

Report

	final.contigs
# contigs (≥ 1000 bp)	1623
# contigs (≥ 5000 bp)	61
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 1000 bp)	3642891
Total length (≥ 5000 bp)	385137
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	2846
Largest contig	9194
Total length	4483316
Reference length	4857432
GC (%)	52.15
Reference GC (%)	52.22
N50	2105
NG50	1923
N75	1208
NG75	999
L50	669
LG50	762
L75	1369
LG75	1624
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	1540
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	86.871
Duplication ratio	1.062
# N's per 100 kbp	0.00
# mismatches per 100 kbp	596.06
# indels per 100 kbp	0.24
Largest alignment	9194
NA50	2105
NGA50	1923
NA75	1207
NGA75	999
LA50	669
LGA50	762
LA75	1370
LGA75	1624

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

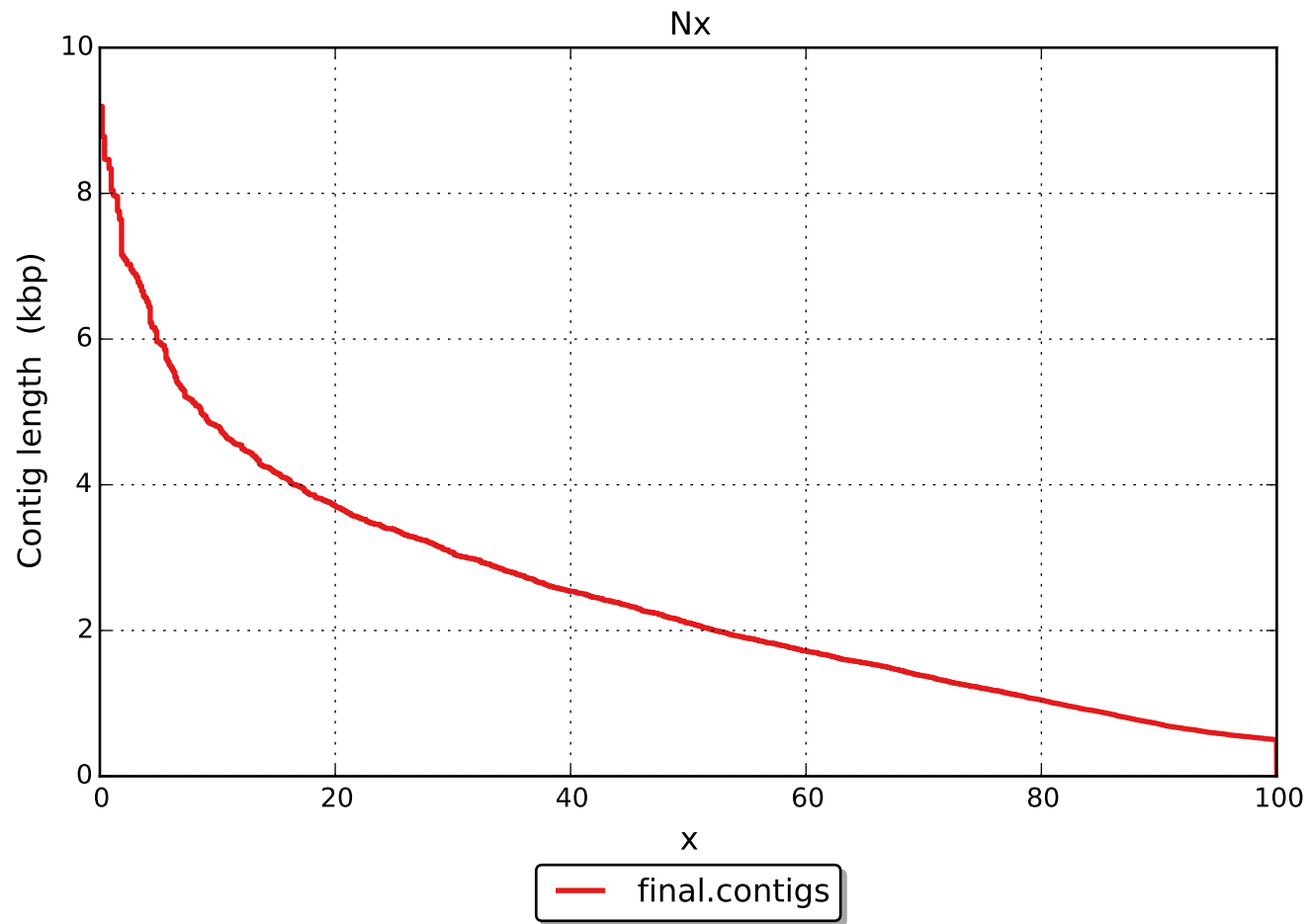
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	1540
# local misassemblies	1
# mismatches	25152
# indels	10
# short indels	10
# long indels	0
Indels length	13

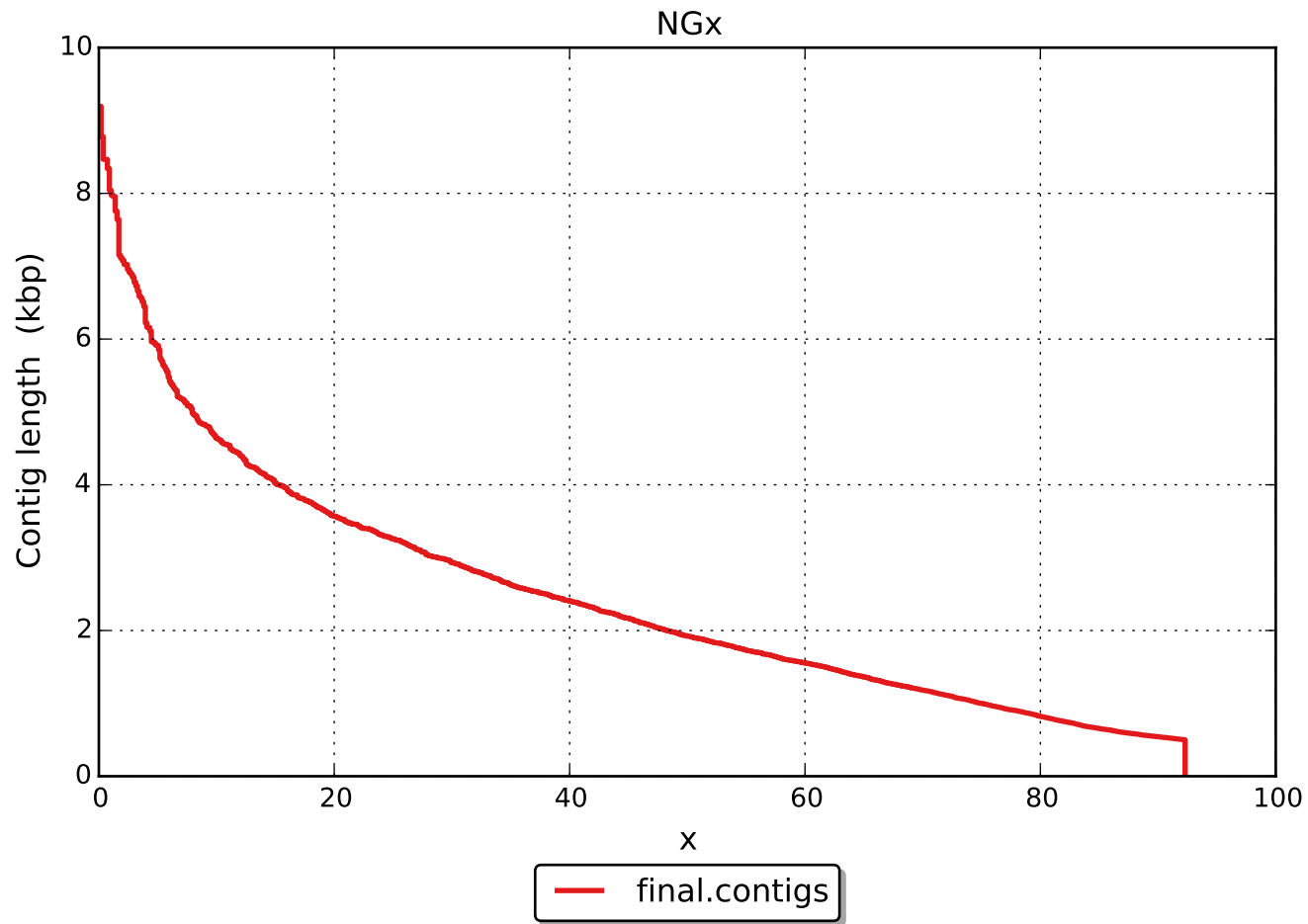
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

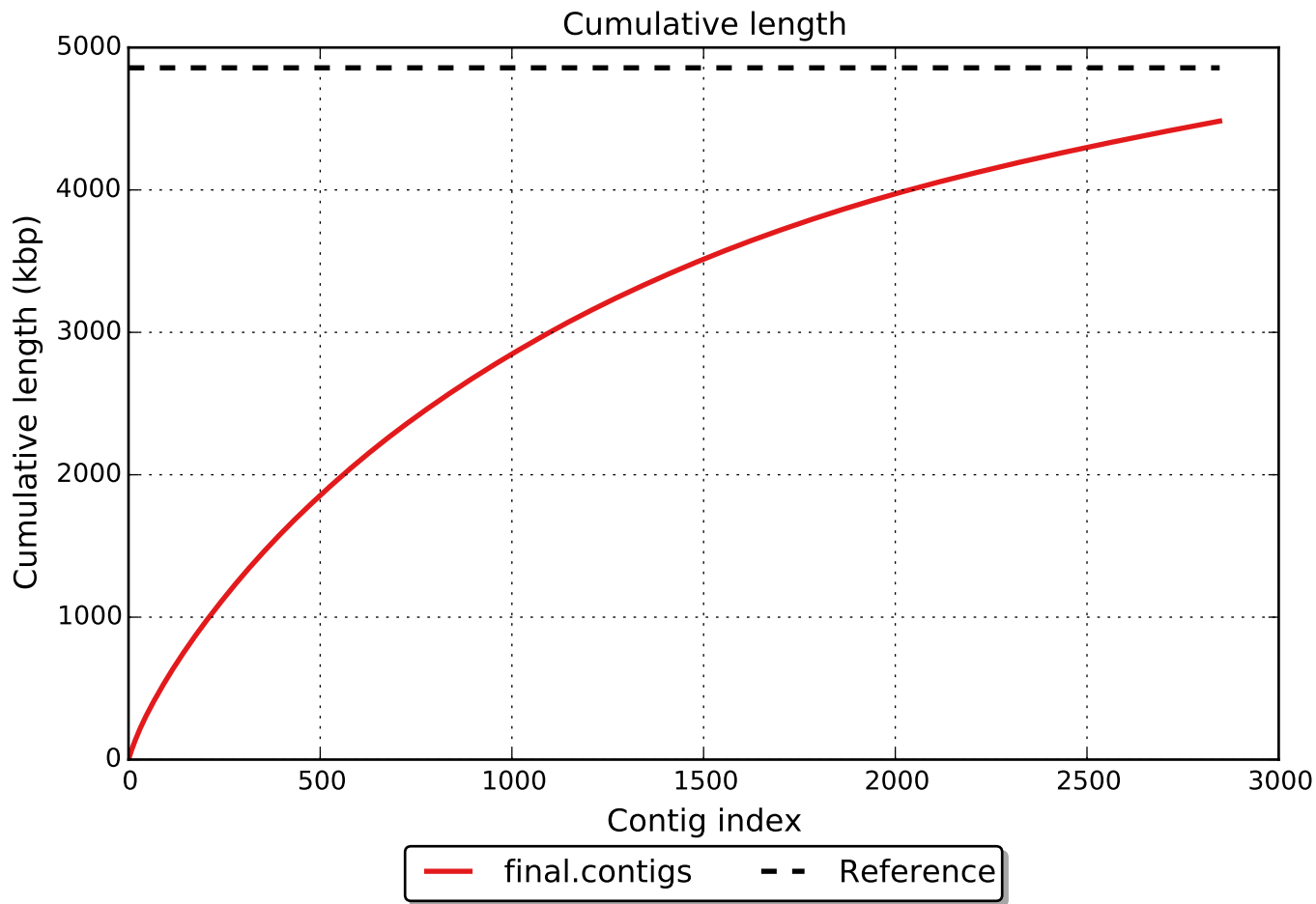
Unaligned report

	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

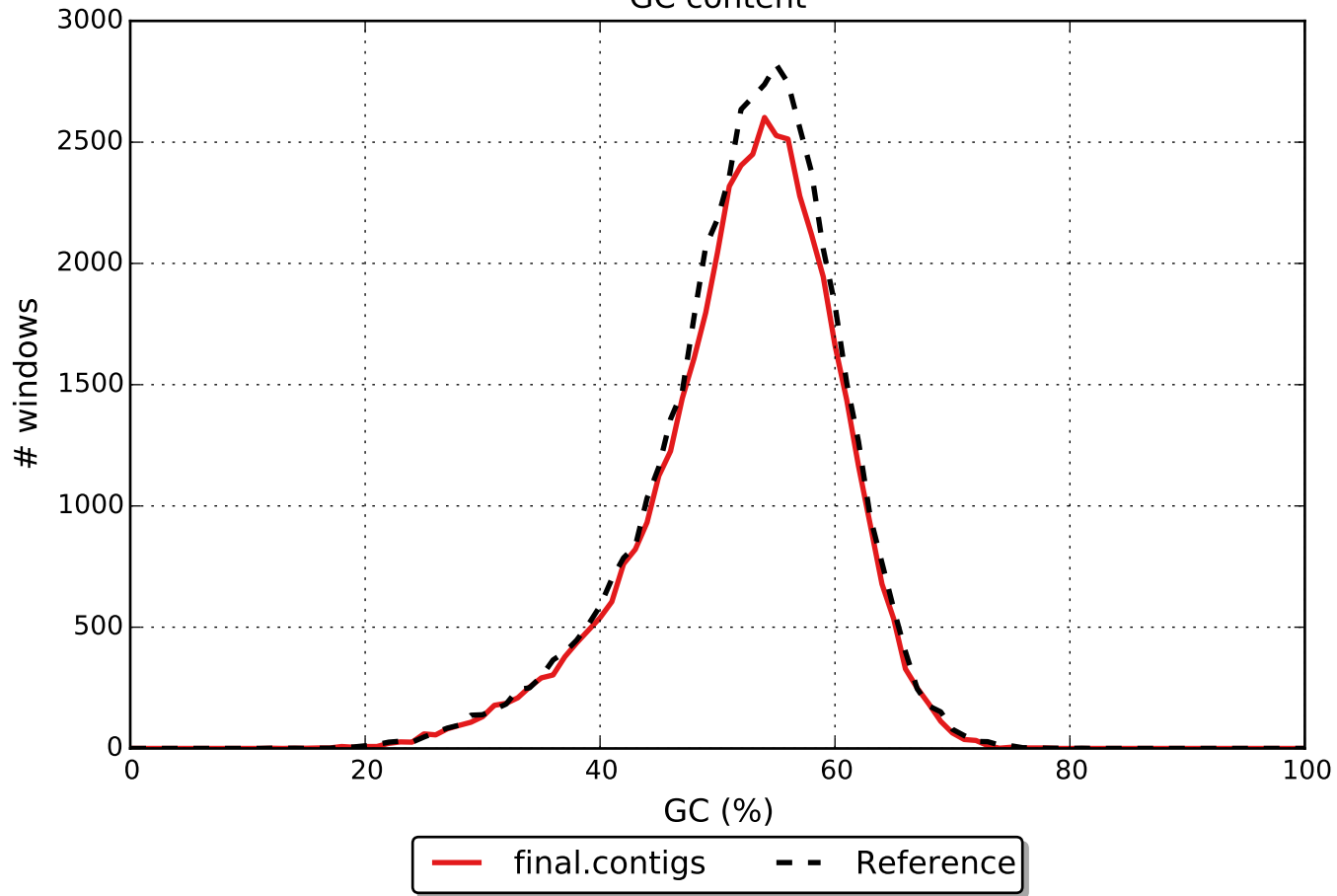
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).





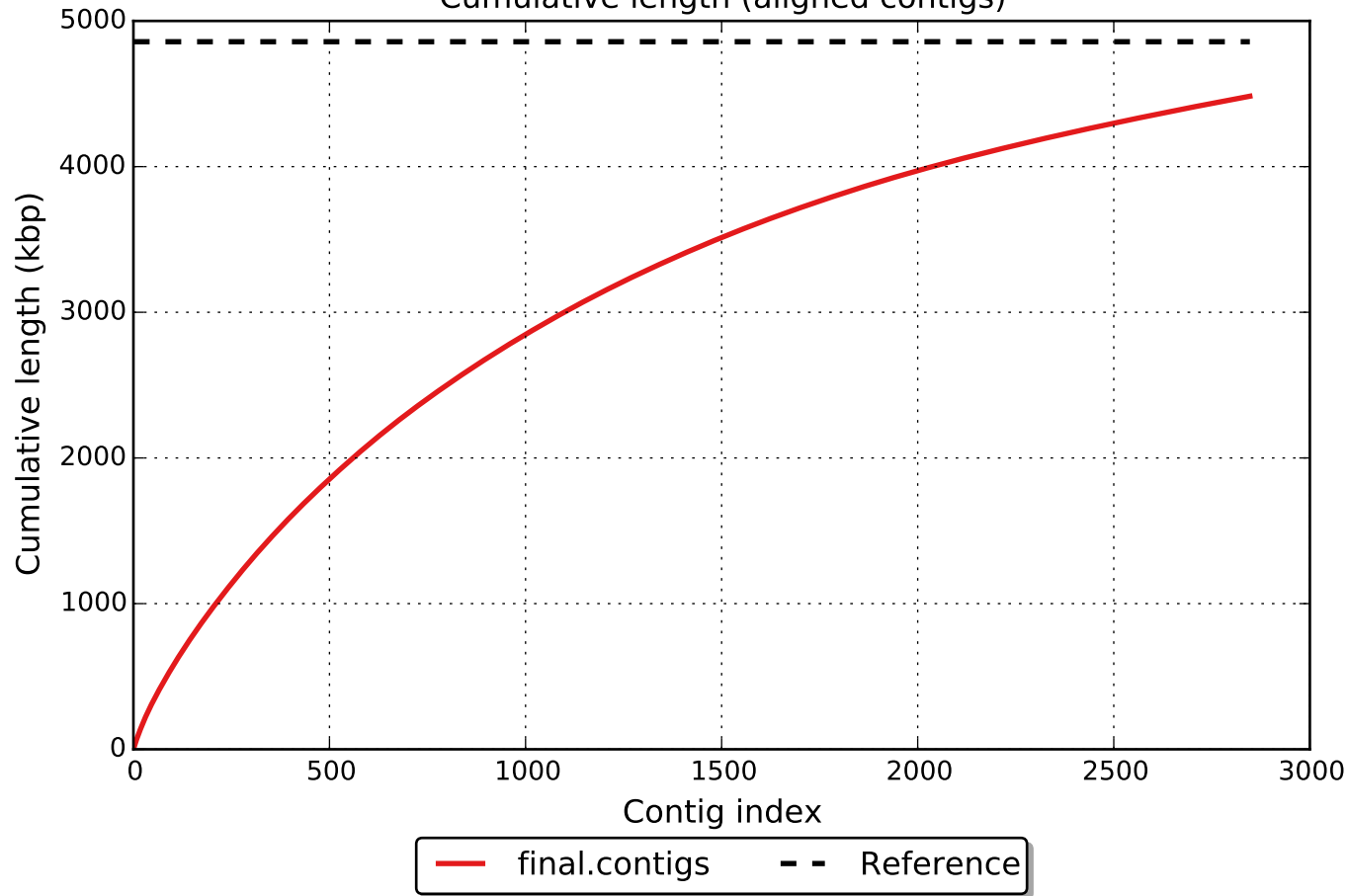


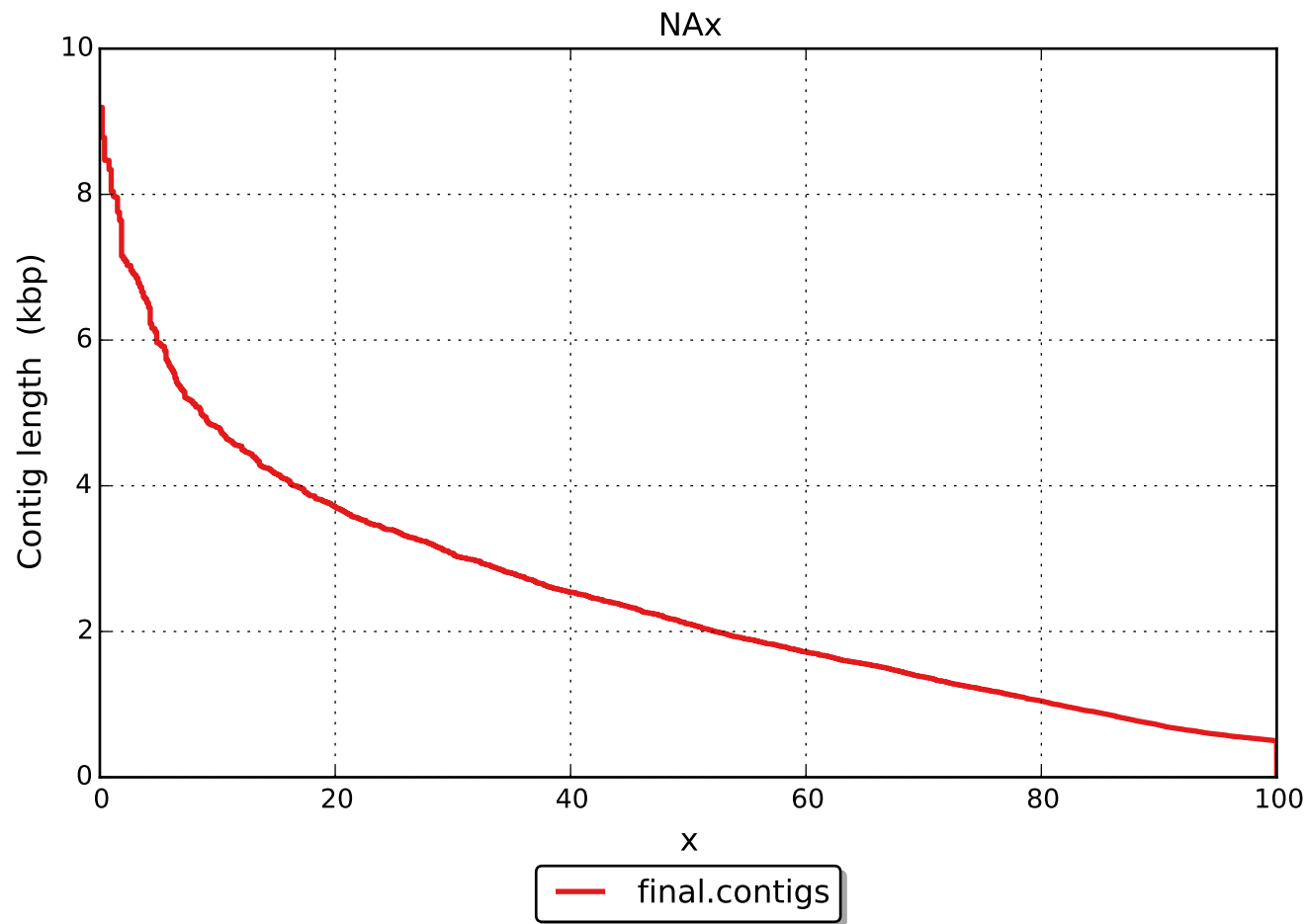
GC content





Cumulative length (aligned contigs)





NGAx

