In utero tobacco smoke exposure, DNA methylation and asthma in Latino children.

Andreas M. Neophytou;[a,b] Sam S. Oh;[c] Donglei Hu;[c] ; Scott Huntsman;[c] Celeste Eng;[c] José R. Rodríguez-Santana;[d] Rajesh Kumar;[e, f] John R. Balmes;[a, c] Ellen A. Eisen;[a] Esteban G. Burchard.[c]

ONLINE DATA SUPPLEMENT

Supplemental Table S1: Demographic characteristics of the study sample of 572 Latino children with DNA methylation data and the entire GALA II asthma case control study.

Characteristic, n (%)	Subsample (N=572)	GALA II (N=4702)
Asthma status	310 (54.2)	2374 (50.5)
Male	286 (50)	2306 (49.0)
Age, mean±sd	12.5±3.4	13.3±3.5
Maternal smoking during pregnancy	80 (14.0)	210 (4.5)
Maternal education[*]		
Less than high school	225 (39.7)	1651 (35.5)
High school grad. or equivalent	153 (27.0)	1243 (26.7)
At least some college	189 (33.3)	1754 (37.7)
Current SHS exposure in the home (any)[*]	128 (23.5)	860 (21.0)
Recruitment region		
Chicago	176 (30.8)	696 (14.8)
Houston	49 (8.6)	385 (8.2)
New York	52 (9.1)	577 (12.3)
Puerto Rico	192 (33.6)	2123 (45.2)
SF Bay Area	103 (18.0)	921 (19.6)
Ethnicity		
Mexican	276 (48.2)	1556 (13.5)
Other Latino	77 (13.5)	827 (17.6)
Puerto Rican	219 (38.3)	2319 (49.3)
Cases only		
Asthma control		
Controlled	88 (28.4)	527 (26.1)
Partially controlled	106 (34.2)	685 (33.9)
Uncontrolled	116 (37.4)	811 (40.1)

[*] Data on maternal education and current SHS exposures were not complete. Percentages based on participants with complete data

Supplemental Table S2: Mean±SD and IQRs for DNA methylation at selected CpG loci (as percentages).

CpG locus (gene)[*]	Mean (SD)	IQR
cg18132363 (*LINC00473*)[*]	42.1±6.1	8.7
cg26764244 (*GNG12*)	19.7±4.1	5.1
cg13822849 (*OLFM1*)	19.5±3.4	4.1
cg05575921 (*AHRR*)	87.0±3.4	3.9
cg22549041 (*CYP1A1*)	33.6±9.8	13.2
cg26889659 (*EXOC2*)	67.9±10.8	14.2
cg25189904 (*GNG12*)	47.1±5.4	6.6

[*]Gene for CpG locus cg18132363 is the nearest (within 10Mb) genes to the locus as opposed to a mapped gene