

Peer-Reviewed Publications

*Authors contributed equally

71. Lo T, Coombe L, Lin D, **Warren RL**, et al. 2020. Complete chloroplast genome sequence of a black spruce (*Picea mariana*) from Eastern Canada. *Microbiol Resour Announc*. <https://doi.org/10.1128/MRA.00877-20>.
70. **Warren RL** and Birol I. 2020. HLA predictions from the bronchoalveolar lavage fluid and blood samples of eight COVID-19 patients at the pandemic onset. *Bioinformatics*. <https://doi.org/10.1093/bioinformatics/btaa756>
69. Nip KM, Chiu R, Yang C, Chu J, Mohamadi H, **Warren RL**, Birol I. 2019. RNA-Bloom enables reference-free and reference-guided sequence assembly for single-cell transcriptomes. *Genome Res*. <http://www.genome.org/cgi/doi/10.1101/gr.260174.119>
68. Hafezqorani S, Yang C, Nip KM, **Warren RL**, Birol I. 2020. Trans-NanoSim characterizes and simulates nanopore RNA-seq data. *GigaScience*. 9:1-7 <https://doi.org/10.1093/gigascience/giaa061>
67. 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*. <https://doi.org/10.1093/gbe/evaa108>
66. Coombe L, Nikolić V, Chu J, Birol I, **Warren RL**. 2020. ntJoin: Fast and lightweight assembly-guided scaffolding using minimizer graphs. *Bioinformatics*. 36:3885. <https://doi.org/10.1093/bioinformatics/btaa253>
65. Law WD, **Warren RL**, McCallion AS. 2020. Establishment of an eHAP1 human haploid cell line hybrid reference genome assembled from short and long reads. *Genomics*. <https://doi.org/10.1016/j.ygeno.2020.01.009>
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63. Lin D, Coombe L, Jackman SD, Gagaloova KK, **Warren RL**, et al. 2019. Complete chloroplast genome sequence of an Engelmann spruce (*Picea engelmannii*) genotype from western Canada. *Microbiol Resour Announc*. 8:e00382-19. DOI: 10.1128/MRA.00382-19.
62. Lin D, Coombe L, Jackman SD, Gagaloova KK, **Warren RL**, et al. 2019. Complete chloroplast genome sequence of a white spruce (*Picea glauca*, genotype WS77111) from eastern Canada. *Microbiol Resour Announc*. 8:e00381-19. DOI: 10.1128/MRA.00381-19.

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*. 35:4430. <https://doi.org/10.1093/bioinformatics/btz400>
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
57. Coombe L*, Zhang J*, Vandervalk B, Chu J, Jackman S, Birol I, **Warren RL**. 2018. ARKS: chromosome-scale scaffolding of human genome drafts with linked read kmers. *BMC Bioinformatics*. 19:234 doi:10.1186/s12859-018-2243-x
56. **Warren RL**. 2018. Visualizing genome synteny with xmatchview. *Journal of Open Source Software* 3:497 doi:10.21105/joss.00497
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.
53. Jones SJM, Taylor GA, Chan S, **Warren RL**, Hammond SA, Bilobram S, et al. 2017. The Genome of the Beluga Whale (*Delphinapterus leucas*). *Genes*. 8:378.
52. Hammond SA, **Warren RL**, Vandervalk BP, Kucuk E, Khan H, Gibb EA, Pandoh P, Kirk H, Zhao Y, Jones M, Mungal AJ, Coope R, Pleasance S, Moore RA, Holt RA, Round JM, Ohora S, Walle BV, Veldhoen N, Helbing CC, Birol I. 2017. The North American bullfrog draft genome provides insight into hormonal regulation of long noncoding RNA. *Nature Comm*. 8:1433 doi:10.1038/s41467-017-01316-7

51. Yeo S*, Coombe L*, Chu J, **Warren RL***, Birol I. 2017. ARCS: Scaffolding genome drafts with linked reads. *Bioinformatics*. 34:725-731. doi:10.1093/bioinformatics/btx675
50. Hasan NA, **Warren RL**, Epperson LE, Malecha A, Alexander DC, Turenne CY, MacMillan D, Birol I, Pleasance S, Coope R, Jones SJM, Romney MG, Ng M, Chan T, Rodrigues M, Tang P, Gardy JL, Strong M. 2017. Complete Genome Sequence of Mycobacterium chimaera SJ42, a Nonoutbreak Strain from an Immunocompromised Patient with Pulmonary Disease. *Genome Announc*. 5:e00963-17. doi: 10.1128/genomeA.00963-17.
49. Yang C, Chu J, **Warren RL**, Birol I. 2017. NanoSim: nanopore sequence read simulator based on statistical characterization. *GigaScience*. 6:1
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
47. Jackman SD, Vandervalk BP, Mohamadi H, Chu J, Yeo S, Hammond SA, Jahesh G, Khan H, Coombe L, **Warren RL**, Birol I. 2017. ABySS 2.0: resource-efficient assembly of large genomes using a Bloom filter. *Genome Res*. 27:768
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
45. **Warren RL**. 2016. RAILS and Cobbler: Scaffolding and automated finishing of draft genomes using long DNA sequences. *The Journal of Open Source Software*. doi: 10.21105/joss.00116
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39. **Warren RL**, Yang C, Vandervalk BP, Behsaz B, Lagman A, Jones SJ, Birol I. 2015. LINKS: Scalable, alignment-free scaffolding of draft genomes with long reads. *GigaScience*. 4:35
38. Paulino D*, **Warren RL***, Vandervalk BP, Raymond A, Jackman SD, Birol I. 2015. Sealer: a scalable gap-closing application for finishing draft genomes. *BMC Bioinformatics*. 16:230
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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33. Watson CT, Steinberg KM, Graves-Lindsay TA, **Warren RL**, Malig M, Schein JE, Wilson RK, Holt R, Eichler E, Breden F. 2014. Sequencing of the human IG light chain loci from a hydatidiform mole BAC library reveals locus-specific signatures of genetic diversity. *Genes Immun*. 16:24–34
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2. Molday RS, **Warren R**, Loewen C, Molday L. 1999. Cyclic GMP-gated channel and peripherin/rds-rom-1 complex of rod cells. In: Rhodopsin and Phototransduction. *Novartis Found Symp*. 224:249-261. Publisher: John Wiley & Sons, N.Y.

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 (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)