



Data Set Group: GSE15745 GPL6104 NIH Human Brain ILM humanRef-8 v2.0 (May10) RMA

Data Set: GSE15745 NIH Human Brain Prefrontal Cortex ILM humanRef-8 v2.0 (May10) RankInv

GN Accession: GN482

GEO Series: [GSE15745](#)

Title: Integration of GWAS SNPs and tissue specific expression profiling reveal discrete eQTLs for human traits in blood and brain.

Organism: [Human \(hg19\)](#)

Group: Brain-Normal-NIH-Gibbs

Tissue: Prefrontal Cortex mRNA

Dataset Status: Public

Platforms: [Illumina humanRef-8 v2.0 expression beadchip \(GPL6104\)](#)

Normalization: RankInv

Contact Information

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Download datasets and supplementary data files

- [GN482_MeanDataAnnotated_rev081815.txt \(23M\)](#)
- [GN482_StdError_rev081815.txt \(450K\)](#)

Summary:

Summary from GEO Series [GSE36192](#) and [GSE: GSE36194](#) "A fundamental challenge in the post-genome era is to understand and annotate the consequences of genetic variation, particularly within the context of human tissues. We describe a set of integrated experiments designed to investigate the effects of common genetic variability on mRNA expression distinct human brain regions. We show that brain tissues may be readily distinguished based on expression profile. We find an abundance of genetic cis regulation mRNA expression. We observe that the largest magnitude effects occur across distinct brain regions. We believe these data, which we have made publicly available, will be useful in understanding the biological effects of genetic variation."

Experiment Type:

North American Brain Expression Consortium and UK Human Brain Expression Database: Gene Expression. Genome-wide association studies have nominated many genetic variants for common human traits, including diseases, but in many cases the

underlying biological reason for a trait association is unknown. Subsets of genetic polymorphisms show a statistical association with transcript expression levels, and have therefore been nominated as expression quantitative trait loci (eQTL). However, many tissue and cell types have specific gene expression patterns and so it is not clear how frequently eQTLs found in one tissue type will be replicated in others. In the present study we used two appropriately powered sample series to examine the genetic control of gene expression in blood and brain. We find that while many eQTLs associated with human traits are shared between these two tissues, there are also examples where blood and brain differ, either by restricted gene expression patterns in one tissue or because of differences in how genetic variants are associated with transcript levels. These observations suggest that design of eQTL mapping experiments should consider tissue of interest for the disease or other traits studied. Published by Elsevier Inc.

Citation:

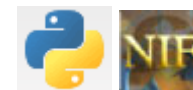
Please review and cite: Gibbs JR, Hernandez DG, Dillman A, Ryten M, Trabzuni D, Traynor BJ, Nalls MA, Arepalli S, Ramasamy A, van der Brug MP, Troncoso J, Johnson R, O'Brien R, Zielke HR, Zonderman A, Ferrucci L, Longo DL, Smith C, Walker R, Weale M, Hardy JA, Cookson MR, Singleton AB. **PMID: 22433082.**

Study Id:

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WWW service initiated January, 1994 as **The Portable Dictionary of the Mouse Genome** and June 15, 2001 as WebQTL. This site is currently operated by **Rob Williams, Lei Yan, Pjotr Prins, Zachary Sloan, Arthur Centeno**. Design and code by Pjotr Prins, Lei Yan, Zach Sloan, Arthur Centeno, Kenneth Manly, Jintao Wang, Danny Arends, Christian Fischer, Sam Ockman, Xiaodong Zhou, Christian Fernandez, Ning Liu, Rudi Alberts, Elissa Chesler, Evan G. Williams, Alexander G. Williams, and Robert W. Williams, and **colleagues**.



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