

Report

	final.contigs
# contigs (≥ 0 bp)	863
# contigs (≥ 1000 bp)	485
Total length (≥ 0 bp)	1245381
Total length (≥ 1000 bp)	970292
# contigs	863
Largest contig	8613
Total length	1245381
Reference length	641799
GC (%)	26.31
Reference GC (%)	26.30
N50	1746
NG50	2810
N75	1055
NG75	2194
L50	217
LG50	80
L75	450
LG75	145
# misassemblies	33
# misassembled contigs	32
Misassembled contigs length	76798
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	589
Genome fraction (%)	94.983
Duplication ratio	2.042
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1734.58
# indels per 100 kbp	2.30
Largest alignment	7611
NA50	1648
NGA50	2624
NA75	1009
NGA75	2098
LA50	228
LGA50	84
LA75	471
LGA75	152

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	33
# relocations	33
# translocations	0
# inversions	0
# possibly misassembled contigs	1
# misassembled contigs	32
Misassembled contigs length	76798
# local misassemblies	0
# mismatches	10574
# indels	14
# short indels	14
# long indels	0
Indels length	14

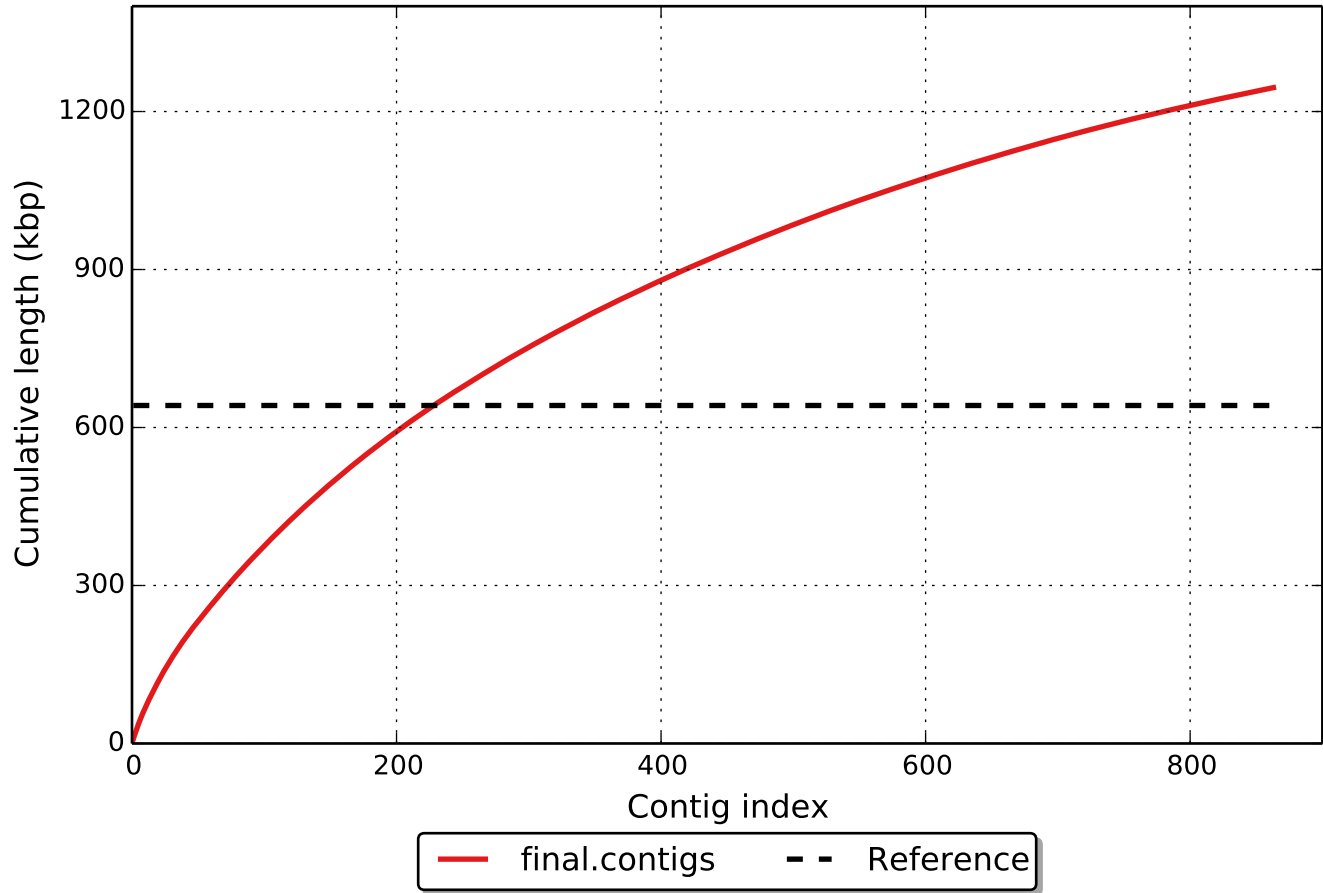
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

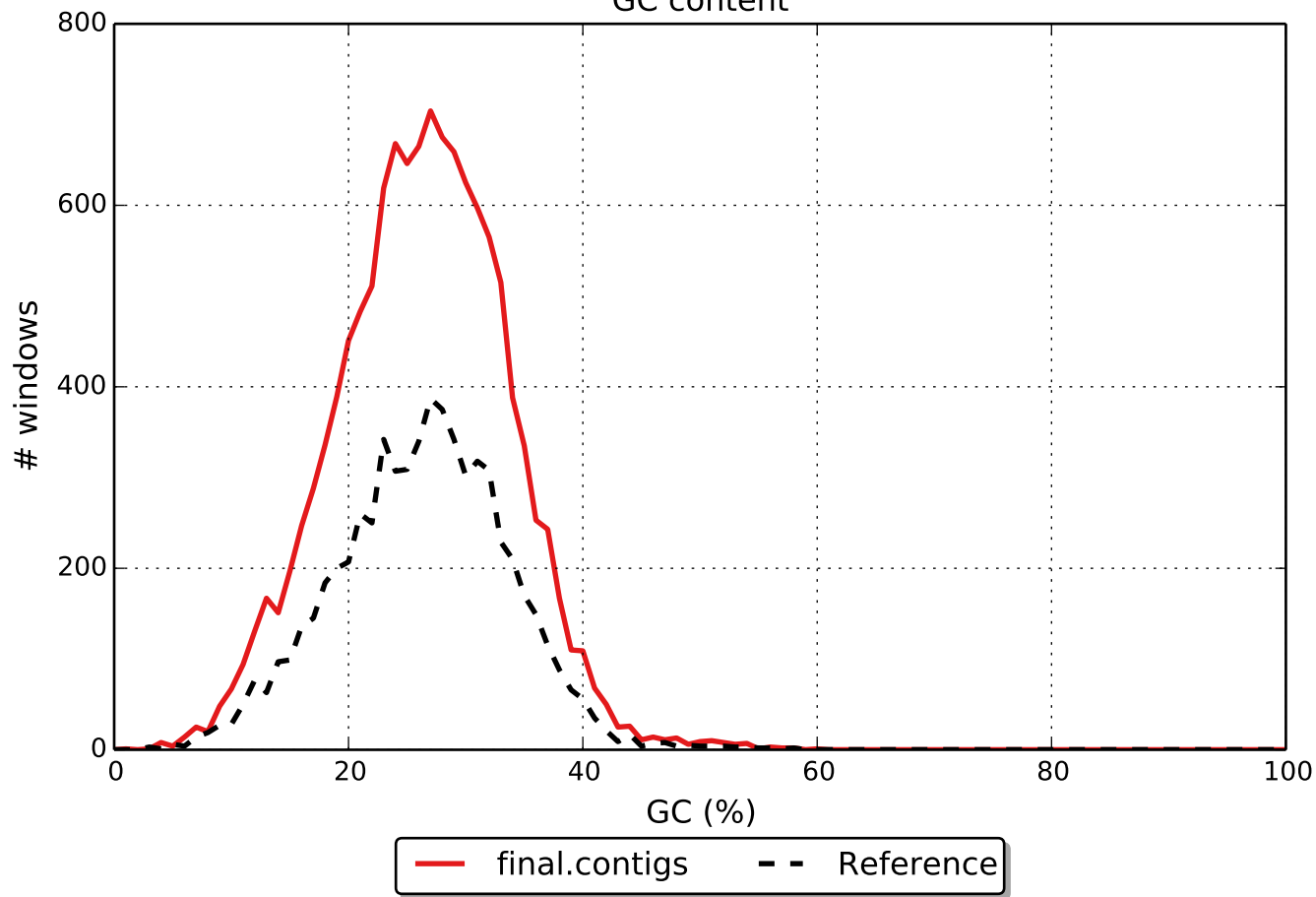
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	1
Partially unaligned length	589
# N's	0

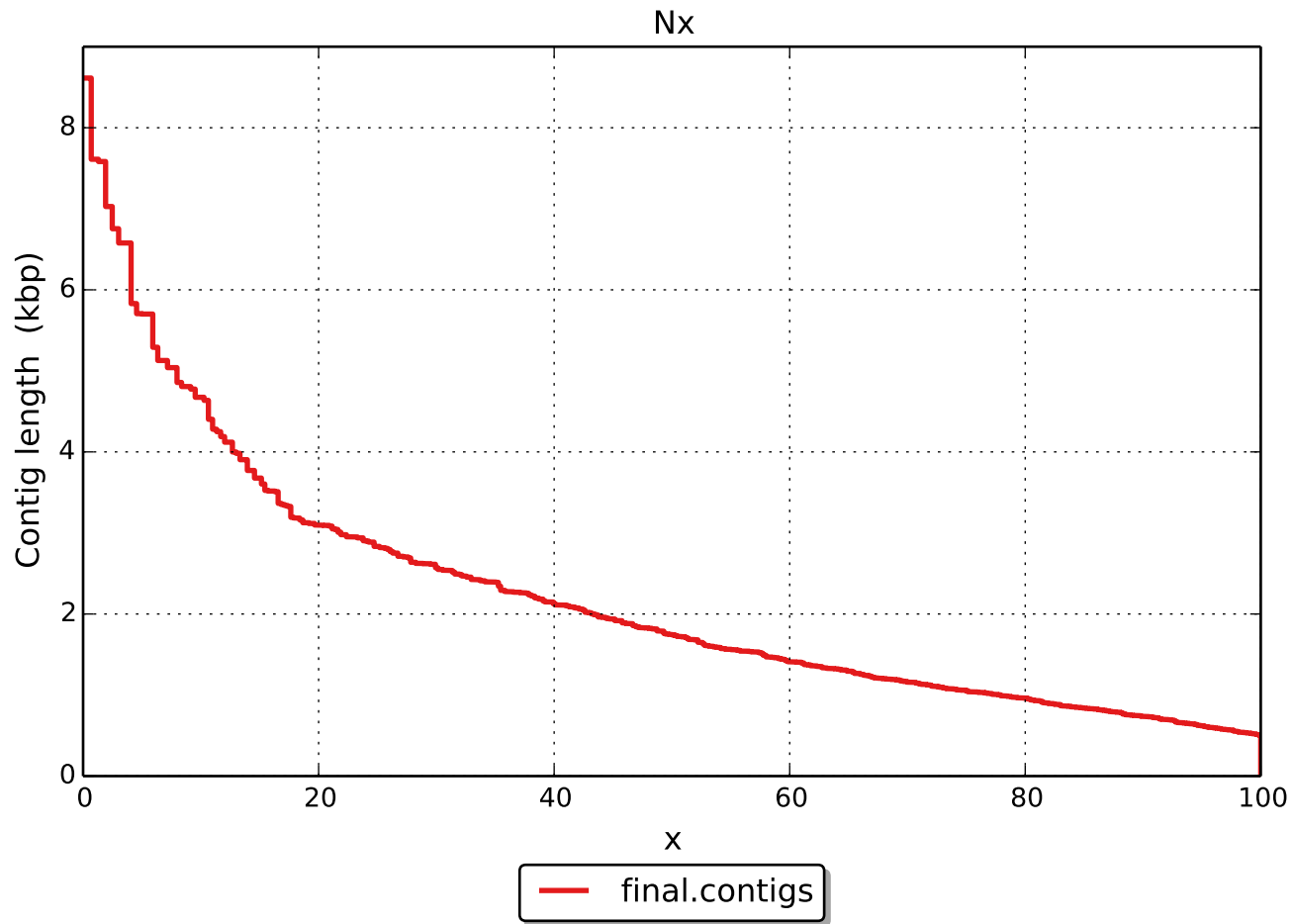
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Cumulative length

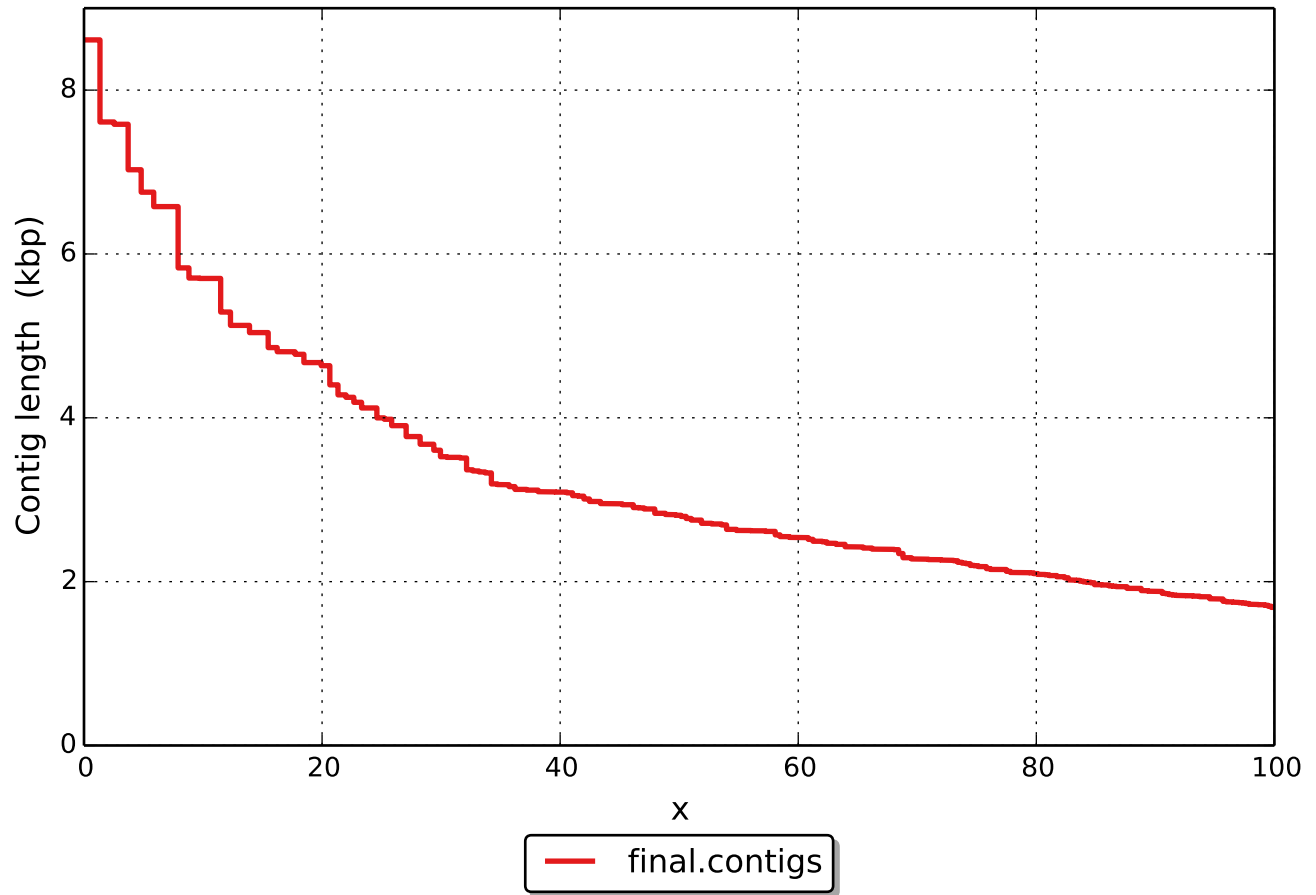


GC content

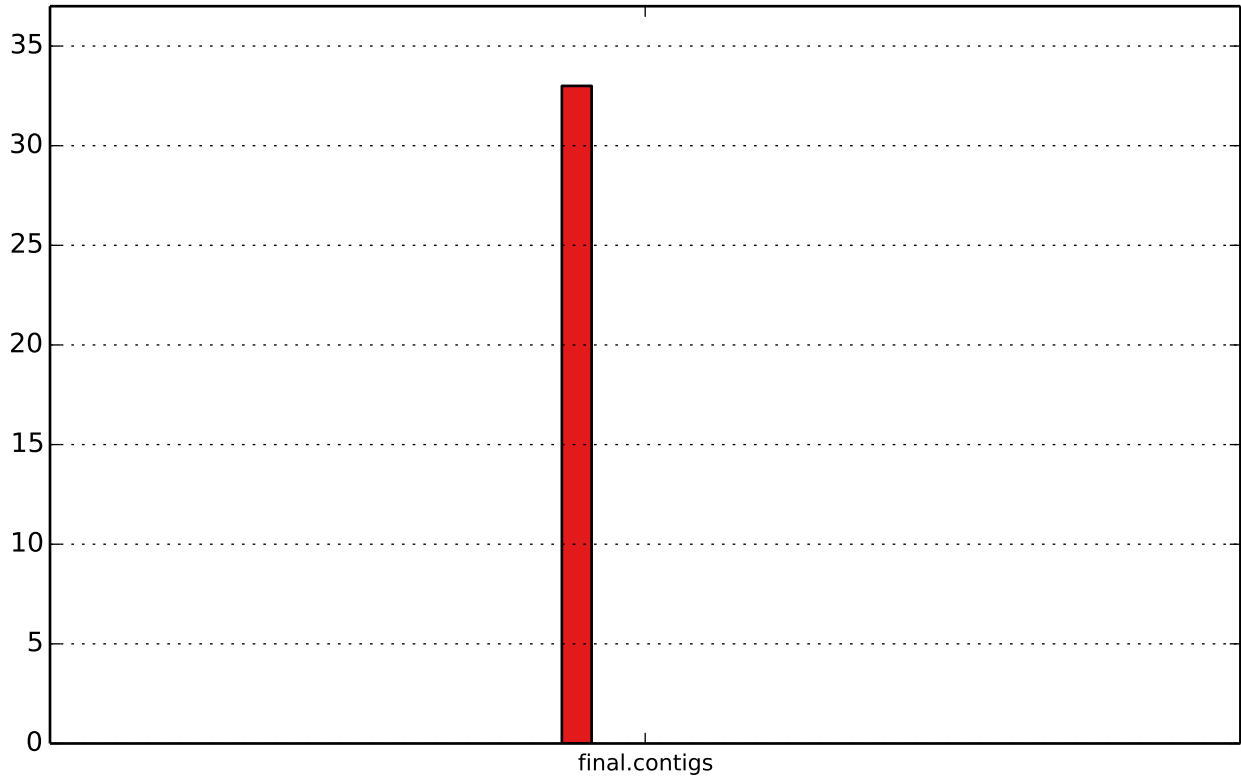




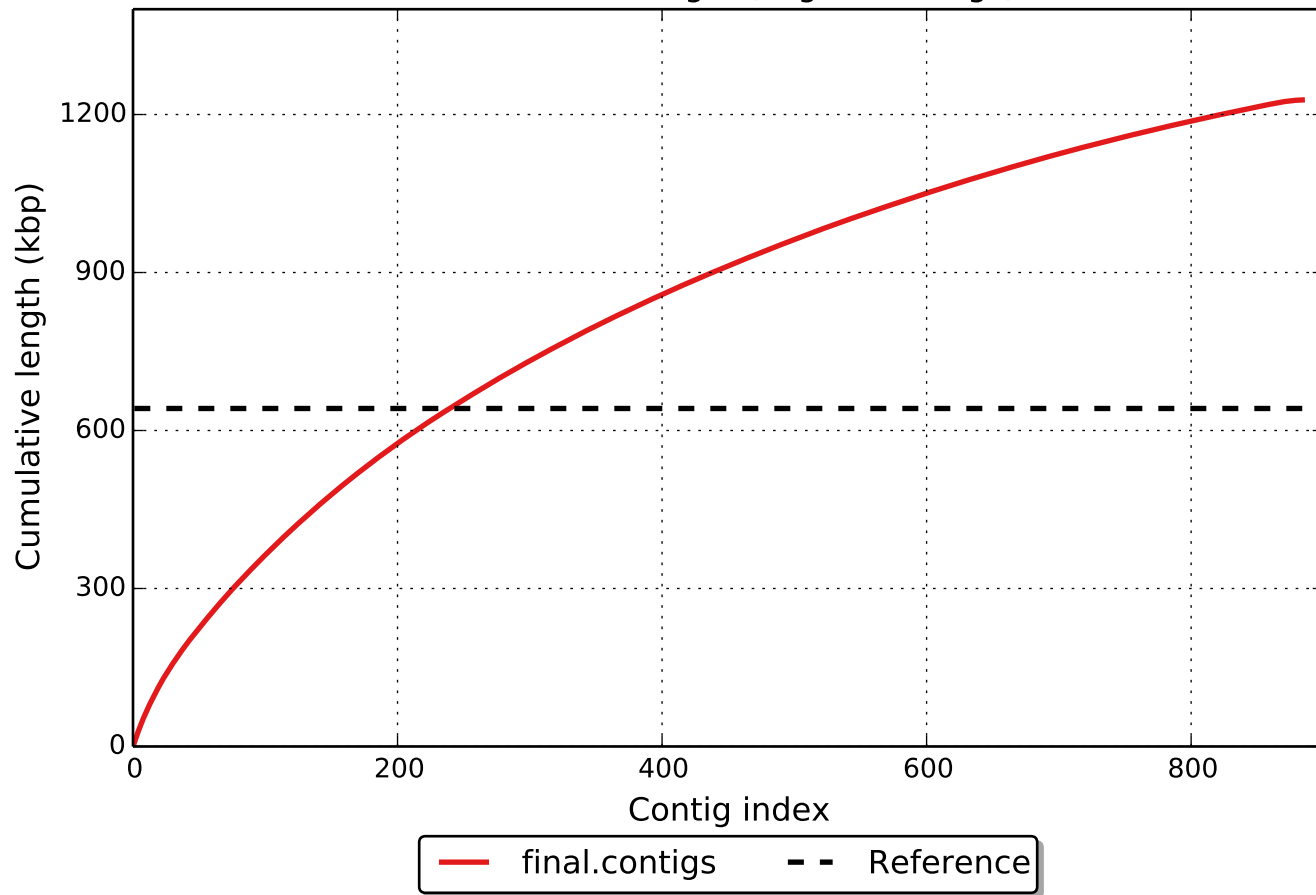
NGx

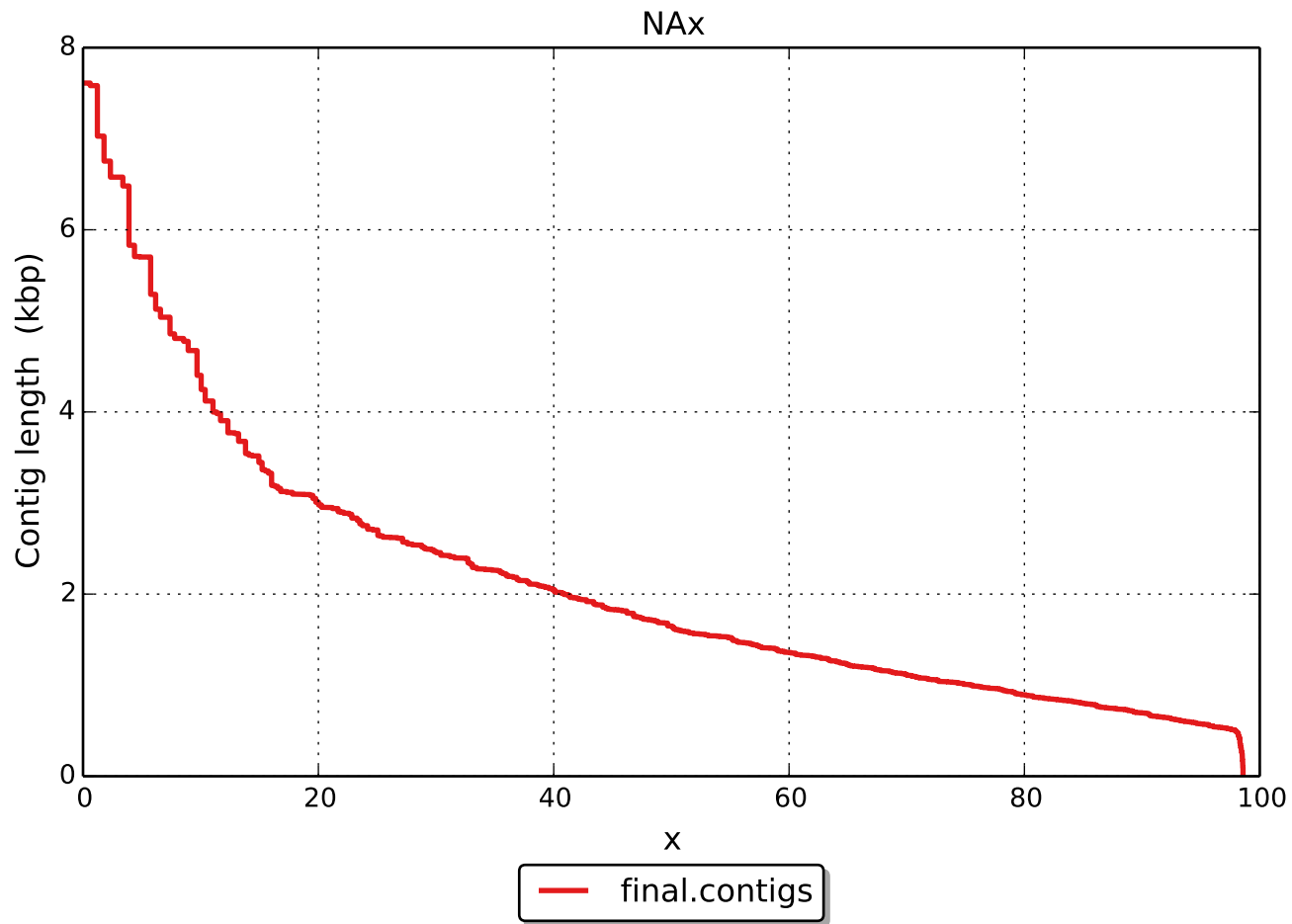


Misassemblies



Cumulative length (aligned contigs)





NGAx

