

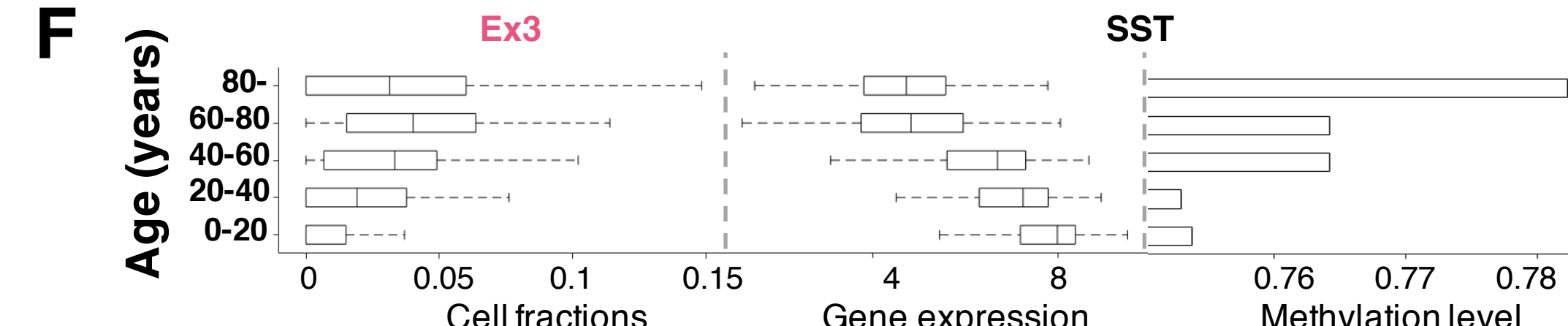
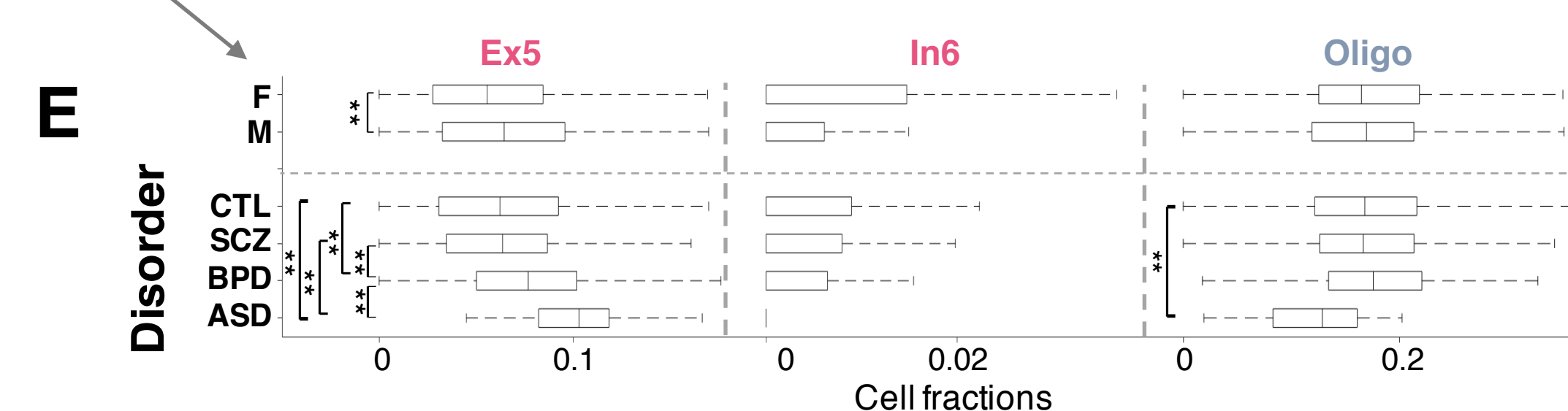
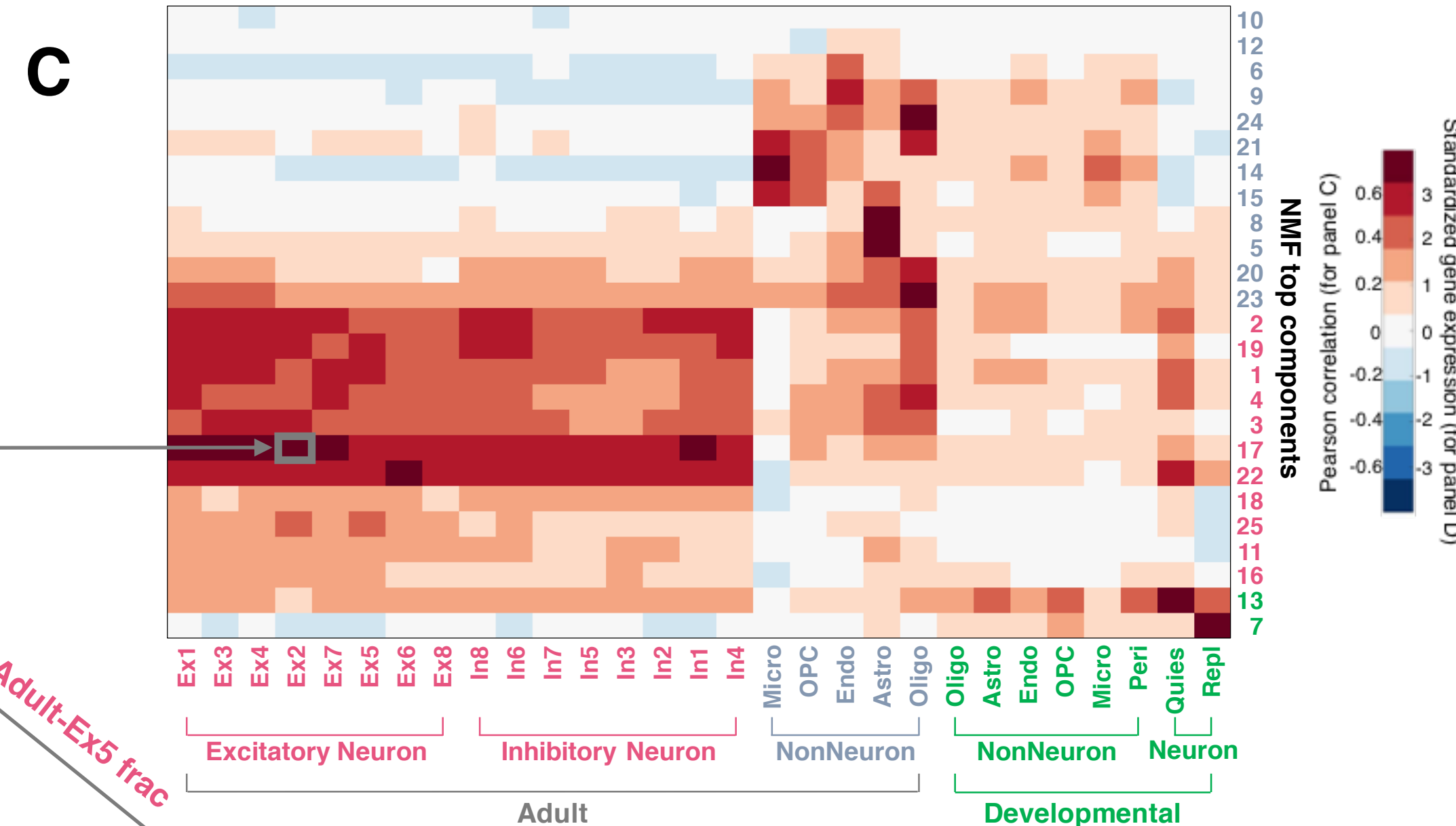
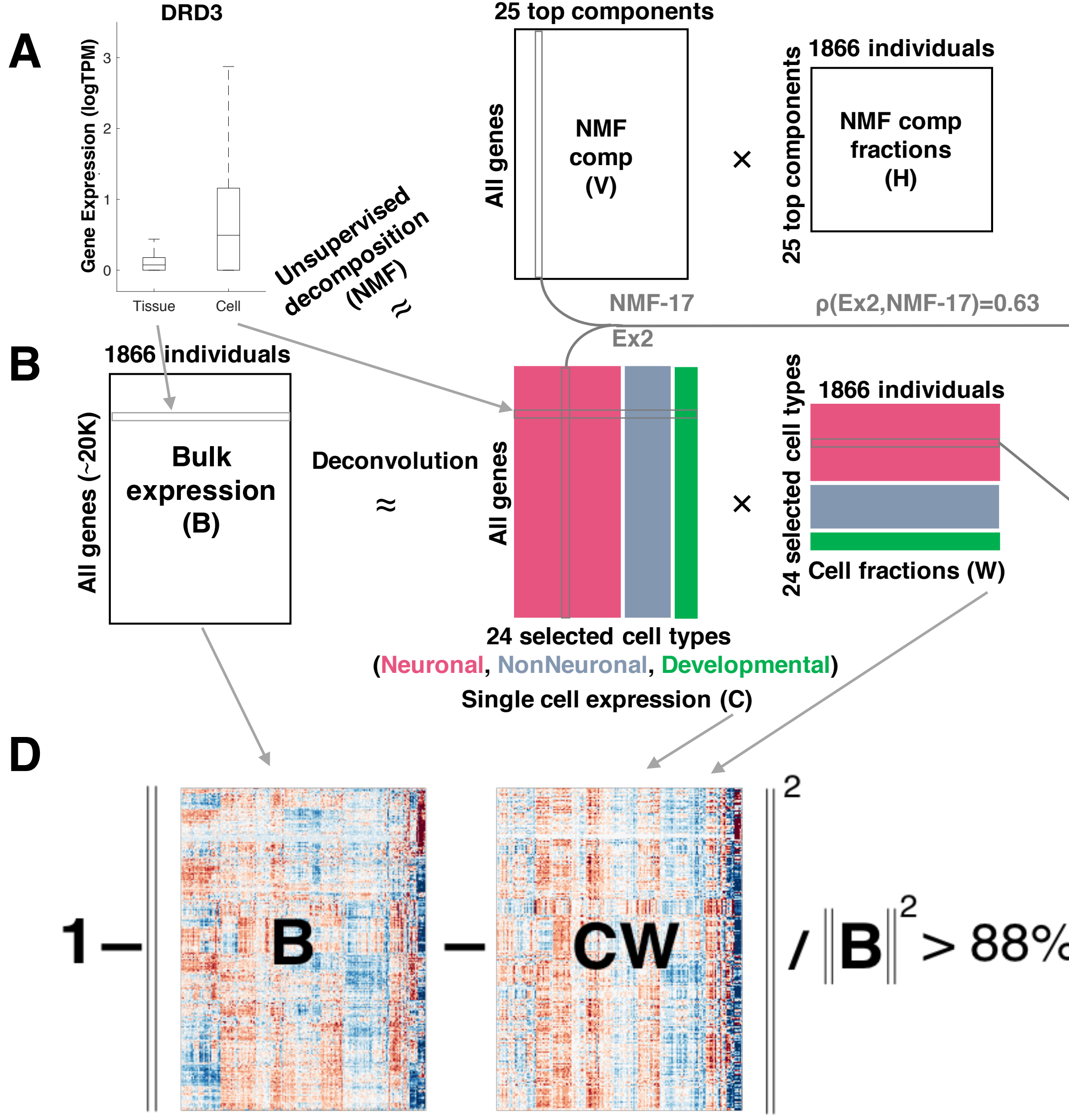
Tissue

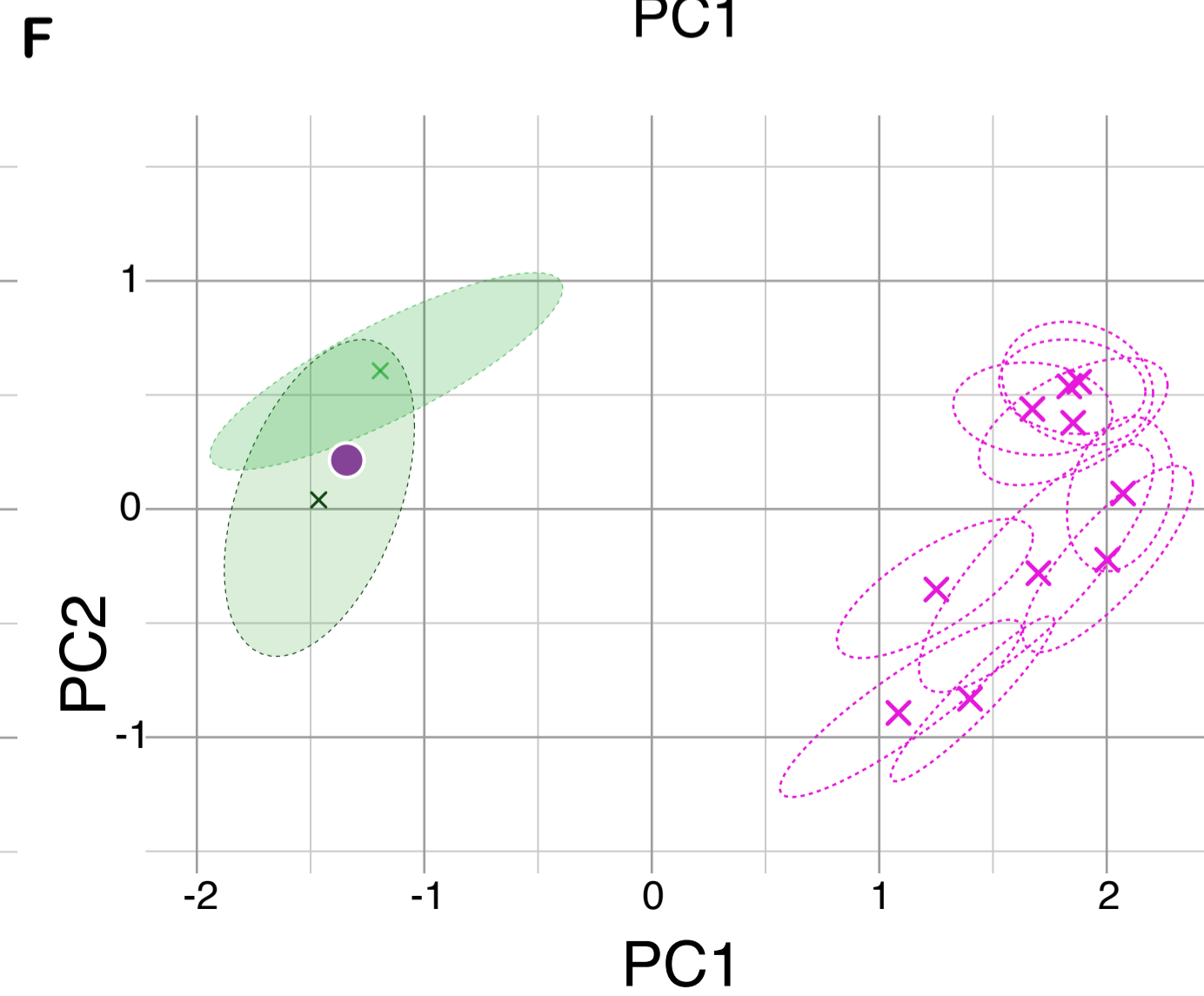
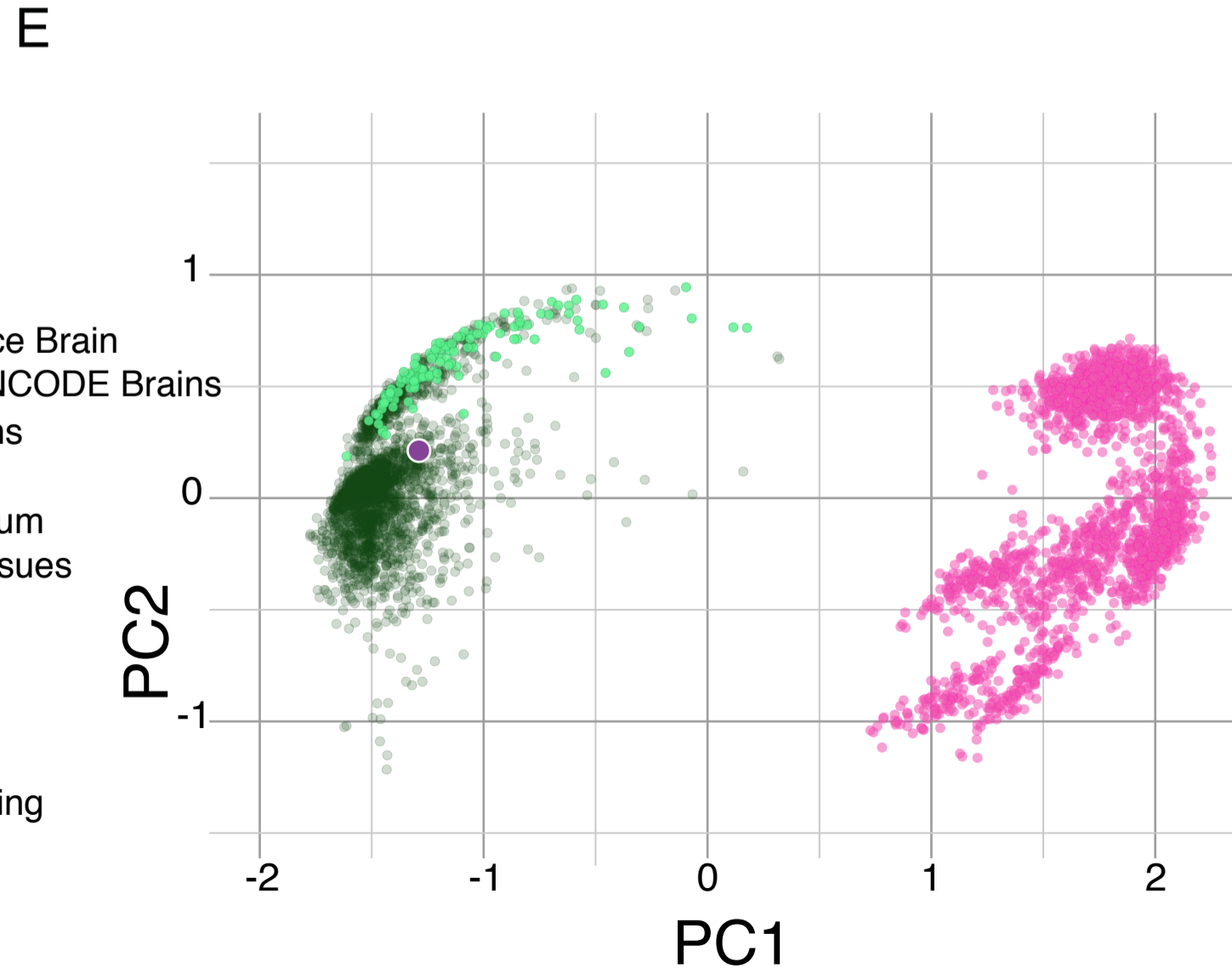
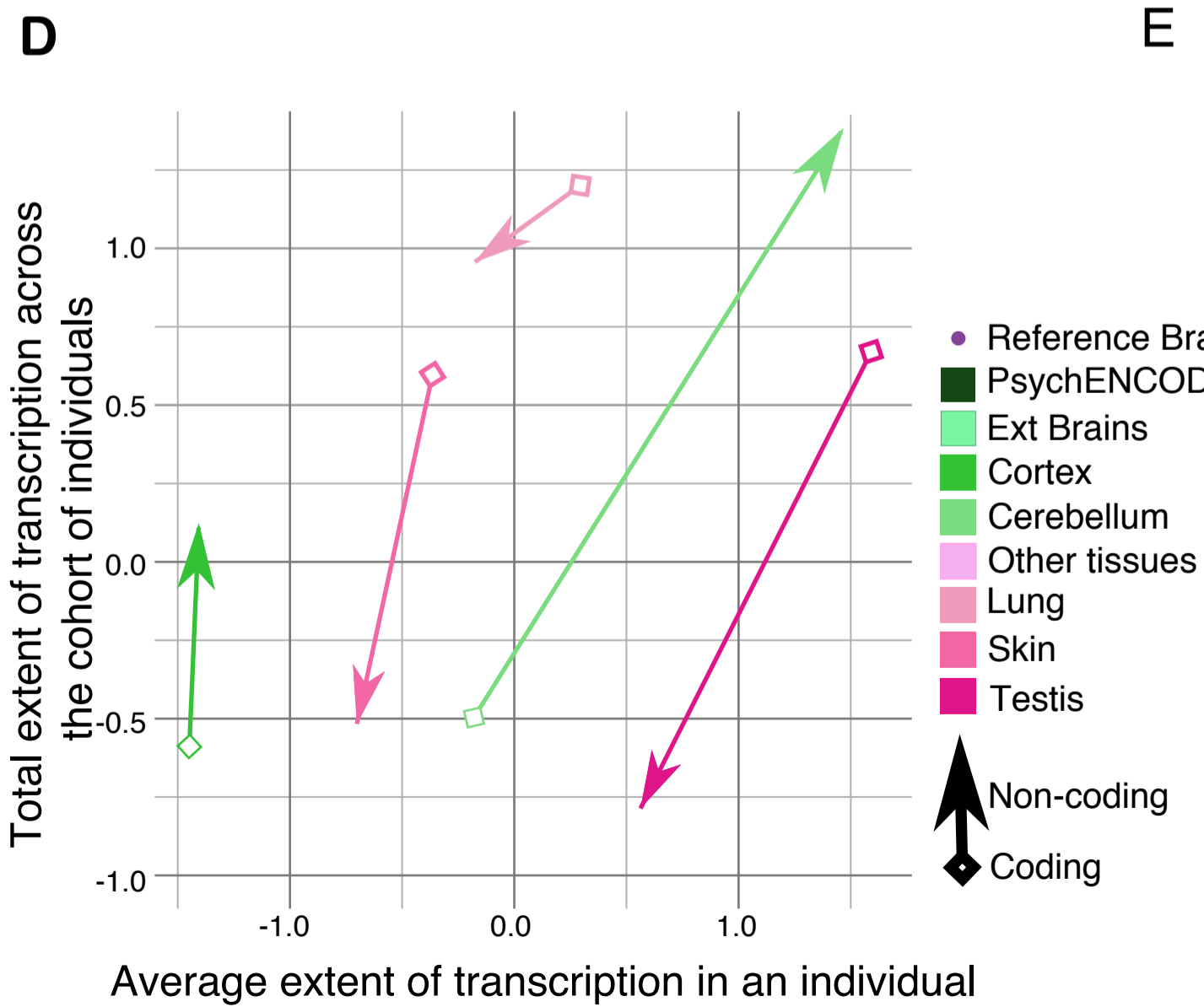
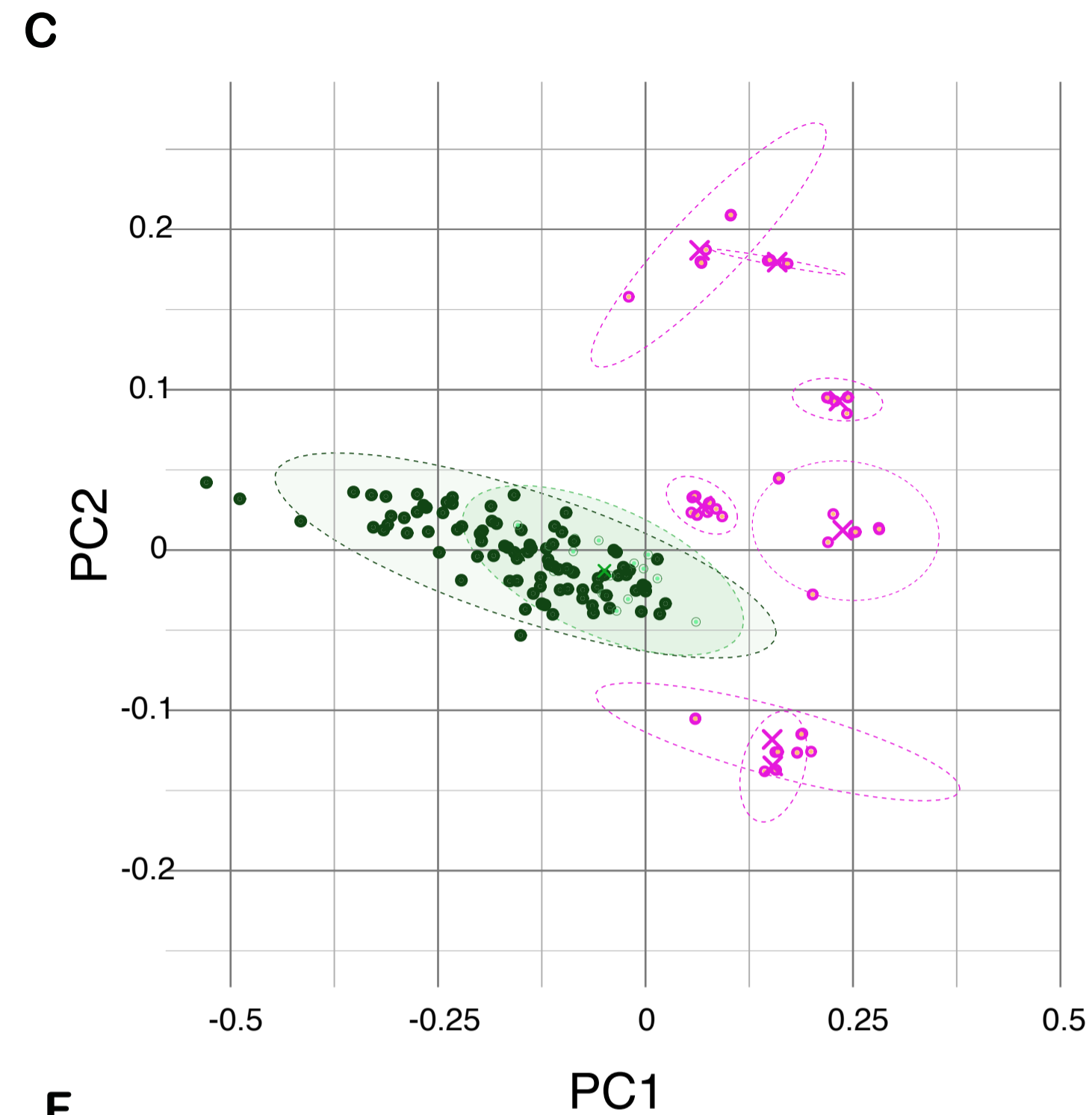
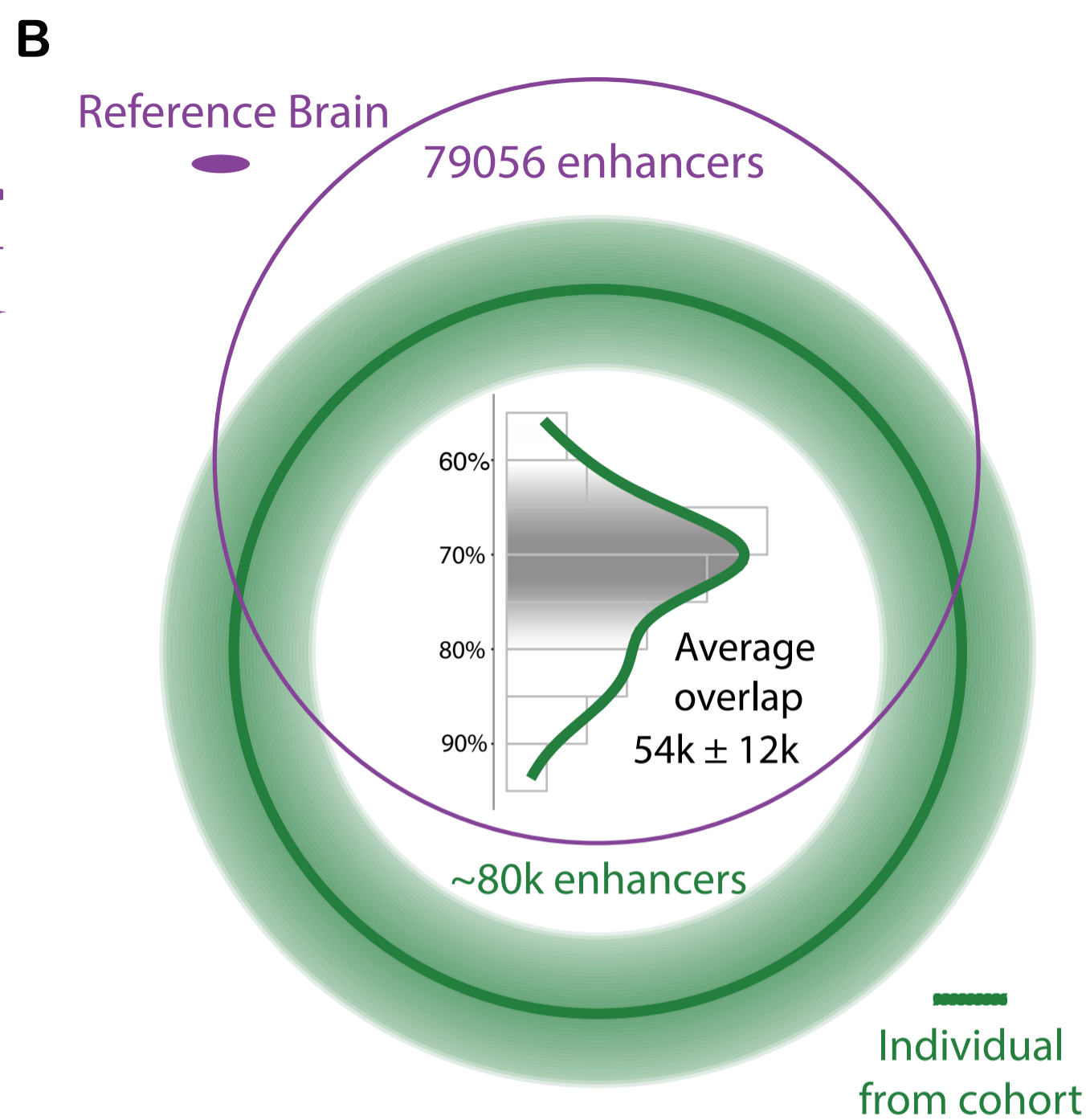
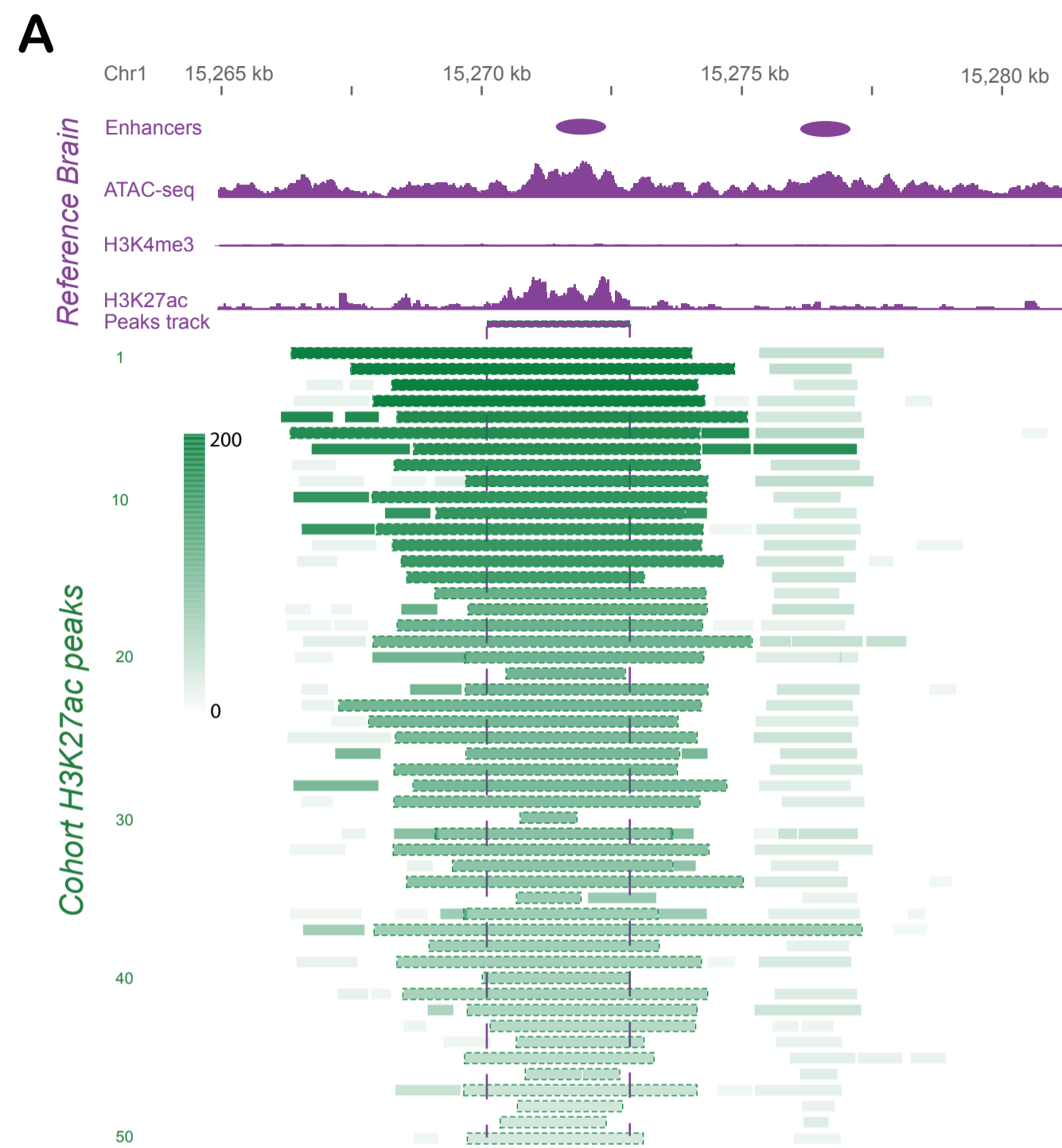
Prefrontal Cortex - PFC (26,769)

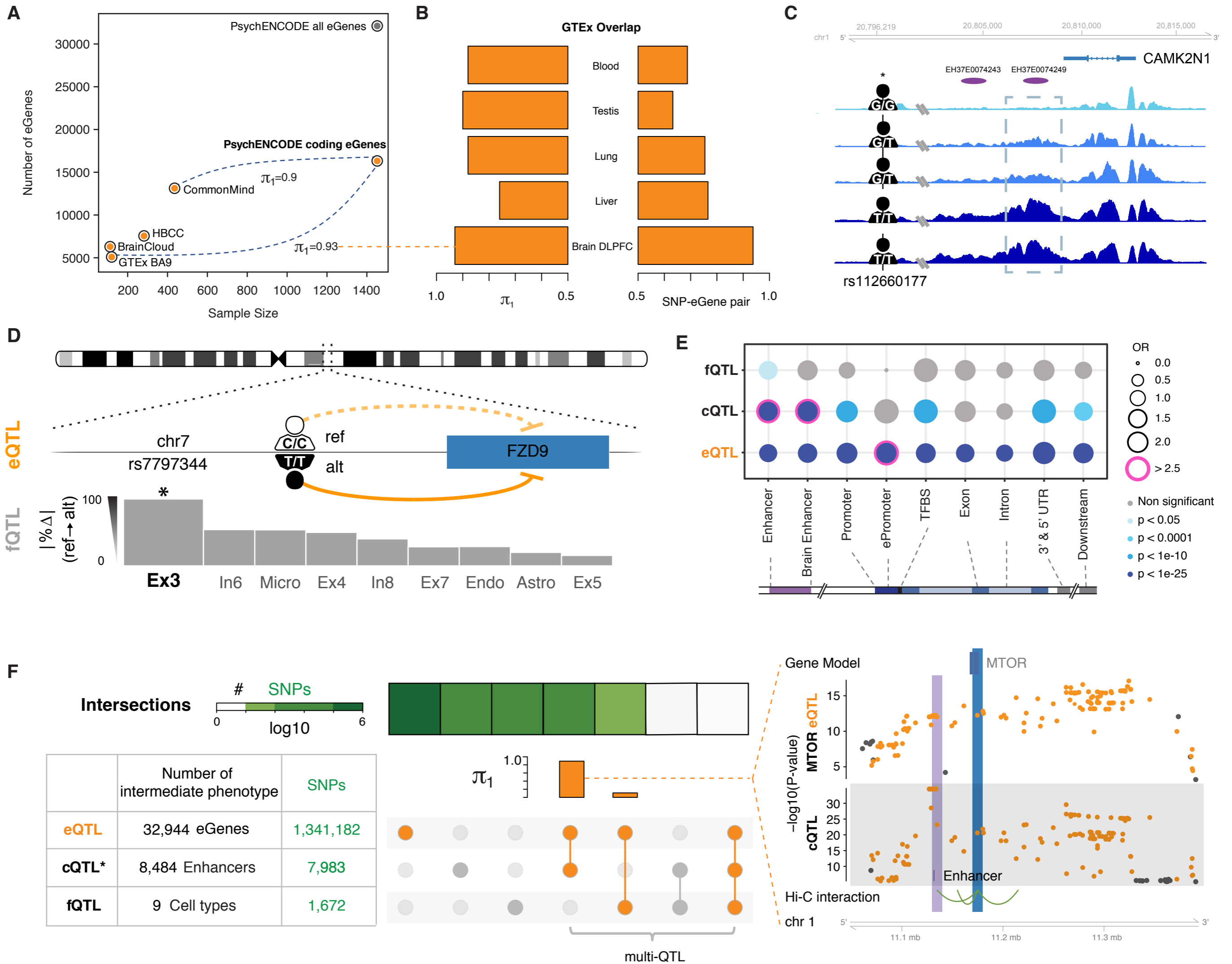
Temporal Cortex - TC (2,153)

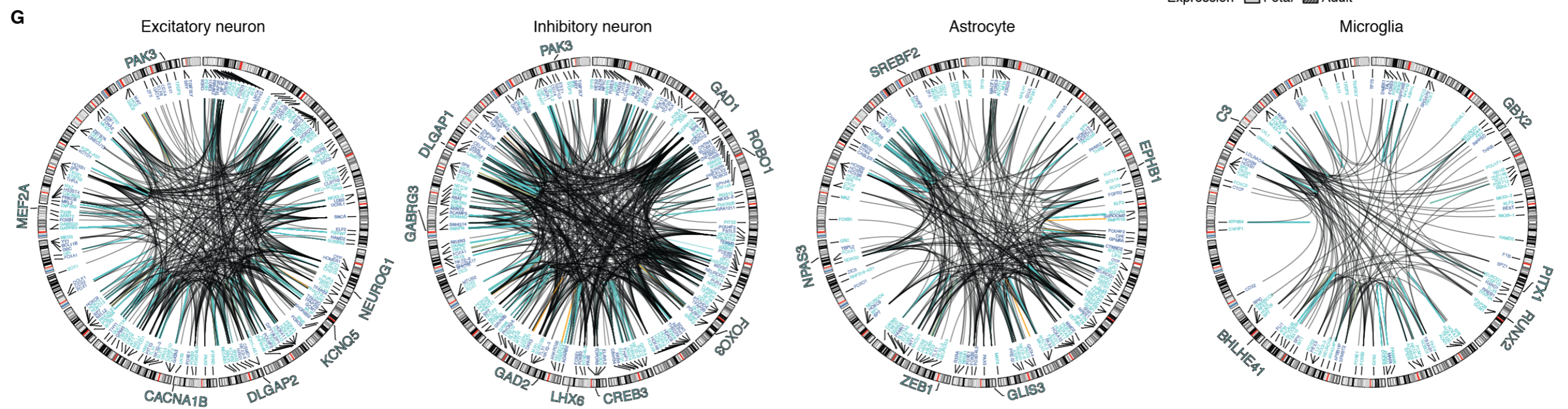
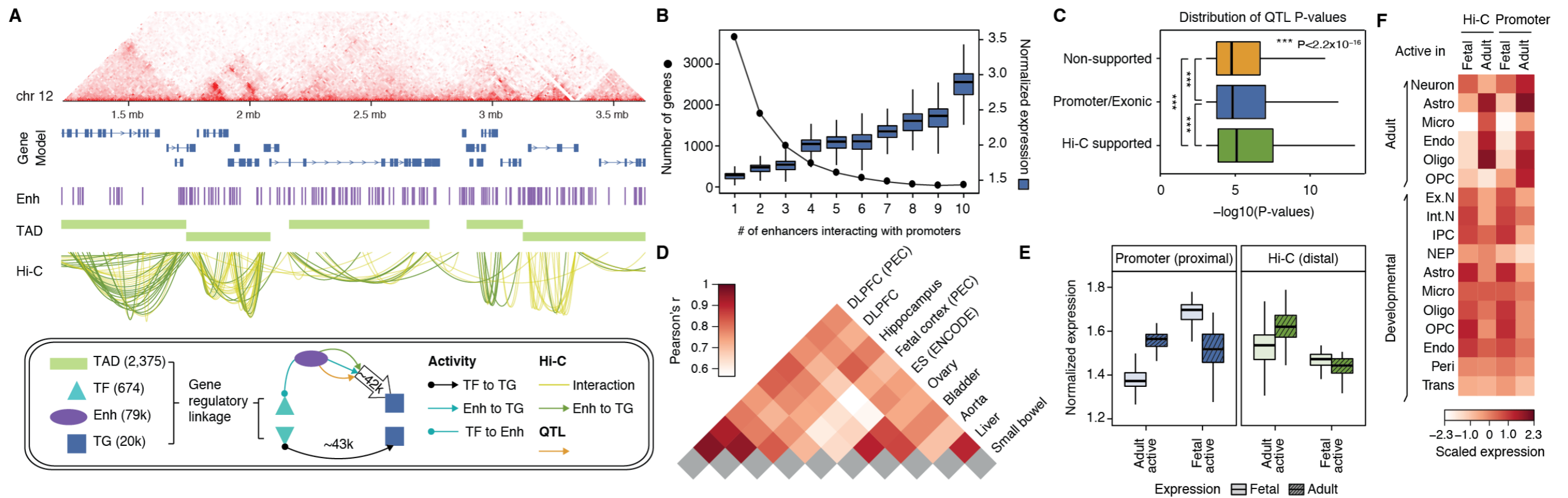


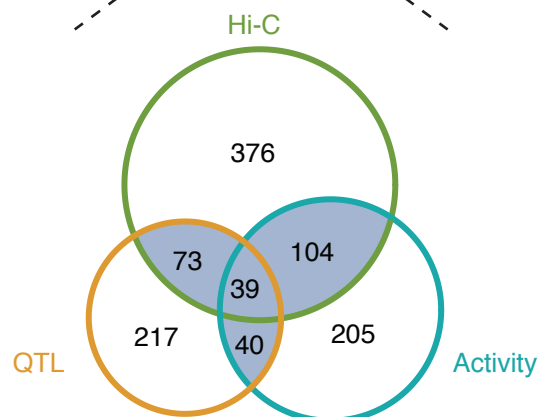
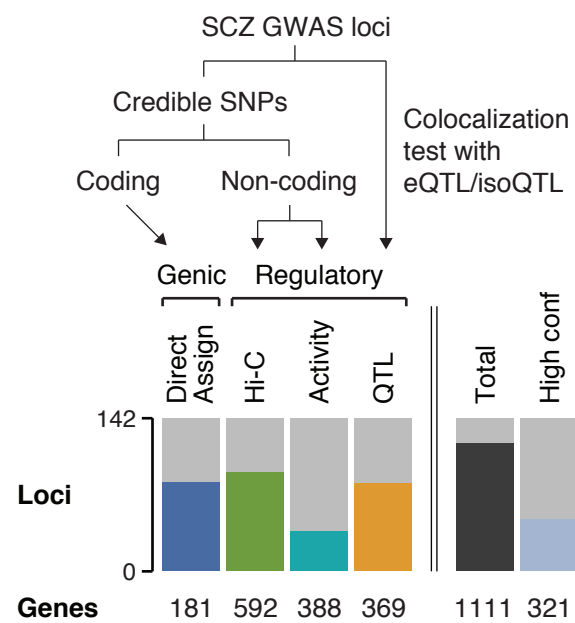
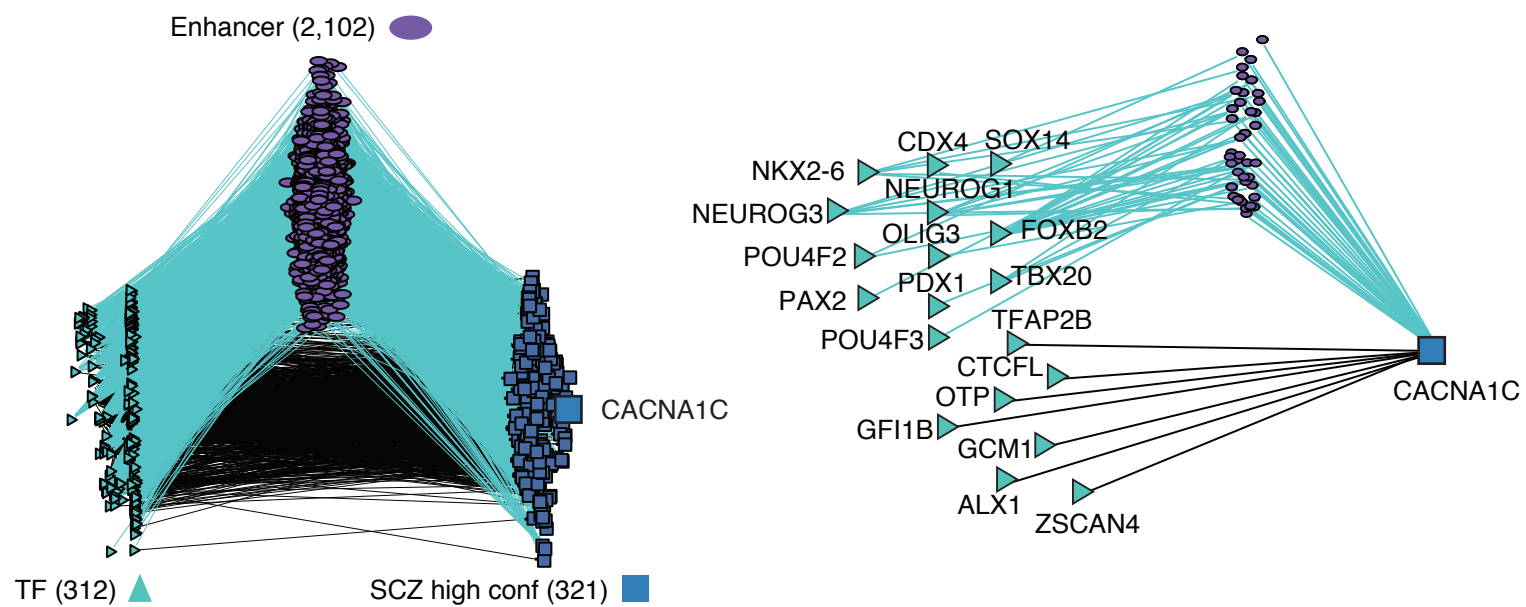
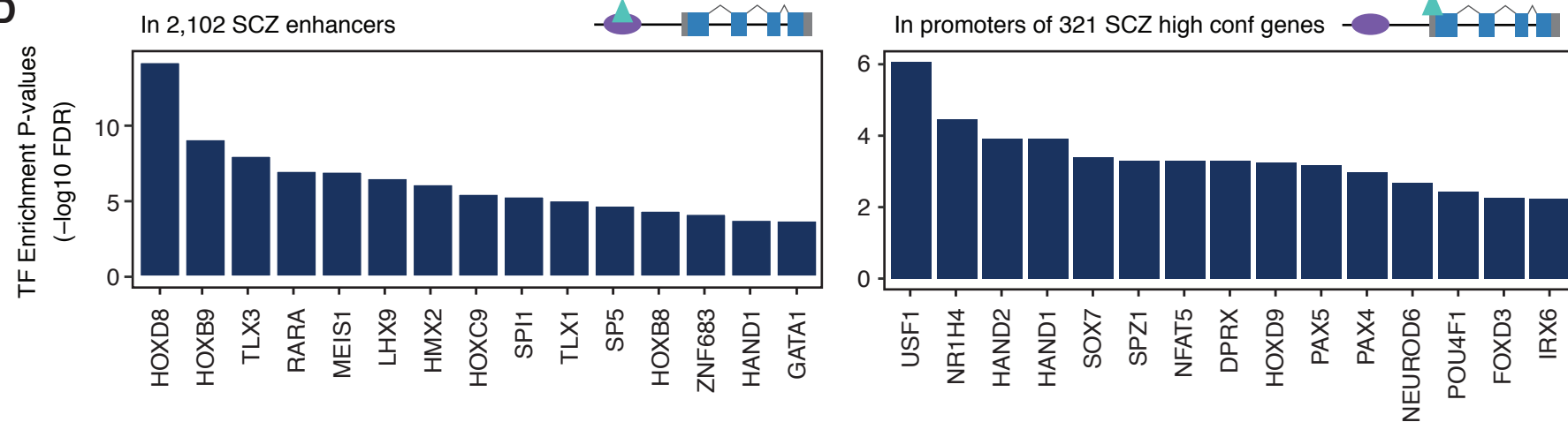
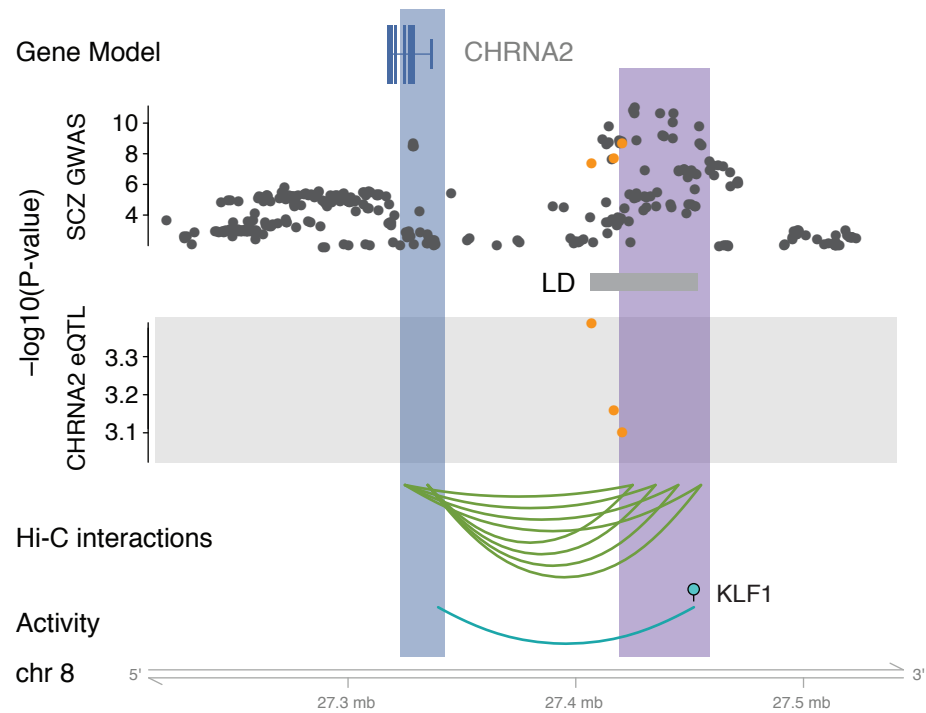
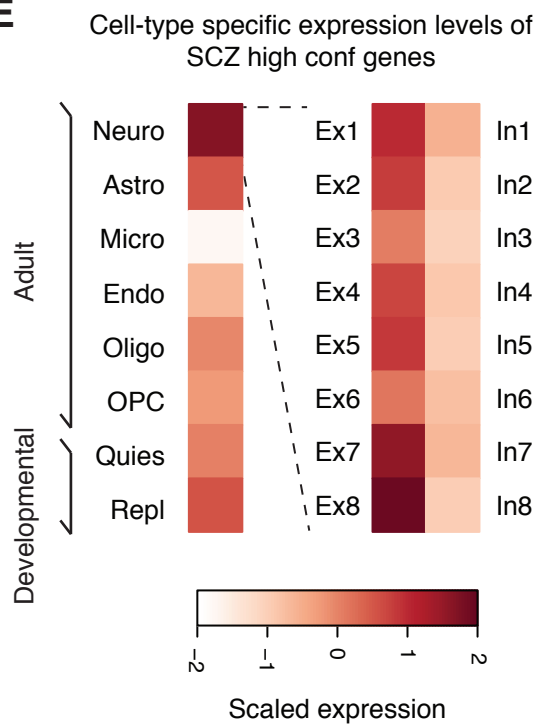
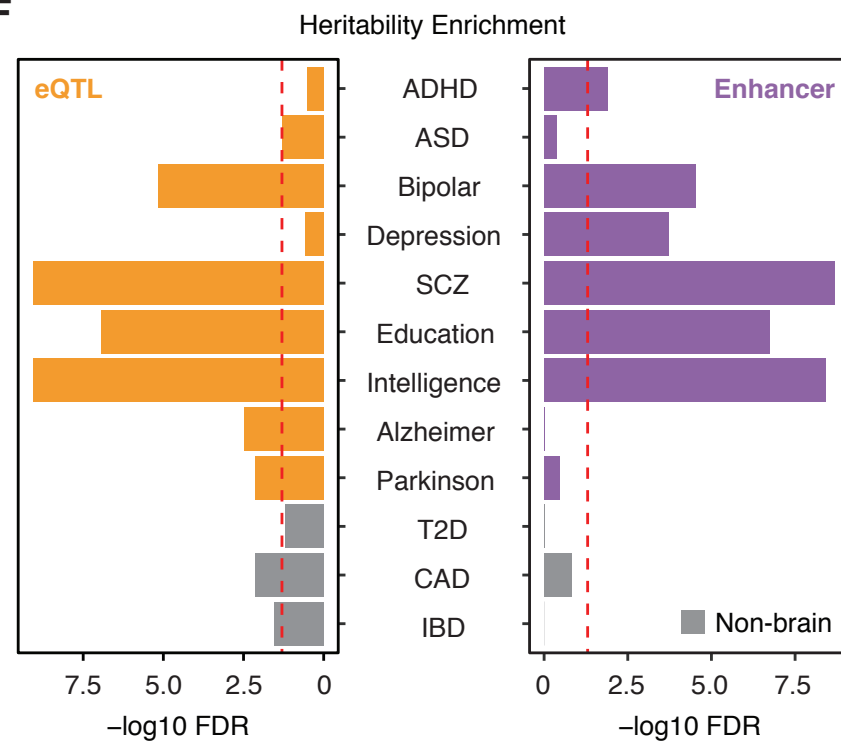
Cerebellum - CB (348)



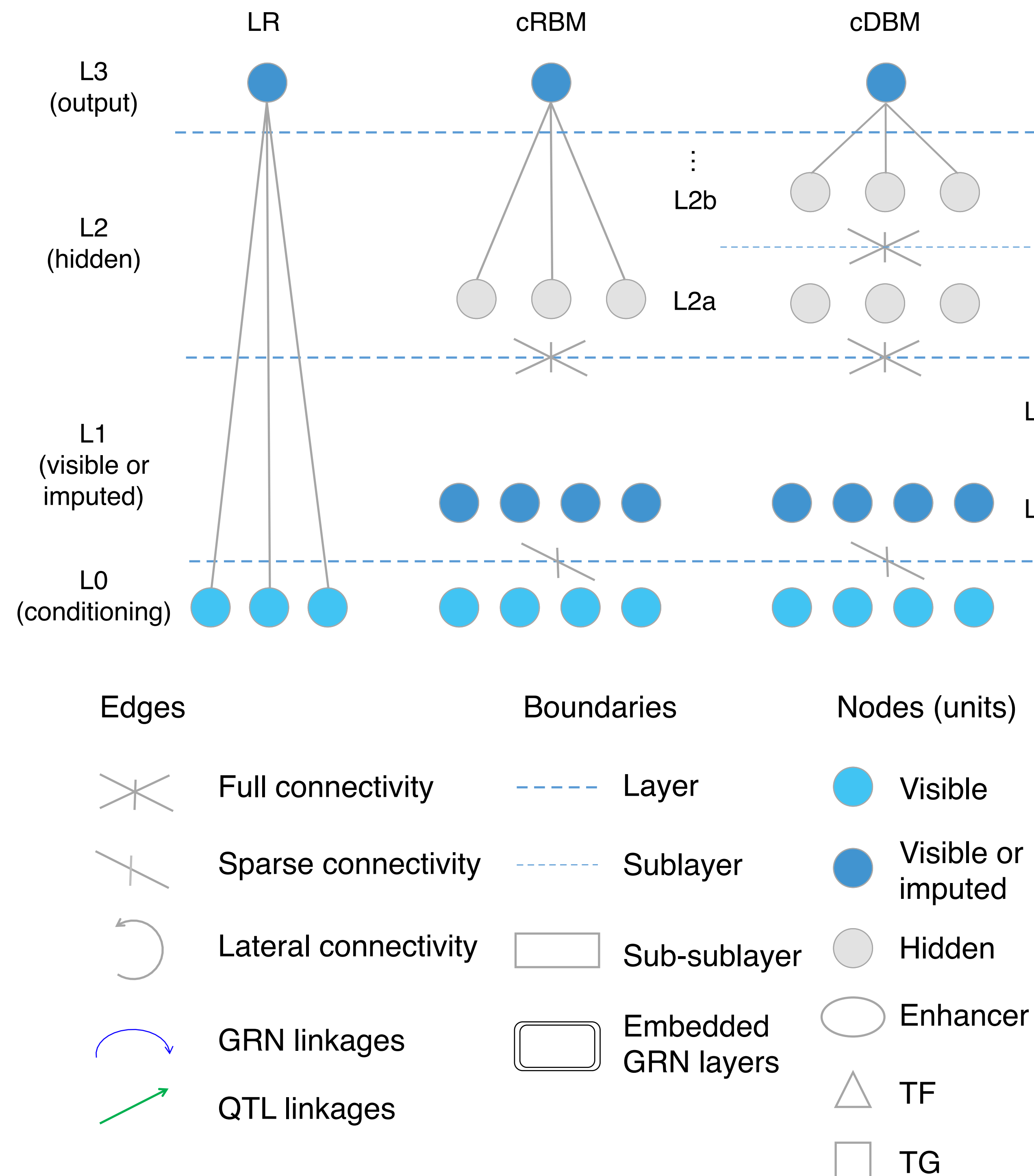




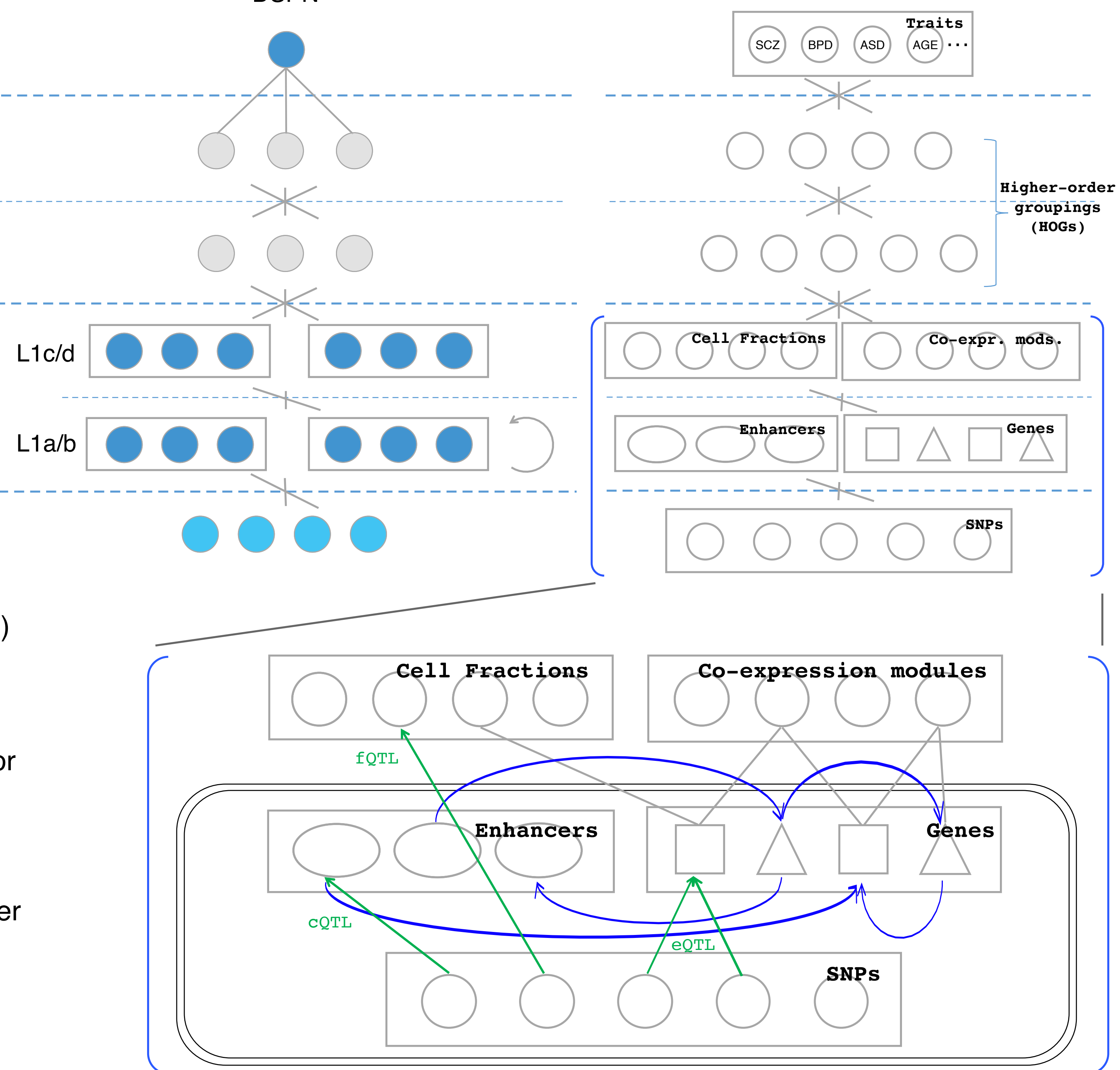


A**B****D****C****E****F**

A



B



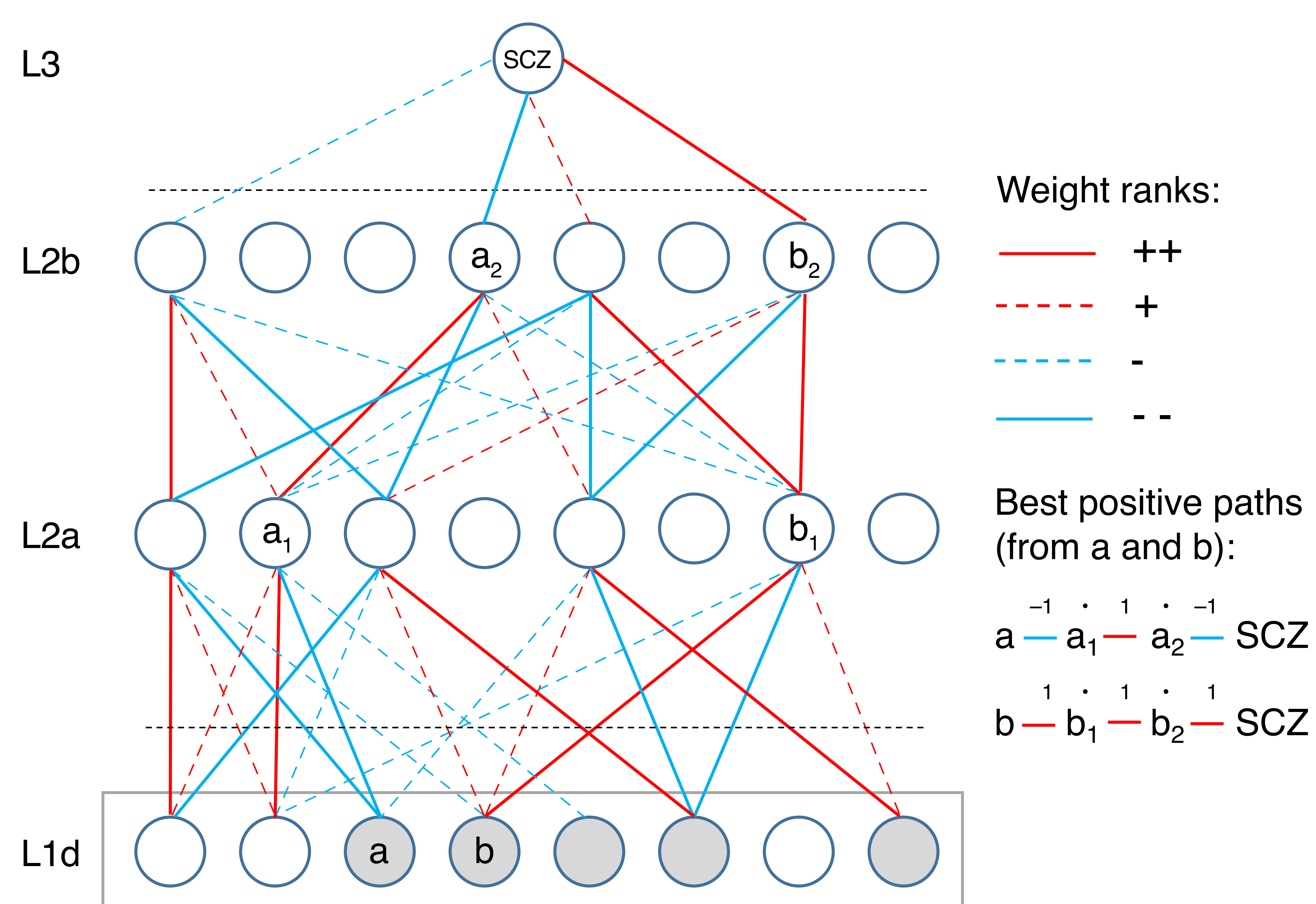
C

Method	SCZ	BPD	ASD	AVG (SCZ+BPD+ASD)	GEN	ETH	AGE
LR-gene	54.6% (0.5%)	56.7% (2.5%)	50.0% (0.0%)		50.0%	99.0%	61.9% (AOD)
LR-trans	63.0% (4.8%)	63.3% (6.3%)	51.7% (1.8%)	59.3% (4.3%)	69.7%	86.0%	81.2%
cRBM	70.0% (31.0%)	71.1% (22.6%)	63.3% (10.8%)	68.1% (21.5%)	71.5%	89.0%	83.1%
DSPN-impute	59.0% (1.8%)	67.2% (10.7%)	58.8% (3.2%)	61.7% (5.2%)			
DSPN-full	73.6% (32.8%)	76.7% (37.4%)	68.3% (11.3%)	72.9% (27.2%)	71.5%	94.3%	86.9%

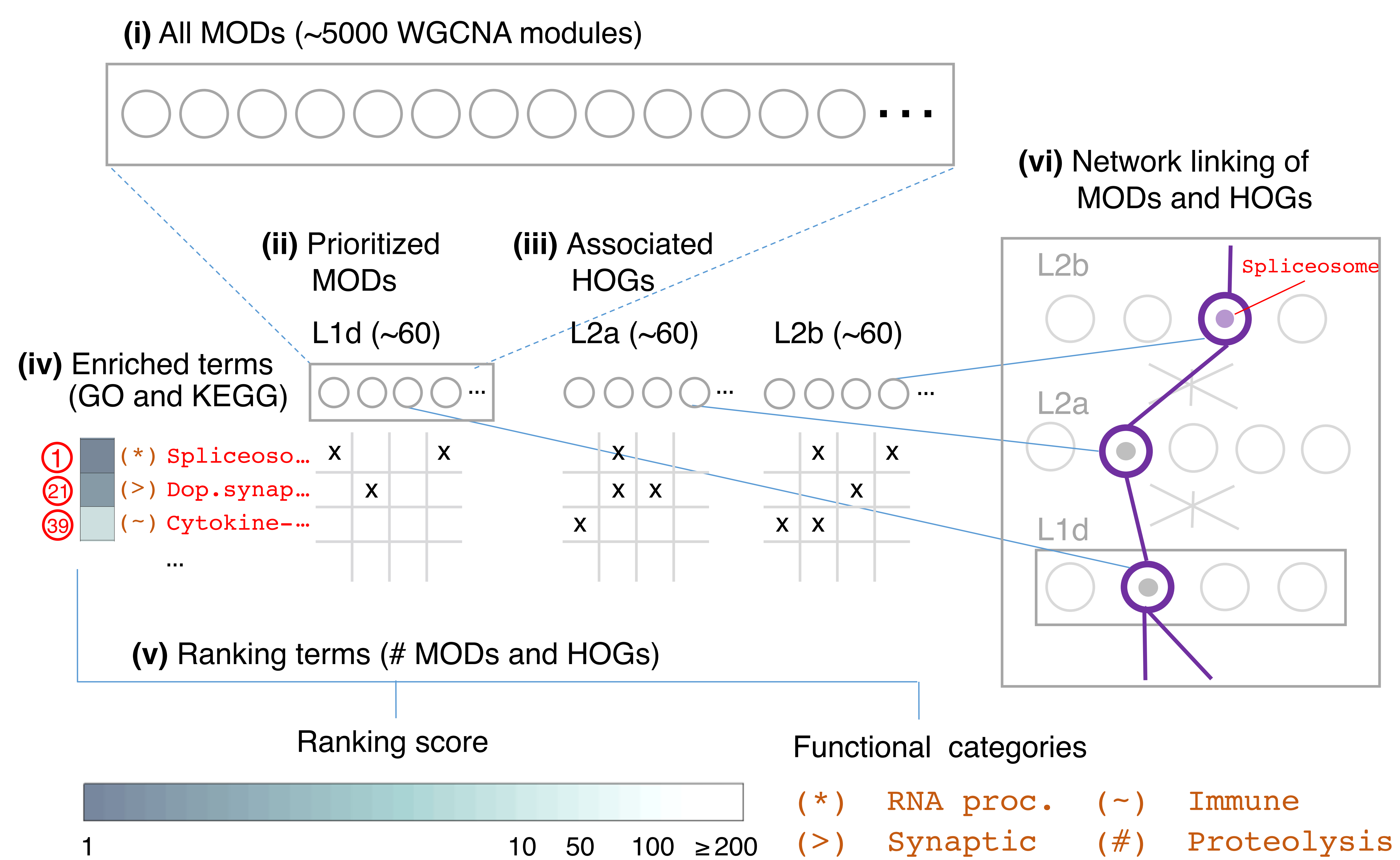
Model complexity	increasing	increasing	constant	increasing
Predictors	genotype	transcriptome	genotype->transcriptome	genotype->transcriptome

Unbracketed figures show test-set performance accuracy, with chance at 50%; bracketed figures show variance explained on liability scale

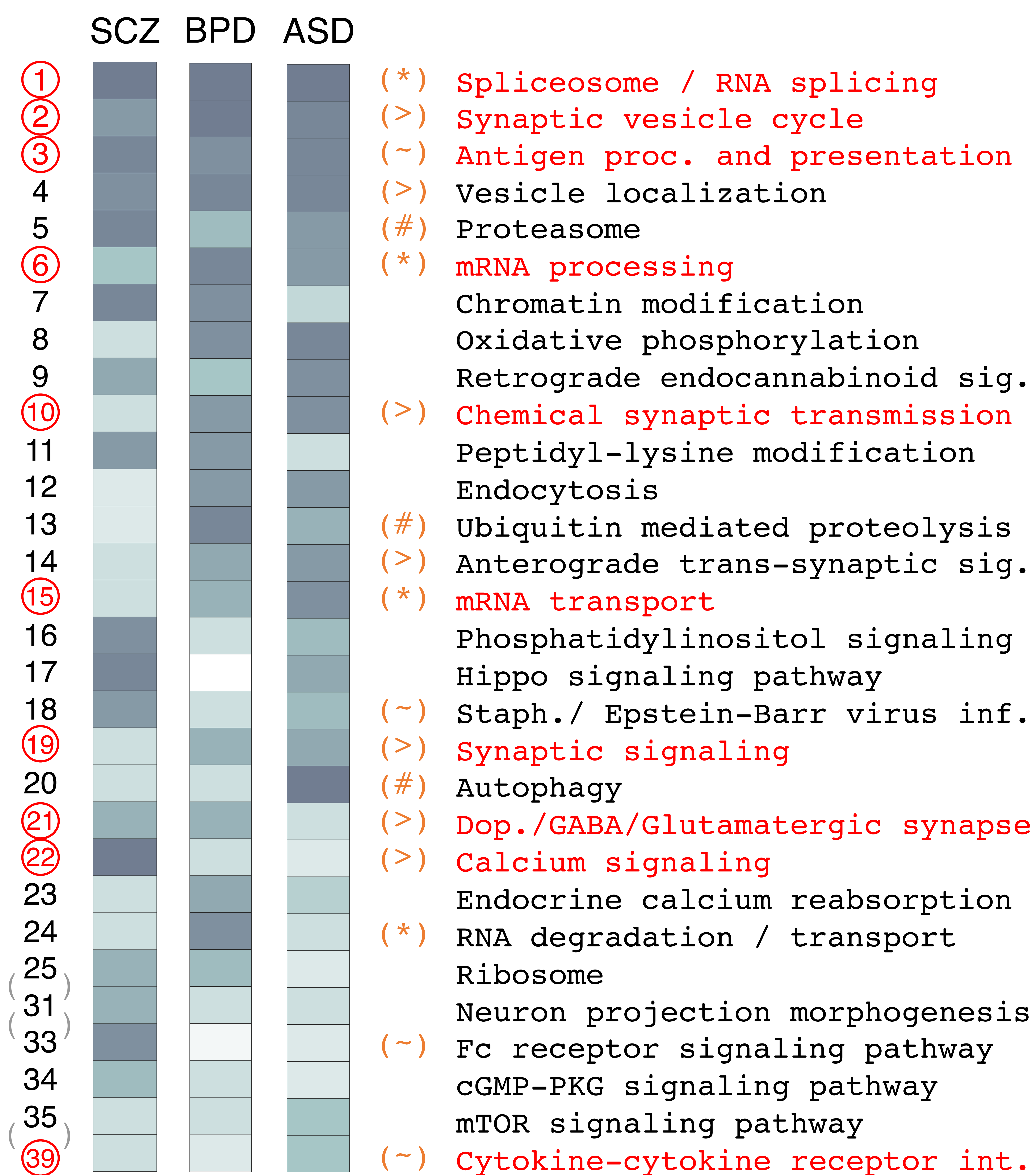
A



B



C



D

