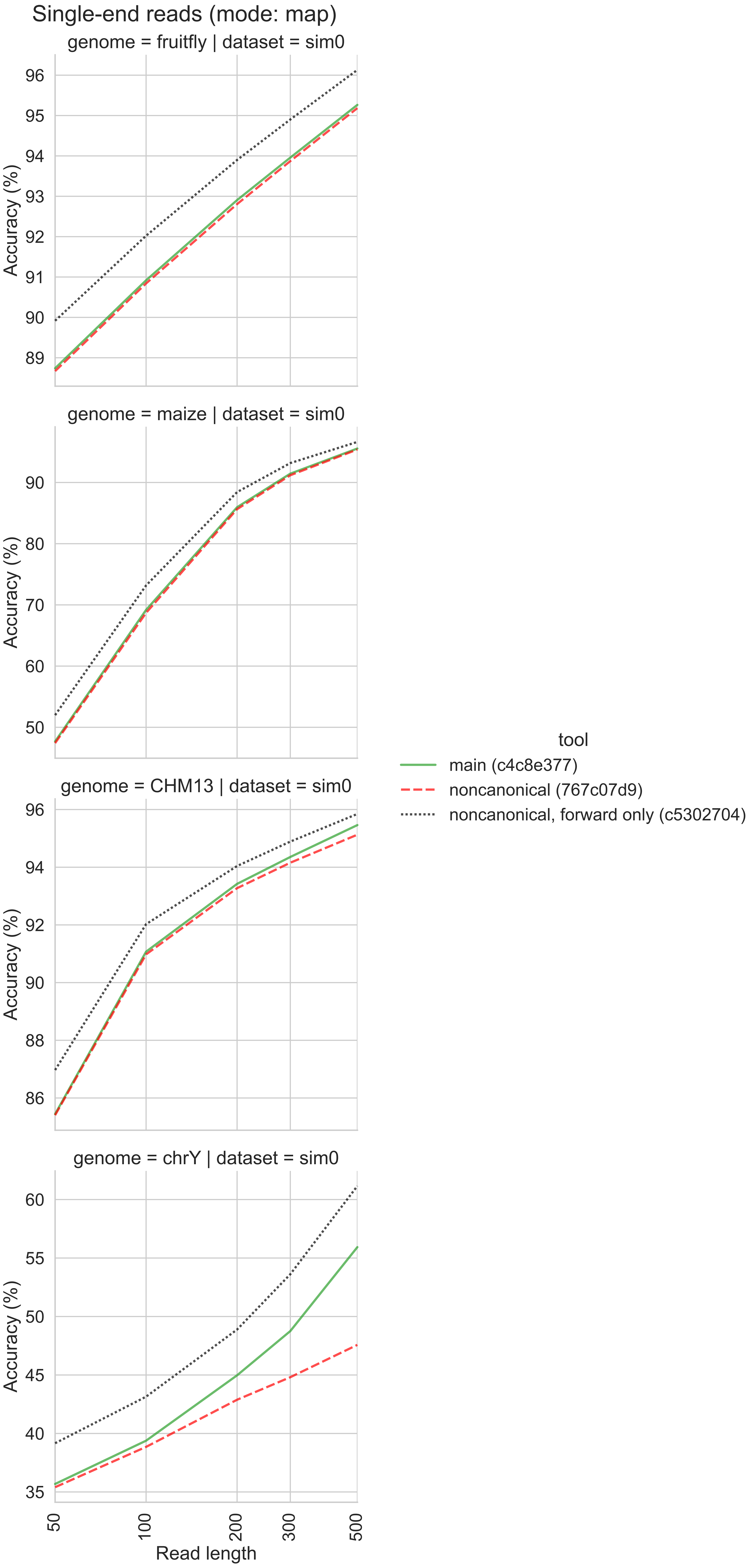
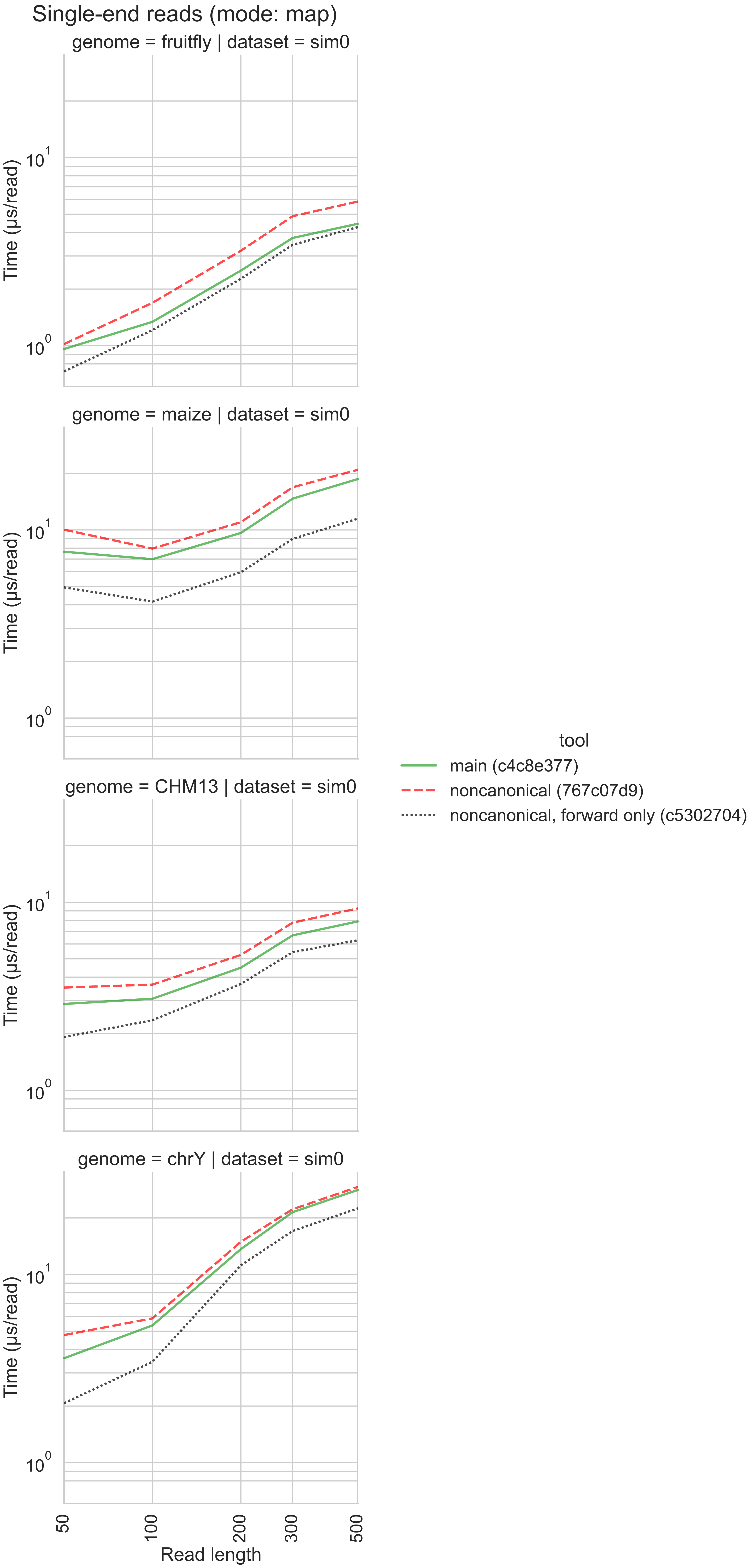

Single-end reads (mode: map)
genome = fruitfly | dataset = sim0
genome = maize | dataset = sim0
genome = CHM13 | dataset = sim0
genome = chrY | dataset = sim0
Accuracy (%)
89
90
91
92
93
94
95
96
50
60
70
80
90
86
88
90
92
94
96
35
40
45
50
55
60
Read length
50
100
200
300
500
tool
main (c4c8e377)
noncanonical (767c07d9)
noncanonical, forward only (c5302704)


Single-end reads (mode: map)
genome = fruitfly | dataset = sim0
genome = maize | dataset = sim0
genome = CHM13 | dataset = sim0
genome = chrY | dataset = sim0
Time (µs/read)
10^1
10^0
50
100
200
300
500
Read length
tool
main (c4c8e377)
noncanonical (767c07d9)
noncanonical, forward only (c5302704)