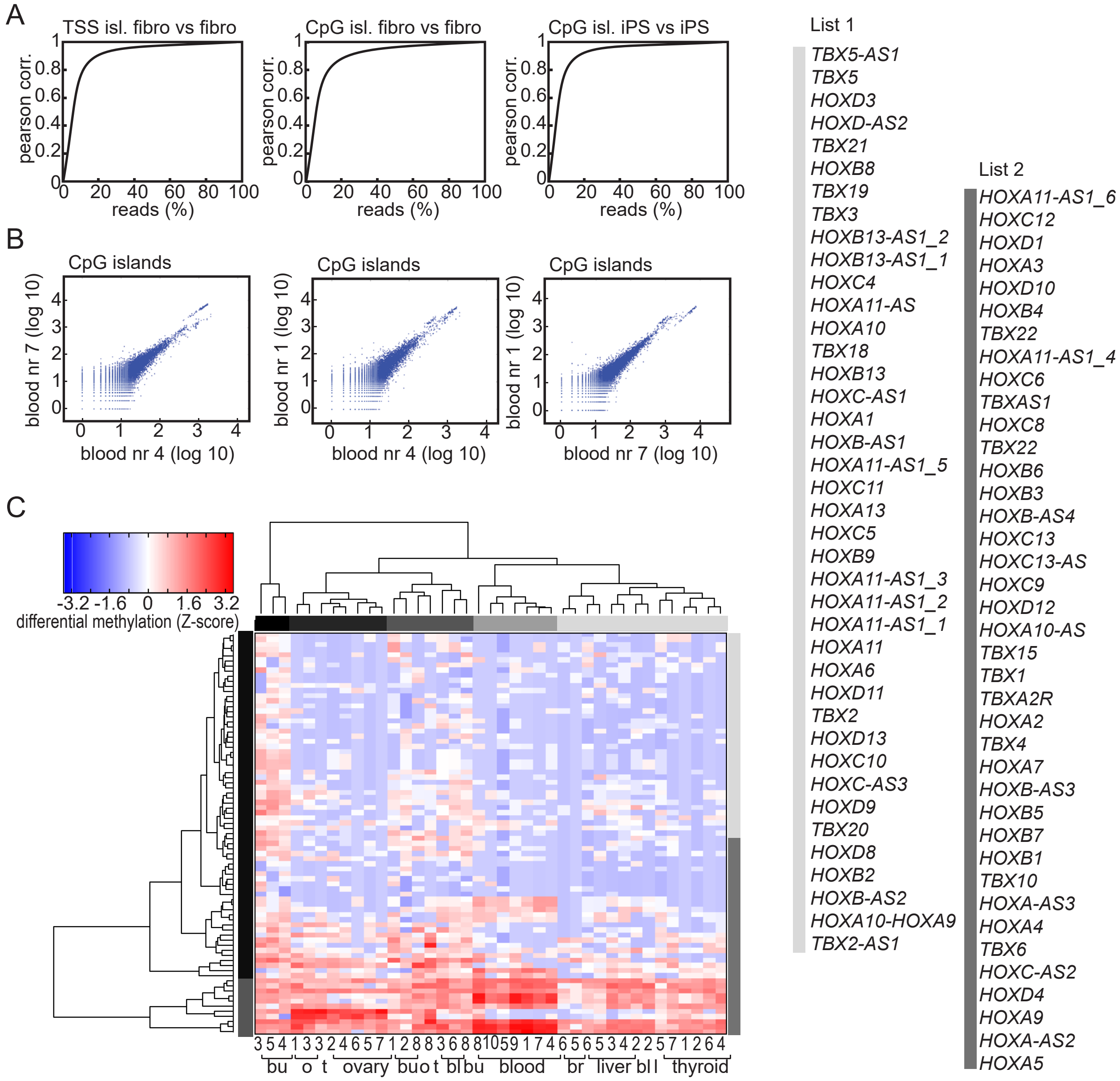

Supplemental Fig S5. Tissue and patient specific DMRs.

a) Pearson correlation analysis of CpG islands and TSSs upon in silico dilution starting with 150 million reads.

b) Correlation analysis of CpG island read counts between blood samples of different patients.

c) Unsupervised hierarchical clustering of tissues based on differentially methylated TSS in the *HOXA-D* and *TBX* gene loci called by Chi-squared testing and Bonferroni correction, color grades are based on the Z-scores of the read count.