

## BioNano Genomics IrysSolve® Output Compression Tool for IrysView®

### *Sharing results of BioNano Genomics IrysSolve De Novo Assembly and Hybrid Scaffold for Importing into IrysView*

This document provides instructions for compressing and sharing output results of the BioNano Genomics IrysSolve pipelines for *de novo* assembly and hybrid scaffold. These scripts have not been fully validated and are currently not supported by BioNano. The scripts are available for download at the BioNano Genomics' GITHUB and the BioNano Genomics' Community User Forums, and are made available to help facilitate the use of IrysView software and aid in the future development of fully validated and supported tools that might be incorporated into future versions of Irys® System Software.

#### **Disclaimer:**

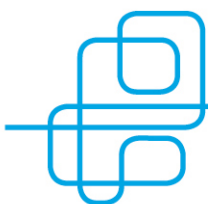
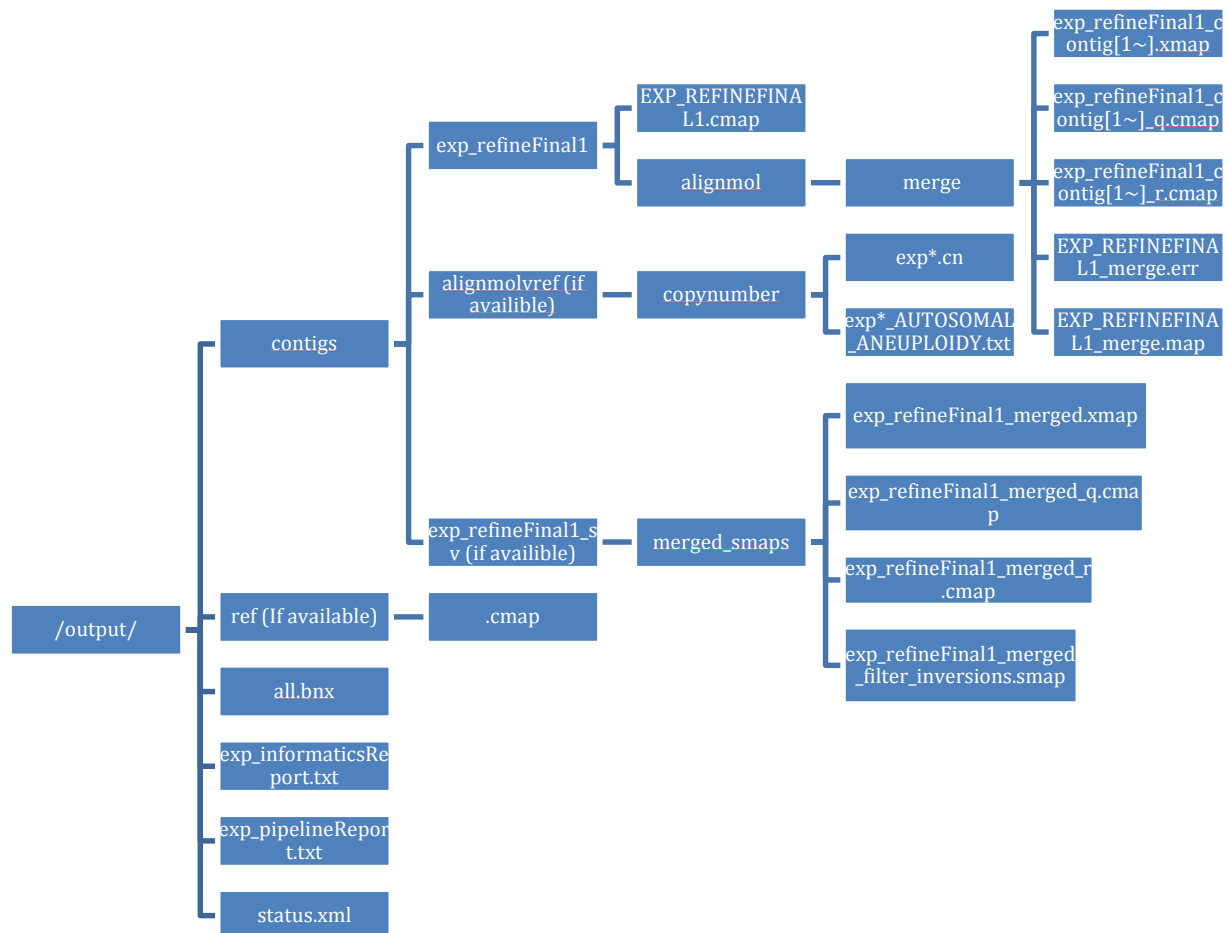
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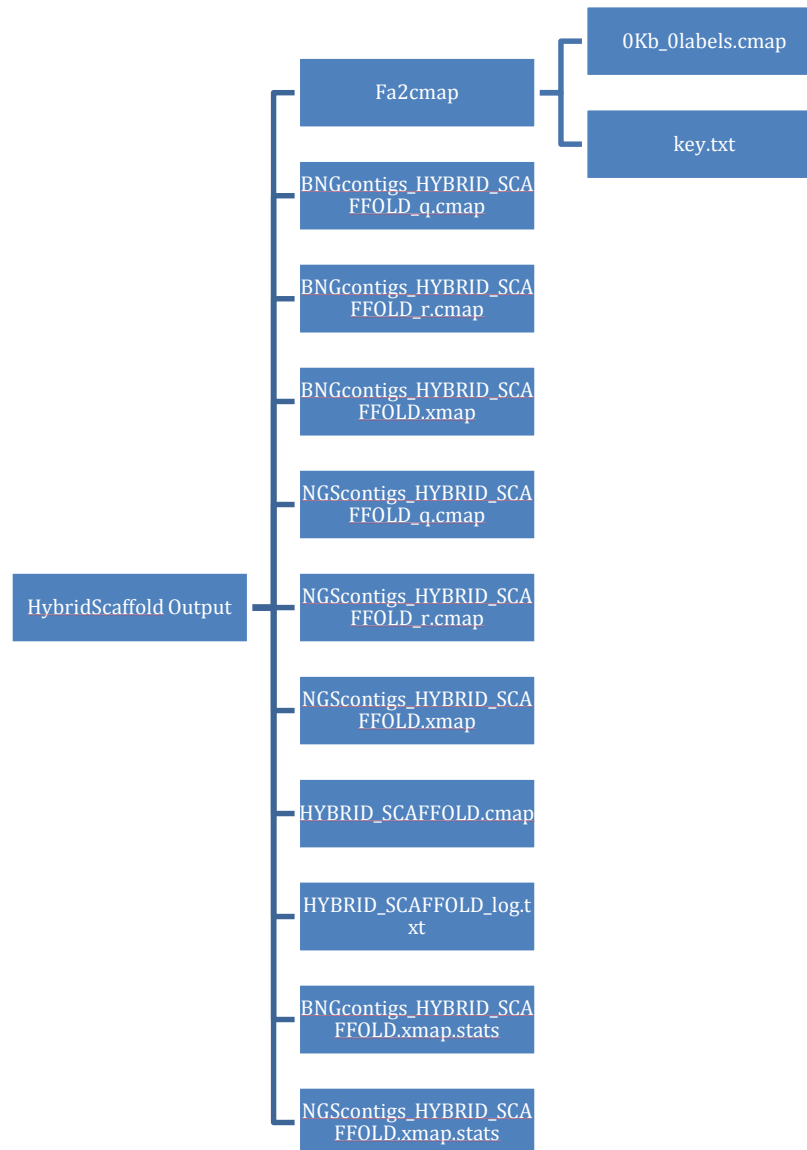
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Expected structure and required files of *de novo* assembly “output” folder:



Expected structure and required files of hybrid scaffold “output” folder:



Download the Linux compression script to compress *de novo* assembly results or hybrid scaffold results. The path and parameter examples in the instructions below are for the hybrid scaffold.

For more information about the usage for each script, access the help for each script using the “-h” parameter: eg: “./compressHybridScaffold\_forIrysView.sh --help”

#### Instructions for Compressing:

- 1) To compress denovo assembly, download: [https://github.com/BioNano-Genomics/Unofficial-scripts-and-tools/blob/master/IrysSolve\\_output\\_compression\\_tool/compressDeNovo\\_forIrysView.sh](https://github.com/BioNano-Genomics/Unofficial-scripts-and-tools/blob/master/IrysSolve_output_compression_tool/compressDeNovo_forIrysView.sh)
  - 2) To compress hybrid scaffold, download: [https://github.com/BioNano-Genomics/Unofficial-scripts-and-tools/blob/master/IrysSolve\\_output\\_compression\\_tool/compressHybridScaffold\\_forIrysView.sh](https://github.com/BioNano-Genomics/Unofficial-scripts-and-tools/blob/master/IrysSolve_output_compression_tool/compressHybridScaffold_forIrysView.sh)
  - 3) Copy the compression script to a location on a Linux system that has access to the “output” folder.
  - 4) Change the permissions of the folder to enable executable privileges: eg: “chmod 755 compressHybridScaffold\_forIrysView.sh”
  - 5) The script requires minimum input parameters:
    - a. --targetFolder : path/to/hybrid/scaffold/output
    - b. --outputFolder : path/to/compressFileOutput/folder
    - c. --prefix : name\_for\_output\_file
- Optional parameters:
- a. --gzip : force tar.gz gzip output
  - b. --verbose : verbose output
- 6) Execute the script on the target folder: eg: “./compressHybridScaffold\_forIrysView.sh --targetFolder ./output/ --outputFolder ./ --prefix denovoCompressTest --gzip --verbose”
  - 7) The compressed file generated with name “prefix” can be shared for import into IrysView.

#### Instructions for Importing:

- 1) Download the compressed file, “.tar.bz2” or “.tar.gz”.
- 2) Uncompress the file to a temporary folder using 7-Zip: <http://www.7-zip.org/>
- 3) From IrysView, use the “Import” feature (pg. XXX in IrysView 2.3 User Guide) to import the “output” folder from the uncompressed folder.

