

Descriptions of Supplementary Data files

Supplementary Data 1

Number of female and male samples per cohort used in the discovery phase.

Supplementary Data 2

Characteristics of the four female-specific loci identified in the discovery cohort.

Supplementary Data 3

The 48 sentinel variants corresponding to the 48 loci identified in female samples, and tested for an effect in males. For each variant, the table associated *P*-values for females and males, the number of associated CpGs, the nearest gene, and mean effect sizes over the associated CpGs.

Supplementary Data 4

Test-statistics for the association of three sentinel variants with X-chromosomal DNA methylation, both uncorrected and corrected for nearby X-chromosomal genetic variants.

Supplementary Data 5

All variants known to affect blood composition^{19,20} and their associated *P*-values relating to the association with X-chromosomal DNA methylation. None of the variants reach statistical significance after correction for multiple testing, indicating these variants do not confound the analysis through blood composition.

Supplementary Data 6

Re-testing the four female-specific sentinel variants corrected for nearby (1Mb) variants known to affect blood composition^{19,20}, or without correcting for the latent factors.

Supplementary Data 7

Results from the replication analysis of the four sentinel variants in independent cohorts.

Supplementary Data 8

Results from *cis*-eQTL mapping, relating the sentinel variants of the three replicated, female-specific sentinel variants to nearby genes (<250Kb).

Supplementary Data 9

Results from *trans*-meQTL mapping of the three sentinel variants on all individual X-chromosomal CpGs.

Supplementary Data 10

X-chromosomal CpGs and the significant associations to nearby X-chromosomal genes (<250Kb).

Supplementary Data 11

Trans-meQTL mapping of the three sentinel variants on all autosomal CpGs *in trans* (>5Mb).