

# K=3

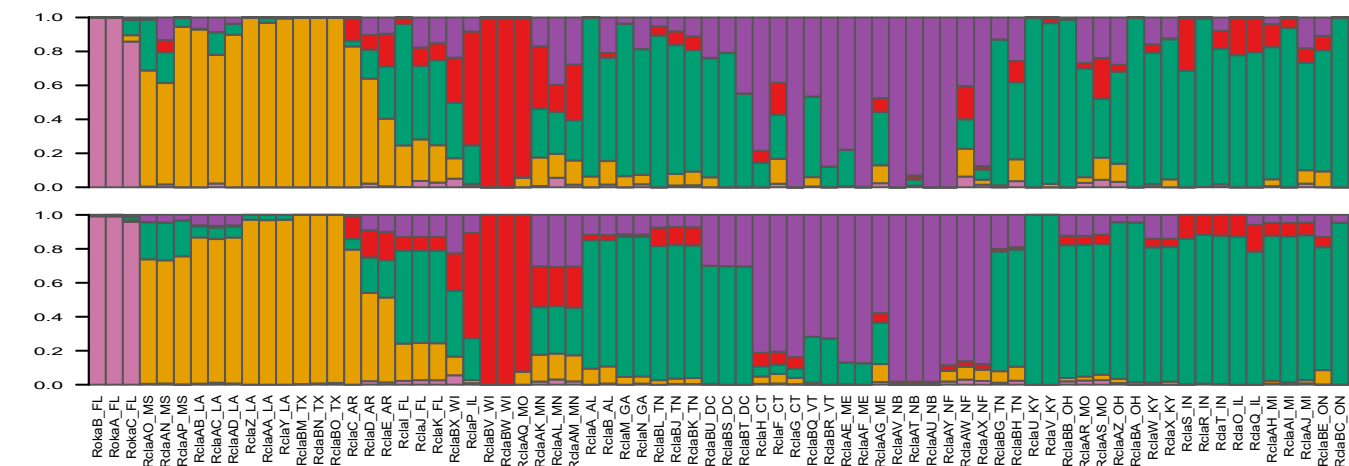
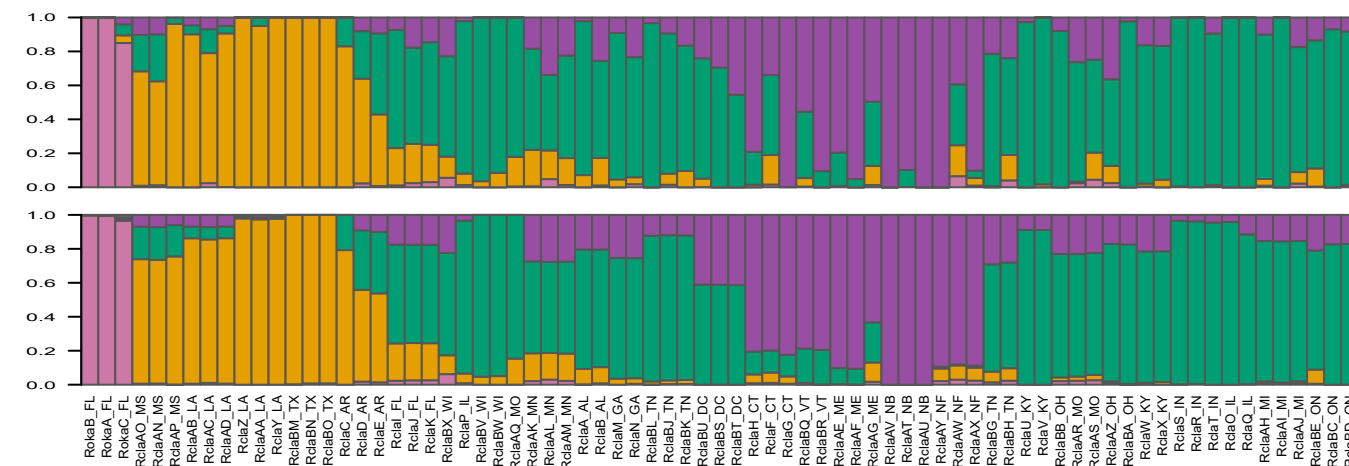
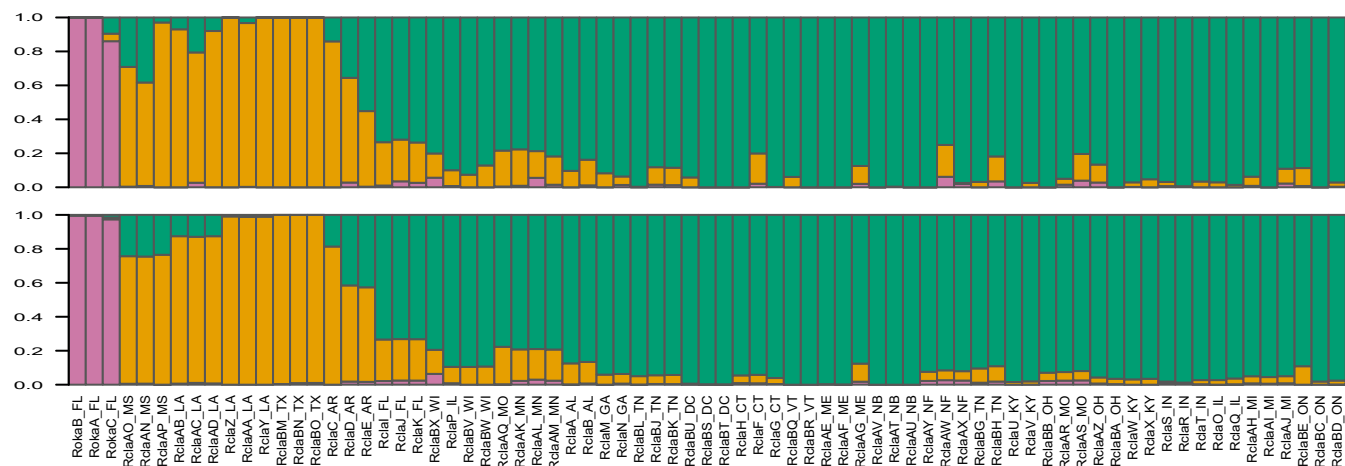
# K=4

# K=5

<50% missing genotypes per SNP

LEA

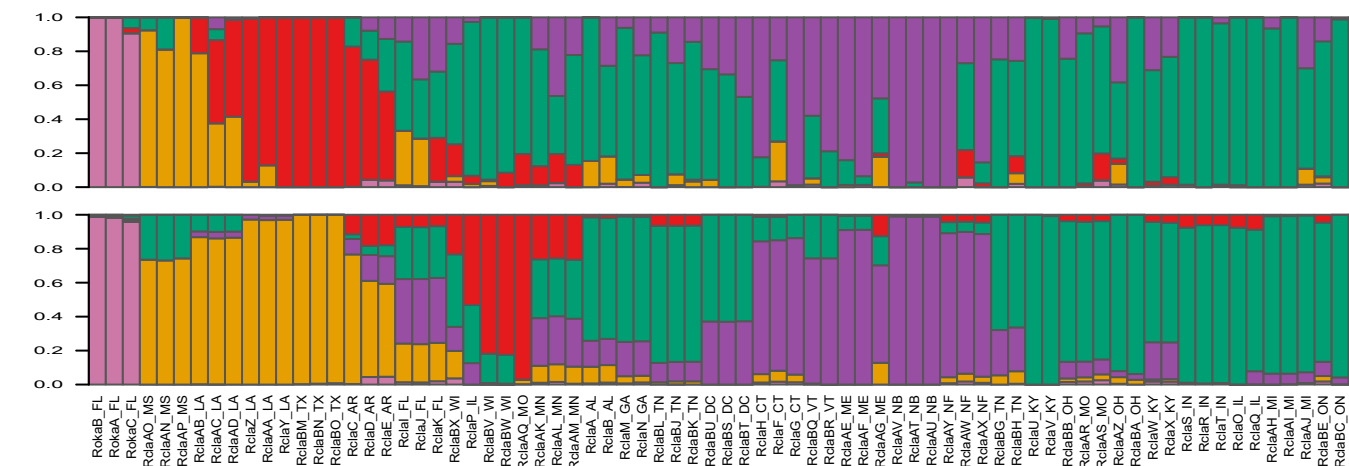
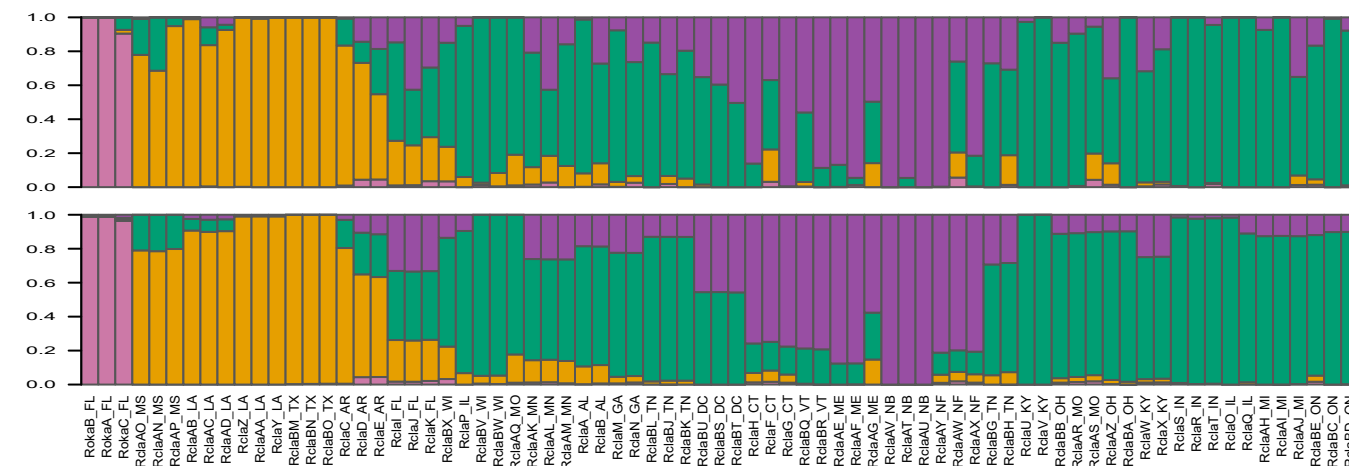
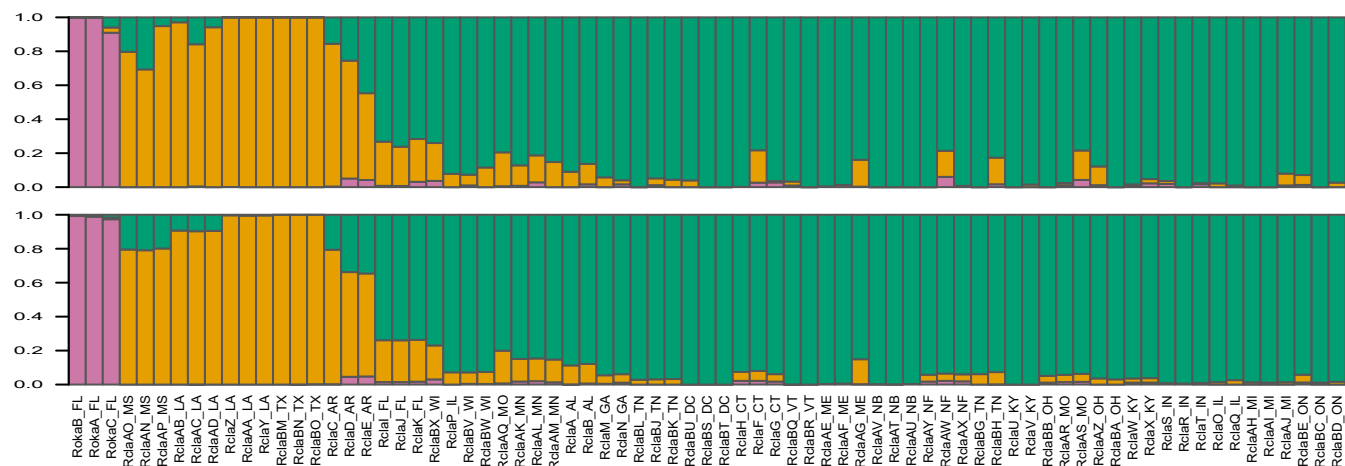
tess3R



<40% missing genotypes per SNP

LEA

tess3R



<30% missing genotypes per SNP

LEA

tess3R

