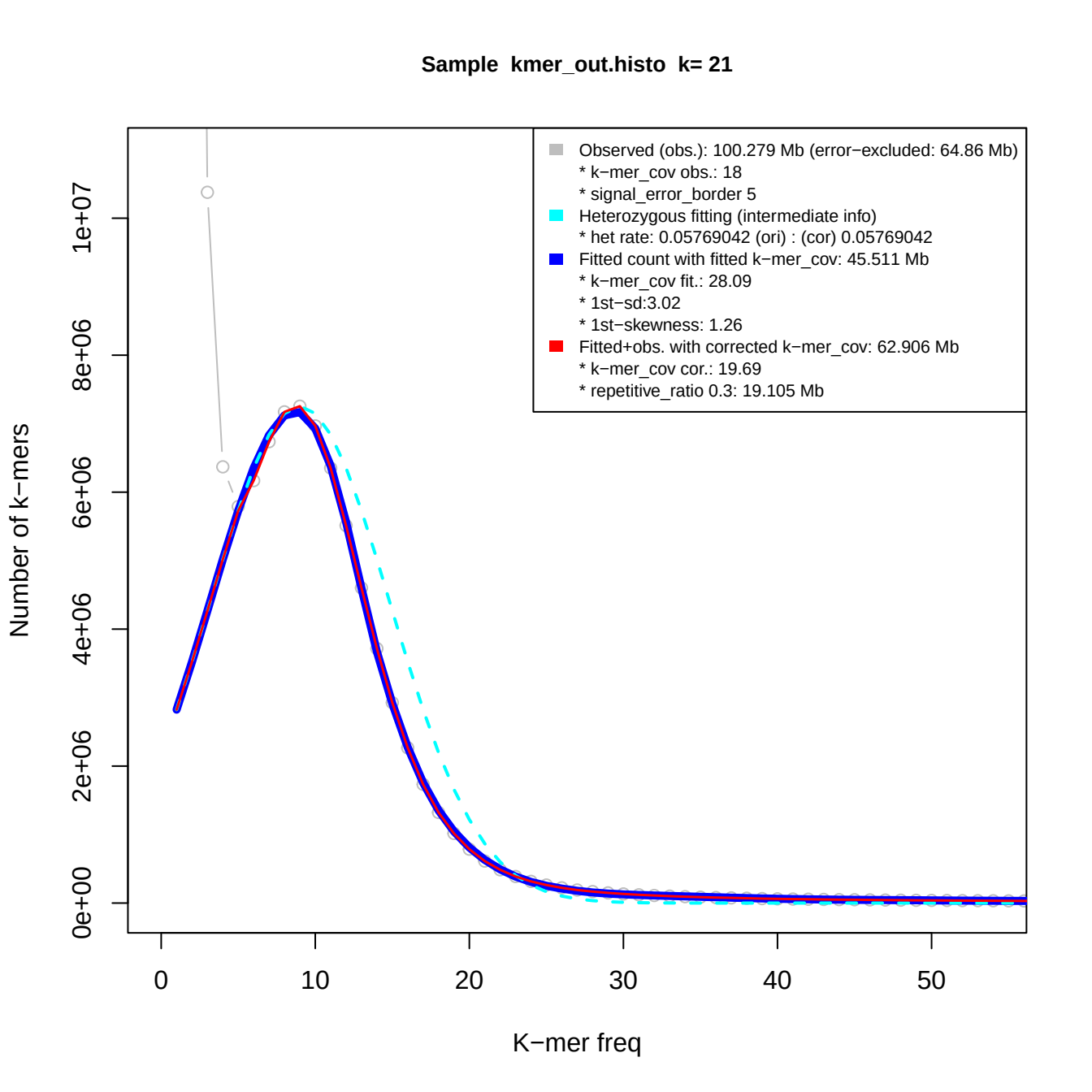
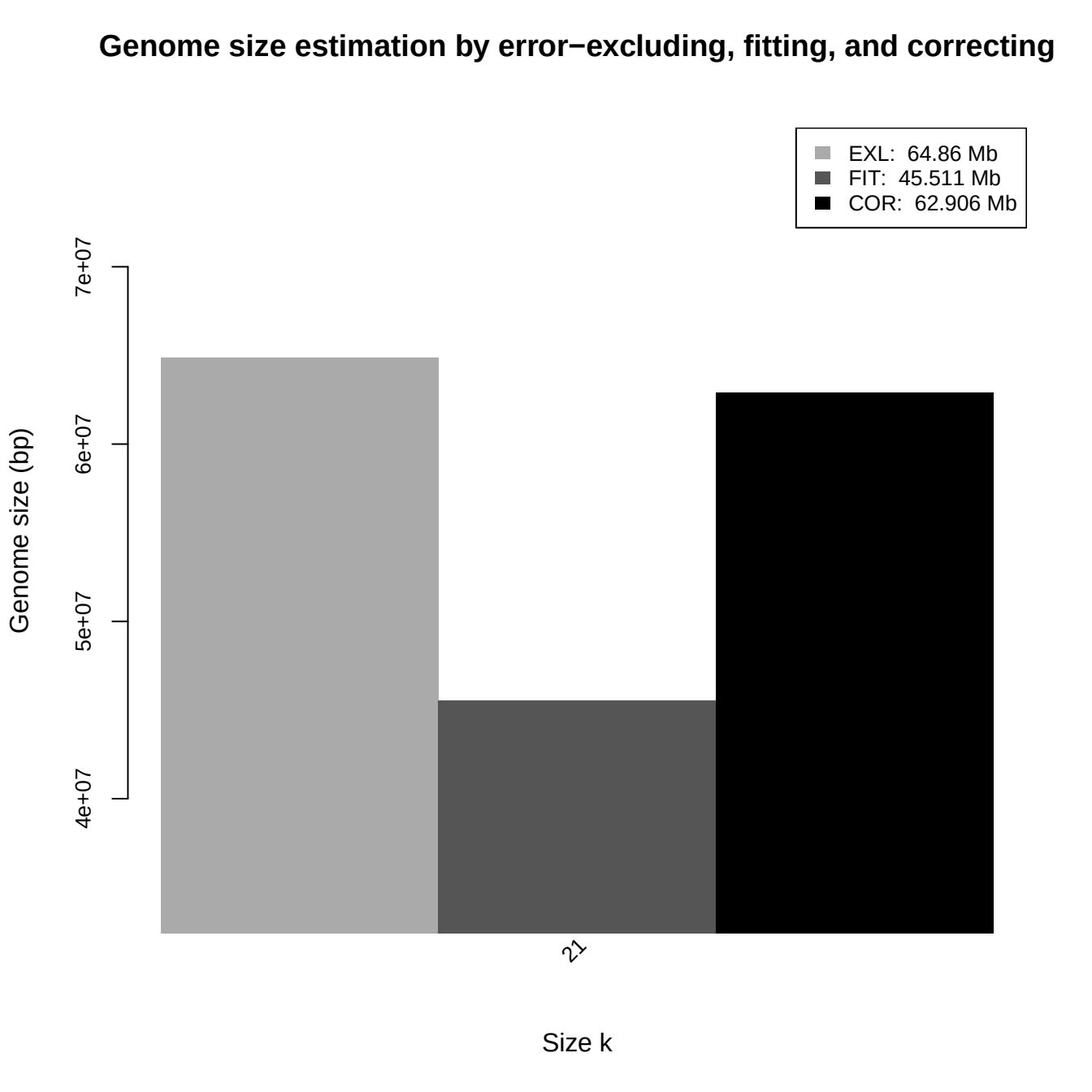

Sample kmer_out.histo k= 21
Observed (obs.): 100.279 Mb (error−excluded: 64.86 Mb)
* k−mer_cov obs.: 18
* signal_error_border 5
Heterozygous fitting (intermediate info)
* het rate: 0.05769042 (ori) : (cor) 0.05769042
Fitted count with fitted k−mer_cov: 45.511 Mb
* k−mer_cov fit.: 28.09
* 1st−sd:3.02
* 1st−skewness: 1.26
Fitted+obs. with corrected k−mer_cov: 62.906 Mb
* k−mer_cov cor.: 19.69
* repetitive_ratio 0.3: 19.105 Mb
Number of k−mers
0e+00
2e+06
4e+06
6e+06
8e+06
1e+07
0
10
20
30
40
50
K−mer freq


Genome size estimation by error−excluding, fitting, and correcting
EXL: 64.86 Mb
FIT: 45.511 Mb
COR: 62.906 Mb
Genome size (bp)
4e+07
5e+07
6e+07
7e+07
21
Size k