



Supplemental Fig S3: Concordance of DNA methylation measured by different assays in two cell types.

We measure the concordance of DNA methylation values between samples (at loci with ≥ 10 read coverage) using the root-mean-square error (RMSE), with lower error values (blue) indicating higher concordance between measurements. There is a clear difference between the values for the IMR-90 and GM12878 cell types, with X-WGBS clustering with WGBS results using older technology. When Bismark was used as an alternative analytical approach to bwa-meth, the results were more concordant by sample and assay than by analytical approach, indicating that the two analytical approaches generated similar results.