# How many tagging SNPs does it take to cover the whole human genome?

# God knows the answer

# Non-African population

CEPH

Hapmap phase I: ~294.000
Hapmap phase II: ~ 530.000

$r^2>=0.8$
MAF>=0.05

# African population

Yoruba

Hapmap phase I: ~474.000
Hapmap phase II: ~ 1.06 milj

$r^2>=0.8$
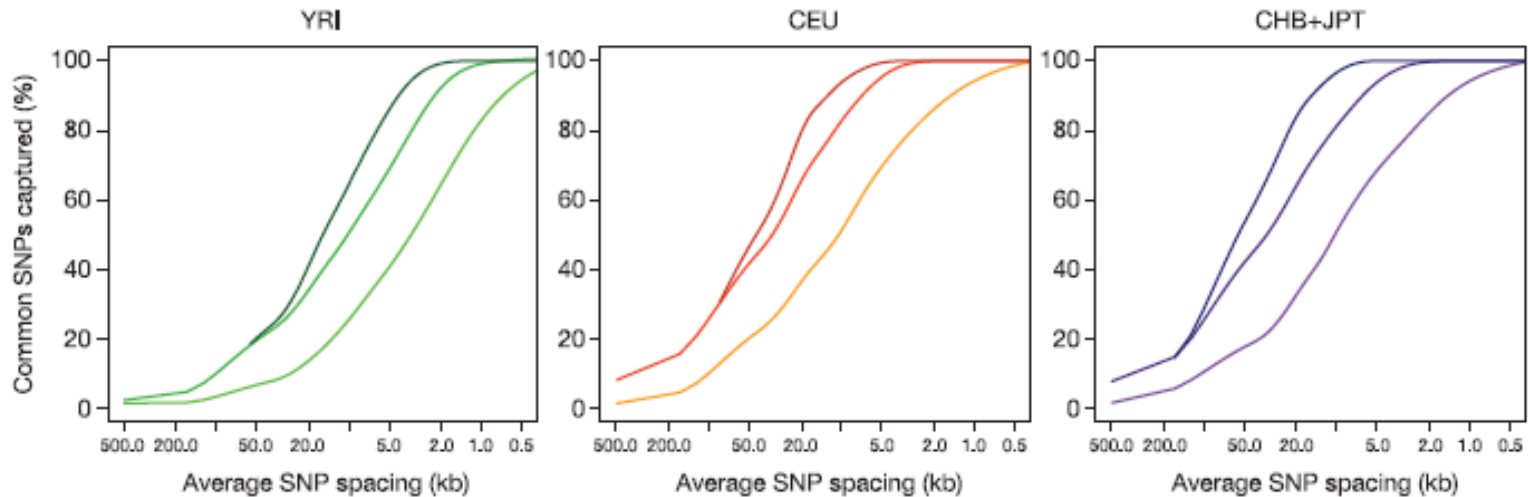MAF>=0.05

# tagSNP density



**Figure 14 | Tag SNP information capture.** The proportion of common SNPs captured with $r^2 \geq 0.8$ as a function of the average tag SNP spacing is shown for the phased ENCODE d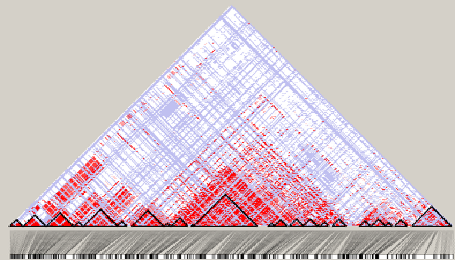ata, plotted (left to right) for tag SNPs prioritized by Tagger (multimarker and pairwise) and for tag SNPs picked at random. Results were averaged over all the ENCODE regions.

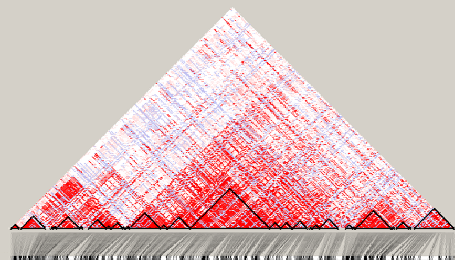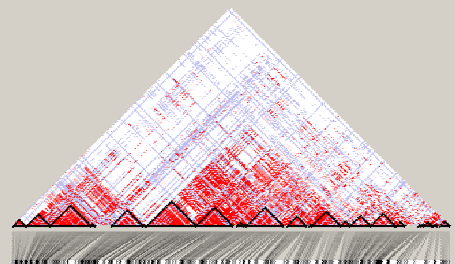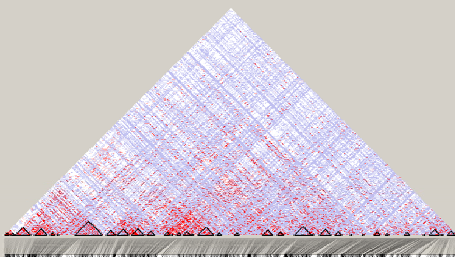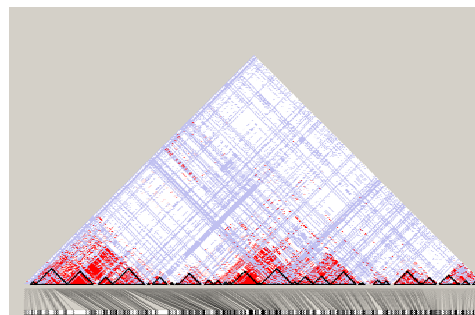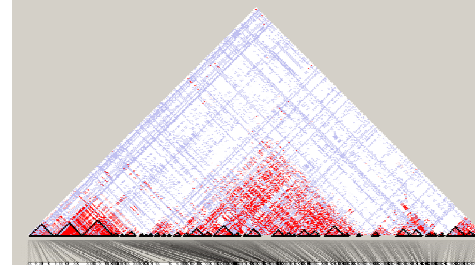# CEPH tagSNPs on Estonian population sample
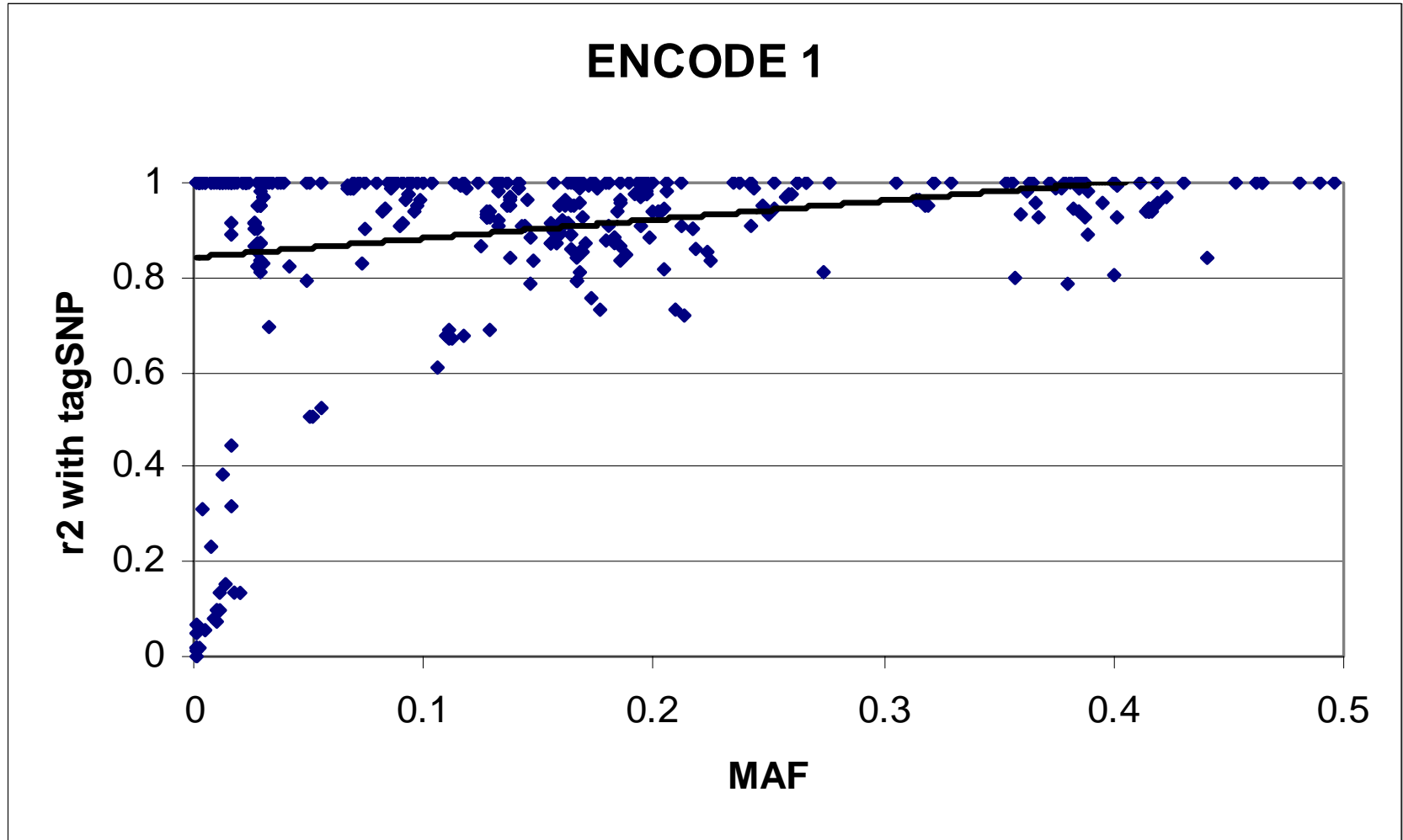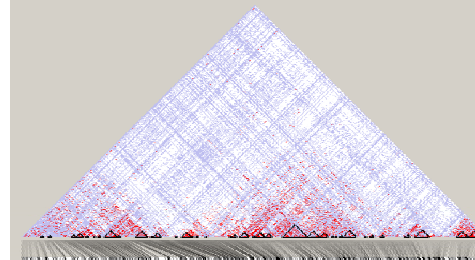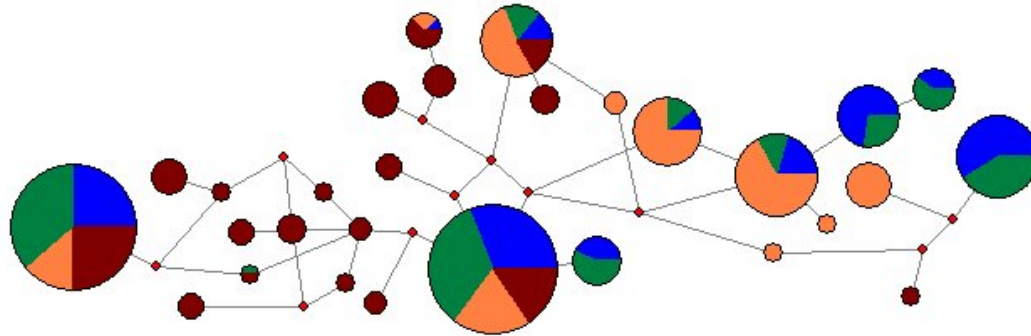
A)

CEU

EST

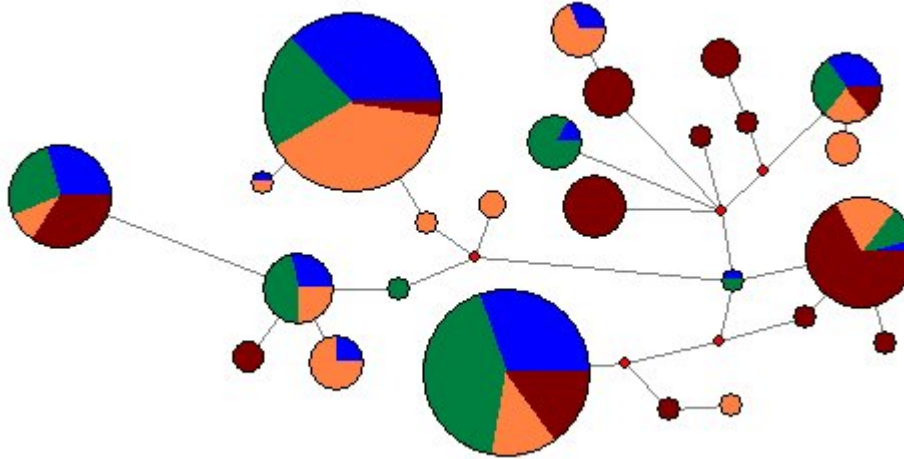CHB/JPT

YRI

B)

CEU

EST
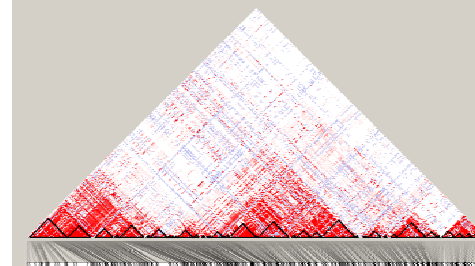
CHB/JPT

YRI

ENC 1)



ENC 2)



Blue – EST-, green – CEU-, orange - CHB/JPT-, brown – YRI