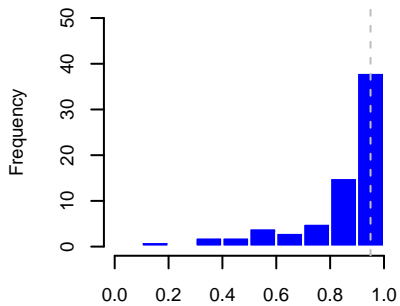
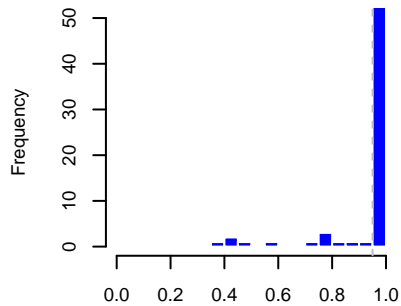
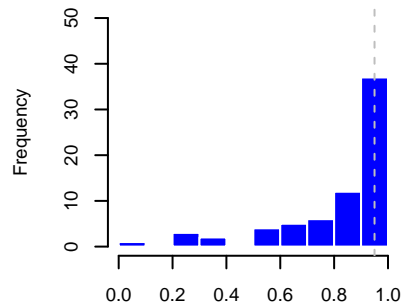


F-score

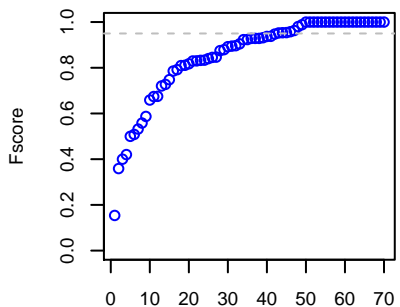
F-score
av = 0.886 (inc = 0.974)

Precision

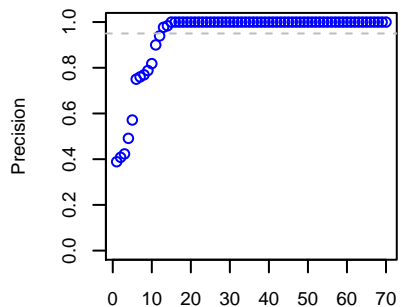
Precision
av = 0.958 (inc = 0.956)

Recall

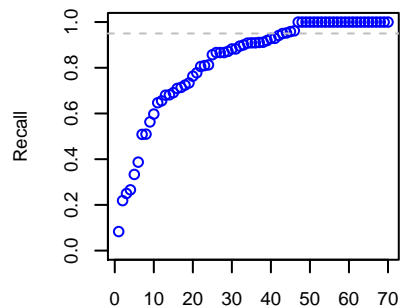
Recall
av = 0.847 (inc = 0.999)

Fscore

Index
n(>=.95) = 28

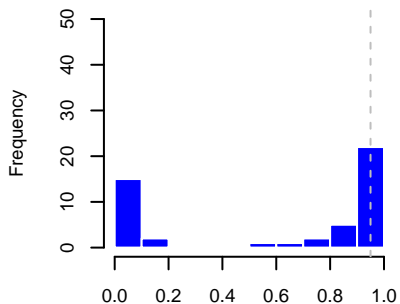
Precision

Index
n(>=.95) = 58

Recall

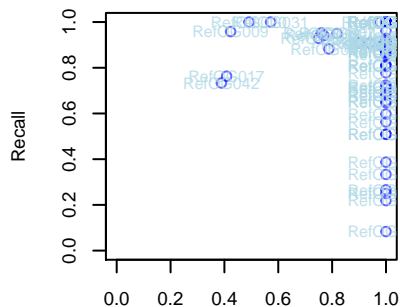
Index
n(>=.95) = 28

Rand index

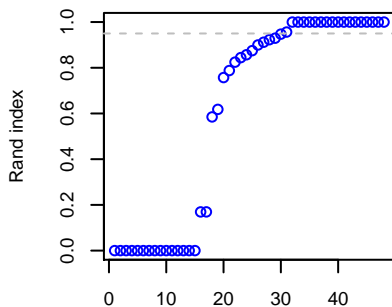


av = NaN (inc = NaN) | med = 0.866

Precision & recall

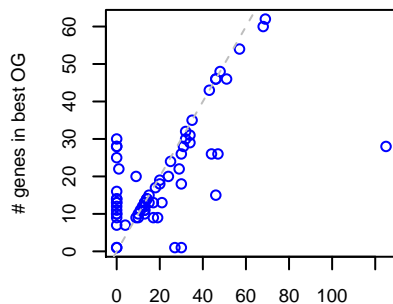


Rand index



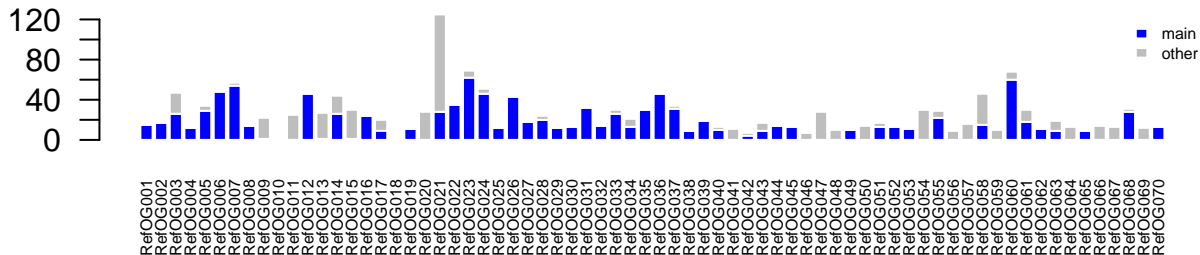
n(>=0.95) = NA

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

