

Peer-Reviewed Publications *Authors contributed equally

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	All	Since 2020
Citations	14808	6877
h-index	44	36
i10-index	83	70

114. Lauren Coombe, **René L Warren**, Inanc Birol. 2025. ntSynt-viz: Visualizing synteny patterns across multiple genomes. *bioRxiv* 2025.01.15.633221; <https://doi.org/10.1101/2025.01.15.633221>
113. **René L. Warren**, Inanc Birol, CGEn HostSeq Initiative. 2025. Concordance and dissonance: A genome-wide analysis of self-declared versus inferred ancestry in 10,250 participants from the HostSeq cohort. *bioRxiv* 2025.06.10.658783; doi: <https://doi.org/10.1101/2025.06.10.658783>
112. Lauren Coombe, Parham Kazemi, Johnathan Wong, Inanc Birol, **René L Warren**. 2026. Multi-genome synteny detection using minimizer graph mappings. *BMC Biology*. <https://doi.org/10.1186/s12915-025-02455-w>
111. **René L Warren**, Lauren Coombe, Johnathan Wong, Parham Kazemi, Inanc Birol. 2025. ntRoot: Computational Inference of Human Ancestry at Scale from Genomic Data. *Bioinformatics Advances*, 5:1, vba287, <https://doi.org/10.1093/bioadv/vba287>
110. Salehi A, Yanai A, Richter A, Li C, Sutherland D, Coombe L, Kotkoff M, **Warren RL**, Hoang LMN, Birol I. 2025. Antimicrobial Peptides with High Bioactivity Against MDR Isolates: Addressing Public Health Concerns. *Microbial Pathogenesis*. <https://doi.org/10.1016/j.micpath.2025.107893>
109. Lopez MLD, **Warren RL**, Allison MJ, Coombe L, Imbery JJ, Birol I, Helbing CC. 2025. Conserved sequence identification within large genomic datasets using unikseq2: Application in environmental DNA assay development. *Molec. Ecol. Res.*; <https://doi.org/10.1111/1755-0998.70014>
108. Langlois V, Lopez ML, Allison M, Imbery J, Couillard J, Acharya-Patel N, Bergman L, Bonderud M, Brochu M, Castonguay, M, Coombe L, Dema A, Groenwold E, Lee H, Ma I, Ren Y, Knowles G, Sandre F, To TA, **Warren RL**, Yang C, Birol I, Helbing C. 2025. Environmental DNA (eDNA) Quantitative Polymerase Chain Reaction-Based Assays for Surveying 125 Taxa of Importance to North America. *Environmental DNA*, 7: e70139 <https://doi.org/10.1002/edn3.70139>
107. Acharya-Patel N, Cram K, Groenwold ET, Lee H, Keller AG, Bomback B, Lyons S, **Warren RL**, Coombe L, Lowe CJ, Bergman LC, Bishay F, Birol I, Macdonald TA, Helbing CC. 2025. Monitoring marine pollution effects through targeted environmental DNA (eDNA) testing in the Pacific northwest. *Marine Pollution Bulletin*, 216, 118036. <https://doi.org/10.1016/j.marpolbul.2025.118036>

106. Warren RL, Birol I. 2025. Streaming long-read sequence alignments for HLA predictions using HLAminer. *Current Protocols*. 5, e70124. <https://doi.org/10.1002/cpz1.70124>
105. Zhang E, Coombe L, Wong J, Warren RL, Birol I. 2025. GoldPolish-target: targeted long-read genome assembly polishing. *BMC Bioinformatics* 26, 78. <https://doi.org/10.1186/s12859-025-06091-7>
104. Li C, Sutherland D, Salehi A, Richter A, Lin D, Aninta SI, EbrahimiKondori H, Yanai A, Coombe L, Warren RL, Kotkoff M, Hoang LMN, Helbing CC, Birol I. 2025. Mining the UniProtKB/Swiss-Prot database for antimicrobial peptides. *Protein Science*. <https://doi.org/10.1002/pro.70083>
103. Lopez MLD, Yang CL, Coombe L, Warren RL, Allison MJ, Imbery JJ, Birol I, Helbing CC. 2025. mtGrasp: Streamlined reference-grade mitochondrial genome assembly and standardization to enhance metazoan mitogenome resources. *Methods in Ecology and Evolution*, 00, 1–10. <https://doi.org/10.1111/2041-210X.14506>
102. Li C, Sutherland D, Richter A, Coombe L, Yanai A, Warren RL, Kotkoff M, Hof F, Hoang LMN, Helbing C, Birol I. 2024. *De novo* synthetic antimicrobial peptide design with a recurrent neural network. *Protein Science*. <https://doi.org/10.1002/pro.5088>
101. EbrahimiKondori H, Sutherland D, Yanai A, Richter A, Salehi A, Li C, Coombe L, Kotkoff M, Warren RL, Birol I. 2024. Structure-aware deep learning model for peptide toxicity prediction. *Protein Science*. <https://doi.org/10.1002/pro.5076>
100. Acharya-Patel N, Groenwold E, Lemay MA, Clemente-Carvalho R, Morien E, Dudas S, Rubidge E, Yang CL, Coombe L, Warren RL, Frid A, Birol I, Helbing CC. 2024. Comparison of environmental DNA and SCUBA diving methods to survey keystone rockfish species on the Central Coast of British Columbia, Canada. *Ecol. Indic.* 160, 111830. <https://doi.org/10.1016/j.ecolind.2024.111830>
99. Warren RL, Abraham R, Calingo M, Garant JM, Jones SJM, Birol I; CGEn HostSeq Initiative. Establishing association between HLA-C*04:01 and severe COVID-19. *HLA*. 2024 Jan;103(1):e15355. <https://doi.org/10.1111/tan.15355> PMID: 38273454.
98. Wong J, Kazemi P, Coombe L, Warren RL, Birol I. 2023. aaHash: recursive amino acid sequence hashing. *Bioinformatics Advances*, vbad162, <https://doi.org/10.1093/bioadv/vbad162>
97. Lo T, Coombe L, Gagalova KK, Marr A, Warren RL, Kirk H, Pandoh P, Zhao Y, Moore RA, Mungall AJ, Ritland C, Pavly N, Jones SJM, Bohlmann J, Bousquet J, Birol I, Thomson A. 2023. Assembly and annotation of the black spruce genome provide insights on spruce phylogeny and evolution of stress response. *G3 Genes|Genomes|Genetics*, jkad247, <https://doi.org/10.1093/g3journal/jkad247>

96. Li JX, Fernandez KX, Ritland C, Jancsik S, Engelhardt DB, Coombe L, **Warren RL**, van Belkum MJ, Carroll AL, Vederas JC, Bohlmann J, Birol I. 2023. Genomic virulence features of Beauveria bassiana as a biocontrol agent for the mountain pine beetle population. *BMC Genomics* 24, 390. <https://doi.org/10.1186/s12864-023-09473-4>
95. Allison MJ, **Warren RL**, Lopez ML, Acharya-Patel N, Imbery JJ, Coombe L, Yang CL, Birol I, Helbing CC. 2023. Enabling robust environmental DNA assay design with “unikseq” for the identification of taxon-specific regions within whole mitochondrial genomes. *Environmental DNA*, 00, 1-16. <https://doi.org/10.1002/edn3.438>
94. Nip KM, Hafezqorani S, Gagalova KK, Chiu R, Yang C, **Warren RL**, Birol I. 2023. Reference-free assembly of long-read transcriptome sequencing data with RNA-Bloom2. *Nat. Commun.* 14, 2940. <https://doi.org/10.1038/s41467-023-38553-y>
93. Wong J, Coombe L, Nikolić V, Zhang E, Nip KM, Sidhu P, **Warren RL**, Birol I. 2023. Linear time complexity de novo long read genome assembly with GoldRush. *Nat. Commun.* 14, 2906. <https://doi.org/10.1038/s41467-023-38716-x>
92. Yoo S, Garg E, Elliott LT, Hung RJ, Halevy AR, Brooks JD, Bull SB, Gagnon F, Greenwood C, Lawless JF, Paterson AD, Sun L, Zawati MH, Lerner-Ellis J, Abraham R, Birol I, Bourque G, Garant JM, Gosselin C, Li J, Whitney J, Thiruvahindrapuram B, Herbrick JA, Lorenti M, Reuter MS, Adeoye OO, Liu S, Allen U, Bernier FP, Biggs CM, Cheung AM, Cowan J, Herridge M, Maslove DM, Modi BP, Mooser V, Morris SK, Ostrowski M, Parekh RS, Pfeffer G, Suchowersky O, Taher J, Upton J, **Warren RL**, Yeung R, Aziz N, Turvey SE, Knoppers BM, Lathrop M, Jones S, Scherer SW, Strug LJ. HostSeq: a Canadian whole genome sequencing and clinical data resource. *BMC Genom Data*. 2023 May 2;24(1):26. <https://doi.org/10.1186/s12863-023-01128-3> PMID: 37131148
91. Yang C, Lo T, Nip KM, Hafezqorani S, **Warren RL**, Birol I. 2023. Characterization and simulation of metagenomic nanopore sequencing data with Meta-NanoSim. *GigaScience J.* 12, giad013. <https://doi.org/10.1093/gigascience/giad013>
90. Li C, **Warren RL**, Birol I. 2023. Models and data of AMPlify: a deep learning tool for antimicrobial peptide prediction. *BMC Res. Notes.* 16, 11. <https://doi.org/10.1186/s13104-023-06279-1>
89. Coombe L, **Warren RL**, Wong J, Nikolic V, Birol I. 2023. ntLink: a toolkit for de novo genome assembly scaffolding and mapping using long reads. *Curr. Protocols.* <https://doi.org/10.48550/arXiv.2301.08785>
88. Richter A, Sutherland D, Ebrahimikondori H, Babcock A, Louie N, Li C, Coombe L, Lin D, **Warren RL**, Yanai A, Kotkoff M, Helbing CC, Hof F, Hoang LMN, Birol I. 2022. Associating Biological Activity and Predicted Structure of Antimicrobial Peptides from Amphibians and Insects. *Antibiotics*. 11(12):1710. <https://doi.org/10.3390/antibiotics11121710>

87. Nikolic V, Kazemi P, Coombe L, Wong J, Afshinfard A, Chu J, **Warren RL**, Birol I. 2022. btllib: A C++ library with Python interface for efficient genomic sequence processing. *Journal of Open Source Software*. 7(79), 4720, <https://doi.org/10.21105/joss.04720>
86. Shalev TJ, El-Dien OG, Yuen MMS, Shengqiang S, Jackman SD, **Warren RL**, Coombe L, van der Merwe L, Stewart A, Boston LB, Plott C, Jenkins J, He G, Yan J, Yan M, Guo J, Breinholt JW, Neves LG, Grimwood J, Rieseberg LH, Schmutz J, Birol I, Kirst M, Yanchuk AD, Ritland C, Russell JH, Bohlmann J. 2022. The western redcedar genome reveals low genetic diversity in a self-compatible conifer. *Genome Res.* gr.276358.121, <https://doi.org/10.1101/gr.276358.121>
85. **Warren RL**. 2022. HLA predictions from long sequence read alignments, streamed directly into HLAMiner. *arXiv*. <https://doi.org/10.48550/arXiv.2209.09155>
84. Kazemi P, Wong J, Nikolic V, Mohamadi H, **Warren RL**, Birol I. 2022. ntHash2: recursive spaced seed hashing for nucleotide sequences. *Bioinformatics*. btac564. <https://doi.org/10.1093/bioinformatics/btac564>
83. **Warren RL**. 2022. PASS: De novo assembler for short peptide sequences. *arXiv*. <https://doi.org/10.48550/arXiv.2208.05598>
82. Lin D, Sutherland D, Aninta SI, Louie N, Nip KM, Li C, Yanai A, Coombe L, **Warren RL**, Helbing C, Hoang LMN, Birol I. 2022. Mining Amphibian and Insect Transcriptomes for Antimicrobial Peptide Sequences with rAMPPage. *Antibiotics*. 11:952. <https://doi.org/10.3390/antibiotics11070952>
81. Gagalova KK, **Warren RL**, et al. 2022. Spruce giga-genomes: structurally similar yet distinctive with differentially expanding gene families and rapidly evolving genes. *The Plant Journal*. <https://doi.org/10.1111/tpj.15889>
80. Nikolic V, Afshinfard A, Chu J, Wong J, Coombe L, Nip KM, **Warren RL**, Birol I. 2022. RResolver: efficient short-read repeat resolution within ABySS. *BMC Bioinformatics*. 23:246. <https://doi.org/10.1186/s12859-022-04790-z>
79. Afshinfard A, Jackman SD, Wong J, Coombe L, Chu J, Nikolic V, Dilek G, Malkoç Y, **Warren RL**, Birol I. 2022. Physlr: Next-Generation Physical Maps. *DNA* 2:116-130. <https://doi.org/10.3390/dna2020009>
78. Li JX, Coombe L, Wong J, Birol I, **Warren RL**. 2022. ntEdit+Sealer: Efficient targeted error resolution and automated finishing of long-read genome assemblies. *Curr. Protocols*. 2:e442. <https://doi.org/10.1002/cpz1.442>
77. Li C, Sutherland D, Hammond SA, Yang C, Taho F, Bergman L, Houston S, **Warren RL**, Wong T, Hoang LMN, Cameron CE, Helbing CC, Birol I. 2022. AMPlify: attentive deep learning model for discovery of novel antimicrobial peptides effective against WHO priority pathogens. *BMC genomics*. 23:77. <https://doi.org/10.1186/s12864-022-08310-4>

76. Stephenson M, Nip KM, Hafezqorani S, Gagalova K, Yang C, **Warren RL**, Birol I. 2021. RNA-Scoop: interactive visualization of transcripts in single-cell transcriptomes. *NAR Genomics and Bioinformatics*. 3:lqab105. <https://doi.org/10.1093/nargab/lqab105>
75. Coombe L, Li JX, Lo T, Wong J, Nikolic V, **Warren RL**, Birol I. 2021. LongStitch: high-quality genome assembly correction and scaffolding using long reads. *BMC Bioinformatics*. 22:534. <https://doi.org/10.1186/s12859-021-04451-7>
74. **Warren RL**, Birol I. 2021. HLA alleles measured from COVID-19 patient transcriptomes reveal associations with disease prognosis in a New York cohort. *PeerJ*. 9:e12368. <http://doi.org/10.7717/peerj.12368>
73. Chen E, Chu J, Zhang J, **Warren R**, Birol I. 2021. GapPredict: A Language Model for Resolving Gaps in Draft Genome Assemblies. *IEEE/ACM Trans Comput Biol Bioinform*. <https://doi.org/10.1109/TCBB.2021.3109557>
72. **Warren RL** and Birol I. 2021. Interactive SARS-CoV-2 mutation timemaps. *F1000Res*. 10:68. <https://doi.org/10.12688/f1000research.50857.1> PMID: 34136131
71. **Warren RL** and Birol I. 2020. Retrospective in silico HLA predictions from COVID-19 patients reveal alleles associated with disease prognosis. *medRxiv*. 10.27.20220863; <https://doi.org/10.1101/2020.10.27.20220863>
70. Lo T, Coombe L, Lin D, **Warren RL**, et al. 2020. Complete chloroplast genome sequence of a black spruce (*Picea mariana*) from Eastern Canada. *Microbiol Resour Announc*. <https://doi.org/10.1128/MRA.00877-20>
69. **Warren RL** and Birol I. 2020. HLA predictions from the bronchoalveolar lavage fluid and blood samples of eight COVID-19 patients at the pandemic onset. *Bioinformatics*. <https://doi.org/10.1093/bioinformatics/btaa756>
68. Nip KM, Chiu R, Yang C, Chu J, Mohamadi H, **Warren RL**, Birol I. 2020. RNA-Bloom enables reference-free and reference-guided sequence assembly for single-cell transcriptomes. *Genome Res*. <http://www.genome.org/cgi/doi/10.1101/gr.260174.119>
67. Hafezqorani S, Yang C, Nip KM, **Warren RL**, Birol I. 2020. Trans-NanoSim characterizes and simulates nanopore RNA-seq data. *GigaScience*. 9:1-7. <https://doi.org/10.1093/gigascience/giaa061>
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. *Genome Biol Evol*. <https://doi.org/10.1093/gbe/evaa108>
65. Coombe L, Nikolić V, Chu J, Birol I, **Warren RL**. 2020. ntJoin: Fast and lightweight assembly-guided scaffolding using minimizer graphs. *Bioinformatics*. 36:3885. <https://doi.org/10.1093/bioinformatics/btaa253>

64. 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>
63. Lin D, Coombe L, Jackman SD, Gagalova KK, **Warren RL**, et al. 2019. Complete chloroplast genome sequence of an Engelmann spruce (*Picea engelmannii*) genotype from western Canada. *Microbiol Resour Announc*. 8:e00382-19. <https://doi.org/10.1128/MRA.00382-19>
62. Lin D, Coombe L, Jackman SD, Gagalova 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. <https://doi.org/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*. 35:4430. <https://doi.org/10.1093/bioinformatics/btz400>
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 <https://doi.org/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. <https://doi.org/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. <https://doi.org/10.1186/s12859-018-2243-x>
56. **Warren RL**. 2018. Visualizing genome synteny with xmatchview. *Journal of Open Source Software* 3:497. <https://doi.org/10.21105/joss.00497>
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*. <https://doi.org/10.1093/bioinformatics/btx839>
54. Jones SJ, Haulena M, Taylor GA, Chan S, Bilobram S, **Warren RL**, et al. 2017. The Genome of the Northern Sea Otter (*Enhydra lutris kenyoni*). *Genes*. 8:379.
53. Jones SJM, Taylor GA, Chan S, **Warren RL**, Hammond SA, Bilobram S, et al. 2017. The Genome of the Beluga Whale (*Delphinapterus leucas*). *Genes*. 8:378.

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.* 8:1433. <https://doi.org/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*. 34:725-731. <https://doi.org/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. <https://doi.org/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. <https://doi.org/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*. 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*. <https://doi.org/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. 2016. 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*. <https://doi.org/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. <https://doi.org/10.1186/s13742-015-0076-3>
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. <https://doi.org/10.1111/tpj.12886>
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. <https://doi.org/10.1186/s13073-015-0142-6>
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. <https://doi.org/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. <https://doi.org/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. <https://doi.org/10.1101/gr.165985.113>
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. <https://doi.org/10.1186/2049-2618-1-16>
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. <https://doi.org/10.1186/gm396>
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. <https://doi.org/10.1101/gr.126516.111>
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. <https://doi.org/10.1371/journal.pone.0019816>
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. <https://doi.org/10.1101/gr.115428.110>
22. D'Souza CA, Kronstad JW, Taylor G, **Warren R**, et al. 2011. Genome Variation in *Cryptococcus gattii*, an Emerging Pathogen of Immunocompetent Hosts. *mBio*. <https://doi.org/10.1128/mBio.00342-10>

21. Warren RL and Holt RA. 2010. A census of predicted mutational epitopes suitable for immunologic cancer control. *Hum Immunol.* 71:245-254.
20. Shah SP, Morin RD, Khattra J, Prentice L, Pugh T, Burleigh A, Delaney A, Gelmon K, Giuliany R, Senz J, Steidl C, Holt RA, Jones S, Sun M, Leung G, Moore R, Severson T, Taylor GA, Teschendorff AE, Tse K, Turashvili G, Varhol R, Warren RL, Watson P, Zhao Y, Caldas C, Huntsman D, Hirst M, Marra MA, Aparicio S. 2009. Mutational evolution in a lobular breast tumour profiled at single nucleotide resolution. *Nature.* 461:809-813. <https://doi.org/10.1038/nature08489>
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. <https://doi.org/10.1101/gr.092924.109>
17. Warren RL, Nelson BH, Holt RA. 2009. Profiling model T cell metagenomes with short reads. *Bioinformatics.* 25:458-464. <https://doi.org/10.1093/bioinformatics/btp010>
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.
13. Warren RL, Sutton GG, Jones SJ, Holt RA. 2007. Assembling millions of short DNA sequences using SSAKE. *Bioinformatics.* 23:500-501. <https://doi.org/10.1093/bioinformatics/btl629>
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. <https://doi.org/10.1186/1472-6750-6-43>
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, Romanuk 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, Lanning 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.
5. **Warren R**, Hsiao WW, Kudo H, Myhre M, Dosanjh M, Petrescu A, Kobayashi H, Shimizu S, Miyauchi K, Masai E, Yang G, Stott JM, Schein JE, Shin H, Khattri J, Smailus D, Butterfield YS, Siddiqui A, Holt R, Marra MA, Jones SJ, Mohn WW, Brinkman FS, Fukuda M, Davies J, Eltis LD. 2004. Functional characterization of a catabolic plasmid from polychlorinated-biphenyl-degrading *Rhodococcus* sp. strain RHA1. *J. Bacteriol.* 186:7783-7795.
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

3. BIROL, Inanc; LIN, Diana; **WARREN, René, Louis**; SUTHERLAND, Darcy; LI, Chenkai; HOANG, Linda; YANAI, Anat; EBRAHIMIKONDORI, Hossein; RICHTER, Amelia; HELBING, Caren, C; HOF, Fraser. WIPO (PCT) Patent Appln No. CA2024/050914, ANTIMICROBIAL PEPTIDES
- 2 BIROL, Inanc, LIN, Diana, **WARREN, René, Louis**, SUTHERLAND, Darcy, LI, Chenkai, HOANG, Linda, YANAI, Anat, FRASER, Erin - U.S. Patent Application No. 63/487,920 filed March 2, 2023, and in PCT Patent Application No. PCT/CA2023/050941 filed July 13, 2023. Antimicrobial Peptides.
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

20. Pacific Symposium on Biocomputing, Kona, Hawaii, USA. January 2025. (Poster: **ntRoot: Human ancestry inference at scale from genomic data**)
19. 27th Annual International Conference on Research in Computational Molecular Biology (RECOMB), Istanbul, Turkey, April 2023 (Poster: **Unique region identification in genomes using a k-mer approach**)
18. 29th Intelligent Systems for Molecular Biology (ISMB), Virtual/online. July 2021 (Speed talk: **SARS-CoV-2 variant timemaps**)
17. 27th Intelligent Systems for Molecular Biology (ISMB), Basel, Switzerland. July 2019 (Poster: **ntEdit: ultra fast, scalable genome sequence polishing**)
16. 22nd Annual International Conference on Research in Computational Molecular Biology (RECOMB), Paris, France, April 2018 (Poster: **Chromosome-scale scaffolding human genomes with linked read k-mers**)
15. 21st Annual International Conference on Research in Computational Molecular Biology (RECOMB), Hong Kong, May 2017 (Selected talk: **ARCS: Genome scaffolding with linked reads**)
14. American Society of Human Genetics (ASHG), Vancouver, Canada, October 2016 (Poster: **HLAminer v2: HLA predictions by targeted assembly with ABySS**)
13. 24th Intelligent Systems for Molecular Biology (ISMB), Orlando, Florida, USA. July 2016 (Invited talk – highlights track : **A scalable genome assembly toolkit**)
12. 23rd Intelligent Systems for Molecular Biology (ISMB), Dublin, Ireland. July 2015 (Invited talk – late breaking research track. Selected talk - HiTSeq): **LINKS: Scaffolding genome assemblies with nanopore reads**
11. Student Biotechnology Network, Vancouver, Canada. February 2015 (Invited talk: **My bioinformatics career journey**)
10. Pacific Symposium on Biocomputing, Kona, Hawaii, USA. January 2015 (Poster: **High-performance computing for assembly and analysis of big genomics data**)
9. Pacific Symposium on Biocomputing, Kona, Hawaii, USA. January 2012 (Poster: **HLAminer: Derivation of HLA types from shotgun sequence datasets**)
8. Sequencing, Finishing and Analysis in the Future, Santa Fe, New Mexico, USA. June 2010 (Invited Talk: **Sequencing human IgH from H. mole**)
7. Advances in Genome Biology and Technology, Marco Island, Florida, USA. February 2009 (Posters: **SSAKE v3.2.1 and T Cell Receptor Sequencing**)

6. Pacific Symposium on Biocomputing, Kona, Hawaii, USA. January 2008 (Poster: **SSAKE v3.0**)
5. Synthetic Biology 3.0 conference, Zurich, Switzerland. June 2007 (Invited talk: ***H. influenzae* genome reconstruction in *E. coli***)
4. 5th CSHL/Wellcome Trust Genome Informatics meeting. Cold Spring Harbor, New-York, USA. October 2005 (Poster: **Physical map-assisted whole-genome shotgun sequence assemblies**)
3. 7th Annual Conference on Computational Genomics. Reston, Virginia, USA. October 2004 (Poster: ***Rhodococcus* sp. RHA1 whole genome sequencing**)
2. Genomes 2004: International Conference on Microbial Genomes analysis. Hinxton, UK. April 2004 (Poster: ***Rhodococcus* sp. RHA1 whole genome sequencing**)
1. 3rd CSHL/Wellcome Trust Genome Informatics meeting. Cold Spring Harbor, New-York, USA. May 2003 (Poster: **Sequence Assembly Manager**)