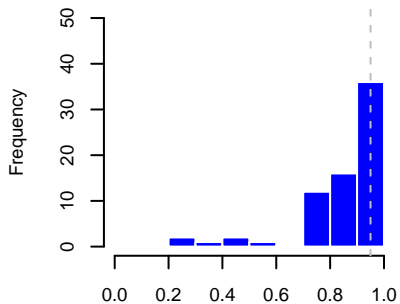
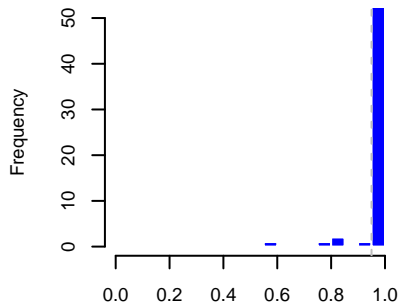
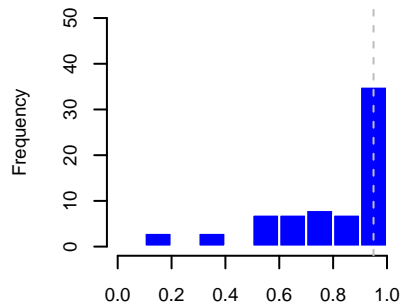


F-score

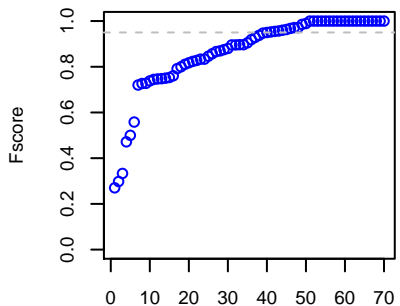
F-score
av = 0.824 (inc = 0.903)

Precision

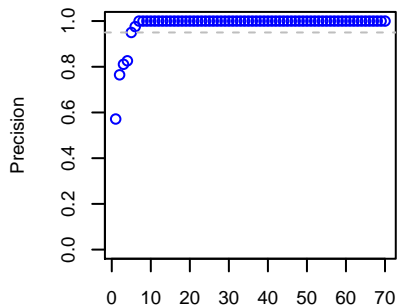
Precision
av = 0.981 (inc = 0.980)

Recall

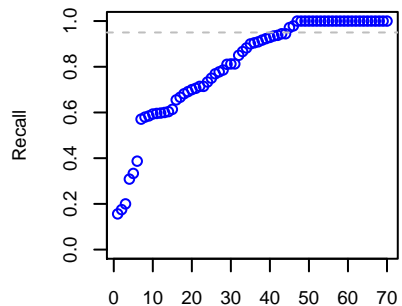
Recall
av = 0.756 (inc = 0.887)

Fscore

Index
n(>=.95) = 31

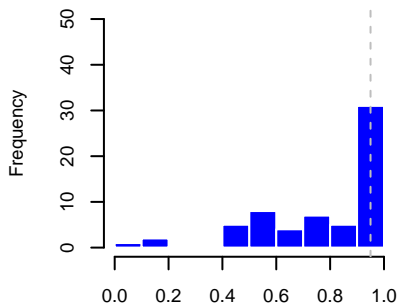
Precision

Index
n(>=.95) = 66

Recall

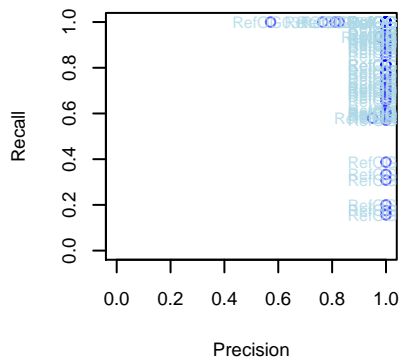
Index
n(>=.95) = 26

Rand index

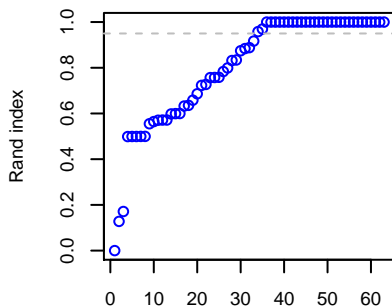


av = NaN (inc = NaN) | med = 0.888

Precision & recall

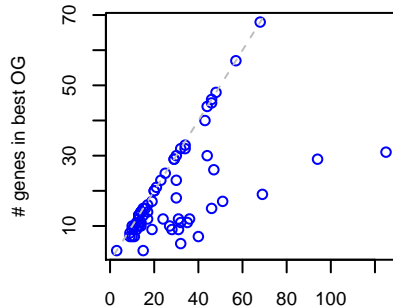


Rand index



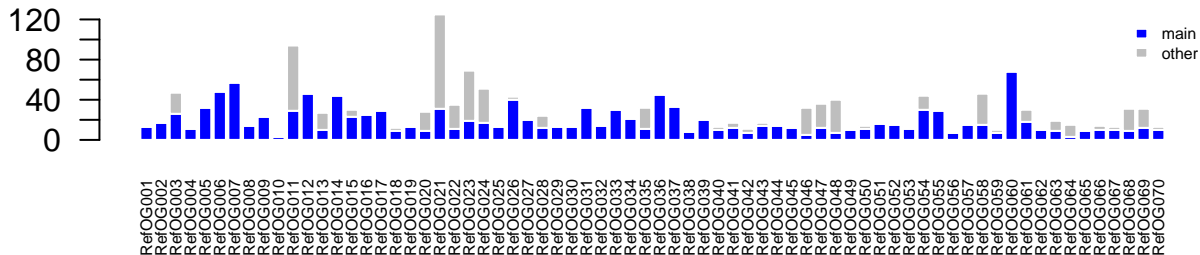
n(>=0.95) = NA

size OGs



n(best = all) = 24 (p=0.957 | r=1.000)
n(best < all) = 46 (p=0.998 | r=0.706)

number of reference genes in main and other OGs



num OGs per refOG

