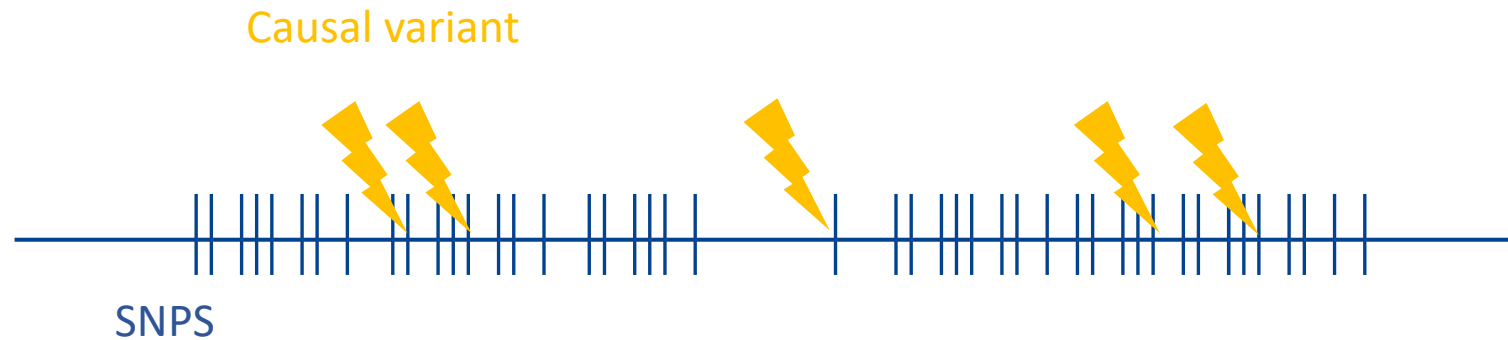


# Imputation to whole genome sequence variants in pigs

**T. H. Le, O. F. Christensen, P. Sarup, B.  
Guldbrandtsen, G. Sahana**

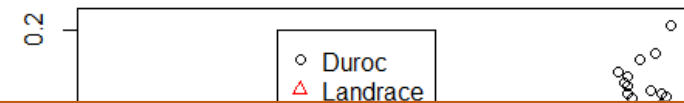
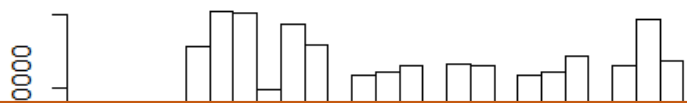
# Imputation to whole genome sequence variants in pigs

Why sequence?

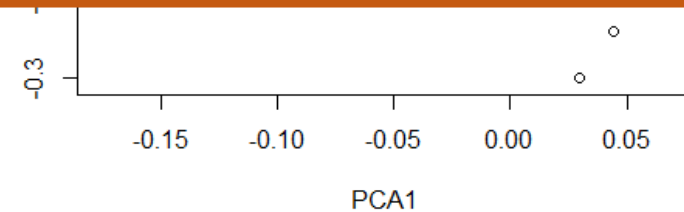
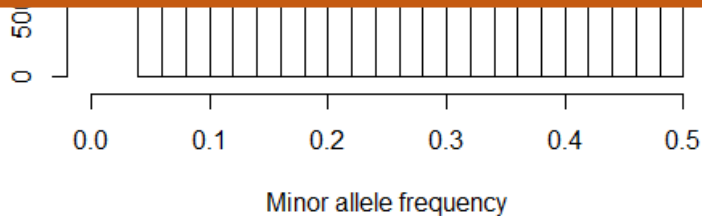


# Imputation to whole genome sequence variants in pigs

91 Duroc + 27 Landrace Sequenced  
5,889,814 variants



Additional sequence data from 25 Landrace and 50 Yorkshire pigs are being generated



Average imputation accuracy 60K -> WGS 0.83 per SNP