

Peer-Reviewed Publications

*Authors contributed equally

53. Khan H, Mohamadi H, Vandervalk BP, **Warren RL**, Chu J, Birol I. 2017. ChopStitch: exon annotation and splice graph construction using transcriptome assembly and whole genome sequencing data. *Bioinformatics*. TBD
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*. 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*. 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
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
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
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
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
28. **Warren RL**, Choe G, Freeman DJ, Castellarin M, Munro S, Moore R, Holt RA. 2012. Derivation of HLA types from shotgun sequence datasets. *Genome Med*. 4:95
27. Castellarin M*, **Warren RL***, Freeman JD, Dreolini L, Krzywinski M, Strauss J, Barnes R, Watson P, Allen-Vercoe E, Moore RA, Holt RA. 2012. *Fusobacterium nucleatum* infection is prevalent in human colorectal carcinoma. *Genome Res*. 22:299-306

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25. **Warren RL**, Holt RA. 2011. Targeted assembly of short sequence reads. *PLoS ONE* 6(5):e19816
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21. **Warren RL** and Holt RA. 2010. A census of predicted mutational epitopes suitable for immunologic cancer control. *Hum Immunol.* 71:245-254
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19. Pel J, Broemeling D, Mai L, Poon HL, Tropini G, **Warren RL**, Holt RA, Marziali A. 2009. Nonlinear electrophoretic response yields a unique parameter for separation of biomolecules. *Proc Natl Acad Sci U S A.* 106:14796-14801
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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16. **Warren RL**, Freeman JD, Levesque RC, Smailus DE, Flibotte S, Holt RA. 2008. Transcription of foreign DNA in *Escherichia coli*. *Genome Res*. 18:1798-1805
15. Smailus DE, **Warren RL**, Holt RA. 2008. Constructing large DNA segments by iterative clone recombination. *Syst. Synth. Biol.* 1:139-144
14. Holt RA, **Warren R**, Flibotte S, Missirlis PI, Smailus DE. 2007. Rebuilding microbial genomes. *Bioessays*. 29:580-590
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12. Mullick A, Xu Y, **Warren R**, Koutroumanis M, Guilbault C, Broussau S, Malenfant F, Bourget L, Lamoureux L, Lo R, Caron AW, Pilote A, Massie B. 2006. The Cumate gene-switch: a system for regulated expression in mammalian cells. *BMC Biotechnology*. 6:43
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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7. Bakkeren G, Jiang G, **Warren RL**, Butterfield Y, Shin H, Chiu R, Linning R, Schein J, Lee N, Hu G, Kupfer DM, Tang Y, Roe BA, Jones S, Marra M, Kronstad JW. 2006. Mating factor linkage and genome evolution in basidiomycetous pathogens of cereals. *Fungal Genetics and Biology*. 43:655-666
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4. **Warren R**, Molday RS. 2002. Regulation of the rod photoreceptor cyclic nucleotide gated channel. *Adv Exp Med Biol*. 514:205-223
3. Molday RS, **Warren R**, Molday LL. 2000. Purification and biochemical analysis of the cGMP-gated channel and Na/Ca-K exchanger of rod photoreceptors. *Methods Enzymol*. 315:831-847
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

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)