**PsychENCODE Consortium Workshop**

July 7, 2017

National Institutes of Health

31 Center Drive

Bethesda, MD 20892

Room 6C10

8:30 am - 5:30 pm

**8:30 - 9:00 am**: **Check-in**

**9:00 AM – 12:00 PM: Morning Session** (**Chairs**: Nenad Sestan and Schahram Akbarian)

**Individual project updates** – 15 minutes per project

**9:00 – 9:15**: Update of Duke/UNC project – *Gregory Crawford, Ph.D., Duke*

*University*

**9:15 – 9:30**: Comparative transcriptome and gene regulation in iPSC derived

organoids and dono ridentical brain tissue – *Flora Vaccarino, M.D., Yale University*

**9:30 – 9:45**: Translation regulation and chromatin accessibility in

Schizophrenia – *Annie Shieh, University of Illinois at Chicago*

**9:45 – 10:00**: Cell type specific DNA methylation changes in the developing

and aging frontal cortex – *Andrew Jaffe, Ph.D., Lieber Institute for Brain Development*

**10:00 – 10:15**: A Comprehensive Profiling of Epigenome and Chromatin

Contacts in Cultured Neuronal Cells Derived from Olfactory Neuroepithelium to Study Molecular Mechanisms of Schizophrenia – *James Knowles, M.D., Ph.D., SUNY Downstate Medical Center*

**10:00 – 10:15**: Update of lncRNA projects – *Dalila Pinto, Ph.D., Icahn School of*

*Medicine at Mount Sinai*

**10:15 – 10:30**: **Break**

**10:30 - 11:00 am**: Summary of data availability – *Mette Peters, Ph.D., Sage*

*Bionetworks*

**10:45 – 11:00**: Functional Genomics of Human Brain Development and Autism

– *Nenad Sestan, M.D., Ph.D., Yale University*

**11:00 – 11:15**: Cell-type-specific H3K27ac and DNA methylation profiling

of adult human prefrontal cortex - *Stella Dracheva, Ph.D., Icahn School of Medicine at Mt. Sinai*

**11:15 – 11:30**: PRESENTATION TITLE

**11:30 – 11:45**: PRESENTATION TITLE

**11:45 – 12:00**: PRESENTATION TITLE

**12:00 - 12:15**: PRESENTATION TITLE

**12:00 – 5:30 PM: Afternoon Session** (**Chairs**: Greg Crawford and Pamela Sklar)

**12:00 – 12:30: Lunch (on your own)**

**12:30 – 2:00: Capstone project breakout groups**

* **Group 1:**
  + **Capstone Project 1:** Cross – disorder gene expression analyses in autism, schizophrenia, and bipolar disorder – Chairs: *Daniel Geschwind, Chunyu Liu, Kevin White*
  + **Capstone Project 4**: Integrative analysis (with CommonMind, ENCODE, GTEx, and Roadmap) – *Mark Gerstein, Jim Knowles*
* **Group 2:**
  + **Capstone Project 2**:Adult and disease epigenetic map – Chairs: *Pamela Sklar, Zhiping Weng*
  + **Capstone Project 3a**: Transcriptome and eQTL analyses across human brain development – Chair: *Nenad Sestan*
    - **Capstone project 3b**: Analysis of prompters/enhancer elements across early development: Construction of a Developmental EpiMap – Chair: *Flora Vaccarino*

**2:00 – 3:00: Reconvene from breakout groups**

**3:00 – 3:15: Break**

**3:15 – 4:15: Single cell analysis vs. other methods**

**4:15 - 5:15: Plan for capstone publications and policies and**

**Consortium data sharing policies**

1. Individual group plans for analysis and publications (see the individual group plans per the last face to face below)
   1. How they fit within the scope of capstone projects
   2. Collaboration with other consortia
   3. Publications in progress form each lab related to PsychENCODE
2. Revisit publication policies
   1. Individual project papers
   2. Joint analyses papers
   3. Citing PsychENCODE Consortium as an author

**5:15 - 5:30: Closing remarks**

**5:30: Adjourn**

**Addendum**

**Individual Analysis Plans**:

**Schahram Akbarian**

▪ ChIP-seq methods paper. Accepted

▪ Exploration of region specific epigenomic signal (me3 and ac27) in the normal human brain

**Greg Crawford**

▪ Analysis of ATAC-seq from 300 DLPFC [CMC samples](http://www.synapse.org/#!Synapse:syn2759792/wiki/69613) (150 cases and 150 controls), originating from the MSSM brain bank, to identify chromatin QTLs, with a focus on comparing to existing CMC RNA-seq and GWAS data. Plan to include STARR-seq data targeting a few GWAS loci to quantify some of the regulatory elements identified.

▪ ATAC-seq on the ACC is being generated from the same individuals, but will not be analyzed before after the DLPFC

**Stella Dracheva**

▪ Analysis of the neuron subtype-specific H3K27ac mark in the normal human brain

▪ Analysis of the neuron subtype-specific DNA methylation in the normal human brain (Published in 2016)

**Peggy Farnham**

▪ Analysis of inter individual and case-control differences in CNON cells (+ Jim Knowles)

▪ Analysis of chromatin domains and their ability to refine GWAS loci

**Dan Geschwind**

▪ Replication of microarray findings in RNA-seq - submitted

▪ Cross-disorder comparison using microarray data

▪ Characterization of Hi-C in fetal brain and utility in annotation of human specific gene annotation - submitted

**Mark Gerstein**

▪ Characterization of repetitive elements across disease and during development

▪ Characterization of allelic genes between individual brain regions

**Andrew Jaffe**

▪ RNA-seq methods paper. Other ways of looking at transcripts than gene and transcript counts and new measures of RNA quality

▪ Analysis WGBS from 80 DLPFC samples across development. Plan to integrate with expression changes to identify functional epigenetic trajectories. Will compare tissue homogenate to NeuN+ fractions

**Jim Knowles**

▪ NOME seq methods paper

▪ Differential gene expression between SCZ (81) and control (65) in CNON cells. (not directly PEC)

▪ microRNA analysis in SCZ and control CNON cells

**Chunyu Liu**

▪ Co-expression networks in SCZ, BD and controls using lncRNA and coding RNAs

▪ A study of technical vs population variation. Looking for data with technical replicates

**Dalila Pinto**

▪ IsoSeq methods paper

▪ Analysis of lncRNA in the CMC cohort (SZC and control)

▪ Analysis of lncRNA in ASD (waiting for total dataset since relatively small)

**Nenad Sestan**

▪ Create a RNA-seq and ChIP-seq reference maps of human development

▪ Create a RNA-seq reference map in human and macaque single cells

**Pamela Sklar**

▪ Characterization of RNAseq in Schizophrenia: Differential expression, coexpression networks, refinement of GWAS loci

▪ Study of post-mortem human human SCZ brains: Characterize the extent and nature of inter-individual variation, and neuronal vs. non-neuronal variation in these marks; common SNPs that influence chromatin states (epiQTLs - cis or trans); test for association with risk for SCZ and variation in epigenetic marks, refine SCZ SNP associations by prioritizing individual genes and causal alleles in nominally-associated GWAS regions

**Flora Vaccarino**

▪ Compare transcriptome and gene regulatory elements in iPSC-generated organoids with prenatal human brain tissue from the same individual.

▪ Provide a genome-wide catalogue of brain-specific transcripts and their transcription regulatory elements at different stages stages of early human neuronal differentiation

**Peter Zandi**

▪ RNA-seq in BD to define GWAS loci

▪ Differential expression in BD vs control at the gene and network level

**Authorship Principles**:

▪ All papers from individual groups (or, collaboration between individual groups) that have been entirely or partially funded through the PsychENCODE grants will include ‘PsychENCODE Federation’ as an author

▪ Individual, or collaborating, groups will determine authorship as appropriate. If individual group data processed by the DAC are used, individual DAC members will be co-authors

▪ Capstone projects will include ‘PsychENCODE Consortium’ as an author