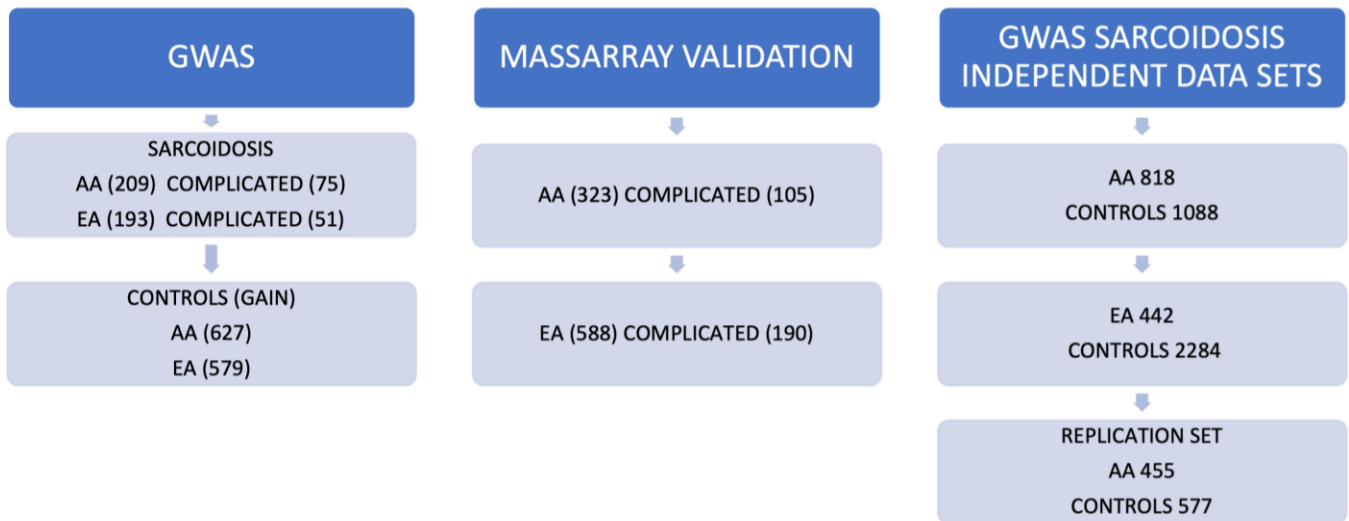
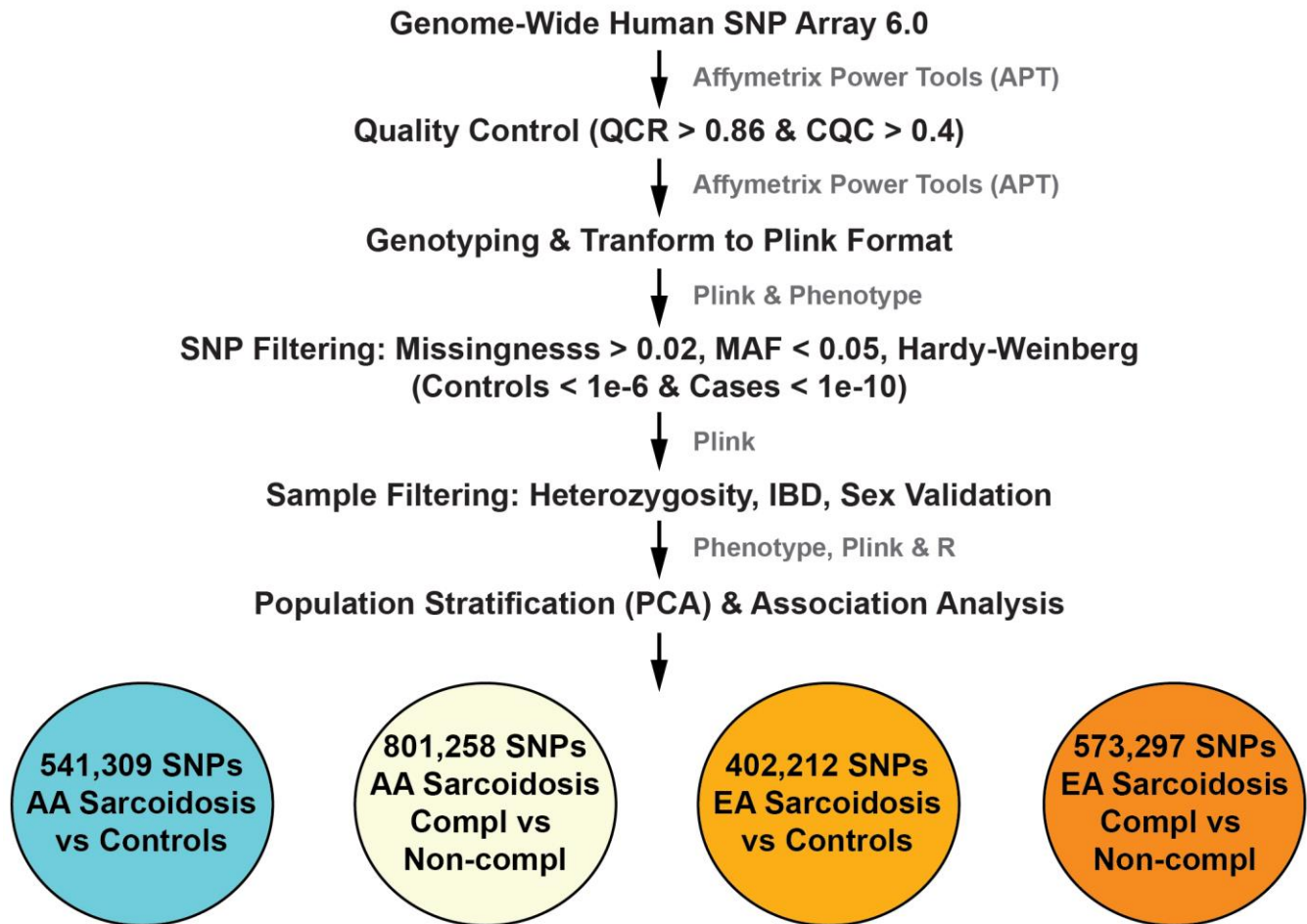


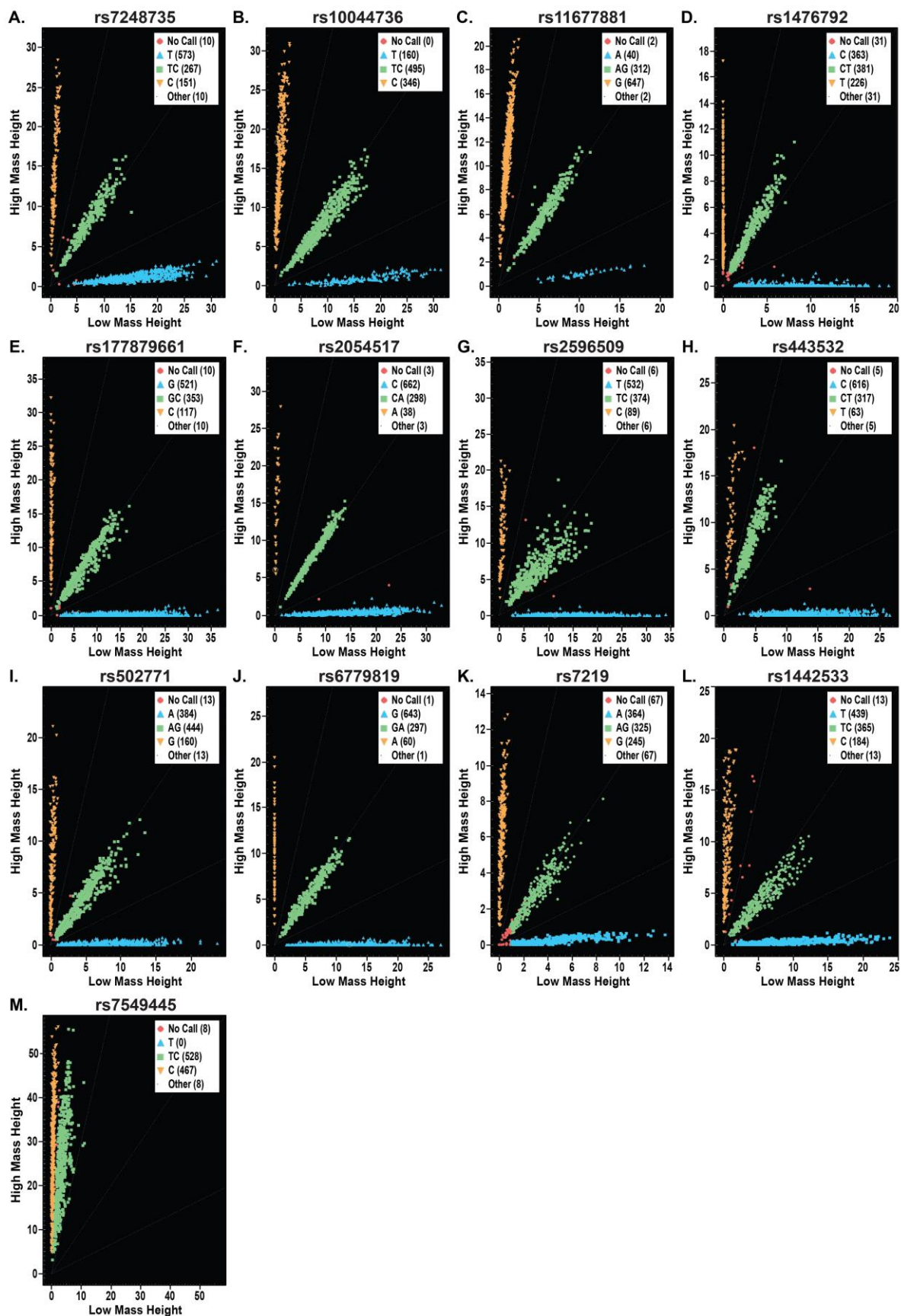
Supplementary Figures



Supplementary Figure S1. The different data sets and cohorts included in the study.



Supplementary Figure S2. The analytical process utilized to analyze the Sarcoidosis Discovery Cohort GWAS. The Affymetrix Genome-Wide Human SNP Array 6.0 containing 946,000 probes for the detection of copy number variation, using Affymetrix Power Tools for automated initiation of data processing, QC, genotyping, results generation and data transformation. Allele and genotype calling data was formatted to PLINK 1.9, to determine variant associations with sarcoidosis with each GWAS sarcoidosis data sets, initially processed together and then separately applying logistic regression and additive genetic models.



Supplementary Figure S3. Scatter plots showing the mass intensity of each allele of the 13 validated SNPs. Axis indicate the mass height, with x-axis representing the low mass height and y-axis the high mass eight. Triangles indicate the genotype call for homozygous and squares the heterozygous genotype, no successful call is indicated in red circles.