

Supplementary Information

Identification of 55,000 Replicated DNA Methylation QTL

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Figure S1: Distance of *cis* mQTL SNP from target CpG site. Most of the significant *cis* mQTL SNP are located within 100Kbp from the target CpG. However, substantial numbers of *cis* mQTL are still observed at 1-2Mbp away from the target CpG site.

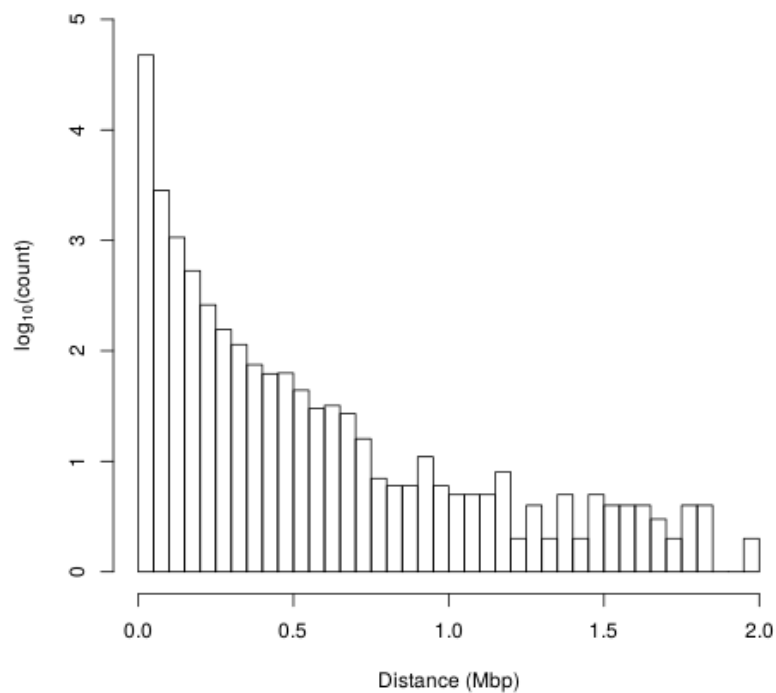


Figure S2: Location of significant mQTL in the BSGS (left) and LBC (right) cohorts. There is a substantial overlap in significant mQTL between the two groups.

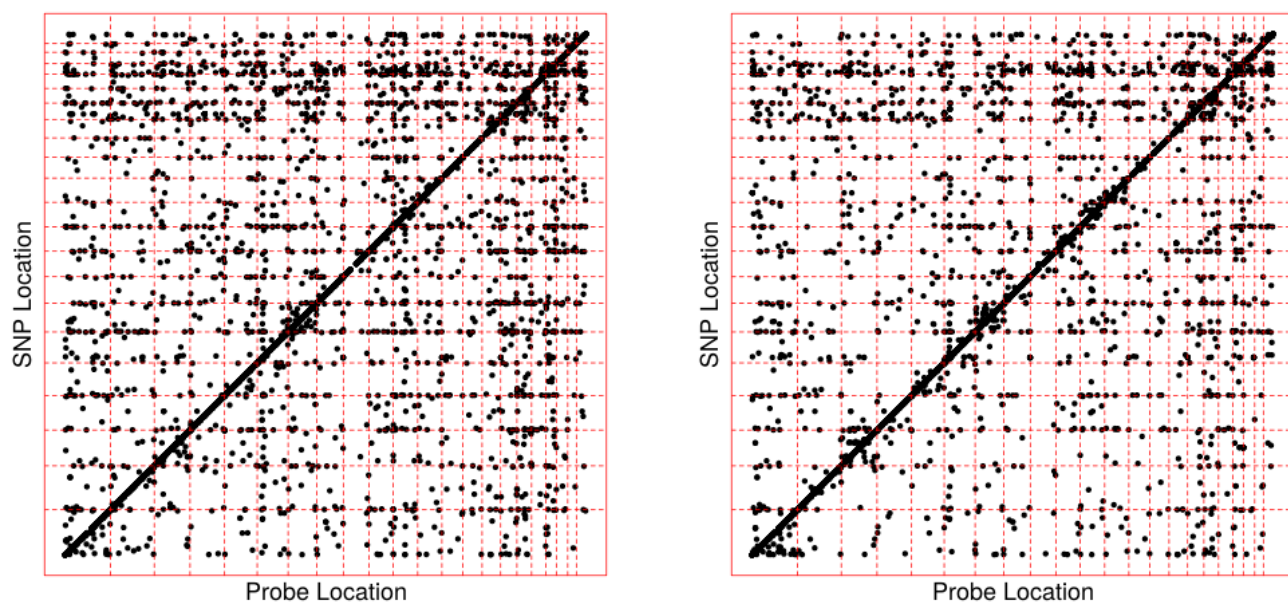
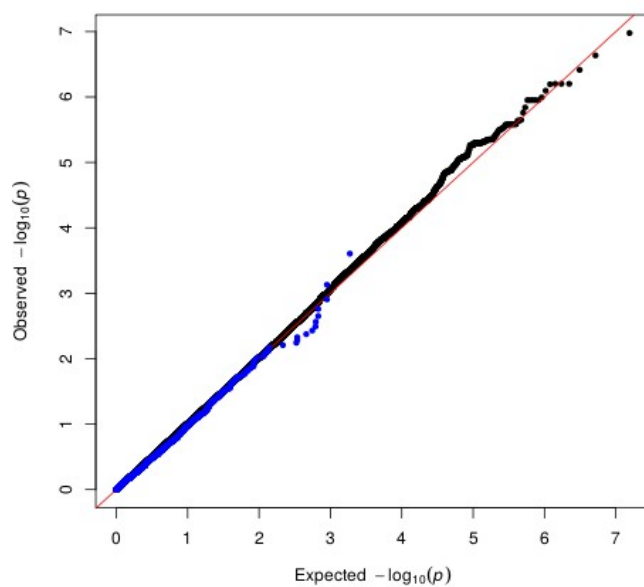
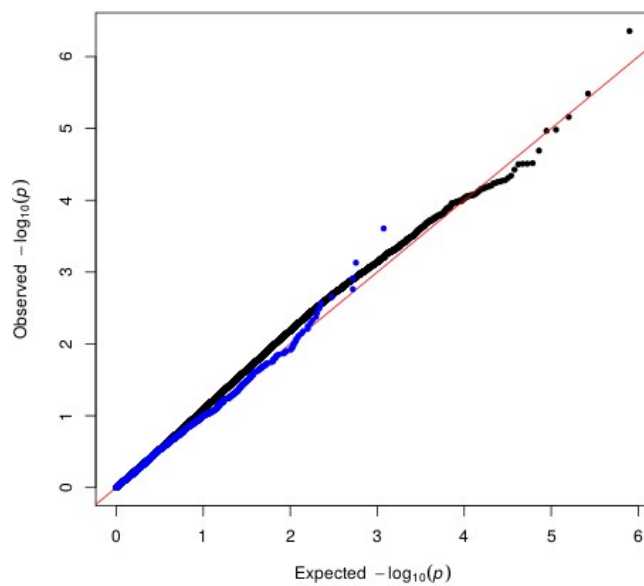


Figure S3: No association between *trans* mQTL SNP and methylation with telomere length in the LBC. Both the SNPs (a) and methylation (b) from *trans* mQTL showed no inflation in their average test statistics for association with telomere length. Black dots are for SNPs/methylation probes genome wide and SNPs/probes from *trans* mQTL are coloured blue.

(a)



(b)



Supplementary Table 1: List of replicated mQTL. Excel spreadsheet containing the list of all 52,916 *cis* and 2,025 *trans* mQTL identified and replicated in the BSGS and LBC cohorts. All genomics positions are given with hg19 locations.

Supplementary Table 2: Correlation between the absolute value of the mQTL effect size and the absolute value of the SNP effect size or log-odds ratio for a number of complex traits and disease. Significant correlations are observed for all traits tested but this is driven purely by the relationship between average effect size and allele frequency.

Trait	Raw Effect Sizes		Standardized Effect Sizes	
	Correlation	P-value	Correlation	P-value
Height	0.048	2×10^{-8}	-0.004	0.69
BMI	0.072	$< 2 \times 10^{-16}$	0.002	0.42
Schizophrenia	0.082	$< 2 \times 10^{-16}$	0.004	0.26
Ulcerative colitis*	0.045	8×10^{-6}	-0.024	0.99
Crohn's Disease*	-0.010	0.82	0.001	0.45
Coronary Artery Disease	0.050	8×10^{-9}	-0.020	0.99
Type 2 Diabetes	0.100	$< 2 \times 10^{-16}$	0.004	0.34
Rheumatoid Arthritis*	0.092	$< 2 \times 10^{-16}$	-0.007	0.87
Educational Attainment	0.050	1×10^{-8}	0.004	0.34

* Excluding the HLA region of chromosome 6