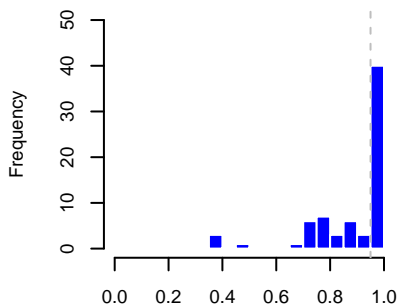
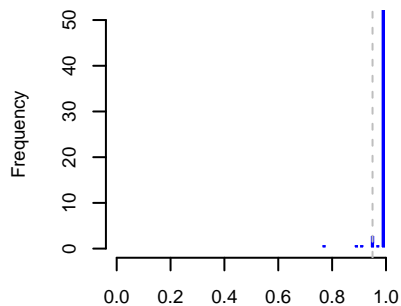
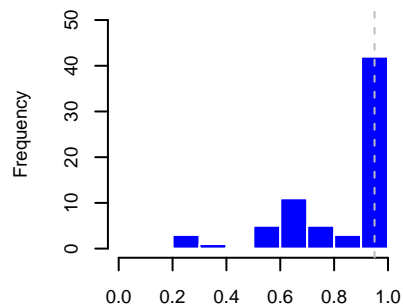


F-score

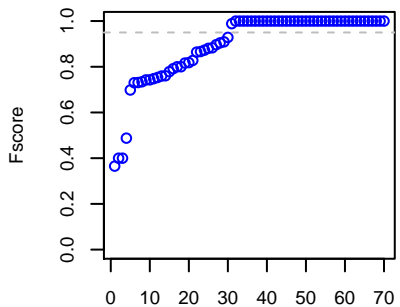
F-score
av = 0.834 (inc = 0.928)

Precision

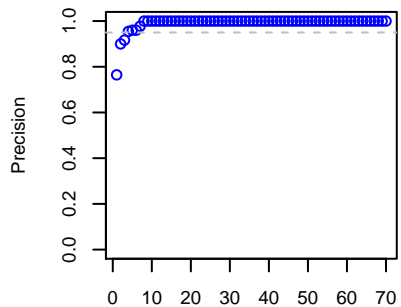
Precision
av = 0.992 (inc = 0.993)

Recall

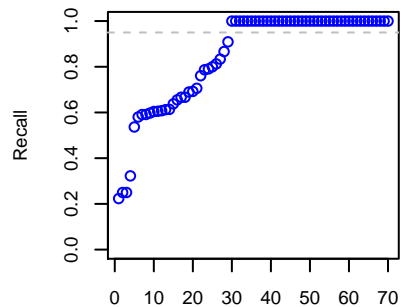
Recall
av = 0.760 (inc = 0.912)

Fscore

Index
n(>=.95) = 40

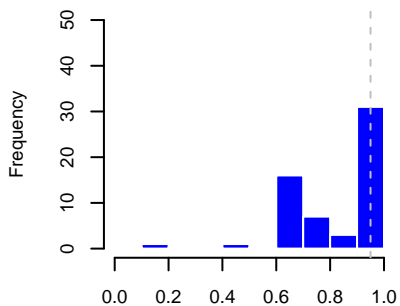
Precision

Index
n(>=.95) = 67

Recall

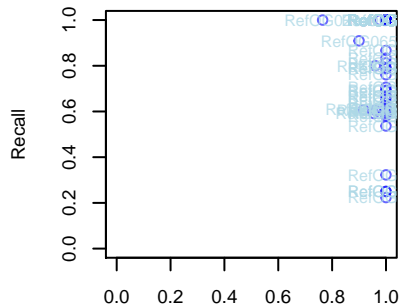
Index
n(>=.95) = 41

Rand index



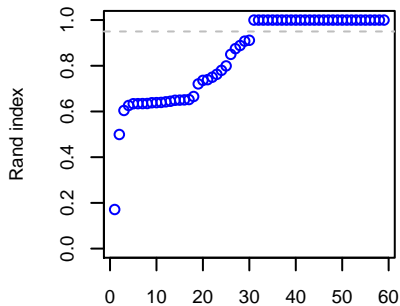
av = NaN (inc = NaN) | med = 0.912

Precision & recall



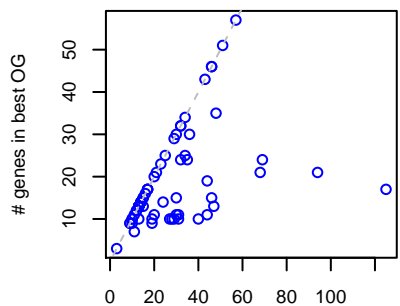
Precision

Rand index



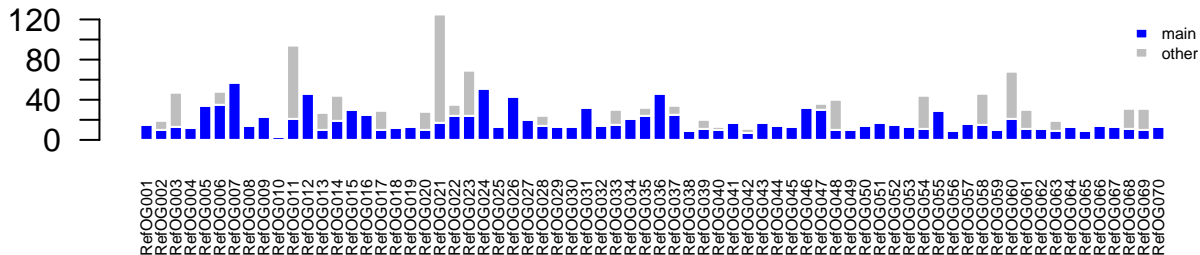
Index
n(>=0.95) = NA

size OGs



n(best < all) = 42 (p=0.998)
n(best = all) = 41 (p=0.994 | r=1.000)
n(best > all) = 29 (p=0.989 | r=0.630)

number of reference genes in main and other OGs



num OGs per refOG

