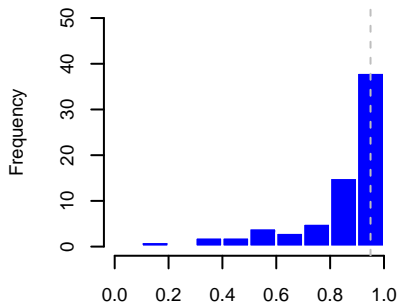
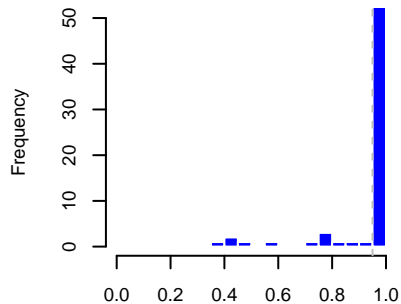
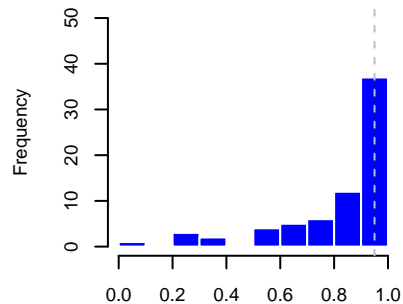


**F-score**

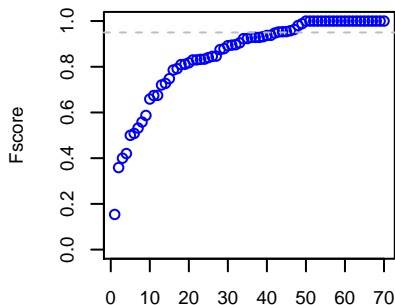
F-score  
av = 0.886 (inc = 0.974)

**Precision**

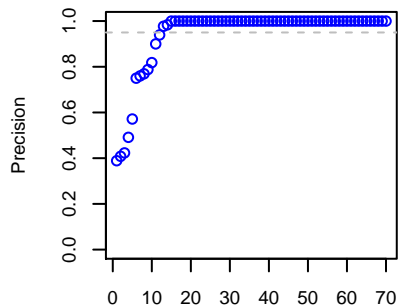
Precision  
av = 0.958 (inc = 0.956)

**Recall**

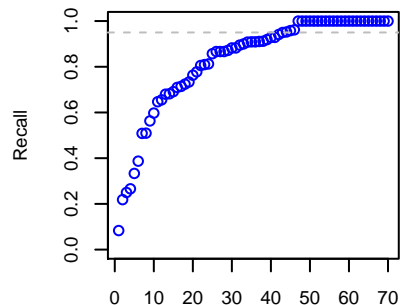
Recall  
av = 0.847 (inc = 0.999)

**Fscore**

Index  
n(>=.95) = 28

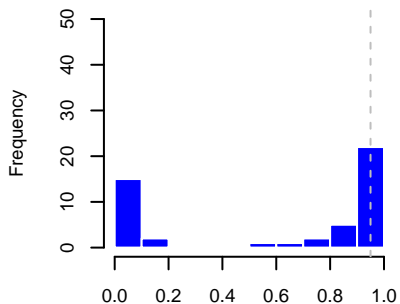
**Precision**

Index  
n(>=.95) = 58

**Recall**

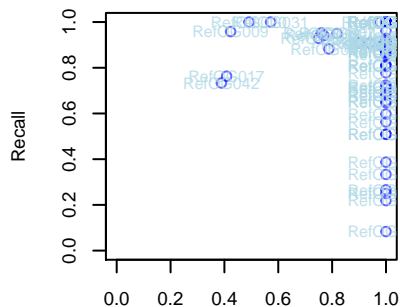
Index  
n(>=.95) = 28

# Rand index

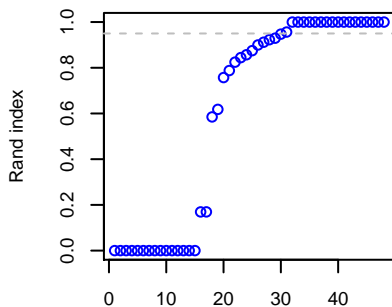


av = NaN (inc = NaN) | med = 0.866

# Precision & recall

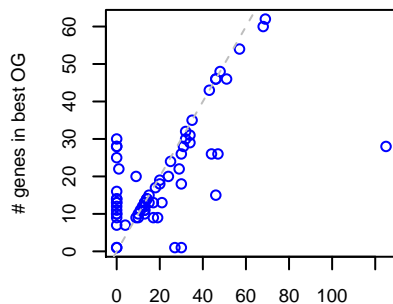


# Rand index



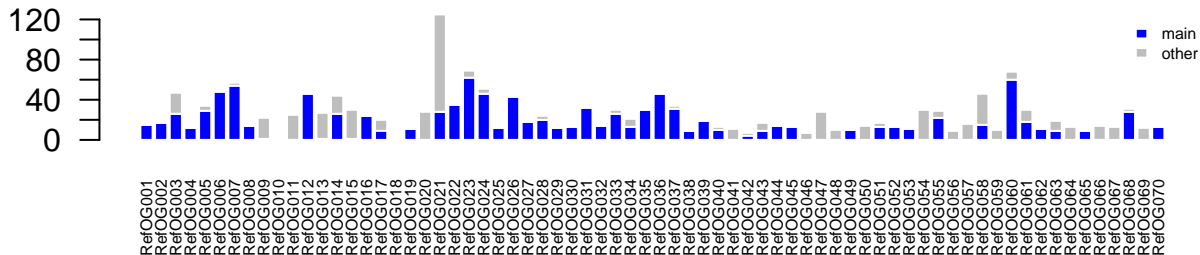
n(>=0.95) = NA

# size OGs



n(best = all) = 17 (p=0.973 | r=1.000)  
n(best < all) = 33 (p=0.961 | r=0.816)

## number of reference genes in main and other OGs



## num OGs per refOG

