# Supplementary Figures

**Figure S1**: Sample drop out during QC for A) DNA methylation array and B) RNAsequencing samples. The upper tier (dark blue) shows the total numbers of included subjects and the bottom tier (in green) shows the total numbers of samples analysed in this study. Samples are  broken down by subject groups. : PersA_ICS Persistent asthma with ICS use PersA_no_ICS Persistent asthma without ICS use, ClinR Clinical Remission, ComR Complete Remission, H Healthy Controls. A) The middle tiers (light blue) show drop out of samples due to failed DNA extraction (no DNA), failure to meet the MethylAid QC criteria (MethylAid QC) and genotype mismatch between methylation array and independent SNP array (genotype mismatch). B) The middle tiers (light blue) show drop out of samples due to failed RNA extraction (no RNA), failure during sample processing (sample processing) and failure to meet QC criteria after sequencing (QC).

A)



B)
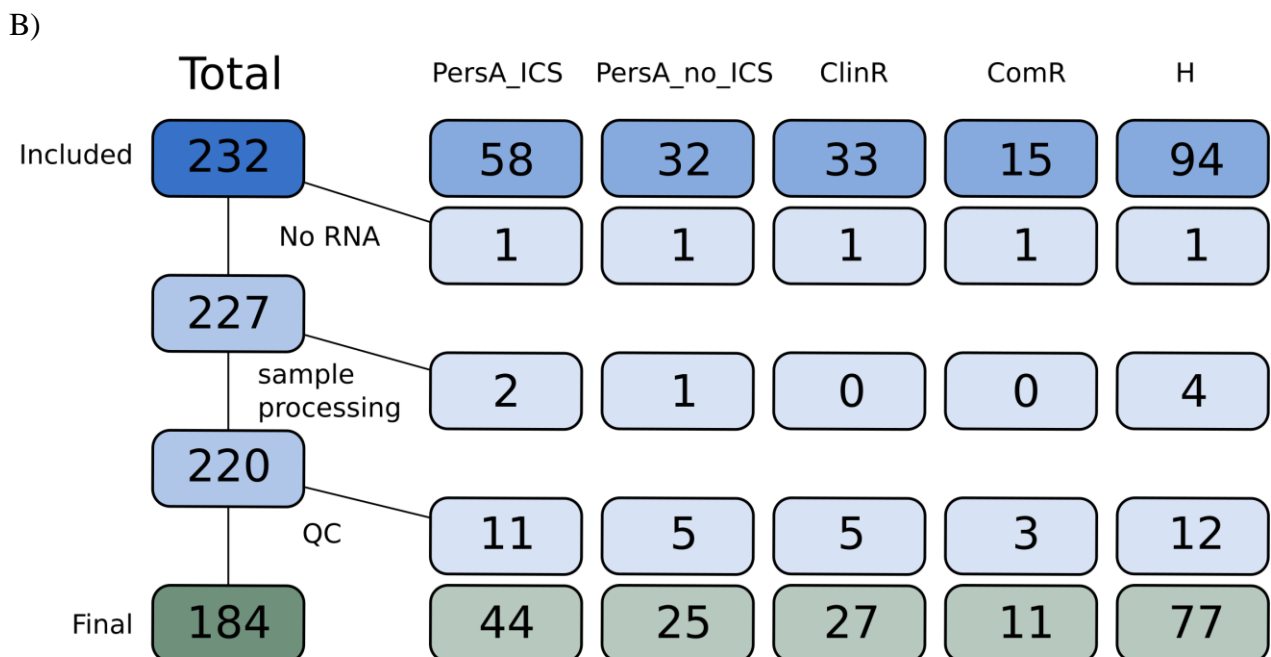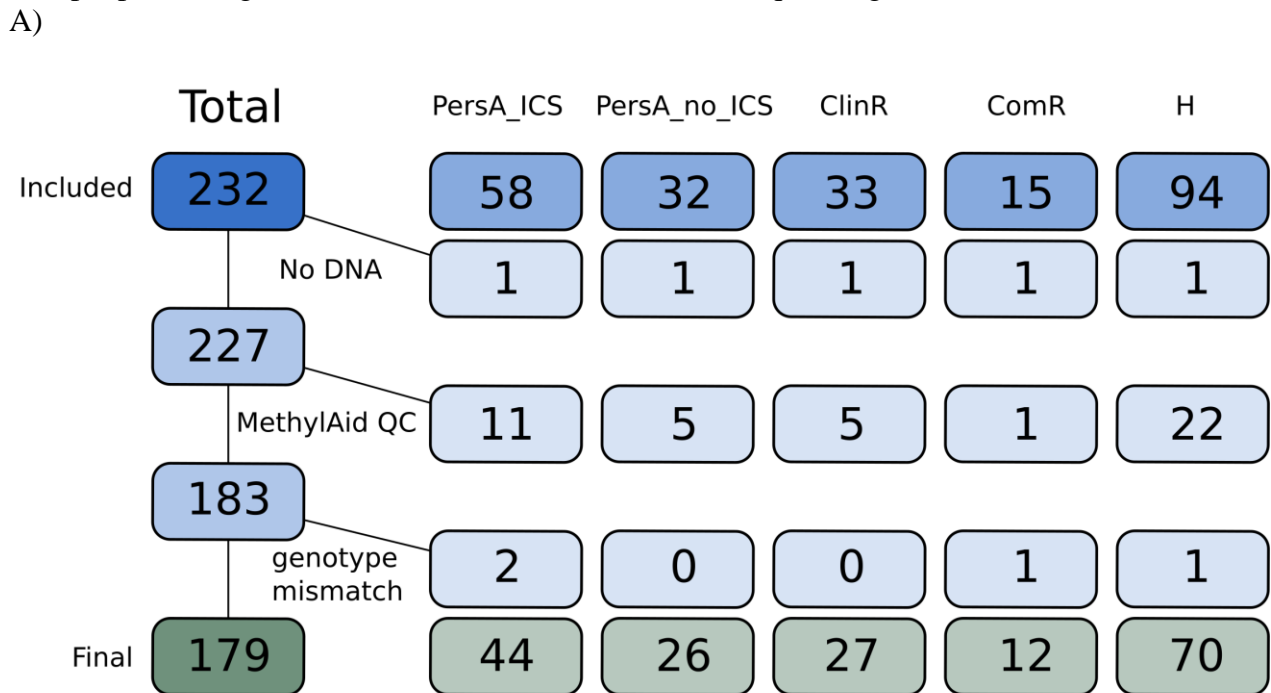
**Figure S2**: Summary statistics of the effect of adding cell type composition on differential methylation of a subset of CpG-sites. Figure (A) shows the -log10 transformed *P*-values from the contrasts that were assessed in the manuscript. The leftmost four CpG-sites are the tophits from the contrast remission *versus* asthma and the remaining sites come from the contrast remission *versus* healthy. See the MS for details. Plotted are the uncorrected *P*-values (red, also reported in Table 2A and 2B) and the *P*-values from the analysis including surrogate variables (blue). Figure (B) shows the -log10 transformed *P*-values for the surrogate variables for the same CpG-sites as in (A).

A)
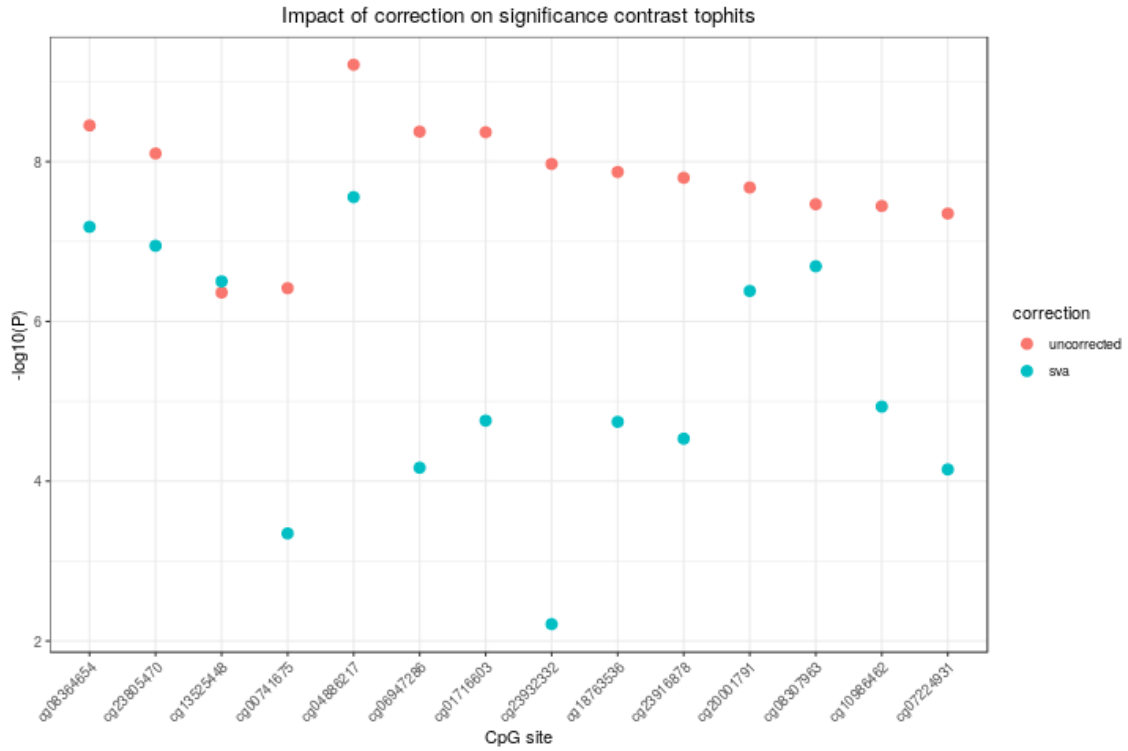


B)
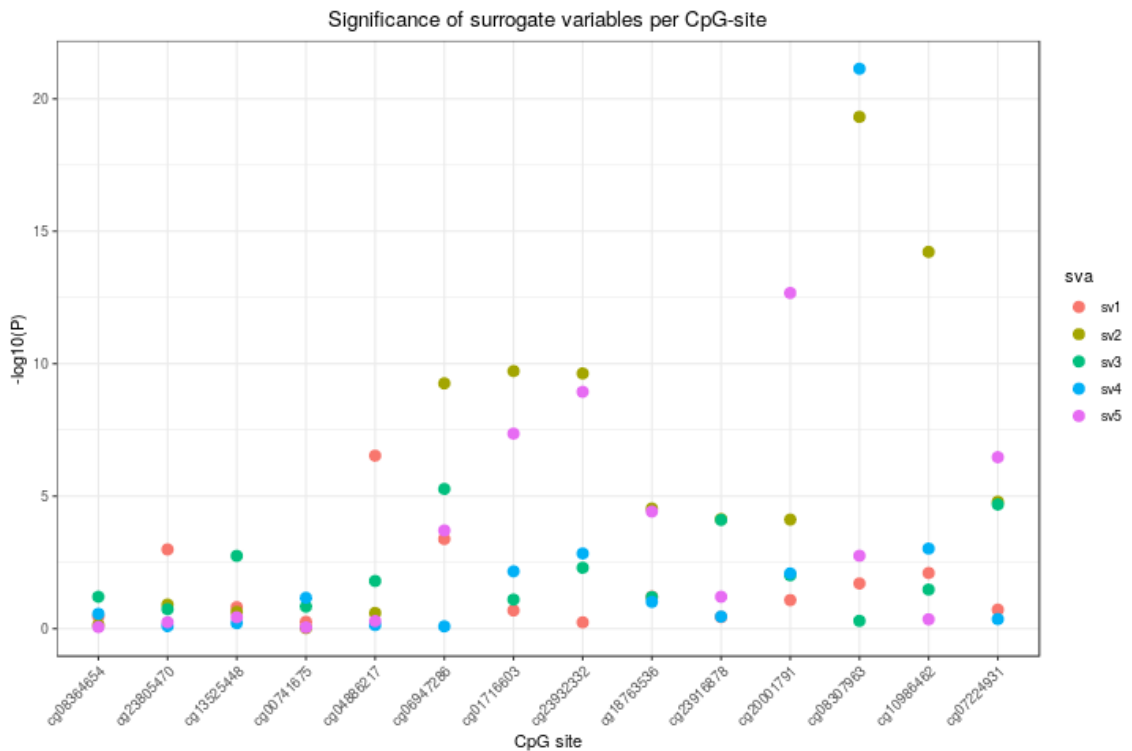
**Figure S3**: Quantile-quantile plots of observed *P*-values plotted against the expected *P*-values from a uniform distribution. Plots show data from the contrast (A) remission versus asthma and (B) remission versus healthy. The lambda values from chi-square statistics are reported in the figures. Lambda values differing from 1 indicate systematic bias, but may have a biological source (e.g. driven by differences cell composition).
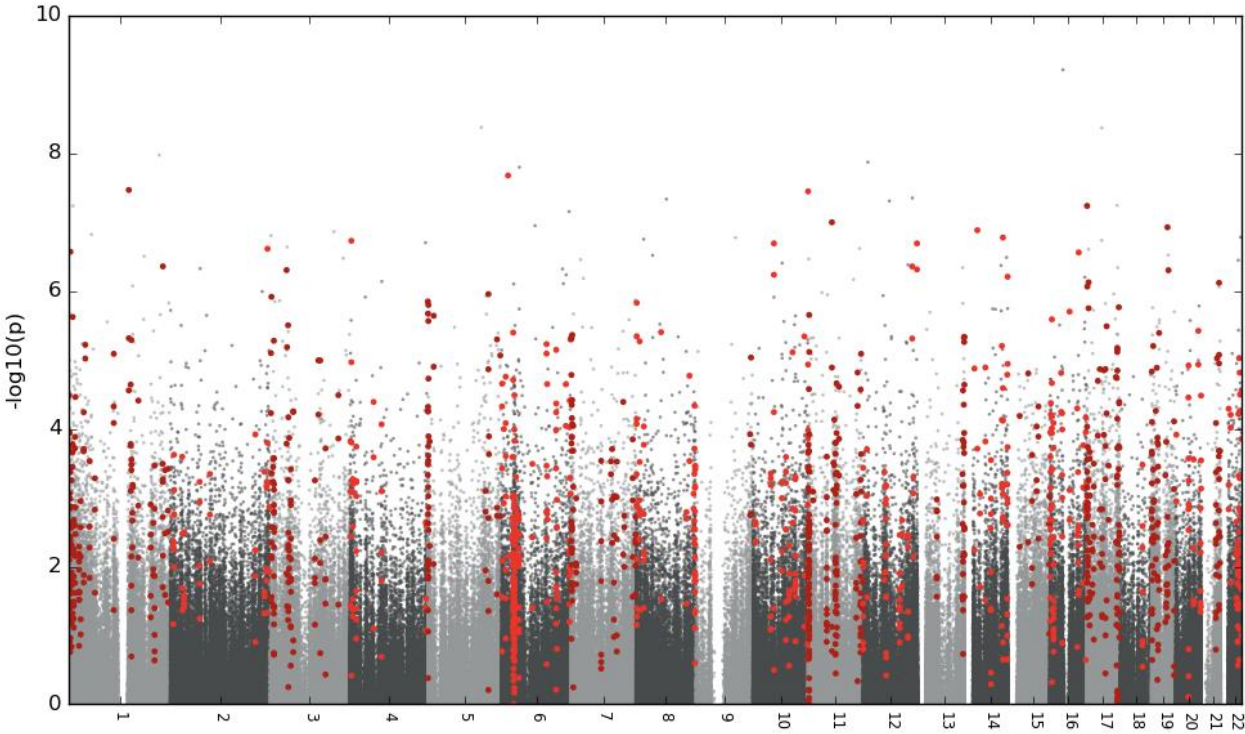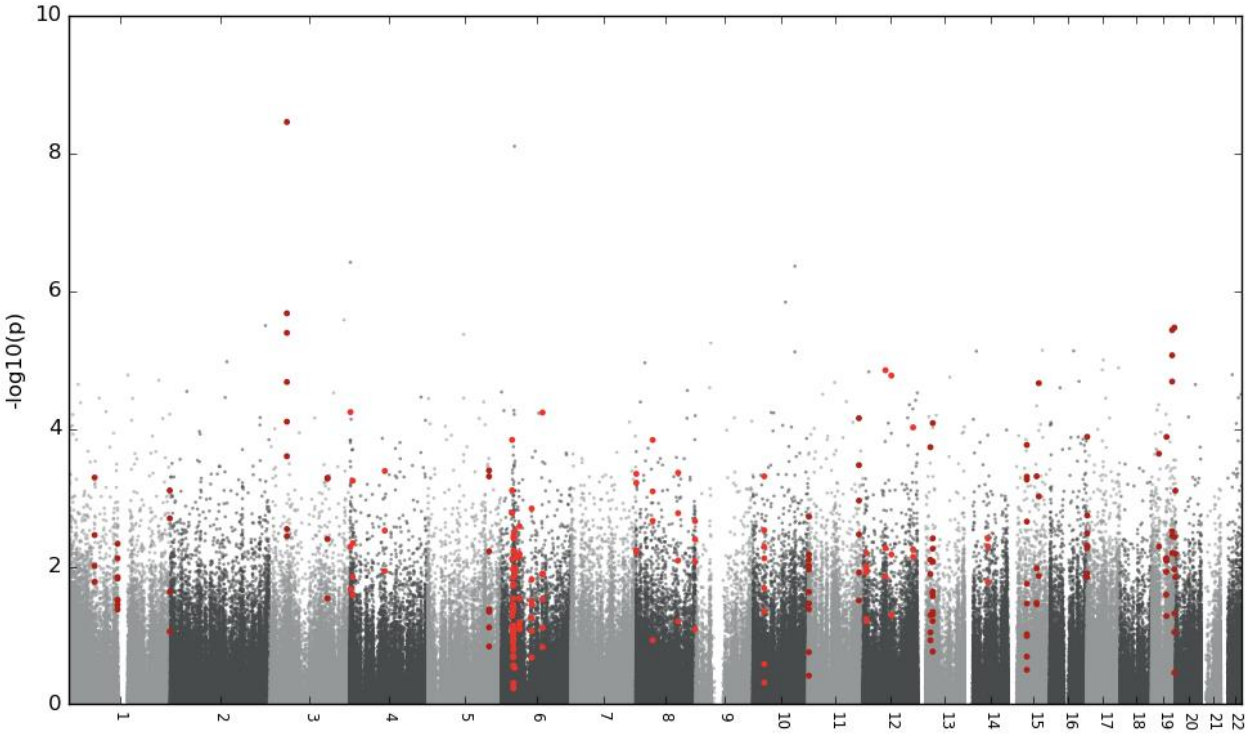
A)
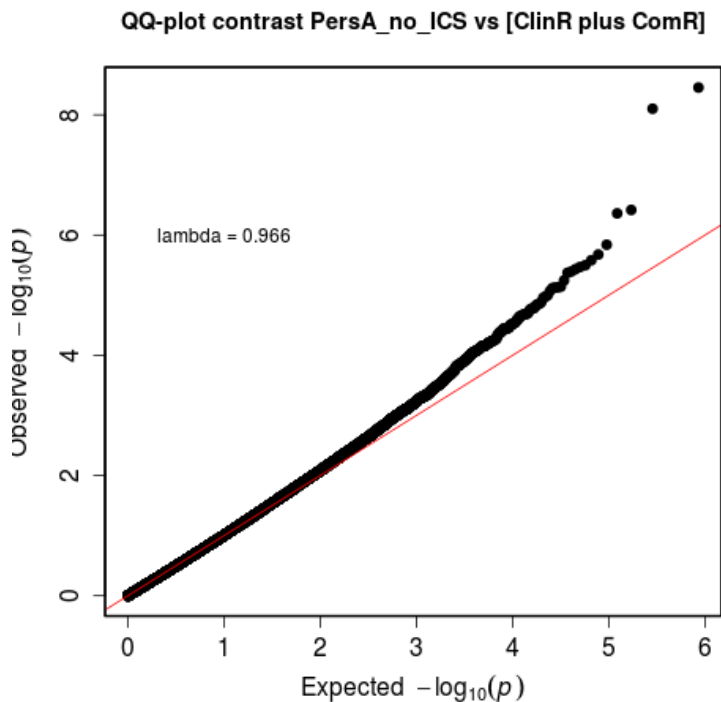


B)
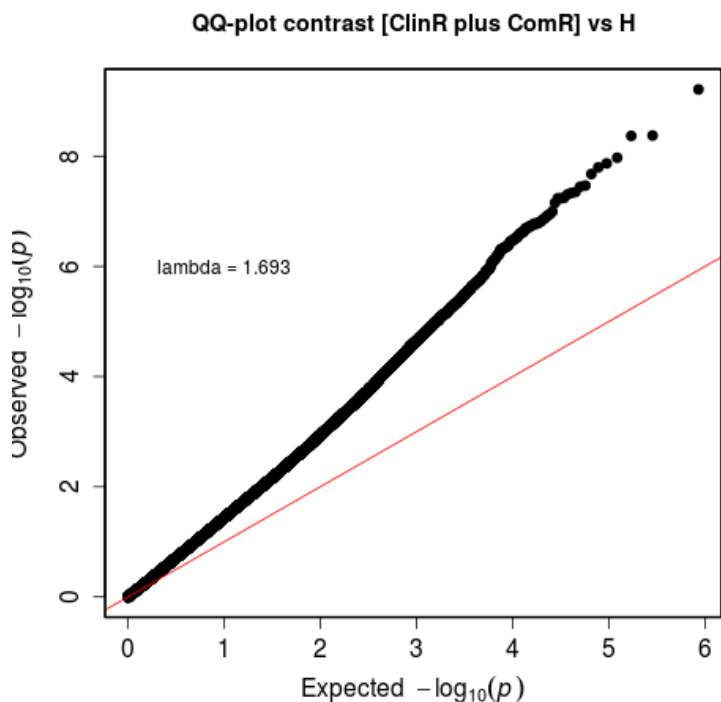
**Figure S4:** Manhattan plots of DMRs as output of the comb-p program. A) Asthma versus Remission. B) Remission versus Healthy.

**Figure S5:** Overlap in genomic position of individual CpGs with DMRs. A) Asthma versus Remission. B) Remission versus Healthy.