Report

	final.contigs
# contigs (>= 0 bp)	4547
# contigs (>= 1000 bp)	1497
Total length (>= 0 bp)	4471828
Total length (>= 1000 bp)	2343789
# contigs	4547
Largest contig	7611
Total length	4471828
Reference length	5478683
GC (%)	50.22
Reference GC (%)	50.49
N50	1037
NG50	874
N75	723
NG75	574
L50	1392
LG50	1922
L75	2697
LG75	3869
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	76.425
Duplication ratio	1.068
# N's per 100 kbp	0.00
# mismatches per 100 kbp	400.47
# indels per 100 kbp	0.07
Largest alignment	7611
NA50	1037
NGA50	874
NA75	723
NGA75	574
LA50	1392
LGA50	1922
LA75	2697
LGA75	3869

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).
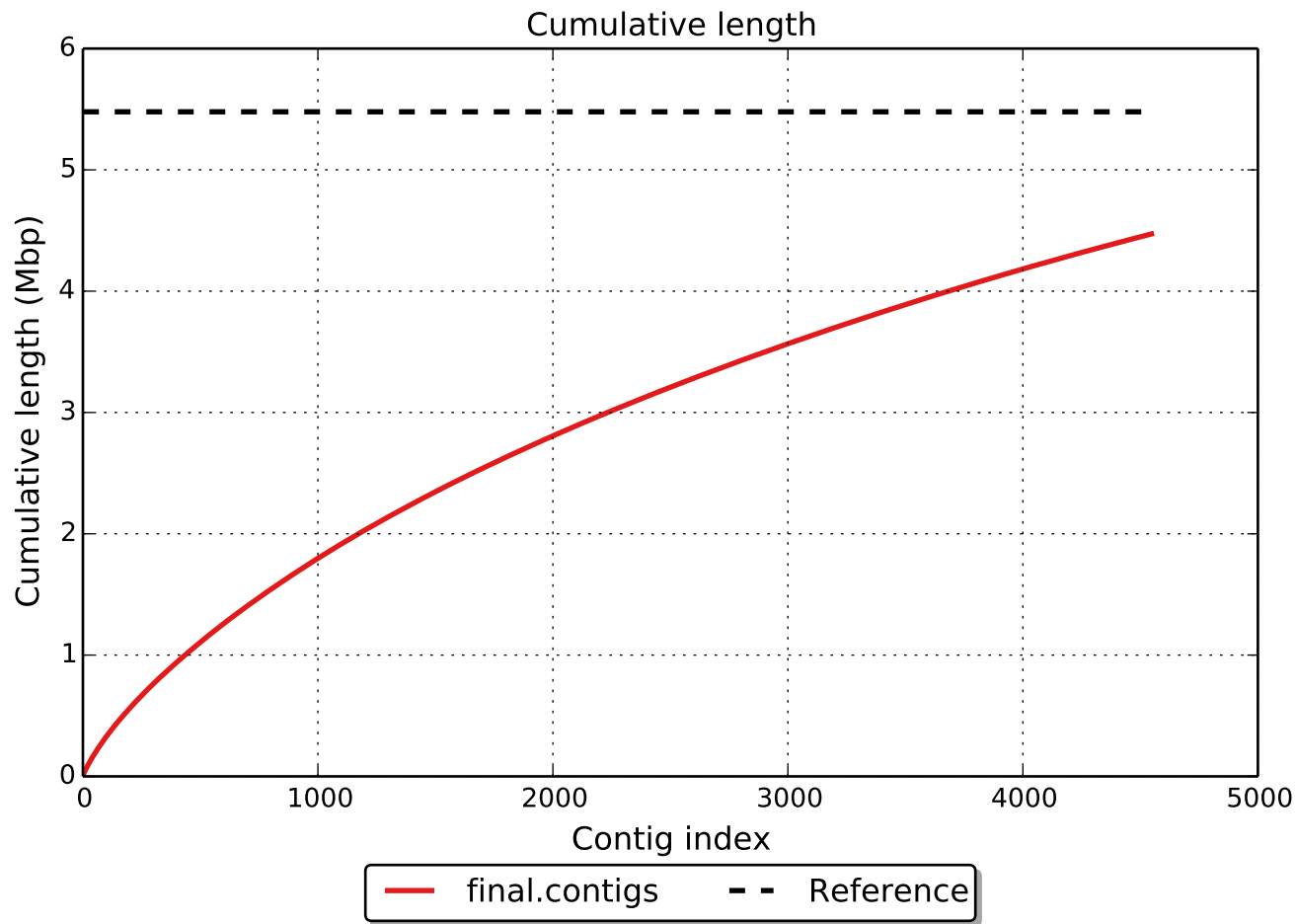
Misassemblies report

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	16768
# indels	3
# short indels	2
# long indels	1
Indels length	8

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).
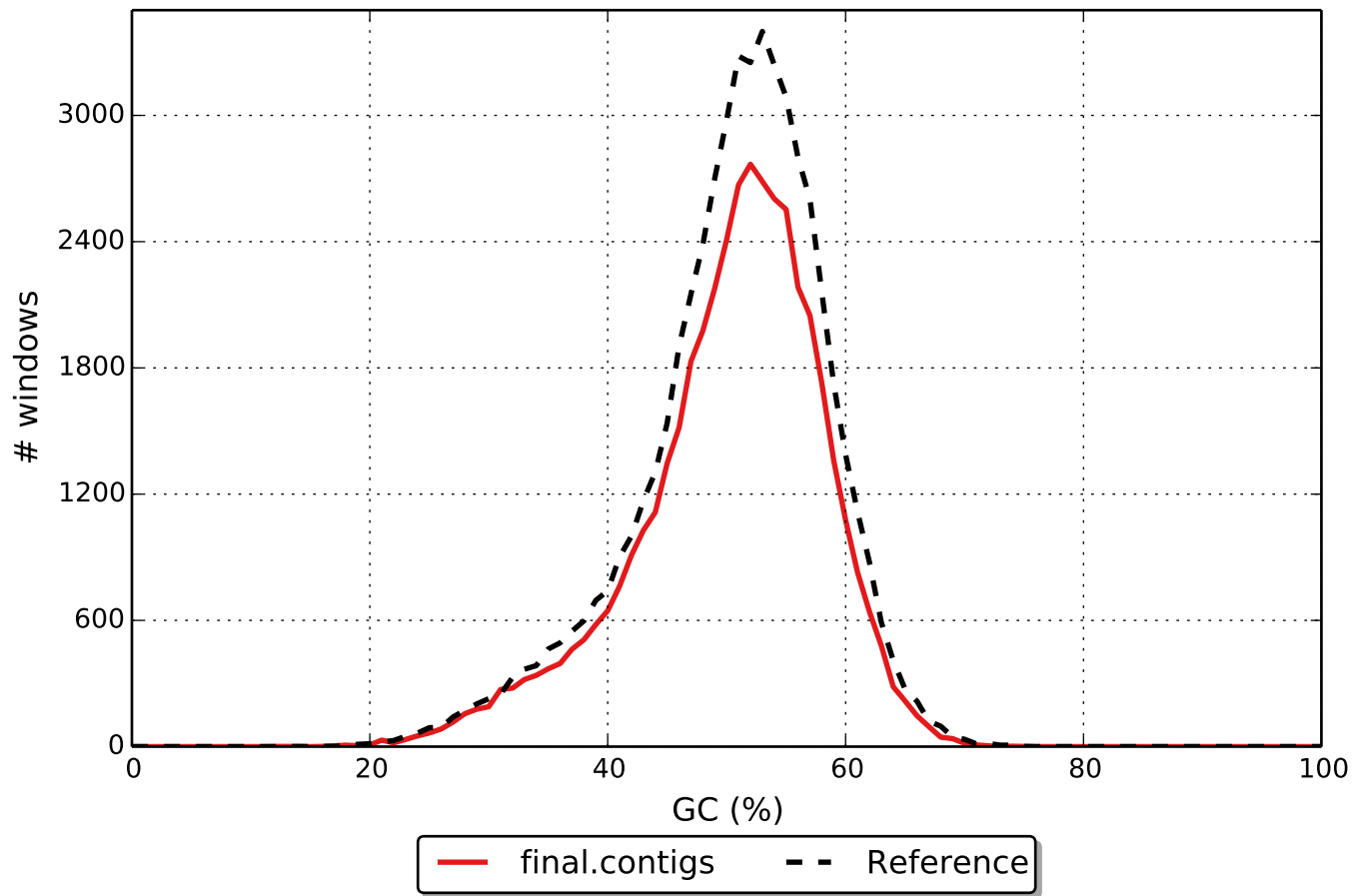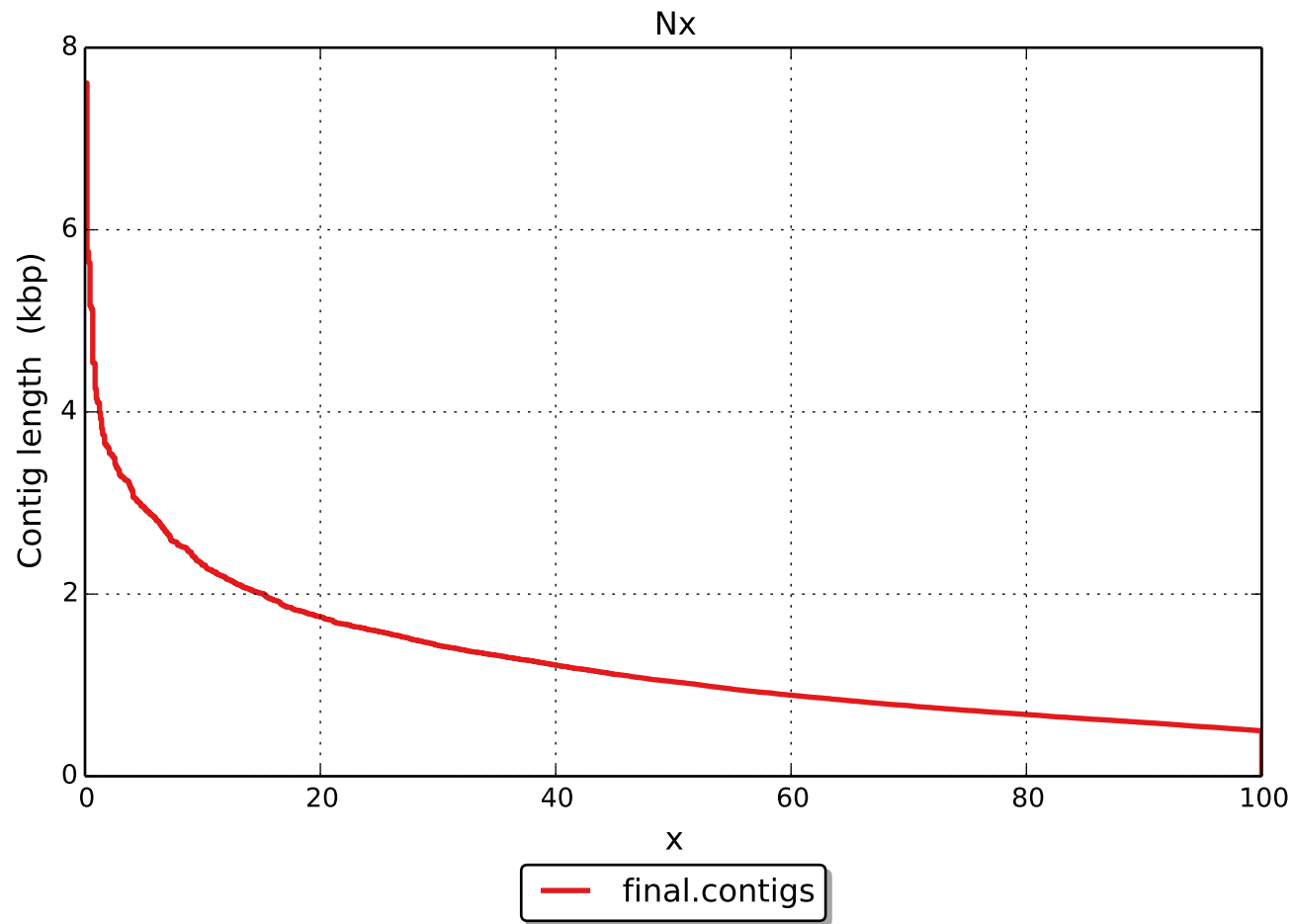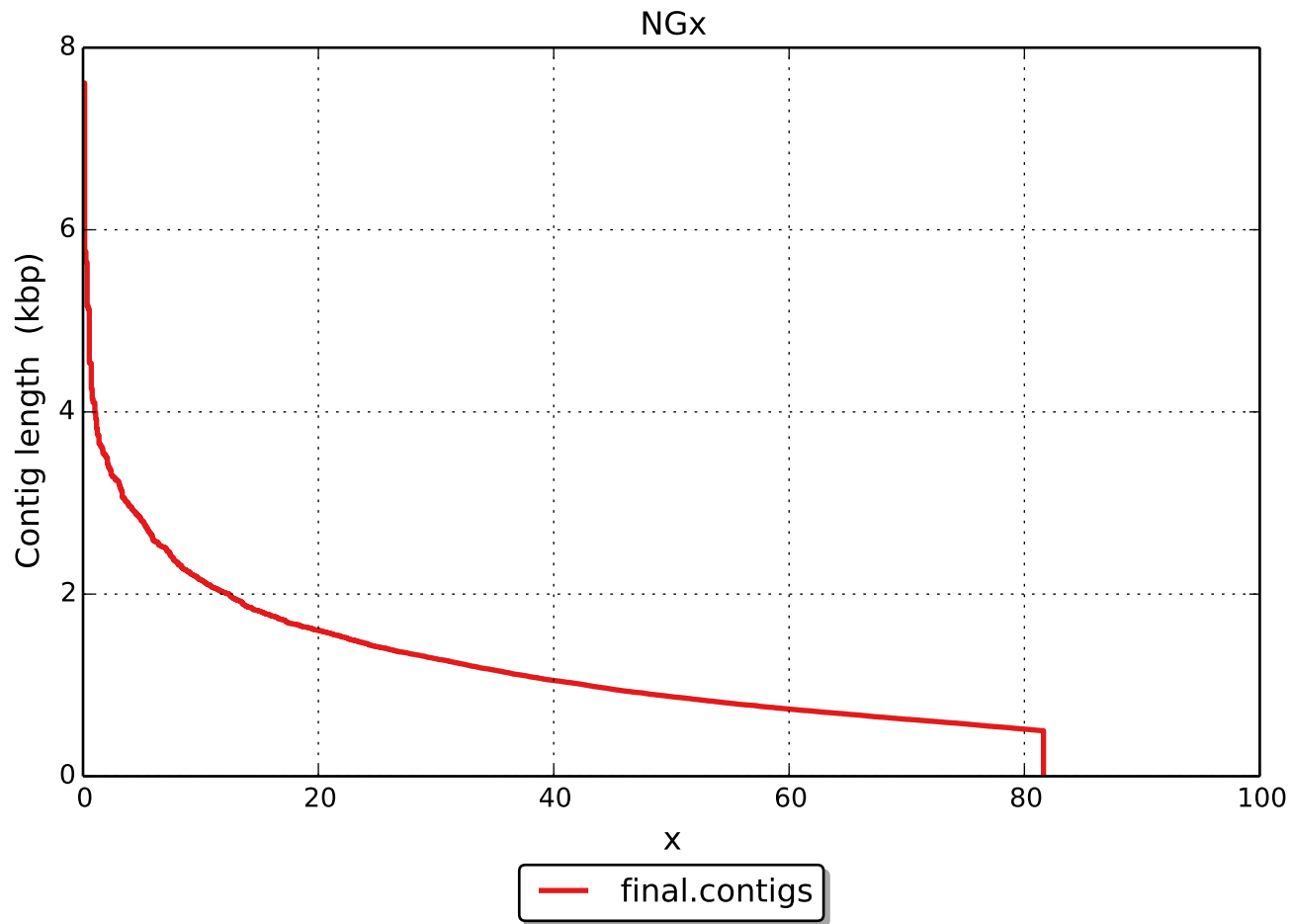
Unaligned report

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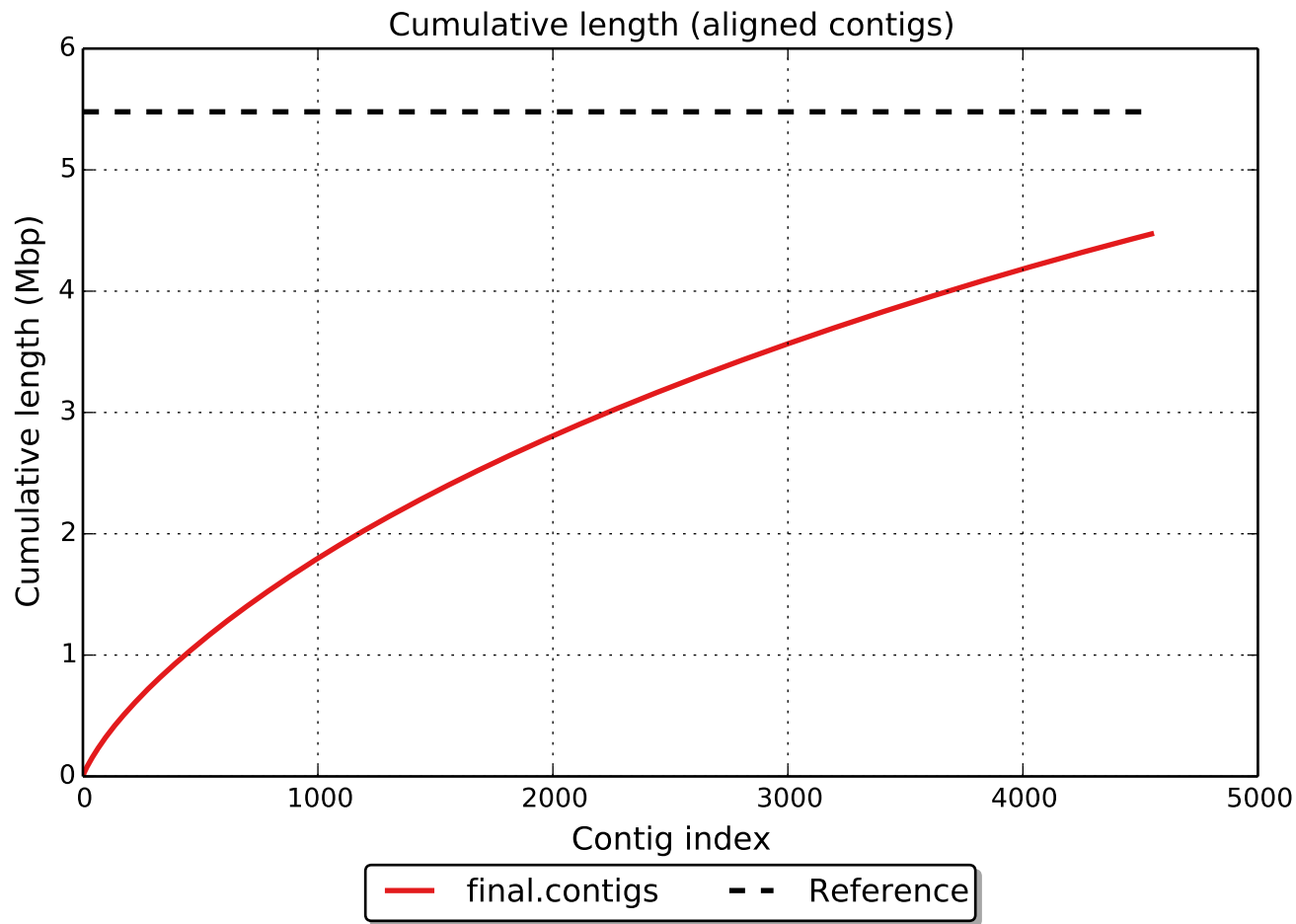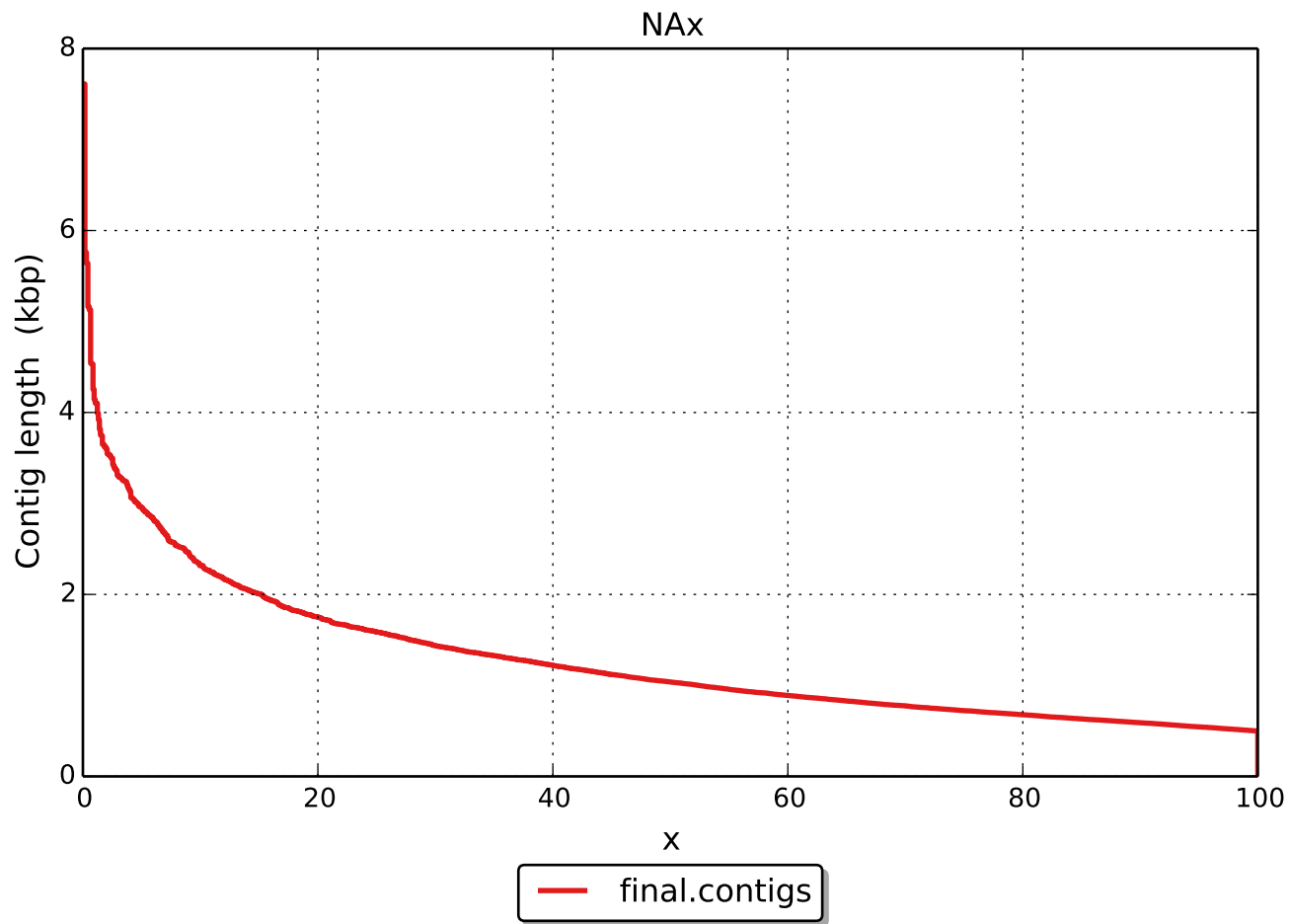(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Cumulative length

GC content

windows vs GC (%)

final.contigs ——— Reference - - -

Misassemblies

final.contigs

Cumulative length (aligned contigs)