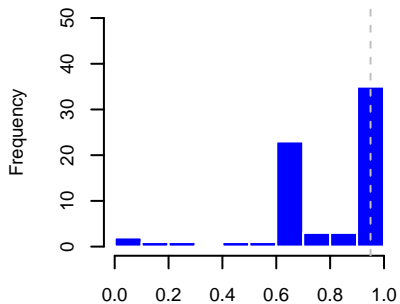
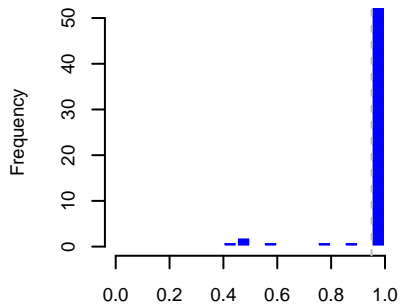
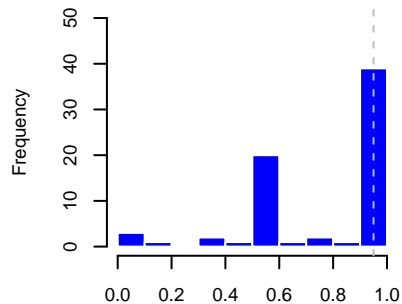


F-score

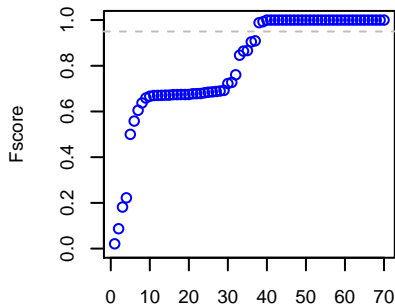
F-score
av = 0.837 (inc = 0.991)

Precision

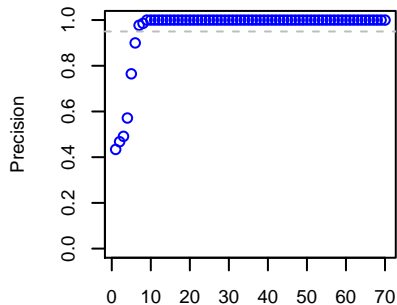
Precision
av = 0.986 (inc = 0.986)

Recall

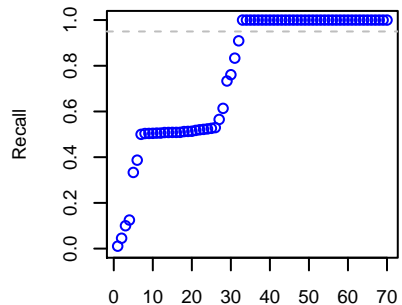
Recall
av = 0.765 (inc = 0.999)

Fscore

Index
n(>=.95) = 33

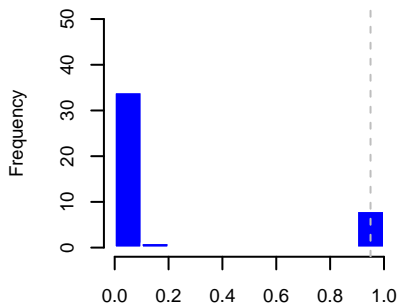
Precision

Index
n(>=.95) = 64

Recall

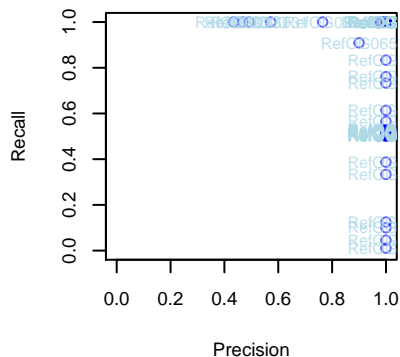
Index
n(>=.95) = 38

Rand index

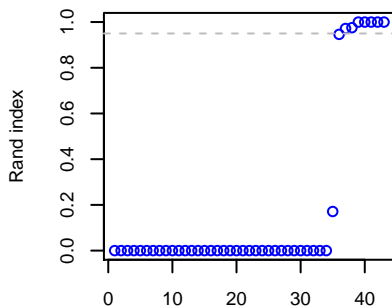


av = NaN (inc = NaN) | med = 0.000

Precision & recall

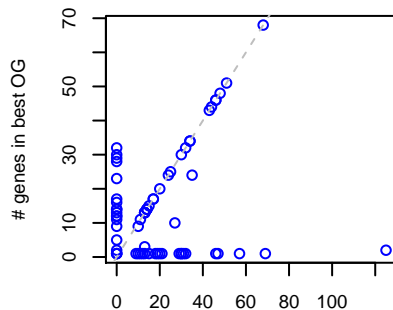


Rand index



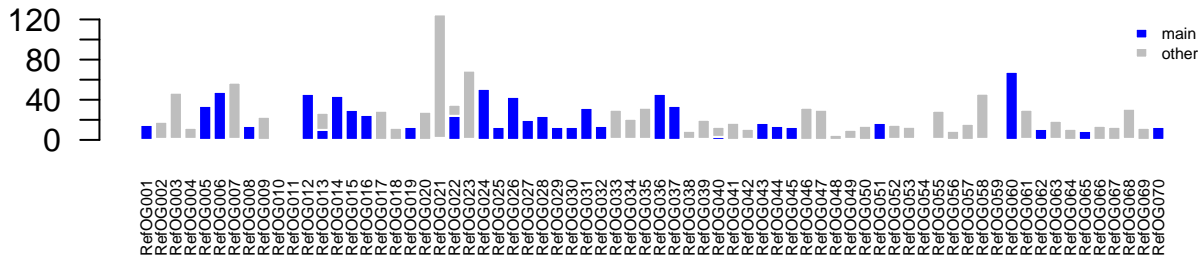
Index
n(>=0.95) = NA

size OGs



n(best < all) = 17 (p=0.882)
n(best = all) = 27 (p=0.974 | r=1.000)
n(best > all) = 24 (p=0.996 | r=0.545)

number of reference genes in main and other OGs



num OGs per refOG

