User Guide

Access dsRNA data from mitotic and early meiotic yeast cells via the Sense/Antisense double stranded RNA Viewer (SensR)

Last update 19/01/2023

Uniform Resource Locator (URL): http://vm-gb.curie.fr/mprimig/SensR/

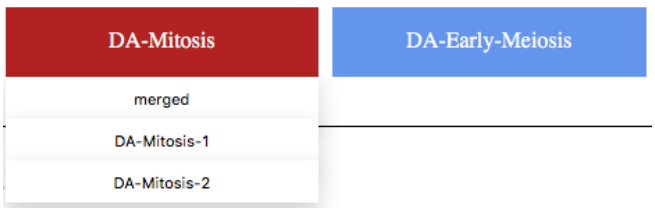
Note: this tool is accessible via a hypertext transfer protocol (http) that is not secure.

Reference: Szachnowski et al. in preparation

Compare dsRNA formation at loci encoding overlapping sense/antisense RNAs in mitotic and early meiotic yeast cells

1. SensR provides access to information about double-stranded RNAs (dsRNAs) formed by partially or completely overlapping sense/antisense RNAs. We compared samples from mitotic cells cultured in rich medium (YPD) and early meiotic cells cultured in sporulation medium (SPII). The approach is based on a budding yeast strain that contains Dicer and Argonaute transgenes, which encode proteins that cleave dsRNAs into defined fragments that are detected by a special DNA strand-specific small RNA-Sequencing protocol and mapped back onto the genome.
2. Go to http://vm-gb.curie.fr/mprimig/SensR/
3. Press the **Start** button in the welcome page and select the samples for which you want to display data by clicking on the rectangles. Note that wild type (WT) samples are negative controls while Dicer/Argonaute (DA) samples yield *bona fide* dsRNA signals.

4. Select *merged* if you want to display the averaged signals or individual samples



5. Select options to visualize the data. For example, select *fill* for a filled diagram, *stranded* to show DNA-strand specific data, *linear* to display untransformed signals and opt for *normalized* data display. Alternatively, select *heatmap* or *line* as options.

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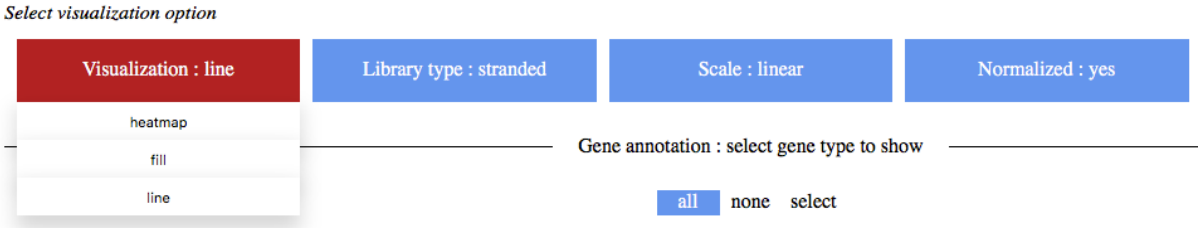
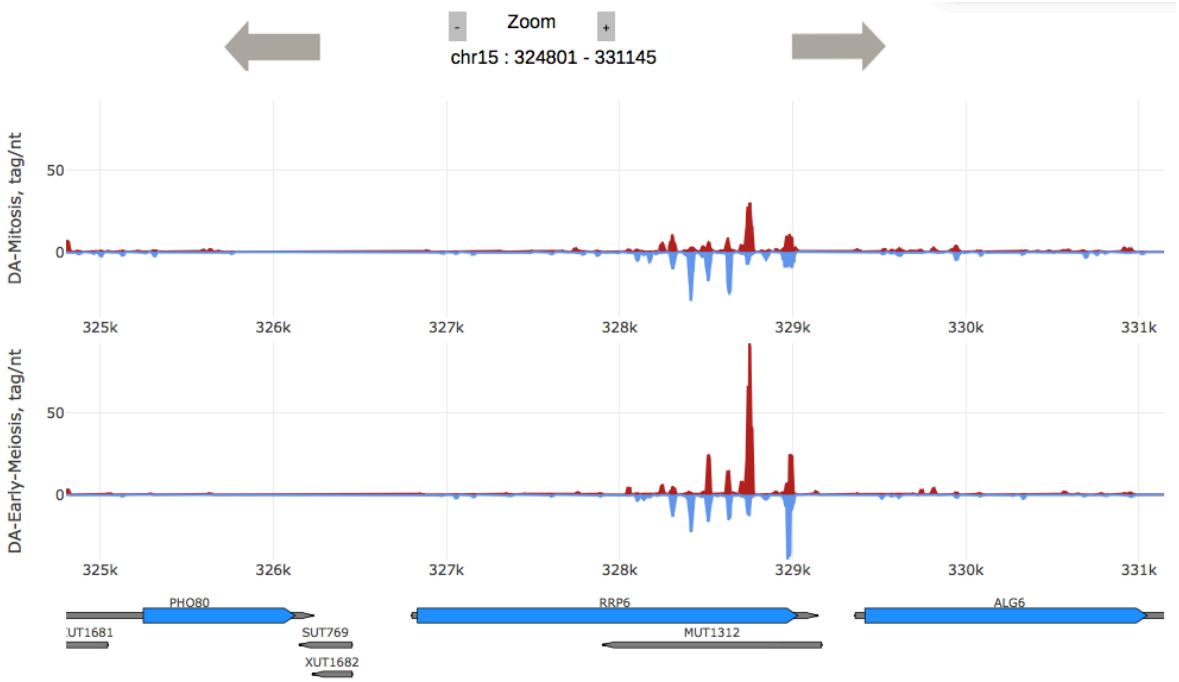


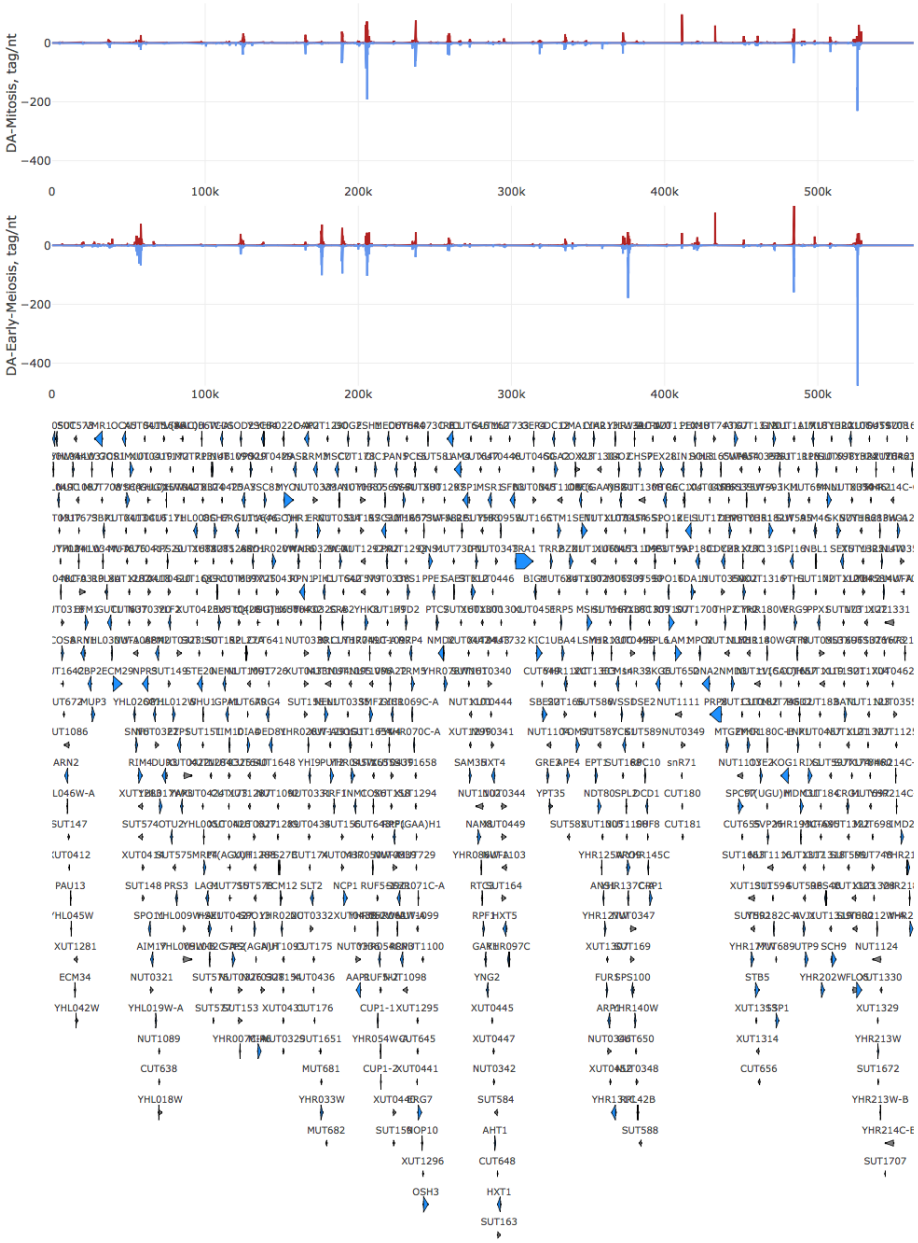
6. Select the chromosome in the popup menu (chr01) and enter the *genome coordinates* (left) or the *standard* or *systematic* gene name (right) in the query text fields and press the **GO!** button.

7. In the *filled* graph view, top and bottom strand-specific signals are given in red and blue, respectively. The diagram plots genome coordinates (x-axis) against normalized tags per nucleotide (tag/nt) signal units (y-axis). Protein coding and non-coding genes are given as blue and grey rectangles, respectively. UTRs are shown as lines. Arrowheads indicate the direction of transcription. You can interpret the dsRNA signal in the context of current genome annotation data. Note that the dsRNA signal corresponds to current *RRP6*/MUT1312 annotation. This is frequently not the case; try for example *SET1*/XUT1302. You will notice that the dsRNA extends the overlapping region. This is likey due to XUT1302 being longer than previously thought, or another as yet unknown lncRNA might be expressed downstream of XUT1302. You can compare dsRNA data to RNA-Sequencing data obtained with mitotic diploid yeast cells reported in Xie *et al*., RNA Biol 2019 at http://vm-gb.curie.fr/mprimig/5FU/index.htm.



8. You can walk along the chromosomes by clicking on the grey arrows at the top. Click on the - and + symbols to zoom in and out. Click on the bottom right camera icon to download the plot as an image file in png format.

9. You can view an entire chromosome by selecting its number and entering genome coordinates; for example, chr8: 1 – 562643 (or any number larger than the chromosome if you do not know the precise coordinates). If you do not wish to display the genes you can select “none” in the gene annotation section.



10. You can also combine the mitotic and meiotic data into one color-coded graph by selecting the *line* rather than the *filled* view. Use the zoom function or provide genome coordinates or gene names to focus on smaller regions or loci of interest.