S8 Table

Summary results of genome-wide *cis*-eQTL analysis

Test		Gene	Transcript	Exon	Junction	Intron
TOTAL	**SNPs**	1745261	2813231	3337666	3264551	3611418
	Genes	14546	13783	14042	10564	13469
	Targets	14546	63438	141117	127404	93747
	Distinct SNP-Gene pairs	3016012	6759383	10220224	9090904	9603702
	Total SNP-Target pairs	3016012	9072417	31227090	24439851	17057283
SIGNIFICANT (FDR < 0.05)	**SNPs**	458654	429686	1256346	935370	1144452
	Genes	8351	8874	12918	9659	11111
	Targets	8351	17218	89099	63839	42950
	Distinct SNP-Gene pairs	610696	586659	2158552	1417712	1756270
	Total SNP-Target pairs	610696	763559	7524183	935370	2972825
PERCENTAGE SIGNIFICANT	**SNPs**	26.28	15.27	37.64	28.65	31.69
	Genes	57.41	64.38	92.00	91.43	82.49
	Targets	57.41	27.14	63.14	50.11	45.81
	Distinct SNP-Gene pairs	20.25	8.68	21.12	15.59	18.29
	Total SNP-Target pairs	20.25	8.42	24.10	3.83	17.43

The results of this table are depicted in S11 Fig. A genome-wide *cis*-eQTL analysis was performed as described in methods for all common SNPs (MAF > 5%) against gene quantifications profiled at gene-, transcript-, exon-, junction-, and intron-level. 'TOTAL' referes to the total number of elements tested in a genome-wide setting. The number of SNPs is different per quantification type as the analysis is run in *cis*, meaning only expression elements within +/-500kb of each SNP are considered; therefore, if there is no expression element within this distance, the SNP is not included in the analysis. 'Genes' referes to the number of distinct (unique) genes tested against, and 'targets' refers to the number of individual genes, transcripts, exons, junctions, and introns tested against measured using the corresponding profiling type. 'SIGNIFICANT' refers to the number of SNPs, genes etc. that pass a genome-wide false discovery rate (FDR) multiple testing threshold of 5%. 'PERCENTAGE SIGNIFICANT' refers to the percentage of SNPs, genes etc. that are significant as a percentage of the total tested.