JBrowse ITCR 2020

JavaScript cancer genome browser
This talk has a webpage

[jbrowse.org/demos/itcr2020/]
Studying structural variants with JBrowse 1

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<td>Translocation</td>
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<td>-</td>
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</tr>
</tbody>
</table>

Perumal et al, 2020

Brassica nigra

Perumal et al, 2020

jbrowse.org/demos/itcr2020/
JBrowse 2 features

• General features
  • Modern web: React, web workers, npm modularity, TypeScript
  • Synteny views; protein integration
  • Web-based administration

• Cancer-motivated features
  • Whole-genome Circos style overviews
  • Split views of breakpoints combining evidence and features
  • Data adapters for GDC portal GraphQL API

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GDC GraphQL API

GraphQL GDC API track colored by variant score

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Breakpoint view showing inter-chromosomal connections (NGMLR mapping) plus translocation TRA variant call given by Sniffles variant caller

[jbrowse.org/demos/itcr2020/](jbrowse.org/demos/itcr2020/)
Synteny views

[jbrowse.org/demos/itcr2020/](http://jbrowse.org/demos/itcr2020/)

Long read vs reference

Duplication
Multiple breakpoint overviews

Tabular and circular views (translocations called by Sniffles on SKBR3 breast cancer cell line)

Long read vs ref in feature browser

Long read vs reference in dotplot

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Insight into complex events

A complex set of breakpoints. The view is chaotic, but shows the genomic origin of an amplification (30x → 900x coverage)

Synteny plot matching gene markers and larger blocks (this dataset is two plant genomes but could e.g. be tumor vs reference)

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Features inspired by* IGV

*shamelessly borrowed from

Show soft-clipped bases

Sort by base pair

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JBrowse roadmap

- July 2020: Beta versions of JBrowse web & JBrowse embedded
- Jan 2021: Polished version of JBrowse web
- Mid-2021: Polished version of JBrowse SV inspector

jbrowse.org/demos/itcr2020/
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JBrowse core team

Lincoln Stein  Scott Cain  Robin Haw  Andrew Duncan  Ian Holmes

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