**Main Text, last paragraph**

To minimize the possibility of LD between sites used in the analysis as much as possible, we used the approximately independent LD blocks in Europeans76 as in Section “Mixture weights for covariance structure between male and female effects”. Namely, we subdivided the genome into 1703 LD blocks such that we expect sites from different LD blocks will have little to no LD between them. We iterated over the 1703 blocks and identified all post-filtering sites which fell within each block; we then randomly sampled one of these sites within each LD block and used this sample of (up to) 1703 sites to perform the weighted linear regression of on The slope and SE of this regression line was our estimate of A. We replicated this estimation process 1,000 times to generate 1,000 estimates of A. We then used the estimates of slope divided by the SE of these estimates to generate 1,000 Z-scores for A. The point estimate Z-score presented in Fig. 6D is the mean of the 1,000 replicates. **To get the error bar, we resampled with replacement among all of the LD blocks which had at least one post-filtering site within them, then resampled one point from each of these resampled LD blocks. We then recalculated A, SE of A, and Z-scores for A. This was replicated 1,000 times, and the error bar represents the 5th and 95th percentile of these 1,000 re-sampled Z-scores.** In the main text, we focus on the results performed this estimation for Ashkenazi Jewish, Finnish, and Non-Finnish European populations as the other ancestry groups in gnomAD are more genetically diverged from the UKB White British sample and the GWAS estimates are expected to be less portable67,79, similar to the UK Biobank sample

**Supp Text S8, after second paragraph**

We downloaded gnomAD VCF files from the gnomAD browserfor all autosomes and used VCFTools14to parse the file. We filtered the data toexclude insertions or deletions, and only kept bi-allelic SNPs. We further removed missing data (3,698 sites). These filtering steps resulted in 2,285,169 remaining sites. In an effort to avoid confounding results that could arise from population substructure, we split the data into the different ancestry groups labeled by gnomAD and worked with the data in each subpopulation separately from this point forward. We removed sites with less than 1,000 alleles in each ancestry group independently. The number of loci we removed at this step depended on the sample size of each group, as we removed fewer loci from large populations and more loci in small populations (Table S1). This step resulted in the complete removal of the Amish and Middle Eastern populations because their low sample sizes.

**It has been reported that some sex-specific affects mapping to loci on the autosomes may actually be due to mismapping of the autosomal region to regions of the sex chromosomes. To account for this, we ran an additional filtering step for every imputed locus in the GWAS dataset. Using the GRCH37 assembly—the same as used in the UK Biobank—we found the sequence 150bp up- and down-stream of each polymorphism site. We then used 3 sliding 150bp windows and ran a Mega-BLAST through NCBI’s command-line BLAST tool to find regions of identity between the autosomes and either sex chromosome. Following thresholds laid out in Kasimatis et al., we then filtered out all autosome sites with a greater than 90% identity to the sex chromosomes.**