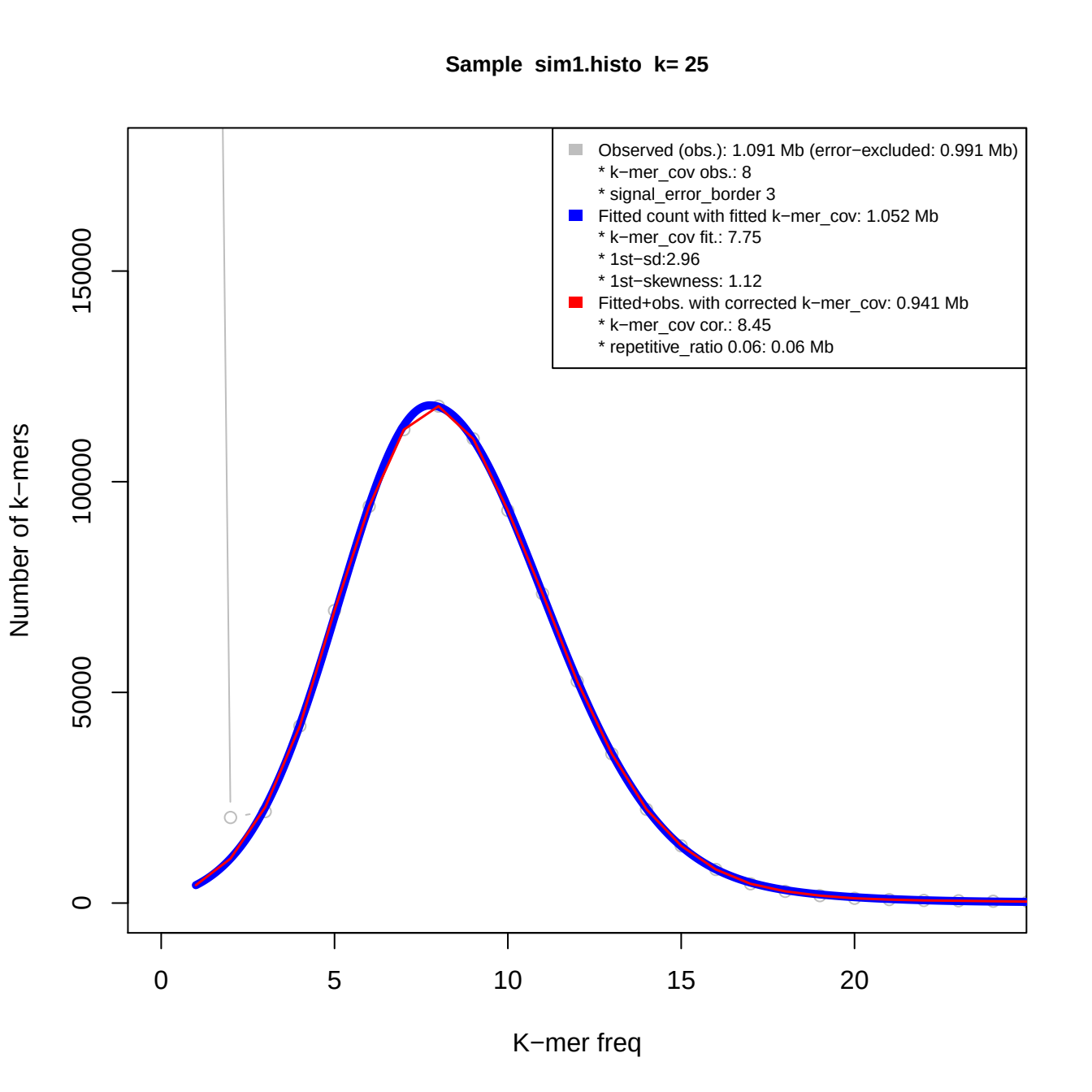
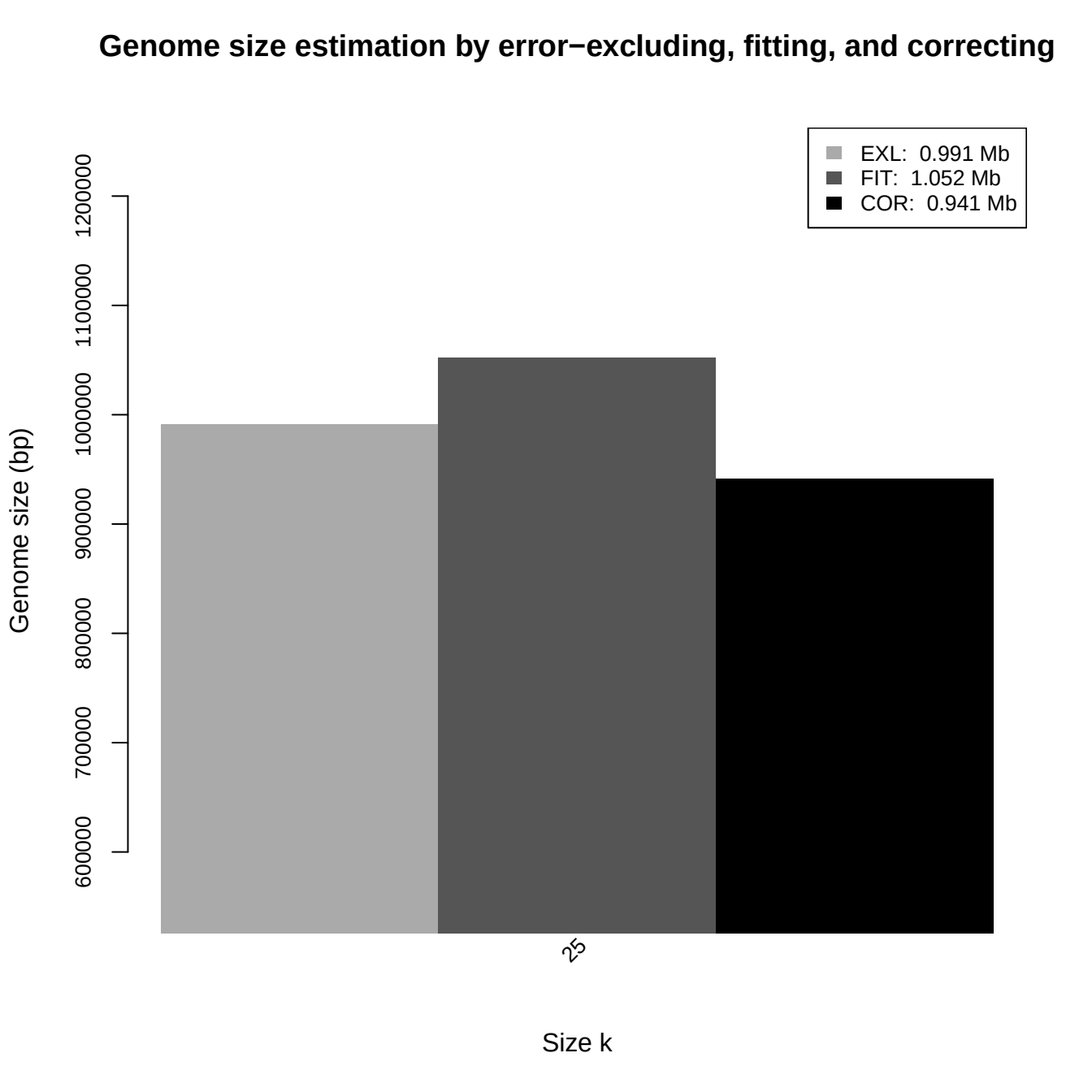

Sample sim1.histo k= 25
Observed (obs.): 1.091 Mb (error−excluded: 0.991 Mb)
* k−mer_cov obs.: 8
* signal_error_border 3
Fitted count with fitted k−mer_cov: 1.052 Mb
* k−mer_cov fit.: 7.75
* 1st−sd:2.96
* 1st−skewness: 1.12
Fitted+obs. with corrected k−mer_cov: 0.941 Mb
* k−mer_cov cor.: 8.45
* repetitive_ratio 0.06: 0.06 Mb
Number of k−mers
0
50000
100000
150000
0
5
10
15
20
K−mer freq


Genome size estimation by error−excluding, fitting, and correcting
EXL: 0.991 Mb
FIT: 1.052 Mb
COR: 0.941 Mb
Genome size (bp)
600000
700000
800000
900000
1000000
1100000
1200000
25
Size k