

Report

	final.contigs
# contigs (≥ 0 bp)	560
# contigs (≥ 1000 bp)	155
Total length (≥ 0 bp)	769306
Total length (≥ 1000 bp)	590588
# contigs	275
Largest contig	25883
Total length	669346
Reference length	1283598
GC (%)	26.32
Reference GC (%)	26.30
N50	4473
NG50	604
N75	2222
L50	44
LG50	225
L75	98
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	51.214
Duplication ratio	1.018
# N's per 100 kbp	0.00
# mismatches per 100 kbp	432.32
# indels per 100 kbp	0.00
Largest alignment	25883
NA50	4473
NGA50	604
NA75	2222
LA50	44
LGA50	225
LA75	98

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	2842
# indels	0
# short indels	0
# long indels	0
Indels length	0

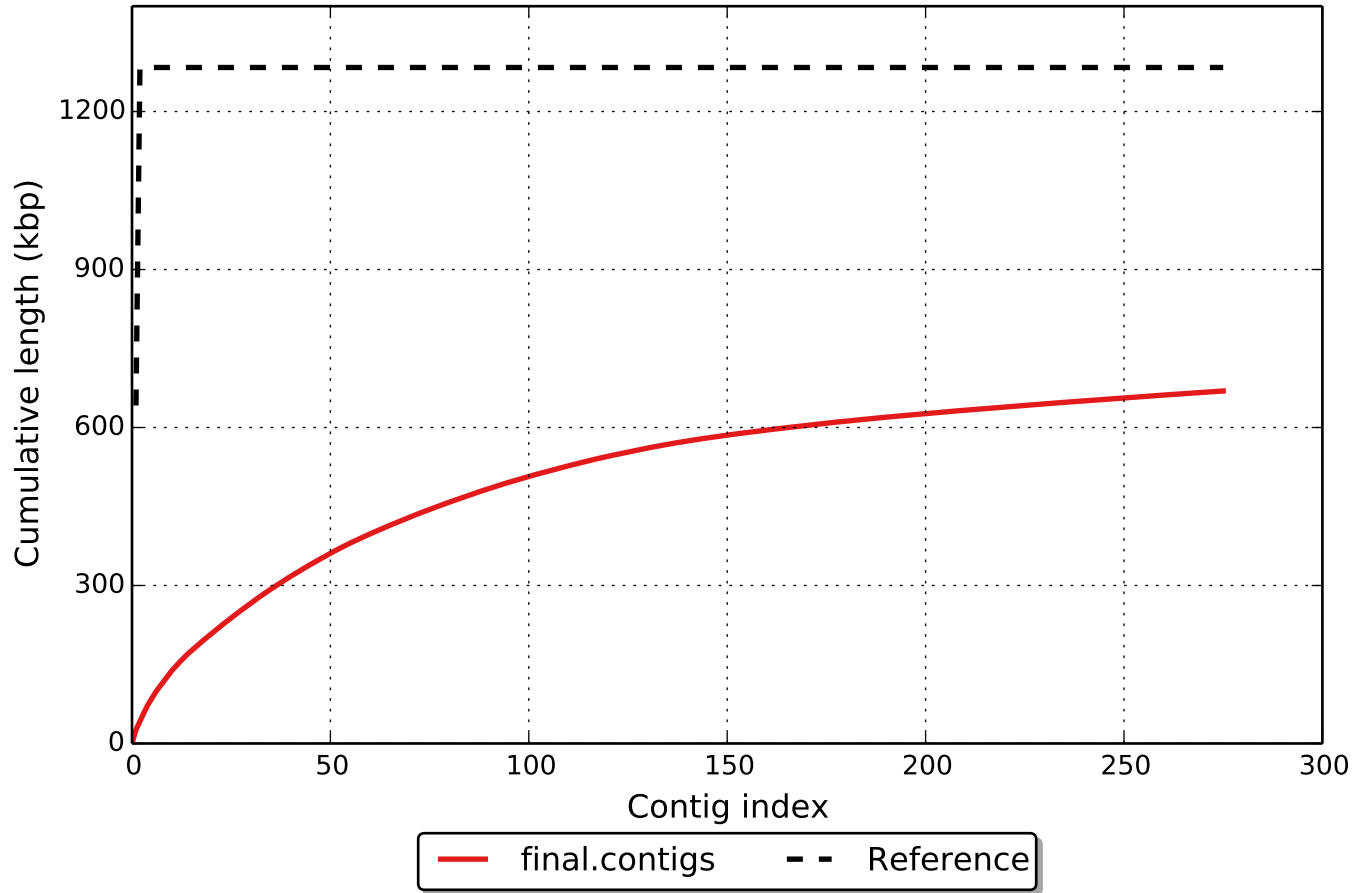
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

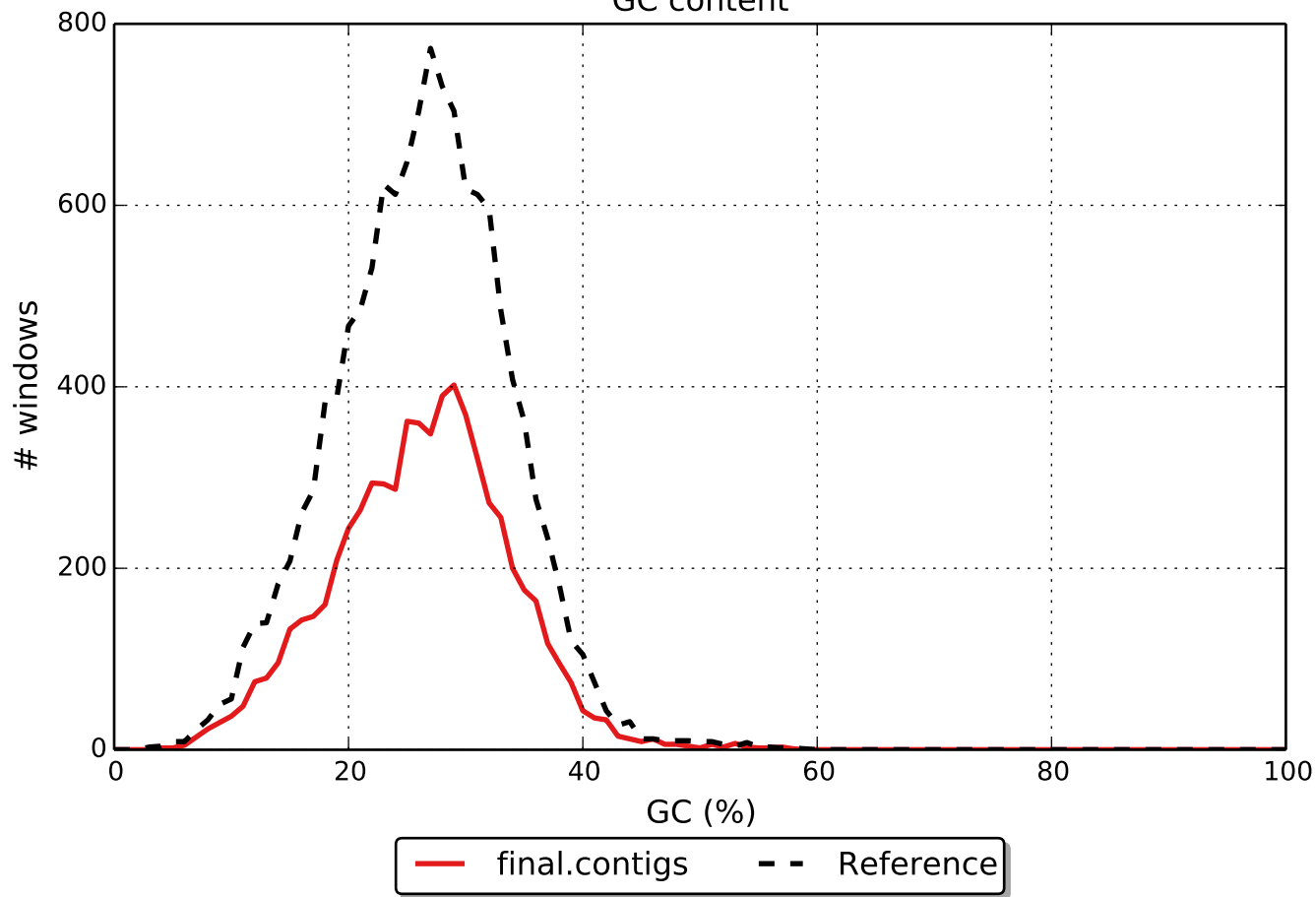
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

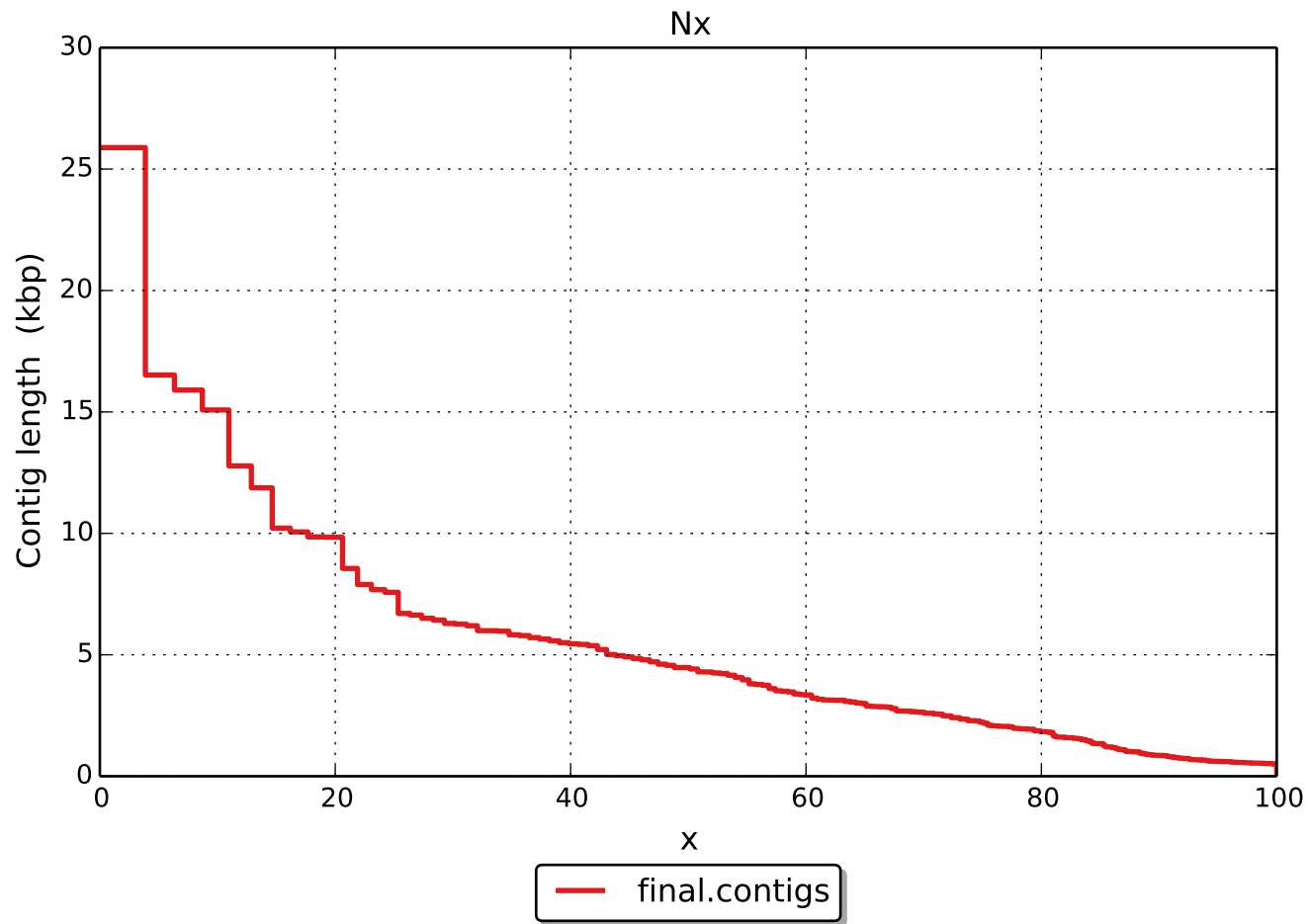
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

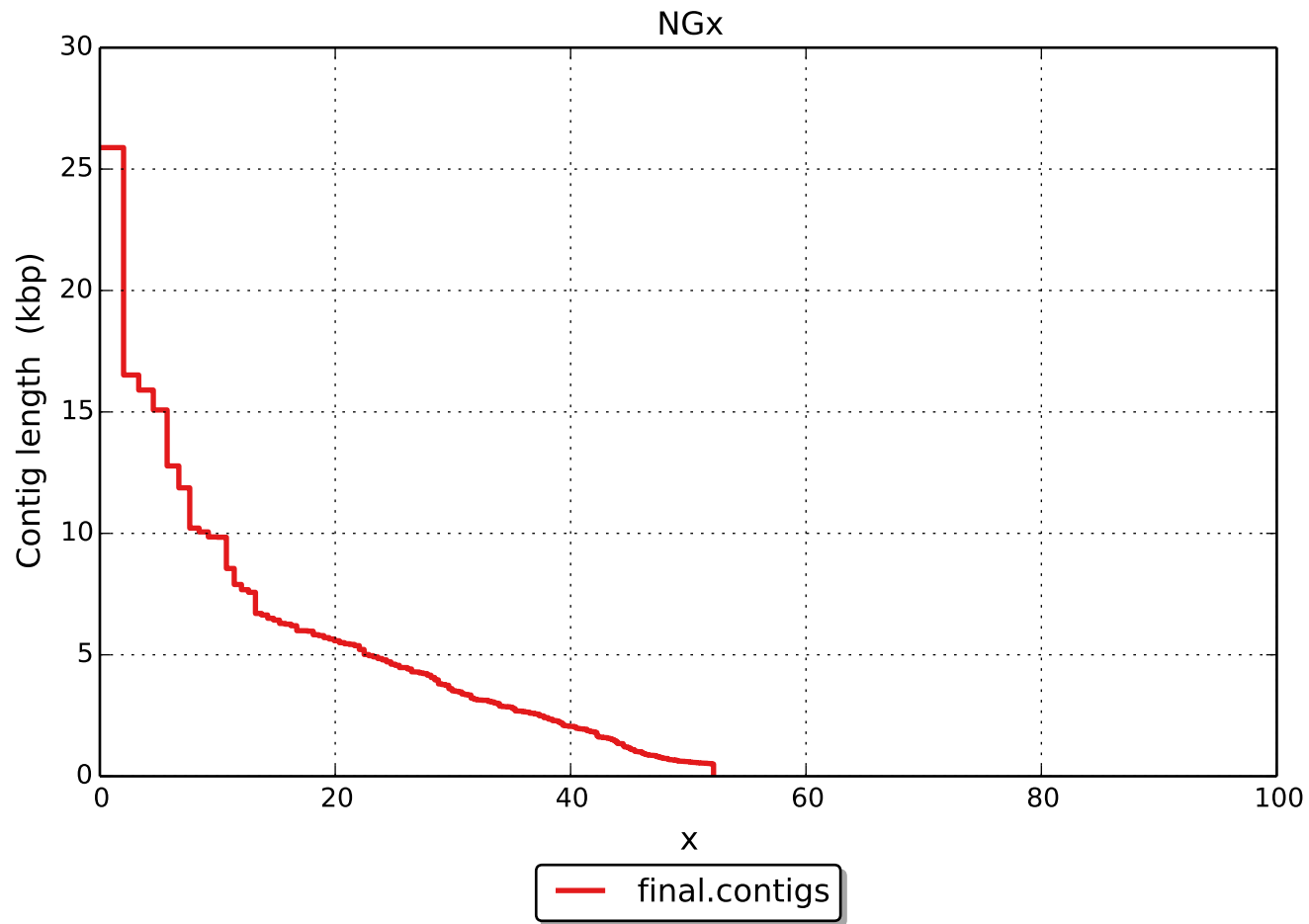
Cumulative length



GC content



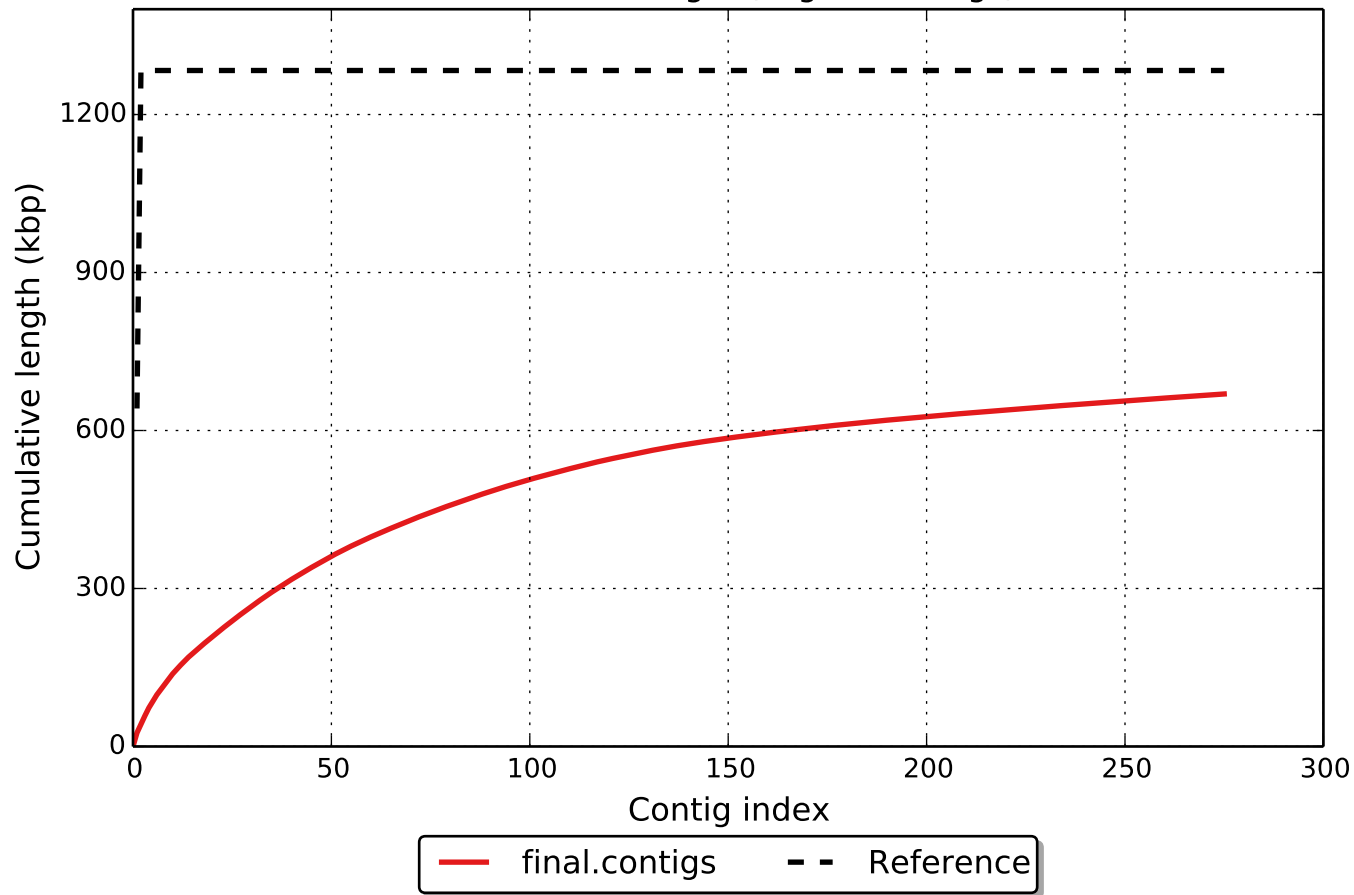


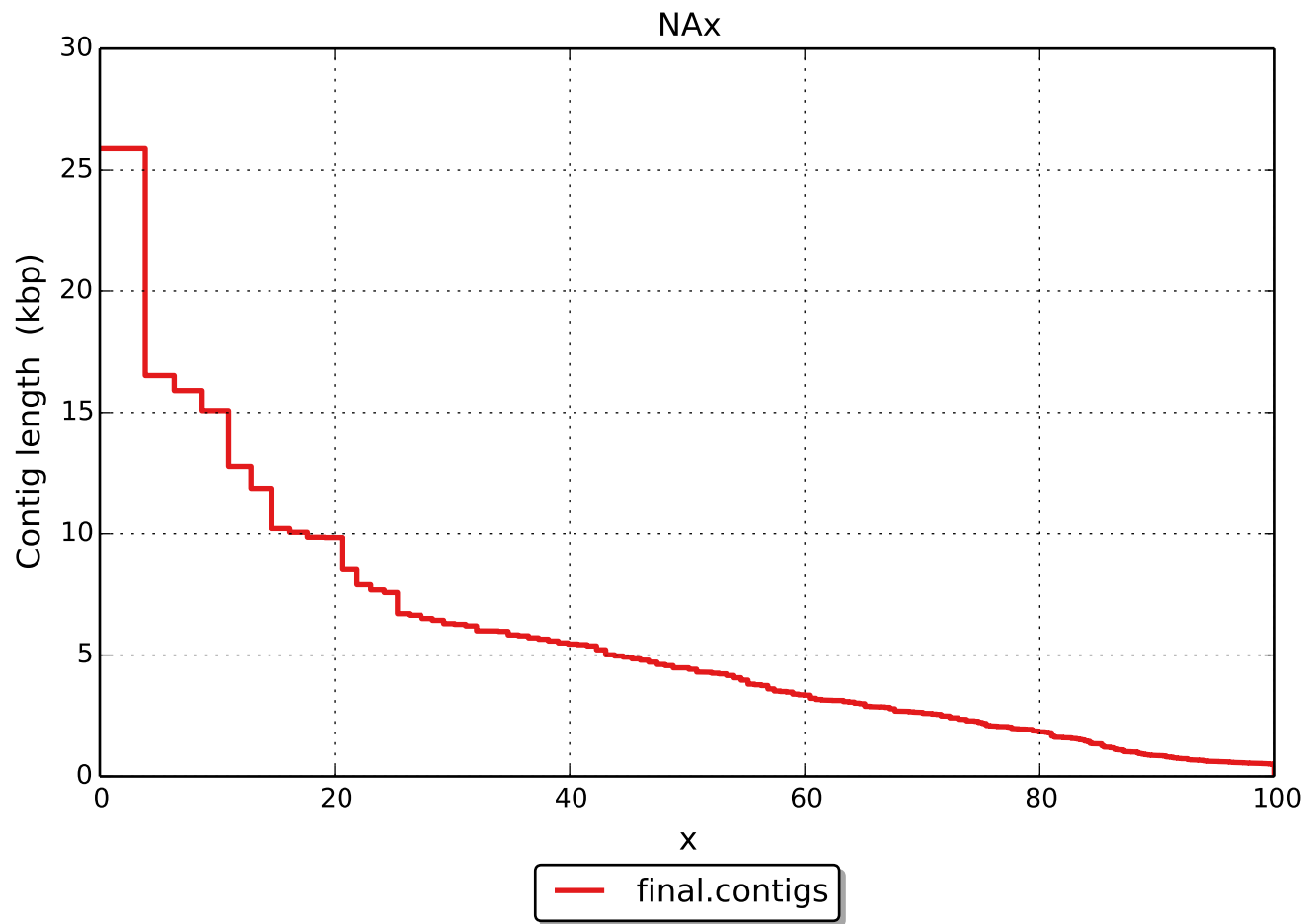


Misassemblies

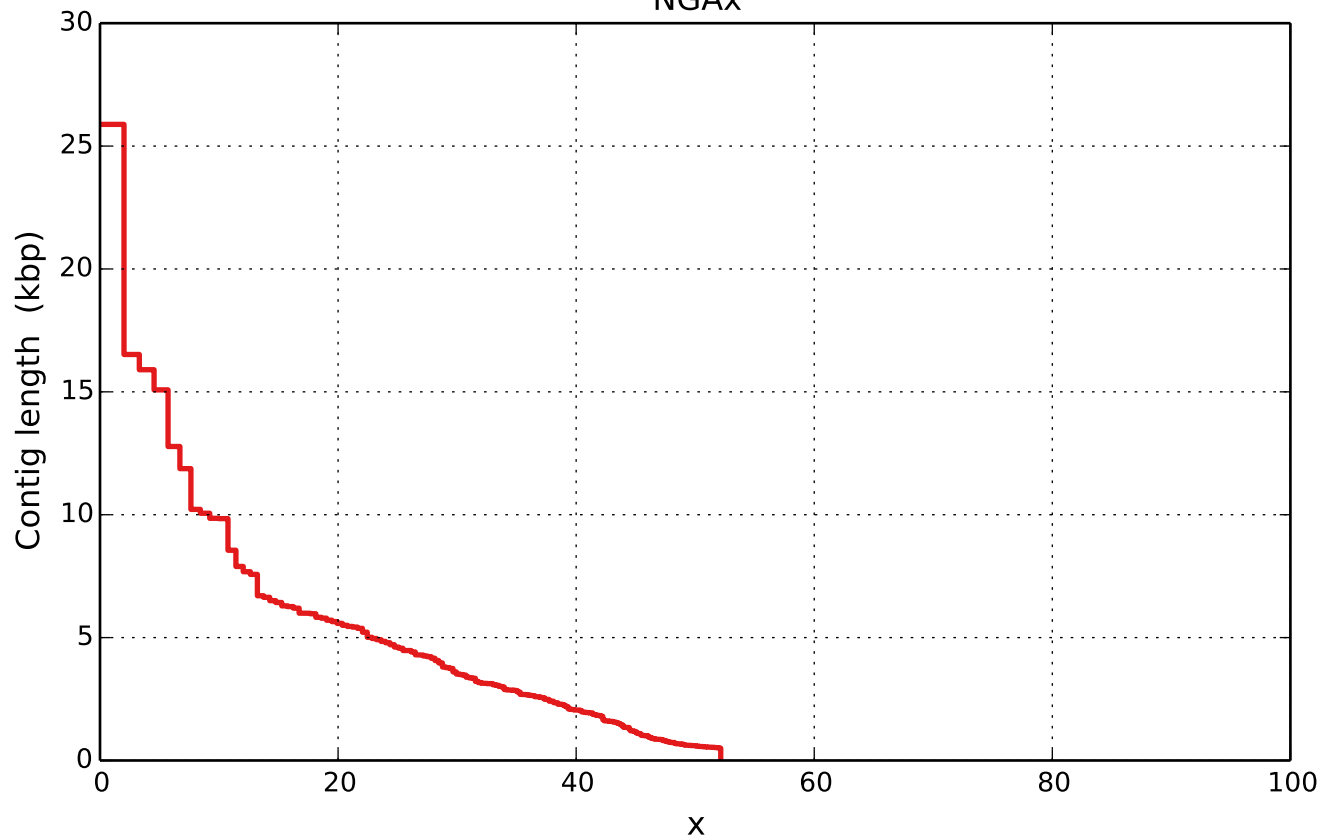


Cumulative length (aligned contigs)





NGAx



— final.contigs