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Important file formats

.cmap - short for consensus map these files store either *in silico* maps or genome maps (see “Important terms” section below)

.xmap - these files store alignments of two CMAP files

.bed - BED format files store coordinates of features (e.g. contigs within a scaffold or alternately gaps within a scaffold, where gaps are runs of Ns)

.bnx - these files store Bionano single molecule maps with quality scores

.tiff - these files store raw molecule images taken on the Irys platform

_key.txt - key of original FASTA file headers and the corresponding number in the CMAP file of *in silico* maps

Important terms

single molecule map - an individual molecule described in a BNX file

***in silico* map** - an individual map in a CMAP file created from a FASTA sequence file

genome map - an individual map in a CMAP file created from assembled BioNano single molecule maps

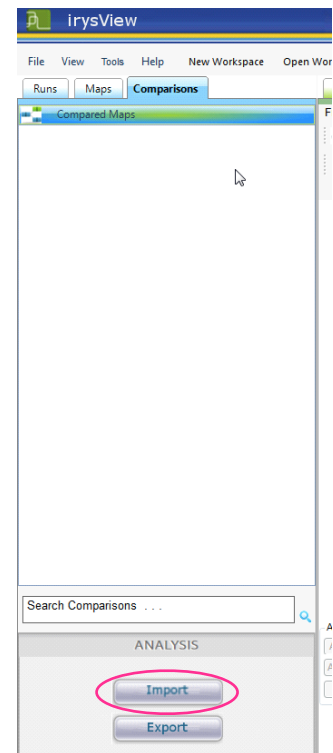


Fig 1: Importing XMAP files (Make sure the blue "Comparisons" tab is selected).

Viewing alignments

To view XMAPs included in your files move the **ENTIRE** folder that the XMAP is in to a Windows machine. Select the green "Data" tab when the blue "Comparisons" tab is also selected. Import the XMAP file you wish to view into IrysView using the import button circled in the screen shot (Figure 1). Remember to move all of these files to your Windows machine and save them in the same folder but only select the XMAP to import and view alignments in IrysView.

Detailed training and installation instructions for IrysView are available here:
<http://www.bnxinstall.com/training/docs/IrysViewSoftwareInstallationGuide.pdf>
<http://www.bnxinstall.com/training/docs/IrysViewSoftwareTrainingGuide.pdf>

Viewing putative structural variants and/or gaps

To view structural variant calls move the **ENTIRE** directory named "merged_smaps" to your Windows machine. Import the file ending in "_sv.xmap" into IrysView. Use "File -> Import -> SV -> Add" in the upper right corner of the window for the green "Data" tab when the blue "Comparisons" tab is also selected to import the file ending in ".smap" (Figure 2).

I have included a bed file with your gaps as features the file ending in "_gaps.bed". You can view this at the same time as the SV-detect results or your standard alignment (in the "align_in_silico" folder) using "File -> Import -> BED -> Add". If viewing SV-detect results also use the same BED import button to add the file ending in "_merged.bed" from the "merged_smaps" folder.

After importing load alignments for viewing (Figure 3). The final view should be similar to Figure 4.

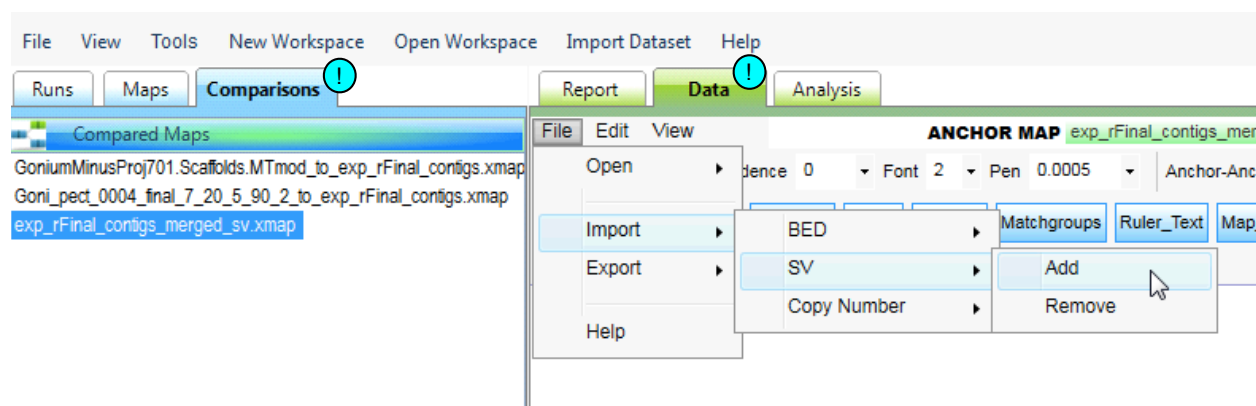


Fig 2: Importing track files (BED files and SMAPs which correspond with indels (red and green) or gaps (purple)). Remember (❗) to make sure the green "Data" tab and the blue "Comparisons" tab are selected to view standard alignments. The XMAP you want to view should be highlighted in blue in the box on the left of the screen.

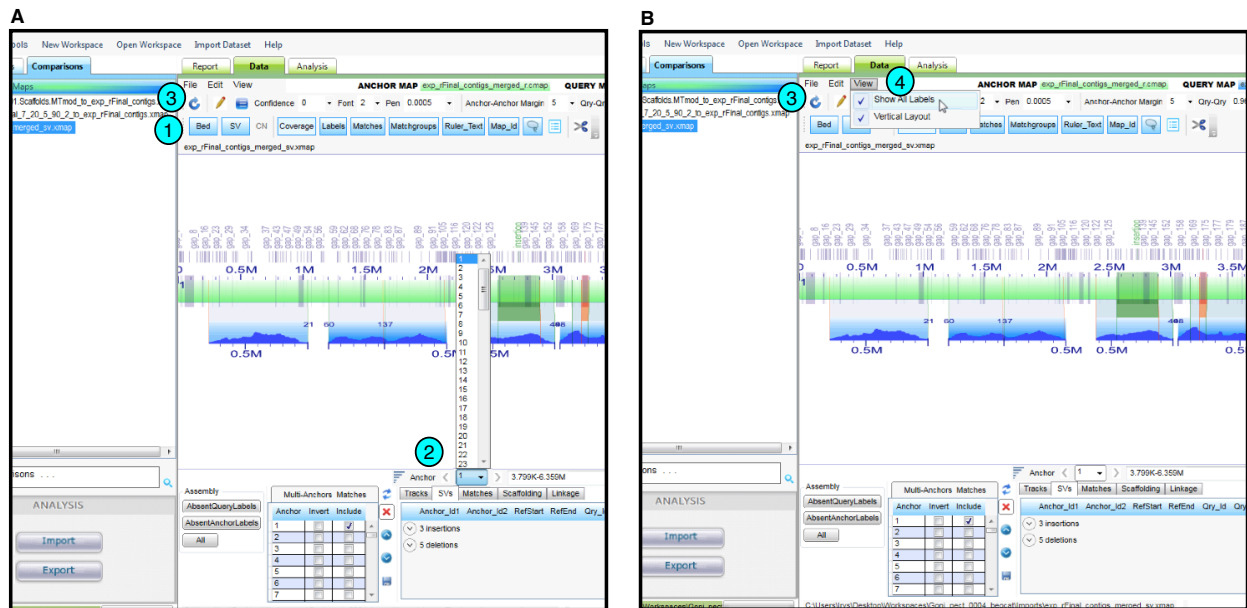


Fig 3: (A) Visualize alignments and BED file annotations. Click “BED” and/or “SV” button(s) (1). Step 2: import reference, also referred to as anchor, map from pop-up menu (2). Step 3: if annotations do not load automatically click the blue curved arrow (3) indicated to refresh and re-select your reference/anchor map. (B) If labels and matches between labels fail to draw un-click and re-click “View->Show All Labels” (4) then click the blue curved arrow (3) indicated to refresh and finally re-select your reference/anchor map. When BED files are loaded, as in the image above, indels are annotated as red or green translucent squares and gaps are indicated as lavender translucent squares.

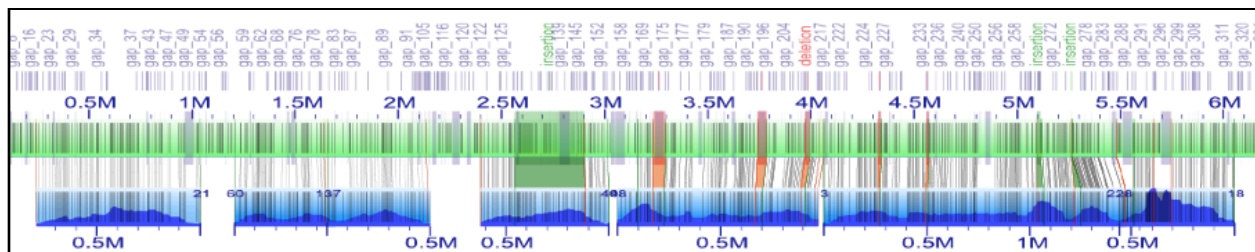


Fig 4: Now you should see the alignment to your selected reference/anchor map as well as any annotation tracks that you have loaded. Here you can see BED files and SMAPs which correspond with indels (translucent red and green) or gaps (translucent lavender)). Reference/anchor *in silico* maps (solid green) are from the user provided FASTA file. Query genome maps (solid light blue) are assembled from BioNano single molecule maps. Single molecule map coverage of genome maps is also shown (dark blue).

Further training and installation instructions for IrysView are available here:
<http://www.bnxinstall.com/training/docs/IrysViewSoftwareInstallationGuide.pdf>
<http://www.bnxinstall.com/training/docs/IrysViewSoftwareTrainingGuide.pdf>

For further information on file formats, refer to the included BNX, CMAP, and XMAP file format specs in “file format.zip”.