In the last years, genome-wide association studies have allowed to identify multiple genetic variants associated with atherosclerosis. In this review, we highlight the identification of genomic variants associated with coronary artery disease and myocardial infarction as well as large-vessel stroke. We will focus on genetic variants that displayed overlap for these atherosclerotic diseases. Current research is focusing on the identification of the functional mechanisms underlying these associations. As frequent variants are often only associated with small increases in risk, the search for the identification of rare variants with large increases in risk is ongoing. Whole-exome sequencing recently revealed rare variants dramatically increasing cardiovascular risk. Taken together, the developments of the past few years light the vision of improved prevention and therapy of coronary artery disease and stroke.