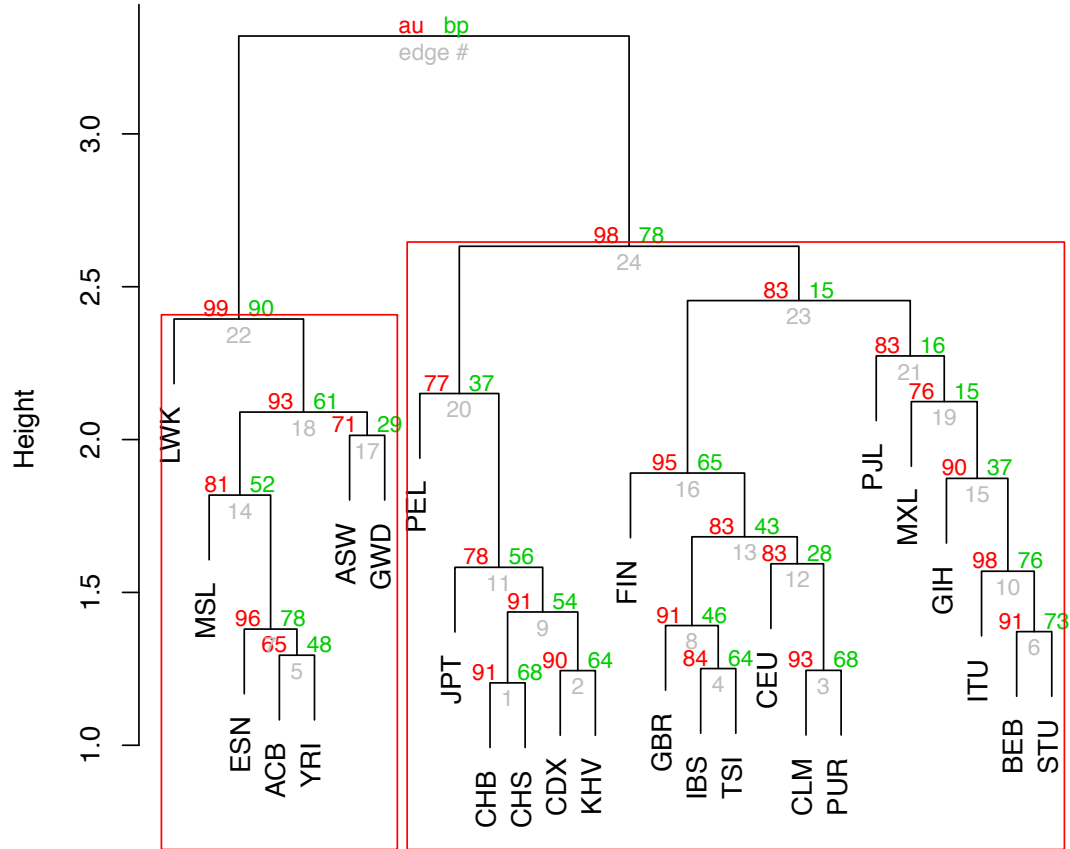


Figure 1 – Simplified flowchart of the retroduplication calling pipeline.

A)

Cluster dendrogram with AU/BP values (%)



Distance: manhattan
Cluster method: average

B)

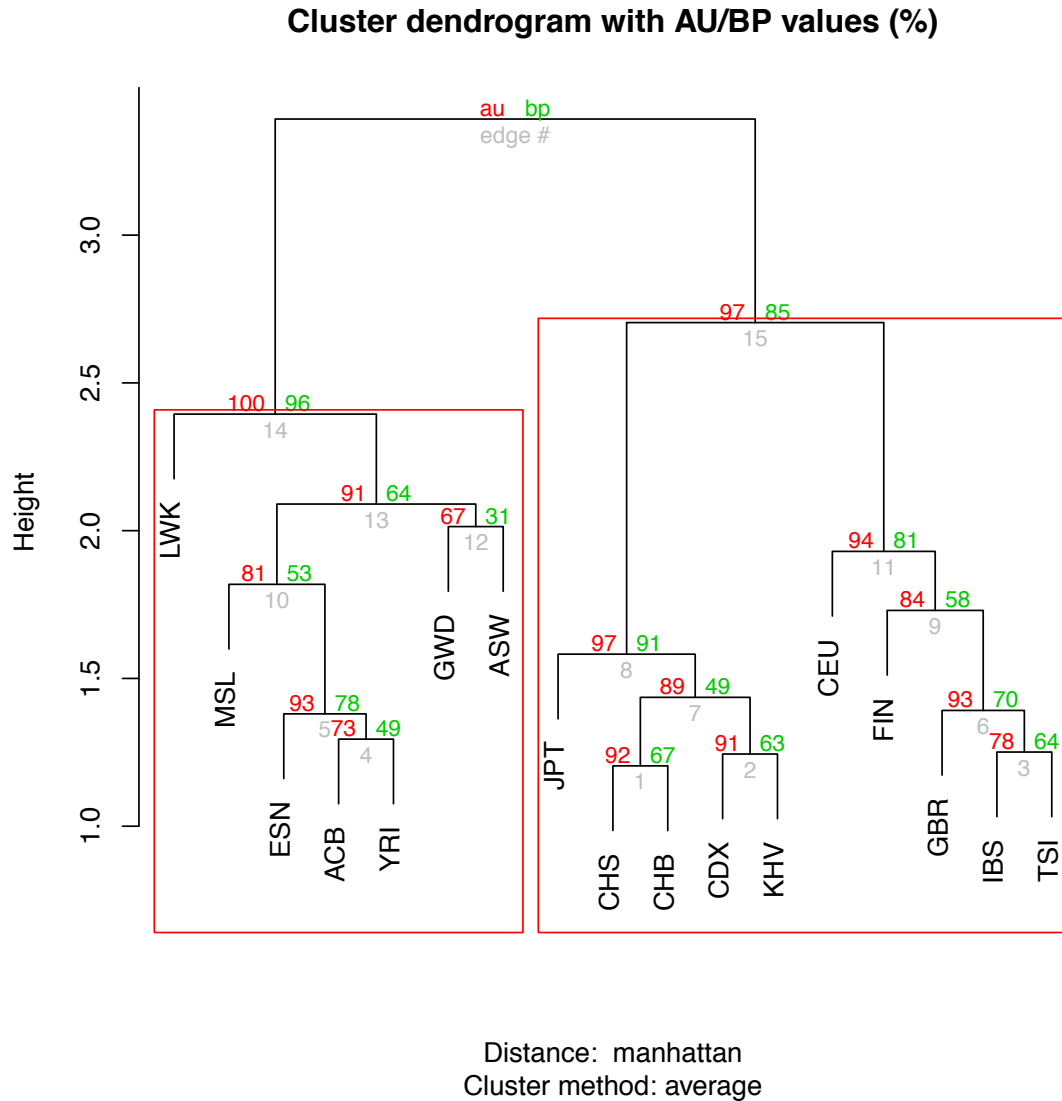


Figure 2 – Phylogenetic trees built based on novel retroduplications. A – The phylogenetic tree of all 26 populations enrolled in the 1000 Genome Project. B – The phylogenetic tree of 17 non-mixed population. Red number: AU (approximately unbiased) probability value. Green number: BP value, i.e. the frequency of the cluster appearing in bootstrap replicates. In the rectangulars, we highlight clusters with $AU \geq 0.95$. Bootstrap resampling was performed 1000 times for generating the trees shown in A and B.