

Report

	final.contigs
# contigs (>= 1000 bp)	580
# contigs (>= 5000 bp)	333
# contigs (>= 10000 bp)	155
# contigs (>= 25000 bp)	18
# contigs (>= 50000 bp)	1
Total length (>= 1000 bp)	4691740
Total length (>= 5000 bp)	3995466
Total length (>= 10000 bp)	2701985
Total length (>= 25000 bp)	563905
Total length (>= 50000 bp)	51384
# contigs	622
Largest contig	51384
Total length	4724919
Reference length	4641652
GC (%)	50.80
Reference GC (%)	50.78
N50	11772
NG50	12256
N75	6895
NG75	7098
L50	124
LG50	121
L75	256
LG75	247
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	16627
Genome fraction (%)	99.869
Duplication ratio	1.016
# N's per 100 kbp	0.00
# mismatches per 100 kbp	28.99
# indels per 100 kbp	0.09
Largest alignment	51384
NA50	11754
NGA50	12199
NA75	6809
NGA75	7039
LA50	125
LGA50	122
LA75	259
LGA75	250

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

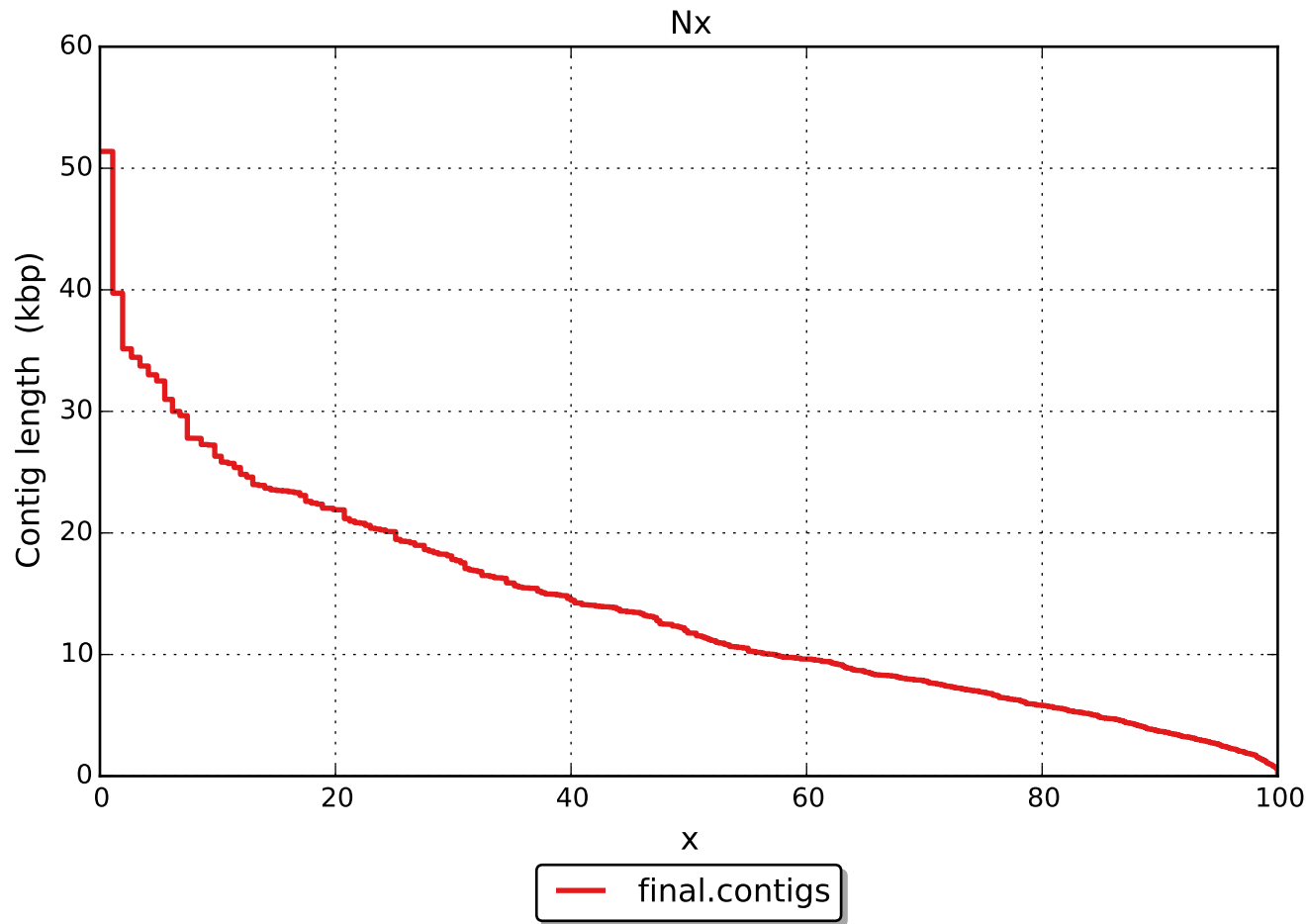
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	1
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	1344
# indels	4
# short indels	4
# long indels	0
Indels length	4

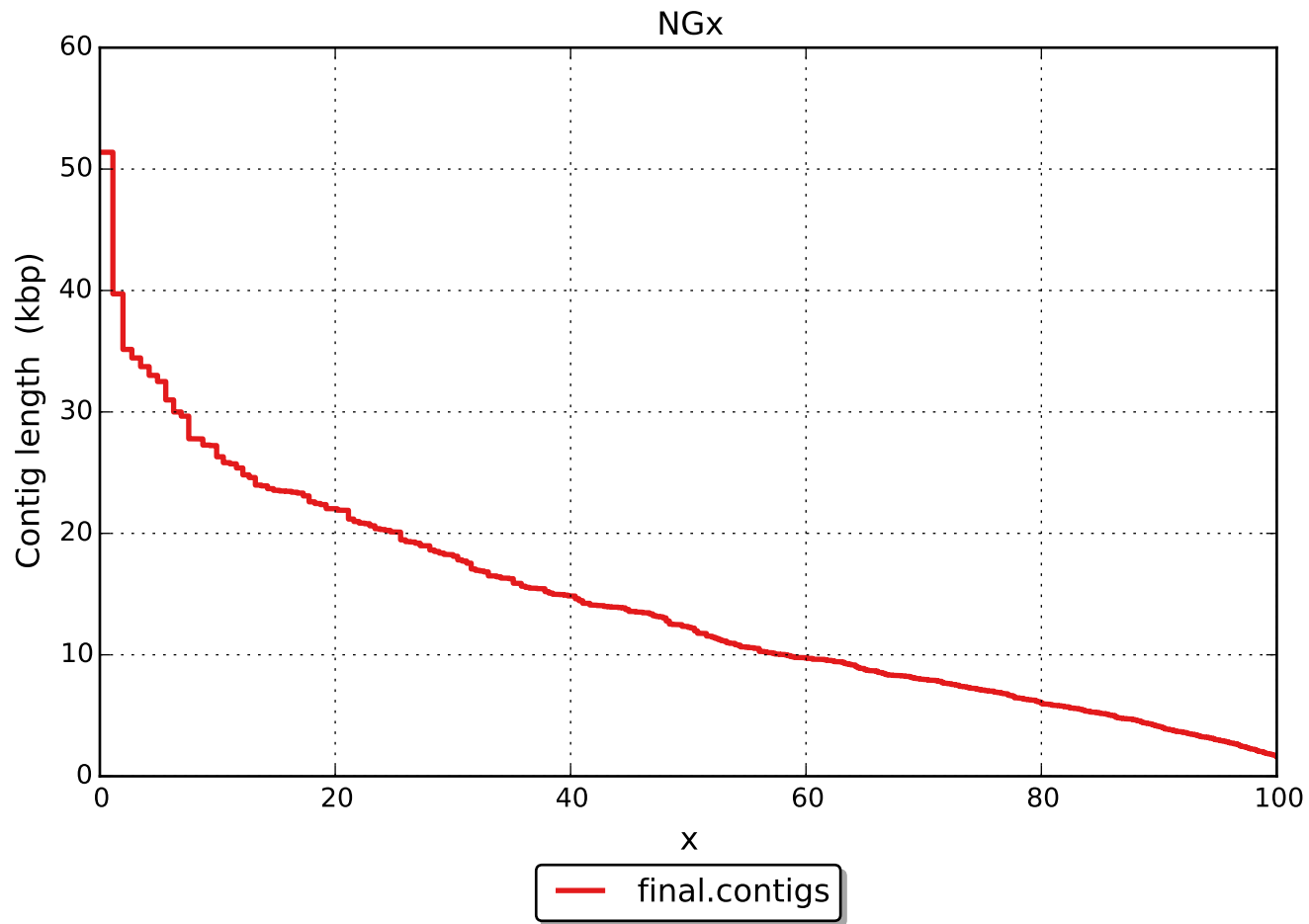
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

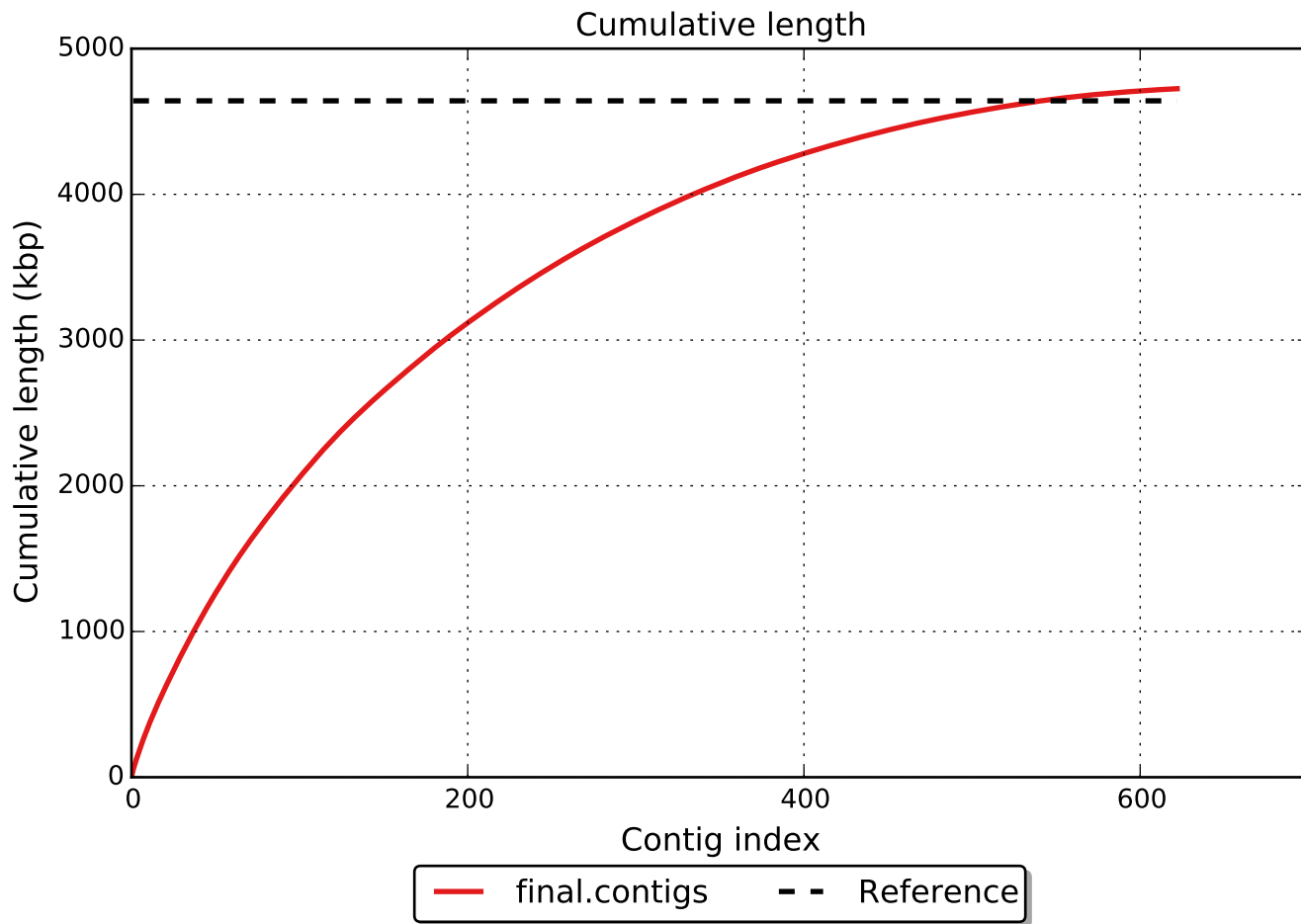
Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	1
Partially unaligned length	16627
# N's	0

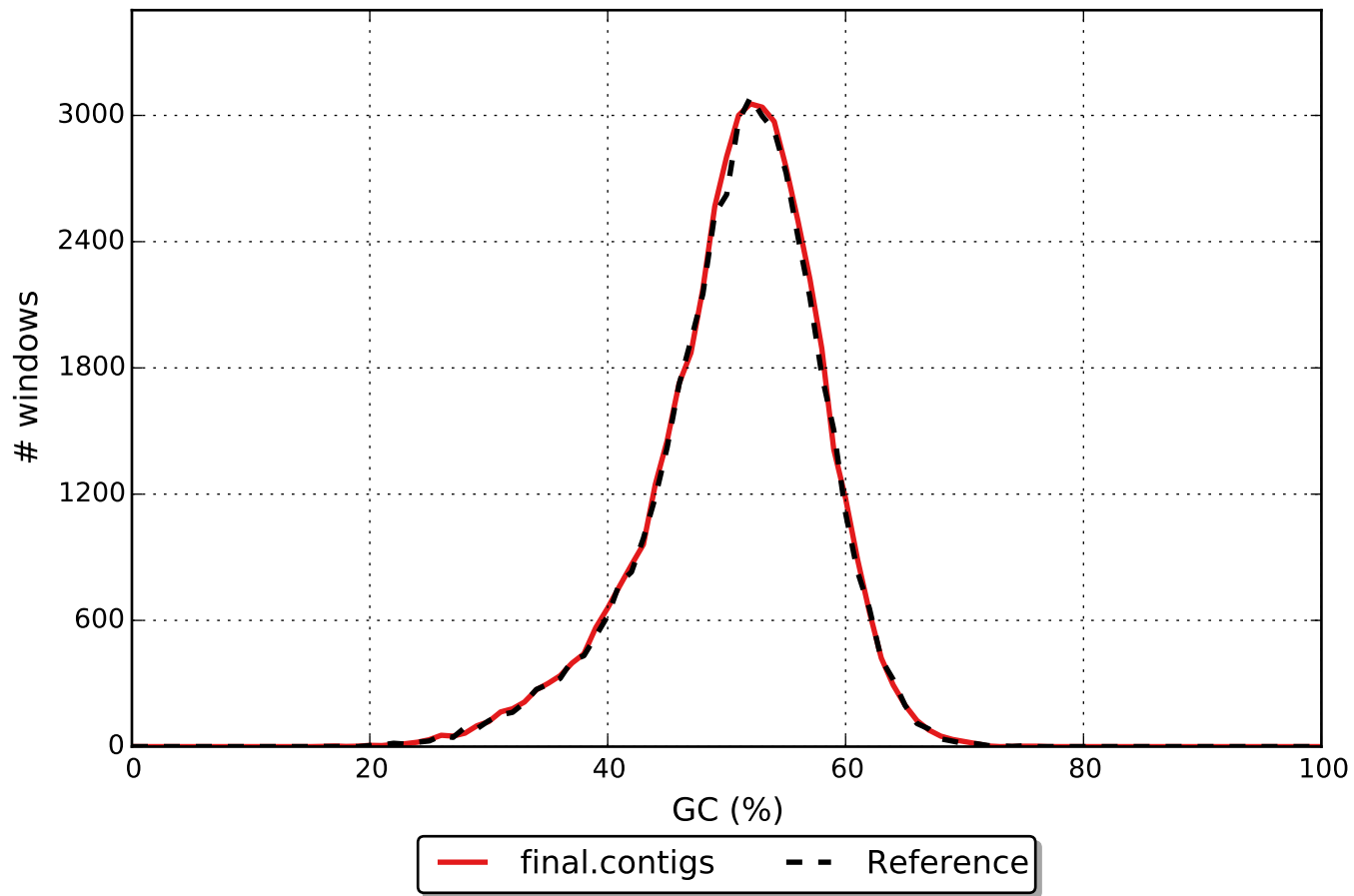
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).







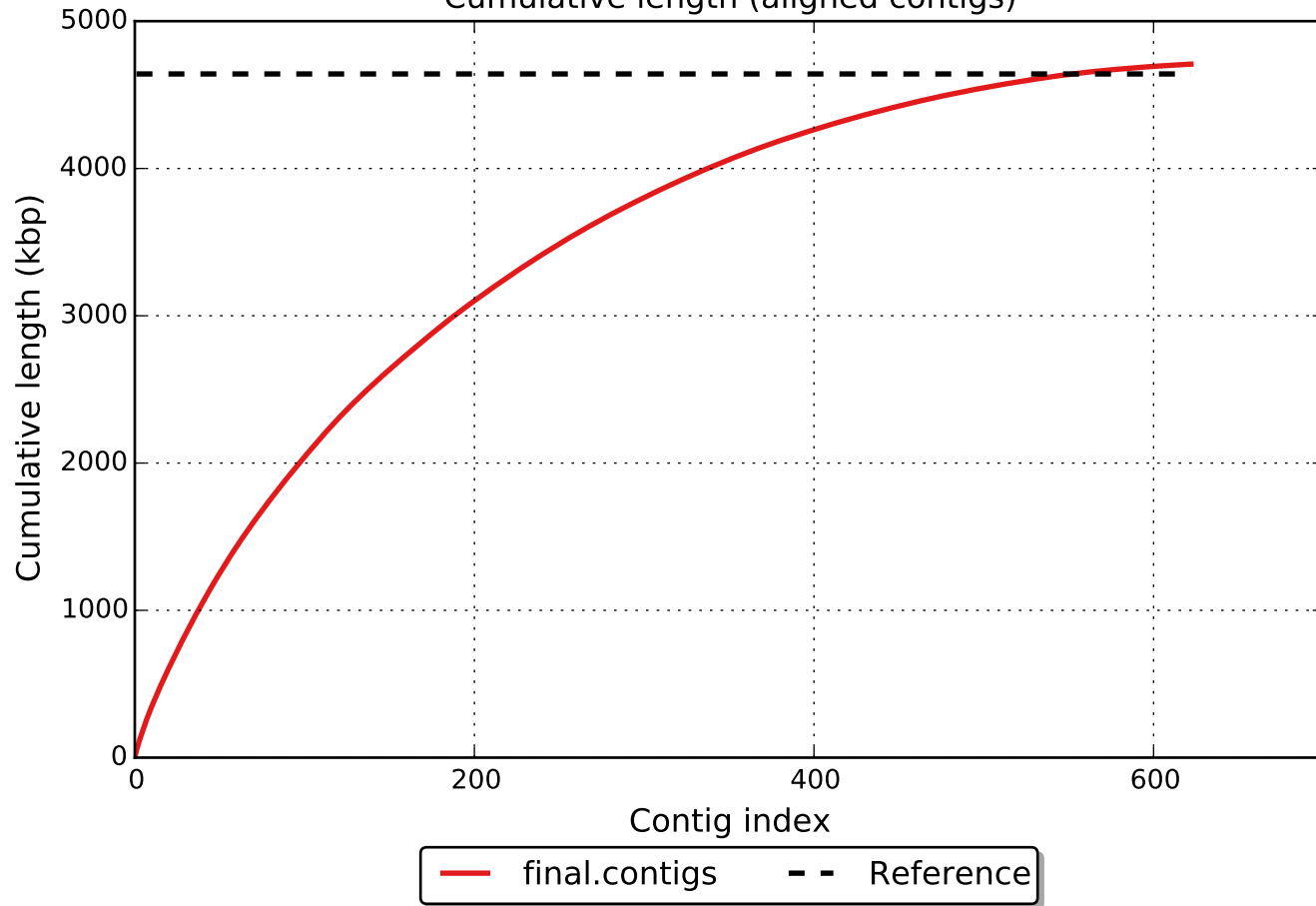
GC content

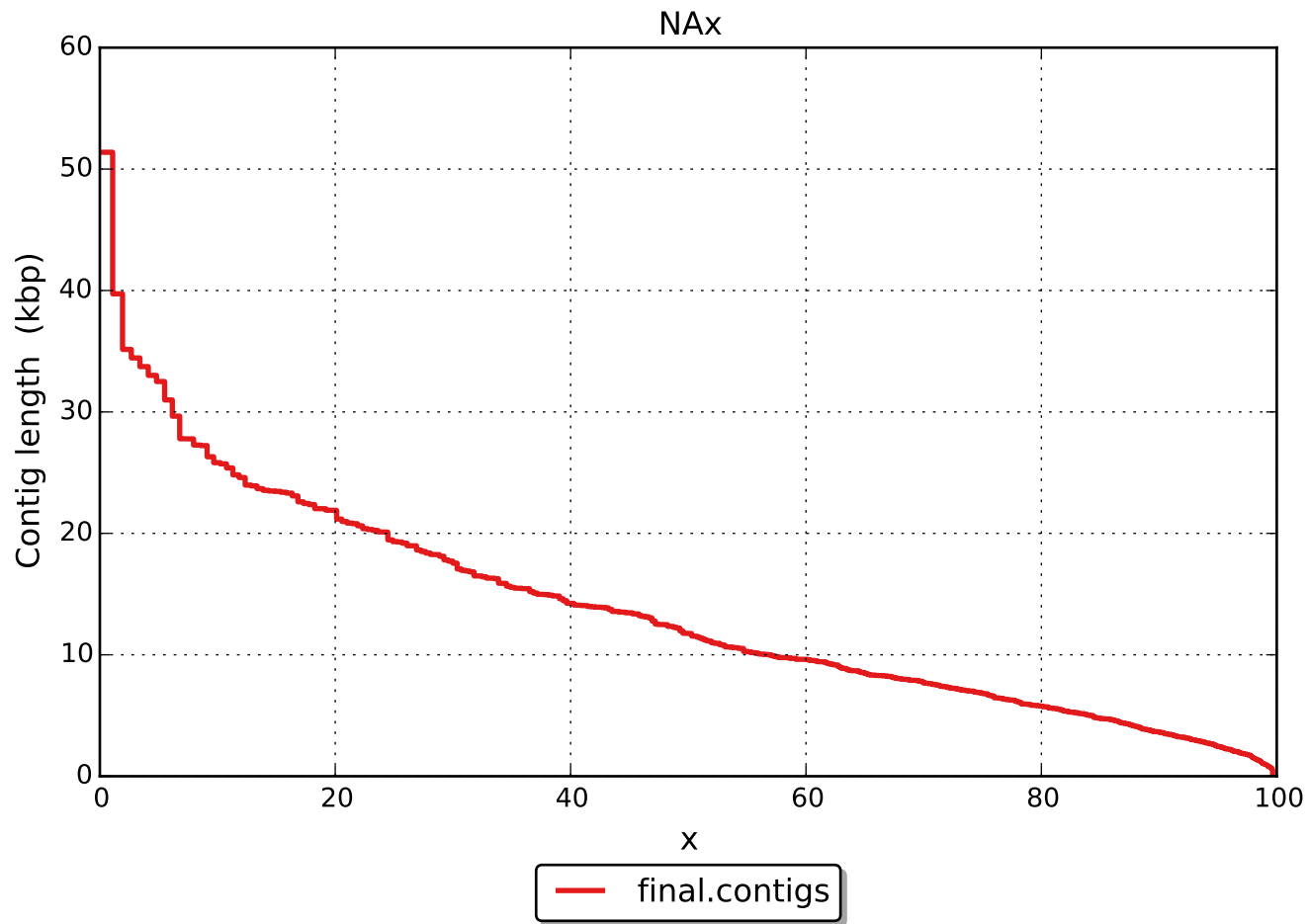


Misassemblies



Cumulative length (aligned contigs)





NGAx

