

Fig. S1 | Overview of the e/meQTL and co-localization studies in AECs treated with RV. (A) Experimental design used to identify treatment-specific e/meQTLs in upper AECs from 104 individuals. (B) Sample composition. (C) Venn diagram showing the overlap of asthma and CRS status of the 104 study participants.

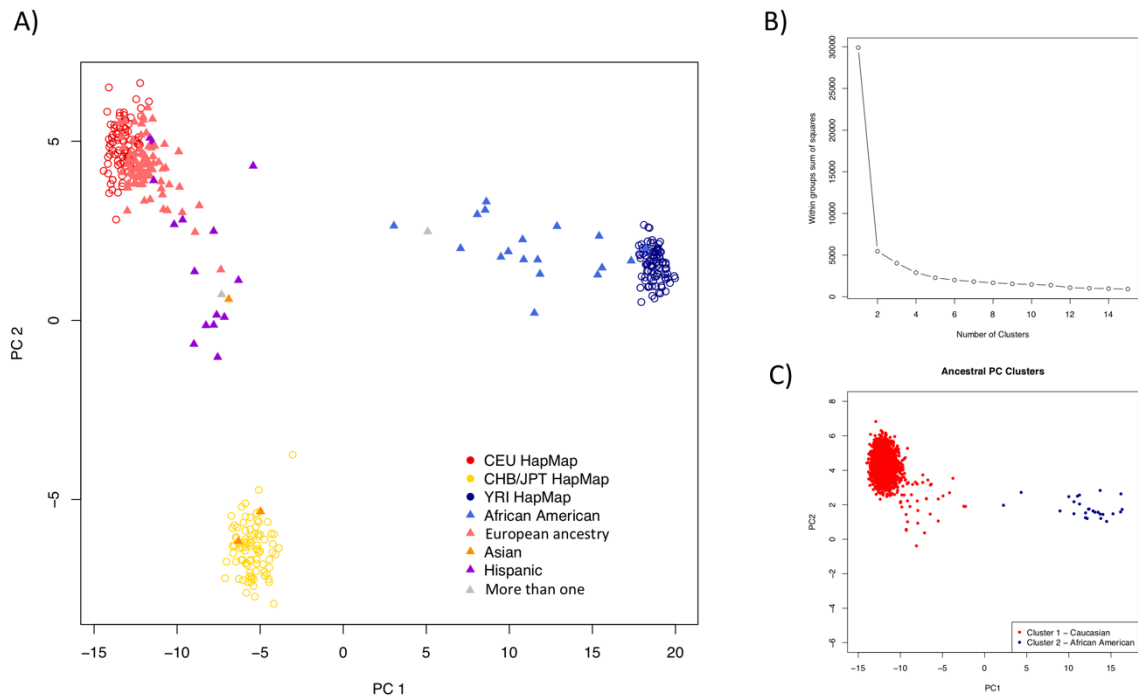


Fig. S2 | PCA and k-means clustering of genotypes. (A) PCA plot of study participant's genotypes (circles) projected on HapMap genotypes (squares). **(B)** Scree plot of k-means clustering of ancestral PCs in which the within groups sum of squares (y-axis) is plotted against the number of potential group clusters (x-axis); using the 'elbow criterion', it is determined that two clusters are best representative of how many clusters study samples can be grouped into for imputation. **(C)** PCA plot of study participants grouped into two cluster for genotype imputation, European (red), and African American (Blue), according to the k-means clustering criterion.

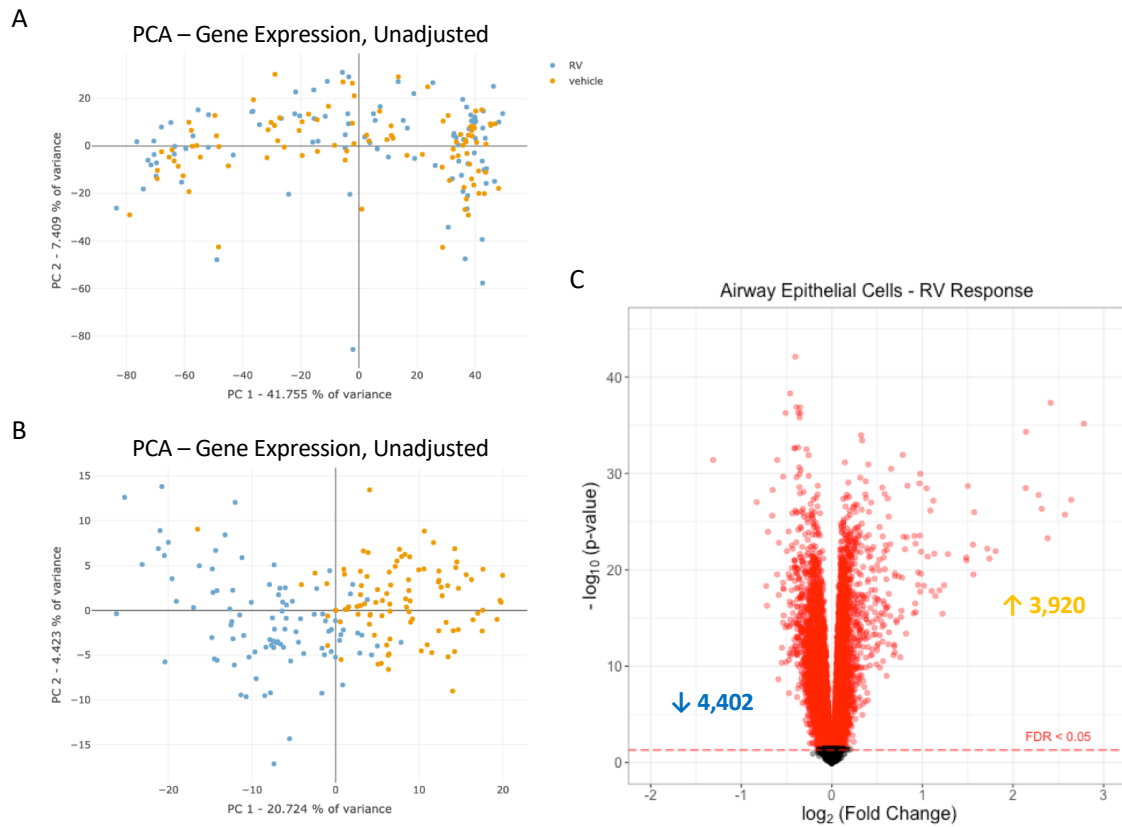


Fig. S3 | PCA of gene expression in vehicle and RV-treated AECs. (A) PCA plot of epithelial cell gene expression from 95 individuals treated with vehicle and RV before regressing out covariates. (B) PCA plot of gene expression in vehicle- and RV-treated cells after regressing out covariates. (C) Volcano plot showing treatment responses in epithelial cells were detected in the combined sample with 8,322 differentially expressed genes identified at a $\text{FDR} \leq 0.05$.

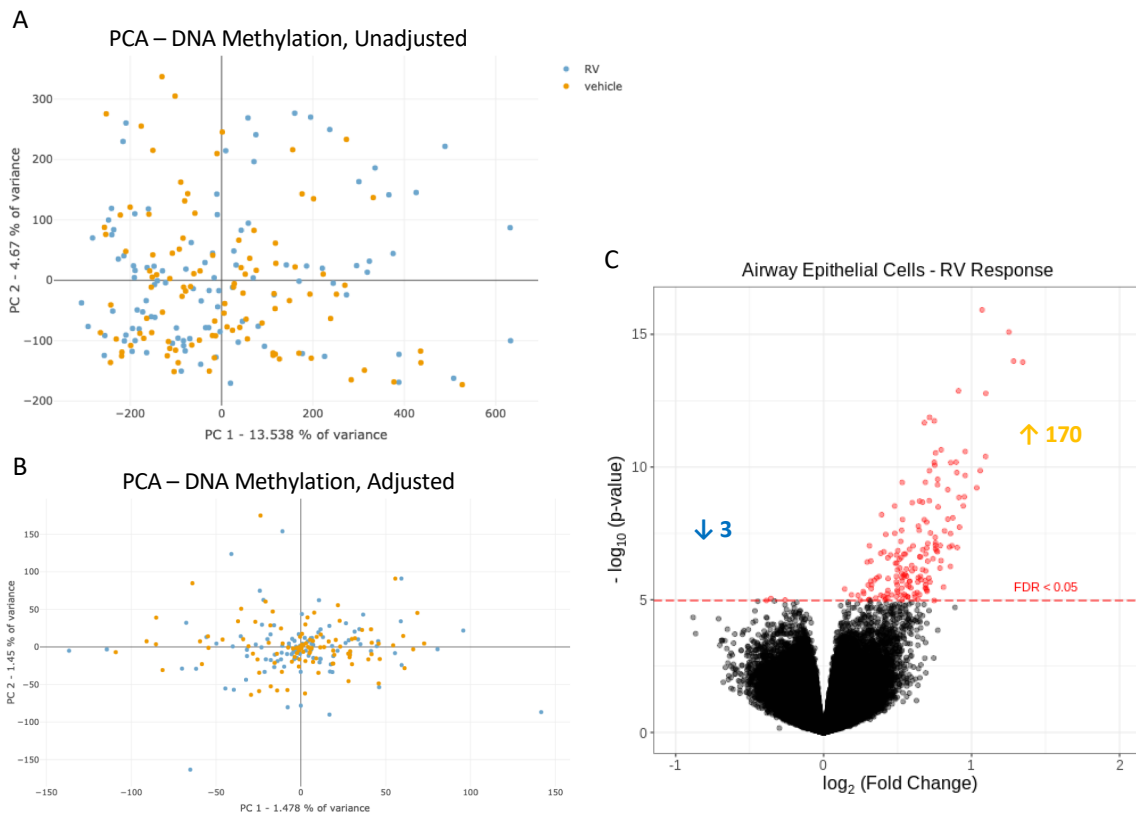


Fig. S4 | PCA of DNA methylation in vehicle- and RV-treated cultured AECs. (A) PCA plot of cultured airway epithelial DNA methylation from 103 individuals treated with vehicle and RV before regressing out covariates. (B) PCA plot of DNA methylation in vehicle- and RV-treated cells after regressing out covariates. Tables showing p-values of correlation with PCs and covariates before (C) Volcano plot showing treatment responses were detected in the combined sample with 173 differentially methylated CpGs at a FDR<0.05.

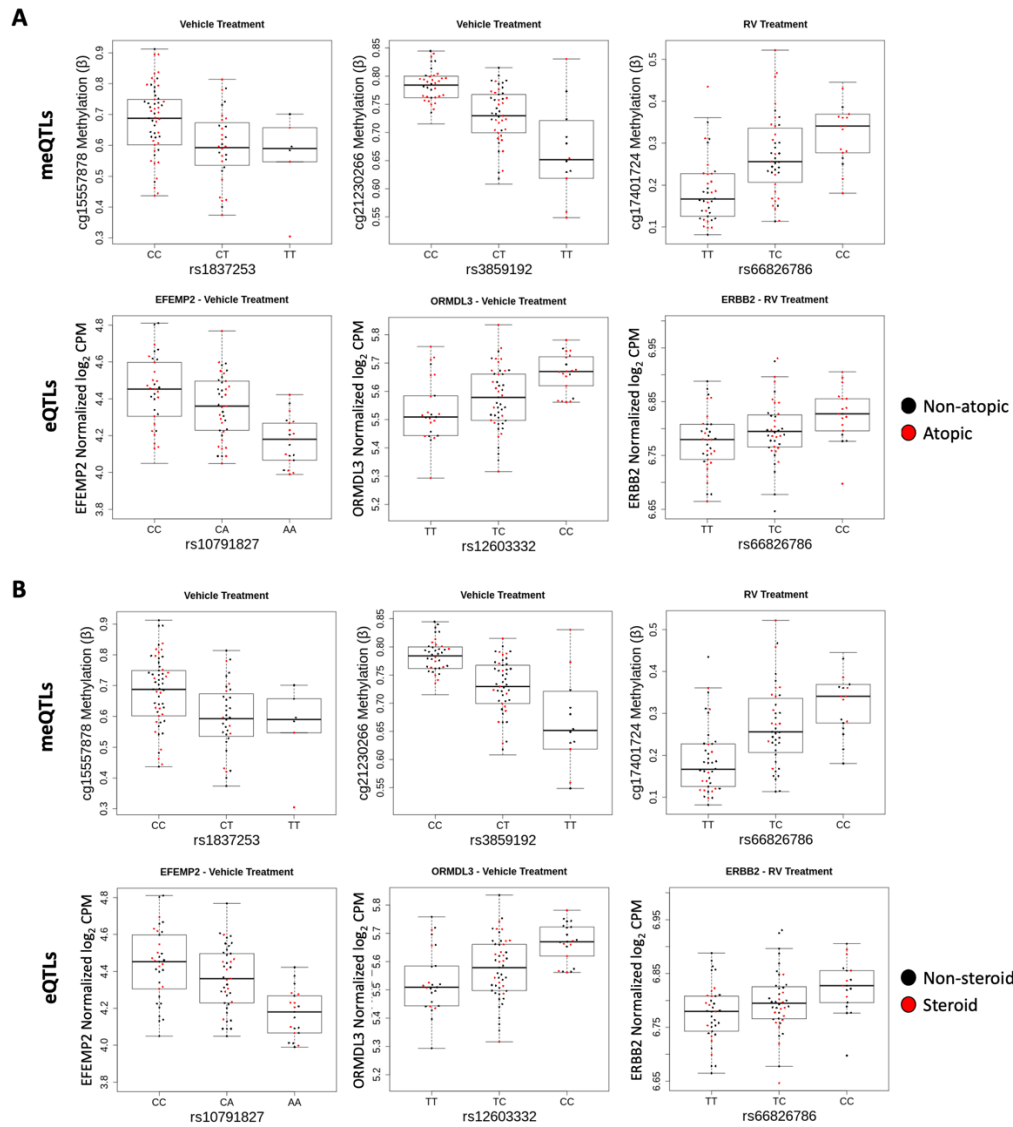


Fig. S5 | Molecular QTLs highlighting atopic samples. Box plots showing examples of eQTLs and meQTLs from vehicle- and RV-treated AECs highlighted in this study. A quality control measure showing that genotype-specific gene expression and DNAm levels were similar between the atopic and non-atopic individuals (A) and between individuals who used steroid medications vs those who did not (B). The box plots show that the molecular QTLs highlighted in this study were not confounded by either atopy or steroid use.

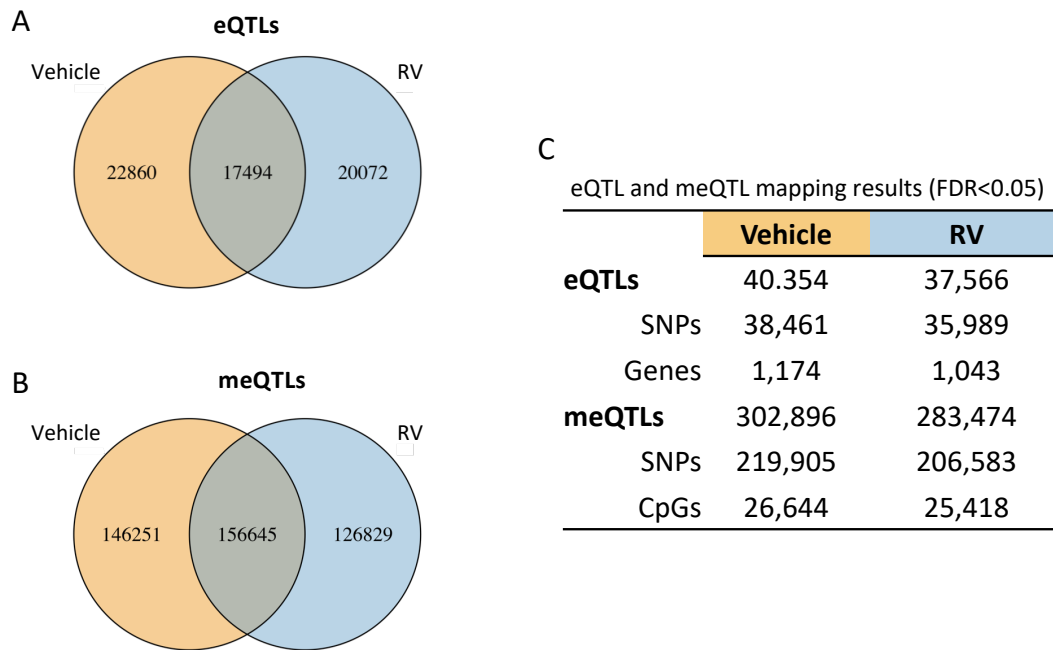


Fig. S6 | Summary results for molecular QTL mappings. Venn diagrams of eQTLs (**A**) and meQTLs (**B**) in each condition (FDR<0.05). (**C**) Summary of eQTL and meQTL mapping results for each treatment condition. The number of SNPs associated with the gene expression of at least one gene or CpG and the number of genes or CpGs whose expression or DNA methylation levels was associated with at least one SNP.

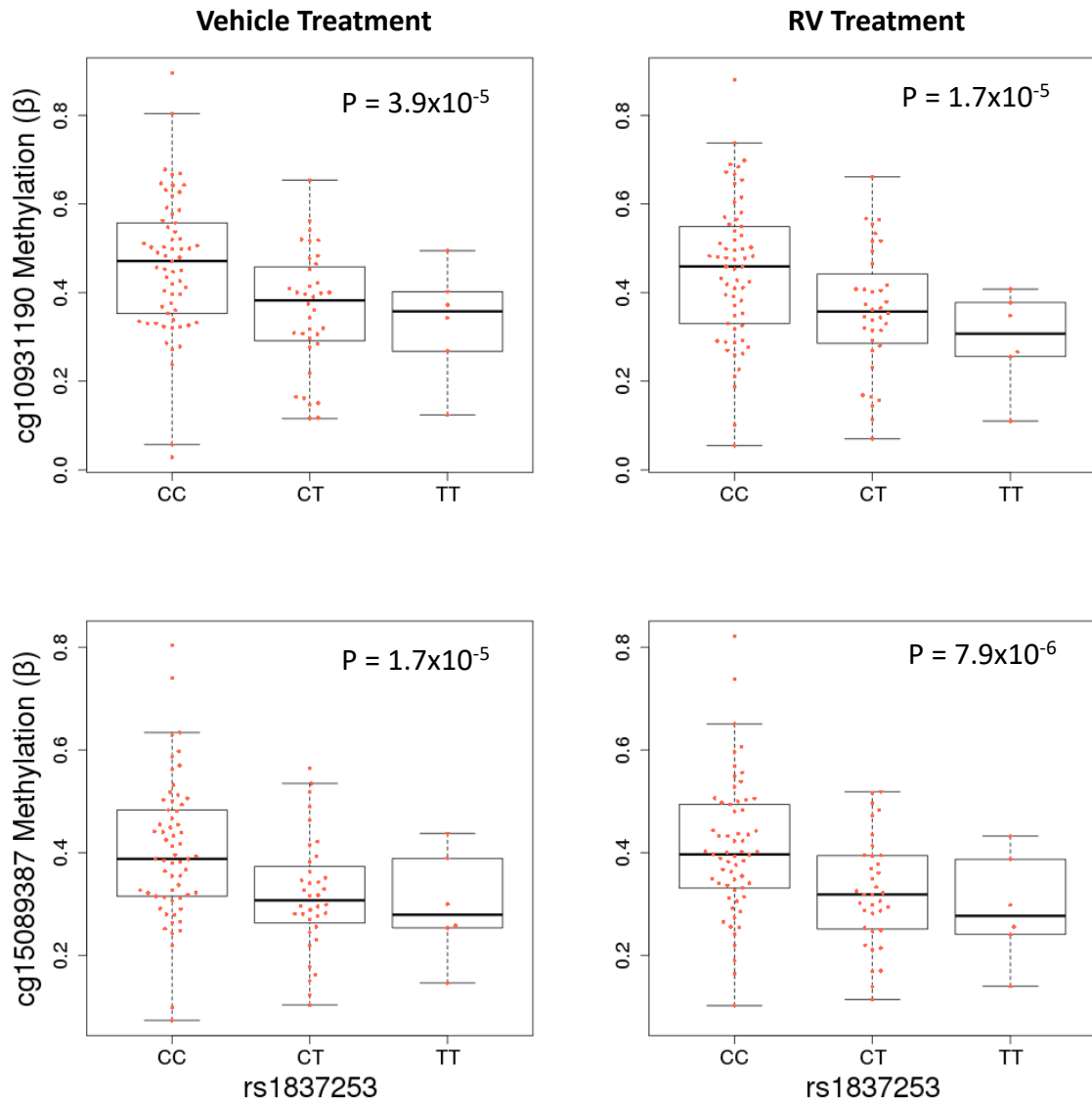


Fig. S7 | meQTLs at rs1837253 located in the first untranslated exon of the *TSLP* gene. Box plots of two meQTLs that were identified in both the vehicle- (left) and RV-treated (right) AECs were co-localized with the asthma risk variant (rs1837253) in adult onset and childhood onset asthma GWASs.