Sample sim1.histo k= 18

Observed (obs.): 1.448 Mb (error−excluded: 1.349 Mb)
* k−mer_cov obs.: 9
* signal_error_border 3
Fitted count with fitted k−mer_cov: 1.437 Mb
* k−mer_cov fit.: 8.74
* 1st−sd:3.15
* 1st−skewness: 1.15
Fitted+obs. with corrected k−mer_cov: 1.275 Mb
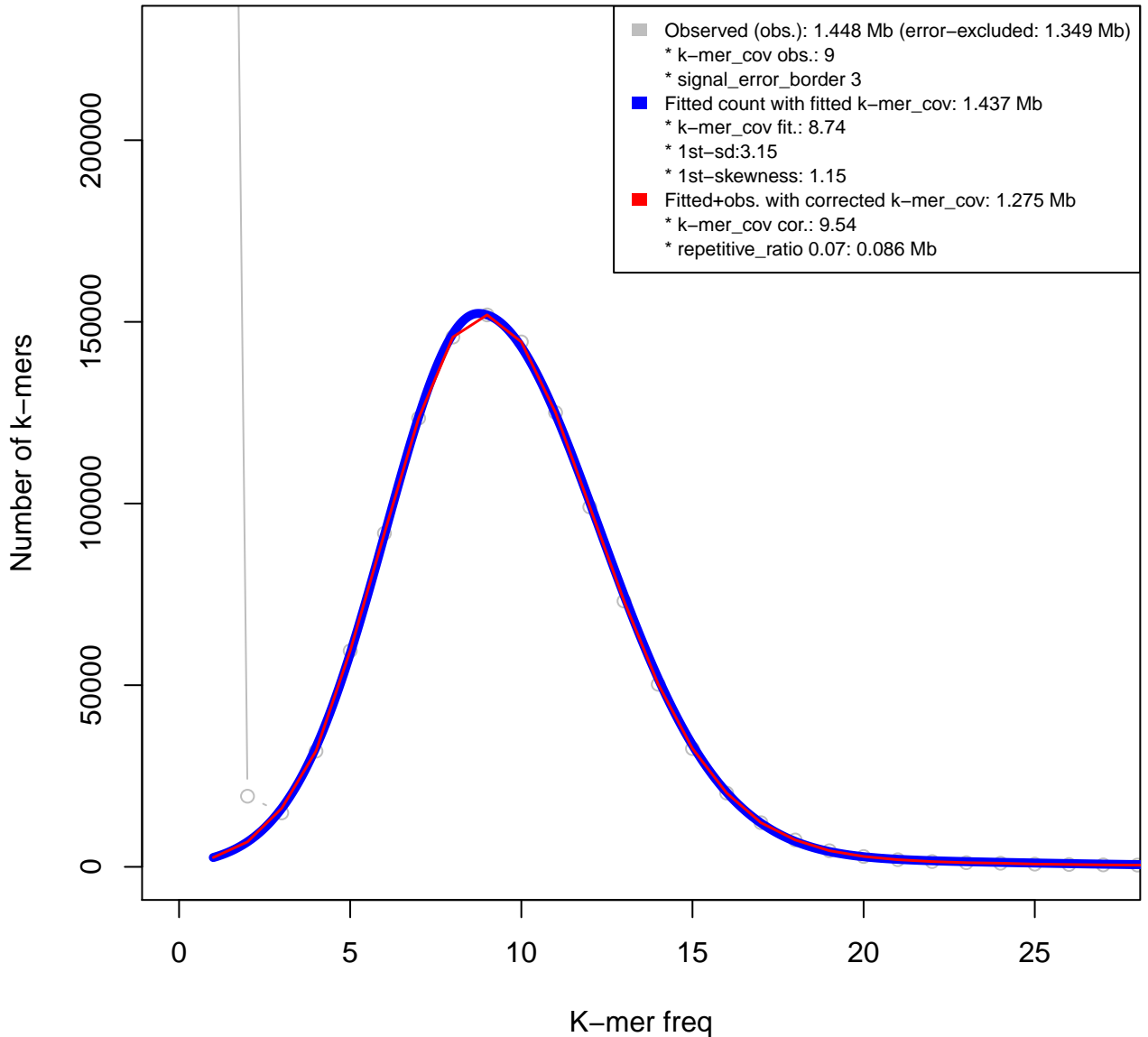* k−mer_cov cor.: 9.54
* repetitive_ratio 0.07: 0.086 Mb

Genome size estimation by error−excluding, fitting, and correcting