

# Viewing Data with IGV and HMV


## Viewing Data with the Integrative Genomics Viewer


Once you have run a query for [gene expression](#), or have run analyses for [copy number](#), or analyses for genomic data, you can view results in the Integrative Genomics Viewer (IGV).

The IGV is a high-performance visualization tool for interactive exploration of large, integrated datasets. It supports a wide variety of data types including sequence alignments, microarrays, and genomic annotations.



### IGV information

For more information about the Integrative Genomics Viewer or to connect independently to the IGV home page, see [Integrative Genomics Viewer](#) .

You may also want to refer to the [IGV User Guide](#) .

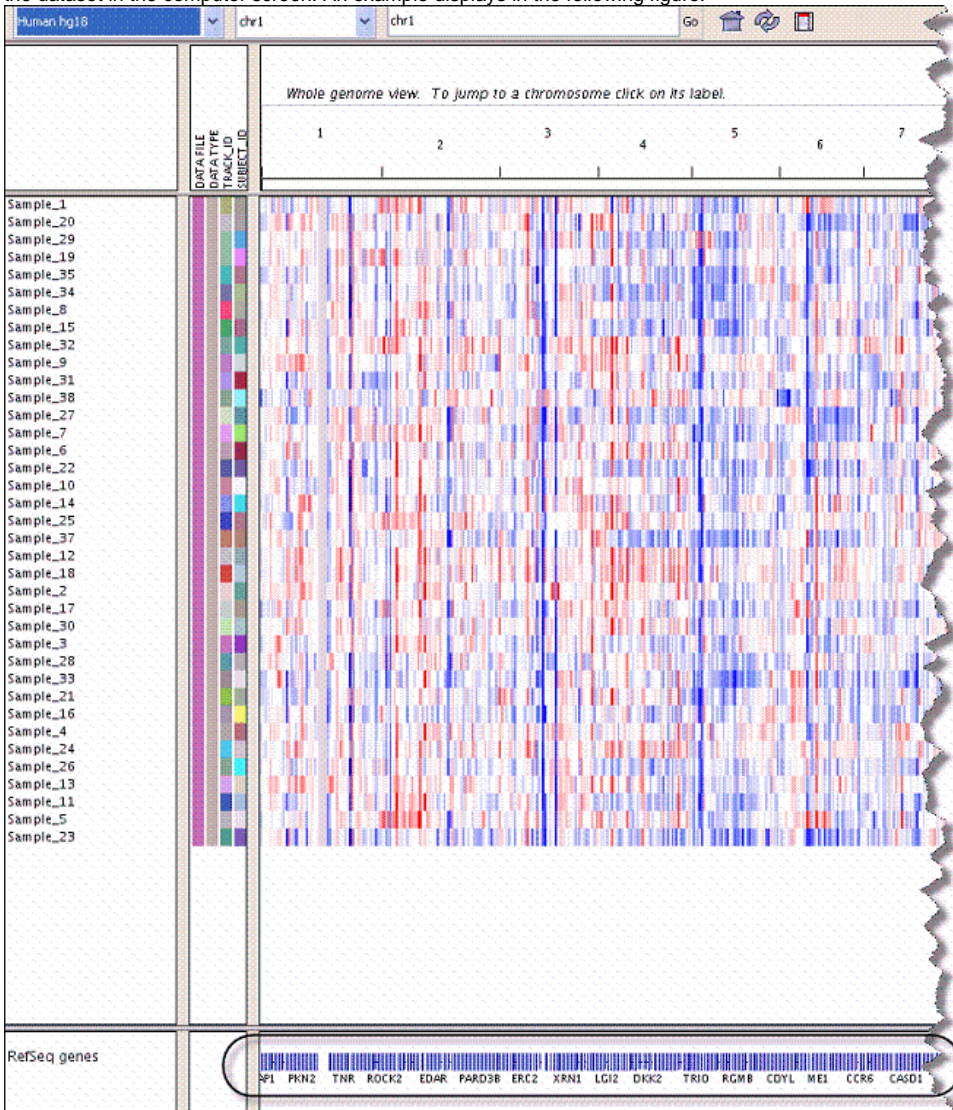
. The IGV viewer and the NCI Heat Map viewer both require you to install a version of Java containing Java Web Start. For more information, see [Java for IGV and Heat Map Viewer](#).

There are two ways to integrate caIntegrator with the IGV. To configure the connection to IGV, follow one of these methods.

#### Method 1 IGV

1. With the appropriate study open, at the bottom of the Query Results page, click the **View in Integrative Genomics Viewer** button.
2. If you click the button at the bottom of the page with any of the query results line items selected, caIntegrator creates IGV files, with a monitor informing you of this. After the files are created, click the **Launch Integrative Viewer** hypertext link.

3. Follow the instructions through the intermediate dialog boxes. After clicking **Open** with the Java program listed, the IGV . jnlp opens, displaying the dataset in the computer screen. An example displays in the following figure.



4. Move your mouse to hover over the genes graphic at the bottom of the page, indicated in the figure.

5. Click the mouse when you've identified a gene of interest.

This opens the genome site at UCSC, where you can learn more about the gene. The following figures exhibits the kind of metadata you can expect from the UCSC genome site.

<a href="#">Home</a>	<a href="#">Genomes</a>	<a href="#">Genome Browser</a>	<a href="#">Blat</a>	<a href="#">Tables</a>	<a href="#">Gene Sorter</a>	<a href="#">PCR</a>	<a href="#">Session</a>	<a href="#">FAQ</a>	<a href="#">Help</a>
----------------------	-------------------------	--------------------------------	----------------------	------------------------	-----------------------------	---------------------	-------------------------	---------------------	----------------------

### Human Gene GABRG1 (uc003gxb.1) Description and Page Index

**Description:** gamma-aminobutyric acid A receptor, gamma 1  
**RefSeq Summary (NM\_173536):** The protein encoded by this gene belongs to the ligand-gated ionic channel family. It is involved in and opening an integral chloride channel. This gene is clustered with three other family members on chromosome 4. [provided by RefSeq, Sep 2011]  
**Strand:** - **Genomic Size:** 88296 **Exon Count:** 9 **Coding Exon Count:** 9

<b>Page Index</b>	<a href="#">Sequence and Links</a>	<a href="#">UniProtKB Comments</a>	<a href="#">Genetic Associations</a>	<a href="#">CTD</a>	<a href="#">Microarray</a>
<a href="#">RNA Structure</a>	<a href="#">Protein Structure</a>	<a href="#">Other Species</a>	<a href="#">GO Annotations</a>	<a href="#">mRNA Descriptions</a>	<a href="#">Pathways</a>
<a href="#">Other Names</a>	<a href="#">Model Information</a>	<a href="#">Methods</a>			

### Sequence and Links to Tools and Databases

<a href="#">Genomic Sequence (chr4:45,732,544-45,820,839)</a>		<a href="#">mRNA (may differ from genome)</a>		<a href="#">Protein (465 aa)</a>	
<a href="#">Gene Sorter</a>	<a href="#">Genome Browser</a>	<a href="#">Protein FASTA</a>	<a href="#">Proteome Browser</a>	<a href="#">VisiGene</a>	<a href="#">Table Schema</a>
<a href="#">CGAP</a>	<a href="#">Ensembl</a>	<a href="#">Entrez Gene</a>	<a href="#">ExonPrimer</a>	<a href="#">GeneCards</a>	<a href="#">GeneNetwork</a>
<a href="#">Gepis Tissue</a>	<a href="#">H-INV</a>	<a href="#">HGNC</a>	<a href="#">HPRD</a>	<a href="#">HuGE</a>	<a href="#">Jackson Lab</a>
<a href="#">OMIM</a>	<a href="#">PubMed</a>	<a href="#">Stanford SOURCE</a>	<a href="#">Treefam</a>	<a href="#">UniProtKB</a>	<a href="#">User annotations</a>

### Comments and Description Text from UniProtKB

**ID:** [GABRG1\\_HUMAN](#)  
**DESCRIPTION:** RecName: Full=Gamma-aminobutyric acid receptor subunit gamma-1; AltName: Full=GABA(A) receptor subunit gamma-1  
**FUNCTION:** GABA, the major inhibitory neurotransmitter in the vertebrate brain, mediates neuronal inhibition by binding to and opening an integral chloride channel. This gene is clustered with three other family members on chromosome 4. [provided by RefSeq, Sep 2011]  
**SUBUNIT:** Generally pentameric. There are five types of GABA(A) receptor chains: alpha, beta, gamma, delta, and rho.  
**SUBCELLULAR LOCATION:** Cell junction, synapse, postsynaptic cell membrane; Multi-pass membrane protein. Cell surface.  
**PTM:** May be palmitoylated (By similarity).  
**MISCELLANEOUS:** This subunit carries the benzodiazepine binding site.  
**SIMILARITY:** Belongs to the ligand-gated ionic channel (TC 1.A.9) family.  
**WEB RESOURCE:** Name=Protein Spotlight, Note=Forbidden fruit - Issue 56 of March 2005; URL="http://www.expasy.org/spotlights/issue56/ffruit.html"

### Genetic Association Studies of Complex Diseases and Disorders

**Genetic Association Database:** [GABRG1](#)  
**CDC HuGE Published Literature:** [GABRG1](#)

### Comparative Toxicogenomics Database (CTD)

The following chemicals interact with this gene

- [D004026](#) Disulfiram

1. With the appropriate study open, click **Integrative Genomics Viewer** on the left sidebar. This opens the View IGV Selector page, shown in the following figure.

**View IGV Selector**

Enter Integrative Genomics Viewer parameters and click **View**.

**Platform**

Gene Expression Platform: AgilentG4502A\_07\_3 ▼

Copy Number Platform: 022522\_D\_F\_20090107 ▼

**Annotations - Default**

- ☐ Age
- ☐ Death Date
- ☐ Disease
- ☐ Followup Month
- ☐ GENDER

Select All Unselect All

Cancel View

2. In the drop-down list, select the **Gene Expression Platform** for the data you want to view.
3. Select the **Copy Number Platform** ID.
4. The Annotations - Default panel displays existing annotation fields for the gene expression data in the open study. Select those fields you want to view when you open the IGV. Use the buttons for convenience if you want to **Select All** or **Unselect All**, when all are checked.
5. Click **View** to see the data in the Integrative Genomic Viewer. calIntegrator creates IGV files of the data.
6. After the files are created, click the **Launch Integrative Viewer** hypertext link that appears.
7. Continue with Step 3 in [Method 1 IGV](#).

## Viewing Data with Heat Map Viewer

Once you have run a query for [gene expression](#), or for [copy number](#), or have run analyses on genomic data, you can view results in the Heat Map Viewer (HMV).



### HMV information

For more information about the Heat Map Viewer or to connect independently to the HMV home page, see [Heat Map Viewer documentation](#) or [HMV documentation](#). The IGV viewer and the NCI Heat Map viewer both require you to install a version of Java containing Java Web Start. For more information, see [Java for IGV and Heat Map Viewer](#).

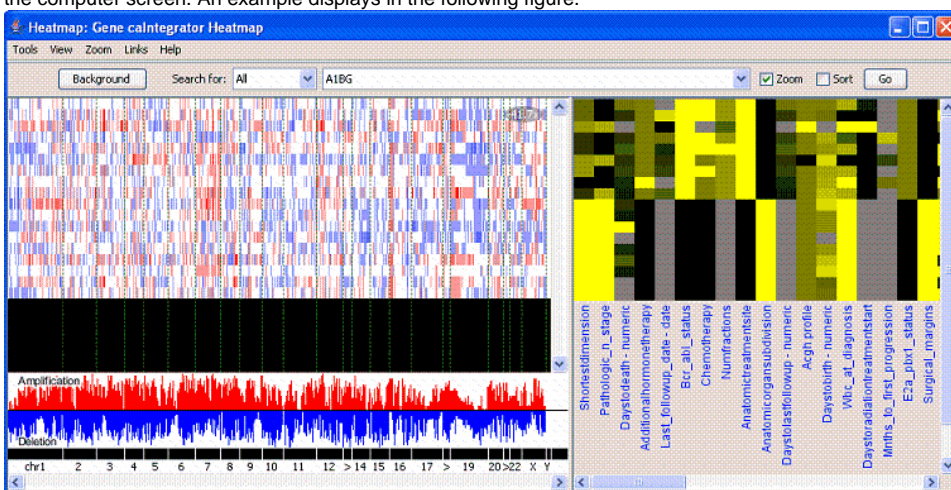
There are two ways to integrate calIntegrator with the Heat Map Viewer. To configure the connection, follow one of these methods.

#### Method 1 HMV

1. With the appropriate study open, at the bottom of the Query Results page, click the **View in Heat Map Viewer** button.
2. If you click the button at the bottom of the page with any of the query results line items selected, calIntegrator creates HMV files, with a monitor informing you of this. After the files are created, click the **Launch Heat Map Viewer** hypertext link.



- Follow the instructions through the intermediate dialog boxes. After clicking **Open** with the Java program listed, the runs, displaying the dataset in the computer screen. An example displays in the following figure.



#### Method 2 HMV

- With the appropriate study open, click **Heat Map Viewer** on the left sidebar. This opens the View Heat Map Viewer Selector page, shown in the following figure.

- Select the appropriate **Copy Number Platform** in the drop down list.
- The Annotations - Default panel displays existing annotation fields for the gene expression data in the open study. Select one or more annotations in the annotation list. For convenience, you can use the **Select All** or **Unselect All** buttons.
- Click **View** to view the data you select in Heat Map Viewer. calIntegrator creates Heat Map Viewer files of the data.
- After the files are created, click the **Launch Heat Map Viewer** hypertext link that appears.
- Continue with Step 3 in [Method 1 HMV](#).



#### HMV help files

For interpretation of the results and using HMV features, see the help files opened from HMV.

## Java for IGV and Heat Map Viewer

To use the IGV and the NCI Heat Map viewer, described in [Viewing Data with the Integrative Genomics Viewer](#) and [Viewing Data with Heat Map Viewer](#), you must install a version of Java containing Java Web Start. You must install recent versions of the Java Development Kit (JDK 1.5.0 aka JDK 5.0 or newer) or Java Runtime Environment (JRE 1.5.0 aka JRE 5.0 or newer). The easiest option is to install [JRE 5.0](#).

Without Java Web Start, when you click **Launch Integrative Genomics Viewer** or **Launch Heat Map Viewer**, a dialog box displays in your browser giving you the option to save or open with `igv.jnlp` (IGV) or `retrieveFile.jnlp` (HMV). Clicking the **Open** option starts the Java Web Start Launcher (default), installing the Java app so that you can view the files.



#### Upon first launch

The first time you launch the IGV or HMV with Java properly installed, regardless of browser type, a warning may appear: the "the digital signature cannot be verified". Click **Run** to proceed with opening the viewer.