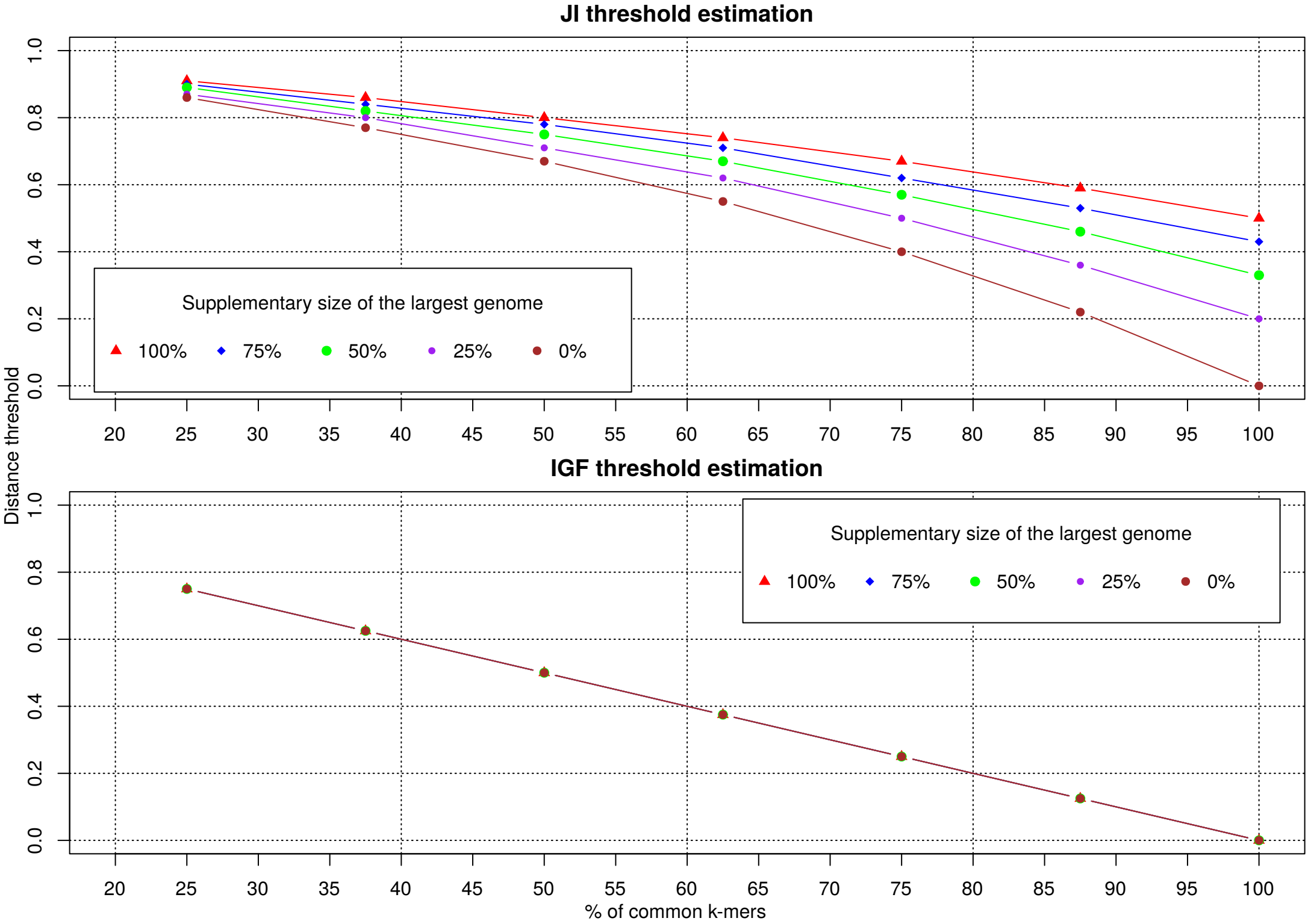
JI threshold estimation
Distance threshold
0.0
0.2
0.4
0.6
0.8
1.0
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
Supplementary size of the largest genome
100%
75%
50%
25%
0%
IGF threshold estimation
Distance threshold
0.0
0.2
0.4
0.6
0.8
1.0
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
% of common k-mers
Supplementary size of the largest genome
100%
75%
50%
25%
0%