**24 hippocampal gene co-expression modules**

Co-expression analysis, human surgical hippocampus samples (fresh frozen, n=122 TLE patients)

Conserva7on, of, co-expression, in, several, gene, expression, datasets,
human non-diseased hippocampus samples (post-mortem, n=63)
mouse non-diseased hippocampus samples (fresh-frozen, n=100)
UKBEC (post mortem, 4 brain regions, n=102)

**Cross-species and cross-brain regions conserved gene co-expression modules**

Enrichment of association with cognitive abilities
GWAS
- Discovery (GS:SFHS) n=6,732
- Replication (LBC1936) n=1,003

Enrichment for disease ascertained de novo mutations
WES
- (ASD, SCZ, ID, EE, DDD)
Total parent-offspring trios n=6,871

**Convergent gene co-expression module for cognitive abilities and neurodevelopmental diseases**

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Supplementary Figure 1

Schematic overview of study design

We hypothesized that gene regulatory networks starting from the human hippocampus could be informative for genes and pathways relevant to diverse cognitive abilities and neurodevelopmental disease. Hippocampus gene-regulatory networks were inferred *a priori*, without reference to cognitive phenotypes using fresh-frozen hippocampus samples that had been surgically removed from 122 patients undergoing temporal lobectomy for epilepsy. Conservation of modules was then tested using distinct expression datasets from non-diseased post-mortem hippocampus samples (n=63) and healthy mouse hippocampus samples (n=100). From this, we identified 4 cross-species conserved hippocampal gene co-expression modules whose co-expression relationships are unrelated to epilepsy (M1, M3, M11 and M19). We then used independent gene expression datasets to show that these modules were conserved widely across the human cortex and expressed under tight developmental regulation during brain development. The modules were then integrated with GWAS data relating to four cognitive abilities (general fluid cognitive ability, processing speed, crystallized cognitive ability and verbal delayed recall) in two independent community cohorts (GS:SFHS and LBC1936), and *de novo* mutation data from parent-offspring trios across five neurodevelopmental disorders (ASD, SCZ, ID, EE, DDD) to reveal convergent gene co-expression modules for healthy human cognitive abilities and neurodevelopmental disease. Full details relating to datasets, experimental methods and references are provided in the manuscript. TLE=temporal lobe epilepsy; ASD=autism spectrum disorder; SCZ=schizophrenia; ID=intellectual disability; DDD=Deciphering Development Disorders Cohort (http://www.ddduk.org). UKBEC=UK Brain Expression Consortium (http://www.braineac.org). WES= whole-exome sequencing.