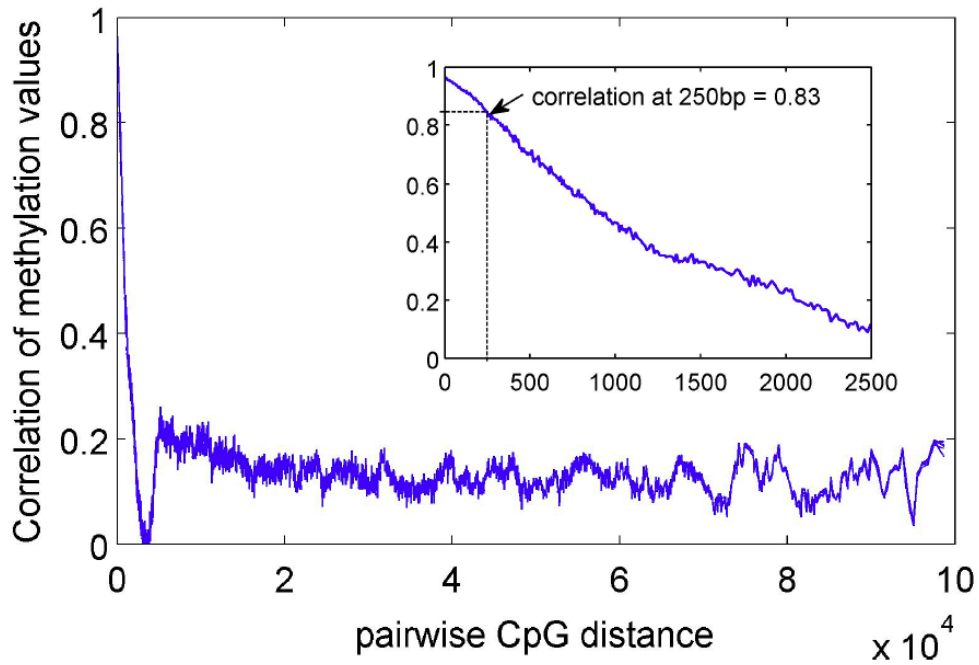
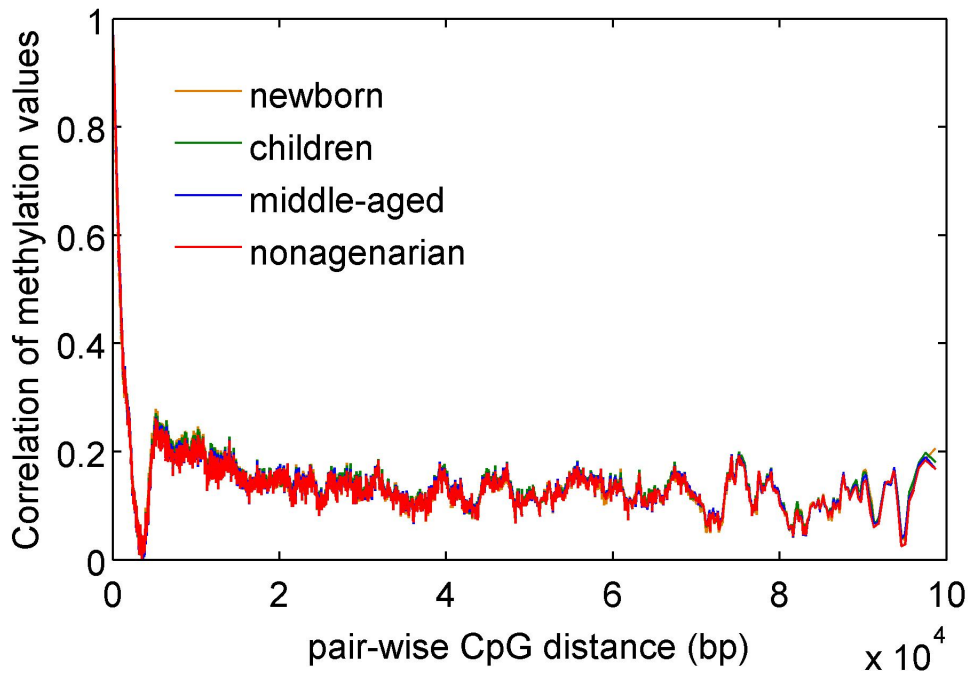


**Supplementary Figure 1. CpGs typed on infinium 450K array are irregularly spaced in the genome:** Frequency distribution of distance (bp) between neighbouring CpGs on the Infinium 450K array. The inset shows a zoomed in region of distances less than 5000 bp, where the majority of CpGs reside.

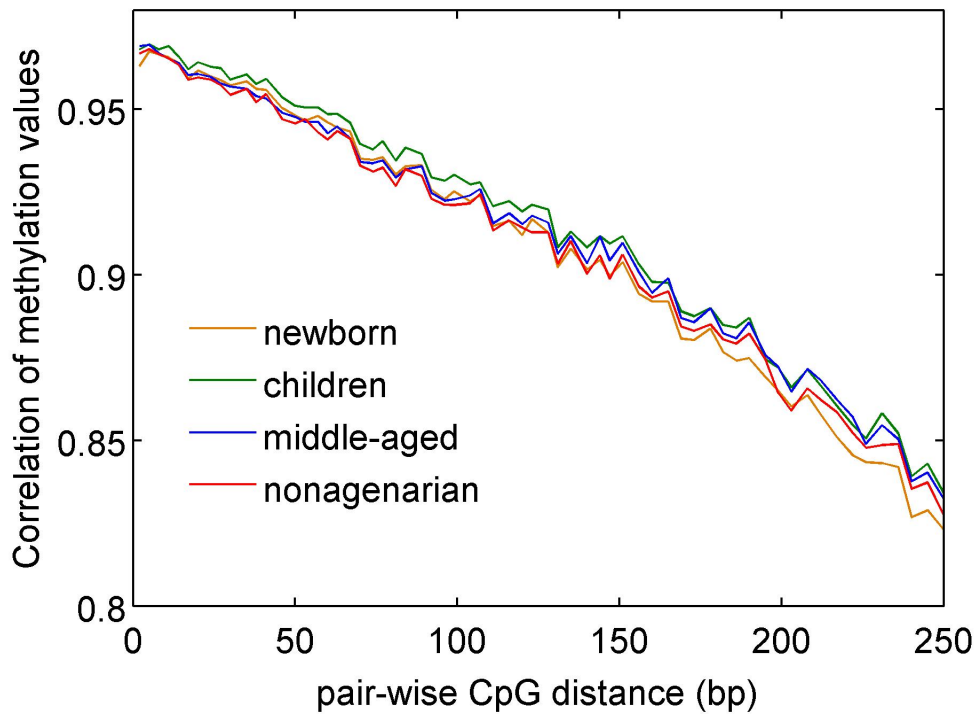


**Supplementary Figure 2. Correlation of CpG methylation levels of probes within close distances is discernable of the Infinium 450K array:** Pearson correlation of pair-wise Infinium 450K measured methylation levels (y-axis) with distance between the probes (bp) (x-axis). The inset shows a zoomed-in region of distances < 2500bp, where the correlation ranges from approximately 0.9 to 0.1.

a

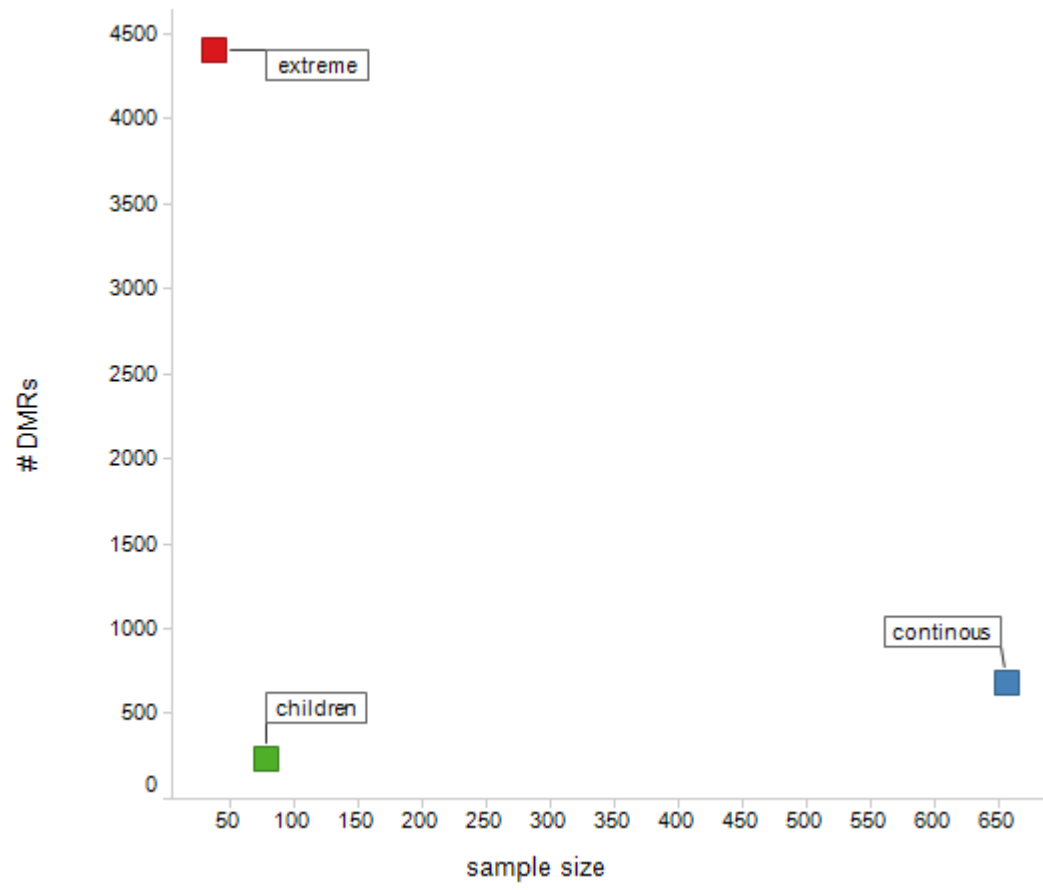


b

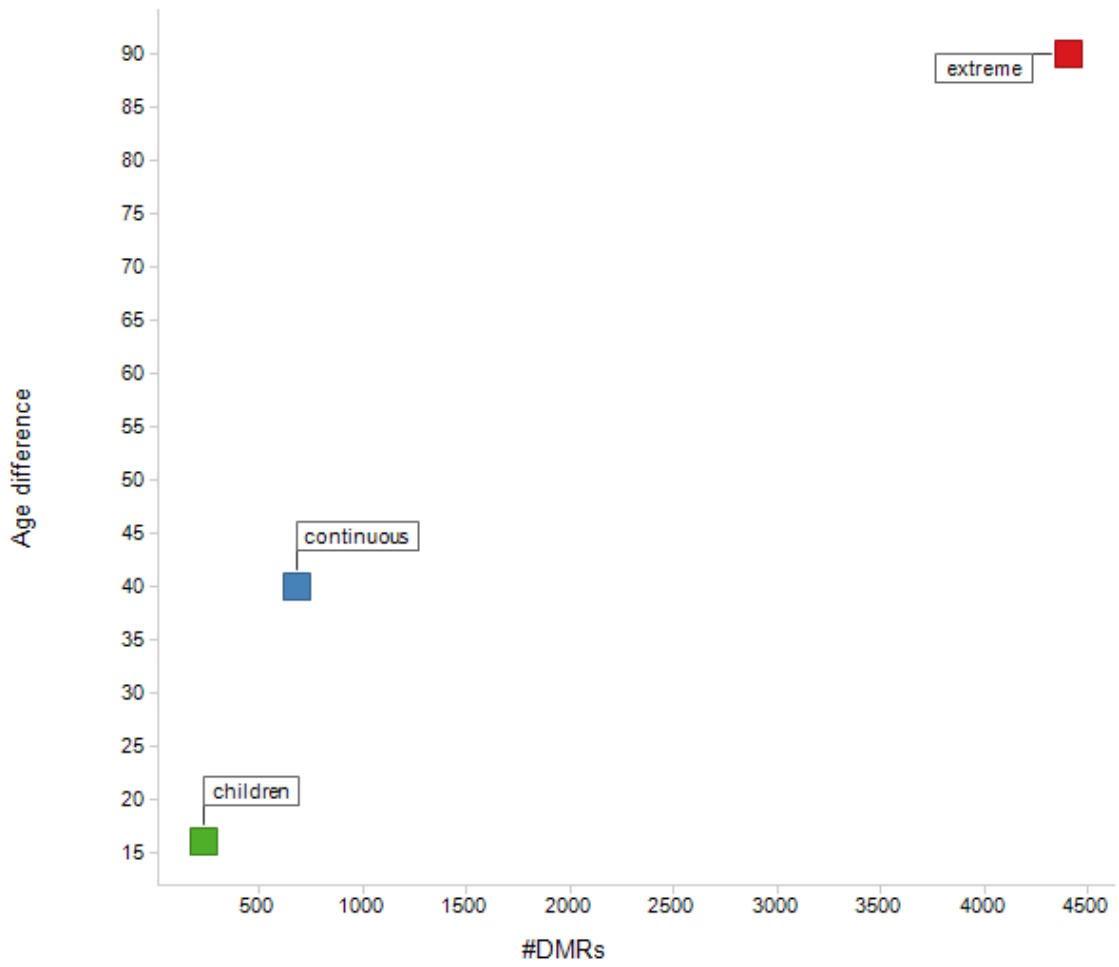


**Supplementary Figure 3.** Correlation of CpG methylation levels with distance for different age groups: a) Pearson correlation of pair-wise Infinium 450K measured methylation levels (y-axis) with distance (bp) (x-axis). b) The figure shows a zoomed-in region of distance < 250bp.

a

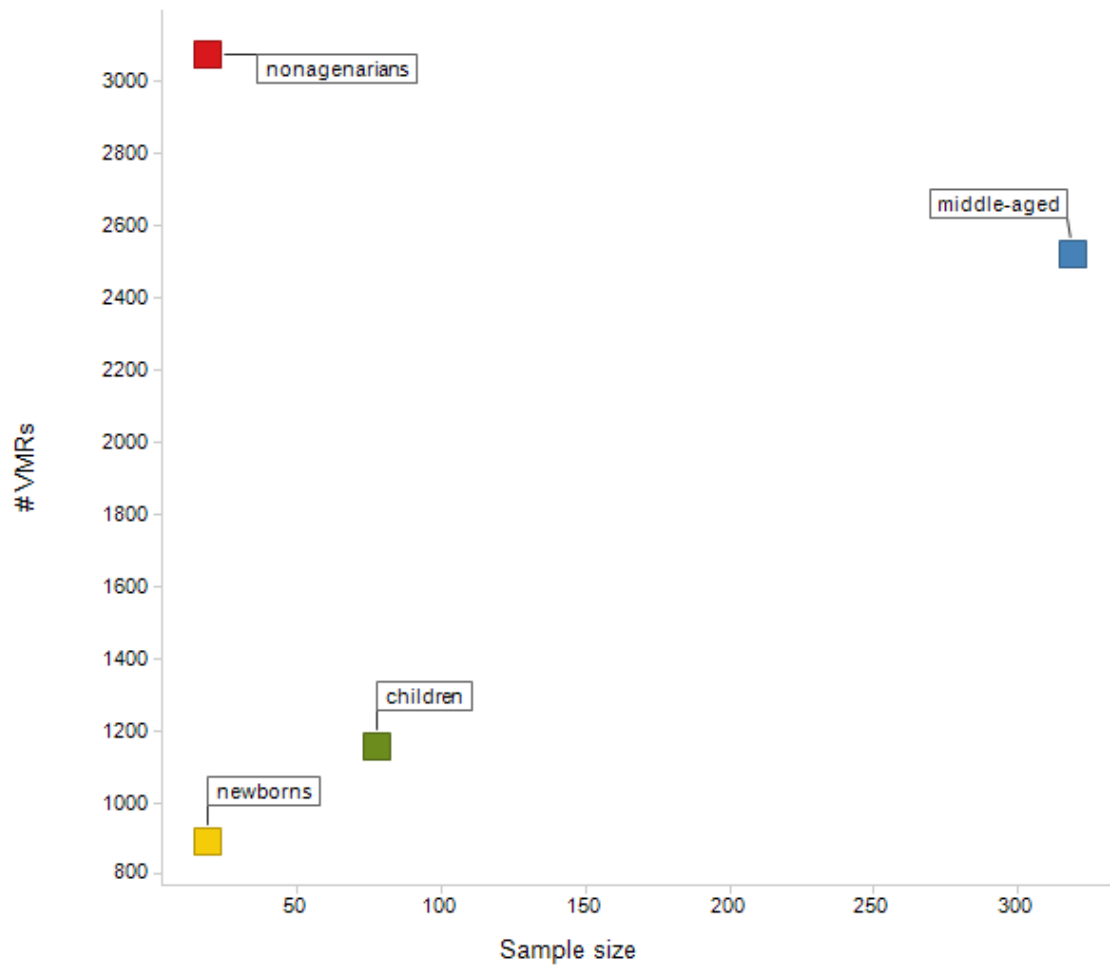


b

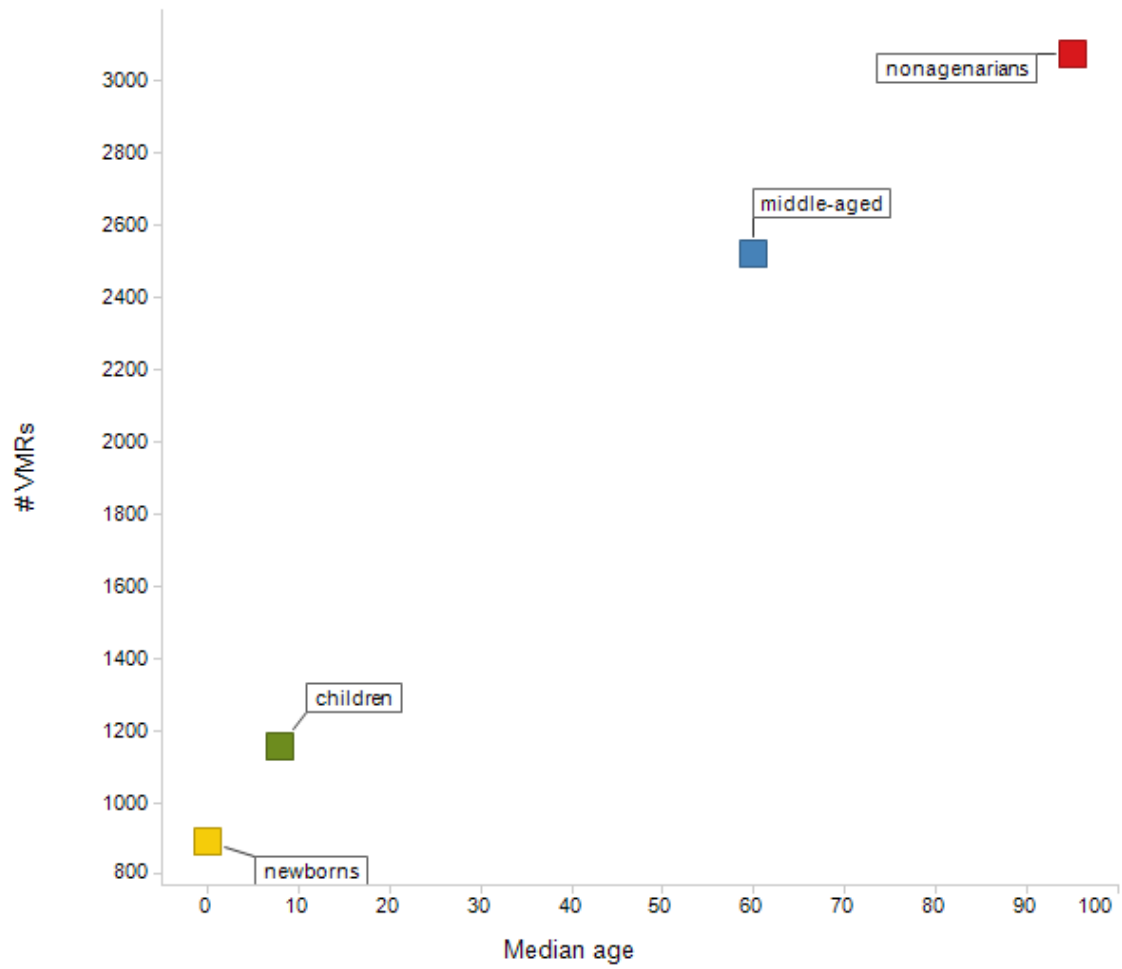


**Supplementary Figure 4.** Relationship between number of significant DMRs identified and a) sample size or b) age difference in sample set

a

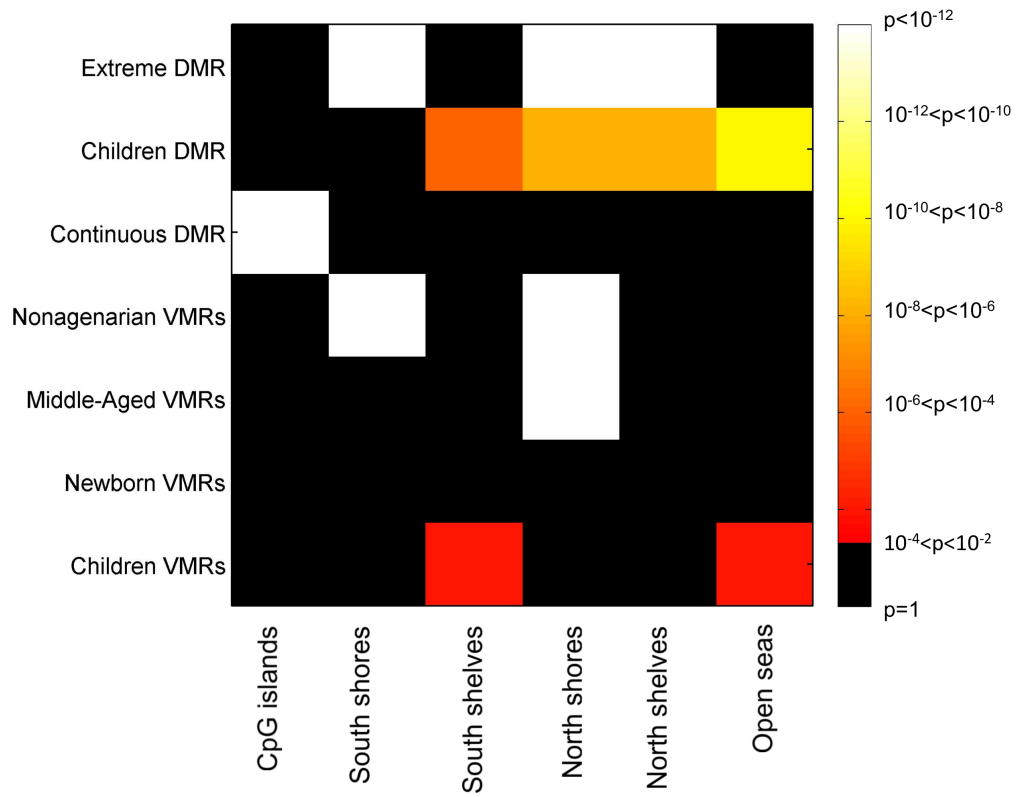


b



**Supplementary Figure 5.** Relationship between number of significant VMRs identified and a) sample size or b) median subject age in sample set





**Supplementary Figure 6. Heat-map of CpG island enrichment results.** Genomic regions of varying proximity to CpG islands are indicated on the x-axis and region lists on the y-axis. Cells are coloured for p-value of enrichment.