

Supplemental Data 4: Partial least squares regression (PLSR) between cell deconvolution PCA and the methylation PCA scores.

Both transcriptome and methylation data from 21 samples were used. An initial PCA was created using cell deconvolution data established with the transcriptome data. Then a second PCA was created with methylation data. Each PCA, methylation and cell deconvolution contained matching samples, and samples as indicated UC (red), N (blue). The methylation data was limited to promoters (2000 bp downstream to 200bp upstream) from all transcripts expressed in the transcriptome work ($\log_2 FC > 5$).

