Sample 21mer_no_cut.histo k= 21

Number of k-mers (y-axis), K-mer freq (x-axis)

Legend:
- Observed (obs.): 200.557 Mb (error−excluded: 132.937 Mb)
  - * k−mer_cov obs.: 9
  - * signal_error_border 5
- Fitted count with fitted k−mer_cov: 142.525 Mb
  - * k−mer_cov fit.: 9.14
  - * 1st−sd:4.91
  - * 1st−skewness: 0.78
- Fitted+obs. with corrected k−mer_cov: 157.912 Mb
  - * k−mer_cov cor.: 7.85
  - * repetitive_ratio 0.45: 71.75 Mb
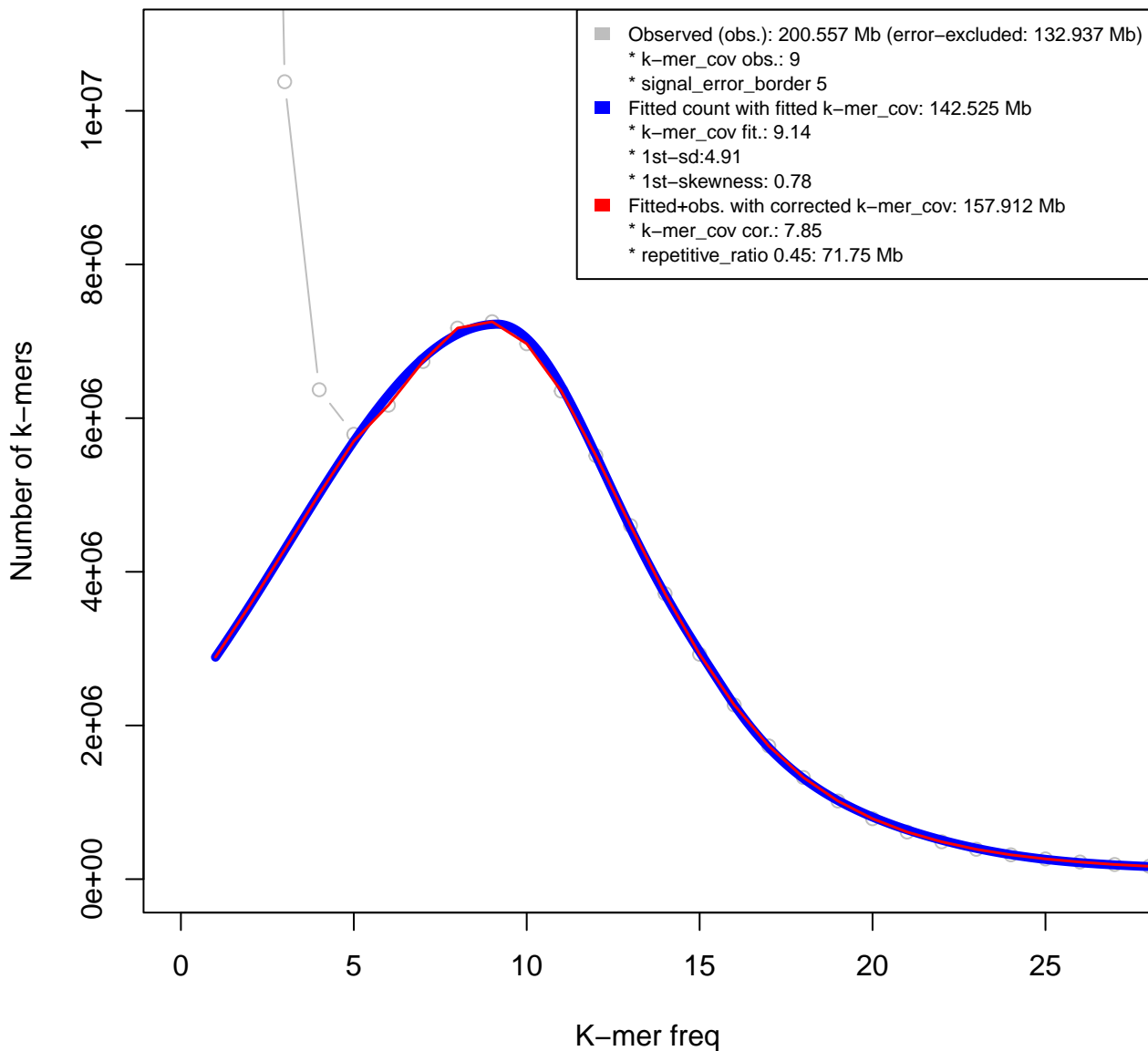
Genome size estimation by error−excluding, fitting, and correcting

Legend:
- EXL: 132.937 Mb
- FIT: 142.525 Mb
- COR: 157.912 Mb

Y-axis: Genome size (bp)

X-axis: Size k (21)