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Gencove gets Phase I SBIR grant to validate polygenic risk score estimation

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The grant will be used to validate methods for accurate calculation of polygenic risk scores from low-pass sequencing data that allow for population-scale screening applications, with a first application to coronary artery disease

Gencove, the leading low-pass sequencing platform announced that the receipt of a Phase I grant from the National Human Genome Research Institute under the auspices of the Small Business Innovation Research (SBIR) program of the National Institutes of Health. The grant will be used to validate methods for accurate calculation of polygenic risk scores from low-pass sequencing data that allow for population-scale screening applications, with a first application to coronary artery disease.

As clinical evidence for the benefit of screening patients for polygenic risk of diseases continues to accumulate, there will be increasing need for a scalable and flexible assay to measure these scores. Gencove's low-pass genome sequencing combined with its imputation algorithms can address the technological challenge to provide a highly accurate estimate of a polygenic risk score across ethnic groups using an assay that can scale financially and operationally to entire health care systems. Low-pass sequencing is an approach to combine the throughput and cost-effectiveness of genotyping arrays with the accuracy and population portability of whole genome sequencing.

Regarding this award, Gencove's CEO Joe Pickrell said, "The flexibility, operational efficiency, cost-effectiveness, and population-agnostic nature of low-pass sequencing make it a great choice for calculating polygenic risk scores at scale."