

MetaBrain

14 datasets

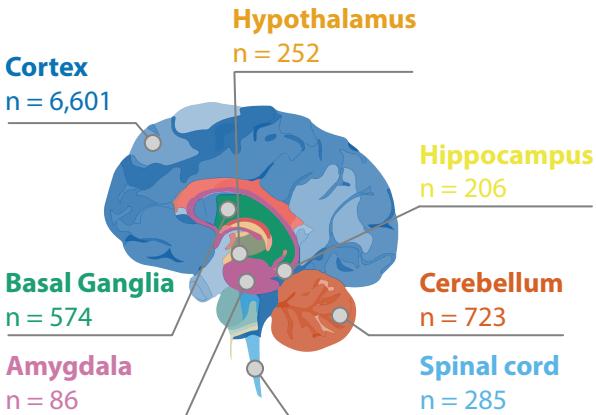
6,518 individuals

8,727 RNA-seq samples

Re-align and harmonize

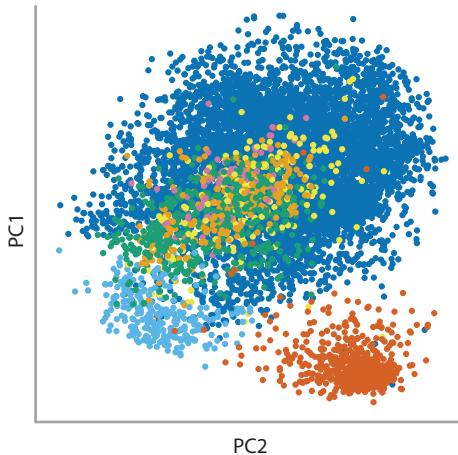
7 brain regions

collected across multiple datasets



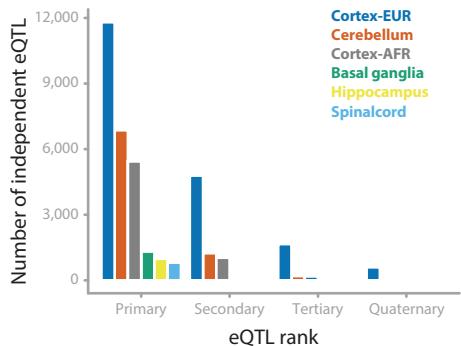
Principal component analysis

distinguishes brain regions



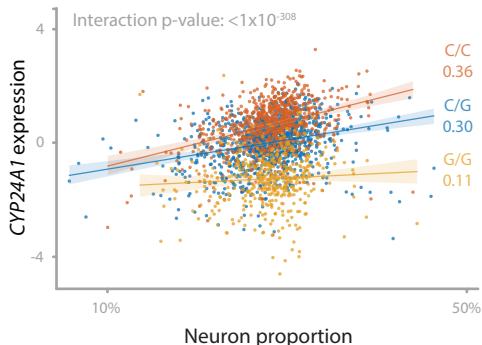
Cis-eQTL analysis

e.g. identifies multiple independent associations per gene in different brain regions



Interaction eQTL analysis

e.g. identifies neuron dependent eQTL for multiple sclerosis associated SNP and *CYP24A1*



Trans-eQTL analysis and Coregulation network

e.g. identifies 35 trans-eQTLs for SNP associated with frontotemporal dementia

