#### capstone 4 call 20180602 ####

Response: <http://goo.gl/jp1Xpv> <https://bit.ly/2LgvZrX>

Draft: <http://goo.gl/f228aK>

Supplement: <http://goo.gl/A6wmmN>

1st submission dropbox (Apr 10 2018): <https://www.dropbox.com/sh/ge42shs3souywja/AABsATLJGieIo8eiLSSppPUwa?dl=0>

# ## immediate todos

- DW & DC - think about splitting up the response a bit more & DC to show DW the encodec - assign to people

- PE et al. think about the website

- PE & DW - think about a presentation for the update GRN

- people can start filling in quick responses

- DC, SL, XS - think about the trans eQTL -residual-multivariate phenotypes

- XS - CBC think about cbc single cell

- MTG - think about CBC

- DW & SL & Hyg. - slides for Fri.

#

# ## LINK

http://bit.ly/mglab-capstone4-response

# ## Website

Fix up adult.psychencode.org - look a better - twitter bootstrap

Zhiping to host brain enhancers on CREs on SCREEN + encodec

JZ + MTG - get her cre list => psych screen

DW, DC - http://encodenets.gersteinlab.org/ - could make the networks browseable

What to ask Mette to do - PE, SL

# ### Schedule

Mon. - send the manuscript, not the suppl. + ref. Reports to Lora

5 or 6 June

Brain day w/ Hyg. & SL call in

8 June - pres.

- the six fig of paper

- put the referee reports - w/ some highlights

- slide (made DW) summarizing Laura's comments - GWAS, portal

16 June to ~10 Jul. - MG out of it

25 July - resubmission

<https://cts.sciencemag.org/scc/#/login>

# ### for/from Laura - May not relevant

Dear Laura,

Great thanks for sending the decision on the manuscript.

We have two quick questions:

1) Do you want a word document of the paper to mark up? You seem to have requested for the other capstone papers and we're wondering if you want it for our paper as well.

2) Many of the referees complained about the "denseness" of the text and fact that many of the supporting materials are in the supplement. They suggested that we move some of these materials to the maintext.

\*\* GWAS coordinate

Also per the reviewer who saw all 3 papers (reviewer #4) please note specific comments to be addressed: [All papers] do some form of GWAS hit enrichment in their expression data - it seems they should coordinate to present a unified robust discovery on this front, esp given that many the same authors are on all 3 papers. Also which data elements overlap these 3 studies?

SL & Hyg. - capstone DC & 4

\*\*\* Brainspan GWAS: Putative promoters and enhancers (H3K27ac peaks) specific for DFC or CBC were enriched for SNP heritability identified through partitioned LD score regression analysis from Genome Wide Association Studies (GWAS) for schizophrenia (SCZ), autism spectrum disorder (ASD), attention-deficit hyperactive disorder (ADHD), IQ, and neuroticism (NEUROT) but not for non-neural disorders or traits such as height, cholesterol levels, or diabetes. Solid color indicates significance for Bonferroni adjusted P-value and faint color indicates nominal significance at P<0.05.



26. B. M. Neale, P. Sklar, *Curr Opin Neurobiol* **30**, 131-138 (2015).

27. Network Pathway Analysis Subgroup of Psychiatric Genomics Consortium, *Nat Neurosci* **18**, 199-209 (2015).

28. Schizophrenia Working Group of the Psychiatric Genomics Consortium, *Nature* **511**, 421-427 (2014).

Need to respond

SL - nenad

Hyg. - Dan

\*\*\* There is adult bulk RNAseq in all of them - was this the same data?

PE & SL - Dan

Sort of!

is the single cell data used in each case the same?

Discussion pt. w/ Nenad

YES

Capstone1 used a diff. Of Lake

So DC capstone

Each of the papers has a fig 1 that details data used in the individual paper, but it is not possible to understand the bigger picture of which data sets are used across multiple studies (and which of these studies have already been published elsewhere). While it is clear that the raw and "pipeline processed" data from these studies is available through the PsychENCODE portal, it is my strong opinion that the more highly processed data elements used to detail individual findings in this report (and more generally in all large data resource annoucements of this type) should be made more easily accessible to readers. Each time an analysis is done and a finding reported, the processed data involved should be easily and directly accessible to any reader.

Referee has ignore adult.psychencode.org

Discussing on the call

# ## Laura's comments on the text (from aat8464\_ArticleContent\_v2.docx)

### 1

This tool can utilize the richly structured data of the resource to identify interactions between genotype and molecular phenotypes at multiple layers[LZ1] , as well as predict high-level[LZ2] traits.

 [LZ1]It’s not clear to me what this means in this context. Please rephrase/ clarify.

 [LZ2]What is a high-level trait? Please define.

### 2

We designed [Adult.PsychENCODE.org](http://adult.psychencode.org/) as a large, coherently structured resource of data of brain functional genomics (*1*). Broadly, it organizes data hierarchically, with a base of raw data files (of which individual genotyping and raw next-generation sequencing of transcriptomics and epigenomics have restricted access[LZ1]

I assume this access restriction is for privacy of the participants? Can you just say that here and [LZ1]briefly note here how one would be able to get access

Please see the checklist and supplemental template for formatting the supplemental materials Figures should be labeled sequentially as they appear in the text and in supplemental materials EG Fig 1A, 1B, 2, 3, S1, S2, S3. Please do not number them according to the sections of text with which they are associated.

### 3

 The results constitute a matrix, C of expression signatures, which are mostly concordant with what has been published (Fig. S2.4 and Conclusion[LZ1] ). A number of genes had expression levels that varied more across cell types than they did across individuals in a population (e.g., dopamine rec

 [LZ1]Please see the checklist and supplemental template for formatting the supplemental materials Figures should be labeled sequentially as they appear in the text and in supplemental materials EG Fig 1A, 1B, 2, 3, S1, S2, S3. Please do not number them according to the sections of text with which they are associated.

### 4

To investigate chromatin variability across the population, we uniformly processed the H3K27ac data from PFC, temporal cortex (TC), and cerebellum (CB) on a cohort of 50 individuals [LZ1] (*15*). Aggregating ChIP-seq data across the cohort resulted in a total of 37,761 H3K27ac "peaks"

 [LZ1]Are they a mix of populations or primarily people of European descent? This is information that would be worth noting

For example, particular excitatory and inhibitory neurons exhibited different fractions[LZ1] between male and female samples (i.e., Ex3 and In8).

 [LZ1]?Differed in number? If not please rephrase/ clarify

### 5

For gene expression, our RCA comparison revealed that the brain separates from the other tissues in the first component (Fig. 3E). [LZ1] Inter-tissue comparisons exhibits more differences than intra-tissue assessments (Fig. S4.1-4). A different picture emerged for chromatin. Comparisons showed that the chromatin levels at all regul

 [LZ1]Does RCA use Principle components- the axis of Fig 3E suggests this and to avoid confusion I’d make this clear above when it is described

### 6

Also, an appreciable number of eQTLs were enriched on the promoter of a different gene than the one regulated, suggesting e-promotor activity [LZ1] (*27*). For the overlap among different QTL

 [LZ1]Please briefly define what this means

### 7

TFs via enhancers. The SCZ-genes represent an increase from the reported 22 genes across 19 loci from a smaller QTL set (*8, 28*) and a larger number than can be linked by genomic proximity (176[LZ1] , Fig. 5D). The majority of the 734 SCZ-genes were not in linkage disequilibrium with the index SNPs ( ~6

 [LZ1]What is this number- your genes, or those previously associated? Please clarify.

### 8

**Acknowledgment**[LZ1]

We would like to acknowledge the National Institute of Mental Health (NIMH) for funding. Also, we acknowledge program staff, in particular T. Lehner, L. Bingaman, D. Panchision, A. Arguello and G. Senthil, for providing ins

 [LZ1]Please see the checklist for how the structure the acknowledgments

### 9

fig 3

Analysis for gene expression data of PsychENCODE samples are shown in dark green. The brain samples from GTEx are shown in light green[LZ1] , and other tissue samples are shown in magenta. **(F)** The center (cross) and ranges of transcription for different tissue clusters (dashed ellipses) are shown on an RCA scatterplot of (**E**).Finally, **(D)** The transcriptional diversity for coding (circle) and non-coding (triangle) regions among the tissue samples (inter-sample on x-axis) is shown compared to the diversity on cumulative tissue samples (y-axis) for tissue types including cerebellum, cortex, lung, skin, and testes, from PolyA RNA-seq data.[LZ2]

 [LZ1]These greens are difficult to distinguish on my display, perhaps a different color choice (keeping in mind potentially color vision deficient individuals) for one will help with the visualizations?

 [LZ2]D should be listed before E and F, both here and in the text

####### P2P response #######

Response: <http://goo.gl/jp1Xpv>

Draft: <http://goo.gl/f228aK>

Supplement: <http://goo.gl/A6wmmN>

1st submission dropbox (Apr 10 2018): <https://www.dropbox.com/sh/ge42shs3souywja/AABsATLJGieIo8eiLSSppPUwa?dl=0>

Point-by-Point response letter for revision

# Reviewer 1

## -- Ref 1.0a –resource as foundation for building knowledge--

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| --- | --- |
| ReviewerComment | Wang et al. presents the production and analysis of a large corpus of genomics data on the human brain as part of the PsychENCODE project. The analysis includes, in addition, brain data produced by other projects, creating likely the most comprehensive molecular resource of the human brain to date. I am a strong supporter of large-scale genomics projects. The resources that they generate serve as a foundation over which, through thework of many, knowledge is built about biological phenomena—without such a foundation, building such a knowledge would be much more costly. |
| AuthorResponse |  |
| Excerpt From Revised Manuscript |  |

## -- Ref 1.0b –overall--

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| ReviewerComment | It is often difficult to identify a specific breakthrough in genomic projects, and sometimes, under pressure to highlight them, findings may be over-emphasized. This is not a mistake in Wang et al. The value of the genomics projects is in both the data that they produce,and the methods they pioneer to produce, and analyze the data, and to report the findings. **In this regard, Wang et al. is, in my opinion, a very good large-scale functional****genomics project. The authors produce substantial data, they enhance their data, by pooling it together with other data, they develop methods to look at data in novel ways, and they present and summarize their data and their findings through high-content graphical descriptions.** Regarding specifically the last two points, I liked particularly their integrative deep-learning model (DSPN), through which the authors attempt to linkgenomic variants to organismic phenotypes (mostly brain disorders) through intermediate phenotypes. This will become increasingly relevant, as data on intermediate phenotypes (i.e biological imaging at different levels) will accumulate within the next years. Regardingthe presentation of the data and findings I acknowledge the effort by the authors to create figures that synthesize a large amount of information; some of these figure require a lot of effort by the reader, and, in some cases, some additional guidance through the captionswould be further acknowledge (see my specific comments, below). In addition, the paper includes some relevant resources and insights regarding cell composition, regulatory elements, eQTLs and GWAS. |
| AuthorResponse |  |
| Excerpt From Revised Manuscript |  |

## -- Ref 1.0c –Integration of additional data types and website--

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| ReviewerComment | As with all large genomic-scale projects, there is always some degree of arbitrarity in the angle that is chosen to present and analyze the data. For instance, the paper ignores comparisons with increasingly available primate brain genomic data, or, while the authors acknowledge that DSPN could be used to integrate neuroimaging data, no effort is made to integrate ample available neuroimaging data with associated genomics data. **I am not****suggesting that these analyses should be performed, maybe they are, but it is overall unclear to me what additional analysis of the data (these or others) are followed in more detail in companion papers (although some can be guessed from the references).** %%% coordinate **[[ WEBSITE ]]**%%% coordinate **What I find quite poor, compared to other genome projects is the Adult.PsychENCODE page. There are no query options, links to browsers that can be used by researchers interested****in particular genes or genomic regions, no good data visualization tools, etc. It looks to me just a data repository. Also access to many data requires a synapse account.** |
| AuthorResponse |  |
| Excerpt From Revised Manuscript |  |

## -- Ref 1.1 –data protocols--

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| ReviewerComment | I do not have strong issues with the paper itself; what follows is a number of comments/suggestions:1**. I could not find information on the protocols employed for obtaining the data used by the consortium. What was the depth of the RNA-Seq or what genotyping platform was employed, etc?.** I understand that data has been generated specifically for this project(according to Table S2.1), but this is not described in the paper, nor references to other papers describing this data are given. |
| AuthorResponse | Point out in suppl.  |
| Excerpt From Revised Manuscript |  |

## -- Ref 1.2 –single cell deconvolution--

$$$ XS to handle

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| ReviewerComment | 2. Transcriptome Analysis. The authors employ a method to estimate cellular composition in bulk tissue RNA-Seq based on the expression signatures that they infer from single cell data. One important result is that a large fraction of the variance of gene expression across tissue samples can be explained by changes in the cellular composition of the samples. The authors estimate that this is about 85%. This has implications for analysis of differential gene expression, since it means, in particular that changes in gene expression detected between different conditions (cell types, tissues, species, etc.) may actually reveal changes in cellular composition. **As a measure of “goodness” of their estimates of cellular proportions, the authors compute the R^2. Am I correct in assuming that in the way R^2 is computed in the paper, the underlying assumption is that expression variance is constant across all genes? If so, wouldn’t it make sense to provide the R^2 at the sample level (how well the expression for a single individual is explained with the estimated cell types, and see the distribution of these R^2 values, instead of calculating a global one).**$$$ split $$$Moreover, the authors used an alternative method, CIBERSORT, which apparently, it does not perform as well as their method (R^2=0.81, compared to 0.88 for their method. Although the wording is sort of confusing, because they say the variance is the R^2, which is actually the fraction of variance explained (also in the manuscript this number is 0.85)). **Given the previous comments, maybe the authors could compute in addition the root square mean error (RMSE). In any case, I think that it would useful to know how correlated the two methods are (i.e. whether they tend to produce the same decomposition of not).** |
| AuthorResponse |  |
| Excerpt From Revised Manuscript |  |

## -- Ref 1.3 –cell fraction changes across brain regions--

$$$ XS - could we do this on CBC ?

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| ReviewerComment | 3. Related to the above, another interesting result of the paper is that the authors found changes in the cell fractions associated to phenotypes and disorders. However, it is not clear to me whether these changes are inferred over all brain samples, or over specificregions (i.e. only the Prefrontal Cortex). **I believe that it would be of interest to investigate whether the changes occur similarly across different brain subregions.** |
| AuthorResponse |  |
| Excerpt From Revised Manuscript |  |

## -- Ref 1.4 –enhancers of temporal cortex vs. cerebellum--

$$$ MTG to think about

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| ReviewerComment | 4. Enhancers. **I found surprising that the number of enhancers is much large in temporal cortex than in cerebellum (~43,000 compared to ~27,000). Any hypothesis about this?** |
| AuthorResponse | Cortex has lots of cell types CBC is more homog.  |
| Excerpt From Revised Manuscript |  |

## -- Ref 1.5 –coloring tissues in comparative analysis--

$$$ Minor

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| ReviewerComment | 5. Figure 3E. Is it not possible to distinguish the colors corresponding to the different tissues—even zooming in the figure. Also, what is the population of samples near (0,-2)? |
| AuthorResponse |  |
| Excerpt From Revised Manuscript |  |

## -- Ref 1.6 –clarification of transcriptomic diversity on Figure 3--

$$$ Minor

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| ReviewerComment | 6. **I believe that the description of some figures and results could be improved. For instance, in Figure 3d it took me a while to understand what does “Transcriptome diversity” mean.** I believe it simply means % of (100bp windows in) the genome transcriptionally active (although in the main text it appears to implicitly mean the number of genes transcribed); and “Inter sample transcriptome diversity” just the average transcriptome diversity. Moreover, the caption of Figure 3d mentions triangles and circles, which do not appear in the figure. |
| AuthorResponse |  |
| Excerpt From Revised Manuscript |  |

## -- Ref 1.7 –replicability of GTEx eQTLs for non-brain tissues--

$$$ SL to put in results to the suppl. (target genes)

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| ReviewerComment | 7. QTL analysis. The authors claim a high replicability between their eQTLs and the GTEx brain eQTLs. To use this as support for the psychENCODE eQTLs, **I believe that it would be of interest to show that this replicability is smaller when compared to eQTLs from GTEx tissues other than brain.** |
| AuthorResponse |  |
| Excerpt From Revised Manuscript |  |

## -- Ref 1.8 –multivariate phenotypes for isoQTLs and fQTLs--

$$$ DC & SL & XS ??

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| ReviewerComment | 8. The authors use standard univariate approaches for isoform and cell fraction QTLs. These however are intrinsically multivariate phenotypes, in which the values of the different variables add to one (in the case of isoforms, if abundances are relative proportions). Testing them independently ignores the strong dependency between them. **There are now a number of methods that test associations with multivariate phenotypes, which are probably more appropriate in these cases.** |
| AuthorResponse |  |
| Excerpt From Revised Manuscript |  |

## -- Ref 1.9 –cell fractions for trans-eQTLs--

$$$ SL, Hyg. , DC - what to do ? I agree ?

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| ReviewerComment | **9. I am not sure I understand how the cell-type differences are factored out to identify 200,729 trans-eQTLs which “represent variant-expression associations largely unexplained by changing proportions of cell types”. I do not think this is explained in the****supplementary information.** **Also, why not a similar approach (i.e. using the cell fractions as co-variates) to identify cis-eQTLs truly associated to changes in gene expression and not to cell fractions?** |
| AuthorResponse |  |
| Excerpt From Revised Manuscript |  |

## -- Ref 1.10 –Figure captions on gene regulatory networks--

$$$ minor

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| ReviewerComment | 10. Regulatory Networks. Figure S6.1 The caption is confusing. I think that there is no description for panel C and panel D is missing. Also in Figure S6.2, maybe it is obvious, but what do CP and GZ stand for? In Figure 5F. what are the orange dots? |
| AuthorResponse |  |
| Excerpt From Revised Manuscript |  |

## -- Ref 1.11 –DSPN drawbacks, figure captions and binarization--

%%% JW

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| ReviewerComment | 11. Integrative deep-learning model. Figure 6D in general shows that DSPN improves phenothype prediction over other simpler methods, such as logistic regression, that do nottake into account intermediate phenotypes. However, this is not the case for ethnicity, in which DSPN performs worse than using only genotype information. Obviously, ethnicity is fully determined by genotype, and adding additional information may mask the genotype signal. **Maybe the authors could comment under which circumstances DSPN may not be the optimal approach.** $$$ split **Also, the figure is an example of the need of some better explanation.** As employed by the authors DSPN predicts binary phenotypes. But in Fig 6D one of the phenotypes investigated is age. It is not obvious from the caption of the text that age is being binarized |
| AuthorResponse |  |
| Excerpt From Revised Manuscript |  |

# Reviewer 2

## -- Ref 2.1 –Overall--

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| ReviewerComment | In this manuscript, the authors describe an impressive wealth of data generated within the PsychENCODE consortium, including genotype, transcriptome, chromatin (including Hi-C) and single cell data from over 1800 individuals. These data were then integratedwith existing functional genomic resources to build a unique resource for functional genomics in brain research. The authors not only catalogue the findings but also underline the relevance of this resource by presenting more extended functional annotation ofschizophrenia GWAS hits and by using these data to develop a deep learning model that integrate these molecular layers with genotypes and increases disease prediction. |
| AuthorResponse |  |
| Excerpt From Revised Manuscript |  |

## -- Ref 2.2 –single cell and bulk RNA-seq--

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| ReviewerComment | Overall, from the wealth of data, the authors present more detail on relating single cell gene expression data to bulk RNA seq. **This analysis, especially with the power of large sample sizes is highly relevant for the community.** |
| AuthorResponse |  |
| Excerpt From Revised Manuscript |  |

## -- Ref 2.3 –epigenomics--

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| ReviewerComment | The second focus is on enhancers. Here there is a limitation as only two chromatin marks are investigated in depth. **This should be presented as a limitation. This also introduces a limitation into the transcriptome epigenome comparison.** |
| AuthorResponse | We should ack.  |
| Excerpt From Revised Manuscript |  |

## -- Ref 2.4 –details for fQTLs--

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| ReviewerComment | The QTL analyses are very detailed and present for the first time QTL ranging from expression, chromatin, splicing-isoform, and cell-fraction QTLs, with interesting intersection presented. **As for the cell fraction QTLs, this is very novel, but more detail on****this analysis needs to be given to better understand how the SNPs drive this specific QTL.** |
| AuthorResponse |  |
| Excerpt From Revised Manuscript |  |

## -- Ref 2.5 –providing gene regulatory linkages--

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| --- | --- |
| ReviewerComment | The data presented so far are then integrated into regulatory network, investigating dual to multi-QTL. **Here some more detail should be given on the mentioned full regulatory network beyond the number of linkages.** These networks are then linked to GWAS data, showing strong enrichment for brain disorders and highlighting new candidate genes for schizophrenia. This important analysis seems somewhat buried in the supplements and this reviewer could not really find a link to the list of these genes. **[[[ $$$ split ]]****Also in this section CACNA1C is mentioned as an example but CHRNA2 is then shown in the figure (5F).** |
| AuthorResponse |  |
| Excerpt From Revised Manuscript |  |

## -- Ref 2.6 –samples and datasets for DSPN--

|  |  |
| --- | --- |
| ReviewerComment | Finally, the authors present an integrative deep learning model and apply it to differentiate between cases and controls using multilayer molecular data. **Again it would be helpful if the authors could briefly explain in the main text what kind of samples and data were used to test the full models vs. just genotype alone.** |
| AuthorResponse |  |
| Excerpt From Revised Manuscript |  |

## -- Ref 2.7 –enhance the links between main text and supplement--

|  |  |
| --- | --- |
| ReviewerComment | Overall, the authors present data and analyses from a unique resource leading to novel insights about regulatory elements in brain and their relationship to psychiatric disease. **The depth of analysis – from bulk sequencing to single cell with multiple layers of****molecular information is unique, especially paired with the large sample size and the work definitely deserves publication in a journal for a broad audience such as Science.** Overall, however, the paper is extremely dense and a lot of very important information is now onlyin the supplement. **Here additional brief summary sentences in the main text may help to enhance the link between the main text and the supplements and could avoid that readers miss some important results.** |
| AuthorResponse |  |
| Excerpt From Revised Manuscript |  |

## -- Ref 2.8 –website--

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| ReviewerComment | Most importantly, **the authors have made their data and analyses available to the public in a very well designed and intuitive website,** so that this resource can be easily accessed by other researchers. |
| AuthorResponse |  |
| Excerpt From Revised Manuscript |  |

# Reviewer 3

## -- Ref 3.0 –Overall--

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| --- | --- |
| ReviewerComment | The manuscript from Wang et al, entitle “comprehensive functional genomic resource and integrative model for the adult brain” provides for a comprehensive presentation of new genomic resources from the PsychENCODE consortium, including ~5,500 datasets from~1900 individuals. Through a series of analyses, the authors assess i- the source of intersample heterogeneity in expression profiles, arguing for changes in proportion of cell types accounting for over 85% of the variation, ii- define the cis-regulatory landscape and iii - report QTLs for expression, chromatin, splicing and cell-type-proportion changes in the reference brain. Finally, taking all the data into account, the authors present a new method to decipher disease predisposition and extend the list of genes targeted by GWAS hits for psychiatric disorders.Overall, this manuscript provides a comprehensive analysis of the PsychENCODE data, addressing the primary needs in analyzing such large genomic datasets. It also provides biological insight into population heterogeneity, exploiting single-cell RNA-seq to capture the contribution of changes in the proportion of cell types between samples to justify inter-sample variation. It also addresses the functional characterization of genetic risk to psychiatric diseases. |
| AuthorResponse |  |
| Excerpt From Revised Manuscript |  |

## -- Ref 3.1 –elaborating data samples and supplements--

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| --- | --- |
| ReviewerComment | 1. This manuscript is rich in information and would benefit from ensuring that all critical information be presented in the main text. Currently the reader has to rely heavily on the supplementary section to adequately understand the work. In addition, the following shouldbe considered:1.1 The type and number of samples available for each dataset should be clearly mentioned especially when multiple resources have been combined together for different analysis.1.2. Every section should mention the exact supplementary section being referred toinstead of just by ref(15).1.3 All supplementary figures should be referenced in the text. |
| AuthorResponse |  |
| Excerpt From Revised Manuscript |  |

## -- Ref 3.2 –source code for deep learning model--

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| ReviewerComment | 2. The source code of the deep-learning model should be made available. |
| AuthorResponse |  |
| Excerpt From Revised Manuscript |  |

## -- Ref 3.3 –Figure 3 legends and captions--

|  |  |
| --- | --- |
| ReviewerComment | 3. Legend to figure 3 needs to be revised. For instance, “Panels E and F are drown similarly to D” should read “similarly to B”. Also, Panel D need to be explained before E and F. Also, the figure states “(D) … for coding (circle) and noncoding (triangle)…” whileonly diamonds are presented in the figure. The legend should also include a description of the meaning for the arrows. |
| AuthorResponse |  |
| Excerpt From Revised Manuscript |  |

## -- Ref 3.4 –binarization in DSPN--

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| ReviewerComment | 4. The DSPN model uses a conditional deep boltzmann machine which requires binarized representations of the data used as also stated by the authors. It should be explained how gene expression and enhancer activity were binarized to fit the model. |
| AuthorResponse |  |
| Excerpt From Revised Manuscript |  |

## -- Ref 3.5 –quantitative description for cell types--

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| ReviewerComment | 5. Recommend a quantitative as opposed to qualitative report of the results in the text. For instance, on page 6 “…the proportions of excitatory neuron Ex4 and Ex5 were associated with the most”, this last word should be replaced by a quantitative assessment. (also consider completing that sentence with “fQTLs”). |
| AuthorResponse |  |
| Excerpt From Revised Manuscript |  |

## -- Ref 3.6 –data size for Figure 5C--

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| ReviewerComment | 6. Figure 5C, the number of data points should be clearly mentioned for each boxplot on the figure. |
| AuthorResponse |  |
| Excerpt From Revised Manuscript |  |

## -- Ref 3.7 –adding genotype information on Fig. 4B--

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| ReviewerComment | 7. Figure 4B, consider adding the genotype next to the H3K27ac signal on the figure |
| AuthorResponse |  |
| Excerpt From Revised Manuscript |  |

## -- Ref 3.8 –Referring “Roadmap” project --

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| ReviewerComment | 8. Change “Epigenomics Roadmap” on page 3 first paragraph to “Roadmap Epigenomics Project (Roadmap)” and maintain the use of “Roadmap” in subsequent sections |
| AuthorResponse |  |
| Excerpt From Revised Manuscript |  |

## -- Ref 3.9 –Figure resolution--

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| ReviewerComment | 9. The resolution on Figure 1, 3, 4 and 5 was poor. Please provide better quality figures. |
| AuthorResponse |  |
| Excerpt From Revised Manuscript |  |

## -- Ref 3.10 –Fig. S3.2--

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| ReviewerComment | 10. Supplementary figure 3.2, page 22, y-axis add “b” in “number” |
| AuthorResponse |  |
| Excerpt From Revised Manuscript |  |

# Reviewer 4 [anchor]

## -- Ref 4.1 –accessibility of processed data--

%%% website

|  |  |
| --- | --- |
| ReviewerComment | The authors use bulk and single cell RNAseq, H3K27ac, and Hi-C data to explore the molecular structure of the adult human brain.While it is clear that the raw and "pipeline processed" data from these studies is available through the PsychENCODE portal, **it is my strong opinion that the more highly processed data elements used to detail individual findings in this report (and more generally in all large data resource announcements of this type) should be made more easily accessible to readers.** Each time an analysis is done and a finding reported, the processed data involved should be easily and directly accessible to any reader. In particular, the cell typedata derived from the single cell data, the list of 80K enhancers in the reference brain as well as the 120K enhancers in the larger collection, the various QTLs identified, the Hi-C maps and regulatory networks, genes linked to GWAS variants - **all of these processed****data elements can be useful tools in additional in silico analysis and should be at the finger tips of readers.** |
| AuthorResponse |  |
| Excerpt From Revised Manuscript |  |

## -- Ref 4.2 –clarification of deep learning model--

$$$ we have clarified on the website

|  |  |
| --- | --- |
| ReviewerComment | Perhaps particular attention can be paid to the deep learning model in this manner. The authors stress its interpretability. **The structure, utility and exact location (for download) of input, intermediate, and output elements of this approach should be made clear to enable such secondary use of this analysis.** |
| AuthorResponse |  |
| Excerpt From Revised Manuscript |  |

## -- Ref 4.3 –fetal GWAS variants for disorders--

$$$ Hyg. - think about a figure.

|  |  |
| --- | --- |
| ReviewerComment | In the "Linking GWAS variants to genes" section, **it should be noted that the linking of GWAS variants to genes in this report uses only data from the adult brain, while much of risk for schizophrenia, ASD and bipolar disorder has been mapped to fetal development.**Therefore, this analysis may be missing a large proportion of the relevant expression and epigentic information to make these links. |
| AuthorResponse |  |
| Excerpt From Revised Manuscript |  |

## -- Ref 4.4 –NMF consistency--

%%% minor

|  |  |
| --- | --- |
| ReviewerComment | A minor point: the NMF algorithm used is not noted in either the main text or methods - what algorithm was used and does it produce stable/consistent results across multiple runs? |
| AuthorResponse |  |
| Excerpt From Revised Manuscript |  |