

Report

	final.contigs
# contigs (≥ 0 bp)	631
# contigs (≥ 1000 bp)	439
Total length (≥ 0 bp)	1284116
Total length (≥ 1000 bp)	1140822
# contigs	631
Largest contig	11378
Total length	1284116
Reference length	641799
GC (%)	26.29
Reference GC (%)	26.30
N50	2787
NG50	4314
N75	1631
NG75	3510
L50	149
LG50	55
L75	301
LG75	96
# misassemblies	41
# misassembled contigs	39
Misassembled contigs length	143887
# local misassemblies	0
# unaligned contigs	6 + 6 part
Unaligned length	10565
Genome fraction (%)	97.923
Duplication ratio	2.026
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1943.44
# indels per 100 kbp	2.23
Largest alignment	10913
NA50	2541
NGA50	4063
NA75	1516
NGA75	3267
LA50	159
LGA50	59
LA75	324
LGA75	102

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	41
# relocations	40
# translocations	0
# inversions	1
# possibly misassembled contigs	3
# misassembled contigs	39
Misassembled contigs length	143887
# local misassemblies	0
# mismatches	12214
# indels	14
# short indels	14
# long indels	0
Indels length	14

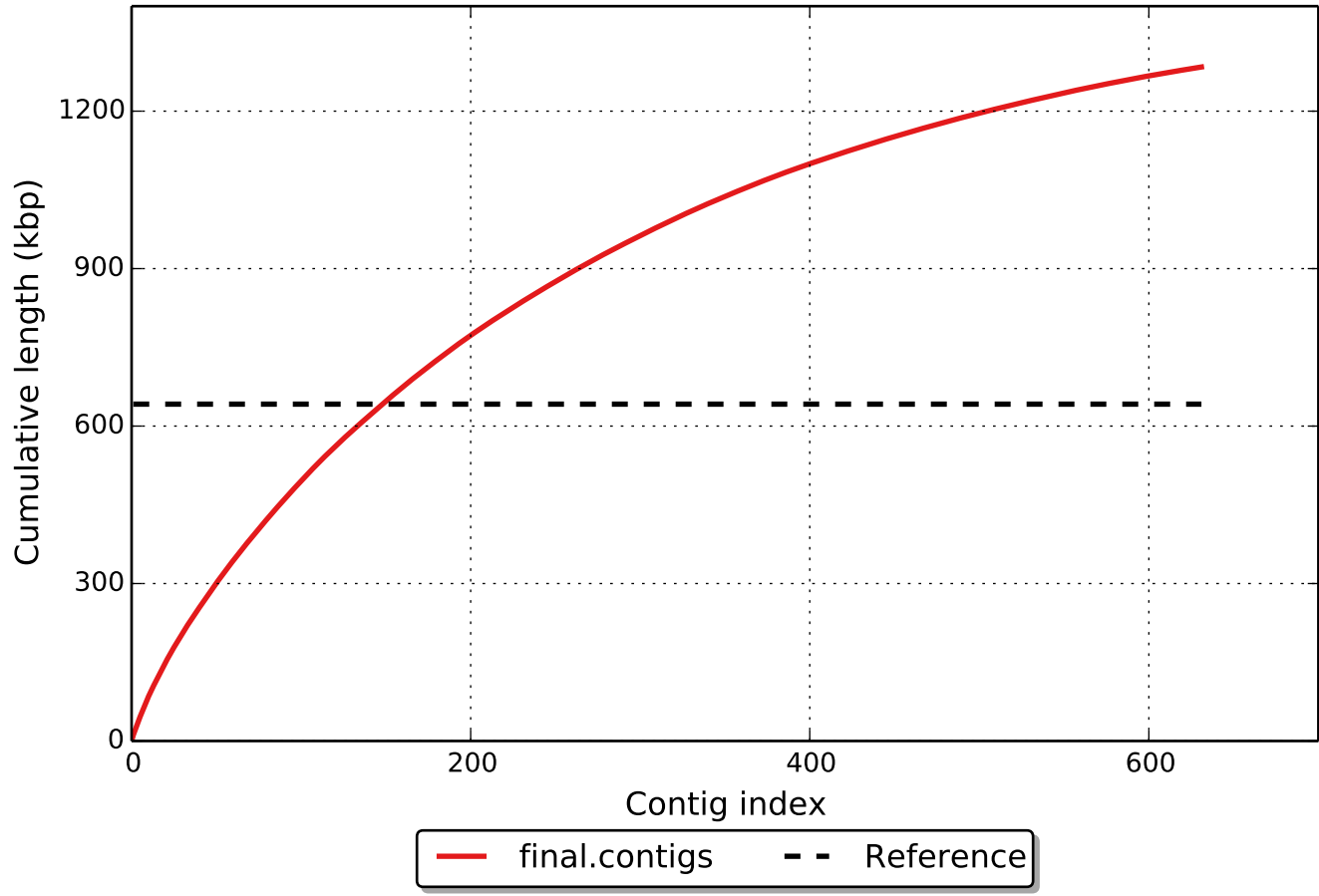
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

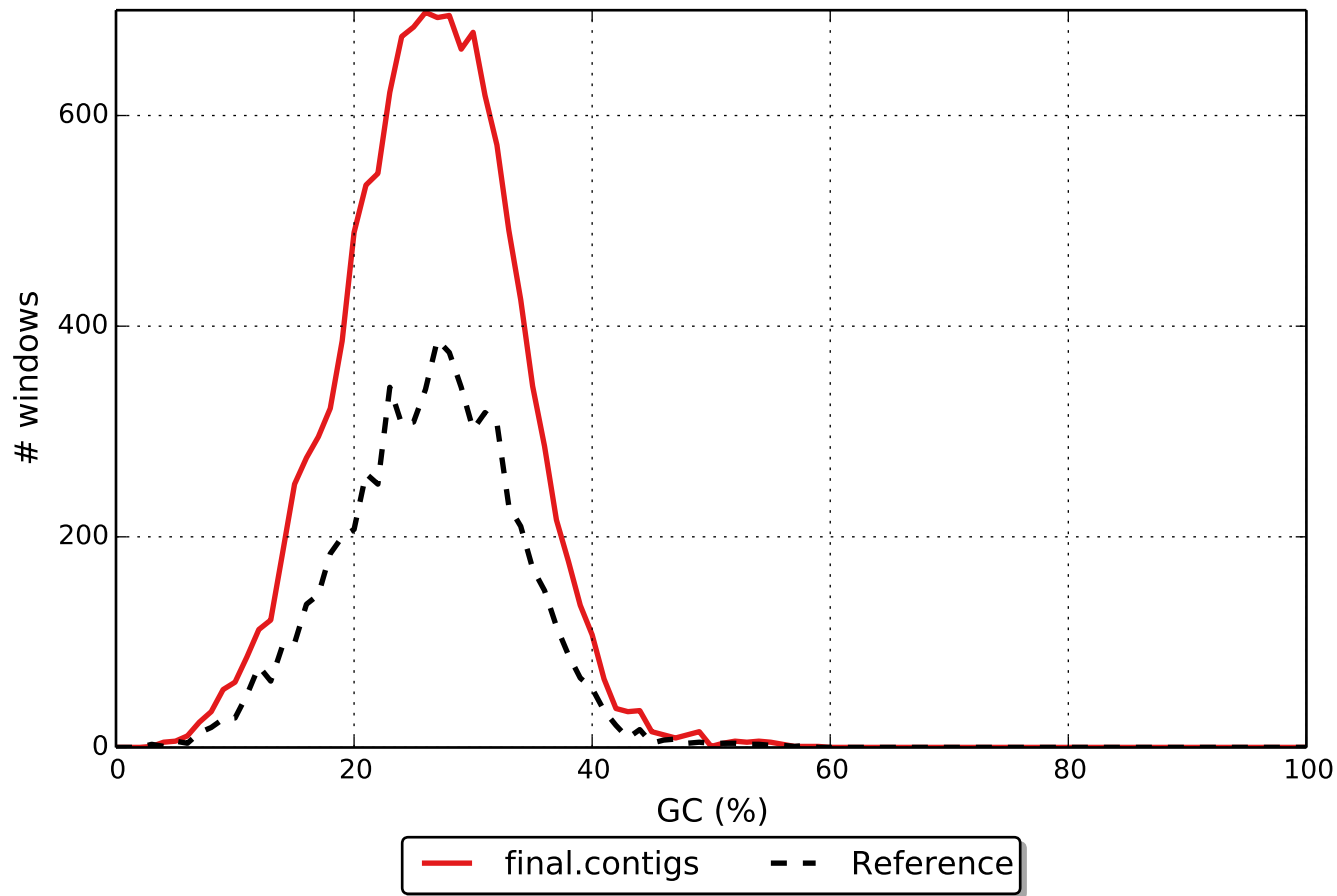
	final.contigs
# fully unaligned contigs	6
Fully unaligned length	6285
# partially unaligned contigs	6
# with misassembly	0
# both parts are significant	3
Partially unaligned length	4280
# N's	0

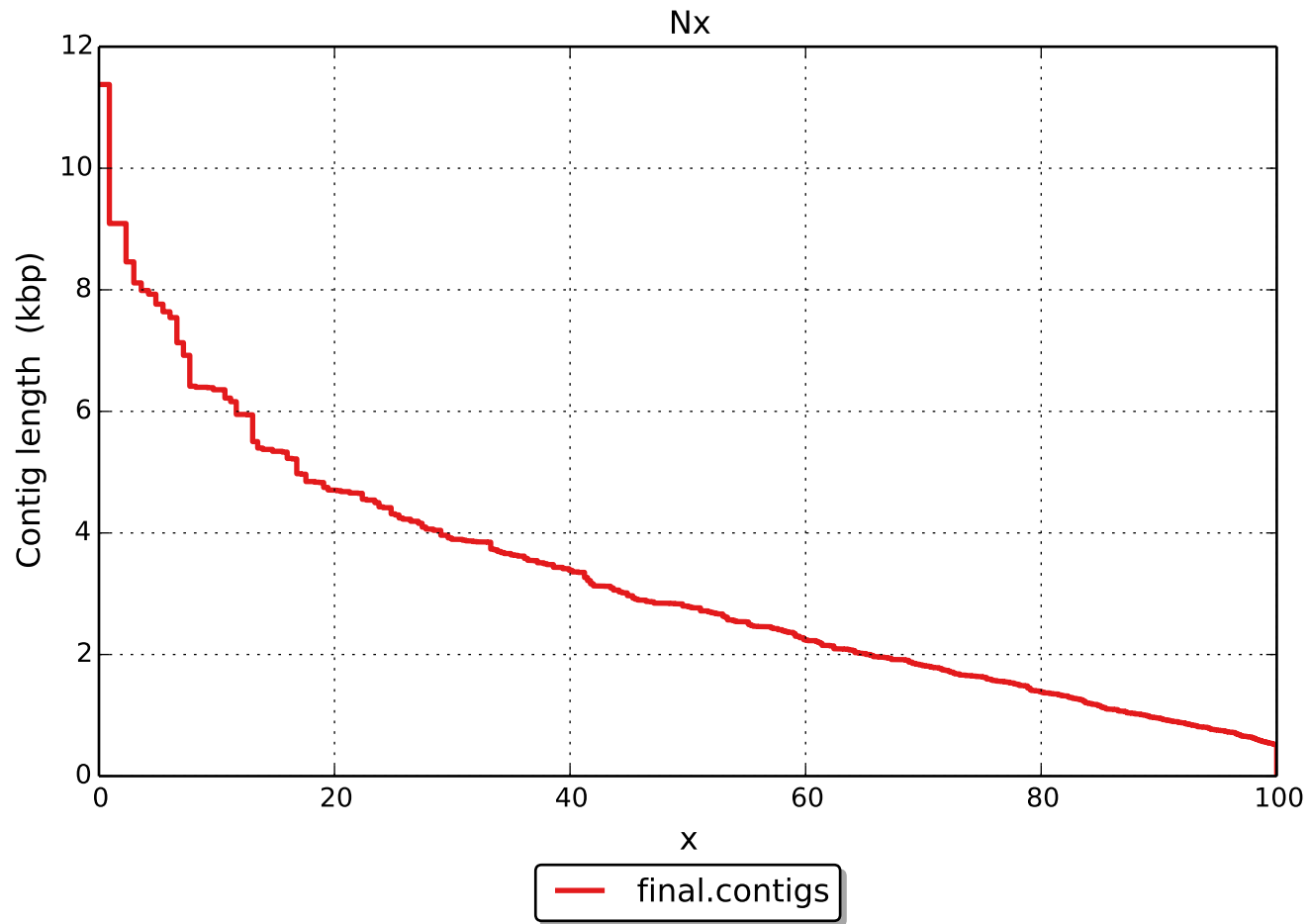
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

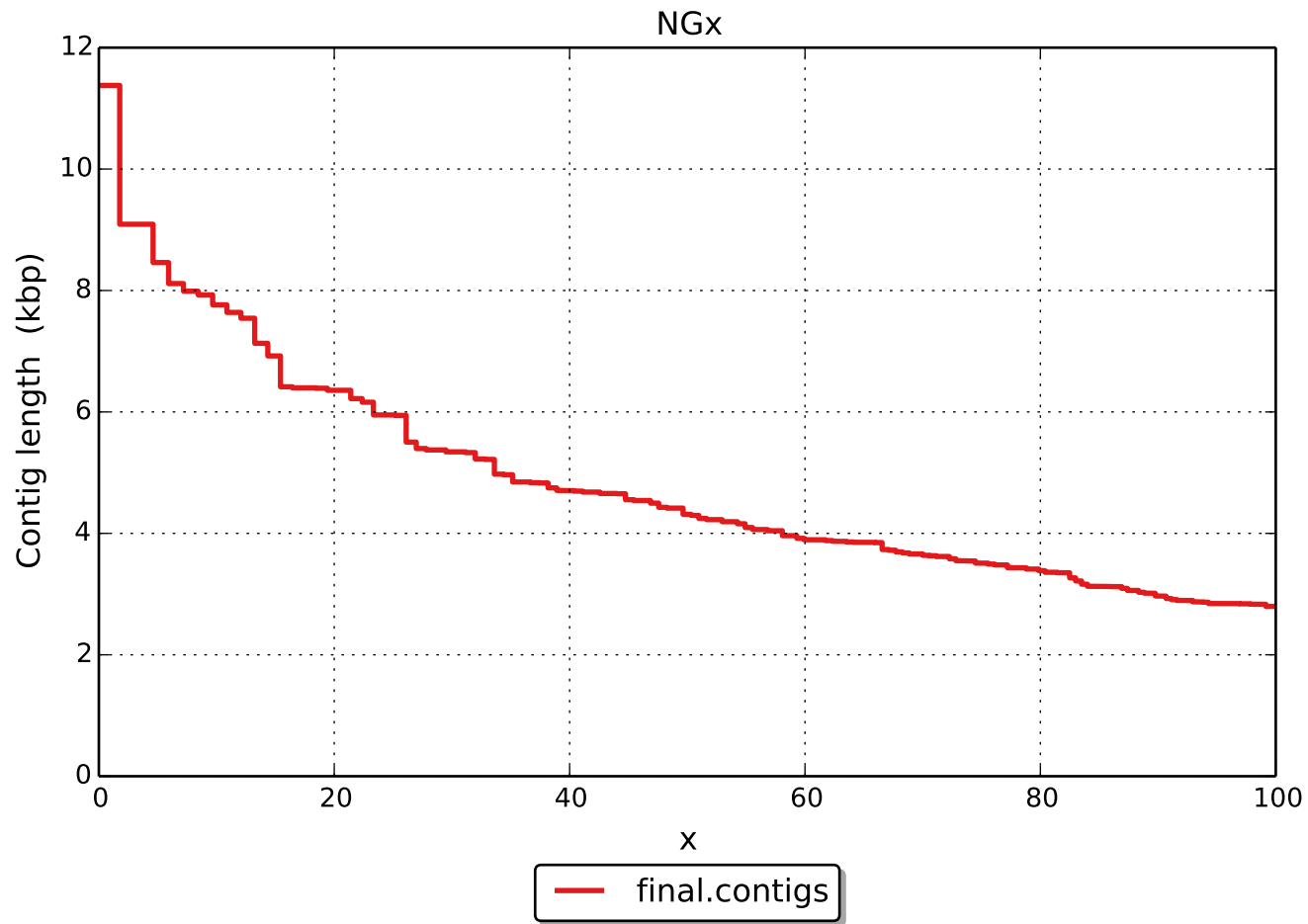
Cumulative length



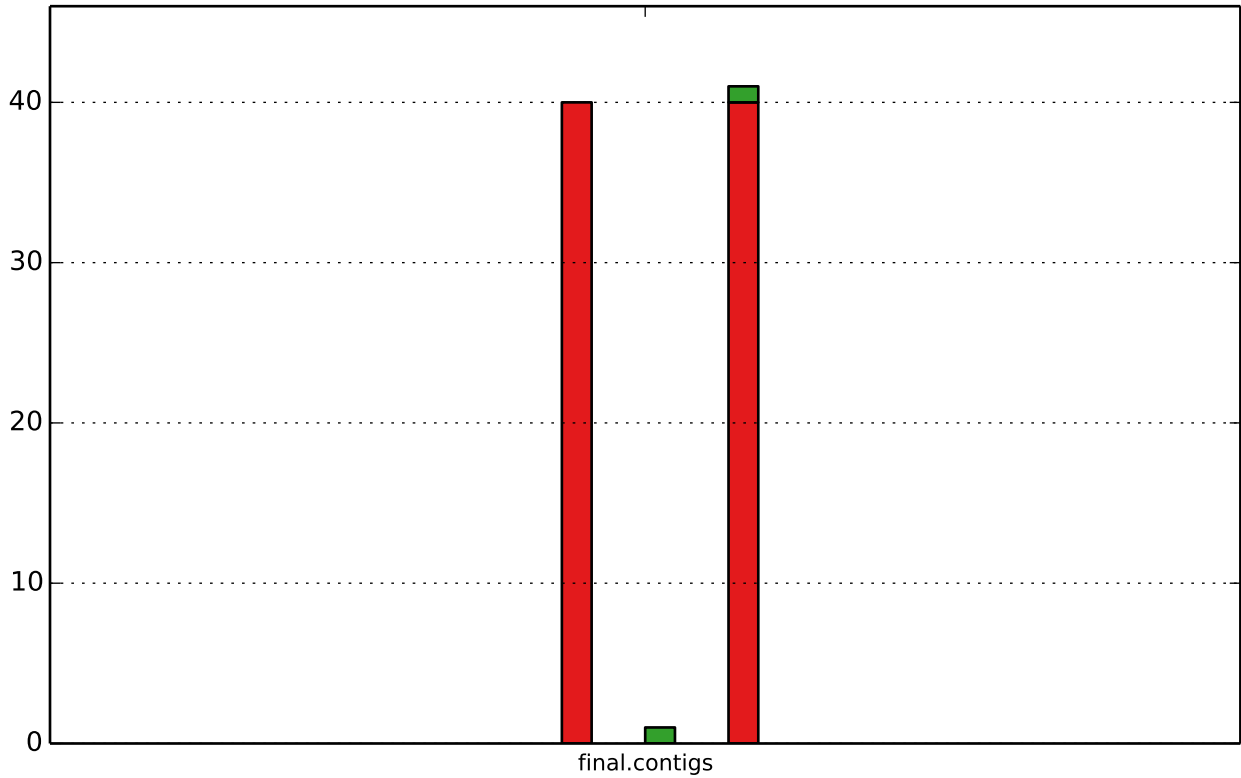
GC content



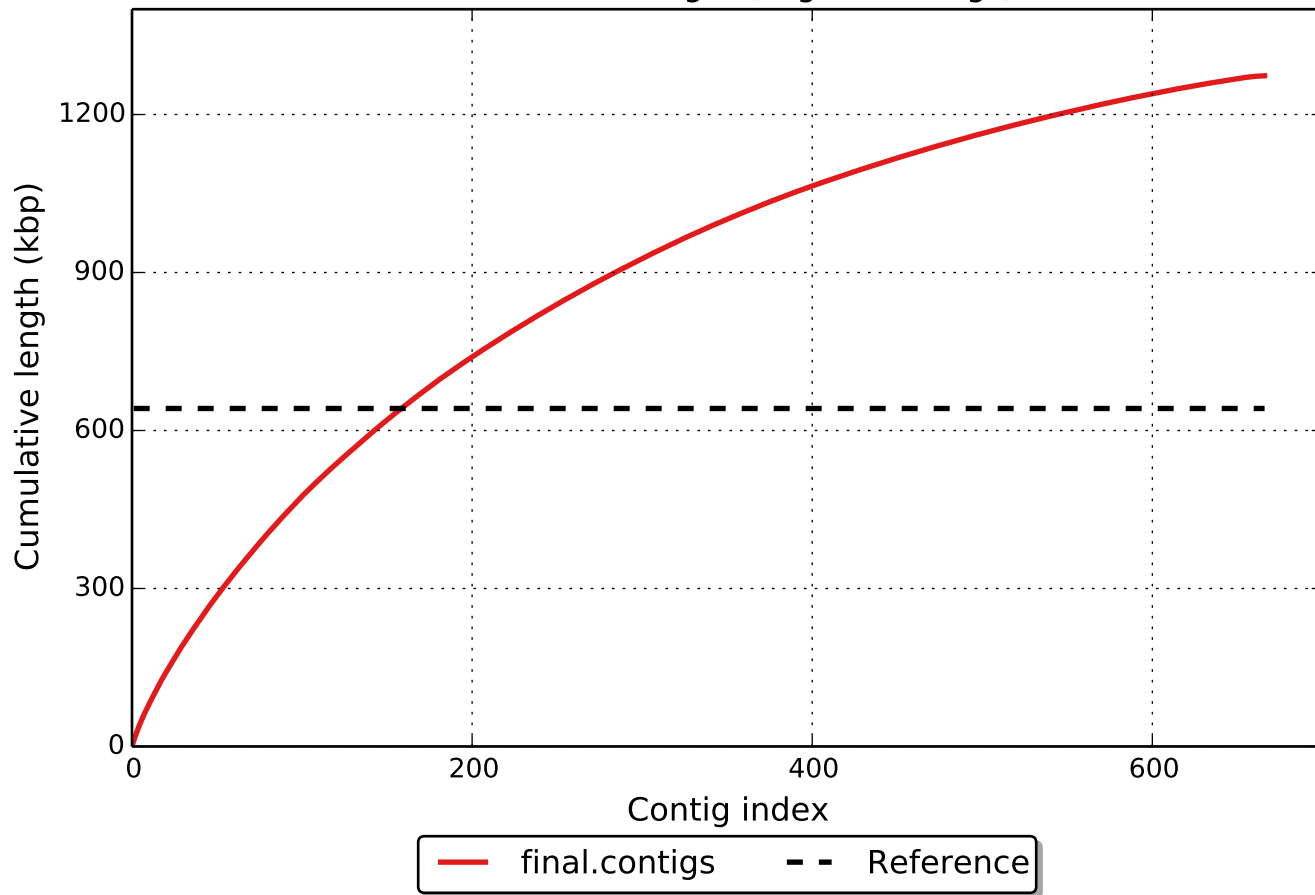


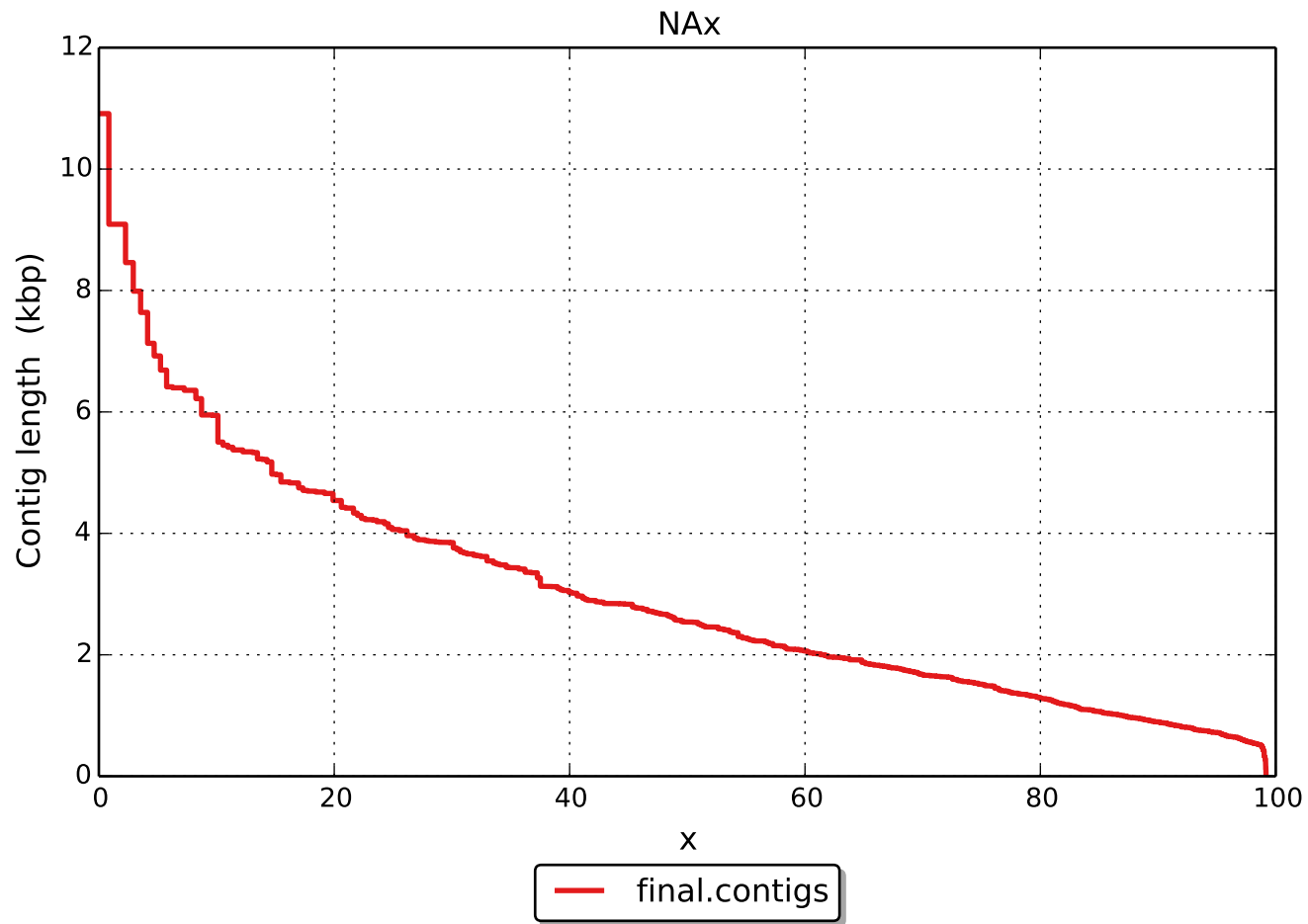


Misassemblies



Cumulative length (aligned contigs)





NGAx

