Principle and main process

GWAS usually compare the DNA of two groups of samples. One group is composed of samples which have the disease (The traits perform on them.), with another group composed of samples which don't and they are usually called controls. Each sample's SNPs will be read by SNP arrays. If there exist a specific variant which is frequent in samples with the disease, that SNP is said to be "associated" with the disease. In that way, associated SNPs will be used to mark a region of the genome which probably can explain the appearance of the disease. What we should also know is that GWAS look through the entire genome rather than test few regions. Most published GWA studies were designed to identify SNPs associated with common diseases. However, the technique can also be used to identify genetic variants related to quantitative traits such as height [8] or cardiographic QT interval.[9] Apart from these, GWAS have other application even in economy, and I don't explain more here. What you should know is GWA studies have a broader application than discovery of individual SNPs associated with discrete disease endpoints.

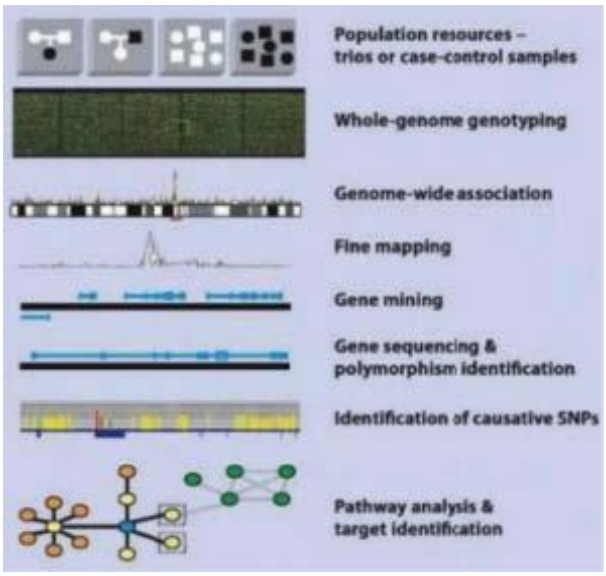
A classical GWA studies mainly have four process: The typical GWA study has four parts:

(1) Set up the samples group for investigation. Select a large number of individuals with the disease or trait of interest and a suitable comparison group;[6]

(2) DNA extraction and isolation, genotyping, and data review to ensure high genotyping quality;

(3) Choose appropriate statistical tests for analysis the relationship between the SNPs and the disease/trait; and

(4) Replication of identified associations in an independent population samples or examination of functional implications experimentally.[7]


Population resources –
trios or case-control samples
Whole-genome genotyping
Genome-wide association
Fine mapping
Gene mining
Gene sequencing &
polymorphism identification
Identification of causative SNPs
Pathway analysis &
target identification