# Supplemental Material to:

David Martino, Jihoon E Joo, Alexandra Sexton-Oates,
Thanh Dang, Katrina Allen, Richard Saffery,
and Susan Prescott

# Epigenome-wide association study reveals longitudinally stable DNA methylation differences in CD4+ T cells from children with IgE-mediated food allergy

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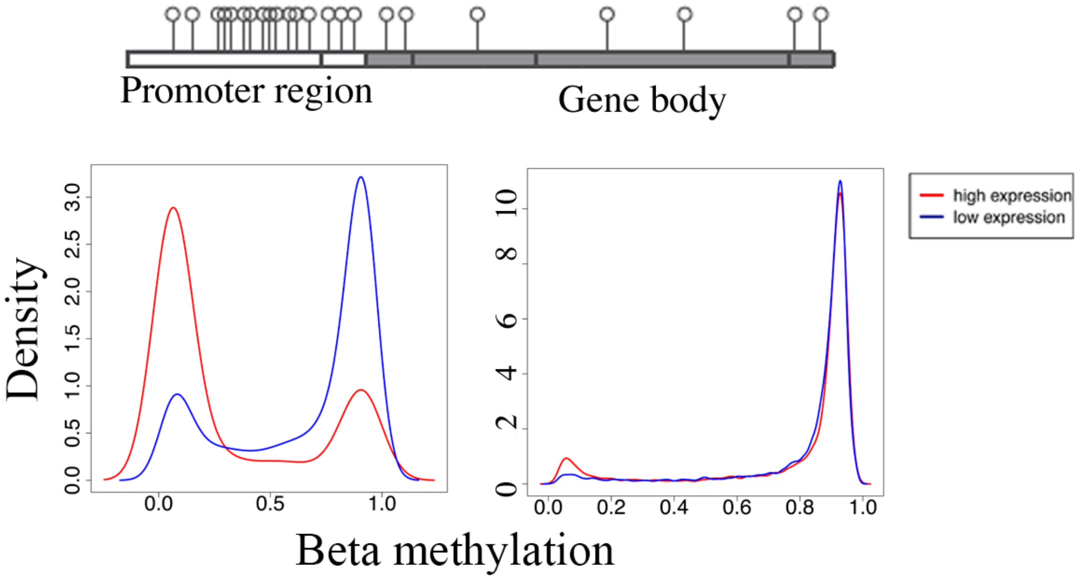

**Supplementary Figure 1- Relationship between DNA methylation and gene expression according to location in gene coding region.** DNA methylation data and gene expression data were mapped to the hg19 reference genome and merged by shared ENTREZ ID. CpG localized to either 'Promoter region' or 'Gene body', as annotated in the manifest (v2) was analyzed separately. For these respective classes, we first divided expressed genes into those with high expression (75% or higher quartile of gene expression distribution, labeled red) and low expression levels (25% or lower quartile, blue). We then identified their corresponding methylation probes and compared the distribution of DNA methylation levels for CpGs in highly expressed genes, versus lowly expressed genes using weighted kernel density plots. The relationship between DNA methylation and gene expression is anti-correlated in the promoter region whereby highly expressed genes tend to be mostly un-methylated and genes with low expression tend to be mostly methylated. This relationship is not clear in the gene body suggesting additional levels of complexity.

# Table S2.

| Characteristic | | Food Allergy | Healthy | P value |
|---|---|---|---|---|
| Gender* | (n(%)) | | | |
| | Male | 9 (75) | 4 (33) | * 0.042 |
| | Female | 3 (25) | 8 (67) | |
| | | | | |
| Delivery method* (n(%)) | | | | |
| | Vaginal | 7 (58) | 6 (60) | 0.622 |
| | Caesarian | 4 (33) | 2 (20) | |
| | | | | |
| Pets at home* (n(%)) | | | | |
| | Yes | 6 (50) | 4 (40) | 0.658 |
| | No | 6 (50) | 6 (60) | |
| | | | | |
| Breastfed* | (n(%)) | 12 (100) | 10 (100) | |
| | Yes | 0 (0) | 0 (0) | |
| | No | | | |
| | | | | |
| Childhood Infection by 12months* (n(%)) | | 11 (92) | 9 (90) | 0.899 |
| | Yes | 1 (8) | 1 (10) | |
| | No | | | |
| | | | | |
| Daycare/playgroup attendance* (n(%)) | | | | |
| | Yes | 8 (67) | 3 (30) | 0.095 |
| | No | 4 (33) | 7 (70) | |
| | | | | |
| Gestation* (w(SE)) | | 39 (0.8) | 39 (1.0) | 0.429 |
| Birthweight* (g(SD)) | | 3670 (262) | 3454 (509) | 0.203 |
| Length* (g(SD)) | | 51 (2.2) | 50 (2.6) | 0.535 |
| Headcircumference* (cm(SD)) | | 35 (1.1) | 34 (1.6) | 0.248 |
| Number of siblings* (n(SD)) | | 0.5 (0.19) | 0.9 (0.23) | 0.123 |
| Age of first weaning* (m(SD)) | | 9.5 (1.0) | 7.5 (2.3) | 0.137 |
| Age egg introduced* (m(SD)) | | 10.3 (0.4) | 9.9 (0.6) | 0.569 |

| *Clinical Outcomes* | | Food Allergy | | Healthy | |
|---|---|---|---|---|---|
| Sensitization † (n(%)) | | 12months | 2.5 years | 12 months | 2.5 years |
| | Egg | 10 (91) | 6 (86)** | 0(0) | 0(0) |
| | Cow's Milk | 1 (9) | 1 (14) | 0(0) | 0(0) |
| | Peanut | 2 (18) | 3 (43) | 0(0) | 0(0) |
| | Multiple Sensitization (2 or more allergens) | 3 (27) | 3 (43) | 0(0) | 0(0) |
| | Not sensitized | 0(0) | 0(0) | 12 (100) | 12 (100) |
| | | | | | |
| Allergic Symptoms on exposure* ((n%)) | | | | | |
| | Respiratory involvement | 6 (50) | 9 (81) | 0(0) | 0(0) |
| | Angiodema | 11 (92) | 10 (100) | 0(0) | 0(0) |
| | Urticaria | 7 (54) | 2 (20) | 0(0) | 0(0) |
| | Asymptomatic | 0 (0) | 0 (0) | 12 (100) | 12 (100) |
| | | | | | |
| Maternal History of Atopy * (n(%)) | | 12 (100) | 12 (100) | 10 (84) | 10 (84) |

† Determined by skin prick test

* Determined by questionnaire data

** SPT Data on 7/12 children at 2.5 years

Statistical comparisons were made using the Pearsons Chi squared test for categorical data, and the Students *t* test for continous data.

Supplementary table 3 - primer sequences used for validation

| Assay name | Assay Type | strand | forward primer | reverse primer |
|---|---|---|---|---|
| KCNN3 | sequenom | F | aggaagagagGAGGTTTATTATAGGGAATGATTAAGTGA | cagtaatacgactcactatagggagaaggctTAAATAACCAAAACCAAAACTTCCA |
| NAPRT1 | sequenom | F | aggaagagagGGTTATAGGTGGGGGTTTTTGT | cagtaatacgactcactatagggagaaggctCTAACCTCTACCAAACCACCATAA |
| CACNA1B | pyromark | F | TGGGAGGAGGATAGTAAATGG | CACACCCAAACTCCTAAAC |