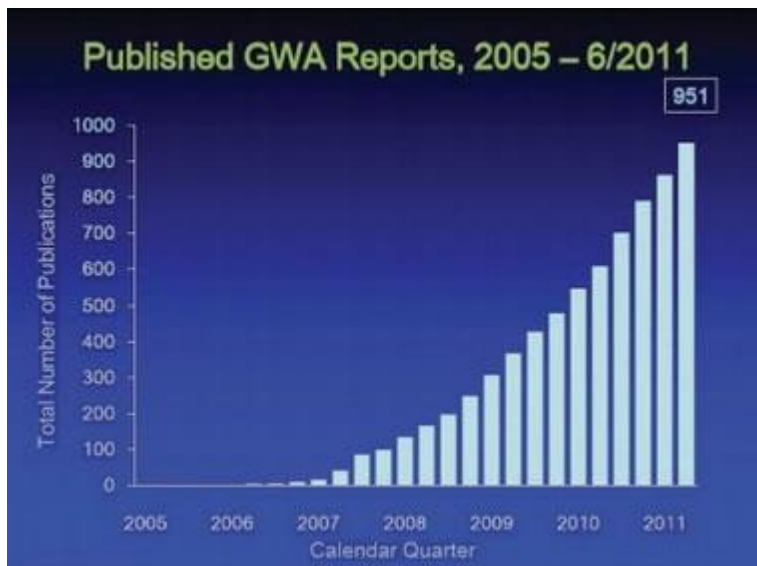


## Development

Except the conceptual framework, there are two key elements which boost the development of GWAS. One was the appearance of the biobanks. Biobanks contain plentiful resource of human genetic material, thus, it greatly decreases cost and difficulty of samples for study. Another one was the International HapMap Project which from 2003 had identified a majority of the common SNPs which are interrogated in a GWA study.<sup>3</sup> Besides, the Human Genome Project, the SNP Consortium, and the 1000 genome Projects are all helpful for the development of GWAS. In 2005, Science reported the first successful GWAS which is about investigated patients with age---related molecular degenerations. GWAS typically focus on associations between single---nucleotide polymorphisms (SNPs) and traits like major diseases. It found two SNPs which had significantly altered allele frequency when comparing with healthy controls.<sup>4</sup> In 2007, Saxena with many organization reported that they found out many locus which are associated with T2DM; In 2008, more than 30 sensitive genes locus were reported to be associated with Crohn disease by Barrett and other researchers.



GWA studies have successfully identified common genetic determinants of coronary artery disease, atrial fibrillation, blood pressure, blood lipid concentration, diabetes, obesity, smoking behavior, plasma homocysteine, and intracranial aneurysm.<sup>5</sup> Below is a illustration of the SNPs associated with disease of human---beings which are found by GWAS.

