README of Scripts for SAS for Zhu et al.

FilterINFO.R = Script to get the FST values from the Allele Frequency values from Gnomad, split up by ancestry group

FSTvGWAS.R = Script to get the Var{GxS} values from the GWAS effect sizes, then puts these values and the FST values from FilterINFO.R into one table for regression later

NewFSTvGWASpfilt.R = Script to run a weighted regression of FST vs Var{GxS} 1000 times, getting a slope of the regression for each iteration

zscores.R = Script to get Zscores for all of the slopes generated by NewFSTvGWASpfilt.R

ZscoreCI.R = Script to get the confidence intervals of the mean Zscores from zscores.R, by resample bootstrapping from these means 10,000 times

sex\_selection\_plotNewFST.R = Script to plot the results for the figures, including both the example regressions and the mean Zscores plots (outputs both an unrefined version of the plots and the r metadata which was used to generate the final plots)