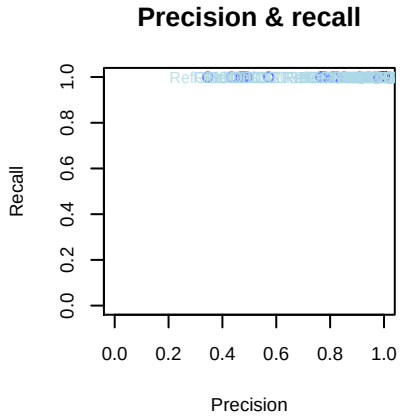
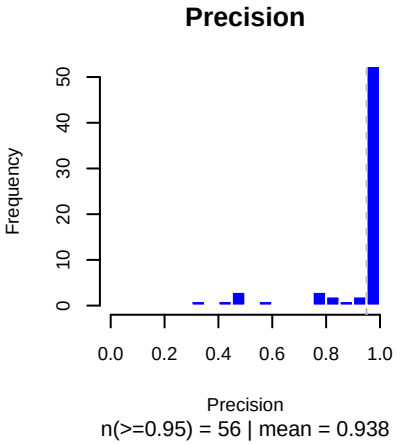
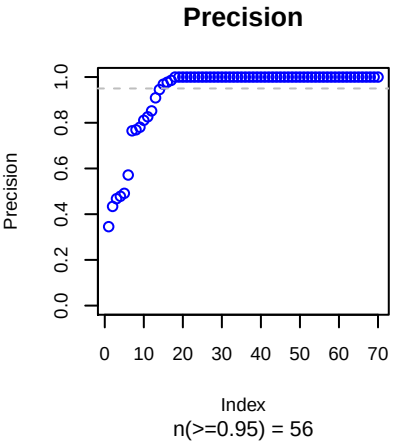
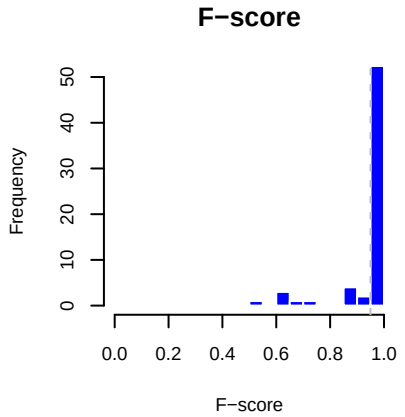
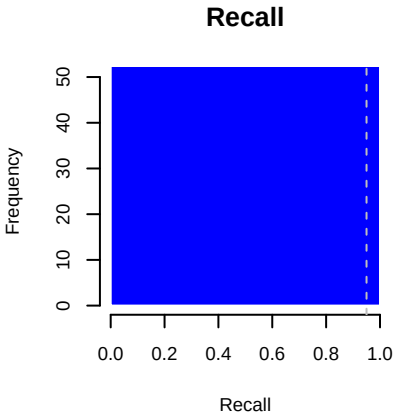
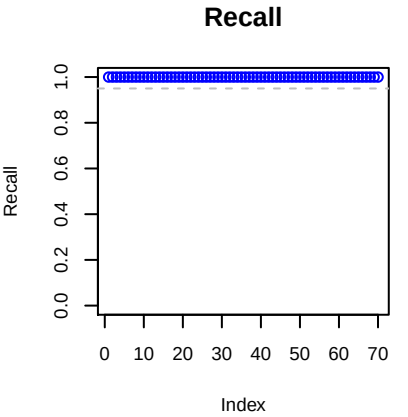

Precision & recall
Recall
Precision
0.0
0.2
0.4
0.6
0.8
1.0

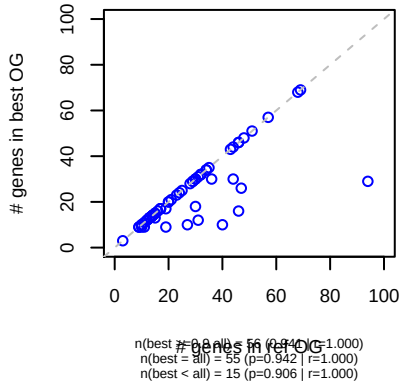

Precision
Frequency
Precision
0
10
20
30
40
50
0.0
0.2
0.4
0.6
0.8
1.0
n(>=0.95) = 56 | mean = 0.938

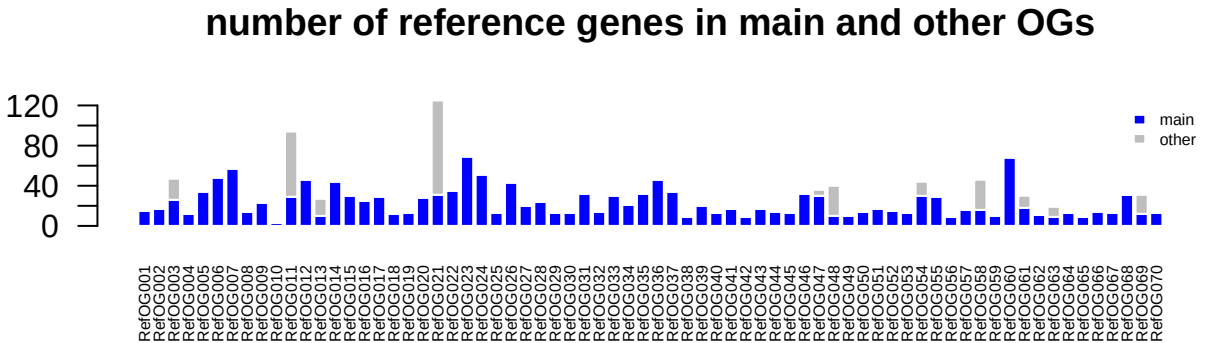

Precision
Precision
Index
0
10
20
30
40
50
60
70
n(>=0.95) = 56

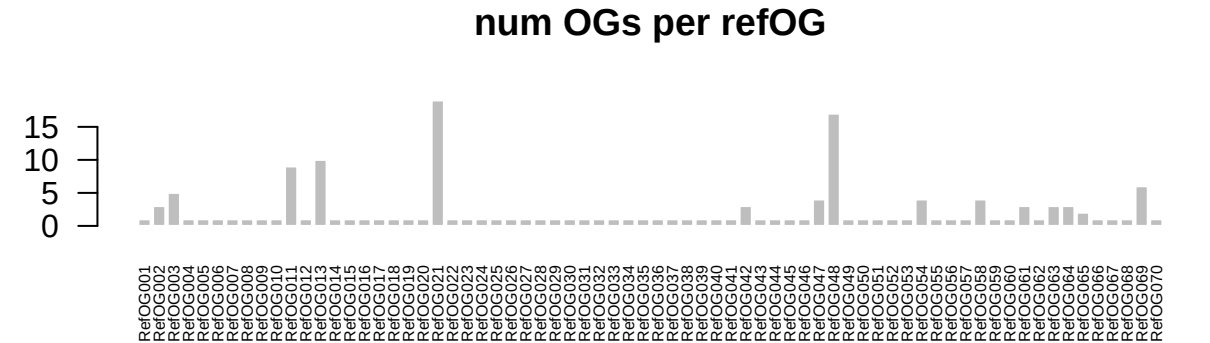

F−score
Frequency
F−score
n(>=0.95) = 58 | mean = 0.961


Recall
Frequency
Recall
n(>=0.95) = 70 | mean = 1.000


Recall
Recall
Index
n(>=0.95) = 70


genes in best OG
0
20
40
60
80
100
0
20
40
60
80
100
# genes in ref OG
n(best = all) = 55 (p=0.942 | r=1.000)
n(best < all) = 15 (p=0.906 | r=1.000)


number of reference genes in main and other OGs
120
80
40
0
main
other
RefOG001
RefOG002
RefOG003
RefOG004
RefOG005
RefOG006
RefOG007
RefOG008
RefOG009
RefOG010
RefOG011
RefOG012
RefOG013
RefOG014
RefOG015
RefOG016
RefOG017
RefOG018
RefOG019
RefOG020
RefOG021
RefOG022
RefOG023
RefOG024
RefOG025
RefOG026
RefOG027
RefOG028
RefOG029
RefOG030
RefOG031
RefOG032
RefOG033
RefOG034
RefOG035
RefOG036
RefOG037
RefOG038
RefOG039
RefOG040
RefOG041
RefOG042
RefOG043
RefOG044
RefOG045
RefOG046
RefOG047
RefOG048
RefOG049
RefOG050
RefOG051
RefOG052
RefOG053
RefOG054
RefOG055
RefOG056
RefOG057
RefOG058
RefOG059
RefOG060
RefOG061
RefOG062
RefOG063
RefOG064
RefOG065
RefOG066
RefOG067
RefOG068
RefOG069
RefOG070


num OGs per refOG
15
10
5
0
RefOG001
RefOG002
RefOG003
RefOG004
RefOG005
RefOG006
RefOG007
RefOG008
RefOG009
RefOG010
RefOG011
RefOG012
RefOG013
RefOG014
RefOG015
RefOG016
RefOG017
RefOG018
RefOG019
RefOG020
RefOG021
RefOG022
RefOG023
RefOG024
RefOG025
RefOG026
RefOG027
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