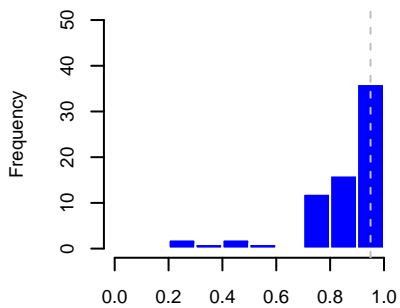
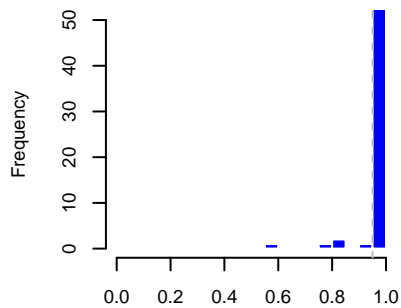
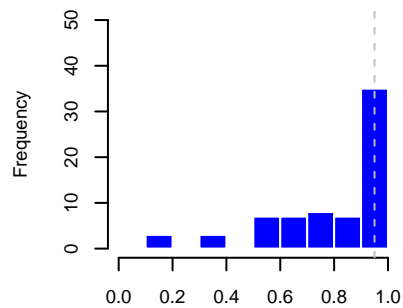


F-score

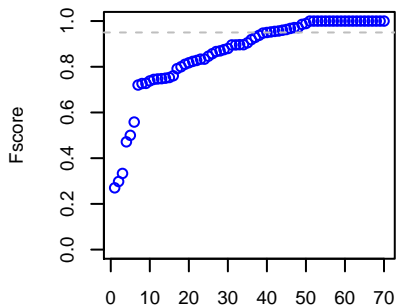
F-score
av = 0.885 (inc = 0.985)

Precision

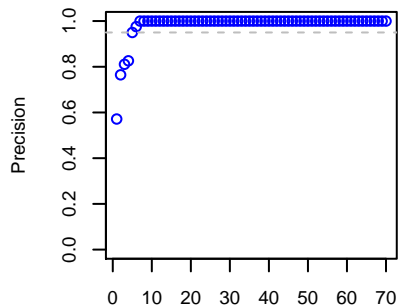
Precision
av = 0.976 (inc = 0.975)

Recall

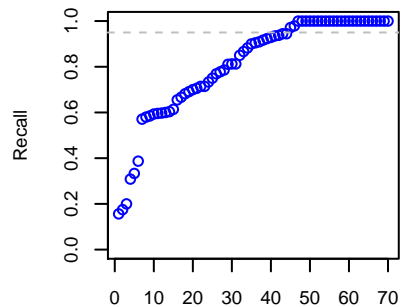
Recall
av = 0.834 (inc = 1.000)

Fscore

Index
n(>=.95) = 31

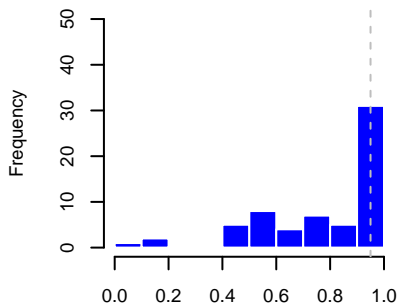
Precision

Index
n(>=.95) = 66

Recall

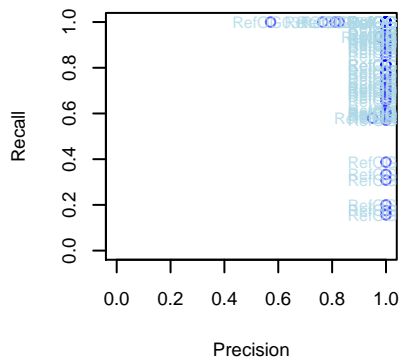
Index
n(>=.95) = 26

Rand index

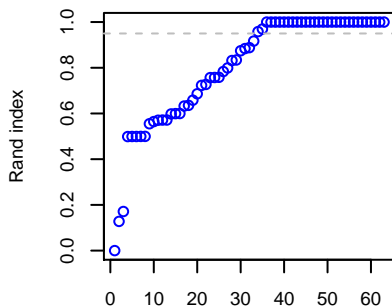


av = NaN (inc = NaN) | med = 0.888

Precision & recall

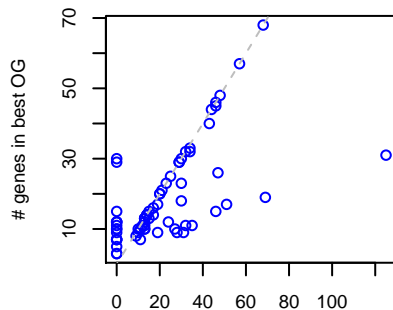


Rand index



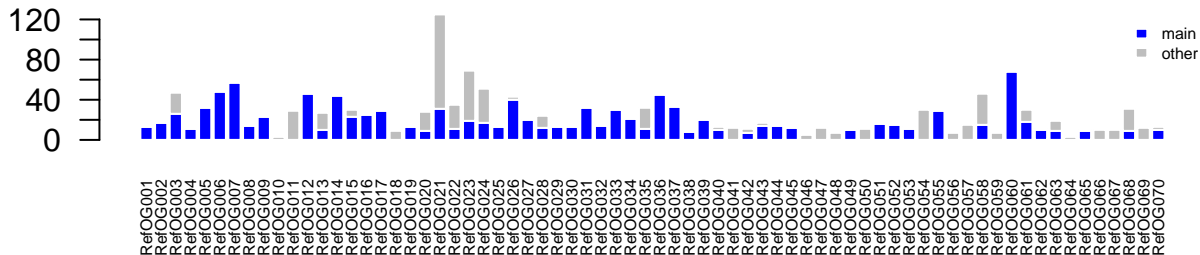
Index
n(>=0.95) = NA

size OGs



genes in best OG
n(best = all) = 23 (p=0.955 | r=1.000)
n(best < all) = 31 (p=0.998 | r=0.777)

number of reference genes in main and other OGs



num OGs per refOG

