



JCVI: A versatile toolkit for comparative genomics analysis

Haibao Tang¹, Vivek Krishnakumar², Xiaofei Zeng³, Zhougeng Xu⁴, Adam Taranto⁵, Johnathan S. Lomas⁶,
Yixing Zhang¹, Yumin Huang¹, Yibin Wang³, Won Cheol Yim⁶, Jisen Zhang⁷, Xingtang Zhang³

¹Fujian Provincial Key Laboratory of Haixia Applied Plant Systems Biology, Haixia Institute of Science and Technology and College of Life Sciences, Fujian Agriculture and Forestry University, Fuzhou, Fujian, China

²J. Craig Venter Institute, Rockville, Maryland, USA

³National Key Laboratory for Tropical Crop Breeding, Shenzhen Branch, Guangdong Laboratory for Lingnan Modern Agriculture, Genome Analysis Laboratory of the Ministry of Agriculture, Agricultural Genomics Institute at Shenzhen, Chinese Academy of Agricultural Sciences, Shenzhen, Guangdong, China

⁴National Key Laboratory of Plant Molecular Genetics (NKLPMG), CAS Center for Excellence in Molecular Plant Sciences (CEMPS), Institute of Plant Physiology and Ecology (SIPPE), Chinese Academy of Sciences (CAS), Shanghai, China

⁵School of BioSciences, The University of Melbourne, Melbourne, Victoria, Australia

⁶Department of Biochemistry and Molecular Biology, University of Nevada, Reno, Nevada, USA

⁷State Key Lab for Conservation and Utilization of Subtropical Agro-Biological Resources, Guangxi Key Lab for Sugarcane Biology, Guangxi University, Nanning, Guangxi, China



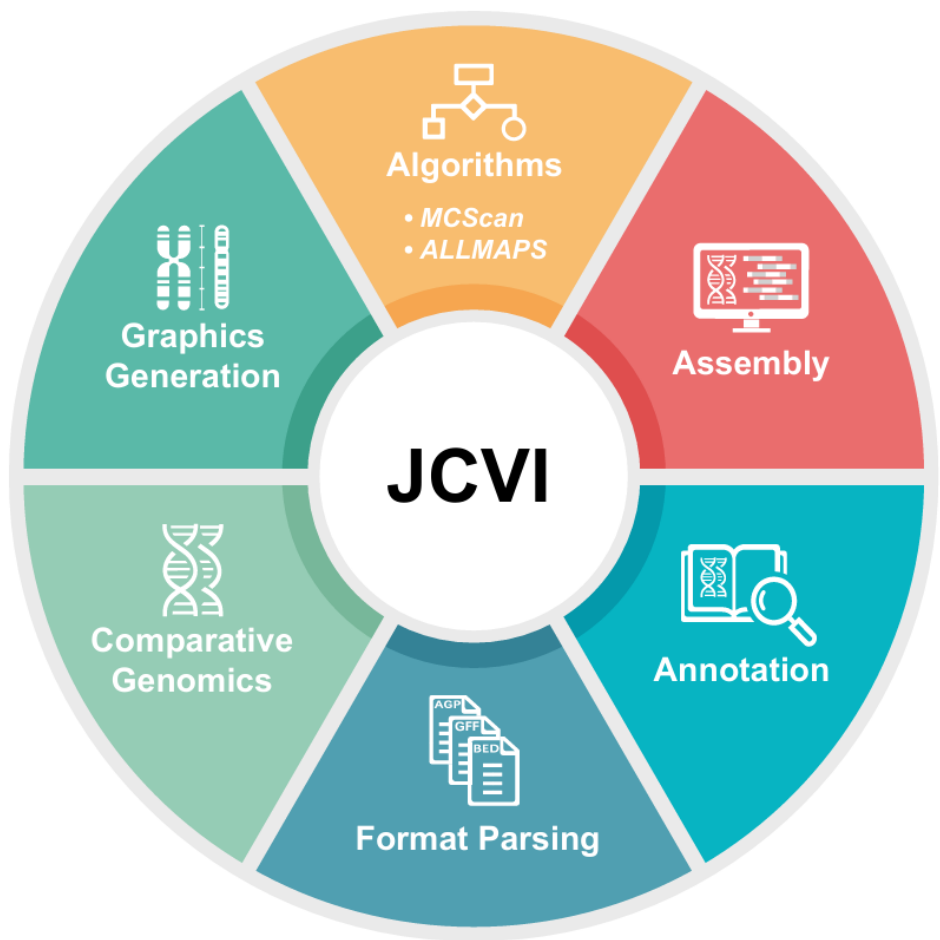
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Introduction

JCVI: The integrated suite of tools



module

- algorithms
- apps
- formats
- graphics
- utils
- assembly
- annotation
- compara

visualization

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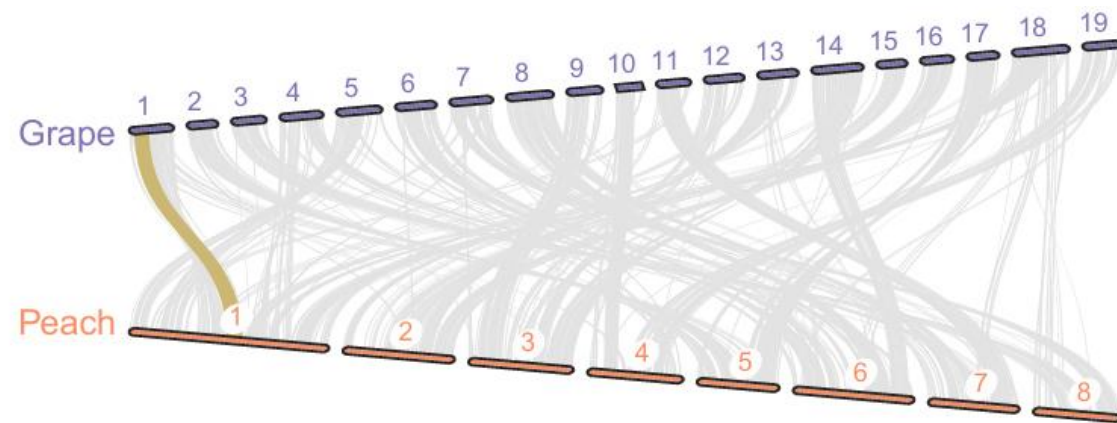
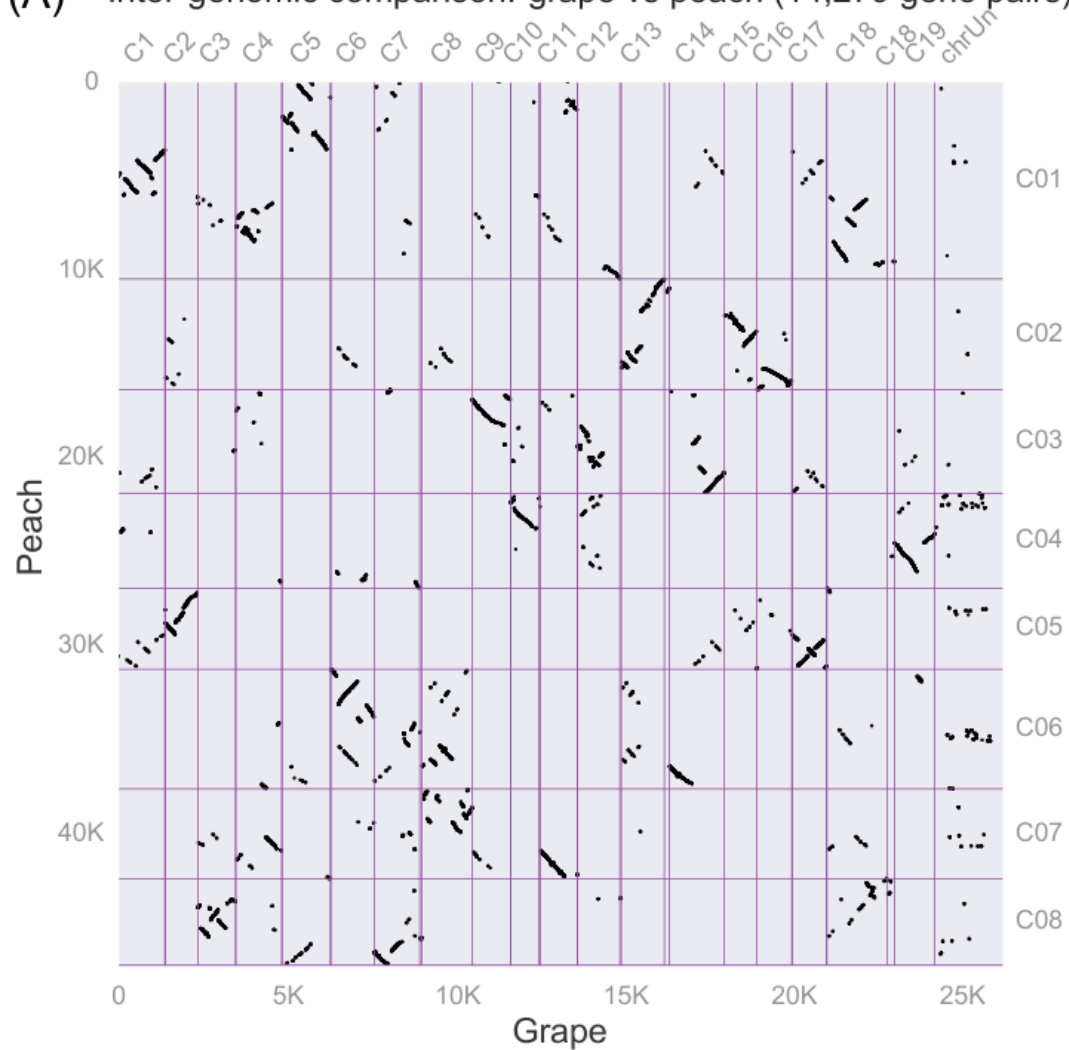
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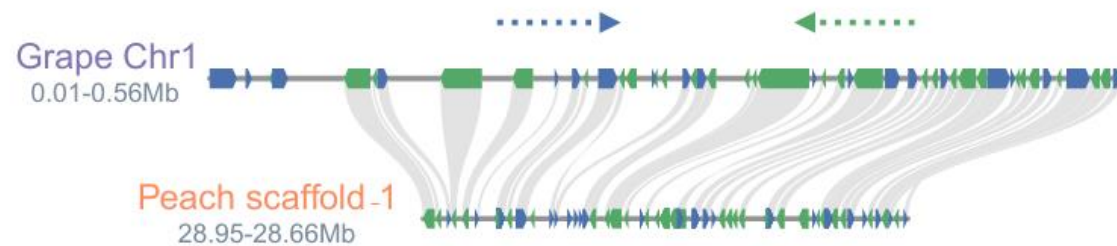


Case I: Synteny inference and visualization with MCscan

(A) Inter-genomic comparison: grape vs peach (14,279 gene pairs)



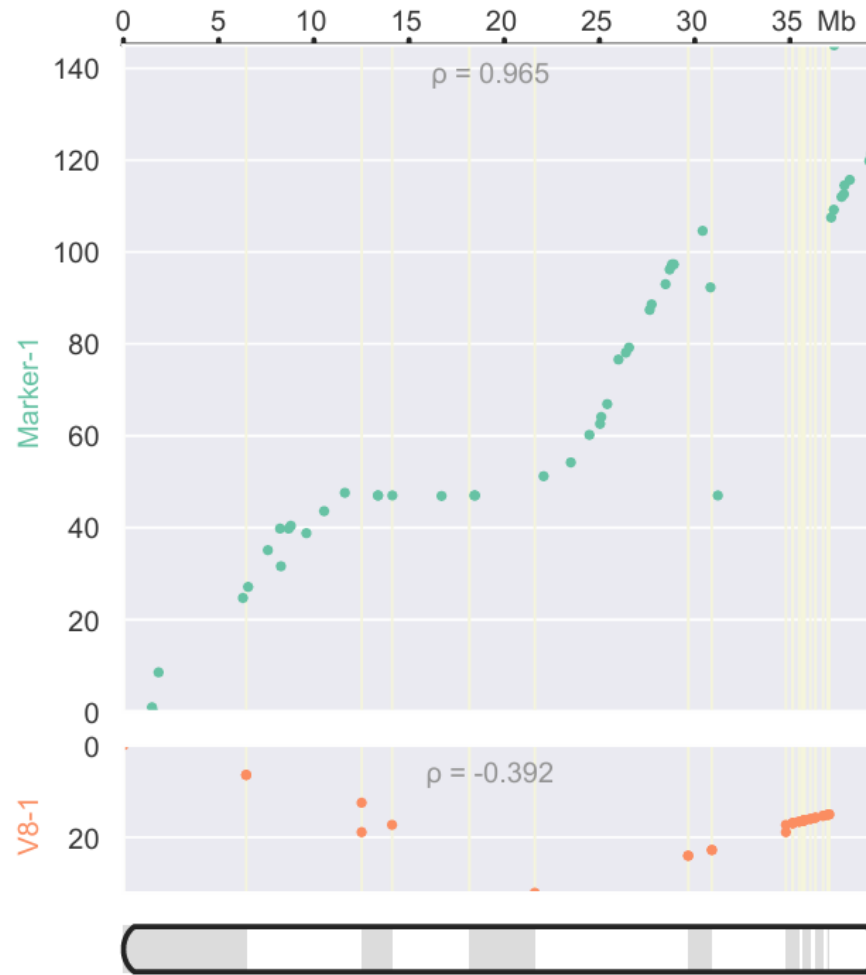
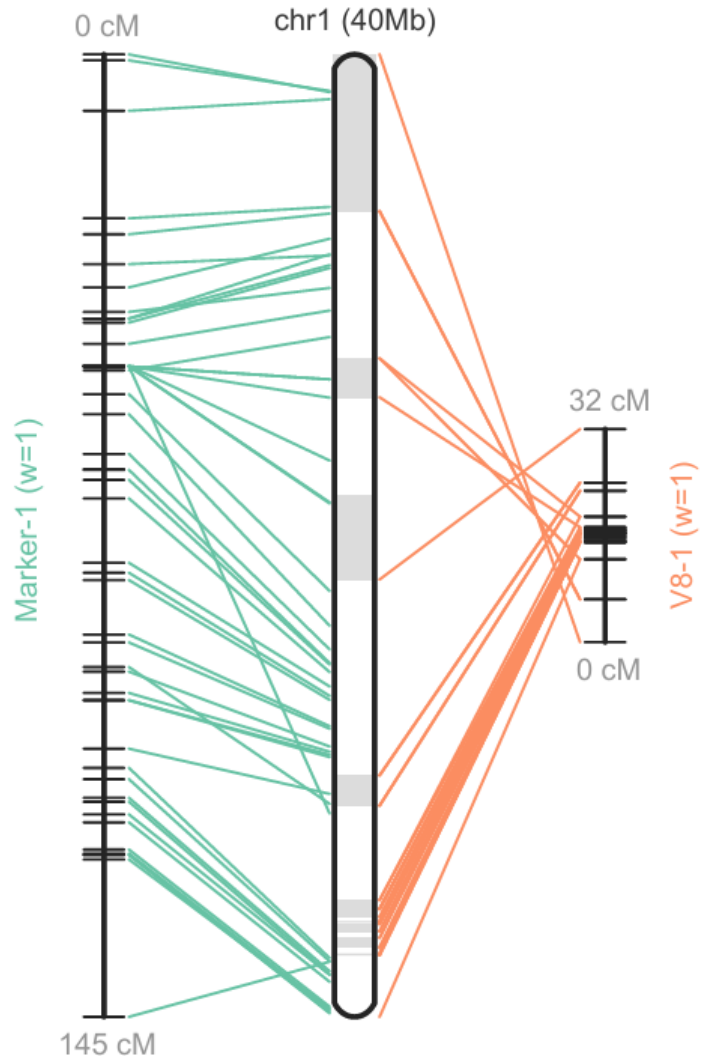
(C)



compara`



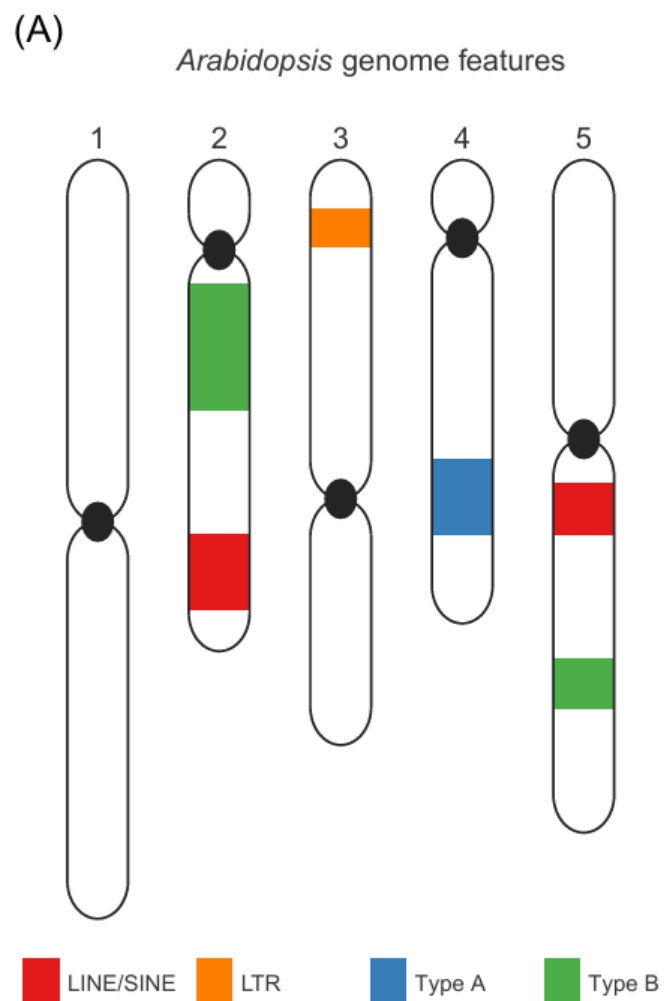
Case II: Map-based assembly and alignment with ALLMAPS



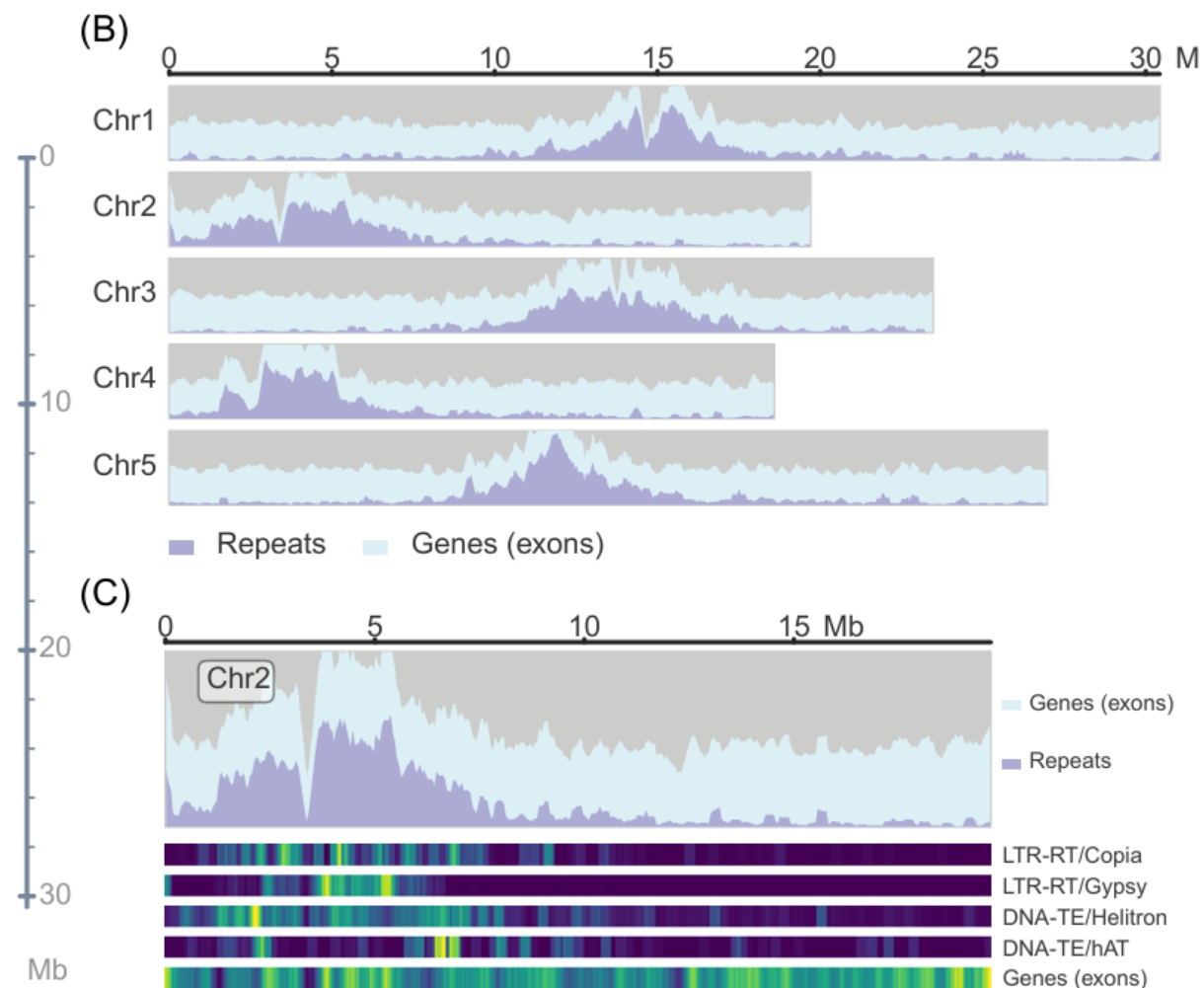
``assembly.allmaps``



Case III: Genome features and landscape plotting

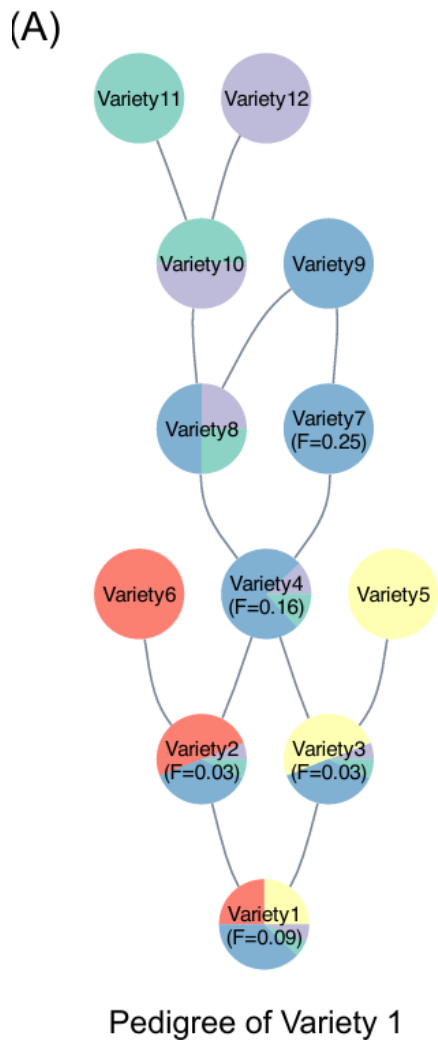


`graphics.chromosome`

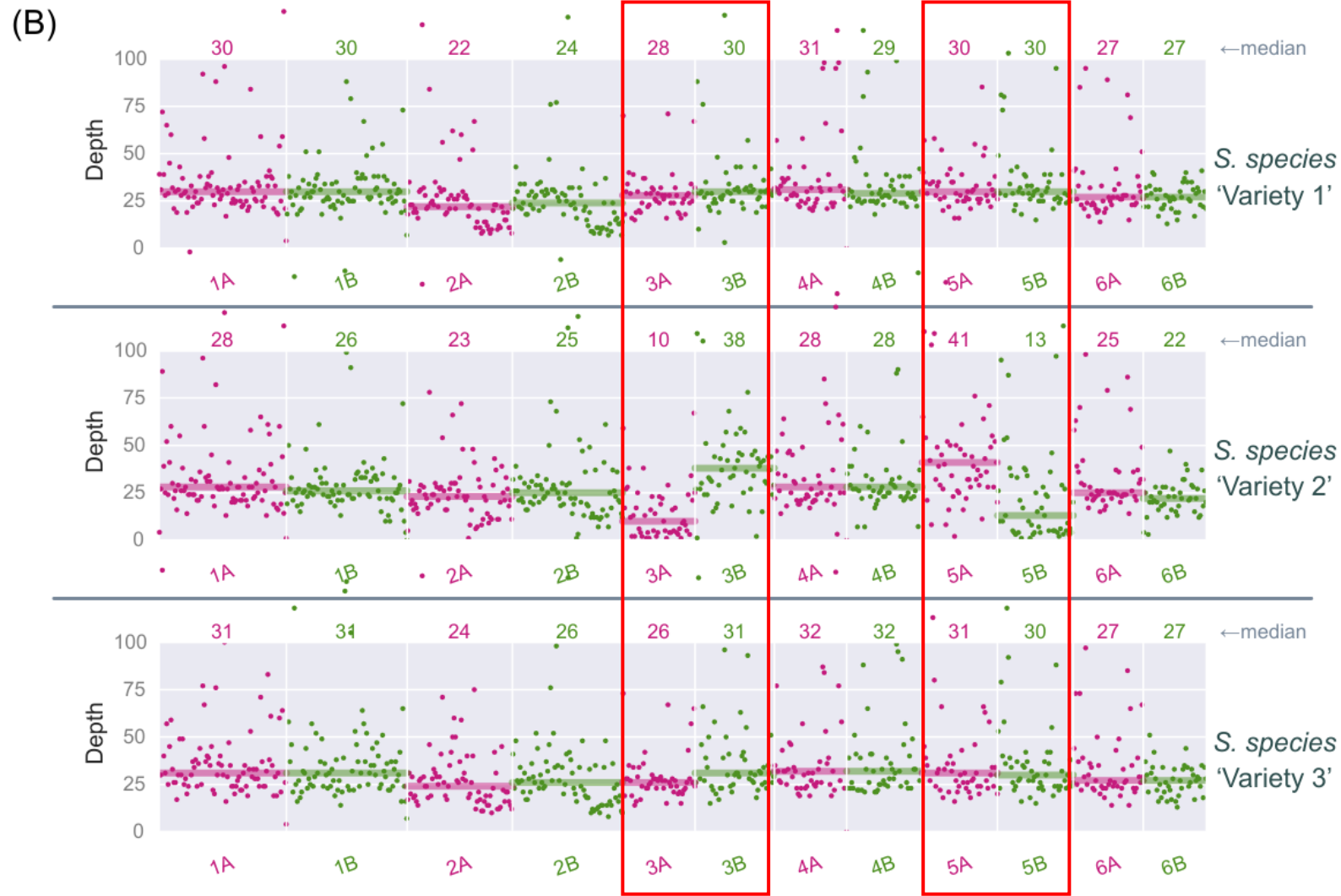


`\graphics.landscape``

Case V: Pedigree and genome diversity



`\compara.pedigree``



`\graphics.landscape``

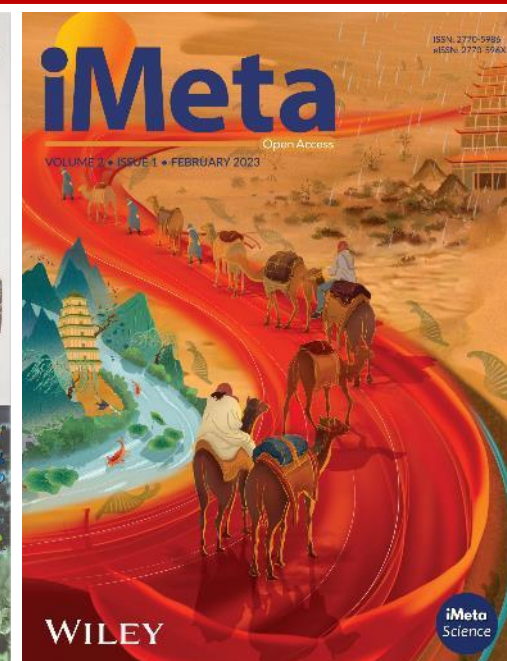
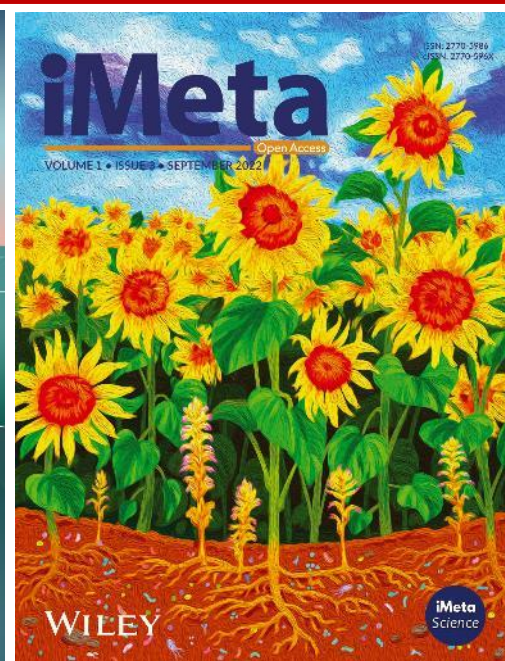


Conclusion

- ❑ JCVI offers powerful tools for synteny analysis, chromosome mapping, and other visual representations. It is a comprehensive toolkit specifically designed for comparative genomics.
- ❑ The synteny inference in JCVI is based on adaptive seeds via LAST, which avoids artificial factors from repeats, and ALLMAPS employs a more complex approach to reconcile differences between different data types, enabling iterative sorting and orienting of the genome.
- ❑ The combined use of ALLMAPS, ALLHIC, MCscan, and genome build quality control tools within JCVI provides a more thorough approach.
- ❑ Website: <https://github.com/tanghaibao/jcvi>

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