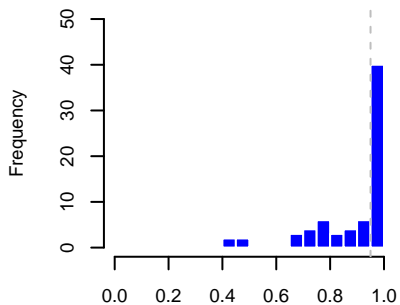
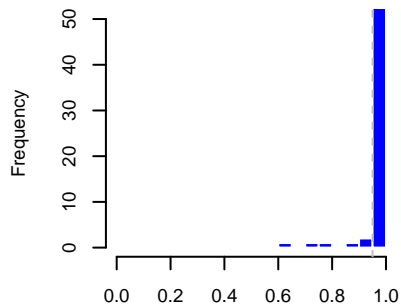
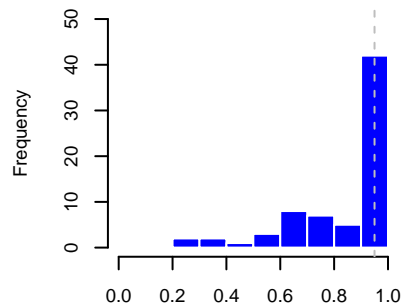


**F-score**

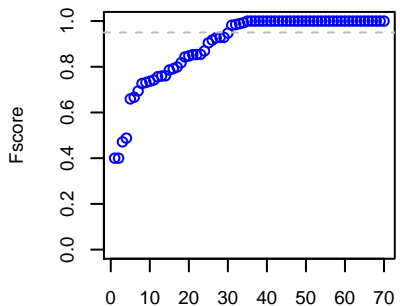
F-score  
av = 0.897 (inc = 0.989)

**Precision**

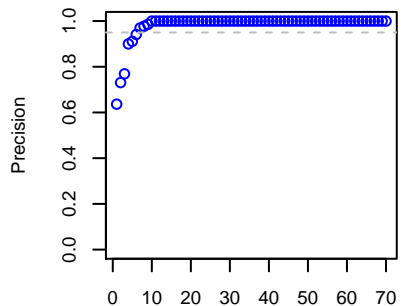
Precision  
av = 0.980 (inc = 0.981)

**Recall**

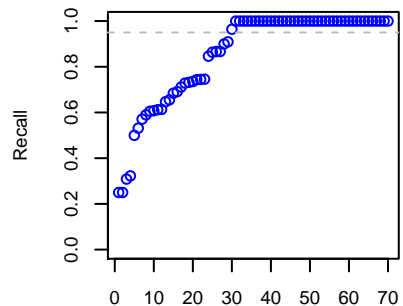
Recall  
av = 0.843 (inc = 0.999)

**Fscore**

Index  
n(>=.95) = 40

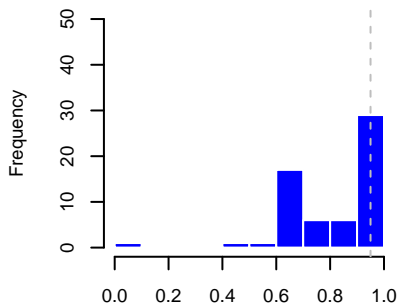
**Precision**

Index  
n(>=.95) = 64

**Recall**

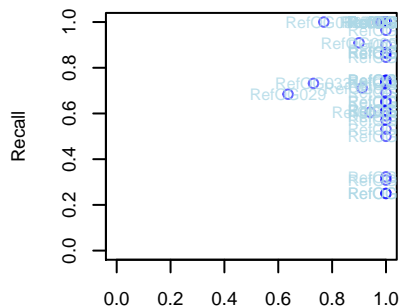
Index  
n(>=.95) = 41

## Rand index

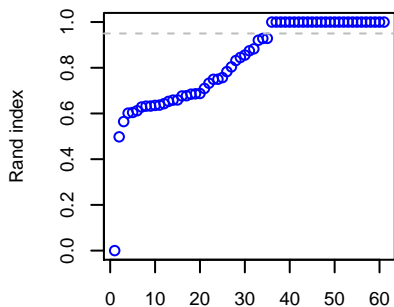


av = 0.785 (inc = 0.785) | med = 0.874

## Precision & recall

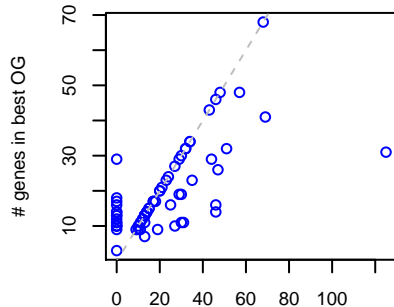


## Rand index



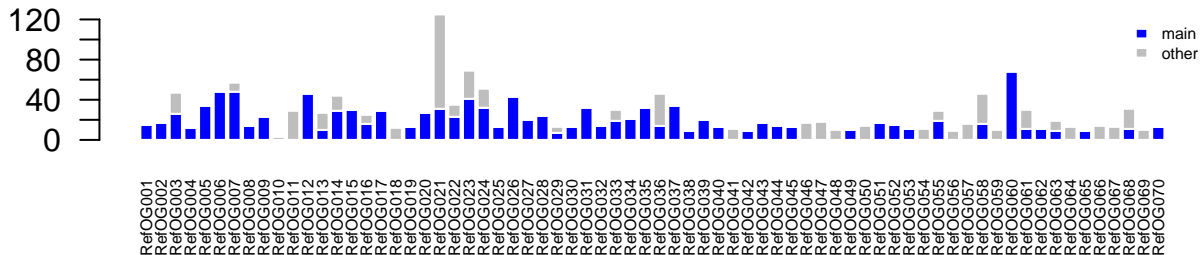
Index  
n(>=0.95) = NA

## size OGs



n(best = all) = 33 (p=0.991 | r=0.999)  
n(best < all) = 21 (p=0.958 | r=0.722)

## number of reference genes in main and other OGs



## num OGs per refOG

