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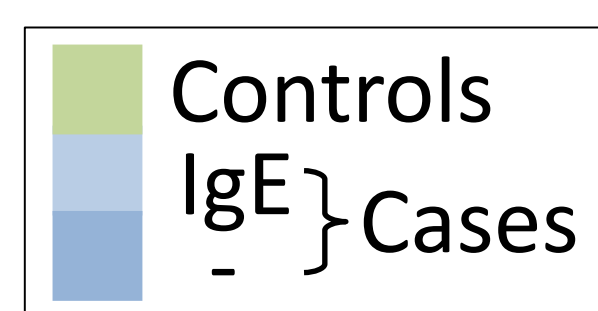
HLA and asthma in the Consortium on Asthma among African-ancestry Populations in the Americas (CAAPA)

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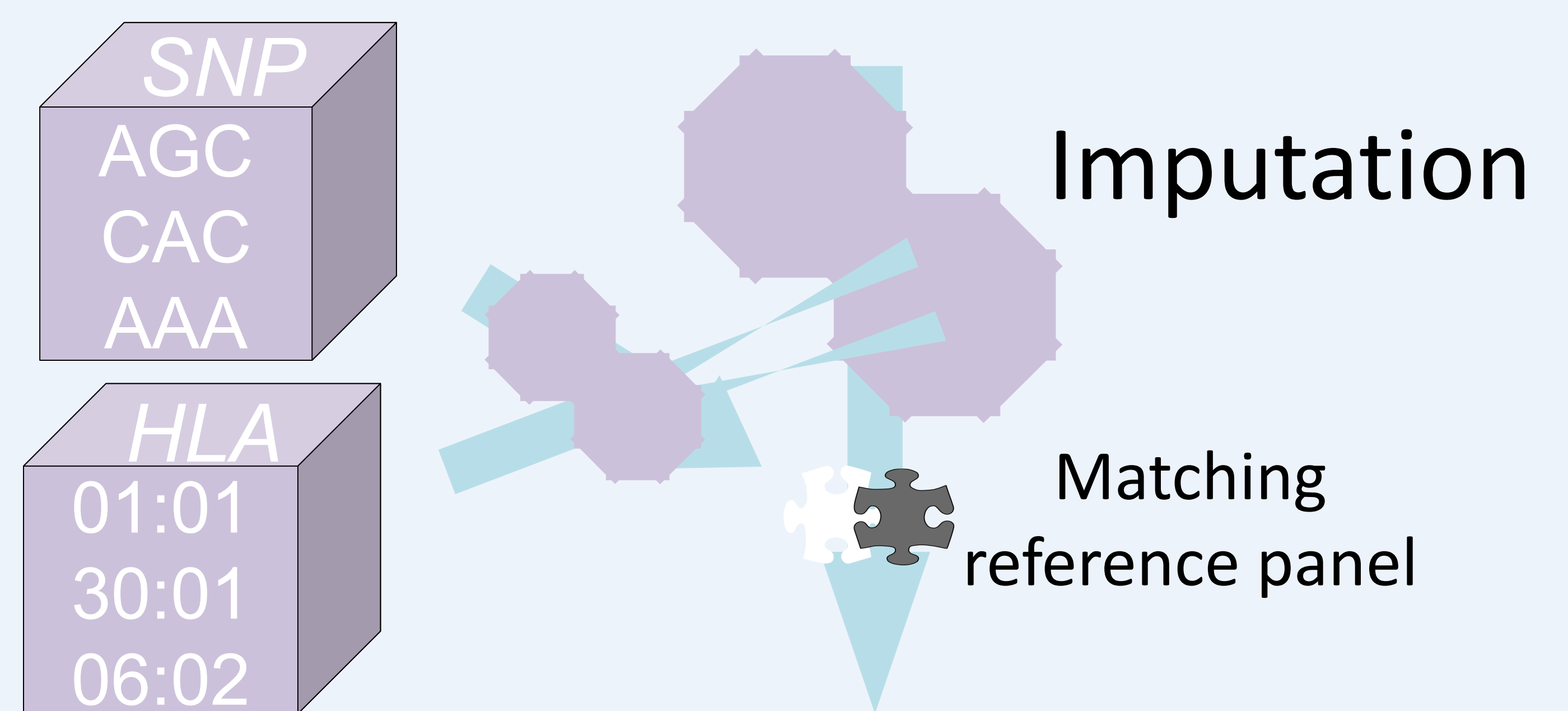
	Previously		Here
Design	Candidate genes	GWAS	CAAPA
cohort type	Small	Big	Big
Advantages	Biological meaning	Power	Both

10 African American asthma cohorts



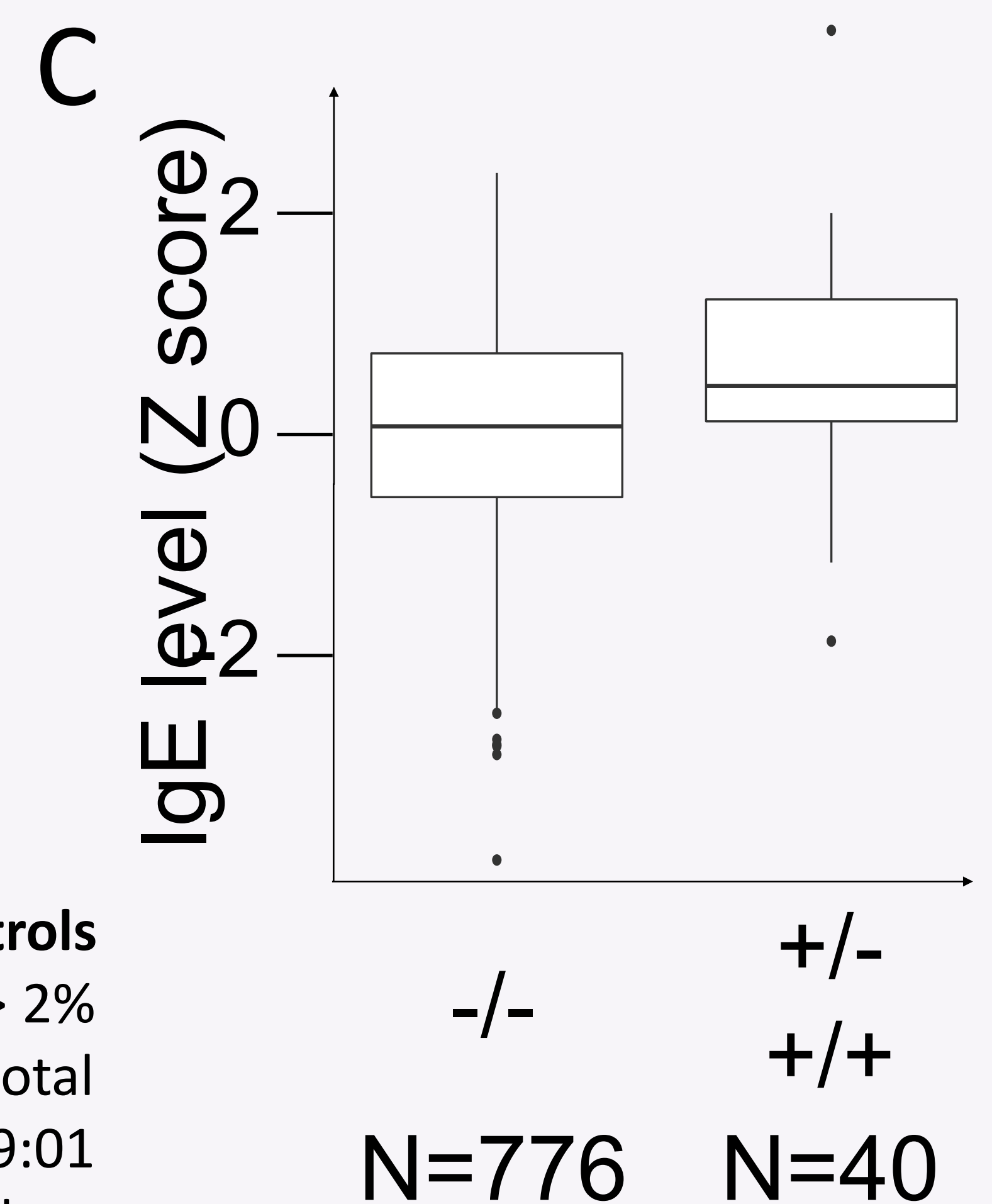
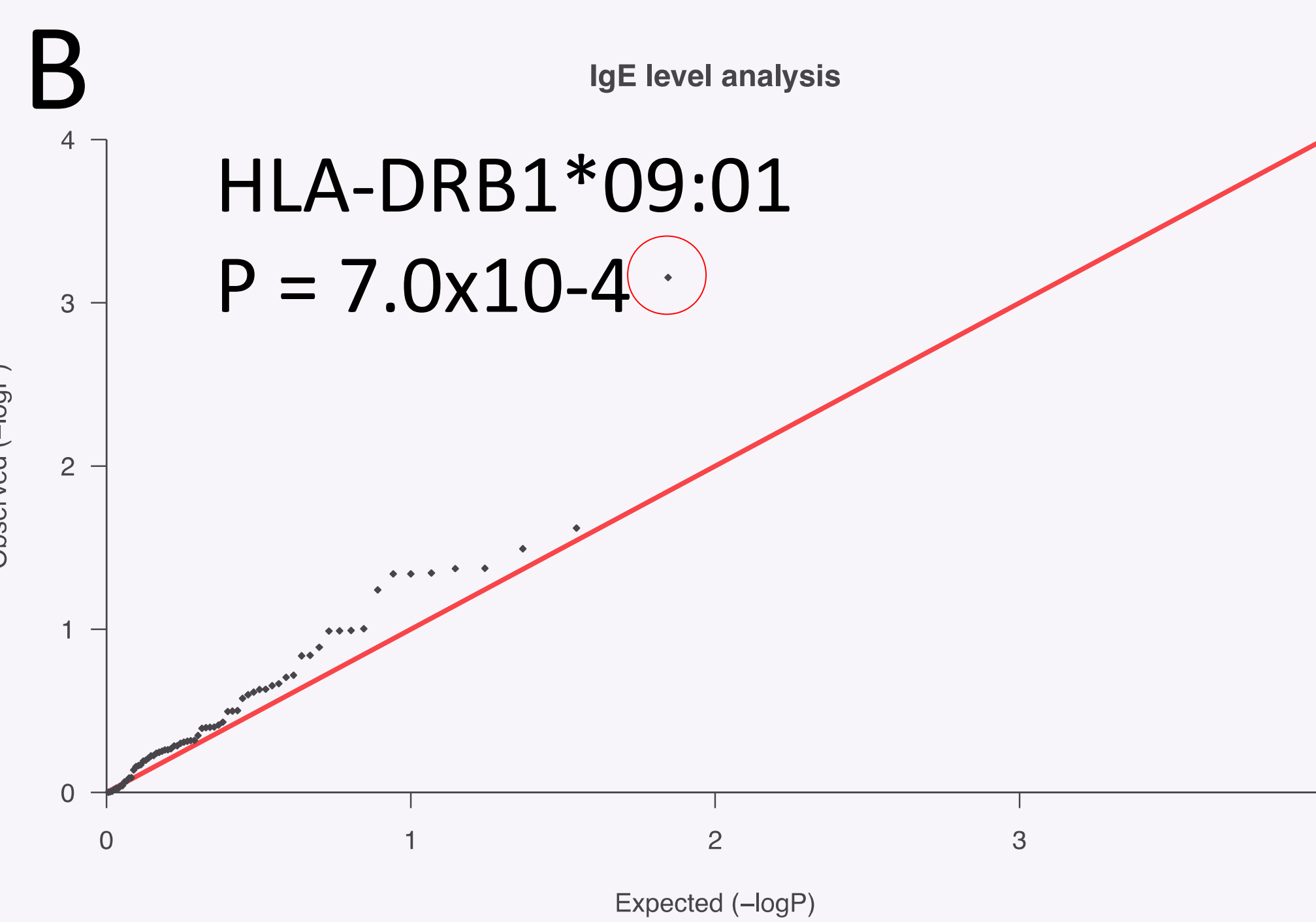
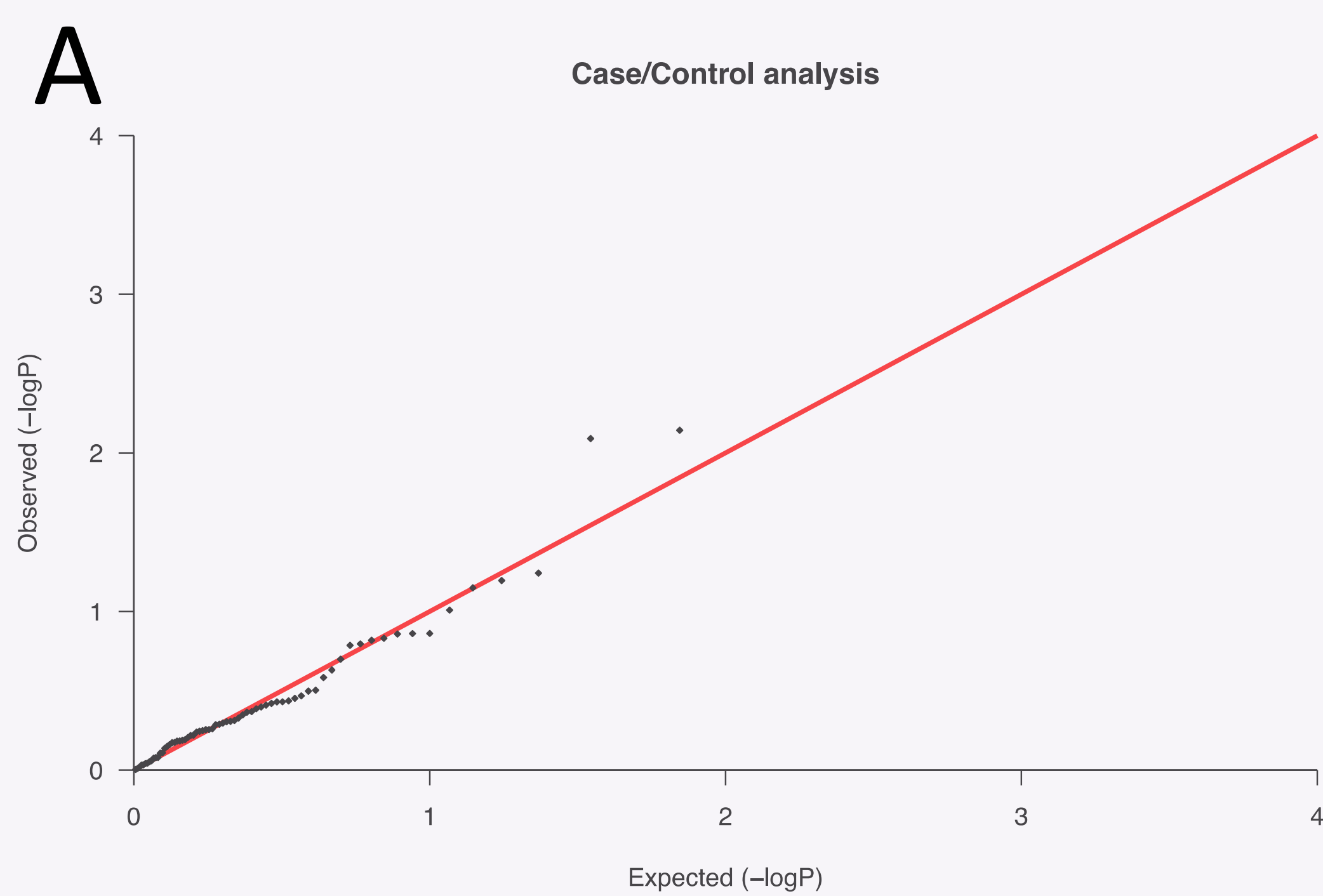
Innovative computational statistical inference

Genotypes			HLA allele
A	G	C	?
C	A	C	?
A	A	A	?



HLA alleles are inferred from the SNPs using a large HLA reference panel

HLA allele
01:01
30:01
06:02



QQplots of P values obtained in a meta-analysis (allelic regression model) comparing HLA alleles in a) **cases and controls** and in b) **IgE level as continuous variable**. Analysis was corrected with local ancestry. HLA alleles with a frequency > 2% are represented. Imputed HLA with a post-probability < 0.5 were excluded from the analysis. c) Box plot comparing total IgE level between Asthmatics with 1 or 2 HLA-DRB1*09:01 allele (+/- and +/+) and Asthmatics without HLA-DRB1*09:01 allele (-/-). IgE level is expressed in Z score. The N representing the number of individuals in each group is depicted on the graph. The P value of the meta-analysis from the dominant regression model is depicted on the graph.

We identified for the first time an *HLA* allele associated with asthma severity amongst African Americans. Our report emphasizes that by leveraging powerful computational methods, specific/extreme phenotypes, and population diversity, we can explore *HLA* gene polymorphisms in depth and reveal the full extent of complex disease associations.