Integrative Genomics Viewer IGV

Tom Carroll MRC Clinical Sciences Centre

- Introduction to IGV.
 - What is IGV.
 - How to run IGV.
- Navigating IGV.
 - The IGV user interface.
 - Moving around genomes.
- Loading and visualising data.
 - Genome information and annotation.
 - User supplied data.
 - Sample information.
 - External data.
- Displaying genomics data
 - Basic visualisation.
 - Data dependent visualisation.

What is IGV?

- Created by the Broad institute.
- Genome browser.
 - Visualises genomic data (expression, ChIP, resequencing, multiple alignment, shRNA)
 - Handles most common genomic data types.
- Java Desktop application
 - No dependence on server
 - Loads data locally or from URL, consumes memory and CPU.

How to run IGV?





http://www.broadinstitute.org/ software/igv/download



Home > Downloads **Downloads** Integrative Genomics Viewer (IGV) (Version 2.3) Install IGV Options for installing and running IGV: 1. (Mac only) Download and run the Mac applcation; or 2. (All systems) Use the Java Web Start buttons (Mac users: see below for limitations); or 3. (All systems) Download the binary distribution and run IGV from the command line. 1. Mac Application Download and unzip the Mac App archive, then double-click the IGV application to run it. The Download application can be moved to the "Applications" folder, or anywhere else. Note: This requires Java Mac App 7. Mac users with Java 6 (JRE 1.6) should use the binary distribution archive or the Java Web Start buttons below. 2. Java Web Start The buttons below use Java Web Start (JWS) to install and launch IGV directly from our web site. *Mac Users: The Java Web Start option is not recommended for Mac OSX Mountain Lion or higher. Using it requires that you set Gatekeeper security to its lowest level, and it is possible that even this will not be enough. Chrome: Chrome does not automatically launch the Java Webstart files by default. Instead, the launch buttons below will

download a "jnlp" file. This should appear in the lower left corner of the browser. Double-click the downloaded file to run.

ava

- Download to computer.
- Runs locally.
- Archived versions available

3. Binary Distribution

Download and unzip the binary distribution archive in a folder of your choosing. IGV is launched from a command prompt -- follow instructions in the "readme" file. To launch igv on Mac or Linux platforms use the shell script "igv.sh". On Windows use "igv.bat".

Download Binary Distribution

igvtools

Utilities for preprocessing data files.

• igvtools_2.3.40.zip

Other IGV Versions

Development Snapshot Build Latest development snapshot; built at least nightly.

Archived Versions

- Runs from webstart.
- Always runs latest version of IGV.

2. Java Web Start

The buttons below use Java Web Start (JWS) to install and launch IGV directly from our web site.

*Mac Users: The Java Web Start option is not recommended for Mac OSX Mountain Lion or higher. Using it requires that you set Gatekeeper security to its lowest level, and it is possible that even this will not be enough.

Chrome: Chrome does not automatically launch the Java Webstart files by default. Instead, the launch buttons below will download a "jnlp" file. This should appear in the lower left corner of the browser. Double-click the downloaded file to run.

Windows users: To run with more than 1.2 GB of memory you must install 64-bit Java. *Most Windows installs do not include 64-bit Java by default, even if the operating system is 64-bit.* Attempting to use the 2GB or greater launch options with 32-bit Java will result in the error "could not create virtual machine".

Launch with 750 MB Launch Maxim for Wir Java.	Launch h with 1.2 GB hum usable memory ndows OS with 32-bit	unch Launch with 2 GB Launch with 10 GB m usable memory t MacOS. For large memory machines with 64-bit Jay	va.
---	--	--	-----

IGV GUI

📫 IGV 2.3	File	Genomes	View	Tracks	Regions	Tools	Geno	meSpace	He	lp		4	2	ļ. 🗖) *	((;	1	00% 🗲	ЪТ	ue 09:!	56 -	Thoma	as Carr	oll	Q !!	Ξ
$\Theta \Theta \Theta$										IGV																	
Human hg19		All		\$				Go	Ê		Þ	¢		×								—					+
		1	I	2	3	4	I	5	6	Ī	7	8	1	9	I	10 I	11	12 	1: !	3 I	14 	15 I	16 	7 18 	19 20	21 22	
RefSeq Genes		latt		dista	<u></u>	14. s			.		ulu	<u>Uma</u>	- 4			لىمى		<u></u>	<u></u>		ل الدميا	<u>u</u>			.	d d bbi	
2 tracks loaded																									194	A of 415N	Л

- IGV GUI:-
 - Sample information panel <1>
 - Genome Navigation panel <2>
 - Data panel <3>
 - Attribute panel <4>





- Menu bar
 - File, Load data/sample information.
 - Genome, Load and manage genomes.
 - View, Display preferences.
 - Tracks, Group/sort/filter data tracks.
 - **Regions**, Create region/gene lists.
 - Tools, Access to Integrated tools (IGVtools/ Bedtools).
 - GenomeSpace, Export/import from Genomespace

Moving around genomes

- Cytoband selection and zooming
- Scrolling
- Selection of region of interest

$\bigcirc \bigcirc \bigcirc \bigcirc$	IGV
Human hg19	AII ÷ Go ☆ ★ ♥ □ ★ ♥ □
	$ \begin{array}{ cccccccccccccccccccccccccccccccccccc$
RefSeq Genes	here have not a set of the here and the set of the set of the here have a set of the here here and the here and
2 tracks loaded	172M of 415M

Whole genome view

● ● ●	IGV
Human hg19	÷ All ÷ Go 👚 • 🖗 🖩 💥 🖵
	1 3 5 7 9 11 13 15 17 19 21 2 4 6 8 10 12 14 16 18 20 22
RefSeq Genes	aka kalenda menanda ana sebara ana aka kalenda ana kalenda akalenda aka kalenda aka kalenda aka kalenda aka ka
2 tracks loaded	172M of 415M



Zooming

🗭 ⊖ 🕀							IG	V									
Mouse mm9		‡ Ch	r1	÷	chr	1					Go	Ê	•	r de	, 🔲	жĘ	
		qA2	qA4	qB	qC1.1	. qC2	2 0	qC4	qD	qE1.2	qE2.3	qE	4 qF	qG2	qH2.2	qH4	qH6
		⊲ 20 mb 		40 mb 		60 mb 	1	80 mb 	- 162	mb 100 mb	1	120 mb 		140 mb 	, I	160 mb 	
Refseq genes		8L16Rik	Gm597	Aff3	Tmeff2	Abi2	lkzf2	Pax3	Sp100	Slco4c1	Bcl2	Tsn	Mgat5	Ptprc	Pla2g	4a Tnr	Uck2
tracks loaded	chr1:2	26,791,616														216M of	396M

Scrolling

00				IGV		
Mouse mm9	♣ chr1	chr1:68,125,345	L97,077,344 Go 👚	 ▶ ∅ □ × □ 	E]
	qA1 qA2 qA3	qA5 qB qC	1.1 qC1.3 qC3 qC4	qC5 qD qE1.1 qE2.2	qE3 qE4 qF qG1 qH1	qH2.3 qH4 qH5 qH6
	80 mi	5 100 	mb 120 	mb 128 mb − I 128 mb − I 140 mb 1 I I	160 mb	180 mb
Refseq genes	bb4 Tnp1 Pax3	Ins1 Sp110 Iqca Bok Gin	1 Cdh20 Cdh7 Cntnap5	a Dpp10 Lct Elk4 Igfn1 Cfh Glrx	2 Pla2g4a ler5 Rfwd2 Scyl3 Pbx1 lgs	10000000000000000000000000000000000000
			4			
		1				
2 tracks loaded chr	1:138,699,823					209M of 359M

Jump to Region





"Bookmarking" regions of interest

- Regions may be added to "Regions of interest"
- These act as bookmarks for areas of particular interest

Ś	IGV 2.3	File	Genomes	View	Tracks	Regions	Tools	Genome	eSpace	e He	lp		4	2	
• •	\bigcirc					Region	Navigato	or			IGV	1			
Мо	use mm9		¢ chr	6	¢ chr	Gene Li	sts Regions	5	Go	Î	•	•	Ø [X 🖵
			q/	A1	qA2 qA	Import	Regions	 1υ2.1 γυ2.3	3	qB3		qC1	L qC	2	qC3 c
			122,656	¢b		122	2,658 kb 				122,66 	60 kb	— 10 kl	b —	I
000)						IGV								
Mous	e mm9	¢ cł	nr6 🛊	chr6:122,65	5,586-122,66	5,796 Go 1	≝ ◄ ►	🤣 🖪 🔅	¥ 🖵						
			qA1 qA2 6 kb	qA3.1 qA3	3.3 qB1 qB2 122,658 kb 1 Show All C hr Start nr6 122	.1 qB2.3 qB3	122,660 kb 1 ns of Interest Remove dd a new regio 665796	1 qC2 (qC3	qD1 122					
				S	View earch	🖞 Zoom to Regio	n	Clear Search)						

"Book marked" Region Of Interest

Mouse mm9	¢ chr6	¢ chr6:122	,646,455-12	2,674,926	Go 音 🖣	▶ @]	X 🖵		
	qA1	qA2 qA3.1	qA3.3 qB1	qB2.1 qB7 3	qB3	qC1 qC2	qC3 qD1	qD2 qD	qE1
		122,650 kb 				122,660 kb 		,	
Pefece conc						· · · ·			

Loading data in IGV

Loading Genome Information

 Most genomes can be selected from dropdown.





 Genomes not included may be downloaded from repository



Loading genome annotation

- For supported genomes, gene positions are automatically included in "feature" panel.
- Additional gene positions can be loaded into IGV in gff format.



Loading sample data.

- Most common formats can be loaded into IGV through file menu
- Acceptable data formats include:-
 - BED (.bed)
 - BAM and index (.bam with .bai/.bam.bai)
 - BigWig (.bw)
 - BedGraph/Wig (.bedGraph, .wig)

And many more...

Loading sample metadata

- IGV allows the inclusion of information on samples.
- Sample

 information is
 then included in
 sample
 information panel.



• Example Sample Information file

http://www.broadinstitute.org/igvdata/exampleFiles/exampleSampleInfo.txt

		PARTICIPAN						Primary/	Hypermutat
TRACK_ID	Data_Type	T_ID	SAMPLE_ID	GENDER	T/N	Tumor_type	Treated	Secondary	ed
EX-01-001	Expression	P-01-P001	P-01-S001	М	Tumor	GBM	Y	Primary	Y
	CopyNumbe								
CN-01-002	r	P-01-P001	P-01-S001	М	Tumor	GBM	Υ	Primary	Υ
MU-01-003	Mutation	P-01-P001	P-01-S002	М	Tumor	GBM	Y	Primary	Y
EX-01-004	Expression	P-01-P002	P-01-S003	М	Normal	GBM	Y	Secondary	Y
	CopyNumbe								
CN-01-005	r	P-01-P002	P-01-S004	М	Tumor	GBM	Y	Secondary	N
EX-01-006	Expression	P-01-P002	P-01-S004	М	Tumor	GBM	Y	Secondary	Ν
ME-01-007	Methylation	P-01-P002	P-01-S004	М	Tumor	GBM	Y	Secondary	N
EX-01-008	Expression	P-01-P003	P-01-S006	F	Tumor	GBM	N	Primary	Y
EX-01-009	Expression	P-01-P004	P-01-S009	F	Tumor	GBM	N	Primary	Y
EX-01-0010	Expression	P-01-P005	P-01-S0011	М	Control				

Using sample information.

- Sample information can include discrete and continuous.
- Can be used to "sort" and "filter" tracks.
- Can split tracks across panels by "group"



Loading external data and annotation

Load data from a URL.

• As with UCSC, IGV supports data hosted on external servers.

• Data accessible from a URL such as HTTP and FTP can be loaded using the **"Load from URL".**

File Genomes	View Tra	cks	Regions	Tools	Gen	omeSp	ace	He	р			2	<u>ب</u>		5 \$	((i·	D
Load from File			IGV	– Sessio	n: /Us	ers/tca	rroll	/Docu	imen	ts/te	este/t	rackt	able	s/RNA	Pol2ig	v.xml	
Load from URL.	·· •						Go			►	Ż		¥				
Load from Serv Load from DAS Load from ENC	er ODE																
New Session Open Session Save Session		2	2	3	4	; 	5	6	i		7	8	1	9	10 		11
Save Image Exit	_																
	FileGenomesLoadfrom File.Loadfrom URL.Loadfrom DASLoadfrom ENCNew SessionOpen SessionOpen SessionSave SessionSave ImageExit	File Genomes View Transmitted Load from File Load from URL * Load from Server Load from DAS * Load from ENCODE * New Session Open Session Save Image * Exit *	File Genomes View Tracks Load from File Image Image <th>File Genomes View Tracks Regions Load from File IGV Load from URL • Load from Server • Load from DAS • Load from ENCODE 2 New Session 2 Save Image • Exit •</th> <th>File Genomes View Tracks Regions Tools Load from File IGV - Sessio IGV - Sessio Load from URL • • • Load from Server Load from DAS • • Load from ENCODE 2 3 New Session 2 3 Save Image 1 1 1 Exit • • • •</th> <th>File Genomes View Tracks Regions Tools Gen Load from File IGV - Session: /Us Load from URL Image <td< th=""><th>File Genomes View Tracks Regions Tools GenomeSp Load from File IGV - Session: /Users/tca Load from URL * * * Load from Server Load from DAS * * * Load from ENCODE 2 3 4 * New Session 2 3 4 * Save Session 1 1 1 * * Exit * * * * * *</th><th>File Genomes View Tracks Regions Tools GenomeSpace Load from File IGV - Session: /Users/tcarroll Load from URL I Load from Server Go Load from DAS I Load from ENCODE 2 New Session 2 Open Session 2 Save Image I Exit I</th><th>File Genomes View Tracks Regions Tools GenomeSpace Hele IGV - Session: /Users/tcarroll/Docu Load from URL Load from Server Load from DAS Load from ENCODE New Session Open Session Save Image Exit</th><th>File Genomes View Tracks Regions Tools GenomeSpace Help Load from File IGV - Session: /Users/tcarroll/Documen Load from URL Go Image Image</th><th>File Genomes View Tracks Regions Tools GenomeSpace Help Load from File IGV - Session: /Users/tcarroll/Documents/te Load from URL Go Load from Server Go Load from DAS Load from ENCODE New Session Open Session Save Image Exit</th><th>File Genomes View Tracks Regions Tools GenomeSpace Help I Load from File IGV - Session: /Users/tcarroll/Documents/teste/t Load from URL Go Image Image Image Load from DAS 2 3 4 5 6 Load from ENCODE 2 3 4 5 6 Save Session 2 3 4 5 6 Load from ENCODE Image Image Image Image Image</th><th>File Genomes View Tracks Regions Tools GenomeSpace Help M 2 Load from File IGV - Session: /Users/tcarroll/Documents/teste/trackt Load from URL Go Image Image Image Load from DAS Image Image Image Image Image Save Image Image Image Image Image Image</th><th>File Genomes View Tracks Regions Tools GenomeSpace Help M 2 Image Load from File Load from URL Load from DAS Load from ENCODE New Session Open Session Save Image Exit</th><th>File Genomes View Tracks Regions Tools GenomeSpace Help M 2 Image Imag</th><th>File Genomes View Tracks Regions Tools GenomeSpace Help M 2 Image Imag</th><th>File Genomes View Tracks Regions Tools GenomeSpace Help M 2 Image Imag</th></td<></th>	File Genomes View Tracks Regions Load from File IGV Load from URL • Load from Server • Load from DAS • Load from ENCODE 2 New Session 2 Save Image • Exit •	File Genomes View Tracks Regions Tools Load from File IGV - Sessio IGV - Sessio Load from URL • • • Load from Server Load from DAS • • Load from ENCODE 2 3 New Session 2 3 Save Image 1 1 1 Exit • • • •	File Genomes View Tracks Regions Tools Gen Load from File IGV - Session: /Us Load from URL Image Image <td< th=""><th>File Genomes View Tracks Regions Tools GenomeSp Load from File IGV - Session: /Users/tca Load from URL * * * Load from Server Load from DAS * * * Load from ENCODE 2 3 4 * New Session 2 3 4 * Save Session 1 1 1 * * Exit * * * * * *</th><th>File Genomes View Tracks Regions Tools GenomeSpace Load from File IGV - Session: /Users/tcarroll Load from URL I Load from Server Go Load from DAS I Load from ENCODE 2 New Session 2 Open Session 2 Save Image I Exit I</th><th>File Genomes View Tracks Regions Tools GenomeSpace Hele IGV - Session: /Users/tcarroll/Docu Load from URL Load from Server Load from DAS Load from ENCODE New Session Open Session Save Image Exit</th><th>File Genomes View Tracks Regions Tools GenomeSpace Help Load from File IGV - Session: /Users/tcarroll/Documen Load from URL Go Image Image</th><th>File Genomes View Tracks Regions Tools GenomeSpace Help Load from File IGV - Session: /Users/tcarroll/Documents/te Load from URL Go Load from Server Go Load from DAS Load from ENCODE New Session Open Session Save Image Exit</th><th>File Genomes View Tracks Regions Tools GenomeSpace Help I Load from File IGV - Session: /Users/tcarroll/Documents/teste/t Load from URL Go Image Image Image Load from DAS 2 3 4 5 6 Load from ENCODE 2 3 4 5 6 Save Session 2 3 4 5 6 Load from ENCODE Image Image Image Image Image</th><th>File Genomes View Tracks Regions Tools GenomeSpace Help M 2 Load from File IGV - Session: /Users/tcarroll/Documents/teste/trackt Load from URL Go Image Image Image Load from DAS Image Image Image Image Image Save Image Image Image Image Image Image</th><th>File Genomes View Tracks Regions Tools GenomeSpace Help M 2 Image Load from File Load from URL Load from DAS Load from ENCODE New Session Open Session Save Image Exit</th><th>File Genomes View Tracks Regions Tools GenomeSpace Help M 2 Image Imag</th><th>File Genomes View Tracks Regions Tools GenomeSpace Help M 2 Image Imag</th><th>File Genomes View Tracks Regions Tools GenomeSpace Help M 2 Image Imag</th></td<>	File Genomes View Tracks Regions Tools GenomeSp Load from File IGV - Session: /Users/tca Load from URL * * * Load from Server Load from DAS * * * Load from ENCODE 2 3 4 * New Session 2 3 4 * Save Session 1 1 1 * * Exit * * * * * *	File Genomes View Tracks Regions Tools GenomeSpace Load from File IGV - Session: /Users/tcarroll Load from URL I Load from Server Go Load from DAS I Load from ENCODE 2 New Session 2 Open Session 2 Save Image I Exit I	File Genomes View Tracks Regions Tools GenomeSpace Hele IGV - Session: /Users/tcarroll/Docu Load from URL Load from Server Load from DAS Load from ENCODE New Session Open Session Save Image Exit	File Genomes View Tracks Regions Tools GenomeSpace Help Load from File IGV - Session: /Users/tcarroll/Documen Load from URL Go Image Image	File Genomes View Tracks Regions Tools GenomeSpace Help Load from File IGV - Session: /Users/tcarroll/Documents/te Load from URL Go Load from Server Go Load from DAS Load from ENCODE New Session Open Session Save Image Exit	File Genomes View Tracks Regions Tools GenomeSpace Help I Load from File IGV - Session: /Users/tcarroll/Documents/teste/t Load from URL Go Image Image Image Load from DAS 2 3 4 5 6 Load from ENCODE 2 3 4 5 6 Save Session 2 3 4 5 6 Load from ENCODE Image Image Image Image Image	File Genomes View Tracks Regions Tools GenomeSpace Help M 2 Load from File IGV - Session: /Users/tcarroll/Documents/teste/trackt Load from URL Go Image Image Image Load from DAS Image Image Image Image Image Save Image Image Image Image Image Image	File Genomes View Tracks Regions Tools GenomeSpace Help M 2 Image Load from File Load from URL Load from DAS Load from ENCODE New Session Open Session Save Image Exit	File Genomes View Tracks Regions Tools GenomeSpace Help M 2 Image Imag	File Genomes View Tracks Regions Tools GenomeSpace Help M 2 Image Imag	File Genomes View Tracks Regions Tools GenomeSpace Help M 2 Image Imag



Loading external data and annotation

Load data from a server.

- Unlike UCSC, IGV comes with few external tracks.
- External tracks (relevant to the genome) can be loaded from the IGV server or Encode-IGV server.

🗯 IGV 2.3	File	Genomes	View	Tracks	Region	s Tools	Genom	eSpace	He	lp	
$\Theta \Theta \Theta$										IGV	'
Human hg19	Loa Loa	Load from File Load from URL		•	-1			Go	Ê		•
	Loa	ad from Serv	'er	server	cks or sam	pie informa	tion from a		-		
	Loa	ad from DAS						_			
	Loa	ad from ENC	ODE								
	Ne	w Session									
	Op	en Session		2	3	4	5	6		7	
	Sav	e Session				1		1	- 1		1
	Sav	e Image									
	Exi	t									



Viewing data

- IGV associates common file formats with default display methods.
- Most of the time IGV will make a sensible choice how we wish to display data.

Accepted formats and default display.

Information on accepted file formats and default display can be found at http://www.broadinstitute.org/software/igv/RecommendedFileFormats

Recommended File Formats

The following table lists recommended file formats for data types. Tip: Using jgvtools to convert a source data file to a binary TDF file can reduce loading time and improve performance.

Source Data	Recommended File Formats
ChIP-Seq, RNA-Seq	TDF format. Use the <u>igvtools</u> package (count command) to generate a binary read count density file in TDF format. Load the resulting TDF file into IGV.
Copy number	CN format, SNP format
	Log values : If copy number data contains negative values, IGV assumes they are scaled log values and displays them without modification. If copy number data contains all positive values, IGV assumes they are unscaled. It centers the unscaled values around 2 (1 for allele specific files), log transforms them (logValue = log2(copyNumber / 2)), and displays the log values.
Gene expression data	GCT format RES format

Bed/bigBed

- Basic
 - Tab-delimited
 Chrom,Start,End
- Bed6
- bigBed (recommended)



Wig, BedGraph and BigWig

- Wig/bedGraph require high memory load
- Recommended format is bigWig



BAM alignment files

- BAM files contain alignment information.
- Require an accompanying .bai index file for display



Finer control of display

• IGV allows for customization of track display.

– Menu bar -> View -> Preferences

– Select track (right click)

Display preferences

General

General Tracks Mutations Charts Alignments Probes Proxy Advanced IonTorrent
Distinguish missing data
Distinguish regions with zero values from regions with no data on plots (e.g. bar charts). Regions with no data are indicated with a gray background.
Display all tracks in a single panel
Show attribute panel
Show default track attributes
Display default track attributes (NAME, DATA_TYPE, and DATA_FILE) in the attribute panel.
Show region boundaries
Zoom to features This option controls the behavior of feature searchs. If true, the zoom level is changed as required to size the view to the feature size. If false the zoom level is unchanged.
Sequence resolution threshold (bp/pixel): 2
Resolution in base-pairs per pixel at which sequence track becomes visible.
Feature flanking region (bp or %): 2000
Added before and after feature locus when zooming to a feature. Also used when defining panel extents in gene/loci list views. A negative number is interpreted as a percentage.
Background color click to change):
Default font: Arial 10 Change
OK Can

Tracks

$\bigcirc \bigcirc \bigcirc$	
General Tracks Mutations Charts Alignments Probes Proxy Advanced	IonTorrent
Default Track Height Charts (Pixels) 40 Default height of chart tracks (barcharts, sca	atterplots, etc)
Default Track Height, Other (Pixels) 15 Default height of all other tracks	
Irack Name Attribute	
Name of an attribute to be used to label tracks. If provided tracks will be labeled with the	
corresponding attribute to be used to label tracks. If provided tracks will be labeled with the	
Expand Feature Tracks	
Show Expand Icon	
Normalize Coverage Data	
Applies to coverage tracks computed with igytools (.tdf files). If selected coverage values are sca	aled by
(1,000,000 / totalCount), where totalCount is the total number of features of alignments.	
	OK Cancel

Alignments

Ger	neral Tracks Mutatio	ns Charts	Alignments	Probes Proxy Advan	ced IonTorrent
Visibility ran	nge threshold (kb): 30	Nom	ninal window siz	e at which alignments bec	come visible
🗹 Downsar	mple reads Max read	l count: 100	per v	vindow size (bases): 50	
Filter and sh	ading options				
Coverage	e allele-freq threshold	0.2	Mapping qua	lity threshold: 0	
🗹 Filter du	plicate reads		🗹 Show cen	ter line	
🗹 Filter ver	ndor failed reads		Show cov	erage track	
E Filter sec	condary alignments		Show soft	-clipped bases	
🗌 Filter su	pplementary alignments		🗌 Flag unm	apped pairs	
🗹 Shade mi	ismatched bases by qualit	y: 5 to	20		
🗌 Flag inse	ertions larger than:			bases	
🗌 Filter alig	gnments by read group	URL or path	to filter file		
Splice Juncti	ion Track Options				
Show jur	nction track Min flanki	na width: 0		Min junction coverage:	1
Show fla	nking regions	ly math.		init junction coverage.	1
nsert Size O	ptions	of maired align	mante huinfarre	dincert size Base nair va	luce est default
alues. If "co	ompute" is selected values	are computed fi	rom the actual s	ize distribution of each lib	orary.
Dofaults	Minimum (bp):		Compute	Minimum (porcontilo):	0.5
Defaults	Mininum (bp). 50		Compute	Minimum (percentite).	0.5
	Maximum (bp): 100	0		Maximum (percentile):	99.5

Track display options

Read Packing, grouping, sorting, colouring options.

				IGV	
Mouse mm9	chr16	035-92,701,026	Go 👚	- ►	🤣 🖪 🗙 🖵
	DP_CTCFDupMarked.bam	qB1 qB2	qB3	qB4	qB5 qC1.1
	Rename Track Copy read details to clipboard Group alignments by	92,698,000 bp			3,985 bp 92,699,000 bp I
DP CTCFDupMarked.bam	Sort alignments by	no color			
	 ✓ Shade base by quality ✓ Show mismatched bases Show all bases 	✓ read strand read group sample tag			
DP_CTCFDupMarked.bam	View as pairs Go to mate View mate region in split screen Set insert size options	bisulfite mode	•		
	Re-pack alignments ✓ Show coverage track Load coverage data	-			
	✓ Collapsed Expanded Squished	_			
	Select by name Clear selections				
	Copy read sequence Copy consensus sequence	_			
	Sashimi Plot				
	Remove Track	_			

Track display options Graph/interval files

Track colour/appearance

00								IGV					
Mouse m	1m9	*	chr16	*	chr16:92,688,	883-92,7	07,039	Go 👚	►	Ø (i x		
	DNAseDupMa	a y	ormalised.bv	qA1	qA2	qB1	qB2	qB3 92,6	qB4 96 kb	1 1 9	qB5 8 kb 2,698 kb	qC1.1	92,70
DNAseDupMark DNAseDupMark DNAseDup ised.bw	Rename T Change T Change T Change T Change F Type of Graph Heatmap ✓ Bar Chart Points Line Plot	rack rack rack rack ont S	 Color (Pos Color (Neg Height ize	<mark>itive Va</mark> gative Va	lues) alues)								
	Windowing Fu Minimum ✓ Mean Maximum None Set Data F	nction 1 Range											
	Set Bata Set Heatm Log scale ✓ Autoscale ✓ Show Dat	nap So a Ran	cale Ige										
Refseq genes	Create Ov Separate	verlay Track	Track s			Runx1	• •	• •	< (F	tunx1	• •	
	Kaplan-M Remove T	leier I rack	Plot			-							
5 tracks	Save imag	ge),340										

Graph type

000	•									10	SV				
Mous	se mm9	*	chr16	*	chr1	6:92,688,	883-92,7	707,039	Go		►	Ŵ		X	
				qA1		qA2	qB1	qB2	qB3		qB4		qB5	, —	qC1.1
	Total Tracks Sele	cted: 3	92			2,692 kb	I	92,694 kb	I	92,696 k	b	1	92,698	kb	I
DNAseDup	Rename Trac Change Trac Change Trac Change Trac Change Font	ck k Colo k Colo k Heig Size.	or (Positiv or (Negat Jht	ve Values ive Value	s) es)										
DNAseDup	Type of Graph								\sim	~~ <u> </u>			\bigvee	\searrow	$\overline{}$
DNAseDup	 ✓ Heatmap ✓ Bar Chart Points ✓ Line Plot 														
	Windowing Function Minimum ✓ Mean Maximum None	on													
	Set Data Ran Set Heatmap Log scale ✓ Autoscale ✓ Show Data R	ge Scale ange													
Refseq ge	Create Overl Separate Tra	ay Tra .cks	ck			-	Runx1	< <	• •		<	<	∢ Runx′	+	+ +
	Kaplan-Meie	r Plot.													
	Remove Trac	:ks													
5 tracks	Save image	8:92,691	,746												

Data Scaling.



Autoscaling adjusts to track's visible signal maximum



Some cool features.

IGV can display splicing information



...and Sashimi plots (http://www.broadinstitute.org/igv/Sashimi)



IGV can overlay tracks too.





IGV includes a simple toolset IGVTools

- IGVTools can be used to postprocess genomics data.
- Includes indexing, sorting and genome graph creation.





Where to get help?

- <u>http://www.broadinstitute.org/igv/UserGuide</u>
- https://groups.google.com/forum/#!forum/igv-help