

**Peer-Reviewed Publications**

\*Authors contributed equally

49. Yeo S, Coombe L, Chu J, **Warren RL**, Birol I. XXXX. ARCS: Assembly Roundup by Chromium Scaffolding. TBD
48. Kucuk E, Chu J, Vandervalk BP, Hammond SA, **Warren RL**, Birol I. XXXX. Kollector: transcript-guided de novo targeted assembly of genes. TBD
47. Jackman SD, Vandervalk BP, Mohamadi H, Chu J, Yeo S, Hammond SA, Jahesh G, Khan H, Coombe L, **Warren RL**, Birol I. 2016. ABySS 2.0: resource-efficient assembly of large genomes using a Bloom filter. *bioRxiv* 068338; doi: <http://dx.doi.org/10.1101/068338>
46. Chu J, Mohamadi H, **Warren LR**, Yang C. Birol I. XXXX. Overlapping long and error-prone sequence reads: Current innovations and challenges in developing sensitive, specific and scalable algorithms. TBD
45. Yang C, Chu J, **Warren LR**, Birol I. 2016. NanoSim: nanopore sequence read simulator based on statistical characterization. *Bioinformatics*. TBD
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. Connector 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
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*.

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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:  $\alpha$ -Proteobacteria Predominate Independent of Host Immune Status. *PLoS One* 8(1):e54673
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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
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
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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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
  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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  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
  6. **Warren RL**, Butterfield YS, Morin RD, Siddiqui AS, Marra MA, Jones SJM. 2005. Management and visualization of whole genome shotgun assemblies using SAM. *Biotechniques.* 38:715-720
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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
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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**

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)