Future Perspectives
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The work performed in the thesis has wide applications in the context of asthma biology. Although most of the issues have been well addressed there are certain areas that could not be completed due to time and other limitations. These could be taken up as leads for further research.

The identified compounds that could differentiate the cases from controls and the subtypes of asthma require validation in another cohort to be used as biomarker signatures for diagnosis and differentiation. Validation of the clinical characteristics of the identified phenotypes could have it far-reaching impacts.

Finally developing sensors for these breath prints, which could be used, for diagnosis and prognosis of these diseases is probably the best fitting translational application of our work. Although ambitious, yet these breath-prints could be used in electronic noses that are already there in the market although with limited clinical applications.

The GWAS although carried out in a small discovery cohort, gave us interesting initial leads. The analysis needs to be extended by validating the associated SNPs obtained in a larger cohort to increase the power of the study and also functionally confirming their role in asthma pathogenesis.

This study offers important implications and suggests new paradigm shifts. First, by following and tracking different metabolites one could have a comprehensive view of the metabolic fluxes in diseases and healthy states. Genomics helps one monitor different genes’ expression in different states. Knowledge of the transcripts in a system also could help us gauge the different regulatory modifications such alternative splicing etc. that might control the ultimate protein signatures reflected through proteomic studies. A longitudinal –omics analysis of a large number of individuals (both healthy and diseased) may be extremely valuable to dissecting the disease and its various subtypes, as well providing information into the molecular mechanism of its onset and susceptibility.

Finally, we believe that the wealth of data generated from this study will serve as a valuable resource to the community in the developing field of personalized medicine. Such detailed integrated studies are the need of the hour. These generate larger
repertoires of valuable data which helps one visualize the complete picture and stitch the different parts of a complex physiology. A database with all the clinical, molecular, phenotypic, physiologic, genetic information of the different subtypes of the disease might well be a treasure trove for diagnostics, monitoring, and treatment of diseased states to the medical fraternity.

To sum up in the lines of Sir Richard Feynman the famous physicist “Nature uses only the longest threads to weave her patterns, so that each small piece of her fabric reveals the organization of the entire tapestry.” It is the threads we have to unveil to actually appreciate the patterns of physiology.