

## Life Sciences Reporting Summary

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Please do not complete any field with "not applicable" or n/a. Refer to the help text for what text to use if an item is not relevant to your study. [For final submission](#): please carefully check your responses for accuracy; you will not be able to make changes later.

### ▶ Experimental design

#### 1. Sample size

Describe how sample size was determined.

N=495 (Discovery) - This was established based on the brain tissue on hand and the money available for sequencing. However, we have previously shown that developmental changes in brain expression require much smaller sample sizes; previous eQTL analyses and power calculation by GTEx suggested that this sample size was well-powered for eQTLs; previous analyses and power calculations suggested this sample size was well-powered for case-control expression differences.

#### 2. Data exclusions

Describe any data exclusions.

We only included samples from the two main ethnicities in our brain collection - Caucasian and African American.

#### 3. Replication

Describe the measures taken to verify the reproducibility of the experimental findings.

We have downloaded and uniformly processed and quantified data from the CommonMind Consortium and the GTEx project. We also report replication p-values and statistics for expression features differentially expressed in schizophrenia and also for eQTLs identified in the DLPPFC

#### 4. Randomization

Describe how samples/organisms/participants were allocated into experimental groups.

This was an observational study from postmortem human brain tissue and thus subjects were not randomized into outcome groups. Subjects were diagnosed using medical records and next-of-kin interviews as described in the paper.

#### 5. Blinding

Describe whether the investigators were blinded to group allocation during data collection and/or analysis.

Investigators were not blinded to group allocation since the study was observational

Note: all in vivo studies must report how sample size was determined and whether blinding and randomization were used.

## 6. Statistical parameters

For all figures and tables that use statistical methods, confirm that the following items are present in relevant figure legends (or in the Methods section if additional space is needed).

n/a Confirmed

- The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement (animals, litters, cultures, etc.)
- A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
- A statement indicating how many times each experiment was replicated
- The statistical test(s) used and whether they are one- or two-sided  
*Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
- A description of any assumptions or corrections, such as an adjustment for multiple comparisons
- Test values indicating whether an effect is present  
*Provide confidence intervals or give results of significance tests (e.g. P values) as exact values whenever appropriate and with effect sizes noted.*
- A clear description of statistics including central tendency (e.g. median, mean) and variation (e.g. standard deviation, interquartile range)
- Clearly defined error bars in all relevant figure captions (with explicit mention of central tendency and variation)

See the web collection on [statistics for biologists](#) for further resources and guidance.

## ► Software

Policy information about [availability of computer code](#)

## 7. Software

Describe the software used to analyze the data in this study.

TopHat2 (v2.0.4 and v2.0.9), R/Bioconductor (limma, GenomicRanges, MatrixEQTL, sva, clusterProfiler, derfinder, derfinderPlot, minfi, crlmm), featureCounts (v1.4.3-p1), StringTie (v1.1.2), regtools (v0.1.0), CuffMerge (v 2.2.1), plink (v1.9), bwtool. More information is available at our GitHub repository: [https://github.com/LieberInstitute/brainseq\\_phase1](https://github.com/LieberInstitute/brainseq_phase1)

For manuscripts utilizing custom algorithms or software that are central to the paper but not yet described in the published literature, software must be made available to editors and reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). [Nature Methods guidance for providing algorithms and software for publication](#) provides further information on this topic.

## ► Materials and reagents

Policy information about [availability of materials](#)

## 8. Materials availability

Indicate whether there are restrictions on availability of unique materials or if these materials are only available for distribution by a third party.

No unique materials were used - sequencing data will be made available as described below

## 9. Antibodies

Describe the antibodies used and how they were validated for use in the system under study (i.e. assay and species).

No antibodies were used

## 10. Eukaryotic cell lines

a. State the source of each eukaryotic cell line used.

No eukaryotic cell lines were used

b. Describe the method of cell line authentication used.

No eukaryotic cell lines were used

c. Report whether the cell lines were tested for mycoplasma contamination.

No eukaryotic cell lines were used

d. If any of the cell lines used are listed in the database of commonly misidentified cell lines maintained by [ICLAC](#), provide a scientific rationale for their use.

No eukaryotic cell lines were used

## ► Animals and human research participants

Policy information about [studies involving animals](#); when reporting animal research, follow the [ARRIVE guidelines](#)

## 11. Description of research animals

Provide all relevant details on animals and/or animal-derived materials used in the study.

No animals were used

## 12. Description of human research participants

Describe the covariate-relevant population characteristics of the human research participants.

These 495 samples were from postmortem donors which are not considered human subjects - however, demographic data on these donors is available in Table S1. Briefly, this overall cohort was 65.9% Male and 48.7% Caucasian with an average age of 37.0 (including 50 prenatal samples). 175/495 subjects were patients diagnosed with schizophrenia.