

9/5/14 Used PSIKO for population structure

2 redundant lines in sequencing; ran both and kept the ones with most complete allele calls (one of each; much better in both cases)

30,891 SNPs (after removing $MAF < 0.05$)

100,650 GEMs (after removing < 0.4 RPKM)

OREGIN disease traits

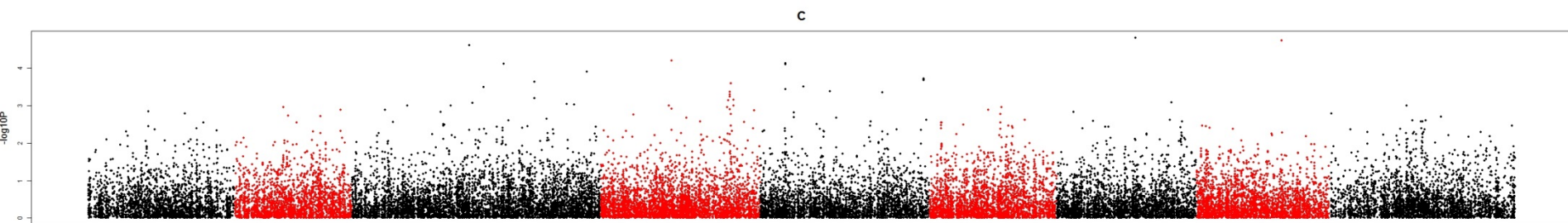
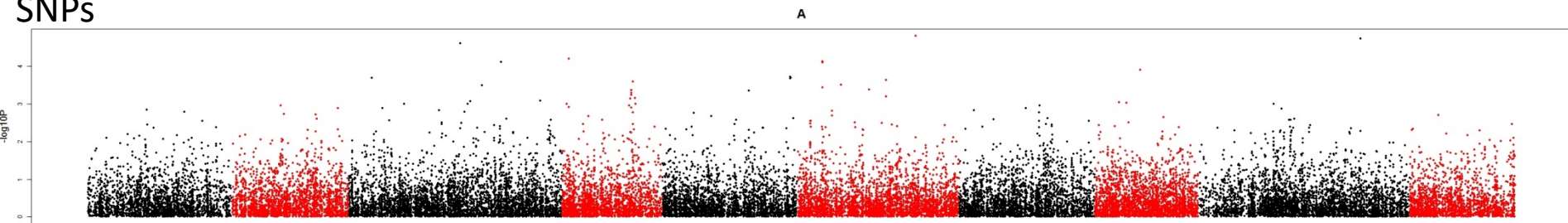
Low N = 0kg/ha

High N = 30kg/ha

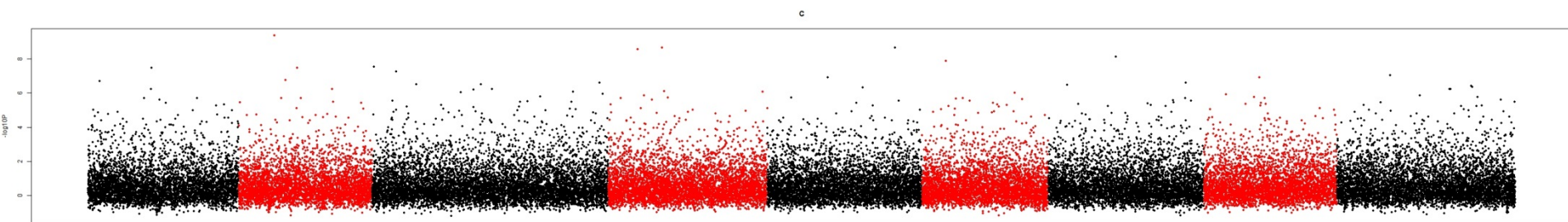
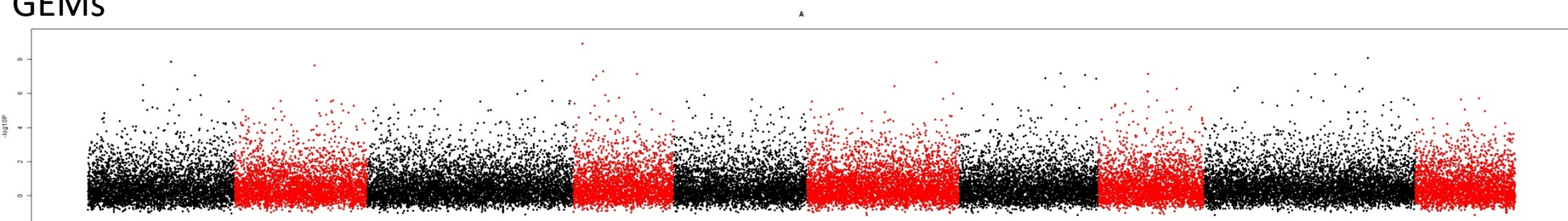
Phoma Incidence, Phoma Severity and Leaf Miner Incidence

91 accessions in analysis

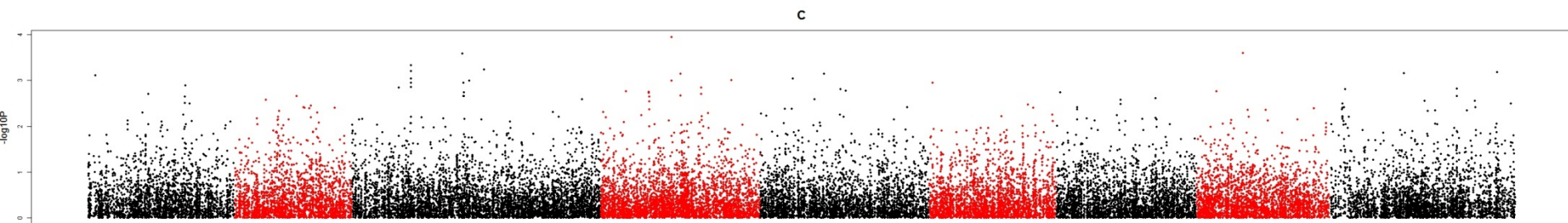
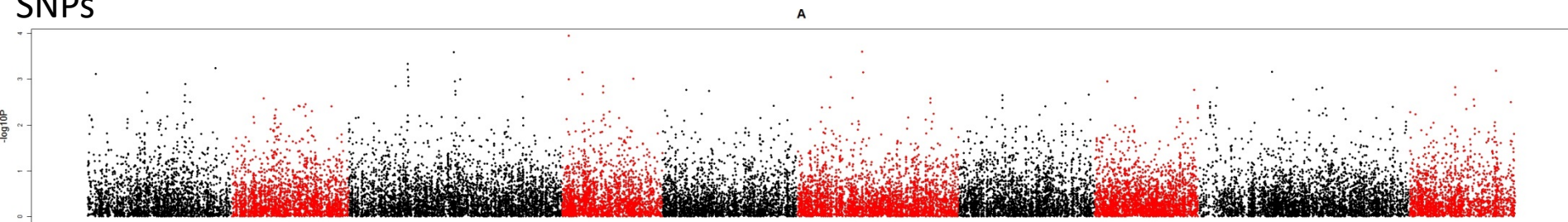
SNPs



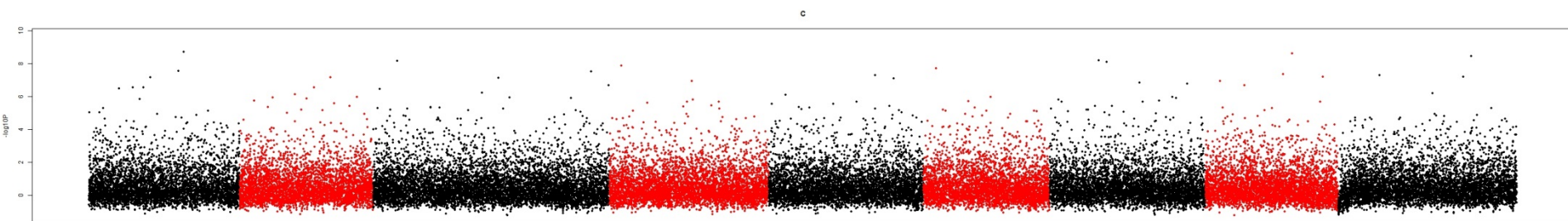
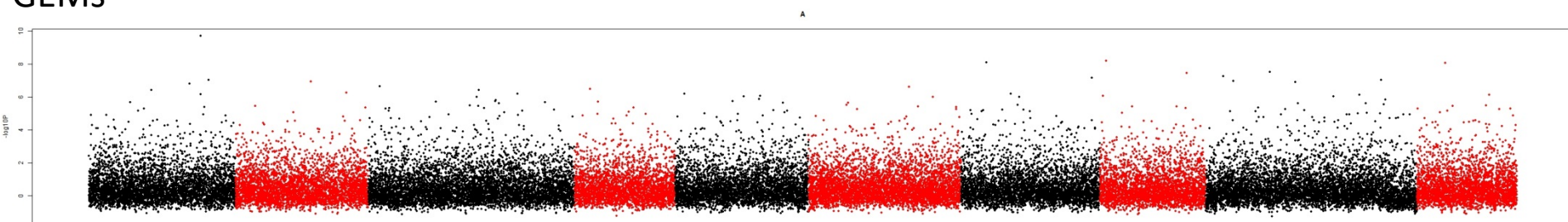
GEMs



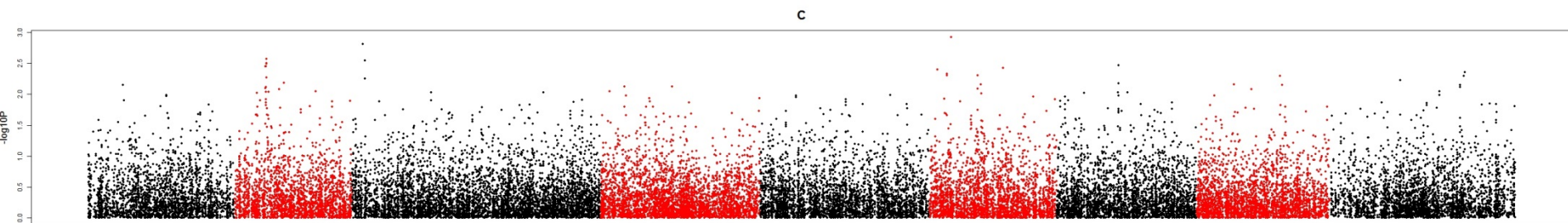
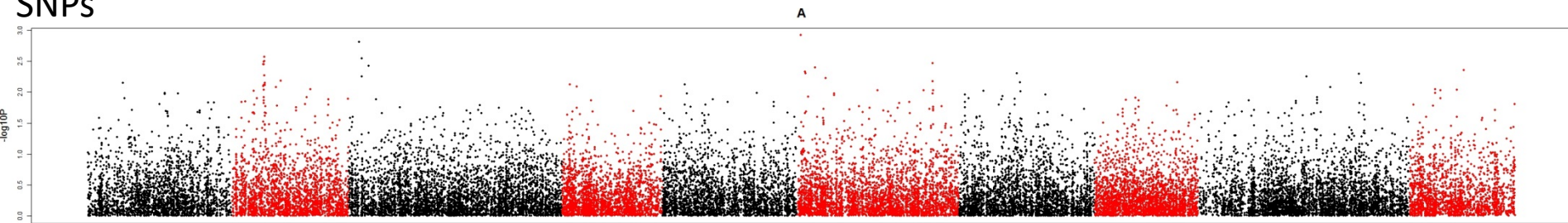
SNPs



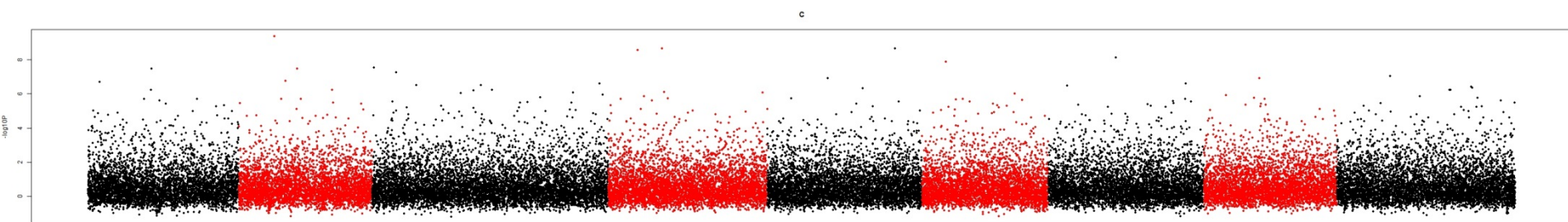
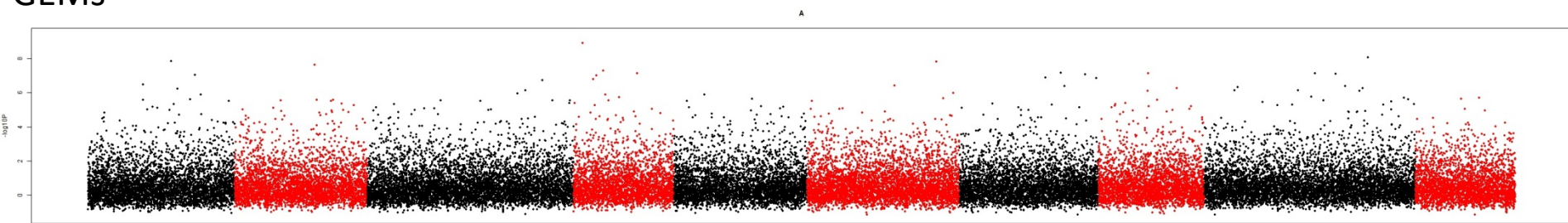
GEMs



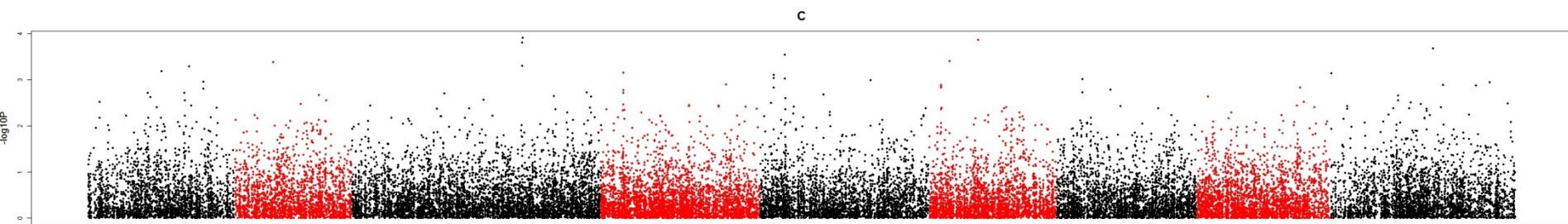
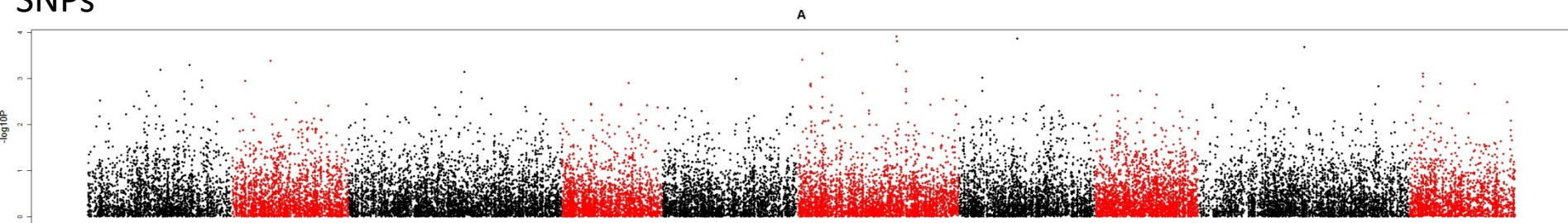
SNPs



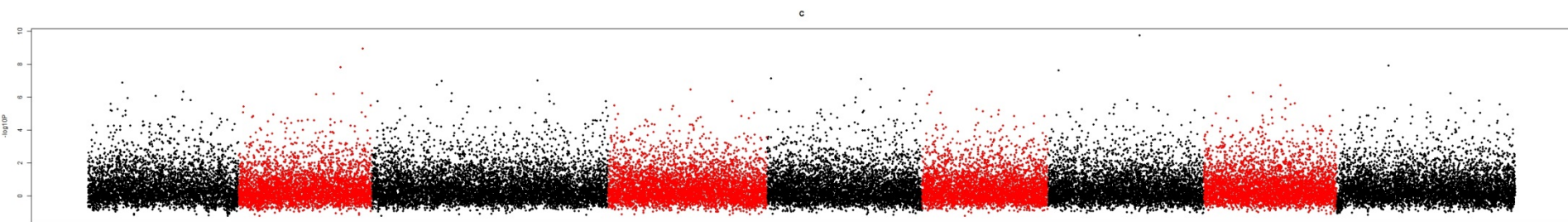
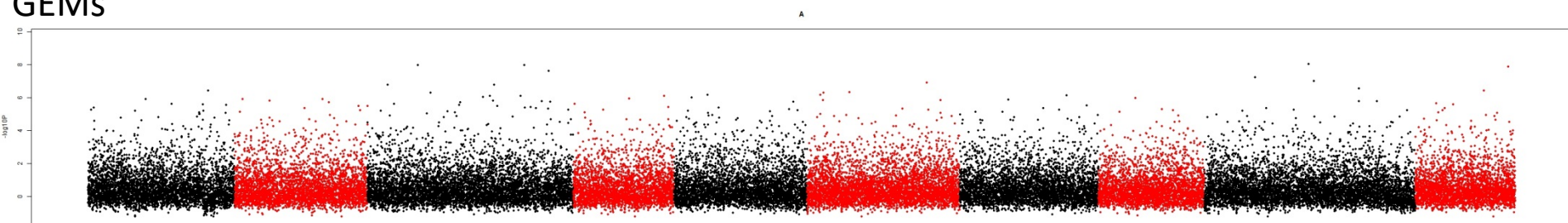
GEMs



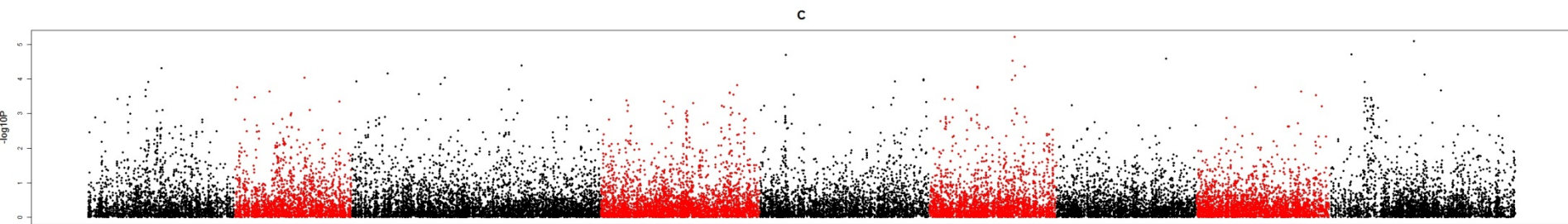
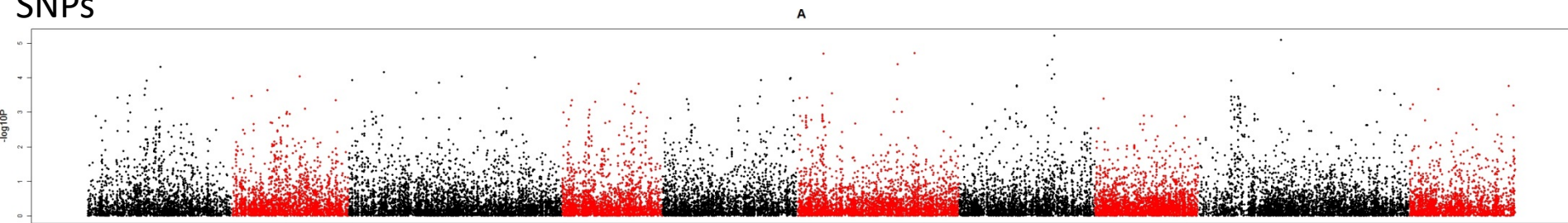
SNPs



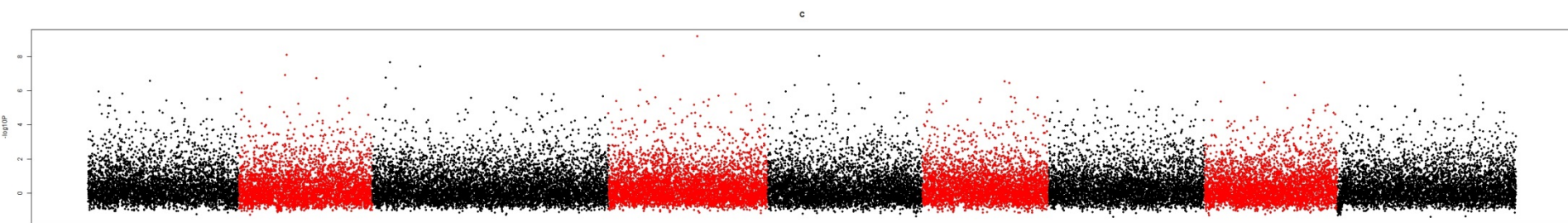
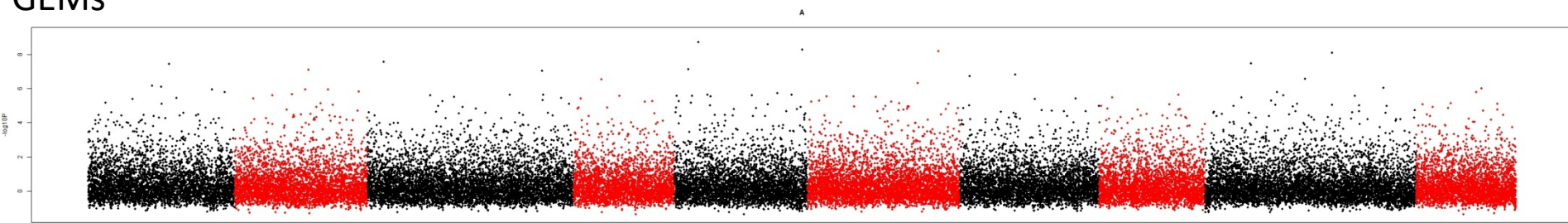
GEMs



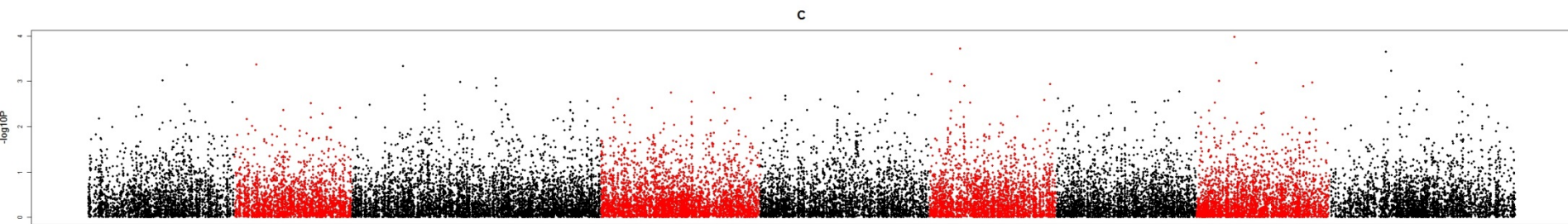
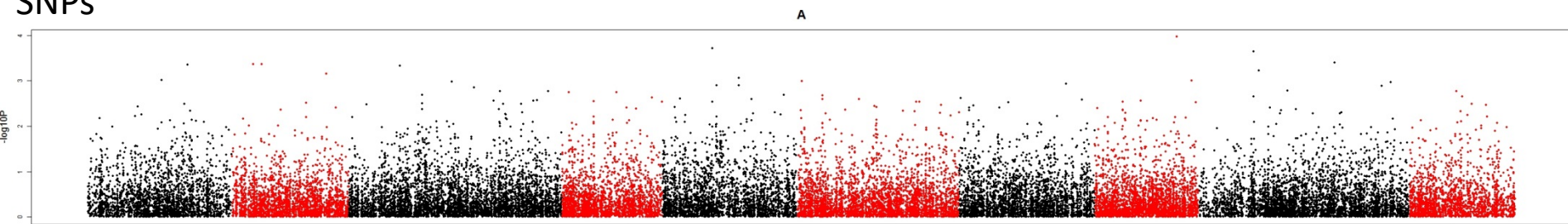
SNPs



GEMs



SNPs



GEMs

