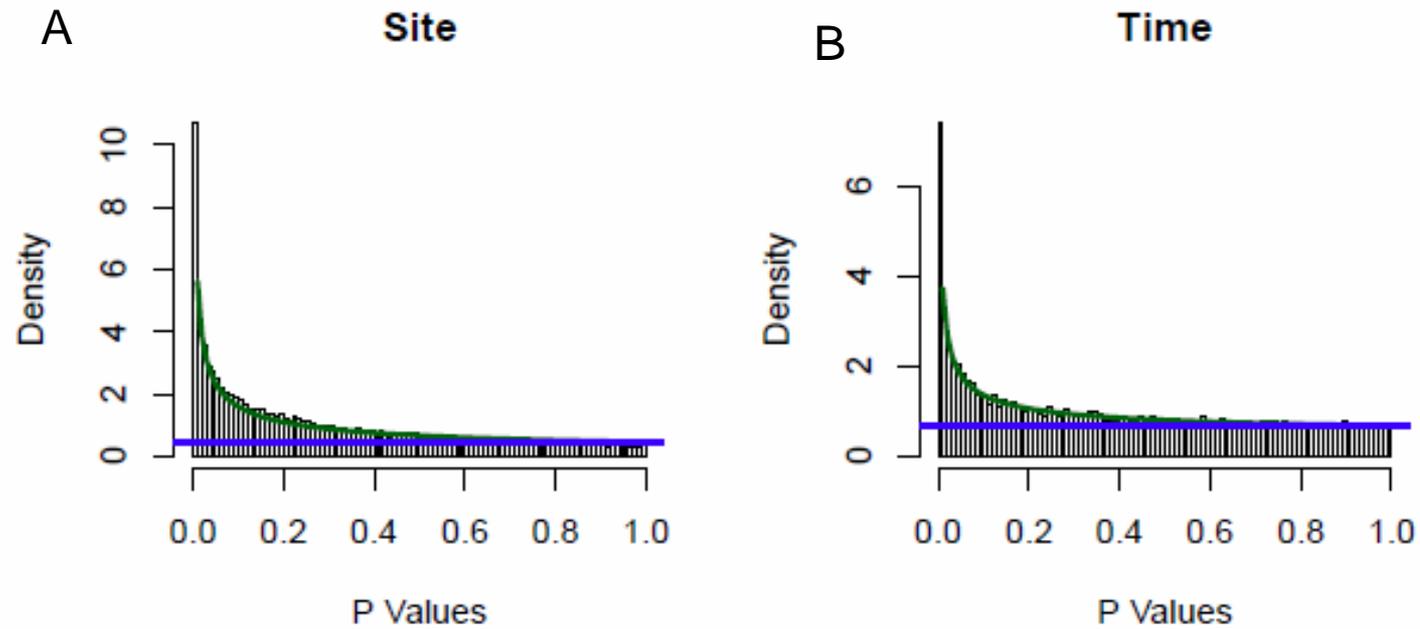
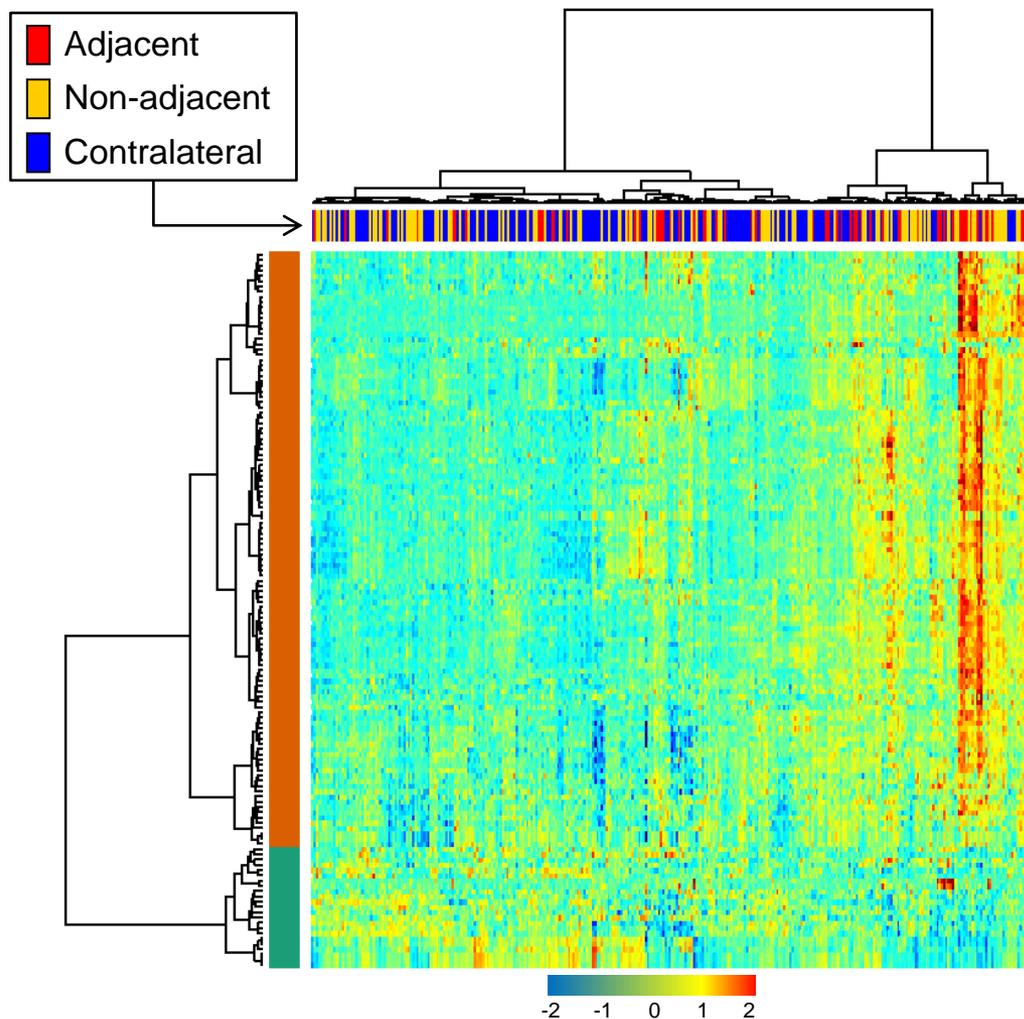


Supplementary figure 1



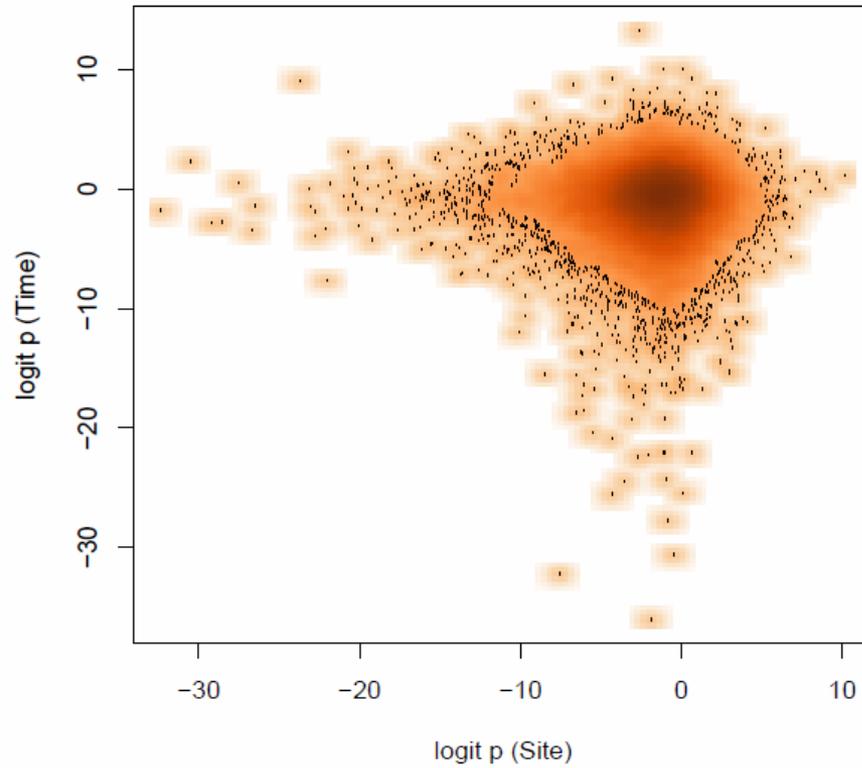
Supplementary figure 1. Histograms of the p-values for site- and time-dependent differential expression. BUM models were fitted to the p-values, indicated by the superimposed curves, for both site- and time-linked expression differences in the statistical model incorporating all airway samples (n=391) after which histograms were plotted to demonstrate the distribution of the p-values.

Supplementary figure 2



Supplementary figure 2. Site-dependent differential gene expression patterns identified by expression profiling of airways excluding main carinas. Heat map depicting two-dimensional clustering of airway samples (n=331) excluding main carinas and genes (n=136) that were determined to be differentially expressed by site in the mixed-effects model based on a 1% FDR cut-off. Differentially expressed genes were grouped into two clusters with 113 genes (upper cluster) exhibiting relatively increased expression in adjacent airways and were found to separate airway samples into two group with significantly dissimilar number of adjacent airways ($p=0.000266$ of the Fisher's exact test for count data).

Supplementary figure 3



Supplementary figure 3. Smoothened scatter plot of transformed p-values for site and time effects.