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## Abstract

Large numbers of inbred laboratory rat strains have been developed for a range of complex disease phenotypes. To gain insights into the evolutionary pressures underlying selection for these phenotypes, we sequenced the genomes of 27 rat strains, including 11 models of hypertension, diabetes, and insulin resistance, along with their respective control strains. Altogether, we identified more than 13 million single-nucleotide variants, indels, and structural variants across these rat strains. Analysis of strain-specific selective sweeps and gene clusters implicated genes and pathways involved in cation transport, angiotensin production, and regulators of oxidative stress in the development of cardiovascular disease phenotypes in rats. Many of the rat loci that we identified overlap with previously mapped loci for related traits in humans, indicating the presence of shared pathways underlying these phenotypes in rats and humans. These data represent a step change in resources available for evolutionary analysis of complex traits in disease models.