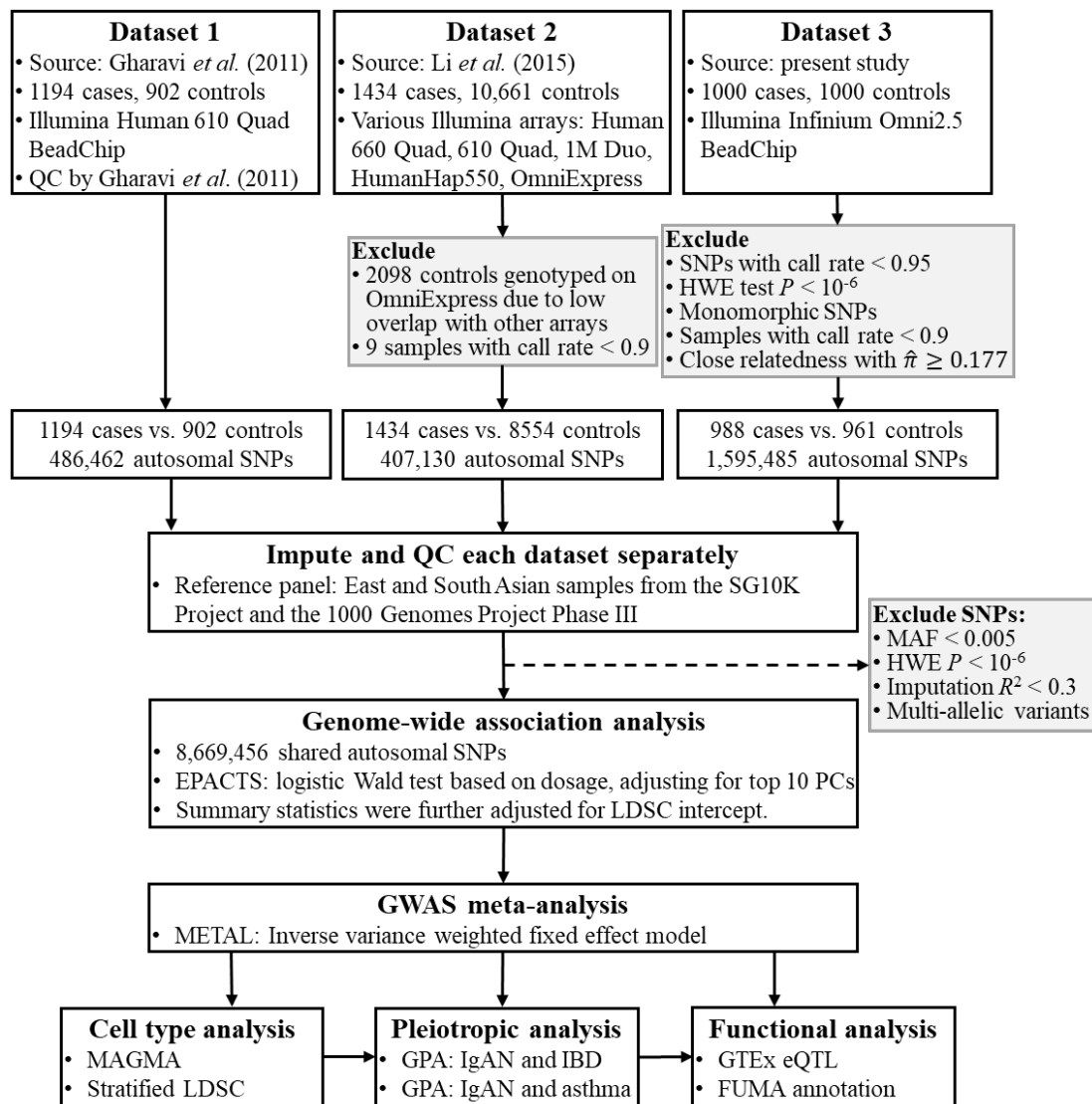
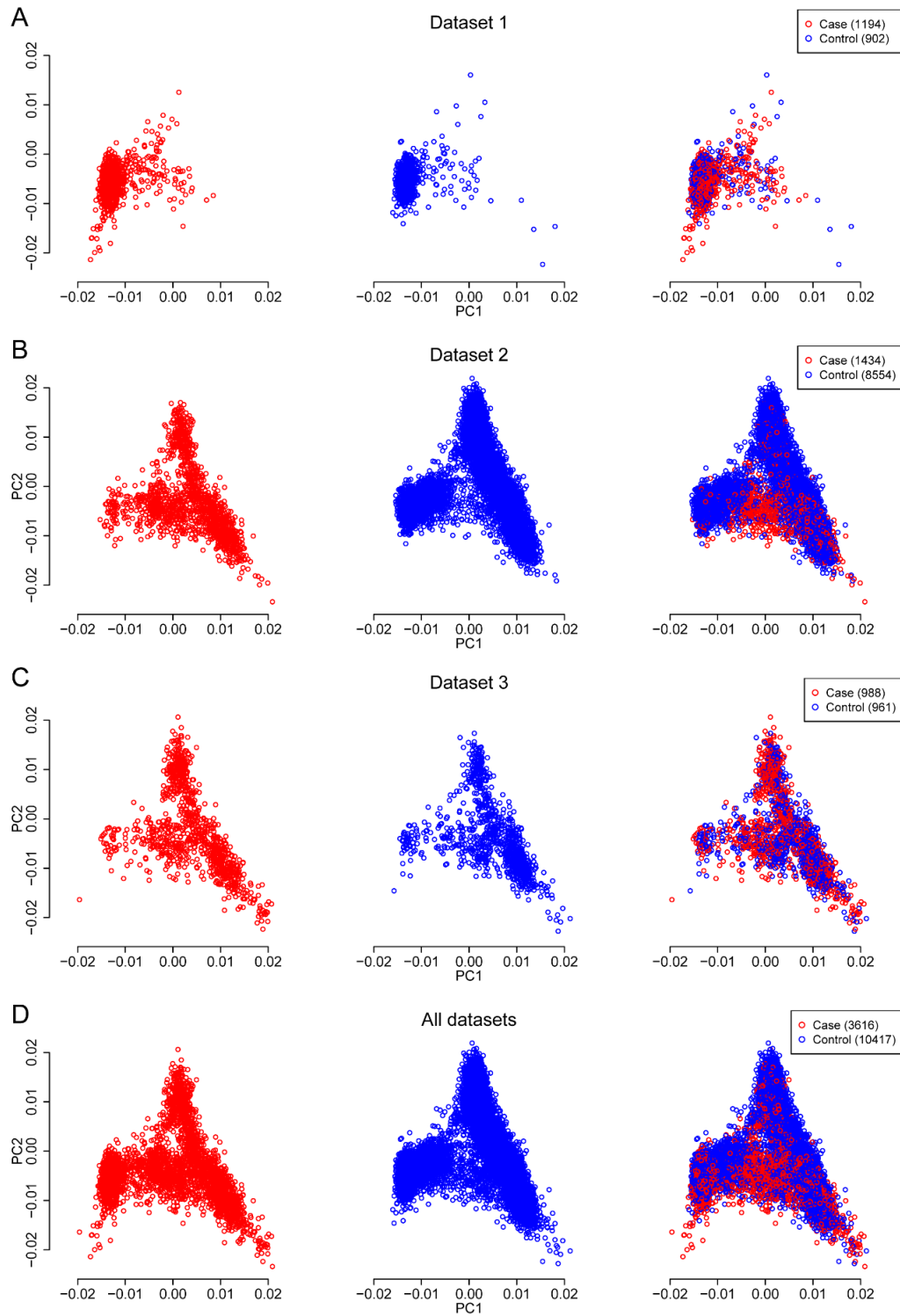


**Supplementary Figure 1. Flowchart of the present study.**

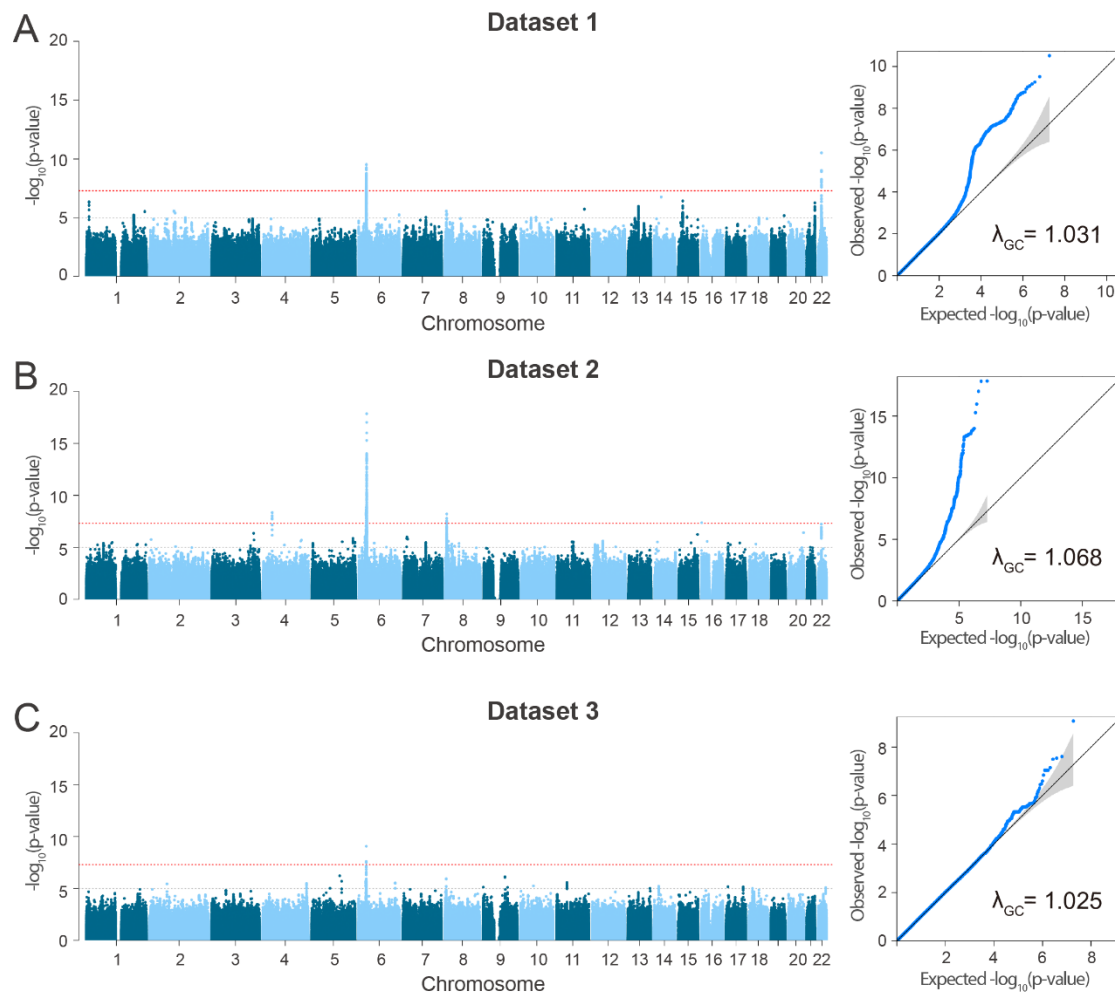


**Supplementary Figure 2. Population structure of GWAS samples for IgAN.** (A) PCA of samples in dataset 1. (B) PCA of samples in dataset 2. (C) PCA of samples in dataset 3. (D) PCA of all samples.

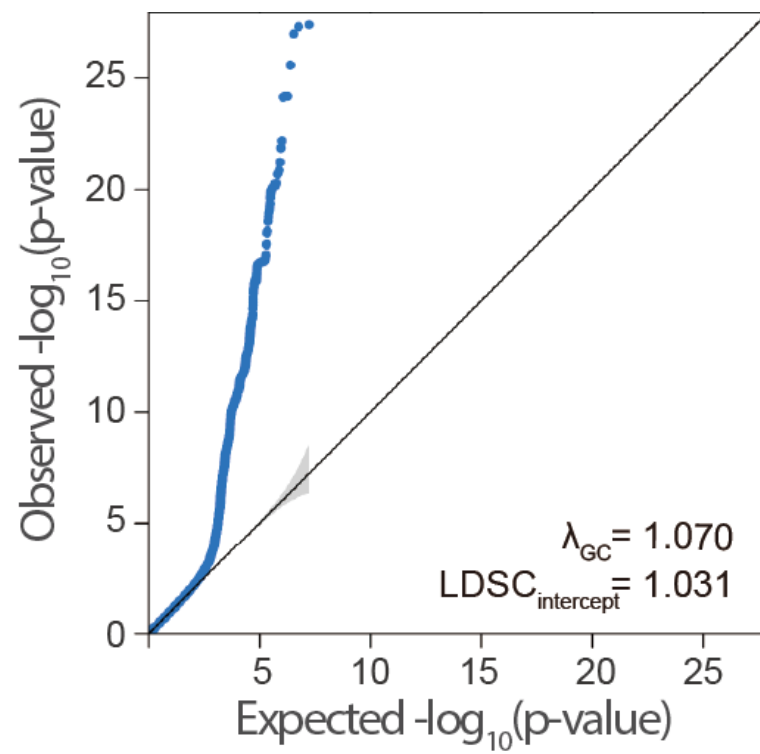


**Supplementary Figure 3. GWAS results for IgAN in three Chinese datasets. (A)**

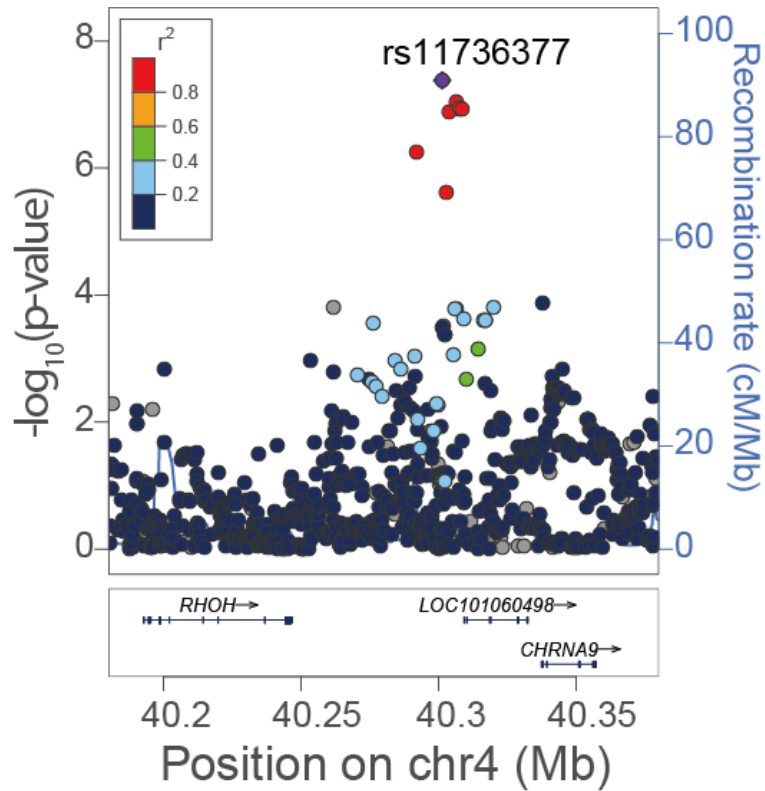
Dataset 1. (B) Dataset 2. (C) Dataset 3. The left panel is the Manhattan plot where the red dash line indicates the genome-wide significance level at  $P = 5 \times 10^{-8}$  and the grey dash line indicates the suggestive significance level at  $P = 1 \times 10^{-5}$ . The right panel is the QQ plot where the grey region represents 95% confidence interval under the null hypothesis of no association.



**Supplementary Figure 4. QQ plot of GWAS meta-analysis  $P$  values.** The grey region represents 95% confidence interval under the null hypothesis of no association.

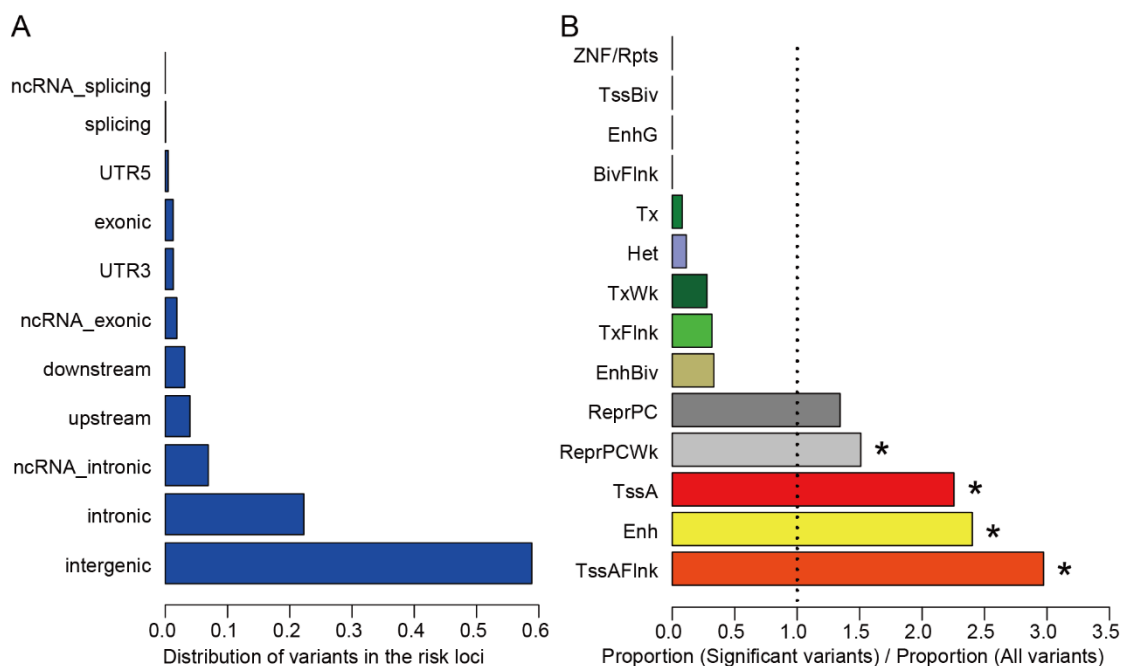


**Supplementary Figure 5. Regional plot of the novel locus at 4p14.** The lead variant is indicated by the purple diamond, while neighboring variants are colored by their LD with the lead variant based on East Asian samples from 1000 Genomes Project. Grey color indicates no LD information.

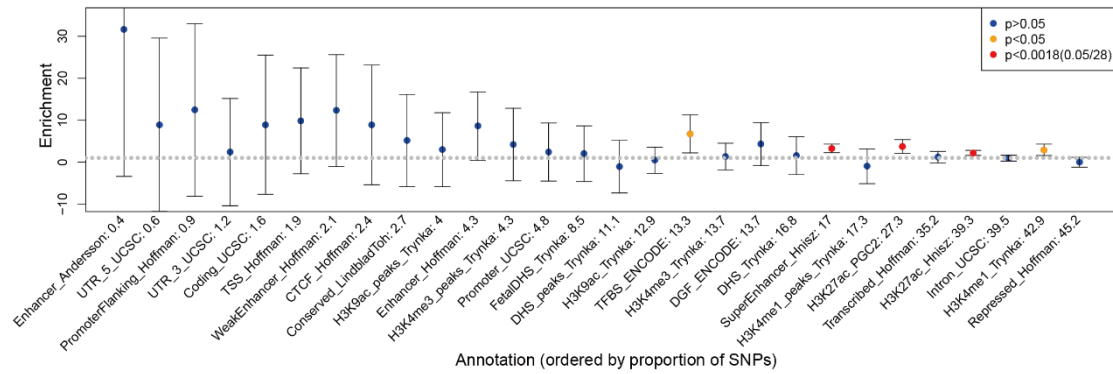


**Supplementary Figure 6. Genomic annotation of variants in IgAN associated loci.**

(A) Genomic distribution of the variants ( $P < 1 \times 10^{-5}$ ) in IgAN suggestive associated loci. (B) Annotation distribution of significant variants ( $P < 5 \times 10^{-8}$ ) in different chromatin states of the Th17 cells PMA-I stimulated CD4+CD25-IL17+. Asterisks indicate significant enrichment by Fisher's exact test ( $P < 0.05/14$ ). The associated region was defined as the region 500 kb around the lead variant reaching the suggestive significant threshold (A:  $P < 1 \times 10^{-5}$ ) or significant threshold (B:  $P < 1 \times 10^{-8}$ ). TssA: active transcription start site, TssAFlnk: flanking active transcription start site, TxFlnk: transcription at gene 5' and 3', Tx: strong transcription, TxWk: weak transcription, EnhG: genic enhancers, Enh: enhancers, ZNF/Rpts: ZNF genes and repeats, Het: heterochromatin, TssBiv: bivalent/poised transcription start site, BivFlnk: flanking bivalent TSS/Enh, EnhBiv, bivalent enhancer, ReprPC: repressed PolyComb, ReprPCWk: weak repressed PolyComb.



**Supplementary Figure 7. Heritability enrichment of 28 functional annotations calculated with the stratified LDSC.** The dot indicates the estimated enrichment, whereas the dashed line represents 95% confidence intervals. TSS, transcription start site; CTCF, CCCTC binding factor; DGF, digital genomic footprint; TFBS, transcription factor binding site; DHS, DNase I hypersensitivity site.



Supplementary Figure 8. Locus Compare plots for the colocalization analysis.

