CNVnator with JBrowse

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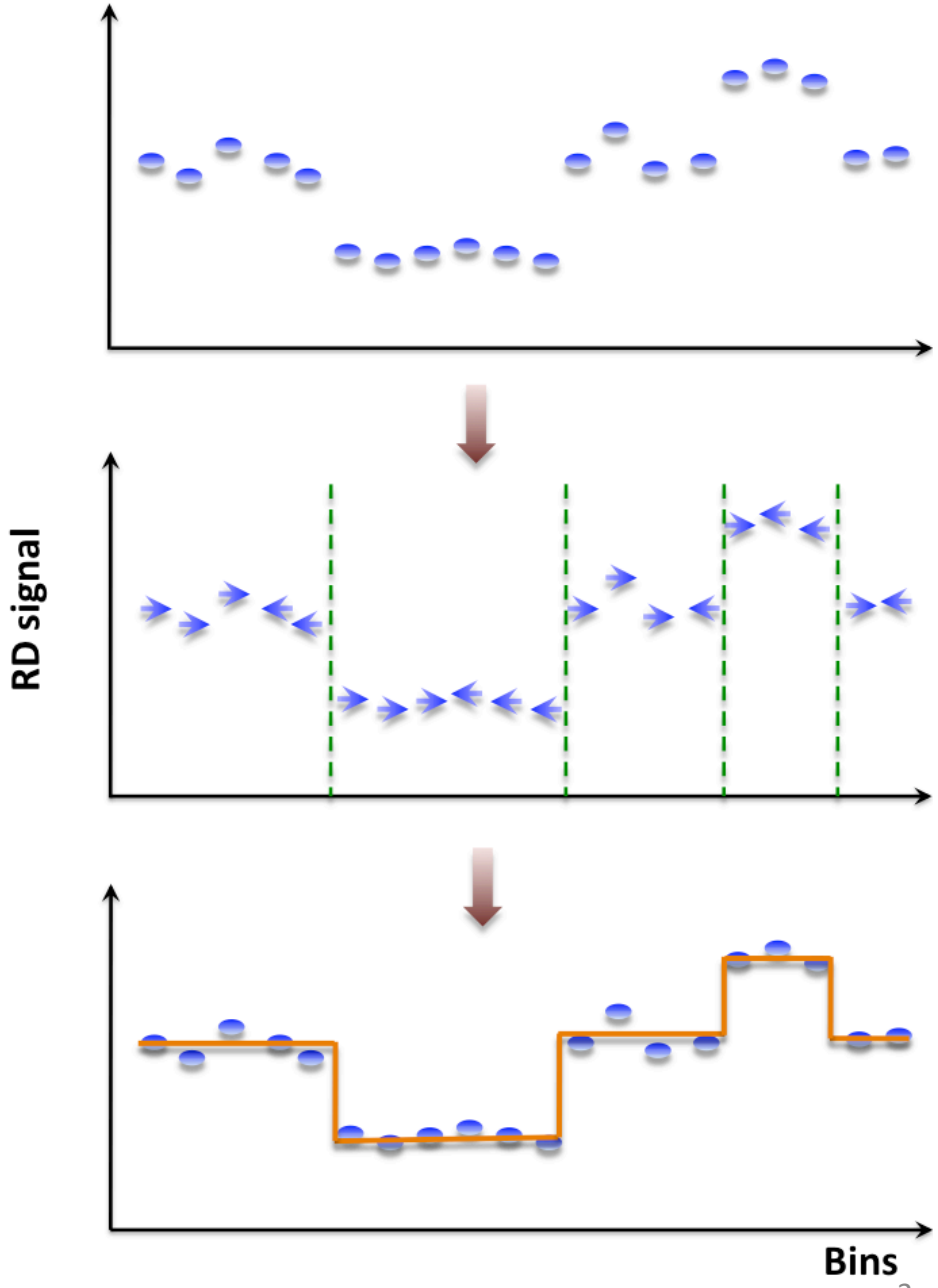
CNVnator and CNVpytor

CNVnator: mean-shift approach

- Derived from image-processing applications
- For each bin, attraction (mean-shift) vector points the direction of bins with most similar RD signal
- Not model-based, with minimum assumptions and parameters
  - Local segmentation
  - No prior assumptions about number, sizes, frequency and density of CNV regions
- Achieves discontinuity-preserving smoothing
- <u>Highest sensitivity to find CNVs detected by aCGH and fosmid end sequencing</u>



Abyzov et al., Genome Research, 2011
Mills et al., Nature, 2011

CNVpytor: a Python extension of CNVnator

- GitHub: https://github.com/abyzovlab/CNVpytor

- Easy to install

```
> pip install cnvpytor
> cnvpytor -download
```

- Can be used as python module with all functionalities

```
import cnvpytor
```

- Can be used in Jupyter notebook
- Installable in Colab Google

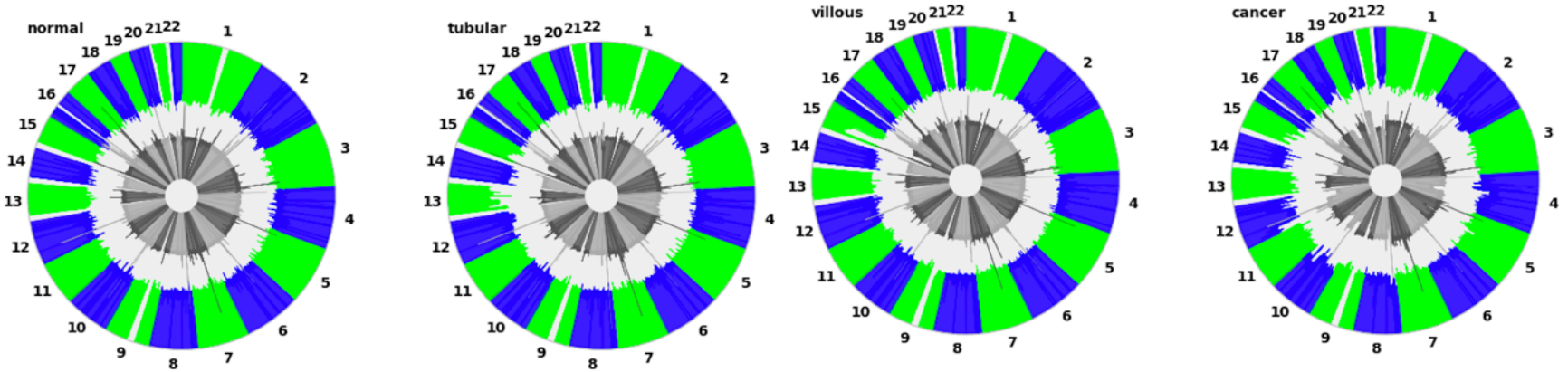
- HDF5 format to store data:
  - RD & BAF information *.pytor* file takes less than 50Mb

- Interactive plotting command line interface with tab completion

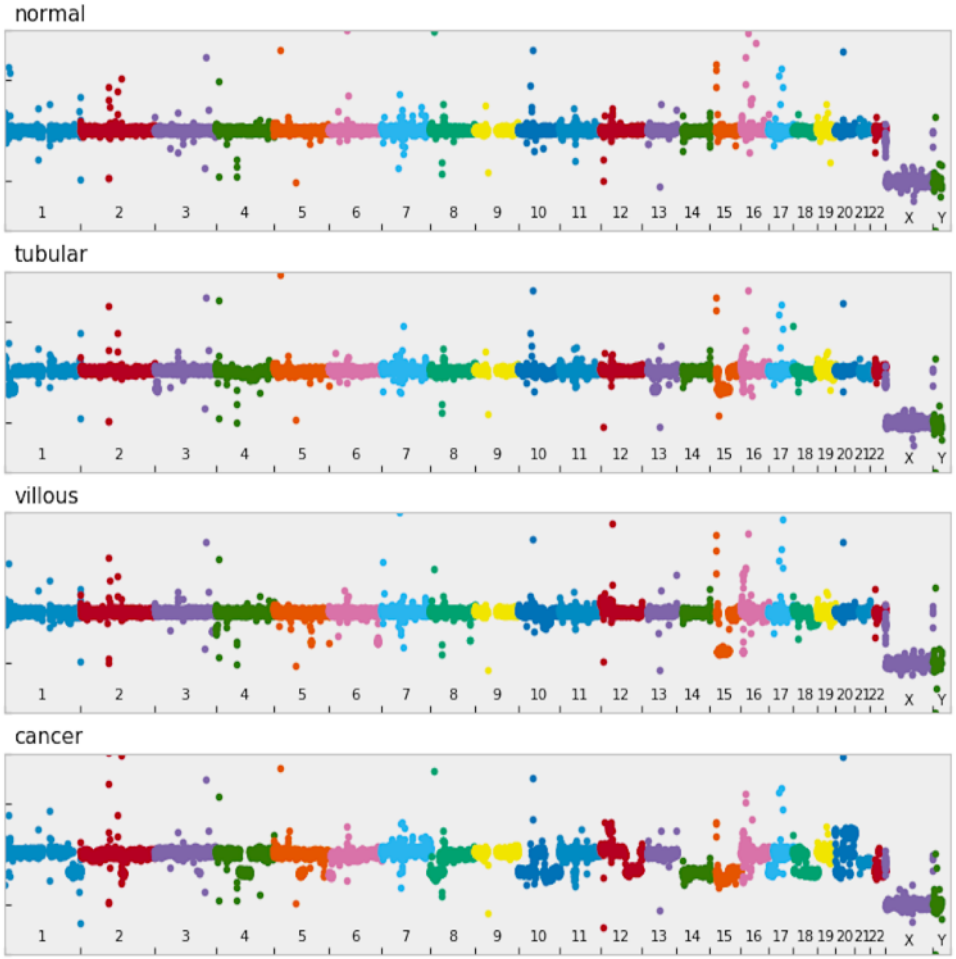
- Different plot styles and image formats

Plotting

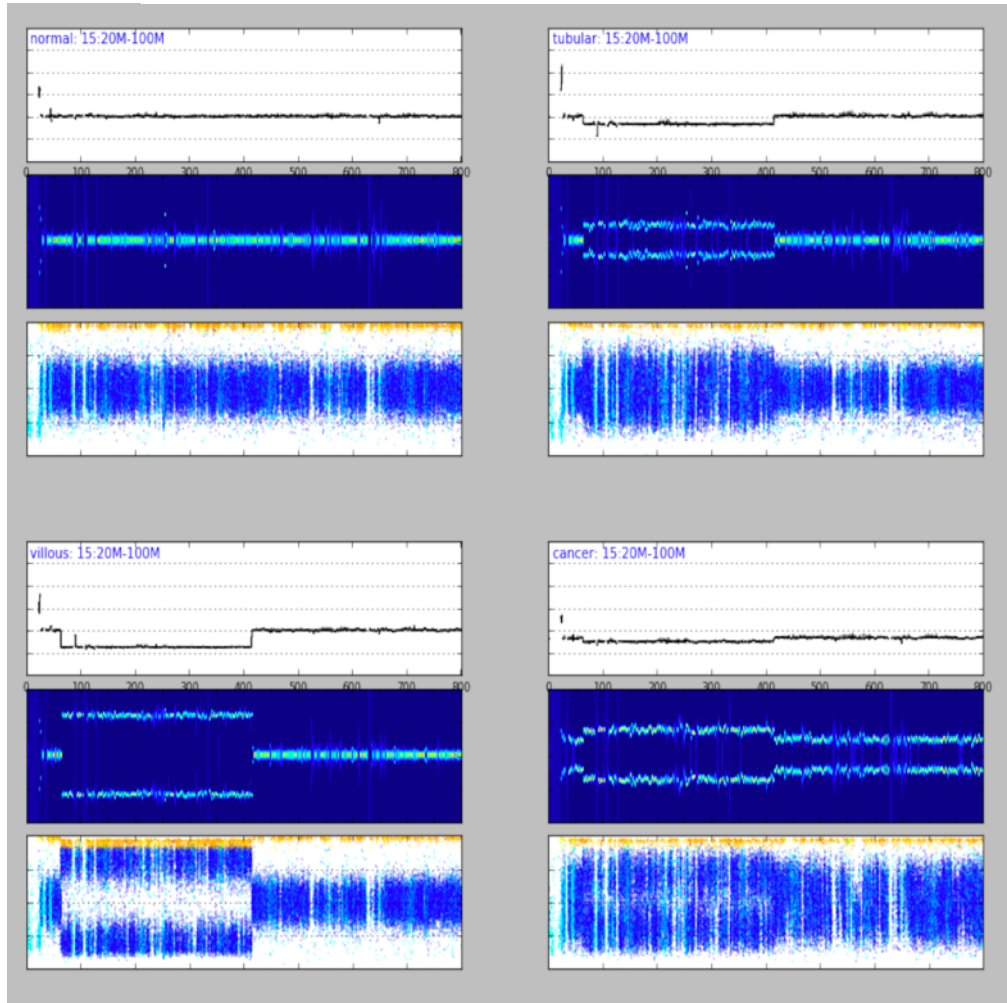
Circular plots



Manhattan plot



Multiple signals in genomic regions

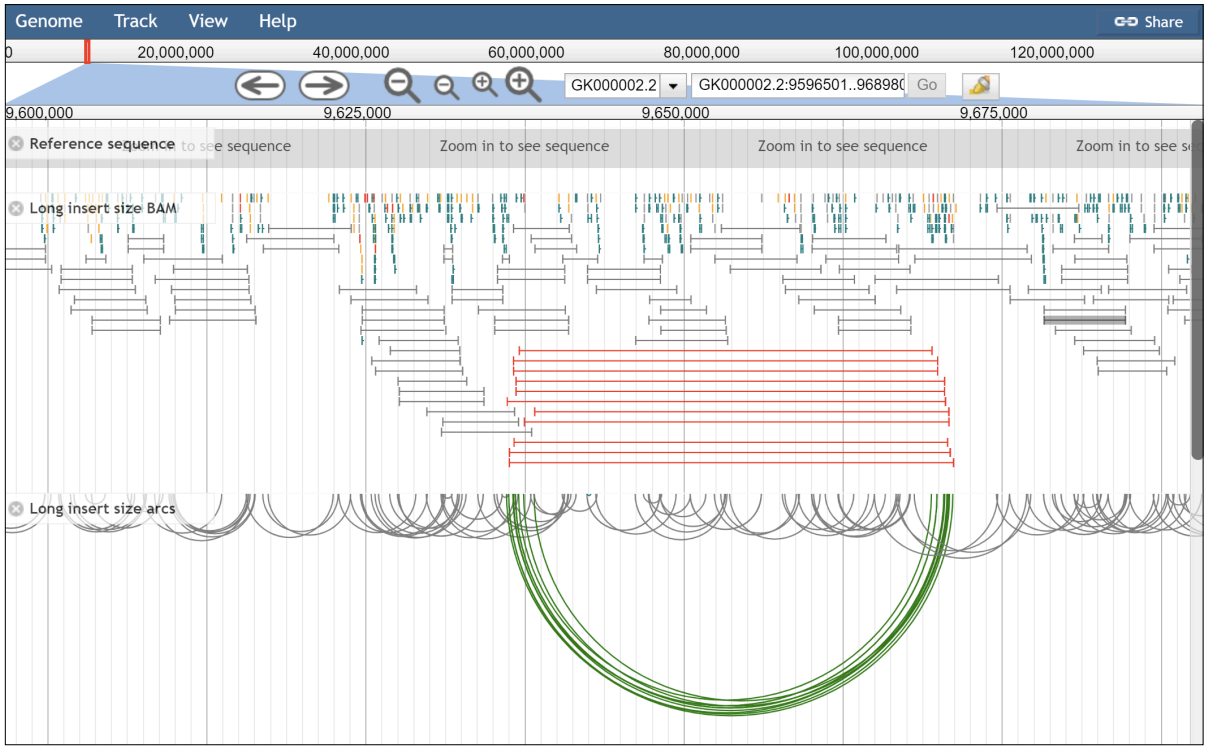


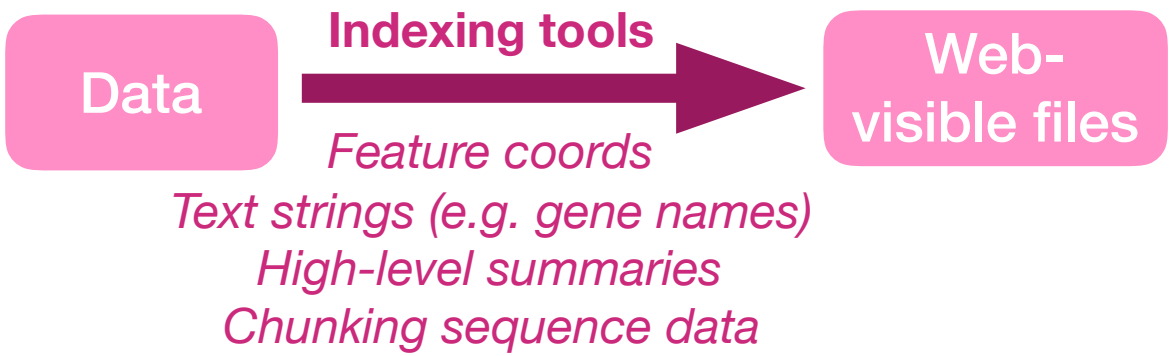
JBrowse

courtesy of Ian Holmes

JBrowse is...

- A general-purpose genome browser
- Written entirely in JavaScript
- Web-publishable as a static site (low cost, high security)
- Fluent in most common bioinformatics formats





courtesy of Ian Holmes

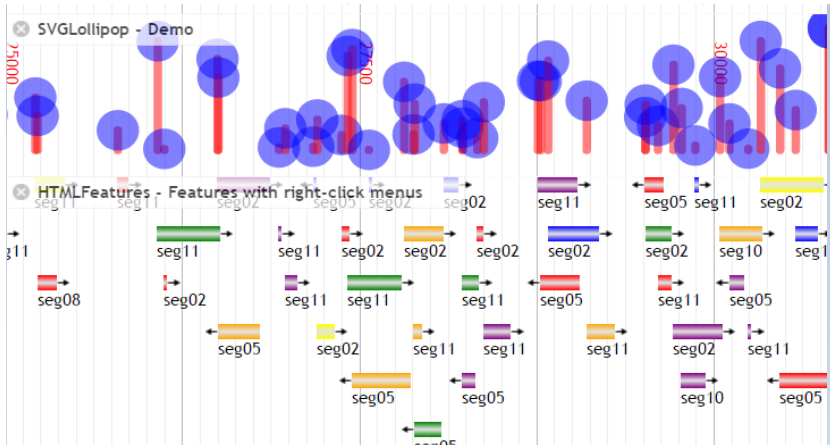
Apps & sites using JBrowse

- Sequencing analysis pipelines: GenSas, DNASubway, InterMine, SeqWare…
- Collaborative online genome annotation: WebApollo, Afra
- Model orgs (AGR), non-models (i5k, Phytozome), cancer (Cosmic), many "small" genome projects

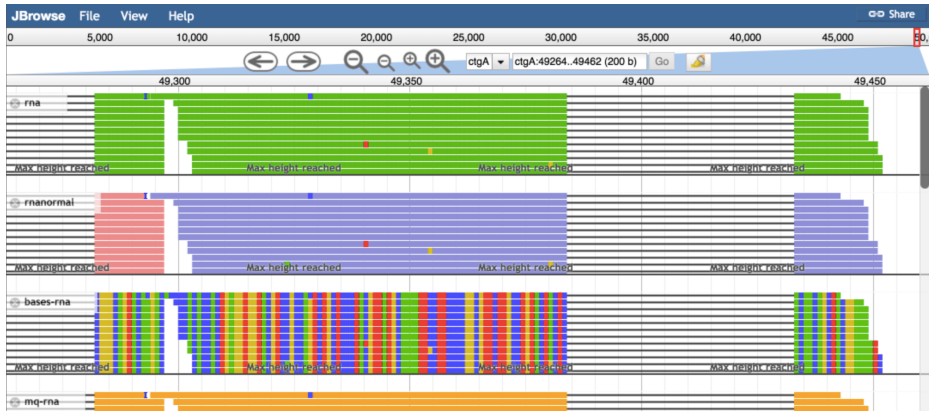
ALLIANCE of GENOME RESOURCES

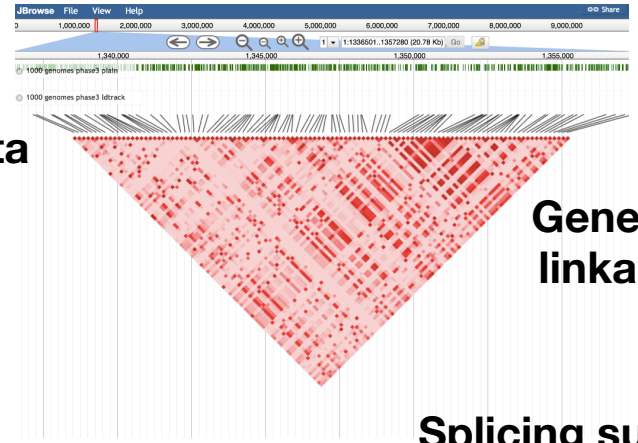
courtesy of Ian Holmes

JBrowse plugin registry

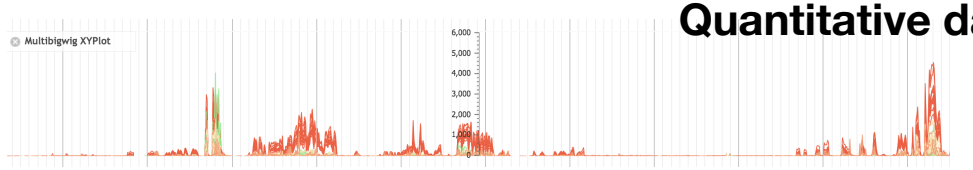


Population genomics





Variants

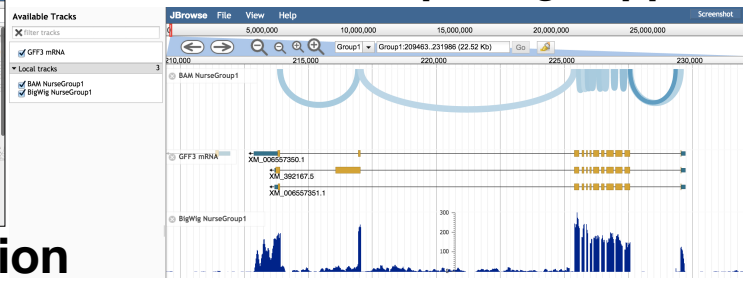


Quantitative data

Genetic linkage

Dynamix: AI that prioritizes deep track lists
Apollo: Google Docs for genome curators
Plugins for Galaxy, CoGe…

~50 plugins as of January 2020



Splicing support

Paired-end visualization

courtesy of Ian Holmes

Integrating CNVpytor and JBrowse

How to integrate

Arijit Panda

- Install CNVpytor with pyBigWig dependency
- Install JBrowse with MultiBigwig and MultiScaleBigwig plugins

  - Export file generation

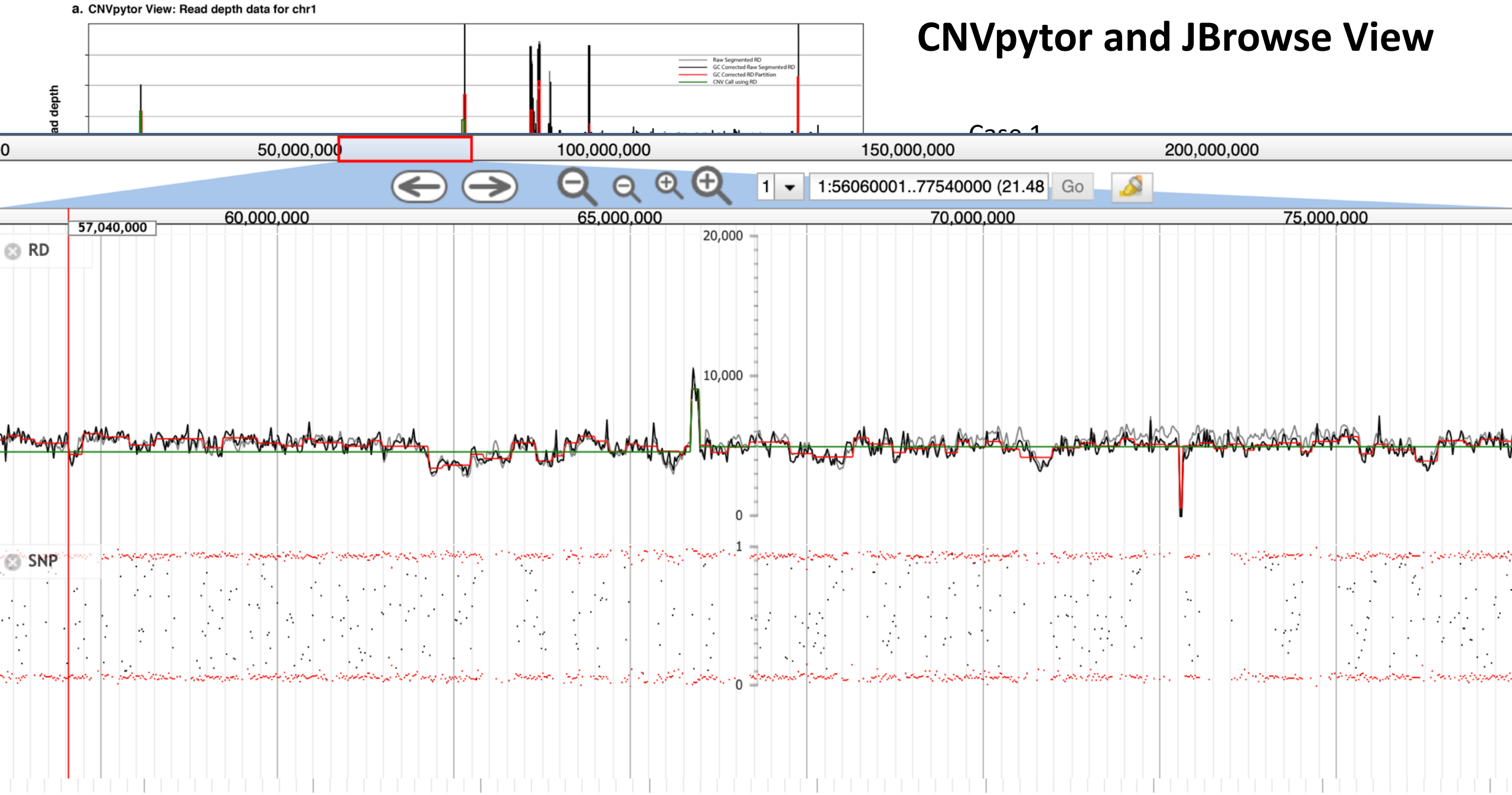
    ```
    CNVpytor –root [root files] –export jbrowse [Directory Name(optional)]
    ```

  - Visualization

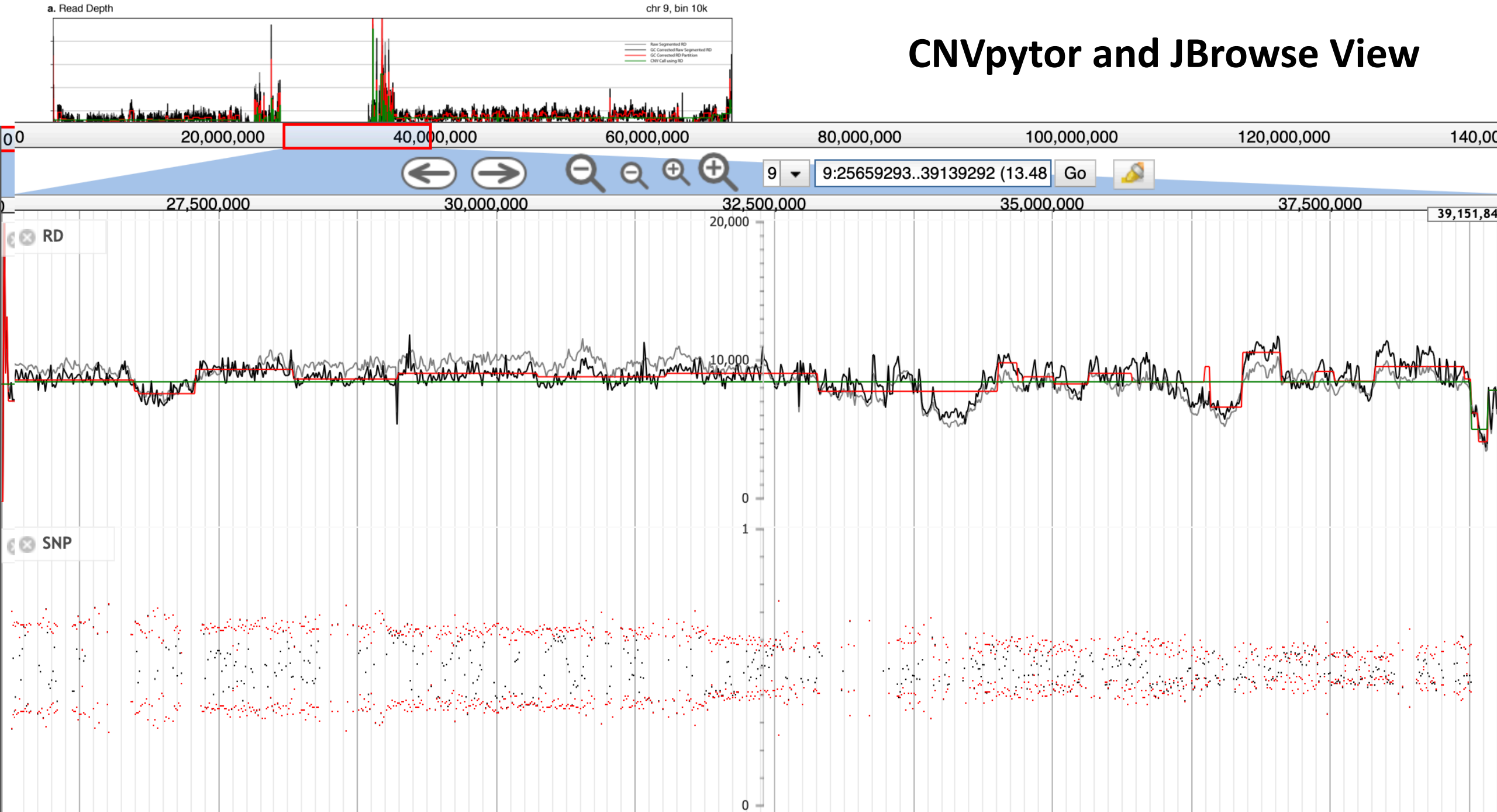
    ```
    http://localhost/jbrowse/?data=[Directory Name]
    ```

    Note:
    If export directory is not the JBrowse Installed directory, then the user need to copy to JBrowse directory

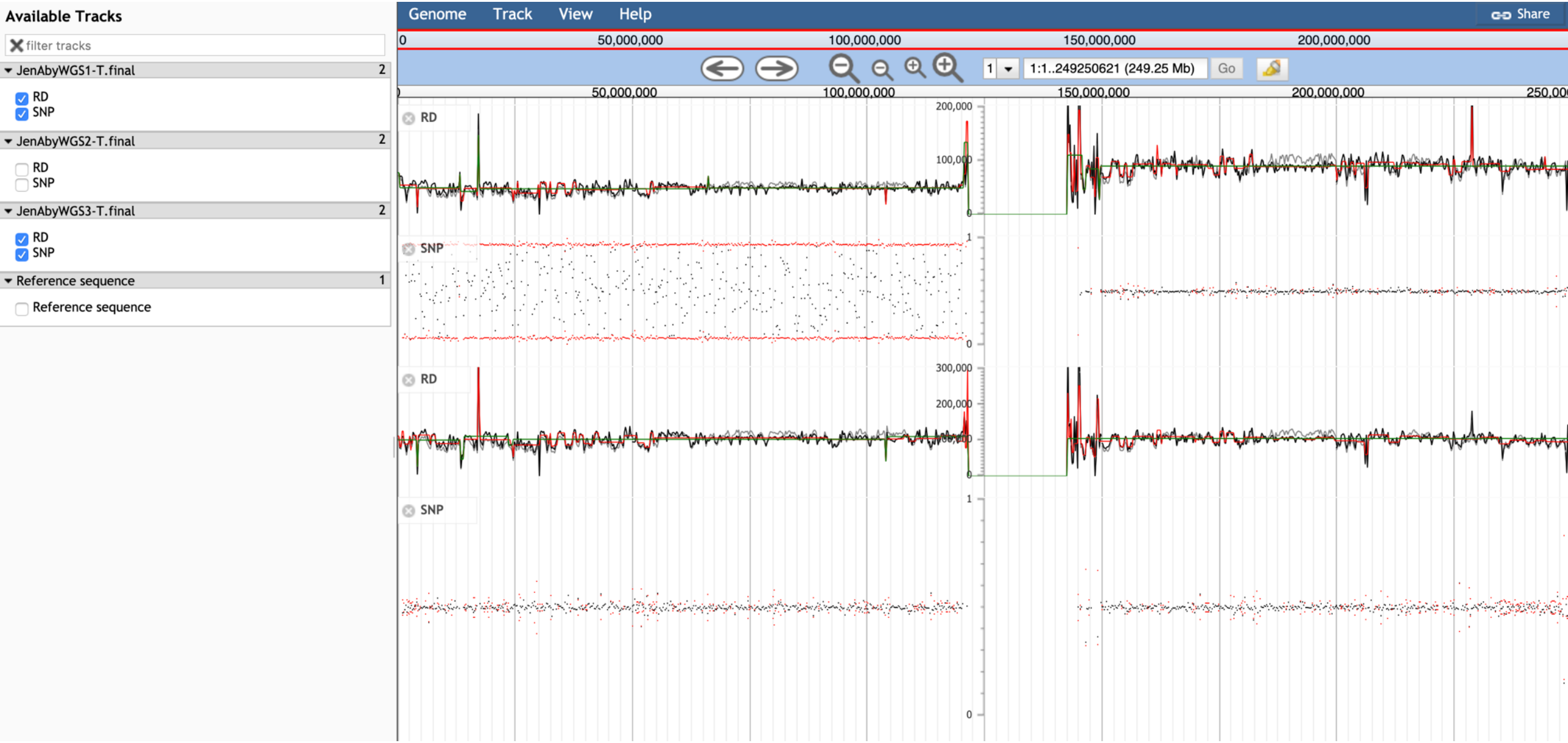
CNVpytor and JBrowse View



CNVpytor and JBrowse View



CNVpytor and JBrowse View with Multiple cases



Future developments

- Porting some of CNVpytor’s segmentation and calling functionality into JBrowse
- Improvements and maintenance