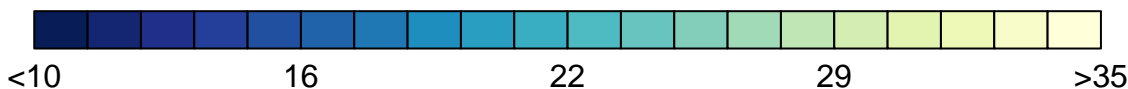
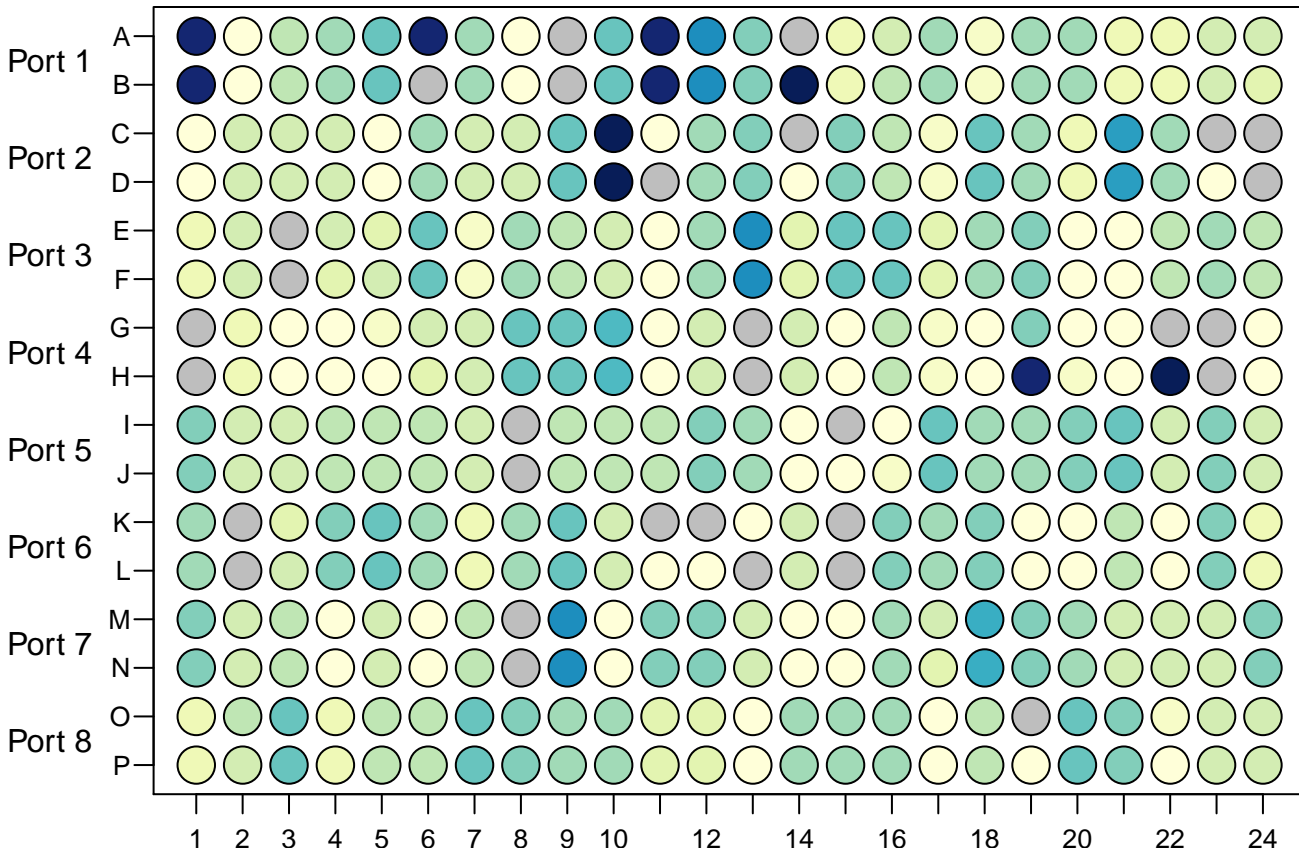
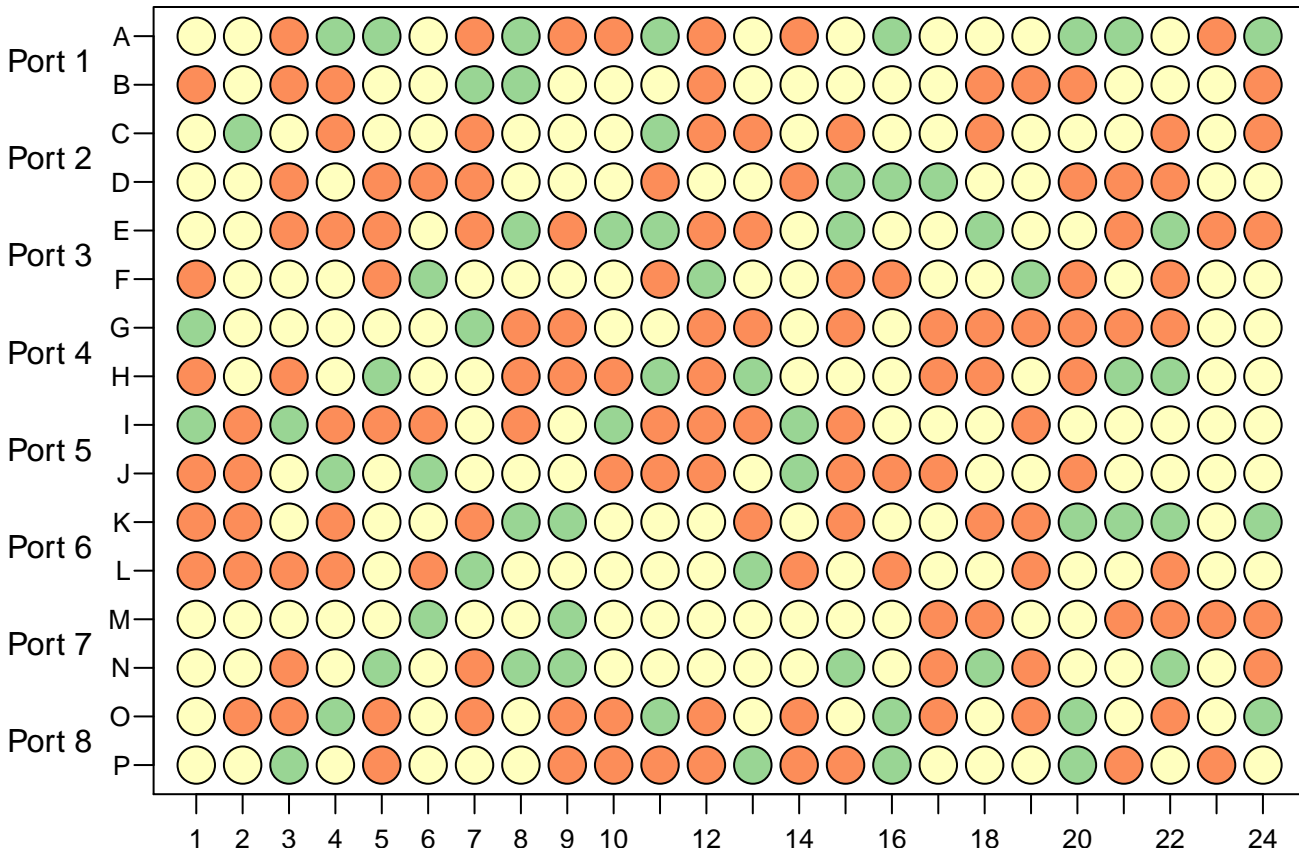


sample1

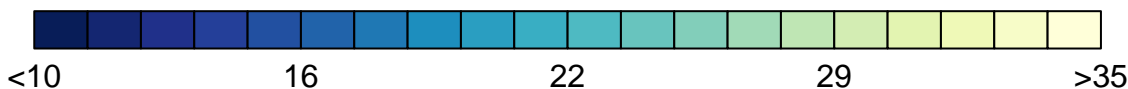
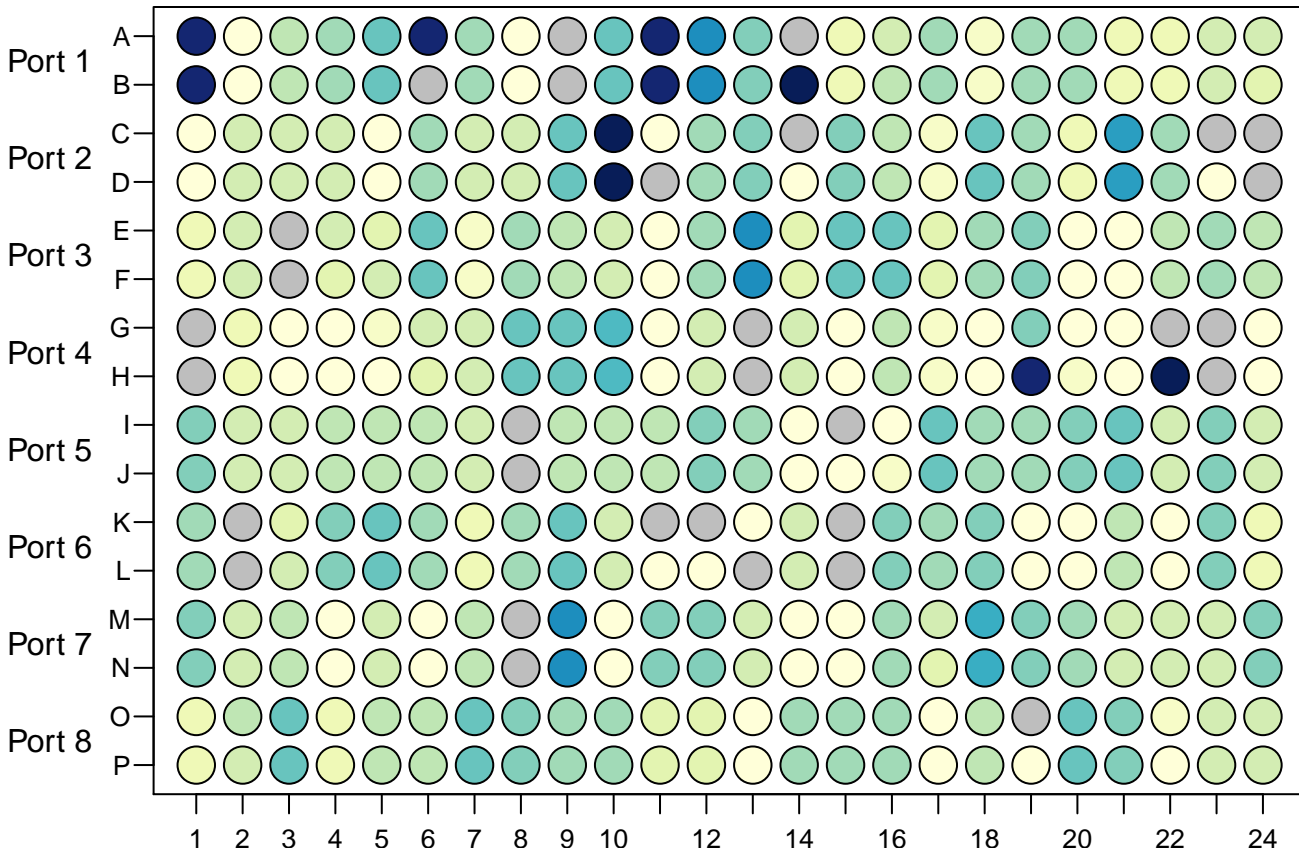


# sample1

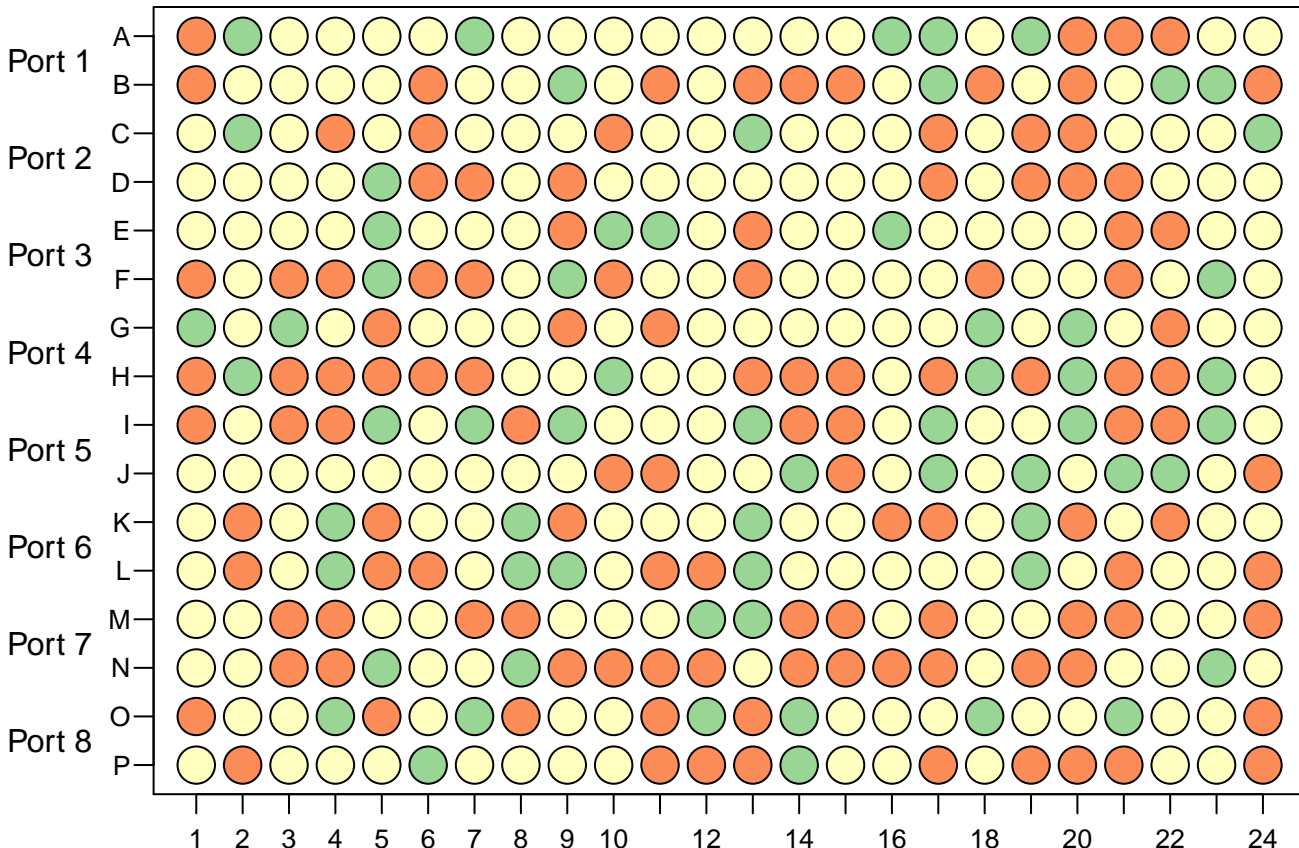


Kinase Marker TF

sample1

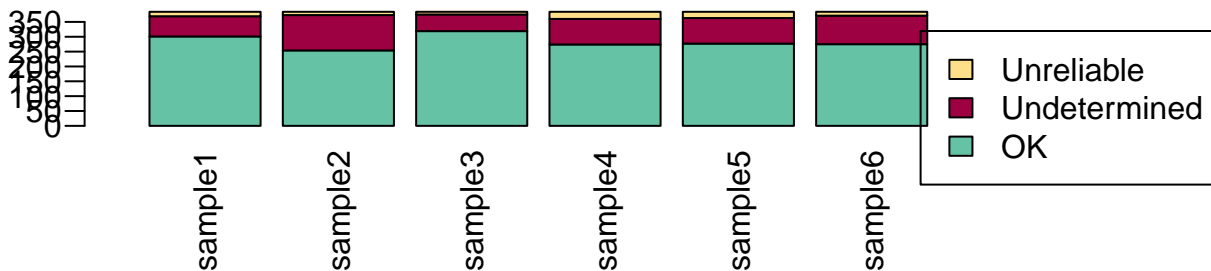
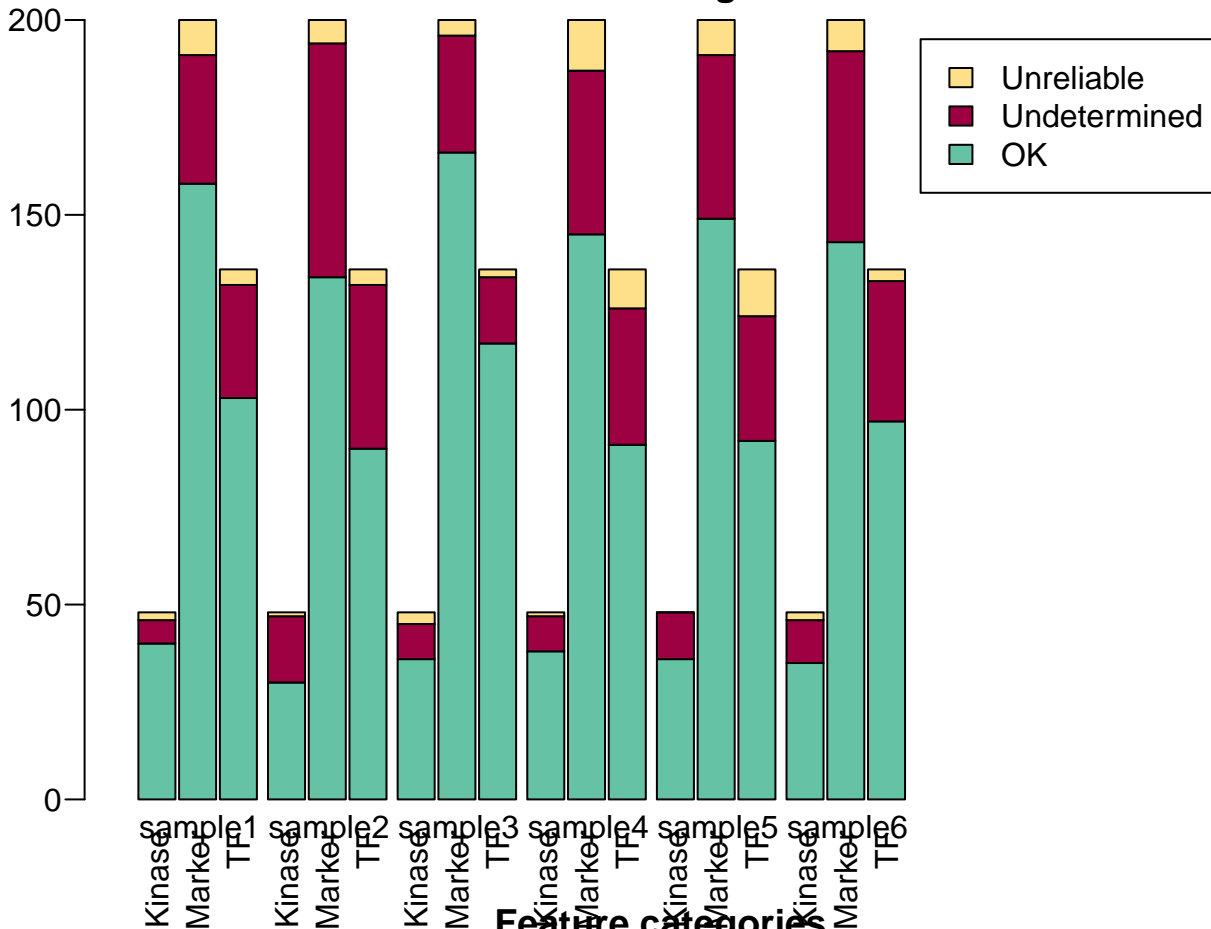


# sample1



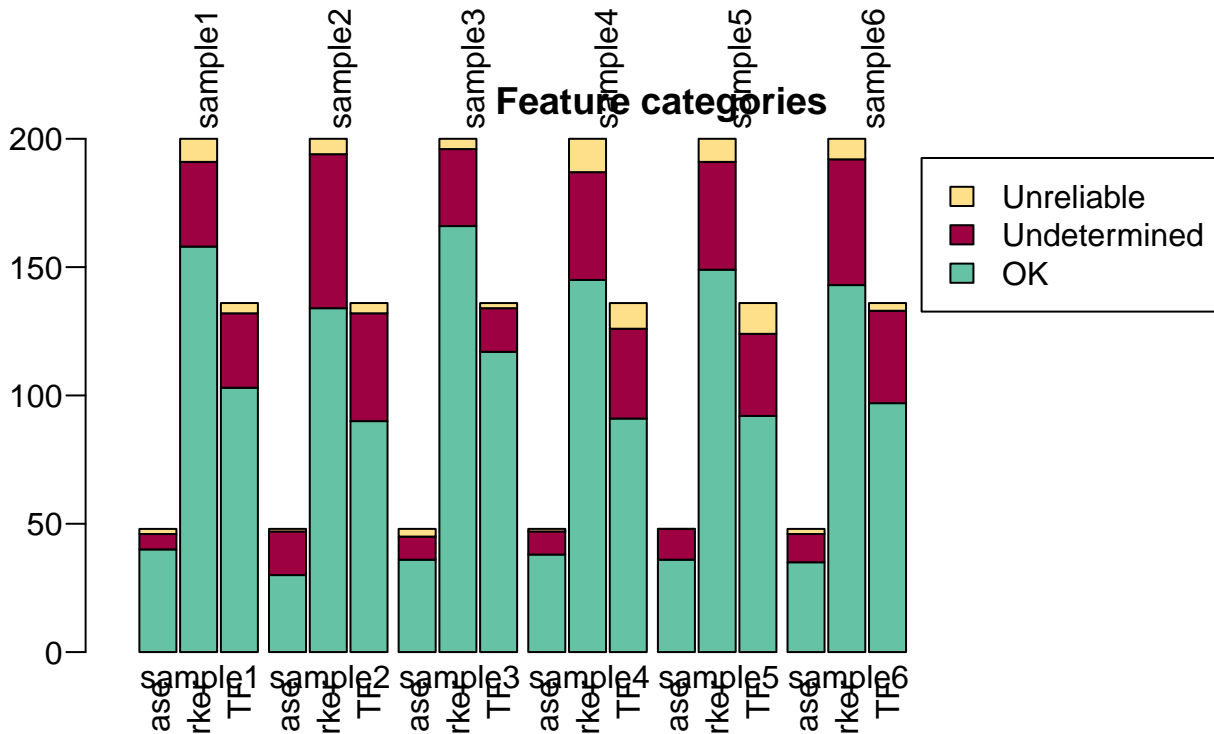
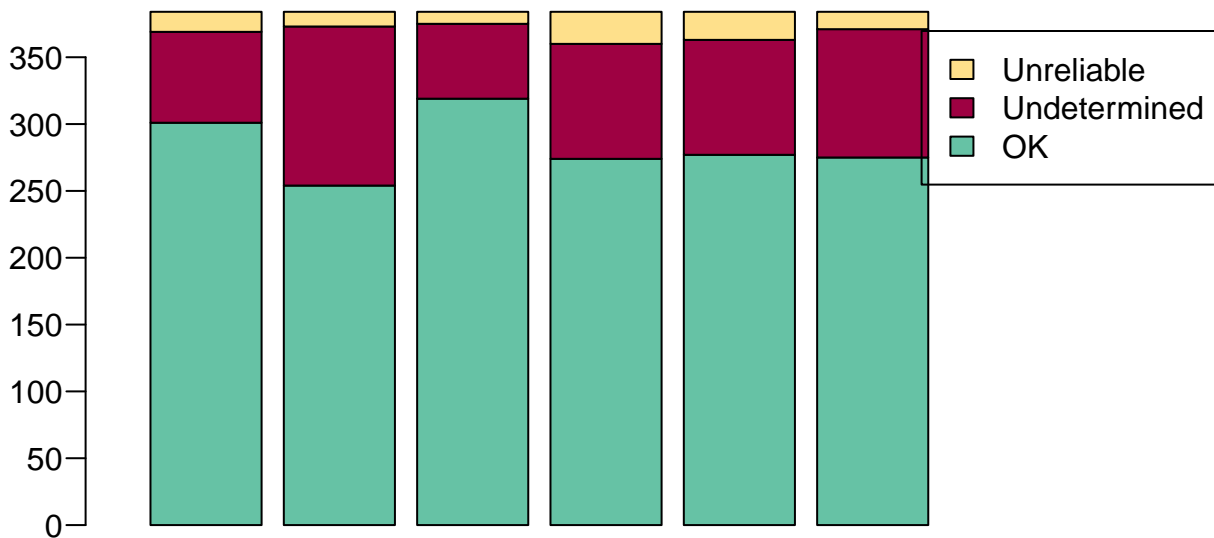
Kinase Marker TF

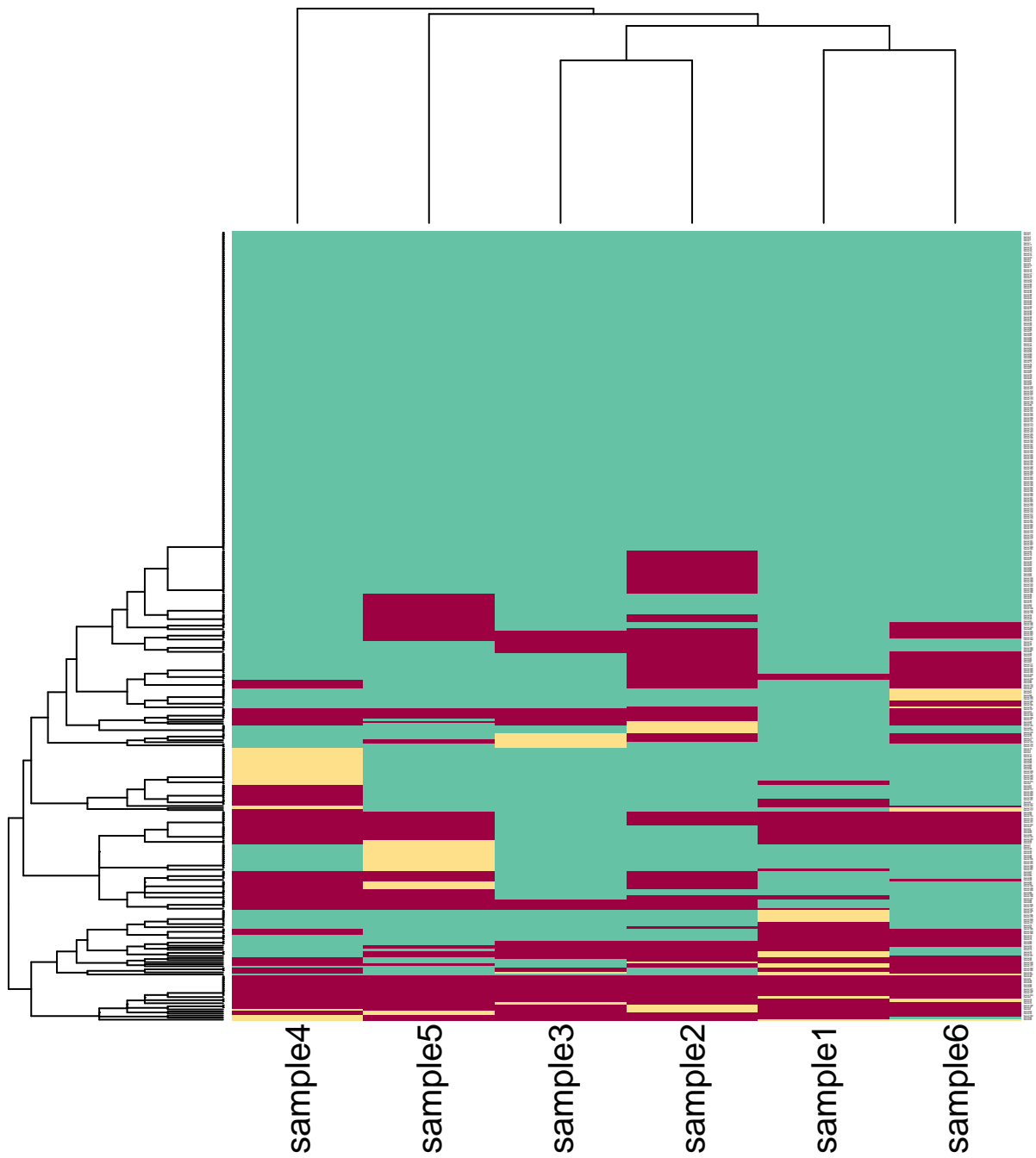
# Feature categories

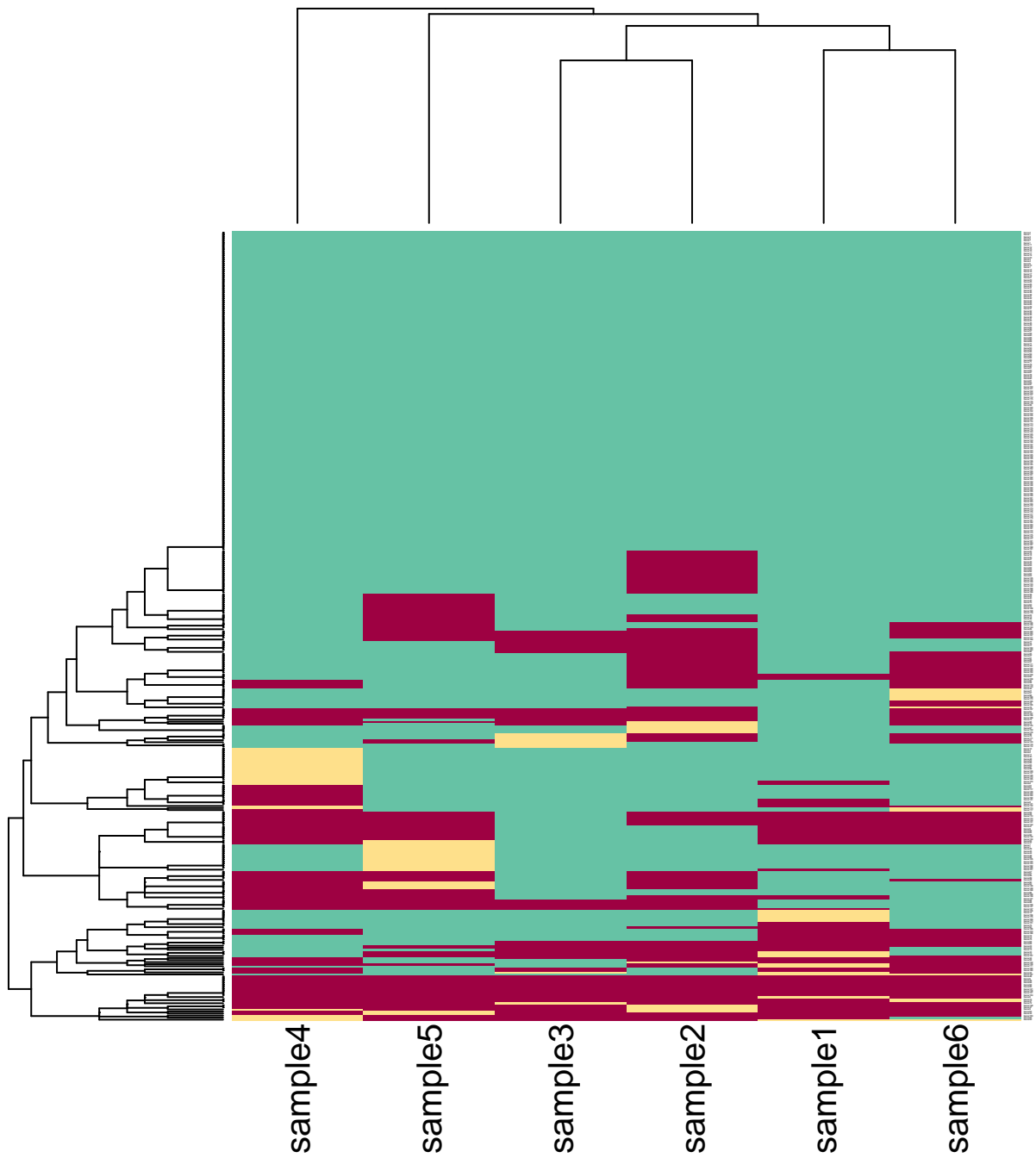




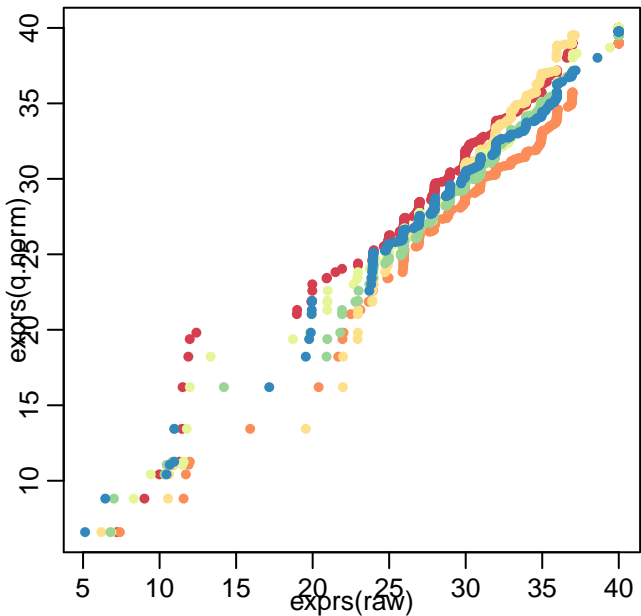
# Feature categories



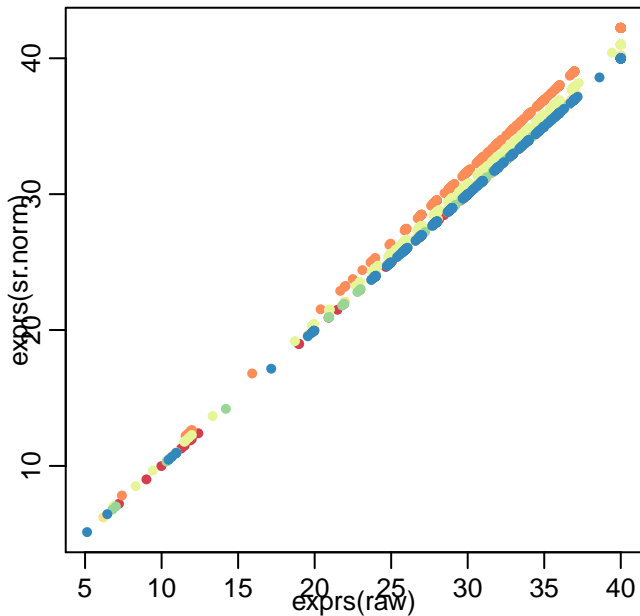




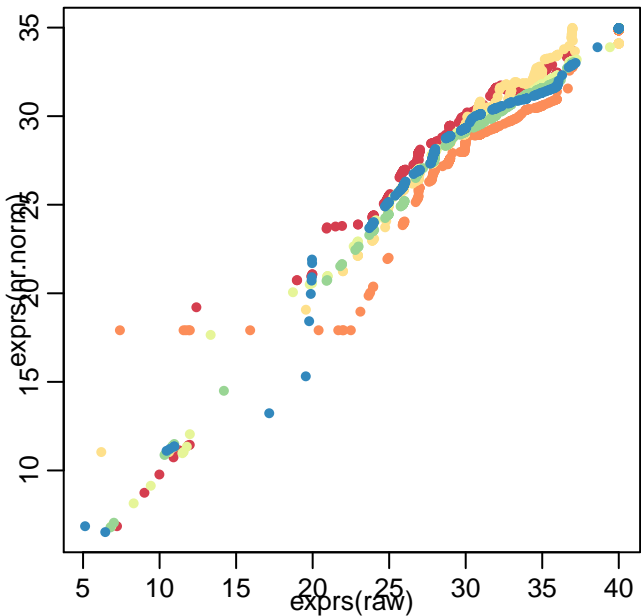
**Quantile normalisation**



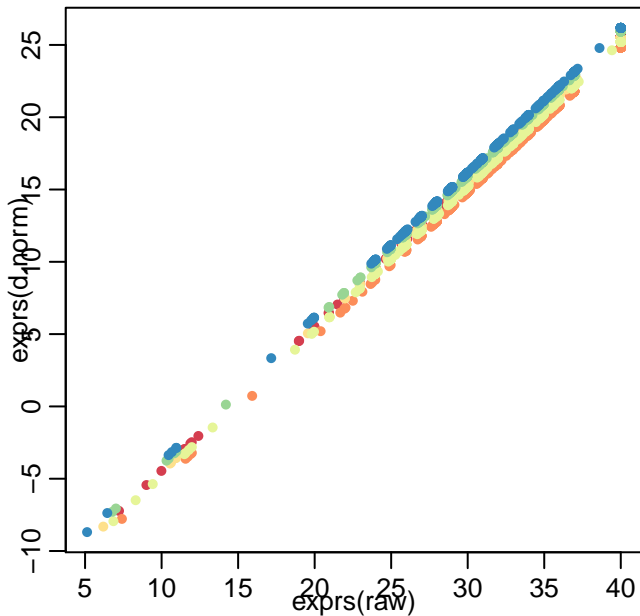
**Rank invariant scaling**

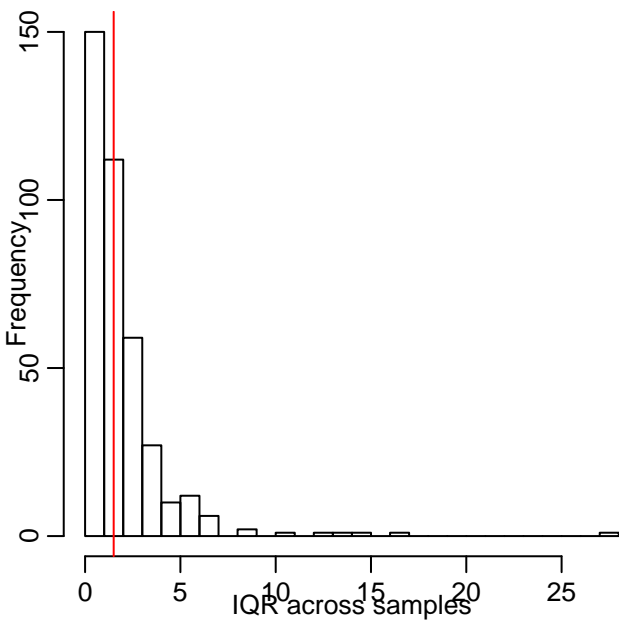


**Rank invariant normalisation**

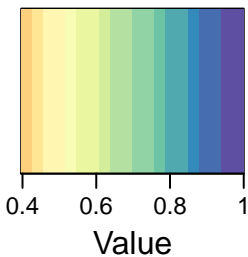


**deltaCt normalisation**

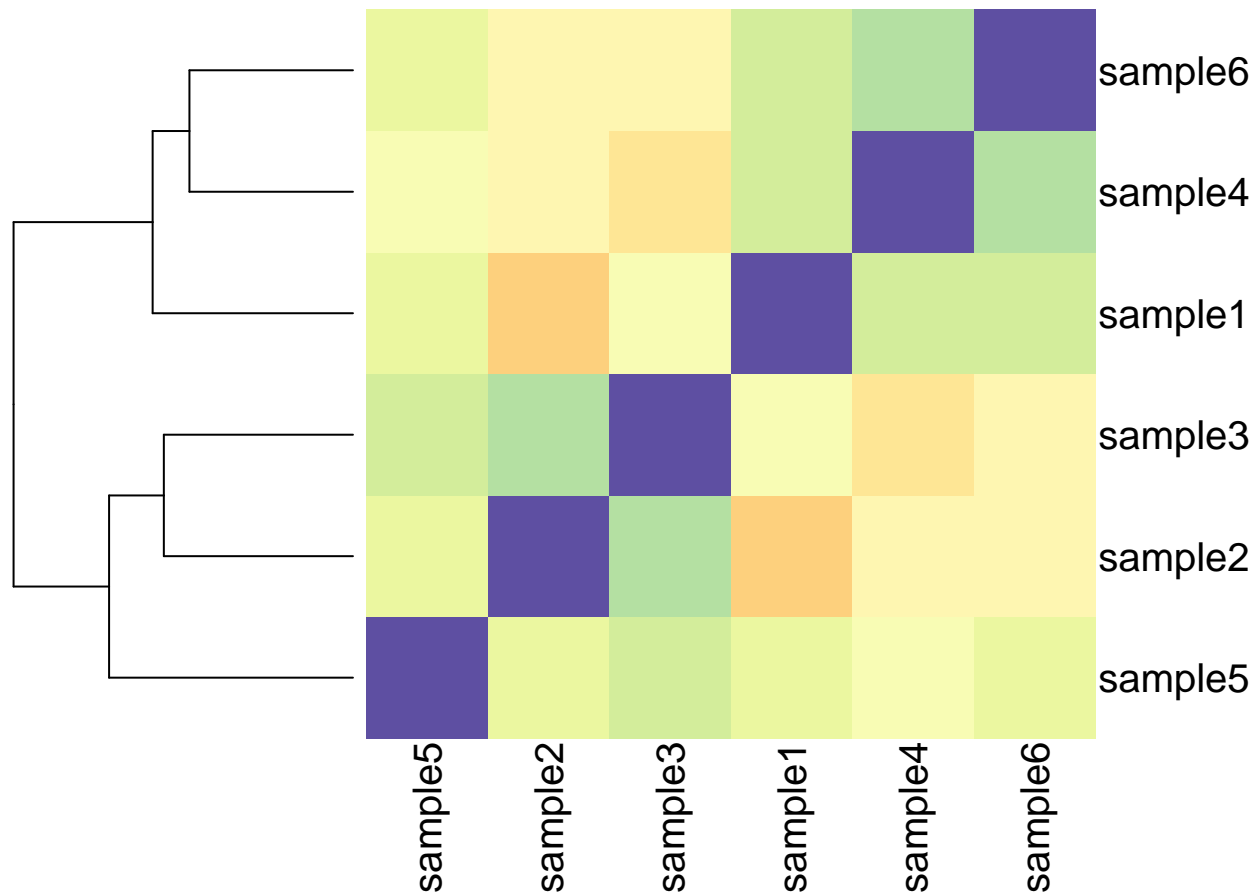




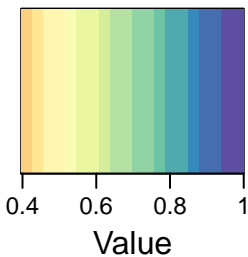
Color Key



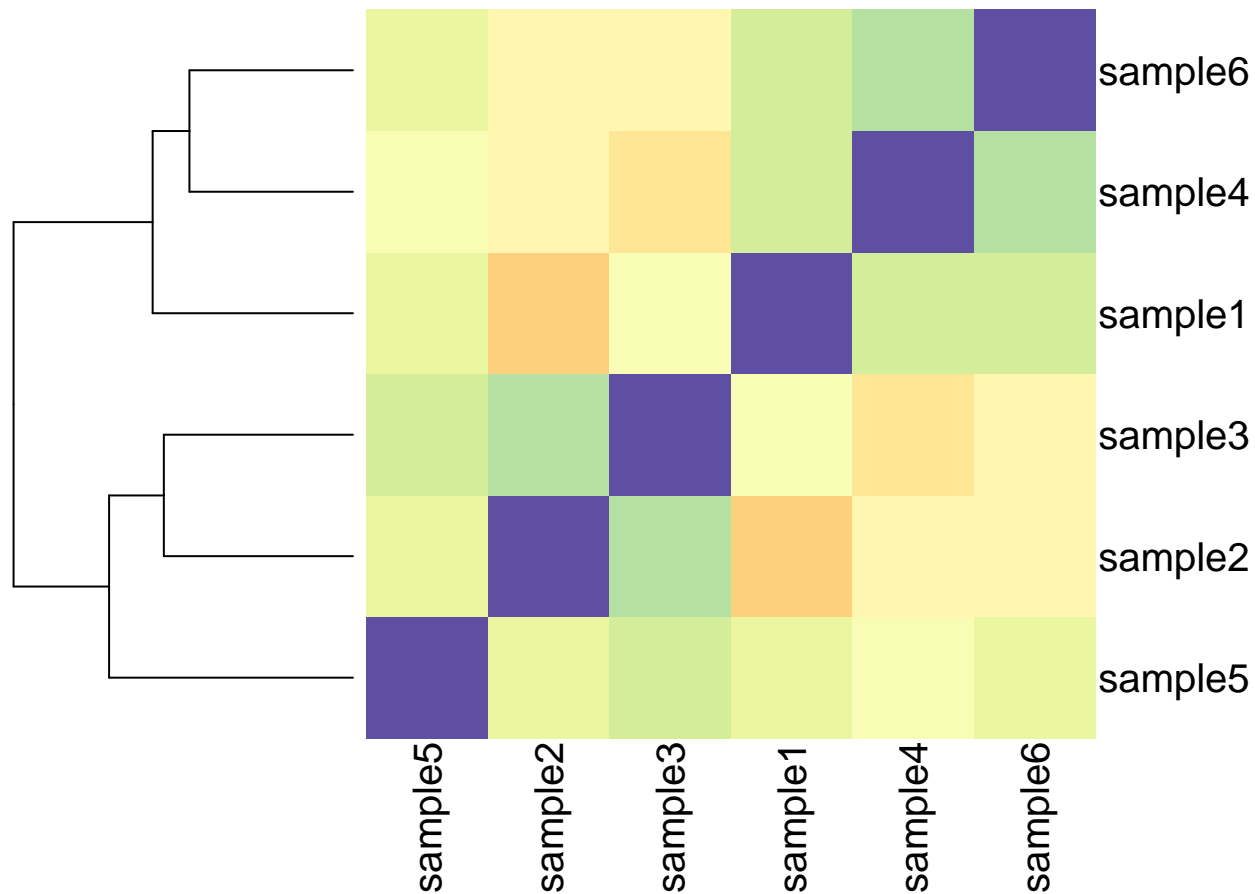
Ct correlation

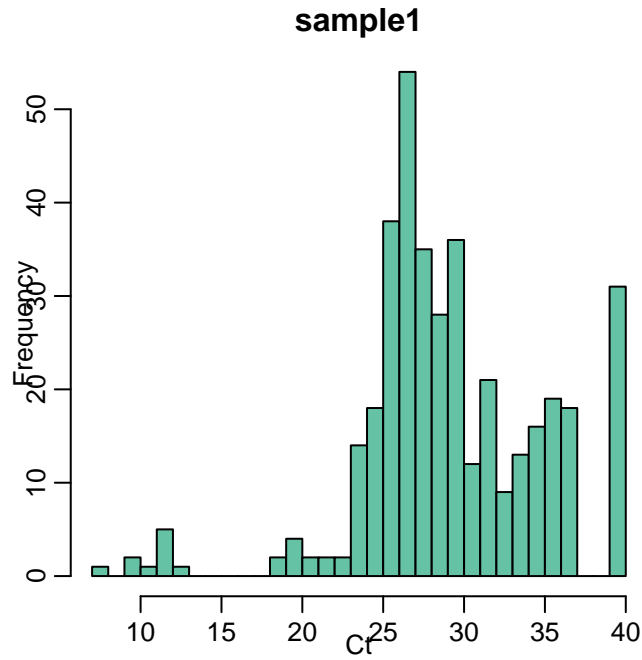
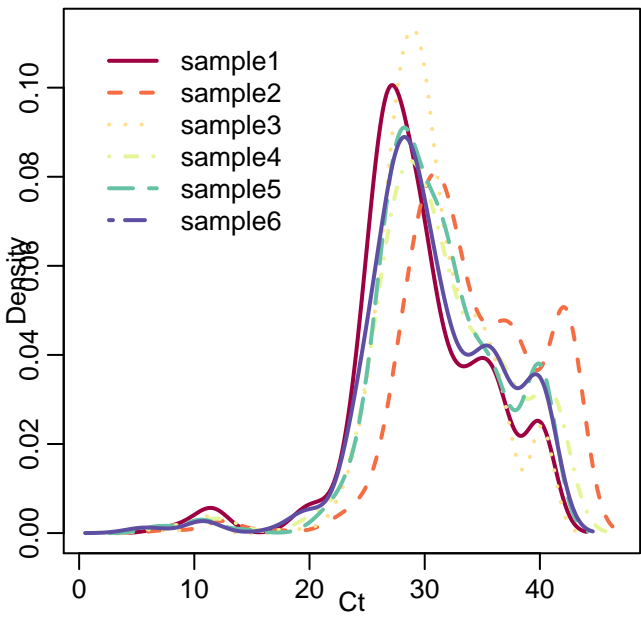


Color Key

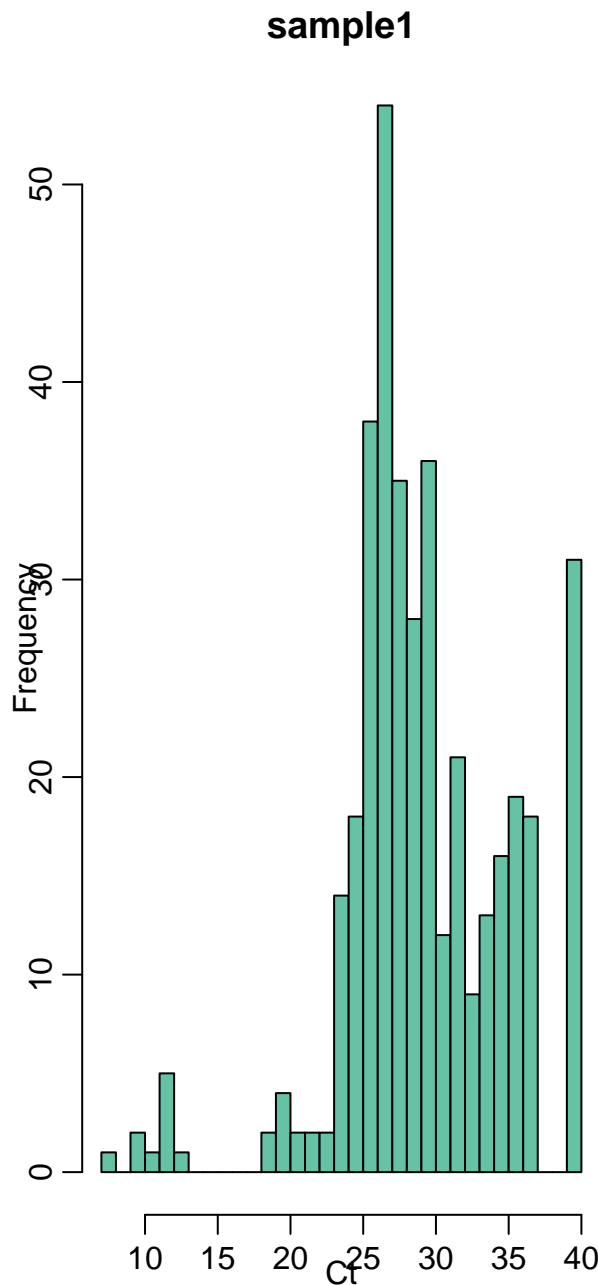
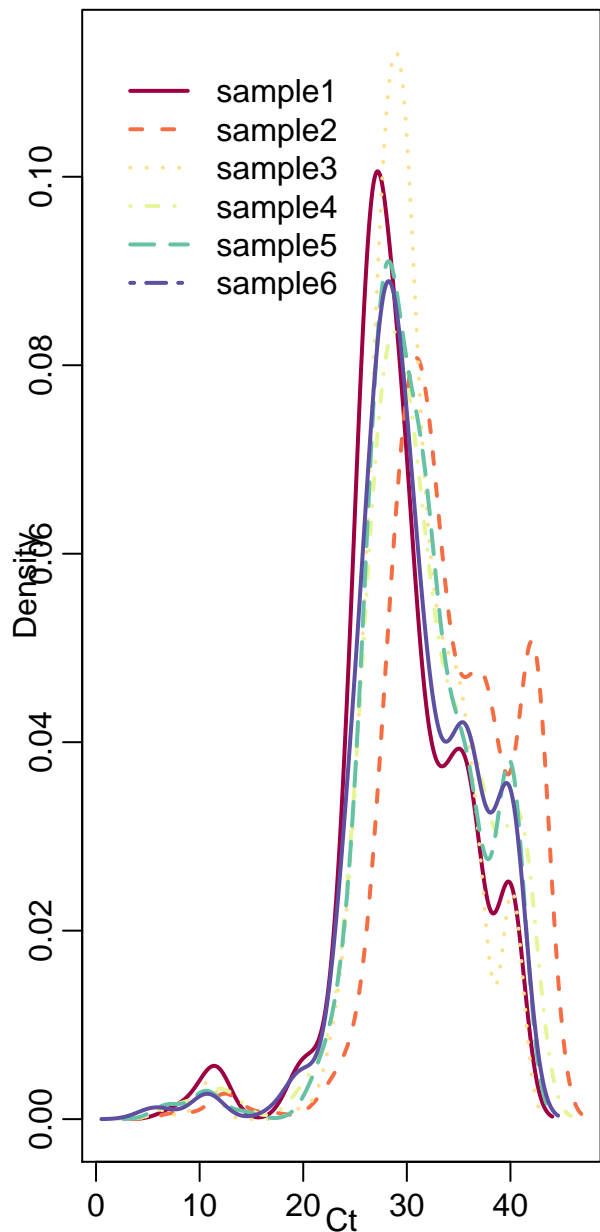


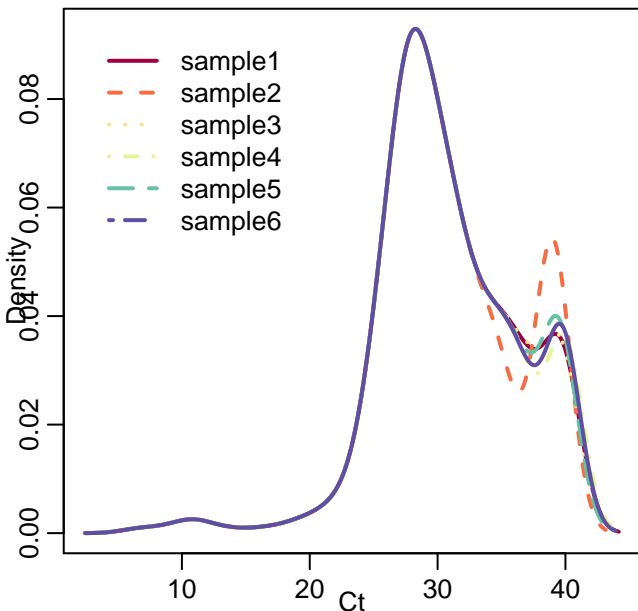
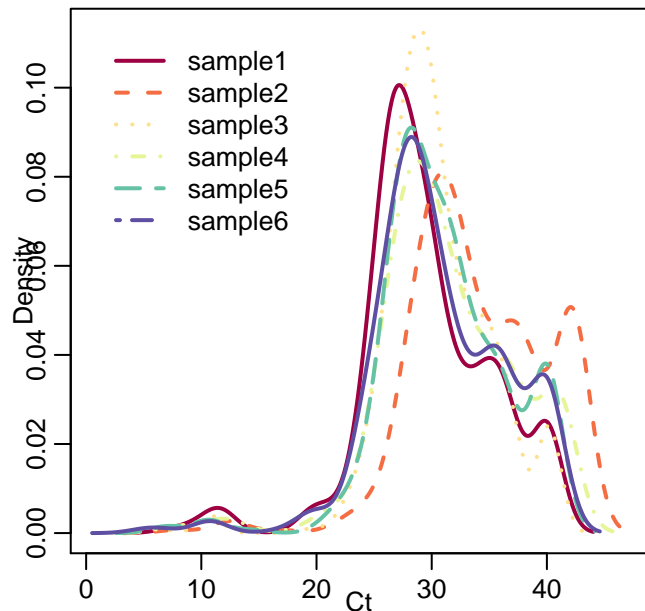
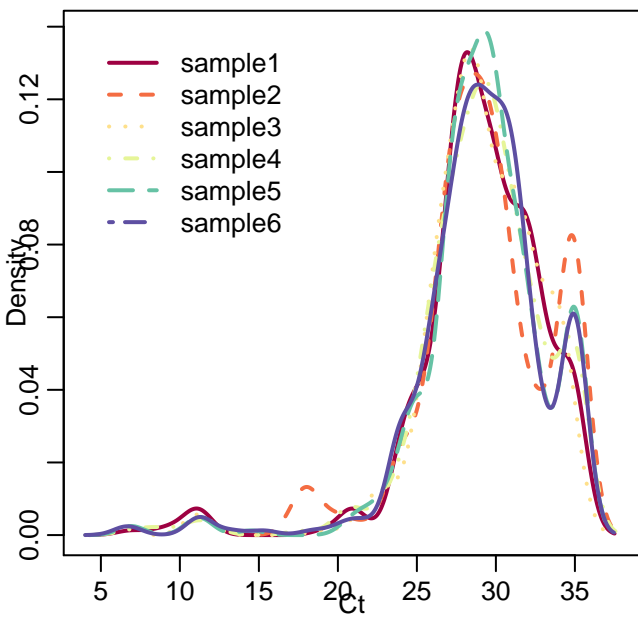
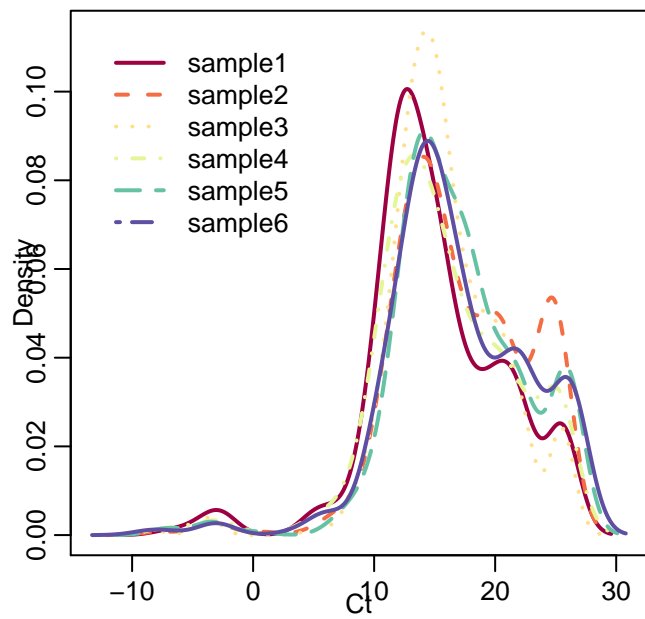
Ct correlation

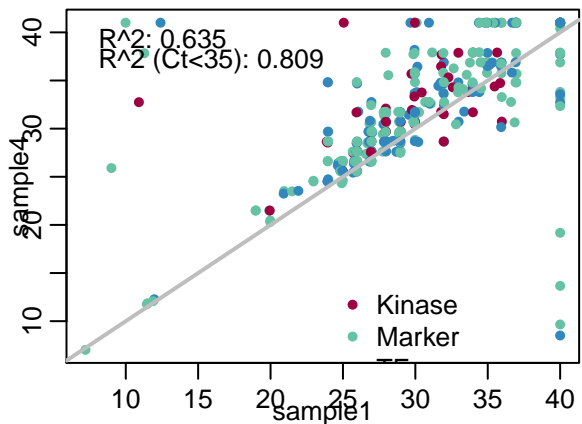
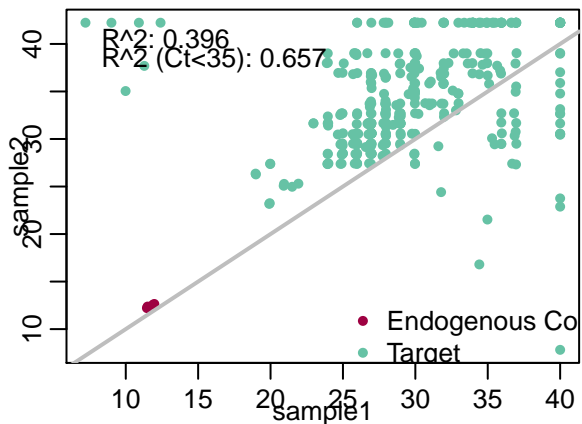
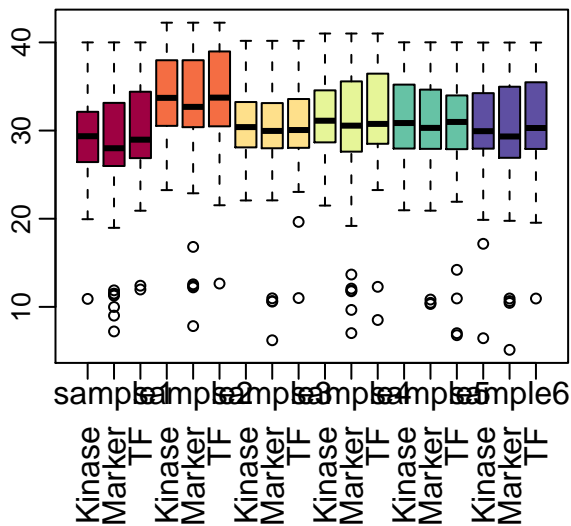
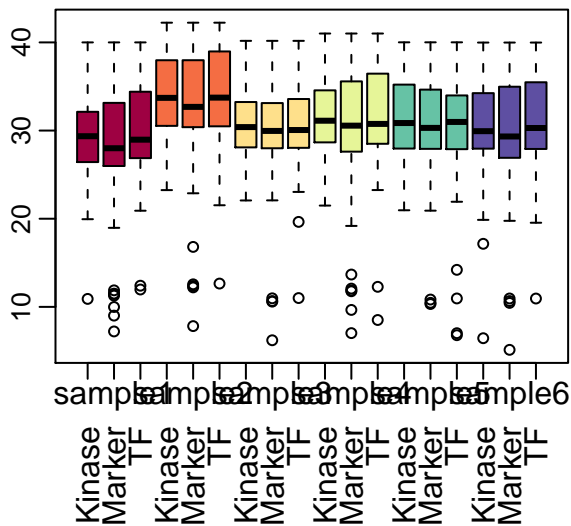


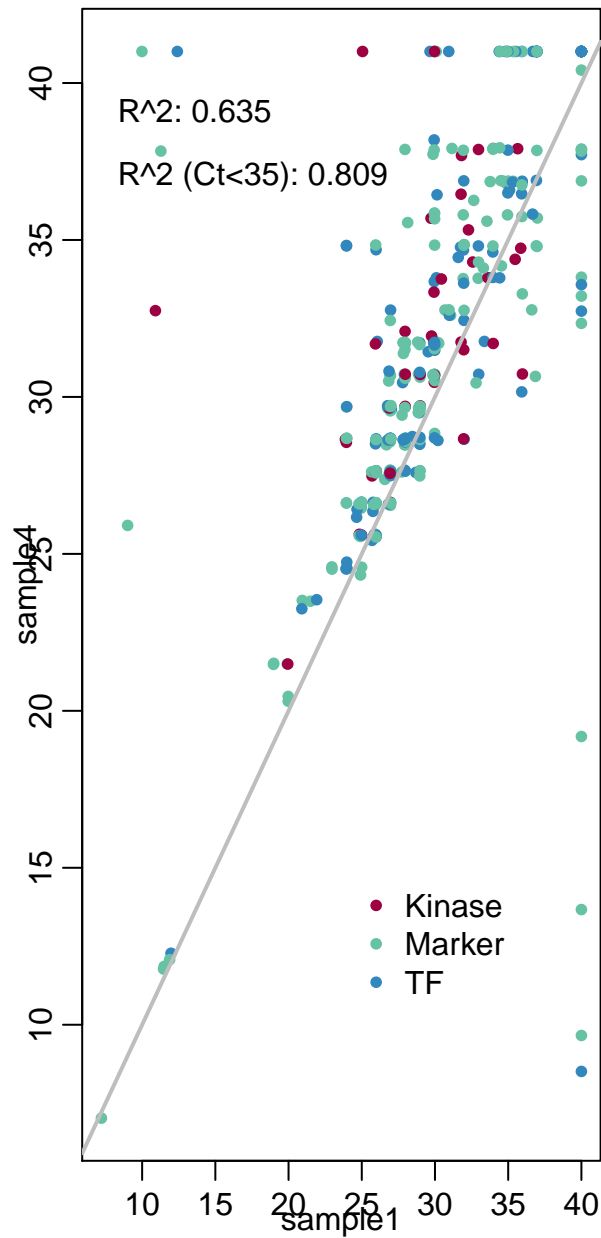
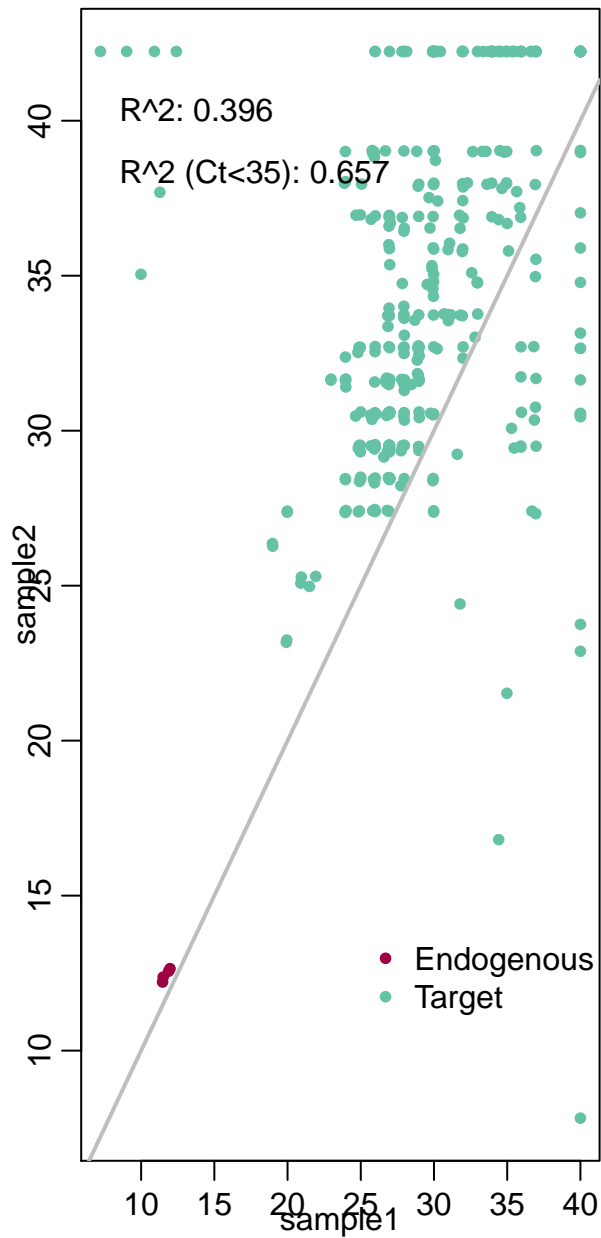


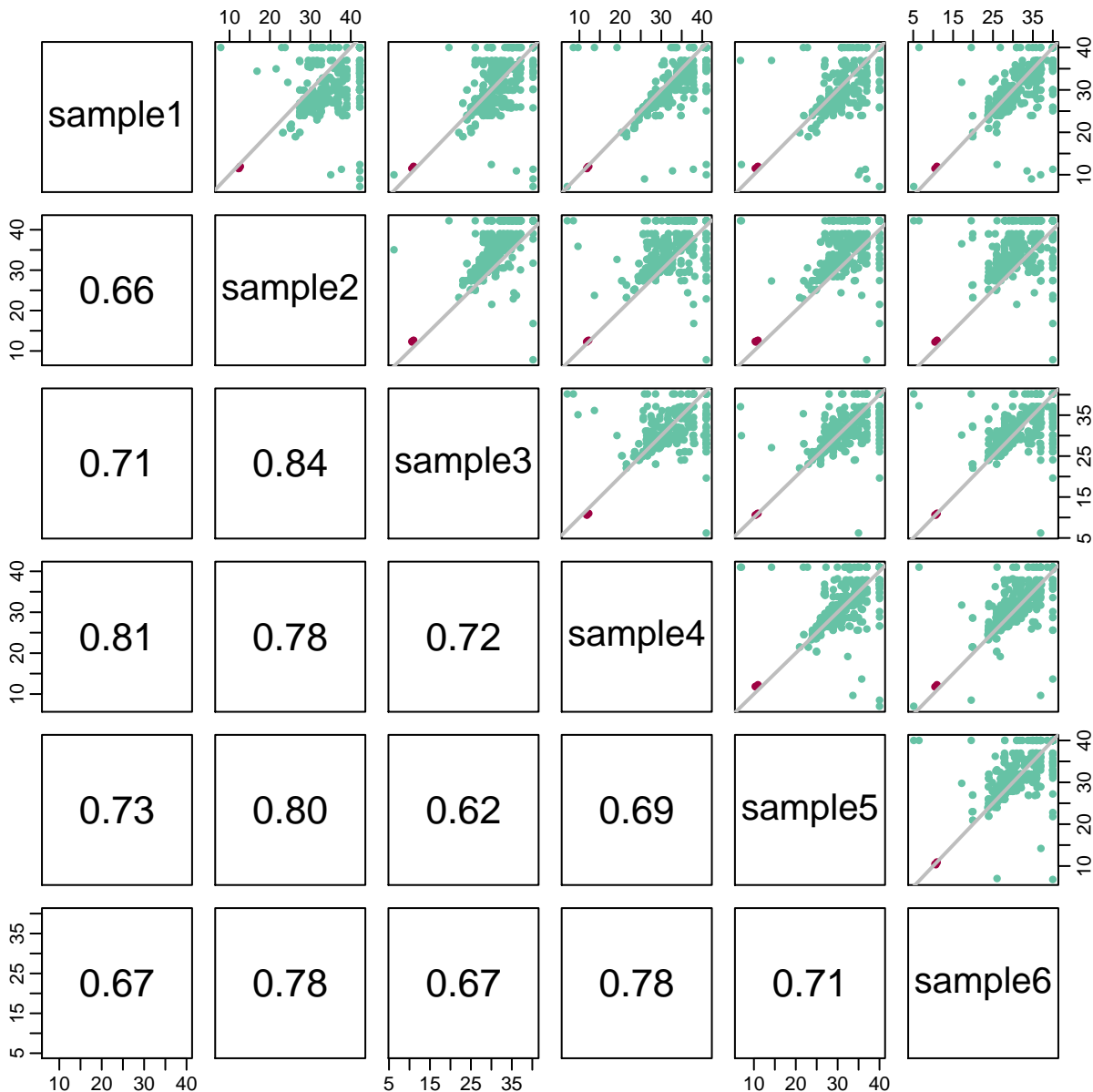


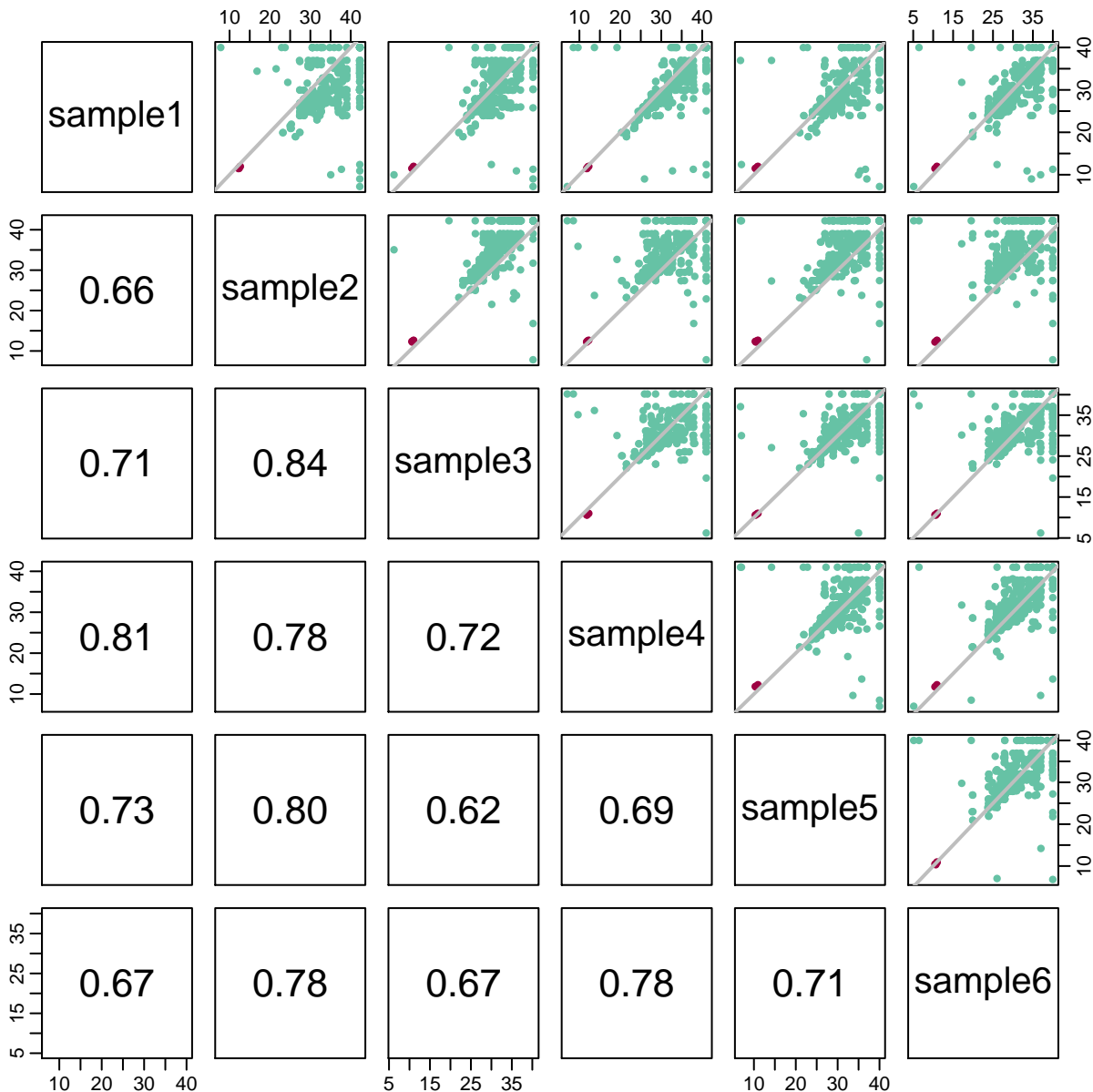


**quantile****scale.rankinvariant****norm.rankinvariant****deltaCt**

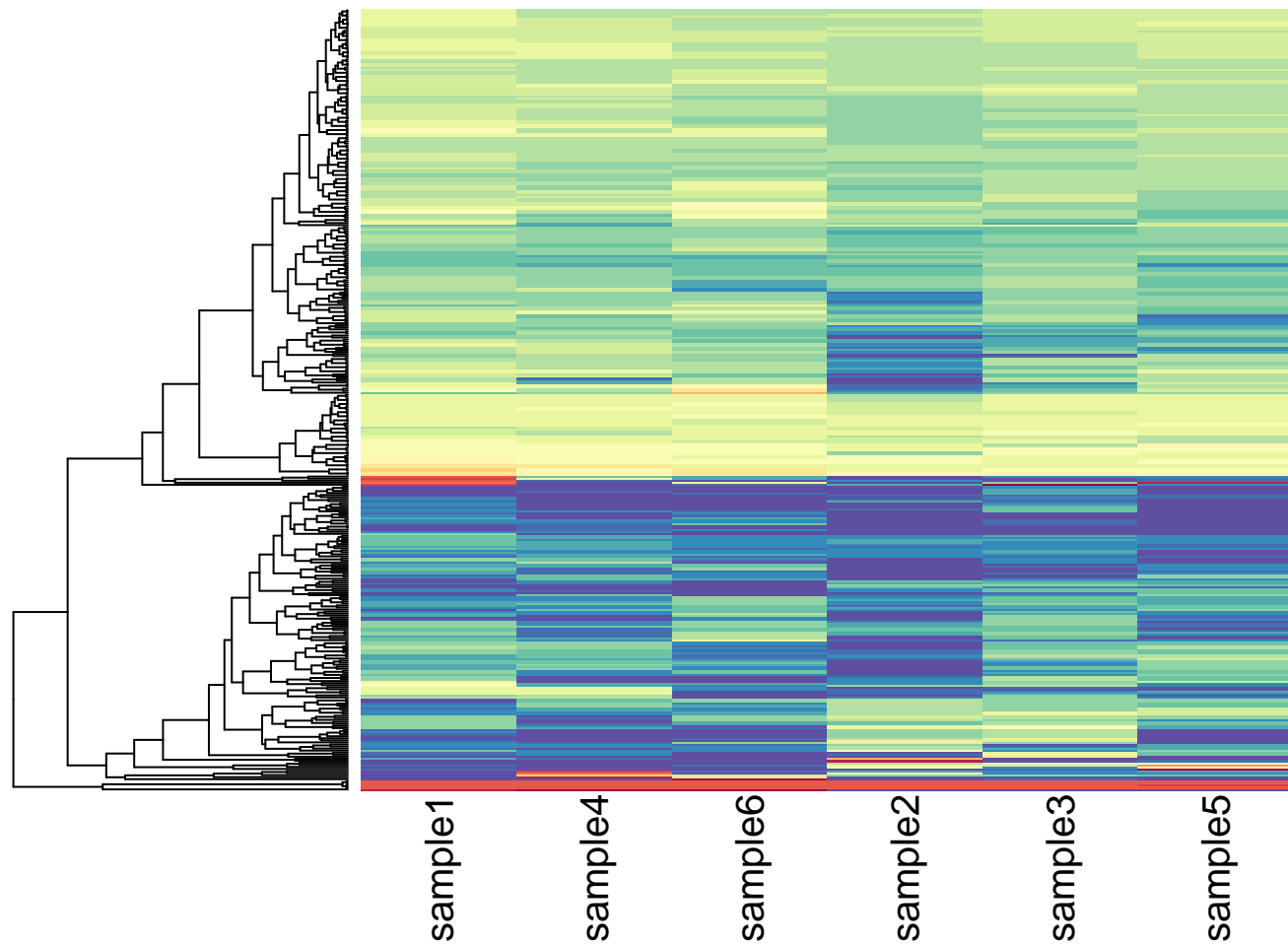
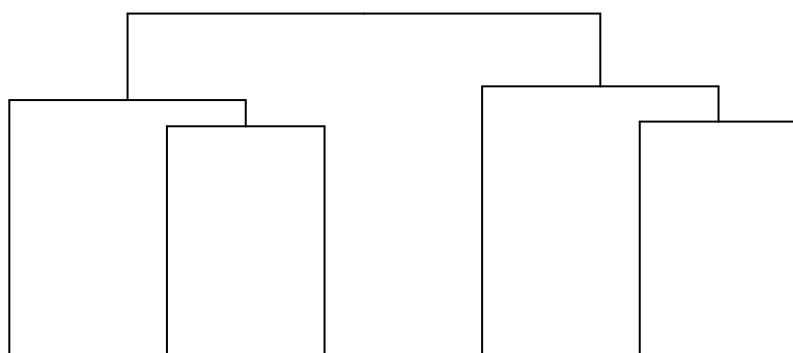
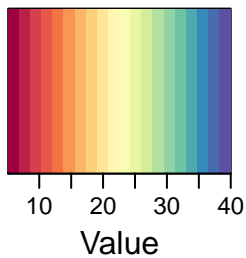




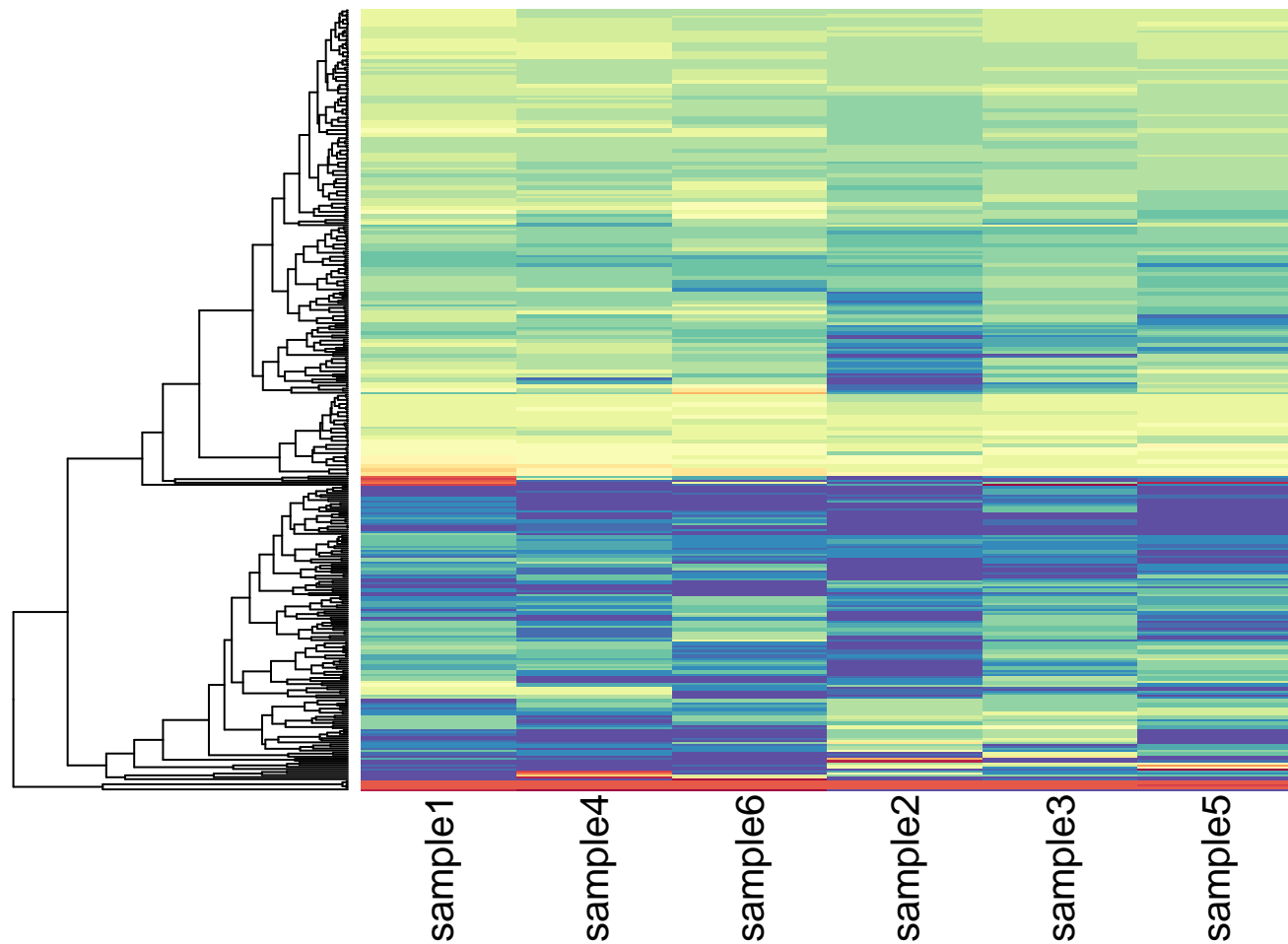
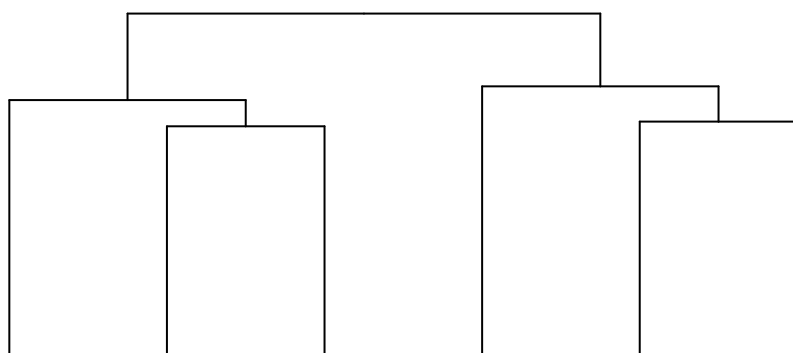
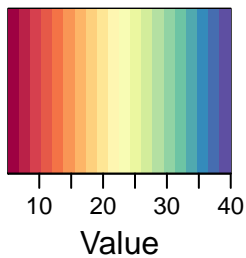




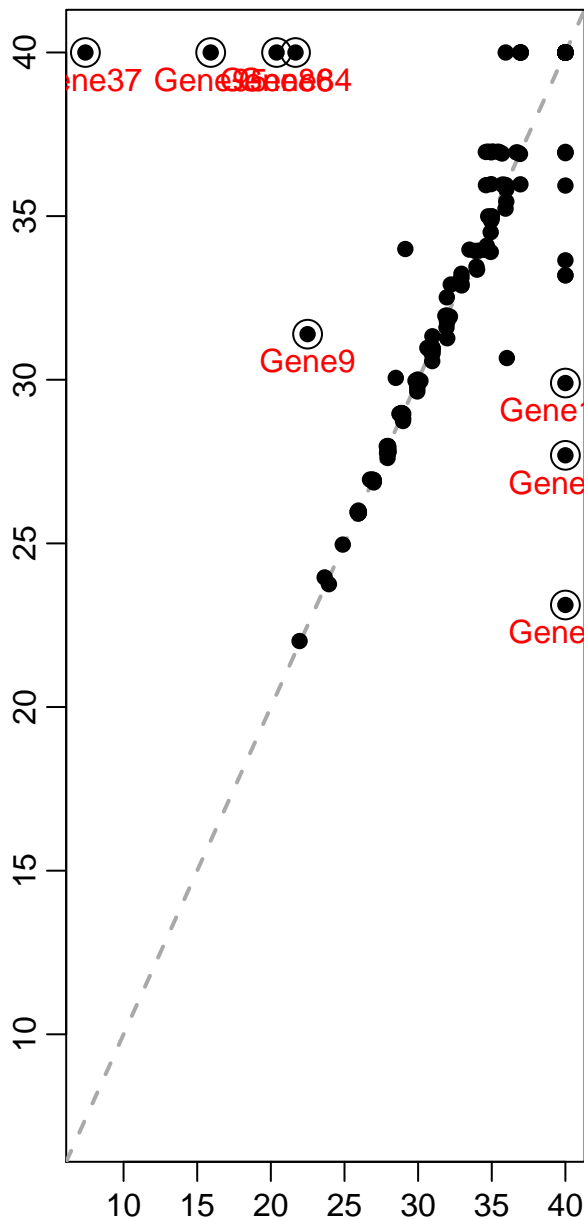
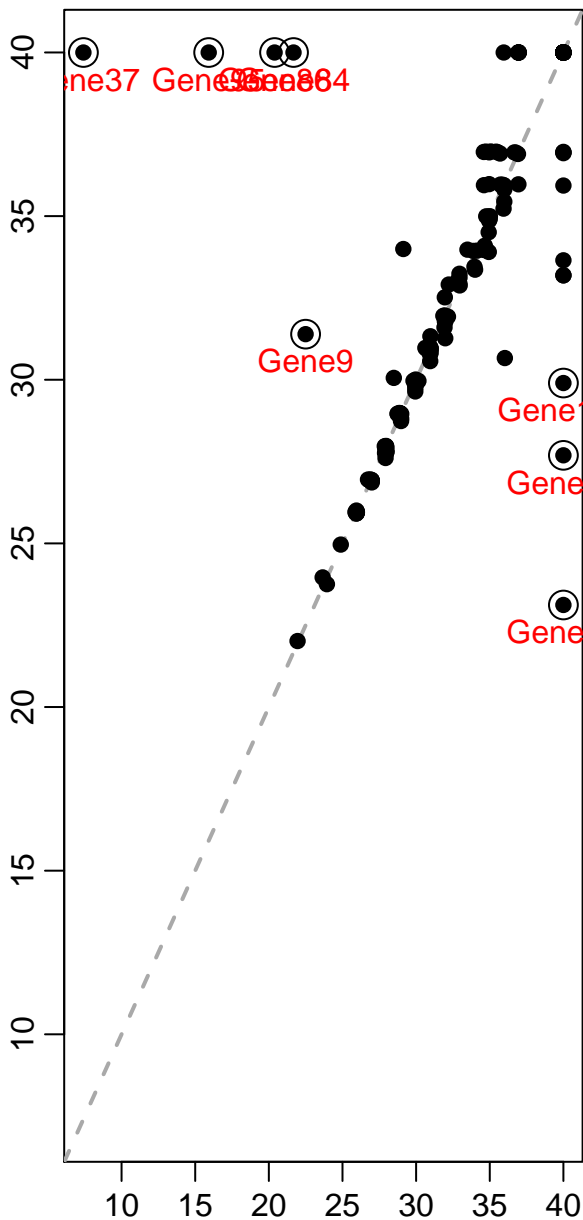
Color Key

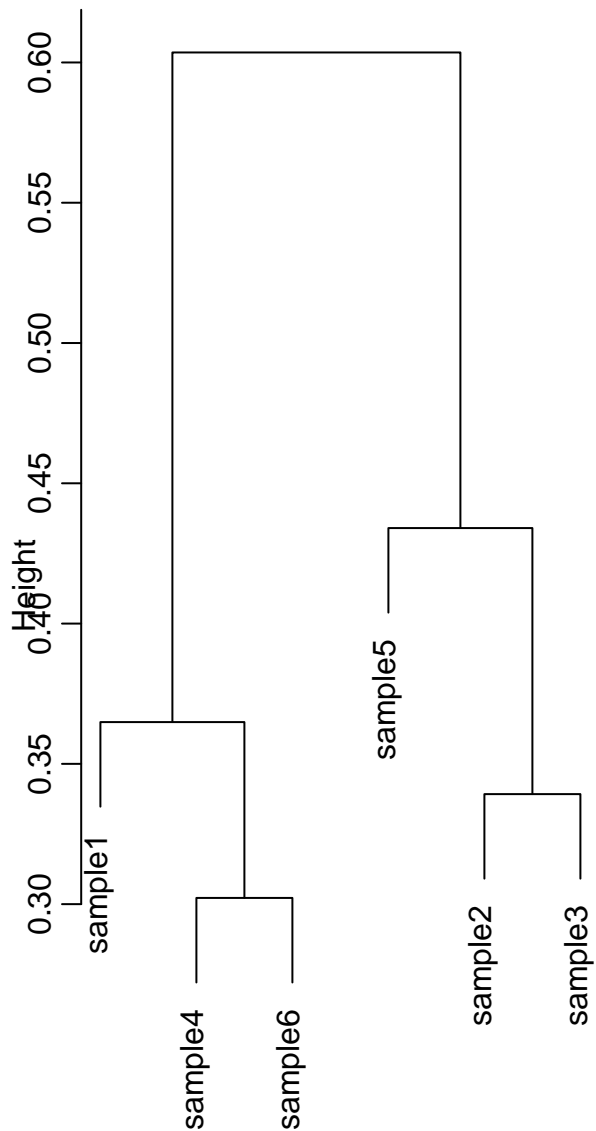


Color Key

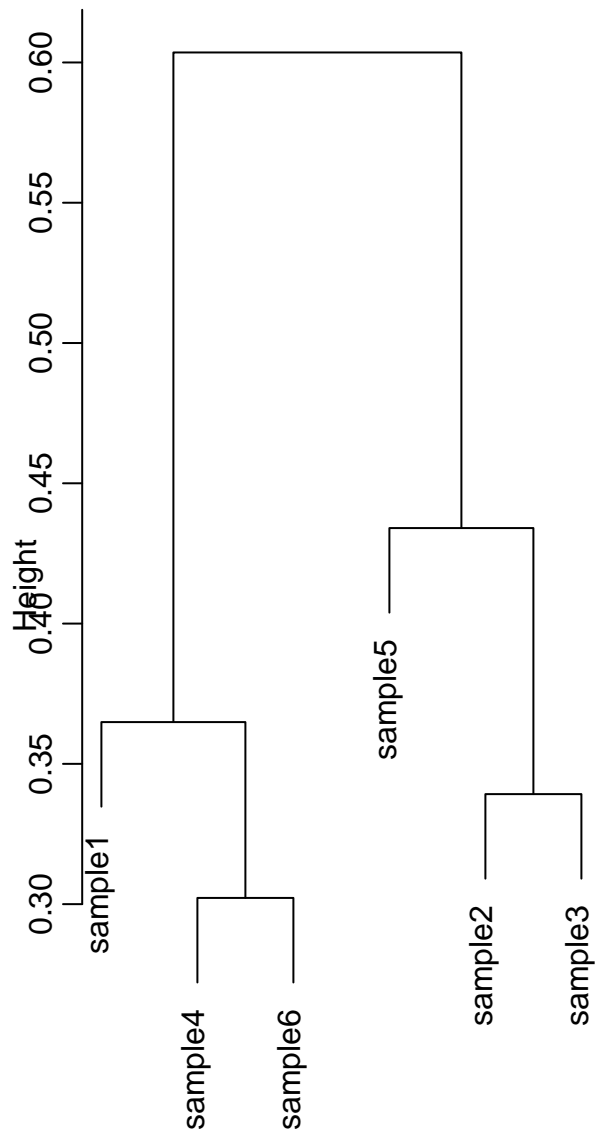




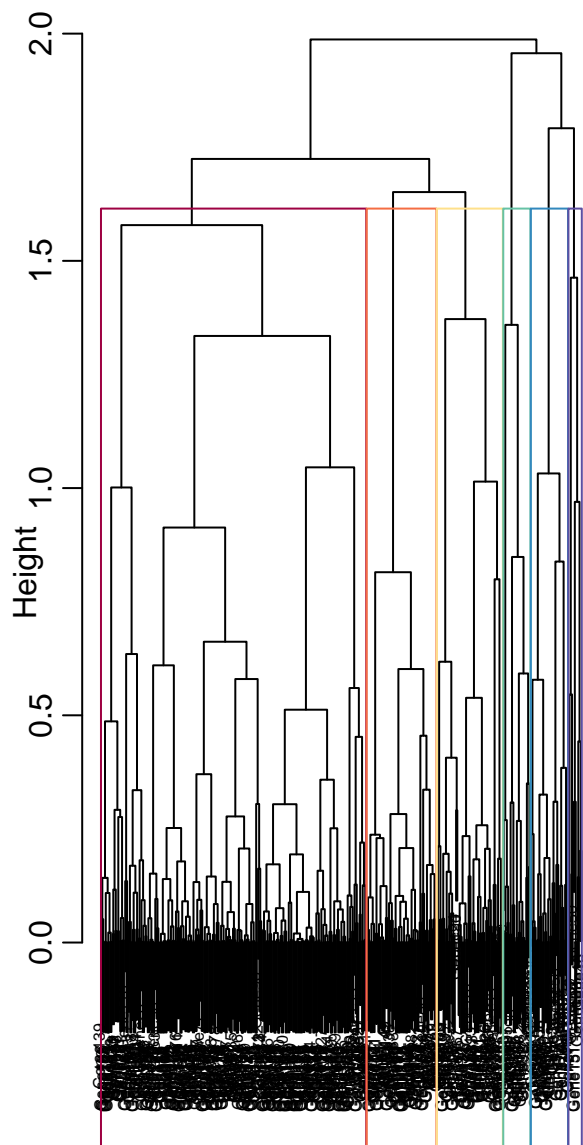




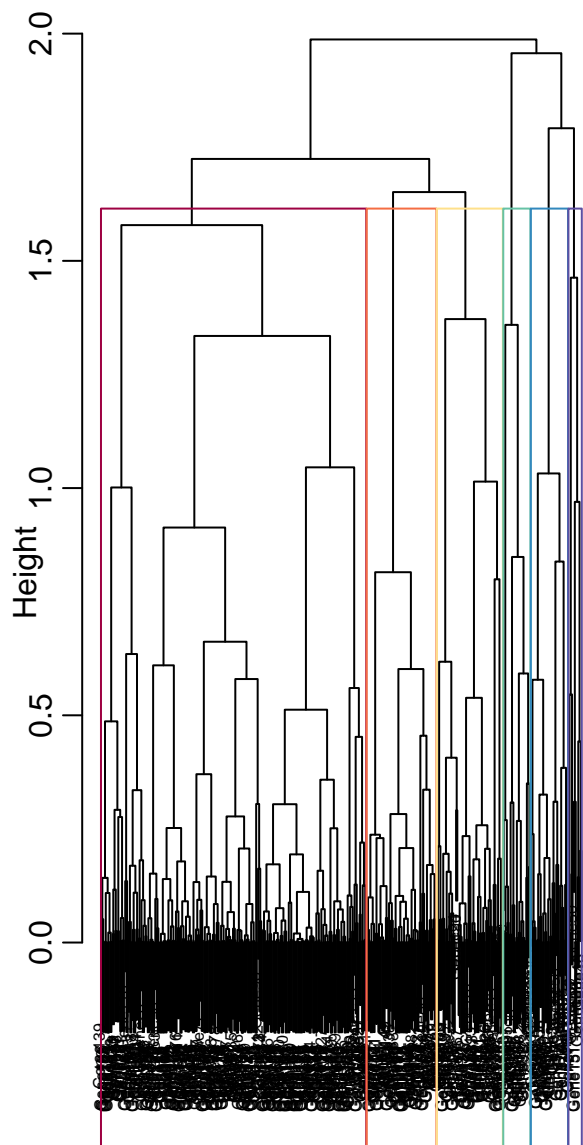
Cluster dendrogram



Cluster dendrogram



Cluster dendrogram

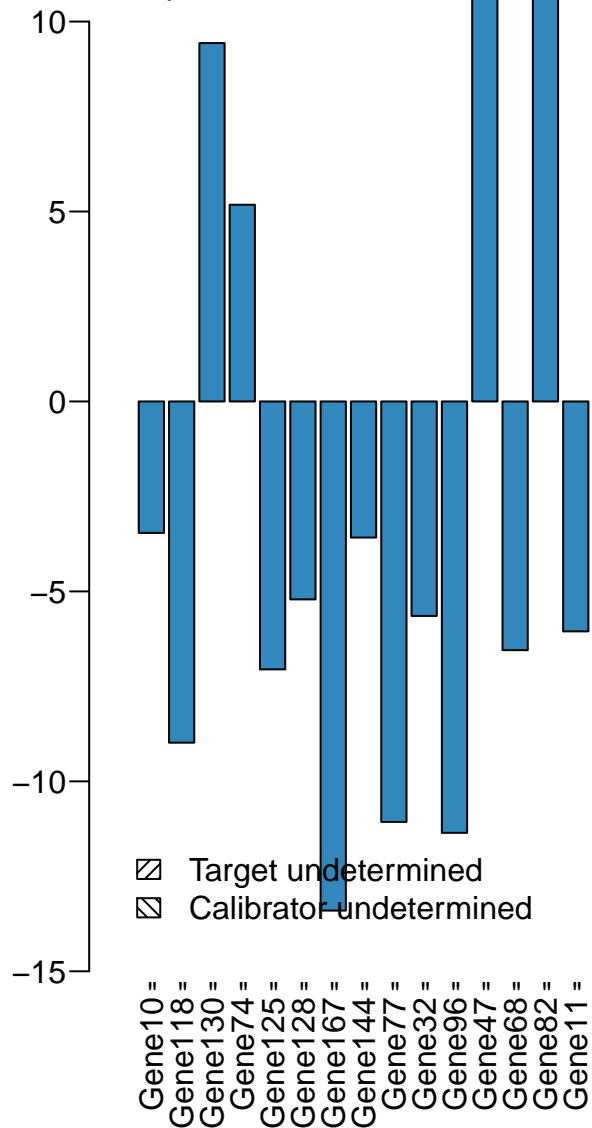


Cluster dendrogram

# Relative quantification

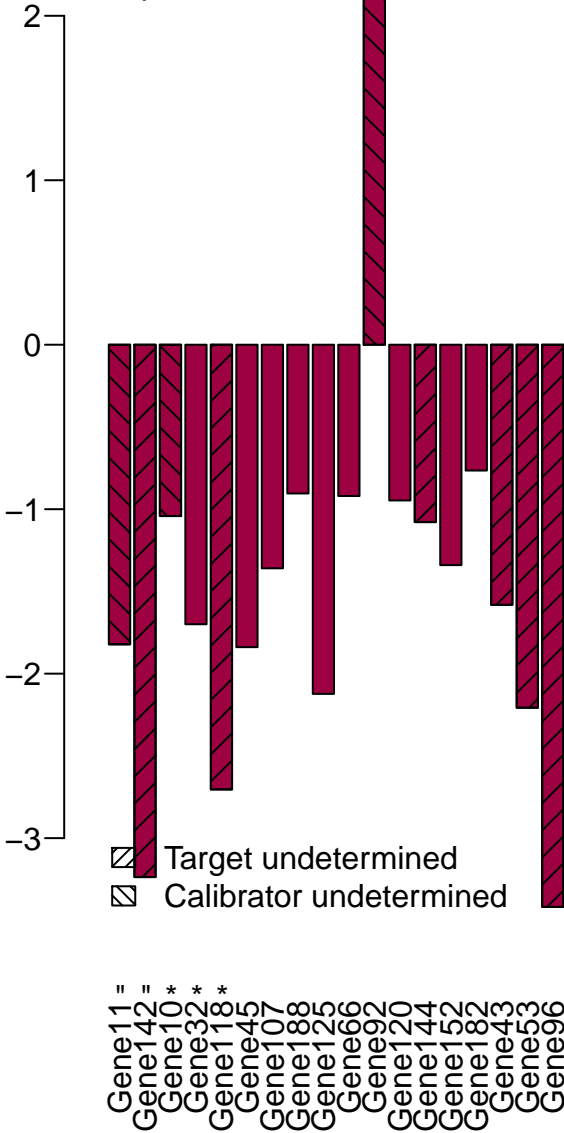
\* p-value < 0.05

" p-value < 0.01



Comparison: LS-C

\* p-value < 0.05  
" p-value < 0.01



# Relative quantification

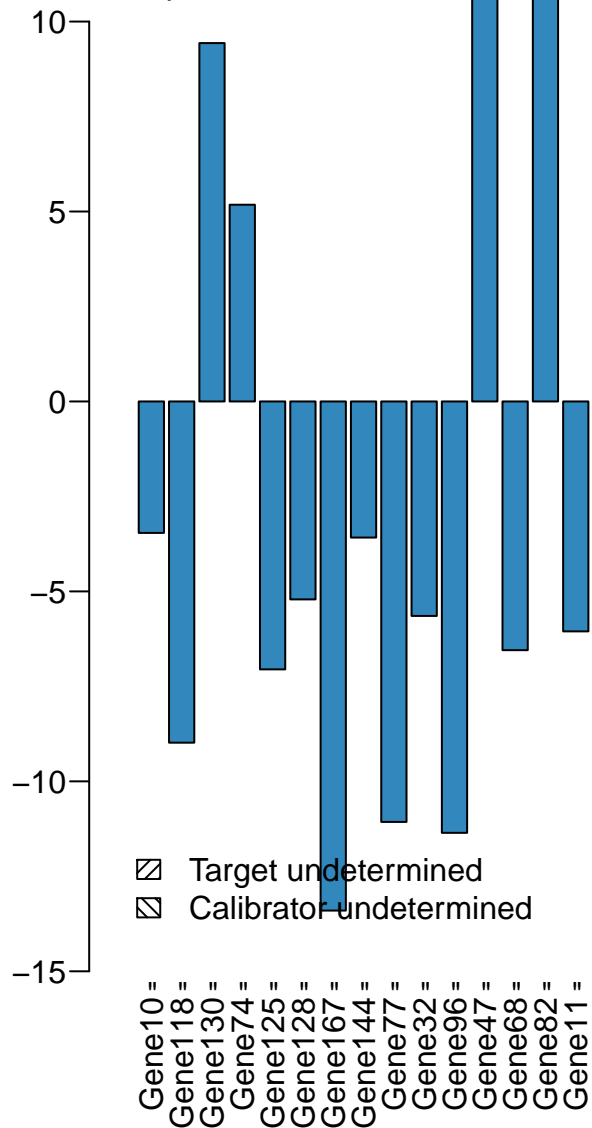
\* p-value < 0.05

" p-value < 0.01

Target undetermined

Calibrator undetermined

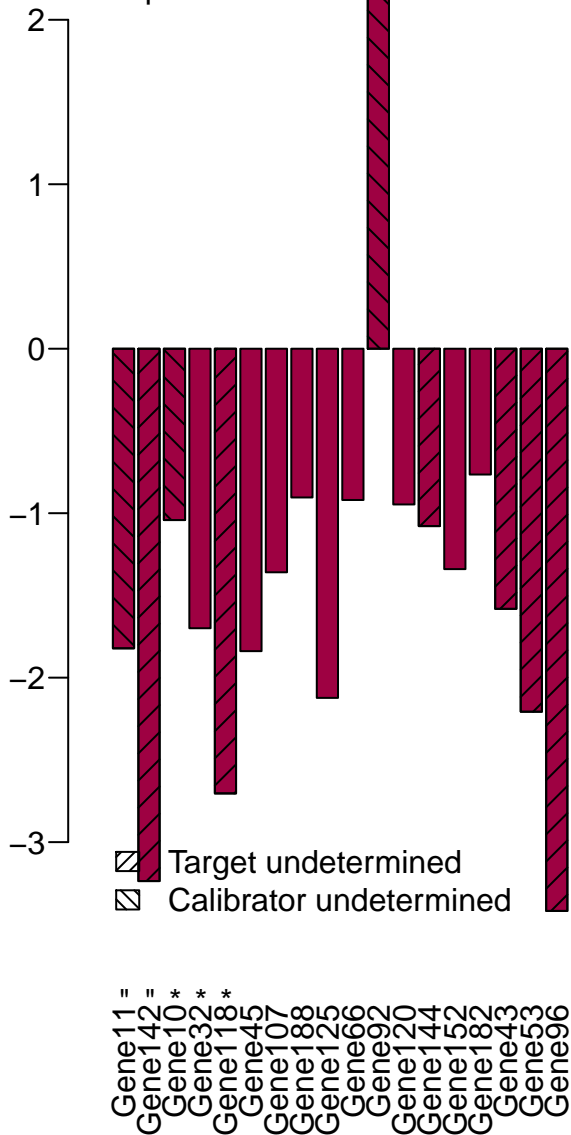
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Gene118 =  
Gene130 =  
Gene74 =  
Gene125 =  
Gene128 =  
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Gene77 =  
Gene32 =  
Gene96 =  
Gene47 =  
Gene68 =  
Gene82 =  
Gene11 =



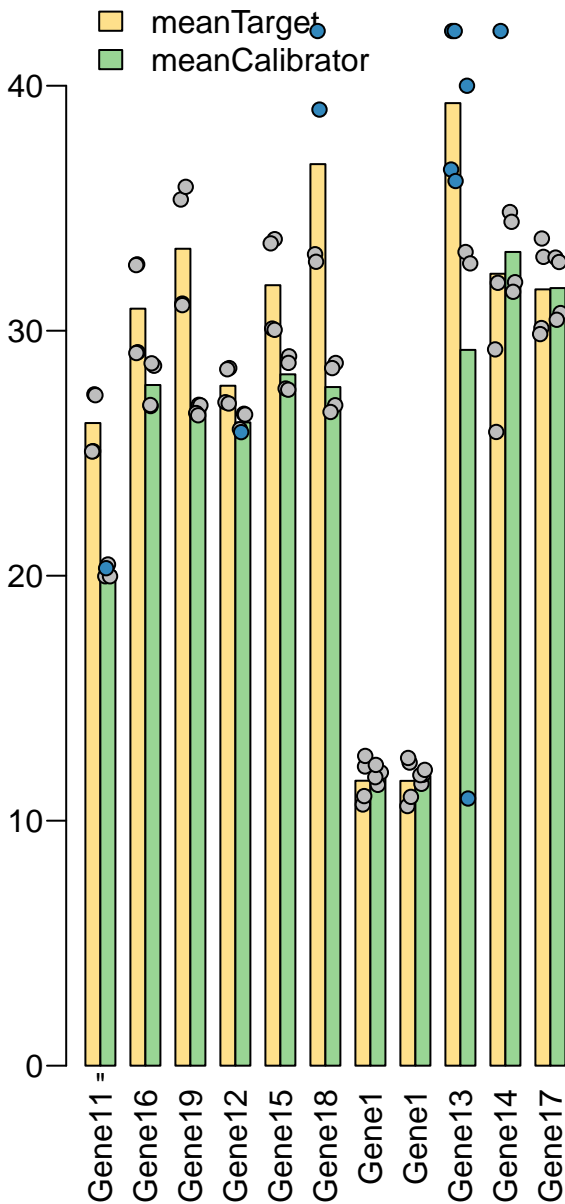
# Comparison: LS-C

\* p-value < 0.05

" p-value < 0.01

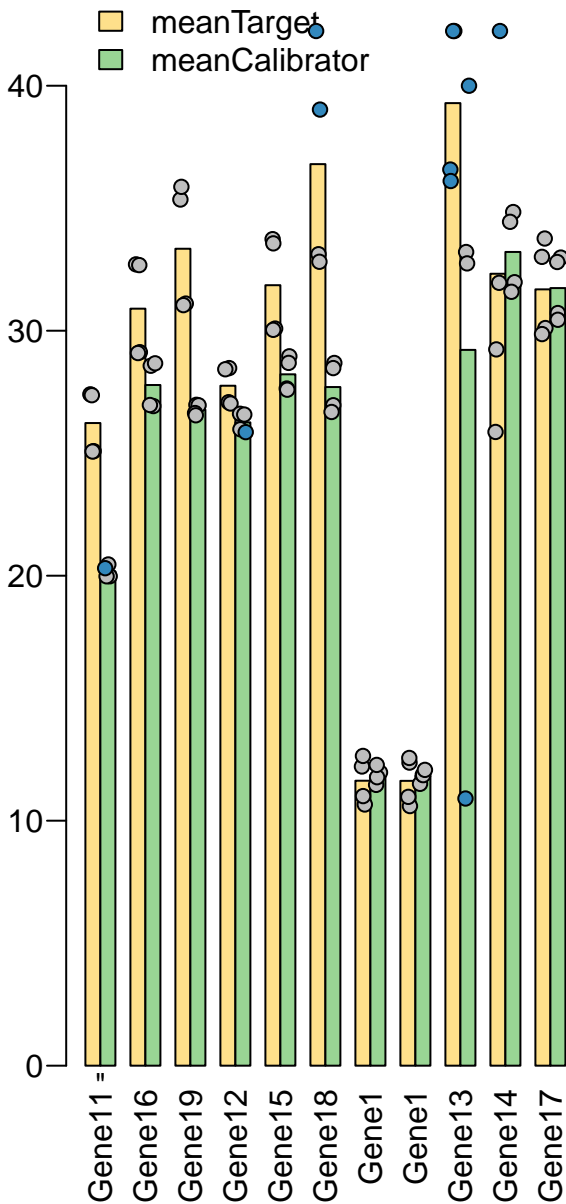


# Comparison: LS-C

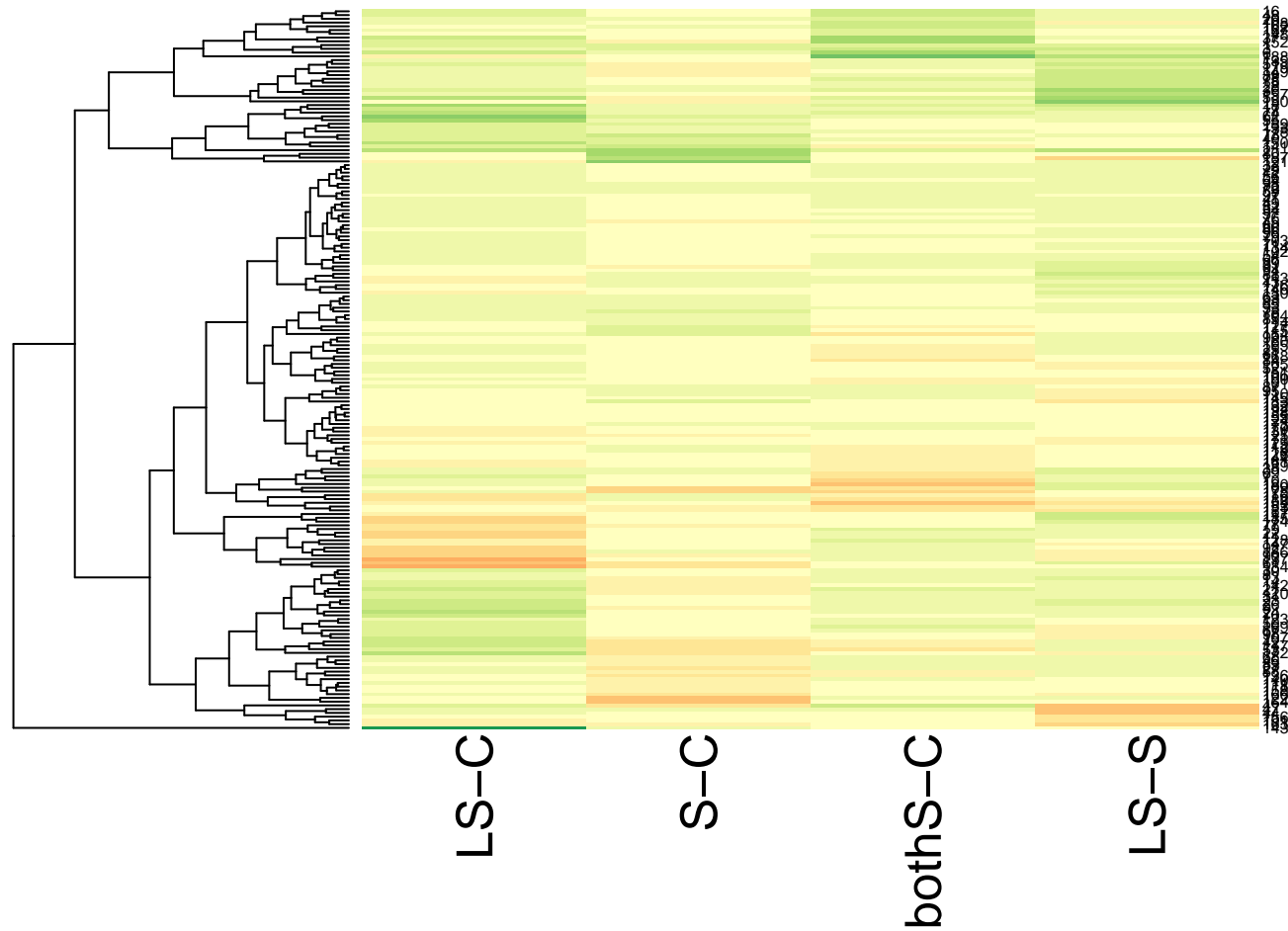
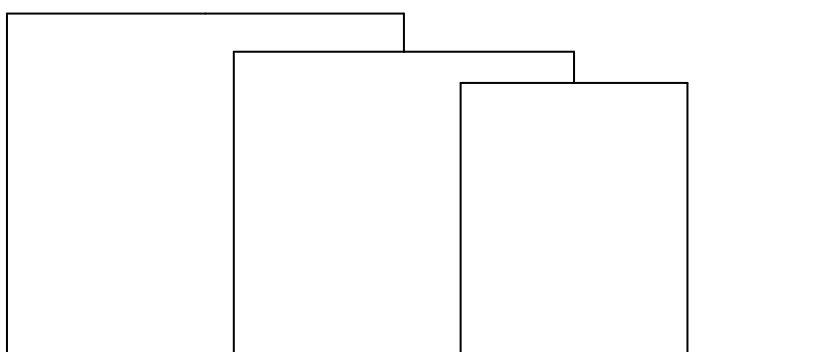
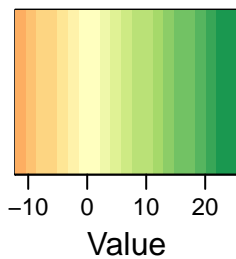




# Comparison: LS-C



Color Key



Color Key

