

Table E1 Correlation of Methylation sites

Correlation
Matrix¹

	CPG1	CPG2	CPG3	CPG4	CPG5	CPG6	CPG7	CPG8
CPG1	1	0.38	0.54	0.42	0.35	0.43	0.39	0.45
CPG2		1	0.20	0.21	0.18	0.28	0.24	0.29
CPG3			1	0.60	0.52	0.56	0.44	0.44
CPG4				1	0.73	0.59	0.56	0.52
CPG5					1	0.64	0.60	0.45
CPG6						1	0.79	0.76
CPG7							1	0.75
CPG8								1

Clade 1

Clade 2

Clade 3

Values denote Pearson correlation coefficients for 177 subjects

Table E2. The association between percent methylation at *ADRB2* and asthma outcomes, stratified by sample type

Dyspnea				
	Combined sample		Saliva	Blood
Predictor	OR (95%CI) ^a N=177	p-value	OR (95%CI) ^b N=136	OR (95%CI) ^b N=41
Average methylation of <i>ADRB2</i>	0.2 (0.1 – 0.6)	0.002	0.3 (0.1 – 0.8)	0.01 (<0.1 – 0.6)
Clade 1	0.2 (0.04 – 0.7)	0.01	0.2 (0.04 – 1.0)	0.003 (<0.1 – 1.0)
Clade 2	0.4 (0.2 – 0.8)	0.01	0.5 (0.2 – 1.2)	0.1 (0.02 – 0.9)
Clade 3	0.4 (0.2 – 0.7)	0.004	0.4 (0.2 – 0.9)	0.04 (<0.1 – 0.8)

^aadjusted for age, race, gender, preterm birth, family history of asthma, diagnosis of eczema and sample type

^badjusted for age, race, gender, preterm birth, and diagnosis of eczema. Family history of asthma omitted due to model instability.

OR: Odds ratio; 95%CI: 95% Confidence Interval of the odds ratio point estimate