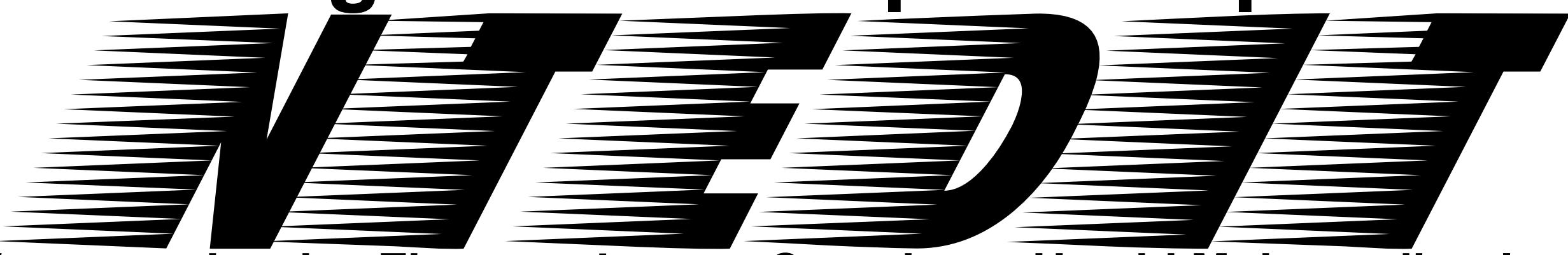
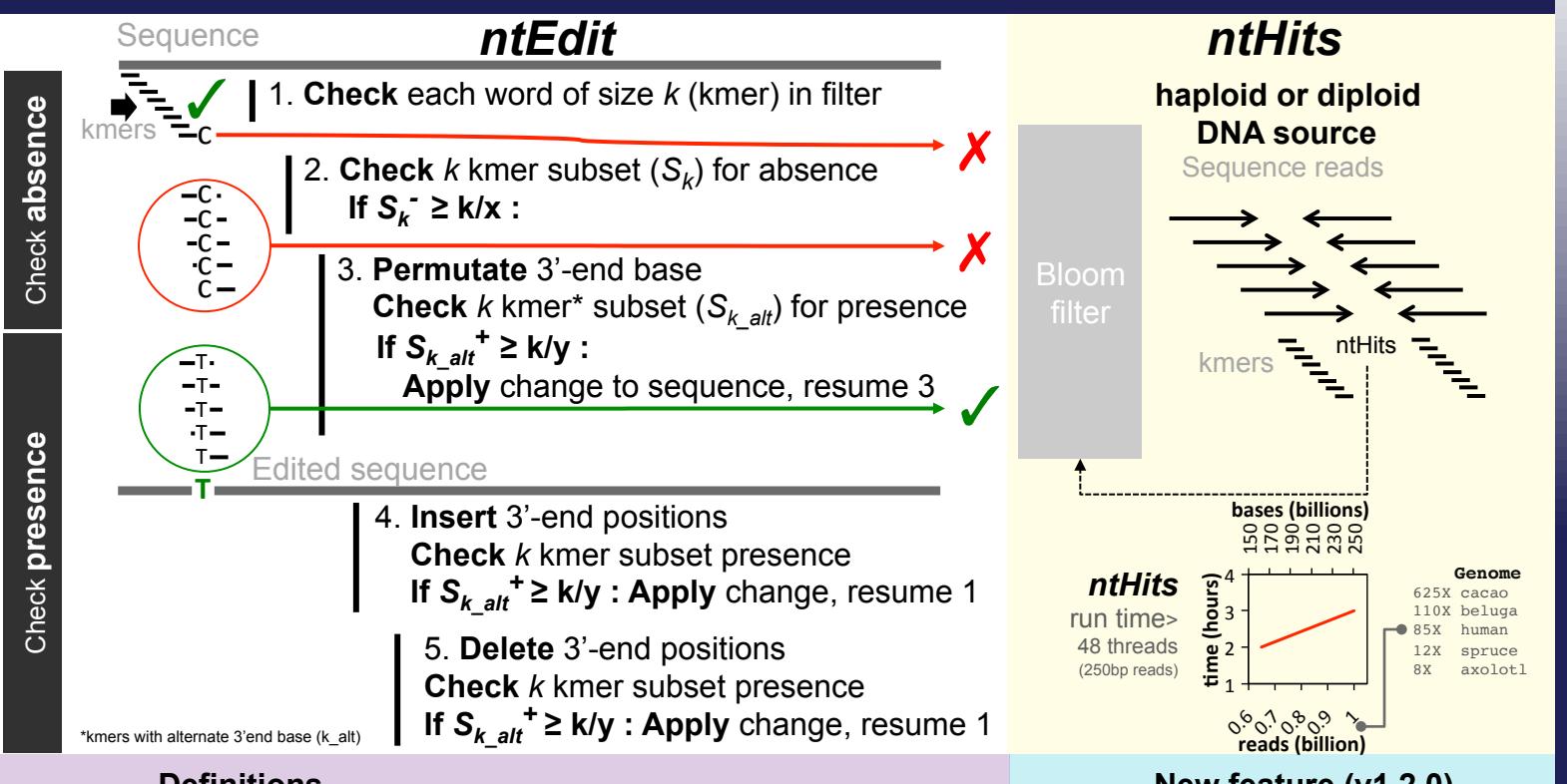


scalable genome sequence polishing

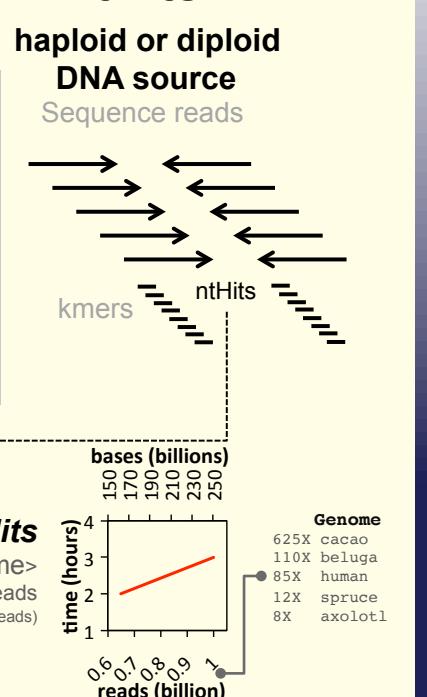


René Warren • Jessica Zhang • Lauren Coombe • Hamid Mohamadi • Inanç Birol

Method



ntHits



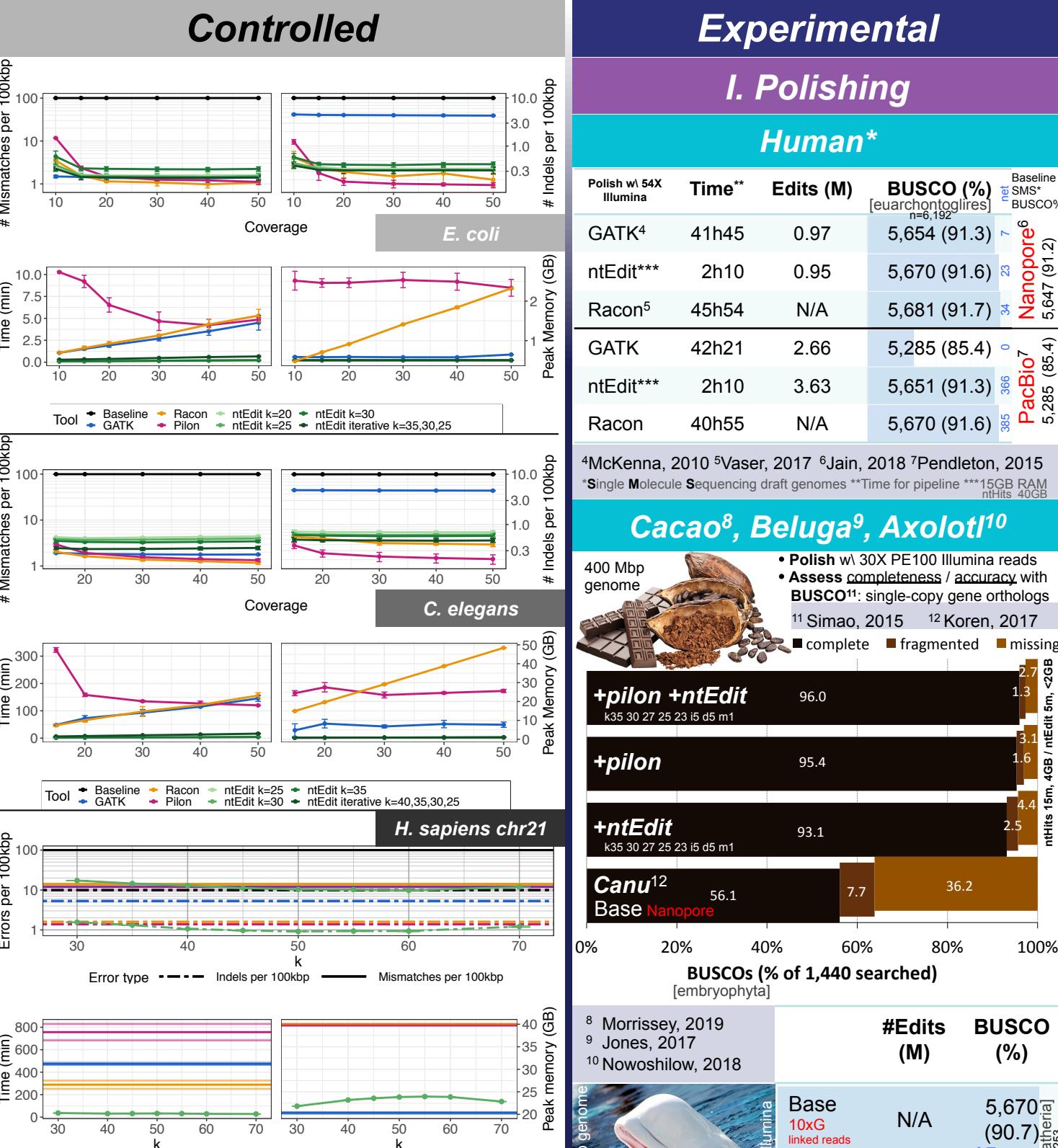
New feature (v1.2.0)

-m option editing mode 0-2 [default=0]

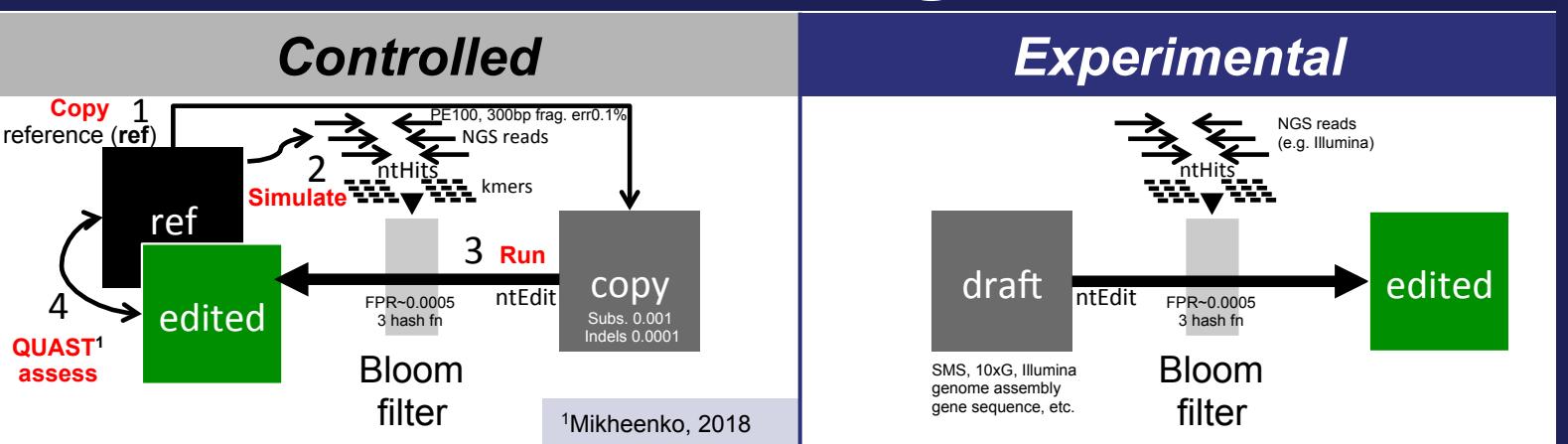
0: best substitution, or first supported indel
1: best substitution, or best indel
2: best edit overall (exhaustive)

Results

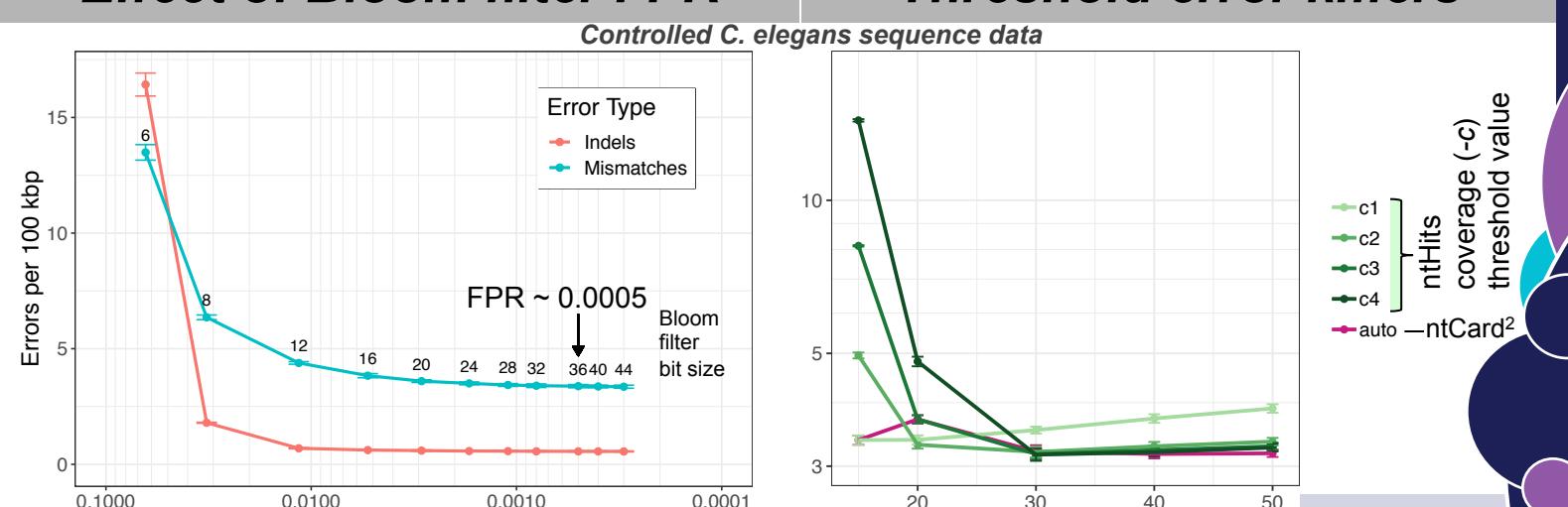
Controlled



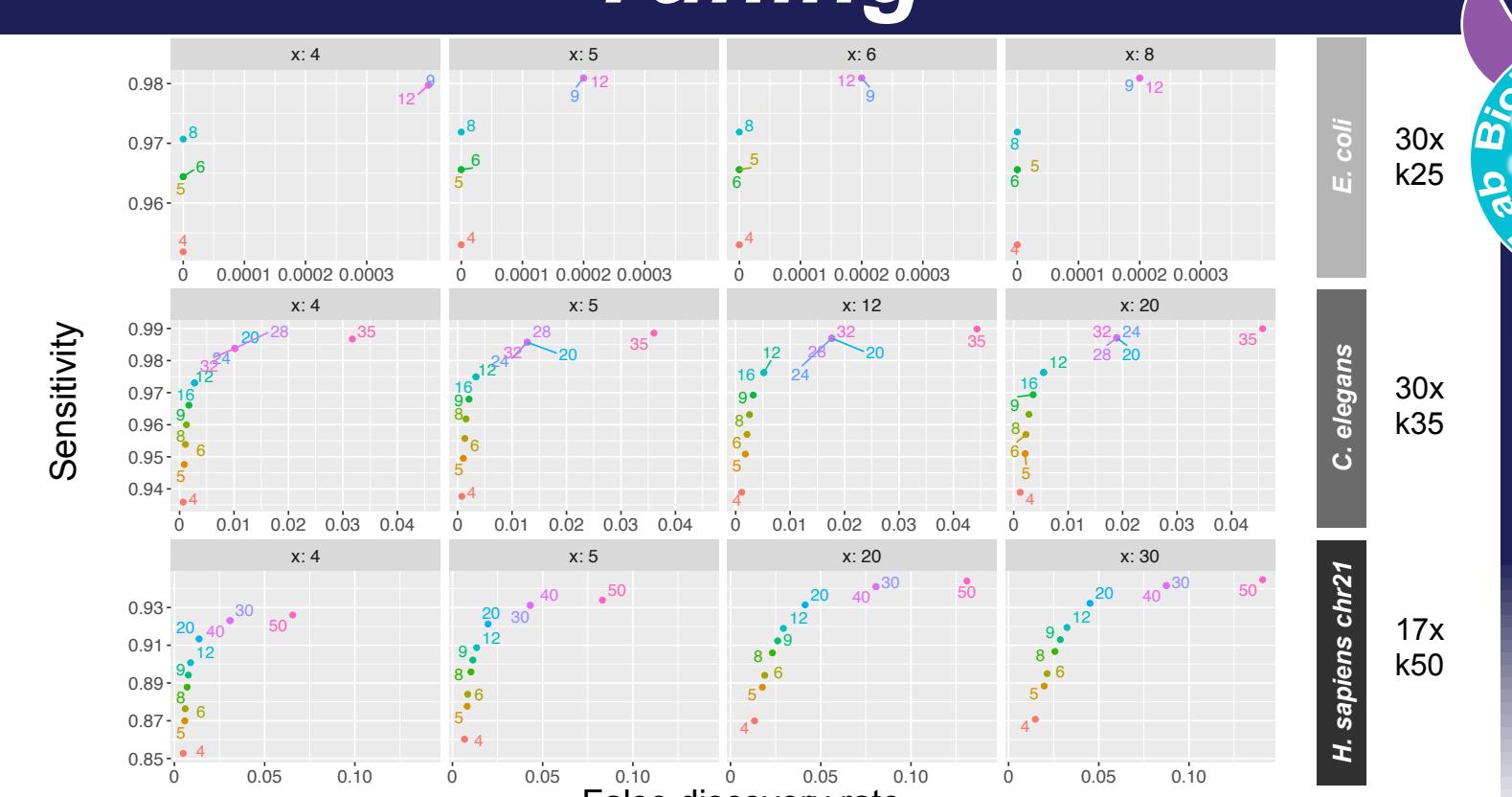
Testing



Effect of Bloom filter FPR

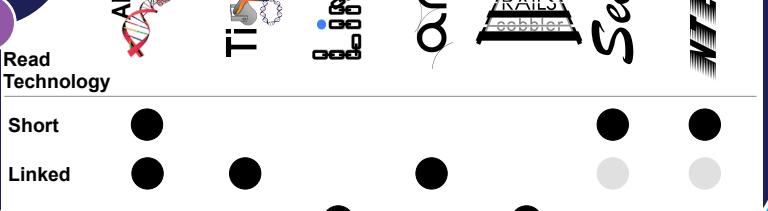
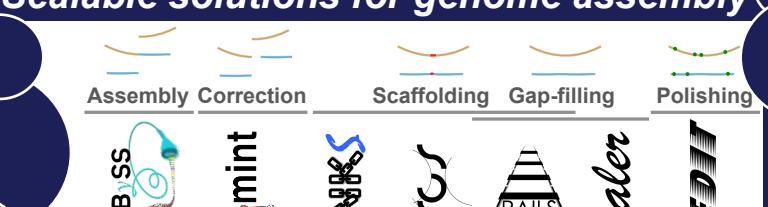


Tuning



Summary

Scalable solutions for genome assembly



Acknowledgements

Reference

Warren et al. 2019. *Bioinformatics*. DOI: 10.1093/bioinformatics/btz400

Software

<https://github.com/bcgsc/nthits>
<https://github.com/bcgsc/ntedit>



<http://birol-lab.ca>
<http://renewarren.ca>

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