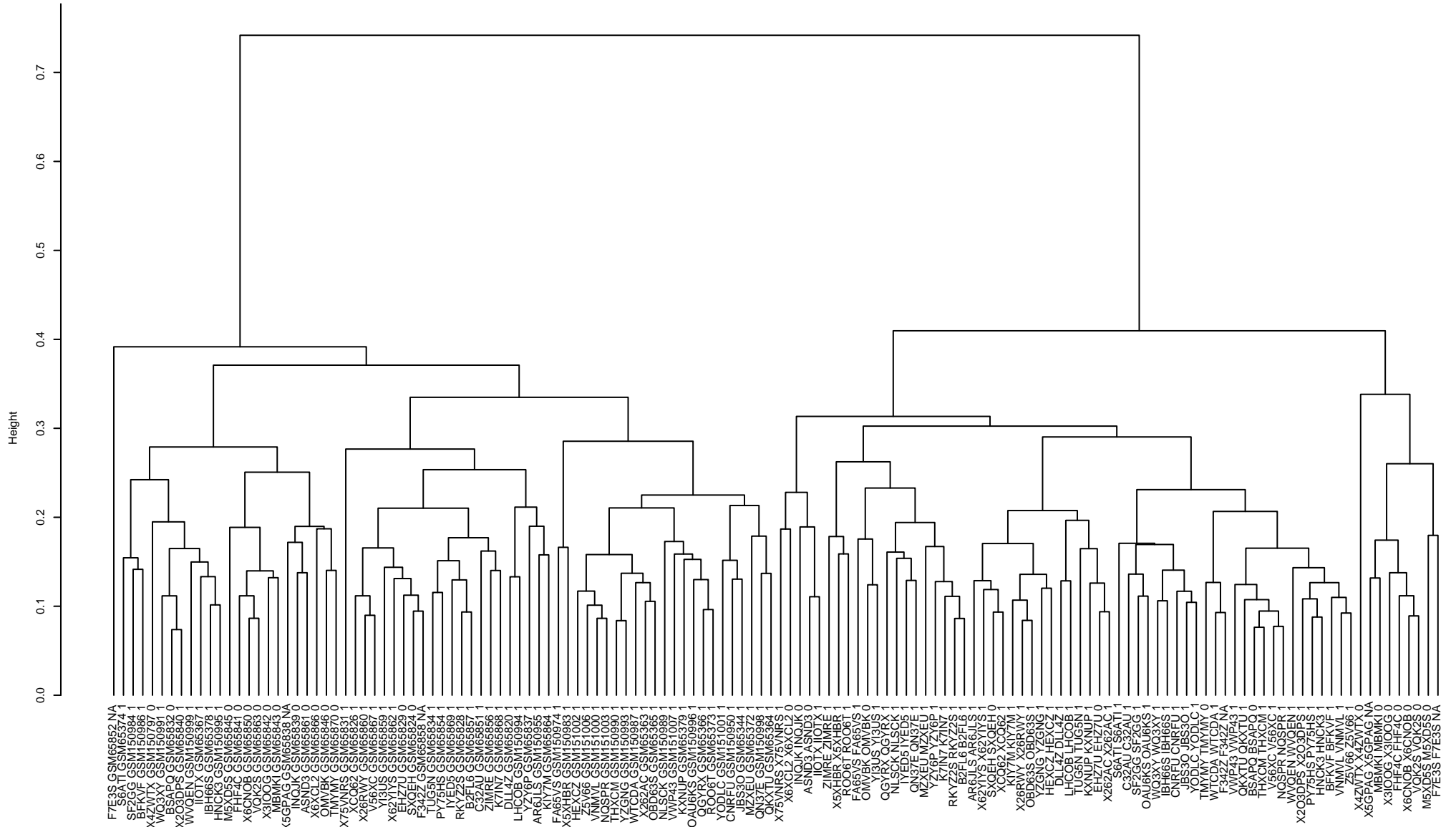
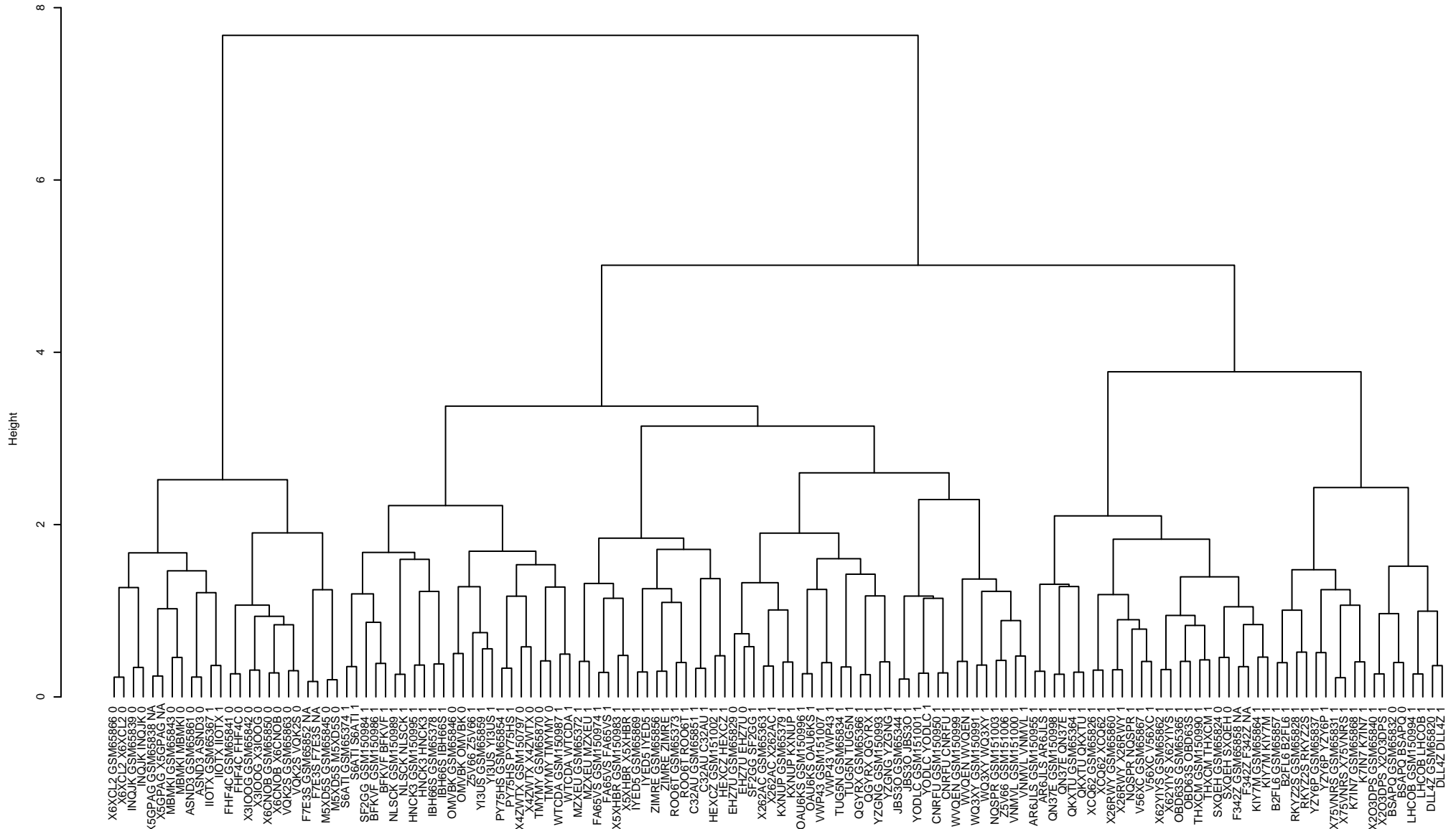


Samples clustering before quantile scaling



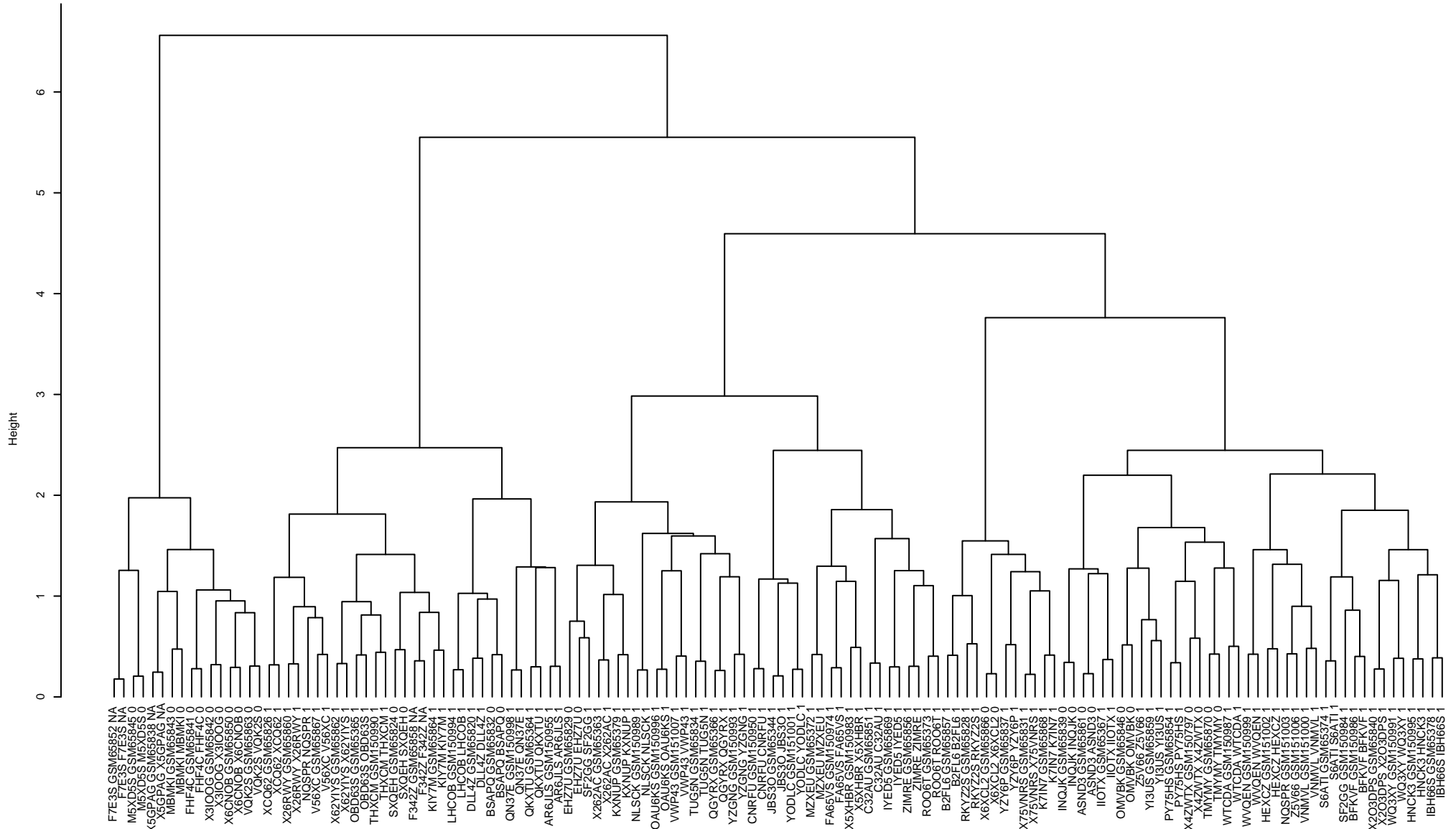
dd
hclust("complete")

Cluster Dendrogram

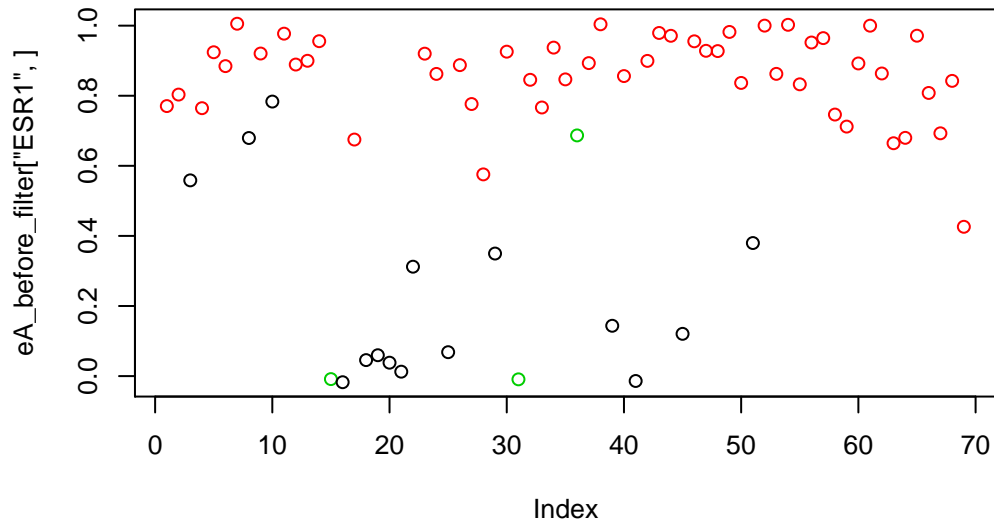
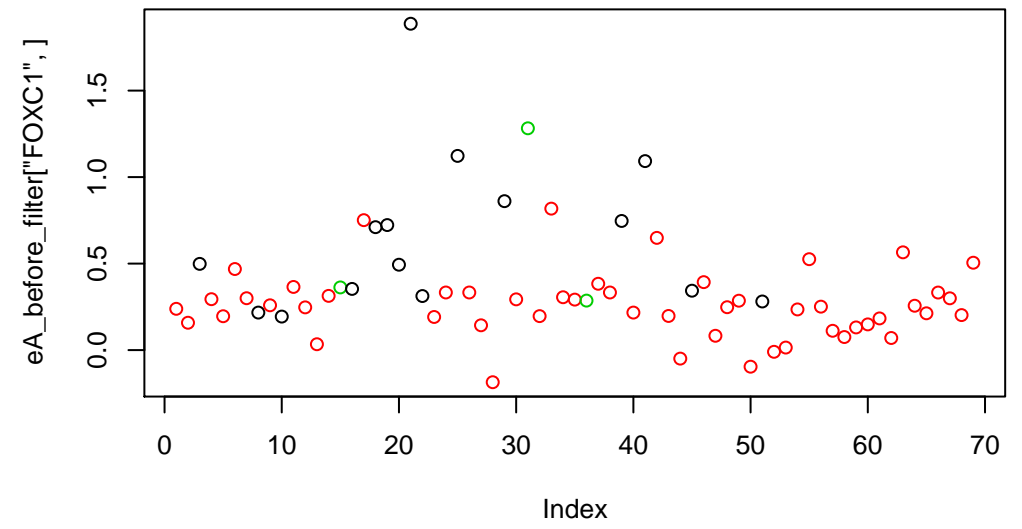
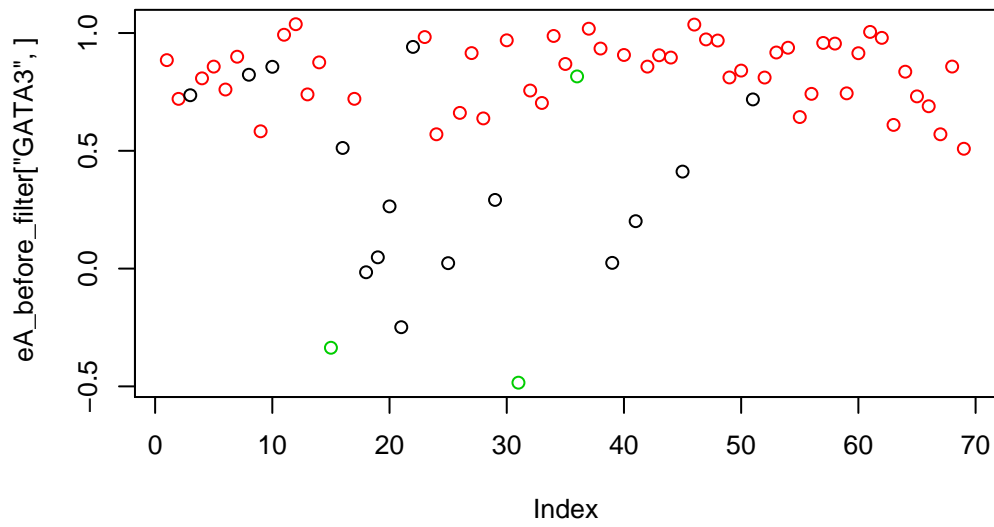
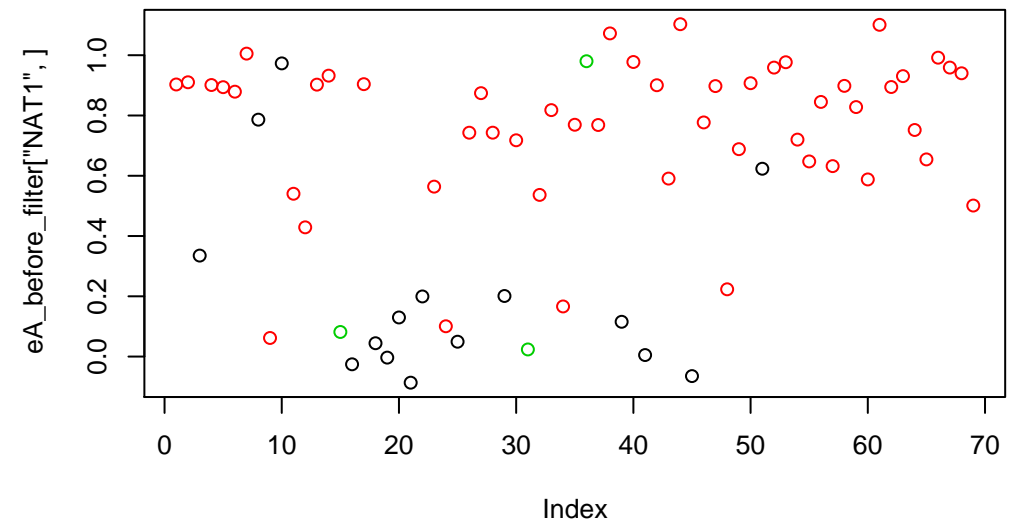


dd
hclust (*, "ward")

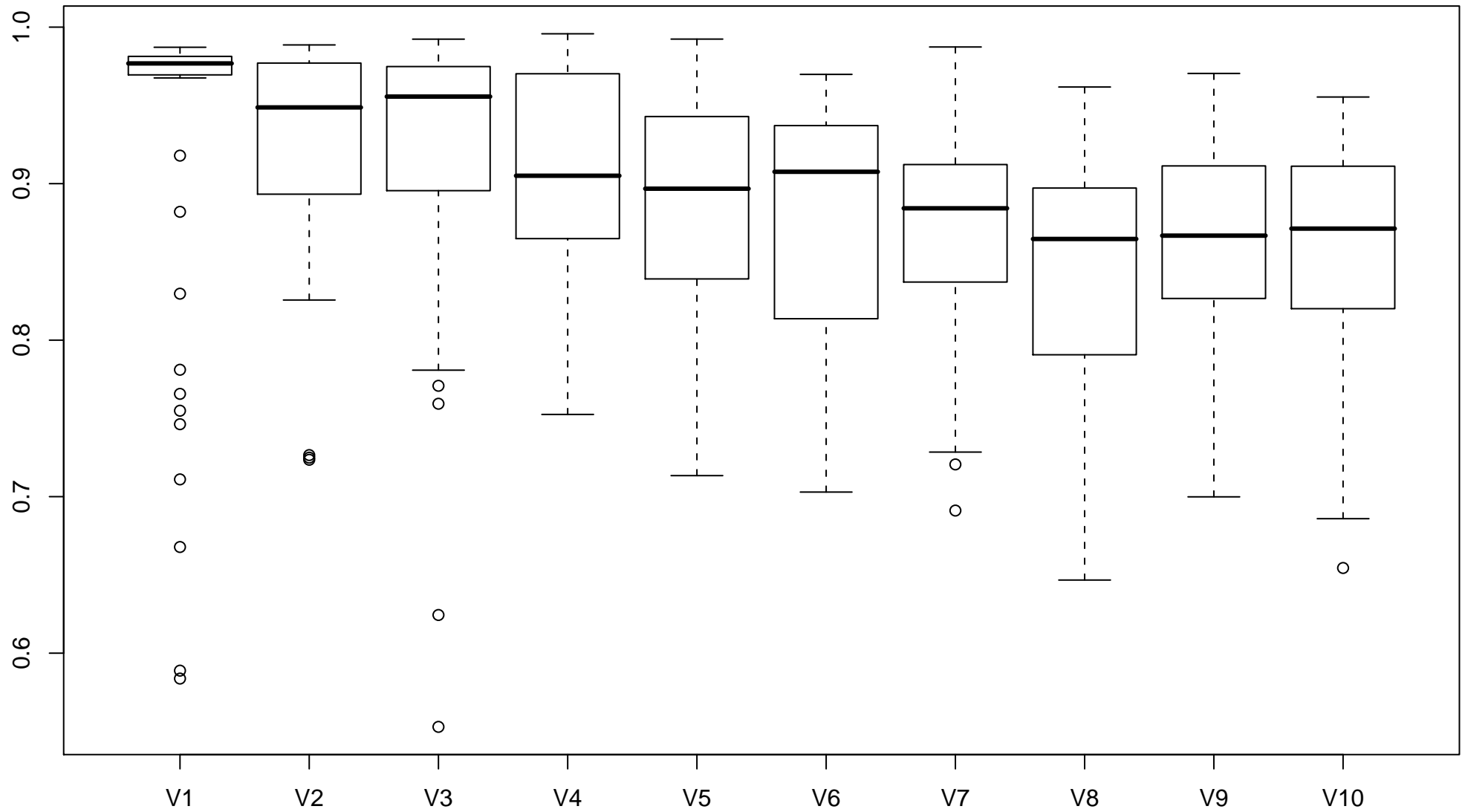
Cluster Dendrogram



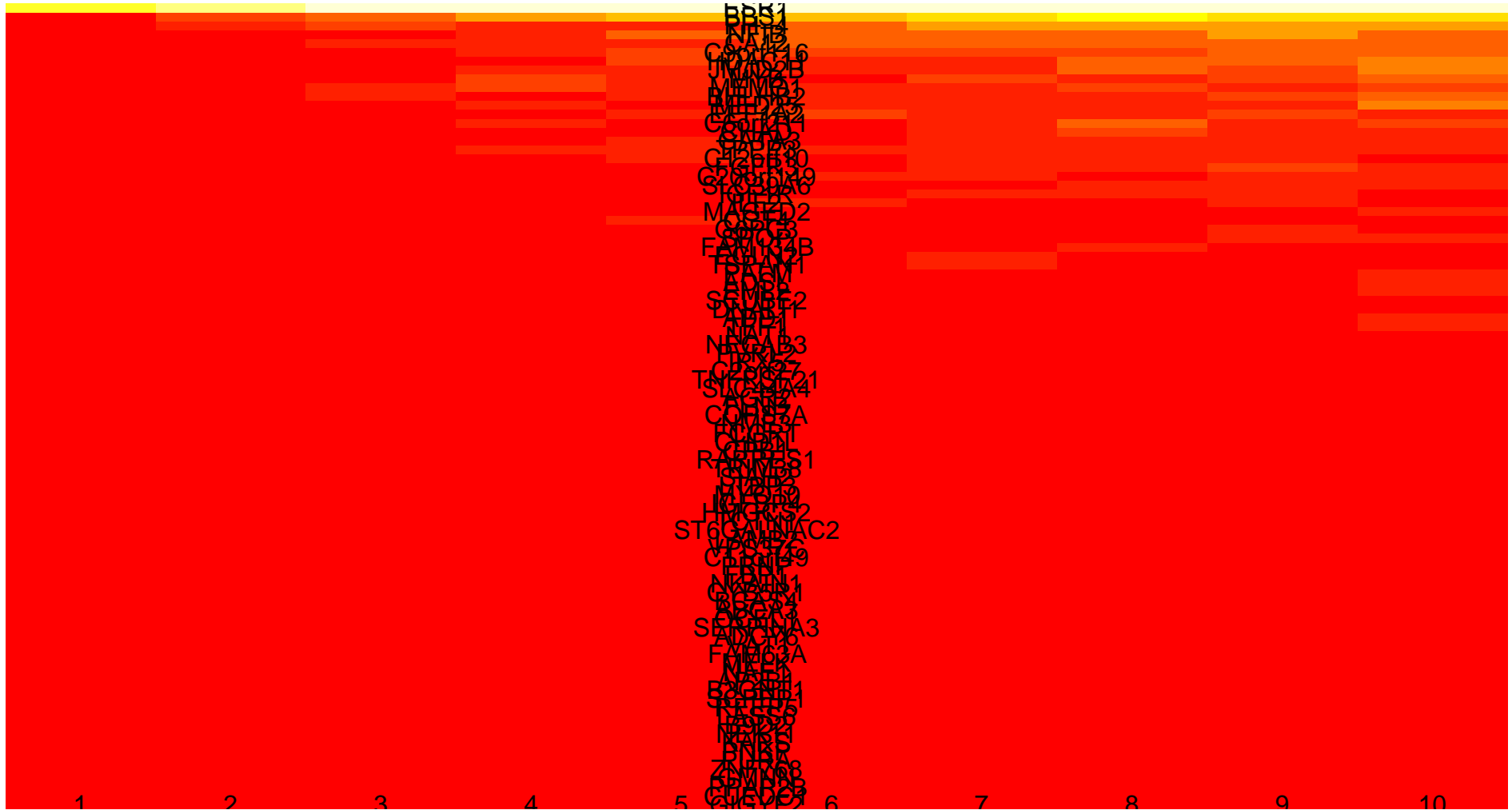
dd
hclust ("", "ward")

ESR1**FOXC1****GATA3****NAT1**

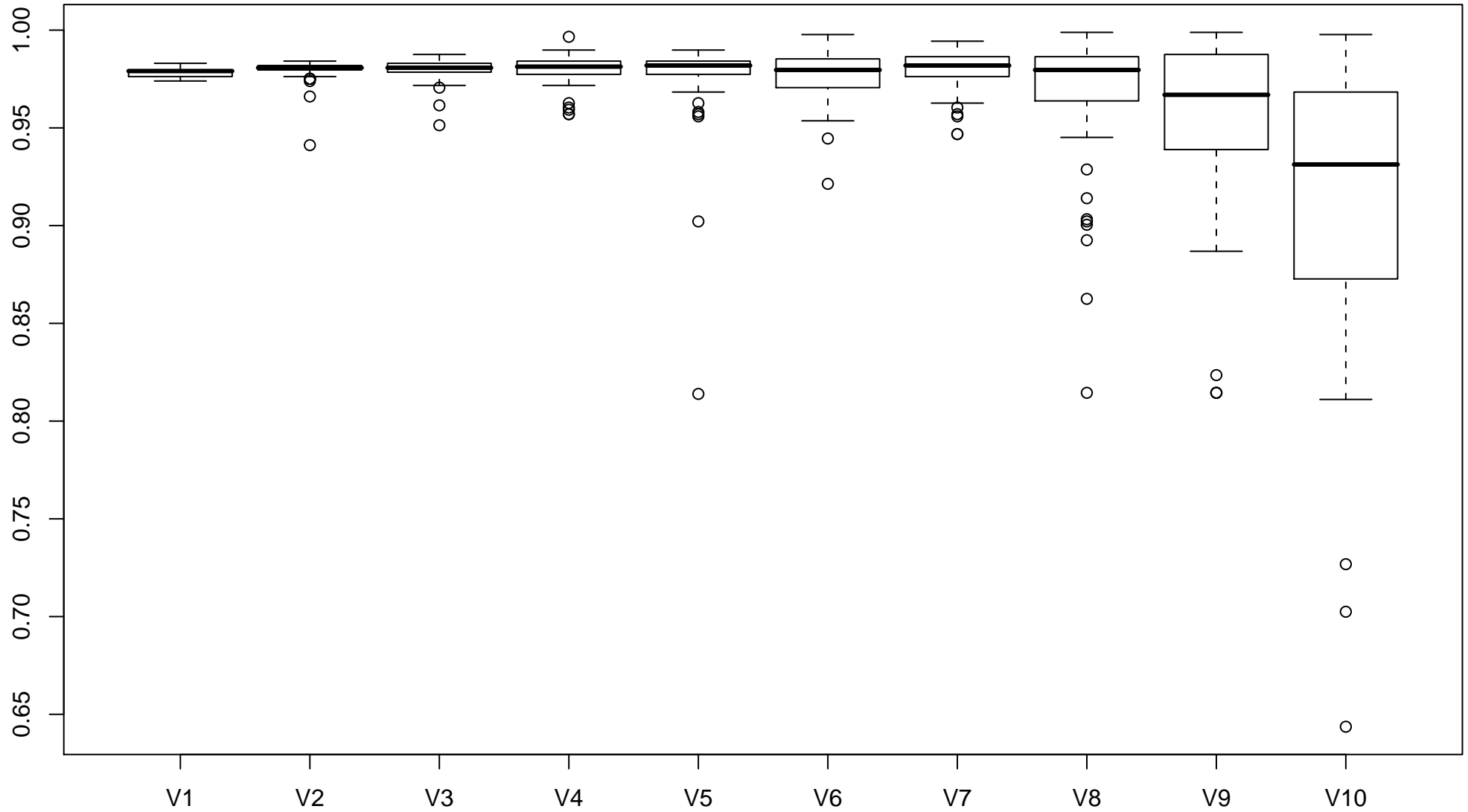
AUC=f(#genes in classifier); prop. of Affy samples (train set): 0



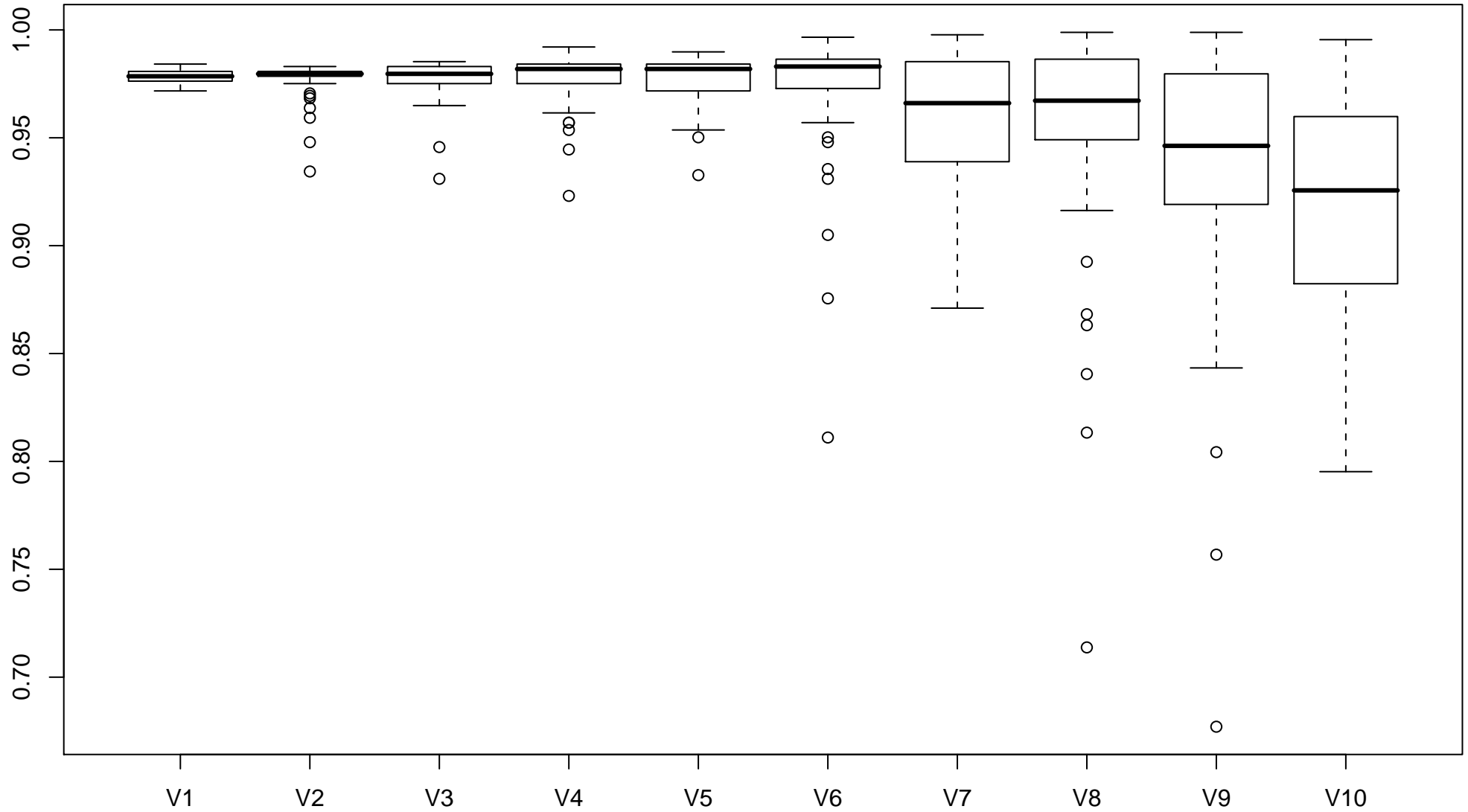
Genes most often selected in classifiers; prop. of Affy samples (train set): 0



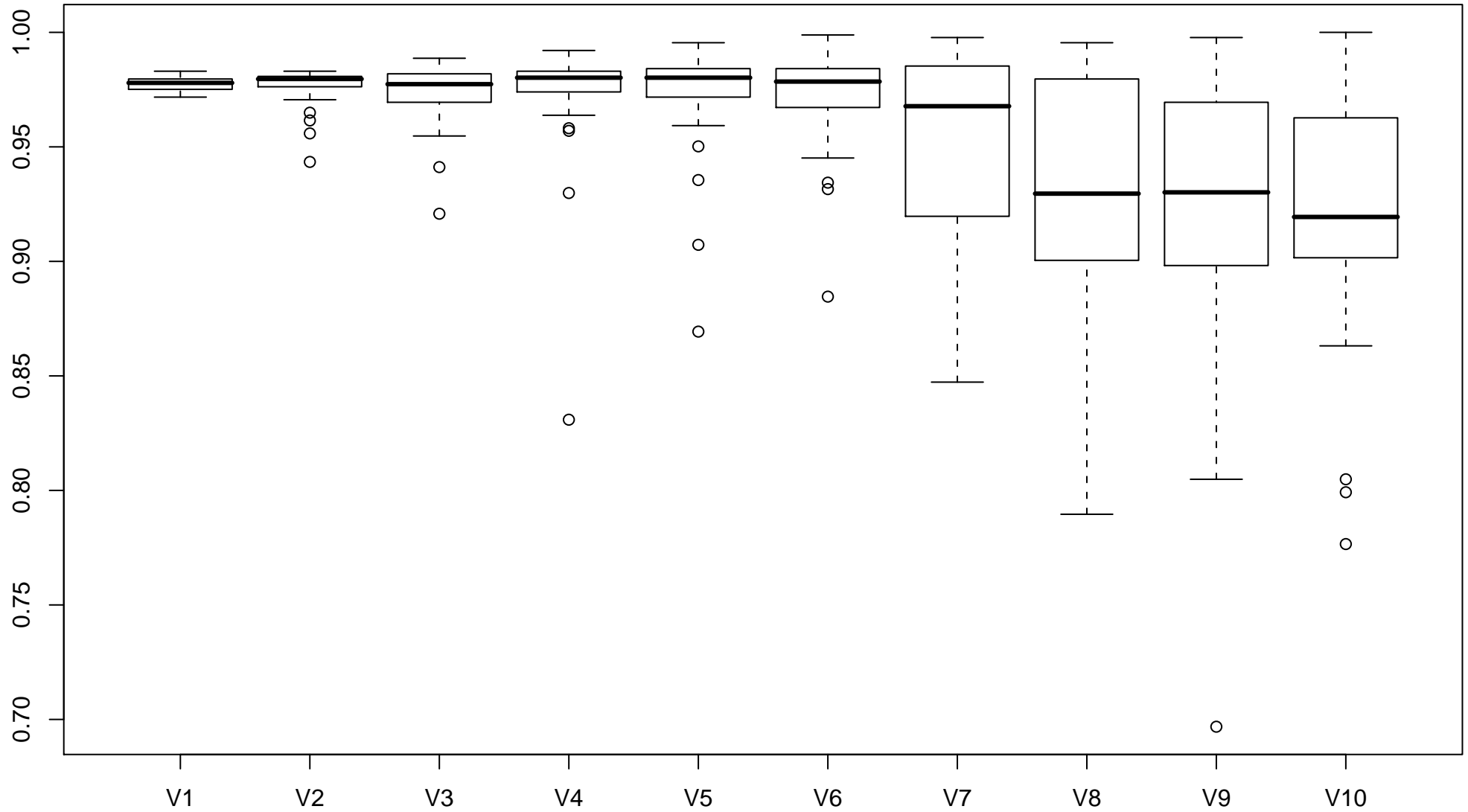
AUC=f(#genes in classifier); prop. of Affy samples (train set): 0.1



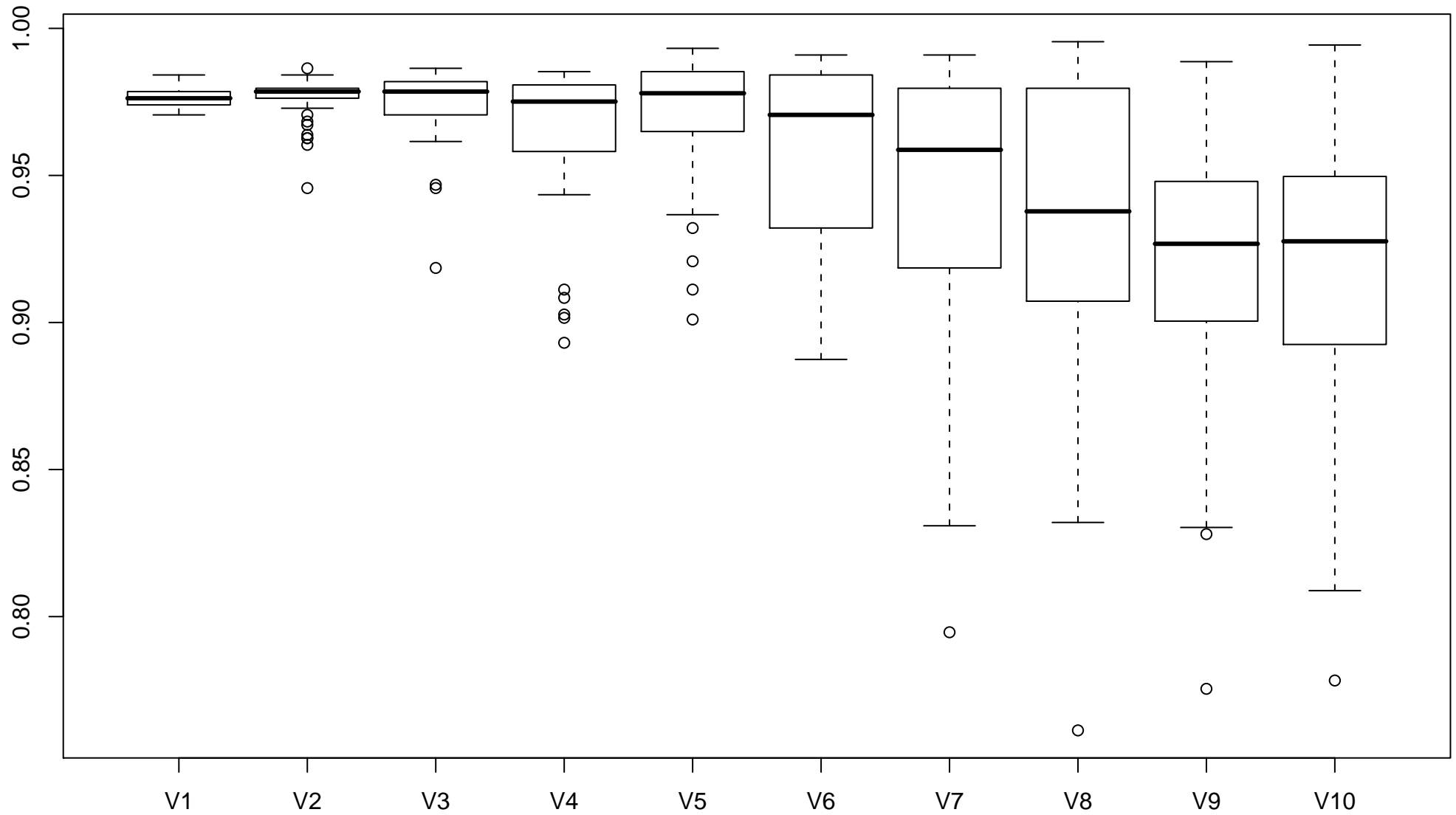
AUC=f(#genes in classifier); prop. of Affy samples (train set): 0.2



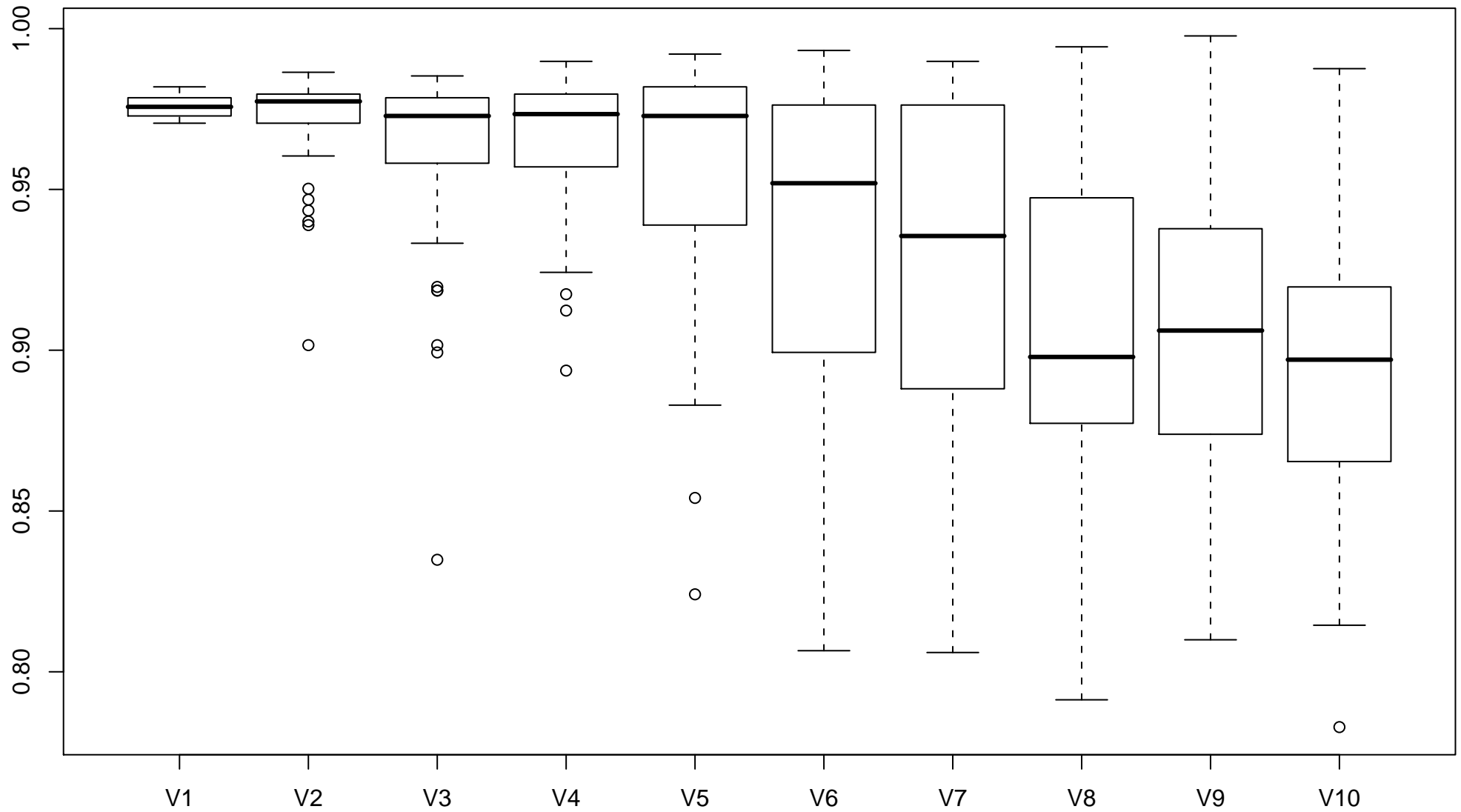
AUC=f(#genes in classifier); prop. of Affy samples (train set): 0.3



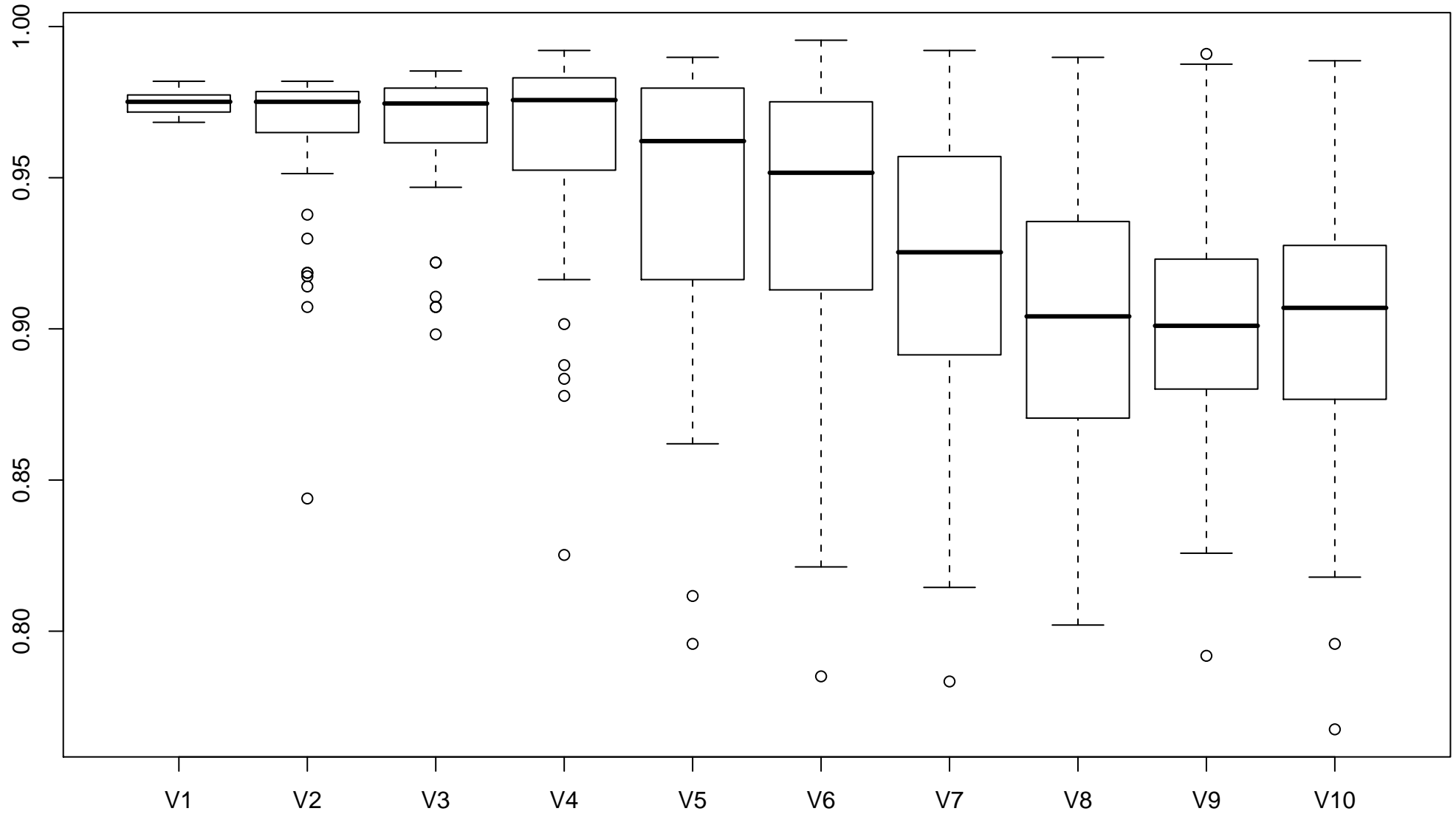
AUC=f(#genes in classifier); prop. of Affy samples (train set): 0.4



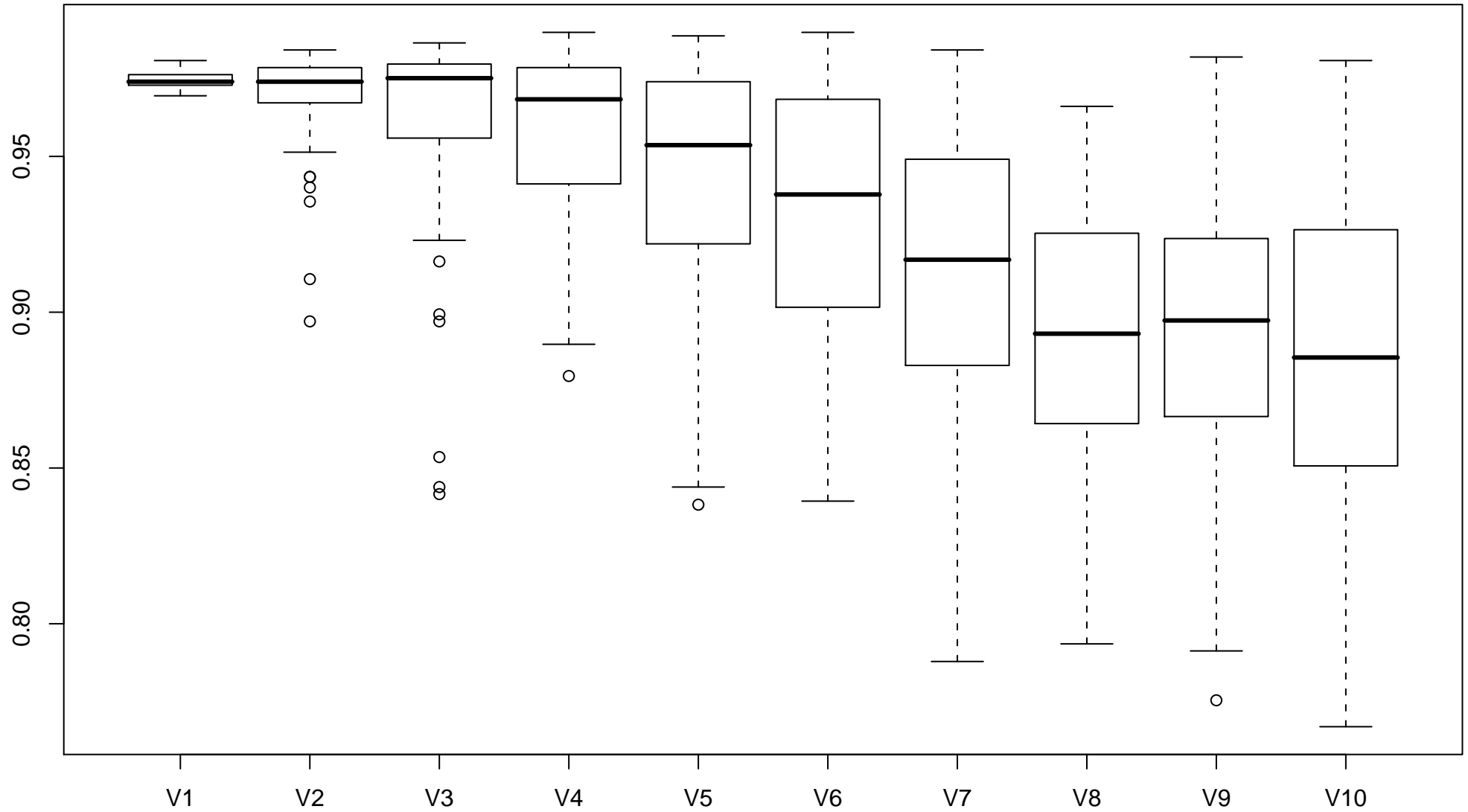
AUC=f(#genes in classifier); prop. of Affy samples (train set): 0.5



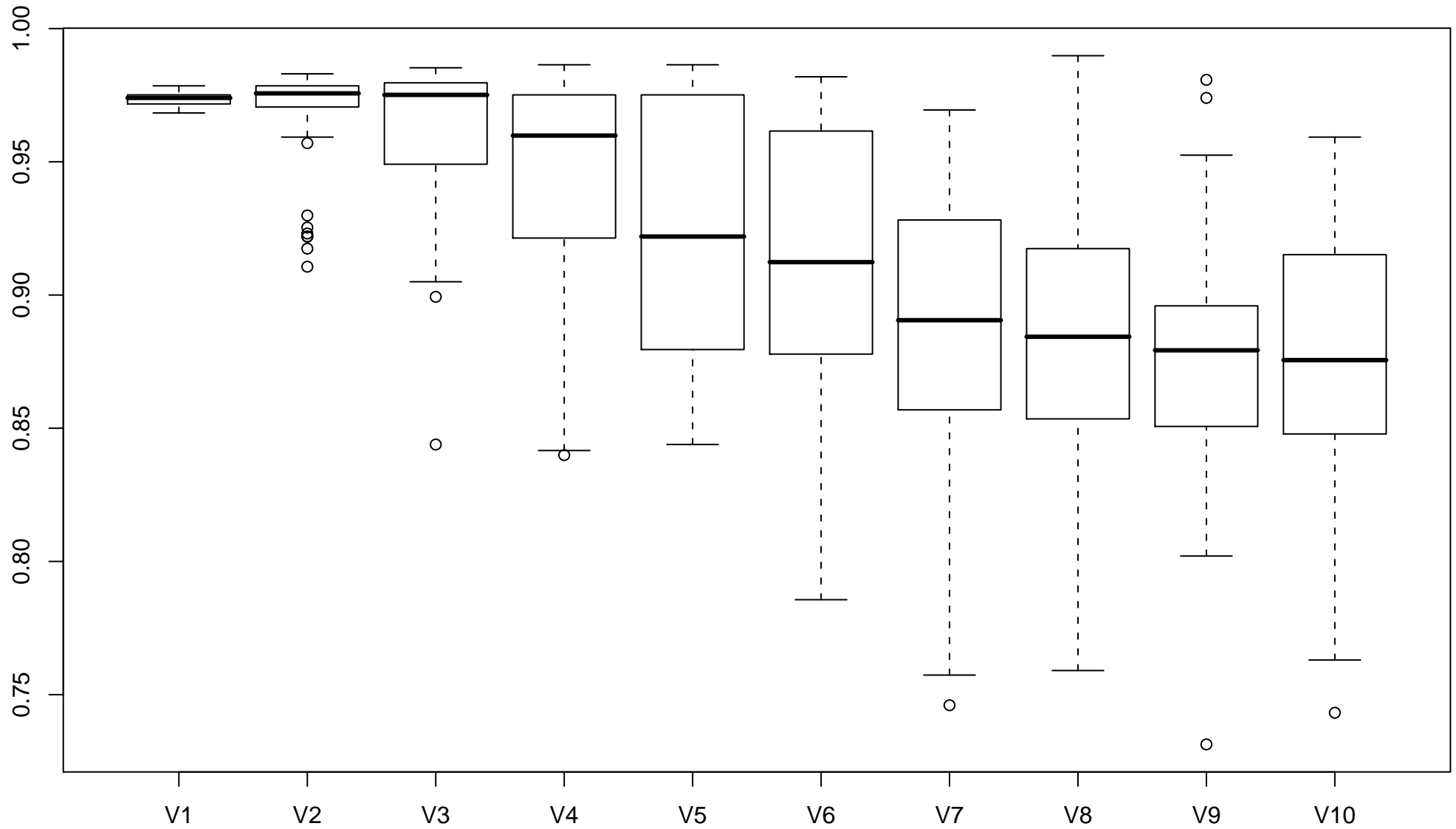
AUC=f(#genes in classifier); prop. of Affy samples (train set): 0.6



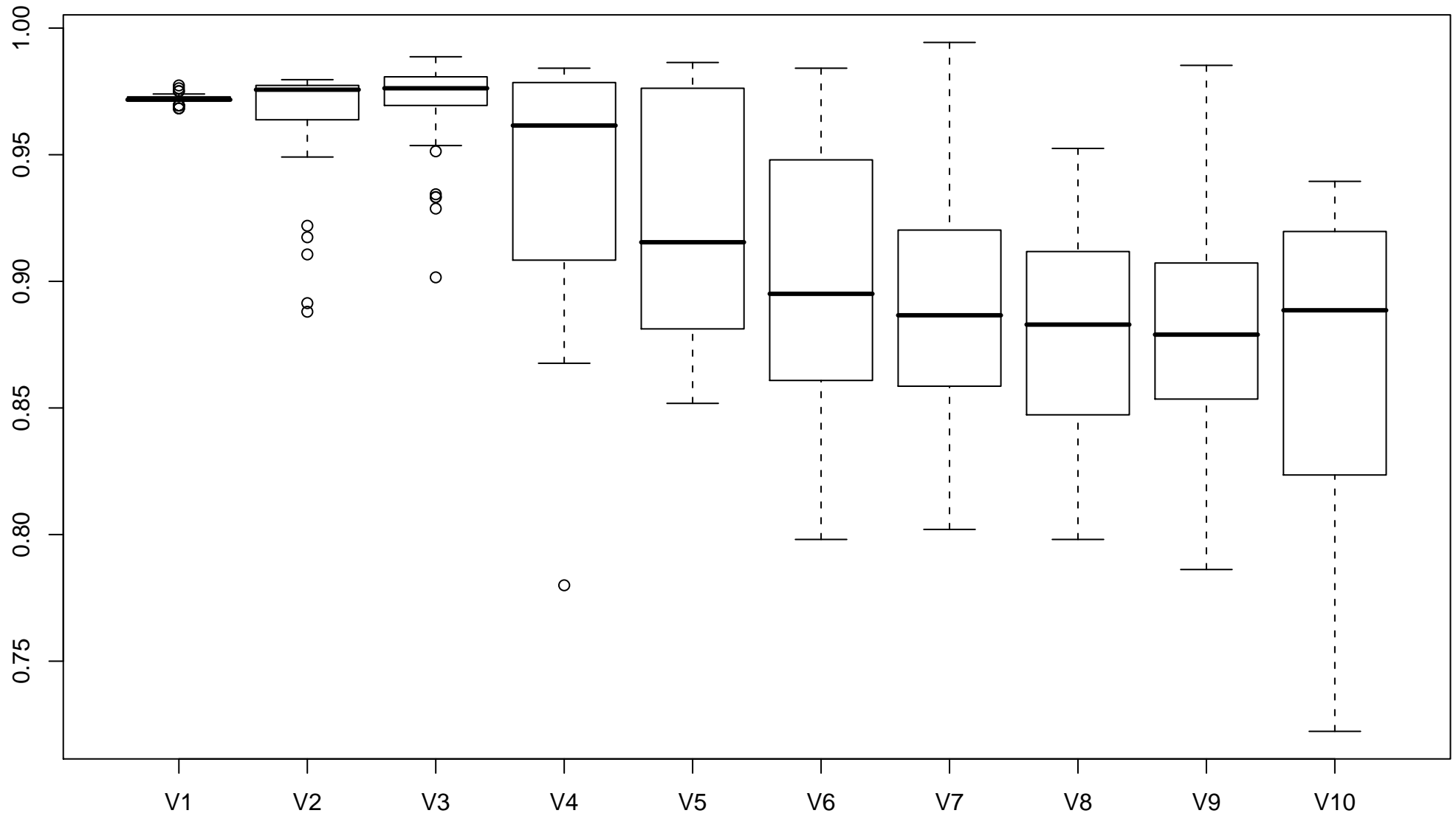
AUC=f(#genes in classifier); prop. of Affy samples (train set): 0.7



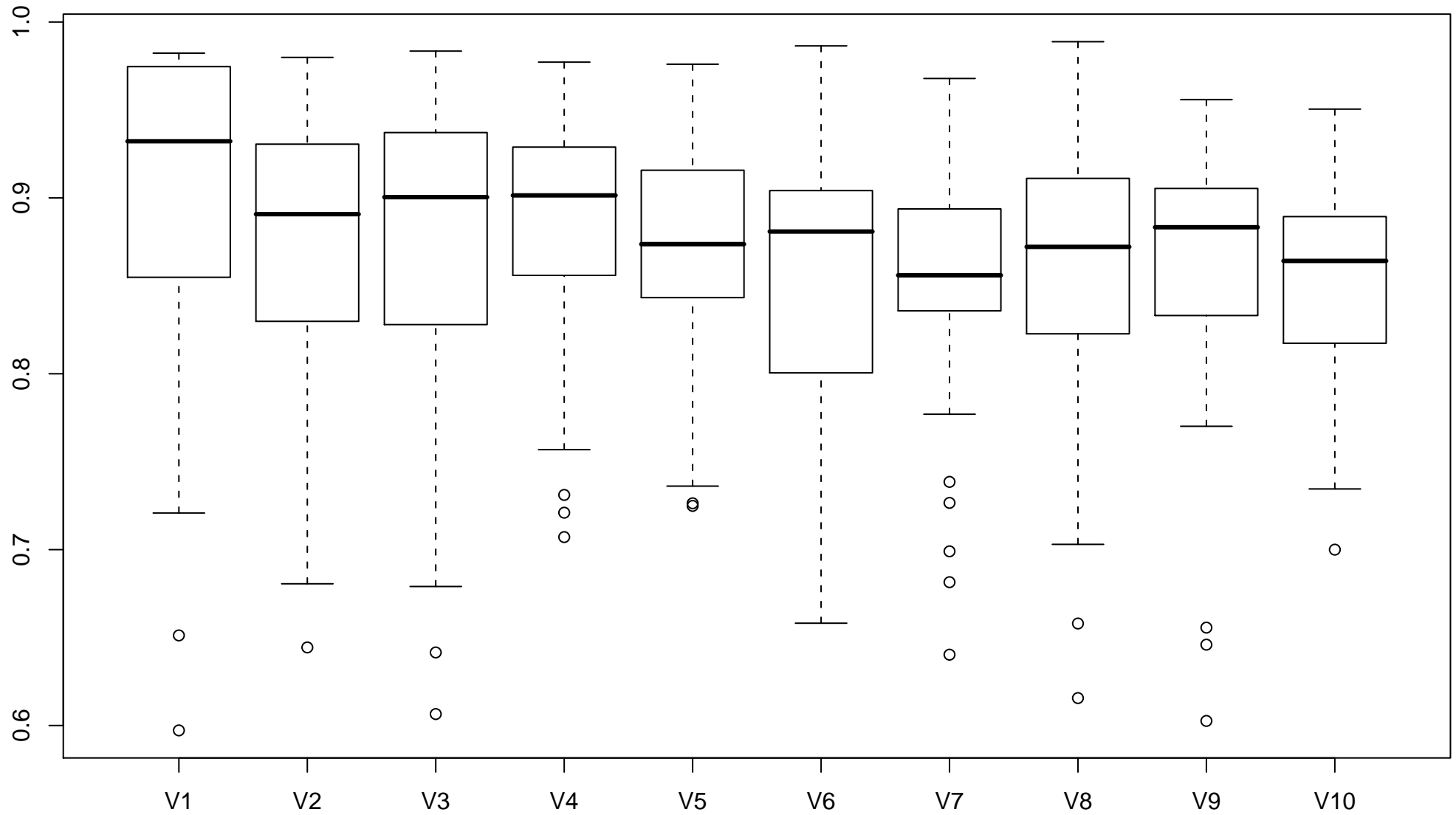
AUC=f(#genes in classifier); prop. of Affy samples (train set): 0.8



AUC=f(#genes in classifier); prop. of Affy samples (train set): 0.9



AUC=f(#genes in classifier); prop. of Affy samples (train set): 1



AUC=f(#genes in classifier); Overall

