Table 1. Summary of genes exhibiting *cis*-controlled expression QTL in multiple tissues in the BxH intercross

Primary tissue	**No. of active genes** (*cis*-eQTL lod > 4.3)	**Second Tissue**	**No. of active genes (N*)**	**No. of genes ($M_1^{\dagger}$)** (*cis*-eQTL lod > 4.3)	**Percentage of detection 100*M_1/N (%)**	**No. of genes ($M_2^{\ddagger}$)** (*cis*-eQTL lod > 2.0)	**Percentage of detection 100*M_2/N (%)**
Liver	1,865	Adipose	1,726	877	50.81	1,047	60.66
		Brain	1,062	859	80.89	910	85.69
		Muscle	1,272	827	65.02	927	72.88
Adipose	1,491	Liver	1,166	868	74.44	953	81.73
		Brain	1,019	869	85.28	903	88.62
		Muscle	1,168	885	75.77	958	82.02
Brain	1,754	Liver	1,281	859	67.06	968	75.57
		Adipose	1,627	869	53.41	1,038	63.80
		Muscle	1,296	928	71.60	1,017	78.47
Muscle	1,584	Liver	1,218	827	67.90	945	77.59
		Adipose	1,486	885	59.56	1,027	69.11
		Brain	1,105	928	83.98	970	87.78

This study is designed to estimate the probability of detecting a *cis*-eQTL in a second tissue after it has been detected in a primary tissue. The number of genes actively expressed and *cis*-eQTL detected across multiple tissues are summerized. Whether a gene with a *cis*-eQTL in one tissue can be also detected with a *cis*-eQTL in another tissue will depend on (i) whether the gene is expressed in the second tissue, and (ii) whether the *cis*-regulation also occurs in the second tissue. To select a list of actively expressed genes in a particular tissue, we adopted a vigorous selection procedure (1). We then estimated the percentage of these genes demonstrating significant *cis*-eQTL. We defined a significant *cis*-eQTL as having a lod score > 4.3 where the eQTL mapped within 20-Mb of the physical location of the gene. The results show a range from 53% to 85% for the pair-wise comparisons among the four tissues, suggesting 53-85% of the significant *cis*-eQTL can be detected in two tissues. We then estimated the probability of detecting the *cis*-eQTL in a second tissue with a reduced threshold (lod score > 2.0). The power to detect a *cis*-eQTL in an independent experiment (second tissue) that was detected in a first experiment (primary tissue) with a lod score > 4.3 is estimated to be > 99% at a lod score threshold of 2.0 (follows from application of standard power calculation for point-wise, simple linear regression method). The percentage of *cis*-eQTL that can be detected for genes expressed in the second tissue is now calculated to be 63-88%. Overall, our data suggest that, for a gene exhibiting significant *cis*-eQTL in one tissue, it is likely that it also exhibits *cis*-regulation in another tissue if it is actively expressed in that tissue. *N, the number of actively expressed genes; †M_1, the number of genes with *cis*-eQTL lod > 4.3; ‡M_2, the number of genes with *cis*-eQTL lod > 2.0.

1. Yang X, Schadt EE, Wang S, Wang H, Arnold AP, Ingram-Drake L, Drake TA，Lusis AJ (2006) *Genome Res.* 16：995-1004.