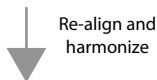




MetaBrain

15 datasets
6,518 individuals
8,727 RNA-seq samples



7 brain regions

Hypothalamus
n = 252

Cortex
n = 6,601

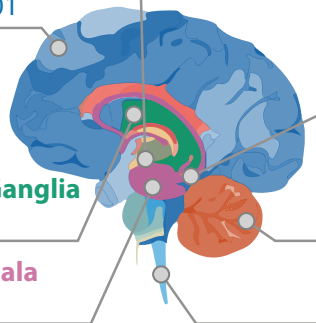
Hippocampus
n = 206

Basal Ganglia
n = 574

Cerebellum
n = 723

Amygdala
n = 86

Spinal cord
n = 285

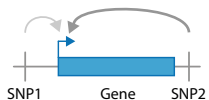


Cis-eQTLs



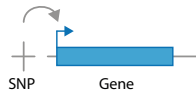
27,226 primary *cis*-eQTLs

Secondary eQTLs



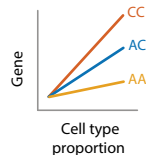
16,192 non-primary *cis*-eQTLs

Trans-eQTLs



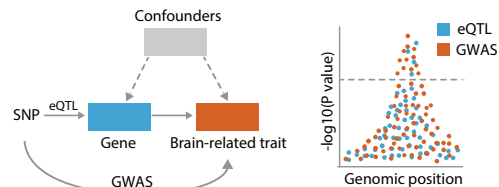
2,589 *trans*-eQTLs

Interaction eQTLs



1,515 interaction eQTLs

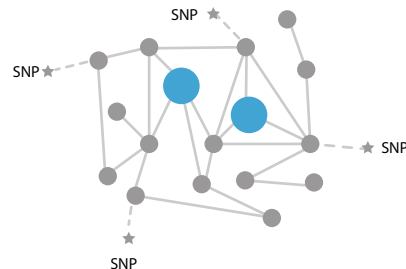
Mendelian randomization and colocalization



439 prioritized genes for 27 brain related traits

Gene
prioritization

Co-regulation network



208 genes prioritized for 5 traits