User Guide

Sense/Antisense double stranded RNA Viewer (SensR)

Last update 21/10/2024

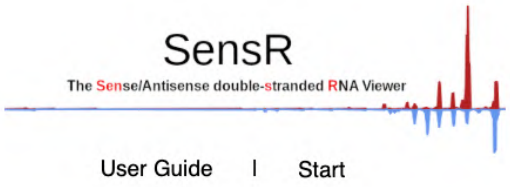
Uniform Resource Locator (URL): https://sensr.genouest.org

Note: this tool is accessible via a secure hypertext transfer protocol (https)

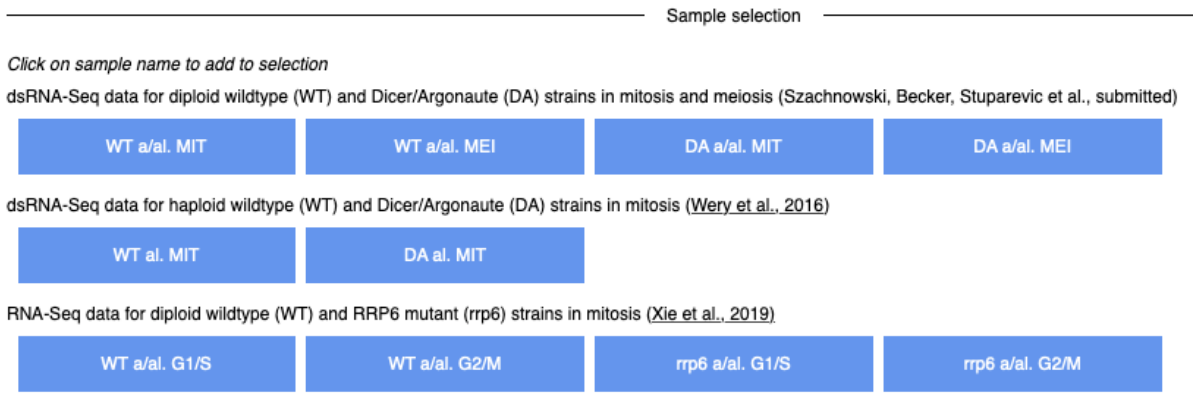
Reference: Szachnowski et al. submitted

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 - MIT) and meiotic cells cultured in sporulation medium (SPII - MEI). The approach is based on a budding yeast strain that contains Dicer (DCR1) and Argonaute (AGO1) transgenes from *Naumovozyma castellii*. The DA strain cleaves dsRNAs into small fragments of 19-23 bases that are detected by a special DNA strand-specific small RNA-Sequencing protocol and mapped back onto the genome.
2. Go to https://sensr.genouest.org.



3. Press the **Start** button in the welcome page and select the samples from three different studies as indicated 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.



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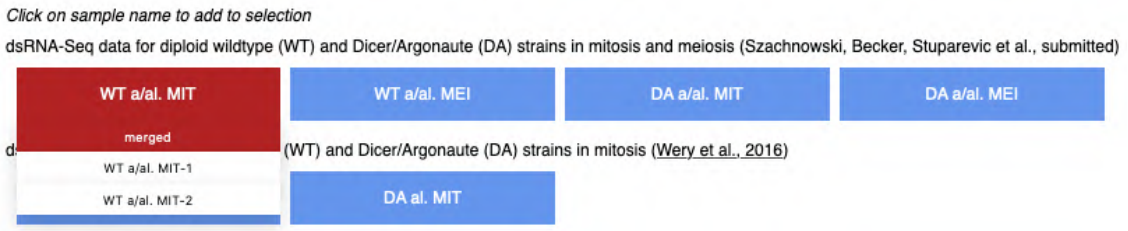
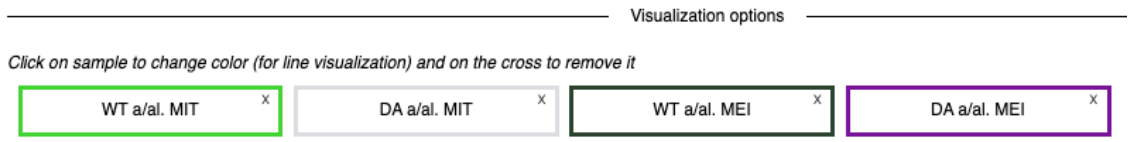
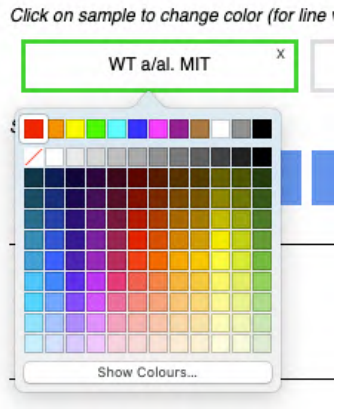
4. Select *merged* in the popup menu if you want to display the averaged signals or select individual samples



5. Edit the sample display in the *Visualization options* section. Click on the cross in the top right corner to remove a sample.



Click on the rectangle to select the color for a given sample. This is required for the line view but not the filled line and heatmap options.



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.

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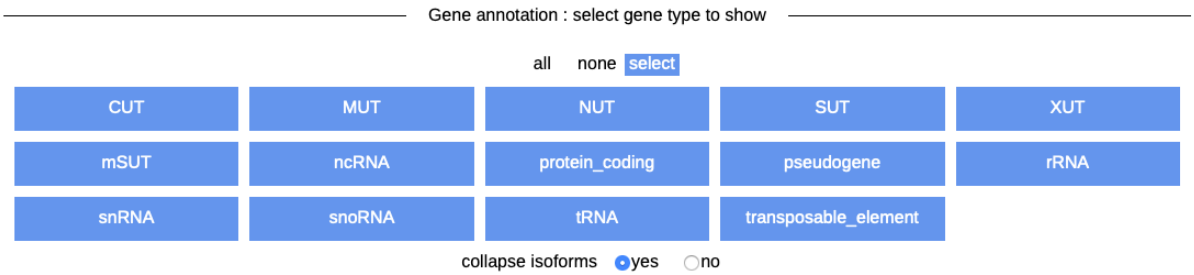
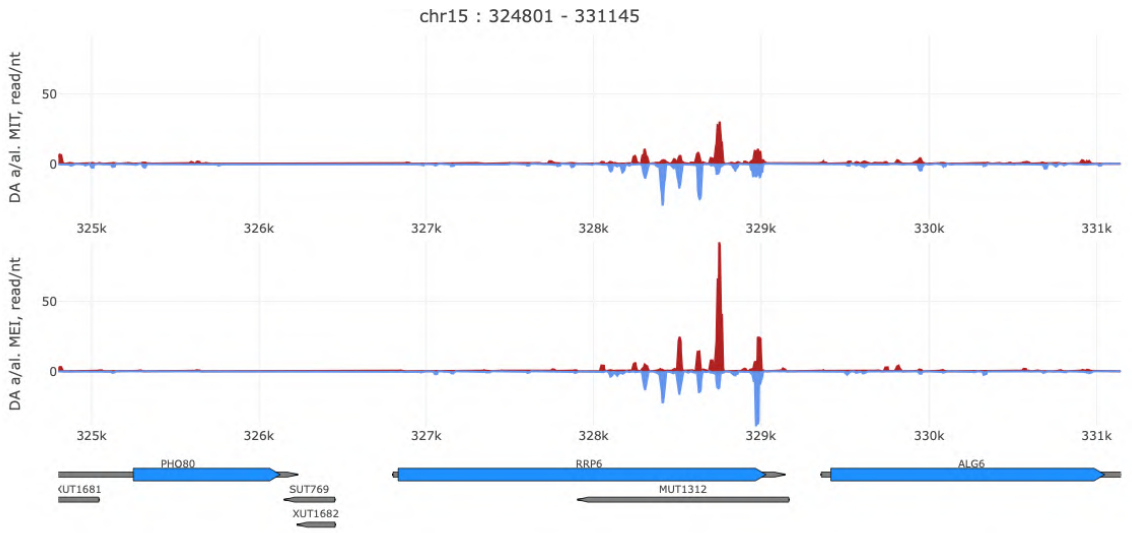
6. You can display all, none or a selection of transcript types by clicking on the options in the gene annotation section.



7. 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.

8. 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 reads per nucleotide (read/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. Alternatively, 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 by selecting the samples in the start page or, if you wish to interpret the complete dataset at https://5fur.genouest.org.



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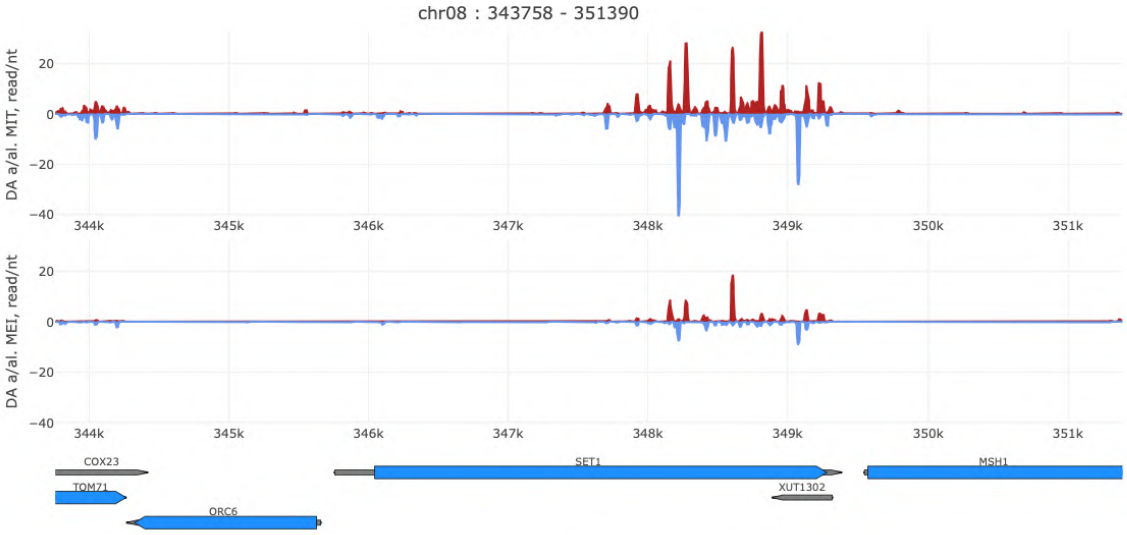
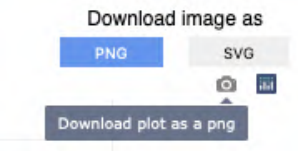
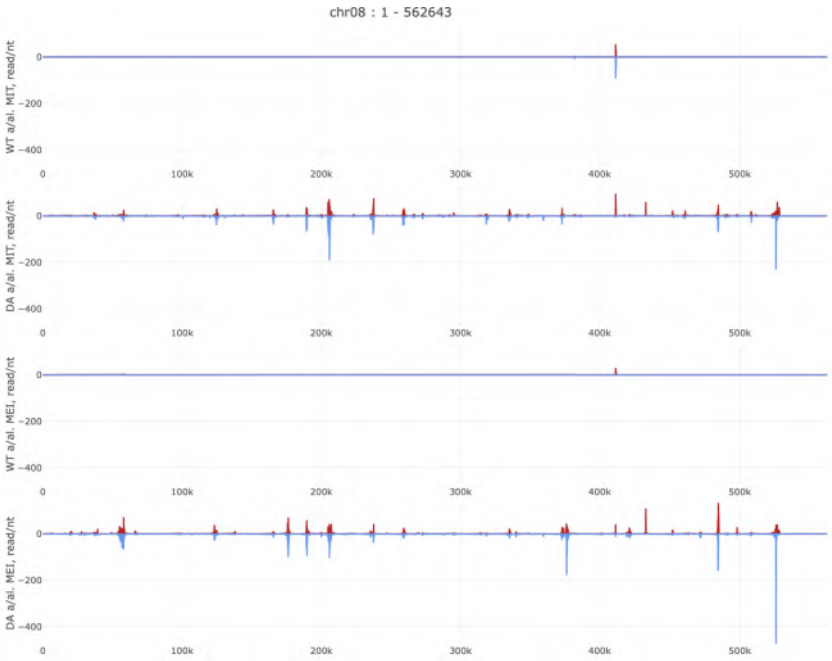


9. You can walk along the chromosomes by clicking on the grey arrows at the top. Click on the - and + symbols to zoom out and in.

10. You can download the data as images. First, select the PNG or vectorized SVG format and then click on the camera icon to download the plot, which includes the selected genome coordinates.



11. 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).



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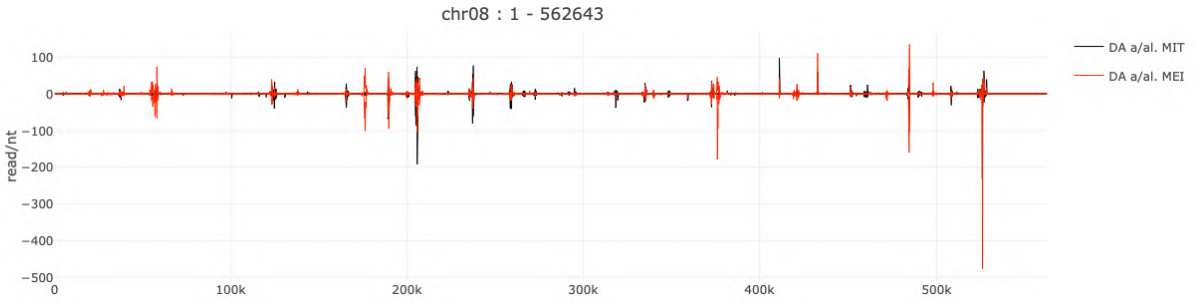
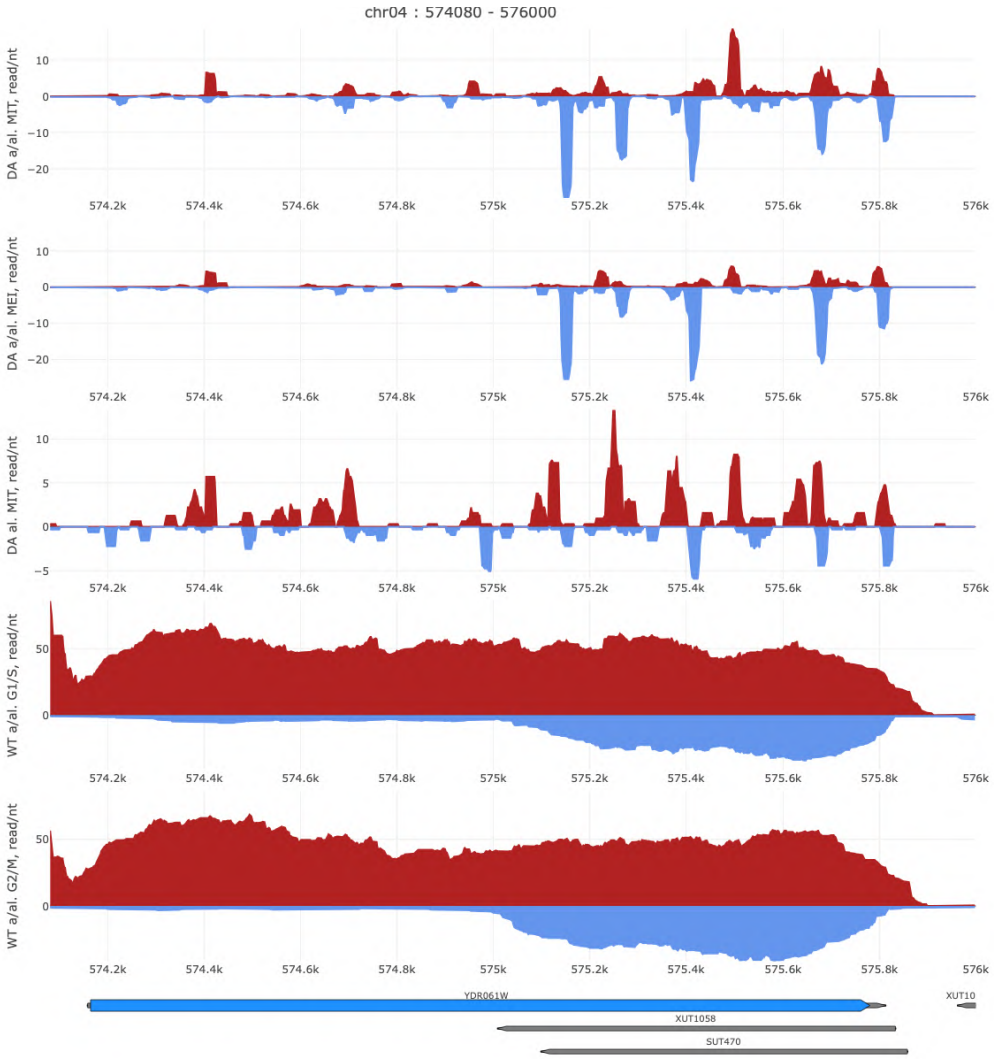
12. You can also combine the mitotic and meiotic data into one color-coded graph by selecting the *line* rather than the *filled* view. Mitotic and meiotic signals are shown in black and red, respectively.



13. To combine dsRNA and RNA-Seq expression data, select appropriate strains (e.g. diploid DA a/al. MIT and MEI, haploid DA al. for dsRNA data and diploid WT a/al. G1/S & G2S for RNA expression data), select *filled* diagram, *linear* data and enter a target locus, for example YDR061W. Then home in on the locus to avoid squashing the graph due to highly expressed neighbouring genes by selecting the coordinates 574080-576000.



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