ITCR grant:
The Integrative Genomics Viewer (IGV): Visualization Supporting Cancer Research
PI: Jill P. Mesirov, UC San Diego

Collaborative Set-Aside Project
with Karchin Lab, Johns Hopkins University

ITCR PI Meeting, April 7 2017
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Integrative Genomics Viewer (IGV)

> Provides visual exploration of genomic data.
> Frequently used for visual inspection of data underlying putative variants called by computational methods.
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> Frequently used for visual inspection of data underlying putative variants called by computational methods.

Goal of our collaborative set-aside project:
Provide IGV users with tools to help assess the functional significance of somatic mutations and germline polymorphisms they view in IGV.
Cancer-related Annotation of Variants Toolkit (CRAVAT)

Provides predictive scores for germline variants, somatic mutations and relative gene importance, as well as annotations from published literature and databases.

Mutation Position Imaging Toolkit (MuPIT)

Maps SNVs from genomic coordinates onto protein structures and provides an interactive visualization tool.
Direct links from IGV to CRAVAT

1. Click on a variant in IGV track (.bam, .vcf, .maf tracks) ➔ Open window with CRAVAT annotations

2. Click on a variant in IGV track (.bam, .vcf, .maf tracks) ➔ Launch CRAVAT analysis
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User enters CRAVAT analysis options
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User enters CRAVAT analysis options
Direct links from IGV to MuPIT

1. Click on a **variant** in IGV track (.bam, .vcf, .maf tracks) ➔ View **variant** in MuPIT 3D protein structure viewer

2. Click **anywhere** in any IGV data track ➔ View **locus** in MuPIT 3D protein structure viewer

3. Click on **exon** in IGV gene annotation track ➔ View **gene** in MuPIT 3D protein structure viewer
Direct links from IGV to MuPIT

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2. Click **anywhere** in any IGV track → View **locus** in MuPIT 3D protein structure viewer

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IGV Desktop and igv.js