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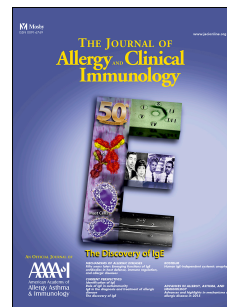
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# Accepted Manuscript

An epigenome-wide association study of total serum immunoglobulin E in Hispanic children

Wei Chen, PhD, Ting Wang, PhD, Maria Pino-Yanes, PhD, Erick Forno, MD, MPH, Liming Liang, PhD, Qi Yan, PhD, Donglei Hu, PhD, Daniel E. Weeks, PhD, Andrea Baccarelli, MD, PhD, Edna Acosta-Perez, PhD, Celeste Eng, MS, Yueh-Ying Han, PhD, Nadia Boutaoui, PhD, Catherine Laprise, PhD, Gwyneth A. Davies, MD, Julian M. Hopkin, MD, Miriam F. Moffatt, DPhil, William O.C.M. Cookson, MD, Glorisa Canino, PhD, Esteban G. Burchard, MD, MPH, Juan C. Celedón, MD, DrPH, FAAAAI



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2 **children**

3

4 Wei Chen, PhD<sup>1§</sup>, Ting Wang, PhD<sup>1§</sup>, Maria Pino-Yanes, PhD<sup>2</sup>, Erick Forno, MD, MPH<sup>1</sup>,  
5 Liming Liang, PhD<sup>3</sup>, Qi Yan, PhD<sup>1</sup>, Donglei Hu, PhD<sup>4</sup>, Daniel E. Weeks, PhD<sup>5</sup>, Andrea  
6 Baccarelli, MD, PhD<sup>6</sup>, Edna Acosta-Perez, PhD<sup>7</sup>, Celeste Eng, MS<sup>4</sup>, Yueh-Ying Han, PhD<sup>1</sup>,  
7 Nadia Boutaoui, PhD<sup>1</sup>, Catherine Laprise, PhD<sup>8</sup>, Gwyneth A. Davies, MD<sup>9</sup>, Julian M. Hopkin,  
8 MD<sup>9</sup>, Miriam F. Moffatt, DPhil<sup>10</sup>, William O.C.M. Cookson, MD<sup>10</sup>, Glorisa Canino, PhD<sup>7</sup>,  
9 Esteban G. Burchard, MD, MPH<sup>4\*</sup>, Juan C. Celedón, MD, DrPH, FAAAAI<sup>1\*</sup>

10

11 <sup>1</sup>Division of Pediatric Pulmonary Medicine, Allergy, and Immunology, Children's Hospital of  
12 Pittsburgh of UPMC, University of Pittsburgh, Pittsburgh, PA

13 <sup>2</sup>Instituto de Salud Carlos III, CIBER de Enfermedades Respiratorias, Madrid, Spain

14 <sup>3</sup>Departments of Epidemiology and Biostatistics, Harvard School of Public Health, Boston,  
15 MA

16 <sup>4</sup>Department of Therapeutic Sciences and Bioengineering, University of California at San  
17 Francisco, San Francisco, CA

18 <sup>5</sup>Departments of Human Genetics and Biostatistics, Graduate School of Public Health,  
19 University of Pittsburgh, Pittsburgh, PA

20 <sup>6</sup>Department of Environmental Medicine, Harvard School of Public Health, Boston, MA

21 <sup>7</sup>Behavioral Sciences Research Institute and Department of Pediatrics, University of Puerto Rico,  
22 San Juan, PR

23 <sup>8</sup> Université du Québec à Chicoutimi, Saguenay, Québec, Canada

25 <sup>10</sup> National Heart and Lung Institute, Imperial College, London, UK

26 <sup>\$</sup>These authors equally contributed to this work.

27 <sup>\*</sup>These authors equally supervised this work.

28

29 **Corresponding Author:**

30 Juan C. Celedón, M.D., Dr.P.H.

31 Division of Pulmonary Medicine, Allergy and Immunology

32 Children's Hospital of Pittsburgh of UPMC

33 4401 Penn Avenue, Pittsburgh, PA 15224

34 Phone: 412.692.8429

35 Fax: 412.692.7636

36 Email: [juan.celedon@chp.edu](mailto:juan.celedon@chp.edu)

37

38 **Author Contributions:** Study concept and design: E.G.B., and J.C.C.; data collection, and

39 material and technical support: N.B., E.A-P., C.E., C.L., G.A.D., J.M.H., M.M., W.O.C.,

40 and G.C.; statistical analysis: W.C., T.W., M.P-Y., A.B., D.H., E.F., Q.Y., D.W. and L.L.;

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42 approved the final version of the manuscript prior to submission.

43

44 **Word count:** 3,455

45

46

48 **Background:** Total immunoglobulin E (IgE) is a therapeutic target in allergic diseases. DNA  
49 methylation in white blood cells (WBCs) was associated with total IgE in an epigenome-wide  
50 association study (EWAS) of Caucasians. Whether DNA methylation of eosinophils explains  
51 those findings is insufficiently understood.

52 **Methods:** We tested for association between genome-wide DNA methylation in WBCs and total  
53 IgE in two studies of Hispanic children: the Puerto Rico Genetics of Asthma and Lifestyle Study  
54 (PR-GOAL, n = 306) and the Genes-environments and Admixture in Latino Americans (GALA  
55 II, n = 573). Whole-genome methylation of DNA from WBCs was measured using the Illumina  
56 Infinium HumanMethylation450 BeadChip. Total IgE was measured using the UniCAP 100  
57 system. In PR-GOAL, WBC types (i.e. neutrophils, eosinophils, basophils, lymphocytes, and  
58 monocytes) in peripheral blood were measured using Coulter-Counter techniques. In GALA II,  
59 WBC types were imputed. Multivariable linear regression was used for the analysis of DNA  
60 methylation and total IgE, which was first conducted separately for each cohort, and then  
61 combining results from the two cohorts in a meta-analysis.

62 **Results:** CpG sites in multiple genes, including novel findings and results previously reported in  
63 Caucasians, were significantly associated with total IgE. However, adjustment for WBC types  
64 resulted in markedly fewer significant sites. Top findings from this adjusted meta-analysis were  
65 in genes *ZFPM1* ( $P=1.5\times 10^{-12}$ ), *ACOT7* ( $P=2.5\times 10^{-11}$ ), and *MND1* ( $P=1.4\times 10^{-9}$ ).

66 **Conclusions:** In an EWAS adjusted for WBC types (including eosinophils), methylation  
67 changes in genes enriched in pathways relevant to asthma and immune responses were  
68 associated with total IgE among Hispanic children.

69 **Abstract word count:** 250

70

72 *ACOT7*, and *MND1* are associated with total IgE. *ACOT7* and *ZFPM1* have been implicated in  
73 the pathogenesis of asthma or atopy.

74  
75 **Capsule Summary:** In an EWAS adjusted for WBC types, few DNA methylation changes were  
76 significantly associated with total IgE among Hispanic children. Future EWAS of total IgE  
77 should account for DNA methylation of WBC types, particularly eosinophils.

78  
79 **Key words:** EWAS, total IgE, Hispanics, children.

80  
81 **Abbreviations:**

82 EWAS: epigenome-wide association study

83 IgE: immunoglobulin E

84 WBC: white blood cell

85 PR-GOAL: Puerto Rico Genetics of Asthma and Lifestyle Study

86 GALA II: Genes-environments and Admixture in Latino Americans study

87 eQTM: expression Quantitative Trait Methylation

88 PC: principle component

90 Allergic diseases affect millions of people worldwide. In subjects with allergic diseases,  
91 secretion of interleukin (IL)-4 and IL-13 by T helper 2 (Th2) cells increases production of total  
92 immunoglobulin E (IgE) by B cells. Total IgE is a key intermediate phenotype and a therapeutic  
93 target in allergic diseases such as asthma and allergic rhinitis<sup>1</sup>.

94  
95 Genome-wide association studies have identified SNPs linked with total IgE, but their joint  
96 estimated effect accounts for a very small proportion of the trait's heritability<sup>2-5</sup>. Environmental  
97 exposures affect total IgE<sup>6,7</sup>, and thus epigenetic mechanisms such as DNA methylation may  
98 explain the "missing heritability" of total IgE.

99  
100 A recent epigenome-wide association study (EWAS) using DNA from white blood cells (WBCs)  
101 reported that methylation in several genes is implicated on total IgE level in Caucasians<sup>8</sup>, with  
102 methylation of three genes (*LPCAT2*, *IL5RA*, and *ZNF22*) accounting for ~13% of total IgE  
103 variance. Whether those findings are explained by DNA methylation of eosinophils (which play  
104 a major role in allergic inflammation) or other WBC is insufficiently understood.

105  
106 In the United States, Puerto Ricans are heavily affected with allergic diseases, while Mexican  
107 Americans have a lower but non-negligible burden from allergies<sup>9-11</sup>. We report the first EWAS  
108 of total IgE with adjustment for (percentage of) WBC types, as well as the first EWAS of total  
109 IgE in Hispanics.

110

## 111 **METHODS**

112 Please also see the Online Supplement.

115 *Puerto Rico Genetics Of Asthma and Lifestyle Study (PR-GOAL)*: From March of 2009 to June of  
116 2010, 678 children with and without asthma (defined as physician-diagnosed asthma and at least  
117 one episode of wheeze in the prior year) were recruited in San Juan (Puerto Rico), as described  
118 elsewhere<sup>12</sup>. Eligibility criteria included age 6 to 14 years and having four Puerto Rican  
119 grandparents. Of the 562 subjects who had blood samples with sufficient DNA for genome-wide  
120 genotyping, 306 subjects had additional data (including WBC count, total IgE, and a genome-wide  
121 study of DNA methylation) and were thus included in this analysis. Total serum IgE was measured  
122 using the UniCAP 100 system (Pharmacia & Upjohn, Kalamazoo, MI), and total WBC count and  
123 percentages of the five possible cell types (i.e. neutrophils, eosinophils, basophils, lymphocytes,  
124 and monocytes) in peripheral blood were measured using Coulter-Counter techniques. There were  
125 no significant differences in age, gender, asthma status or total IgE between subjects with available  
126 DNA who were (n=306) and were not (n=256) included in the current analysis.

127 Following bisulfite conversion of DNA from WBCs using the EZ DNA methylation kit (Zymo  
128 Research, Irvin CA), whole-genome DNA methylation levels were measured using the  
129 HumanMethylation 450K BeadChip system (Illumina, San Diego, CA). In brief, 200 ng of  
130 bisulfite-converted DNA was whole-genome amplified for 23 hours, followed by end-point  
131 fragmentation. The fragmented DNA was precipitated, denatured, and hybridized to the  
132 BeadChips for 18 hours at 48°C. The BeadChips were then washed, and the hybridized primers  
133 were extended and labeled prior to scanning the BeadChips using the Illumina iScan system  
134 (Illumina, San Diego, CA).



136 the HumanOmni2.5 BeadChip platform [Illumina Inc., San Diego, CA), as previously  
137 described<sup>12</sup>. Genome-wide gene expression in a subset of 121 whole-blood samples was  
138 measured at the University of Pittsburgh Genomics and Proteomics Core Laboratories, using the  
139 Illumina HumanHT-12 v4 Expression BeadChip, as described in our previous work<sup>13</sup>.

140 Written parental consent was obtained for participating children, from whom written assent was  
141 also obtained. The study was approved by the Institutional Review Boards of the University of  
142 Puerto Rico (San Juan, PR), Brigham and Women's Hospital (Boston, MA) and the University  
143 of Pittsburgh (Pittsburgh, PA).

144 *Genes-environments & Admixture in Latino Americans (GALA II)*: The GALA II study is a  
145 multicenter case-control study of asthma in 1,858 Latino children and adolescents<sup>14</sup>. Cases and  
146 healthy controls were recruited from five centers throughout the U.S. (Chicago, Bronx, Houston,  
147 San Francisco Bay Area, and Puerto Rico). Subjects were eligible if they were 8 to 22 years of  
148 age, self-identified all four grandparents as Latino, and had <10 pack-years of smoking history.  
149 Asthma was defined as physician-diagnosed asthma and report of symptoms and medication use  
150 in the previous two years. Participants were classified into three Latino subgroups (Puerto Rican,  
151 Mexican and other Latino), according to the self-reported ancestry of their four grandparents. All  
152 participants were genotyped on the Axiom<sup>®</sup> LAT1 array (World Array 4, Affymetrix, Santa  
153 Clara, CA), as described elsewhere<sup>15</sup>. A subset of 573 participants (219 Puerto Ricans, 269  
154 Mexicans and 85 other Latinos) with data for genome-wide DNA methylation and total IgE were  
155 included in the current analysis; there were no significant differences in age, gender, asthma  
156 status or total IgE between subjects who were (n=573) and were not (n=1,285) included in the  
157 analysis. Total serum IgE was measured using the ImmunoCAP<sup>™</sup> 100 system (Phadia,

159 HumanMethylation 450K BeadChips to measure methylation levels.

160

161 The study was approved by the Institutional Review Boards of the University of California at  
162 San Francisco and all other participating centers. All children and their parents provided written  
163 informed assent and consent, respectively.

164

### 165 **Preprocessing and quality control for 450K DNA methylation data**

166 We performed the same preprocessing and quality control for 450K DNA methylation data in  
167 PR-GOAL and GALA II. We read methylation data from the raw IDAT files using the R  
168 package *methyumi*, and calculated the  $\beta$ -value for each CpG as  $\beta = M/(M + U + \alpha)$ , where M  
169 and U represent methylated and un-methylated signal intensities at the specific site and  $\alpha$  is an  
170 arbitrary offset (usually 100) intended to stabilize  $\beta$ -values where fluorescent intensities are low.  
171 Next, the methylation data were preprocessed by color balance adjustment, background  
172 correction and quantile-normalization with the *lumi* R package, and followed by Beta-Mixture  
173 Quantile (BMIQ) normalization with the *wateRmelon* package. This normalization strategy first  
174 quantile-normalized the intensities of methylation signals among all arrays, and then used BMIQ  
175 dilation to normalize the  $\beta$ -values within each array<sup>16-18</sup>.

176

177 In each data set, we removed poor-quality probes with detection P-value > 0.01 in at least 20%  
178 of the samples. We also removed 11,656 probes with CpG loci located on sex chromosomes and  
179 19,344 probes that had rs\* names or located at 0 distance to known SNPs, according to the  
180 Illumina product annotation of Infinium HD Methylation SNP List. This QC process left 454,552

182 (considering extreme values as noise signals and to reduce multiple tests), which left 188,368  
183 CpGs for data analysis.

184

### 185 **Comparison to previous findings in Caucasians (see also Online Supplement)**

186 We compared our results in Hispanic children to those of Liang et al. in Caucasians<sup>8</sup>. The  
187 comparison sample consists of three cohorts of Caucasians (Table E1), as follows: (1) The  
188 Medical Research Council Asthma (MRCA) panel, a cohort of 355 subjects (183 male) with  
189 mean age of 28 years (range 2-61 years), of whom 175 had doctor-diagnosed asthma, (2) a subset  
190 of the Poblogaeth Asthma Prifysgol Abertawe (PAPA) study, including 149 subjects (77 male,  
191 34 with doctor-diagnosed asthma) with mean age of 21 years (range, 18 to 30 years), selected  
192 equally from the top and bottom deciles of the total IgE distribution from the entire PAPA study  
193 of 1,614 unselected volunteers, and (3) a subset of the Saguenay-Lac-Saint-Jean (SLSJ) asthma  
194 familial collection, including 160 subjects (80 male) with mean age of 29 years (range 5-79  
195 years), of whom 69 had asthma. MRCA used the Illumina HumanMethylation 27K chip, while  
196 PAPA and SLSJ used the Illumina HumanMethylation 450K chip. We used the results presented  
197 in the original report, more detailed information can be found in Liang et al.<sup>8</sup>. Of note, we could  
198 not directly compare effect sizes across our study and those studies (which used transformed  
199 methylation values), but the directions of effect estimates were comparable across studies.

200

### 201 **Statistical analysis**

202 Total IgE was transformed to a log<sub>10</sub> scale as a natural value in medical studies for data analysis.

203 Linear regression was used for the multivariable analysis of DNA methylation and total IgE,

205 (or plate), population subgroup (in GALA II) and the first five principal components (PCs) of the  
206 genotypic data, i.e., EWAS regression model (1) is:  $\text{Log}_{10}\text{Ige} \sim \text{CpG methylation} + \text{Age} +$   
207  $\text{Gender} + \text{Asthma} + \text{Batch} + \text{Population} + 5 \text{ PCs}$ . PCs were calculated using common SNPs  
208 (minor allele frequency  $> 5\%$ ) by using EIGENSTRAT<sup>19</sup>, separately for PR-GOAL and GALA  
209 II. We next performed a meta-analysis to combine summary statistics from PR-GOAL and  
210 GALA II, using inverse variance weighting to generate the combined effect size and P-value for  
211 each CpG site. A Bonferroni-corrected  $P < 2 \times 10^{-7}$  was used as the cutoff for genome-wide  
212 statistical significance.

213  
214 We then carried out a similar multivariable analysis of DNA methylation and total IgE in PR-  
215 GOAL, with additional adjustment for the percentages of WBC types (only neutrophils,  
216 eosinophils, lymphocytes, and monocytes are included, since the sum of the percentages of these  
217 four cell types determines the percentage of the fifth possible type) to uncover IgE regulatory  
218 pathways that are independent of eosinophil count. Hence, our EWAS regression model (2) is:  
219  $\text{Log}_{10}\text{Ige} \sim \text{CpG methylation} + \text{Age} + \text{Gender} + \text{Asthma} + \text{Batch} + \text{Population} + 5 \text{ PCs} +$   
220  $\text{Percentages of 4 WBC types}$ . Since WBC percentages were not available in GALA II, cell type  
221 percentages were inferred based on the method described by Houseman et al.<sup>20</sup>. In brief, a Lasso  
222 regression model for each of the five cell types was first trained from the observations of cell  
223 percentage and DNA methylation in PR-GOAL, and then the most predictive 200 CpG sites (see  
224 Table E2) for the five cell types were selected as reference CpGs for the application of a multiple  
225 imputation method<sup>21</sup> to impute the cell percentages, which were adjusted for in the multivariable  
226 analysis of GALA II. Of note, we validated the performance of the Houseman imputation-based

228 significantly and highly correlated (see Figure E1). Thus, methodologically, this imputation  
229 should work for GALA II samples, whose imputed WBC types are likely valid and without  
230 significant bias.

231  
232 Next, we conducted a meta-analysis of total IgE in PR-GOAL and GALA II, after additional  
233 adjustment for WBC types. Genes containing the top 1000 CpG sites associated with total IgE in  
234 this meta-analysis were examined in a KEGG pathway enrichment analysis, using Fisher's exact  
235 test, the multiple testing p-values were adjusted with FDR. Moreover, we performed an  
236 expression Quantitative Trait Methylation (eQTM) analysis for the top 20 findings from the meta-  
237 analysis adjusted for WBC types (using PR-GOAL data), to test for association between DNA  
238 methylation and cis-gene (< 1M bases) expression in whole blood, adjusting for age, sex, asthma  
239 status (and WBC types), i.e. Gene expression ~ CpG methylation + Age + Gender + Asthma + 5  
240 PCs +(Percentages of 4 WBC types).

241

## 242 **RESULTS**

243 The characteristics of participants in the **Puerto Rico Genetics Of Asthma and Lifestyle Study**  
244 (**PR-GOAL**) and the **Genes-environments & Admixture in Latino Americans Study (GALA II)**  
245 are shown in **Table I**. Compared to participants in GALA II, those in PR-GOAL were younger  
246 and had a higher total IgE. DNA methylation levels were similar across studies (Figure E2).

247

248 We conducted a multivariable linear regression analysis of DNA methylation and total IgE, first  
249 separately for each cohort, and then combining results from the two cohorts in a meta-analysis.

251 at FDR < 0.01 (See Manhattan and QQ plots in Figure E3). Table E3 lists the top 200 CpG sites  
252 (by P-value) in this meta-analysis, as well as their results of separate analysis for each cohort.  
253 The direction of association between CpG sites and total IgE was consistent across studies. PR-  
254 GOAL had 640 significant CpGs with  $P < 2 \times 10^{-7}$ , while GALA II had 404 significant CpGs, and  
255 their correlation of overall effect size or  $-\log_{10}(P\text{-value})$  were also significant (Figure E4). In a  
256 sensitivity analysis, we performed a mega-analysis by combining the datasets from PR-GOAL  
257 and GALA II into a single dataset, using a similar approach to that for the meta-analysis, with  
258 additional adjustment for study site. This mega-analysis yielded similar results to those from the  
259 meta-analysis (Table E3).

260  
261 Next, we compared the results of our meta-analysis unadjusted for WBC types with those from  
262 an EWAS of total IgE in Caucasians<sup>8</sup>. In spite of differences in ethnicity and age, most of the top  
263 significant CpG sites in our EWAS had the same direction of association as in Caucasians (Table  
264 E3). Of the top 200 CpG sites in our meta-analysis, 189 were also associated with total IgE (at  $P$   
265 < 0.01) in either the PAPA or SLSJ study; and all 9 CpG sites that overlapped with those in the  
266 MRCA study (which had fewer CpG sites from the Illumina 27K Chip) were significantly  
267 associated with total IgE in that study. Moreover, we confirmed the top findings from the  
268 previous EWAS in Caucasians<sup>8</sup> in our study (Table E4).

269  
270 We then repeated the multivariable meta-analysis of our study cohorts after adjustment for WBC  
271 types. **Fig 1** shows Manhattan and QQ plots of results in this adjusted meta-analysis, the number  
272 of significant CpG sites is markedly reduced comparing to the unadjusted results (Figure E3).

274 cg21220721) of them were significantly associated with total IgE at  $P < 2 \times 10^{-7}$ , and the top two  
275 CpGs overlap with those from the meta-analysis without adjusting for WBC types. Partial  
276 regression plots in **Fig 2** show the associations between CpG methylation values and total IgE,  
277 conditional on all other covariates, for the top four genes. Table E5 lists the top 200 CpG sites as  
278 well as the results of this cell-adjusted analysis for each cohort, and similar results were obtained  
279 when a mega-analysis was conducted instead of a meta-analysis.

280  
281 We then performed a KEGG pathway enrichment analysis on the genes closest to the top 1000  
282 CpG sites from the meta-analysis adjusted for WBC types. Of the seven pathways enriched for  
283 these genes at  $FDR \leq 0.01$  (Table III), the first one (“hsa05310 Asthma”) is highly related to  
284 total IgE. Some significant pathways are relevant to immune responses, such as “hsa04612  
285 Antigen processing and presentation”, “hsa05320 Autoimmune thyroid disease” and “hsa04672  
286 Intestinal immune network for IgA production”.

287  
288 Next, we performed eQTM analyses for the twenty CpG sites in **Table II** and their cis-genes,  
289 using the DNA methylation and gene expression data from PR-GOAL. From the analysis  
290 unadjusted for WBC types, cg25087851 methylation was significantly associated with  
291 expression of the gene for the prostaglandin D2 receptor 2 (*PTGDR2*,  $P = 5.16 \times 10^{-17}$ , see Table  
292 E7)). cg25087851 is 473 nucleoside bases upstream of *PTGDR2*, which encodes a G-protein-  
293 coupled receptor that is preferentially expressed in CD4+ effector Th2 cells. This receptor  
294 mediates pro-inflammatory chemotaxis of eosinophils, basophils, and Th2 lymphocytes  
295 generated during allergic inflammation<sup>22</sup>, and a *PTGDR2* antagonist reduces eosinophilic airway

297 site (cg12227660) was significantly associated with expression of the gene polyamine oxidase  
298 (*PAOX*,  $P = 2.04 \times 10^{-13}$ ); cg12227660 is 131,071 bases upstream of *PAOX*. *PAOX* particles can  
299 be used as a drug delivery vehicle for the treatment of acute inflammatory diseases such as  
300 asthma and acute lung injury<sup>24,25</sup>. After adjusting for cell types, the observed associations  
301 between methylation of CpG sites and gene expression became non-statistically significant,  
302 following a pattern similar to that for the EWAS results (Table E7).

303  
304 GALA II participants belong to three Latino subgroups, captured by PCA of genotypic data,  
305 while the effect of population composition on DNA methylation is negligible, according to PCA  
306 of methylation data (Figure E5). Since PR-GOAL participants are all Puerto Rican, we  
307 conducted a secondary EWAS of total IgE after selecting only Puerto Ricans from GALA II ( $n =$   
308 219). Figure E6 shows the Manhattan and QQ plots for all CpG sites, and the results of top 200  
309 sites are listed in Table E8 for the EWAS without cell type adjustment and Table E9 for the  
310 EWAS with cell type adjustment. Findings in this analysis in Puerto Ricans were similar to those  
311 in all Hispanics, the correlations of resultant effect size or  $-\log_{10}(P_{val})$  were significant (Figure  
312 E7); and the 4 significant CpG sites in the meta-analyses with adjustment for WBC types were  
313 the same as those in all Hispanics.

## 314 315 **DISCUSSION**

316 Our meta-analysis without adjustment for WBC types identified 1,326 CpG sites that achieved a  
317 genome-wide significant association with total IgE at  $P < 2 \times 10^{-7}$ . There are some novel findings  
318 on top of the results (Table E3), including methylation in the genes for microRNA 202 (*MIR202*),



320 in cultured airway epithelial cells of monkeys in response to ozone exposure and  
321 lipopolysaccharide (LPS) treatment<sup>26</sup>, and is decreased in bronchoalveolar lavage (BAL) of  
322 patients with sarcoidosis<sup>27</sup>. *LPINI*, which has been implicated in lipid metabolism and  
323 rhabdomyolysis, encodes a magnesium-ion-dependent phosphatidic acid phosphohydrolase  
324 enzyme. Expression of *LPINI* is low in subjects with atopic eczema, who often have other atopic  
325 diseases such as allergic asthma and allergic rhino-conjunctivitis<sup>28</sup>.

326  
327 After additional adjustment of our meta-analysis for WBC types, there was a marked reduction  
328 in the number of CpG sites associated with total IgE. Since only eosinophils were consistently  
329 and significantly associated with total IgE in our study (Table IV), our overall findings suggest  
330 that DNA methylation in eosinophils explain most results for DNA methylation and total IgE in  
331 the analyses unadjusted for WBC types, thus emphasizing the importance of adjusting for cell  
332 types in future studies.

333  
334 Our four genome-wide significant findings in the meta-analysis adjusted for WBC types were  
335 not among the top 62 top loci associated with total IgE (at FDR <0.005, with consistent direction  
336 of association across cohorts) in the meta-analysis of three cohorts included in the prior EWAS  
337 of total IgE in Caucasians<sup>8</sup>. These four CpG sites were located in the genes for zinc-finger  
338 protein multi-type 1 (*ZFPM1*), acyl-CoA thioesterase 7 (*ACOT7*), and meiotic nuclear division 1  
339 (*MND1*). *ZFPM1* suppresses expression of interleukin 4 (IL-4) and induces expression of IFN- $\gamma$   
340 in CD4+ T cells, thus reducing Th2 cell differentiation<sup>29</sup>. Moreover, WBC DNA methylation in  
341 both *ZFPM1* and *ACOT7* has been associated with asthma<sup>30</sup>, and WBC DNA methylation of

343 or high total IgE ( $\geq 200$  kU/L) across two Caucasian cohorts included in a prior study<sup>31</sup>. In that  
344 study, DNA methylation of acyl-CoA thioesterase 7 (*ACOT7*) was significantly associated with  
345 atopy or high total IgE in the discovery cohort but not in a replication cohort. Thus, herein we  
346 first report consistent evidence of a genome-wide significant association between *ACOT7*  
347 methylation and total IgE.

348  
349 Of the top findings in our analysis unadjusted for cell types, CpG sites in *ZFPM1*, *ACOT7*,  
350 *MIR202*, *EVL*, *PTGDR2* and *PGR2* remained among the top twenty results in the analysis  
351 adjusted for WBC types. While not genome-wide significant, the WBC-adjusted analysis  
352 revealed some new genes among our top twenty findings, including *MND1*, sprouty RTK  
353 signaling antagonist 2 (*SPRY2*), major histocompatibility complex, class II, DQ beta 2 (*HLA-*  
354 *DQB2*) and ETS variant 6 (*ETV6*) genes. *SPRY2* differentially regulates lymphoid and myeloid  
355 cell functions relevant to allergic asthma<sup>32</sup>. *HLA-DQB2* is biologically relevant to immune  
356 responses and has previously associated with asthma<sup>33</sup>. *ETV6-ABL* gene rearrangement can  
357 result in chronic myeloid leukemia associated with eosinophilia<sup>34</sup>.

358  
359 We recognize several study limitations. First, WBC types were not measured in GALA II.  
360 Although we applied validated methods to perform imputation of WBC percentages, the  
361 imputation uncertainty may still have reduced our statistical power. It is unlikely to have biased  
362 our results. Second, WBC types such as lymphocytes include multiple cell types (e.g., Th1, Th2,  
363 Th17) and we lack data to identify whether methylation of a specific cell type accounts for our  
364 findings in the meta-analysis adjusted for cell types. Third, we had data for gene expression in  
365 whole-blood (and not WBCs) in only a subset of participants in PR-GOAL, likely reducing our

367 expression. Finally, we lack functional analyses, but our top CpG sites are located within  
368 biologically plausible genes, as demonstrated by combined evidence from prior publications, and  
369 the results from our enrichment and eQTM analyses.

370  
371 In summary, we demonstrate novel WBC DNA methylation changes associated with total IgE in  
372 an EWAS of Hispanic children, while replicating prior findings in Caucasians<sup>8</sup>. Our findings also  
373 emphasize the importance of adjusting for cell types (particularly eosinophils) in future studies  
374 of WBC DNA methylation and total IgE or related phenotypes (e.g., asthma).

375

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388

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485 **Fig 1.** Manhattan and QQ plots for the results of meta-analyses adjusting for WBC types. The  
486 Manhattan plot shows the chromosomal locations of  $-\log_{10}(\text{P-value})$  for association at each CpG  
487 site; the solid line illustrates a threshold of  $\text{P-value}=2\times 10^{-7}$  and the dashed line illustrates a  
488 threshold of  $\text{FDR}=0.01$ . The QQ plot shows observed versus expected  $-\log_{10}(\text{P-value})$  for  
489 association at all loci. The gray area illustrates the 95% confidence band.

490 **Fig 2.** Partial regression plots of CpG methylation and total IgE for the top four genes in the  
491 meta-analysis adjusting for WBC types. The x and y axis respectively stand for the residuals of  
492 regressing methylation and IgE against all other covariates, which are adjusted in the  
493 multivariable regressions. The solid and hollow circles indicate GALA II and PR-GOAL  
494 samples.

495

<b>Study</b>	<b>PR-GOAL (n=306)</b>	<b>GALA II (n=573)</b>
Age (years)	9 (6-15)	13 (8-22)
Gender (female)	131 (42.8%)	287 (50.1%)
Asthma	173 (56.5%)	311 (54.3%)
Total IgE (IU/mL)	694 (2-10178)	371 (1-8545)
Average global genetic ancestry		
European	63%	53%
African	25%	17%
Native American	12%	30%

497 \* Data shown as mean (range) for continuous variables and number (percentage) for categorical variables

498 \*\* PR-GOAL: Puerto Rican Genetics of Asthma and Lifestyle Study

499 \*\*\* GALA II: Genes-environments & Admixture in Latino Americans Study

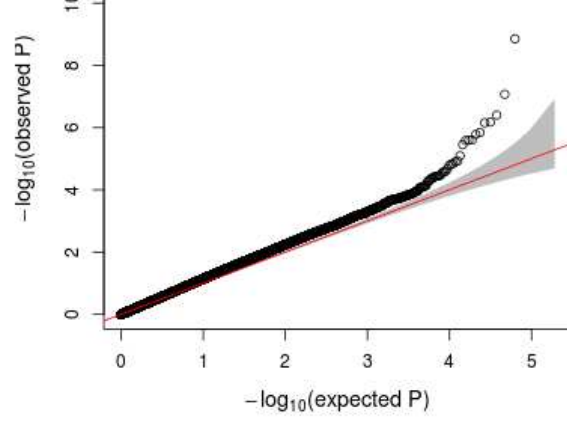
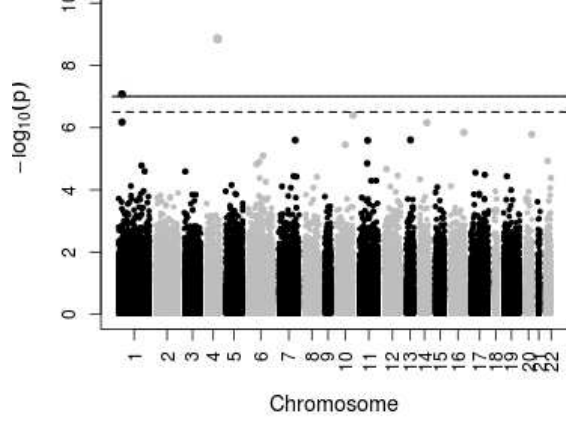
ProbeID	Gene	CHR	Position	PR-GOAL		GALA II		Meta-analysis		
				Effect*	P-value	Effect	P-value	Effect	P-value	FDR
cg04983687	<i>ZFPM1</i>	chr16	88558223	-5.27	4.69×10 <sup>-7</sup>	-3.82	3.61×10 <sup>-7</sup>	-4.31	<b>1.53×10<sup>-12</sup></b>	<b>2.88×10<sup>-7</sup></b>
cg09249800	<i>ACOT7</i>	chr1	6341287	-6.81	5.32×10 <sup>-8</sup>	-6.09	1.06×10 <sup>-4</sup>	-6.53	<b>2.55×10<sup>-11</sup></b>	<b>2.41×10<sup>-6</sup></b>
cg12614529	<i>MND1</i>	chr4	154269418	-5.25	7.38×10 <sup>-5</sup>	-4.67	4.39×10 <sup>-6</sup>	-4.88	<b>1.40×10<sup>-9</sup></b>	<b>8.76×10<sup>-5</sup></b>
cg21220721	<i>ACOT7</i>	chr1	6341230	-5.31	1.26×10 <sup>-7</sup>	-1.84	1.92×10 <sup>-3</sup>	-2.74	<b>8.45×10<sup>-8</sup></b>	<b>3.98×10<sup>-3</sup></b>
cg12227660	<i>MIR202</i>	chr10	135061670	-4.26	1.21×10 <sup>-3</sup>	-3.89	9.19×10 <sup>-5</sup>	-4.02	3.96×10 <sup>-7</sup>	1.49×10 <sup>-2</sup>
cg11699125	<i>ACOT7</i>	chr1	6341327	-5.77	5.34×10 <sup>-6</sup>	-3.19	1.43×10 <sup>-2</sup>	-4.52	6.68×10 <sup>-7</sup>	1.88×10 <sup>-2</sup>
cg01000631	<i>EVL</i>	chr14	100610667	-4.65	1.68×10 <sup>-4</sup>	-3.88	1.09×10 <sup>-3</sup>	-4.25	6.97×10 <sup>-7</sup>	1.88×10 <sup>-2</sup>
cg08940169	<i>ZFPM1</i>	chr16	88540241	-5.49	8.37×10 <sup>-5</sup>	-4.13	4.14×10 <sup>-3</sup>	-4.83	1.43×10 <sup>-6</sup>	3.38×10 <sup>-2</sup>
cg01458054	<i>HELZ2</i>	chr20	62200603	-3.34	2.75×10 <sup>-3</sup>	-2.99	1.78×10 <sup>-4</sup>	-3.11	1.66×10 <sup>-6</sup>	3.48×10 <sup>-2</sup>
cg15017119	<i>SPRY2</i>	chr13	82585793	-4.84	7.04×10 <sup>-5</sup>	-2.96	5.45×10 <sup>-3</sup>	-3.78	2.49×10 <sup>-6</sup>	4.06×10 <sup>-2</sup>
cg00405825	<i>HIPK2</i>	chr7	139474807	4.10	2.84×10 <sup>-3</sup>	3.35	2.47×10 <sup>-4</sup>	3.58	2.54×10 <sup>-6</sup>	4.06×10 <sup>-2</sup>
cg25087851	<i>PTGDR2</i>	chr11	60623918	-4.43	2.41×10 <sup>-3</sup>	-4.30	3.29×10 <sup>-4</sup>	-4.35	2.58×10 <sup>-6</sup>	4.06×10 <sup>-2</sup>
cg12103951	<i>WAPL</i>	chr10	88162314	0.77	7.00×10 <sup>-2</sup>	1.28	1.18×10 <sup>-5</sup>	1.12	3.55×10 <sup>-6</sup>	5.15×10 <sup>-2</sup>
cg12427941	<i>TJAP1</i>	chr6	43457177	5.40	7.88×10 <sup>-3</sup>	4.56	3.11×10 <sup>-4</sup>	4.79	7.99×10 <sup>-6</sup>	1.08×10 <sup>-1</sup>
cg06623197	<i>MTMR3</i>	chr22	30400763	2.99	5.23×10 <sup>-3</sup>	1.64	3.59×10 <sup>-4</sup>	1.86	1.18×10 <sup>-5</sup>	1.48×10 <sup>-1</sup>
cg12296550	<i>HLA-DQB2</i>	chr6	32728862	0.54	5.89×10 <sup>-2</sup>	0.91	4.77×10 <sup>-5</sup>	0.77	1.26×10 <sup>-5</sup>	1.48×10 <sup>-1</sup>
cg15700636	<i>PRG2</i>	chr11	57156050	-5.59	9.80×10 <sup>-4</sup>	-4.41	4.07×10 <sup>-3</sup>	-4.94	1.41×10 <sup>-5</sup>	1.57×10 <sup>-1</sup>
cg13074835	<i>NFKBIL1</i>	chr6	31515196	-2.05	1.22×10 <sup>-1</sup>	-3.32	3.72×10 <sup>-5</sup>	-2.98	1.51×10 <sup>-5</sup>	1.58×10 <sup>-1</sup>
cg15492834	<i>C1orf226</i>	chr1	162351057	-5.26	1.55×10 <sup>-3</sup>	-3.11	1.79×10 <sup>-3</sup>	-3.68	1.66×10 <sup>-5</sup>	1.64×10 <sup>-1</sup>
cg20481287	<i>ETV6</i>	chr12	12224457	-2.10	3.73×10 <sup>-2</sup>	-2.58	1.95×10 <sup>-4</sup>	-2.43	2.14×10 <sup>-5</sup>	2.02×10 <sup>-1</sup>

\*Effect is the regression parameter for methylation data (beta value) at each CpG site

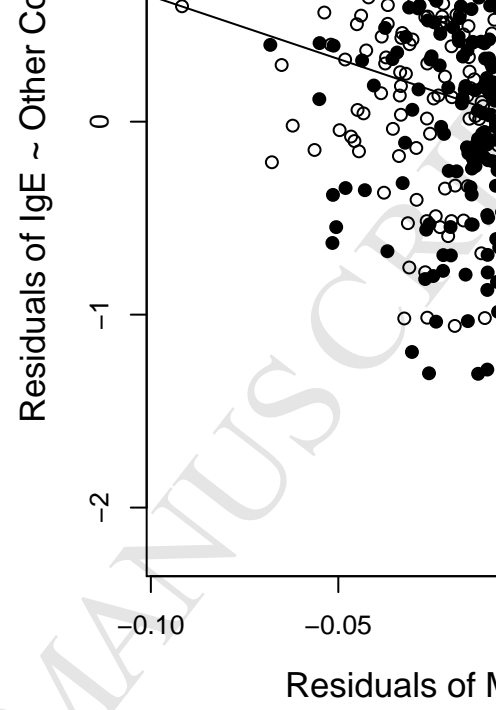
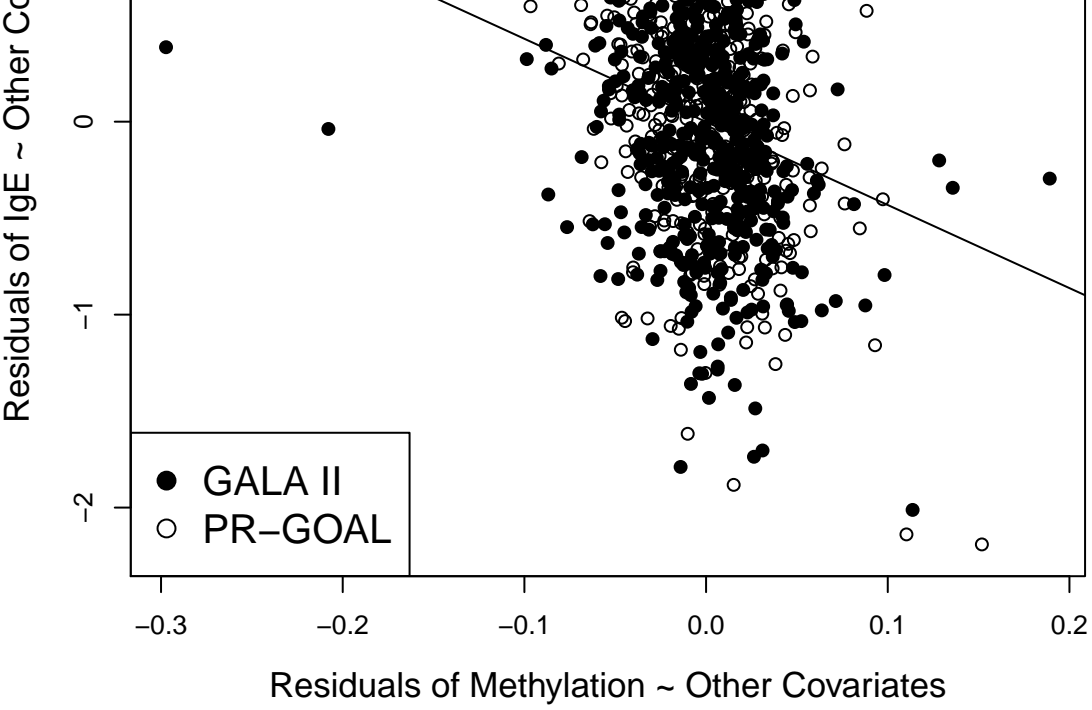
Pathway	Odds Ratio	P-value	FDR	Included.Genes
hsa05310 Asthma	7.41	$1.72 \times 10^{-05}$	0.002	<i>PRG2,HLA-DOA,HLA-DQA1,HLA-DQB1,IL4,HLA-DRB5,IL13,HLA-DQA2,HLA-DPA1</i>
hsa05330 Allograft rejection	6.06	$6.46 \times 10^{-05}$	0.004	<i>HLA-DOA,HLA-DQA1,HLA-G,HLA-DQB1,IL4,HLA-DRB5,HLA-DQA2,GZMB,HLA-DPA1</i>
hsa04612 Antigen processing and presentation	4.15	$2.02 \times 10^{-04}$	0.009	<i>HLA-DOA,PSME3,HSPA2,HLA-DQA1,HLA-G,HLA-DQB1,CTSB,TAP2,HLA-DRB5,HLA-DQA2,HLA-DPA1</i>
hsa05320 Autoimmune thyroid disease	4.88	$2.66 \times 10^{-04}$	0.009	<i>HLA-DOA,HLA-DQA1,HLA-G,HLA-DQB1,IL4,HLA-DRB5,HLA-DQA2,GZMB,HLA-DPA1</i>
hsa05332 Graft-versus-host disease	5.22	$3.89 \times 10^{-04}$	0.01	<i>HLA-DOA,HLA-DQA1,HLA-G,HLA-DQB1,HLA-DRB5,HLA-DQA2,GZMB,HLA-DPA1</i>
hsa04750 Inflammatory mediator regulation of TRP channels	3.29	$4.25 \times 10^{-04}$	0.01	<i>ADCY4,PRKCE,PIK3CG,PLA2G4C,IL1RAP,ADCY8,TRPM8,ADCY5,PRKCA,PPP1CA,PRKCB,PIK3CB,ADCY3</i>
hsa05323 Rheumatoid arthritis	3.43	$5.06 \times 10^{-04}$	0.01	<i>ATP6V0A2,HLA-DOA,HLA-DQA1,TNFSF11,CSF2,HLA-DQB1,ATP6V0E2,HLA-DRB5,TGFB3,HLA-DQA2,ANGPT1,HLA-DPA1</i>

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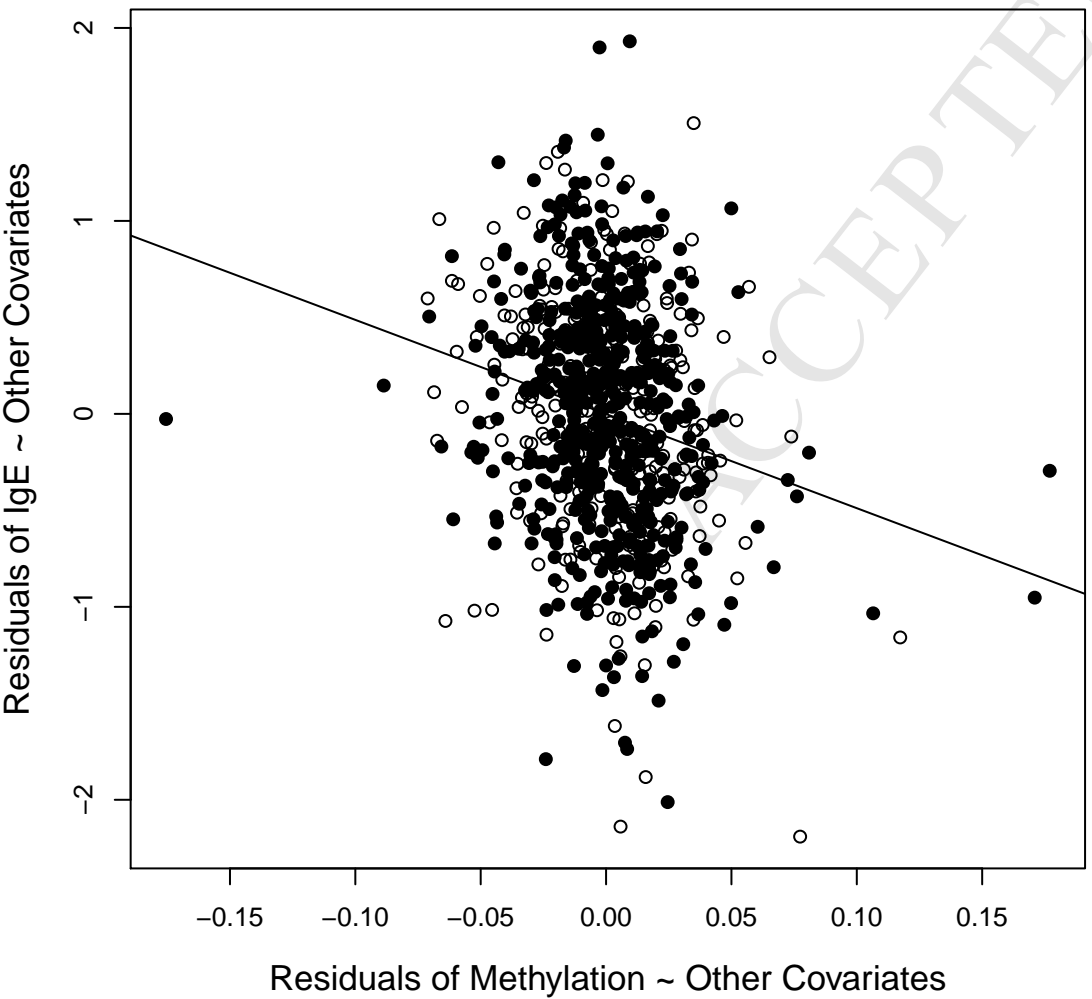
IgE ~ Cell Percentage	PR-GOAL						GALA II					
	Control		Case		All		Control		Case		All	
	Effect	P-value	Effect	P-value	Effect	P-value	Effect	P-value	Effect	P-value	Effect	P-value
Neutrophil	-0.007	0.216	-0.009	0.091	-0.008	0.050	-0.007	0.061	-0.004	0.319	-0.008	0.007
Lymphocyte	-0.011	0.076	-0.001	0.885	-0.008	0.057	0.001	0.792	-0.009	0.055	-0.002	0.573
Monocyte	0.045	0.128	-0.023	0.419	0.007	0.756	0.021	0.237	-0.012	0.566	-0.008	0.575
Eosinophil	0.116	<b>2.1×10<sup>-15</sup></b>	0.040	<b>6.0×10<sup>-05</sup></b>	0.067	<b>2.1×10<sup>-16</sup></b>	0.112	<b>5.1×10<sup>-11</sup></b>	0.090	<b>4.2×10<sup>-15</sup></b>	0.108	<b>1.0×10<sup>-29</sup></b>
Basophil	0.491	0.047	-0.058	0.756	0.194	0.200	0.449	0.010	0.115	0.519	0.258	0.050



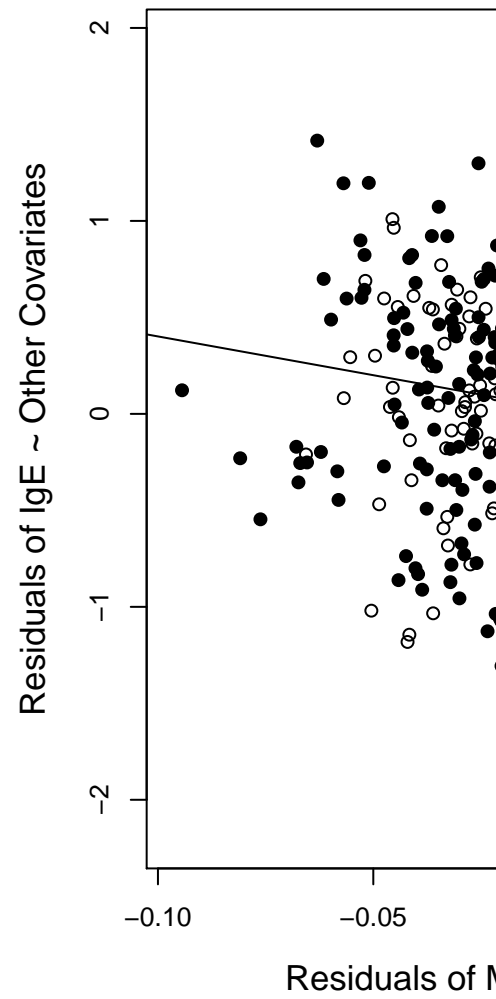
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**Partial Regression Plot for MND1 (cg12614529)**



**Partial Regression**



# **An epigenome-wide association study of total serum immunoglobulin E in Hispanic children**

Wei Chen, PhD<sup>1§</sup>, Ting Wang, PhD<sup>1§</sup>, Maria Pino-Yanes, PhD<sup>2</sup>, Erick Forno, MD, MPH<sup>1</sup>, Liming Liang, PhD<sup>3</sup>, Qi Yan, PhD<sup>1</sup>, Donglei Hu, PhD<sup>4</sup>, Daniel E. Weeks, PhD<sup>5</sup>, Andrea Baccarelli, MD, PhD<sup>6</sup>, Edna Acosta-Perez, PhD<sup>7</sup>, Celeste Eng, MS<sup>4</sup>, Yueh-Ying Han, PhD<sup>1</sup>, Nadia Boutaoui, PhD<sup>1</sup>, Catherine Laprise, PhD<sup>8</sup>, Gwyneth A. Davies, MD<sup>9</sup>, Julian M. Hopkin, MD<sup>9</sup>, Miriam F. Moffatt, DPhil<sup>10</sup>, William O.C.M. Cookson, MD<sup>10</sup>, Glorisa Canino, PhD<sup>7</sup>, Esteban G. Burchard, MD, MPH<sup>4\*</sup>, Juan C. Celedón, MD, DrPH<sup>1\*</sup>

<sup>1</sup>Division of Pediatric Pulmonary Medicine, Allergy, and Immunology, Children's Hospital of Pittsburgh of UPMC, University of Pittsburgh, Pittsburgh, PA

<sup>2</sup>Instituto de Salud Carlos III, CIBER de Enfermedades Respiratorias, Madrid, Spain

<sup>3</sup>Departments of Epidemiology and Biostatistics, Harvard School of Public Health, Boston, MA

<sup>4</sup>Department of Therapeutic Sciences and Bioengineering, University of California at San Francisco, San Francisco, CA

<sup>5</sup>Departments of Human Genetics and Biostatistics, Graduate School of Public Health, University of Pittsburgh, Pittsburgh, PA

<sup>6</sup>Department of Environmental Medicine, Harvard School of Public Health, Boston, MA

<sup>7</sup>Behavioral Sciences Research Institute and Department of Pediatrics, University of Puerto Rico, San Juan, PR



<sup>9</sup>Institute of Life Science, Swansea University Medical School, Swansea, UK

<sup>10</sup>National Heart and Lung Institute, Imperial College, London, UK

\*These authors equally supervised this work.

**Corresponding Author:**

Juan C. Celedón, M.D., Dr.P.H.

Division of Pulmonary Medicine, Allergy and Immunology

Children's Hospital of Pittsburgh of UPMC

4401 Penn Avenue, Pittsburgh, PA 15224

Phone: 412.692.8429

Fax: 412.692.7636

Email: [juan.celedon@chp.edu](mailto:juan.celedon@chp.edu)

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Table E2. Reference CpG sites for WBC type imputation

Table E3. Results for the top 200 CpG sites in the meta-analysis of PR-GOAL and GALA II, unadjusted for WBC types

Table E4. Results for the top CpG sites reported in a previous EWAS of total IgE (without adjustment for WBC types)

Table E5. Results for the top 200 CpG sites in the meta-analysis of PR-GOAL and GALA II, adjusting for WBC types

Table E6. eQTM results for the top 20 CpG sites in the meta-analysis adjusting for WBC types

Table E7. Top 200 CpG sites in the meta-analysis unadjusted for WBC types, in Puerto Ricans only

Table E8. Top 200 CpG sites in the meta-analysis adjusting for WBC types, in Puerto Ricans only

Figure E1. Performance of WBC type imputation in PR-GOAL data

Figure E2. Comparison of mean and standard deviation of DNA methylation between PR-GOAL and GALA II

Figure E3. Manhattan and QQ plots for the results of meta-analyses unadjusted for WBC types

Figure E4. Consistency of EWAS results between PR-GOAL and GALA II

Figure E5. PCA of genotypic and methylation data in GALA II

Figure E6. Manhattan and QQ plots for the results of meta-analyses, in Puerto Ricans only

Figure E7. Consistency of meta-analyses results, including all Latino participants or Puerto Ricans only

	<b>PR-GOAL</b>	<b>GALA II</b>	<b>MRCA</b>	<b>PAPA</b>	<b>SLSJ</b>
Number of Samples	306	573	355	149	160
Age, Mean (range)	9 (6-15)	13 (8-22)	28 (2-61)	21 (18-30)	29 (5-79)
Gender_Female, N (%)	131 (42.8%)	287 (50.1%)	172 (48.5%)	72 (48.3%)	80 (50.0%)
Asthma, N (%)	173 (56.5%)	311 (54.3%)	175 (49.3%)	34 (22.8%)	69 (43.1%)
Total IgE, IU/ml	647 (2-10178)	371 (1-8545)	320 (1-4,999)	663 (0-18800)	412 (2-7653)
Methylation_Platform	450K	450K	27K	450K	450K
Population	Hispanics	Hispanics	Caucasians	Caucasians	Caucasians

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cg00286717	C11orf42	chr11	6225537	cg13895148	LY86	chr6	6762233
cg00441741	METTL8	chr2	172290573	cg14011971	ANK3	chr10	61997974
cg00446123	ZGPAT	chr20	62367888	cg14083146	RALGAPA2	chr20	20694136
cg00551892	ZNF530	chr19	58123307	cg14160422	SLC44A2	chr19	10735548
cg00578437	MAPK1	chr22	22217249	cg14165142	CDC25B	chr20	3778655
cg00678239	NEAT1	chr11	65190227	cg14177140	2-Mar	chr1	220956859
cg00786138	RERE	chr1	8470722	cg14252486	NFIA	chr1	61331027
cg00882883	FBRSL1	chr12	133052863	cg14350544	FBP2	chr9	97349564
cg01000631	EVL	chr14	100610667	cg14535274	POLQ	chr3	121151186
cg01258949	C11orf49	chr11	47092992	cg14597739	LTA	chr6	31539998
cg01330991	DNAH2	chr17	7648108	cg14608454	NDOR1	chr9	140106083
cg01445399	LINC01140	chr1	87596934	cg14654886	EVC2	chr4	5710319
cg01827012	TRRAP	chr7	98603440	cg14709239	INHBB	chr2	121098464
cg01870113	NDOR1	chr9	140106010	cg14769121	SMURF1	chr7	98722470
cg01901579	DICER1	chr14	95615731	cg14973204	FBRSL1	chr12	133052753
cg01942646	NR0B2	chr1	27240694	cg15535471	HIPK2	chr7	139332087
cg01963696	ELANE	chr19	851650	cg15625636	GPR65	chr14	88472437
cg02133716	PVT1	chr8	128981622	cg15700636	PRG2	chr11	57156050
cg02326551	NOC2L	chr1	892704	cg15704662	CASC8	chr8	128388831
cg02497428	METTL9	chr16	21665138	cg15983520	GPT	chr8	145729106
cg03370752	TMEM138	chr11	61136373	cg16068833	UBXN11	chr1	26644515
cg03399239	FAM160B2	chr8	21952741	cg17018980	IQCE	chr7	2613413
cg03448301	CHRM1	chr11	62678778	cg17078393	LCK	chr1	32717002
cg03461678	PLOD3	chr7	100859600	cg17116895	FYN	chr6	112133054
cg03467256	HPCAL1	chr2	10556515	cg17141902	NINJ1	chr9	95897216
cg03507593	NCOR2	chr12	124939480	cg17322118	LOC646626	chr1	85743732
cg03555710	PFKFB3	chr10	6220879	cg17585031	KSR1	chr17	25798942
cg03562367	USP25	chr21	17106209	cg17756730	FASLG	chr1	172608644
cg03661164	EZH2	chr7	148560646	cg17758696	ST3GAL1	chr8	134548281
cg03727333	SGMS1	chr10	52379467	cg17829017	ZFAT	chr8	135612538
cg03945895	PRDM2	chr1	14111352	cg17851165	SDHAP3	chr5	1548899
cg04173586	DOT1L	chr19	2167496	cg18103150	DNHD1	chr11	6518907
cg04260633	TTYH3	chr7	2687305	cg18424841	SLCO4A1	chr20	61315444
cg04340595	CLSTN1	chr1	9789174	cg18634090	COL23A1	chr5	177964789
cg04674060	CHD3	chr17	7792063	cg18643199	SH2D4B	chr10	82363313
cg05184016	ZNF862	chr7	149543136	cg18659081	PARVG	chr22	44588350
cg05235171	TMPRSS4	chr11	117958104	cg18752987	MAD1L1	chr7	2099773
cg05431947	PARVA	chr11	12621248	cg18777299	STIM2	chr4	26994740
cg05579652	CACNA1C	chr12	2173351	cg18783781	SLC25A33	chr1	9599067
cg05580512	LPCAT1	chr5	1463045	cg18920397	LY9	chr1	160765805
cg05613273	NARF	chr17	80419874	cg19380303	KIF7	chr15	90172193
cg05689267	TAP2	chr6	32798439	cg19468534	OIP5	chr15	41623761
cg05690260	SEL1L3	chr4	25836272	cg19743891	UBXN11	chr1	26644573
cg05898907	CLDND1	chr3	98242685	cg19914554	CD7	chr17	80275401
cg06112967	SP110	chr2	231085725	cg20267828	THEMIS	chr6	128222390
cg06173319	PRDM7	chr16	90148775	cg20363347	MYEOV	chr11	69061473
cg06494464	GGT1	chr22	24992604	cg20792833	PTPRCAP	chr11	67205195
cg06818532	BBX	chr3	107318032	cg20952652	UXS1	chr2	106757367
cg07173760	CLC	chr19	40229266	cg20997661	PKNOX2	chr11	125120940

cg07522227	ZNF69	chr19	12001680	cg21352837	CYS1	chr2	10199417
cg07731455	LSM3	chr3	14220336	cg21404108	ABHD5	chr3	43769400
cg07813265	CDC14A	chr1	100820528	cg21463763	HSPA12B	chr20	3713341
cg07828169	8-Sep	chr5	132114623	cg21535980	ABR	chr17	1083183
cg08157194	SLC25A17	chr22	41185264	cg21575634	STX2	chr12	131310417
cg08224773	FAM167A	chr8	11311868	cg21773162	ZAP70	chr2	98330087
cg08362785	MKL1	chr22	40814878	cg21816942	MAP1LC3C	chr1	242121827
cg08698796	CELF1	chr11	47561199	cg22082267	OR8K1	chr11	56112153
cg08773180	PRG2	chr11	57157607	cg22160073	HBG2	chr11	5653405
cg08796342	TC2N	chr14	92334029	cg22163130	FAM19A2	chr12	62586665
cg08886063	VPS53	chr17	600398	cg22235258	EHF	chr11	34675402
cg09072634	MAD2L2	chr1	11737212	cg22528044	SCN9A	chr2	167232679
cg09691317	UVSSA	chr4	1379690	cg22610434	CD1C	chr1	158259914
cg09834503	HECTD1	chr14	31679612	cg22799499	COL9A2	chr1	40773045
cg10161121	FASLG	chr1	172628020	cg22996170	JUNB	chr19	12895529
cg10526374	ASCL2	chr11	2292525	cg23189692	EIF4G1	chr3	184050393
cg10624395	FDX1	chr11	110350574	cg23231026	SLC2A11	chr22	24225988
cg10652507	LINC01094	chr4	79584115	cg23296836	FGF20	chr8	16870927
cg10704177	INADL	chr1	62209607	cg23356302	MIR1247	chr14	101993498
cg10732094	ERCC1	chr19	45957466	cg23510807	LFNG	chr7	2567893
cg11007850	HS6ST1	chr2	129216138	cg23828876	PCYT1A	chr3	196001706
cg11162249	NUDT16	chr3	131100713	cg23842205	RBM14-RBM4	chr11	66394024
cg11206634	SFT2D3	chr2	128458399	cg24254196	CHSY1	chr15	101719523
cg11310939	3-Mar	chr5	126257116	cg24353535	ASCL2	chr11	2293048
cg11610626	THEMIS	chr6	128222053	cg24368962	SIK2	chr11	111570978
cg11831003	HBG2	chr11	5646029	cg24376793	PPP1R12B	chr1	202545589
cg11957777	ERCC3	chr2	128015142	cg24427660	PNPLA2	chr11	818892
cg12094903	PSMB8	chr6	32808689	cg24459209	PRG3	chr11	57148215
cg12179219	MIAT	chr22	27149381	cg24710320	HRASLS	chr3	192958832
cg12216435	COPG1	chr3	128995479	cg25192081	JAK1	chr1	65308244
cg12222277	SKI	chr1	2191658	cg25270424	OSBPL3	chr7	24965657
cg12614529	MND1	chr4	154269418	cg25305879	UXS1	chr2	106814630
cg12675714	C4orf46	chr4	159592618	cg25420477	PCBP1	chr2	70319121
cg12769657	TMEM9	chr1	201140721	cg25554496	GNA13	chr17	63036095
cg12810837	CLEC2D	chr12	9822287	cg25872816	ZNF516	chr18	74168914
cg12872357	RAB32	chr6	146863647	cg25952192	TTC39C	chr18	21656374
cg13167816	FITM1	chr14	24601808	cg26167930	FAM96A	chr15	64363681
cg13233042	ATL3	chr11	63432489	cg26252077	NFIA	chr1	61607055
cg13388830	PPRC1	chr10	103910870	cg26341831	TMEM63A	chr1	226036279
cg13430807	MTMR11	chr1	149903315	cg26396815	BANK1	chr4	102878132
cg13466180	CALR	chr19	13054470	cg26449074	ZC3H15	chr2	187351671
cg13533976	FAM117A	chr17	47865880	cg26601310	PRR5L	chr11	36397123
cg13562353	CCL27	chr9	34662773	cg26774971	TMEM181	chr6	158994407
cg13583115	YPEL5	chr2	30369314	cg26818464	PRKCQ	chr10	6618723
cg13606287	RIC1	chr9	5672070	cg26865494	DOCK1	chr10	129172573
cg13696436	EBF3	chr10	131695094	cg27260636	MSANTD4	chr11	105892993
cg13720639	SIPA1L1	chr14	72061746	cg27658026	CALHM3	chr10	105239085
cg13781408	AATK	chr17	79095700	ch.13.80513820F	SPRY2	chr13	81615819

**Table E3. Results for the top 200 CpG sites in the meta-analysis of PR-GOAL and GALA II, u types**

#	ProbeID	Gene	CHR	Position	PR-GOAL		GALA II		Mega-analysis		Meta-analysis			MRC
					Eff <sup>a</sup>	Pval	Eff	Pval	Eff	Pval	Eff	Pval	FDR	
1	cg04983687	ZFPM1	chr16	88558223	-4.7	2.0E-19	-4.6	7.8E-23	-4.6	1.2E-40	-4.7	1.3E-40	1.5E-35	NA
2	cg09249800	ACOT7	chr1	6341287	-5.4	1.6E-20	-6.8	3.8E-22	-5.8	1.1E-39	-6.0	1.6E-40	1.5E-35	NA
3	cg11699125	ACOT7	chr1	6341327	-4.9	5.3E-19	-5.9	1.4E-19	-5.1	2.9E-35	-5.3	1.1E-36	7.0E-32	NA
4	cg25087851	PTGDR2	chr11	60623918	-5.7	3.3E-16	-7.1	3.8E-21	-6.2	2.2E-35	-6.3	2.7E-35	1.0E-30	NA
5	cg12227660	MIR202	chr10	135061670	-6.2	2.7E-16	-6.4	1.3E-20	-6.0	1.1E-34	-6.3	2.7E-35	1.0E-30	NA
6	cg01000631	EVL	chr14	100610667	-4.8	9.8E-18	-6.9	1.2E-19	-5.2	6.2E-33	-5.5	1.1E-34	3.4E-30	NA
7	cg08940169	ZFPM1	chr16	88540241	-6.1	1.3E-17	-7.4	6.4E-19	-6.5	1.4E-34	-6.7	1.3E-34	3.5E-30	NA
8	cg15700636	PRG2	chr11	57156050	-6.2	1.4E-16	-7.5	8.9E-20	-6.6	3.9E-34	-6.8	2.0E-34	4.7E-30	NA
9	cg21220721	ACOT7	chr1	6341230	-4.8	2.9E-20	-3.6	2.7E-16	-4.0	8.1E-34	-4.1	2.7E-34	5.7E-30	NA
10	cg10142874	LPIN1	chr2	11917623	-6.1	6.4E-16	-7.0	9.9E-19	-6.4	6.9E-33	-6.5	6.9E-33	1.2E-28	NA
11	cg04290133	GUSB	chr7	65439512	-5.5	2.1E-14	-8.4	2.1E-21	-6.3	5.1E-31	-6.7	7.1E-33	1.2E-28	NA
12	cg12077754	HK2	chr2	75089669	-4.7	2.2E-14	-5.8	5.5E-20	-5.0	1.7E-30	-5.3	1.9E-32	3.0E-28	NA
13	cg01901579	DICER1	chr14	95615731	-5.6	2.2E-14	-7.0	1.1E-19	-6.1	3.5E-32	-6.2	4.3E-32	6.2E-28	NA
14	cg26547058	SLC45A4	chr8	142243143	-6.7	1.6E-15	-6.9	4.0E-18	-6.6	7.7E-32	-6.8	4.8E-32	6.4E-28	NA
15	cg06528816	TTC7A	chr2	47242277	-5.3	9.1E-15	-6.3	7.1E-19	-5.8	9.0E-33	-5.8	8.2E-32	1.0E-27	NA
16	cg07970948	ZNF862	chr7	149543165	-4.8	1.4E-15	-5.4	9.2E-18	-4.9	1.8E-31	-5.0	1.3E-31	1.4E-27	NA
17	cg24491618	KCNH2	chr7	150649807	-5.6	3.0E-16	-7.7	9.0E-18	-6.2	4.6E-31	-6.4	1.3E-31	1.4E-27	NA
18	cg18550847	EVL	chr14	100610570	-4.9	3.9E-16	-6.1	3.2E-17	-5.2	1.1E-30	-5.4	2.1E-31	2.2E-27	NA
19	cg16263722	MECR	chr1	29523841	-6.5	1.5E-15	-6.8	2.1E-17	-6.4	2.5E-30	-6.6	2.5E-31	2.5E-27	NA
20	cg08776942	SNN	chr16	11729131	-6.6	4.1E-15	-7.7	8.9E-18	-6.9	1.5E-30	-7.1	4.1E-31	3.9E-27	NA
21	cg16409452	EVL	chr14	100610186	-5.3	4.2E-15	-7.9	9.6E-18	-6.0	1.6E-29	-6.2	3.9E-30	3.5E-26	NA
22	cg01998785	LPCAT2	chr16	55542709	-5.5	3.9E-13	-6.9	7.2E-19	-5.9	1.3E-29	-6.2	4.5E-30	3.8E-26	-0.6
23	cg02985445	BRI3	chr7	97908505	-6.9	4.0E-16	-6.0	1.3E-15	-6.0	9.9E-29	-6.4	4.9E-30	4.0E-26	NA
24	cg23706836	MCPH1	chr8	6407997	-4.7	8.1E-15	-5.5	6.2E-17	-5.0	4.2E-30	-5.1	5.5E-30	4.3E-26	NA
25	cg20885063	ATPAF2	chr17	17939419	-5.8	8.5E-16	-6.6	1.5E-15	-6.1	2.4E-30	-6.2	1.2E-29	8.7E-26	NA
26	cg16362140	DAP	chr5	10708717	-5.6	5.1E-16	-6.3	3.1E-15	-5.7	1.2E-28	-5.9	1.4E-29	1.0E-25	NA

#	ProbeID	Gene	CHR	Position	PR-GOAL		GALA II		Mega-analysis		Meta-analysis			MRC	
					Eff	Pval	Eff	Pval	Eff	Pval	Eff	Pval	FDR	Coef	
27	cg13645296	DAPK2	chr15	64275810	-6.6	1.4E-16	-5.3	2.4E-14	-5.7	1.0E-28	-5.9	5.3E-29	3.7E-25	NA	
28	cg18666454	KCNH2	chr7	150651937	-5.2	1.0E-13	-7.0	2.3E-17	-5.9	1.6E-29	-6.0	6.3E-29	4.3E-25	NA	
29	cg04497992	PRR35	chr16	616212	-7.3	1.7E-16	-5.3	1.5E-14	-5.7	1.1E-28	-6.1	8.2E-29	5.3E-25	NA	
30	cg13576859	FBP1	chr9	97403129	-6.2	7.8E-15	-6.3	1.7E-15	-6.1	1.5E-28	-6.2	9.7E-29	6.1E-25	NA	
31	cg21045547	SOGA1	chr20	35422703	-6.8	1.9E-13	-9.4	2.0E-17	-7.5	5.2E-28	-7.8	1.5E-28	9.2E-25	NA	
32	cg07562835	ITGB4	chr17	73734756	-7.3	7.3E-14	-7.0	4.9E-16	-6.6	4.6E-26	-7.1	2.6E-28	1.5E-24	NA	
33	cg23147443	KCNH2	chr7	150649655	-5.1	1.5E-16	-5.3	2.4E-13	-5.0	6.7E-28	-5.2	2.7E-28	1.5E-24	NA	
34	cg17988187	DCTN1	chr2	74612222	-5.6	1.1E-13	-6.7	2.8E-16	-6.0	1.0E-28	-6.1	3.3E-28	1.8E-24	NA	
35	cg08889930	MCM2	chr3	127317798	-6.9	7.7E-14	-8.0	7.5E-16	-7.2	2.6E-27	-7.4	5.4E-28	2.9E-24	NA	
36	cg06070625	MITF	chr3	69812798	-5.8	1.4E-13	-6.7	5.2E-16	-6.0	1.1E-27	-6.2	7.0E-28	3.6E-24	NA	
37	cg18650626	MAD1L1	chr7	1914073	-4.1	2.5E-15	-4.6	3.9E-14	-4.2	1.6E-27	-4.3	7.9E-28	4.0E-24	NA	
38	cg11456013	AMD1	chr6	111192760	-5.7	5.6E-14	-7.2	1.1E-15	-6.0	8.5E-27	-6.3	9.7E-28	4.8E-24	NA	
39	cg20840540	TRERF1	chr6	42363749	-7.3	2.8E-12	-9.1	2.8E-17	-7.8	7.6E-27	-8.2	1.1E-27	5.2E-24	NA	
40	cg00944309	ELOVL7	chr5	60142446	-5.9	5.3E-15	-6.2	2.9E-14	-6.0	9.8E-28	-6.1	1.1E-27	5.3E-24	NA	
41	cg26787239	IL4	chr5	132008525	-7.9	5.0E-13	-11.9	3.0E-17	-9.1	6.4E-27	-9.4	1.3E-27	5.8E-24	-0.6	1
42	cg25939647	GPR176	chr15	40173065	-5.4	2.8E-16	-4.9	9.8E-13	-4.9	5.0E-26	-5.2	2.1E-27	9.4E-24	NA	
43	cg01445399	LINC01140	chr1	87596934	-6.4	2.9E-13	-7.5	1.3E-15	-6.9	2.4E-28	-6.9	3.9E-27	1.7E-23	NA	
44	cg00114012	SLC2A8	chr9	130158144	-5.9	3.8E-14	-5.7	1.6E-14	-5.5	5.5E-26	-5.8	4.3E-27	1.8E-23	NA	
45	cg20673965	IRGC	chr19	44220148	-6.4	1.3E-13	-6.6	7.5E-15	-6.0	5.1E-25	-6.5	7.0E-27	2.9E-23	NA	
46	cg06391412	FOXP1	chr3	71295684	-6.2	6.2E-14	-7.2	1.4E-14	-6.5	3.1E-27	-6.6	8.8E-27	3.6E-23	NA	
47	cg03131767	ABCB9	chr12	123446272	-6.3	3.1E-13	-7.1	3.8E-15	-6.8	1.3E-28	-6.7	1.0E-26	4.1E-23	NA	
48	cg12819873	PRG2	chr11	57157632	-6.5	9.9E-14	-7.6	1.1E-14	-6.8	2.3E-26	-7.0	1.1E-26	4.3E-23	NA	
49	cg14978242	SERINC5	chr5	79501131	-6.3	4.4E-15	-5.6	5.0E-13	-5.9	2.8E-27	-5.9	1.9E-26	7.3E-23	NA	
50	cg07781995	LINC01140	chr1	87655840	-7.5	1.0E-15	-7.6	3.3E-12	-7.4	1.8E-26	-7.5	2.3E-26	8.6E-23	NA	
51	cg21067750	PHGR1	chr15	40641778	-7.2	3.5E-13	-8.6	9.1E-15	-7.4	2.7E-24	-7.8	3.4E-26	1.3E-22	NA	
52	cg08773180	PRG2	chr11	57157607	-5.7	6.1E-16	-5.5	8.6E-12	-5.5	1.0E-25	-5.6	3.6E-26	1.3E-22	NA	
53	cg04420917	LGALS4	chr19	39303993	-6.8	1.9E-12	-7.4	3.7E-15	-6.7	1.5E-24	-7.1	5.2E-26	1.9E-22	NA	
54	cg21627181	SLC17A4	chr6	25754190	-7.0	2.3E-13	-7.8	6.3E-14	-7.0	2.5E-24	-7.3	1.2E-25	4.0E-22	-0.4	1

#	ProbeID	Gene	CHR	Position	PR-GOAL		GALA II		Mega-analysis		Meta-analysis			MRC	
					Eff	Pval	Eff	Pval	Eff	Pval	Eff	Pval	FDR	Coef	
55	cg25173129	EPX	chr17	56269410	-6.0	3.4E-13	-7.3	3.0E-14	-6.3	4.8E-25	-6.6	1.2E-25	4.0E-22	NA	
56	cg14613878	TLDC2	chr20	35504198	-6.0	8.2E-17	-4.0	2.3E-11	-4.6	3.5E-25	-4.8	1.4E-25	4.6E-22	NA	
57	cg21919729	CTSB	chr8	11719367	-5.6	9.6E-13	-5.5	2.8E-14	-5.3	1.4E-24	-5.5	1.8E-25	6.0E-22	NA	
58	cg07177867	LYSMD2	chr15	52030746	-6.5	1.2E-12	-7.8	1.5E-14	-6.8	1.8E-24	-7.1	2.0E-25	6.2E-22	NA	
59	cg00170714	MLX	chr17	40724562	-6.3	3.8E-12	-6.9	7.1E-15	-6.6	5.0E-26	-6.6	2.0E-25	6.2E-22	NA	
60	cg02427831	SIGLEC8	chr19	51961937	-6.8	2.7E-13	-7.1	2.9E-13	-6.5	1.2E-22	-7.0	5.4E-25	1.7E-21	NA	
61	cg20836212	VKORC1L1	chr7	65419185	-4.7	3.0E-13	-4.4	2.7E-13	-4.4	8.3E-25	-4.6	5.9E-25	1.8E-21	NA	
62	cg22919538	NME6	chr3	48334413	-8.1	2.3E-14	-8.0	4.1E-12	-7.6	1.8E-23	-8.0	6.2E-25	1.9E-21	NA	
63	cg25224369	IQSEC1	chr3	12918528	-6.5	7.5E-15	-5.4	8.2E-12	-5.7	3.4E-24	-6.0	6.4E-25	1.9E-21	NA	
64	cg10159529	IL5RA	chr3	3152530	-5.7	6.1E-13	-7.0	9.3E-14	-6.0	1.7E-24	-6.2	6.7E-25	2.0E-21	-0.6	5
65	cg07908654	WBP4	chr13	41631052	-5.6	2.8E-12	-6.3	4.5E-14	-5.9	9.3E-26	-5.9	1.0E-24	2.9E-21	NA	
66	cg13628444	MED27	chr9	134883788	-6.3	1.0E-12	-6.7	1.5E-13	-6.3	1.8E-24	-6.5	1.1E-24	3.1E-21	NA	
67	cg01649647	MYL9	chr20	35177530	-8.2	2.4E-15	-5.9	2.5E-11	-6.6	3.2E-24	-6.9	1.5E-24	4.2E-21	NA	
68	cg17540765	RECQL5	chr17	73631586	-6.3	3.0E-11	-6.5	8.3E-15	-6.1	9.3E-24	-6.4	1.7E-24	4.6E-21	NA	
69	cg26235490	ABR	chr17	1047567	-7.3	4.1E-14	-7.0	8.0E-12	-6.8	3.4E-24	-7.2	2.2E-24	6.0E-21	NA	
70	cg06906869	NEK3	chr13	52734154	-7.3	2.1E-13	-7.1	1.6E-12	-6.9	2.2E-24	-7.2	2.2E-24	6.0E-21	NA	
71	cg25488567	FAM26F	chr6	116781307	-6.8	5.3E-14	-7.2	6.6E-12	-6.6	6.1E-23	-7.0	2.4E-24	6.4E-21	NA	
72	cg13562011	EXD3	chr9	140308660	-6.7	9.4E-15	-6.4	4.1E-11	-6.4	2.0E-24	-6.6	2.5E-24	6.7E-21	NA	
73	cg01310029	IL5RA	chr3	3152374	-6.6	2.7E-13	-7.2	2.4E-12	-6.6	1.8E-23	-6.9	4.7E-24	1.2E-20	NA	
74	cg26865494	DOCK1	chr10	129172573	-7.4	3.9E-12	-8.3	2.1E-13	-7.4	6.8E-23	-7.8	6.2E-24	1.6E-20	NA	
75	cg01330991	DNAH2	chr17	7648108	-5.4	1.9E-13	-5.9	5.3E-12	-5.4	2.5E-23	-5.6	7.0E-24	1.7E-20	NA	
76	cg13312337	DCTN1	chr2	74612759	-8.8	1.6E-15	-5.8	1.5E-10	-6.7	5.7E-23	-7.0	1.5E-23	3.6E-20	NA	
77	cg25643253	VKORC1L1	chr7	65419190	-4.8	1.2E-10	-5.1	1.9E-14	-4.8	1.4E-22	-5.0	1.5E-23	3.6E-20	NA	
78	cg15146567	ZNF662	chr3	42948626	-5.4	3.5E-13	-4.3	3.5E-12	-4.4	2.2E-21	-4.7	1.5E-23	3.7E-20	NA	
79	cg12555233	MAN2A2	chr15	91455366	-7.7	1.3E-10	-8.5	2.0E-14	-7.5	1.7E-21	-8.1	2.0E-23	4.7E-20	NA	
80	cg02359181	GPI	chr19	34860339	-6.4	3.6E-11	-8.1	4.4E-14	-7.1	5.6E-24	-7.2	2.0E-23	4.8E-20	NA	
81	cg14226212	MUSK	chr9	113530240	-5.8	1.1E-09	-7.6	1.7E-15	-6.4	4.8E-22	-6.7	3.0E-23	7.0E-20	NA	
82	cg16177693	NR0B2	chr1	27240669	-6.1	2.8E-14	-4.9	9.6E-11	-5.3	1.5E-23	-5.4	3.2E-23	7.3E-20	NA	



#	ProbeID	Gene	CHR	Position	PR-GOAL		GALA II		Mega-analysis		Meta-analysis			MRC	
					Eff	Pval	Eff	Pval	Eff	Pval	Eff	Pval	FDR	Coef	
83	cg10298741	ZFH3	chr16	73019173	-6.5	3.4E-13	-6.4	1.8E-11	-6.3	6.6E-23	-6.5	3.8E-23	8.6E-20	NA	
84	cg04321303	PGAM2	chr7	44107504	-5.3	1.7E-12	-5.2	3.8E-12	-4.9	6.0E-21	-5.3	4.2E-23	9.3E-20	NA	
85	cg04217850	SLC25A26	chr3	66428294	-7.2	4.0E-10	-9.3	7.9E-15	-8.0	6.5E-23	-8.2	4.5E-23	1.0E-19	NA	
86	cg17521120	SIGLEC8	chr19	51961666	-7.2	8.5E-17	-4.5	8.8E-09	-5.4	3.0E-22	-5.7	7.5E-23	1.6E-19	NA	
87	cg11987455	ERMAP	chr1	43290834	-6.6	2.7E-11	-7.5	4.9E-13	-6.8	5.7E-22	-7.0	1.0E-22	2.2E-19	NA	
88	cg06009042	ANXA6	chr5	150480839	-5.2	7.2E-09	-7.6	4.7E-16	-6.1	3.2E-22	-6.4	1.0E-22	2.2E-19	NA	
89	cg12614529	MND1	chr4	154269418	-4.7	8.6E-12	-4.1	2.4E-12	-4.2	3.4E-22	-4.4	1.6E-22	3.3E-19	NA	
90	cg12172163	PROZ	chr13	113825954	-6.2	9.3E-13	-5.5	3.8E-11	-5.8	9.9E-24	-5.8	2.6E-22	5.4E-19	NA	
91	cg19434937	EMG1	chr12	7104184	-5.8	4.1E-16	-3.3	1.8E-09	-4.0	7.3E-22	-4.2	3.0E-22	6.3E-19	NA	
92	cg03492094	SEMA4D	chr9	91994786	-5.5	2.6E-10	-5.8	2.3E-13	-5.4	6.0E-22	-5.7	3.8E-22	7.7E-19	NA	
93	cg06866208	FAM65A	chr16	67560245	-7.3	7.9E-15	-5.2	2.3E-09	-6.0	3.6E-22	-6.2	4.4E-22	8.9E-19	NA	
94	cg09636525	TADA2B	chr4	7052612	-7.3	3.2E-10	-8.2	1.9E-13	-7.3	3.0E-21	-7.8	4.4E-22	8.9E-19	NA	
95	cg05219423	CELF2	chr10	11291279	-6.4	1.4E-13	-5.3	3.7E-10	-5.6	1.1E-21	-5.8	4.7E-22	9.3E-19	NA	
96	cg11385906	INTS9	chr8	28745680	-5.9	1.2E-10	-6.5	7.1E-13	-5.7	5.2E-20	-6.2	5.9E-22	1.2E-18	NA	
97	cg26791242	LINC01140	chr1	87596895	-5.6	2.6E-14	-4.6	2.2E-09	-4.8	8.1E-21	-5.1	6.0E-22	1.2E-18	NA	
98	cg03060158	IP6K2	chr3	48755856	-7.1	4.3E-10	-8.5	1.6E-13	-7.8	1.6E-23	-7.8	6.2E-22	1.2E-18	NA	
99	cg16046667	SOGA1	chr20	35422698	-4.3	6.9E-10	-5.3	1.0E-13	-4.6	1.7E-21	-4.8	6.9E-22	1.3E-18	NA	
100	cg07819010	AMBRA1	chr11	46619375	-5.9	1.9E-15	-3.6	5.5E-09	-4.4	3.4E-21	-4.6	9.7E-22	1.8E-18	NA	
101	cg23943829	IL4	chr5	132009111	-8.2	1.1E-11	-8.8	2.5E-11	-8.0	6.8E-20	-8.5	1.8E-21	3.4E-18	NA	
102	cg11396585	TAPBP	chr6	33273477	-9.2	7.9E-15	-6.5	1.0E-08	-7.4	3.7E-20	-7.8	2.0E-21	3.8E-18	NA	
103	cg27469152	EPX	chr17	56282313	-5.8	1.4E-13	-4.3	7.9E-10	-4.8	5.4E-22	-4.9	2.1E-21	3.9E-18	NA	
104	cg26953137	MRPL45P2	chr17	45573695	-6.0	1.2E-09	-7.5	1.8E-13	-6.5	5.0E-21	-6.7	2.3E-21	4.1E-18	NA	
105	cg09535526	ZFPM1	chr16	88558065	-5.7	3.3E-13	-4.3	4.6E-10	-4.6	2.9E-19	-4.9	2.4E-21	4.3E-18	NA	
106	cg14025883	PLGRKT	chr9	5436224	-5.0	1.9E-09	-7.7	2.6E-14	-5.8	2.5E-20	-6.1	2.4E-21	4.3E-18	NA	
107	cg00414077	TLDC2	chr20	35504511	-7.8	7.7E-16	-3.9	2.1E-09	-4.8	1.2E-20	-5.1	3.2E-21	5.6E-18	NA	
108	cg26457013	TMEM86B	chr19	55740188	-7.2	1.1E-13	-5.5	2.0E-09	-5.9	1.3E-20	-6.3	3.2E-21	5.6E-18	-0.5	1
109	cg05465955	COASY	chr17	40715236	-5.4	8.5E-12	-3.9	2.0E-11	-4.2	2.5E-20	-4.4	3.3E-21	5.6E-18	NA	
110	cg06154903	EHD1	chr11	64642558	-4.5	3.6E-14	-3.4	7.9E-09	-3.7	1.5E-19	-3.9	4.2E-21	7.3E-18	NA	

#	ProbeID	Gene	CHR	Position	PR-GOAL		GALA II		Mega-analysis		Meta-analysis			MRC	
					Eff	Pval	Eff	Pval	Eff	Pval	Eff	Pval	FDR	Coef	
111	cg20290167	METRNL	chr17	81040724	-5.6	3.8E-11	-5.3	2.0E-11	-5.4	2.4E-21	-5.5	4.6E-21	7.9E-18	NA	
112	cg18972349	THEMIS2	chr1	28195327	-8.1	3.8E-15	-4.6	5.3E-09	-5.3	2.4E-19	-5.9	5.0E-21	8.5E-18	NA	
113	cg06647928	ENC1	chr5	73612203	-6.0	1.8E-12	-4.5	1.8E-10	-4.7	1.2E-18	-5.1	5.7E-21	9.5E-18	NA	
114	cg10387956	CELF6	chr15	72646210	-5.9	6.0E-10	-7.5	8.7E-13	-6.6	2.4E-21	-6.6	6.0E-21	9.8E-18	NA	
115	cg21239317	CCDC126	chr7	23640510	-6.2	1.6E-10	-6.8	5.6E-12	-6.3	4.1E-21	-6.5	6.3E-21	1.0E-17	NA	
116	cg08808720	KIF5C	chr2	149639914	-6.2	9.6E-10	-8.8	3.0E-13	-7.1	1.7E-20	-7.3	6.7E-21	1.1E-17	NA	
117	cg20151107	FAM53B	chr10	126331425	-7.6	5.0E-13	-7.0	2.1E-09	-6.9	1.7E-19	-7.3	6.8E-21	1.1E-17	NA	
118	cg02473287	YWHAQ	chr2	9752386	-6.3	1.1E-12	-5.5	8.9E-10	-5.6	1.9E-19	-5.9	7.1E-21	1.1E-17	NA	
119	cg26774971	TMEM181	chr6	158994407	-6.4	1.1E-12	-6.0	1.1E-09	-6.0	7.2E-21	-6.2	7.9E-21	1.2E-17	NA	
120	cg24202817	PFKFB3	chr10	6220943	-7.8	2.0E-11	-6.5	4.8E-11	-6.9	1.3E-21	-7.0	8.6E-21	1.3E-17	NA	
121	cg20263853	RERE	chr1	8824177	-5.2	2.6E-09	-6.2	4.4E-13	-5.5	5.4E-20	-5.7	9.9E-21	1.5E-17	NA	
122	cg16107105	KCNH2	chr7	150646704	-5.8	4.7E-08	-9.4	3.6E-15	-7.1	9.8E-20	-7.4	1.2E-20	1.9E-17	NA	
123	cg00582671	SAMD11	chr1	872235	-5.6	5.7E-13	-3.8	6.5E-10	-4.3	1.6E-20	-4.5	1.2E-20	1.9E-17	NA	
124	cg18944099	GPANK1	chr6	31629199	-6.1	4.5E-11	-6.1	4.5E-11	-5.8	1.0E-19	-6.1	1.2E-20	1.9E-17	NA	
125	cg02170785	EXD2	chr14	69650830	-5.8	3.8E-10	-7.2	3.5E-12	-6.2	2.3E-20	-6.4	1.3E-20	2.0E-17	NA	
126	cg18783781	SLC25A33	chr1	9599067	-6.5	5.2E-13	-5.8	4.2E-09	-6.1	5.2E-21	-6.2	1.5E-20	2.2E-17	-0.6	5
127	cg25368824	IL4	chr5	132009352	-6.3	2.8E-11	-6.2	1.1E-10	-6.0	5.8E-20	-6.2	1.9E-20	2.9E-17	NA	
128	cg23642826	ZBTB48	chr1	6645463	-6.9	6.3E-11	-5.6	3.8E-11	-5.7	1.1E-18	-6.1	2.1E-20	3.1E-17	NA	
129	cg05720226	ST7	chr7	116786597	-5.7	3.5E-08	-7.0	6.7E-14	-6.1	1.1E-19	-6.4	2.2E-20	3.2E-17	NA	
130	cg26789365	PPP2R2D	chr10	133743048	-5.7	3.2E-09	-8.1	3.8E-13	-6.5	4.7E-20	-6.7	2.8E-20	4.1E-17	NA	
131	cg00844155	VAMP1	chr12	6576111	-7.4	2.1E-11	-6.5	1.9E-10	-6.5	4.5E-19	-6.9	3.0E-20	4.4E-17	NA	
132	cg09565310	MCC	chr5	112541553	-5.3	4.2E-09	-7.1	5.0E-13	-5.8	4.3E-19	-6.1	3.1E-20	4.4E-17	NA	
133	cg06315149	PRKCZ	chr1	2036398	-6.3	6.1E-14	-4.3	2.0E-08	-5.0	1.6E-20	-5.2	3.7E-20	5.2E-17	NA	
134	cg14769121	SMURF1	chr7	98722470	-6.0	5.4E-13	-4.0	1.9E-09	-4.6	7.0E-21	-4.8	4.0E-20	5.6E-17	NA	
135	cg16905199	LINC00869	chr1	149676378	-7.1	1.0E-10	-6.3	6.0E-11	-6.5	7.2E-21	-6.7	4.2E-20	5.8E-17	NA	
136	cg22312249	TMEM104	chr17	72779428	-5.5	3.4E-11	-5.0	1.8E-10	-5.0	6.9E-20	-5.2	4.2E-20	5.8E-17	NA	
137	cg21498475	SLC8B1	chr12	113737469	-6.6	3.0E-14	-3.6	4.4E-09	-4.3	7.9E-20	-4.6	4.3E-20	5.9E-17	NA	
138	cg25135457	COASY	chr17	40715244	-6.6	1.2E-09	-7.4	5.7E-12	-6.6	8.8E-19	-7.0	4.5E-20	6.2E-17	NA	

#	ProbeID	Gene	CHR	Position	PR-GOAL		GALA II		Mega-analysis		Meta-analysis			MRC	
					Eff	Pval	Eff	Pval	Eff	Pval	Eff	Pval	FDR	Coef	
139	cg00869582	SNX29	chr16	12564745	-6.4	2.1E-10	-6.8	4.1E-11	-6.5	1.0E-20	-6.6	5.2E-20	7.0E-17	NA	
140	cg12279125	MYOM2	chr8	2129970	-4.7	1.3E-10	-4.1	5.5E-11	-3.8	6.1E-17	-4.4	5.3E-20	7.2E-17	NA	
141	cg02826233	CDK2	chr12	56365894	-9.0	2.7E-11	-7.7	2.6E-10	-8.0	8.6E-20	-8.3	5.4E-20	7.3E-17	NA	
142	cg06756385	EVL	chr14	100610488	-4.9	2.5E-10	-4.4	3.5E-11	-4.3	7.0E-19	-4.6	5.7E-20	7.5E-17	NA	
143	cg26873132	DENND5A	chr11	9191490	-7.1	2.5E-08	-9.2	2.1E-13	-8.0	2.2E-20	-8.1	6.0E-20	7.9E-17	NA	
144	cg19851574	RPS6KA2	chr6	167178233	-3.1	3.9E-10	-2.8	2.4E-11	-2.7	6.3E-19	-2.9	6.1E-20	8.0E-17	NA	
145	cg16599817	PRKCZ	chr1	2036283	-5.7	1.2E-14	-3.2	2.2E-08	-4.0	1.8E-20	-4.1	6.2E-20	8.0E-17	NA	
146	cg05958985	ZFPM1	chr16	88558237	-6.3	4.5E-11	-4.9	1.3E-10	-5.2	2.8E-19	-5.4	6.5E-20	8.4E-17	NA	
147	cg08268892	ARID1B	chr6	157131429	-6.7	6.2E-13	-5.2	9.8E-09	-6.1	1.0E-21	-5.9	7.2E-20	9.2E-17	NA	
148	cg03519593	EPX	chr17	56274597	-6.7	2.2E-10	-7.5	5.4E-11	-6.9	2.0E-19	-7.1	8.1E-20	1.0E-16	NA	
149	cg02930951	CEBPB	chr20	48806066	-5.8	4.6E-09	-6.6	2.7E-12	-6.0	2.9E-19	-6.2	8.2E-20	1.0E-16	NA	
150	cg04033850	PRPH	chr12	49695016	-8.1	2.6E-11	-7.2	4.8E-10	-7.5	4.9E-20	-7.7	8.6E-20	1.1E-16	NA	
151	cg02475695	PRR35	chr16	616220	-5.7	1.8E-12	-3.8	1.6E-09	-4.3	7.1E-20	-4.6	9.5E-20	1.2E-16	NA	
152	cg12077460	MFHAS1	chr8	8702053	-6.1	4.3E-14	-3.7	2.5E-08	-4.5	4.9E-20	-4.6	1.0E-19	1.3E-16	NA	
153	cg13221796	LINC00441	chr13	48876919	-5.0	8.1E-10	-4.8	2.4E-11	-4.6	3.4E-19	-4.9	1.2E-19	1.4E-16	-0.5	5
154	cg08462941	PTPRS	chr19	5288631	-5.6	6.9E-11	-4.9	2.5E-10	-4.8	1.5E-17	-5.2	1.2E-19	1.4E-16	NA	
155	cg23090159	VKORC1L1	chr7	65419194	-5.2	8.9E-12	-4.3	1.7E-09	-4.6	6.8E-20	-4.7	1.3E-19	1.6E-16	NA	
156	cg14355482	NCAM2	chr21	22373039	-5.3	5.0E-10	-5.7	4.8E-11	-5.3	3.4E-19	-5.5	1.5E-19	1.8E-16	NA	
157	cg01916918	CLU	chr8	27461199	-7.1	1.6E-10	-8.3	1.4E-10	-7.3	5.5E-19	-7.6	1.7E-19	2.0E-16	NA	
158	cg18891604	ETV7	chr6	36319055	-6.3	5.5E-10	-7.6	3.9E-11	-6.9	2.0E-20	-6.9	1.7E-19	2.0E-16	NA	
159	cg08969102	CDKL3	chr5	133563532	-5.1	4.7E-12	-3.3	1.0E-09	-3.7	5.4E-19	-4.0	1.8E-19	2.1E-16	NA	
160	cg21640749	RAB37	chr17	72709731	-6.6	1.1E-11	-5.8	2.3E-09	-5.9	6.1E-19	-6.2	1.8E-19	2.1E-16	-0.3	3
161	cg08404225	IL5RA	chr3	3151899	-5.4	2.4E-11	-4.7	1.1E-09	-4.8	2.2E-18	-5.1	1.8E-19	2.1E-16	-0.3	2
162	cg17041511	CYB561	chr17	61509620	-5.4	3.1E-10	-6.3	7.9E-11	-5.8	5.2E-20	-5.8	1.8E-19	2.1E-16	NA	
163	cg20317437	FUCA1	chr1	24172120	-6.5	1.2E-10	-7.0	2.7E-10	-6.5	3.5E-19	-6.7	2.0E-19	2.3E-16	NA	
164	cg08886063	VPS53	chr17	600398	-6.9	5.7E-11	-7.3	6.0E-10	-6.9	1.8E-19	-7.1	2.1E-19	2.4E-16	NA	
165	cg04305653	TBC1D22A	chr22	47272422	-5.9	1.5E-11	-4.9	1.9E-09	-5.2	5.1E-19	-5.3	2.3E-19	2.7E-16	NA	
166	cg01464484	LOC100130987	chr11	67089352	-9.8	1.4E-10	-9.7	3.9E-10	-9.4	9.8E-19	-9.7	3.1E-19	3.5E-16	NA	

#	ProbeID	Gene	CHR	Position	PR-GOAL		GALA II		Mega-analysis		Meta-analysis			MRC	
					Eff	Pval	Eff	Pval	Eff	Pval	Eff	Pval	FDR	Coef	
167	cg20328327	VKORC1L1	chr7	65419288	-5.0	1.8E-09	-5.6	2.9E-11	-5.1	2.7E-19	-5.3	3.4E-19	3.8E-16	NA	
168	cg13951007	LOC728989	chr1	146503900	-6.7	1.1E-10	-5.9	4.9E-10	-5.8	1.3E-17	-6.3	3.8E-19	4.3E-16	NA	
169	cg24343524	ZC3H11A	chr1	203763352	-6.0	2.5E-08	-8.5	1.1E-12	-7.0	3.5E-19	-7.1	5.2E-19	5.8E-16	NA	
170	cg27000590	SGK223	chr8	8182003	-5.7	1.1E-08	-5.9	8.9E-12	-5.5	4.3E-18	-5.8	5.9E-19	6.5E-16	NA	
171	cg05499338	CMIP	chr16	81517665	-6.4	4.8E-10	-7.3	1.8E-10	-6.7	3.1E-19	-6.8	5.9E-19	6.5E-16	NA	
172	cg12425700	EPGN	chr4	75186779	-5.9	3.2E-13	-3.7	3.3E-08	-4.5	1.3E-19	-4.6	6.8E-19	7.4E-16	NA	
173	cg00068153	CACNA1S	chr1	201028602	-7.0	6.8E-12	-6.3	1.6E-08	-6.5	2.9E-18	-6.7	6.8E-19	7.4E-16	NA	
174	cg18042632	LINC00323	chr21	42520902	-6.2	1.5E-11	-5.7	7.4E-09	-5.8	2.2E-18	-5.9	6.8E-19	7.4E-16	NA	
175	cg21104363	VKORC1L1	chr7	65419248	-4.4	8.7E-10	-4.2	1.4E-10	-4.1	2.5E-18	-4.3	6.9E-19	7.4E-16	NA	
176	cg15482717	FADD	chr11	70053254	-6.1	4.0E-11	-5.1	2.3E-09	-5.6	6.2E-20	-5.6	7.2E-19	7.7E-16	NA	
177	cg19328051	AFG3L2	chr18	12380944	-7.7	3.7E-10	-7.6	3.5E-10	-7.4	1.2E-18	-7.7	7.5E-19	8.0E-16	NA	
178	cg13774539	DCTN1	chr2	74612706	-5.4	1.4E-10	-4.6	6.9E-10	-4.7	9.1E-18	-5.0	7.6E-19	8.0E-16	NA	
179	cg18805734	FAM60A	chr12	31453901	-5.5	6.9E-11	-5.0	2.1E-09	-5.2	3.1E-19	-5.2	9.1E-19	9.6E-16	NA	
180	cg13209388	ACOT7	chr1	6355060	-3.8	2.8E-11	-3.1	4.0E-09	-3.2	2.0E-17	-3.4	9.4E-19	9.9E-16	NA	
181	cg24058805	PDE4B	chr1	66777579	-8.9	1.6E-11	-6.4	3.7E-09	-7.2	4.2E-19	-7.4	9.8E-19	1.0E-15	NA	
182	cg04986931	MGAT3	chr22	39850128	-6.6	5.7E-12	-4.7	9.4E-09	-5.4	5.9E-19	-5.5	9.9E-19	1.0E-15	NA	
183	cg06725287	FOXK2	chr17	80533762	-6.6	6.8E-10	-7.6	2.1E-10	-6.9	6.6E-19	-7.0	1.0E-18	1.1E-15	NA	
184	cg10704177	INADL	chr1	62209607	-4.9	1.8E-13	-2.8	6.0E-08	-3.6	9.3E-20	-3.6	1.3E-18	1.3E-15	NA	
185	cg02245534	METRNL	chr17	81043668	-8.2	3.1E-17	-3.4	2.3E-06	-4.6	1.7E-17	-5.0	1.3E-18	1.3E-15	NA	
186	cg00986350	ZFPM1	chr16	88540396	-5.1	8.0E-10	-4.6	2.8E-10	-4.4	8.3E-17	-4.8	1.4E-18	1.4E-15	NA	
187	cg01764046	HCRTR1	chr1	32082577	-6.9	1.1E-09	-8.8	1.3E-10	-7.3	1.5E-17	-7.7	1.5E-18	1.5E-15	NA	
188	cg07552087	MLST8	chr16	2258457	-5.6	1.0E-09	-4.2	1.2E-10	-4.4	1.8E-17	-4.7	1.5E-18	1.5E-15	NA	
189	cg02765496	PIP5K1B	chr9	71393662	-7.0	2.6E-11	-5.2	5.9E-09	-5.9	3.2E-19	-6.0	2.0E-18	2.0E-15	NA	
190	cg06597413	MYEOV	chr11	69251883	-6.8	2.8E-13	-3.8	5.0E-08	-4.8	1.4E-19	-4.9	2.0E-18	2.0E-15	NA	
191	cg13458609	ENG	chr9	130608923	-6.1	2.2E-15	-2.8	4.6E-07	-3.8	1.8E-18	-4.0	2.1E-18	2.0E-15	NA	
192	cg08165794	PAK6	chr15	40568143	-7.2	6.1E-10	-6.4	5.8E-10	-6.7	8.5E-19	-6.8	2.3E-18	2.3E-15	NA	
193	cg08435683	SLC23A2	chr20	4836338	-3.6	9.4E-09	-3.0	3.5E-11	-2.9	1.6E-15	-3.2	2.4E-18	2.3E-15	NA	
194	cg15817440	C14orf37	chr14	58599910	-6.1	1.4E-08	-7.1	2.5E-11	-6.5	8.4E-19	-6.6	2.4E-18	2.3E-15	NA	

#	ProbeID	Gene	CHR	Position	PR-GOAL		GALA II		Mega-analysis		Meta-analysis			MRC	
					Eff	Pval	Eff	Pval	Eff	Pval	Eff	Pval	FDR	Coef	
195	cg15456821	BEST1	chr11	61717225	-6.6	1.7E-10	-5.0	1.3E-09	-5.5	1.3E-18	-5.6	2.7E-18	2.6E-15	NA	
196	cg22503106	METRNL	chr17	81040906	-4.1	2.8E-08	-5.4	1.0E-11	-4.6	2.0E-18	-4.7	3.3E-18	3.1E-15	NA	
197	cg03606098	NADK	chr1	1690840	-4.4	7.2E-09	-4.3	8.5E-11	-4.3	4.1E-19	-4.3	3.4E-18	3.3E-15	NA	
198	cg16628205	TFR2	chr7	100240094	-6.9	1.9E-08	-9.1	1.7E-11	-7.5	1.3E-17	-7.9	3.7E-18	3.5E-15	NA	
199	cg06495615	ARID3A	chr19	939731	-4.5	9.3E-07	-6.5	2.9E-13	-5.3	1.2E-17	-5.5	4.7E-18	4.5E-15	NA	
200	cg11668148	CELF6	chr15	72636405	-6.7	2.1E-11	-6.2	3.9E-08	-6.4	6.5E-19	-6.5	4.8E-18	4.5E-15	NA	

<sup>a</sup> Effect size: the parameter in our EWAS models. Effect size = 5 means an increase of 1% methylation beta-value associated with a log<sub>10</sub> scaled total IgE level.

<sup>b</sup> Coefficient: the parameter in Liang et al.'s models. Coefficient = 5 means an increase of 1 inverse normal methylation level associated with a log<sub>10</sub> increase of natural logarithm transformed total IgE level. A comparison between our effect size and this coefficient can be made but not on the magnitude.

**Table E4. Results for the top CpG sites reported in a previous EWAS of total IgE (without allotypes)**

#	ProbelID	Gene	CHR	Position	PR-GOAL		GALA II		Mega-analysis		Meta-analysis			MRC	
					Eff <sup>a</sup>	Pval	Eff	Pval	Eff	Pval	Eff	Pval	FDR	Coef <sup>b</sup>	
1	cg01998785	LPCAT2	chr16	55542709	-5.5	3.9E-13	-6.9	7.2E-19	-5.9	1.3E-29	-6.2	4.5E-30	3.8E-26	-0.6	1.
2	cg03693099	CEL	chr9	135936901	-6.7	1.6E-13	-2.8	3.7E-07	-3.6	9.2E-16	-3.9	2.8E-16	2.0E-13	-0.5	1.
3	cg05215575	SMIM22	chr16	4838722	-6.3	2.8E-10	-4.0	1.0E-06	-4.7	7.1E-14	-5.0	6.5E-15	3.6E-12	-0.4	3.
4	cg08404225	IL5RA	chr3	3151899	-5.4	2.4E-11	-4.7	1.1E-09	-4.8	2.2E-18	-5.1	1.8E-19	2.1E-16	-0.3	2.
5	cg09447105	PDE6H	chr12	15126020	-6.1	1.1E-09	-6.5	8.2E-09	-6.0	2.0E-16	-6.2	5.2E-17	4.2E-14	-0.4	2.
6	cg09676390	SSR4P1	chr21	46493345	-3.2	1.2E-05	-1.9	1.7E-04	-2.2	2.1E-08	-2.3	2.4E-08	4.1E-06	-0.5	1.
7	cg10159529	IL5RA	chr3	3152530	-5.7	6.1E-13	-7.0	9.3E-14	-6.0	1.7E-24	-6.2	6.7E-25	2.0E-21	-0.6	5.
8	cg11398517	GTSF1L	chr20	42355625	-6.4	2.9E-11	-4.0	1.0E-07	-4.6	3.9E-16	-4.9	1.3E-16	9.6E-14	-0.4	2.
9	cg13221796	LINC00441	chr13	48876919	-5.0	8.1E-10	-4.8	2.4E-11	-4.6	3.4E-19	-4.9	1.2E-19	1.4E-16	-0.5	5.
10	cg15357945	PRG2	chr11	57158361	-4.6	5.5E-08	-4.5	5.8E-08	-4.3	1.0E-13	-4.6	1.6E-14	8.5E-12	-0.3	2.
11	cg16050349	PIK3CB	chr3	138478129	-6.7	2.9E-09	-5.1	4.9E-08	-5.9	9.3E-17	-5.8	1.3E-15	8.2E-13	-0.3	4.
12	cg18783781	SLC25A33	chr1	9599067	-6.5	5.2E-13	-5.8	4.2E-09	-6.1	5.2E-21	-6.2	1.5E-20	2.2E-17	-0.6	5.
13	cg21627181	SLC17A4	chr6	25754190	-7.0	2.3E-13	-7.8	6.3E-14	-7.0	2.5E-24	-7.3	1.2E-25	4.0E-22	-0.4	1.
14	cg21631409	ALDH3B2	chr11	67449882	-7.3	7.6E-09	-5.7	2.4E-06	-6.1	4.4E-13	-6.4	1.4E-13	6.2E-11	-0.3	2.
15	cg25494227	TMEM52B	chr12	10331614	-7.3	1.9E-08	-3.3	7.1E-05	-4.4	9.7E-11	-4.5	1.7E-10	4.5E-08	-0.4	1.
16	cg26136776	KLF1	chr19	12998426	-6.6	2.7E-09	-6.0	4.1E-08	-6.0	3.8E-15	-6.3	6.4E-16	4.3E-13	-0.4	3.
17	cg26457013	TMEM86B	chr19	55740188	-7.2	1.1E-13	-5.5	2.0E-09	-5.9	1.3E-20	-6.3	3.2E-21	5.6E-18	-0.5	1.
18	cg26787239	IL4	chr5	132008525	-7.9	5.0E-13	-11.9	3.0E-17	-9.1	6.4E-27	-9.4	1.3E-27	5.8E-24	-0.6	1.

<sup>a</sup> Effect size: the parameter in our EWAS models. Effect size = 5 means an increase of 1% methylation beta-value associated with a log<sub>10</sub> scaled total IgE level.

<sup>b</sup> Coefficient: the parameter in Liang et al.'s models. Coefficient = 5 means an increase of 1 inverse normal methylation level associated with a 1 unit increase of natural logarithm transformed total IgE level. A comparison between our effect size and this coefficient can be made but not on the magnitude.

**Table E5. Results for the top 200 CpG sites in the meta-analysis of PR-GOAL and GALA II, a types**

#	ProbelD	Gene	CHR	Position	PR-GOAL		GALA II		Mega-analysis		Meta-analysis			Coe
					Eff <sup>a</sup>	Pval	Eff	Pval	Eff	Pval	Eff	Pval	FDR	
1	cg04983687	ZFPM1	chr16	88558223	-5.3	4.7E-07	-3.8	3.6E-07	-4.2	8.2E-13	-4.3	1.5E-12	2.9E-07	NA
2	cg09249800	ACOT7	chr1	6341287	-6.8	5.3E-08	-6.1	1.1E-04	-5.9	5.2E-10	-6.5	2.6E-11	2.4E-06	NA
3	cg12614529	MND1	chr4	154269418	-5.2	7.4E-05	-4.7	4.4E-06	-4.6	5.2E-09	-4.9	1.4E-09	8.8E-05	NA
4	cg21220721	ACOT7	chr1	6341230	-5.3	1.3E-07	-1.8	1.9E-03	-2.7	6.7E-08	-2.7	8.5E-08	4.0E-03	NA
5	cg12227660	MIR202	chr10	135061670	-4.3	1.2E-03	-3.9	9.2E-05	-3.9	2.9E-07	-4.0	4.0E-07	1.5E-02	NA
6	cg11699125	ACOT7	chr1	6341327	-5.8	5.3E-06	-3.2	1.4E-02	-3.8	2.2E-05	-4.5	6.7E-07	1.9E-02	NA
7	cg01000631	EVL	chr14	100610667	-4.6	1.7E-04	-3.9	1.1E-03	-3.0	1.7E-04	-4.2	7.0E-07	1.9E-02	NA
8	cg08940169	ZFPM1	chr16	88540241	-5.5	8.4E-05	-4.1	4.1E-03	-4.6	2.0E-06	-4.8	1.4E-06	3.4E-02	NA
9	cg01458054	HELZ2	chr20	62200603	-3.3	2.7E-03	-3.0	1.8E-04	-2.8	7.1E-06	-3.1	1.7E-06	3.5E-02	NA
10	cg15017119	SPRY2	chr13	82585793	-4.8	7.0E-05	-3.0	5.5E-03	-3.4	1.4E-05	-3.8	2.5E-06	4.1E-02	NA
11	cg00405825	HIPK2	chr7	139474807	4.1	2.8E-03	3.4	2.5E-04	3.6	1.3E-06	3.6	2.5E-06	4.1E-02	NA
12	cg25087851	PTGDR2	chr11	60623918	-4.4	2.4E-03	-4.3	3.3E-04	-4.1	5.5E-06	-4.4	2.6E-06	4.1E-02	NA
13	cg12103951	WAPL	chr10	88162314	0.8	7.0E-02	1.3	1.2E-05	0.8	3.0E-04	1.1	3.6E-06	5.1E-02	NA
14	cg12427941	TJAP1	chr6	43457177	5.4	7.9E-03	4.6	3.1E-04	3.7	3.4E-04	4.8	8.0E-06	1.1E-01	NA
15	cg06623197	MTMR3	chr22	30400763	3.0	5.2E-03	1.6	3.6E-04	1.4	7.7E-04	1.9	1.2E-05	1.5E-01	NA
16	cg12296550	HLA-DQB2	chr6	32728862	0.5	5.9E-02	0.9	4.8E-05	0.8	1.6E-06	0.8	1.3E-05	1.5E-01	NA
17	cg15700636	PRG2	chr11	57156050	-5.6	9.8E-04	-4.4	4.1E-03	-4.5	4.7E-05	-4.9	1.4E-05	1.6E-01	NA
18	cg13074835	NFKBIL1	chr6	31515196	-2.0	1.2E-01	-3.3	3.7E-05	-2.6	7.8E-05	-3.0	1.5E-05	1.6E-01	NA
19	cg15492834	C1orf226	chr1	162351057	-5.3	1.5E-03	-3.1	1.8E-03	-3.6	1.6E-05	-3.7	1.7E-05	1.6E-01	NA
20	cg20481287	ETV6	chr12	12224457	-2.1	3.7E-02	-2.6	2.0E-04	-1.8	9.9E-04	-2.4	2.1E-05	2.0E-01	NA
21	cg23172671	OPTC	chr1	203482523	1.8	2.4E-02	2.0	3.7E-04	1.7	1.8E-04	2.0	2.5E-05	2.2E-01	NA
22	cg16192821	IQSEC1	chr3	13028642	5.9	6.1E-03	2.7	4.9E-04	2.0	3.0E-03	3.1	2.6E-05	2.2E-01	NA
23	cg02864638	CCDC144NL	chr17	20840716	5.3	3.5E-03	3.4	1.7E-03	2.8	1.2E-03	3.9	2.8E-05	2.3E-01	NA
24	cg07562835	ITGB4	chr17	73734756	-4.1	8.2E-03	-3.7	1.3E-03	-3.3	2.4E-04	-3.8	3.3E-05	2.5E-01	NA
25	cg17306339	ATP6V0A2	chr12	124198578	-3.0	1.7E-03	-2.2	5.2E-03	-2.2	1.6E-04	-2.5	3.5E-05	2.5E-01	NA
26	cg04038179	MIR129-1	chr7	127806902	2.4	4.8E-01	9.1	1.0E-05	6.9	4.9E-05	7.2	3.6E-05	2.5E-01	NA

#	ProbeID	Gene	CHR	Position	PR-GOAL		GALA II		Mega-analysis		Meta-analysis			Co
					Eff	Pval	Eff	Pval	Eff	Pval	Eff	Pval	FDR	
27	cg02901006	CCL25	chr19	8117024	-1.6	1.1E-02	-1.1	9.6E-04	-0.9	1.1E-03	-1.2	3.6E-05	2.5E-01	NA
28	cg24491618	KCNH2	chr7	150649807	-4.4	1.7E-03	-3.9	7.1E-03	-3.1	1.2E-03	-4.1	3.8E-05	2.5E-01	NA
29	cg26547058	SLC45A4	chr8	142243143	-4.2	4.6E-03	-3.4	2.5E-03	-3.7	2.0E-05	-3.7	3.8E-05	2.5E-01	NA
30	cg09435190	TYMP	chr22	50968297	1.7	1.4E-02	1.6	1.0E-03	1.4	3.1E-04	1.6	4.2E-05	2.6E-01	NA
31	cg10296973	HLA-DOA	chr6	32967930	1.3	7.4E-03	0.8	1.1E-03	0.8	2.5E-05	0.9	4.2E-05	2.6E-01	NA
32	cg27659557	OR10G2	chr14	22111727	2.6	4.2E-02	3.7	3.2E-04	2.8	3.8E-04	3.2	4.5E-05	2.7E-01	NA
33	cg26925644	PHLDB1	chr11	118476517	3.1	1.0E-01	5.7	1.1E-04	4.2	2.2E-04	4.7	5.0E-05	2.8E-01	NA
34	cg08882027	MYEOV	chr11	69299509	-4.6	2.2E-03	-3.1	5.6E-03	-3.0	6.7E-04	-3.7	5.1E-05	2.8E-01	NA
35	cg01758512	FUT9	chr6	96463902	4.7	8.2E-03	4.3	2.3E-03	3.5	9.4E-04	4.4	5.6E-05	3.0E-01	NA
36	cg06647928	ENC1	chr5	73612203	-3.1	9.2E-03	-2.5	2.4E-03	-2.0	2.1E-03	-2.7	7.0E-05	3.6E-01	NA
37	cg03726147	DMAP1	chr1	44686022	3.2	2.6E-02	3.0	1.1E-03	2.2	2.8E-03	3.1	7.5E-05	3.7E-01	NA
38	cg08682334	WDR24	chr16	737214	3.2	4.9E-02	3.6	5.8E-04	2.7	1.2E-03	3.5	7.5E-05	3.7E-01	NA
39	cg11725581	USP42	chr7	6140990	1.6	1.2E-02	1.4	2.2E-03	1.2	1.1E-03	1.5	7.8E-05	3.7E-01	NA
40	cg10592478	RARG	chr12	53612641	4.9	2.6E-03	2.7	5.1E-03	2.1	6.5E-03	3.3	7.8E-05	3.7E-01	NA
41	cg25939647	GPR176	chr15	40173065	-4.5	3.7E-04	-2.4	3.6E-02	-2.6	1.5E-03	-3.4	8.2E-05	3.7E-01	NA
42	cg03760919	RUNX1T1	chr8	93103361	-3.4	2.4E-02	-4.0	1.3E-03	-3.1	8.6E-04	-3.8	8.5E-05	3.7E-01	NA
43	cg02985445	BRI3	chr7	97908505	-5.0	8.0E-04	-2.8	1.8E-02	-3.3	1.5E-04	-3.6	8.6E-05	3.7E-01	NA
44	cg25390635	GRAMD4	chr22	47022618	2.2	1.0E-01	4.0	1.9E-04	2.5	1.8E-03	3.3	8.7E-05	3.7E-01	NA
45	cg01401641	TSHZ3	chr19	31839171	-1.4	8.7E-02	-2.0	4.1E-04	-1.7	1.2E-04	-1.8	1.0E-04	4.1E-01	NA
46	cg15361231	GLRX2	chr1	193075191	0.6	4.4E-01	3.3	6.4E-06	1.5	3.7E-03	2.1	1.1E-04	4.1E-01	-0.2
47	cg14799488	MIR4456	chr5	537809	-0.2	4.5E-01	-0.8	4.5E-05	-0.5	1.6E-03	-0.6	1.1E-04	4.1E-01	NA
48	cg05941652	LAMA3	chr18	21273909	2.1	1.3E-01	4.0	2.1E-04	2.7	7.2E-04	3.3	1.1E-04	4.1E-01	NA
49	cg14003143	SGK2	chr20	42194975	-4.5	2.5E-03	-2.6	8.5E-03	-2.9	4.3E-04	-3.2	1.2E-04	4.1E-01	NA
50	cg18451484	HECTD4	chr12	112760326	3.1	7.8E-02	3.3	6.1E-04	1.8	1.2E-02	3.2	1.2E-04	4.1E-01	NA
51	cg11286405	SNORD115-17	chr15	25451255	-4.4	3.2E-04	-1.9	3.3E-02	-2.5	4.2E-04	-2.8	1.2E-04	4.1E-01	NA
52	cg03342543	KIF1A	chr2	241715115	-2.2	1.6E-01	-4.8	1.5E-04	-3.0	1.4E-03	-3.8	1.3E-04	4.1E-01	NA
53	cg17460285	PSME3	chr17	40985453	2.0	1.3E-02	1.9	3.5E-03	1.5	1.8E-03	2.0	1.3E-04	4.1E-01	NA
54	cg15827086	PPP2CA	chr5	133560225	-0.5	7.3E-01	-2.8	4.6E-05	-2.1	3.4E-04	-2.4	1.3E-04	4.1E-01	NA



#	ProbeID	Gene	CHR	Position	PR-GOAL		GALA II		Mega-analysis		Meta-analysis			Coef
					Eff	Pval	Eff	Pval	Eff	Pval	Eff	Pval	FDR	
55	cg18552413	ACKR1	chr1	159174610	-2.6	6.4E-03	-2.0	6.5E-03	-1.0	4.0E-02	-2.2	1.3E-04	4.1E-01	0.0
56	cg03582047	GLP2R	chr17	9729235	2.1	5.9E-02	2.6	8.6E-04	2.0	1.3E-03	2.5	1.4E-04	4.1E-01	NA
57	cg16691158	PSD2	chr5	139140550	-2.7	2.0E-02	-2.7	2.6E-03	-1.9	6.4E-03	-2.7	1.4E-04	4.1E-01	NA
58	cg04071964	ADGRG7	chr3	100328745	-1.8	2.7E-02	-1.7	1.9E-03	-1.4	1.4E-03	-1.7	1.4E-04	4.1E-01	NA
59	cg23706836	MCPH1	chr8	6407997	-2.9	5.3E-03	-2.6	9.4E-03	-2.6	2.3E-04	-2.8	1.4E-04	4.1E-01	NA
60	cg00451113	PRR23A	chr3	138722221	2.9	8.7E-02	4.1	5.8E-04	3.3	4.7E-04	3.7	1.4E-04	4.1E-01	NA
61	cg09022430	MSH2	chr2	47800047	-6.2	2.8E-04	-2.7	5.4E-02	-3.3	1.7E-03	-4.1	1.5E-04	4.1E-01	NA
62	cg05465955	COASY	chr17	40715236	-2.5	1.7E-02	-2.2	3.0E-03	-2.1	1.8E-04	-2.3	1.5E-04	4.1E-01	NA
63	cg03841312	MIRLET7BHG	chr22	46508486	2.0	2.5E-01	5.1	1.1E-04	3.7	3.0E-04	4.0	1.5E-04	4.1E-01	NA
64	cg09360654	TOE1	chr1	45806501	-2.2	1.5E-01	-3.5	3.7E-04	-2.7	6.5E-04	-3.1	1.5E-04	4.1E-01	0.0
65	cg16004593	BTNL2	chr6	32369487	0.6	1.2E-01	0.8	5.0E-04	0.7	3.0E-05	0.7	1.6E-04	4.1E-01	NA
66	cg02800100	AUTS2	chr7	69110945	-2.0	3.1E-02	-2.1	1.9E-03	-1.8	5.4E-04	-2.1	1.6E-04	4.1E-01	NA
67	cg14540650	KDM4C	chr9	6683274	-1.9	2.3E-02	-1.6	2.5E-03	-1.3	1.7E-03	-1.7	1.6E-04	4.1E-01	NA
68	cg24680570	SIPA1L2	chr1	232726838	-2.0	1.3E-01	-3.1	4.3E-04	-2.1	2.5E-03	-2.8	1.7E-04	4.1E-01	NA
69	cg11168614	LOC283585	chr14	87179368	0.6	4.3E-01	2.9	9.2E-06	1.4	3.4E-03	1.8	1.7E-04	4.1E-01	NA
70	cg20314918	SCN2A	chr2	166151447	-1.7	4.8E-02	-2.0	1.3E-03	-1.8	3.1E-04	-1.9	1.7E-04	4.1E-01	NA
71	cg26055446	B3GALT4	chr6	33245990	-3.2	1.2E-02	-2.6	4.9E-03	-2.2	1.6E-03	-2.8	1.8E-04	4.1E-01	NA
72	cg09677763	NUP98	chr11	3817793	-0.6	4.4E-01	-2.0	5.5E-05	-1.3	8.7E-04	-1.5	1.8E-04	4.1E-01	NA
73	cg10142874	LPIN1	chr2	11917623	-4.5	3.5E-03	-3.1	1.4E-02	-3.5	3.0E-04	-3.6	1.8E-04	4.1E-01	NA
74	cg03661164	EZH2	chr7	148560646	-2.9	5.5E-03	-2.3	1.0E-02	-1.9	3.9E-03	-2.6	1.8E-04	4.1E-01	NA
75	cg25546539	TPP1	chr11	6640996	1.3	2.2E-01	2.9	1.7E-04	1.6	4.7E-03	2.3	1.8E-04	4.1E-01	NA
76	cg01047555	SOGA3	chr6	127835990	3.0	6.4E-02	2.9	1.1E-03	1.9	9.4E-03	2.9	1.8E-04	4.1E-01	NA
77	cg08435683	SLC23A2	chr20	4836338	-1.5	7.4E-02	-1.9	9.5E-04	-1.3	3.7E-03	-1.8	1.8E-04	4.1E-01	NA
78	cg19914919	TANK	chr2	161992878	-0.9	3.6E-01	-2.1	1.5E-04	-1.2	9.1E-03	-1.8	1.8E-04	4.1E-01	NA
79	cg05400869	S100A7L2	chr1	153413932	3.3	6.0E-03	1.8	6.0E-03	1.6	4.7E-03	2.2	1.9E-04	4.1E-01	NA
80	cg14531564	SDF4	chr1	1154853	-1.8	8.7E-02	-2.4	8.0E-04	-1.6	3.8E-03	-2.2	1.9E-04	4.1E-01	NA
81	cg15437528	GPRC5C	chr17	72427628	-5.4	1.2E-01	-6.5	6.9E-04	-6.2	1.7E-04	-6.3	1.9E-04	4.1E-01	NA
82	cg18184910	ADGRF2	chr6	47624247	1.5	2.4E-01	2.0	3.7E-04	1.2	7.3E-03	1.9	1.9E-04	4.1E-01	NA

#	ProbeID	Gene	CHR	Position	PR-GOAL		GALA II		Mega-analysis		Meta-analysis			Coef
					Eff	Pval	Eff	Pval	Eff	Pval	Eff	Pval	FDR	
83	cg20080245	OLMALINC	chr10	102137421	3.2	1.6E-01	4.1	5.2E-04	4.0	1.3E-04	3.9	2.0E-04	4.1E-01	NA
84	cg20320283	FOXE3	chr1	47880440	-2.3	5.9E-02	-2.7	1.3E-03	-1.7	1.2E-02	-2.6	2.0E-04	4.1E-01	NA
85	cg02190383	BEST1	chr11	61725666	-4.5	9.4E-03	-3.8	7.2E-03	-3.6	7.3E-04	-4.1	2.0E-04	4.1E-01	NA
86	cg19312305	MIR122	chr18	56117016	-2.6	2.0E-02	-2.5	3.6E-03	-2.2	7.9E-04	-2.6	2.0E-04	4.1E-01	NA
87	cg10288525	LINC00423	chr13	33455187	4.0	6.6E-04	1.6	2.1E-02	2.0	8.1E-04	2.2	2.0E-04	4.1E-01	NA
88	cg03550384	TMEM64	chr8	91803357	-1.4	1.1E-01	-1.5	7.6E-04	-1.2	1.7E-03	-1.5	2.0E-04	4.1E-01	NA
89	cg17713161	HID1	chr17	72951370	-2.1	7.0E-02	-1.9	1.2E-03	-1.6	1.5E-03	-1.9	2.0E-04	4.1E-01	NA
90	cg21054521	SOX1	chr13	112759386	5.0	3.4E-02	4.8	2.3E-03	3.0	1.7E-02	4.8	2.0E-04	4.1E-01	NA
91	cg01649647	MYL9	chr20	35177530	-5.5	5.7E-04	-2.4	3.7E-02	-3.3	3.0E-04	-3.5	2.1E-04	4.1E-01	NA
92	cg01721149	C1orf61	chr1	156394727	2.4	2.2E-02	2.0	3.3E-03	1.8	1.6E-03	2.1	2.1E-04	4.1E-01	NA
93	cg21045547	SOGA1	chr20	35422703	-3.3	2.8E-02	-4.9	2.2E-03	-3.4	1.4E-03	-4.1	2.1E-04	4.1E-01	NA
94	cg04512965	RFX2	chr19	6038846	-2.3	1.7E-02	-1.9	4.4E-03	-1.6	3.4E-03	-2.0	2.1E-04	4.1E-01	NA
95	cg04420917	LGALS4	chr19	39303993	-3.0	2.9E-02	-3.6	2.6E-03	-2.9	9.7E-04	-3.4	2.1E-04	4.1E-01	NA
96	cg16734734	POPDC3	chr6	105624309	-4.5	6.9E-03	-3.4	9.9E-03	-4.0	5.5E-05	-3.9	2.1E-04	4.1E-01	NA
97	cg01520924	HSPA2	chr14	65006170	-0.6	7.8E-01	-5.0	4.7E-05	-4.0	1.5E-04	-4.0	2.2E-04	4.1E-01	-0.1
98	cg13645296	DAPK2	chr15	64275810	-4.7	1.2E-03	-2.3	2.7E-02	-3.2	6.6E-05	-3.1	2.2E-04	4.1E-01	NA
99	cg08889930	MCM2	chr3	127317798	-3.9	8.6E-03	-3.3	9.1E-03	-3.1	1.0E-03	-3.6	2.2E-04	4.1E-01	NA
100	cg20774552	AMBRA1	chr11	46415316	-3.0	3.6E-02	-3.1	2.4E-03	-1.9	1.7E-02	-3.1	2.2E-04	4.1E-01	NA
101	cg20752847	DNAH10	chr12	124248044	2.4	2.6E-02	2.1	3.2E-03	1.6	4.5E-03	2.2	2.2E-04	4.1E-01	NA
102	cg11393173	NHLH2	chr1	116369577	-2.4	1.8E-02	-2.2	4.5E-03	-1.5	8.1E-03	-2.2	2.2E-04	4.1E-01	NA
103	cg25052121	BFSP1	chr20	17539745	3.9	4.5E-03	2.3	1.1E-02	2.1	3.7E-03	2.8	2.2E-04	4.1E-01	NA
104	cg17972162	APOBEC3H	chr22	39496387	-1.9	3.7E-02	-1.9	2.4E-03	-1.5	3.3E-03	-1.9	2.3E-04	4.1E-01	NA
105	cg16190888	ANTXR1	chr2	69428235	-1.8	2.4E-02	-1.6	3.6E-03	-1.4	9.2E-04	-1.7	2.3E-04	4.2E-01	NA
106	cg04821026	POTED	chr21	15068553	2.1	2.2E-02	2.0	4.1E-03	1.7	1.6E-03	2.0	2.4E-04	4.3E-01	NA
107	cg18224977	MIR4417	chr1	5398602	2.5	2.2E-01	4.2	4.1E-04	2.7	6.6E-03	3.7	2.4E-04	4.3E-01	NA
108	cg08654091	PSEN2	chr1	227015418	1.7	3.3E-02	1.7	3.0E-03	1.2	6.3E-03	1.7	2.6E-04	4.4E-01	NA
109	cg26821293	FAM83C	chr20	33880930	-2.6	6.5E-02	-4.2	1.1E-03	-2.9	2.1E-03	-3.5	2.6E-04	4.4E-01	NA
110	cg16815882	KIAA0319L	chr1	35908609	1.5	7.1E-02	2.4	1.1E-03	1.6	1.8E-03	2.0	2.6E-04	4.4E-01	NA

#	ProbeID	Gene	CHR	Position	PR-GOAL		GALA II		Mega-analysis		Meta-analysis			Coe
					Eff	Pval	Eff	Pval	Eff	Pval	Eff	Pval	FDR	
111	cg08187736	IMPAD1	chr8	57912015	3.6	5.7E-03	1.9	8.6E-03	1.7	6.2E-03	2.3	2.7E-04	4.4E-01	NA
112	cg27455540	NT5C1B-RDH14	chr2	18866125	-3.2	6.6E-03	-2.1	1.1E-02	-2.2	8.2E-04	-2.5	2.7E-04	4.4E-01	NA
113	cg02654940	HMGA1	chr6	34206400	-2.3	7.3E-02	-2.8	1.4E-03	-2.5	3.9E-04	-2.6	2.7E-04	4.4E-01	NA
114	cg27121267	CHEK1	chr11	125544292	-1.0	4.1E-01	-3.1	1.5E-04	-1.8	6.5E-03	-2.5	2.7E-04	4.4E-01	NA
115	cg16570273	LINC01257	chr12	131647128	8.0	3.4E-05	2.1	2.0E-01	3.9	1.3E-03	4.5	2.7E-04	4.4E-01	NA
116	cg25366315	BTNL3	chr5	180408809	0.7	2.7E-02	0.5	3.1E-03	0.4	5.4E-03	0.5	2.7E-04	4.4E-01	NA
117	cg11725415	PCGF3	chr4	736485	-2.4	4.8E-07	-0.2	6.3E-01	-0.9	2.6E-03	-1.1	2.7E-04	4.4E-01	NA
118	cg13450944	LRIG1	chr3	66533056	2.4	9.1E-02	3.3	1.1E-03	2.4	2.8E-03	3.0	2.8E-04	4.5E-01	NA
119	cg25332499	BATF2	chr11	64756382	-2.7	1.5E-02	-2.2	6.3E-03	-1.8	2.7E-03	-2.3	2.8E-04	4.5E-01	NA
120	cg20985980	RCC1	chr1	28832113	1.2	3.5E-02	1.6	2.7E-03	1.3	4.5E-04	1.4	2.8E-04	4.5E-01	NA
121	cg21982924	NFKBIL1	chr6	31516059	2.5	8.0E-02	3.4	1.3E-03	2.8	5.1E-04	3.0	2.9E-04	4.6E-01	NA
122	cg08794157	PMP22	chr17	15164627	5.7	3.0E-03	2.9	1.5E-02	2.8	3.1E-03	3.6	3.0E-04	4.6E-01	NA
123	cg06121808	SLC20A1	chr2	113404678	-0.4	6.4E-01	-2.5	6.2E-05	-1.8	3.1E-04	-1.8	3.1E-04	4.7E-01	NA
124	cg00522451	CKAP2L	chr2	113464048	-0.4	7.1E-01	-2.2	1.1E-04	-1.4	4.0E-03	-1.8	3.1E-04	4.7E-01	NA
125	cg17814758	HCN1	chr5	45192536	-3.0	6.5E-03	-2.0	1.4E-02	-2.1	1.0E-03	-2.3	3.2E-04	4.8E-01	NA
126	cg03751829	ZNF99	chr19	22988136	3.2	2.2E-03	1.7	2.7E-02	2.0	9.4E-04	2.2	3.2E-04	4.8E-01	NA
127	cg20717123	P2RX2	chr12	133195520	2.4	2.1E-01	5.2	3.7E-04	3.6	1.6E-03	4.2	3.2E-04	4.8E-01	NA
128	cg19178479	MIR4435-2HG	chr2	112124118	2.4	2.7E-02	2.0	4.3E-03	1.6	4.9E-03	2.1	3.3E-04	4.8E-01	NA
129	cg01688202	SPATA2	chr20	48526714	1.7	9.9E-05	0.5	7.7E-02	0.9	1.2E-04	0.8	3.3E-04	4.8E-01	NA
130	cg26430023	TENM4	chr11	79147209	1.9	6.6E-02	2.6	1.7E-03	1.6	1.0E-02	2.3	3.3E-04	4.8E-01	NA
131	cg13499318	LOC401557	chr9	138154185	-0.8	3.5E-04	-0.3	5.8E-02	-0.4	4.6E-04	-0.5	3.4E-04	4.8E-01	NA
132	cg15590133	IPW	chr15	25338219	-1.2	3.2E-01	-3.1	2.1E-04	-2.2	9.4E-04	-2.5	3.4E-04	4.8E-01	NA
133	cg13978347	ASTN2	chr9	120140243	-2.7	1.4E-01	0.4	2.4E-04	0.4	8.6E-04	0.4	3.5E-04	4.8E-01	NA
134	cg25308381	TEX36-AS1	chr10	127262851	-3.1	2.0E-02	-2.3	5.8E-03	-2.3	7.6E-04	-2.5	3.5E-04	4.8E-01	NA
135	cg08335767	HMGA1	chr6	34206495	-3.9	2.7E-02	-3.3	4.8E-03	-2.9	2.3E-03	-3.5	3.5E-04	4.8E-01	NA
136	cg06379340	UNC80	chr2	210863849	4.5	2.8E-03	2.3	2.0E-02	2.7	7.4E-04	2.9	3.5E-04	4.8E-01	NA
137	cg01973410	BTNL3	chr5	180408813	1.0	1.4E-02	0.7	7.7E-03	0.6	4.1E-03	0.8	3.5E-04	4.8E-01	NA
138	cg15756319	ATP11AUN	chr13	113296447	1.4	1.3E-02	1.3	1.0E-02	1.3	7.9E-04	1.4	3.5E-04	4.8E-01	NA

#	ProbeID	Gene	CHR	Position	PR-GOAL		GALA II		Mega-analysis		Meta-analysis			Coe
					Eff	Pval	Eff	Pval	Eff	Pval	Eff	Pval	FDR	
139	cg26229990	ADCY4	chr14	24801301	-2.3	6.1E-06	-0.4	3.2E-01	-1.0	8.4E-04	-1.1	3.6E-04	4.8E-01	NA
140	cg01709551	ADGRA1	chr10	134892649	1.1	1.4E-01	3.2	2.0E-04	1.8	1.3E-03	2.1	3.6E-04	4.8E-01	NA
141	cg22387550	KPRP	chr1	152733337	2.1	3.2E-01	3.9	4.6E-04	3.1	1.3E-03	3.5	3.6E-04	4.8E-01	NA
142	cg06659727	COL4A1	chr13	110959428	4.4	6.4E-02	4.3	2.3E-03	3.7	1.7E-03	4.4	3.6E-04	4.8E-01	NA
143	cg09862509	IER5	chr1	181069576	-4.3	8.6E-03	-3.2	1.4E-02	-4.0	5.3E-05	-3.6	3.7E-04	4.8E-01	NA
144	cg21521758	RARRES2	chr7	150036287	-3.3	1.7E-02	-2.7	7.5E-03	-2.2	5.3E-03	-2.9	3.7E-04	4.8E-01	NA
145	cg00776252	SYT17	chr16	19178699	2.4	1.1E-03	1.3	7.3E-02	1.6	7.5E-04	1.8	3.7E-04	4.8E-01	NA
146	cg23147443	KCNH2	chr7	150649655	-3.8	3.7E-04	-1.6	1.3E-01	-2.4	1.1E-03	-2.7	3.8E-04	4.8E-01	NA
147	cg07102229	SLC38A4	chr12	47219958	1.1	4.0E-02	1.1	3.7E-03	0.9	5.9E-03	1.1	3.8E-04	4.8E-01	NA
148	cg17327828	SNORD114-12	chr14	101435254	1.2	1.9E-02	0.7	5.2E-03	0.9	7.5E-05	0.8	3.8E-04	4.8E-01	NA
149	cg19851574	RPS6KA2	chr6	167178233	-1.4	1.7E-02	-1.2	8.2E-03	-1.2	4.1E-04	-1.3	3.8E-04	4.8E-01	NA
150	cg01383911	TRIM39	chr6	30297627	-0.8	2.9E-01	-2.4	1.9E-04	-1.5	2.0E-03	-1.8	3.8E-04	4.8E-01	NA
151	cg07757885	PARP8	chr5	50219072	2.3	5.6E-02	2.8	2.6E-03	2.6	2.7E-04	2.6	3.9E-04	4.8E-01	NA
152	cg06399596	FOXC1	chr6	1595676	-1.9	1.1E-02	-1.4	1.2E-02	-1.5	5.0E-04	-1.6	3.9E-04	4.8E-01	NA
153	cg12911256	RNF207	chr1	6265879	-2.3	1.6E-01	-3.9	8.4E-04	-2.6	4.8E-03	-3.4	4.0E-04	4.9E-01	NA
154	cg04293489	DEFB114	chr6	49917881	2.8	4.6E-02	3.8	2.9E-03	3.5	1.2E-04	3.4	4.0E-04	4.9E-01	NA
155	cg12797771	NME7	chr1	169103812	2.7	1.4E-01	3.0	1.3E-03	2.5	1.7E-03	3.0	4.0E-04	4.9E-01	NA
156	cg10919522	ELMSAN1	chr14	74227441	-2.1	1.2E-02	-1.4	1.0E-02	-1.4	2.2E-03	-1.6	4.1E-04	4.9E-01	NA
157	cg16036046	RIT2	chr18	40696164	3.1	3.8E-02	3.7	4.1E-03	2.9	2.2E-03	3.5	4.2E-04	4.9E-01	NA
158	cg10633040	ZNF366	chr5	71915686	-2.0	2.9E-02	-2.1	5.5E-03	-2.0	5.7E-04	-2.1	4.2E-04	4.9E-01	NA
159	cg18775542	STAM	chr10	17682215	5.1	9.2E-05	1.5	1.9E-01	2.2	7.3E-03	3.0	4.2E-04	4.9E-01	NA
160	cg11350504	TUBGCP3	chr13	113121280	0.7	5.6E-01	2.6	1.8E-04	1.6	7.0E-03	2.1	4.3E-04	4.9E-01	NA
161	cg03757017	CYP4F2	chr19	16013630	-3.5	5.7E-02	-4.1	3.0E-03	-3.7	4.8E-04	-3.9	4.3E-04	4.9E-01	NA
162	cg16447058	DAPK2	chr15	64231444	5.6	8.3E-03	3.8	1.5E-02	3.3	5.8E-03	4.4	4.3E-04	4.9E-01	NA
163	cg03169472	B3GALT4	chr6	33246008	-2.6	6.2E-02	-3.2	2.7E-03	-2.4	3.4E-03	-3.0	4.3E-04	4.9E-01	NA
164	cg20126106	TAGLN3	chr3	111718135	2.4	1.8E-01	5.0	5.7E-04	3.4	2.0E-03	4.0	4.3E-04	4.9E-01	0.0
165	cg13460073	SFXN3	chr10	102800939	-1.4	1.5E-01	-2.2	1.0E-03	-1.8	8.2E-04	-1.9	4.4E-04	4.9E-01	NA
166	cg05696877	IFI44L	chr1	79088769	-0.4	4.2E-01	-1.4	1.9E-04	-0.9	2.1E-03	-1.1	4.4E-04	4.9E-01	NA

#	ProbeID	Gene	CHR	Position	PR-GOAL		GALA II		Mega-analysis		Meta-analysis			Coe
					Eff	Pval	Eff	Pval	Eff	Pval	Eff	Pval	FDR	
167	cg26331243	CCDC33	chr15	74550946	-4.1	2.8E-03	-2.4	3.7E-02	-2.6	2.4E-03	-3.1	4.4E-04	4.9E-01	NA
168	cg04290133	GUSB	chr7	65439512	-2.8	6.0E-02	-5.0	1.8E-03	-2.8	6.7E-03	-3.8	4.5E-04	4.9E-01	NA
169	cg10162659	ZFH3	chr16	73068480	-1.5	1.2E-01	-1.9	1.4E-03	-1.6	1.4E-03	-1.8	4.5E-04	4.9E-01	NA
170	cg02826233	CDK2	chr12	56365894	-5.0	1.4E-03	-2.6	6.5E-02	-3.5	4.4E-04	-3.6	4.5E-04	4.9E-01	NA
171	cg00742898	ADAMTSL2	chr9	136431882	4.8	1.0E-03	1.8	2.8E-02	2.1	1.9E-03	2.5	4.5E-04	4.9E-01	NA
172	cg27598761	DIP2C	chr10	537128	2.5	1.6E-02	1.7	8.7E-03	1.7	1.2E-03	1.9	4.5E-04	4.9E-01	NA
173	cg04039397	CD96	chr3	111260783	-0.6	3.3E-01	-1.5	2.8E-04	-1.1	1.2E-03	-1.2	4.5E-04	4.9E-01	0.1
174	cg19718771	C18orf42	chr18	5195201	-2.8	7.6E-02	-4.0	2.0E-03	-3.4	3.9E-04	-3.5	4.5E-04	4.9E-01	NA
175	cg14457074	BTNL3	chr5	180408785	0.7	2.7E-02	0.6	6.3E-03	0.5	7.7E-03	0.7	4.5E-04	4.9E-01	NA
176	cg16618104	CHST11	chr12	104853100	-2.4	1.5E-02	-1.4	7.8E-03	-1.4	1.9E-03	-1.7	4.6E-04	4.9E-01	NA
177	cg15481493	CD44	chr11	35133274	1.7	2.7E-02	2.4	5.5E-03	1.8	1.3E-03	2.0	4.6E-04	4.9E-01	NA
178	cg23155911	3-Mar	chr5	126205009	2.4	9.7E-02	2.8	2.0E-03	2.5	6.2E-04	2.7	4.7E-04	4.9E-01	NA
179	cg19951409	ZNF516	chr18	74175071	4.0	3.7E-02	3.6	4.9E-03	3.2	2.1E-03	3.7	4.7E-04	4.9E-01	NA
180	cg23892310	TBCD	chr17	80816702	3.1	3.8E-02	2.0	3.8E-03	1.5	1.1E-02	2.2	4.7E-04	4.9E-01	NA
181	cg13068215	FMN2	chr1	240286481	1.9	1.7E-01	2.8	1.1E-03	2.0	4.9E-03	2.5	4.7E-04	4.9E-01	NA
182	cg27179101	NCOR2	chr12	124991139	2.2	2.9E-02	2.2	6.3E-03	2.0	1.1E-03	2.2	4.8E-04	4.9E-01	NA
183	cg22715764	PEX14	chr1	10556294	1.3	1.4E-01	1.6	1.5E-03	1.3	1.5E-03	1.5	4.8E-04	4.9E-01	NA
184	cg05218678	ENPP4	chr6	46081541	-2.6	8.5E-03	-1.9	1.9E-02	-1.9	1.6E-03	-2.2	4.9E-04	5.0E-01	NA
185	cg00225830	SHISA9	chr16	13214589	1.3	2.9E-01	3.4	3.1E-04	2.1	4.3E-03	2.6	4.9E-04	5.0E-01	NA
186	cg05442111	NAALAD2	chr11	89901285	-1.7	2.2E-02	-1.7	8.6E-03	-1.6	7.8E-04	-1.7	4.9E-04	5.0E-01	NA
187	cg23342358	PCBP3	chr21	47162272	2.3	1.1E-01	2.3	2.0E-03	1.6	9.7E-03	2.3	4.9E-04	5.0E-01	NA
188	cg13737493	GADD45G	chr9	92216472	-4.4	1.9E-03	-2.1	4.2E-02	-2.2	9.0E-03	-2.9	5.0E-04	5.0E-01	NA
189	cg20281309	GAB2	chr11	78127618	4.7	6.5E-02	5.1	3.2E-03	4.0	3.1E-03	5.0	5.1E-04	5.0E-01	NA
190	cg08776942	SNN	chr16	11729131	-4.3	6.8E-03	-3.0	2.3E-02	-3.0	2.3E-03	-3.5	5.1E-04	5.0E-01	NA
191	cg20139683	POLE	chr12	133250118	-0.3	2.7E-02	-0.3	7.4E-03	-0.3	1.6E-03	-0.3	5.3E-04	5.0E-01	NA
192	cg08880817	BLOC1S5-TXNDC5	chr6	7909642	-2.0	6.9E-02	-2.2	3.2E-03	-1.6	6.3E-03	-2.1	5.3E-04	5.0E-01	NA
193	cg18418928	MDS2	chr1	23953778	1.2	1.5E-01	2.1	1.1E-03	1.3	7.2E-03	1.8	5.4E-04	5.0E-01	NA
194	cg02276274	SUMF1	chr3	3839921	-1.7	1.9E-01	-2.7	1.1E-03	-2.5	2.6E-04	-2.4	5.4E-04	5.0E-01	NA

#	ProbeID	Gene	CHR	Position	PR-GOAL		GALA II		Mega-analysis		Meta-analysis			Coef
					Eff	Pval	Eff	Pval	Eff	Pval	Eff	Pval	FDR	
195	cg17475857	DNMT3B	chr20	31366466	-1.6	1.2E-01	-2.5	1.6E-03	-2.3	1.1E-04	-2.2	5.5E-04	5.0E-01	NA
196	cg14405528	TBC1D22A	chr22	47372700	5.2	7.8E-02	3.7	2.6E-03	2.8	8.7E-03	3.9	5.5E-04	5.0E-01	NA
197	cg02082462	PRTN3	chr19	848001	2.1	5.2E-02	2.5	4.1E-03	2.1	1.2E-03	2.4	5.5E-04	5.0E-01	NA
198	cg08815340	RPP40	chr6	5026435	4.0	4.5E-03	2.1	2.3E-02	2.0	6.9E-03	2.6	5.5E-04	5.0E-01	NA
199	cg14978242	SERINC5	chr5	79501131	-4.0	2.2E-03	-2.0	4.2E-02	-2.8	2.5E-04	-2.7	5.5E-04	5.0E-01	NA
200	cg19180602	RPL38	chr17	72200560	-2.6	1.4E-02	-2.0	1.3E-02	-1.9	2.8E-03	-2.2	5.6E-04	5.0E-01	NA

<sup>a</sup> Effect size: the parameter in our EWAS models. Effect size = 5 means an increase of 1% methylation beta-value associated with a log<sub>10</sub> scaled total IgE level.

<sup>b</sup> Coefficient: the parameter in Liang et al.'s models. Coefficient = 5 means an increase of 1 inverse normal methylation level associated with a log<sub>10</sub> increase of natural logarithm transformed total IgE level. A comparison between our effect size and this coefficient can be made but not on the magnitude.

**Table E6. eQTM results for the top 20 CpG sites in the meta-analysis adjusting for WBC type**

CpG	cis-Gene	Pval_noCT	Pval_CT	CpG	cis-Gene	Pval_noCT	Pval_CT	CpG	cis-Gene	P
cg25087851	PTGDR2	<b>5.16E-17</b>	0.483	cg06623197	MTMR3	0.034	0.962	cg25087851	PRPF19	
cg12227660	PAOX	<b>2.04E-13</b>	0.399	cg13074835	TNF	0.038	0.044	cg12427941	CDC5L	
cg20481287	MANSC1	2.23E-05	0.093	cg11699125	ZBTB48	0.038	0.609	cg12427941	PTCRA	
cg15492834	USF1	9.19E-05	5.41E-04	cg00405825	HIPK2	0.039	0.062	cg25087851	CD5	
cg12227660	ADAM8	1.13E-04	0.637	cg13074835	LSM2	0.040	0.177	cg25087851	VPS37C	
cg20481287	LOC387841	1.51E-04	0.046	cg01458054	STMN3	0.041	0.035	cg25087851	SLC15A3	
cg12296550	HLA_DQB1	1.57E-04	2.04E-04	cg15700636	SLC43A3	0.045	0.643	cg13074835	PBX2	
cg09249800	TNFRSF25	3.00E-04	0.163	cg13074835	DHX16	0.054	0.119	cg12614529	FBXW7	
cg21220721	TNFRSF25	3.22E-04	0.301	cg20481287	LOC643287	0.060	0.596	cg09249800	NOL9	
cg25087851	TMEM216	8.15E-04	0.931	cg08940169	KLHDC4	0.065	0.384	cg15492834	FCGR2A	
cg12296550	DOM3Z	8.96E-04	4.66E-04	cg25087851	MS4A2	0.068	0.084	cg08940169	FAM38A	
cg11699125	TNFRSF25	3.14E-03	0.838	cg06623197	TCN2	0.073	0.995	cg01458054	OPRL1	
cg25087851	CD6	3.74E-03	0.085	cg13074835	AGER	0.079	0.059	cg08940169	ZFPM1	
cg12296550	NOTCH4	6.08E-03	6.88E-04	cg12296550	TAP2	0.079	0.169	cg13074835	C6ORF48	
cg21220721	RPL22	7.47E-03	0.727	cg15492834	HSPA6	0.084	0.436	cg25087851	CCDC86	
cg04983687	SNAI3	9.87E-03	0.833	cg12614529	TMEM154	0.090	0.715	cg15700636	UBE2L6	
cg01000631	EVL	0.013	0.280	cg13074835	LOC729816	0.094	0.257	cg04983687	ZFPM1	
cg09249800	RPL22	0.014	0.497	cg06623197	C22ORF27	0.094	0.196	cg12427941	KLHDC3	
cg12296550	LOC642073	0.014	7.06E-03	cg11699125	KCNAB2	0.094	0.173	cg13074835	LTA	
cg08940169	SNAI3	0.015	0.962	cg12614529	RNF175	0.103	0.861	cg12427941	TJAP1	
cg11699125	RPL22	0.018	0.792	cg13074835	HLA_B	0.110	0.104	cg04983687	FAM38A	
cg04983687	BANP	0.021	0.034	cg25087851	MS4A3	0.111	9.39E-03	cg01458054	HELZ2	
cg08940169	BANP	0.021	0.033	cg13074835	TUBB	0.113	0.230	cg09249800	ACOT7	
cg04983687	KLHDC4	0.022	0.091	cg09249800	KCNAB2	0.131	0.324	cg01000631	SETD3	
cg15492834	COPA	0.023	0.059	cg21220721	KCNAB2	0.133	0.284	cg12103951	WAPL	
cg20481287	ETV6	0.026	0.701	cg13074835	LTB	0.133	0.227	cg21220721	ACOT7	
cg12614529	TLR2	0.032	0.233	cg11699125	NOL9	0.147	0.176	cg11699125	ACOT7	

**Table E7. Top 200 CpG sites in the meta-analysis unadjusted for WBC types, in Puerto Rico**

#	ProbeID	Gene	CHR	Position	PR-GOAL		GALA II		Mega-analysis	
					Effect <sup>a</sup>	Pvalue	Effect	Pvalue	Effect	Pvalue
1	cg04983687	ZFPM1	chr16	88558223	-4.75	1.97E-19	-5.06	1.26E-14	-4.66	3.14E-31
2	cg21220721	ACOT7	chr1	6341230	-4.80	2.93E-20	-4.99	5.06E-13	-4.57	6.75E-30
3	cg09249800	ACOT7	chr1	6341287	-5.44	1.65E-20	-6.87	4.95E-13	-5.49	4.59E-30
4	cg11699125	ACOT7	chr1	6341327	-4.92	5.27E-19	-6.02	2.15E-12	-4.95	4.70E-28
5	cg12227660	MIR202	chr10	135061670	-6.18	2.67E-16	-7.50	1.83E-14	-6.18	1.09E-26
6	cg15700636	PRG2	chr11	57156050	-6.21	1.43E-16	-8.51	3.65E-13	-6.47	6.50E-26
7	cg08940169	ZFPM1	chr16	88540241	-6.13	1.35E-17	-7.49	1.54E-11	-6.22	1.03E-26
8	cg01000631	EVL	chr14	100610667	-4.79	9.82E-18	-6.95	8.58E-12	-4.99	5.20E-26
9	cg25087851	PTGDR2	chr11	60623918	-5.68	3.34E-16	-7.40	3.11E-12	-5.84	4.60E-25
10	cg14084609	EVL	chr14	100610407	-5.48	1.71E-17	-7.70	5.51E-11	-5.71	1.72E-25
11	cg07970948	ZNF862	chr7	149543165	-4.77	1.45E-15	-6.01	1.41E-12	-4.89	7.39E-25
12	cg02985445	BRI3	chr7	97908505	-6.87	4.01E-16	-7.11	1.10E-11	-6.23	1.96E-23
13	cg25939647	GPR176	chr15	40173065	-5.38	2.78E-16	-6.36	1.24E-11	-5.37	7.19E-25
14	cg18550847	EVL	chr14	100610570	-4.88	3.89E-16	-6.74	5.03E-12	-5.07	1.48E-24
15	cg23706836	MCPH1	chr8	6407997	-4.70	8.13E-15	-6.54	3.04E-13	-5.02	7.96E-25
16	cg06528816	TTC7A	chr2	47242277	-5.32	9.11E-15	-7.14	4.16E-13	-5.61	1.02E-24
17	cg13054523	METRNL	chr17	81055722	-7.70	1.25E-17	-7.04	1.41E-09	-6.79	2.62E-23
18	cg16263722	MECR	chr1	29523841	-6.49	1.53E-15	-7.33	1.43E-11	-6.34	7.18E-24
19	cg00114012	SLC2A8	chr9	130158144	-5.89	3.77E-14	-7.49	3.32E-13	-6.08	7.10E-24
20	cg04290133	GUSB	chr7	65439512	-5.55	2.06E-14	-9.40	6.11E-14	-5.95	7.26E-23
21	cg12077754	HK2	chr2	75089669	-4.74	2.18E-14	-6.32	7.32E-13	-4.87	8.18E-23
22	cg16409452	EVL	chr14	100610186	-5.29	4.15E-15	-8.68	8.16E-13	-5.75	8.32E-24
23	cg10142874	LPIN1	chr2	11917623	-6.06	6.35E-16	-6.88	1.39E-10	-6.06	3.41E-24
24	cg20885063	ATPAF2	chr17	17939419	-5.83	8.49E-16	-7.14	9.85E-11	-5.98	4.53E-24
25	cg16362140	DAP	chr5	10708717	-5.63	5.07E-16	-6.88	2.05E-10	-5.65	2.10E-23
26	cg01998785	LPCAT2	chr16	55542709	-5.50	3.86E-13	-7.98	8.40E-14	-5.93	2.58E-23
27	cg05300717	AP5B1	chr11	65546210	-5.78	8.53E-15	-8.74	4.30E-12	-6.11	6.76E-23



#	ProbeID	Gene	CHR	Position	PR-GOAL		GALA II		Mega-analysis	
					Effect	Pvalue	Effect	Pvalue	Effect	Pvalue
28	cg21723861	JUP	chr17	39686628	-7.27	7.63E-14	-10.90	7.25E-13	-7.93	2.52E-23
29	cg23147443	KCNH2	chr7	150649655	-5.10	1.53E-16	-5.81	3.31E-09	-5.02	2.33E-23
30	cg13576859	FBP1	chr9	97403129	-6.19	7.79E-15	-7.38	6.47E-11	-6.16	7.81E-23
31	cg01942646	NR0B2	chr1	27240694	-6.29	2.64E-16	-7.35	2.46E-09	-6.21	4.22E-23
32	cg01649647	MYL9	chr20	35177530	-8.17	2.39E-15	-8.19	5.19E-10	-7.69	4.29E-23
33	cg08776942	SNN	chr16	11729131	-6.55	4.06E-15	-7.88	2.91E-10	-6.58	1.65E-22
34	cg24491618	KCNH2	chr7	150649807	-5.59	2.97E-16	-7.10	3.30E-09	-5.60	1.82E-22
35	cg01901579	DICER1	chr14	95615731	-5.58	2.17E-14	-6.95	6.65E-11	-5.77	9.70E-23
36	cg02970679	EPX	chr17	56269818	-6.26	1.42E-14	-9.02	6.27E-11	-6.58	1.56E-22
37	cg18650626	MAD1L1	chr7	1914073	-4.14	2.54E-15	-4.88	1.41E-09	-4.14	2.78E-22
38	cg08773180	PRG2	chr11	57157607	-5.74	6.08E-16	-5.97	1.10E-08	-5.59	1.55E-22
39	cg26547058	SLC45A4	chr8	142243143	-6.73	1.57E-15	-6.33	6.64E-09	-6.18	1.05E-21
40	cg06391412	FOXP1	chr3	71295684	-6.17	6.20E-14	-8.43	6.37E-11	-6.55	2.09E-22
41	cg17971251	SEC16B	chr1	177907297	-6.48	4.85E-12	-10.62	2.00E-13	-7.21	2.72E-21
42	cg09377531	TRAPPC9	chr8	141046469	-4.69	3.85E-14	-7.25	8.26E-11	-5.00	1.41E-21
43	cg08698681	TNIK	chr3	171091657	-7.34	2.34E-12	-10.74	2.57E-12	-7.94	3.89E-21
44	cg20673965	IRGC	chr19	44220148	-6.42	1.34E-13	-7.44	2.05E-10	-6.14	4.10E-20
45	cg00944309	ELOVL7	chr5	60142446	-5.93	5.25E-15	-6.73	1.08E-08	-5.97	5.27E-22
46	cg18666454	KCNH2	chr7	150651937	-5.24	1.01E-13	-6.87	2.93E-10	-5.42	4.08E-21
47	cg11456013	AMD1	chr6	111192760	-5.73	5.62E-14	-7.44	5.95E-10	-5.71	1.98E-20
48	cg03131767	ABCB9	chr12	123446272	-6.29	3.14E-13	-8.20	1.52E-10	-6.71	4.63E-22
49	cg21067750	PHGR1	chr15	40641778	-7.20	3.46E-13	-9.96	1.05E-10	-7.54	1.32E-20
50	cg20840540	TRERF1	chr6	42363749	-7.30	2.77E-12	-9.43	1.98E-11	-7.70	3.75E-21
51	cg26865494	DOCK1	chr10	129172573	-7.38	3.87E-12	-11.08	4.56E-12	-7.95	2.03E-20
52	cg20315954	PMP22	chr17	15137304	-6.43	9.35E-13	-9.73	1.95E-11	-6.96	1.04E-20
53	cg07781995	LINC01140	chr1	87655840	-7.48	1.02E-15	-8.20	1.25E-07	-7.30	4.41E-21
54	cg17521120	SIGLEC8	chr19	51961666	-7.21	8.47E-17	-5.28	8.63E-07	-5.80	1.58E-19
55	cg06070625	MITF	chr3	69812798	-5.80	1.36E-13	-6.61	3.45E-09	-5.63	8.37E-20

#	ProbeID	Gene	CHR	Position	PR-GOAL		GALA II		Mega-analysis	
					Effect	Pvalue	Effect	Pvalue	Effect	Pvalue
56	cg13312337	DCTN1	chr2	74612759	-8.82	1.63E-15	-6.54	1.41E-07	-7.09	3.42E-19
57	cg21045547	SOGA1	chr20	35422703	-6.76	1.90E-13	-9.59	9.29E-10	-6.91	1.38E-19
58	cg08889930	MCM2	chr3	127317798	-6.94	7.72E-14	-8.17	6.55E-09	-6.89	2.75E-20
59	cg26787239	IL4	chr5	132008525	-7.92	4.97E-13	-13.14	1.07E-10	-8.57	4.37E-20
60	cg07177867	LYSMD2	chr15	52030746	-6.55	1.24E-12	-8.64	2.97E-10	-6.70	2.79E-19
61	cg21627181	SLC17A4	chr6	25754190	-6.99	2.32E-13	-8.50	3.04E-09	-6.94	1.40E-19
62	cg25173129	EPX	chr17	56269410	-6.02	3.35E-13	-8.15	1.29E-09	-6.34	1.61E-20
63	cg13645296	DAPK2	chr15	64275810	-6.64	1.40E-16	-4.44	1.80E-06	-5.31	1.12E-19
64	cg14978242	SERINC5	chr5	79501131	-6.32	4.44E-15	-5.73	2.58E-07	-6.05	2.27E-21
65	cg01445399	LINC01140	chr1	87596934	-6.43	2.94E-13	-7.47	3.86E-09	-6.59	7.43E-21
66	cg06866208	FAM65A	chr16	67560245	-7.29	7.93E-15	-6.62	1.93E-07	-6.62	5.15E-20
67	cg12614529	MND1	chr4	154269418	-4.71	8.59E-12	-5.03	1.85E-10	-4.58	6.92E-20
68	cg02427831	SIGLEC8	chr19	51961937	-6.82	2.73E-13	-7.93	4.99E-09	-6.76	1.13E-19
69	cg10159529	IL5RA	chr3	3152530	-5.65	6.08E-13	-7.59	1.16E-09	-5.83	1.20E-19
70	cg13562011	EXD3	chr9	140308660	-6.72	9.35E-15	-6.97	2.49E-07	-6.62	6.88E-21
71	cg26791242	LINC01140	chr1	87596895	-5.62	2.63E-14	-5.71	1.70E-07	-5.35	1.42E-19
72	cg25488567	FAM26F	chr6	116781307	-6.81	5.34E-14	-8.48	5.77E-08	-6.80	2.66E-19
73	cg04497992	PRR35	chr16	616212	-7.25	1.68E-16	-4.10	1.34E-06	-4.88	2.68E-17
74	cg01330991	DNAH2	chr17	7648108	-5.38	1.86E-13	-7.00	1.71E-08	-5.51	2.20E-19
75	cg12819873	PRG2	chr11	57157632	-6.48	9.89E-14	-7.52	5.78E-08	-6.49	1.22E-19
76	cg14613878	TLDC2	chr20	35504198	-6.04	8.23E-17	-3.38	4.08E-06	-4.09	2.61E-17
77	cg01310029	IL5RA	chr3	3152374	-6.59	2.74E-13	-8.62	1.80E-08	-6.74	2.89E-19
78	cg00170714	MLX	chr17	40724562	-6.33	3.78E-12	-7.57	1.87E-09	-6.42	4.68E-19
79	cg25224369	IQSEC1	chr3	12918528	-6.54	7.49E-15	-5.47	1.06E-06	-5.74	1.68E-18
80	cg22919538	NME6	chr3	48334413	-8.07	2.28E-14	-8.34	4.66E-07	-7.63	1.09E-18
81	cg21919729	CTSB	chr8	11719367	-5.59	9.60E-13	-6.06	1.24E-08	-5.44	8.25E-19
82	cg17988187	DCTN1	chr2	74612222	-5.61	1.07E-13	-6.27	1.18E-07	-5.56	1.44E-19
83	cg07908654	WBP4	chr13	41631052	-5.57	2.80E-12	-7.17	2.62E-09	-5.83	1.76E-19

#	ProbeID	Gene	CHR	Position	PR-GOAL		GALA II		Mega-analysis	
					Effect	Pvalue	Effect	Pvalue	Effect	Pvalue
84	cg06154903	EHD1	chr11	64642558	-4.52	3.62E-14	-4.09	4.47E-07	-4.21	2.35E-19
85	cg04321303	PGAM2	chr7	44107504	-5.30	1.71E-12	-6.00	1.18E-08	-5.20	1.73E-18
86	cg12104982	SAFB2	chr19	5592815	-8.31	5.48E-12	-10.09	3.23E-09	-8.39	1.62E-18
87	cg26235490	ABR	chr17	1047567	-7.32	4.06E-14	-7.02	7.44E-07	-6.53	3.79E-18
88	cg07562835	ITGB4	chr17	73734756	-7.35	7.26E-14	-6.11	3.23E-07	-6.37	6.51E-18
89	cg00711896	ZNF48	chr16	30410051	-6.08	3.19E-12	-7.84	7.11E-09	-6.28	1.12E-18
90	cg08462941	PTPRS	chr19	5288631	-5.59	6.90E-11	-6.74	5.52E-10	-5.63	6.98E-18
91	cg06906869	NEK3	chr13	52734154	-7.26	2.14E-13	-7.07	2.77E-07	-6.63	1.18E-17
92	cg16177693	NR0B2	chr1	27240669	-6.09	2.80E-14	-4.60	1.33E-06	-5.19	1.27E-18
93	cg24836822	KCNH2	chr7	150648840	-5.56	1.18E-11	-7.43	3.14E-09	-5.87	8.84E-19
94	cg14226212	MUSK	chr9	113530240	-5.80	1.08E-09	-8.84	1.58E-11	-6.34	3.31E-17
95	cg20151107	FAM53B	chr10	126331425	-7.57	4.97E-13	-8.43	2.26E-07	-7.39	5.65E-18
96	cg06647928	ENC1	chr5	73612203	-6.05	1.81E-12	-5.62	7.74E-08	-5.55	5.81E-18
97	cg27469152	EPX	chr17	56282313	-5.83	1.39E-13	-4.26	4.75E-07	-4.64	3.49E-17
98	cg13628444	MED27	chr9	134883788	-6.28	1.02E-12	-6.76	1.69E-07	-6.07	7.00E-18
99	cg15146567	ZNF662	chr3	42948626	-5.40	3.45E-13	-4.35	3.44E-07	-4.55	2.56E-17
100	cg11396585	TAPBP	chr6	33273477	-9.19	7.88E-15	-6.98	1.47E-05	-7.90	1.77E-17
101	cg02359181	GPI	chr19	34860339	-6.41	3.62E-11	-9.35	1.65E-09	-6.87	4.85E-18
102	cg20290167	METRNL	chr17	81040724	-5.63	3.79E-11	-6.11	6.11E-09	-5.52	4.28E-18
103	cg05465955	COASY	chr17	40715236	-5.37	8.55E-12	-4.86	2.95E-08	-4.78	2.08E-17
104	cg20263853	RERE	chr1	8824177	-5.17	2.59E-09	-8.34	1.10E-11	-5.80	3.57E-17
105	cg12172163	PROZ	chr13	113825954	-6.19	9.28E-13	-5.81	3.08E-07	-5.66	1.04E-17
106	cg04033850	PRPH	chr12	49695016	-8.12	2.62E-11	-9.33	1.07E-08	-8.03	1.44E-17
107	cg18348836	HOOK1	chr1	60282400	-6.84	2.89E-10	-11.70	8.48E-11	-7.77	6.63E-18
108	cg19434937	EMG1	chr12	7104184	-5.84	4.11E-16	-2.91	1.07E-05	-3.71	5.19E-16
109	cg14611258	GID4	chr17	17946468	-6.54	4.69E-09	-11.75	2.79E-12	-7.46	1.38E-16
110	cg23943829	IL4	chr5	132009111	-8.20	1.14E-11	-9.91	2.59E-08	-8.22	2.22E-17
111	cg18783781	SLC25A33	chr1	9599067	-6.53	5.18E-13	-7.07	8.11E-07	-6.35	8.10E-18

#	ProbeID	Gene	CHR	Position	PR-GOAL		GALA II		Mega-analysis	
					Effect	Pvalue	Effect	Pvalue	Effect	Pvalue
112	cg08268892	ARID1B	chr6	157131429	-6.74	6.16E-13	-5.72	6.75E-07	-6.22	1.16E-18
113	cg07819010	AMBRA1	chr11	46619375	-5.90	1.89E-15	-3.40	2.29E-05	-4.21	7.47E-16
114	cg02245534	METRNL	chr17	81043668	-8.18	3.12E-17	-3.57	4.34E-05	-5.00	2.13E-16
115	cg26457013	TMEM86B	chr19	55740188	-7.20	1.14E-13	-5.47	4.00E-06	-5.94	5.44E-17
116	cg20836212	VKORC1L1	chr7	65419185	-4.72	3.04E-13	-4.05	3.26E-06	-4.30	1.01E-17
117	cg11987455	ERMAP	chr1	43290834	-6.62	2.66E-11	-8.06	3.01E-08	-6.59	7.69E-17
118	cg08808720	KIF5C	chr2	149639914	-6.24	9.56E-10	-11.49	3.66E-11	-7.12	8.06E-17
119	cg01464484	LOC100130987	chr11	67089352	-9.78	1.36E-10	-13.16	4.04E-09	-10.21	9.78E-17
120	cg24202817	PFKFB3	chr10	6220943	-7.77	2.00E-11	-7.19	6.08E-08	-7.17	3.52E-17
121	cg09535526	ZFPM1	chr16	88558065	-5.72	3.30E-13	-4.98	4.04E-06	-5.12	9.42E-17
122	cg03060158	IP6K2	chr3	48755856	-7.09	4.28E-10	-9.27	2.07E-09	-7.57	1.30E-17
123	cg02765496	PIP5K1B	chr9	71393662	-6.98	2.55E-11	-6.84	7.18E-08	-6.49	6.09E-17
124	cg02346442	LOC253573	chr3	186194046	-6.13	1.01E-11	-7.88	1.10E-07	-6.34	1.36E-17
125	cg10298741	ZFH3	chr16	73019173	-6.55	3.36E-13	-5.96	6.93E-06	-5.98	5.76E-17
126	cg00582671	SAMD11	chr1	872235	-5.62	5.71E-13	-3.81	1.36E-06	-4.10	4.52E-15
127	cg04217850	SLC25A26	chr3	66428294	-7.22	4.00E-10	-9.42	4.59E-09	-7.57	8.43E-17
128	cg16599817	PRKCZ	chr1	2036283	-5.71	1.23E-14	-3.16	1.55E-05	-3.89	1.10E-15
129	cg13209388	ACOT7	chr1	6355060	-3.76	2.80E-11	-3.91	1.41E-07	-3.73	1.86E-17
130	cg00844155	VAMP1	chr12	6576111	-7.41	2.14E-11	-7.81	1.88E-07	-7.07	3.44E-16
131	cg26774971	TMEM181	chr6	158994407	-6.42	1.13E-12	-6.23	4.09E-06	-6.03	5.31E-17
132	cg04692506	SLC39A13	chr11	47401027	-7.10	3.93E-11	-6.57	1.11E-07	-6.71	2.94E-17
133	cg05219423	CELF2	chr10	11291279	-6.37	1.36E-13	-4.77	1.95E-05	-5.46	6.27E-17
134	cg17540765	RECQL5	chr17	73631586	-6.28	3.02E-11	-6.65	1.67E-07	-5.96	4.36E-16
135	cg11310939	3-Mar	chr5	126257116	-5.65	6.11E-11	-8.45	2.42E-08	-6.04	1.20E-16
136	cg12074090	MCPH1	chr8	6360436	-6.13	1.56E-10	-8.73	1.24E-08	-6.51	1.48E-16
137	cg00837308	ZNF469	chr16	88473488	-7.04	5.05E-09	-10.73	2.33E-10	-7.77	3.11E-16
138	cg25135457	COASY	chr17	40715244	-6.59	1.16E-09	-9.10	2.03E-09	-6.89	5.97E-16
139	cg00093688	NDOR1	chr9	140113369	-6.88	1.99E-10	-10.07	8.82E-09	-7.23	4.38E-16

#	ProbeID	Gene	CHR	Position	PR-GOAL		GALA II		Mega-analysis	
					Effect	Pvalue	Effect	Pvalue	Effect	Pvalue
140	cg20317437	FUCA1	chr1	24172120	-6.51	1.23E-10	-8.96	2.20E-08	-6.86	1.51E-16
141	cg14025883	PLGRKT	chr9	5436224	-5.02	1.85E-09	-9.06	1.60E-10	-5.64	7.77E-16
142	cg16107105	KCNH2	chr7	150646704	-5.81	4.75E-08	-11.43	2.01E-12	-6.86	2.31E-15
143	cg26953137	MRPL45P2	chr17	45573695	-5.99	1.18E-09	-9.40	1.03E-09	-6.37	2.36E-15
144	cg09212118	GUCA2A	chr1	42630526	-5.31	6.16E-10	-6.01	1.04E-08	-5.41	5.60E-17
145	cg04420917	LGALS4	chr19	39303993	-6.76	1.88E-12	-6.21	4.44E-06	-6.07	8.81E-16
146	cg00390941	PDE6H	chr12	15124659	-8.61	4.05E-09	-13.01	4.79E-10	-9.52	1.45E-16
147	cg09646173	PDE6A	chr5	149317669	-5.31	1.44E-12	-4.41	5.19E-06	-4.65	9.89E-16
148	cg21239317	CCDC126	chr7	23640510	-6.16	1.64E-10	-7.51	4.28E-08	-6.18	4.09E-16
149	cg02170785	EXD2	chr14	69650830	-5.82	3.81E-10	-8.12	1.17E-08	-6.08	1.12E-15
150	cg22312249	TMEM104	chr17	72779428	-5.53	3.44E-11	-5.49	3.53E-07	-5.13	6.83E-16
151	cg13774539	DCTN1	chr2	74612706	-5.44	1.43E-10	-5.66	8.48E-08	-5.19	4.11E-16
152	cg18972349	THEMIS2	chr1	28195327	-8.12	3.77E-15	-3.93	5.71E-05	-5.11	2.04E-14
153	cg23642826	ZBTB48	chr1	6645463	-6.86	6.27E-11	-6.07	2.28E-07	-5.76	1.71E-14
154	cg19851574	RPS6KA2	chr6	167178233	-3.06	3.86E-10	-3.02	4.96E-08	-2.75	5.26E-15
155	cg09820180	LOC100132735	chr6	140168822	-7.70	1.04E-10	-8.48	1.75E-07	-7.42	1.50E-15
156	cg05499338	CMIP	chr16	81517665	-6.45	4.81E-10	-9.01	1.60E-08	-6.99	1.45E-16
157	cg19328051	AFG3L2	chr18	12380944	-7.66	3.73E-10	-10.72	2.18E-08	-8.08	3.88E-16
158	cg01916918	CLU	chr8	27461199	-7.10	1.64E-10	-9.58	6.43E-08	-7.45	2.81E-16
159	cg19618279	COASY	chr17	40715228	-6.19	3.96E-12	-4.57	2.93E-06	-4.92	2.34E-15
160	cg00068153	CACNA1S	chr1	201028602	-6.99	6.78E-12	-9.37	2.62E-06	-7.19	2.41E-16
161	cg02473287	YWHAQ	chr2	9752386	-6.30	1.09E-12	-5.26	2.83E-05	-5.75	4.50E-16
162	cg02826233	CDK2	chr12	56365894	-9.02	2.68E-11	-8.22	1.35E-06	-8.21	1.19E-15
163	cg14355482	NCAM2	chr21	22373039	-5.32	4.95E-10	-7.25	3.66E-08	-5.52	2.09E-15
164	cg09565310	MCC	chr5	112541553	-5.33	4.17E-09	-8.72	1.23E-09	-5.63	2.21E-14
165	cg25332499	BATF2	chr11	64756382	-5.08	7.63E-11	-4.38	5.82E-07	-4.59	4.64E-16
166	cg23791626	PITPNC1	chr17	65542892	-5.23	2.30E-09	-5.84	2.08E-08	-4.63	3.27E-13
167	cg23205629	RNF122	chr8	33421410	-6.40	5.18E-12	-6.20	1.24E-05	-6.04	9.46E-16

#	ProbeID	Gene	CHR	Position	PR-GOAL		GALA II		Mega-analysis	
					Effect	Pvalue	Effect	Pvalue	Effect	Pvalue
168	cg05215575	SMIM22	chr16	4838722	-6.29	2.81E-10	-6.02	2.13E-07	-5.72	4.01E-15
169	cg13753183	APTX	chr9	32989852	-7.94	2.47E-12	-5.60	1.03E-05	-6.42	1.65E-15
170	cg05958985	ZFPM1	chr16	88558237	-6.25	4.50E-11	-5.56	1.42E-06	-5.71	7.10E-16
171	cg26789365	PPP2R2D	chr10	133743048	-5.66	3.16E-09	-9.52	2.47E-09	-6.25	3.36E-15
172	cg00414077	TLDC2	chr20	35504511	-7.81	7.67E-16	-3.09	8.19E-05	-4.29	8.86E-14
173	cg25368824	IL4	chr5	132009352	-6.26	2.85E-11	-7.09	2.72E-06	-6.17	1.31E-15
174	cg18042632	LINC00323	chr21	42520902	-6.19	1.51E-11	-6.30	6.23E-06	-5.96	1.42E-15
175	cg20405742	STMND1	chr6	16933816	-6.11	3.17E-11	-7.20	2.67E-06	-5.90	1.26E-14
176	cg22027879	FTL	chr19	49469965	-5.32	2.73E-09	-10.26	1.18E-09	-5.90	1.11E-14
177	cg08165794	PAK6	chr15	40568143	-7.24	6.09E-10	-7.68	1.69E-07	-7.15	5.44E-16
178	cg03492094	SEMA4D	chr9	91994786	-5.50	2.61E-10	-5.68	4.18E-07	-5.17	6.13E-15
179	cg07914457	NR0B2	chr1	27241853	-6.96	8.41E-10	-6.55	1.46E-07	-6.29	4.31E-15
180	cg25203627	TSNAX-DISC1	chr1	231886200	-7.84	8.19E-11	-10.21	1.06E-06	-7.74	1.33E-14
181	cg11668148	CELF6	chr15	72636405	-6.69	2.13E-11	-6.85	7.02E-06	-6.35	2.59E-15
182	cg11563127	C12orf76	chr12	110506298	-5.48	1.59E-10	-6.41	9.05E-07	-5.51	2.93E-15
183	cg04986931	MGAT3	chr22	39850128	-6.62	5.69E-12	-4.83	1.51E-05	-5.45	6.91E-15
184	cg19609644	FER1L6	chr8	125213448	-4.87	5.11E-10	-7.78	6.60E-08	-5.21	3.31E-15
185	cg03453890	SLC39A4	chr8	145643535	-6.74	2.04E-13	-3.93	1.15E-04	-5.18	3.81E-15
186	cg15817440	C14orf37	chr14	58599910	-6.08	1.38E-08	-9.21	3.10E-09	-6.76	2.61E-15
187	cg12077460	MFHAS1	chr8	8702053	-6.11	4.32E-14	-3.08	1.38E-04	-4.17	2.22E-14
188	cg07686528	JMJD1C	chr10	65198176	-10.50	1.19E-10	-10.43	1.73E-06	-9.86	3.69E-15
189	cg24058805	PDE4B	chr1	66777579	-8.87	1.56E-11	-6.56	6.89E-06	-7.37	5.02E-15
190	cg05541460	MGAT3	chr22	39850774	-5.78	7.33E-11	-6.99	2.25E-06	-5.80	3.63E-15
191	cg18944099	GPANK1	chr6	31629199	-6.06	4.52E-11	-6.07	4.83E-06	-5.80	4.17E-15
192	cg23991413	NBPF20	chr1	145004305	-8.05	1.44E-11	-6.36	1.04E-05	-6.69	4.23E-14
193	cg04305653	TBC1D22A	chr22	47272422	-5.87	1.52E-11	-5.13	1.38E-05	-5.25	6.41E-15
194	cg15456821	BEST1	chr11	61717225	-6.60	1.71E-10	-5.77	1.23E-06	-5.96	4.83E-15
195	cg18151262	MIDN	chr19	1254251	-6.12	3.18E-08	-7.50	5.47E-09	-6.40	2.61E-15

#	ProbeID	Gene	CHR	Position	PR-GOAL		GALA II		Mega-analysis	
					Effect	Pvalue	Effect	Pvalue	Effect	Pvalue
196	cg15482717	FADD	chr11	70053254	-6.11	4.04E-11	-5.11	5.57E-06	-5.33	1.13E-14
197	cg19704630	ATP2A3	chr17	3872385	-9.30	6.19E-09	-12.01	2.67E-08	-9.49	2.34E-14
198	cg15107869	SSR3	chr3	156269381	-5.76	9.35E-12	-3.59	6.89E-06	-4.44	5.02E-15
199	cg08404225	IL5RA	chr3	3151899	-5.37	2.37E-11	-4.83	1.53E-05	-4.90	1.13E-14
200	cg00869582	SNX29	chr16	12564745	-6.39	2.06E-10	-6.95	1.74E-06	-6.21	1.12E-14

<sup>a</sup> Effect size: the parameter in our EWAS models. Effect size = 5 means an increase of 1% methylation beta-value as log<sub>10</sub> scaled total IgE level.

**Table E8. Top 200 CpG sites in the meta-analysis adjusting for WBC types, in Puerto Ricans**

#	ProbeID	Gene	CHR	Position	PR-GOAL		GALA II		Mega-analysis	
					Effect <sup>a</sup>	Pvalue	Effect	Pvalue	Effect	Pvalue
1	cg04983687	ZFPM1	chr16	88558223	-5.27	4.69E-07	-3.77	3.16E-04	-4.40	1.49E-05
2	cg12614529	MND1	chr4	154269418	-5.25	7.38E-05	-5.02	2.10E-05	-4.64	9.54E-05
3	cg21220721	ACOT7	chr1	6341230	-5.31	1.26E-07	-2.71	4.81E-02	-4.25	2.75E-05
4	cg09249800	ACOT7	chr1	6341287	-6.81	5.32E-08	-2.92	1.46E-01	-5.36	1.96E-05
5	cg18775542	STAM	chr10	17682215	5.13	9.19E-05	4.88	1.98E-03	4.00	4.17E-05
6	cg12227660	MIR202	chr10	135061670	-4.26	1.21E-03	-5.13	1.71E-04	-4.38	2.31E-05
7	cg03726147	DMAP1	chr1	44686022	3.20	2.58E-02	5.50	5.38E-06	3.31	2.37E-05
8	cg21939017	ZNF624	chr17	16556559	7.23	2.13E-04	6.47	1.69E-03	5.86	2.01E-05
9	cg04071964	ADGRG7	chr3	100328745	-1.83	2.69E-02	-2.91	1.42E-05	-1.84	2.05E-05
10	cg03671700	CDH8	chr16	62068673	7.77	1.95E-02	12.82	3.35E-05	9.16	5.62E-05
11	cg11699125	ACOT7	chr1	6341327	-5.77	5.34E-06	-2.44	1.14E-01	-4.06	2.12E-05
12	cg25939647	GPR176	chr15	40173065	-4.54	3.73E-04	-4.23	5.77E-03	-3.78	7.09E-05
13	cg11725581	USP42	chr7	6140990	1.62	1.19E-02	2.38	1.33E-04	1.64	1.59E-05
14	cg03751829	ZNF99	chr19	22988136	3.19	2.24E-03	3.44	1.05E-03	3.22	1.71E-05
15	cg16815882	KIAA0319L	chr1	35908609	1.50	7.13E-02	4.41	2.56E-06	2.32	1.23E-05
16	cg15025485	BRD2	chr6	32943839	2.99	6.03E-03	3.09	6.41E-04	2.31	7.59E-05
17	cg07725206	LPAR3	chr1	85251175	2.70	2.73E-04	1.75	9.03E-03	1.70	3.98E-05
18	cg05400869	S100A7L2	chr1	153413932	3.33	5.97E-03	2.59	5.96E-04	2.19	4.04E-05
19	cg08794157	PMP22	chr17	15164627	5.67	3.01E-03	5.24	1.47E-03	5.04	4.00E-05
20	cg07719679	STEAP4	chr7	87936392	4.69	6.49E-05	2.88	5.35E-02	3.72	2.83E-05
21	cg18431765	NIFK-AS1	chr2	122444031	3.28	7.19E-02	6.46	3.46E-05	4.11	3.78E-05
22	cg26853340	C15orf26	chr15	81409649	4.76	6.02E-04	4.00	9.02E-03	3.39	8.00E-05
23	cg17734798	PLXNA4	chr7	132226700	4.24	5.32E-03	4.35	1.26E-03	2.98	1.97E-05
24	cg26427777	ZHX2	chr8	123875181	3.67	8.93E-04	2.40	5.01E-03	2.03	8.35E-05
25	cg01890568	ASIC2	chr17	31437649	-4.32	1.01E-02	-6.37	4.92E-04	-4.84	6.15E-05
26	cg01000631	EVL	chr14	100610667	-4.65	1.68E-04	-3.21	3.53E-02	-3.20	4.02E-05
27	cg01115380	FOXC1	chr6	1552904	-1.63	2.66E-03	-1.51	2.63E-03	-1.29	1.98E-05



#	ProbeID	Gene	CHR	Position	PR-GOAL		GALA II		Mega-analysis	
					Effect	Pvalue	Effect	Pvalue	Effect	Pvalue
28	cg20985980	RCC1	chr1	28832113	1.18	3.48E-02	2.76	4.22E-05	1.59	1.57E-02
29	cg25052121	BFSP1	chr20	17539745	3.89	4.47E-03	3.47	1.72E-03	2.92	4.97E-02
30	cg13134634	LMO7	chr13	76207486	2.92	1.64E-02	3.56	4.89E-04	2.35	1.70E-02
31	cg11090641	MAP3K12	chr12	53883045	4.21	2.05E-03	4.42	4.05E-03	3.66	2.65E-02
32	cg23087300	KIRREL2	chr19	36348415	2.22	1.59E-02	3.24	3.96E-04	2.27	3.66E-02
33	cg16084190	BEST1	chr11	61716821	2.81	4.26E-02	4.66	1.38E-04	2.54	3.30E-02
34	cg01458054	HELZ2	chr20	62200603	-3.34	2.75E-03	-3.57	3.26E-03	-3.32	3.54E-02
35	cg02898904	PLD5	chr1	242690733	3.95	1.68E-02	5.04	5.13E-04	3.72	6.66E-02
36	cg16570273	LINC01257	chr12	131647128	7.95	3.40E-05	3.58	1.28E-01	5.31	2.40E-02
37	cg23172671	OPTC	chr1	203482523	1.80	2.39E-02	3.11	2.29E-04	1.98	4.68E-02
38	cg23904441	TNFSF11	chr13	43147624	2.72	3.74E-02	4.11	2.12E-04	2.41	2.66E-02
39	cg24265957	EXT1	chr8	119080372	2.90	4.25E-05	1.07	2.23E-02	1.10	2.22E-02
40	cg09011316	ARHGEF19	chr1	16544950	2.11	8.70E-02	3.13	1.15E-04	1.84	4.26E-02
41	cg00742898	ADAMTSL2	chr9	136431882	4.84	1.03E-03	2.87	5.38E-03	2.33	4.06E-02
42	cg16192821	IQSEC1	chr3	13028642	5.92	6.15E-03	2.96	7.45E-04	2.27	2.47E-02
43	cg10584766	C19orf67	chr19	14196219	9.24	7.87E-03	6.64	1.18E-03	5.35	1.99E-02
44	cg18109571	SOGA3	chr6	127835189	3.91	8.62E-03	4.62	1.32E-03	3.00	2.58E-02
45	cg06623197	MTMR3	chr22	30400763	2.99	5.23E-03	1.83	1.42E-03	1.72	6.46E-02
46	cg05203346	HMHB1	chr5	143278195	3.93	4.95E-03	6.12	1.60E-03	4.31	9.22E-02
47	cg04512965	RFX2	chr19	6038846	-2.29	1.66E-02	-2.90	7.04E-04	-2.13	7.18E-02
48	cg21113478	DCLK3	chr3	36782467	-1.95	3.52E-02	-3.38	2.07E-04	-1.90	2.30E-02
49	cg20706134	PCDH20	chr13	61990025	3.15	2.55E-04	2.01	3.73E-02	2.20	3.75E-02
50	cg15676988	OR5B21	chr11	58281496	2.90	1.36E-03	2.40	9.02E-03	2.55	7.01E-02
51	cg17444090	SIPA1L2	chr1	232735450	-1.09	4.17E-02	-2.23	1.15E-04	-1.24	7.00E-02
52	cg14531564	SDF4	chr1	1154853	-1.75	8.69E-02	-4.08	4.68E-05	-2.40	7.33E-02
53	cg08940169	ZFPM1	chr16	88540241	-5.49	8.37E-05	-2.86	9.59E-02	-4.44	1.94E-02
54	cg17223170	LOC642366	chr5	50468642	2.82	4.76E-04	1.88	2.18E-02	2.01	4.57E-02
55	cg02560085	PCDHA1	chr5	140220810	1.35	1.06E-02	1.71	1.22E-03	1.25	7.17E-02

#	ProbeID	Gene	CHR	Position	PR-GOAL		GALA II		Mega-analysis	
					Effect	Pvalue	Effect	Pvalue	Effect	Pvalue
56	cg24737193	PTPN2	chr18	12778029	2.11	8.40E-04	1.65	1.61E-02	2.15	2.33E-02
57	cg13975098	RGS10	chr10	121303635	0.74	4.71E-01	4.78	8.22E-07	1.67	1.29E-02
58	cg05083067	OR51D1	chr11	4661335	-3.26	6.81E-03	-4.27	1.89E-03	-3.54	5.43E-02
59	cg08657939	MYEOV	chr11	69295007	4.81	1.80E-04	1.85	1.01E-02	1.68	2.87E-02
60	cg02854937	LINC01342	chr1	1079879	5.74	9.47E-03	6.87	1.72E-03	5.70	1.88E-02
61	cg19721730	BCL2L12	chr19	50173685	6.26	1.09E-03	4.19	1.15E-02	4.53	1.97E-02
62	cg08659487	HGC6.3	chr6	168386798	3.67	3.81E-02	3.97	5.26E-04	2.32	9.67E-02
63	cg26684601	JPH3	chr16	87638542	3.88	6.02E-03	2.98	2.74E-03	2.12	6.56E-02
64	cg10320884	TRRAP	chr7	98590914	3.25	7.28E-02	4.76	2.43E-04	2.96	3.52E-02
65	cg19904322	AATBC	chr21	45249837	4.61	2.82E-03	2.55	3.40E-03	2.35	1.70E-02
66	cg02292364	ZNF514	chr2	95824277	2.26	2.69E-02	2.25	8.03E-04	1.49	4.90E-02
67	cg09945482	PTPN2	chr18	12777974	1.60	9.56E-04	1.43	2.19E-02	1.74	2.88E-02
68	cg25154038	RADIL	chr7	4841835	4.78	1.33E-02	3.37	1.26E-03	2.54	4.28E-02
69	cg25447202	RGS12	chr4	3409885	4.11	1.45E-02	3.16	1.32E-03	2.35	3.41E-02
70	cg16618104	CHST11	chr12	104853100	-2.35	1.52E-02	-2.02	1.43E-03	-1.59	1.69E-02
71	cg11793759	LRCOL1	chr12	133176828	1.58	6.53E-03	2.61	1.96E-03	1.58	7.12E-02
72	cg12556309	TRIM39	chr6	30304289	1.85	7.00E-02	2.90	2.59E-04	1.74	4.43E-02
73	cg25390635	GRAMD4	chr22	47022618	2.15	1.01E-01	5.05	7.04E-05	2.84	1.43E-02
74	cg06193766	DIP2C	chr10	375391	1.92	3.59E-04	1.12	3.96E-02	1.09	2.19E-02
75	cg00114012	SLC2A8	chr9	130158144	-3.08	2.88E-02	-4.49	6.63E-04	-3.32	4.51E-02
76	cg09995736	MIR331	chr12	95702136	6.21	1.71E-04	3.66	1.15E-01	5.44	3.13E-02
77	cg13068215	FMN2	chr1	240286481	1.86	1.67E-01	4.23	7.08E-05	3.07	2.22E-02
78	cg10111845	MED13L	chr12	116714901	4.73	4.09E-03	4.92	6.03E-03	4.97	2.88E-02
79	cg05975928	HBG2	chr11	5442511	2.80	5.42E-02	5.30	2.39E-04	2.89	4.00E-02
80	cg22007536	HECW1	chr7	43235712	3.48	2.50E-02	5.89	6.05E-04	3.68	1.00E-02
81	cg12341202	LINC00900	chr11	115531299	-7.97	2.63E-03	-4.53	5.04E-03	-4.12	1.81E-02
82	cg19603836	KIAA1462	chr10	30317688	3.40	2.06E-02	3.81	1.32E-03	2.51	4.31E-02
83	cg01649647	MYL9	chr20	35177530	-5.51	5.68E-04	-3.61	3.67E-02	-4.71	3.33E-02

#	ProbeID	Gene	CHR	Position	PR-GOAL		GALA II		Mega-analysis	
					Effect	Pvalue	Effect	Pvalue	Effect	Pvalue
84	cg10880485	SIX6	chr14	60974384	3.40	6.57E-03	2.92	4.30E-03	2.74	5.37E-03
85	cg27524128	ZHX2	chr8	123734126	1.58	2.25E-01	2.70	1.37E-04	1.57	9.27E-01
86	cg09858281	MROH5	chr8	142456070	-3.25	2.73E-02	-5.31	7.03E-04	-3.69	4.55E-02
87	cg25962840	PSD4	chr2	113930962	-3.91	3.66E-04	-2.20	4.90E-02	-3.07	4.33E-02
88	cg17027138	ANKRD55	chr5	55529228	4.26	3.65E-02	2.89	7.51E-04	1.86	9.40E-01
89	cg04039397	CD96	chr3	111260783	-0.55	3.33E-01	-2.47	6.76E-06	-1.41	3.98E-01
90	cg07803420	DDR1	chr6	30851517	2.68	2.75E-02	3.21	1.13E-03	1.86	7.58E-01
91	cg25062539	IL7	chr8	79718482	4.66	7.53E-03	6.05	3.69E-03	4.48	4.97E-02
92	cg13737493	GADD45G	chr9	92216472	-4.40	1.92E-03	-3.98	1.70E-02	-3.77	3.85E-02
93	cg01295399	CHAT	chr10	50820278	3.33	2.46E-03	2.76	1.28E-02	2.38	1.75E-01
94	cg02190383	BEST1	chr11	61725666	-4.55	9.41E-03	-5.83	3.16E-03	-4.93	1.11E-01
95	cg14778914	ARSG	chr17	66289482	2.87	4.77E-02	5.71	3.06E-04	2.54	1.17E-01
96	cg01140214	CCHCR1	chr6	31110647	3.57	1.44E-02	4.16	2.31E-03	3.45	4.41E-02
97	cg02864638	CCDC144NL	chr17	20840716	5.31	3.46E-03	3.33	6.34E-03	2.81	2.99E-01
98	cg04317047	MIR143HG	chr5	148808388	-3.13	2.68E-02	-3.57	1.38E-03	-2.30	5.52E-01
99	cg05465955	COASY	chr17	40715236	-2.49	1.75E-02	-3.37	1.78E-03	-2.83	9.67E-02
100	cg27041424	VWF	chr12	6232979	-3.17	5.41E-03	-4.20	5.86E-03	-3.10	4.67E-02
101	cg26338867	RBP5	chr12	7282186	-2.16	1.45E-03	-1.55	2.17E-02	-1.80	1.53E-01
102	cg21282452	SREBF2	chr22	42232160	2.00	1.94E-01	3.69	1.72E-04	1.83	1.49E-01
103	cg19851574	RPS6KA2	chr6	167178233	-1.41	1.70E-02	-1.73	2.20E-03	-1.42	3.08E-01
104	cg26557404	MYO5B	chr18	47721899	6.59	1.80E-04	3.06	9.63E-02	4.38	3.69E-02
105	cg04364695	ZMAT4	chr8	40618425	-0.60	3.53E-02	-0.99	7.71E-04	-0.64	1.45E-01
106	cg18708402	LIMCH1	chr4	41343184	3.28	7.19E-03	3.69	5.74E-03	3.10	3.57E-02
107	cg19470962	MRPL4	chr19	10367329	2.56	2.40E-01	6.80	7.24E-05	3.22	1.09E-01
108	cg22210627	GFM1	chr3	158390671	5.54	3.13E-03	5.35	1.38E-02	4.72	6.54E-02
109	cg01609688	TENM4	chr11	80125365	4.44	1.99E-03	2.79	1.39E-02	2.42	4.94E-02
110	cg05713856	SAMD12	chr8	119504312	2.44	3.21E-01	4.09	1.69E-04	2.80	4.19E-01
111	cg18309129	DHX34	chr19	47852304	-3.51	2.51E-02	-3.00	1.74E-03	-2.32	4.43E-02

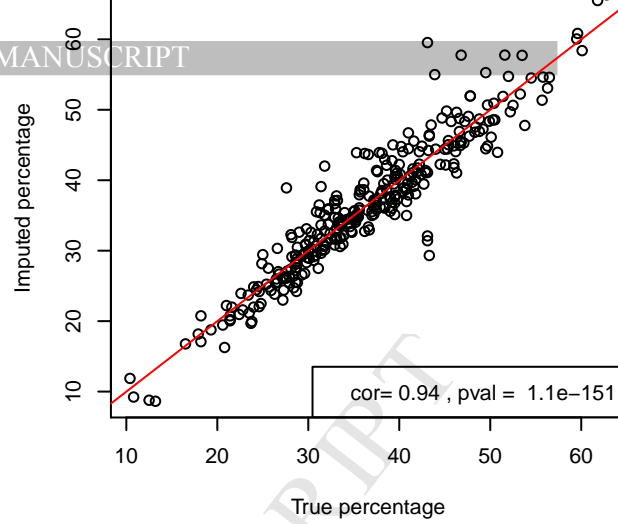
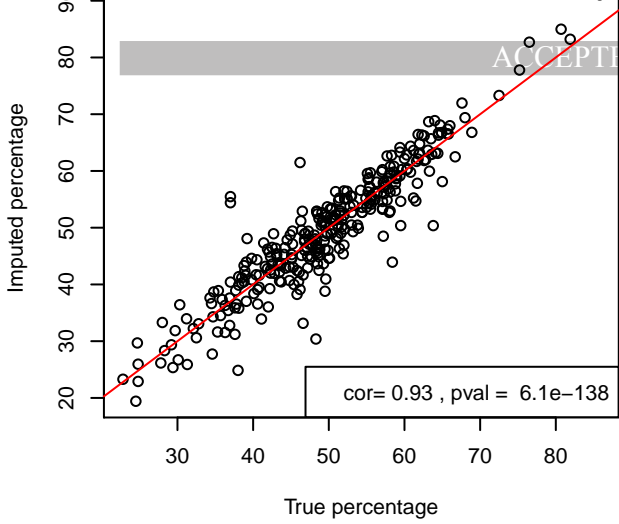
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113	cg22715764	PEX14	chr1	10556294	1.29	1.35E-01	2.48	2.22E-04	1.55	3.14E-01
114	cg13702181	GSTZ1	chr14	77791657	2.00	3.87E-01	5.07	9.36E-05	2.35	2.73E-01
115	cg25514475	UBTD2	chr5	171693762	5.25	9.35E-03	3.47	3.60E-03	3.15	1.44E-01
116	cg26229990	ADCY4	chr14	24801301	-2.34	6.06E-06	-0.43	4.28E-01	-1.39	1.78E-01
117	cg21269781	RHBDL3	chr17	30602727	6.79	1.61E-04	2.83	7.90E-02	3.62	1.73E-01
118	cg08102414	FAM53A	chr4	1570791	2.86	8.85E-04	1.75	3.54E-02	2.22	1.75E-01
119	cg08537737	SLCO5A1	chr8	70743047	2.74	5.04E-03	2.32	8.88E-03	1.69	7.55E-01
120	cg13388253	KLK9	chr19	51505507	1.19	3.30E-02	1.99	9.16E-04	1.38	4.91E-01
121	cg21163717	DOK2	chr8	21769903	-1.25	2.05E-01	-2.99	1.13E-04	-1.68	3.98E-01
122	cg23598886	PTPN2	chr18	12777645	1.34	4.41E-03	1.33	1.13E-02	1.59	2.83E-01
123	cg13649658	EHMT1	chr9	140680393	3.72	7.19E-02	4.58	7.36E-04	2.46	2.00E-01
124	cg10276272	GRIN2A	chr16	10271822	2.98	2.38E-01	4.31	2.60E-04	2.64	6.66E-01
125	cg22987011	IQGAP2	chr5	75753776	-1.45	2.04E-02	-1.92	2.27E-03	-1.50	4.74E-01
126	cg08776660	CRAMP1	chr16	1670473	-1.98	2.47E-02	-2.92	1.66E-03	-2.19	5.17E-01
127	cg08715862	FHOD1	chr16	67275028	2.68	1.91E-01	8.02	5.81E-05	3.92	4.79E-01
128	cg23706836	MCPH1	chr8	6407997	-2.93	5.27E-03	-3.61	9.48E-03	-3.00	2.78E-01
129	cg18520777	VPS13B	chr8	100635039	4.94	8.40E-04	3.14	4.83E-02	3.57	6.40E-01
130	cg02205445	GTDC1	chr2	144648543	4.38	1.46E-02	4.16	3.78E-03	3.18	3.02E-01
131	cg13313047	CABLES1	chr18	20735648	8.53	7.81E-03	5.28	4.70E-03	4.25	5.81E-01
132	cg02985445	BRI3	chr7	97908505	-4.97	8.05E-04	-3.27	6.08E-02	-3.88	2.15E-01
133	cg09304047	ASB3	chr2	53747541	4.31	2.70E-03	2.63	1.38E-02	2.38	4.58E-01
134	cg15700636	PRG2	chr11	57156050	-5.59	9.80E-04	-4.08	5.70E-02	-4.32	8.14E-01
135	cg10717869	SLC41A1	chr1	205780912	2.98	6.73E-03	2.60	8.85E-03	1.99	3.37E-01
136	cg20320283	FOXE3	chr1	47880440	-2.27	5.85E-02	-3.70	7.79E-04	-2.18	5.08E-01
137	cg27455540	NT5C1B-RDH14	chr2	18866125	-3.15	6.55E-03	-3.45	9.52E-03	-3.11	1.91E-01
138	cg13674483	LOC100131347	chr17	37212827	3.50	4.91E-03	2.60	1.10E-02	2.46	9.07E-01
139	cg16524108	FAM161B	chr14	74416111	2.03	1.53E-01	5.48	1.08E-04	3.32	7.81E-01

#	ProbeID	Gene	CHR	Position	PR-GOAL		GALA II		Mega-analysis	
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140	cg14827149	WNT4	chr1	22441051	4.45	4.43E-02	3.22	1.36E-03	1.82	2.48E-03
141	cg24478310	SYCP2L	chr6	10763337	3.49	1.79E-02	3.52	3.70E-03	2.39	7.49E-03
142	cg03550384	TMEM64	chr8	91803357	-1.35	1.13E-01	-1.94	5.78E-04	-1.31	4.01E-03
143	cg26477387	ZNF292	chr6	87973166	1.87	3.31E-03	4.86	4.49E-03	2.00	4.12E-03
144	cg10592478	RARG	chr12	53612641	4.91	2.60E-03	2.75	1.32E-02	2.37	5.43E-03
145	cg12002455	MCMBP	chr10	121609179	4.55	3.50E-03	3.27	1.55E-02	2.85	3.92E-03
146	cg00975680	NUP133	chr1	229618011	2.95	5.59E-02	6.16	4.73E-04	3.77	9.60E-03
147	cg10504062	PCCB	chr3	135968952	-3.57	2.09E-02	-5.64	2.17E-03	-4.27	2.21E-03
148	cg26376346	TGFBR2	chr3	30647378	3.08	2.44E-02	2.83	2.79E-03	2.15	3.75E-03
149	cg00811377	DHX16	chr6	30636608	4.55	3.18E-02	4.22	2.19E-03	2.57	1.66E-03
150	cg10761558	SSBP3	chr1	54842205	-2.99	3.29E-03	-2.78	2.07E-02	-2.75	2.93E-03
151	cg17001401	IL6R	chr1	154425845	4.76	1.04E-02	4.13	6.28E-03	3.29	3.31E-03
152	cg20752847	DNAH10	chr12	124248044	2.42	2.57E-02	2.59	2.70E-03	1.84	3.91E-03
153	cg06647928	ENC1	chr5	73612203	-3.13	9.21E-03	-3.13	7.43E-03	-2.75	7.81E-03
154	cg08295857	BANP	chr16	88096588	2.44	1.71E-01	3.63	4.30E-04	1.87	2.15E-03
155	cg18501230	LOC286083	chr8	1338706	-2.89	1.04E-02	-4.09	5.30E-03	-3.40	1.11E-03
156	cg24765360	EN1	chr2	119611101	3.27	5.50E-02	5.35	8.99E-04	3.72	1.11E-03
157	cg14329508	CSRP2BP	chr20	18168289	3.70	5.97E-02	2.78	1.17E-03	1.63	2.51E-03
158	cg11432069	MCM3AP	chr21	47702262	4.83	2.60E-02	2.93	1.95E-03	1.40	7.10E-03
159	cg25279613	OSBPL3	chr7	24956523	-1.22	1.16E-01	-3.27	1.38E-04	-1.77	1.63E-03
160	cg02737486	MFAP3L	chr4	170917265	-0.69	5.19E-02	-1.21	8.31E-04	-0.87	3.09E-03
161	cg03437273	KRTAP4-3	chr17	39324367	-3.90	6.79E-04	-1.84	3.78E-02	-2.64	1.41E-03
162	cg03987786	LOC100128288	chr17	8264387	-3.14	9.43E-04	-1.99	6.06E-02	-2.51	2.74E-03
163	cg08438392	IFT172	chr2	27708644	2.99	1.51E-01	5.78	3.37E-04	2.83	1.73E-03
164	cg13543576	LINC01347	chr1	243263770	-3.48	2.97E-04	-1.91	2.35E-01	-3.00	1.92E-03
165	cg10828337	FOXP1	chr14	29236476	6.55	2.94E-03	4.77	2.15E-02	4.99	8.68E-03
166	cg26783146	CORO7-PAM16	chr16	4423632	1.83	2.78E-01	3.44	2.68E-04	1.86	1.70E-03
167	cg22109240	KCTD18	chr2	201374010	1.97	4.61E-03	1.65	1.57E-02	1.73	2.62E-03

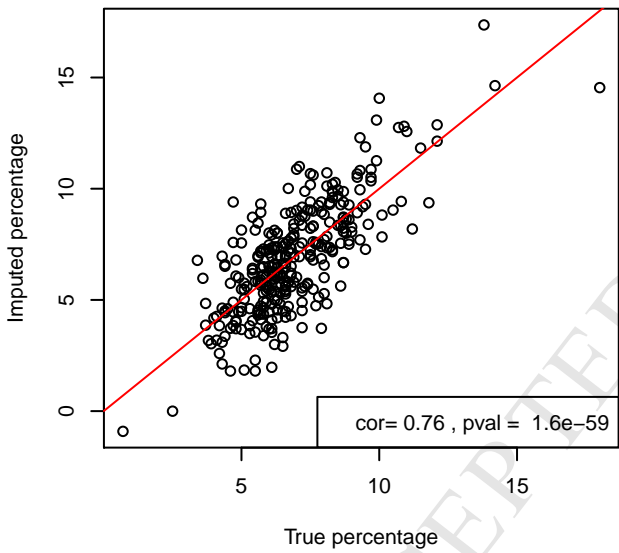
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					Effect	Pvalue	Effect	Pvalue	Effect	Pvalue
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169	cg27180994	URGCP-MRPS24	chr7	43929080	3.14	8.40E-02	4.99	7.37E-04	2.98	7.17E-04
170	cg16135989	UNC5A	chr5	176166629	-0.93	1.60E-01	-1.90	2.99E-04	-1.28	1.49E-04
171	cg16447058	DAPK2	chr15	64231444	5.64	8.34E-03	4.87	8.83E-03	3.99	3.77E-03
172	cg18552413	ACKR1	chr1	159174610	-2.58	6.38E-03	-2.37	1.20E-02	-1.90	1.58E-02
173	cg18544809	PPP2R2C	chr4	6380812	-1.71	9.62E-02	-3.50	4.07E-04	-2.47	5.13E-04
174	cg26784011	NKX2-2	chr20	21497842	4.97	1.15E-02	4.34	6.69E-03	3.78	1.87E-03
175	cg07942135	HOXA3	chr7	27154262	5.41	4.36E-03	2.77	8.04E-03	2.08	1.46E-03
176	cg18878432	HOXB-AS3	chr17	46683409	1.53	2.57E-01	3.67	1.81E-04	1.78	1.94E-04
177	cg03829559	SPTBN1	chr2	54681906	1.75	2.52E-01	3.44	2.76E-04	1.62	2.73E-04
178	cg12817389	ASPH	chr8	62602522	4.49	5.39E-02	2.62	1.20E-03	1.59	2.20E-03
179	cg19951409	ZNF516	chr18	74175071	4.04	3.70E-02	5.36	2.01E-03	3.99	1.50E-03
180	cg05888037	TEX26-AS1	chr13	31506270	-2.54	2.73E-02	-3.14	2.85E-03	-2.33	2.05E-03
181	cg18096987	VGLL4	chr3	11623873	2.91	2.81E-03	1.95	2.22E-02	2.07	8.43E-03
182	cg21301258	RCAN1	chr21	35898717	2.23	2.38E-02	2.55	3.43E-03	1.54	1.17E-03
183	cg18180230	ENDOD1	chr11	94798802	1.68	1.37E-02	4.45	9.64E-04	1.71	2.98E-04
184	cg06066452	PLXNB1	chr3	48470258	1.42	2.10E-01	4.06	1.12E-04	2.18	3.80E-04
185	cg18720687	NXN	chr17	855312	-6.11	4.30E-02	-5.19	1.99E-03	-3.53	8.86E-04
186	cg05941652	LAMA3	chr18	21273909	2.12	1.33E-01	5.25	2.06E-04	2.55	5.61E-04
187	cg12652442	CCDC169-SOHLH2	chr13	36738072	1.62	2.23E-01	3.25	2.93E-04	1.78	1.24E-04
188	cg11860434	LOC100630923	chr7	102067440	-3.58	7.61E-03	-2.19	7.14E-03	-1.66	9.13E-03
189	cg23274951	NDUFS2	chr1	161171632	3.37	1.60E-01	5.18	5.32E-04	3.16	7.97E-04
190	cg07570835	USP48	chr1	22029963	1.56	2.15E-01	3.81	1.87E-04	1.56	4.70E-04
191	cg11819201	FMO6P	chr1	171105925	-3.21	5.49E-03	-2.88	1.55E-02	-2.36	3.14E-02
192	cg11781676	LOC645949	chr2	22416541	4.22	4.11E-03	3.58	2.04E-02	3.07	3.25E-02
193	cg25461865	ENPP3	chr6	131958550	3.59	6.73E-03	2.84	1.17E-02	1.88	1.84E-02
194	cg24261644	CTAGE1	chr18	19997864	4.59	9.12E-03	3.39	8.09E-03	2.82	3.68E-03
195	cg07249888	PCSK6	chr15	101847305	1.67	3.95E-01	5.57	8.94E-05	2.47	2.45E-05

#	ProbeID	Gene	CHR	Position	PR-GOAL		GALA II		Mega-analysis	
					Effect	Pvalue	Effect	Pvalue	Effect	Pvalue
196	cg18139612	LOC653712	chr3	128572244	0.79	4.00E-01	4.43	8.63E-06	1.80	7.43E-02
197	cg10288525	LINC00423	chr13	33455187	4.00	6.62E-04	1.80	4.24E-02	2.68	1.76E-02
198	cg05792273	TRIM39	chr6	30310118	5.11	1.02E-02	4.46	8.43E-03	3.37	6.97E-03
199	cg03099728	ZNF274	chr19	58716135	5.82	1.05E-03	1.89	8.51E-03	1.53	1.09E-02
200	cg07284801	CYFIP2	chr5	156736991	3.04	4.89E-02	3.29	1.96E-03	1.98	1.45E-02

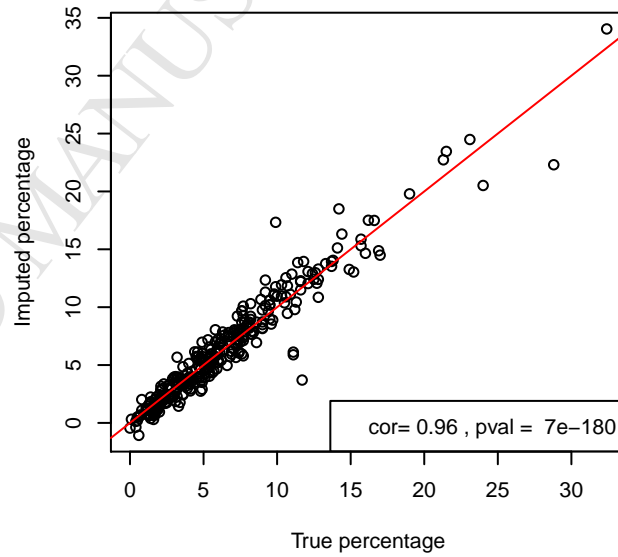
<sup>a</sup> Effect size: the parameter in our EWAS models. Effect size = 5 means an increase of 1% methylation beta-value associated with a 5-fold increase in log<sub>10</sub> scaled total IgE level.



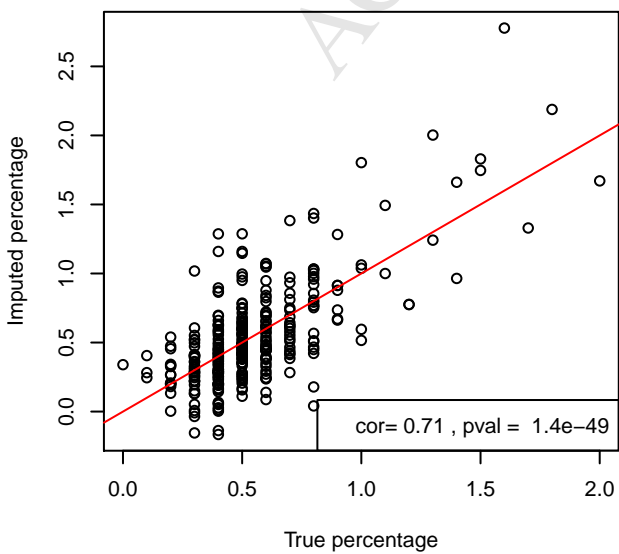
### Monocytes Percentage



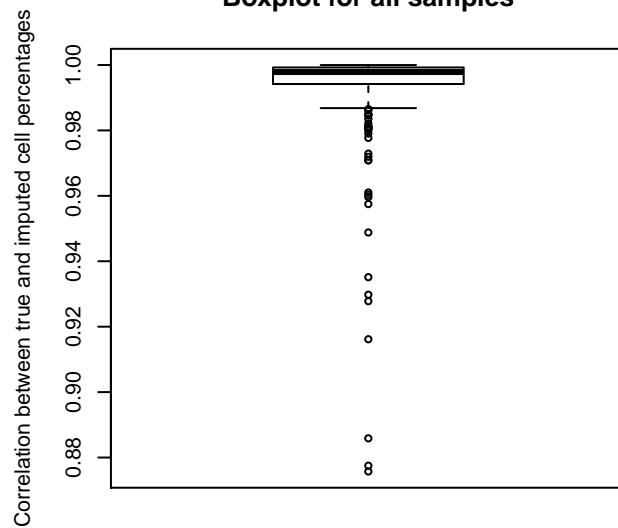
### Eosinophils Percentage



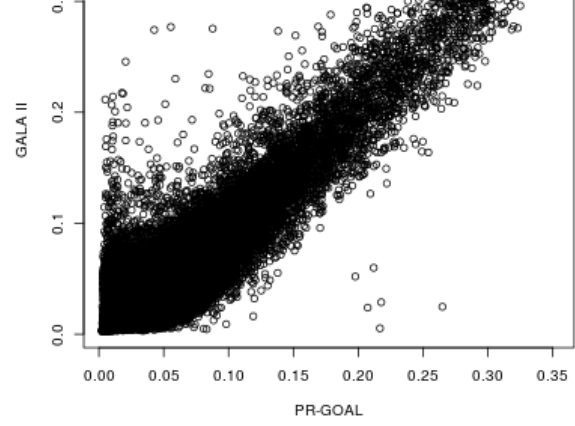
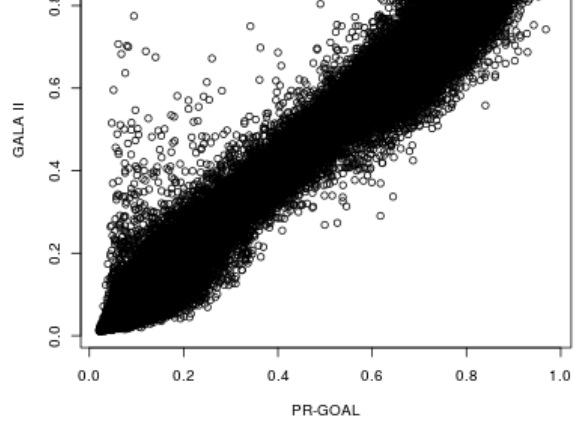
### Basophils Percentage



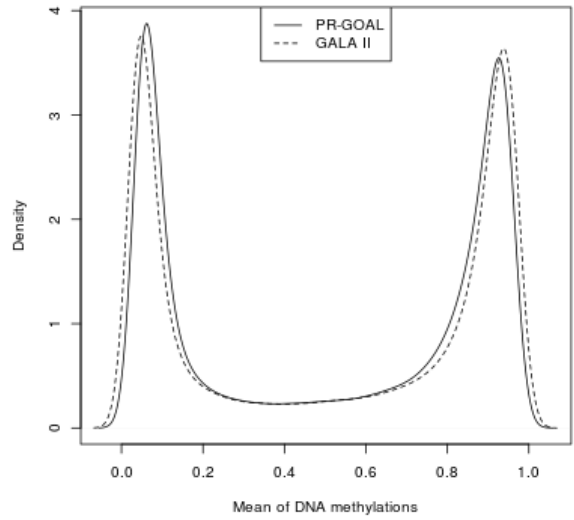
### Boxplot for all samples



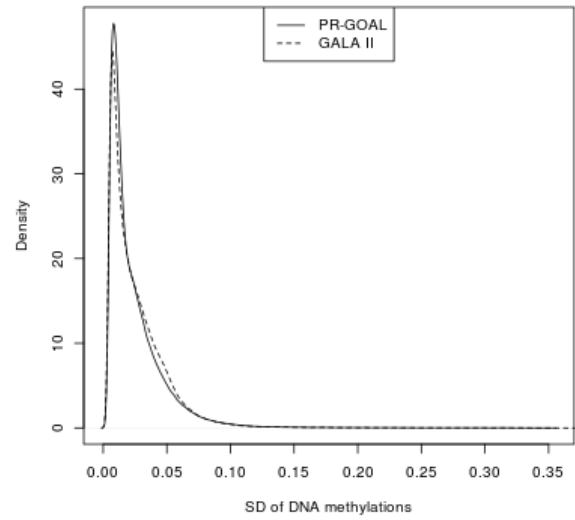




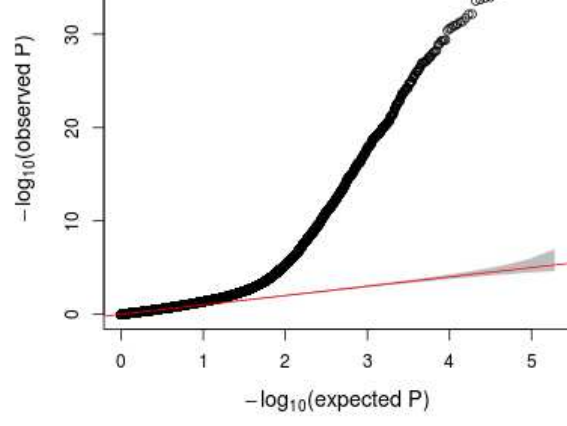
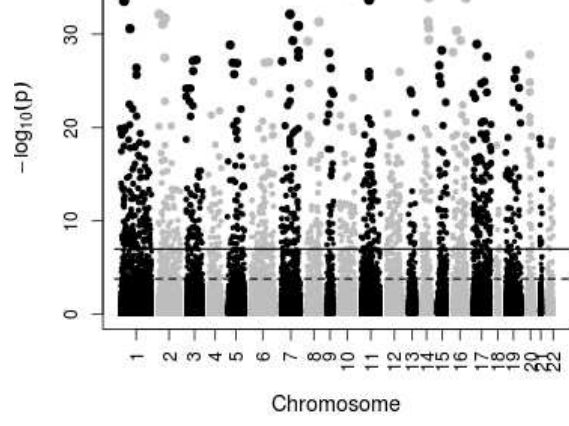
Density of mean methylation



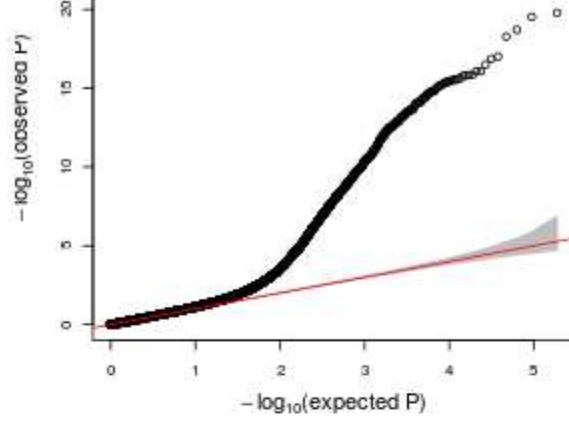
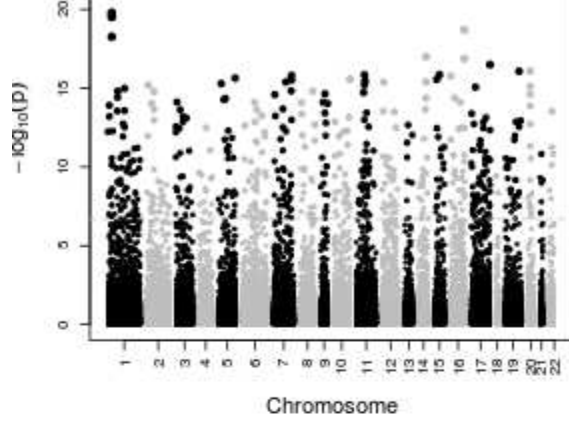
Density of SD of DNA methylation



ACCEPT

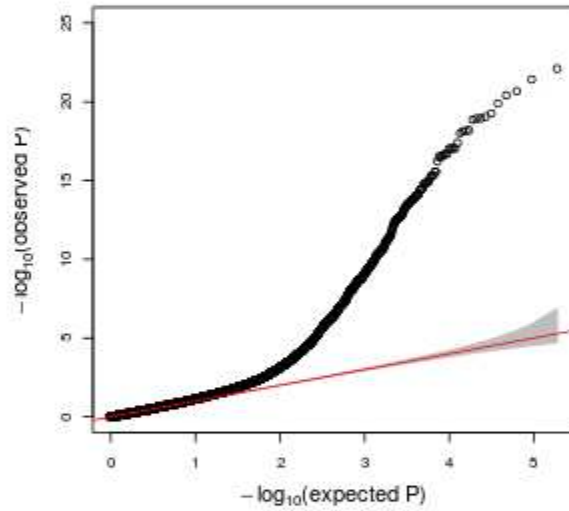
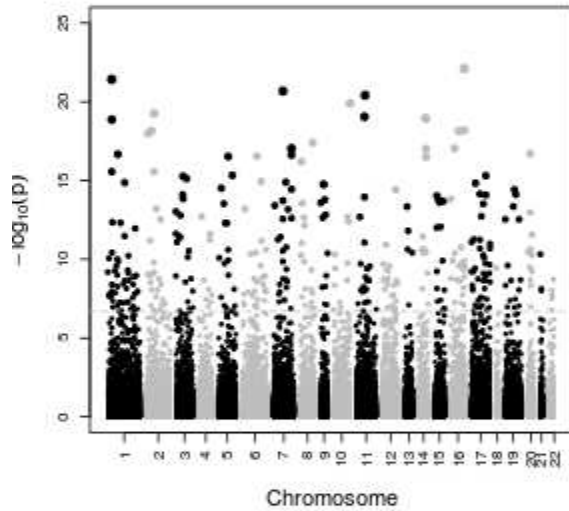


ACCEPTED MANUSCRIPT



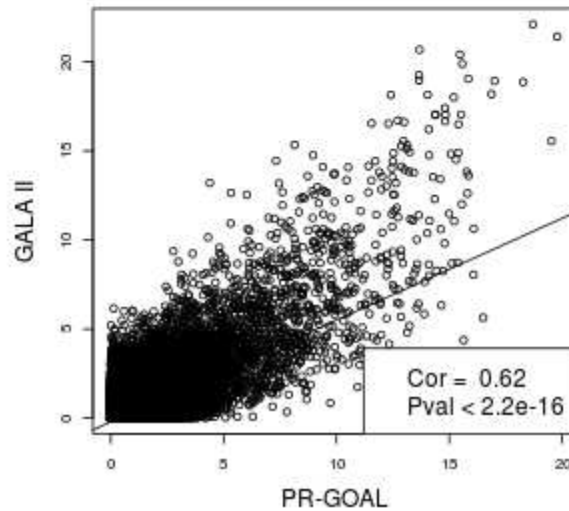
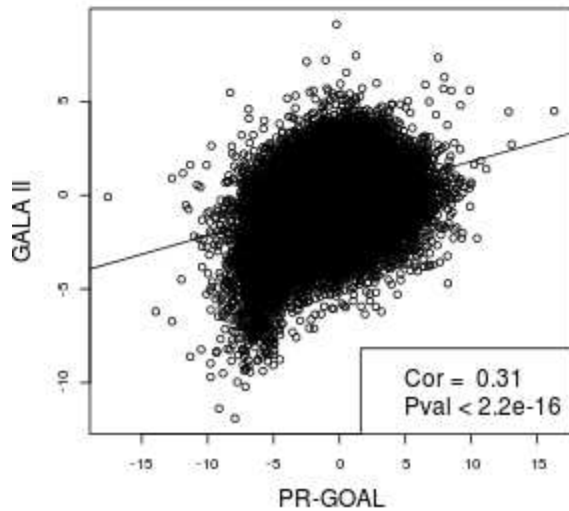
Manhattan plot for GALA II unadjusting for cell types

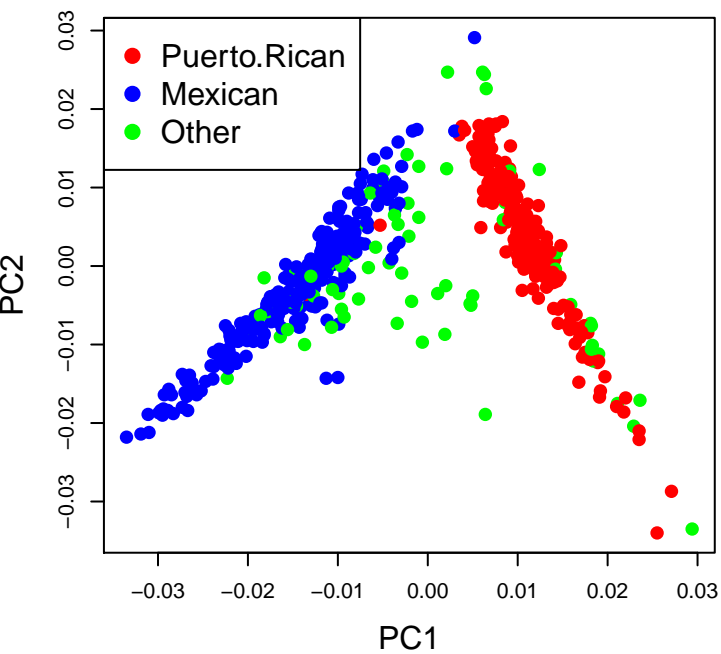
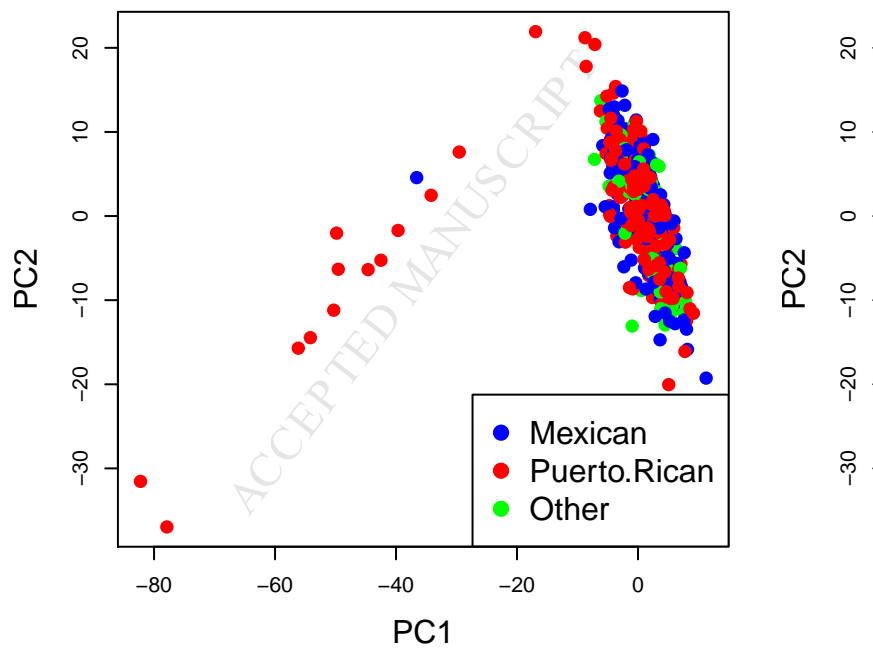
QQ plot for GALA II unadjusting for cell types

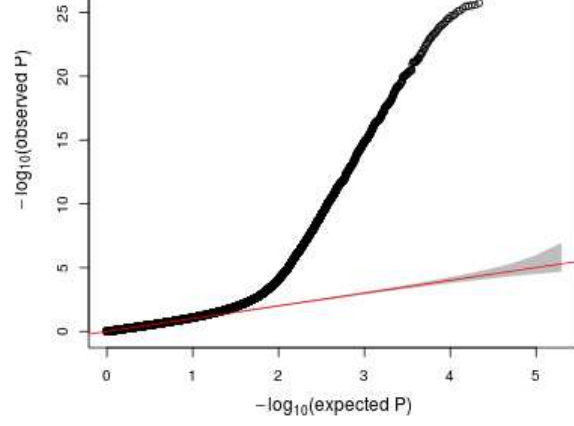
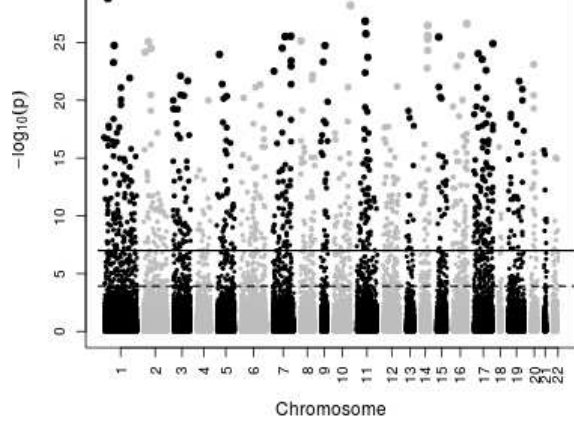


Compare EWAS effect size

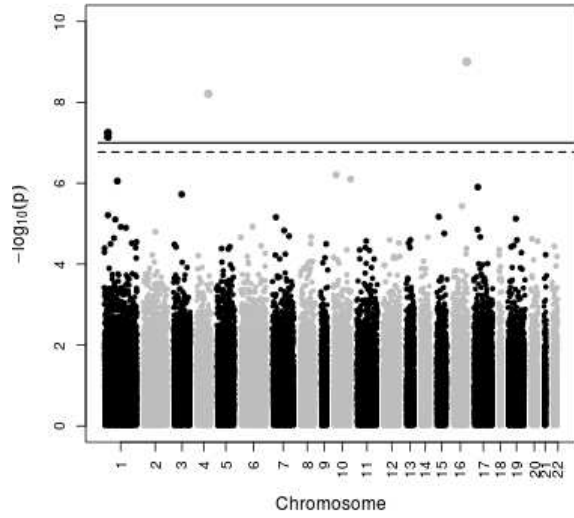
Compare EWAS  $-\log_{10}(P\text{val})$



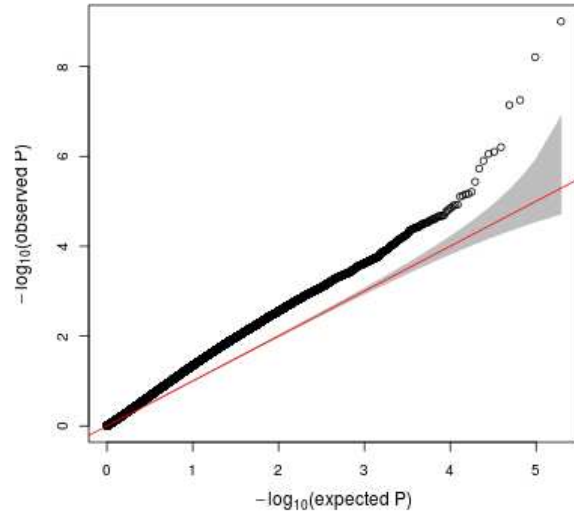
**Population and First 2 PCs of Genotype****Population and First 2 PCs of Methylation**



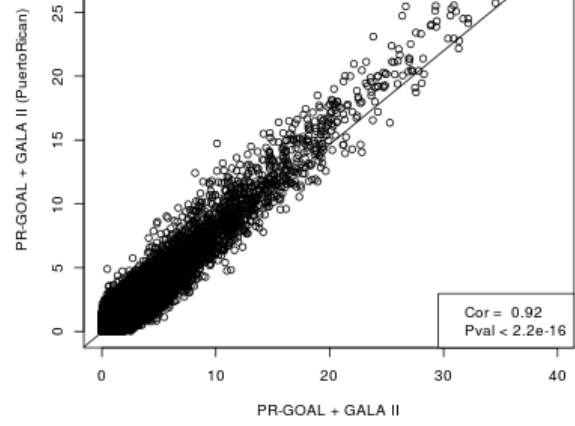
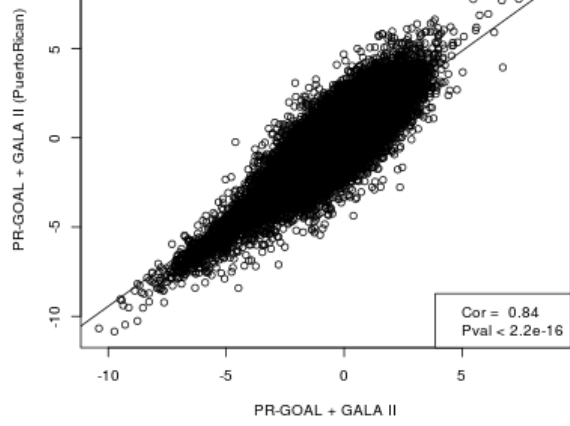
Manhattan plot, adjusting for cell types



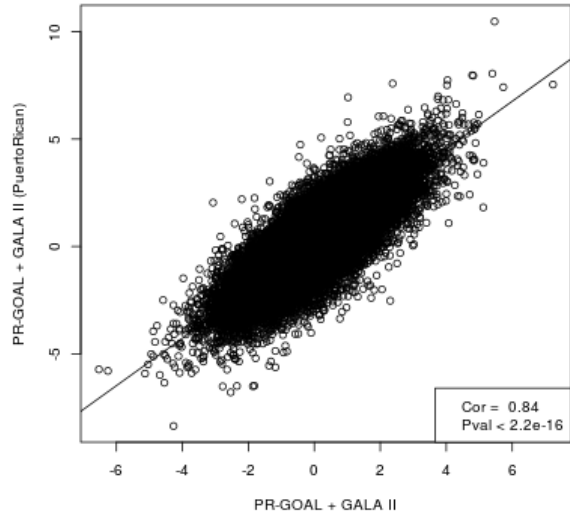
QQ plot, adjusting for cell types



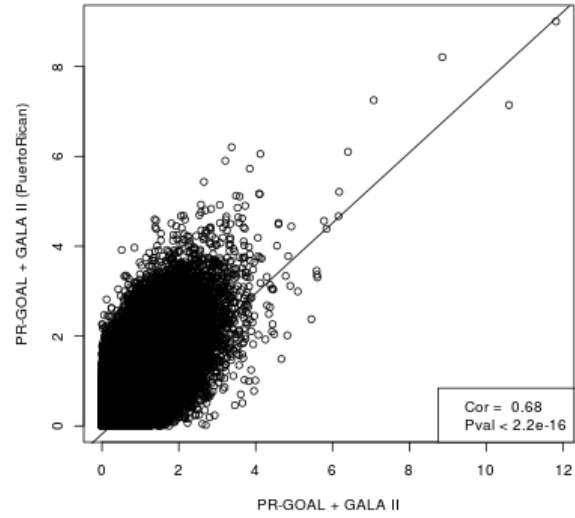
ACCEPT



Compare EWAS Effect Size, with WBC adjustment



Compare EWAS -log10(Pval), with WBC adjustment



ACCEPT