

Study	Sample size	Tissue	n genes mapped by <i>cis</i> eQTLs		Overlapping results	
	n		sign. threshold	n	n	%
This study, two stages	369 + 367	Whole blood	permuted p FDR 0.05	2,211	–	–
Göring <i>et al.</i> [1]	1,240	Lymphocytes	LOD score >3	737	332	45.0
Stranger <i>et al.</i> [2]	270	Lymphoblastoid cell lines	permuted p<0.001	299	122	40.8
Webster <i>et al.</i> [3]	364	Brain cortex	permuted p<0.05	280	103	36.8
Gibbs <i>et al.</i> [4]	600	Four regions in human brain	FDR 0.05	281	146	52.0

Comparison of the number of genes mapped by *cis* eQTLs in the present study and four other studies that have looked into the genetics of gene expression. The number of genes mapped by *cis* eQTLs was based on the significance threshold that was used in each of the studies. eQTL, expression quantitative trait locus; FDR, false discovery rate; LOD, logarithm of odds.

References

1. Göring HHH, Curran JE, Johnson MP, Dyer TD, Charlesworth J, et al. (2007) Discovery of expression QTLs using large-scale transcriptional profiling in human lymphocytes. *Nat Genet* 39: 1208-1216.
2. Stranger BE, Forrest MS, Clark AG, Minichiello MJ, Deutsch S, et al. (2005) Genome-wide associations of gene expression variation in humans. *PLoS Genet* 1: e78.
3. Webster JA, Gibbs JR, Clarke J, Ray M, Zhang W, et al. (2009) Genetic control of human brain transcript expression in Alzheimer disease. *Am J Hum Genet* 84: 445-458.
4. Gibbs JR, van der Brug MP, Hernandez DG, Traynor BJ, Nalls MA, et al. (2010) Abundant quantitative trait loci exist for DNA methylation and gene expression in human brain. *PLoS Genet* 6: e1000952.