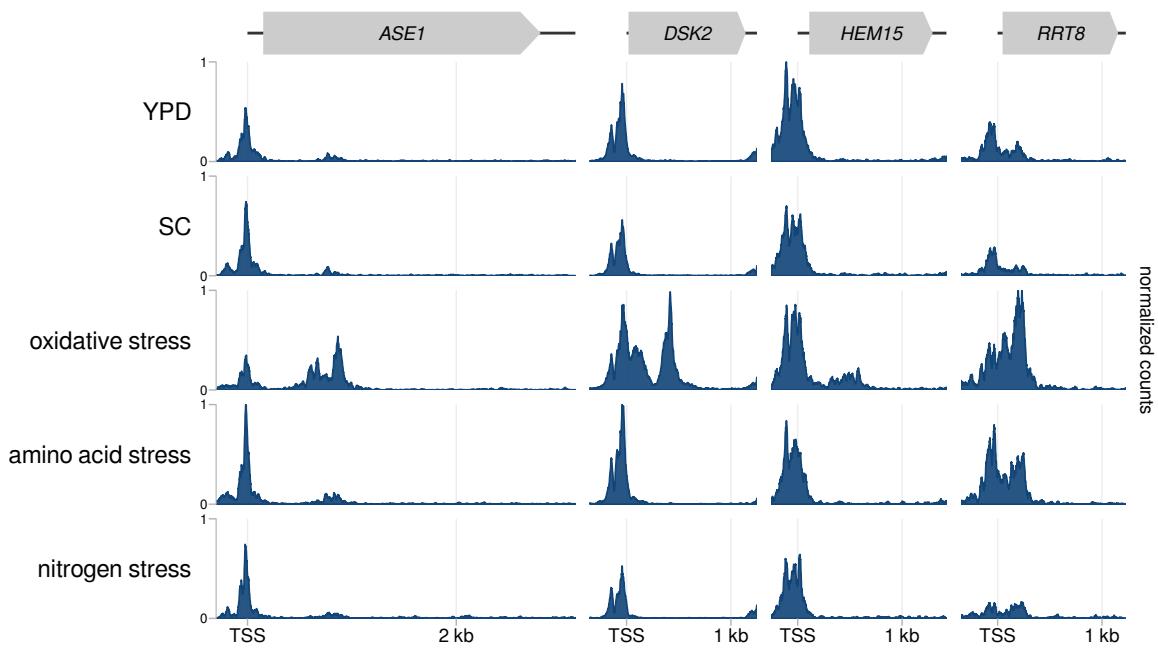


Figure 3.2: Caption asdflkj asldkfjlkj.

## 3.2 Bibliography

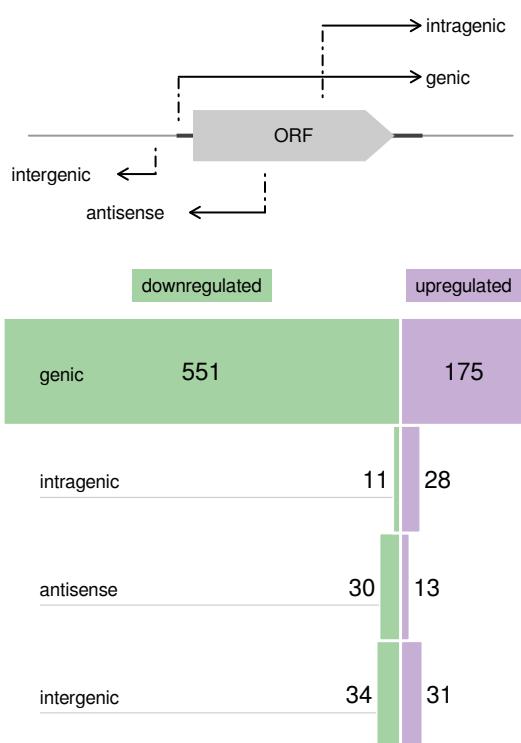


Figure 3.3: Caption dsafklj asldkfjlkj.

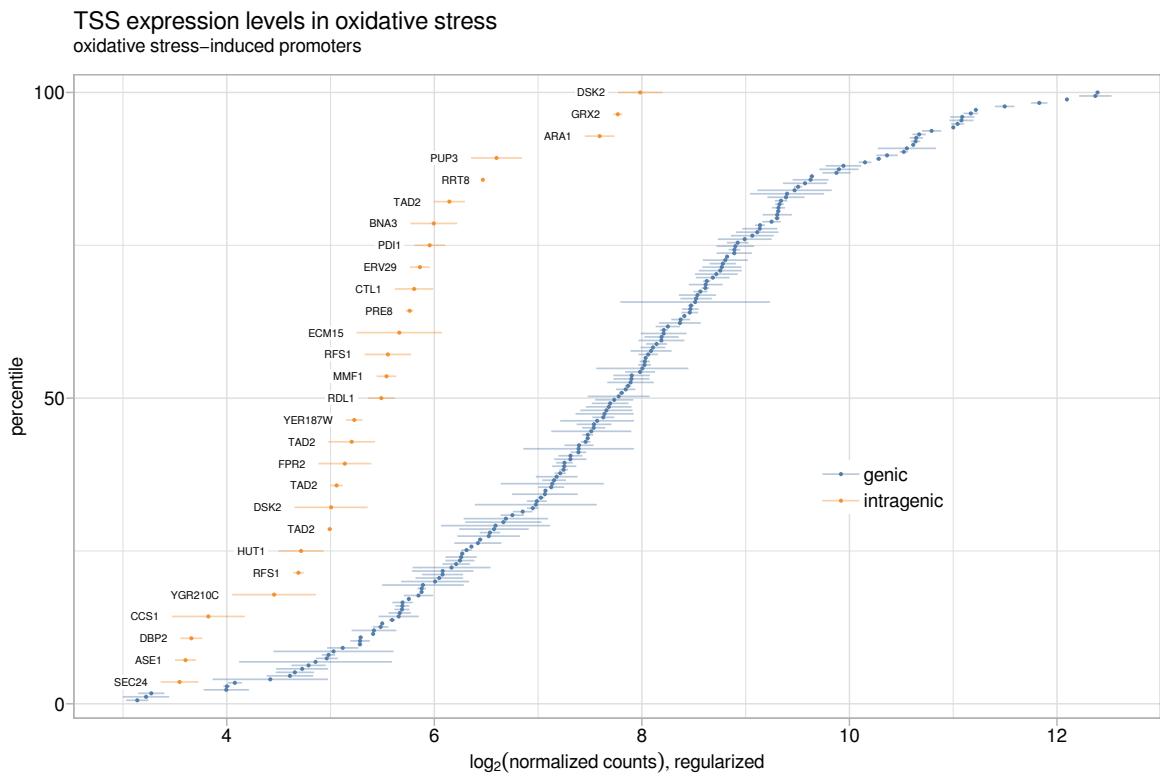


Figure 3.4: Caption dsafklj zzzz.

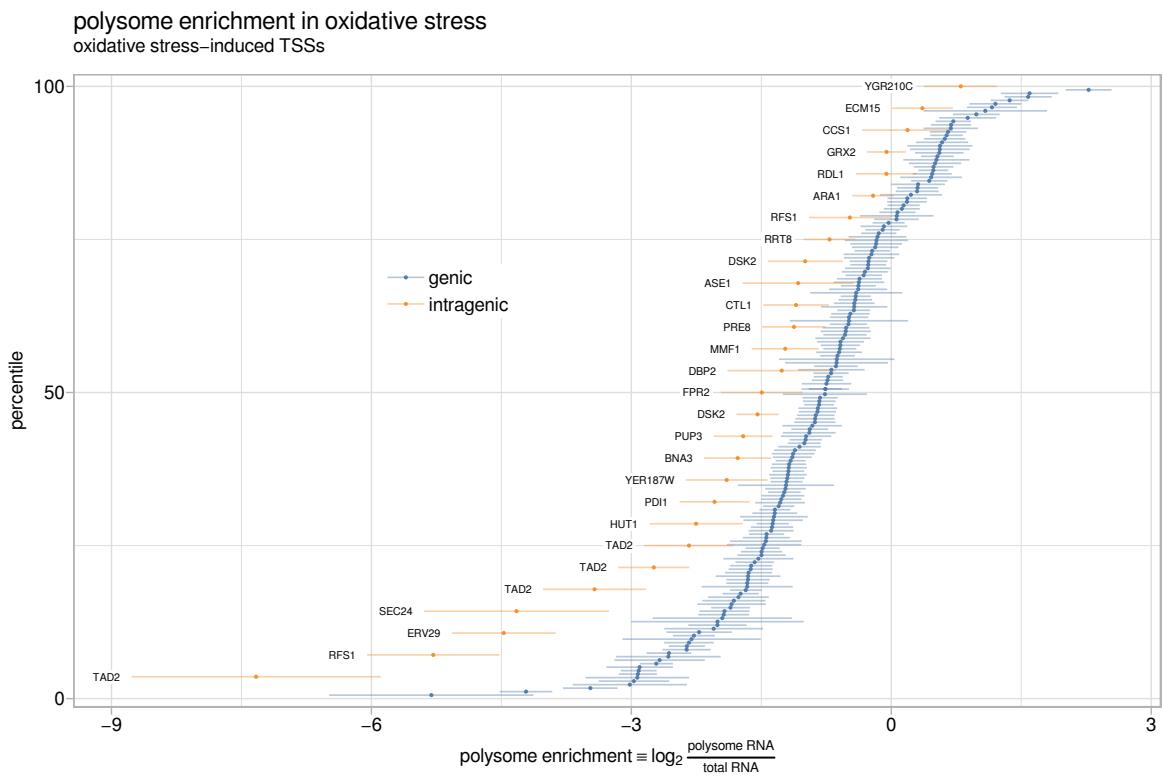


Figure 3.5: Caption wsadasdr zzzz.

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## Vita

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