Table 1 | eQTL Discoveries. eQTL discoveries for genes, transcripts, exons, splicing events and long non-coding RNAs for each of based quantifications (by-transcript and by-exon) and matching array samples are shown using Spearman rank correlation.

Associations	Number of traits	Number of SNPs	Permutation thresholds*	
			0.05	0.01†
Exon quantification	90,064 exons/10,777 genes	1,171,085	3,258	836 (0.13)
Transcript quantification	15,967 transcripts/11,674 genes	1,171,085	1,129	293 (0.40)
Whole gene quantification	11,210 genes	1,171,085	875	256 (0.43)
Long non-coding RNAs	232 exons/102 genes	1,171,085	14	6 (0.17)
Transcript events	6,468 events	1,171,085	416	110 (0.59)
Array-based quantification	21,800 probes/17,420 genes	1,171,397	1,682	539 (0.32)

* Thresholds at the gene level
† False discovery rate (FDR) in parentheses

SNPs (methods described previously[22]). We evaluated association in exons, transcripts and genes and determined the unique number of

To replicate our eQTL discoveries, we com between our study and those obtained from se