User Guide

The 5-FU RNA expression viewer (5-FU^R)

Last update 11/06/2024

Uniform Resource Locator (URL): https://5fur.genouest.org

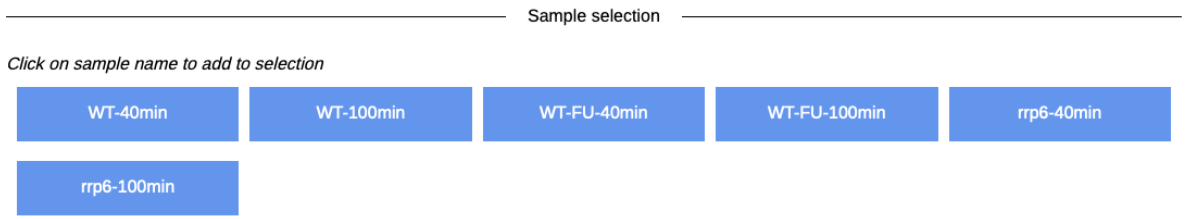
Note: this tool is accessible via a secure hypertext transfer protocol (https)

Reference: Szachnowski et al. in preparation

Reference for RNA-Seq data: Xie *et al.*, RNA Biol 2019.

Compare mRNA and lncRNA levels in untreated and 5-FU treated wild-type cells and rrp6 mutant cells in the diploid JHY222 background

1. 5-FU^R provides access to RNA-Sequencing data for currently annotated mRNAs and different classes of lncRNAs (CUTs, SUTs, XUTs and MUTs). We compared samples from synchronized mitotic cells that were first arrested by starvation and then released into in rich medium (YPD). Duplicate samples were taken at 40-minute (S-phase) and 100-minute (G2/M-phase) time points.
2. Go to https://5fur.genouest.org
3. Press the **Start** button in the welcome page. The entire set of merged (averaged) samples is preselected.



4. Select *individual samples* if you want to display the signals of duplicate samples

5. You can select various options to visualize the dataset using different graphs. First, click on the samples to change their color code (note that the filled diagram includes preset red and blue color codes for top and bottom strand encoded RNAs, respectively. Click on the cross in the top right corner to remove samples. Next, click on the option boxes to open the popup menus and select *fill* for a filled diagram, *stranded* to show DNA-strand specific data, *linear* to display untransformed signals and select *normalized* data display.

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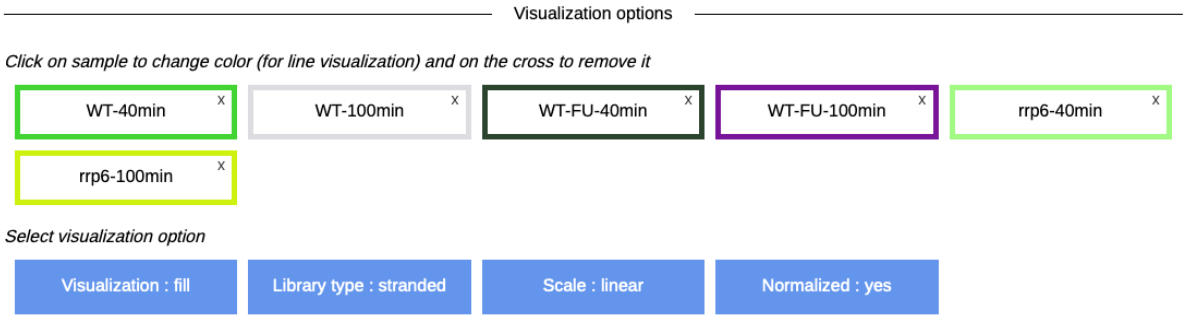
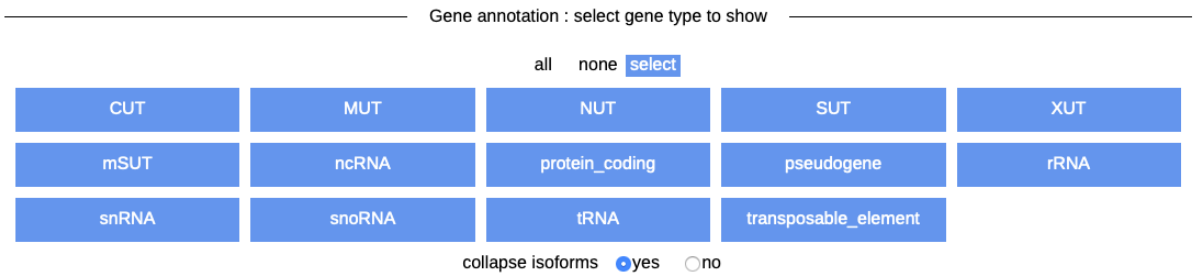
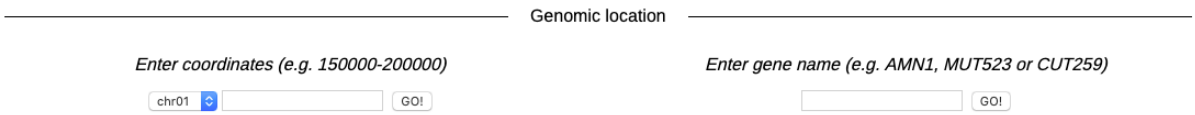


6. You can display all, none or a selection of transcript types by clicking on the options in the gene annotation section.



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 grey bars. Arrowheads indicate the direction of transcription. Alternatively, you can select the line and heatmap views (see below data for *AMN1*)

   You can interpret the RNA expression signal in the context of current genome annotation data. To interpret the biological effect of sense/antisense gene expression, compare the RNA expression data to double-stranded RNA (dsRNA) profiling data obtained with diploid mitotic and meiotic yeast cells at http://sensr.genouest.org.

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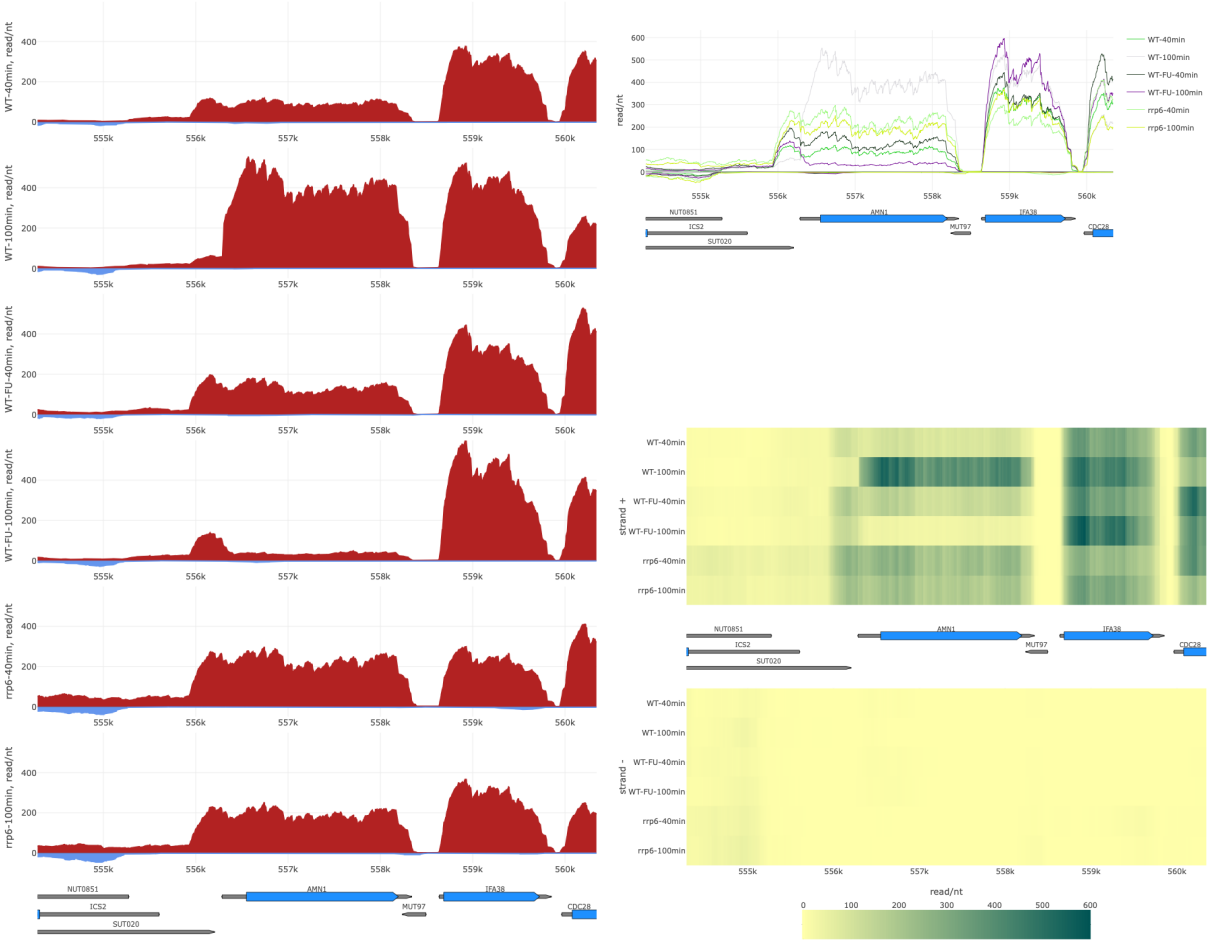
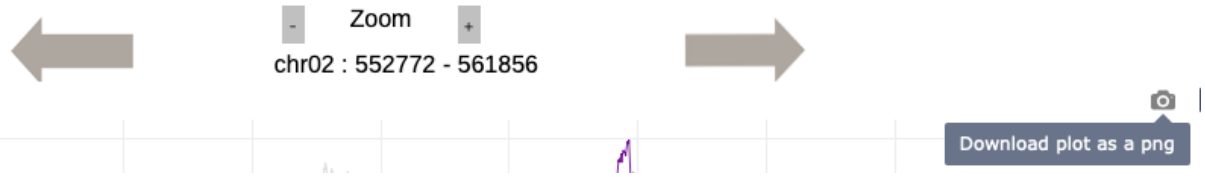


9. Walk along the chromosomes by clicking on the grey arrows at the top. Click on the - and + symbols to zoom out and in. Click on the top right camera icon to download the plot as an image file in png format.



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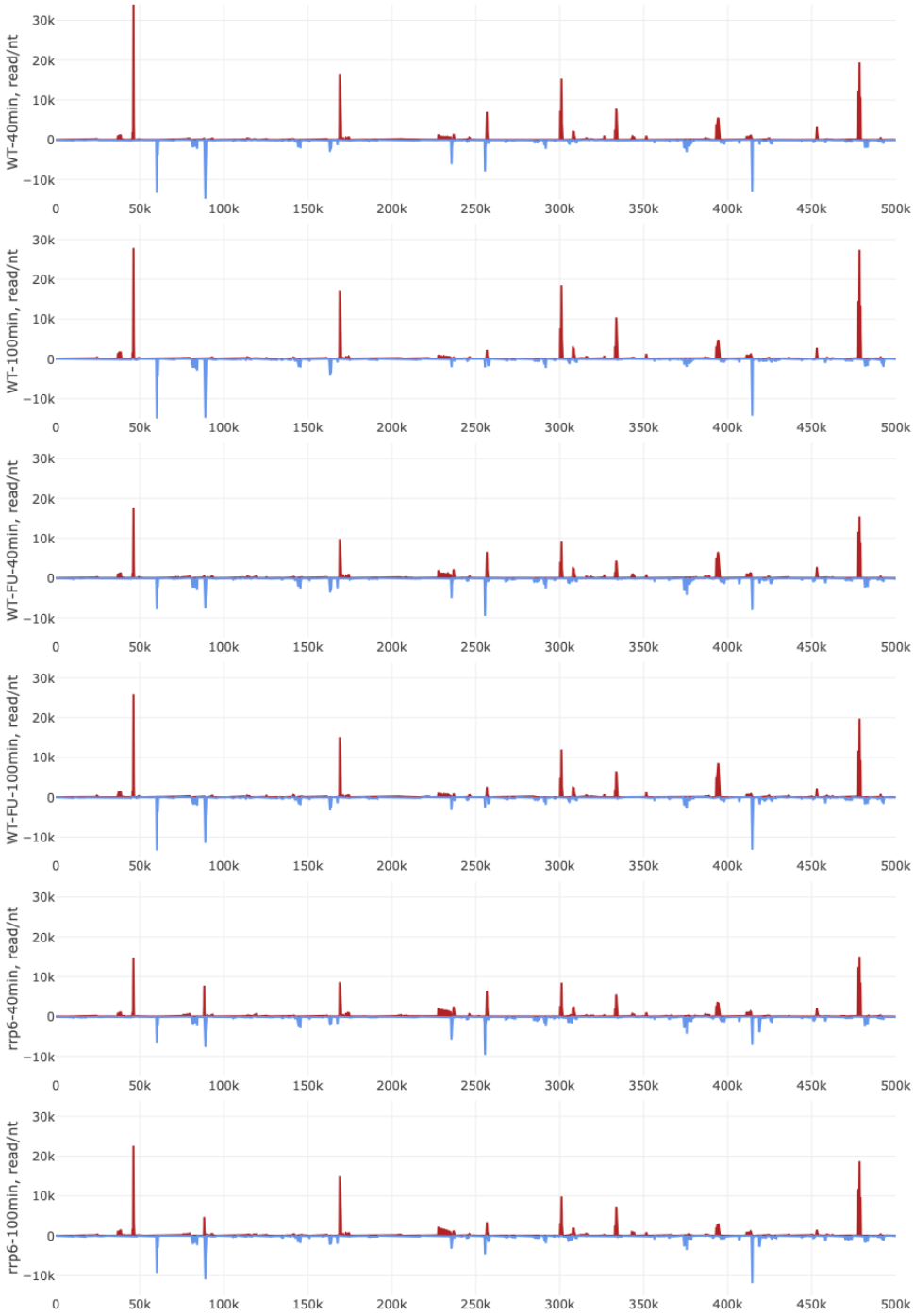
10. You can view gene expression across an entire chromosome by selecting its number and entering genome coordinates; for example, chr2: 1 – 500000 (or any number larger than the chromosome if you do not know the precise coordinates).



11. If you use 5-FU^{R} for your research, please quote Szachnowski et al.

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