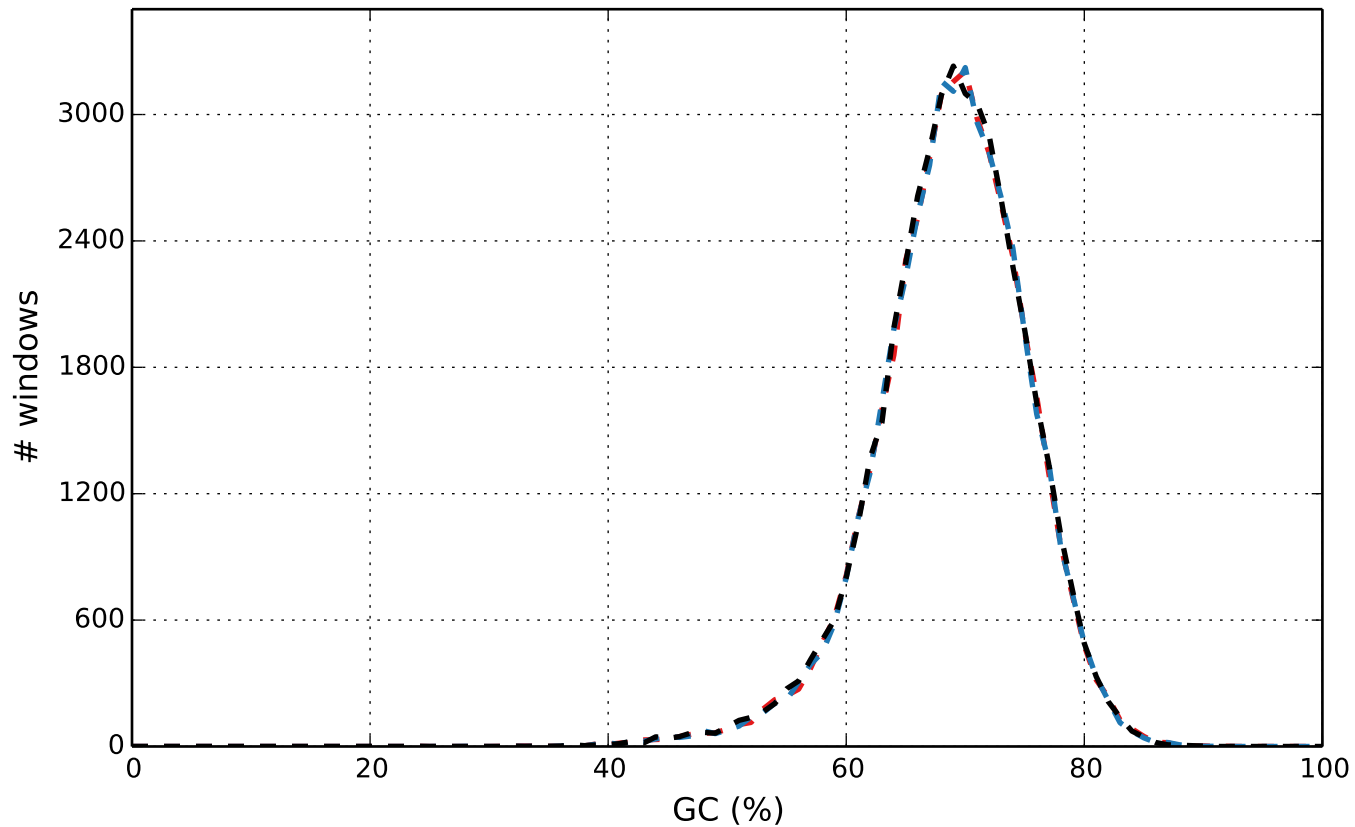# Cumulative length

R.S.-M-Newbler2.8_raw_scf broken   R.S.-M-Newbler2.8_raw_scf   Reference

GC content
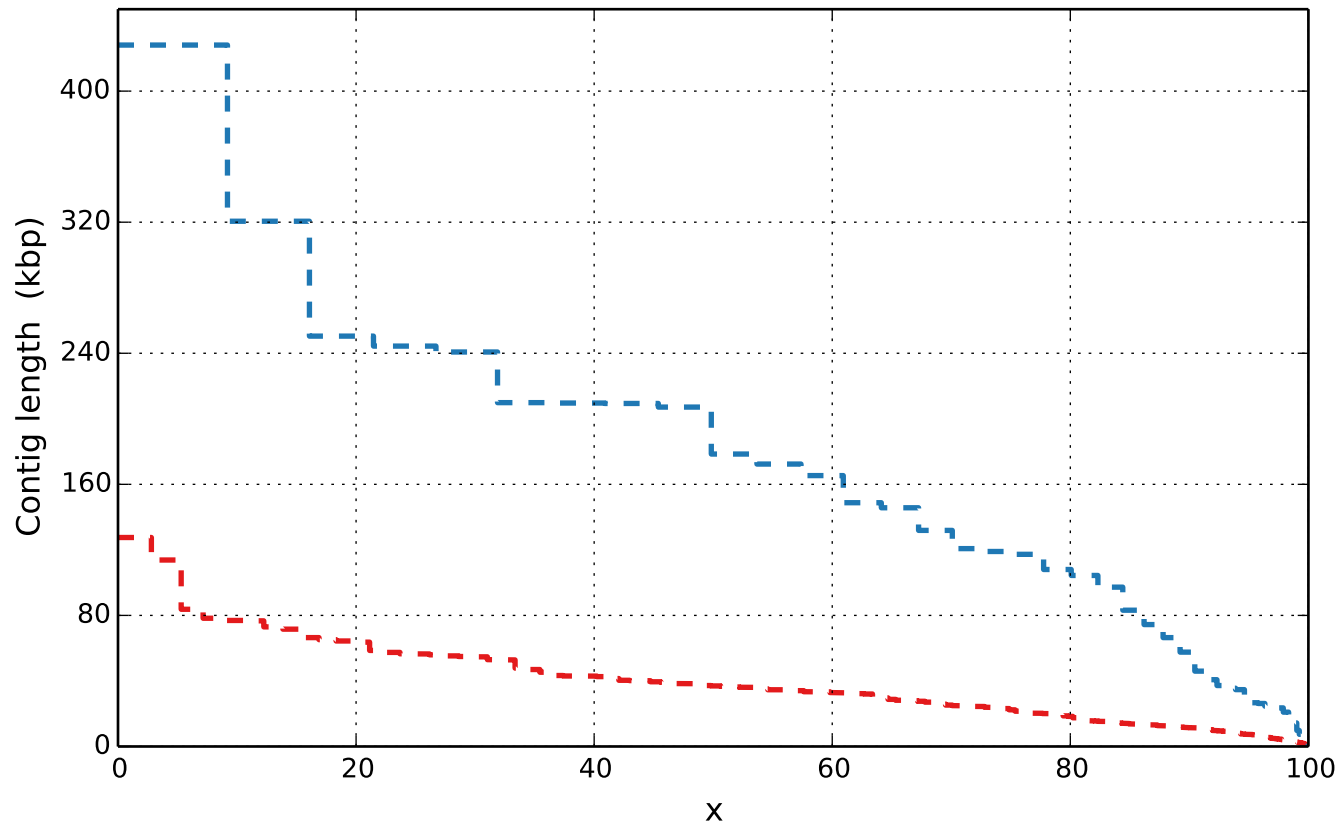
windows

GC (%)

R.S.-M-Newbler2.8_raw_scf broken   R.S.-M-Newbler2.8_raw_scf   Referenc

Nx

Contig length (kbp)

x

- - - R.S.-M-Newbler2.8_raw_scf broken
- - - R.S.-M-Newbler2.8_raw_scf

NGx

Contig length (kbp)

x

R.S.-M-Newbler2.8_raw_scf broken   R.S.-M-Newbler2.8_raw_scf

Cumulative length (aligned contigs)

Legend:
- R.S.-M-Newbler2.8_raw_scf broken
- R.S.-M-Newbler2.8_raw_scf
- Reference

NAx

Contig length (kbp)

x

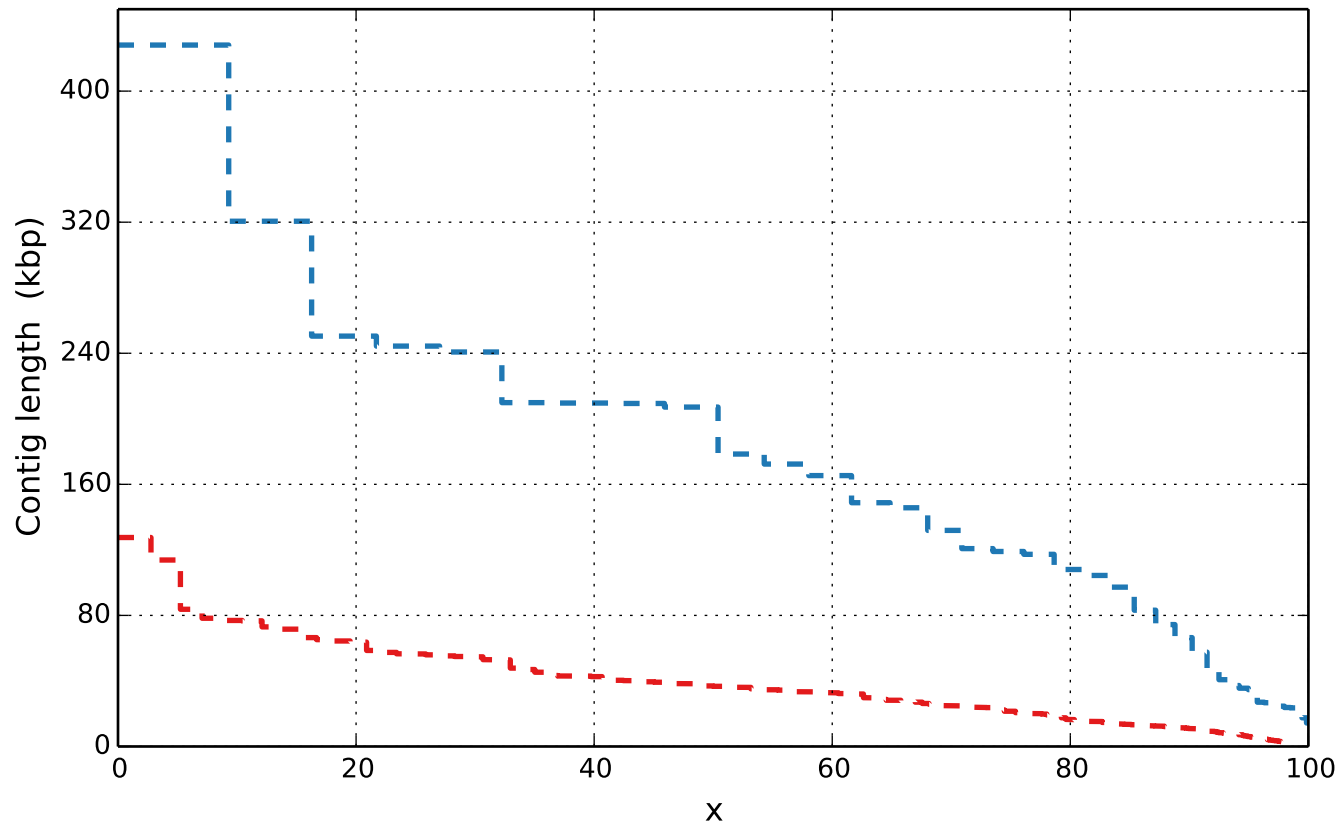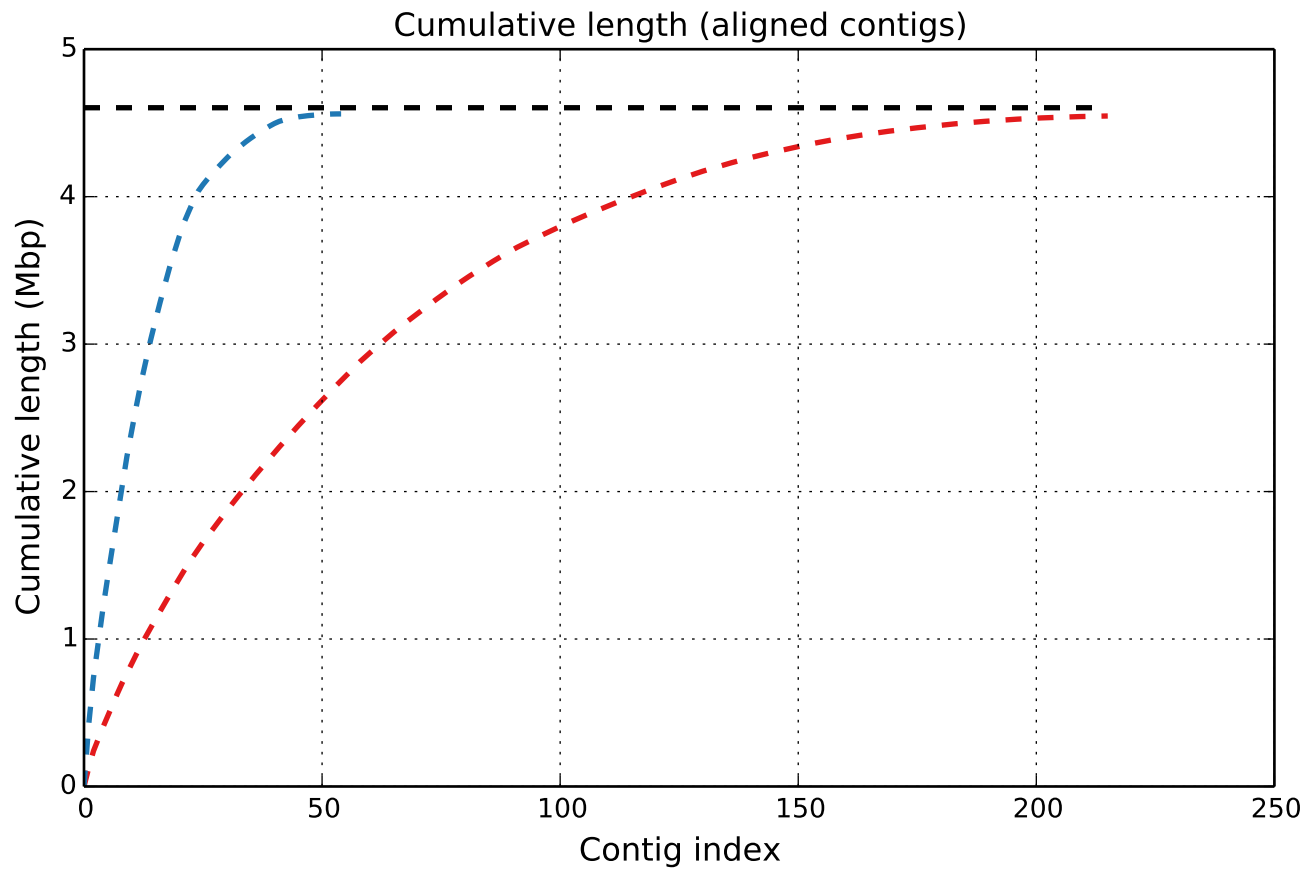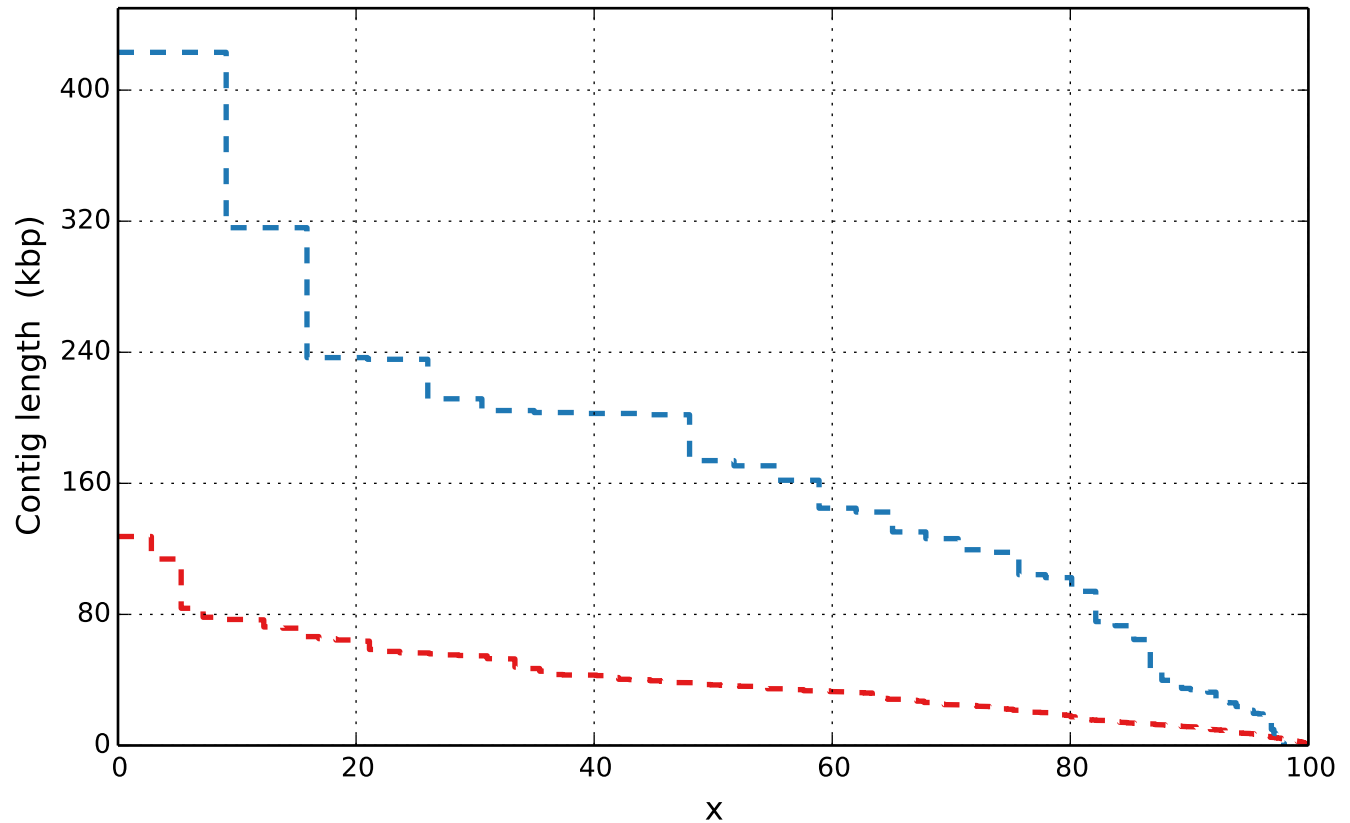R.S.-M-Newbler2.8_raw_scf broken

R.S.-M-Newbler2.8_raw_scf

NGAx

Contig length (kbp)

x

- - - R.S.-M-Newbler2.8_raw_scf broken   - - - R.S.-M-Newbler2.8_raw_scf
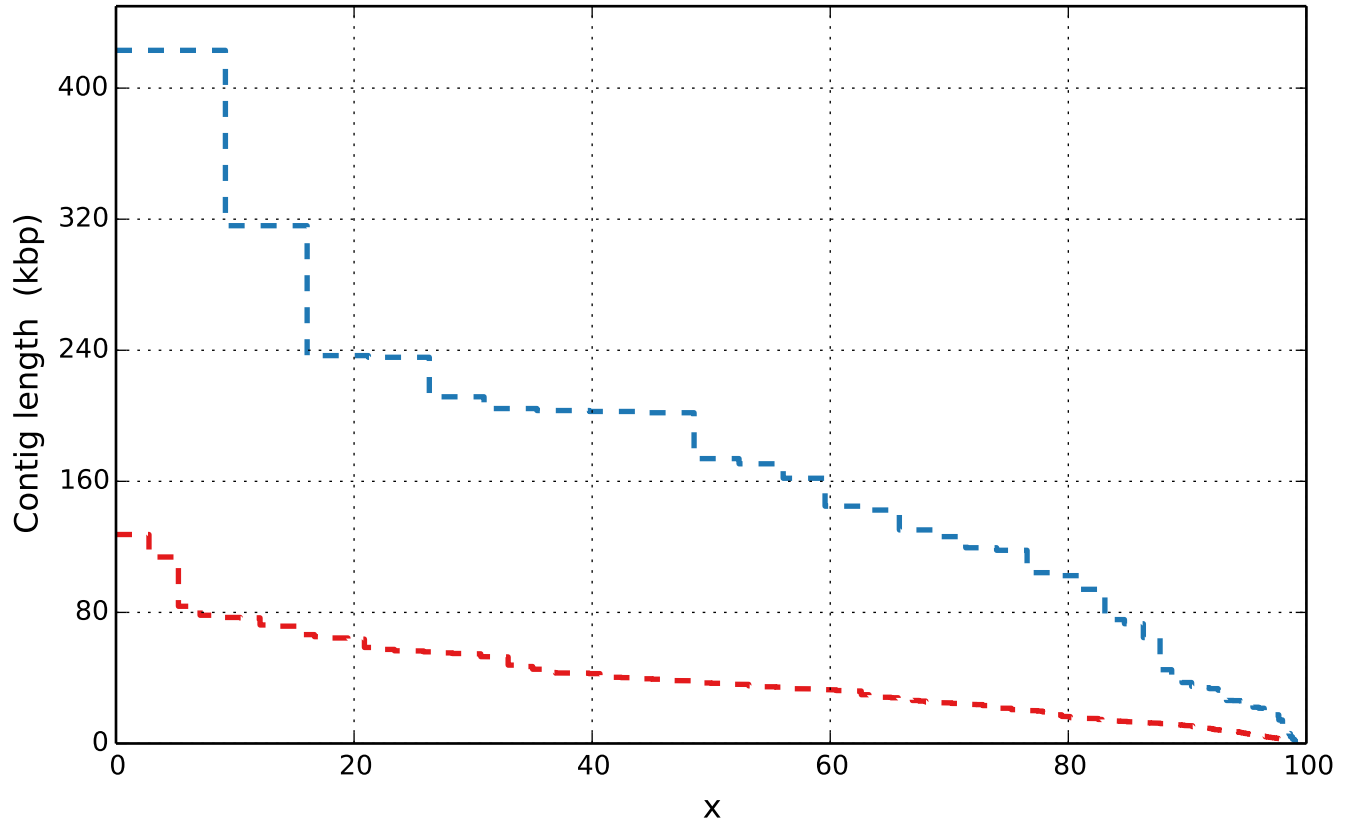
Cumulative # complete genes

Contig index	Cumulative # complete genes

- - - R.S.-M-Newbler2.8_raw_scf broken   - - - R.S.-M-Newbler2.8_raw_scf   - - - Reference

complete genes

+4.255e3

R.S.-M-Newbler2.8_raw_scf broken		R.S.-M-Newbler2.8_raw_scf

Genome fraction, %

100

99

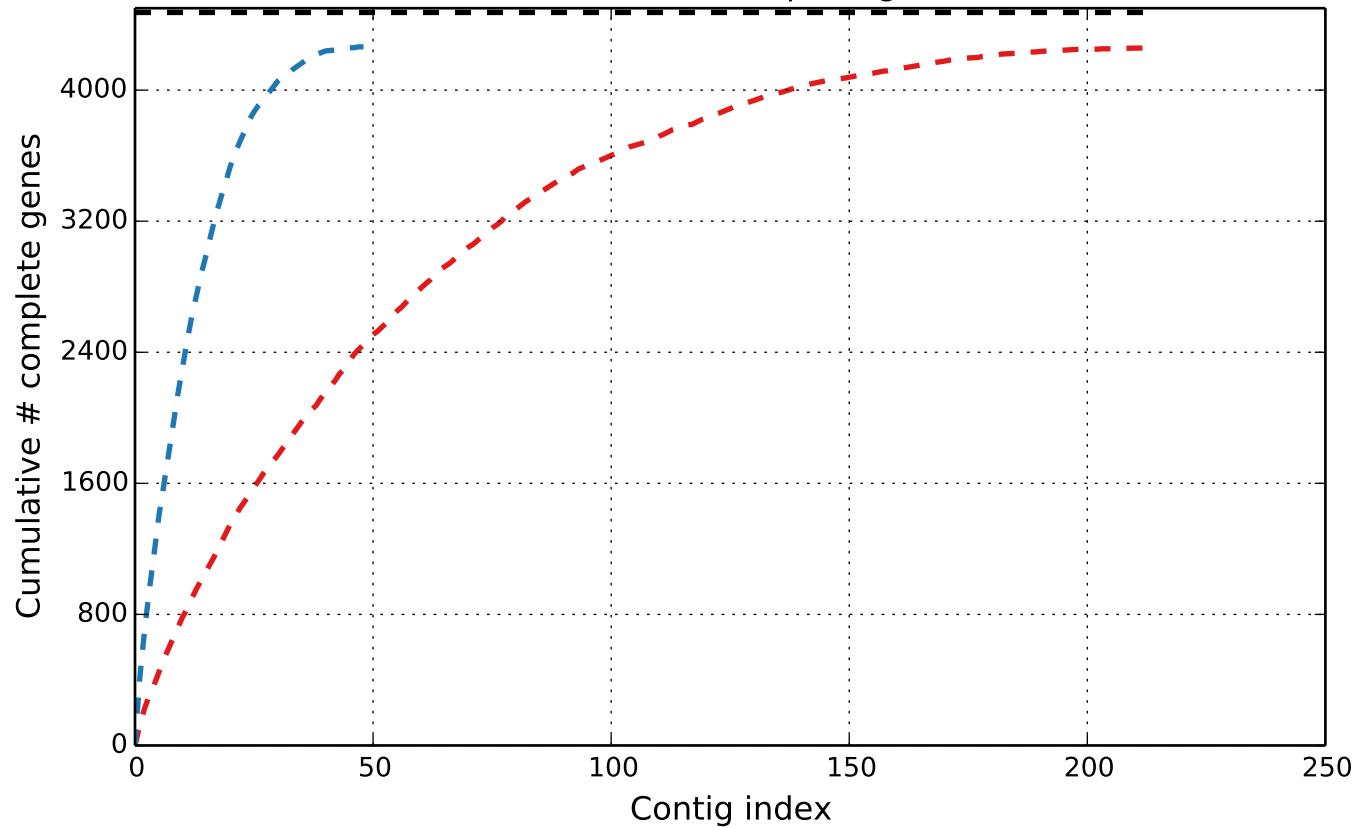R.S.-M-Newbler2.8_raw_scf broken   R.S.-M-Newbler2.8_raw_scf