**General information**

**GWAS summary statistics of allergen component GWAS.**

|  |  |
| --- | --- |
| **Genotyping array**: | The Illumina Infinium Asian Screening Array (illumina). |
| **Sample QC**: | We excluded samples based on the following criteria: (1) a call rate of less than 98%, (2) outliers from the Japanese ancestry estimated by use of principal-component (PC) analysis using the 1000 Genome Project Phase 3, (3) a close familial relationship estimated with PLINK as PI\_HAT more than 0.1875, (4) phenotype-genotype sex discordance. |
| **Variant QC**: | We selected the genotyped variants based on the following criteria: (1) Gentrain score of more than or equal to 0.7, (2) minor allele frequency more than 1%, (3) variant genotyping call rate more than 95%, (4) Hardy–Weinberg-equilibrium P value more than 1.0 × 10-5. |
| **Phasing and imputation**: | shapeit2 and Minimac4 software |
| **Imputation reference**: | JGAS000114 reference panel |
| **Post-imputation QC**: | We selected variants with an imputation quality of Rsq more than 0.7 and minor allele count greater than or equal to 20. |
| **Association test**: | SAIGE software was used with age,　sex, and top 10 principal components as covariates.  |

**Uploaded files**

**GWAS summary statistics of allergen component GWAS**

|  |  |
| --- | --- |
| File name | Descriptions |
| {trait}.txt | Summary results for autosomal variants |

**Columns**

|  |  |  |
| --- | --- | --- |
| # | column name | Descriptions |
| 1 | CHR | Chromosome |
| 2 | POS | Position (hg19) |
| 3 | MarkerID | Variant ID (rs number) |
| 4 | Allele1 | Non-effect allele |
| 5 | Allele2 | Effect allele |
| 6 | BETA | Effect size of effect allele |
| 7 | SE | Standard error |
| 8 | p.value | P value |

 Individual trait except total serum IgE

Alng1.txt: Aln g 1

Alta1.txt: Alt a 1

Amba1.txt: Amb a 1

Arah8.txt: Ara h 8

Betv1.txt: Bet v 1

Betv2.txt: Bet v 2

Blot5.txt: Blo t 5

Canf1.txt: Can f 1

Cora1.0101.txt: Cor a 1.0101

Cora1.0401.txt: Cor a 1.0401

Cryj1.txt: Cry j 1

Cupa1.txt: Cup a 1

Cynd1.txt: Cyn d 1

Derf1.txt: Der f 1

Derf2.txt: Der f 2

Derp1.txt: Der p 1

Derp2.txt: Der p 2

Feld1.txt: Fel d 1

Feld4.txt: Fel d 4

Glym4.txt: Gly m 4

Hevb8.txt: Hev b 8

Jugr2.txt: Jug r 2

Lepd2.txt: Lep d 2

Mald1.txt: Mal d 1

Mera1.txt: Mer a 1

Penm2.txt: Pen m 2

Phlp1.txt: Phl p 1

Phlp12.txt: Phl p 12

Phlp4.txt: Phl p 4

Phlp5.txt: Phl p 5

Plaa2.txt: Pla a 2

2Salbumin.txt: 2S albumin

7Sglobulin.txt: 7S globulin

Argininekinase.txt: Arginine kinase

Berberinebridgeenzyme.txt: Berberine bridge enzyme

Betaexpansin.txt: Beta expansin

Cysteinprotease.txt: Cystein protease

Grassgroup5.txt: Grass group 5

Lipocalin.txt: Lipocalin

Mitegroup5/21.txt: Mite group 5/21

NPC2family.txt: NPC2 family

Pectatelyase.txt: Pectate lyase

Polygalacturonase.txt: Polygalacturonase

PR-10Protein.txt: PR-10 Protein

Profilin.txt: Profilin

Tropomyosin.txt: Tropomyosin

Uteroglobin.txt: Uteroglobin

Total serum IgE

|  |  |  |
| --- | --- | --- |
| # | column name | Descriptions |
| 1 | CHR | Chromosome |
| 2 | POS | Position (hg19) |
| 3 | MarkerID | Variant ID (rs number) |
| 4 | Allele1 | Allele 1 |
| 5 | Allele2 | Allele 2 |
| 6 | Allele | Effect allele |
| 7 | TEST | Test identifier |
| 8 | OBS\_CT | Number of samples in regression |
| 9 | BETA | Regression coefficient |
| 10 | SE | Standard error of effect estimate |
| 11 | T\_STAT | T-statistic |
| 12 | p.value | P value |

total\_IgE.txt: total serum IgE

total\_IgE.txt: total serum IgE