

Second Annual RECOMB Satellite Workshop on Computational Cancer Biology

Poster List

1. Eldrid Borgan, Ole Christian Lingjærde, Hans Kristian Moen Vollan, Hilde Johnsen, Ellen Schlichting, Rolf Kåresen, Torill Sauer and Anne-Lise Børresen-Dale
microRNAs involved in ischemic stress response of breast cancer tissue
2. Mike Smith, Mark Dunning, Simon Tavaré and Andy Lynch
Identification and correction of previously unreported spatial phenomena using raw Illumina BeadArray data
3. Simen Myhre, Bryan Hennessy, Jan Alsner, Jens Overgaard, Gordon Mills, Therese Sørli and Anne-Lise Børresen-Dale
Correlation of copy number, gene and protein expression for breast cancer related genes and proteins
4. Roy Navon, Hui Wang, Israel Steinfeld, Anya Tsalenko, Amir Ben-Dor and Zohar Yakhini
Novel statistics reveal cancer universal microRNA activity
5. Tony Håndstad, Morten Rye, Finn Drabløs and Pål Sætrom
A ChIP-seq based benchmark for transcription factor binding site predictors
6. Anita Sveen, Trude H. Aagesen, Ragnhild A. Lothe and Rolf I. Skotheim
Transcriptome instability, a novel molecular phenotype of colorectal cancer with associations to splicing factor expression levels and patient prognosis
7. Kate Bloch, Andy Evans, Hans Gmuender and Edward A Lock
Comparison of the gene expression profile induced by genotoxic and non-genotoxic carcinogens in the rat kidney cells
8. Moritz Gerstung, Christian Beisel, Peter Wild, Peter Schraml, Holger Moch and Niko Beerenwinkel
Genetic diversity in an evolving carcinoma revealed by ultra-deep sequencing
9. Takaya Saito and Pål Sætrom
A two-step site and mRNA-level model for predicting microRNA targets
10. Stine H. Kresse, Halfdan Rydbeck, Ana H. Barragan-Polania, Ronald Duim, Anne-Marie Cleton-Jansen, Ola Myklebost and Leonardo A. Meza-Zepeda
Integrative analysis of genome-wide genetic and epigenetic changes in human osteosarcomas
11. Heidi Maria Namløs, Stine H Kresse, Ingrid HG Østensen, Ronald Duim, Anne-Marie Cleton-Jansen, Leonardo A Meza-Zepeda and Ola Myklebost
Integrated analysis reveals overexpression of miRNA clusters in osteosarcoma

12. Laurent Thomas, Takaya Saito and Sætrom Pål
Identifying causative variants in microRNA target sites
13. Gautier Stoll, Didier Surdez, Franck Tirode, Karine Laud-Duval, Emmanuel Barillot, Olivier Delattre and Andrei Zinovyev
Ewing sarcoma network model through EWS-FLI1 signaling
14. Paul Geeleher, Eamonn Mulvey, Breege Howley, Vladimir Benes, Nicola Miller, Michael J. Kerin, Howard Fearnhead and Aaron Golden
miRNA Profiling of HER2 Positive Breast Cancers - Correlation between decreased hsa-miR-451 levels and late stage tumour status
15. Junbai Wang and Morigen Morigen
BayesPI - a new model to study protein-DNA interactions: a case study of condition-specific protein binding parameters for Yeast transcription factors
16. Peter Van Loo, Silje Nordgard, Ole Christian Lingjærde, Hege Russnes, Inga Rye, Wei Sun, Victor Weigman, Peter Marynen, Anders Zetterberg, Bjørn Naume, Charles Perou, Anne-Lise Børresen-Dale and Vessela Kristensen
Allele-specific copy number analysis of breast carcinomas
18. Inna Kuperstein, Paola Vera-Licona, Andrei Zinovyev, Gordon Tucker, Thierry Dubois and Emmanuel Barillot
Integrated cell cycle and DNA repair signalling network modelling for identification of key molecular regulators in basal-like breast cancer
19. Terje Kristensen, Vemund Jakobsen, Alvhild Alette Bjørkum, Remy Andre Monsen and Beate Kluge
Protein Data Clustering -some Adaptive Algorithms
20. Gautier Stoll, Didier Surdez, Franck Tirode, Karine Laud-Duval, Emmanuel Barillot, Olivier Delattre and Andrei Zinovyev
Ewing sarcoma network model through EWS-FLI1 signaling
21. Natasa Przulj, Tijana Milenkovic, Oleksii Kuchaiev, Hsiang Ho, Vesna Memisevic, Aleksandar Stevanovic, Anand Ganesan and Jayavani Aruri
Uncovering melanogenesis regulatory pathways from protein-protein interaction networks: the computational method and software tool
22. Vilde D Haakensen, Åslaug Helland, Anne-Lise Børresen-Dale and Ole Christian Lingjærde
GEST: Gene Expression Subtyping Tool
23. Xi Zhao, Therese Sørli, Bjørn Naume, Anita Langerød, Arnaldo Frigessi, Vessela N. Kristensen, Anne-Lise Børresen-Dale and Ole Christian Lingjærde
A multivariate Cox framework for prediction of breast cancer survival based on combined gene signatures
24. Robert Lesurf, Julie Livingstone, Sean Cory and Michael Hallett
Breast Signature Analysis Tool (BreSAT): a framework for investigating the molecular networks of breast cancer