

Launching the Chromosome View

The *Chromosome view* can be invoked from some data nodes on the *Analysis* tab, giving a global overview of the results; or from certain *Task report* or result pages, providing a focused view, i.e. pointing to a specific feature of interest.

Running a Chromosome View Task from a Data Node

On the *Analysis* tab, selecting a data node containing aligned reads, variants, or feature lists, shows *Chromosome view* in the *Exploratory analysis* section of the context-sensitive menu (Figure 1).

If Partek® Flow® has no information on the genome build, you will need to provide the species and genome build in a subsequent dialog (not shown). Otherwise, chromosome view will come up directly.

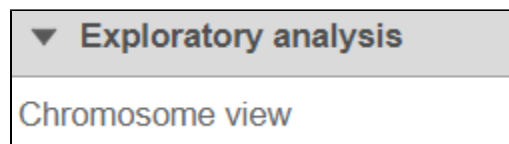


Figure 1. Accessing *Chromosome view* via the context-sensitive menu (the content of the *Visualisation* section depends on the selected data node)

A new *Chromosome view* task node will be added to the canvas (Figure 2) and in order to invoke the viewer <double-click> on the node (you can also select it and then go to **Task report** in the menu). When invoked in this way, the default visualization in the *Chromosome view* is the first 100,000 bases of the first chromosome.

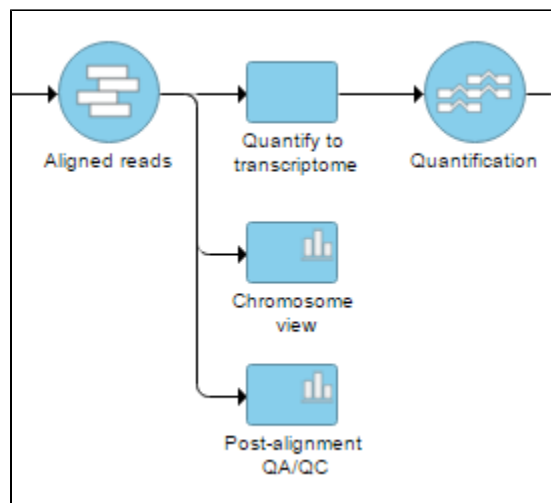



Figure 2. Selecting *Chromosome view* from the context-sensitive menu adds a *Chromosome view* task node to the canvas. To open the view, on it

Browsing directly to a location directly from a Task Report

Another way to get the *Chromosome view* is through a *Task report*. You can launch the viewer by selecting the **chromosome icon**  in the View column (Figure 3) of GSA or *View Variants* reports. In that case, the *Chromosome view* will browse directly to the selected genomic location (i.e. a transcript or a variant, depending on the pipeline).
















	View	Gene ID
1	  	A4GALT
2	  	ACO2
3	  	ADM2
4	  	ADORA2A
5	  	ADORA2A-AS1

Figure 3. Accessing the Chromosome view from results table (mouse-over balloon is visible when hovering over the chromosome icon). The image is an example, based on gene expression pipeline

Depending on the task report used to invoke the *Chromosome view* was invoked, some tracks may be pre-selected and customized. For example, when invoked from a variant table, the reads histogram track will be colored by bases (rather than the default of coloring by sample).

Additional Assistance

If you need additional assistance, please visit [our support page](#) to submit a help ticket or find phone numbers for regional support.

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