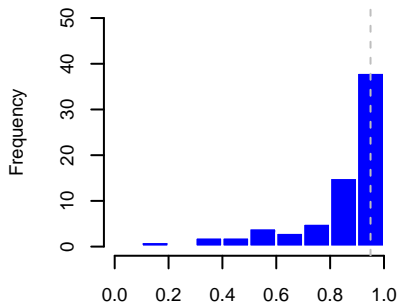
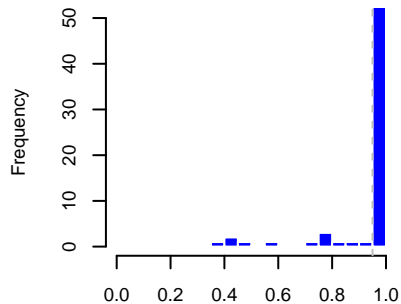
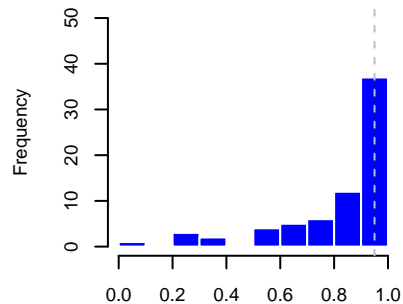


**F-score**

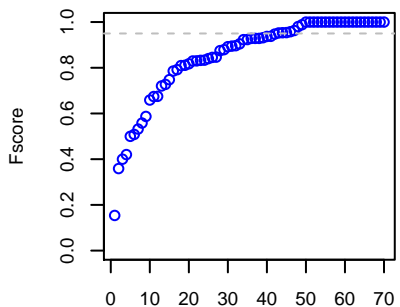
F-score  
av = 0.824 (inc = 0.893)

**Precision**

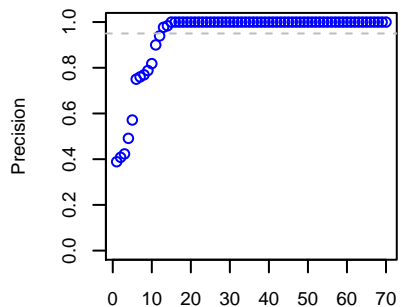
Precision  
av = 0.946 (inc = 0.946)

**Recall**

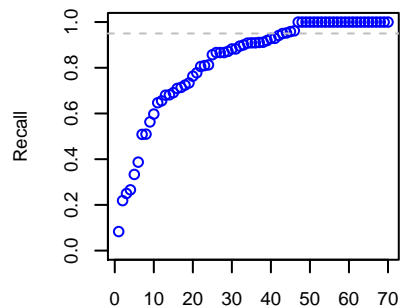
Recall  
av = 0.785 (inc = 0.903)

**Fscore**

Index  
n(>=.95) = 28

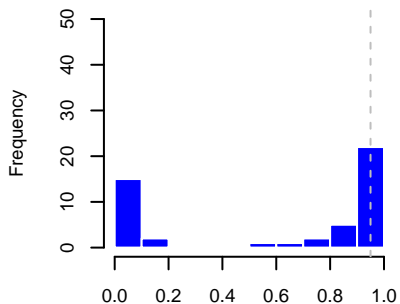
**Precision**

Index  
n(>=.95) = 58

**Recall**

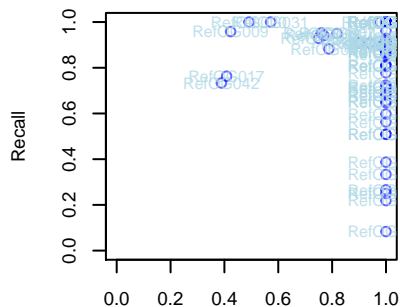
Index  
n(>=.95) = 28

# Rand index

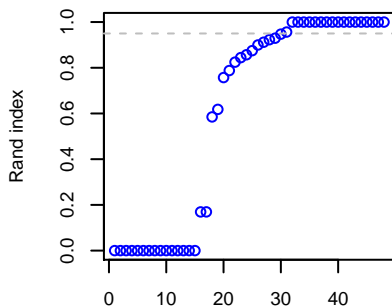


av = NaN (inc = NaN) | med = 0.866

# Precision & recall

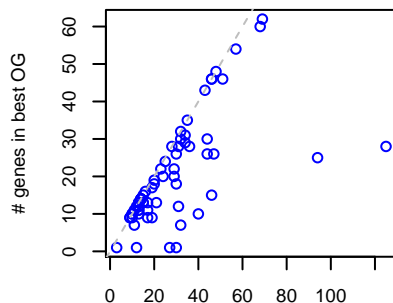


# Rand index



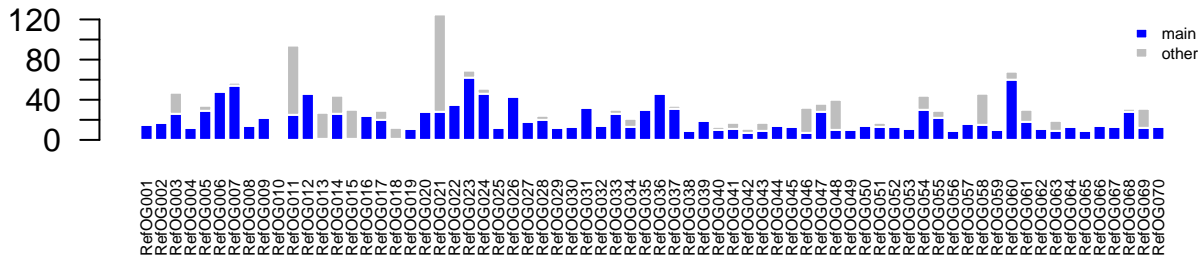
n(>=0.95) = NA

# size OGs



n(best = all) = 26 (p=0.977)  
 n(best = all) = 24 (p=0.960 | r=1.000)  
 n(best < all) = 46 (p=0.933 | r=0.737)

## number of reference genes in main and other OGs



## num OGs per refOG

