Fig. S1: Study Overview



Two main participant data sources were used: whole-genome sequencing (WGS) and imputed genotype data. Gray arrows indicate the main analyses, which are further detailed in the Methods section. Green boxes indicate additional design decisions and which table(s) each analysis is summarized in. There were 4 significant MMSKAT associations (using WGS data), and 4 independent EMMAX GWAS associations (using WGS and imputed genotype data).

Fig. S2: NRG1 Locus Models Manhattan and QQ Plots



AHI analyses of European-Americans and Australians are shown. The Manhattan and QQ plots are based on a meta-analysis of WGS and imputed data. All variants are shown, including variants with low combined p-values that did not meet replication criteria.

Fig. S3: SLC45A2 Locus Models Manhattan and QQ Plots



Average SpO2 analyses of European-Americans and Australians are shown. The Manhattan and QQ plots are based on a meta-analysis of WGS and imputed data. All variants are shown, including variants with low combined p-values that did not meet replication criteria.

Fig. S4: IL18RAP Locus Models Manhattan and QQ Plots



variants with low combined p-values that did not meet replication criteria.



All models with significant IL18RAP loci associations are shown. From top to bottom: Minimum SpO2 all individuals), Minimum SpO2 (all males), Average Desaturation (all individuals), and Average Desaturation (all males). Additional European-American Average Desaturation results listed for comparison in Table S6 did not clear the p < 1e-8 threshold. The Manhattan and QQ plots are based on a meta-analysis of WGS and imputed data. All variants are shown, including

Fig. S5: ATP2B4 Locus Models Manhattan and QQ Plots



Per90 analyses of Hispanic/Latino-Americans are shown. The Manhattan and QQ plots are based on a meta-analysis of WGS and imputed data. All variants are shown, including variants with low combined p-values that did not meet replication criteria.