

Peer-Reviewed Publications

*Authors contributed equally

51. Yeo S*, Coombe L*, Chu J, **Warren RL***, Birol I. 2017. ARCS: Assembly Roundup by Chromium Scaffolding. TBD
50. 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.* TBD
49. Yang C, Chu J, **Warren RL**, Birol I. 2017. NanoSim: nanopore sequence read simulator based on statistical characterization. *Gigascience*. gix010. doi: 10.1093/gigascience/gix010
48. Kucuk E, Chu J, Vandervalk BP, Hammond SA, **Warren RL**, Birol I. 2017. Kollector: transcript-guided de novo targeted assembly of genes. *Bioinformatics*. btx078. doi: 10.1093/bioinformatics/btx078
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.* doi: 10.1101/gr.214346.116
46. Chu J, Mohamadi H, **Warren RL**, Yang C. Birol I. 2016. Overlapping long and error-prone sequence reads: Current innovations and challenges in developing sensitive, specific and scalable algorithms. *Bioinformatics*. doi: 10.1093/bioinformatics/btw811
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
42. Jackman SD, **Warren RL**, Gibb EA, Vandervalk BP, Mohamadi H, Chu J,

- Raymond A, Pleasance S, Coope R, Wildung MR, Ritland CE, Bousquet J, Jones SJM, Bohlmann J, Birol I. 2015. Organellar Genomes of White Spruce (*Picea glauca*): Assembly and Annotation. *Genome Biol Evol.* 8:29
41. Birol I, Chu J, Mohamadi H, Jackman SD, Raghavan K, Vandervalk BP, Raymond A, **Warren RL**. 2015. Spaced Seed Data Structures for De Novo Assembly. *Int J Genomics*. doi: 10.1155/2015/196591
40. Vandervalk BP, Yang C, Xue Z, Raghavan K, Chu J, Mohamadi H, Jackman SD, Chiu R, **Warren RL**, Birol I. 2015. Konnector v2.0: pseudo-long reads from paired-end sequencing data. *BMC Med Genomics*. 8(Suppl 3):S1
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
36. Gibb EA, **Warren RL**, Wilson GW, Brown SD, Robertson G, Morin GB, Holt RA. 2015. Activation of an endogenous retrovirus-associated long non-coding RNA in human adenocarcinoma. *Genome Med*. 7:22
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34. Vandervalk BP, Jackman SD, Raymond A, Mohamadi H, Yang C, Attali DA, Chu J, **Warren RL**, Birol I. 2014. Konnector: Connecting paired-end reads using a bloom filter de Bruijn graph, Bioinformatics and Biomedicine (BIBM), 2014 IEEE International Conference, vol., no., pp.51, 2-5 Nov. 2014 doi: 10.1109/BIBM.2014.6999126
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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
29. Branton WG, Ellestad KK, Maingat F, Wheatley BM, Rud E, **Warren RL**, Holt RA, Surette MG, Power C. 2013. Brain Microbial Populations in HIV/AIDS: α -Proteobacteria Predominate Independent of Host Immune Status. *PLoS One* 8(1):e54673
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26. Moore RA*, **Warren RL***, Freeman JD, Gustavsen JA, Chénard C, et al. 2011. The Sensitivity of Massively Parallel Sequencing for Detecting Candidate Infectious Agents Associated with Human Tissue. *PLoS ONE* 6(5):e19838
25. **Warren RL**, Holt RA. 2011. Targeted assembly of short sequence reads. *PLoS ONE* 6(5):e19816
24. Bhat RK, Ellestad KK, Wheatley BM, **Warren R**, Holt RA, Power C. 2011. Age- and Disease-Dependent HERV-W Envelope Allelic Variation in Brain: Association with Neuroimmune Gene Expression. *PLoS ONE* 6(4): e19176
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
17. **Warren RL**, Nelson BH, Holt RA. 2009. Profiling model T cell metagenomes with short reads. *Bioinformatics*. 25:458-464
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11. Bainbridge MN, **Warren RL**, He A, Bilenky M, Robertson AG, Jones SJ. 2006. THOR: Targeted high-throughput ortholog reconstructor. *Bioinformatics*. 23:2622-2624
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 9. **Warren RL**, Varabei D, Platt D, Huang X, Messina D, Yang SP, Kronstad JW, Krzywinski M, Warren WC, Wallis JW, Hillier LW, Chinwalla AT, Schein JE, Siddiqui AS, Marra MA, Wilson RK, Jones SJ. 2006. Physical map-assisted whole-genome shotgun sequence assemblies. *Genome Res*. 16:768-775
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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 Presentations

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)