

Pangenome data aggregation using genome graphs

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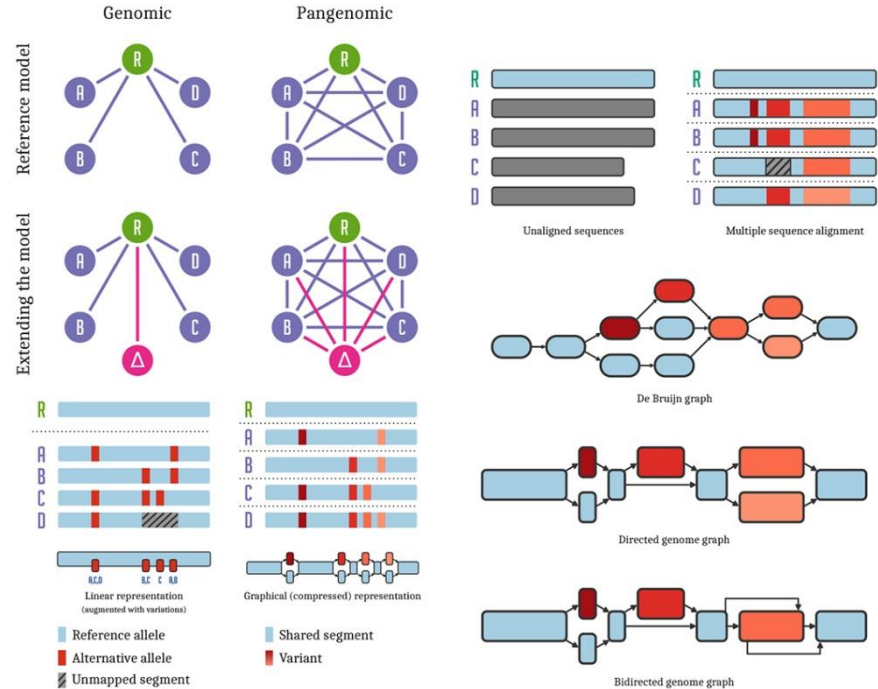


Outline

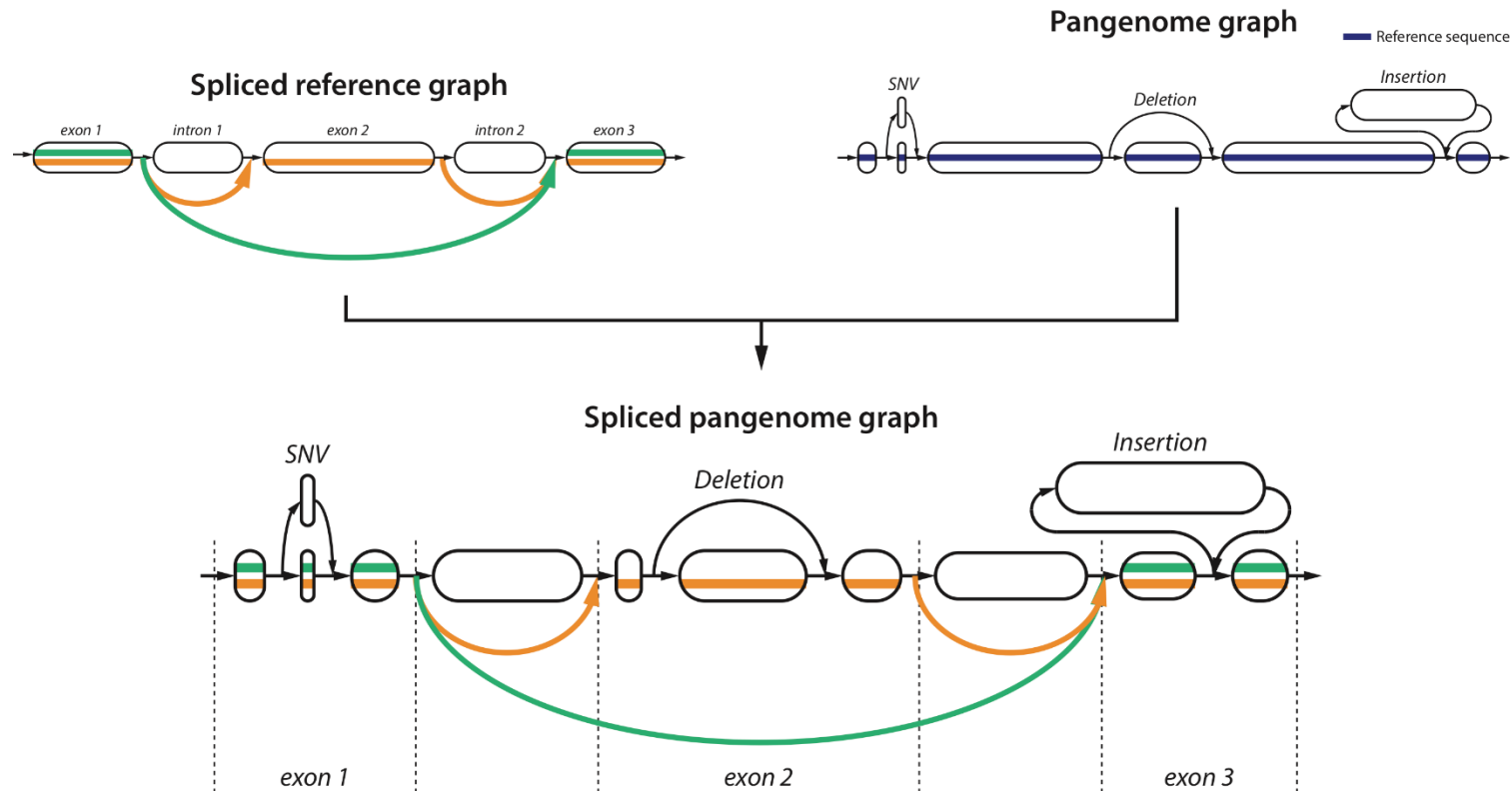
- Pangenome graphs: a genome aggregation approach
- Splice Pangenome graphs: aggregating genomes and transcriptomes
- PAV analysis and visualization
- Pretzel multi-dimensional genome browser

Pangenome graphs: a genome aggregation approach

Pangenome graphs can be used to construct and visualise a compact representation of global diversity within a species, where nodes represent agreement in sequence and edges in the graph represent sequence divergence

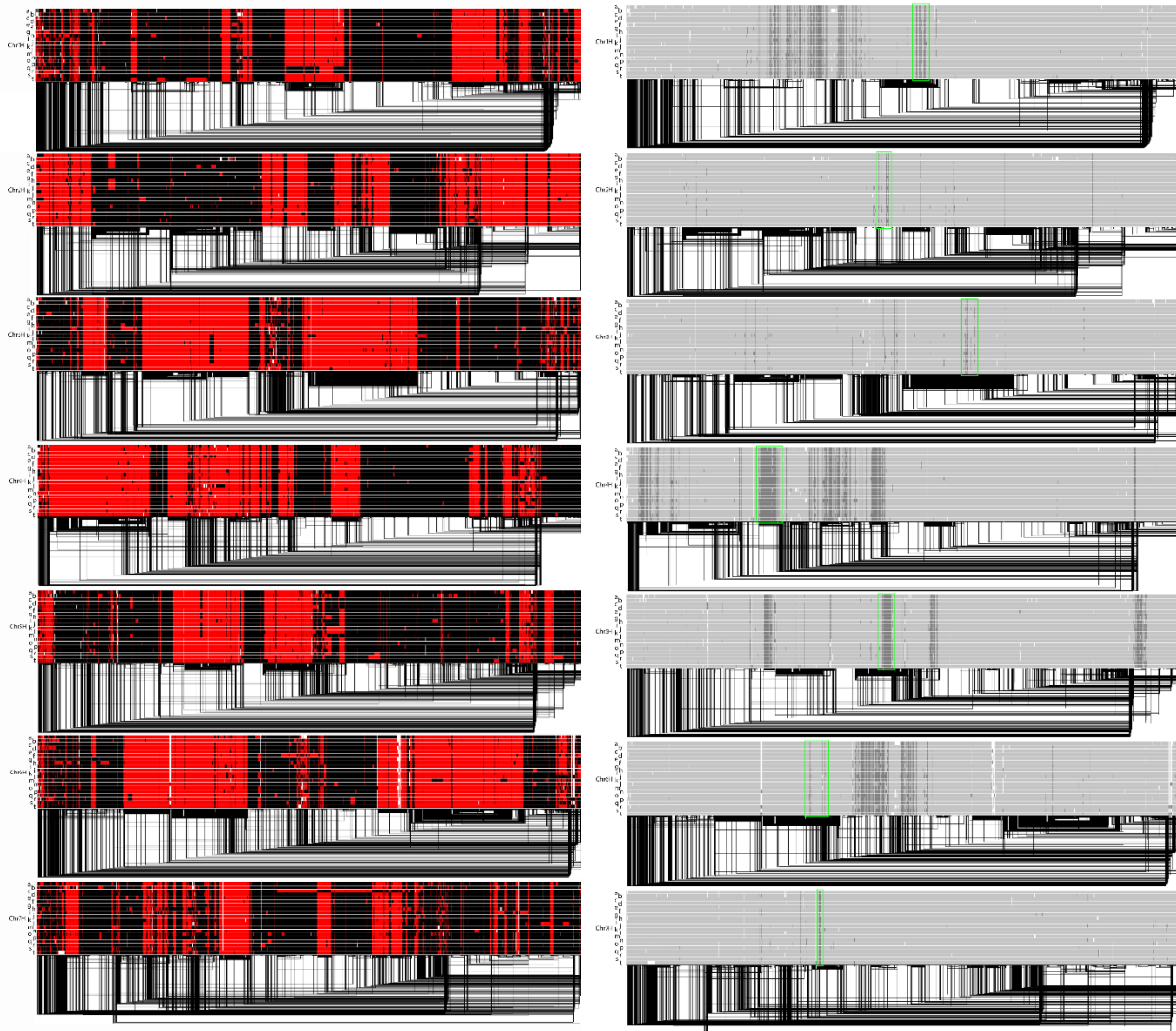


Splice Pangenome graphs: aggregating genomes and transcriptomes



Pangenome graphs

- Visualisation of each chromosome displays global variation from inversions (red blocks) (left image) and node depth showing regions of complexity (right image). Topology of the graph where SV/SNP/INDEL located (black loops/lines)



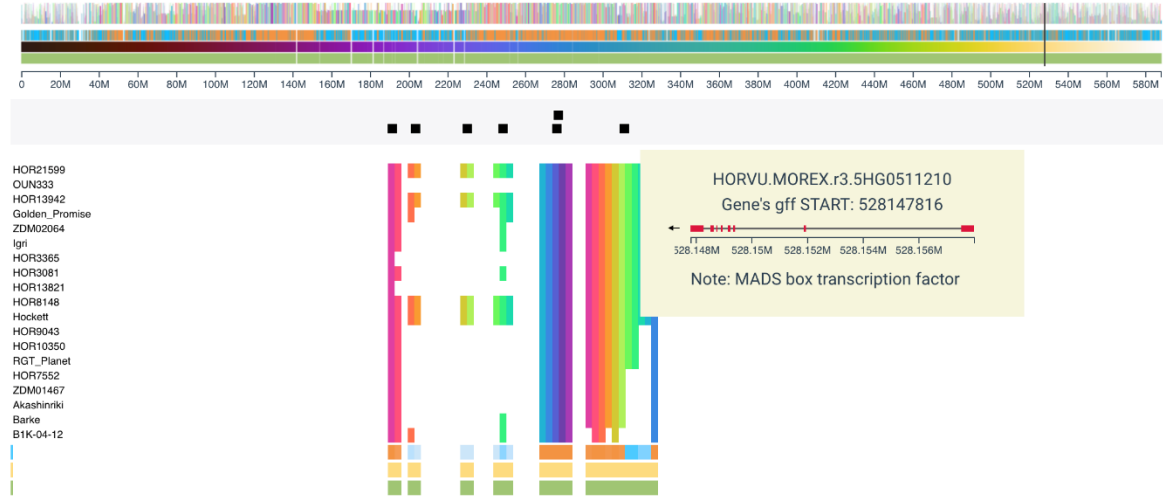
PAV analysis and visualisation

Barley Panache

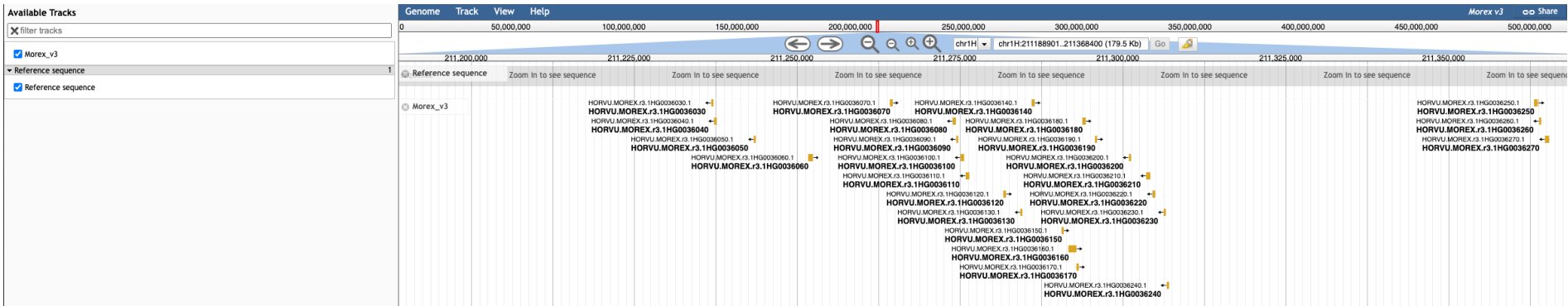
- Linearised pangenome graph with Morex as reference
- PAV binary matrix
- Morex v3 genome annotations

Use case with VRN1:

Involved in the flowering pathway

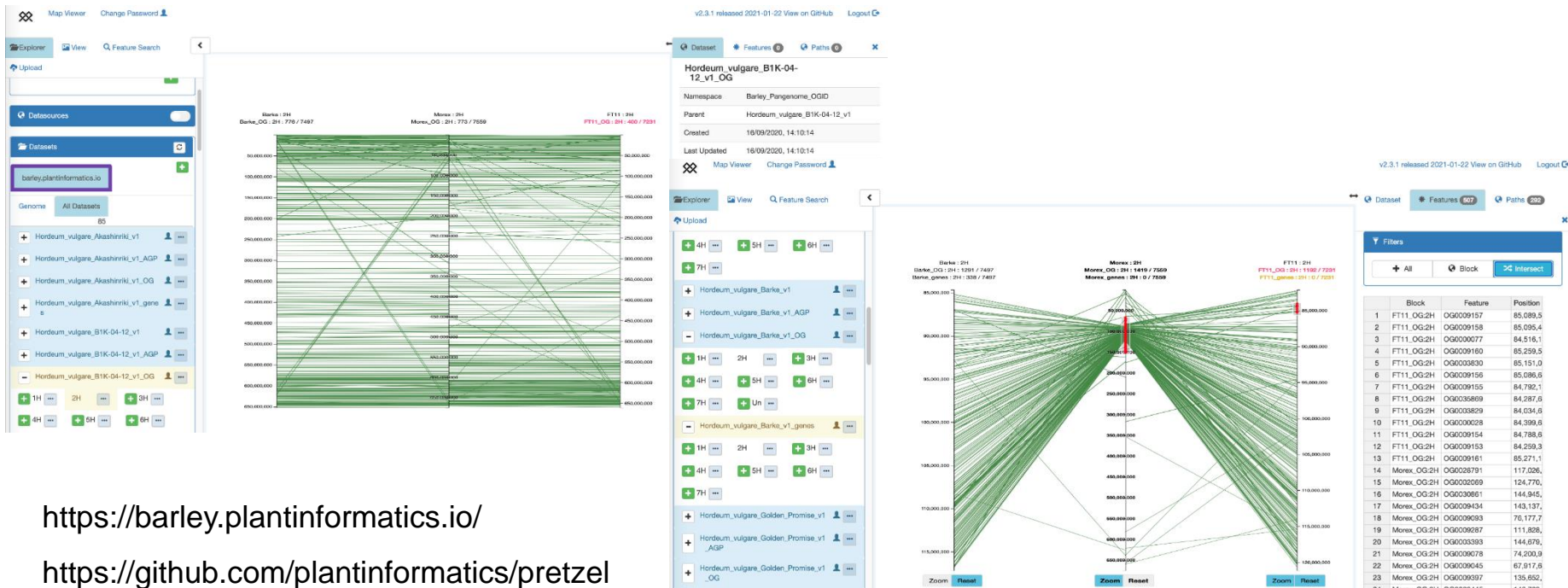


JBrowse linear genome browser



- **Genome browser for each of the 20 accessions with gene and variant call tracks**
- **To be periodically updated with new genomes and tracks**

Pretzel multi-dimensional genome browser

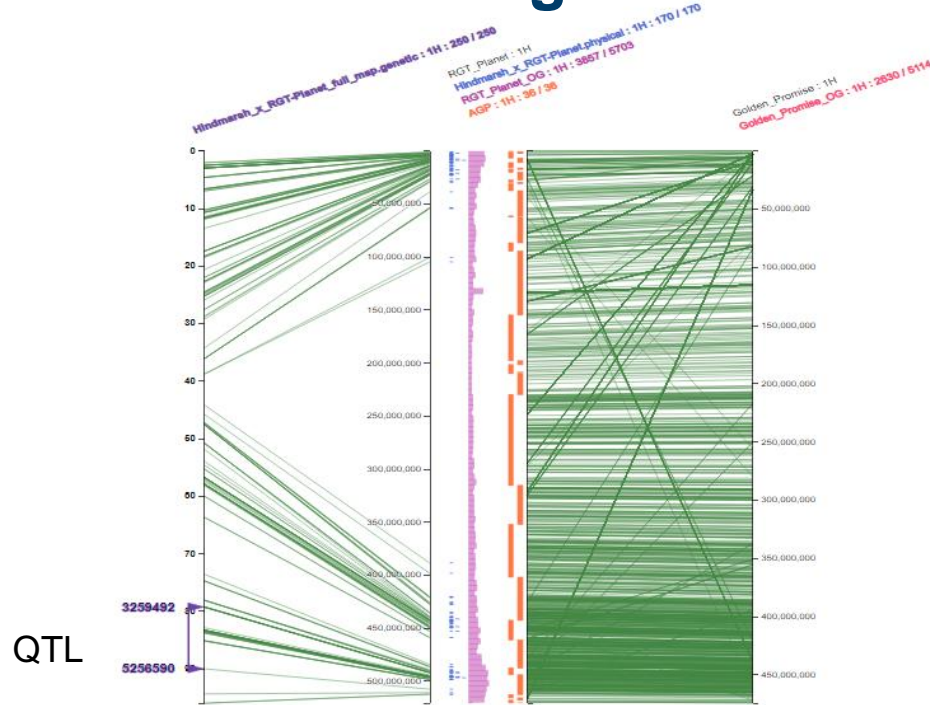


<https://barley.plantinformatics.io/>

<https://github.com/plantinformatics/pretzel>

Pretzel multi-dimensional genome browser

Chromosome-
scale



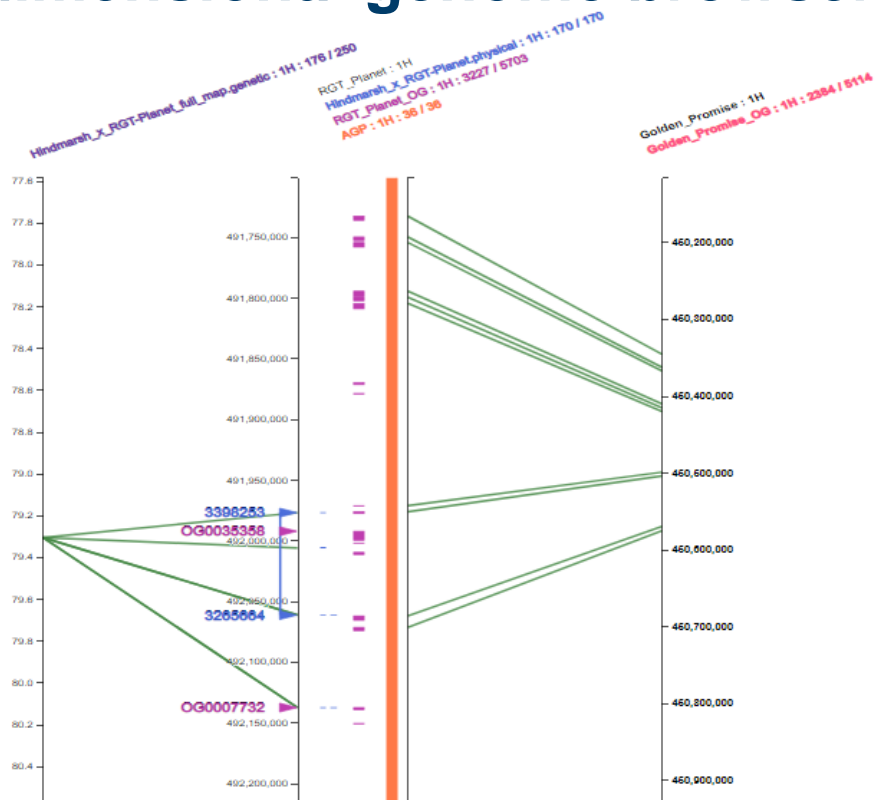
Genetic map – Genome

Genome - Genome

Genetic markers
Ortholog groups (OGs)
AGP structure
Paths between
markers/OGs

Pretzel multi-dimensional genome browser

Megabase-scale

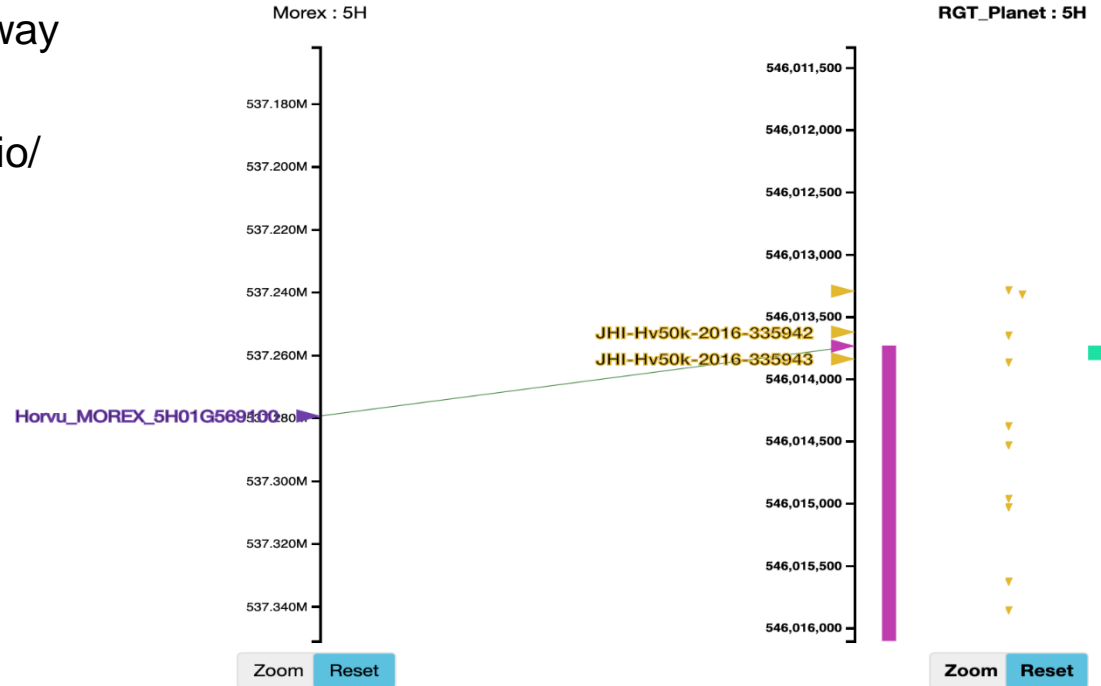


Pretzel multi-dimensional genome browser

Use case with VRN1:

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Acknowledgements

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Thank you!

Questions?

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