

Peer-Reviewed Publications

*Authors contributed equally

50. Yeo S*, Coombe L*, Chu J, **Warren RL***, Birol I. 2017. ARCS: Assembly Roundup by Chromium Scaffolding. 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
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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
35. Birol I, Mohamadi H, Raymond A, Raghavan K, Chu J, Vandervalk BP, Jackman S, **Warren RL**. 2014. Spaced seed data structures, Bioinformatics and Biomedicine (BIBM), 2014 IEEE International Conference, vol., no., pp.15, 2-5 Nov. 2014 doi: 10.1109/BIBM.2014.6999305
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
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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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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
22. D'Souza CA, Kronstad JW, Taylor G, **Warren R**, Yuen M, Hu G, Jung WH, Sham A, Kidd SE, Tangen K, Lee N, Zeilmaker T, Sawkins J, McVicker G, Shah S, Gnerre D, Griggs A, Zeng Q, Bartlett K, Li W, Wang X, Heitman J, Stajich JE, Fraser JA, Meyer W, Carter D, Schein J, Krzywinski M, Kwon-Chung KJ, Varma A, Wang J, Brunham R, Fyfe M, Ouellette BFF, Siddiqui A, Marra M, Jones S, Holt R, Birren BW, Galagan JE and Cuomo CA. 2011. Genome Variation in *Cryptococcus gattii*, an Emerging Pathogen of Immunocompetent Hosts. *mBio*. doi:10.1128/mBio.00342-10

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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
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
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13. **Warren RL**, Sutton GG, Jones SJ, Holt RA. 2007. Assembling millions of short DNA sequences using SSAKE. *Bioinformatics.* 23:500-501
12. Mullick A, Xu Y, **Warren R**, Koutroumanis M, Guilbault C, Broussau S, Malenfant F, Bourget L, Lamoureux L, Lo R, Caron AW, Pilotte 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
10. Bainbridge MN, **Warren RL**, Hirst M, Romanuik T, Zeng T, Go A, Delaney A, Griffith M, Hickenbotham M, Magrini V, Mardis ER, Sadar MD, Siddiqui AS, Marra MA, Jones SJ. 2006. Analysis of the prostate cancer cell line LNCaP

transcriptome using a sequencing-by-synthesis approach. *BMC Genomics*. 7:246

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
8. McLeod MP, **Warren RL**, Hsiao WW, Araki N, Myhre M, Fernandes C, Miyazawa D, Wong W, Lillquist AL, Wang D, Dosanjh M, Hara H, Petrescu A, Morin RD, Yang G, Stott JM, Schein JE, Shin H, Smailus D, Siddiqui AS, Marra MA, Jones SJ, Holt R, Brinkman FS, Miyauchi K, Fukuda M, Davies JE, Mohn WW, Eltis LD. 2006. The complete genome of *Rhodococcus* sp. RHA1 provides insights into a catabolic powerhouse. *Proc Natl Acad Sci U S A*. 103:15582-15587
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
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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 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)