Report

	final.contigs
# contigs (>= 0 bp)	14516
# contigs (>= 1000 bp)	3305
Total length (>= 0 bp)	10906907
Total length (>= 1000 bp)	4828390
# contigs	9297
Largest contig	4582
Total length	9059430
Reference length	11094646
GC (%)	50.38
Reference GC (%)	50.48
N50	1044
NG50	899
N75	742
NG75	579
L50	3013
LG50	4065
L75	5595
LG75	7925
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	2463
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	77.964
Duplication ratio	1.047
# N's per 100 kbp	0.00
# mismatches per 100 kbp	80.13
# indels per 100 kbp	0.16
Largest alignment	4582
NA50	1044
NGA50	899
NA75	741
NGA75	579
LA50	3013
LGA50	4065
LA75	5596
LGA75	7926

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).
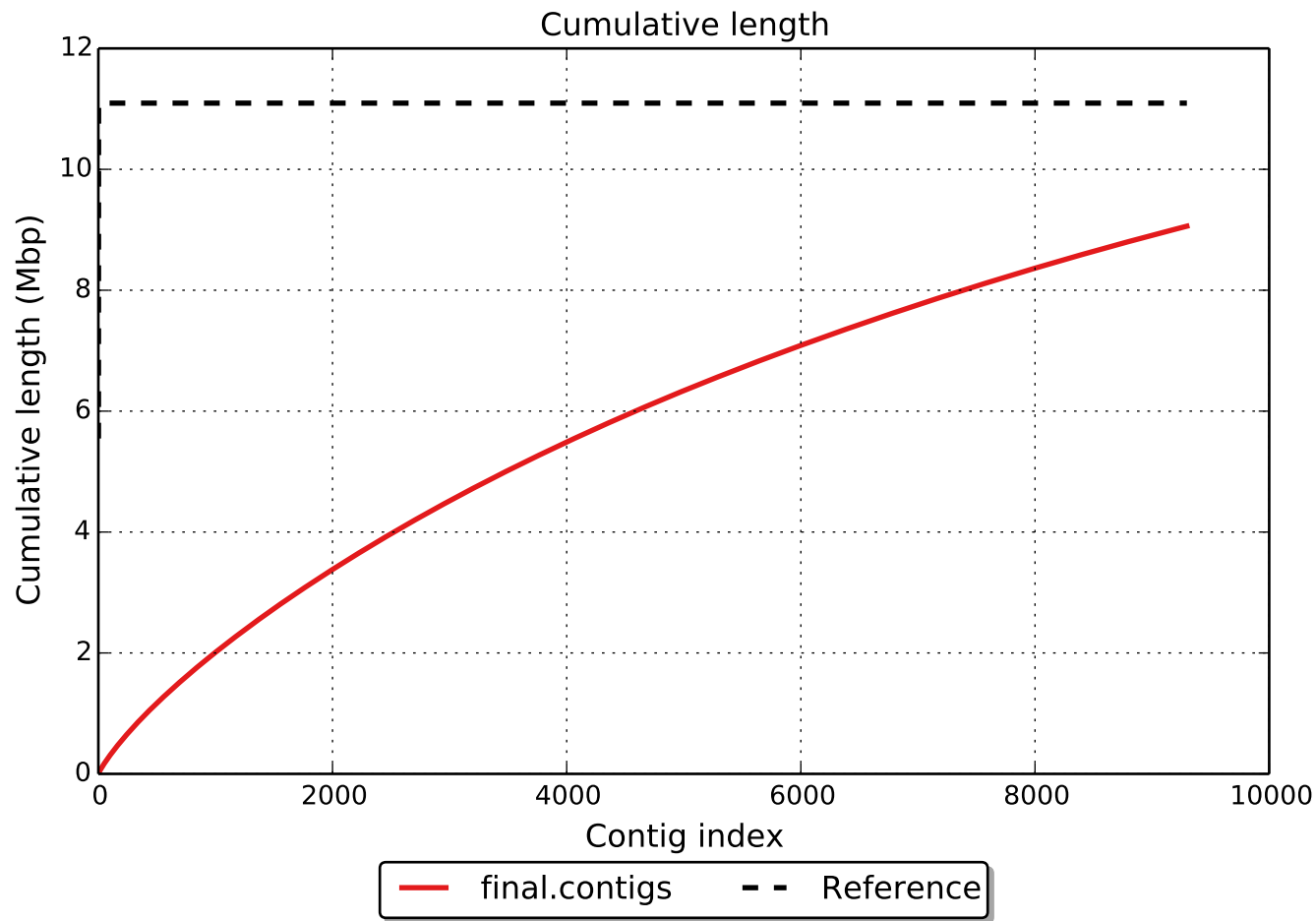
Misassemblies report

	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	2463
# local misassemblies	1
# mismatches	6931
# indels	14
# short indels	14
# long indels	0
Indels length	15

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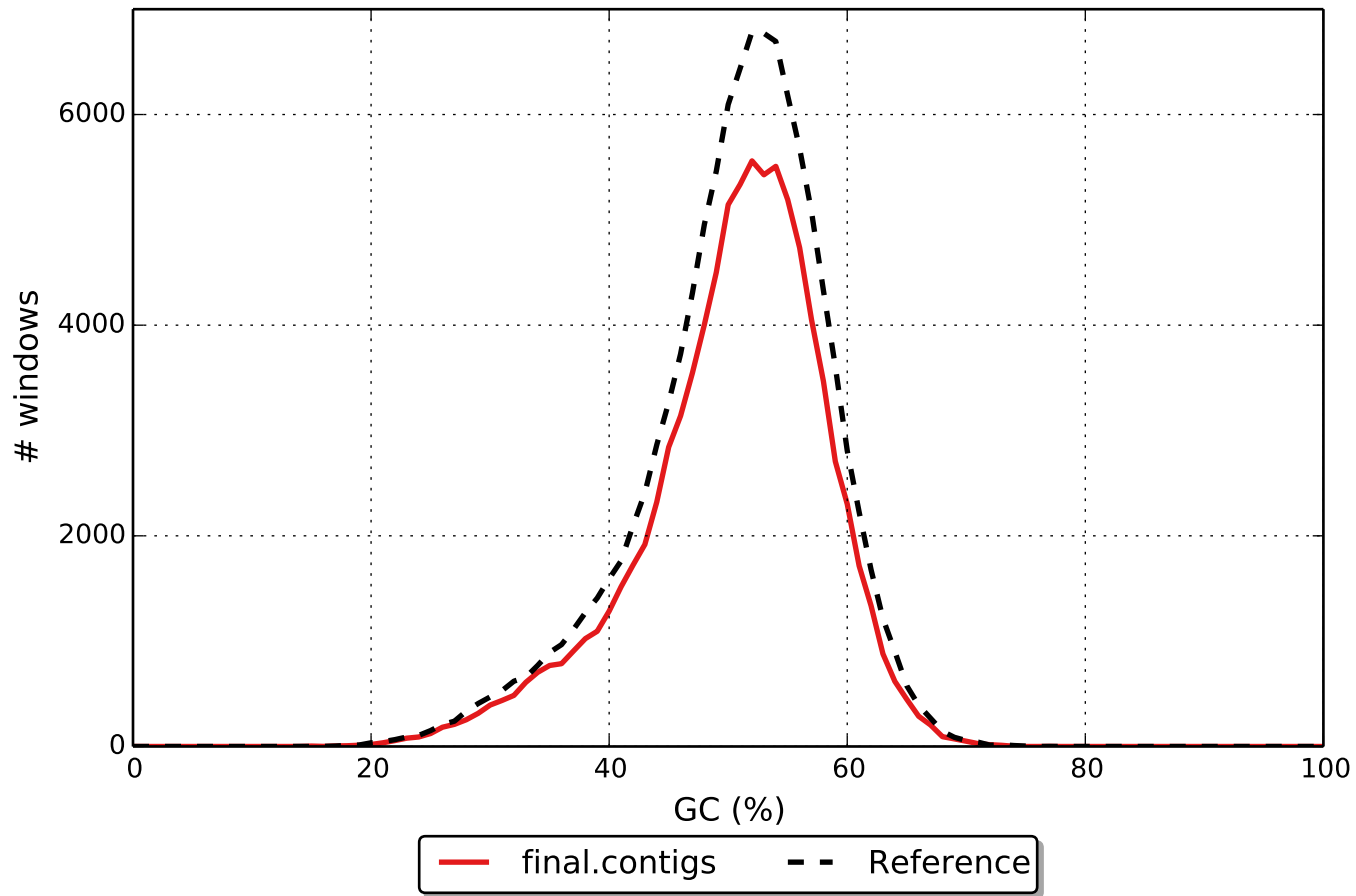(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).
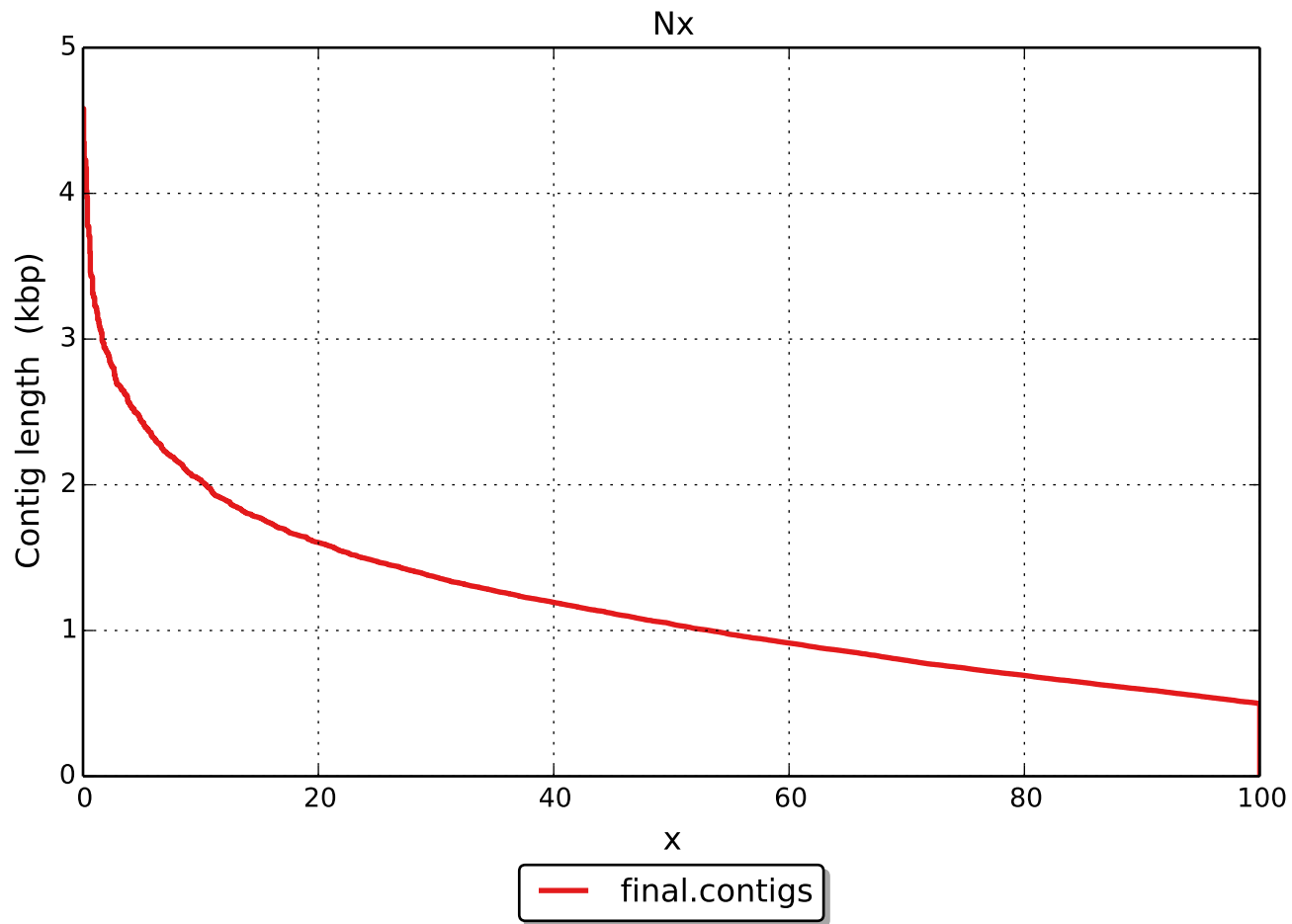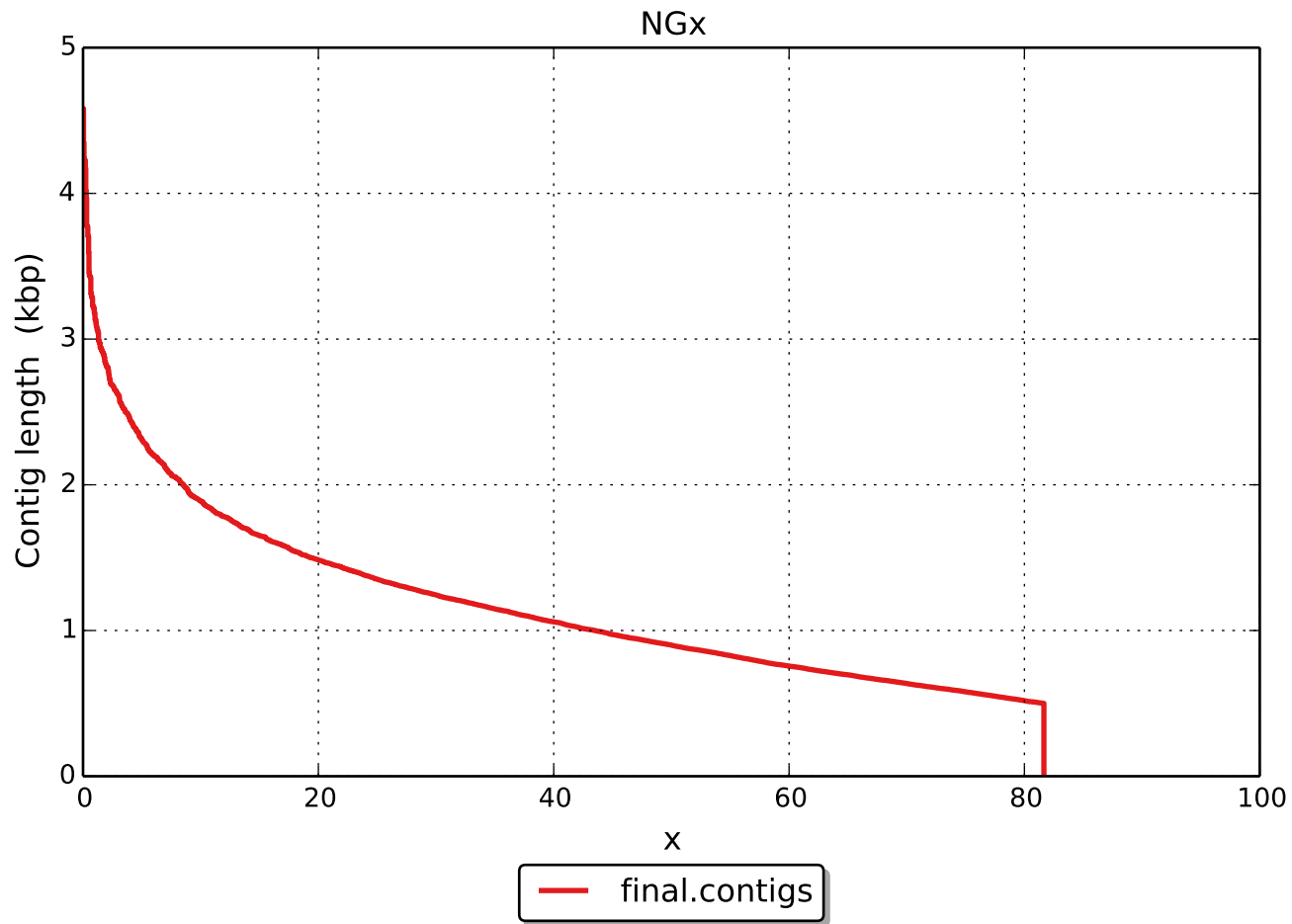
Unaligned report

	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
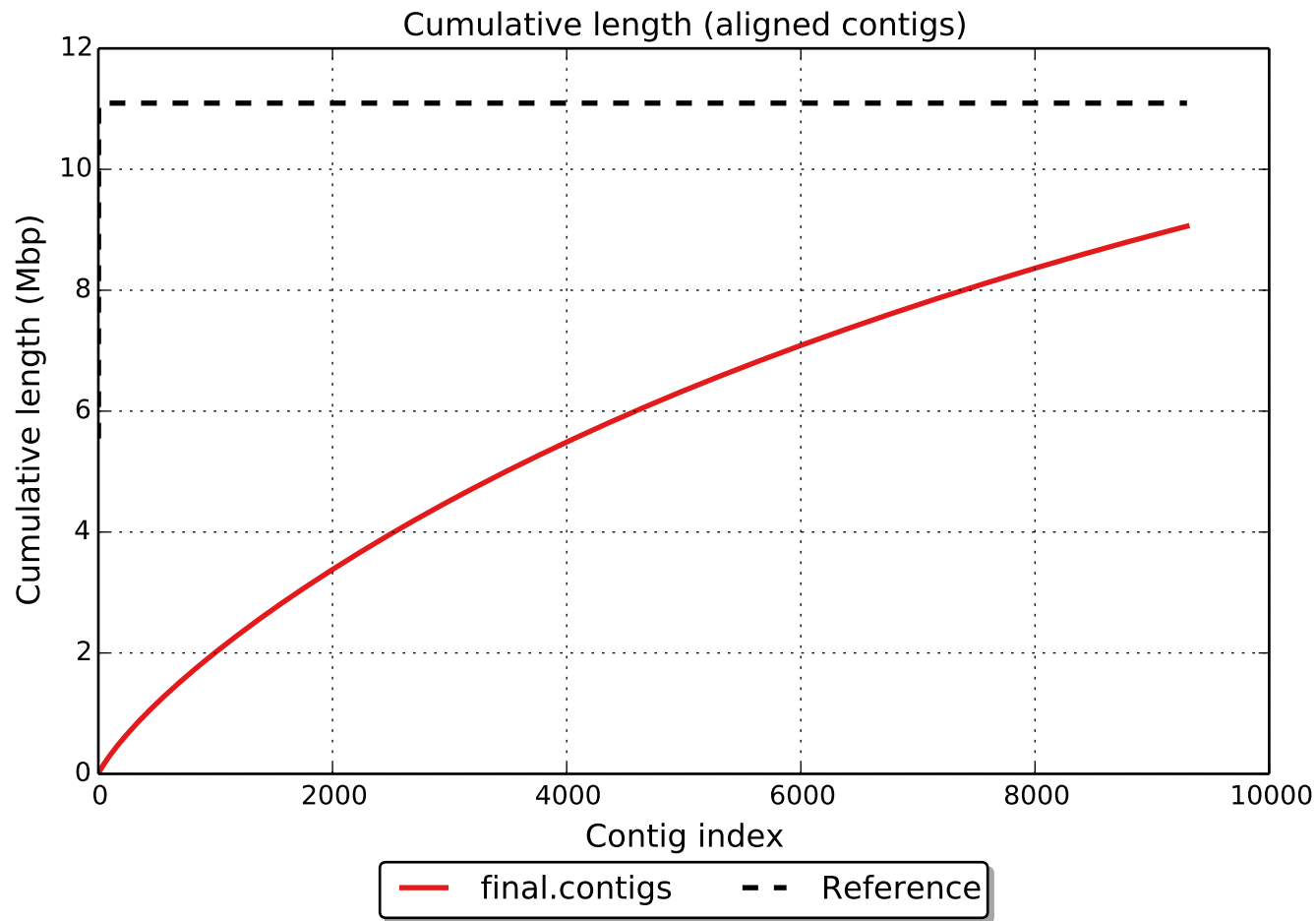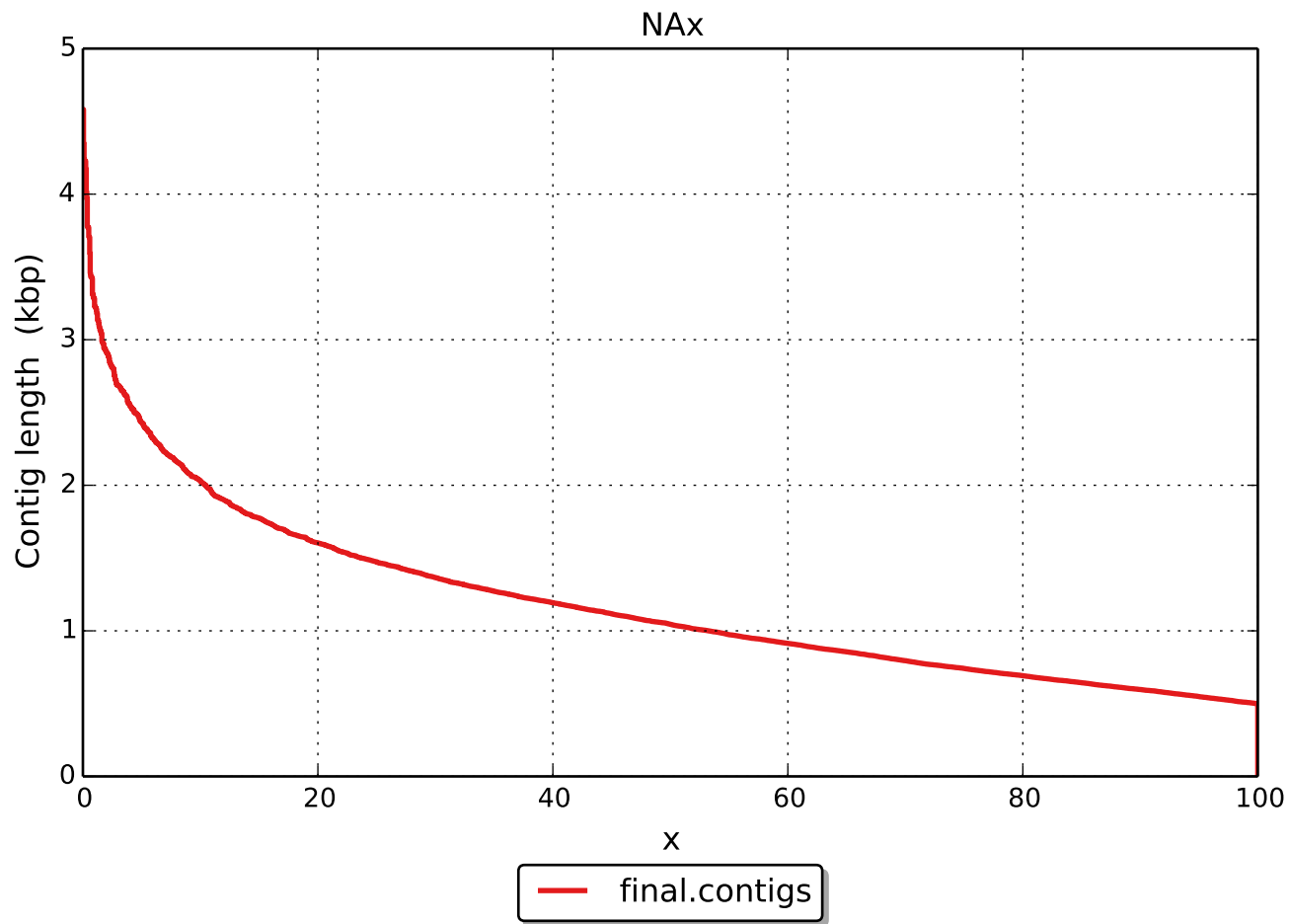(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Cumulative length

GC content

NGx

final.contigs

Misassemblies

Cumulative length (aligned contigs)

NAx