**Table S2:** Loci with previous genome-wide significant associations to asthma (P < 5x10-8) in Japanese populations

|  |  |  |  |
| --- | --- | --- | --- |
| **Gene region a** | **SNP**b | **Reported** | **APCAT** |
| **Risk Allele** | **Freq** | **OR (95% CI)** | **P value** | **SNPs examined in APCAT c** | **Risk Allele** | **OR\_95%\_CI** | **P valued** |
| ***USP38-GAB1*** | rs7686660 | T | 0.27 | 1.16(1.11–1.21) | 1.87E-12 | rs7686660 | T | 0.97 (0.89,1.05) | 8.00E-01 |
| rs4485768 | G | 0.97 (0.89,1.04) | 8.08E-01 |
| rs10015501 | G | 0.97 (0.89,1.05) | 7.61E-01 |
| rs13126430 | A | 0.98 (0.90,1.05) | 7.47E-01 |
| rs13151714 | G | 0.97 (0.89,1.05) | 7.67E-01 |
| ***HLA* region (*NOTCH4*)** | rs404860 | A | 0.5 | 1.21(1.16–1.25) | 4.07E-23 | rs404860 | A | 0.94 (0.83,1.05) | 8.65E-01 |
| ***HLA* region****(*HLA-DPB1*)**  | rs987870 | C | 0.17 | 1.33(1.20–1.47) | 2.3E-10 | rs987870 | C | 0.92 (0.79,1.05) | 8.84E-01 |
| ***IKZF4*** | rs1701704 | G | 0.18 | 1.19(1.14–1.25) | 2.33E-13 | rs1701704 | G | 1.13 (1.05,1.21) | 1.32E-03 |
| rs773108 | G | 1.13 (1.05,1.21) | 1.09E-03 |
| rs773114 | T | 1.12 (1.04,1.19) | 2.03E-03 |
| rs2292239 | G | 1.12 (1.04,1.2) | 3.43E-03 |
| rs11171739 | C | 1.10 (1.03,1.18) | 5.83E-03 |
| rs2069408 | G | 1.08 (1.00,1.16) | 2.91E-02 |
| ***GATA3/TAF3*** | rs10508372 | C | 0.43 | 1.16(1.12–1.21) | 1.79E-23 | rs10508372 | C | 1.08 (0.94,1.23) | 1.40E-01 |
| rs10905491 | T | 1.16 (0.93,1.40) | 8.99E-01 |
| rs10905488 | T | 1.08 (0.94,1.23) | 8.60E-01 |

aGene shown is nearest gene to associated SNP. SNPs from the same locus are grouped together and shaded in the same color. bAll SNPs are from Hirota et al. (2011) (E[20](#_ENREF_20)) except for rs987870, which is from Noguchi et al. (2011) (E[21](#_ENREF_21)). cAll SNPs in LD with r2 > 0.8 with the reported SNP in the Hapmap JPT reference panel were collected, and a “clumped” set of SNPs was generated (only one SNP from a pair within 100 kb and pairwise r2 > 0.8in HapMap CEU). The association results in APCAT are reported for the most strongly associated SNPs in each clump, for each locus. dAPCAT P values are one-tailed with respect to the direction of the risk-increasing allele in the original report.