**PsychENCODE Consortium-Wide Teleconference Call**

November 20, 2015

**Participants**: Geetha Senthil, Thomas Lehner, Flora Vaccarino, Suhn Rhie, Nenad Sestan, Peggy Farnham, Chunyu Liu, Dominic Fitzgerald, Jason Grundstad, Heather Witt, Andrea Beckel-Mitchener, Greg Crawford, Michael Eugenio Junko, Miguel Brown, Shannon Wood, Zhiping Weng, David Panchision, Stella Dracheva, Fides Lay, Mette Peters, Davy Kavanagh, Kay Grennan, Sirisha Pochareddy, Annie Shieh, Anahita Amiri, Gianfilippo Coppola, Robert Gao, Pamela Sklar, Mark Gerstein, Amber Thomas, Tim Reddy, Graham Johnson, Aslihan Dincer, Nancy Francoeur, Alexej Abyzov, Andrew Jaffe, Kevin White, Jim Knowles, Xiao Xu, Daniel Geschwind, Damon Polioudakis, Schahram Akbarian, Menachem Fromer

**Agenda**:

1. Guest presentation – *Manolis Kellis, Ph.D.* (30 mins)
2. Update on harmonizing phenotypic information – *Schahram Akbarian* (10 min)
3. Update from Data Coordination and Analysis Core
4. Available datasets on Synapse and transfer to Bionimbus cluster – *Mette Peters and Kevin White* (10 min)
5. Development of pipelines for RNA-Seq and ChIP-Seq – *Mark Gerstein and Zhiping Weng* (10 min)
6. Uniform processing of datasets timeline (**if possible, please provide slides**) - (10 min)
7. Joint data analysis projects (**please see attachment**) – *Pamela Sklar, Nenad Sestan, and Mark Gerstein* (50 min)

**Guest presentation** – *Manolis Kellis*, *Ph.D.*

Presentation: “Detecting sources of variance in DNA methylation levels in AD”

Please direct any questions on today’s presentations to Dr. Manolis Kellis: manoli@mit.edu.

**Update on harmonizing phenotypic information** – *Mette Peters*

* Mette presented the list of variables that groups decided would be the most valuable to have captured across projects.
* Dominic has been helping Mette with collecting this information. The only things he needs for the RNA-Seq analysis pipeline is the adapter sequence that was used, as well as, the Phred scores for raw scale, and the stranded-ness.
	+ The variables highlighted in blue are the additional variables that were added, in addition to what Schahram provided.
* Additional sample QC and assay variables are needed in terms of the assay information. For most studies, this information has already been provided.
* Mette needs to go through all the meta-data and look at what we need for each group, which she is in the process of doing now.

* RNA-Seq, except for CMC cohort, all need stranded protocol. Mette will follow up with Synapse liaisons, cc-ing Dominic, and will distribute the Clinical Variables spreadsheet to capture the additional information that is needed for each group.
* Mette: We have a list of t-value terms we associated with all the files that indicates where the tissue group came from and also information about the different protocols. We have not provided information on the stranded-ness which we need to collect. We also requested clinical meta-data and the meta-data collected during the assay processing.
	+ Mette will add tabs to the spreadsheet that show what the minimal variables are for the annotations and meta-data files.

**Available datasets on Synapse and transfer to Bionimbus cluster** – *Mette Peters*

* Most of the data is in place for the January 2016 public release. Data below is the data that will be released in January.

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| **PI** | **Study** | **Organism** | **Disease/ Treatment** | **Tissue/Cell Type** | **Life Stage** | **Assay/Assay Target** | **No. samples** |
| Chunyu Liu, Kevin White | BrainGVEX | **Human** | BD, SCZ, C | FC | Adult | **RNA-seq** | 239 |
| Peggy Farnham, James Knowles | CNON | **Human** | SCZ, C | CNON cells | Adult | ChIP-seq/ H3K27ac,H3K4me1,H3K4me3 | 6 |
| Greg Crawford, Patrick Sullivan | MouseHAL | Mouse | Haloperidol treated, C | STR |  | ATAC-seq | 15 |
| Greg Crawford, Patrick Sullivan |  | **Human** | SCZ, C | DLPFC/ACC | Adult | ATAC-seq | 8-20? |
| Stella Dracheve, Schahram Akbarian | EpiGABA | **Human** | C | PFC/GLU.GABAneurones | Adult | **RNA-seq**/ERRBS | 10 |
| Dalila Pinto | lncRNA Pilot | **Human** | C | DLPFC/A549,SH-SY5Y | Adult | IsoSeq, SeqCap | 12 |
| Daniel Geschwind | ASD | **Human** | ASD, C | C, PFC, TC | Adult | **RNA-seq**, ChIP-seq/ H3K27ac, (H3K4me3) | 205 |
| Andrew Jeffe | C | **Human** | C | DLPFC | Fetal | WGBS | 3 |
| Nenad Sestan, Matthew State, | ASD | **Human** | ASD, C | CBC, DFC | Fetal, Infant, Adult | ChIP-seq/H3K27ac | 18 |
| Nenad Sestan, Matthew State, | NPH | Macaque |  | CBC, DFC, DLPFC | Adult | **RNA-seq** | 9 |
| Pamela Sklar, Schahram Akbarian | EpiMap | **Human** | C | DLPFC, ACC/ NeuN+/- | Adult | ChIP-seq/H3K27ac,H3K4me3 | 129 |
| Flora Vaccarino, Matthew State, Mark Gerstein, Sherman Weissman | iPSC | **Human** | C | iPSC lines /NeuN+/- | Fetal, Adult | ChIP-seq/H3K27ac,H3K4me3 , **RNA-seq** | 6 |