Figure S5. Heatmap showing the overlap between sample-types for all identified differentially methylated positions. Taking all sites identified as having a significantly different level of DNA methylation compared to whole blood in at least one sample type (n = 611,070; ANOVA $P < 9 \times 10^{-8}$) we counted the number each of individual sample types characterized by differential DNAm ($P < 0.05$). Each box in this heatmap represents the percentage of significant DMPs that are shared between two sample types.