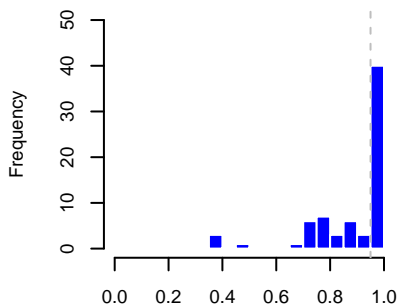
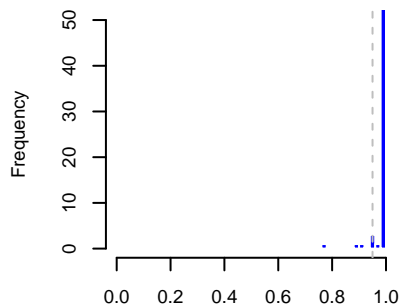
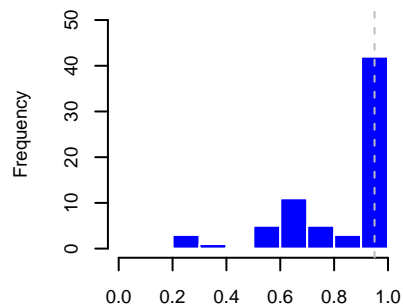


**F-score**

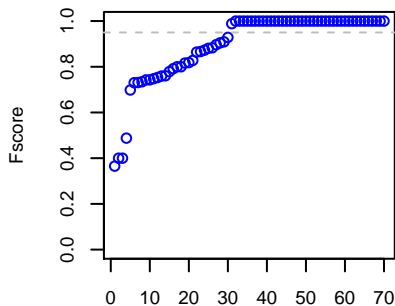
F-score  
av = 0.876 (inc = 0.994)

**Precision**

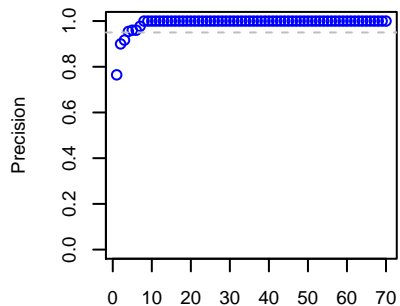
Precision  
av = 0.990 (inc = 0.991)

**Recall**

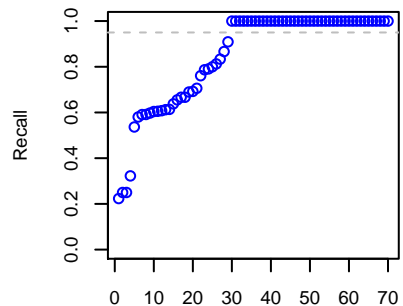
Recall  
av = 0.806 (inc = 0.997)

**Fscore**

Index  
n(>=.95) = 40

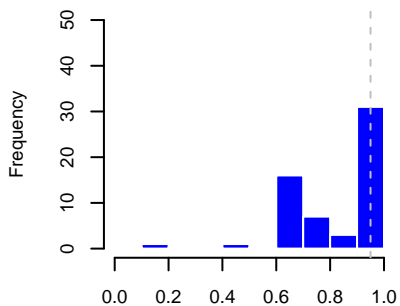
**Precision**

Index  
n(>=.95) = 67

**Recall**

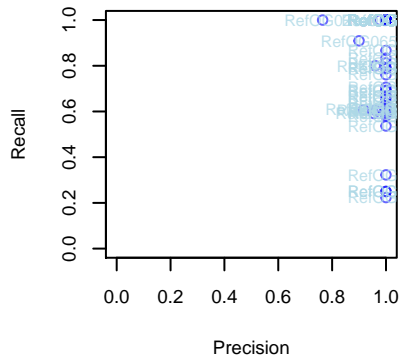
Index  
n(>=.95) = 41

## Rand index

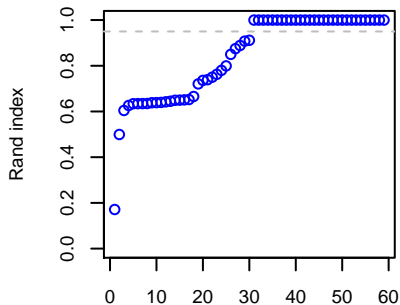


av = 0.833 (inc = 0.833) | med = 0.912

## Precision & recall

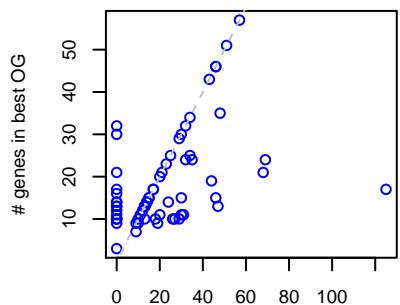


## Rand index



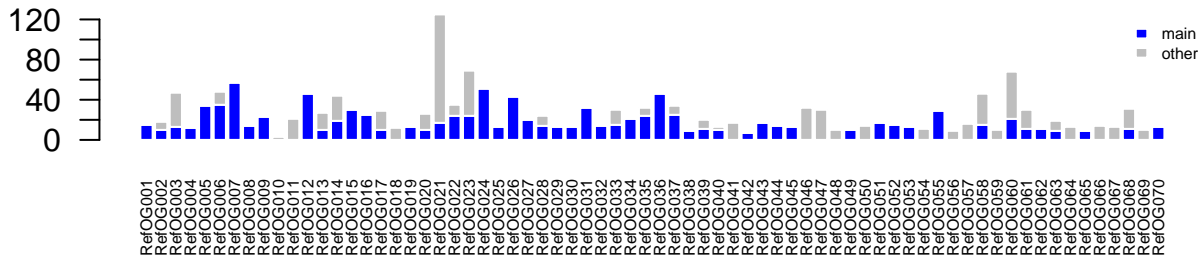
n(>=0.95) = NA

## size OGs



n(best = all) = 48 (p=0.990 | r=0.930)  
n(best = all) = 31 (p=0.992 | r=1.000)  
n(best < all) = 23 (p=0.987 | r=0.675)

## number of reference genes in main and other OGs



## num OGs per refOG

