**Sample sim_m23_2.histo k= 23**

Number of k-mers

K-mer freq

Observed (obs.): 13.889 Mb (error-excluded: 12.784 Mb)
* k-mer_cov obs.: 8
* signal_error_border 3
Fitted count with fitted k-mer_cov: 13.601 Mb
* k-mer_cov fit.: 8.03
* 1st-sd:3.24
* 1st-skewness: 1.16
Fitted+obs. with corrected k-mer_cov: 11.504 Mb
* k-mer_cov cor.: 8.91
* repetitive_ratio 0.15: 1.716 Mb
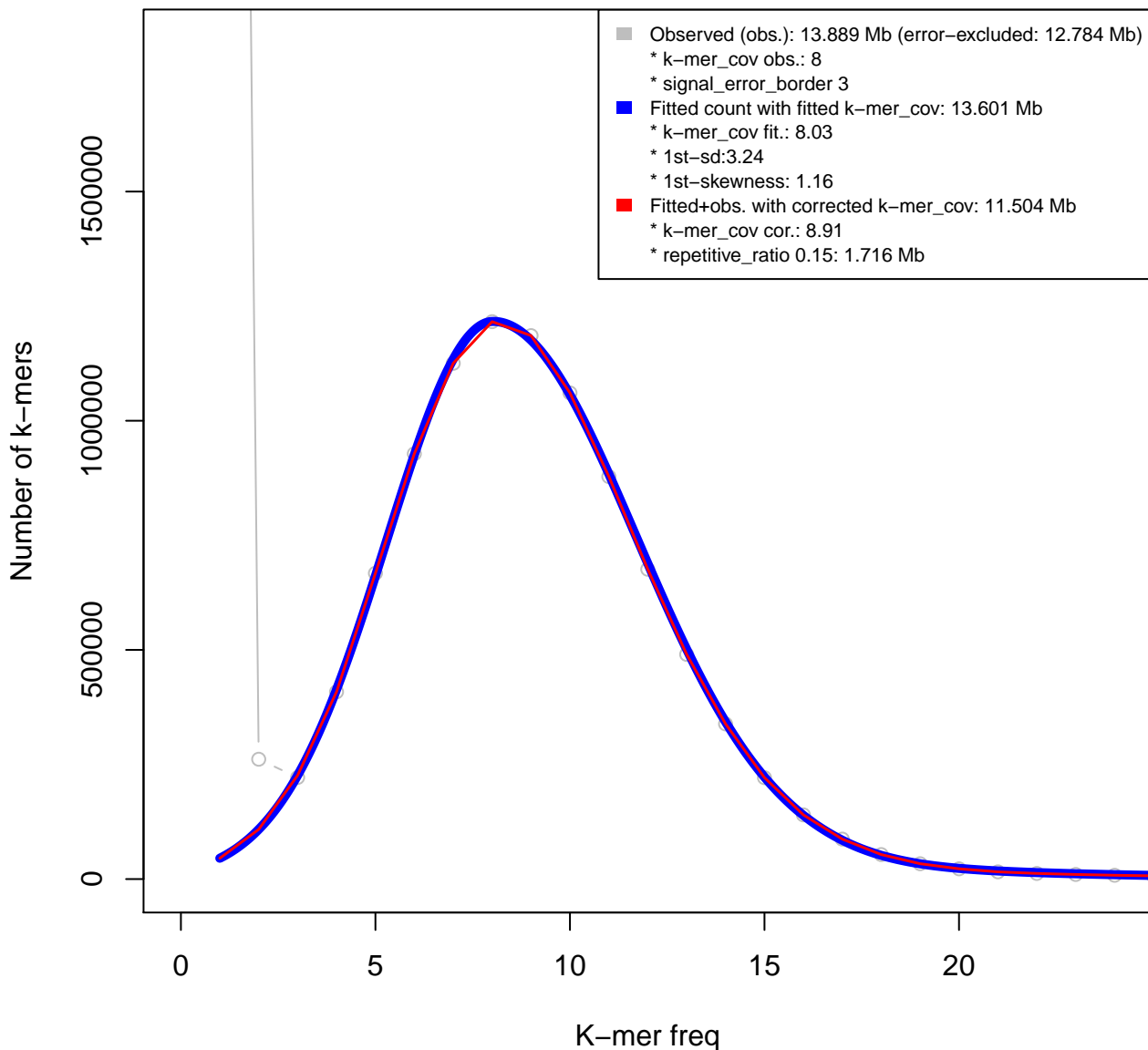
**Genome size estimation by error−excluding, fitting, and correcting**

Legend:
- EXL: 12.784 Mb
- FIT: 13.601 Mb
- COR: 11.504 Mb

Y-axis: Genome size (bp)
X-axis: Size k

$2^3$