Table S2. Study Quality Criteria (17 studies included in the current review)

	Rusiecki et al. (2008) [1]	Pavanello et al (2009) [2]	Wright et al. (2010) [3]	Kim et al (2010) [4]	Yang et al. (2012) [5]	Hossain et al. (2012) [6]	Hanna et al. (2012) [7]	Li et al (2013) [8]	Goodrich et al. (2013) [9]	Zhang et al. (2013) [10]	Lind et al. (2013) [11]	Tajuddin et al. (2013) [12]	Alegria-Torres et al. (2013) [13]	Sanders et al. (2014) [14]	Tellez-Plaza et al. (2014) [15]	Watkins et al. 2014 [16]	Itoh et al. 2014 [17]
All studies																	
Was exposure assessed at the individual level?	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
Was exposure assessed using a biomarker?	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
Were QC data (reliability or validity and LOD) in biomarker data provided?	▨	■	■	■	□	■	▨	□	▨	□	▨	□	■	▨	■	□	■
Did the authors provide any information on QC control for DNA methylation assessment methods?	■	■	■	■	□	■	■	■	■	■	□	■	□	▨	■	□	■
Was the intensity of search of DNA methylation changes independent of exposure status?	■	□	■	■	□	■	■	□	■	□	■	■	■	■	■	■	■
Were the data collected in a similar manner for all participants?	■	□	■	■	■	■	■	□	■	■	■	■	■	■	■	■	■
Were the same exclusion criteria applied to all participants?	□	□	□	■	■	■	□	□	■	■	■	■	■	■	■	■	■
Was the time period over which collected samples for DNA methylation and exposure status determination the same?	■	□	■*	■	■	■	■	■	■	■*	■	■	■	■	■**	■**	■
Was the interviewer blinded with respect to the DNA methylation or exposure status of the person interviewed?	■	□	■	■	□	■	■	□	■	□	■	■	■	■	■	■	■
Did the authors present internal comparisons within study participants?	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
Did the authors address potential confounding factors for DNA methylation in addition to age, sex and cell heterogeneity?	▨	□	■	▨	□	▨	▨	□	▨	▨	▨	■	▨	■	■	▨	■
Studies with micro-array DNA methylation data. Did the authors provide any information on the following items?																	
a. Criteria for samples allocation in the array	-	-	-	-	-	-	□	-	-	-	-	-	-	□	-	-	-
b. Criteria for a priori probes exclusion (i.e. if based on low quality scores, presence of SNPs)	-	-	-	-	-	-	■	-	-	-	-	-	-	▨	-	-	-

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* Institute for Biomedical Research Hospital Clinic of Valencia - INCLIVA (Spain) and Department of Environmental Health Sciences, Johns Hopkins Bloomberg School of Public Health (Baltimore, US); maria.tellez@uv.es; mtellez3@jhu.edu

c. Batch effect evaluation and/or correction	-	-	-	-	-	-	□	-	-	-	-	-	-	□	-	-	-
d. Normalization method	-	-	-	-	-	-	■	-	-	-	-	-	-	■	-	-	-
e. Visualization of potential SNP clustering in statistically significant regions	-	-	-	-	-	-	▨	-	-	-	-	-	-	□	-	-	-
f. Validation (replication or sequencing) of significant regions	-	-	-	-	-	-	■	-	-	-	-	-	-	■	-	-	-

■ fulfilled; ▨ partially fulfilled; □ not fulfilled or information not available; - not applicable. * Prospective design although reported associations are cross-sectional. ** Both cross-sectional and prospective associations reported.

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* Institute for Biomedical Research Hospital Clinic of Valencia - INCLIVA (Spain) and Department of Environmental Health Sciences, Johns Hopkins Bloomberg School of Public Health (Baltimore, US); maria.tellez@uv.es; mtellez3@jhu.edu

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