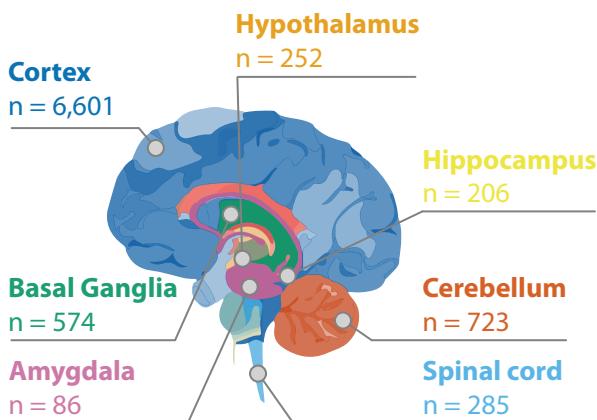


# MetaBrain



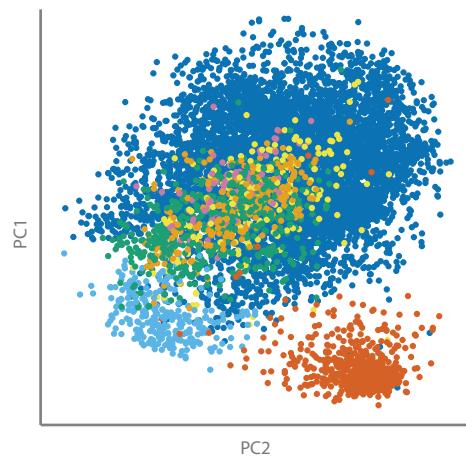
## 7 brain regions

collected across multiple datasets



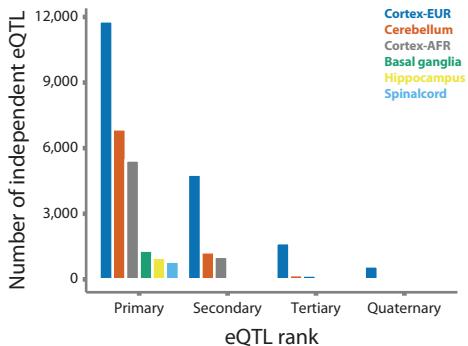
# Principal component analysis

recovers broad brain physiology



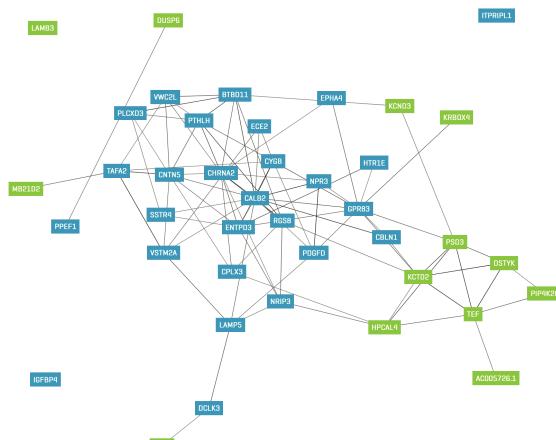
## **Cis-eQTL analysis**

identifies multiple independent associations per gene in different brain regions



## **Trans-eQTL analysis and Coregulation network**

identifies 34 trans-eQTLs for SNP associated with Frontotemporal dementia



## Interaction eQTL analysis

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

