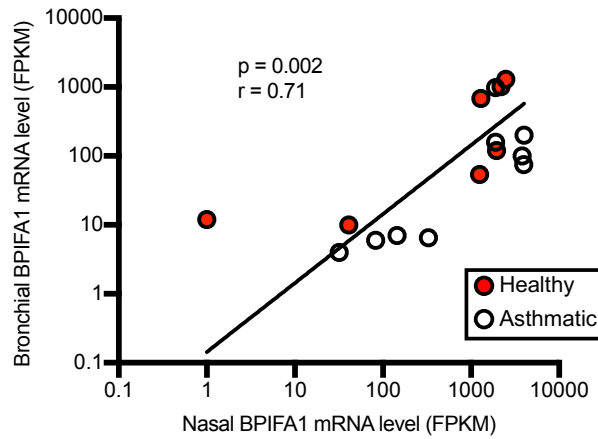
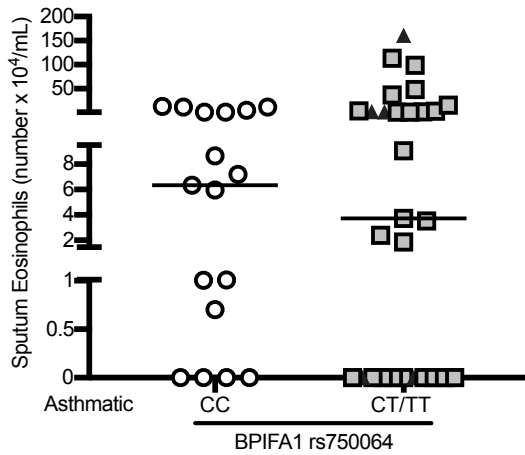


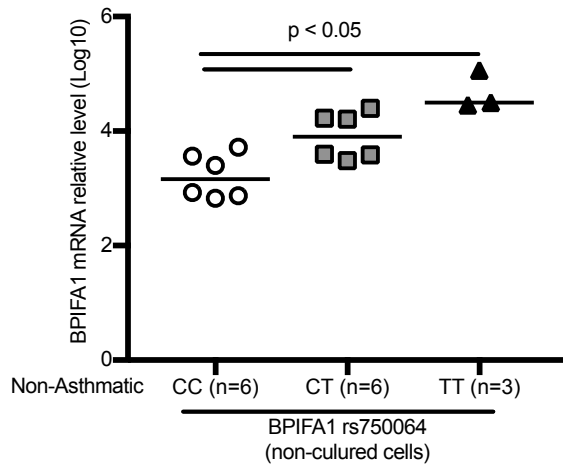
Supplemental Figures



Supplementary Figure 1. Strong positive correlation in BPIFA1 mRNA expression levels between brushed nasal and bronchial epithelium obtained from the same healthy (n=7) and asthmatic (n=9) subjects (age, 19 to 52 years). BPIFA1 mRNA expression was determined from whole transcriptome RNA-sequencing analysis, and is expressed in Fragments Per Kilobase of exon per million fragments mapped (FPKM). A Pearson's correlation analysis was performed.



Supplementary Figure 2. Asthmatics with the BPIFA1 rs750064 CC genotype trend to have higher sputum eosinophils than the CT genotype. Induced sputum was collected from n=46 subjects (n=39 adults, n=7 children). The black line represents the median number.



Supplementary Figure 3. Non-asthmatic subjects (n=6) with the rs750064 CC genotype have significantly less BPIFA1 mRNA expression than subjects with the CT (n=6) and TT (n=3) genotypes. BPIFA1 mRNA expression of non-cultured nasal brushing cells was measured in non-asthmatics who did not have a known lung disease (n=5) or were diagnosed with other lung diseases (n=10). P values represent a Kruskal-Wallis test.