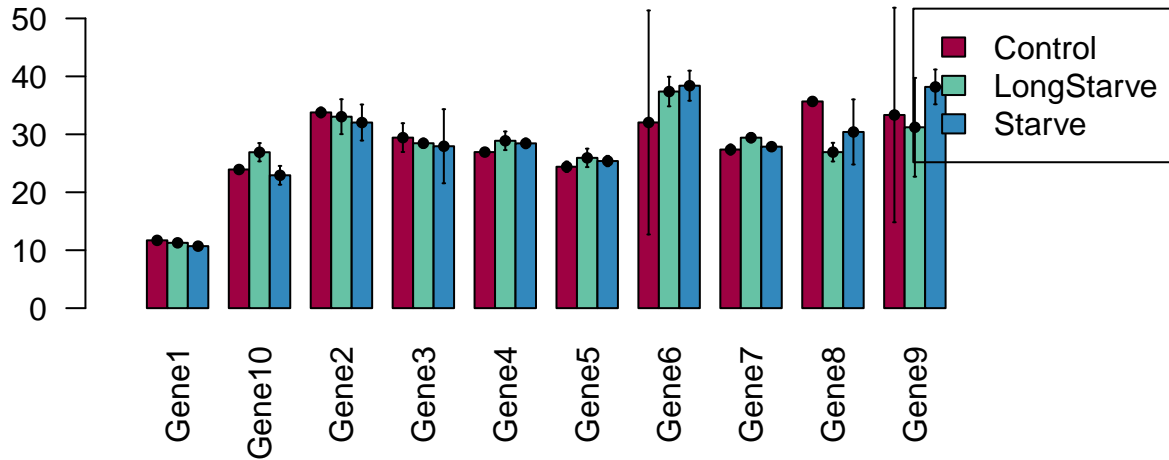
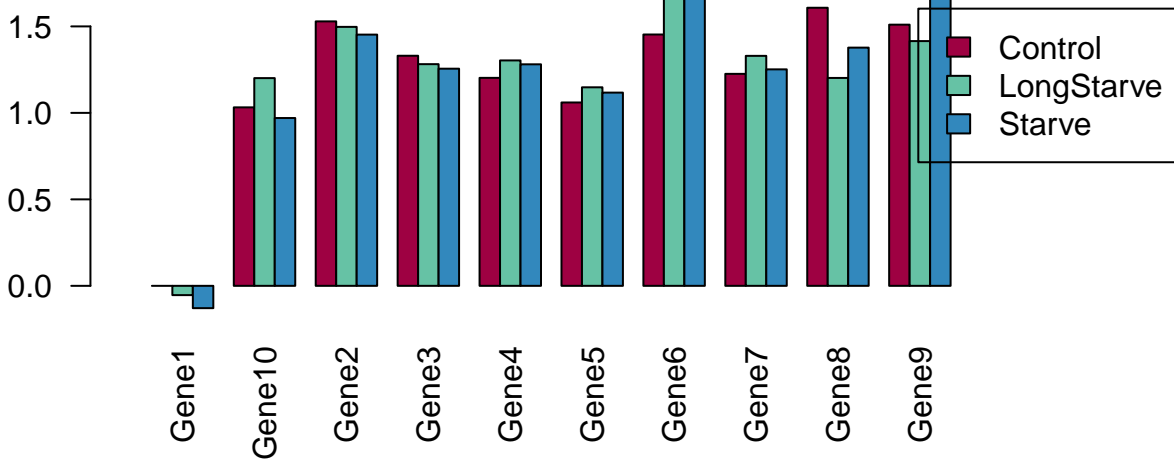


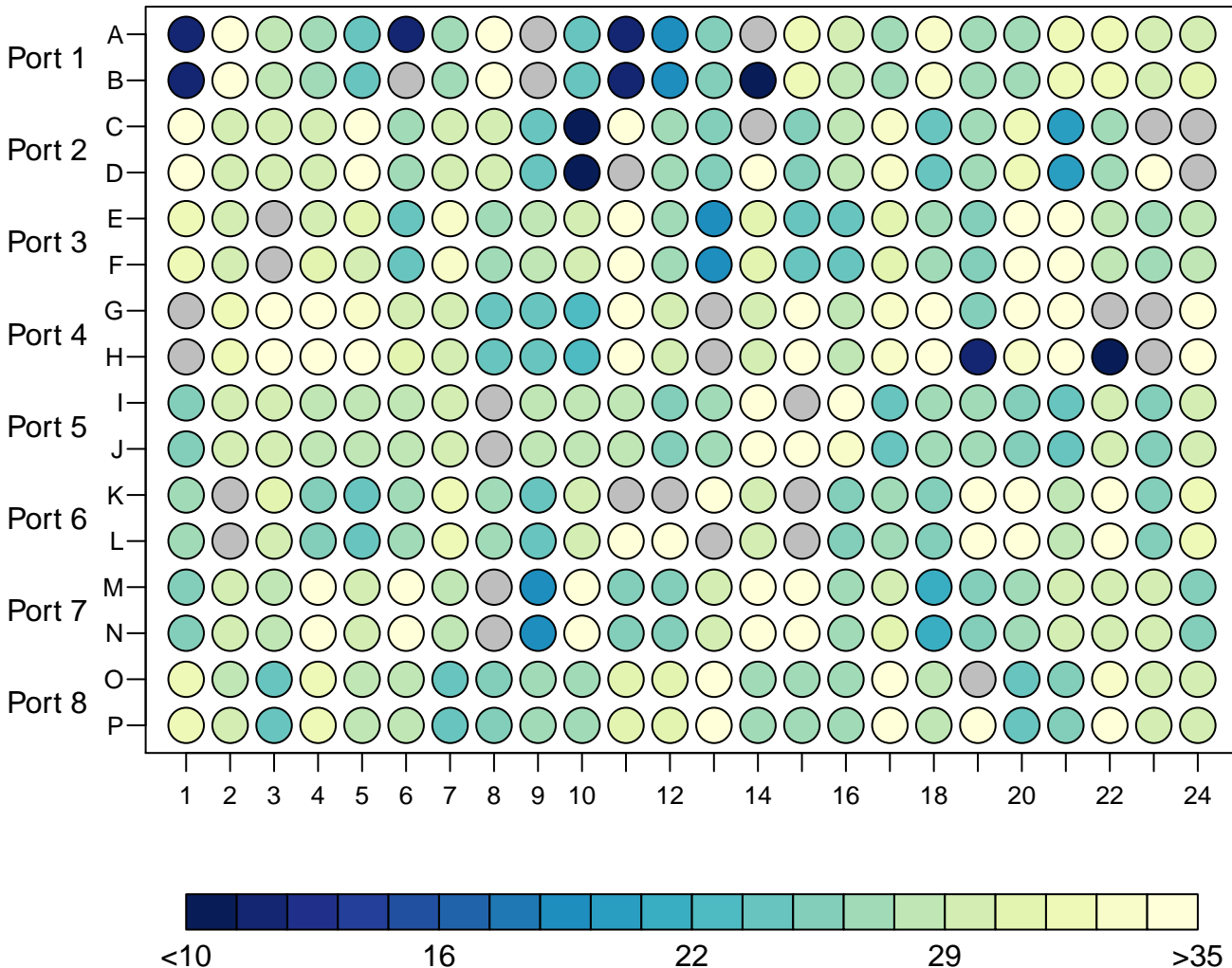
Ct values for samples



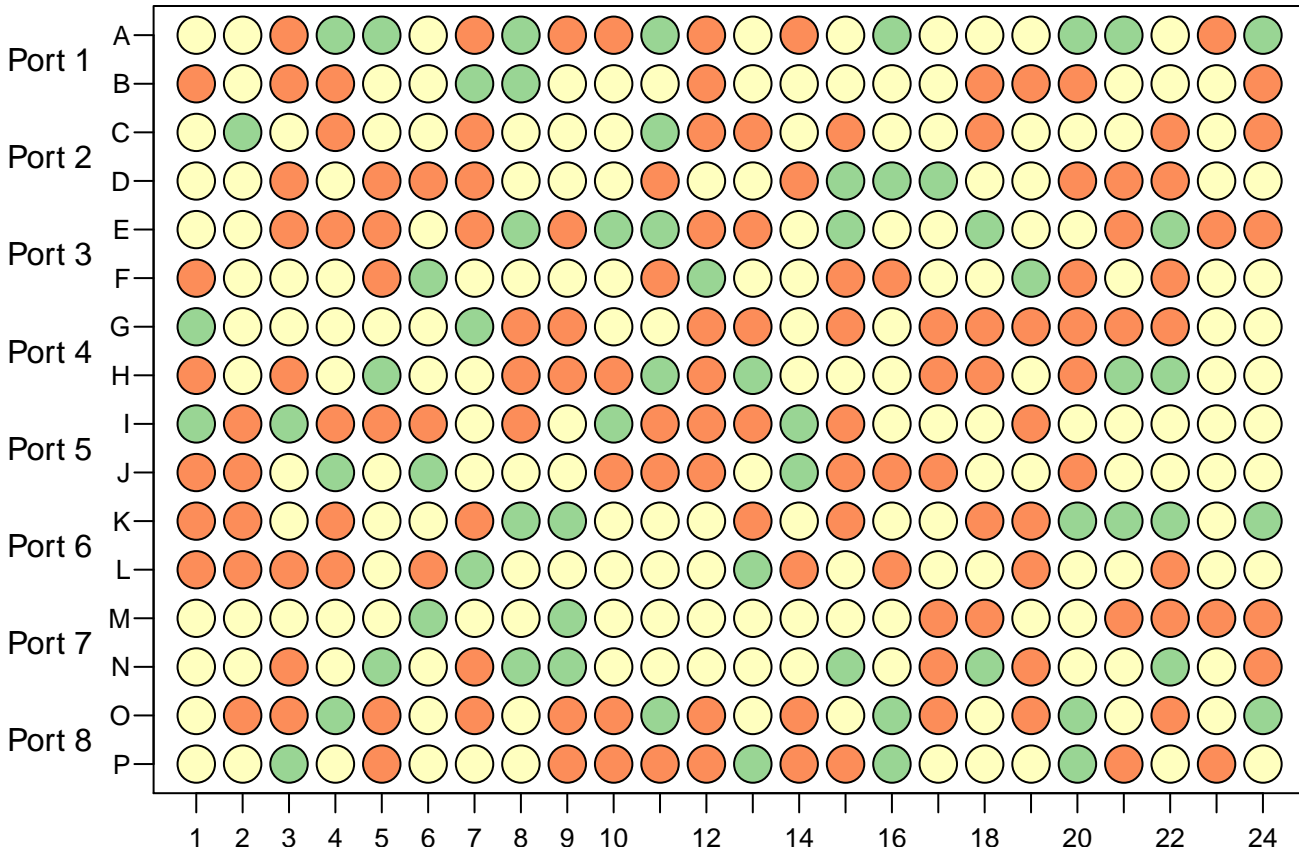
Log2 ratio compared to group Control



sample1

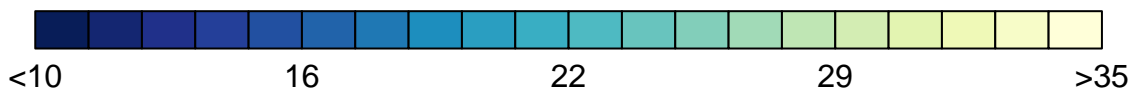
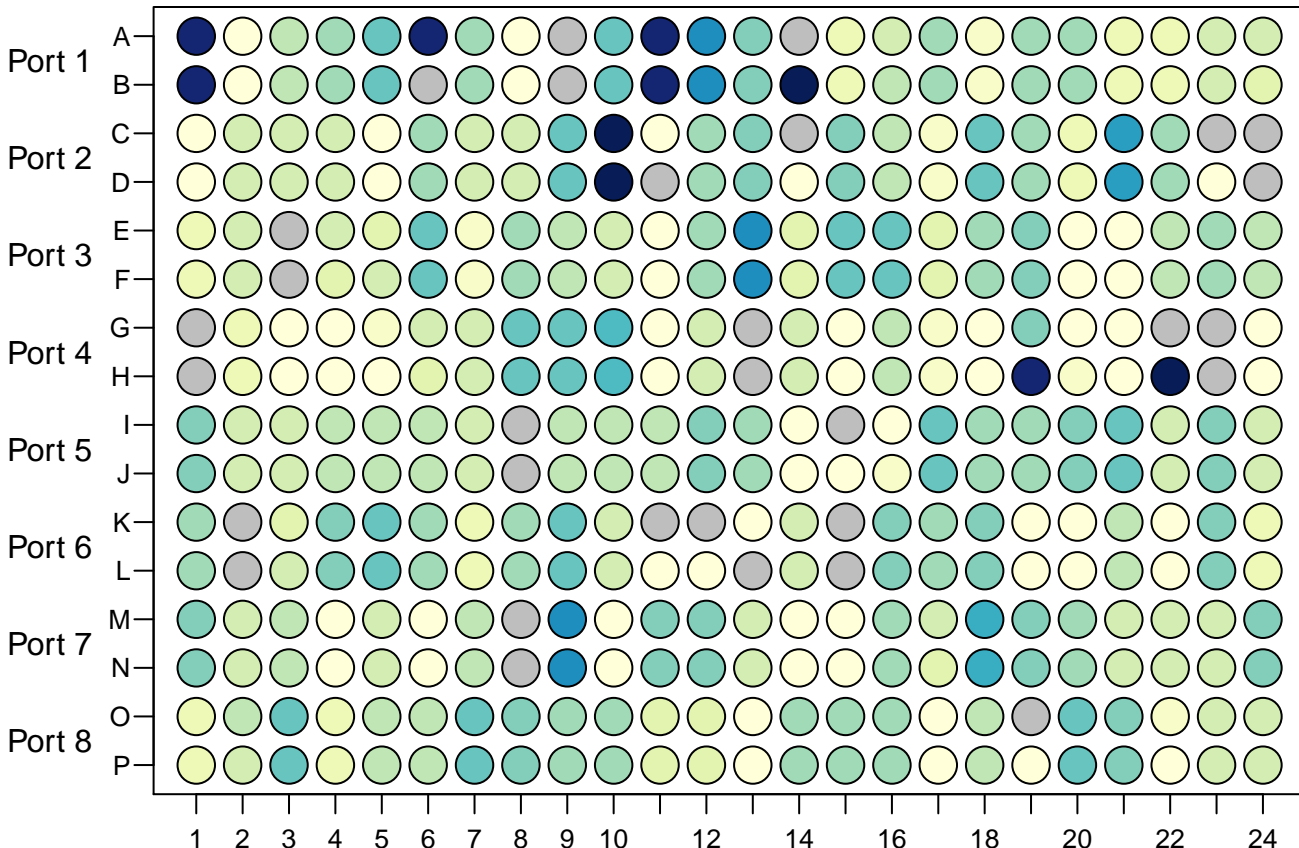


sample1

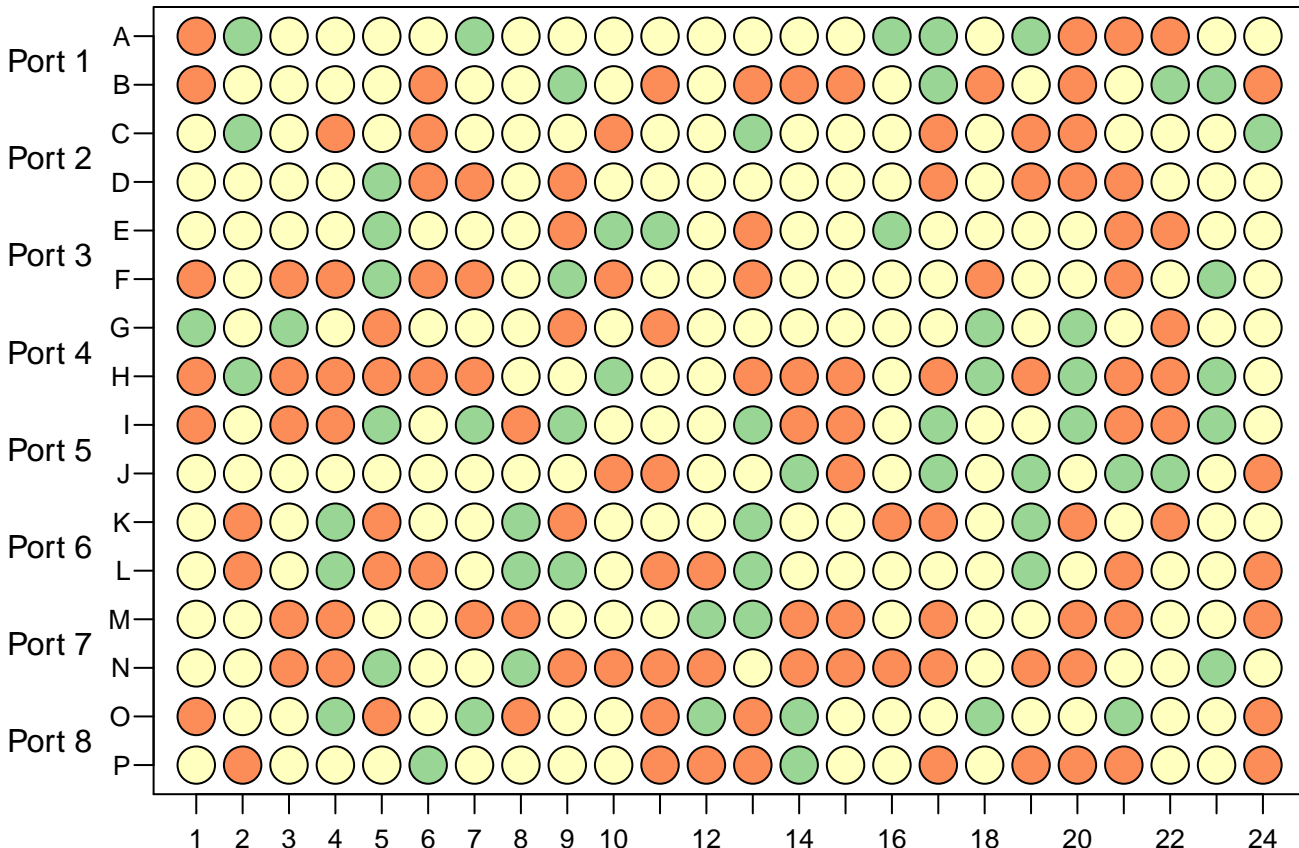


Kinase Marker TF

sample1

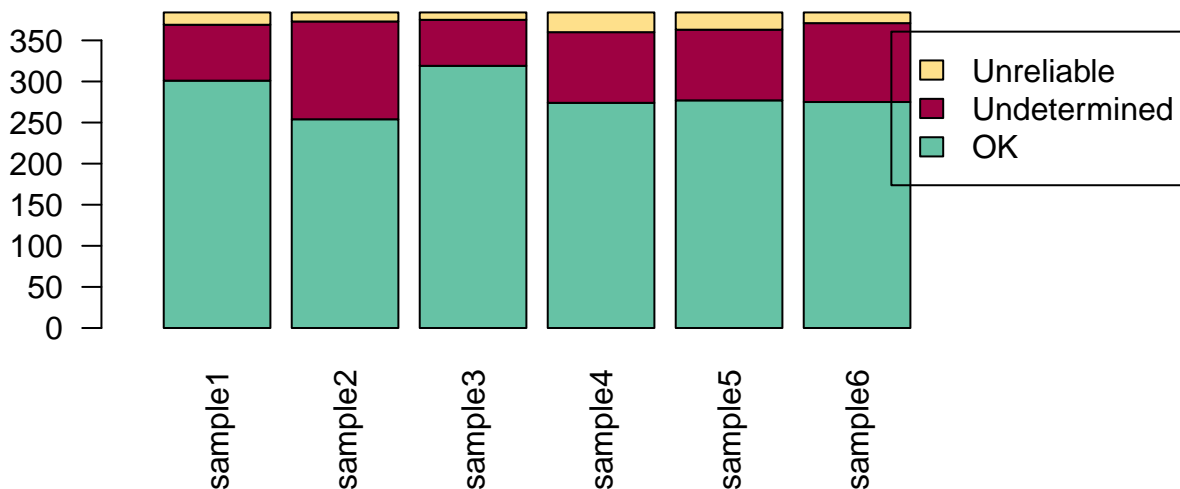


sample1

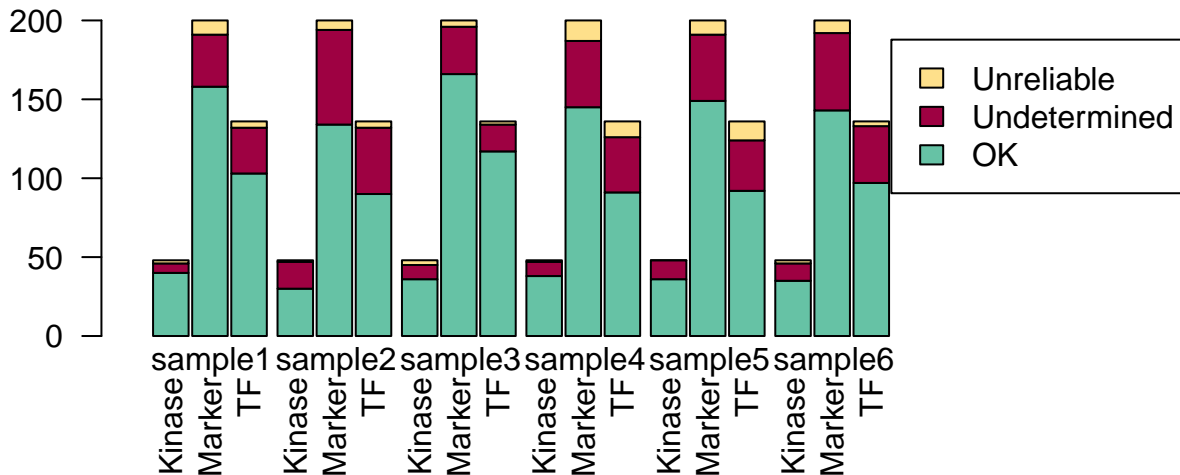


Kinase Marker TF

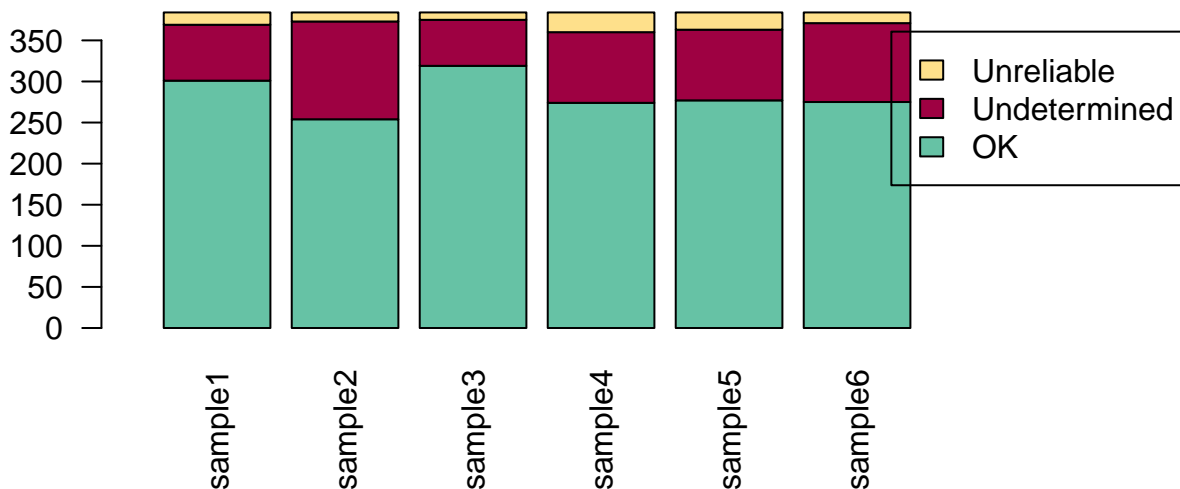
Feature categories



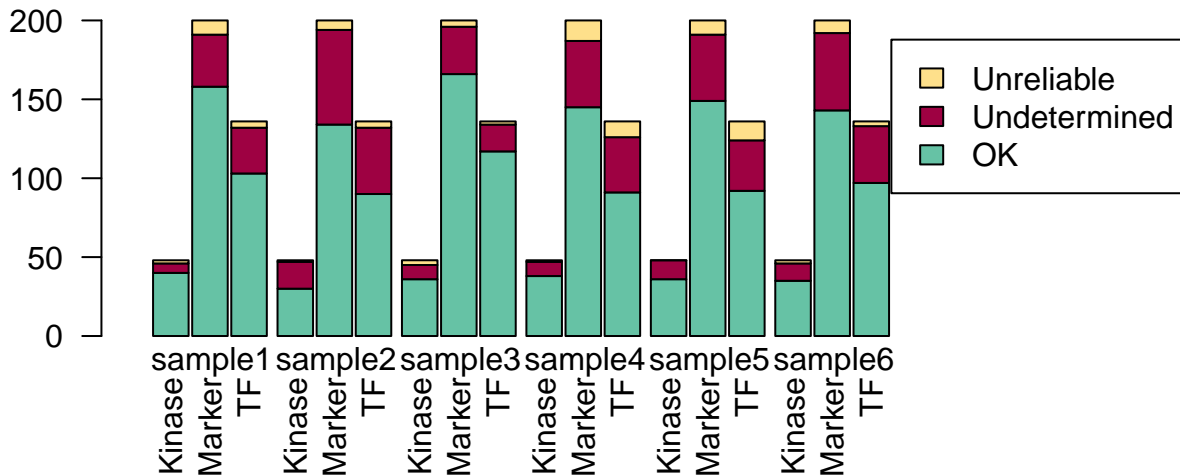
Feature categories

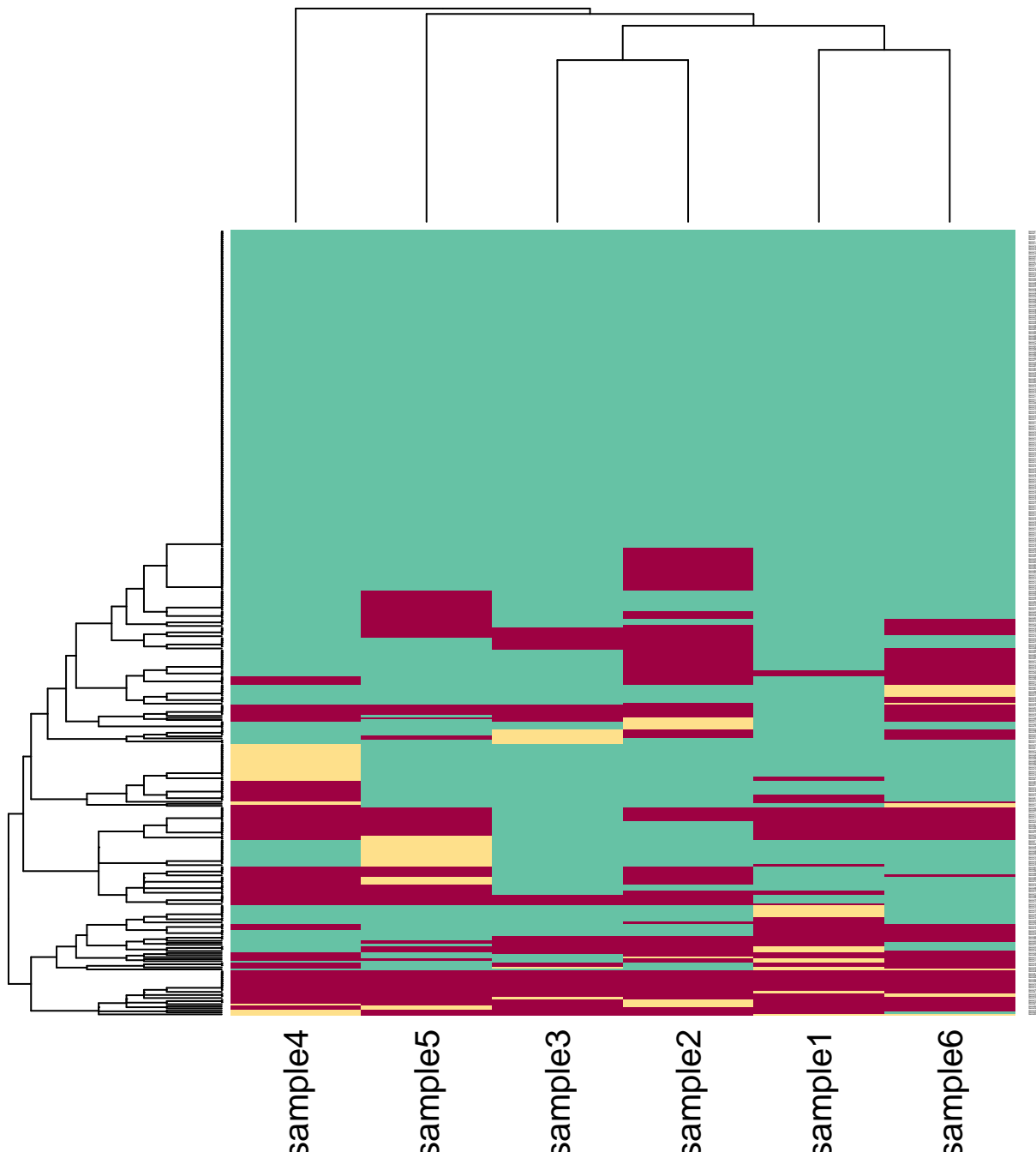


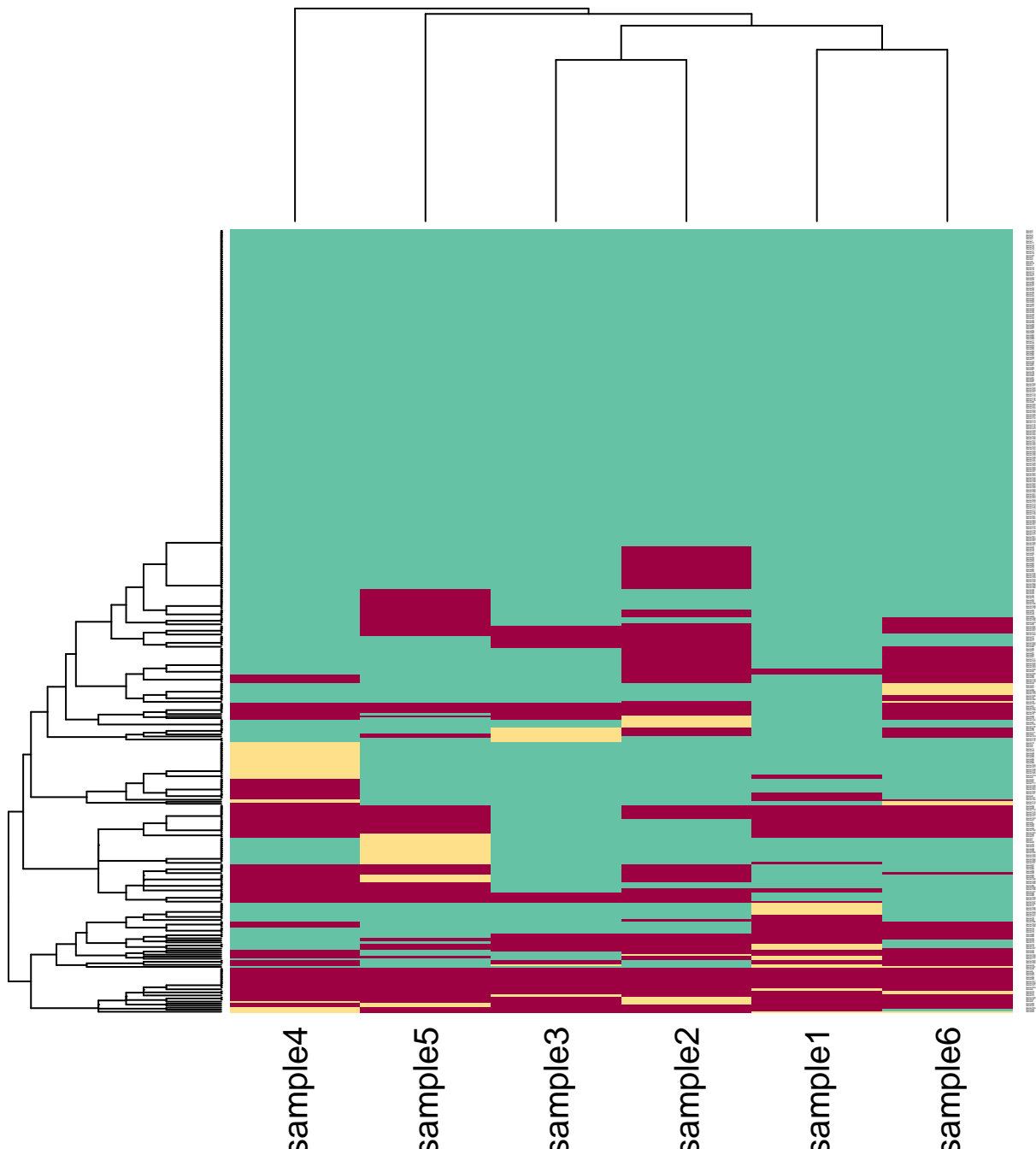
Feature categories



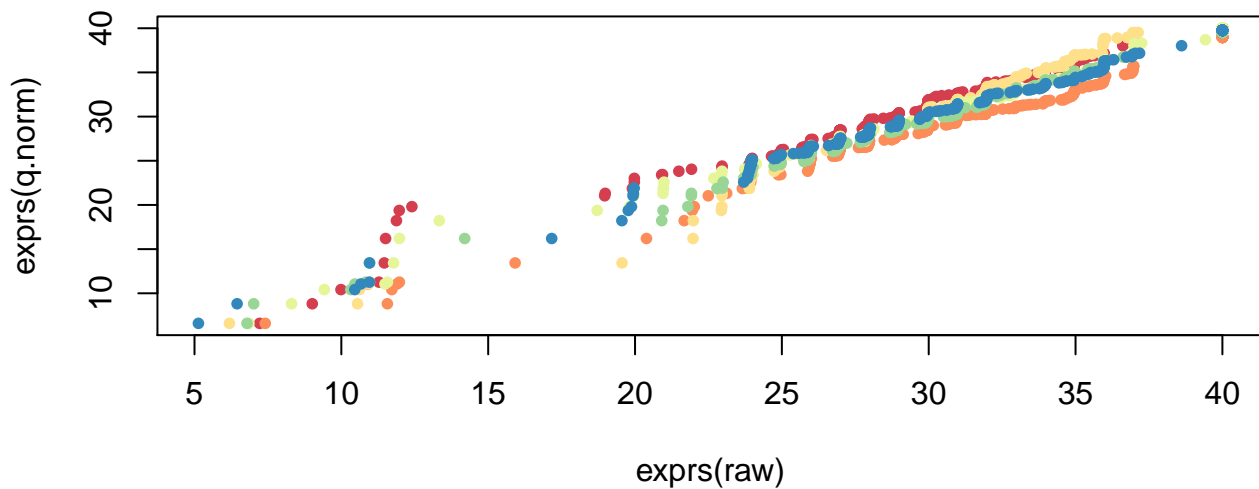
Feature categories

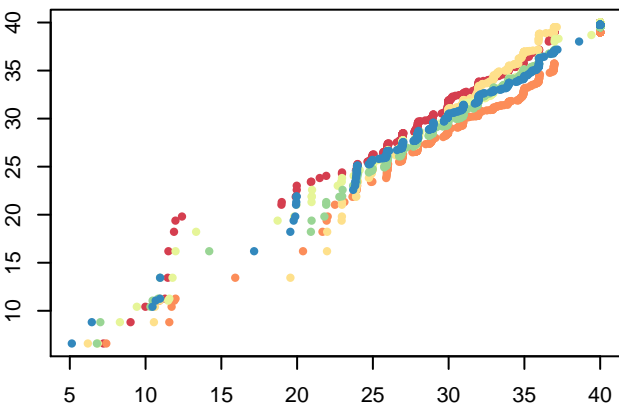
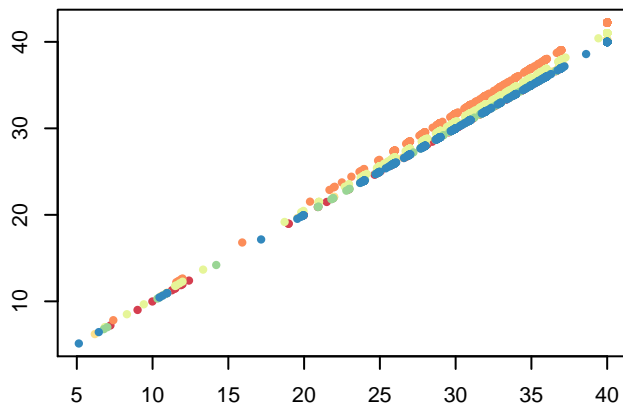
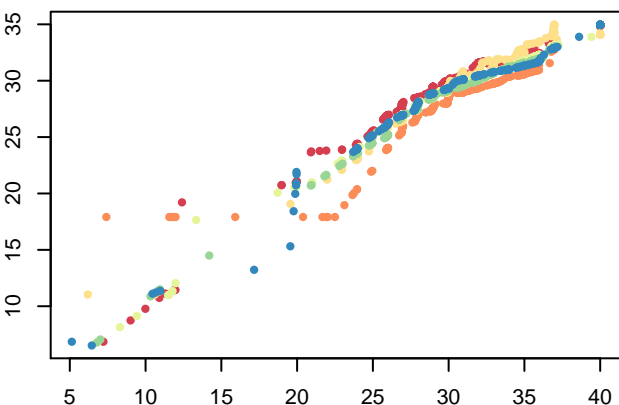
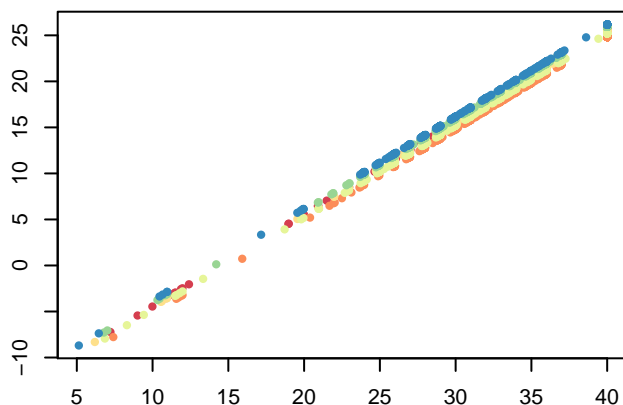
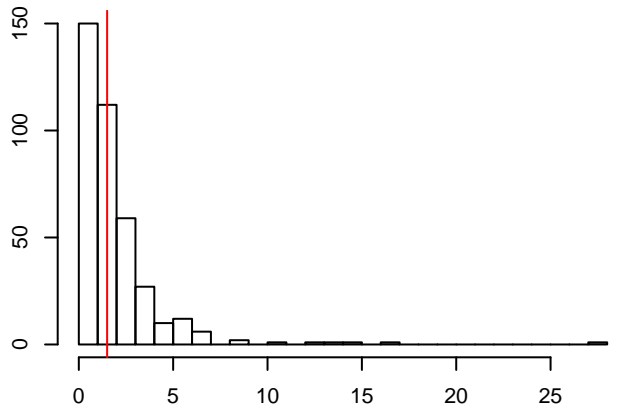
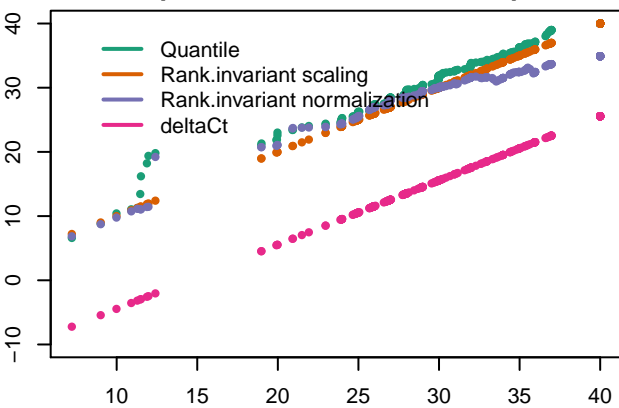


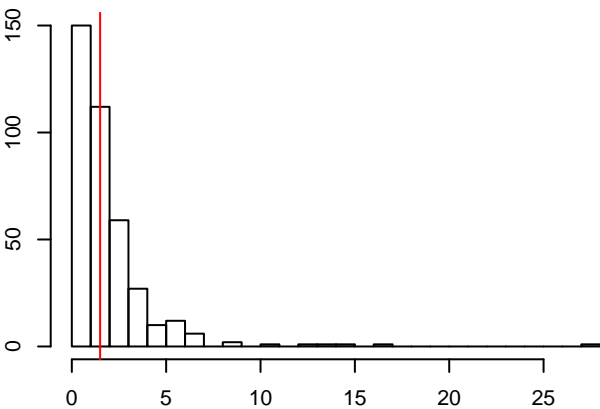




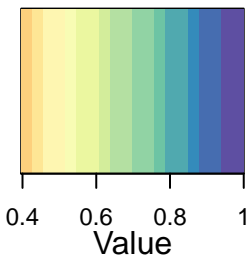
Quantile normalisation



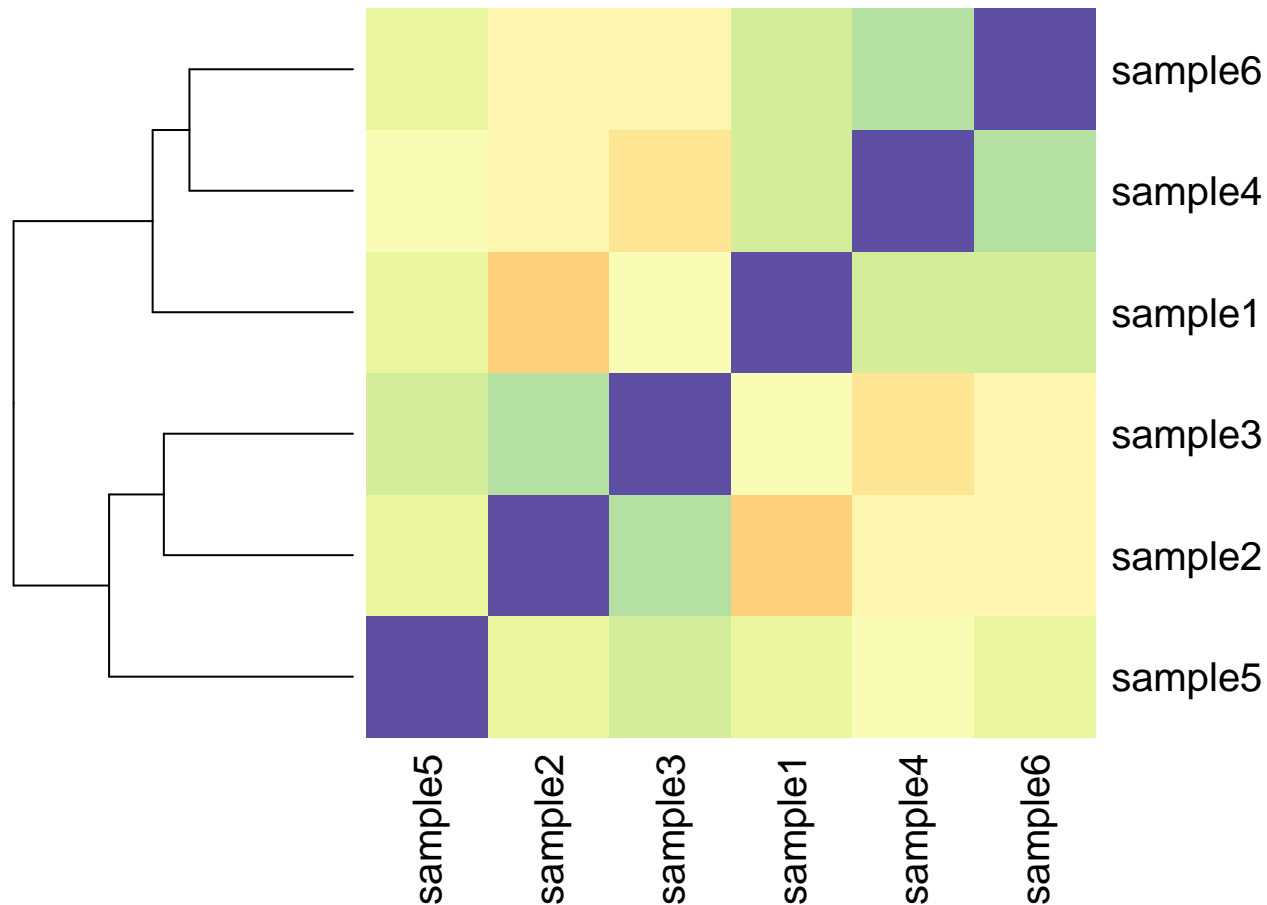
Quantile normalisation**Rank invariant scaling****Rank invariant normalisation****deltaCt normalisation****Comparison of methods for sample 1**



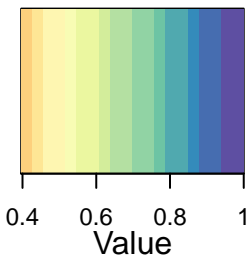
Color Key



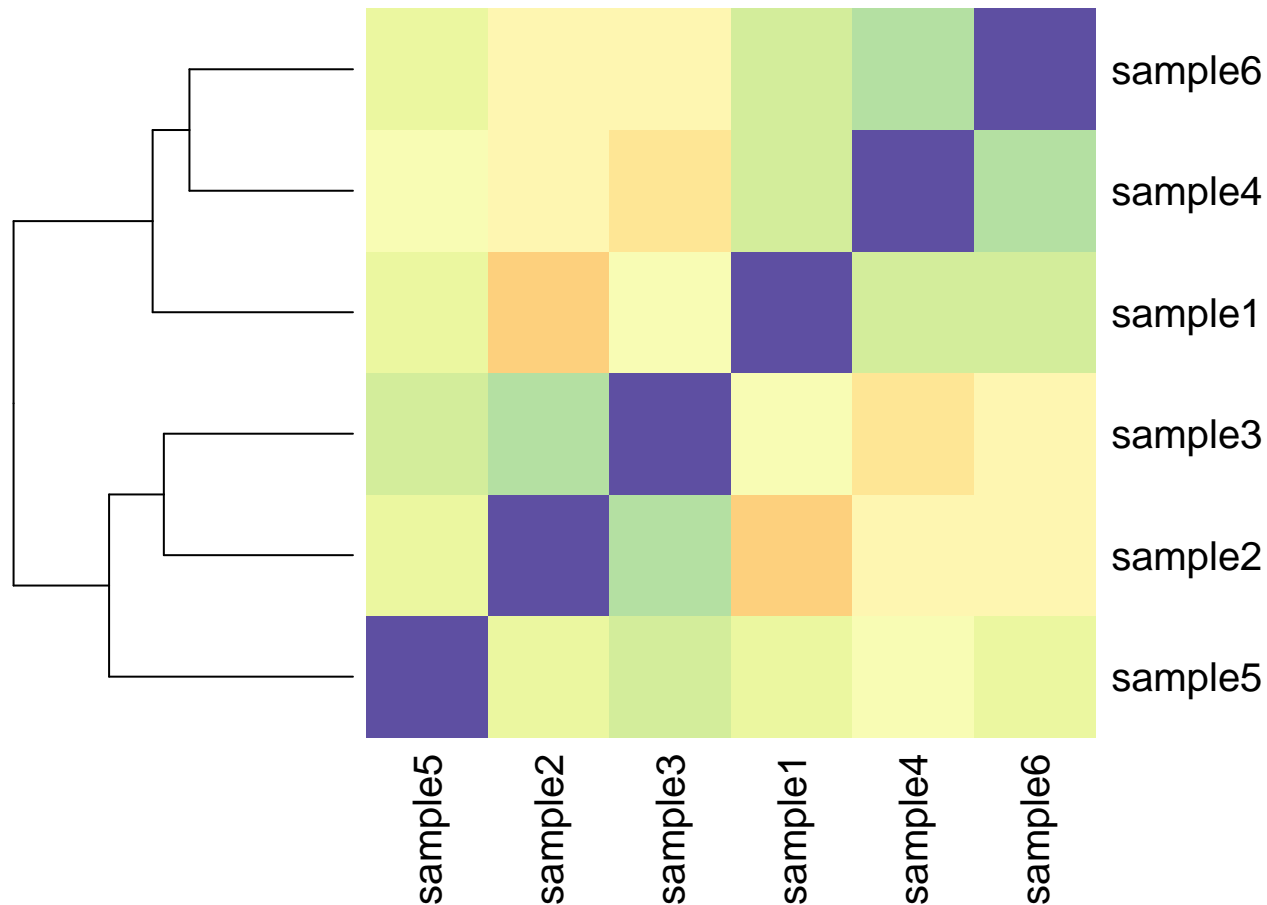
Ct correlation

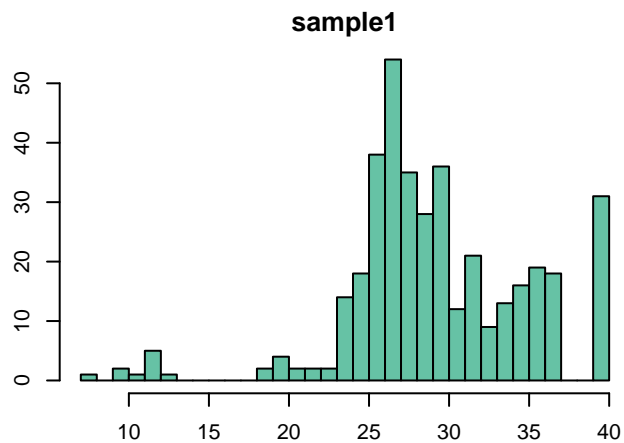
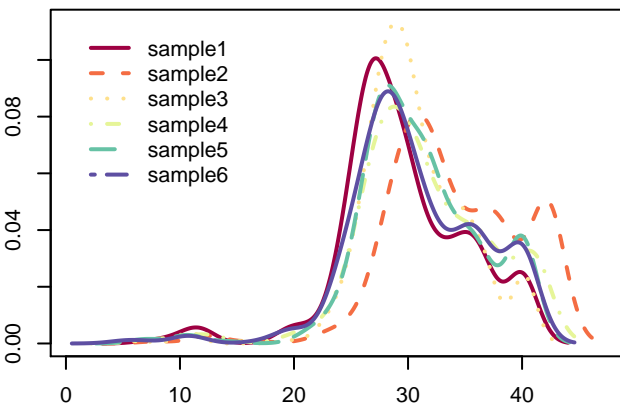


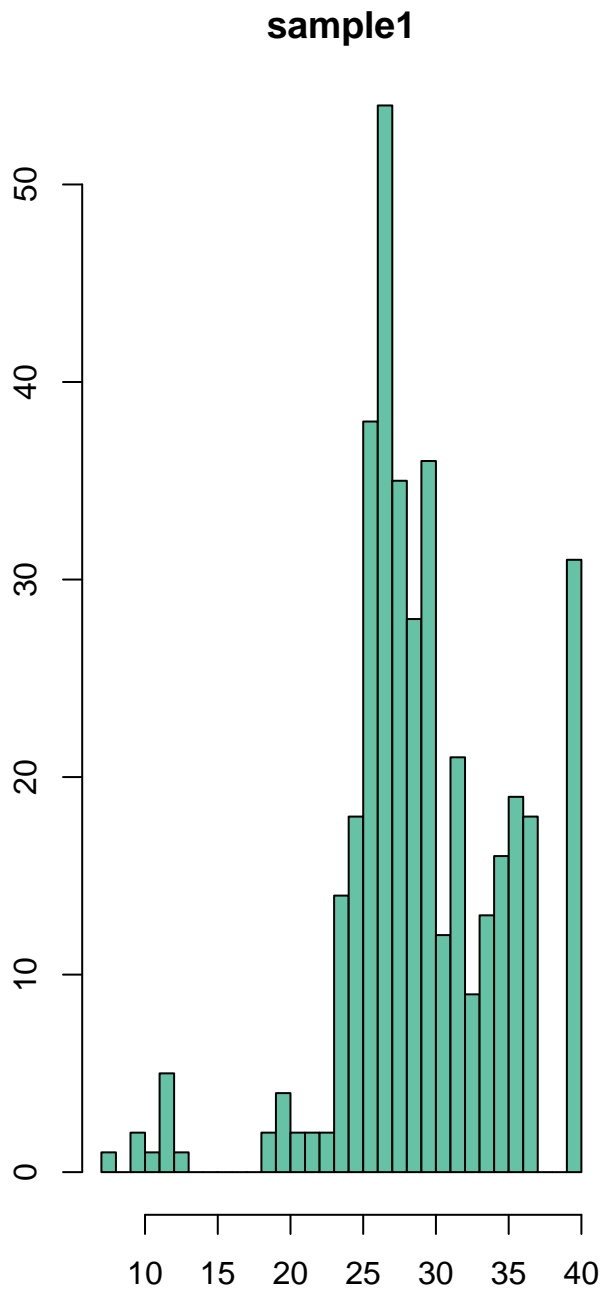
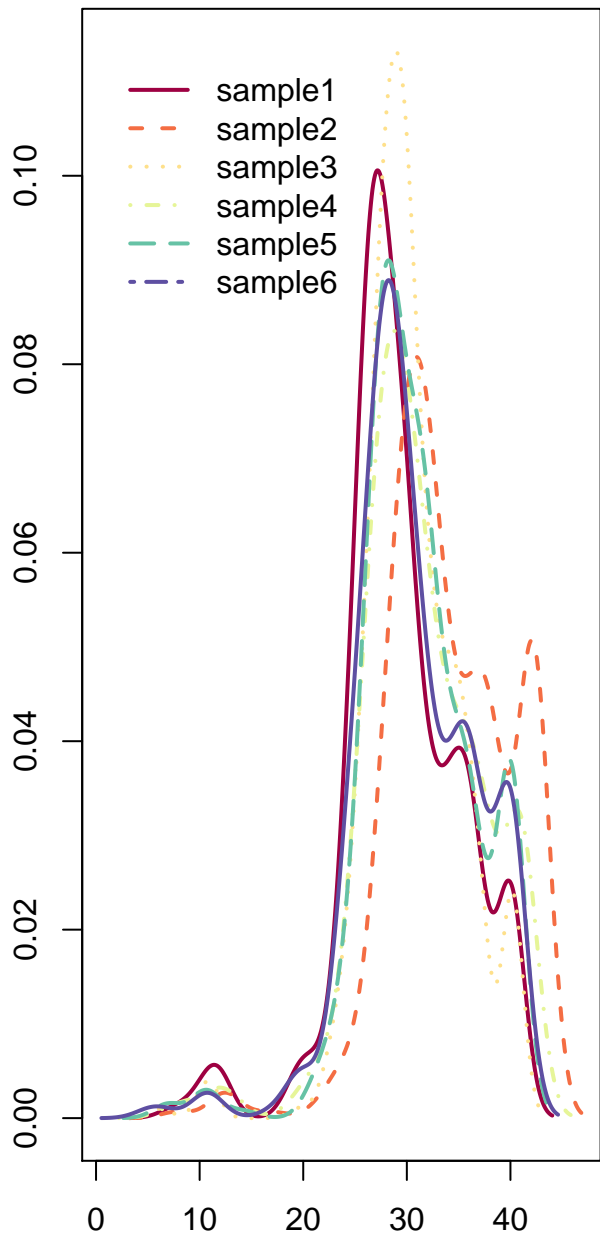
Color Key

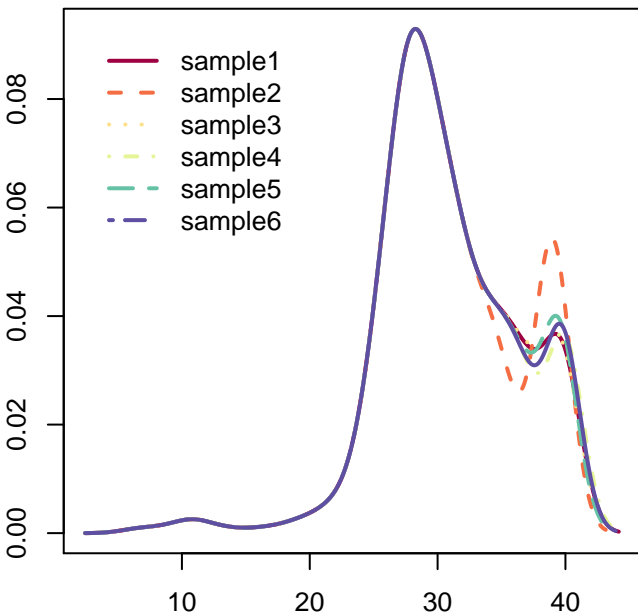
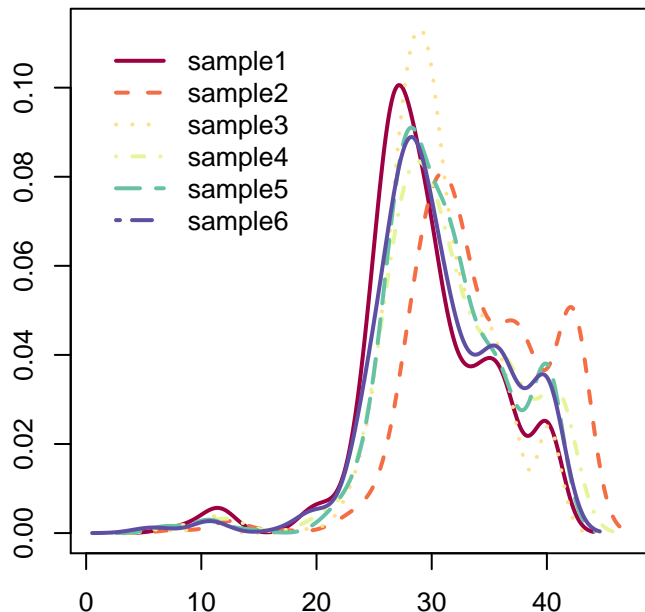
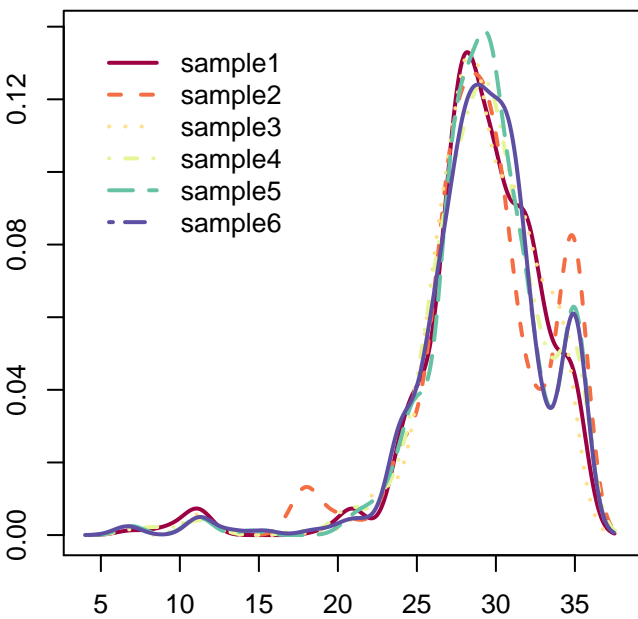
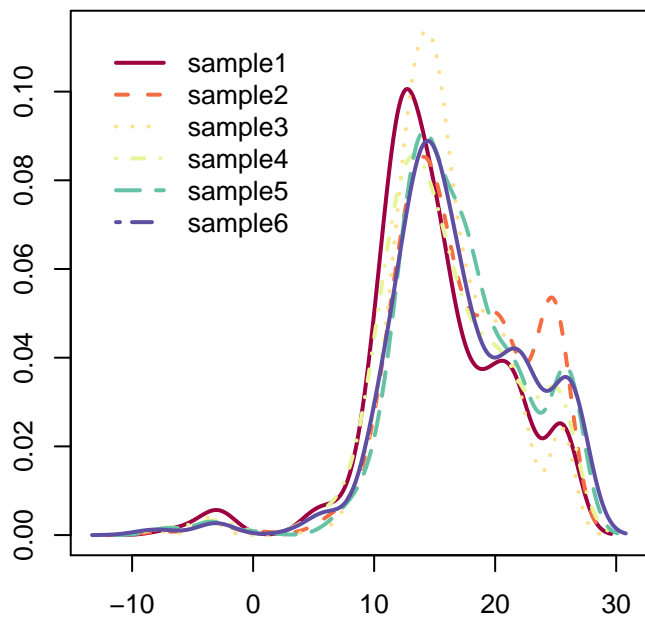


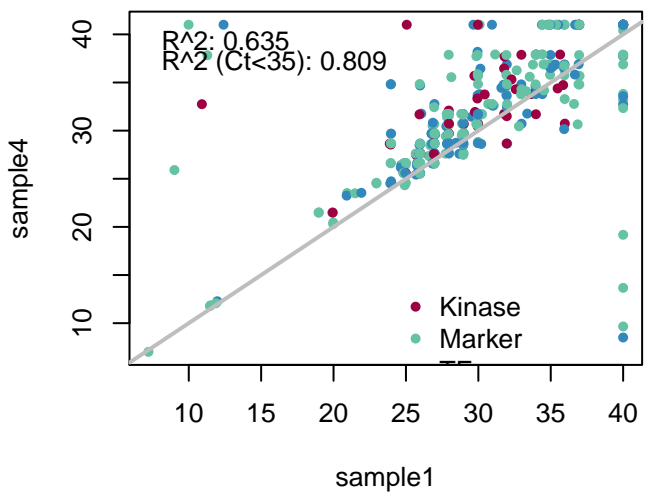
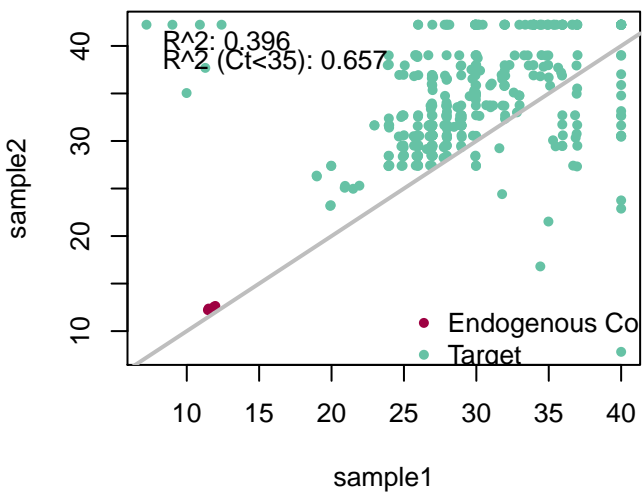
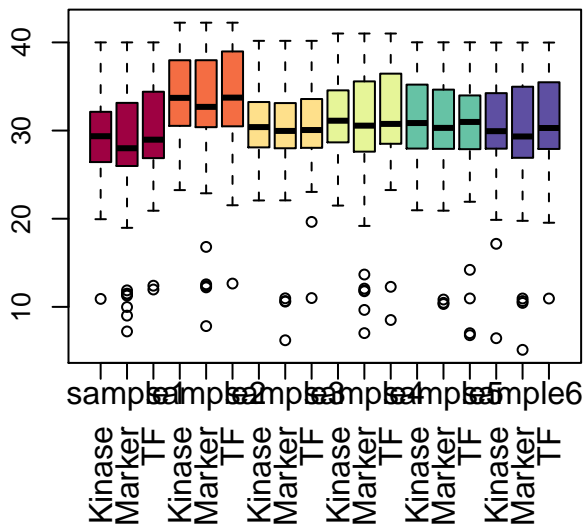
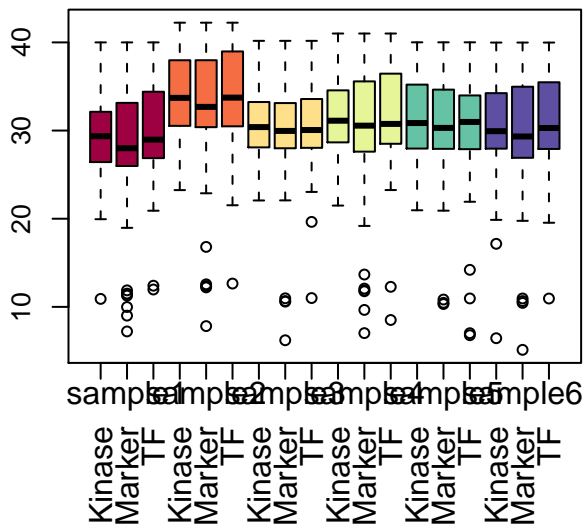
Ct correlation

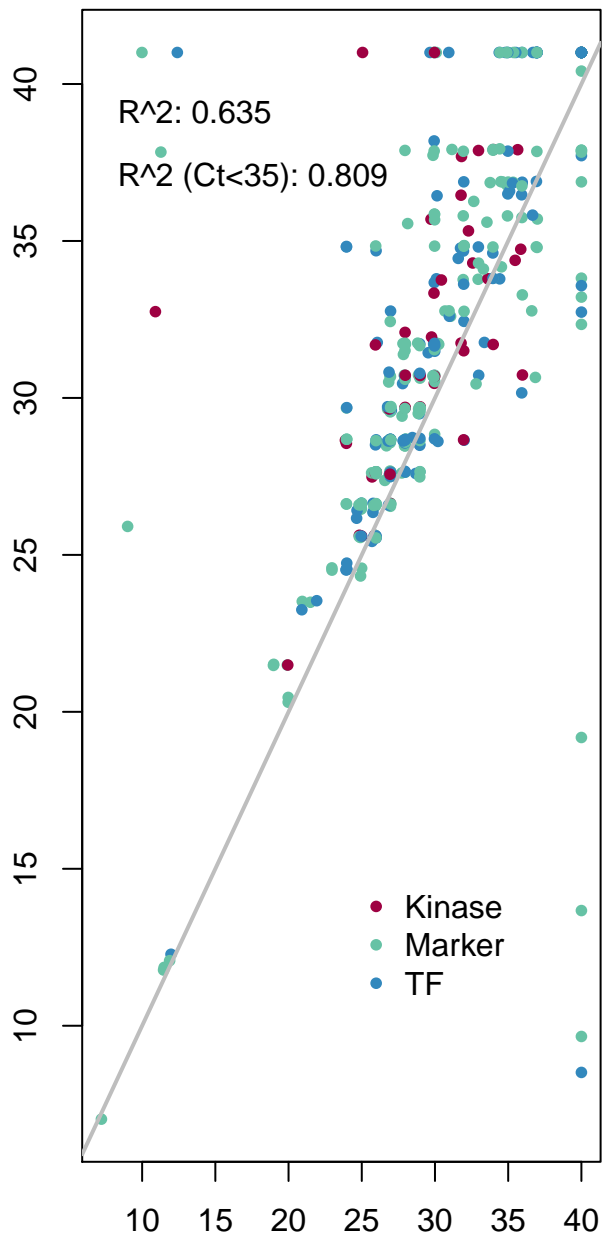
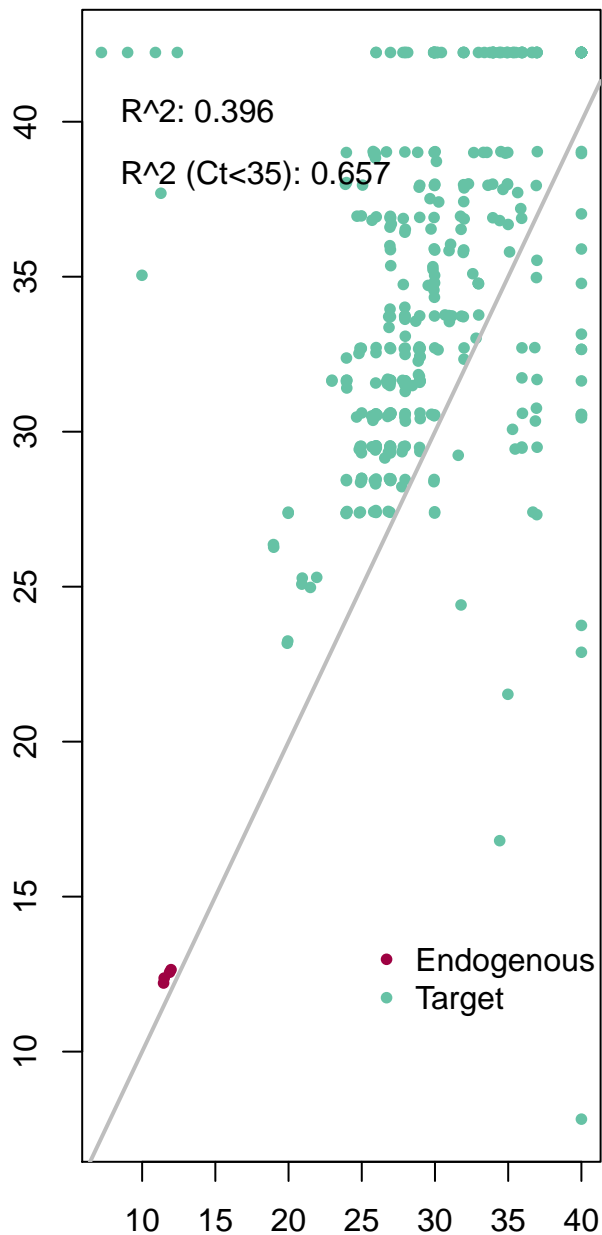


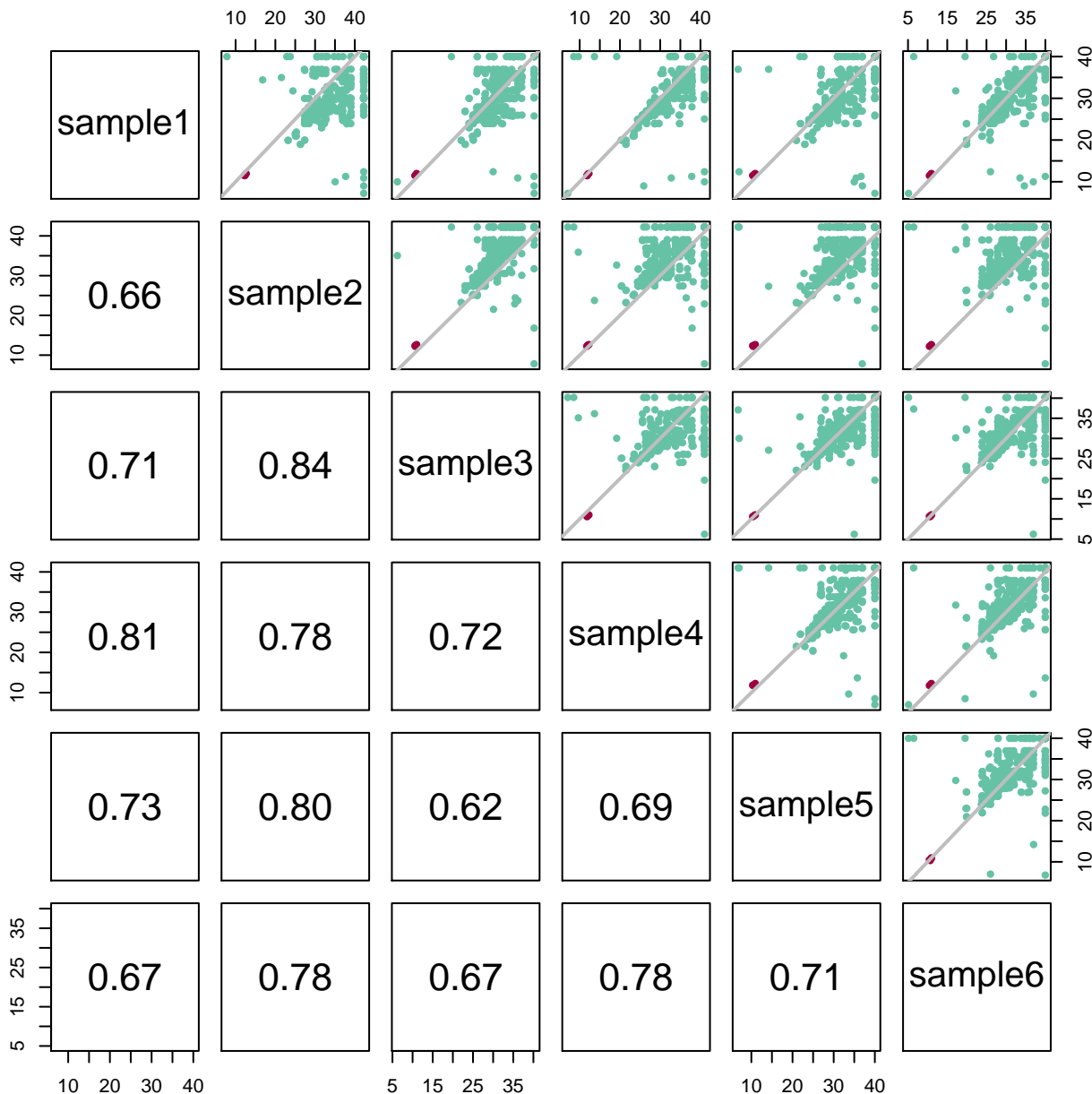


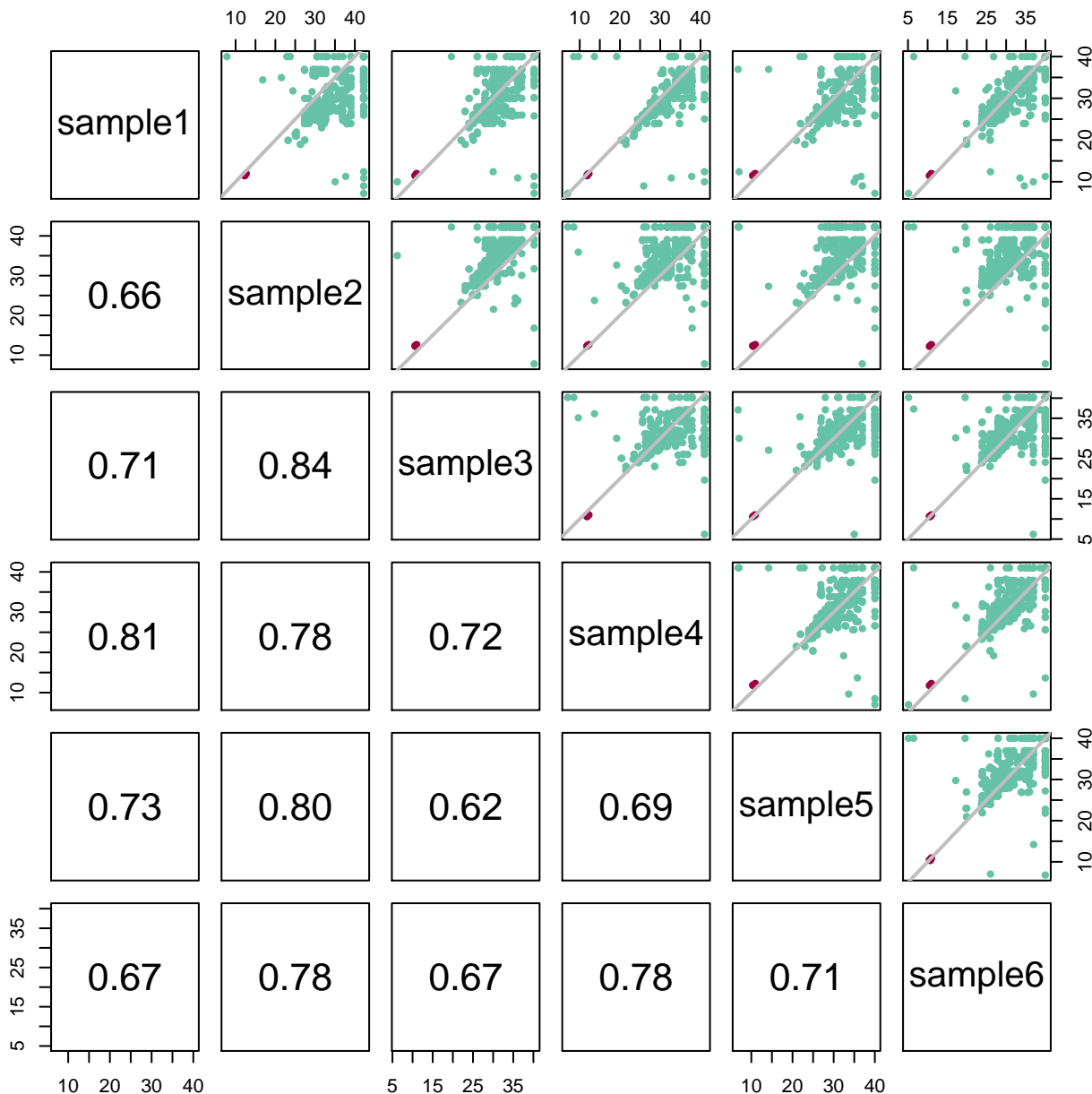


quantile**scale.rankinvariant****norm.rankinvariant****deltaCt**

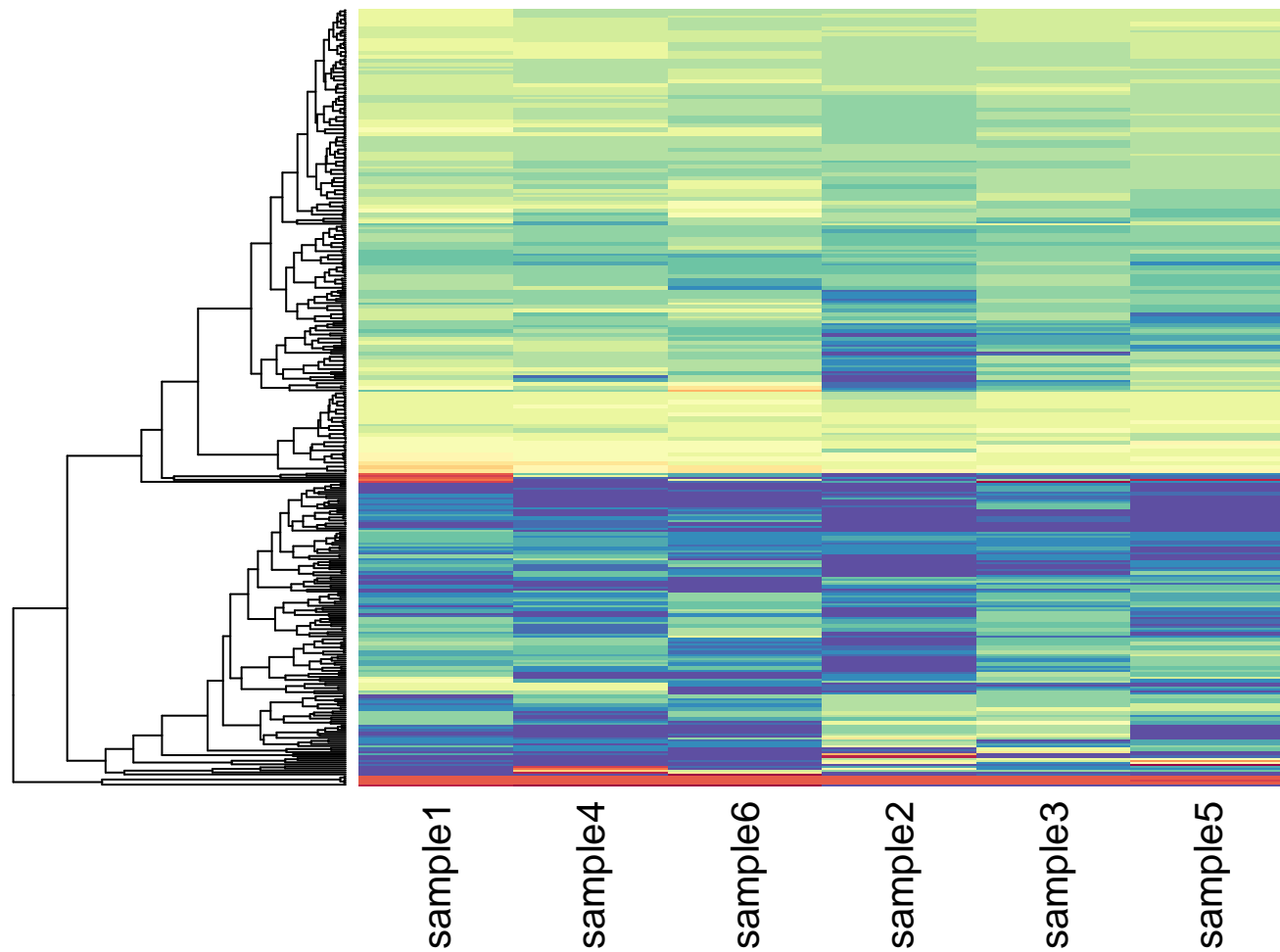
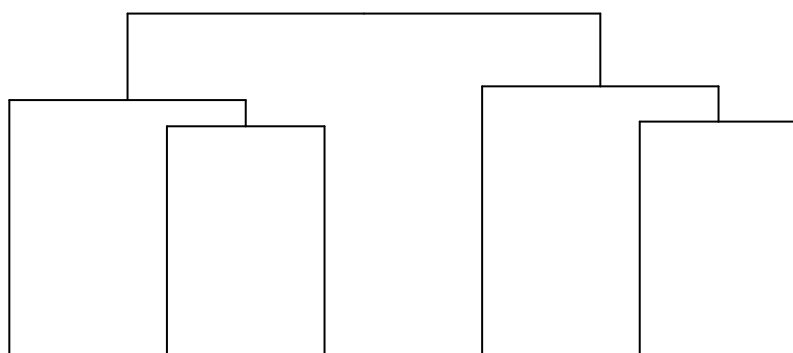
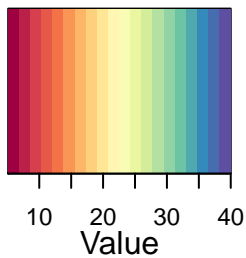




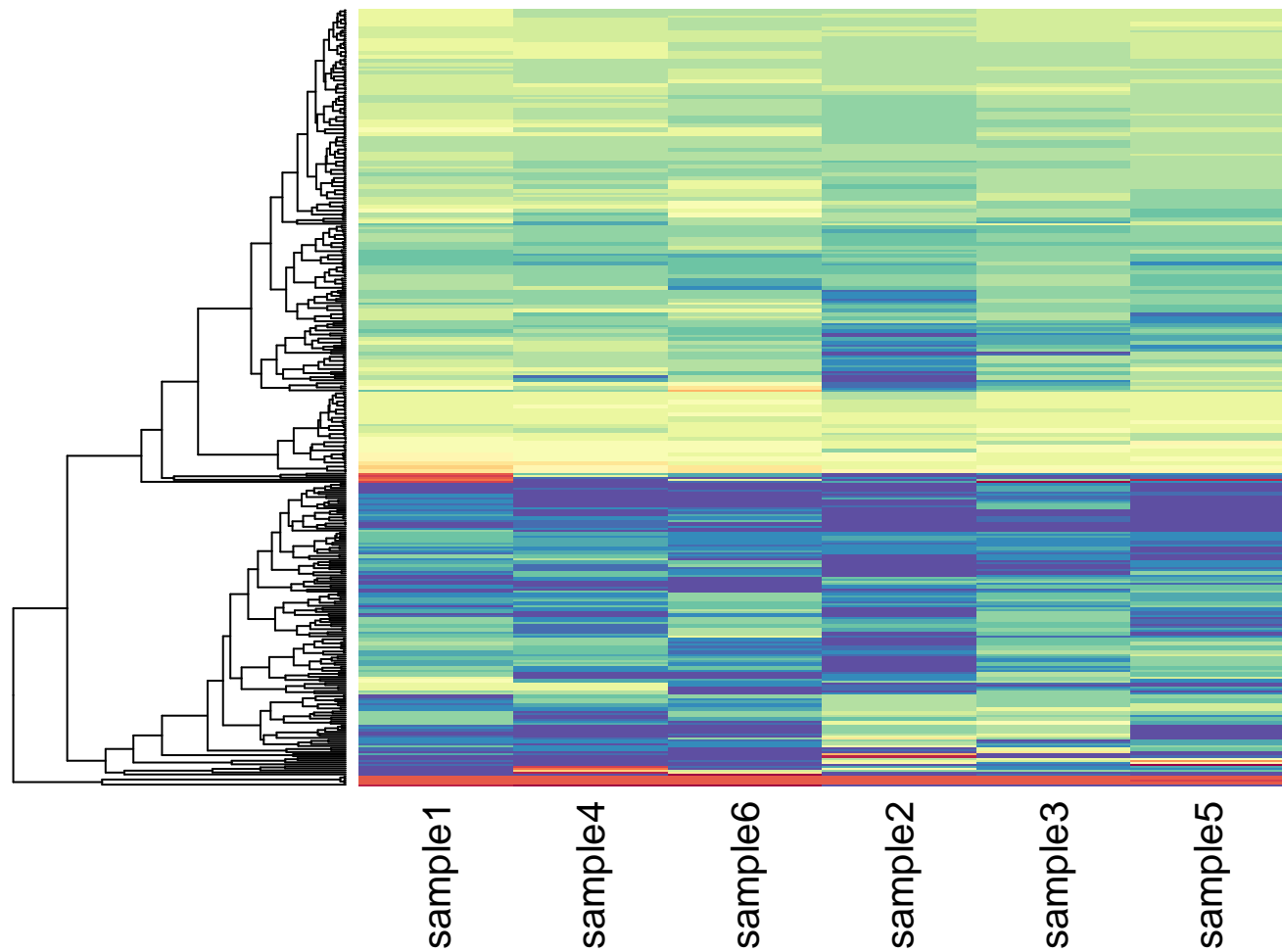
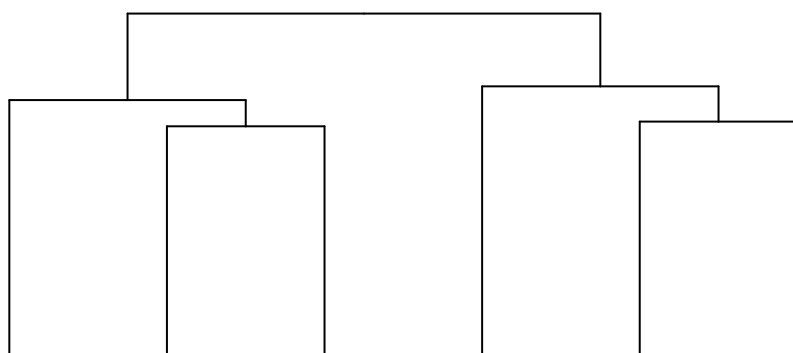
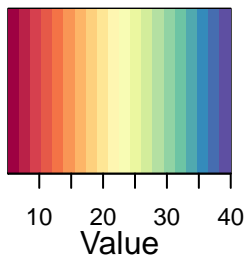


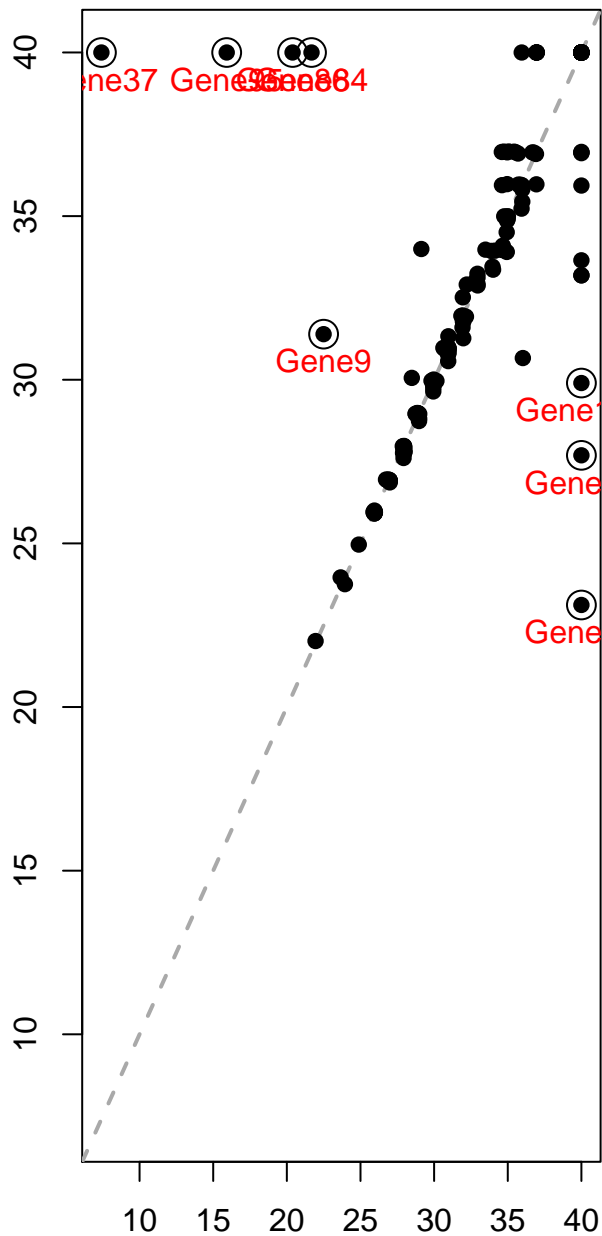
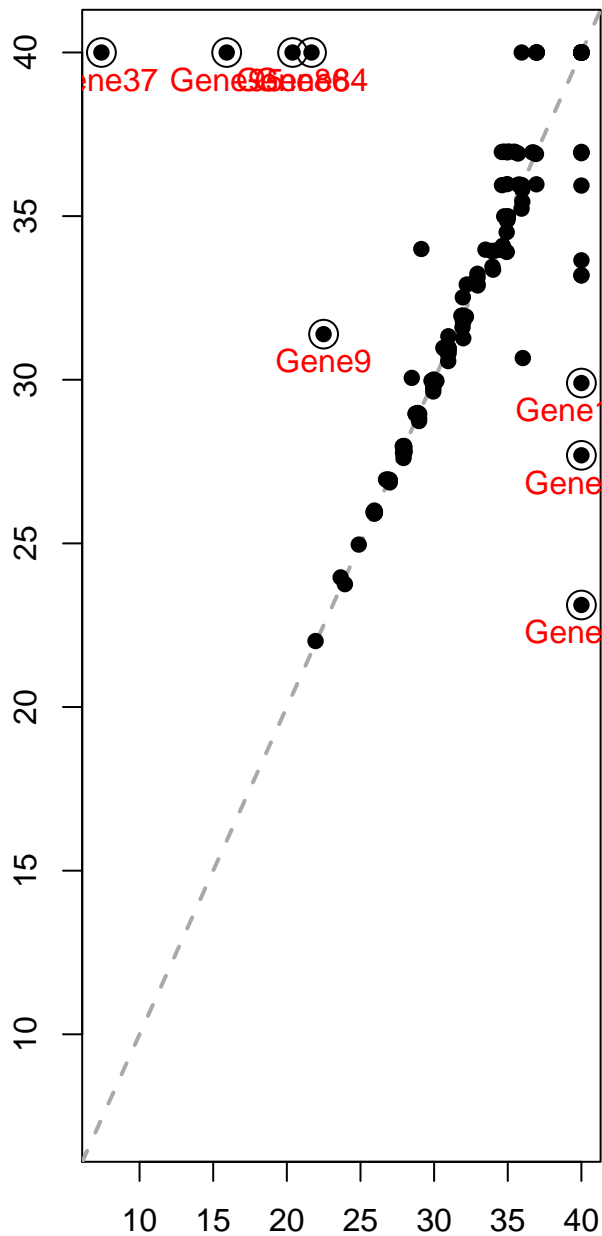


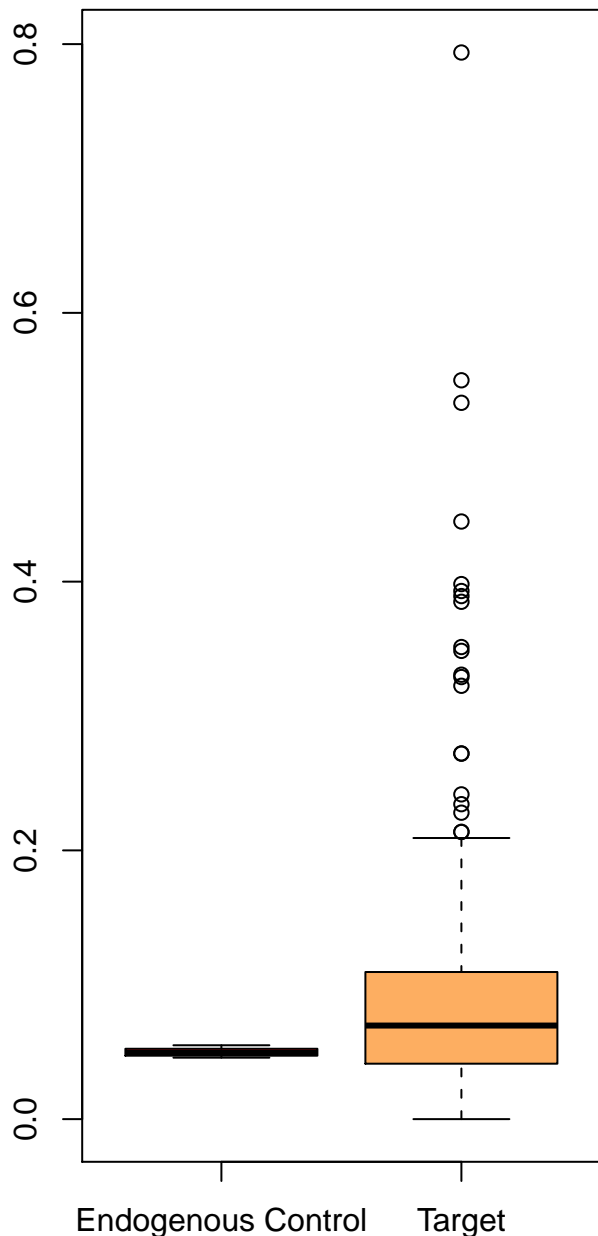
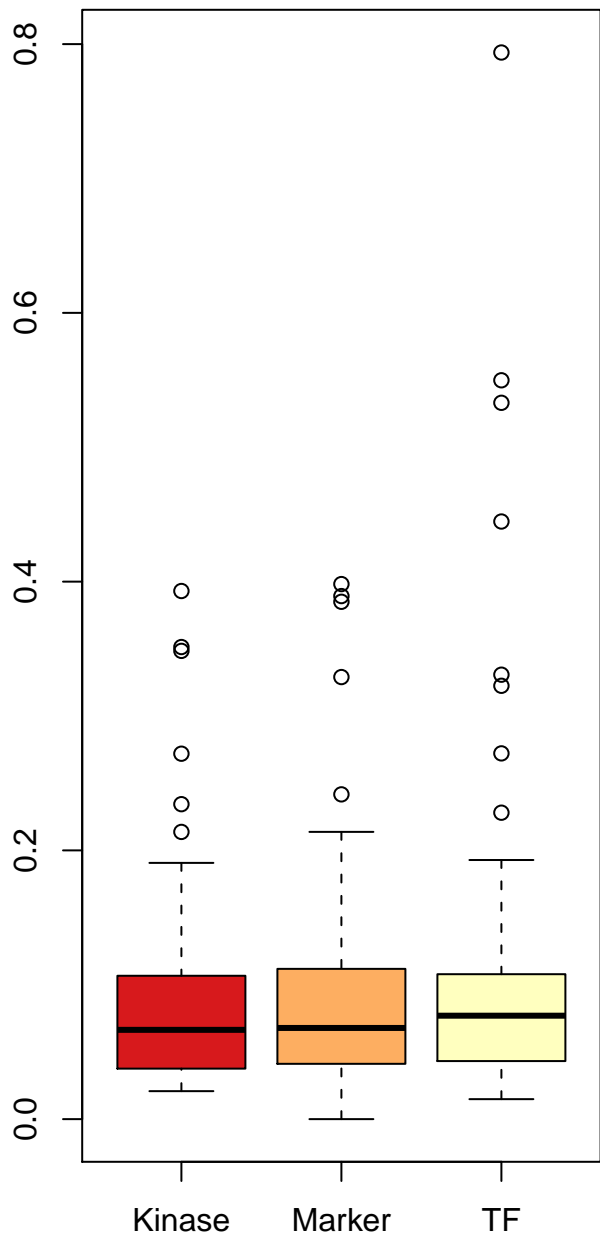
Color Key

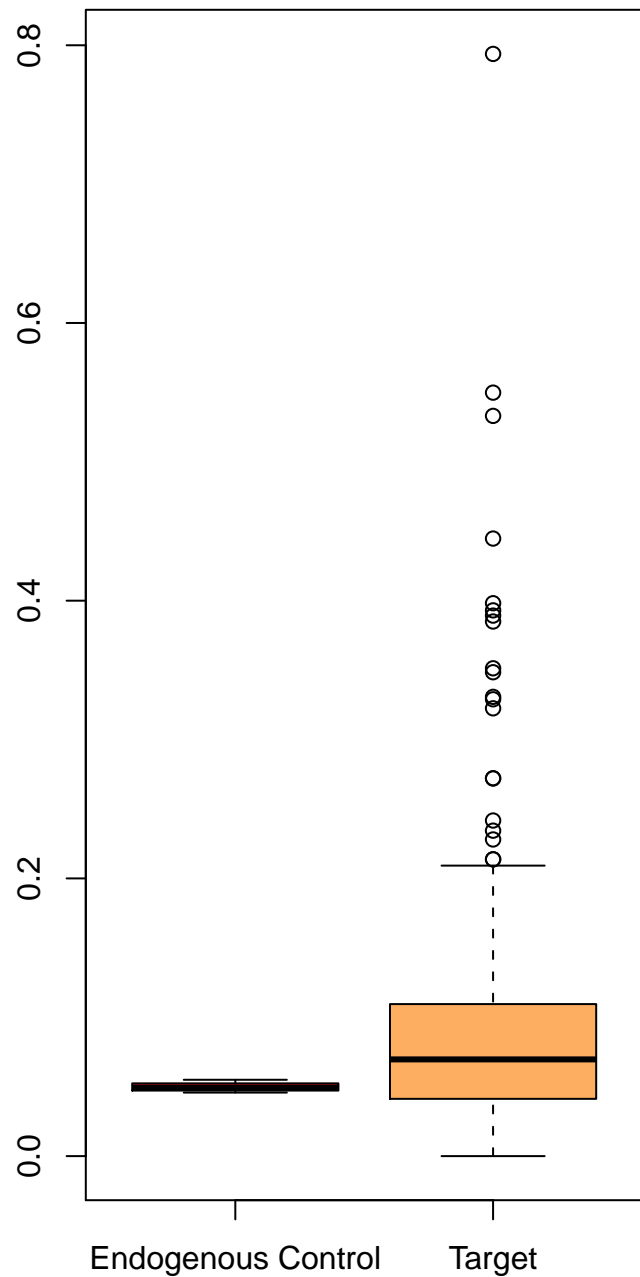
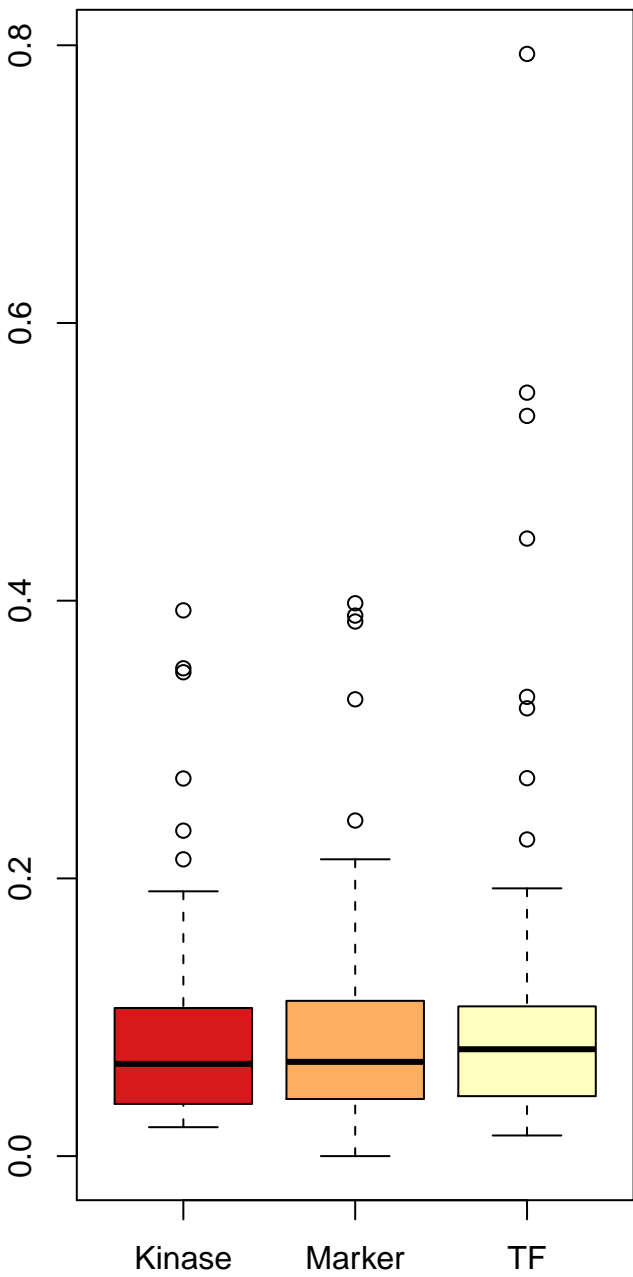


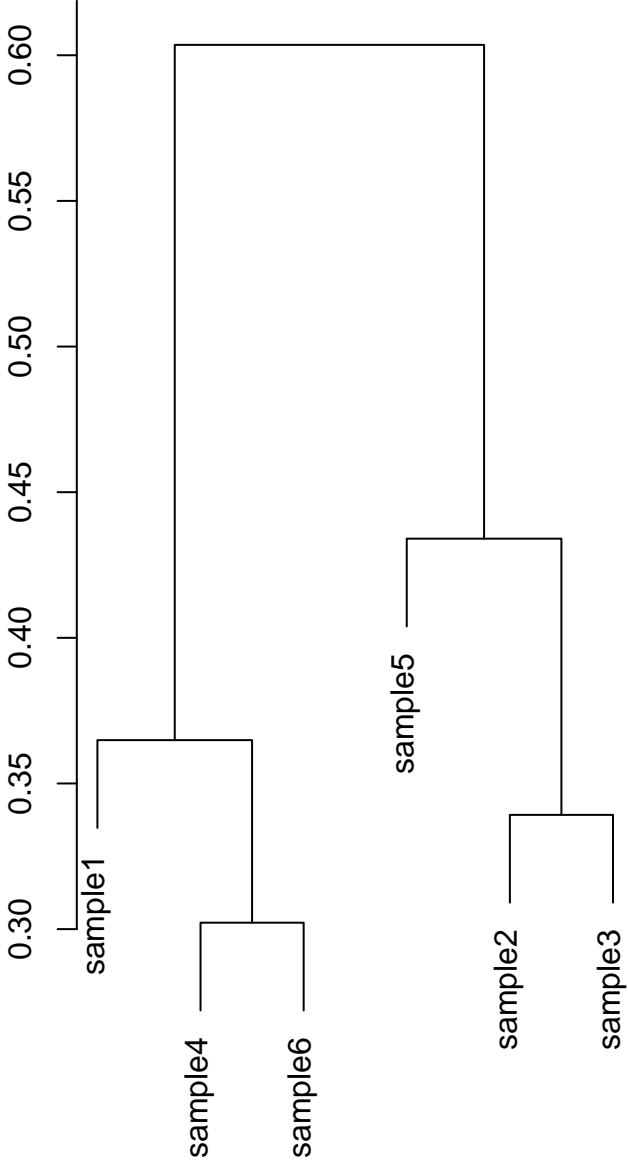
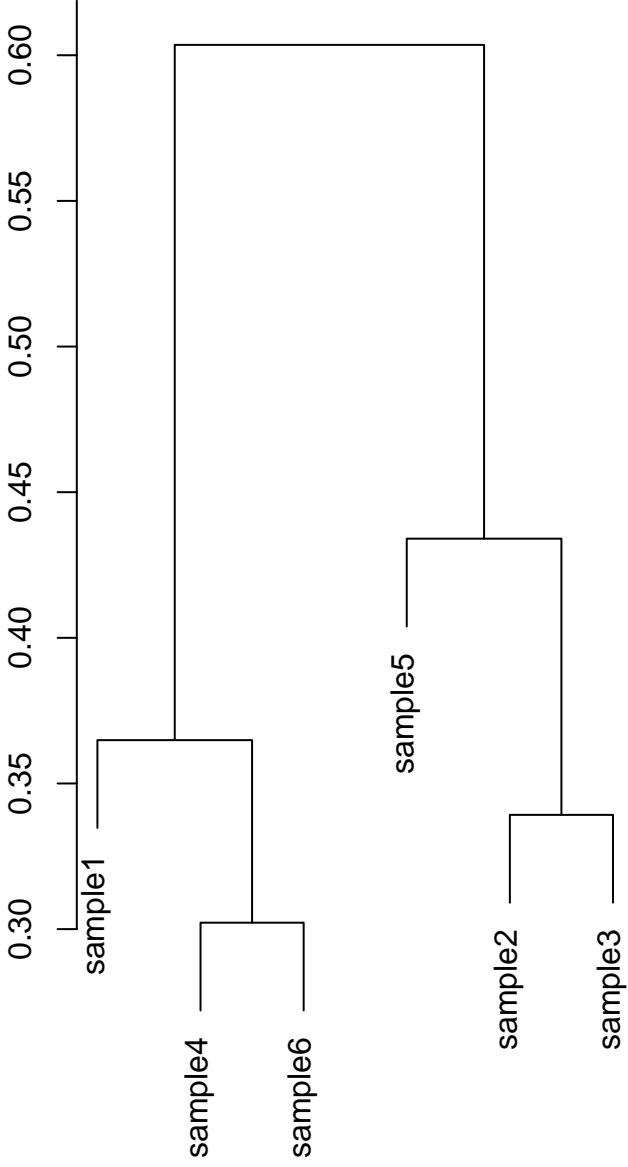
Color Key

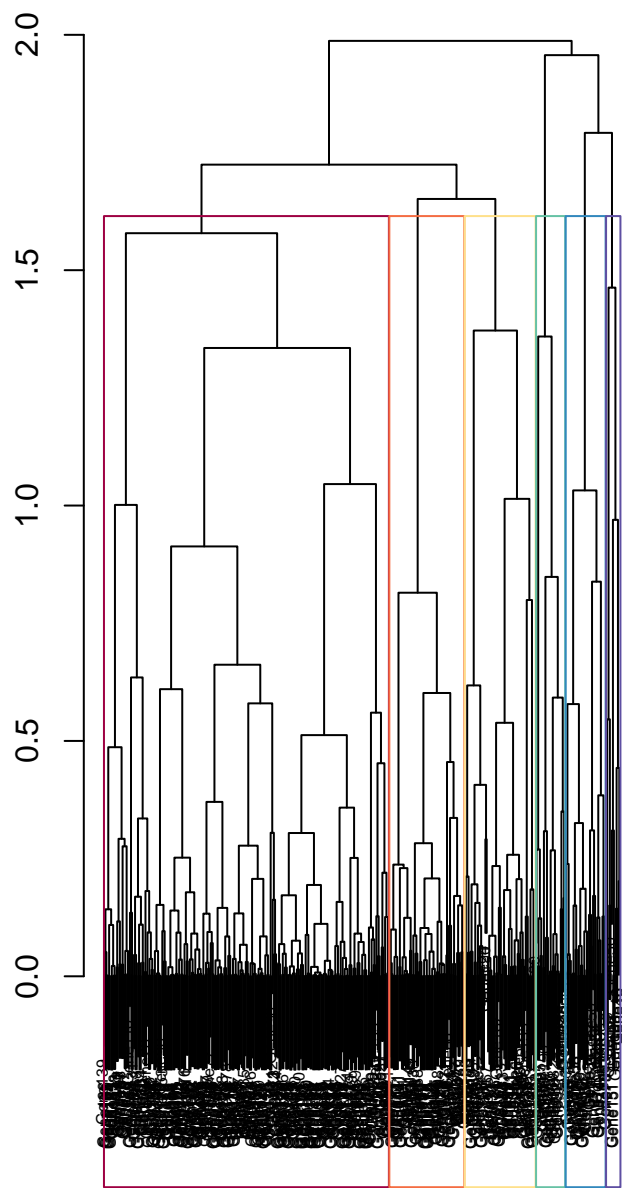
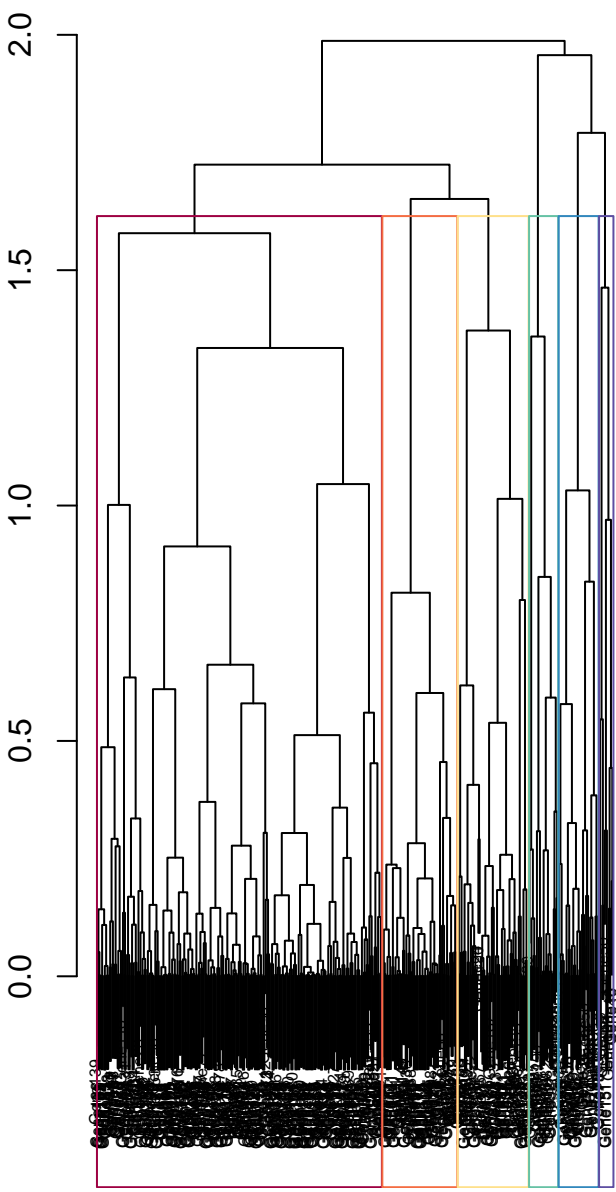


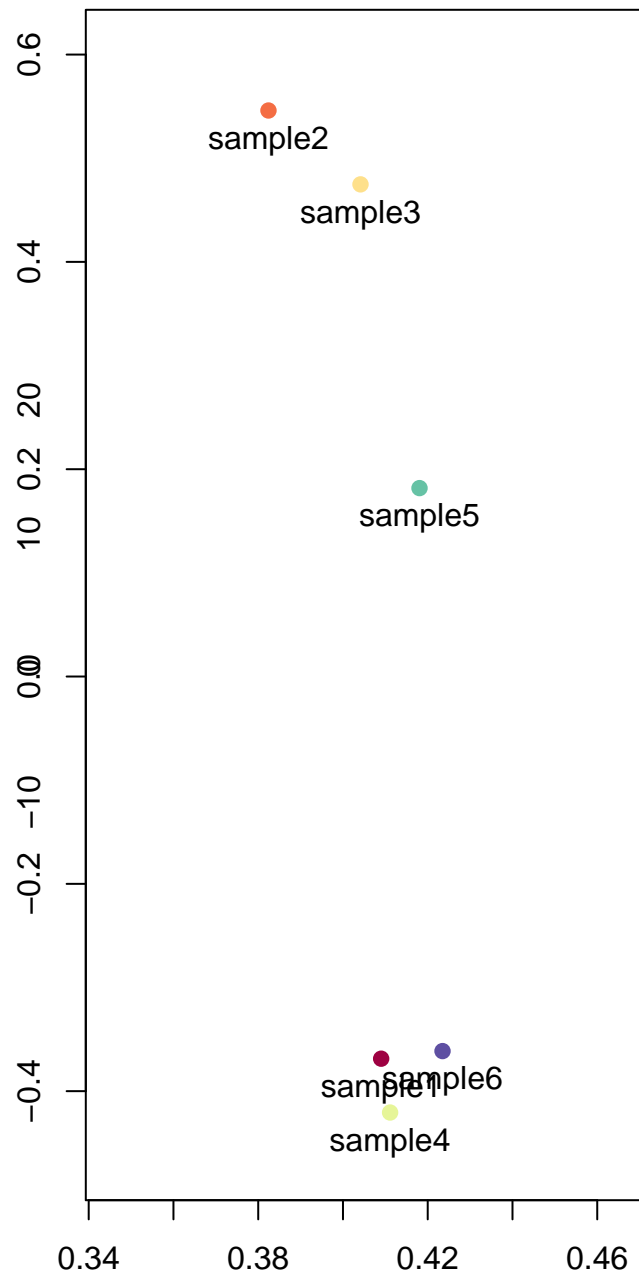
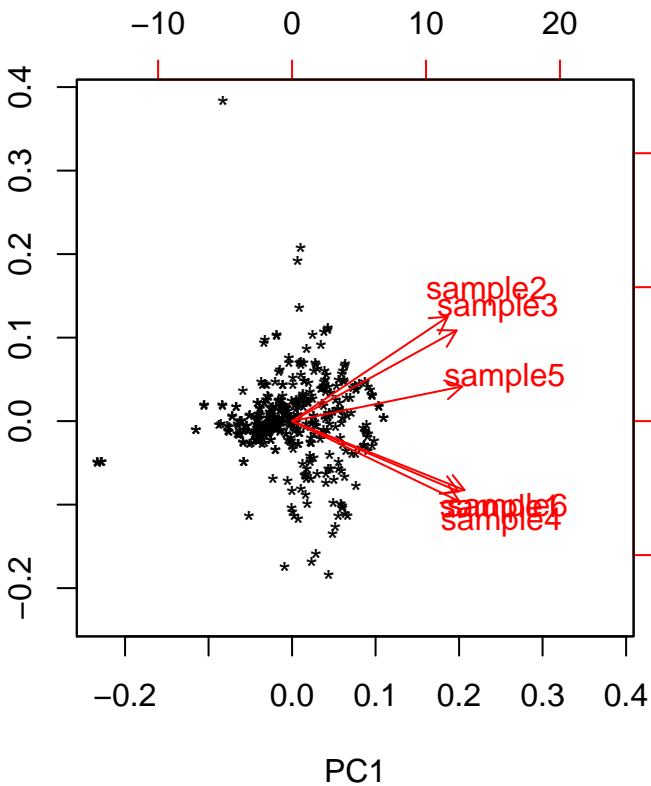


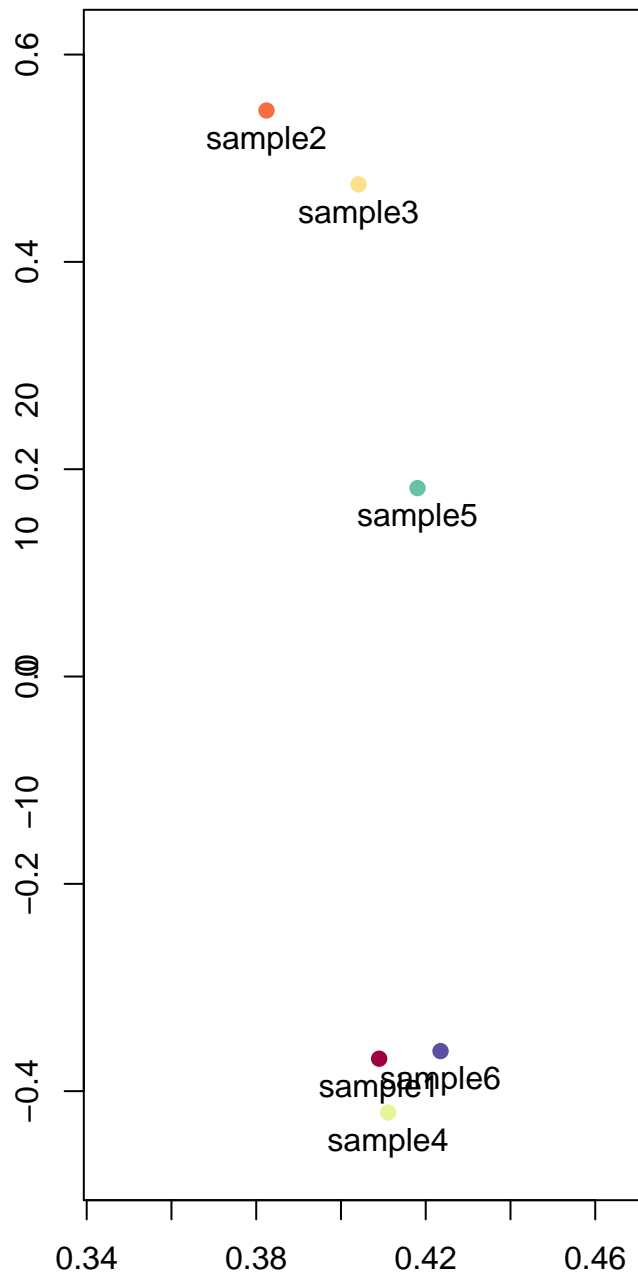
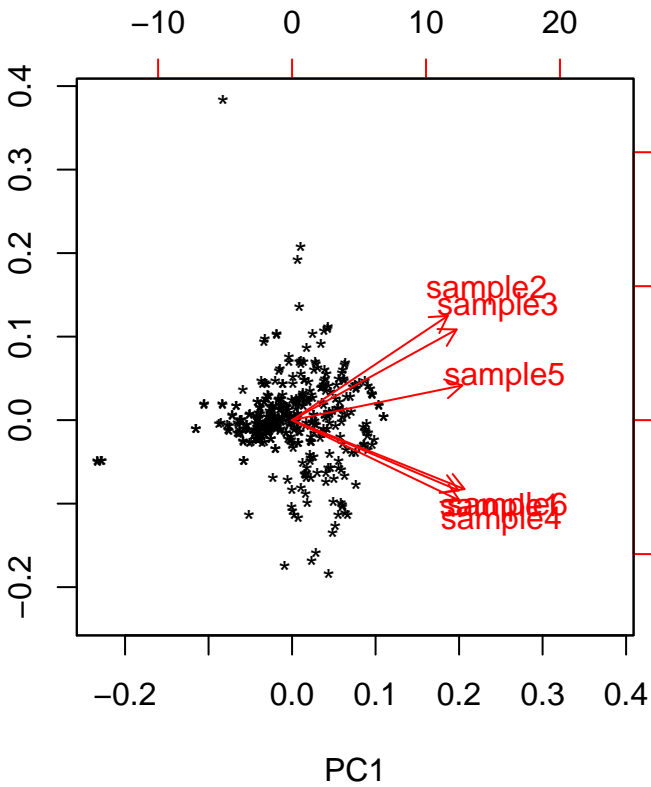








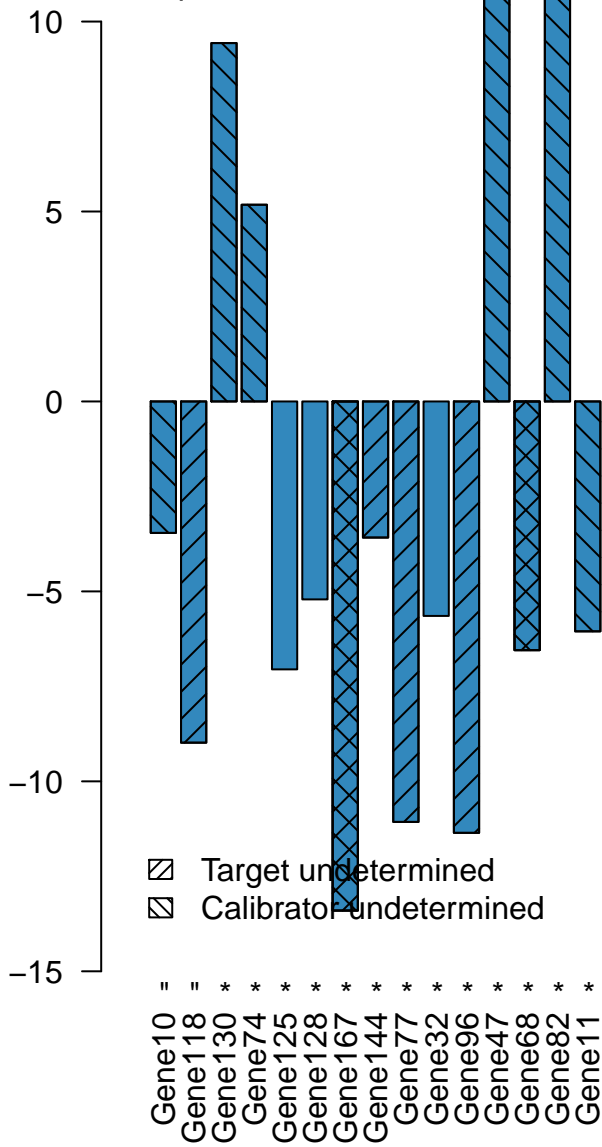




Relative quantification

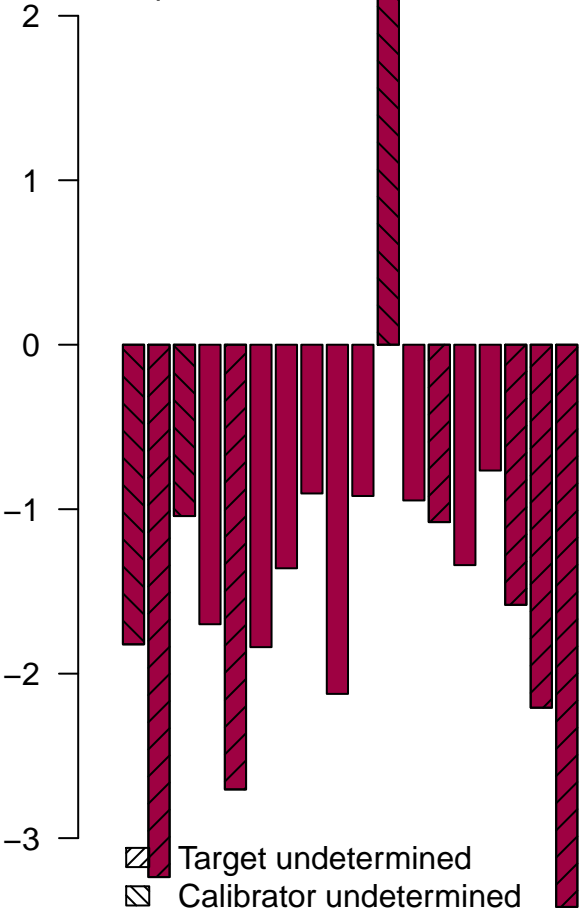
* p-value < 0.05

" p-value < 0.01



Comparison: LS-C

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



Target undetermined
Calibrator undetermined

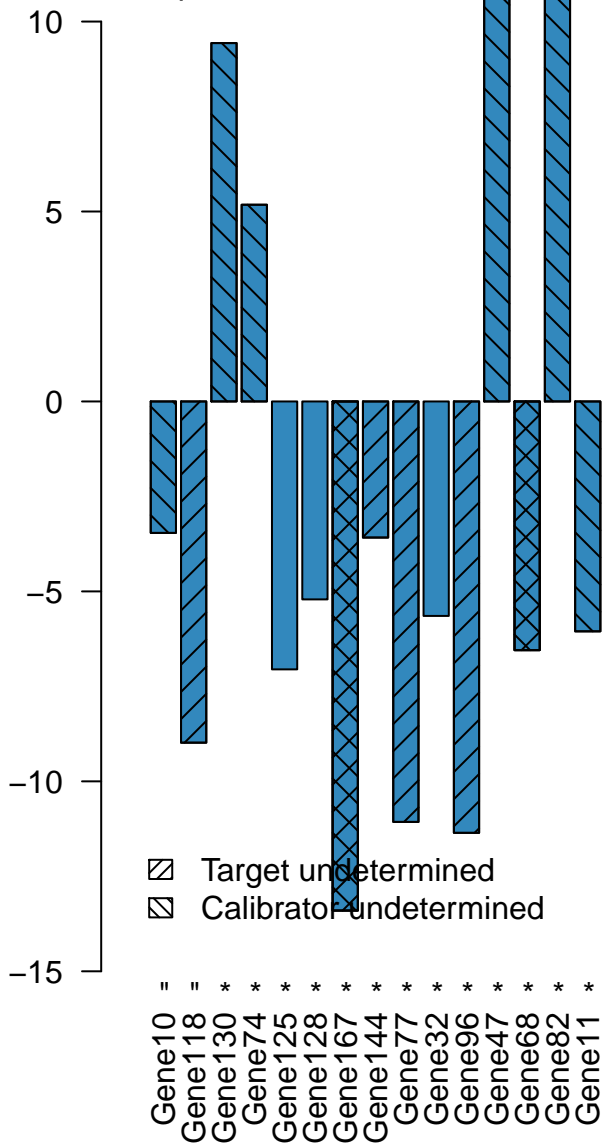
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Gene11
Gene142
Gene10
Gene32
Gene118
Gene45
Gene107
Gene188
Gene125
Gene66
Gene92
Gene120
Gene144
Gene152
Gene182
Gene43
Gene53
Gene96

Relative quantification

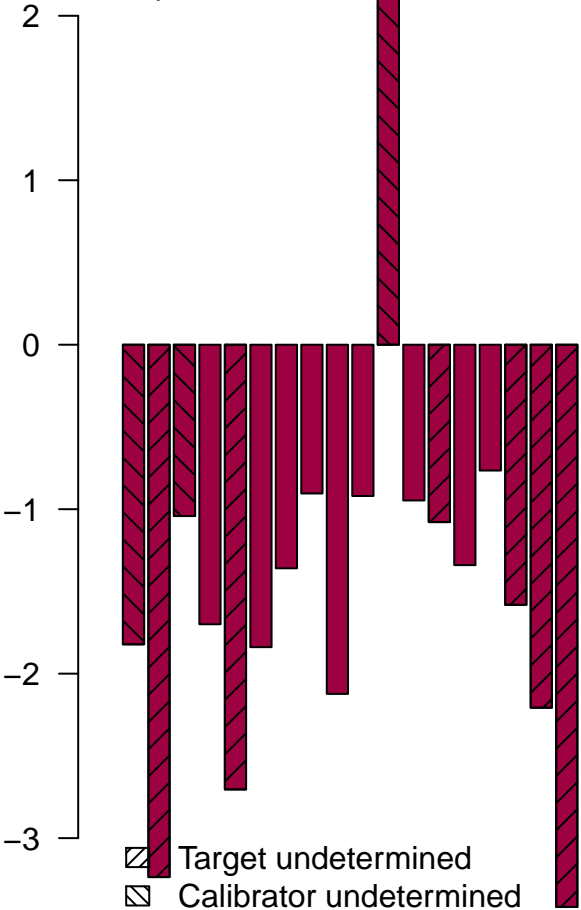
* p-value < 0.05

" p-value < 0.01



Comparison: LS-C

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

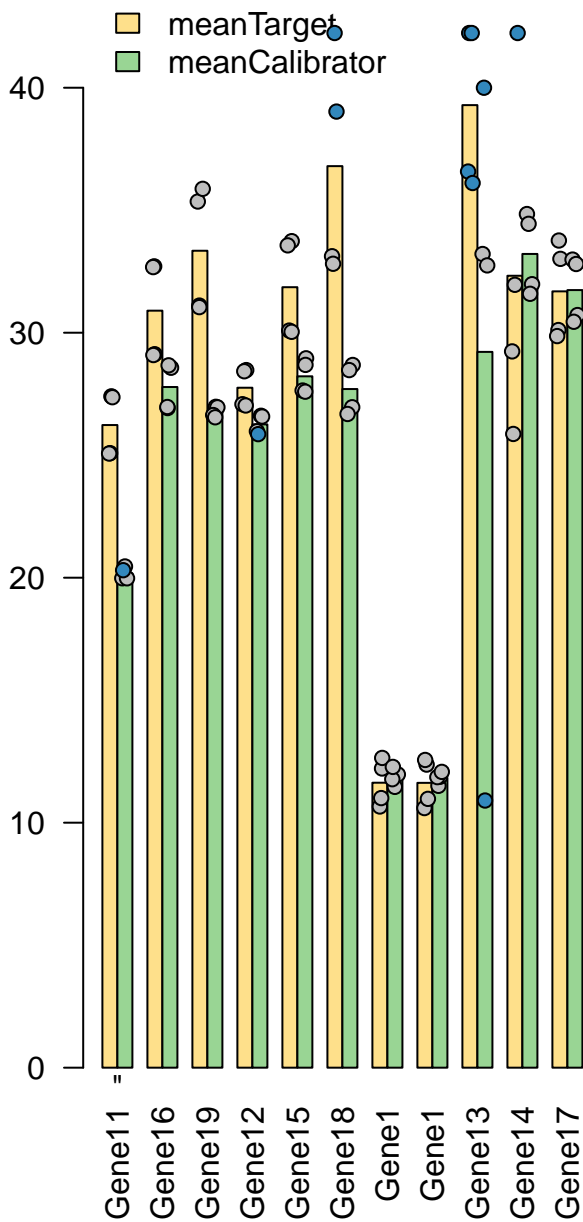


Target undetermined
Calibrator undetermined

= = * * *

Gene11
Gene142
Gene10
Gene32
Gene118
Gene45
Gene107
Gene188
Gene125
Gene66
Gene92
Gene120
Gene144
Gene152
Gene182
Gene43
Gene53
Gene96

Comparison: LS-C



Comparison: LS-C

