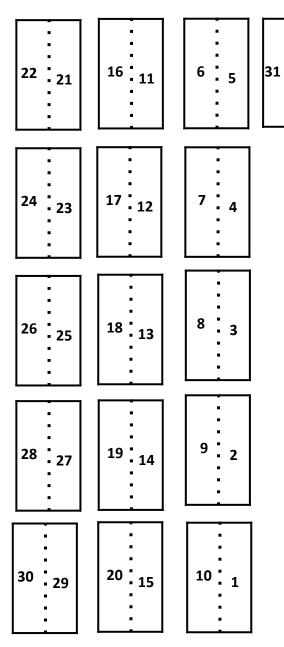
## **Poster Layout Map**

\*Poster Number Matches to Title Number on List to the Right▶\*

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# **2023 Poster Session Participants**

- 1. Thomas Liontis, Dept. of Biochemistry & Cell Biology, MED Clustering Analysis of histopathology scores from pneumonia Inhibition of endogenous small interfering RNAs transgenerationally extends the longevity of insulin/IGF-1 signaling mutants
- 2. GyeungYun Kim, Dept. Biology, CRC U1 snRNP regulates the usage of alternative promoters
- 3. Melissa Inge, Dept. of Biology, CRC Profiling the interactions of epigenetic regulators and their control of various T cells states
- 4. Cameron Dixon, Dept. of Biology, CRC Understanding peripheral disturbances following traumatic injury (TI) using Drosophila melanogaster
- 5. Jaice Rottenberg, Dept. of Biology, CRC Identifying viral protein regulators of host cell growth and death
- **6. Chelsea Stephens,** Dept. of Biology, CRC The Impact of Meg3 Knockdown on Directed Stem Cell Differentiation
- 7. Max Wertheimer, Dept. of Biology, CRC Characterizing the epithelial sheath as a barrier to professional phagocytes during apoptosis in the ovary
- 8. Yuqiao Jiang, Dept. of Biology, CRC Noninvasive transdermal measurement of glomerular filtration rate in a genetically modified mouse model of proteinruic kidney disease
- 9. David Engel, Graduate Program in Genetics and Genomics, kidney fibrosis

Gene co-expression network modules associated with NAFLD and their associated functionalities

- 10. Owen Sanborn, Dept. of Biochemistry, MED Simultaneous miRNA and transcriptome determination at single cell resolution
- 11. Yusuke Koga, Dept. of Computational Biomedicine, MED Comparison of the tumor and lymph node immune microenvironment in early non-small cell lung cancer through multimodal single cell sequencing

12. Amulya Shastry, Dept. of Computational Biomedicine, MED

autopsy samples identifies novel host-response driven pneumonia subclusters.

- 13. Erin Hennessey, Center for Regenerative Medicine, MED Developing a gene therapy approach to treat diseases of alveolar epithelial type II cells
- 14. Robert Fisher, Graduate Program in Genetics and Genomics, MED

Targeting the CoREST Complex Promotes Immunogenic and Tumor Suppressive RNA Splicing

- 15. Angelina Zuger, Dept. of Dermatology, MED Epigenetic Regulation of Targeted Therapy Resistance in Melanoma
- 16. Rachael Thomas, Dept. of Biochemistry and Cell Biology, MED

Investigating the retention of epigenetic marks of X inactivation throughout the cell cycle

- 17. Yichen Liu. Dept. of Medicine. MED Graph neural diffusion in single cell RNA-seq analysis
- 18. Genevieve Kunkel, Dept. of Molecular Biology, MED aiRBP's: Designer RNA-binding Protein generation using Large Language Models
- 19. Simon Lu, Dept. of Computational Biomedicine, MED A novel in-house computational pipeline for single-cell RNA sequencing data analysis reveals a novel molecular mechanism of
- 20. Dmitry Kretov, Dept. of Biochemistry and Cell Biology, MED

Quantitative measurement of RNA - protein interactions in vivo

- 21. Gian Sepulveda Graduate Program in Genetics and Genomics and Dept. of Biochemistry, MED C. elegans DOT-1.1 and mammalian DOT1L regulate MYC/Mondomediated transcription by promoting the transcription factor degradation cycle on chromatin
- 22. Shruti Gupta, Dept. of Biochemistry, MED Global small RNA genomics survey of Aedes aegypti discovers novel persistent viruses in specific mosquito locales

23. Sofia Weaver, Dept. of Biology, CRC

Evidence of Selection in the ADAM19 Gene Region in Savanna Monkeys (Chlorocebus spp.)

- 24. Shinobu Matsuura, Dept. of Medicine, MED Mechanistically Interrogate at the Gene Expression Level the effect of Anti-21 Integrin Antibody on JAK2V617F+ Stem Cells
- 25. Anthony Spinella, Dept. of Biochemistry and Cell Biology, MED

Defining the role of a yap-tead signaling axis in an ageassociated, immune-evasive tumor population in oral squamous cell carcinoma

**26. Pamela Yang, Dept. of Biology, CRC** 

The effects of draper gene knockdown in different tissues on ovarian function in Drosophila melanogaster

- 27. Shannon Fisher, Dept. of Pharmacology, Physiology, & Biophysics, MED Identification of conserved enhancers associated with craniosynostosis risk
- 28. Jackie Turcinovic, Dept. of Virology, Immunology, and Microbiology, MED; Program in Bioinformatics,

Transcriptional markers of disease in survival models of ebolavirus infection in nonhuman primates

- 29. Pooja Savla, Dept. of Bioinformatics, CRC Elucidating the Role of BCL11b in Aneurysm Development: Insights from RNA-sequencing Analysis
- 30. Krupa Sampat, Dept. of Bioinformatics, CRC Interactive meta-analysis web tool for gene expression-based contextual classification of cellular phenotype
- **31.** Aravind Sundaravadivel, Dept. of Biochemistry,

Exploring variants of genetic CJD with Whole Exome Seauencina data

32. Dylan Steiner, Dept. of Computational Biology, MED

Spatially informed profiling of stage I lung adenocarcinoma reveals an extensive gene expression signature of vascular invasion

33. Yi Xu, Zymo Research, Inc.

Universal rRNA Depletion for Transcriptome Analysis of Any Organism with a Streamlined, Autolaunch Platform for **Bioinformatics** 

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