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Title: Next-gen transcriptome analysis (RNA-Seq) of human bronchial biopsies and laser microdissected airway smooth muscle: Asthma vs. controls

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Body: Rationale The pathophysiology of asthma is largely unknown. RNA-Seq allows detailed biological characterization of the airways. We hypothesized that the airway transcriptome is different between asthma and controls. Aim We investigated: a) the difference in transcriptomic profiles of whole endobronchial biopsies between steroid-naïve asthma and controls; b) the feasibility to obtain RNA from airway smooth muscle (ASM) captured by laser microdissection (LCM) suitable for RNA-Seq Methods 4 biopsies per subject (asthma/control: aim a n=4/n=5; aim b n=24/n=12) were incubated in RNAlater. Whole cryosection or LCM-captured ASM was put into TRIzol. cDNA was obtained with Ovation RNA-Seq System and prepared for RNA-Seq (GS FLX+, 454). Results Sample characteristics are shown below.

Sample characteristics

		Whole biopsy	ASM
Concentration (ng/µL)			
	RNA	30-310	2-27
	cDNA	204-321	18-168
RNA-Seq reads mapped (%)[1]			
	Asthma	87	
	Control	88	89[2]

[1]Reference=UCSC hg19; [2]1 subject

The 46 differentially expressed genes between asthma and controls were assigned to networks associated with cell cycle, morphology, and development.

Conclusion Transcriptomic profiles of whole biopsies were different between asthma and controls. LCM-captured ASM is suitable for RNA-Seq. Regulation of airway biological processes in asthma and controls tends to be fundamentally different. These findings may help develop targeted asthma therapy.