

Peer-Reviewed Publications

*Authors contributed equally

70. **Warren RL** and Birol I. 2020. HLA predictions from the bronchoalveolar lavage fluid samples of five patients at the early stage of the Wuhan seafood market COVID-19 outbreak. *arXiv*. 2004.07108.
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66. Jackman SD, Coombe L, **Warren RL**, Kirk H, Trinh E, McLeod T, Pleasance S, Pandoh P, Zhao Y, Coope RJ, Bousquet J, Bohlmann J, Jones SJM, Birol I. 2019. Complete Mitochondrial Genome of a Gymnosperm, Sitka Spruce (*Picea sitchensis*), Indicates Complex Physical Structure. *Genome Biol Evol*. *bioRxiv* 601104; doi: <https://doi.org/10.1101/601104>
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61. **Warren RL**, Coombe L, Mohamadi H, Zhang J, Jaquish B, Isabel N, Jones SJM, Bousquet J, Bohlmann J, Birol I. 2019. ntEdit: scalable genome sequence polishing. *Bioinformatics*. doi:10.1093/bioinformatics/btz400. 35:4430.

60. Helbing CC, Hammond SA, Jackman SH, Houston S, **Warren RL**, Cameron CE, Birol I. 2019. Antimicrobial peptides from *Rana* [Lithobates] *catesbeiana*: Gene structure and bioinformatic identification of novel forms from tadpoles. *Sci. Reports*. 9:1529.
59. Jackman SD, Coombe L, Chu J, **Warren RL**, Vandervalk BP, Yeo S, Xue Z, Mohamadi H, Bohlmann J, Jones SJM, Birol I. 2018. Tigmint: correcting assembly errors using linked reads from large molecules. *BMC Bioinformatics*. 19:393 doi:10.1186/s12859-018-2425-6
58. Xue Z, **Warren RL**, Gibb EA, MacMillan D, Wong J, Chiu R, et al. 2018. Recurrent tumor-specific regulation of alternative polyadenylation of cancer-related genes. *BMC genomics*. 19:536 doi:10.1186/s12864-018-4903-7
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55. Khan H, Mohamadi H, Vandervalk BP, **Warren RL**, Chu J, Birol I. 2018. ChopStitch: exon annotation and splice graph construction using transcriptome assembly and whole genome sequencing data. *Bioinformatics*. doi:10.1093
54. Jones SJ, Haulena M, Taylor GA, Chan S, Bilobram S, **Warren RL**, et al. 2017. The Genome of the Northern Sea Otter (*Enhydra lutris kenyoni*). *Genes*. 8:379.
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48. Kucuk E, Chu J, Vandervalk BP, Hammond SA, **Warren RL**, Birol I. 2017. Kollector: transcript-guided de novo targeted assembly of genes. *Bioinformatics*. 33:1782
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46. Chu J, Mohamadi H, **Warren RL**, Yang C, Birol I. 2017. Innovations and challenges in detecting long read overlaps: an evaluation of the state-of-the-art. *Bioinformatics*. 33:1261
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37. **Warren RL***, Keeling C*, Yuen M, Raymond A, Taylor G, Vandervalk BP, Mohamadi H, Paulino D, Chiu R, Jackman S, Robertson G, Yang C, Hoffmann M, Weigel D, Ritland C, Isabel N, Jaquish B, Yanchuk A, Bousquet J, Jones S, Nelson D, Mackay J, Birol I, Bohlmann, J. 2015. Improved white spruce (*Picea glauca*) genome assemblies and annotation of large gene families of conifer terpenoid and phenolic defense metabolism. *The Plant Journal*. 83:189
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1. Durocher D, Charron F, **Warren R**, Schwartz RJ, Nemer M. 1997. The cardiac transcription factors Nkx2-5 and GATA-4 are mutual cofactors. *EMBO J.* 16:5687-5696

Patents

1. E Allen-Vercoe, R Holt, R Moore, R Warren - US Patent App. 13/877,421, 2011. Detection of fusobacterium in a gastrointestinal sample to diagnose gastrointestinal cancer.

First-Author Conference Presentations

17. 27th Intelligent Systems for Molecular Biology (ISMB), Basel, Switzerland. July 2019 (Poster)
16. 22nd Annual International Conference on Research in Computational Molecular Biology (RECOMB), Paris, France, April 2018 (Poster)
15. 21st Annual International Conference on Research in Computational Molecular Biology (RECOMB), Hong Kong, May 2017 (Selected talk)
14. American Society of Human Genetics (ASHG), Vancouver, Canada, October 2016 (Poster)
13. 24th Intelligent Systems for Molecular Biology (ISMB), Orlando, Florida, USA. July 2016 (Invited talk – highlights track)
12. 23rd Intelligent Systems for Molecular Biology (ISMB), Dublin, Ireland. July 2015 (Invited talk – late breaking research track. Selected talk - HiTSeq)
11. Student Biotechnology Network, Vancouver, Canada. February 2015 (Invited talk)
10. Pacific Symposium on Biocomputing, Kona, Hawaii, USA. January 2015 (Poster)
9. Pacific Symposium on Biocomputing, Kona, Hawaii, USA. January 2012 (Poster)
8. Sequencing, Finishing and Analysis in the Future, Santa Fe, New Mexico, USA. June 2010 (Oral presentation)
7. Advances in Genome Biology and Technology, Marco Island, Florida, USA. February 2009 (2 Posters)
6. Pacific Symposium on Biocomputing, Kona, Hawaii, USA. January 2008

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(Poster)

5. Synthetic Biology 3.0 conference, Zurich, Switzerland. June 2007 (Invited talk)
4. 5th CSHL/Wellcome Trust Genome Informatics meeting. Cold Spring Harbor, New-York, USA. October 2005 (Poster)
3. 7th Annual Conference on Computational Genomics. Reston, Virginia, USA. October 2004 (Poster)
2. Genomes 2004: International Conference on Microbial Genomes analysis. Hinxton, UK. April 2004 (Poster)
1. 3rd CSHL/Wellcome Trust Genome Informatics meeting. Cold Spring Harbor, New-York, USA. May 2003 (Poster)