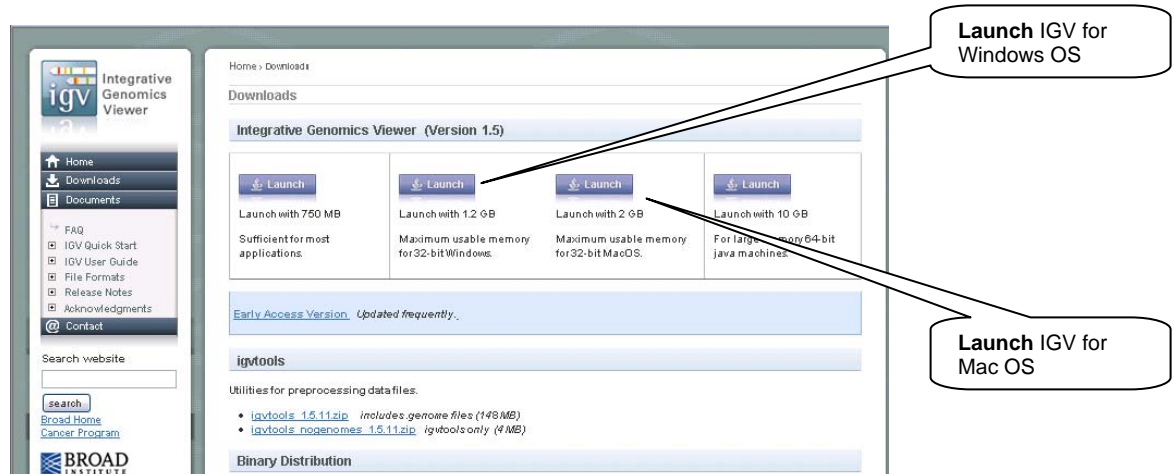


Steps for Integrative Genomics Viewer (IGV) setup and visualization

1. Go to the IGV home page at <http://www.broadinstitute.org/software/igv/home>
2. To download the IGV application, a one-time free registration can be done at <http://www.broadinstitute.org/software/igv/?q=registration>
3. For users with an IGV account, click on the **Downloads** tab from the home page and enter your email address. Logging in will take you to the download page.



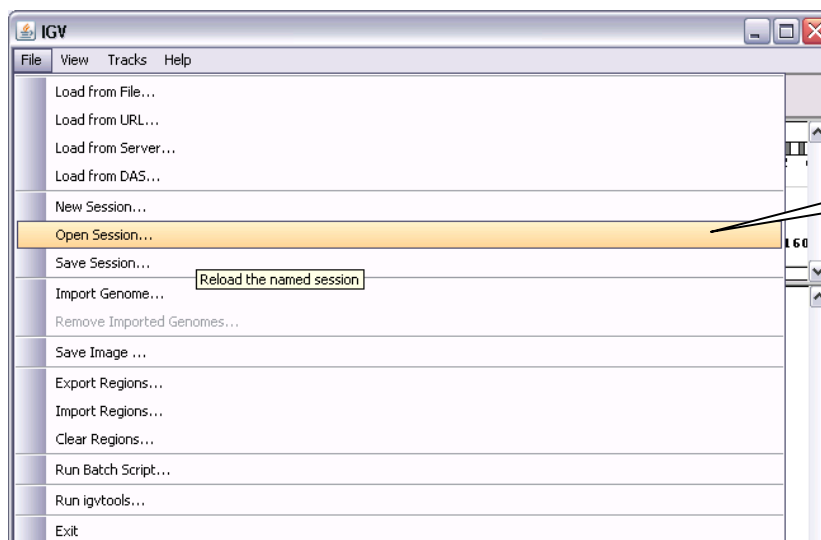
4. Based on your operating system (OS), click on the **Launch** button for 32-bit Windows or 32-bit Mac. This will launch IGV and a short-cut to your desktop will also be created.



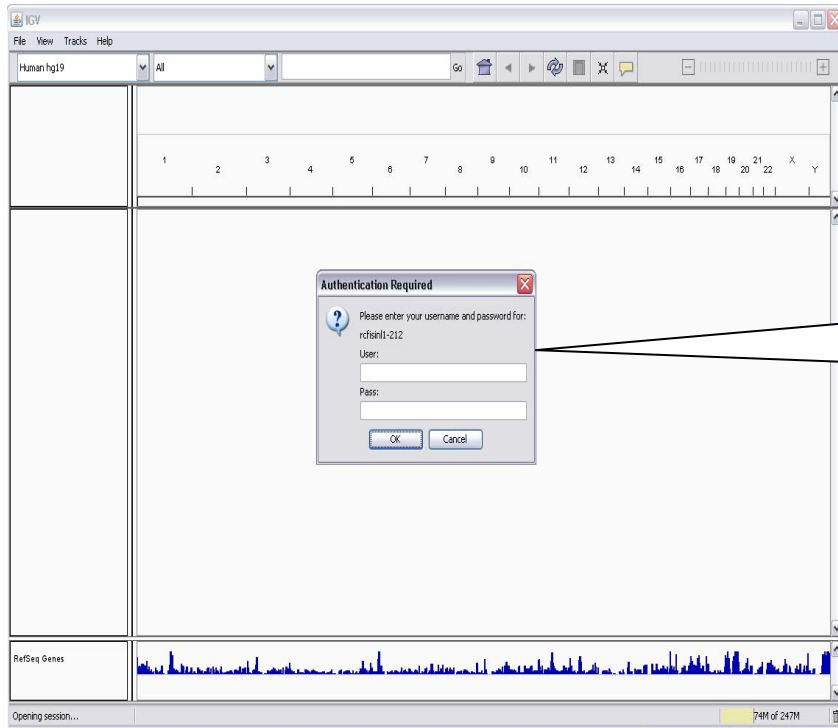


IGV home page

5. Click on **File → Open Session...** and point it to the 'igv_session.xml' file downloaded to your desktop from the BIC delivery folder. This step will load your alignment data and annotation files. Tracks for each sample comprise of the alignment of reads as well as coverage of the location where the reads align.

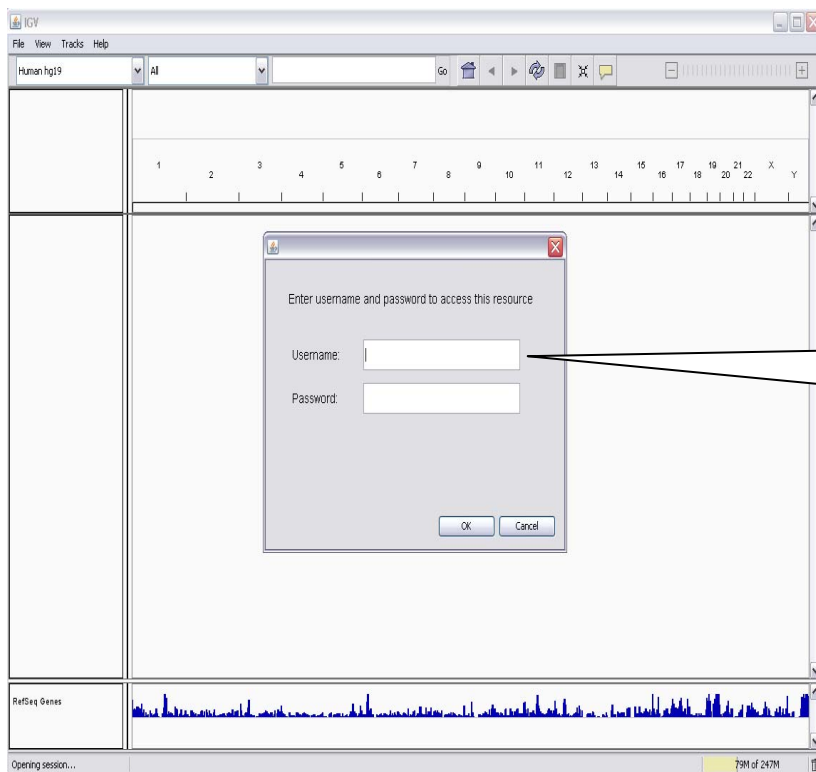


File → Open Session...



First layer of security
Please fill in as follows:-

User: **mfad\your Mayo LANID**
Pass: your password



Second layer of security
Please fill in as follows:-

User: **your Mayo LANID**
Pass: your password

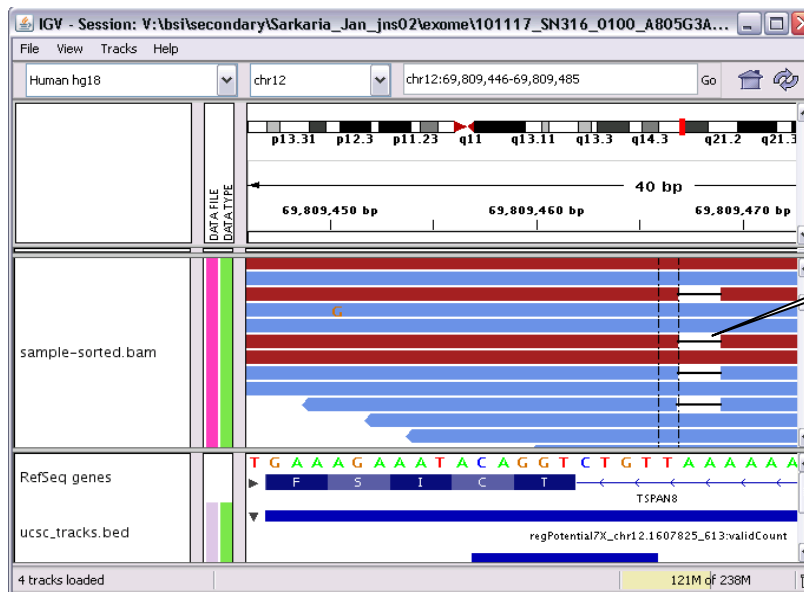
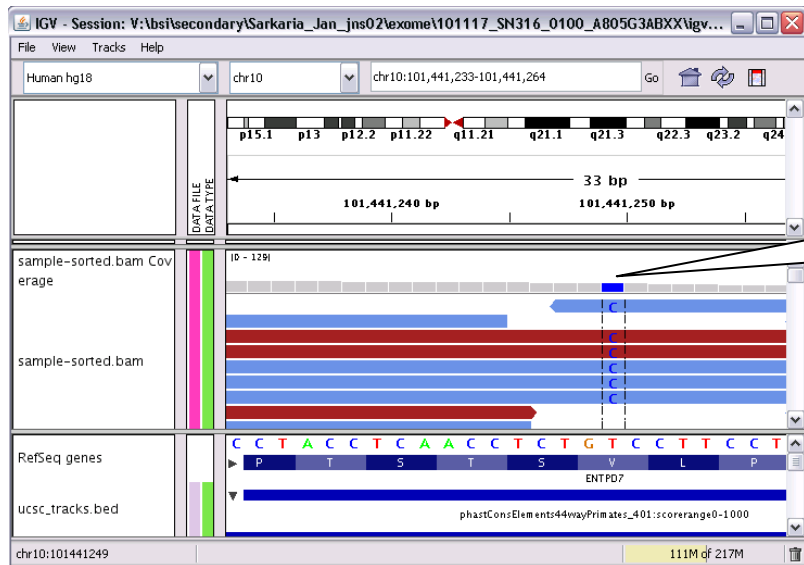


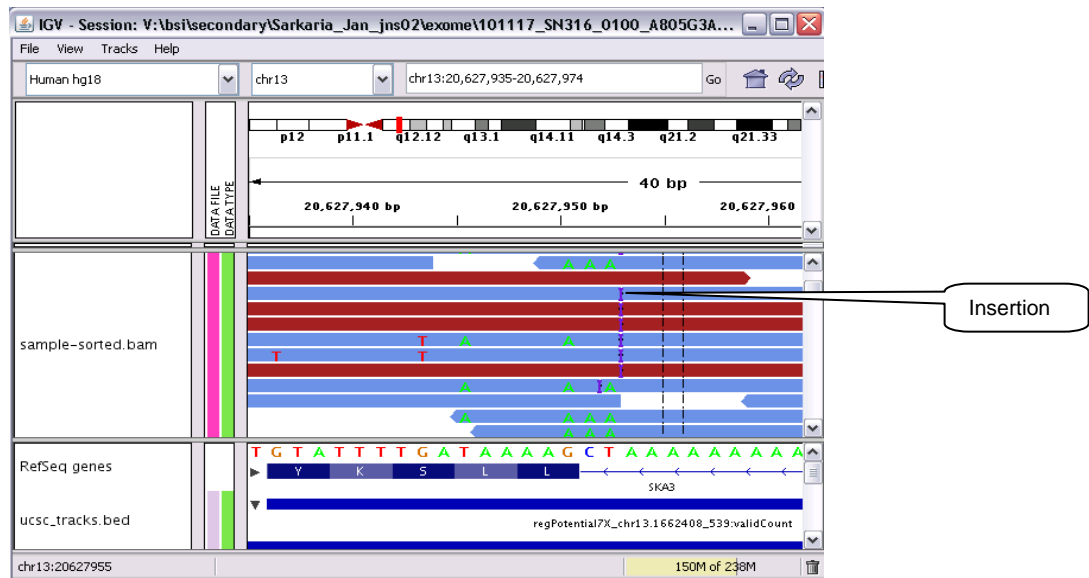
- Open the SNV report or INDEL report (works for both standard and filtered reports) and click on any link in the first column 'IGV link' of the report. IGV will pop up for that specific position where a SNV or INDEL was reported.

IGV link in SNV report

A1	A	B	C	D	E	F	G
1	IGV Link	Chr	Pos	dbSNP130	HapMap_C1	genome	HapMap
2	chr10:100007443	chr10	1E+08	rs1983864	G/T,0.300/	G/T,0.275/	G/T,0.058
3	chr10:100007443	chr10	1E+08	rs1983864	G/T,0.300/	G/T,0.275/	G/T,0.058
4	chr10:100192977	chr10	1E+08	rs5854833	-	G/A,0.008/-	-
5	chr10:100192977	chr10	1E+08	rs5854833	-	G/A,0.008/-	-
6	chr10:100192977	chr10	1E+08	rs5854833	-	G/A,0.008/-	-
7	chr10:100192977	chr10	1E+08	rs5854833	-	G/A,0.008/-	-
8	chr10:100192977	chr10	1E+08	rs5854833	-	G/A,0.008/-	-
9	chr10:100209364	chr10	1E+08	rs1088310	A/T,0.475/A/T,0.475	A/T,0.383	-
10	chr10:100209364	chr10	1E+08	rs1088310	A/T,0.475/A/T,0.475	A/T,0.383	-
11	chr10:101137682	chr10	1.01E+08	rs2298316	A/G,0.100/A/G,0.067	A/G,0.100	-
12	chr10:101441249	chr10	1.01E+08	rs1119024	C/T,0.367/A/C/T,0.325	A/C/T,0.142	-
13	chr10:101441249	chr10	1.01E+08	rs1119024	C/T,0.367/A/C/T,0.325	A/C/T,0.142	-
14	chr10:101534437	chr10	1.02E+08	rs927344	A/T,0.100/A/T,0.025	A/T,0.033	-
15	chr10:101534437	chr10	1.02E+08	rs927344	A/T,0.100/A/T,0.025	A/T,0.033	-
16	chr10:101553805	chr10	1.02E+08	rs2273697	A/G,0.233/A/G,0.267	A/G,0.21	-
17	chr10:101553805	chr10	1.02E+08	rs2273697	A/G,0.233/A/G,0.267	A/G,0.21	-

- Notice that SNVs at any given position follow the color coding of nucleotides A, C, G & T as seen along the RefSeq genes track. Deletions are represented by dashes while Insertions with the letter **I**.





8. More instructions on how to use IGV can be found at their user guide:
<http://www.broadinstitute.org/software/igv/UserGuide>