

Sputum proteomics and airway cell transcripts of current and ex-smokers with severe asthma in U-BIOPRED: an exploratory analysis

Supplementary figures S1 to S3

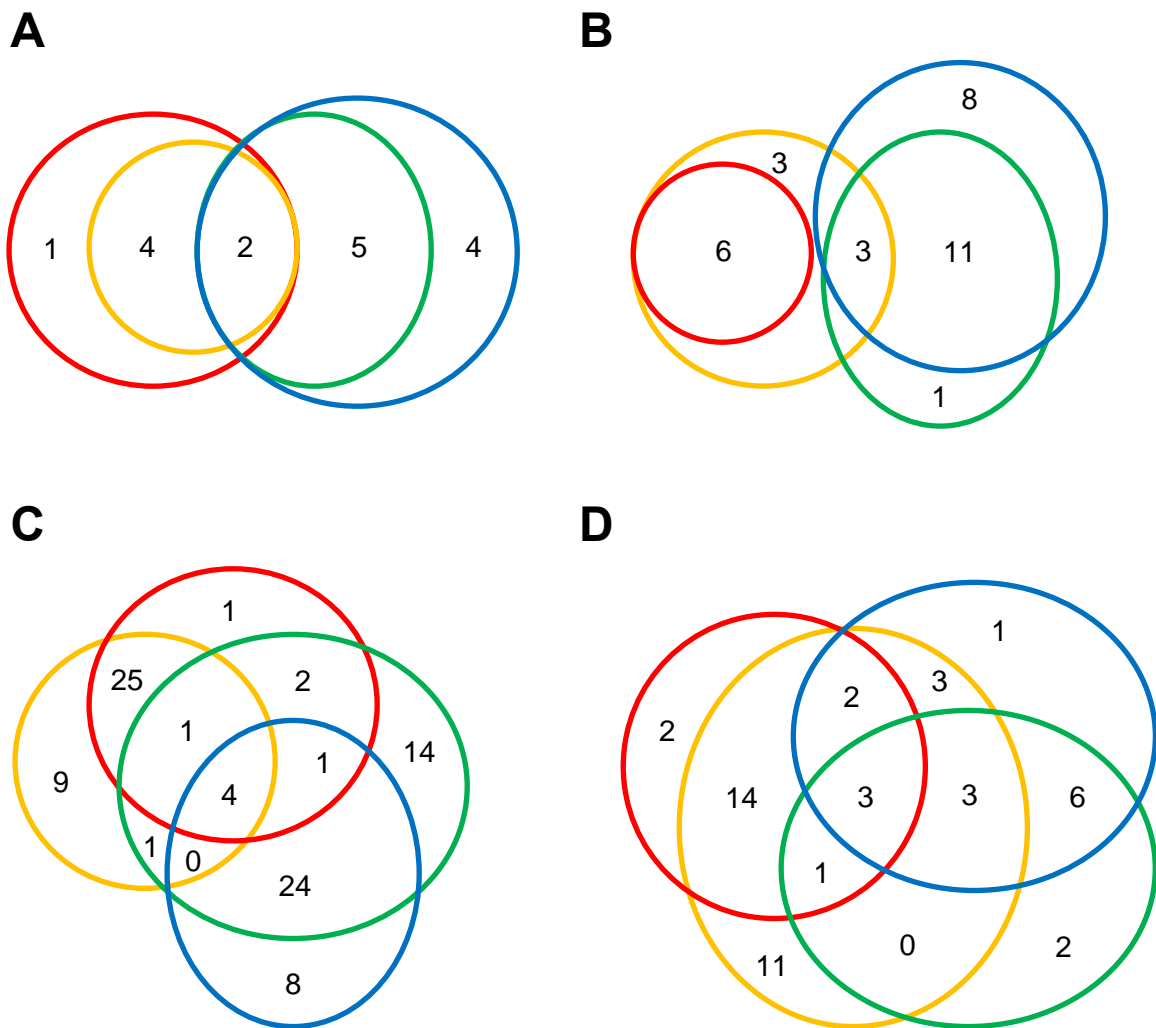


Fig. S1. Venn Diagrams showing the numbers of subjects whose samples were applied for proteomic and transcriptomic analyses.

All subjects whose samples were adequate and used for omics analyses are shown in the diagrams (CSA (A), ESA (B), NSA (C) and NH (D), respectively). Four types of samples are shown as circles with different colours (red circle; bronchial biopsies, orange circle; bronchial brushings, green circle; sputa, and blue circle; sputum SomaLogic, respectively).

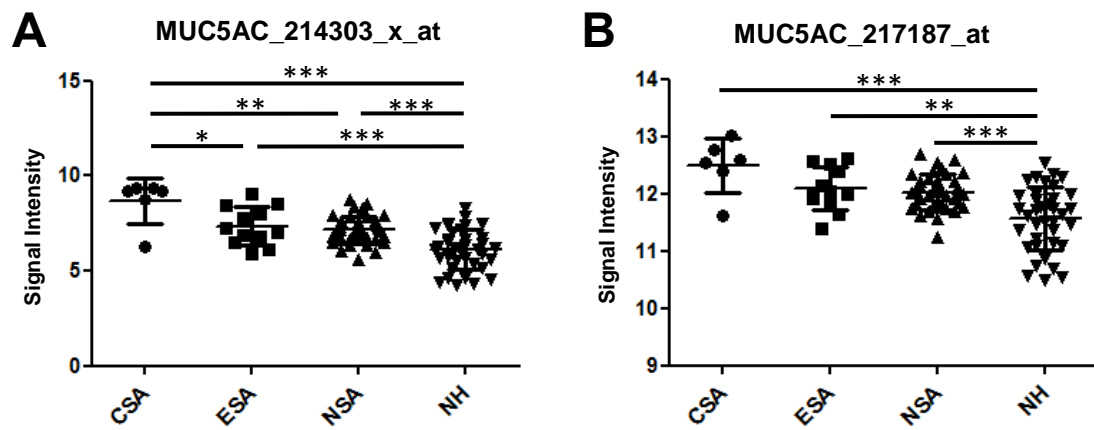


Fig. S2. Gene expression levels of MUC5AC were highest in CSA group.

Dot plots with mean \pm SD showing signal intensity levels of MUC5AC gene expression. Affymetrix probe names were 214303_x_at (A) and 217187_at (B), respectively. * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$.

