

S21 Table eQTLs and matched control variants census in the data set used. The eQTLs and control variants from [1] were projected onto templates of ~2.5 million variants (~9 million variants for analyses involving brain eQTLs) with known pairwise LD.

Tissue	eQTL 2m (9m/Brain*)	Control 2m (9m)
Adipose	4193 (8334/564)	11389 (29385)
Epidermal	4130 (8002/579)	11831 (30072)
LCL	4441 (8623/480)	10172 (26604)
Whole blood	2406 (4898/336)	9341 (20385)
All	13624 (26866/1399)	40194 (101990)
Brain**	(8992)	-

* GTEx [2] eQTLs

** GTEx [2] and CommonMind [3] consensus set

1. Buil A, Viñuela A, Brown A, Davies M, Padioleau I, Bielser D, et al. Quantifying the degree of sharing of genetic and non-genetic causes of gene expression variability across four tissues. *bioRxiv*. 2016;doi:10.1101/053355.
2. GTEx Consortium. The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. *Science*. 2015;348(6235):648–660. doi:10.1126/science.1262110.
3. Fromer M, Roussos P, Sieberts SK, Johnson JS, Kavanagh DH, Perumal TM, et al. Gene expression elucidates functional impact of polygenic risk for schizophrenia. *Nature Neuroscience*. 2016;.