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Editor

Science

 April 8, 2018

Re: Comprehensive functional genomic resource and integrative model for the adult brain

Dear Laura,

 We'd like to submit the enclosed manuscript, “Comprehensive functional genomic resource and integrative model for the adult brain” to *Science*. As you know, we've previously discussed this manuscript in detail. This represents the findings from one of the main PsychENCODE Capstone groups. It synthesizes all the adult brain data from PsychENCODE, including a large-scale volume of population-level chromatin and transcriptome data, and RNA data from single cell studies. This is the only PsychENCODE manuscript to comprehensively model and analyze this scale of chromatin and transcriptome data.

 Thank you for your consideration. Due to potential conflict of interests, we suggest excluding the major PIs of GTEx consortium and other psychiatric studies including Jonathan Pritchard (Stanford) and Stephen B Montgomery (Stanford). Also, we would suggest excluding Mick O’Donovan (Cardiff University) and James Walters (Cardiff University). However, in addition to the anchor reviewers that we suggested in the letter to Dr. Berg on February 27 2018, we list the following suitable reviewers for the manuscript:

1. Bing Ren, University of California San Diego, biren@ucsd.edu, +1 (858) 822-5766
2. Robert J. Klein, Icahn School of Medicine at Mount Sinai, robert.klein@mssm.edu, +1 (212) 241-6500
3. Roderic Guigó, Center for Genomic Regulation, Universitat Pompeu Fabra, roderic.guigo@crg.cat
4. Xiaole Shirley Liu, Dana-Farber Cancer Institute, Harvard School of Public Health, xsliu@jimmy.harvard.edu, +1 (617) 632-2472
5. Thomas Gingeras, Cold Spring Harbor Laboratory, gingeras@cshl.edu, +1 (516) 422-4105

 Note also, we have an extensive supplementary website with all the data files (Adult.psychencode.org). This is online now. Many of the files are open-access. However, some of the link connect to secure-access data. To access this, reviewers will need to establish anonymous Synapse accounts. (Please see attached document on how to do this.)

 We hope that you enjoy reading about the findings detailed herein and look forward to hearing from you in the near future.

 Yours faithfully,

 Mark Gerstein

 Albert L. Williams Professor

 of Biomedical Informatics