




IGV可视化

基因组浏览器总结

- 本地安装UCSC基因组浏览器
- 测序数据可视化 (一)
- IGV基因组浏览器可视化高通量测序数据
- 高通量数据分析必备-基因组浏览器使用介绍 - 1
- 高通量数据分析必备-基因组浏览器使用介绍 - 2
- 高通量数据分析必备-基因组浏览器使用介绍 - 3



比对结果可视化-IGV



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Integrative Genomics Viewer



Overview



The **Integrative Genomics Viewer (IGV)** is a high-performance visualization tool for interactive exploration of large, integrated genomic datasets. It supports a wide variety of data types, including array-based and next-generation sequence data, and genomic annotations.

Funding

Downloads



Download the IGV desktop application and igvtools.

Citing IGV

To cite your use of IGV in your publication:

<http://software.broadinstitute.org/software/igv/>

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Downloads

Did you know that there is also an **IGV web application** that runs only in a web browser, does not use Java, and requires no downloads? See <https://igv.org/app>. Click on the [Help](#) link in the app for more information about using IGV-Web.

Install IGV 2.8.6

See the [Release Notes](#) for what's new in each release.



IGV Mac App

Download and unzip the Mac App Archive, then double-click the IGV application to run it. You can move the app to the *Applications* folder, or anywhere else.



IGV for Windows

Download and run the installer. An IGV shortcut will be created on the Desktop; double-click it to run the application.



IGV for Linux

Download and unzip the Archive. See the downloaded *readme.txt* for further instructions.



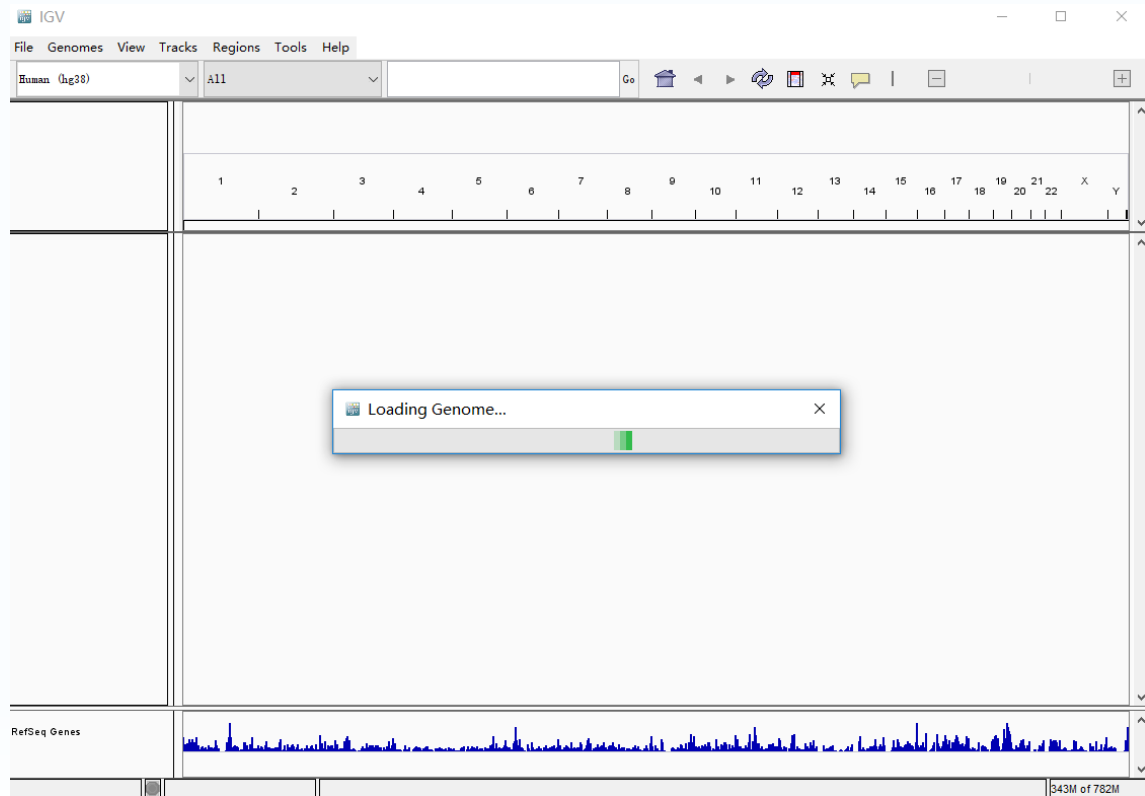
IGV and igvtools to run on the command line (all platforms)

Download and unzip the Archive. **Requires Java 11.** See the downloaded *readme.txt* and *igvtools_readme.txt* for further instructions.

基因组



启动IGV



宏基因组

信宝典

易生信

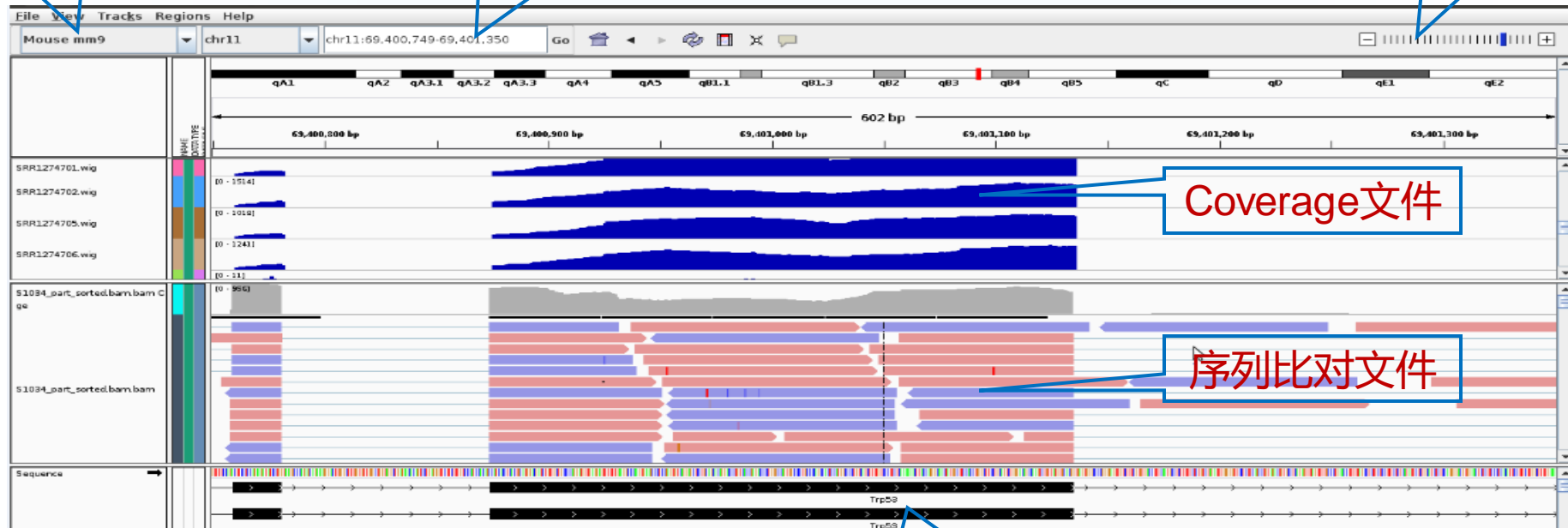
基因组文件的默认位置: C:\Users\Administrator\igv 5



基因组版本

显示区间或基因

区间缩放键

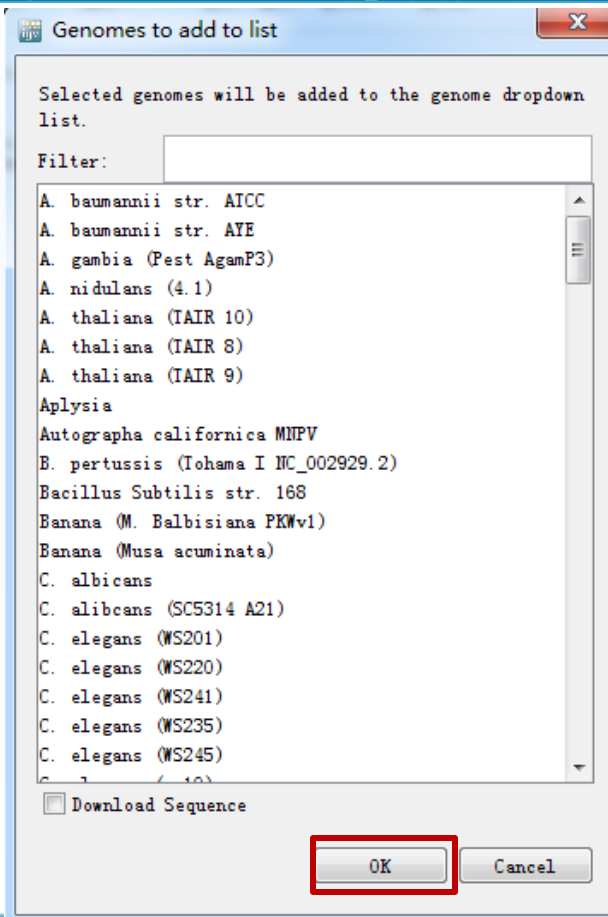
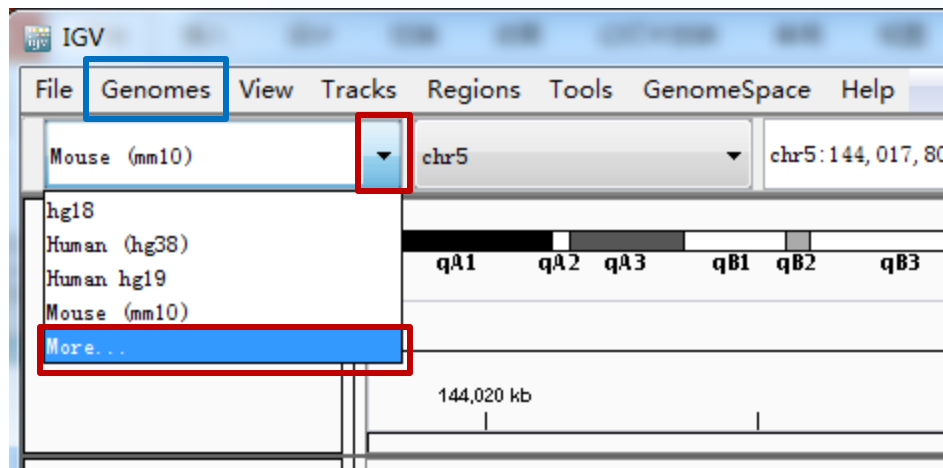


Coverage文件

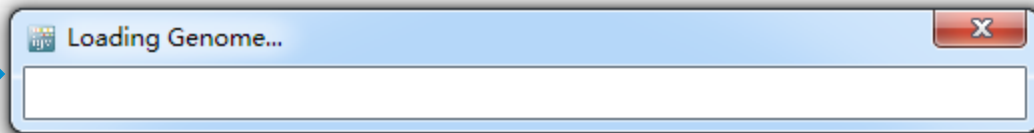
序列比对文件

剪接注释文件

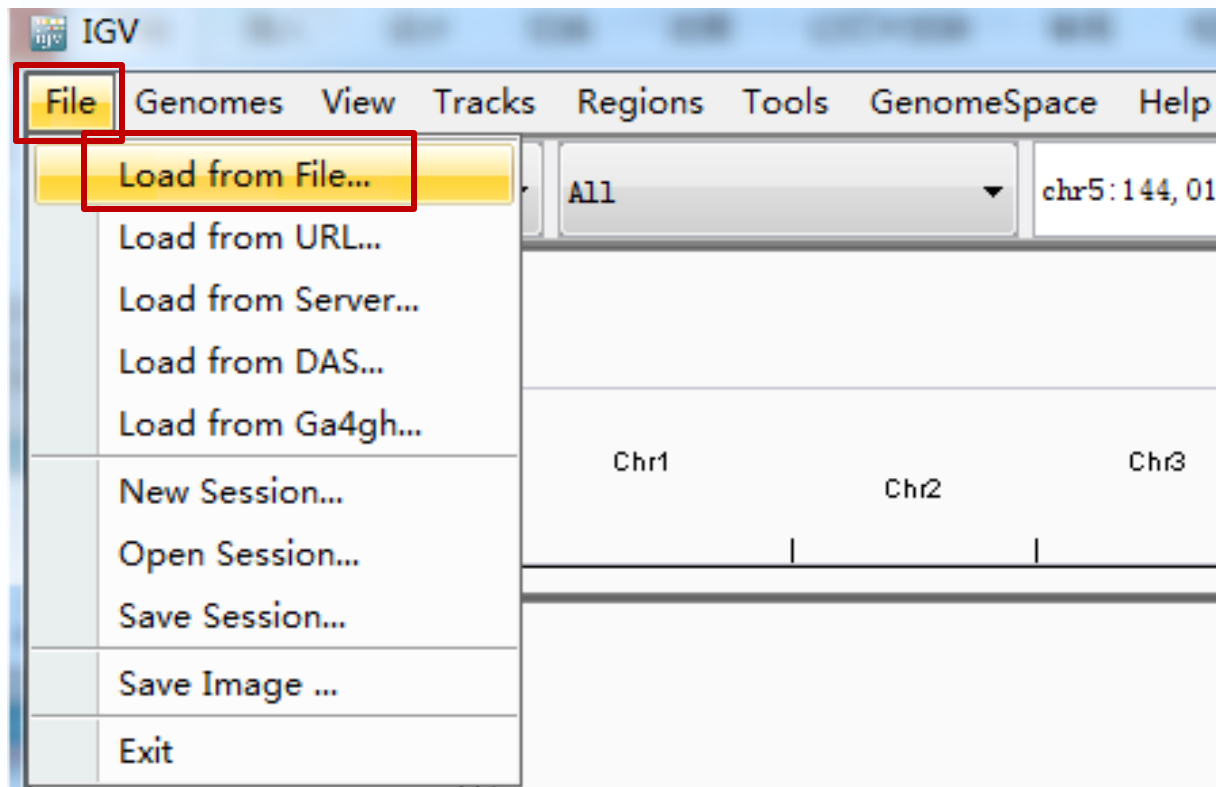
IGV使用步骤 – 加载基因组



基因组



IGV使用步骤 – 导入结果文件



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IGV推荐使用的文件格式

Source Data	File Formats
ChIP-Seq, RNA-Seq	TDF
Copy number	CN format, SNP format
Gene expression data	GCT format, RES format
Genome annotations	GFF or GFF3 format, BED format
GISTIC data	GISTIC format
LOH data	LOH format
Mutation data	MUT format
RNAi data	GCT format
Segmented data	SEG format, CBS format
Sequence alignment data	SAM format, BAM format
Any numeric data	IGV format, TAB format, WIG format

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转换为基因组浏览器可识别格式 BAM to bw/TDF

○ IGVtools

- `igvtools count sample.bam sample.tdf`
- `igvtools count sample.bam sample.tdf,sample.wig`
- `igvtools toTDF sample.norm.wig sample.norm.tdf mm10`

○ 其它工具

- RSeQC的bam2wig.py <http://dldcc-web.brc.bcm.edu/lilab/liguow/CGI/rseqc/build/html/>
- deepTools的bamCoverage <http://deeptools.readthedocs.io>

○ Wig转bigWig

- `mysql --user=genome --host=genome-mysql.cse.ucsc.edu -A -e \`
`"select chrom, size from mm10.chromInfo" > chrom.sizes`
`wigToBigWig in.wig chrom.sizes out.bw`
<http://hgdownload.cse.ucsc.edu/admin/exe/>

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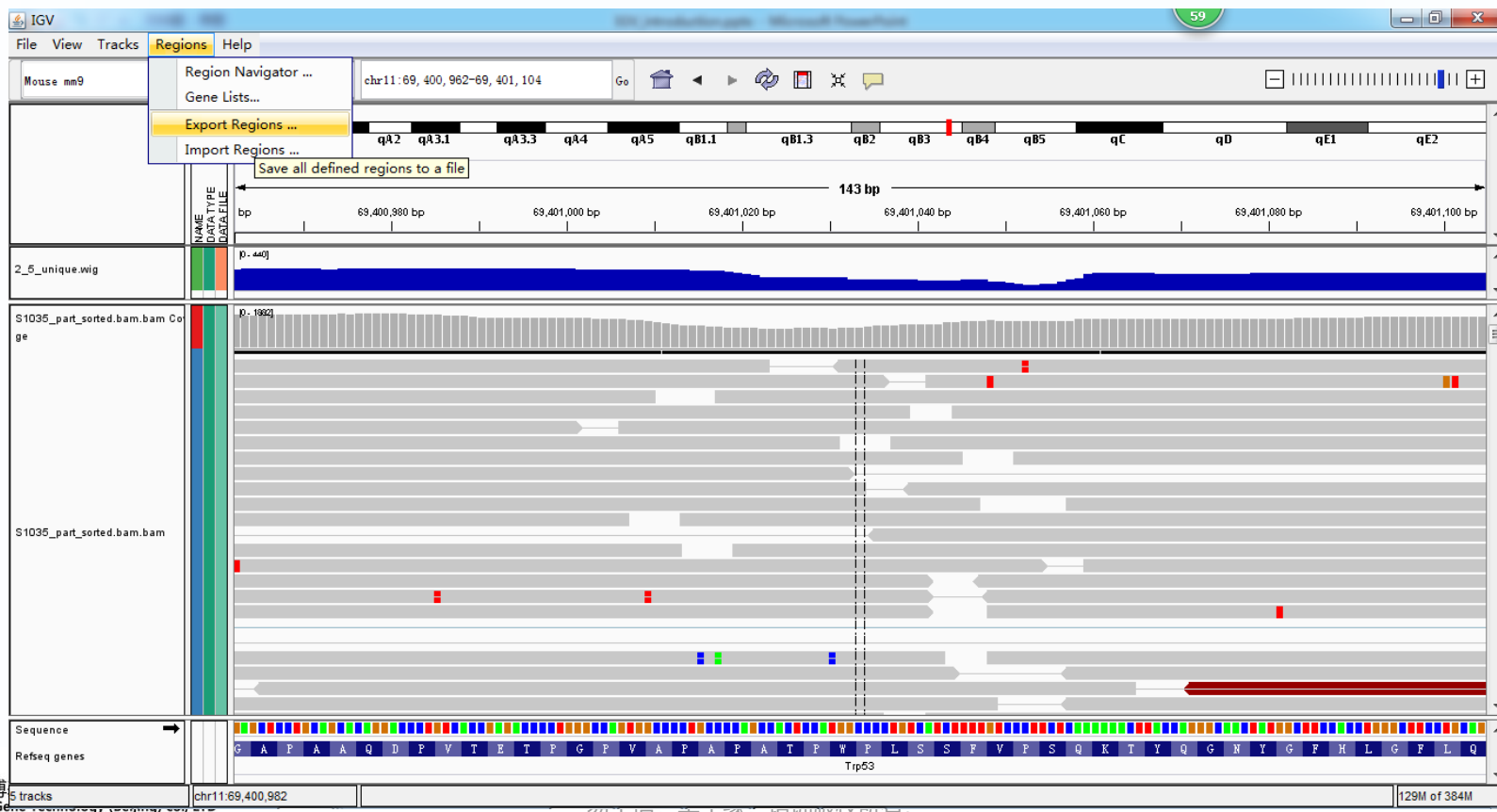
IGV使用步骤 – 更改Track颜色



云基因组



IGV使用步骤 – 输出区域序列



基因组

IGV使用步骤 – 输出区域序列

The screenshot displays the IGV (Integrative Genomics Viewer) interface. The main window shows a genomic track for chromosome 11, specifically the region chr11:69,400,962-69,401,104. The track is labeled 'chr11' and 'chr11:69,400,962-69,401,104'. The track is divided into segments labeled q41, q42, q43.1, q43.3, q44, q45, q81.1, q81.3, q82, q83, q84, q85, qC, qD, qE1, and qE2. The track is labeled 'bp' and '69,400,980 bp'. The track is labeled '2_5_unique.wig' and 'S1035_part_sorted.bam bam Co ge'. The track is labeled 'S1035_part_sorted.bam bam'. The track is labeled 'Sequence' and 'Refseq genes'. The track is labeled 'G A P A A Q D P V T E T P G P V A P A P A T P W P L S S F V P S Q K T Y Q G N Y G F H L G F L Q'. The track is labeled 'Trp53'. The track is labeled '149M of 384M'.

The 'Export Regions of Interest' dialog box is open, showing a list of files to save to. The 'Save' button is highlighted. The dialog box contains the following text:

Export Regions of Interest ...

保存: result1

list.xlsx
NewLncRNA_RIP.pptx
pheno.txt
result.txt
result_2.txt

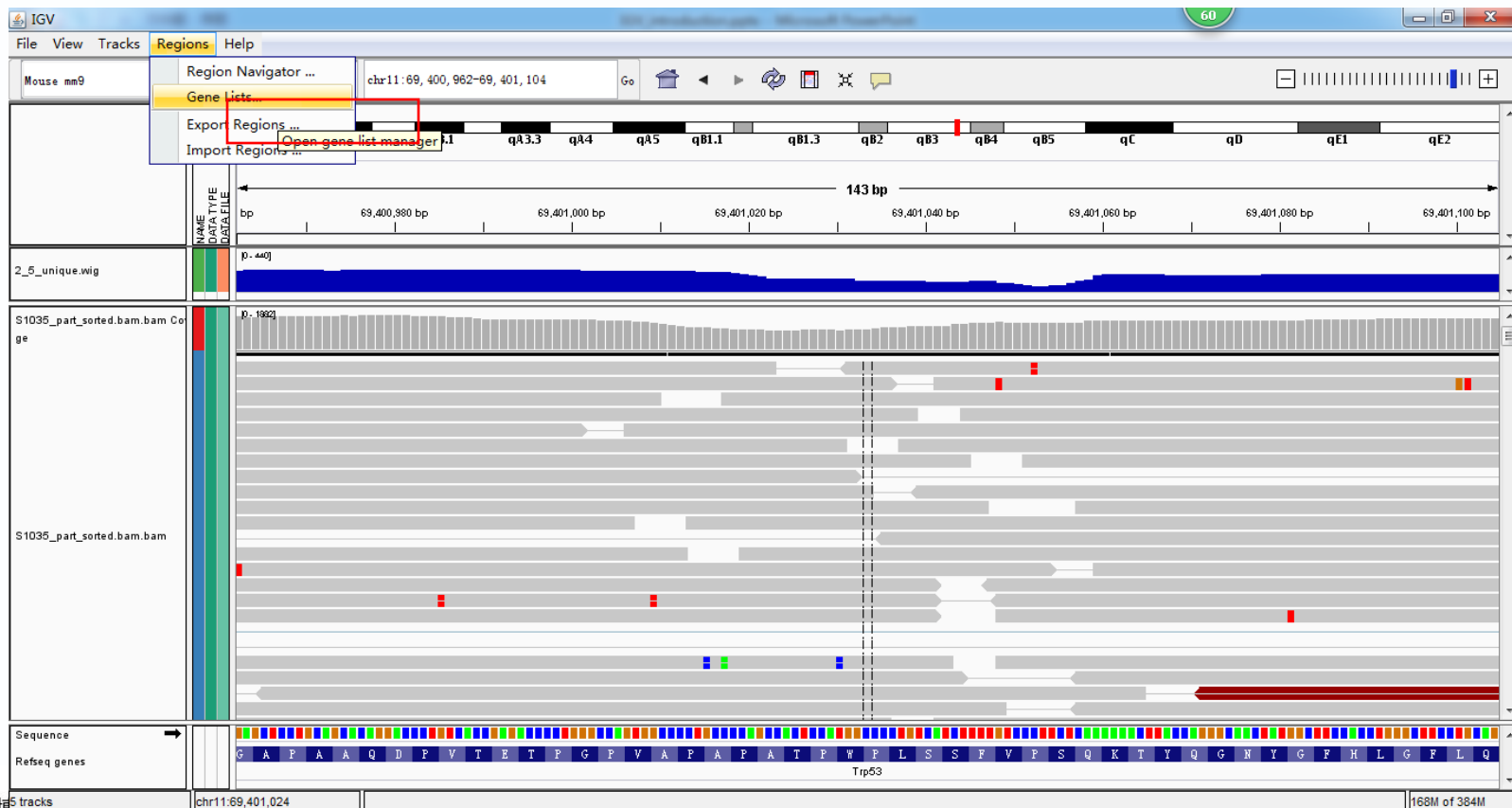
最近使用的项
桌面
我的文档
计算机

文件名: regions.bed
文件类型: 所有文件

保存
取消

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IGV使用步骤 – 多基因同时显示



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IGV使用步骤 – 多基因同时显示

IGV

File View Tracks Regions Help

Mouse mm9 chr11 chr11:69,400,962-69,401,104 Go

NAME DATA TYPE DATA FILE

2_5_unique.wig bp [0-440]

S1035_part_sorted.bam bam Co ge [0-1992]

S1035_part_sorted.bam bam

Sequence Refseq genes

chr11:69,400,967

196M of 384M

Search

Group	List	Loci
All	Proneural dev genes	SOX1
Example gene lists	Microglia markers	SOX2
Reactome canonical pathways	MMR genes	SOX3
KEGG canonical cancer pathways	PI(3)K complex	SOX21
My lists	Oligodendrocytic dev genes	DCX
	P53 signaling	DLL3
	RB signaling	ASCL1
	AKT signaling	TCF4
	RTK/RAS signaling	
	REACTOME_A_THIRD_PROTEOLYTIC_CLEAVAGE_RELEASES_MUC1	
	REACTOME_ABORTIVE_ELONGATION_OF_HIV1_TRANSCRIPT_IN	
	REACTOME_ACETYLCHOLINE_NEUROTRANSMITTER_RELEASE_CYC	
	REACTOME_ACTIVATED_AMPK_STIMULATES_FATTY_ACID_OXIDA	
	REACTOME_ACTIVATED_TAK1_MEDIATES_P38_MAPK_ACTIVATI	
	REACTOME_ACTIVATED_TLR4_SIGNALING	
	REACTOME_ACTIVATION_OF_AIR_IN_RESPONSE_TO_REPLICAT	
	REACTOME_ACTIVATION_OF_BH3_ONLY_PROTEINS	
	REACTOME_ACTIVATION_OF_CHAPERONES_BY_IRE1_ALPHA	
	REACTOME_ACTIVATION_OF_KAINATE_RECEPTORS_UPON_GLU	
	REACTOME_ACTIVATION_OF_NMDA_RECEPTOR_UPON_GUTAMAT	
	REACTOME_ACTIVATION_OF_RAC	
	REACTOME_ACTIVATION_OF_THE_AP1_FAMILY_OF_TRANSCRIP	
	REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMPLEX	

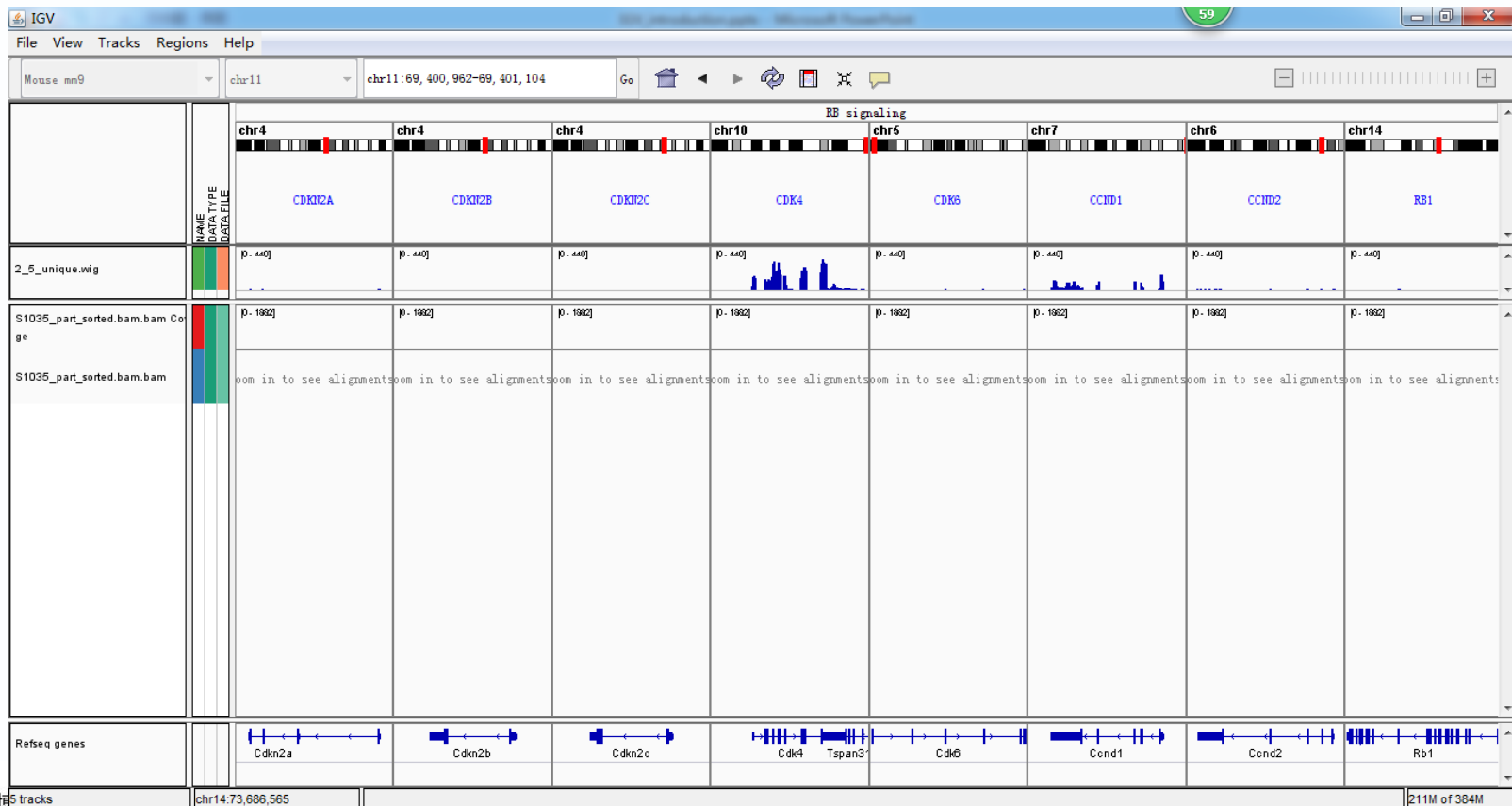
Import Export Delete New Copy Edit Delete Load Close

qE1 qE2

69,401,080 bp 69,401,100 bp

Tip53

IGV使用步骤 – 多基因同时显示



基因组

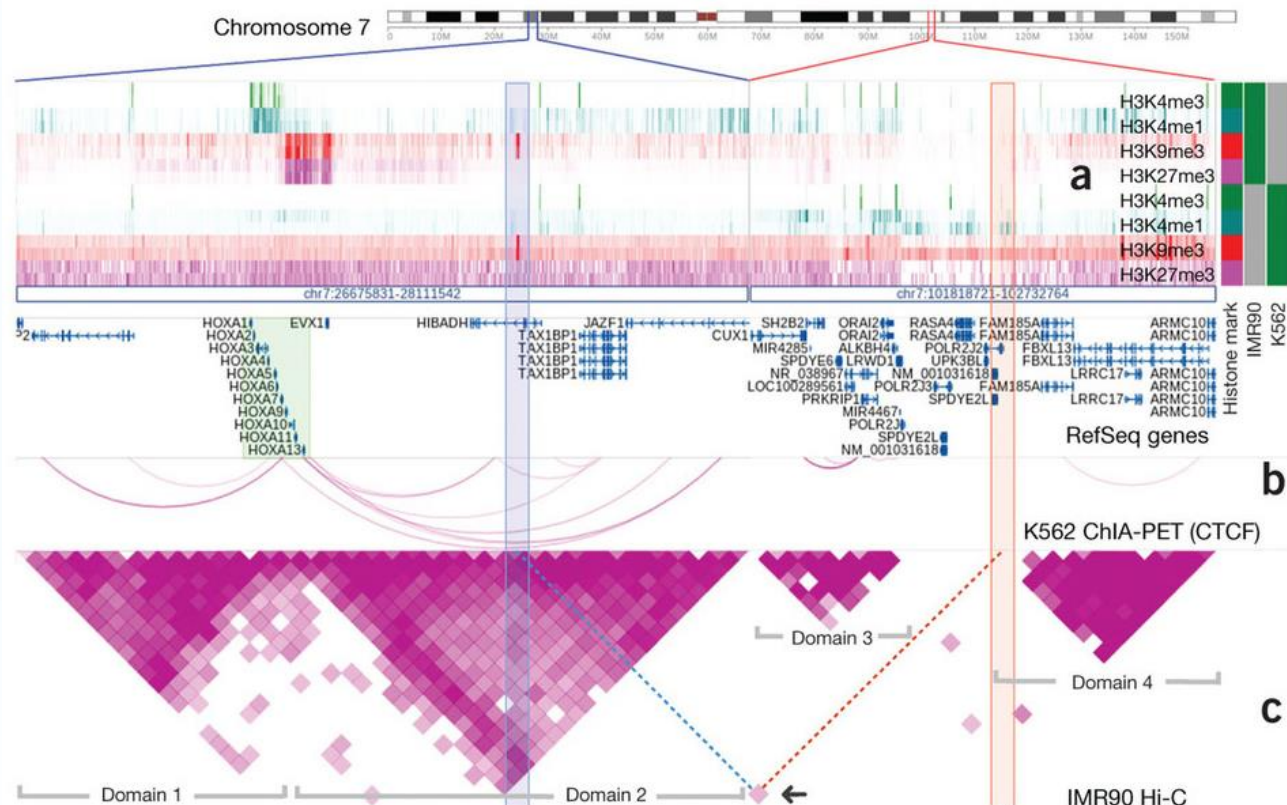
Epigenome Browser

基因表达和调控数据
(组蛋白修饰)

基因注释数据

染色体相互作用数据
(特有功能)

染色体相互作用数据
(特有功能)



Sequencing costs a lot and gains more



长按关注 生信宝典，简单入门，快速晋级



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