

Autosomal genetic control of human gene expression does not differ across the sexes

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Keywords: Gene expression, genetic correlation, sex-specific genetic architecture

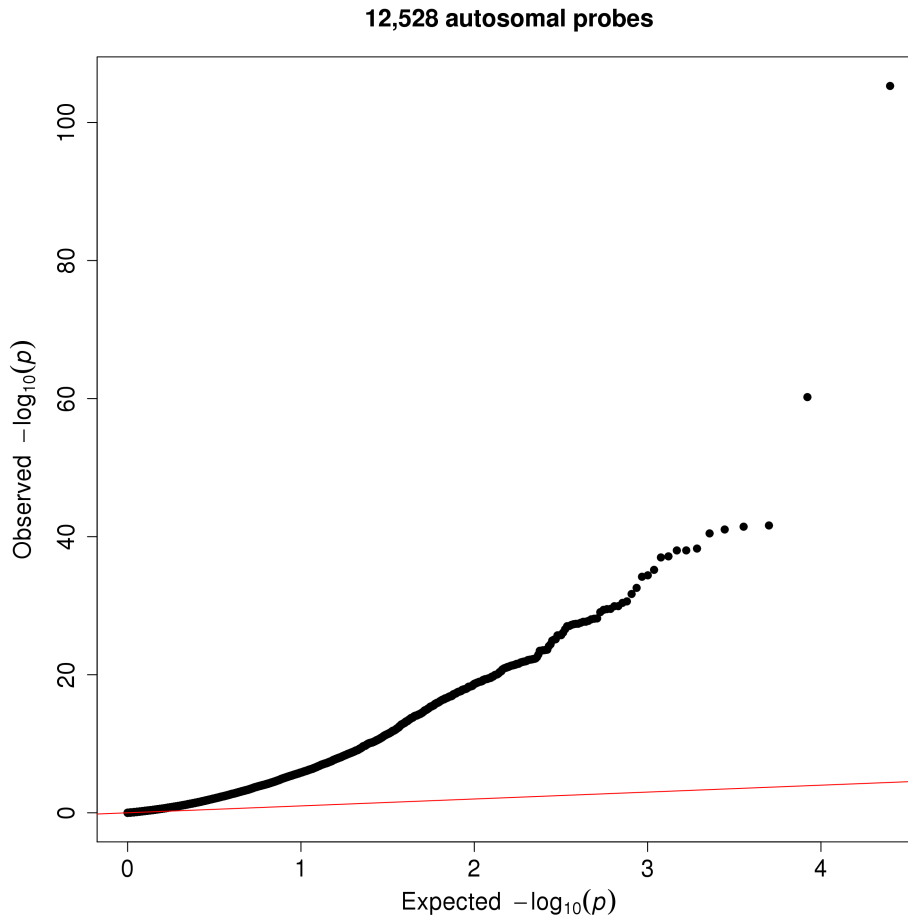


Figure S1: Quantile-quantile plot for expected versus observed P-values testing mean differences in gene expression intensities across the sexes for 12,528 autosomal probes. Extensive sexually dimorphic gene expression is illustrated by a large deviation of the observed test statistics from the expected. A total of 1,413 autosomal probes corresponding to 1,266 unique genes showed significant mean differences in expression intensities across the sexes at a Bonferroni corrected threshold of $P = 3.99 \times 10^{-6}$.

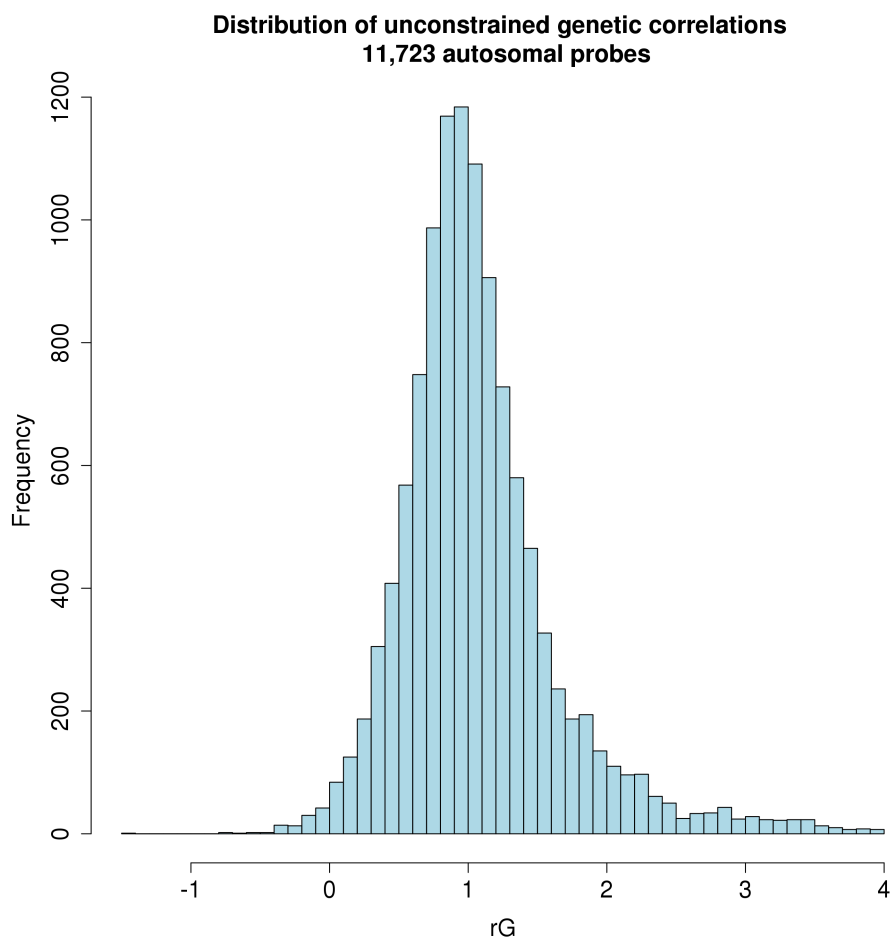


Figure S2: Distribution of 11,723 unconstrained estimates of genetic correlations of autosomal gene expression across males and females from a bivariate GREML analysis. The distribution had median $r_G = 1.01$ across all tested probes.

Validation of predicted cell-type proportions in BSGS (n=623)
Standard least-squares regression approach

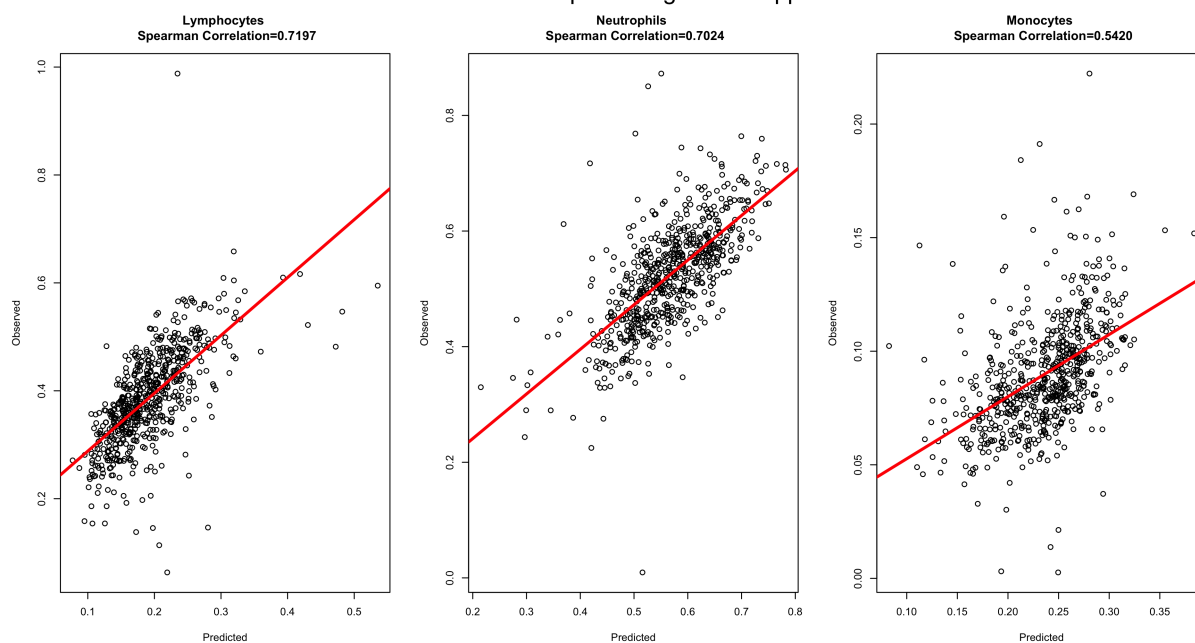


Figure S3: Predicted vs. observed cell-count proportions in $n = 623$ individuals from the BSGS cohort, validating the proposed deconvolution method [40].