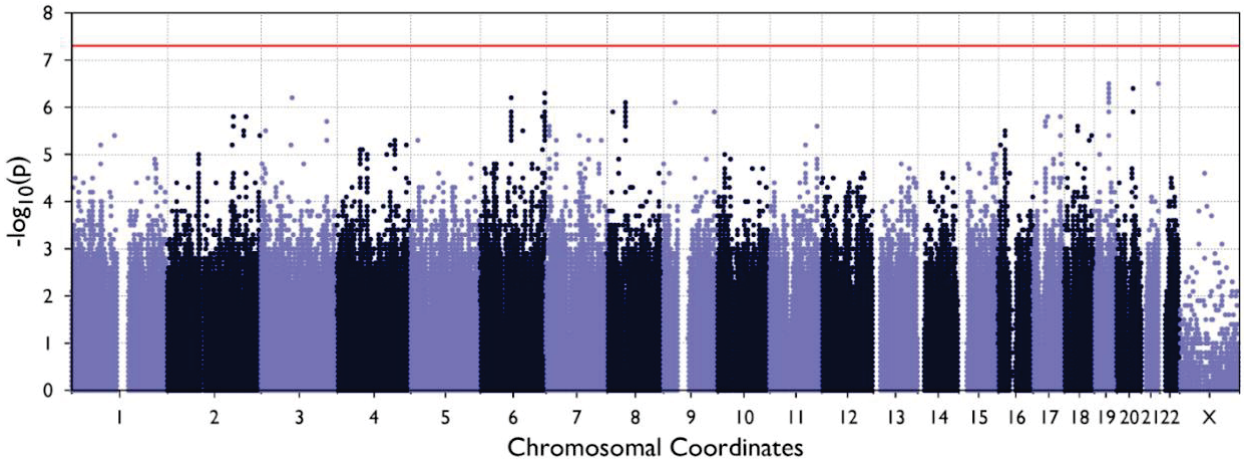
# Supplemental Online Content

Sun Q, Broadaway KA, Edmiston SN, et al. Genetic variants associated with hidradenitis suppurativa. *JAMA Dermatol.* Published online July 26, 2023. doi:10.1001/jamadermatol.2023.2217



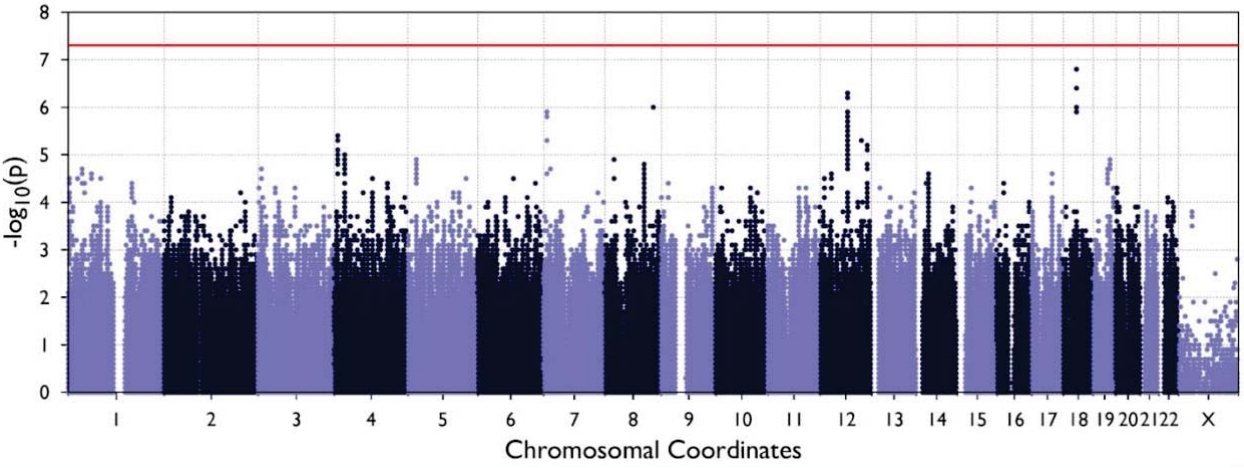
This supplemental material has been provided by the authors to give readers additional information about their work.

## eFigure 1. Genetic variants associated with HS in ProCARE patients and AddHealth controls.



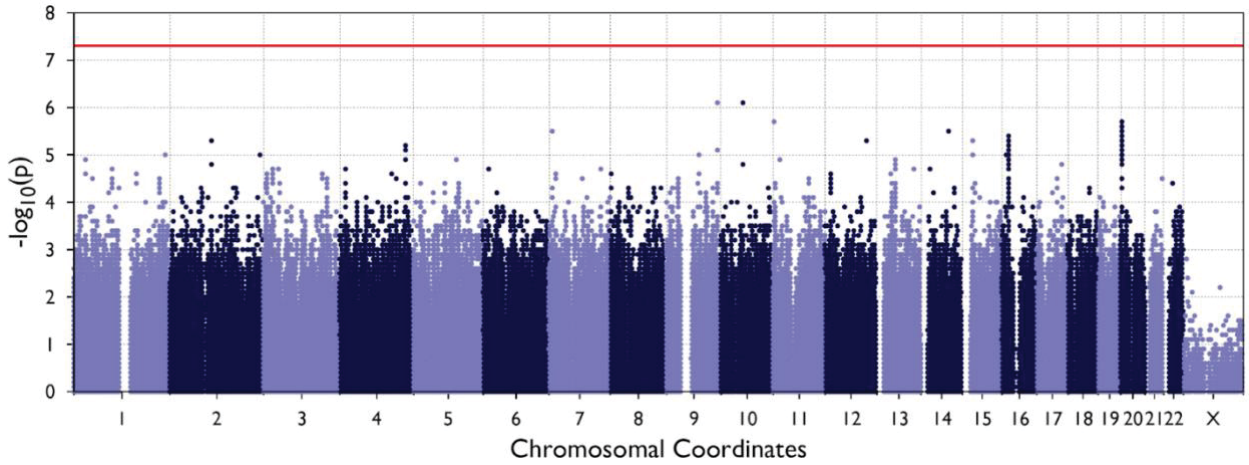

Each dot corresponds to one variant, the X-axis indicates genomic position, and the Y- axis shows the $-\log_{10}$(p-value) of variant association with HS. No variant showed genome-wide significant ($p < 5x10^{-8}$) evidence of association (red line).

## eFigure 2. Genetic variants associated with HS in ProCARE patients and AddHealth controls of primarily European ancestry.



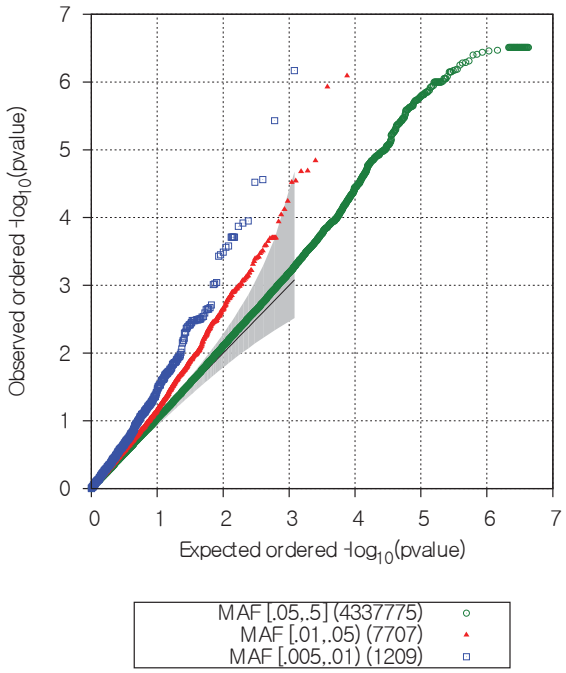

Each dot corresponds to one variant, the X-axis indicates genomic position, and the Y- axis shows the $-\log_{10}$(p-value) of variant association with HS. No variant showed genome-wide significant ($p < 5x10^{-8}$) evidence of association (red line).

## eFigure 3. Genetic variants associated with HS in ProCARE patients and AddHealth controls of primarily African ancestry.



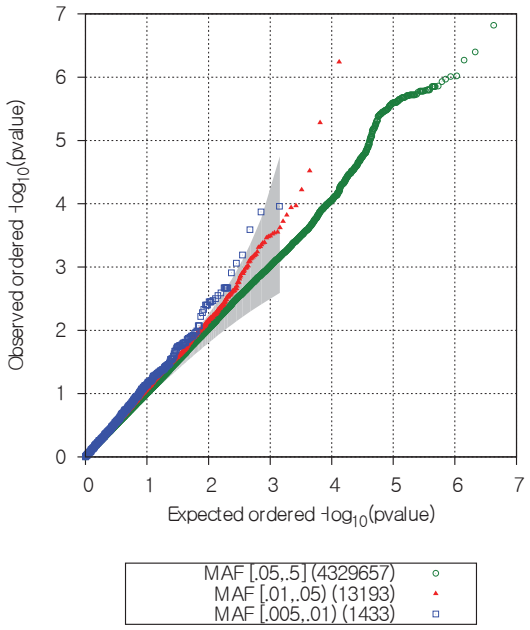

Each dot corresponds to one variant, the X-axis indicates genomic position, and the Y-axis shows the -$\log_{10}$(p-value) of variant association with HS. No variant showed genome-wide significant ($p < 5x10^{-8}$) evidence of association (red line).

## eFigure 4. QQ plot of GWAS for ProCARE patients and AddHealth controls.



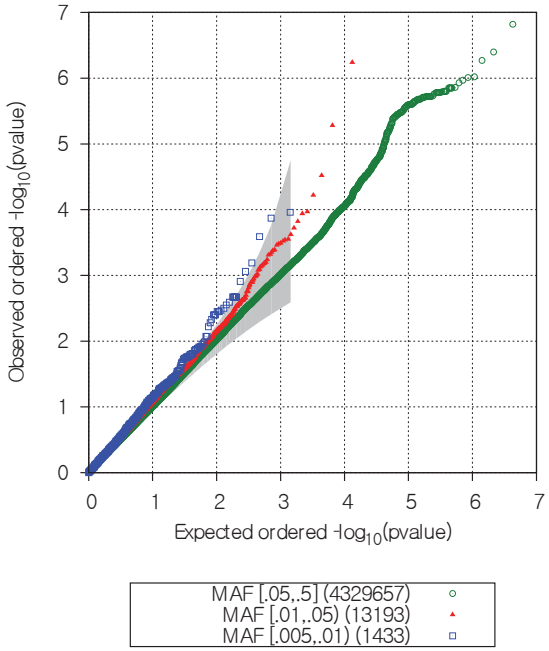

Each dot corresponds to one variant. Variants are grouped into three different MAF categories in different colors. The genomic control coefficient lambda = 1.05.

## eFigure 5. QQ plot of GWAS for ProCARE patients and AddHealth controls of primarily European ancestry.



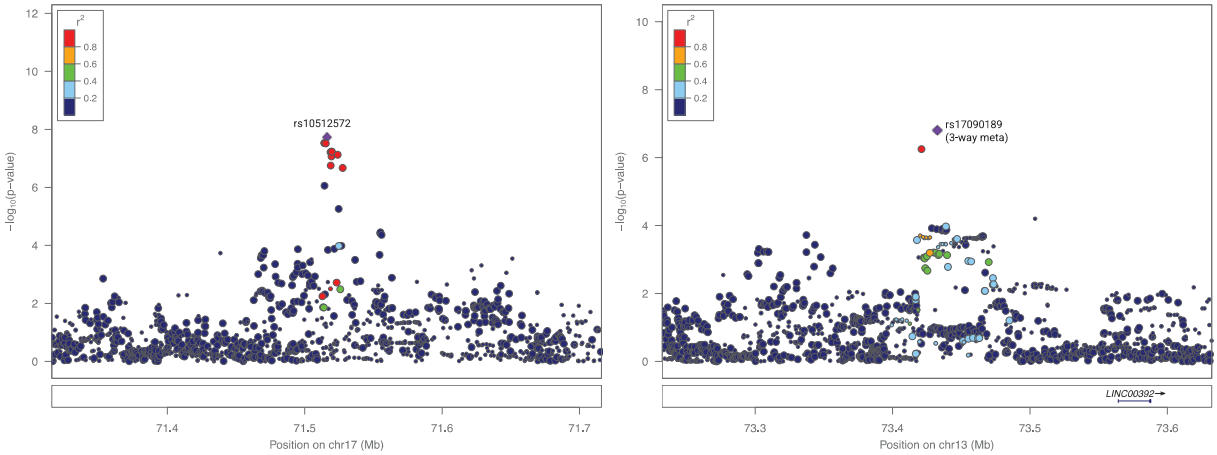

Each dot corresponds to one variant. Variants are grouped into three different MAF categories in different colors. The genomic control coefficient lambda = 1.01.

## eFigure 6. QQ plot of GWAS for ProCARE patients and AddHealth controls of primarily African ancestry.



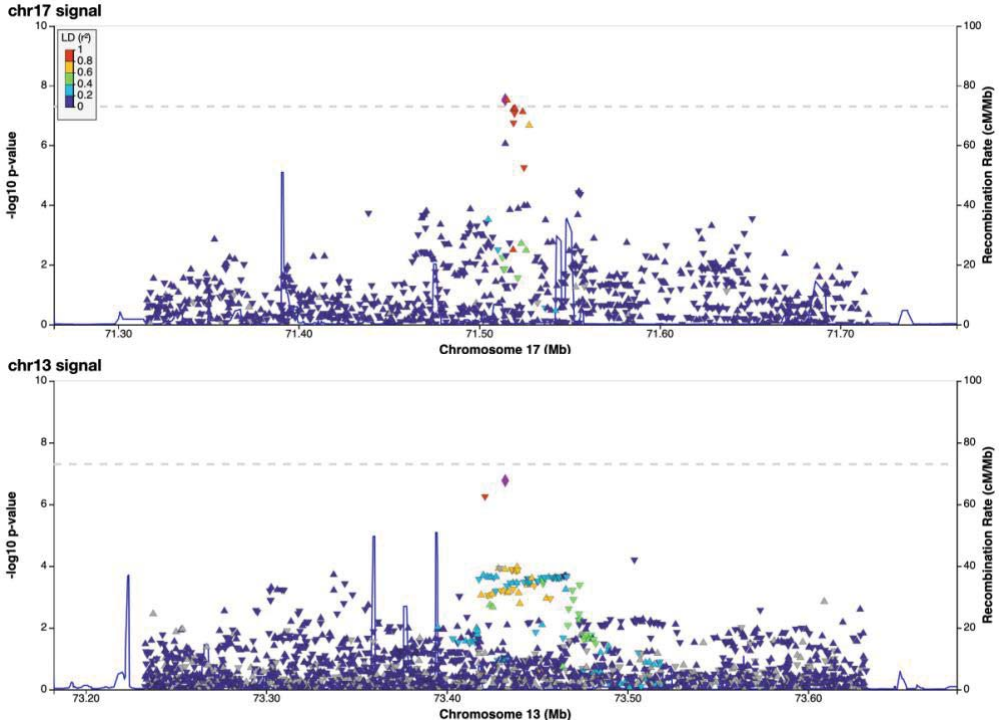

Each dot corresponds to one variant. Variants are grouped into three different MAF categories in different colors. The genomic control coefficient lambda = 1.00.

## eFigure 7. HS association plots for two loci colored based on African LD.




Variants associated with HS in the 3-way meta-analysis located at the chr17 locus (left) and the chr13 locus (right). Each point corresponds to one variant, the X-axis indicates genomic position, the Y- axis shows the -$\log_{10}$(p-value) of variant association with HS, and the size of each point indicates relative sample size analyzed for that variant. Variants are colored according to their linkage disequilibrium (LD) $r^2$ with the most significant variant in each region, which is shown as a purple diamond. LD $r^2$ values are based on TOP-LD African ancestry individuals. The nearest protein-coding genes are not located within the 400-kilobase regions shown.

## eFigure 8. HS association plots for two loci with recombination rates.




Variants associated with HS in the 3-way meta-analysis located at the chr17 locus (top) and the chr13 locus (bottom). Each point corresponds to one variant, the X-axis indicates genomic position, the left Y-axis shows the -$\log_{10}$(p-value) of variant association with HS, the right Y-axis shows the recombination rate, and the size of each point indicates relative sample size analyzed for that variant. Variants are colored according to their linkage disequilibrium (LD) $r^2$ with the most significant variant in each region, which is shown as a purple diamond. LD $r^2$ values are based on 1000G European ancestry individuals. Recombination rates are from 1000G.