

## Peer-Reviewed Publications

\*Authors contributed equally

70. Coombe L, Nikolić V, Chu J, Birol I, Warren RL. 2020. ntJoin: Fast and lightweight assembly-guided scaffolding using minimizer graphs. *Bioinformatics*. <https://doi.org/10.1093/bioinformatics/btaa253>
69. 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>
68. Coombe L, Nikolic V, Chu J, Birol I, **Warren RL**. 2020. ntJoin: Fast and lightweight assembly-guided scaffolding using minimizer graphs. *bioRxiv*. doi: <https://doi.org/10.1101/2020.01.13.905240>.
67. Nip KM, Chiu R, Yang C, Chu J, Mohamadi H, **Warren RL**, Birol I. 2019. RNA-Bloom provides lightweight reference-free transcriptome assembly for single cells. *bioRxiv* 701607; doi: <https://doi.org/10.1101/701607>
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. *bioRxiv* 601104; doi: <https://doi.org/10.1101/601104>
65. Yang C, Li C, Nip KM, **Warren RL**, Birol I. 2019. Termin(A)ntor: Polyadenylation Site Prediction Using Deep Learning Models. *bioRxiv* 710699; doi: <https://doi.org/10.1101/710699>
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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*. 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
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
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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
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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
44. Coombe L\*, **Warren RL\***, Jackman SD, Yang C, Vandervalk BP, Moore RA, Pleasance S, Coope RJ, Bohlmann J, Holt RA, Jones SJM, Birol I. 2016. Assembly of the complete Sitka spruce chloroplast genome using 10X Genomics' GemCode sequencing data. *PLoS ONE.* 11(9): e0163059
43. IJspeert H, Rozmus J, Schwarz K, **Warren RL**, van Zessen D, Holt RA, Pico-Knijnenburg I, Simons E, Jerchel I, Wawer A, Ricarda Lorenz M, Patiroğlu T, Haluk Akar H, Leite R, Verkaik NS, Stubbs AP, van Gent DCC, van Dongen JJM, van der Burg M. 2016. XLF deficiency results in reduced N-nucleotide addition during V(D)J recombination. *Blood.* 128:650
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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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32. Brown SD, **Warren RL**, Gibb EA, Martin SD, Spinelli JJ, Nelson BH, Holt RA. 2014. Neo-antigens predicted by tumor genome meta-analysis correlate with increased patient survival. *Genome Res*. 24:743-50
31. **Warren RL**, Freeman DJ, Pleasance S, Watson P, Moore RA, Cochrane K, Allen-Vercoe E, Holt RA. 2013. Co-occurrence of anaerobic bacteria in colorectal carcinomas. *Microbiome*. 1:16
30. Watson CT, Steinberg KM, Huddleston J, **Warren RL**, Malig M, Schein J, Willsey AJ, Joy JB, Scott JK, Graves TA, Wilson RK, Holt RA, Eichler EE, Breden F. 2013. Complete haplotype sequence of the human

immunoglobulin heavy-chain variable, diversity, and joining genes and characterization of allelic and copy-number variation. *Am J Hum Genet.* 92:530-546

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23. **Warren RL**, Freeman JD, Zeng T, Choe G, Munro S, Moore R, Webb JR, Holt RA. 2011. Exhaustive T-cell repertoire sequencing of human peripheral blood samples reveals signatures of antigen selection and a directly measured repertoire size of at least 1 million clonotypes. *Genome Res.* 21:790-797
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18. Freeman JD\*, **Warren RL\***, Webb JR, Nelson BH, Holt RA. 2009. Profiling the T-cell receptor beta-chain repertoire by massively parallel sequencing. *Genome Res*. 19:1817-1824
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15. Smailus DE, **Warren RL**, Holt RA. 2008. Constructing large DNA segments by iterative clone recombination. *Syst. Synth. Biol.* 1:139-144
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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. 27<sup>th</sup> Intelligent Systems for Molecular Biology (ISMB), Basel, Switzerland. July 2019 (Poster)
16. 22<sup>nd</sup> Annual International Conference on Research in Computational Molecular Biology (RECOMB), Paris, France, April 2018 (Poster)
15. 21<sup>st</sup> 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. 24<sup>th</sup> Intelligent Systems for Molecular Biology (ISMB), Orlando, Florida, USA. July 2016 (Invited talk – highlights track)
12. 23<sup>rd</sup> 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)