







С



Figure 4



Supplemental Figure A





Supplemental Figure C

GO for SCZ genes Schizophrenia GWAS (142 loci) Finemap cytoplasmic mRNA processing body translation repressor activity Credible SNPs (5,996) Colocalization acetylcholine receptor activity test regulation of synaptic plasticity Exonic/Promoter Intergenic/Intronic U12-type spliceosomal complex SNPs (1,420) SNPs (4,576) eQTL positive regulation of type I interferon production Direct cell cycle phase Hi-C E-T network assignment regulation of neuron apoptosis 83 loci 92 loci 32 loci 79 loci negative regulation of protein metabolic process 606 genes 419 genes 182 genes 293 genes regulation of defense response to virus by host response to tropane calcium ion import 119 loci response to isoquinoline alkaloid 1,087 genes mitotic cell cycle 321 high-confident genes response to nicotine 0 1 2 3 4 5 6 7 Z-score

Overlap between: Hi-C vs. E-T network: OR=38.7 P=1.9x10⁻¹¹⁴ Hi-C vs. eQTL: OR=34.3 P=1.4x10-65 eQTL vs. E-T network: OR=23.3 P=3.4x10-51



Overlap between Capstone 4 and CMC eQTL-predicted genes

P=0.87

Hi-C supported sQTL

Promoter/Exonic sQTL



SCZ genes

Bivalent Enhancers

Repressive marks







Figure 6



(d)

	SCZ	BIP	ASD	GEN	ETH	AGE
LR-gen (+GCTA)	54.6% (~3%)	56.7% (~4%)	50% (~2%)	50%	99.0%	61.9%
LR-trans	63.0%	63.3%	51.7%	69.7%	86.0%	81.2%
cRBM	70.3%	71.1%	70%	71.5%	89.0%	83.1%
DSPN-Imput	57.9% (4.5%)	66.7% (22.6%)	65% (7.4%)			
DSPN	73.6% (32.8%)	76.7% (53.8%)	73.3% (21.4%)	73.2%	94.3%	86.9%