

Report

	final.contigs
# contigs (>= 0 bp)	129
# contigs (>= 1000 bp)	123
Total length (>= 0 bp)	1293350
Total length (>= 1000 bp)	1289336
# contigs	127
Largest contig	52933
Total length	1292592
Reference length	1283598
GC (%)	26.30
Reference GC (%)	26.30
N50	16928
NG50	16928
N75	9299
NG75	9306
L50	25
LG50	25
L75	51
LG75	50
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.538
Duplication ratio	1.012
# N's per 100 kbp	0.00
# mismatches per 100 kbp	26.06
# indels per 100 kbp	0.00
Largest alignment	52933
NA50	16928
NGA50	16928
NA75	9299
NGA75	9306
LA50	25
LGA50	25
LA75	51
LGA75	50

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	333
# indels	0
# short indels	0
# long indels	0
Indels length	0

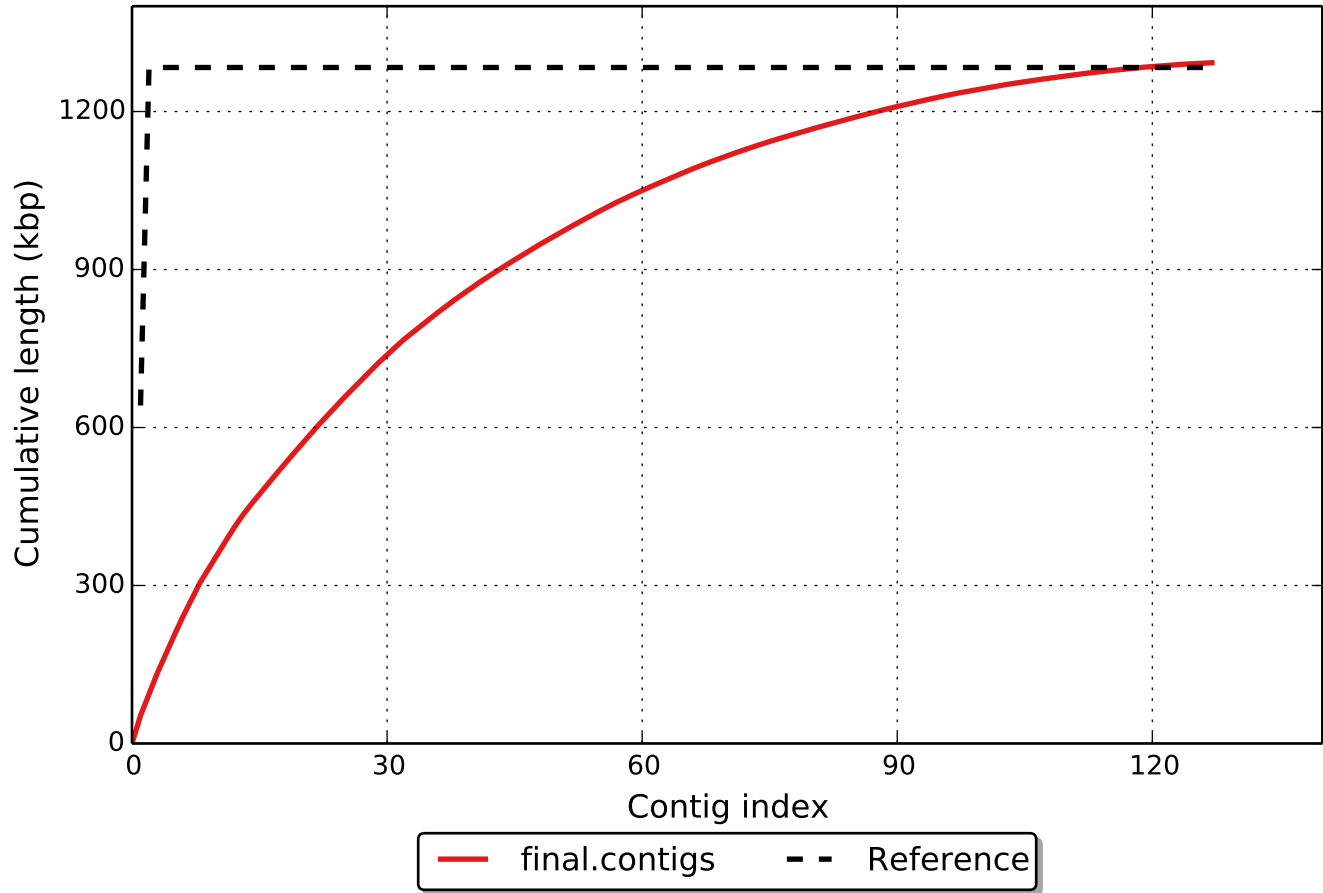
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

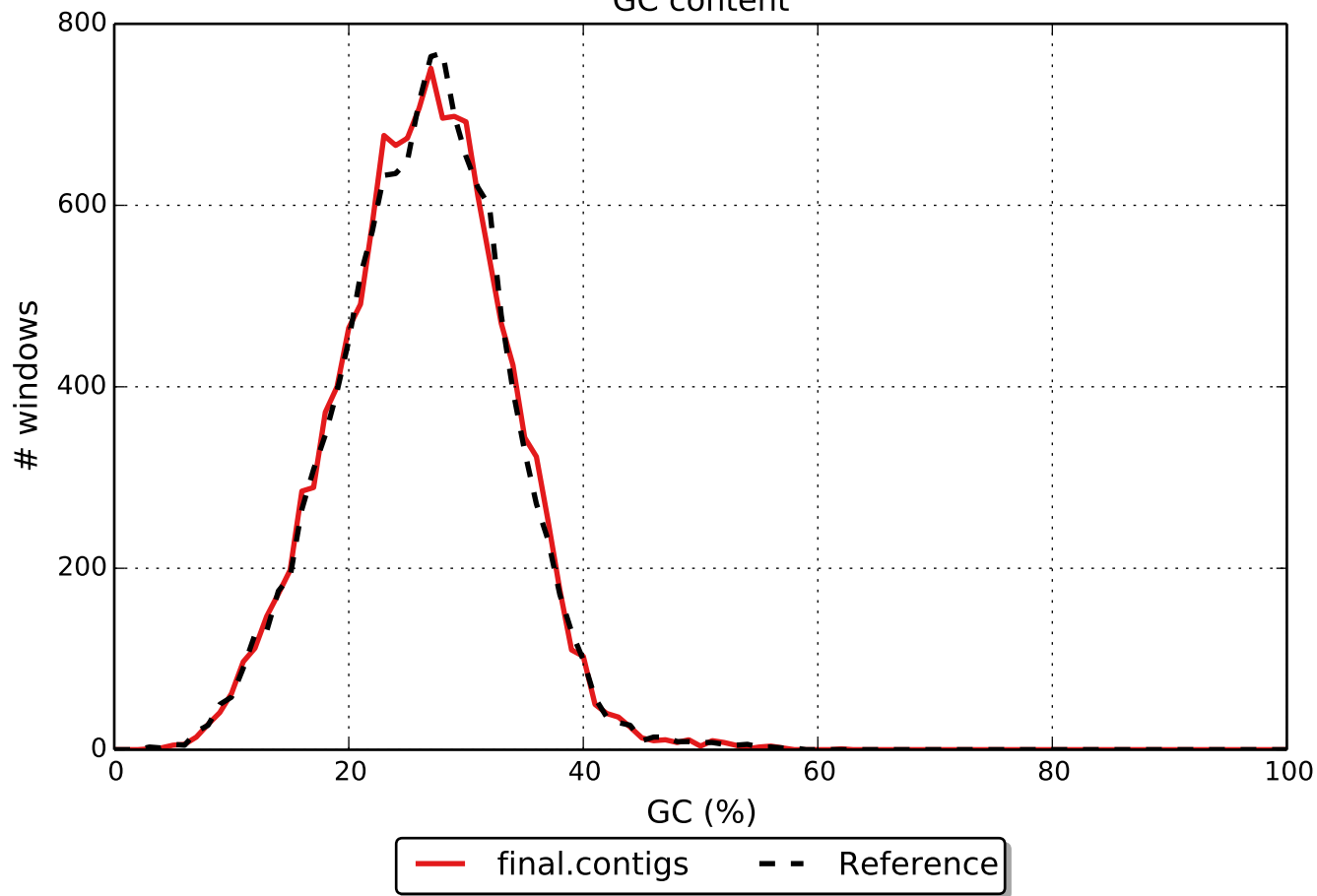
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

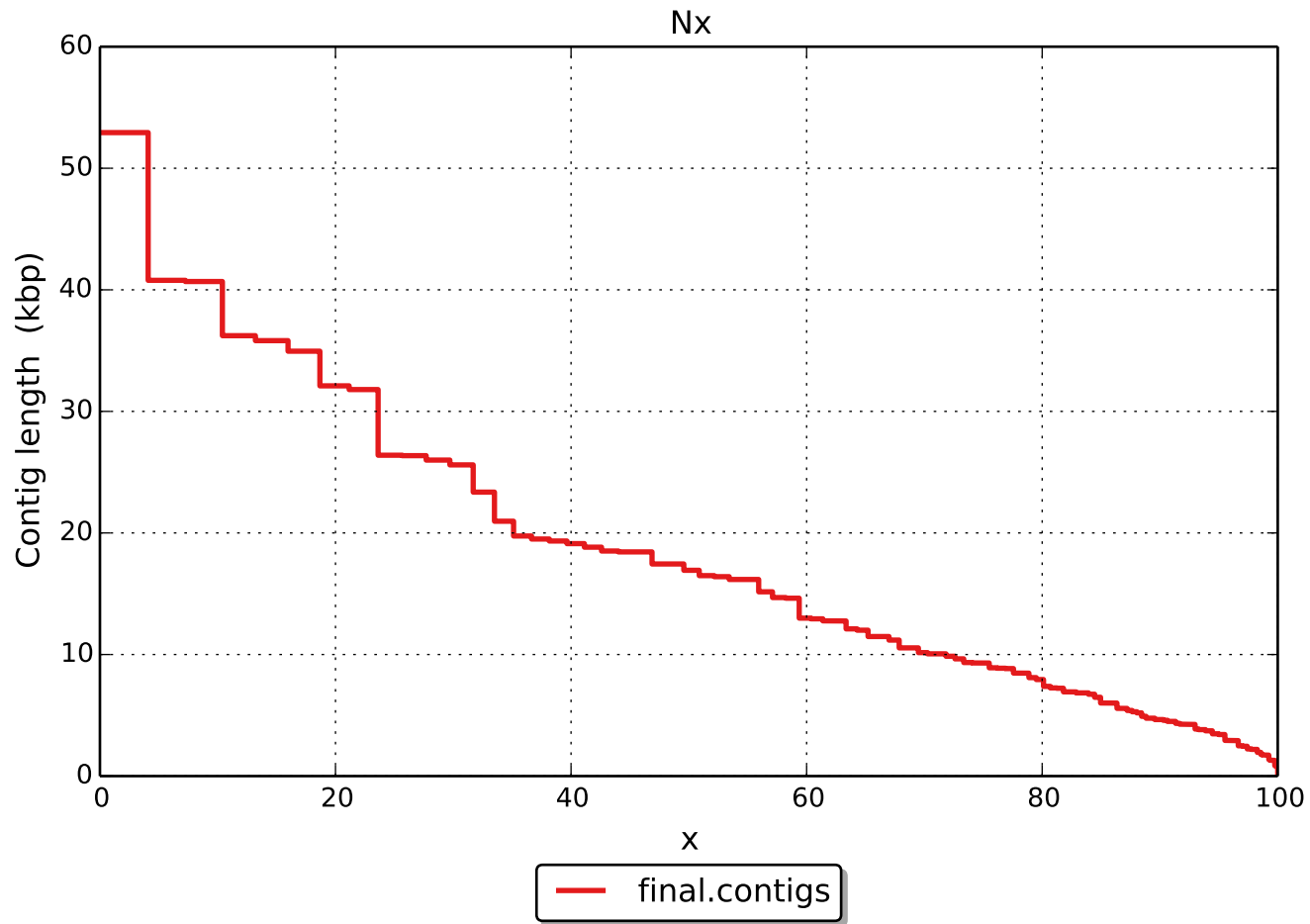
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

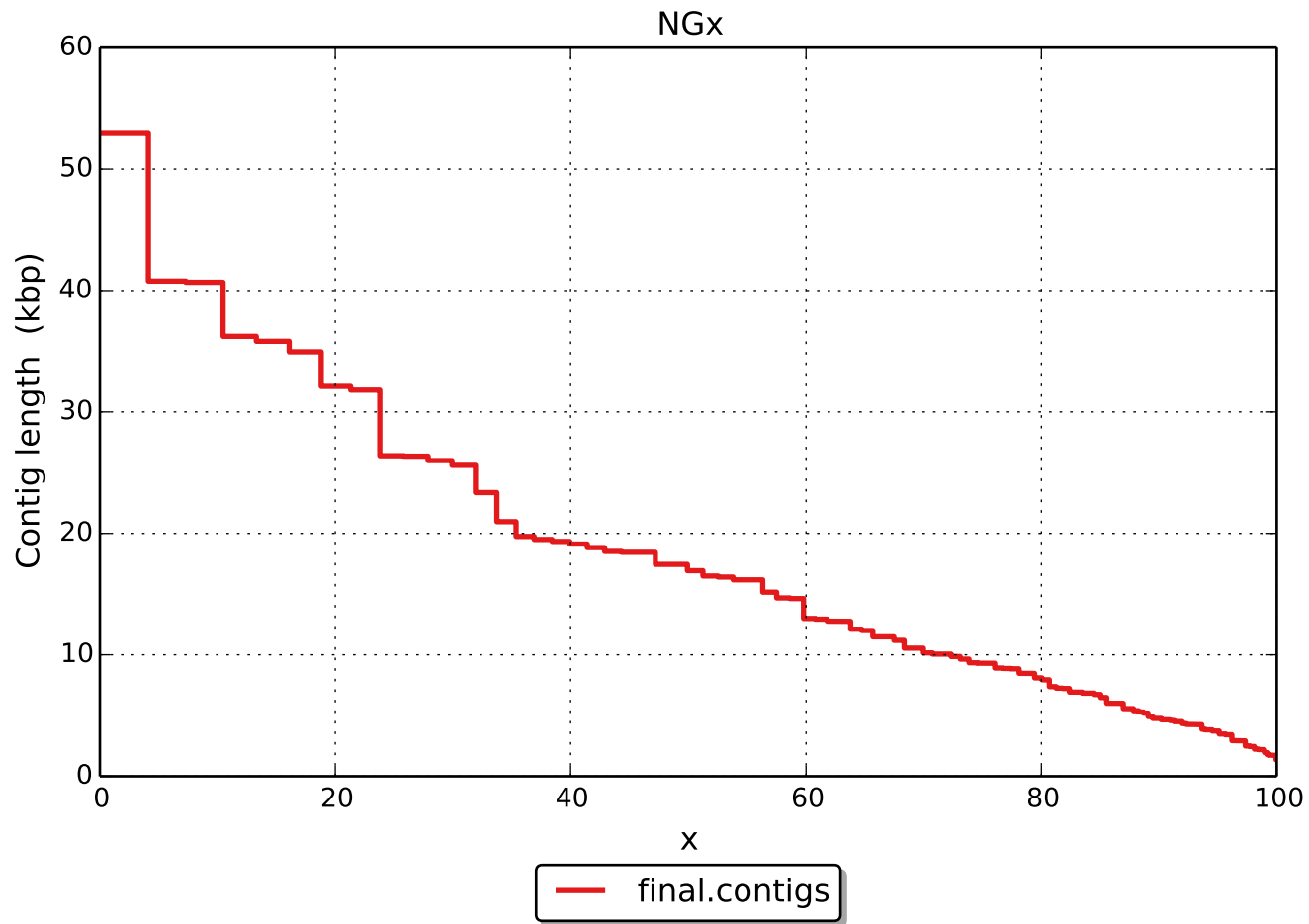
Cumulative length



GC content



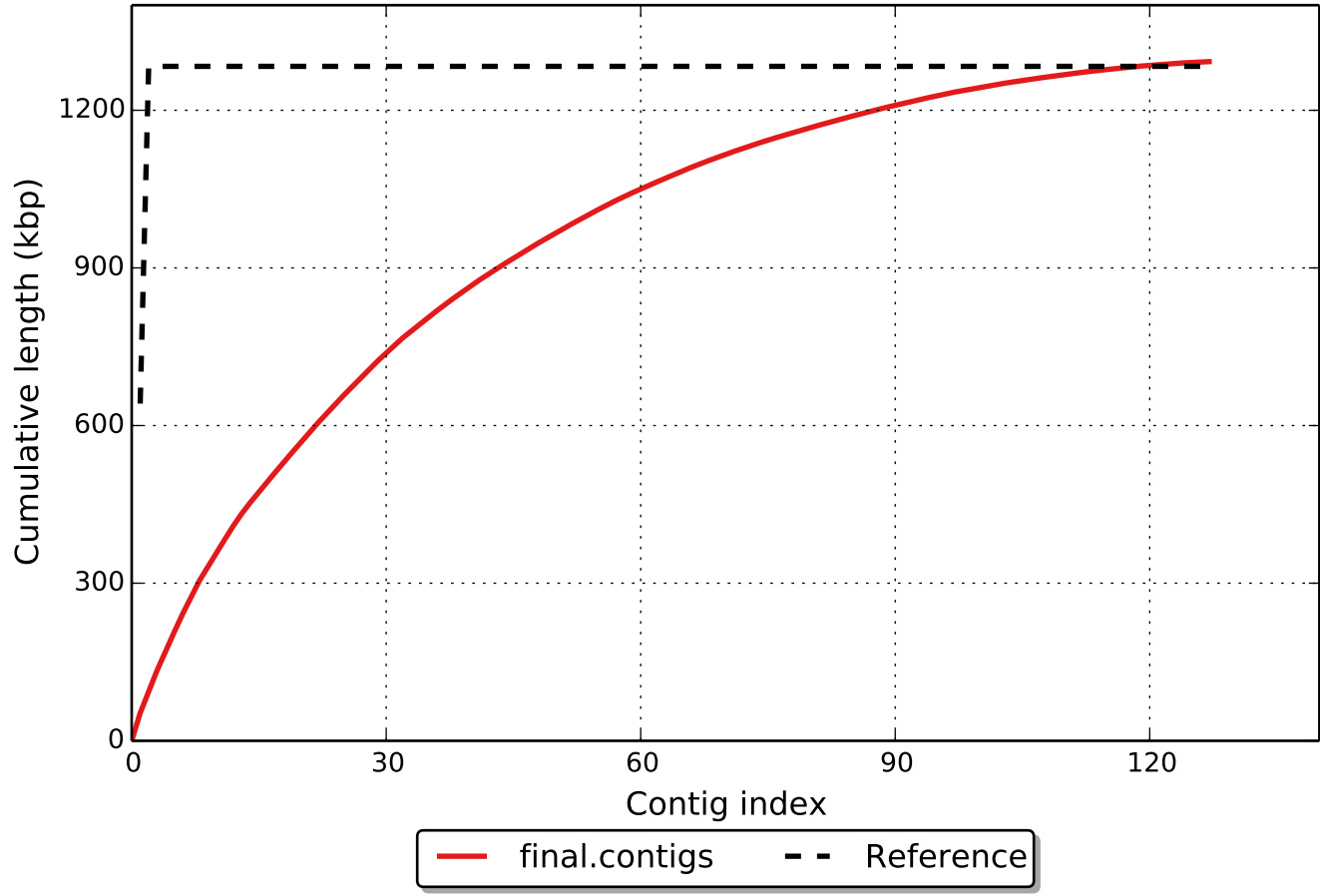


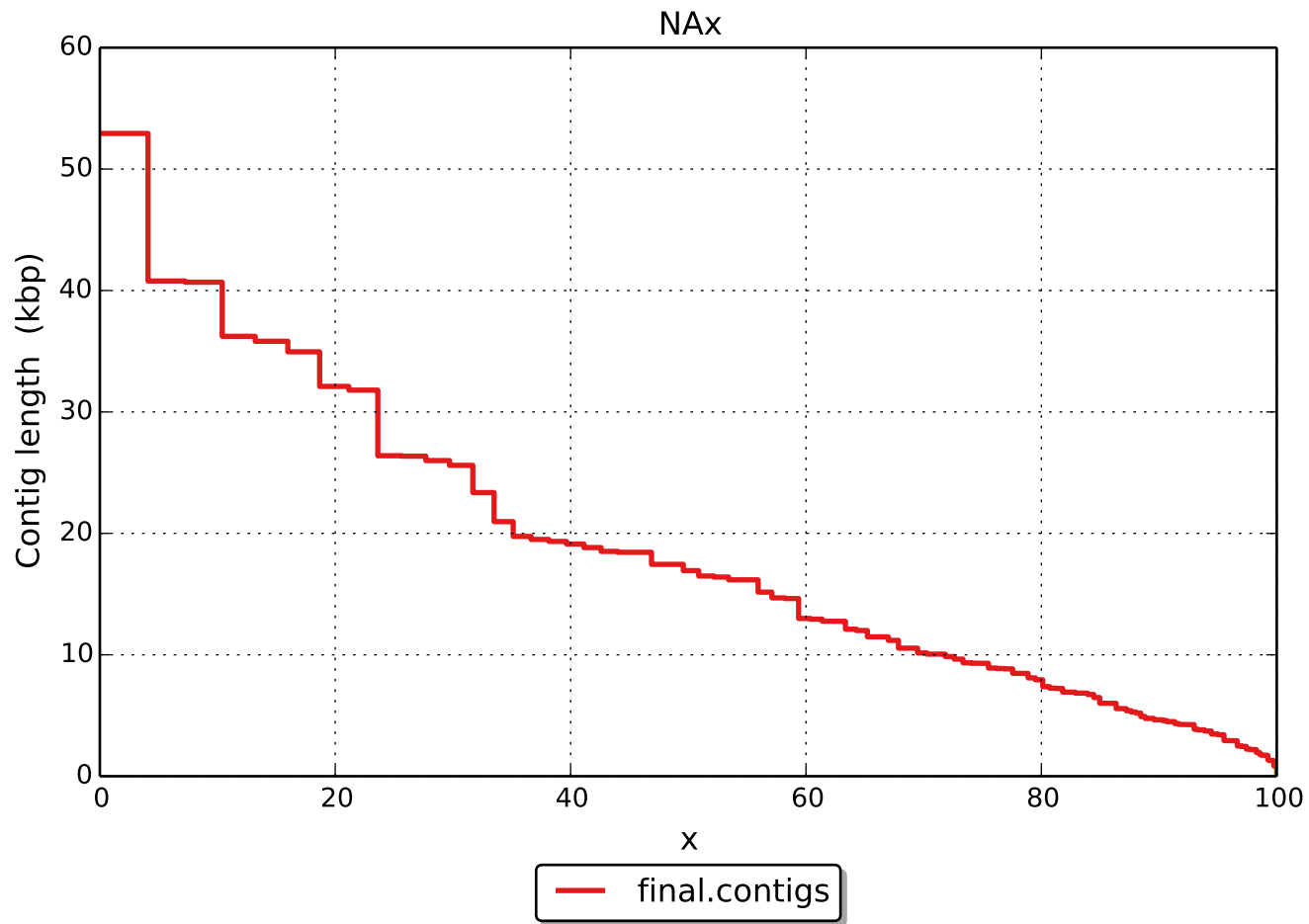


Misassemblies



Cumulative length (aligned contigs)





NGAx

