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Mapping of Gene Expression Reveals CYP27A1 as a Susceptibility Gene for Sporadic ALS

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Study	Sample size n	Tissue	n genes mapped by <i>cis</i> eQTLs		Overlapping results	
			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.

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