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and global DNA methylation patterns

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Table S1. Univariate trends of association of 5-methylcytosine (5-mC) and 5-hydroxymethylcytosine (5-hmC) with dyslipidemia, diabetes, cancer, and cardiovascular disease (CVD).

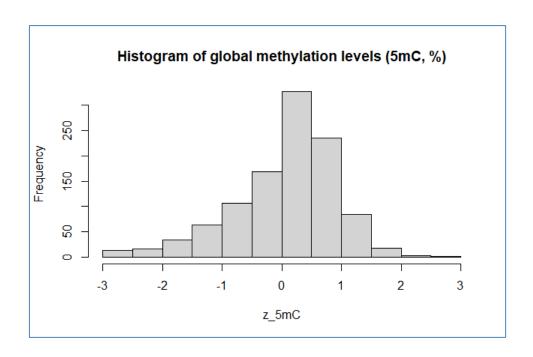
	5mC				5hmC			
	Model 1		Model 2		Model 1		Model 2	
	Beta(SE)	p-value	Beta(SE)	p-value	Beta(SE)	p-value	Beta(SE)	p-value
Dyslipidemia	-0.304(0.106)	<0.01	-0.243(0.134)	0.07	-0.136(0.108)	0.21	-0.089(0.150)	0.55
Diabetes	0.495(0.225)	0.03	-0.037(0.224)	0.87	-0.330(0.230)	0.15	-0.267(0.263)	0.31
Cancer	-0.087(0.159)	0.59	-0.086(0.152)	0.57	-0.018(0.161)	0.91	-0.191(0.169)	0.26
CVD	-0.279(0.115)	0.01	-	-	-0.126(0.115)	0.27	-	-

Model 1: adjusted for age and sex (including prevalent CVD cases).

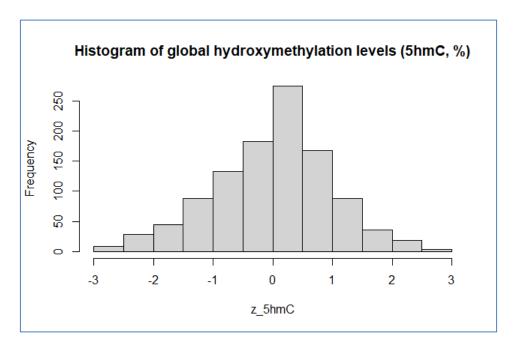
Model 2: adjusted for age and sex (removing prevalent CVD cases from the study population).

Fig. S1 Distributions of global **a)** methylation (5mC, N=1,067) and **b)** hydroxymethylation levels (5hmC, N=1,075) in the analysed subset of the Moli-sani study.

a)

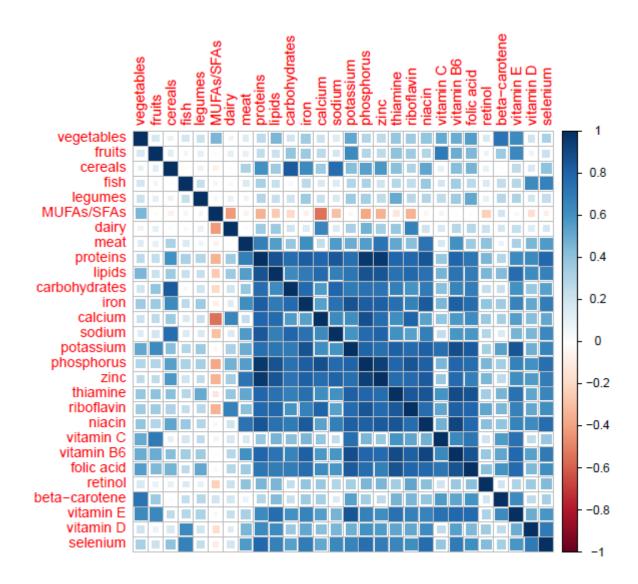


b)



X-axis values are expressed as within-plate standardized proportion (%) of CpG sites carrying the epigenetic modification genome-wide.

Fig. S2 Cross-trait (Pearson's r) correlations of daily intake measures of food groups, macronutrients and micronutrients analysed in the present study.



PARTICIPANT FLOWCHART

24,325 participants randomly recruited in the Moli-sani study in 2005-2010



Randomly selected sub-cohort of 1,160 subjects, after excluding subjects with unreliable questionnaires or missing core variables



1,140 had good quality to perform the methylation analysis



Samples with OD values above thresholds: 1,140 for 5mC and 1,135 for 5hmC



After outliers removal: 1,123 5mC and 1,133 5hmC measures



After removal of prevalent CVD cases: 1,067 5mC and 1,075 5hmC measures