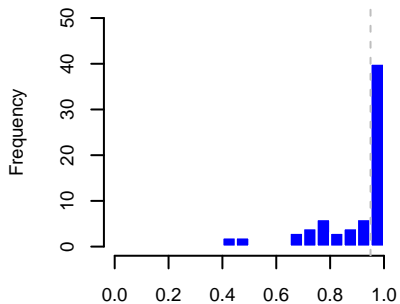
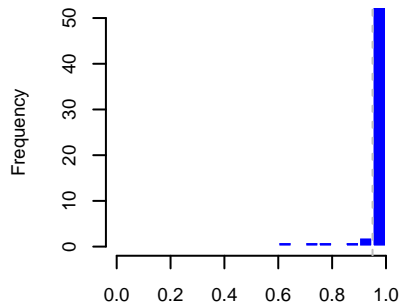
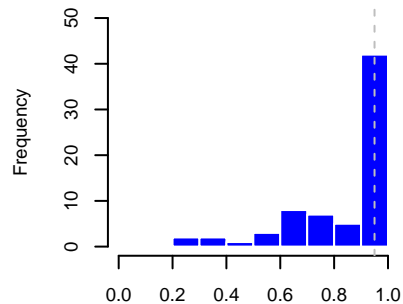


**F-score**

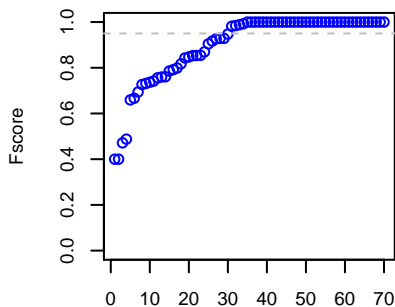
F-score  
av = 0.844 (inc = 0.918)

**Precision**

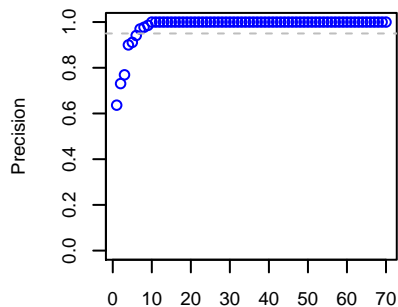
Precision  
av = 0.984 (inc = 0.985)

**Recall**

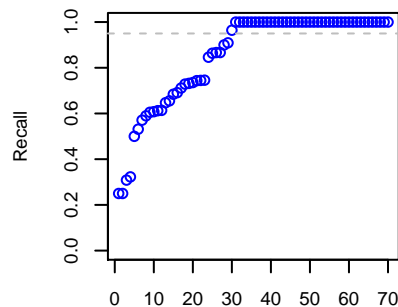
Recall  
av = 0.777 (inc = 0.901)

**Fscore**

Index  
n(>=.95) = 40

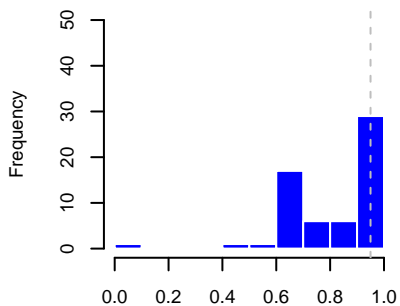
**Precision**

Index  
n(>=.95) = 64

**Recall**

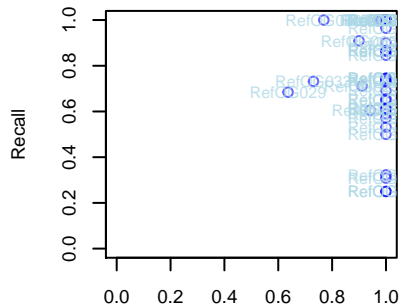
Index  
n(>=.95) = 41

### Rand index



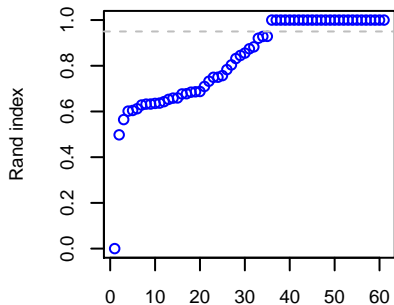
Rand index  
av = NaN (inc = NaN) | med = 0.874

### Precision & recall



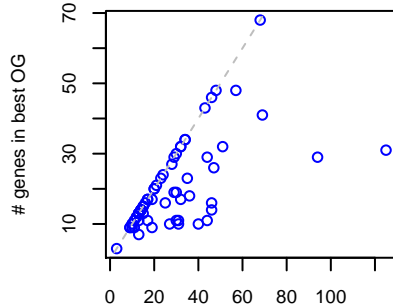
Precision

### Rand index



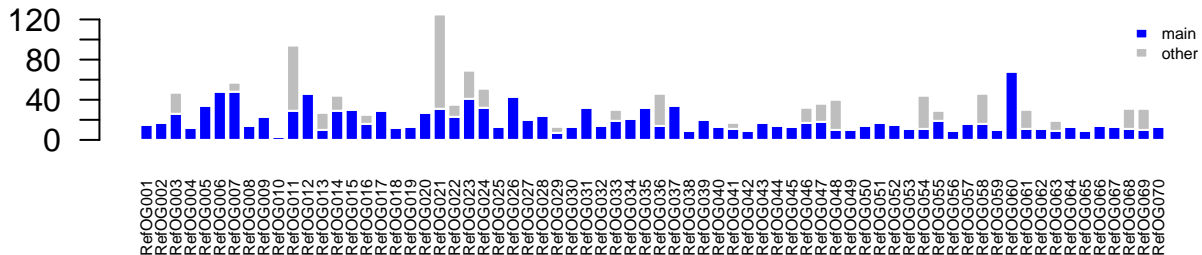
Index  
n(>=0.95) = NA

### size OGs



# genes in best OG  
n(best = all) = 40 (p=0.993 | r=1.000)  
n(best < all) = 30 (p=0.971 | r=0.660)

## number of reference genes in main and other OGs



## num OGs per refOG

