

Posters

- J06 Chromatin state dynamics in genomic regulatory blocks across six human cell lines** • *Presenter:* Chandra Chilamakuri, University of Bergen, Norway; *Last Author:* Boris Lenhard, University of Bergen, Norway
- J07 The Encrypted Germline Genome of the Ciliate Oxytricha** • *Presenter:* Xiao Chen, Princeton University, United States; *Last Author:* Estienne Swart, Princeton University, United States
- J08 Gene Annotator Tool** • *Presenter:* Mary Shimoyama, Medical College of Wisconsin, United States; *Last Author:* Jeff DePons, Medical College of Wisconsin, United States
- J09 RNA-seq and Exome-seq analysis of two Ewing's sarcoma cell lines that show differential drug sensitivity** • *Presenter:* Tabrez Mohammad, Greehey Children's Cancer Research Institute, United States; *Last Author:* Yidong Chen, Greehey Children's Cancer Research Institute, United States
- J10 Whole genome bioinformatics analysis of glycoengineered Pichia pastoris strains with next generation sequencing technologies** • *Presenter:* Jun Zhuang, Merck & Co., Inc, United States; *Last Author:* Jason Hughes, Merck & Co., Inc, United States
- J11 A Novel Algorithm for Accurate and Efficient Alignment of DNA Sequencing Reads** • *Presenter:* Jaegyeon Ahn, Yonsei Univ., Korea, Rep; *Last Author:* Sanghyun Park, Yonsei Univ., Korea, Rep
- J12 Entropy based assessment of cell type-specific and frequent histone modification** • *Presenter:* Tadasu Nozaki, Keio University, Japan; *Last Author:* Masaru Tomita, Keio University, Japan
- J13 Primer3 - New Capabilities and Interfaces** • *Presenter:* Steve Rozen, Duke-NUS Graduate Medical School Singapore, Singapore; *Last Author:* Mairo Remm, University of Tartu, Estonia
- J14 Comprehensive analysis of RNA and DNA differences in non-small cell lung cancer** • *Presenter and Author:* Jinok Yang, Korean Bioinformatics Center/Korea Research Institute of Bioscience & Biotechnology, Korea, Rep
- J15 DNA methylome analysis using reduced representation bisulfite sequencing data** • *Presenter:* Katja Hebestreit, University of Münster, Germany; *Last Author:* Hans-Ulrich Klein, University of Münster, Germany
- J16 Integrative analysis of histone ChIP-seq and gene expression microarray data using Bayesian mixture models** • *Presenter:* Hans-Ulrich Klein, University of Münster, Germany; *Last Author:* Martin Dugas, University of Münster, Germany
- J17 Positioning of synonymous codon and gene translation efficiency among bacteria** • *Presenter and Author:* Satoshi Tamaki, Institute for Advanced Biosciences, Keio University, Japan
- J18 Multiscale Representation of Genomic Signals** • *Presenter:* Theo Knijnenburg, Netherlands Cancer Institute, Netherlands; *Last Author:* Stephen Ramsey, Seattle Biomedical Research Institute, United States
- J19 Direct RNA sequencing of a plant transcriptome highlights complexity of RNA 3'-end formation** • *Presenter:* Alexander Sherstnev, University of Dundee, United Kingdom; *Last Author:* Gordon Simpson, University of Dundee, United Kingdom
- J20 Semi-supervised learning based workflow for predicting recurrence of breast cancer** • *Presenter:* Chihyun Park, Yonsei University, Korea, Rep; *Last Author:* Sanghyun Park, Yonsei University, Korea, Rep
- J21 Improving Color Call Accuracy for Next Generation Sequencing using SVMs** • *Presenter:* Shruthi Viswanath, University of Texas at Austin, United States; *Last Author:* Chengyong Yang, Life Technologies Inc, United States
- J22 A Robust Linear Framework for Transcript Quantification using MultiSplice Features** • *Presenter:* Yan Huang, University of Kentucky, United States; *Last Author:* Jinze Liu, University of Kentucky, United States
- J23 DiffSplice: the Genome-Wide Detection of Differential Splicing Events with RNA-seq** • *Presenter:* Yan Huang, University of Kentucky, United States; *Last Author:* Jinze Liu, University of Kentucky, United States
- J24 FASTG: Representing the True Information Content of a Genome Assembly** • *Presenter:* Ted Sharpe, Broad Institute, United States; *Last Author:* David B. Jaffe, Broad Institute, United States
- J25 RSEM-EVAL: A Probabilistic Transcriptome Assembly Evaluator** • *Presenter:* Bo Li, University of Wisconsin-Madison, United States; *Last Author:* Nathanael Fillmore, University of Wisconsin-Madison, United States
- J26 forestSV: supervised learning for genomic structural variant discovery** • *Presenter:* Jacob Michaelson, University of California, San Diego, United States; *Last Author:* Jonathan Sebat, University of California, San Diego, United States