LPA risk allele associations to coronary artery disease in a heterogenous cohort

Coronary artery disease is the leading cause of death in the United States. Over one hundred loci in the human genome have been confidently associated with coronary artery disease via genome-wide association studies. However, many of these studies have been performed in ancestrally and socioeconomically homogenous populations, especially cohorts of European ancestry. Thus, it is unclear to what extent these published loci can be used to predict disease risk in ancestrally and racially heterogenous populations across different environments in the US. We therefore explore the association strength between previously reported coronary artery disease-associated risk alleles at the *LPA* locus and disease status across various races within a cohort of participants who contributed to the All of Us dataset. Previous research has indicated that coronary artery disease risk conferred by *LPA* is not strongly modified by environmental factors, so allele frequency differences across populations or effect size variation should be studied further in multi-ancestry populations.