universität freiburg

RNAplotter

Manual

Biologie III
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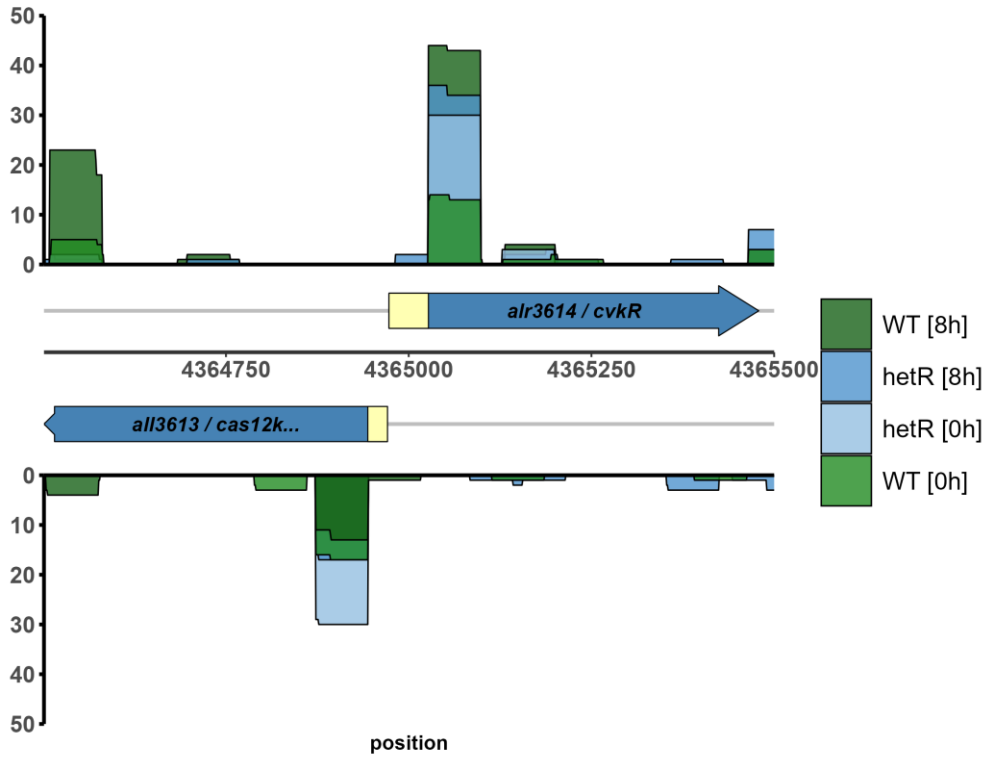
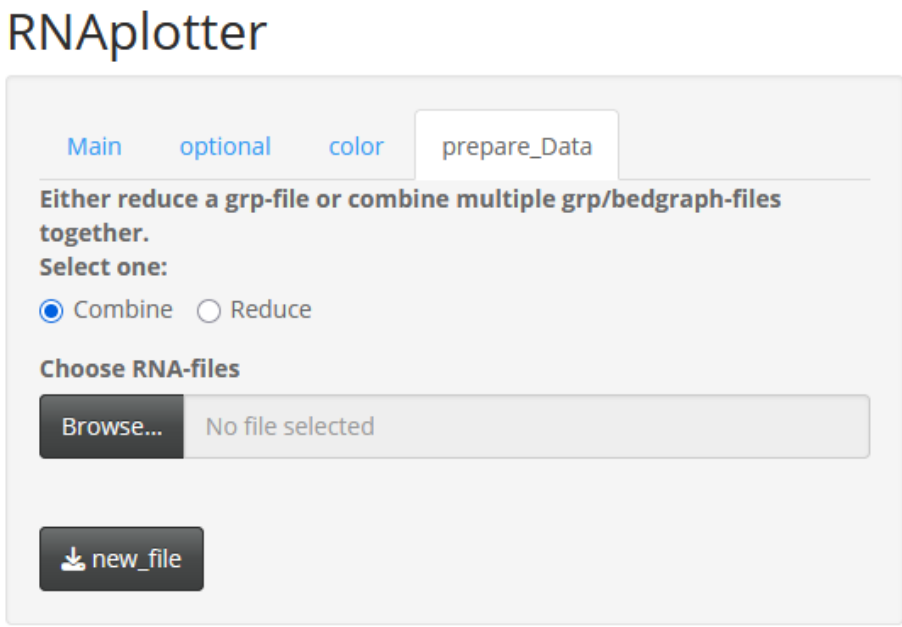
Last update: 29.09.2025



Prepare Data

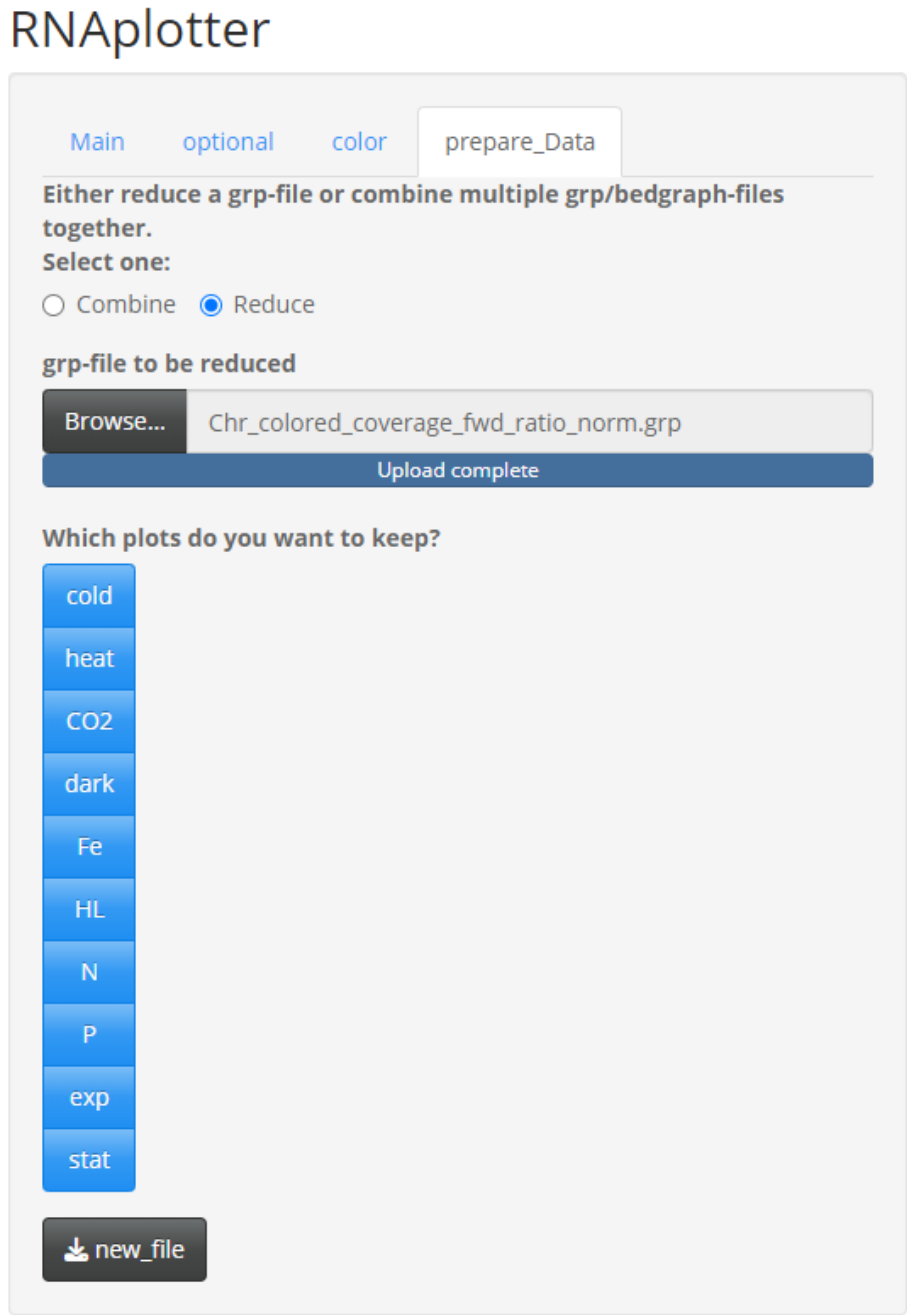
- The data available in BAM files can easily be converted into bedgraph-files by using the bamCoverage program from the deeptools package.
- ***Important***: The bam-file needs to be split into forward and reverse reads.



- Afterwards, the files can be combined via the subpanel *prepare_Data*. To do so, upload the files you want to combine, which can have a bedgraph- or a grp-format. The files will then be turned into a single file in grp-format and the columns will be named after the file-names.
- This needs to be done for fwd- and rev-files.

Prepare Data

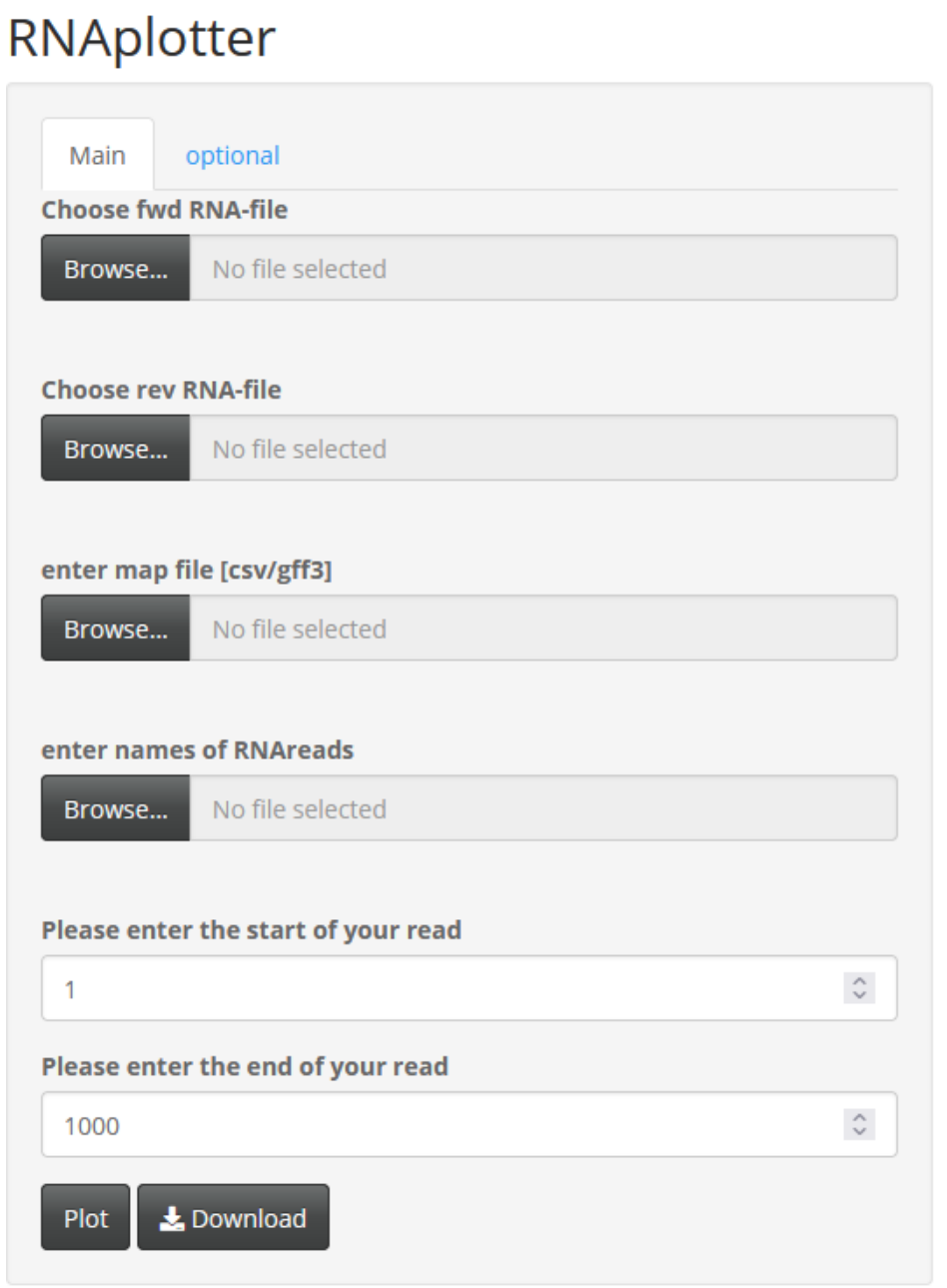
- Existing files can also be split.
- Upload a file and choose the conditions you want to keep. The resulting file will only contain the sequencing data from the choosen conditions.



Input

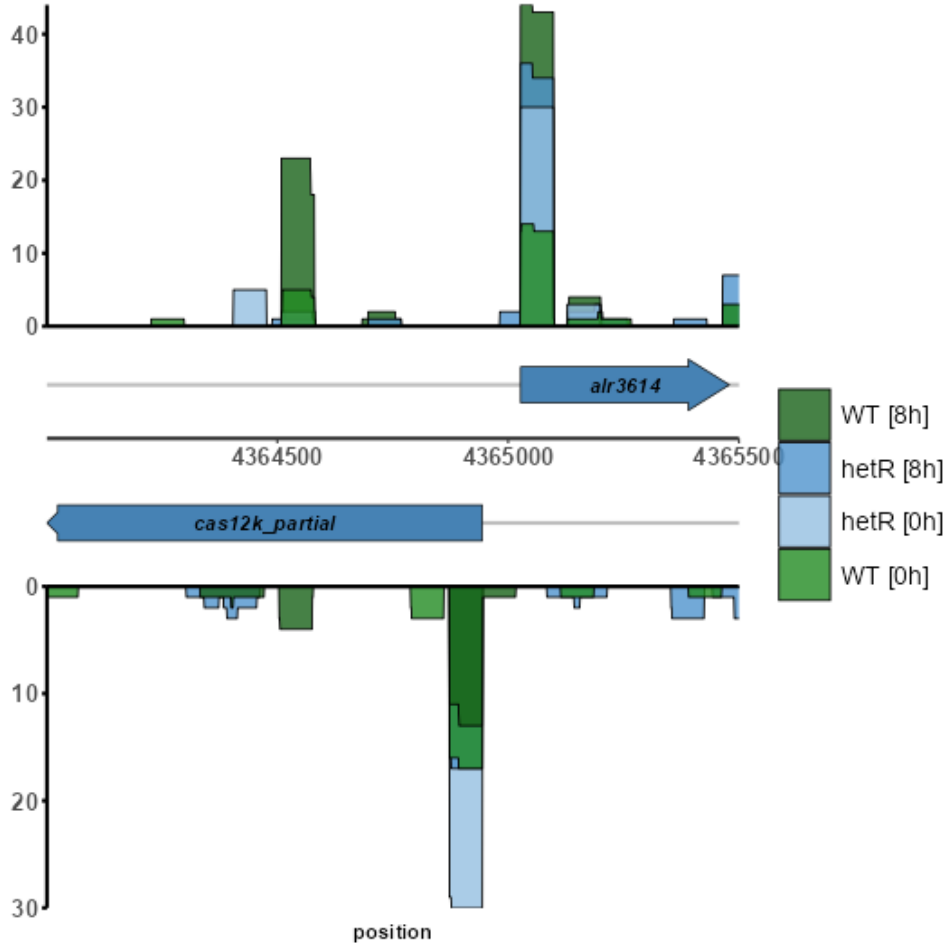
- Insert forward and reverse grp-files of RNAreads
  - It is important, that the order of RNA-plots are equal in both grp-files
- Insert csv/gff/gff3-file with data about the DNA-map
  - Compatible gff3-files can be easily obtained for published nucleotides from the NCBI-database.
- Insert Name file for RNAreads (optional)
  - If no Name-file is given, the program while either use the column name of the grp file or if not given or the names in both grp-files are not the same, the program will just name any plot as “Plot_1”, “Plot_2”,…

All of them can be found in the example folder on Github:
https://github.com/MarcusZiemann/RNAplotter



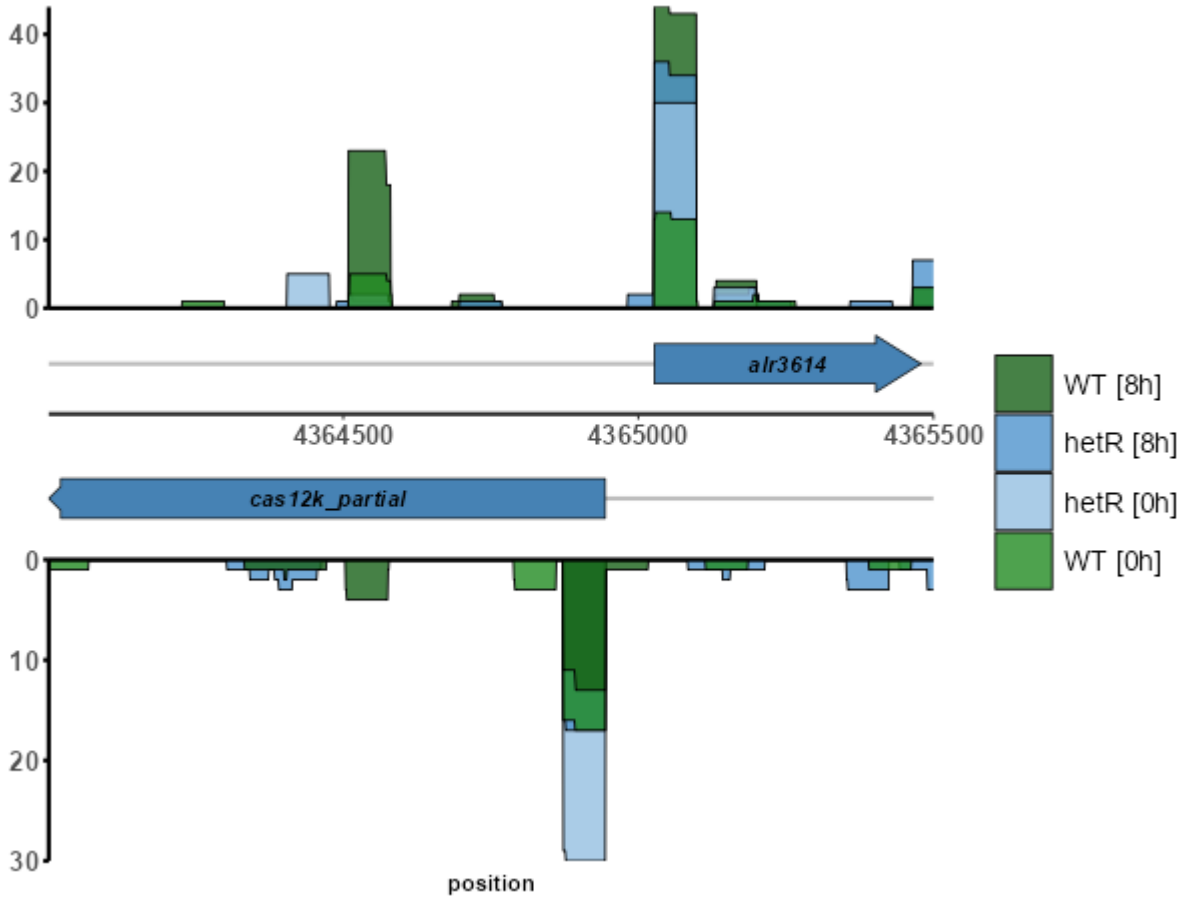
Output - plot

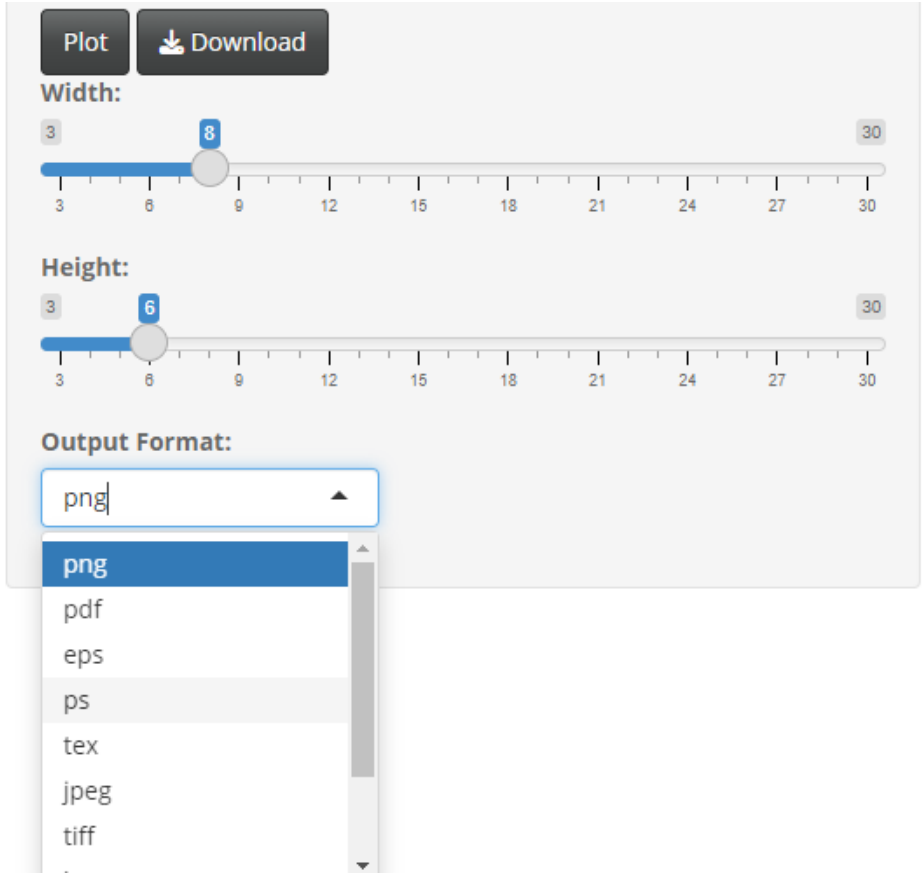
After the upload, the start and end-point can be chosen and the RNA-plot can be plotted in the Application:



Output - plot

The size of the plot can be manipulated and then be downloaded as in different picure formats (by default png):





Output - table

The second mainpanel shows the table of map elements. This table is either the uploaded csv-file or a converted table from an uploaded gff-file. The former are easier to change, so the table can be downloaded as a csv-file, using the “Download table” button.

Plot | table

Show 10 entries Search:

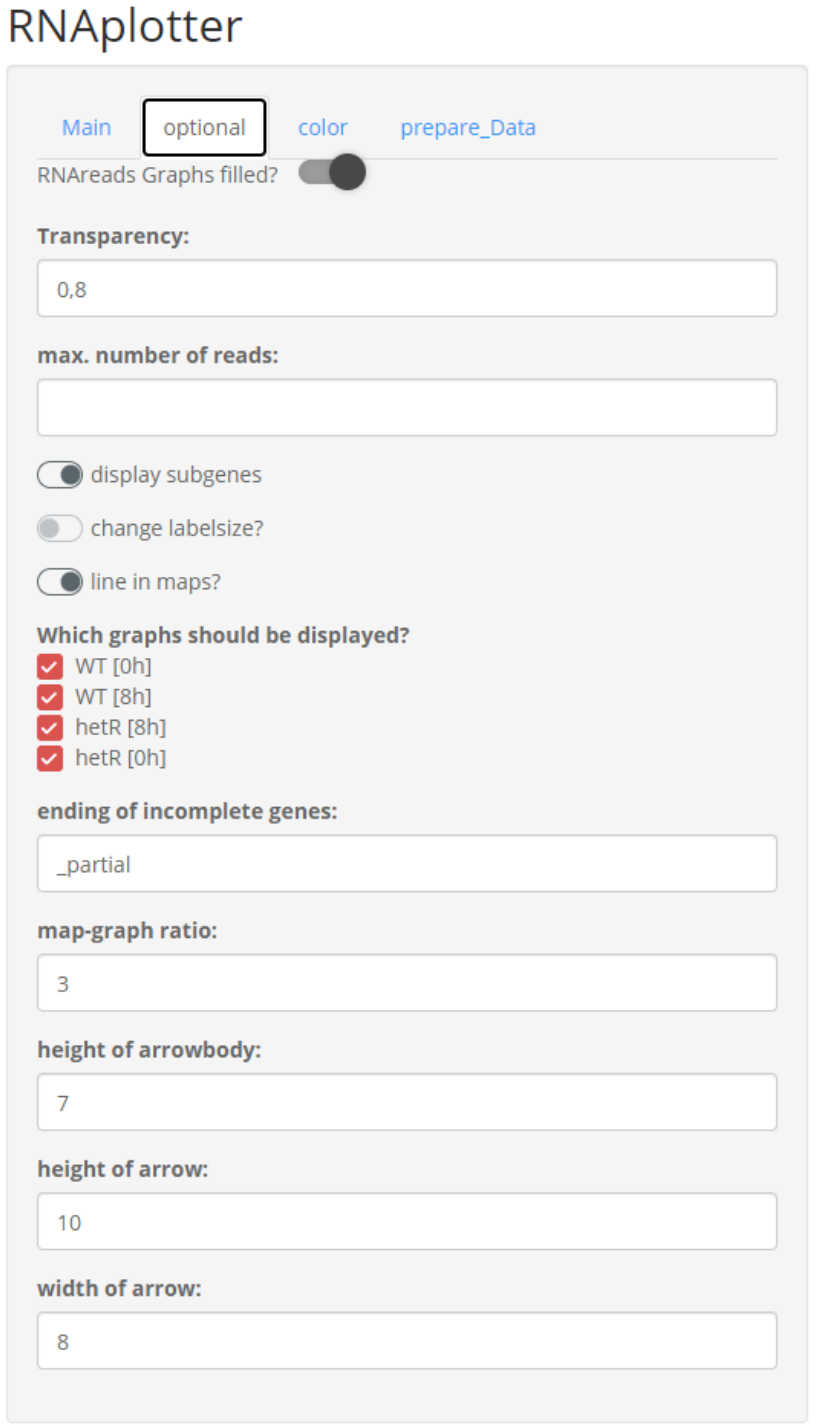
	molecule	gene	start	end	orientation	color	from	to	subcolor	label_type	lane
1	BA000019.2	all0002	981	1718	-1	#4682B4				bold.italic	1
2	BA000019.2	asl0003	2617	2805	-1	#4682B4				bold.italic	1
3	BA000019.2	ssrA	2858	3247	-1	#4682B4				bold.italic	1
4	BA000019.2	atpC	3418	4365	-1	#4682B4				bold.italic	1
5	BA000019.2	atpA	4454	5974	-1	#4682B4				bold.italic	1
6	BA000019.2	atpD	6138	6689	-1	#4682B4				bold.italic	1
7	BA000019.2	atpF	6686	7249	-1	#4682B4				bold.italic	1
8	BA000019.2	atpG	7359	7850	-1	#4682B4				bold.italic	1
9	BA000019.2	atpH	7996	8241	-1	#4682B4				bold.italic	1
10	BA000019.2	atpI	8324	9079	-1	#4682B4				bold.italic	1

Showing 1 to 10 of 5,309 entries Previous 1 2 3 4 5 ... 531 Next

Download table

Optional Input

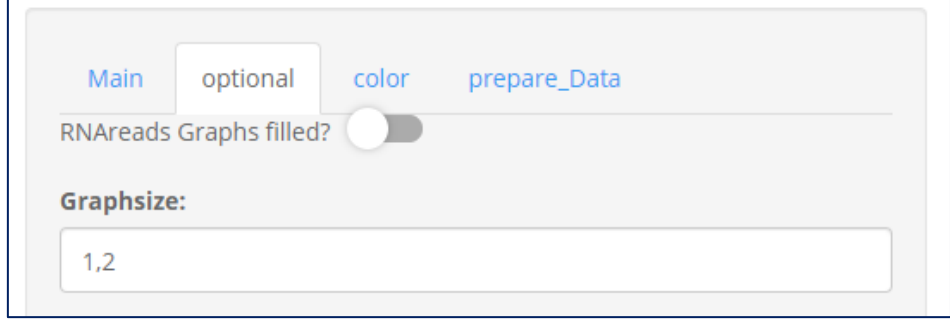
The optional menu gives you further choices for your plotting, like changing the level of transparency of your graph or deleting individual conditions.

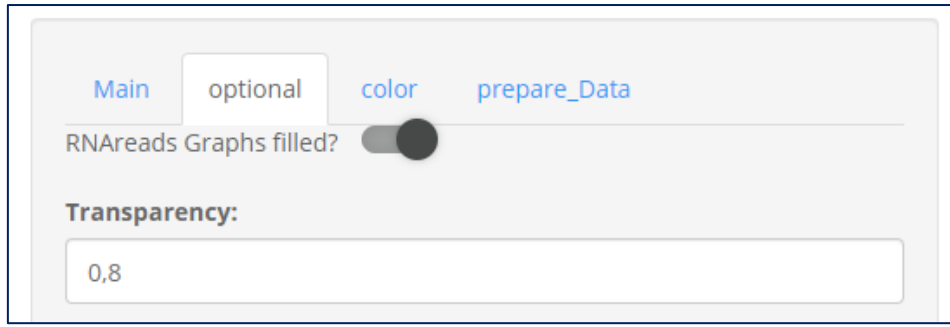


Optional Input

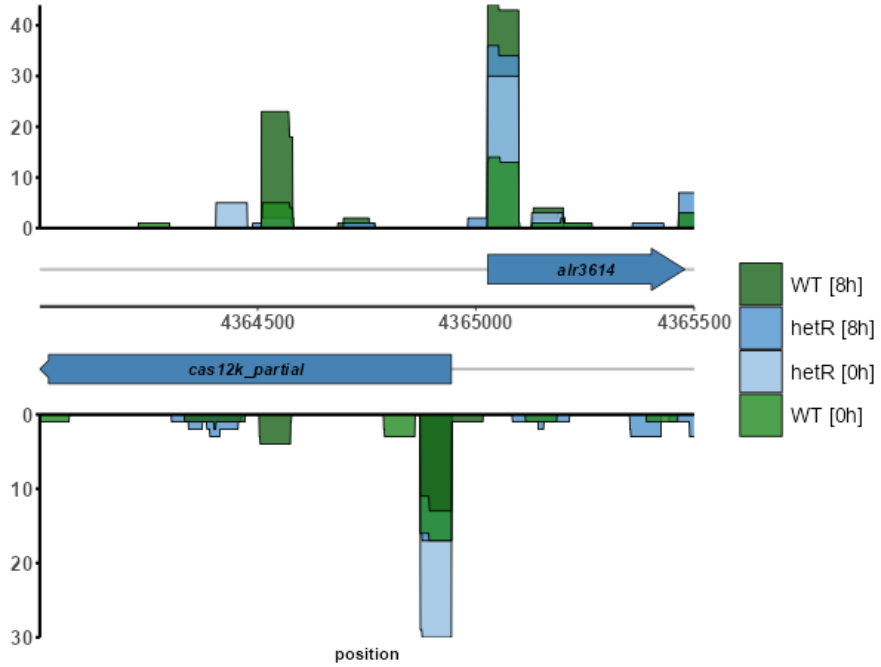
The RNA-reads can be depicted as a line- or area-plot .

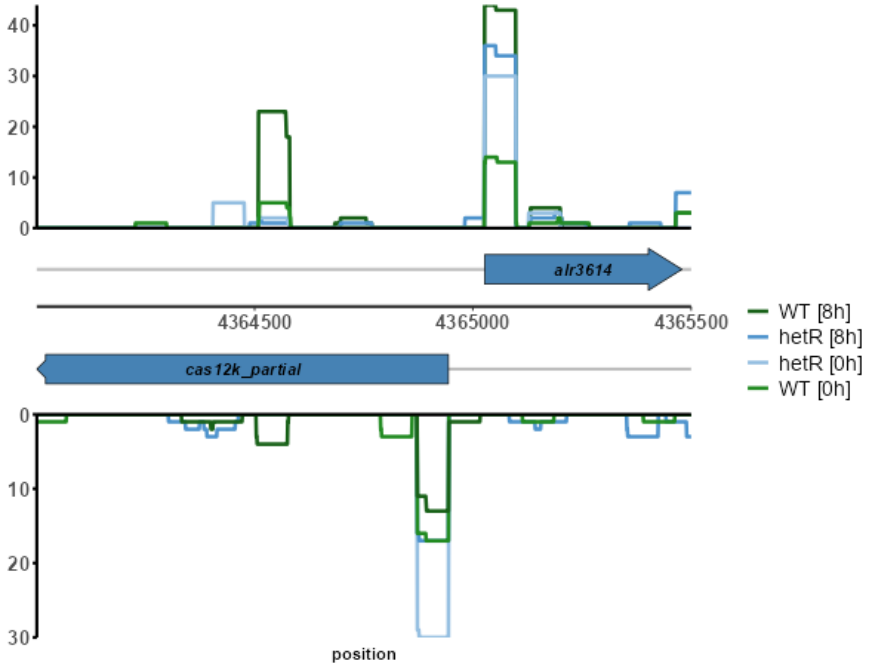
- The area-plot can be changed in transparency
- The line-plot can be changed in linewidth.





Area-plot





Line-plot

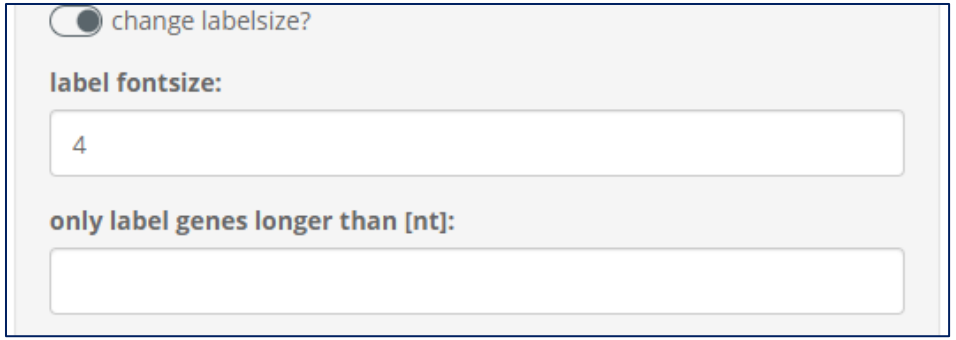
Optional Input

Max. number of reads:

Limits the y-axis on both sequencing plots to a maximum value.

Display subgenes:

Subgenes can be added to the gene map, by setting values in the column “from”, “to” and “subcolor”. The plot will show a different colored area inside a gene. However, if the program should not depict subgenes, set this switch to FALSE.



Line in maps?

Depict a line in the gene map.

Change labelsize:

If this switch is TRUE, the program will ask for map-element font size and the maximum size of map-elements that should be labeled. The program can usually detect if a label is to long for a specific map element, however there are too many variables for this automatization with variable font size.

Optional Input

Which graphs should be displayed?:

Individual sequence runs can be chosen to be depicted.

ending of incomplete genes:

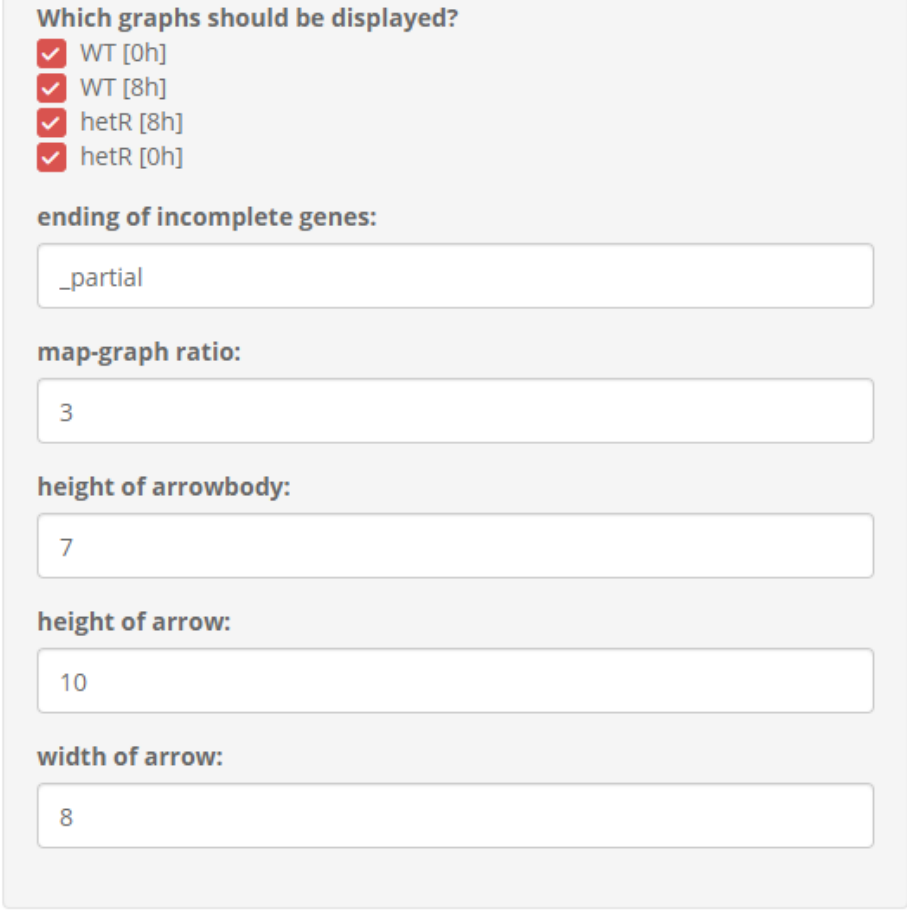
If a map-element is depicted in the plot, but lies partially outside the depicted parameter, the program will add text to clarify, that the element is incomplete. This can be avoided by leaving this input empty.

map-graph ratio:

Here, the height-ratio between gene map and the RNA-sequence graph inside the plot, can be changed.

Height/width of arrow / height of arrowbody:

These input areas can be used to change the gene map arrows in the plot.



Optional Input (color)

The individual color of sequencing conditions can be changed in the “color”-panel.