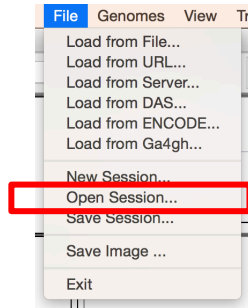# Introduction to the Integrative Genomics Viewer (IGV)

Hands-on exercise: Viewing variants (VCF file)

1. Load data

Click *File > **Open Session***

Then navigate to the downloaded
IGV workshop folder **/ Data / vcf**
and open ***vcf_session.xml***

File | Genomes | View | Tra
Load from File...
Load from URL...
Load from Server...
Load from DAS...
Load from ENCODE...
Load from Ga4gh...
New Session...
Open Session...
Save Session...
Save Image ...
Exit

2. Observe the different data panels

Hover over the **variant sites** and the **genotypes** to see the details.
(If you changed the popup behavior with the 💬 tool, you may have to *click* to see the details)

Observe how the same values in the **sample information** panel are assigned the same color. Try clicking on the sample information column headers to sort by attribute.
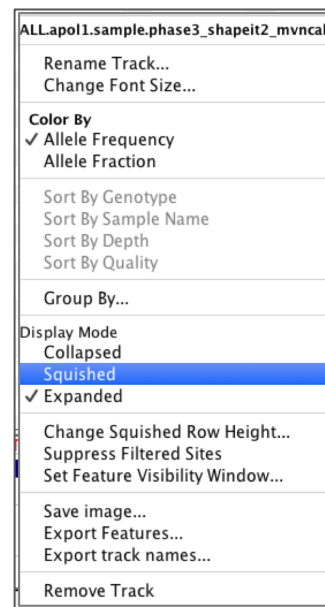
Sample info column headers

Variant sites

Sample information
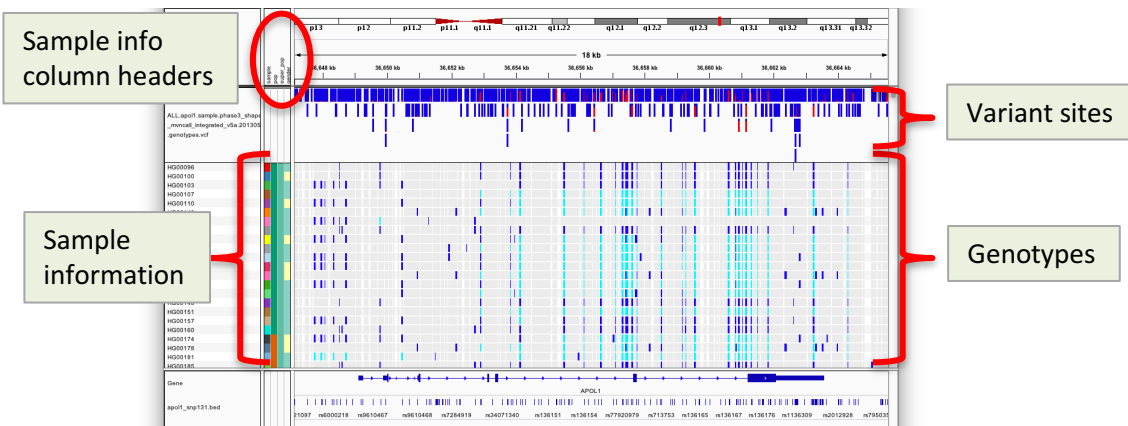
Genotypes

3. Highlight interesting event in gene APOL1

− Type APOL1:S342G in the search box and click ***Go***

APOL1: S342G   Go 🏠 ◄ ► ⟳ ▣ ✕ 💬

− Right-click over genotypes and
select ***Display Mode: Squished***

ALL.apol1.sample.phase3_shapeit2_mvncal
Rename Track...
Change Font Size...

Color By
✓ Allele Frequency
Allele Fraction

Sort By Genotype
Sort By Sample Name
Sort By Depth
Sort By Quality

Group By...

Display Mode
Collapsed
Squished
✓ Expanded

Change Squished Row Height...
Suppress Filtered Sites
Set Feature Visibility Window...

Save image...
Export Features...
Export track names...

Remove Track

3. (continued) Highlight interesting event in gene APOL1

– Right-click over genotypes and select *Group By,* then select attribute **super_pop**.
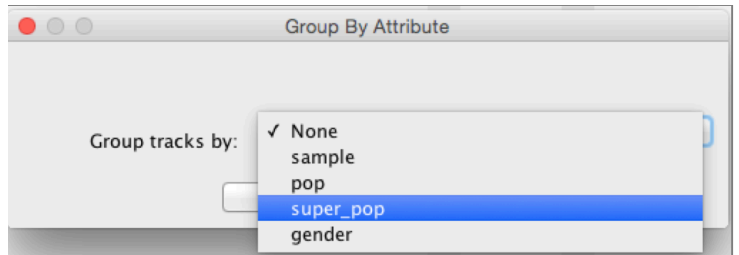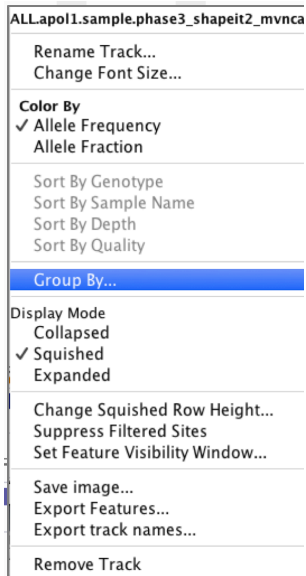
4. Observe differences between groups

Use the scrollbar to scroll down and see all the groups.

Note that the variants at this locus are not present in some population groups and prevalent in others.