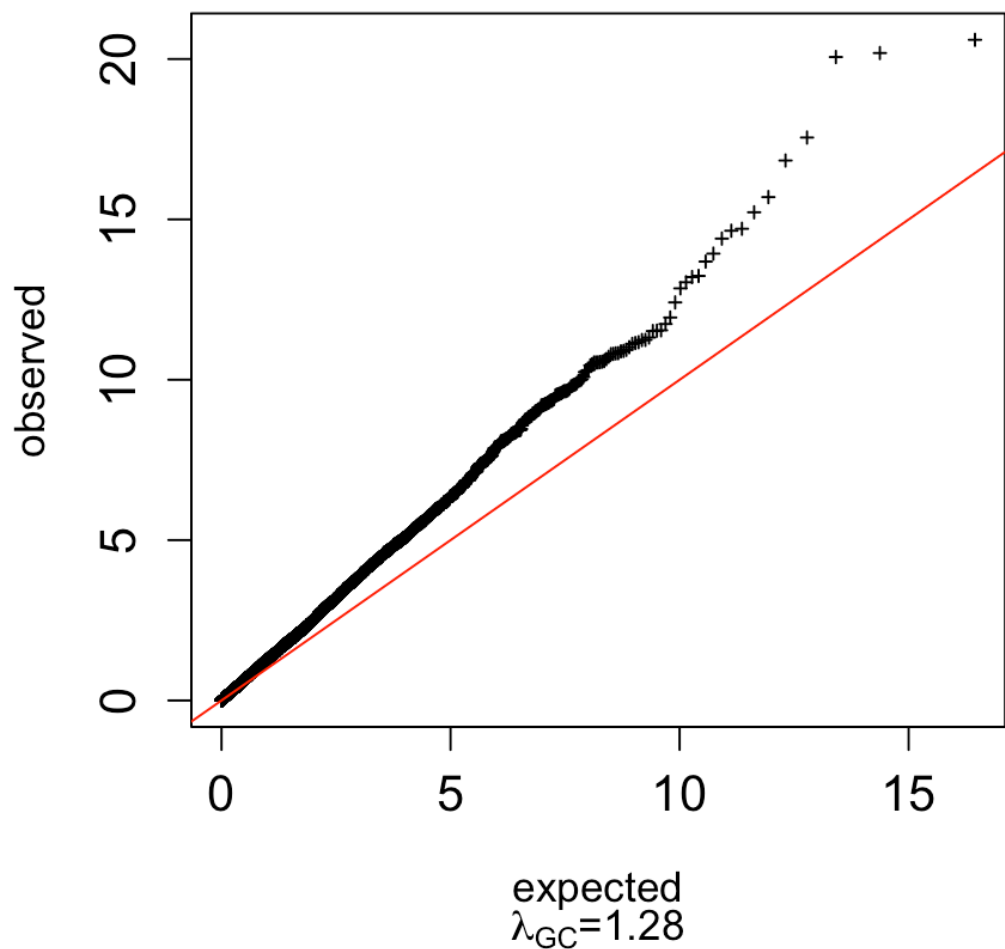


A. QQ-plot of chi-square statistic



B. QQ-plot of chi-square statistic

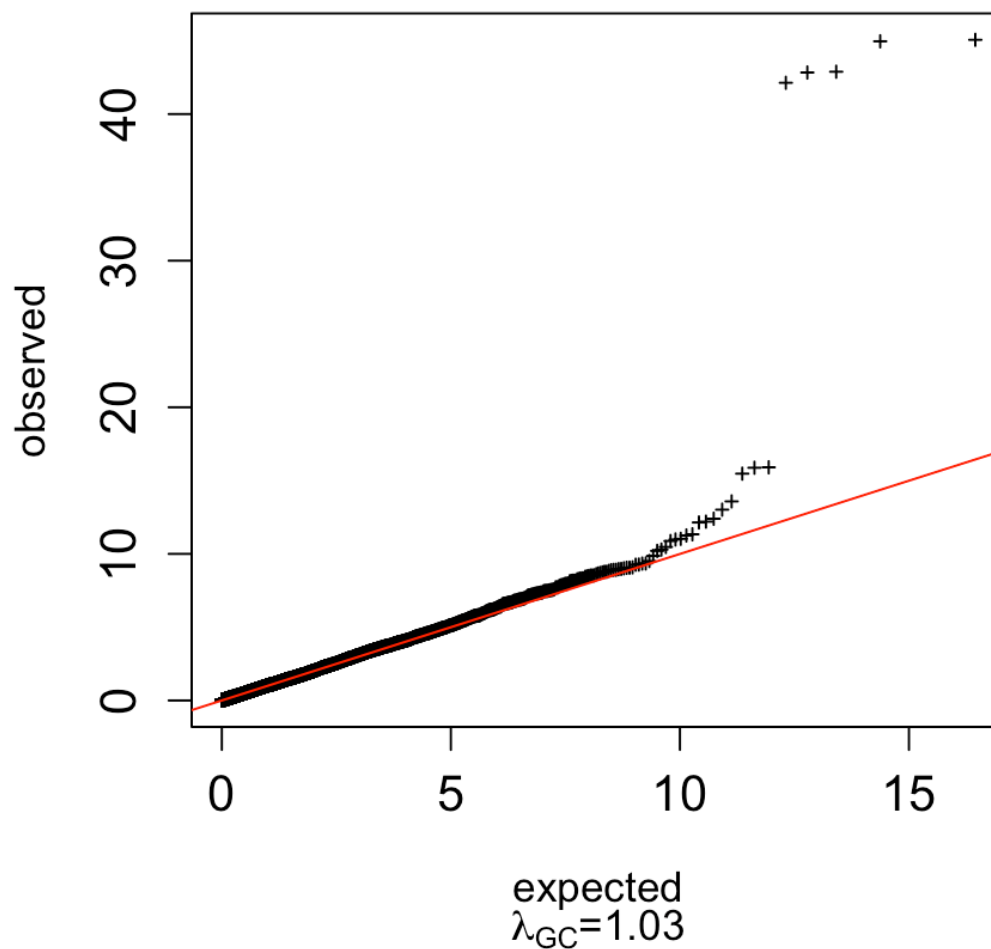
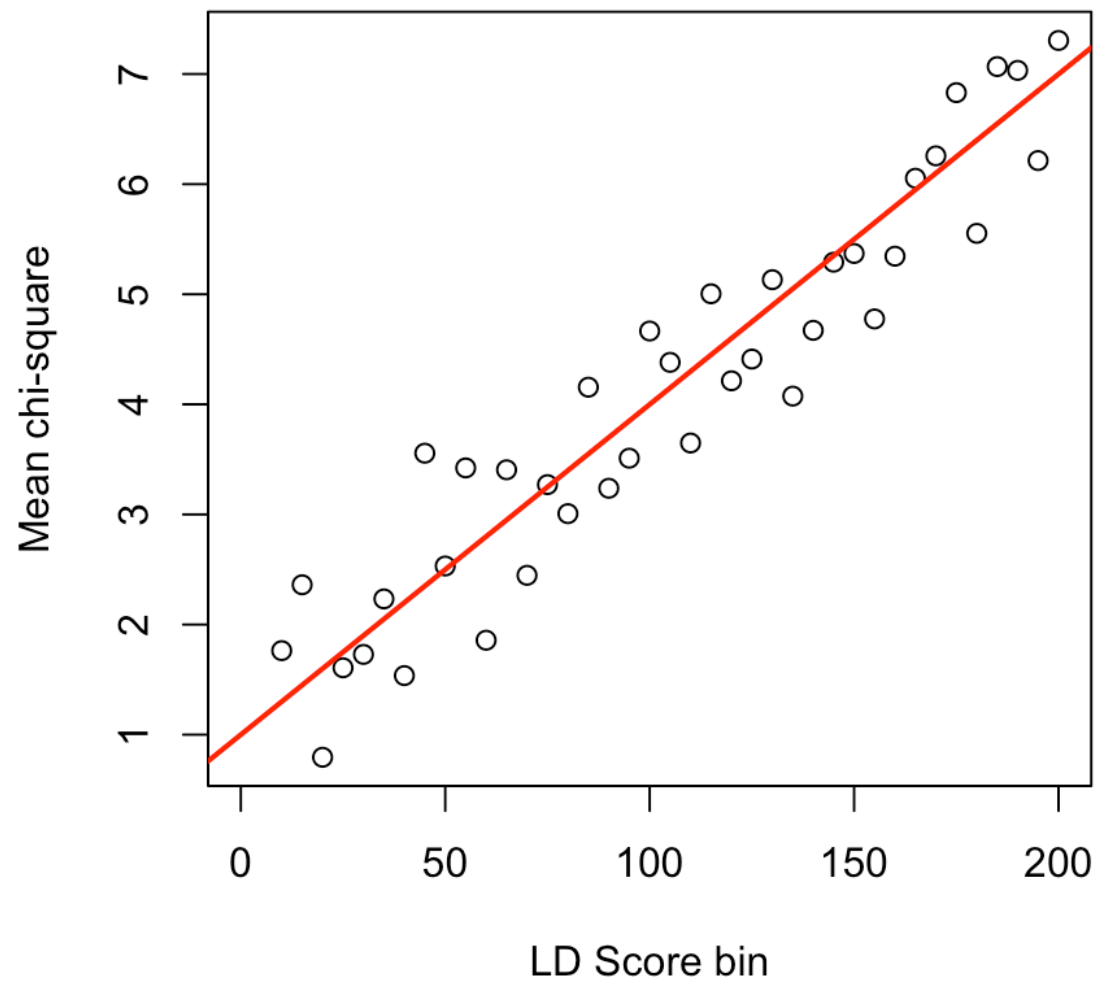


Figure 1. QQ-plots of chi-square association test statistics from two GWAS (GWAS A and GWAS B). Explain what you can infer about these two GWAS based on the information visible in the two plots. (2p)

A.



B.

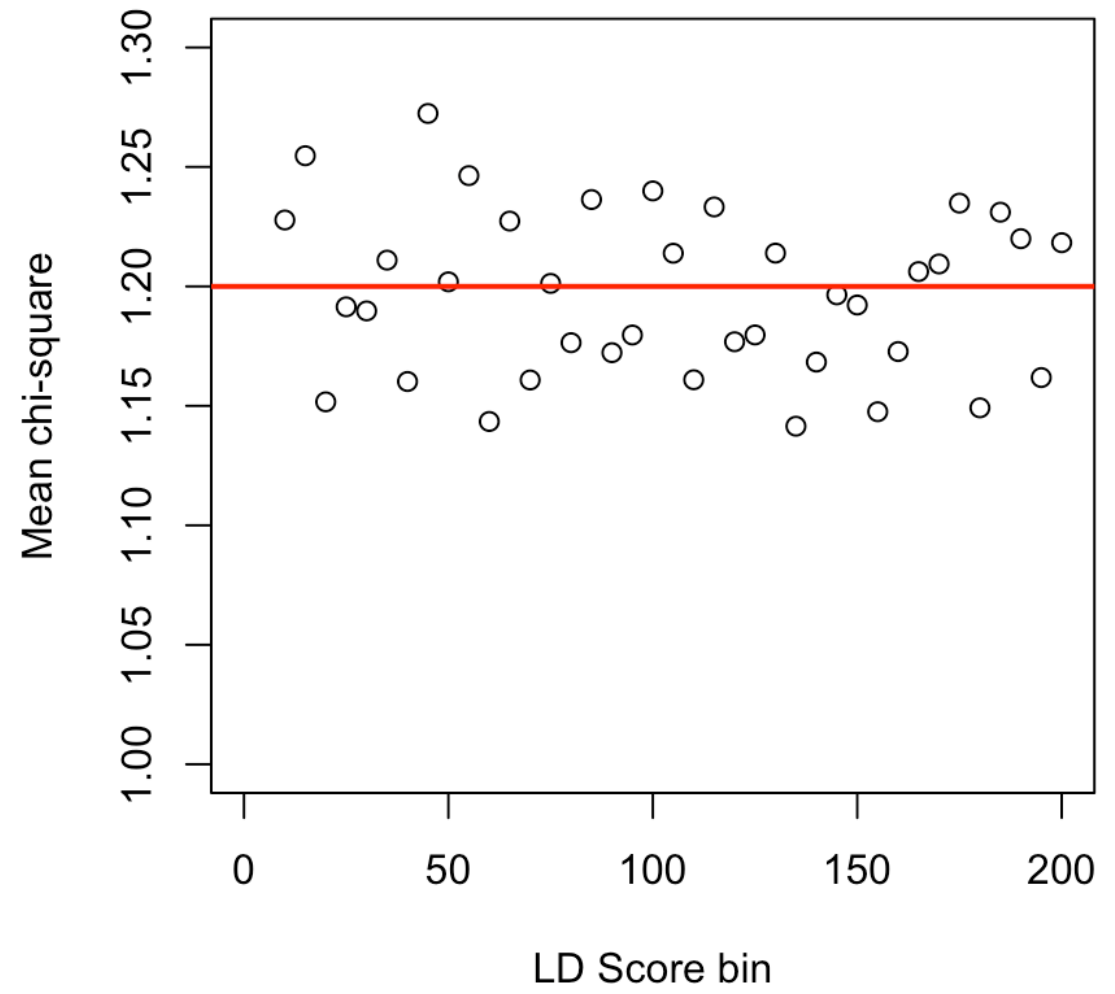


Figure 2. Plots from LD-score regression of two sets of GWAS results (GWAS A and GWAS B). Explain what you can infer about these two GWAS based on the LD-score regression plots. (2p)

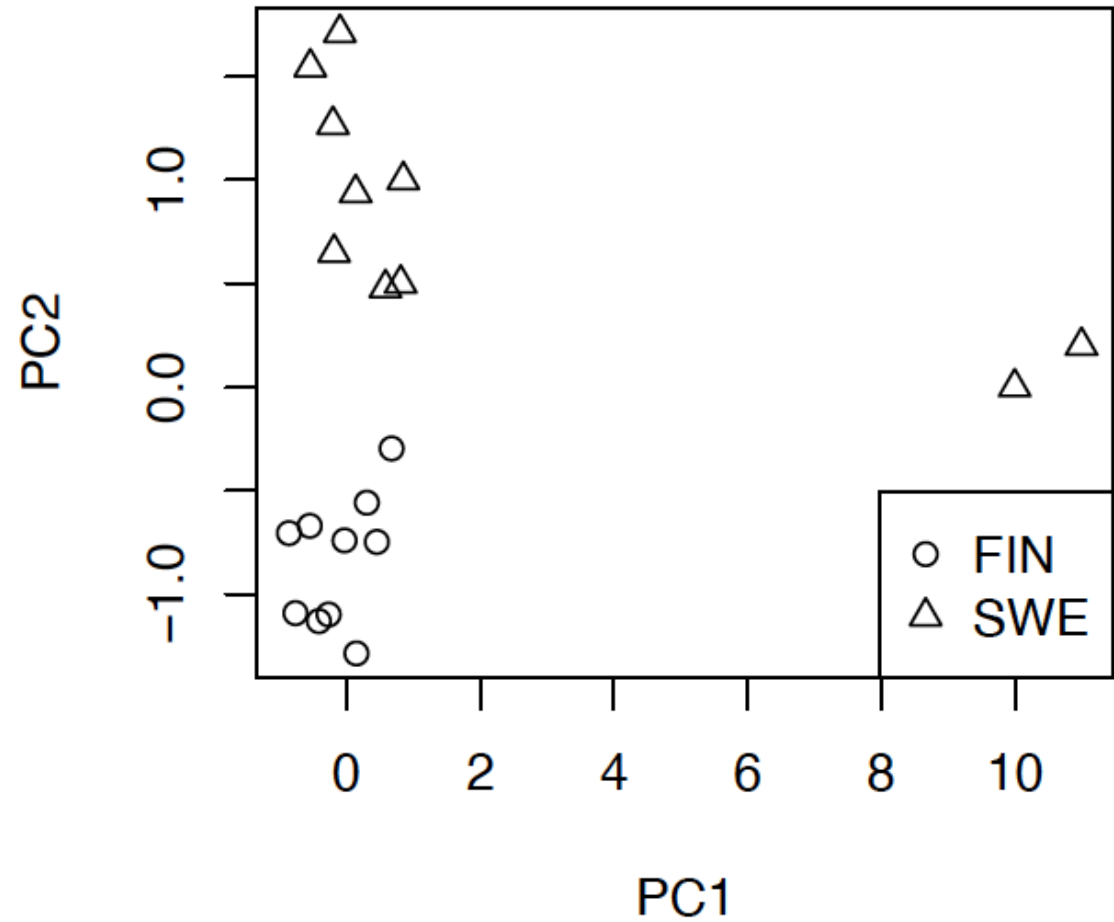


Figure 3. Ten samples from Finland and 10 samples from Sweden have been analyzed by principal components analysis using a genome-wide set of variants. What is a possible source of the problem in this PCA when our goal is to capture the population structure via PCA? (1p) What could you do to overcome the problem when you do not want to completely exclude any samples from further analyses?(1p)