

Brassica/Arabidopsis Comparative Genome Viewer

User's Manual

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Table of Contents

| | |
|---|----|
| Brassica/Arabidopsis Comparative Genome Viewer..... | 1 |
| Table of Contents..... | 2 |
| Table of Figures..... | 2 |
| Introduction..... | 3 |
| The Application..... | 4 |
| Basic Controls..... | 4 |
| The Windows..... | 5 |
| Search Options..... | 10 |

Table of Figures

| | |
|---|----|
| Figure 1 - Bioviz Genome Viewer: Chromosome View..... | 4 |
| Figure 2 - Controls: Scrolling and Scaling..... | 4 |
| Figure 3 - Moving a Window..... | 5 |
| Figure 4 - Minimized Window..... | 5 |
| Figure 5 - Window in Foreground..... | 5 |
| Figure 6 - Search Window..... | 6 |
| Figure 7 - BAC View..... | 6 |
| Figure 8 - Gene List..... | 7 |
| Figure 9 - Gene Info Window..... | 7 |
| Figure 10 - Sequence Window..... | 8 |
| Figure 11 - Displaying EST's in the BAC View..... | 8 |
| Figure 12 - HSP View..... | 9 |
| Figure 13 - BEAST Data..... | 9 |
| Figure 14 - The Search Options..... | 10 |
| Figure 15 - Visual Blast Report..... | 11 |

Introduction

This document contains instructions for use of the Brassica/Arabidopsis Comparative Genome Viewer developed by the bioinformatics team at the Saskatoon Research Centre (SRC) of Agriculture and Agri-food Canada (AAFC). The public version of this viewer is available at www.brassica.ca.

The basis for the SRC Brassica/Arabidopsis Comparative Genome Viewer is the BioViz: Genome Viewer¹ application. BioViz allows the user to see a representation of the Arabidopsis Genome, as annotated by TIGR, in their web browser. This functionality is extended in the comparative viewer to allow visualization of the relationship between the Arabidopsis genome and *Brassica napus* Expressed Sequence Tags (EST's) collected as part of our sequencing program. These tags have been aligned to the BAC's used in the sequencing of the genome and can be viewed on demand.

The viewer was developed using Scalable Vector Graphics (SVG), a World Wide Web Consortium (W3C) recommendation. To use the Comparative Viewer you will require the Adobe SVG plugin, which is available for download from www.adobe.com/svg. While the viewer is functional it is still under development, so any and all feedback would be appreciated. Email: Brassica_Viewer@agr.gc.ca.

The viewer has been tested on Win95/Win98/Win2K with IE 5.5/6.0 and Netscape 4.78. It has not been tested on a Macintosh, though Adobe does provide the SVG plugin for Macintosh. The viewer is not expected to work in Unix/Linux as Adobe does not support the SVG plugin for Unix/Linux.

¹ http://www.svgopen.org/papers/2002/42_lewis_et_al__bioviz_genome_viewer/

The Application

After starting the application you should see the following Chromosome view (Figure 1):

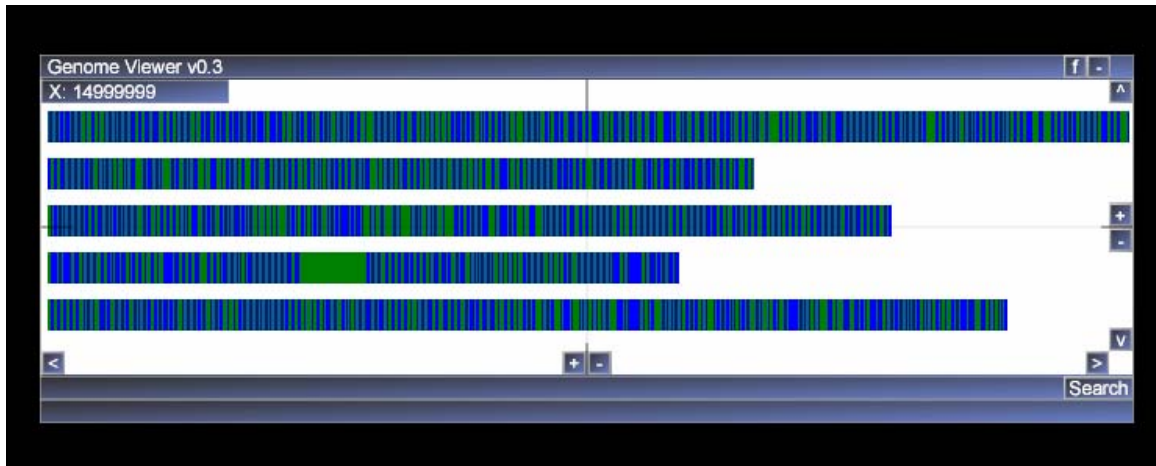


Figure 1 - Bioviz Genome Viewer: Chromosome View

Basic Controls

This initial view contains the majority of the functionality available in the other windows. The windows in BioViz have the functionality that you would expect in a GUI system. The contents of the window can be scrolled or scaled horizontally and vertically using the controls (Figure 2) along the edge of the content, if the controls are not present, the contents of this window can not be scrolled or scaled. Scaling occurs relative to the “crosshairs” of the window (which run between the + / - buttons from one edge to the other).



Figure 2 – Controls: Scrolling and Scaling

Clicking and holding the mouse button on the title bar will cause the window to go dark. Moving the mouse while the window is dark will move the window (Figure 3).

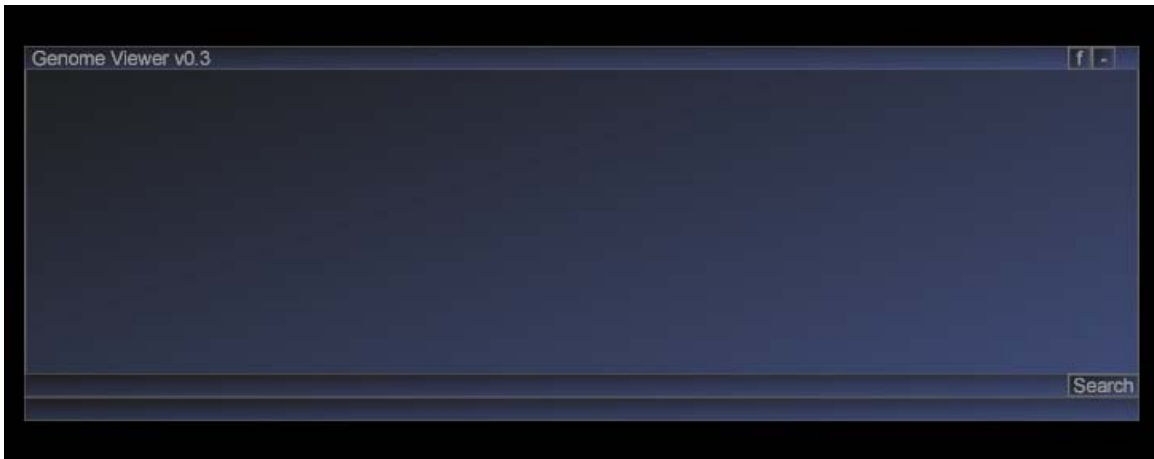


Figure 3 - Moving a Window

The **-** button in the top right of a window can be used to minimize the window. Minimizing a window leaves the title bar, the status bar and the button bar of the window visible so that you can still see status messages, and use the buttons available on the window. (Figure 4)



Figure 4 - Minimized Window

The **f** button at the top right of a window can be used to bring a window to the foreground. So if the window you're interested in is covered by another window, you can bring it to the front. The **X** button at the top right of most windows can be used to close the window (Figure 5).



Figure 5 - Window in Foreground

The Windows

There are a number of views available in the Genome Viewer. The initial chromosome view displays a representation of the five Arabidopsis chromosomes as annotated by TIGR. The button bar for this window contains a search button. Clicking the Search

button will provide a window containing the search menu (Figure 6). The various search options will be explained later in the section on searching.

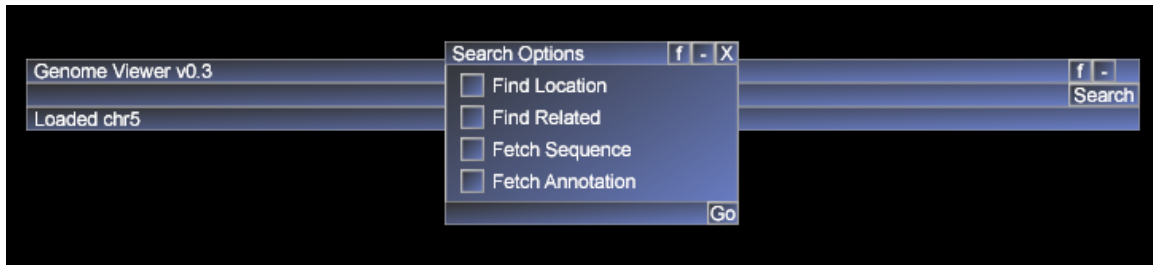


Figure 6 - Search Window

Clicking on one of the BAC's making up the Arabidopsis chromosome will open a window containing the BAC view (Figure 7). The selected BAC is marked red to make it easier to find in the future. Notice that as you mouse over the BAC's their id is displayed on the left side of the status bar (look to the lower left of the BAC View).

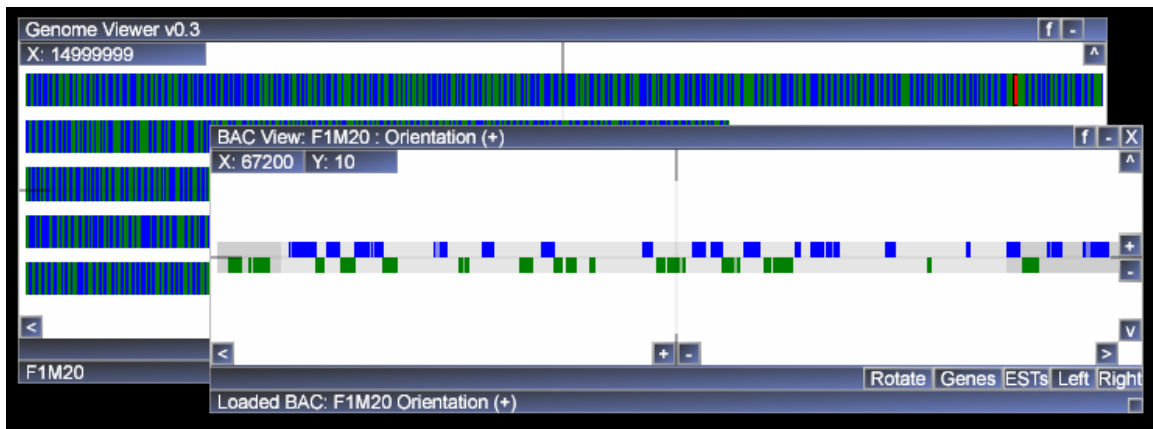


Figure 7 - BAC View

The BAC View contains the representation of the BAC. Displayed on the BAC are the genes annotated by TIGR. The Genes on the top (blue) are in the + direction (relative to the chromosome) and the Genes on the bottom (green) are in the - direction relative to the chromosome. The Left and Right buttons open a window displaying either the Left or Right neighbour of this BAC.

The title bar gives the orientation of the BAC. In this case the orientation is listed as being +, indicating that the BAC annotation and the Chromosome annotation are oriented in the same direction. We chose to orient the BAC's in the same direction as given in the Chromosome annotation so that genes in areas of overlap (the grey ends in the BAC view) would line up with themselves in the neighbouring BAC's. The orientation of the BAC's becomes important when doing certain analysis.

Click the Genes button to get a list of the genes on this BAC (Figure 8). In future versions of the Genome Browser this will be a "live" list and you will be able to click on

the gene to select it. At present you have to select your gene of interest from the BAC representation.

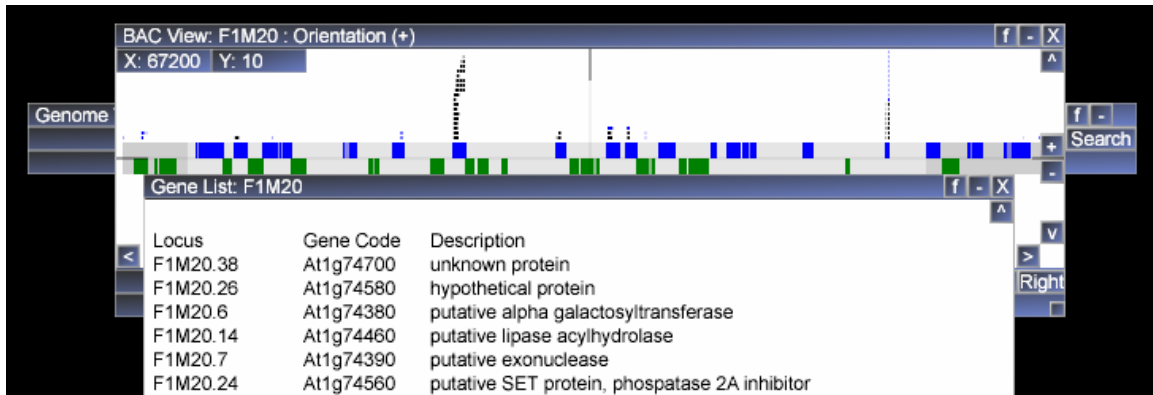


Figure 8 - Gene List

When you click on a gene the Gene Info window pops up with the annotation about this gene from the TIGR dataset (Figure 9). Notice that as you mouse over the genes on the BAC, the gene id is displayed in the status bar of the BAC View.

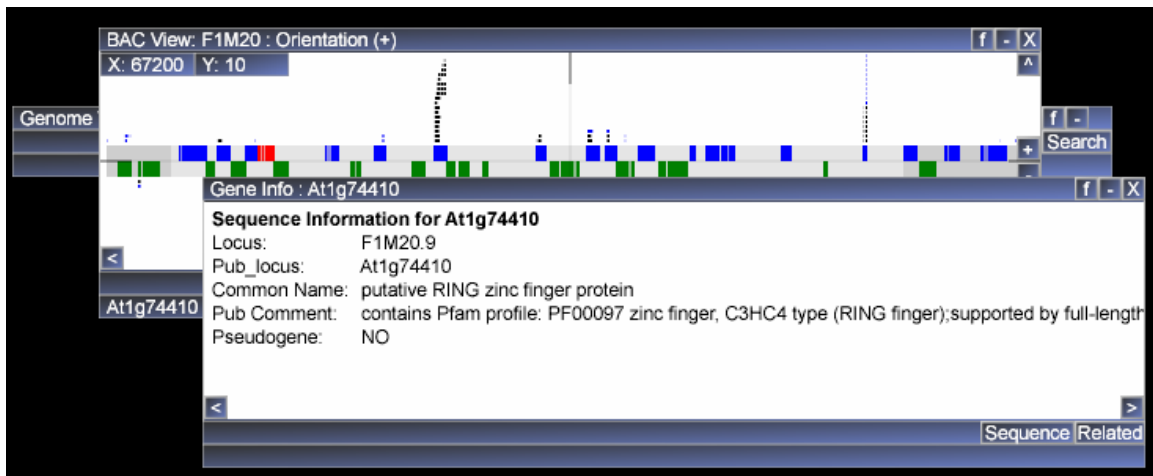


Figure 9 - Gene Info Window

From the Gene Info window it is possible to get the Gene Sequence. Clicking the Sequence button will provide you with a list of sequence options. Selecting the type of sequence you are interested in (Coding, Gene, Protein) and selecting the Go button will popup a window containing the desired sequence (Figure 10). This title bar of this window indicates the source and type of the sequence.

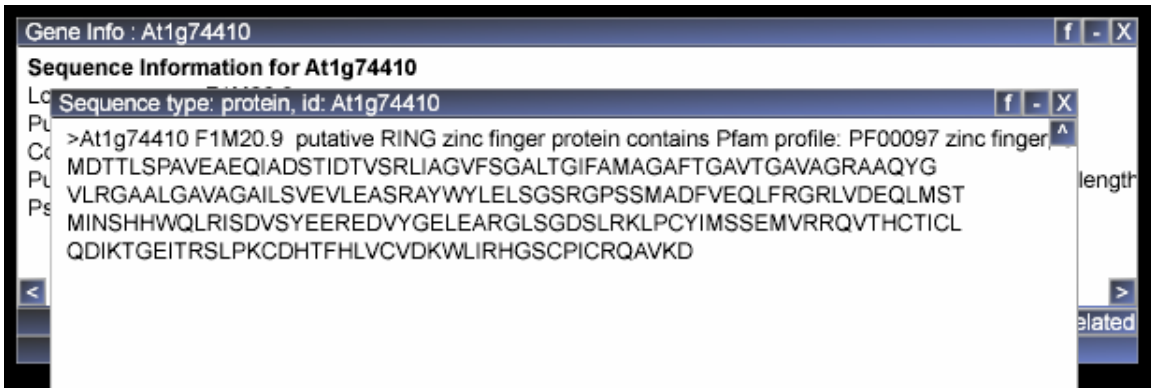


Figure 10 - Sequence Window

Closing the sequence window and the Gene Info windows brings you back to the BAC View. Click the EST button to display the EST's which have homology to this BAC (Figure 11). Notice that as you mouse over the various EST's the id is displayed in the status bar of the BAC view. Black hits indicate primary hits and blue hits indicate non-primary hits. A discussion of how these relationships were produced is provided further on in the manual.

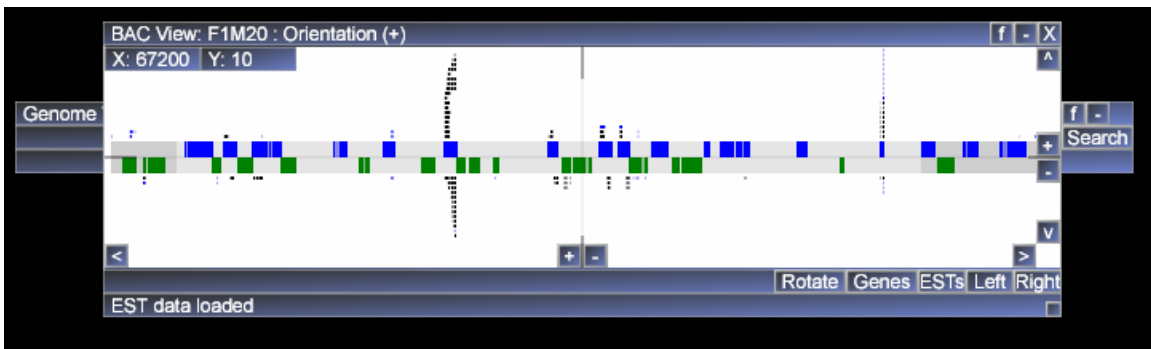


Figure 11 - Displaying EST's in the BAC View

Clicking one of the EST's will open the HSP (High Scoring Pair) View (Figure 12). This window displays the BLAST statistics for each HSP making up this hit. The Next and Prev buttons will cycle you through the HSP's. It is important that the user know that these HSP's are being displayed in order of strongest homology, rather than from left to right.



Figure 12 - HSP View

This is one of the places where the orientation of the BAC is important. The BAC coordinates listed in the HSP View will only agree with those listed in the BAC View if the BAC view lists a + orientation. If the BAC has a - orientation, you will need to rotate it using the rotate button.

The BEAST button will pull information from our BEAST (Brassica EST Analysis and Search Tool) database with the significant hits to the NCBI NT and NR databases. The sequence button returns the EST sequence from the server, however this feature is not available at this time in the public version. (Please email Brassica_EST@agr.gc.ca to enquire about availability of ESTs).

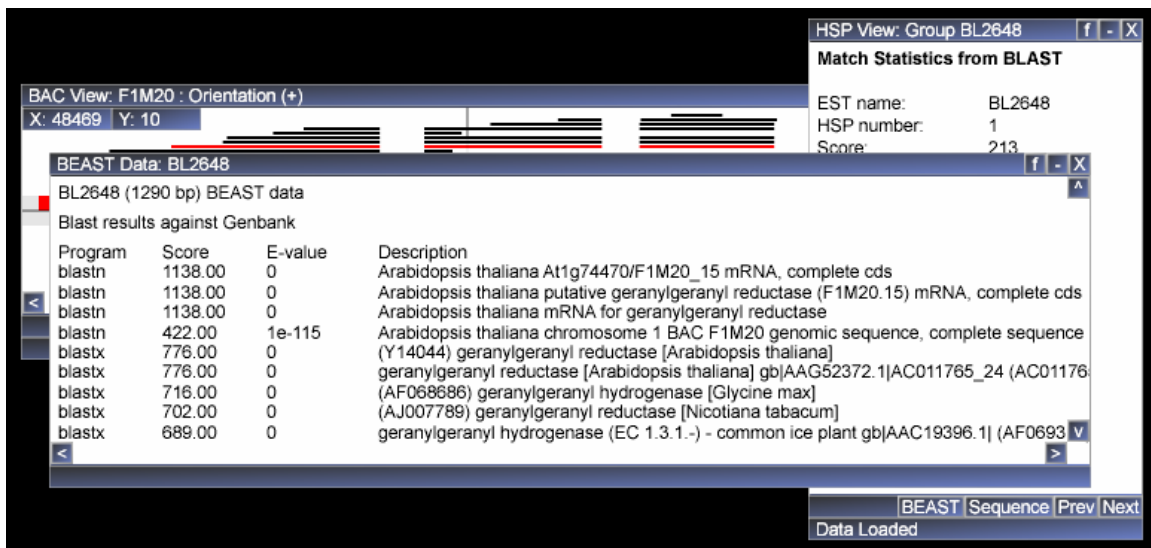


Figure 13 - BEAST Data

Search Options

There are a number of search options available in the BioViz: Genome Viewer (Figure 14).

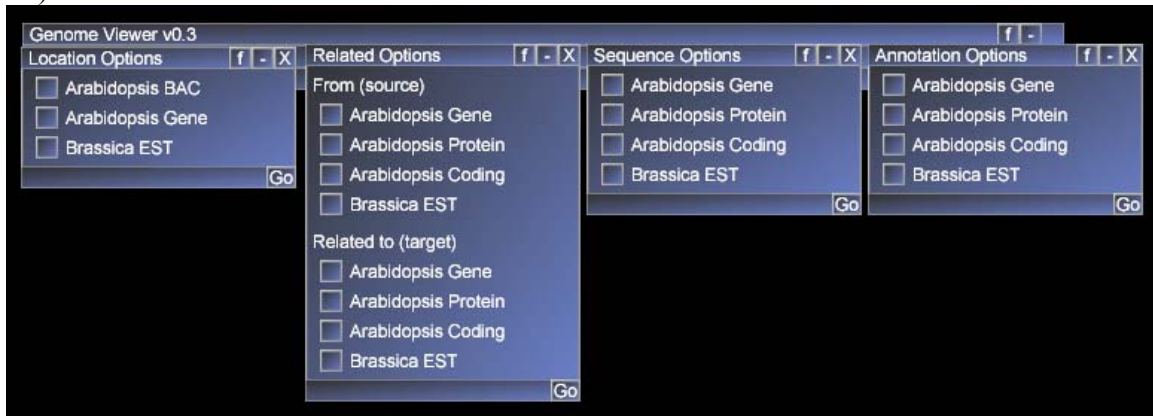


Figure 14 - The Search Options

The first set of options has been dubbed Location Options. Here you can find the location of a feature of interest. Currently you can search for a BAC, a Gene or an EST (Not currently available in the public version, but coming soon). Searching for a BAC opens the BAC View to the desired BAC. Searching for a gene opens the BAC View to the BAC upon which the desired gene is located. Searching for an EST returns a list of BAC's with significant homology to the desired EST. Selecting a BAC from the list will open the BAC View to the desired BAC.

The next set of options allows you to view the relationship between a feature of interest and the elements of a target set. For instance, you could see how one gene is related to all other genes by selecting Arabidopsis Gene to Arabidopsis Gene (Figure 15). Searches involving Brassica ESTs are not available at this time.

Clicking the button next to the Gene Id in the Blast Report View will open the Gene Info window with information about this gene (Figure 9). Clicking one of the bars next to the gene will open the HSP View with statistics about this HSP (Figure 12).

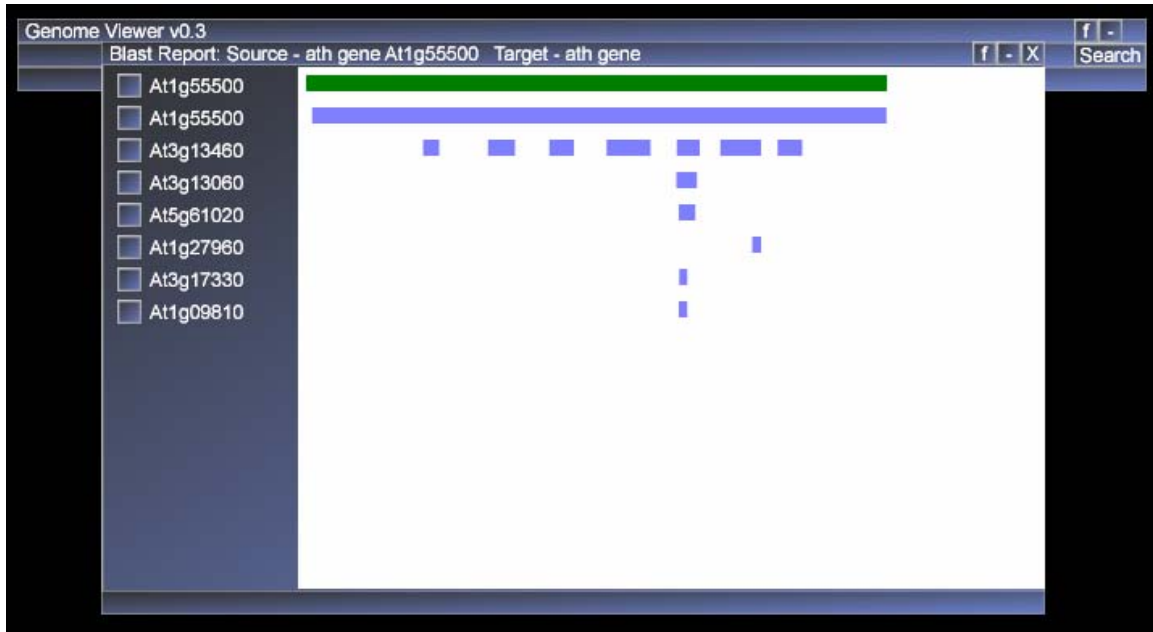


Figure 15 - Visual Blast Report

The next set of options allows you to fetch the sequence for a feature of interest. Allowable feature types are Arabidopsis Gene Sequence, Arabidopsis Coding Sequence, and Arabidopsis Protein Sequence. We are unable to provide the *B. napus* EST sequence in the public version. This option will open a window containing the desired type of sequence (Figure 10).

The final set of options allows the user to fetch the annotation for a feature of interest. Allowable feature types are Arabidopsis Gene Sequence, Arabidopsis Coding Sequence, Arabidopsis Protein Sequence, and Brassica napus BEAST information. This option will display the gene annotation for the desired Arabidopsis type (Figure 9) or BEAST information for the desired *Brassica napus* EST (Figure 13).