Trial/Web Server Login

The trial version of the server does not report all of the results that the fully licensed version does:
-Any number of variants may be submitted.
-The set of variants shown is randomly selected from a larger set of results.
-Up to 20% of all possible results are shown.
-Only a few inactivating or leaky variants are returned.
-No more than 500 variants with changes in information content are displayed.
-User access is anonymous, but IP addresses are tracked.
-The only Server function that is enabled is the Shannon pipeline plugin.
-The full version of the plugin contains none these limitations.

***Please Note**: The server may be accessed without completing steps 1 and 3 below. The server contains results generated from the full version of the plugin which can be viewed without installation of the trial. However, if you would like to examine your own variants (or analyze the sample variants in the _SAMPLE-VARIANTS folder) on the trial server, all of the following steps are required:

1. Uninstall any previously installed Shannon Human Splicing Pipeline plugins.

2. Installation of a CLC bio plugin is required to allow the workbench to connect to a server. This plugin is not created by Cytognomix, it is a CLC bio plugin and simply allows the workbench to connect to any server. If you can already connect to other servers, this step is unnecessary.
- From within the Genomics Workbench, click the plugins button in the top toolbar
- Select “Download Plugins”
- Install the plugin named “CLC Workbench Client Plugin”

3. We will now install the client plugin used to submit and retrieve Shannon pipeline data from the trial server.
- From within the Genomics Workbench, click the plugins button in the top toolbar
- Select “Download Plugins”
- Install the plugin named “Cytognomix Shannon Pipeline Client”

4. Connect to the server
- From within the Genomics Workbench, select file->CLC Server Login
- If necessary, expand the advanced option to uncover 'Server host' and 'Server port'
- Login using the following credentials.
    - User name: trial
    - Password: Cytognomix
    - Server host: 208.75.74.35
    - Server port: 7777

- Click login

5. If desired, you can view some results generated by the full version of the plugin in the folder _SAMPLE-RESULTS-FROM-FULL-VERSION.

6. Your own data in VCF format may be imported at this time. Alternatively, this step may be skipped and sample variants will be examined instead. To examine your own VCF files the data **must** be imported using the following method.

VCF files must be imported. The file must be a standard VCF file with at least the first five columns present. The necessary fields are CHROM, POS, ID, REF, ALT in that order. File headers are not necessary and will be ignored if present. When specifying indels, the reference nucleotide field must include the base preceding the event, which must also be reflected in the position field.
For example, the following lines are acceptable:
5 148835675 . C T
5 148989410 ID1 A G,T
5 148989435 CAGT C (deletion)
5 148989435 C CAAA (insertion)

To import the data, click the import button on the taskbar in the CLC-Bio workbench and select 'Standard Import'. Select the file to be imported and select **force import as type: Shannon Pipeline VCF Format**. The imported object can now be used as input for the Shannon pipeline.

For more instructions regarding the import process, please consult the Shannon Human Splicing Pipeline documentation (Quick start section) on how to import either VCF or Shannon pipeline basic variant. For simplicity, the steps given below will use pre-imported data that are already resident on the Trial Server. However if you import your own data, simply use your imported data as pipeline input instead of sample variants in step 9.

7. In the Genomics Workbench toolbox, expand Shannon Human Splicing Pipeline and double click 'Launch Pipeline'.

8. A wizard will pop up. Select CLC Server and click next.

9. Expand the folder _SAMPLE-VARIANTS to view its contents. Select 'Pre-Imported-hg19-Variants-Ready-to-be-examined-by-the-Shannon-Pipeline' and move it to the 'Selected Elements' region of the wizard. Click next.

10. The pre-imported variants are hg19, so ensure hg19 is selected in 'Genome Build' and click next.

11. Pipeline results should be saved and not opened. This will be selected by default so click next on the Result handling wizard screen.

12. Create a folder to store your results. To do this, highlight the Trial_Server_Data folder and press the +folder button. Name the folder whatever you would like. Highlight your newly created folder and click finish to begin your run.

13. With this data (approximately 5000 variants on 3 different chromosomes), the run will take approximately 30 seconds to complete (if using the pre-imported variants), so be sure to check back to review your results.