

Report

	final.contigs
# contigs (>= 1000 bp)	391
# contigs (>= 5000 bp)	186
# contigs (>= 10000 bp)	64
# contigs (>= 25000 bp)	4
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	2399056
Total length (>= 5000 bp)	1848954
Total length (>= 10000 bp)	982081
Total length (>= 25000 bp)	127222
Total length (>= 50000 bp)	0
# contigs	515
Largest contig	46220
Total length	2480940
Reference length	4857432
GC (▼)	52.34
Reference GC (▼)	52.22
N50	8025
NG50	726
N75	4920
L50	94
LG50	426
L75	189
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (▼)	50.621
Duplication ratio	1.009
# N's per 100 kbp	0.00
# mismatches per 100 kbp	434.51
# indels per 100 kbp	0.00
Largest alignment	46220
NA50	8025
NGA50	726
NA75	4920
LA50	94
LGA50	426
LA75	189

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

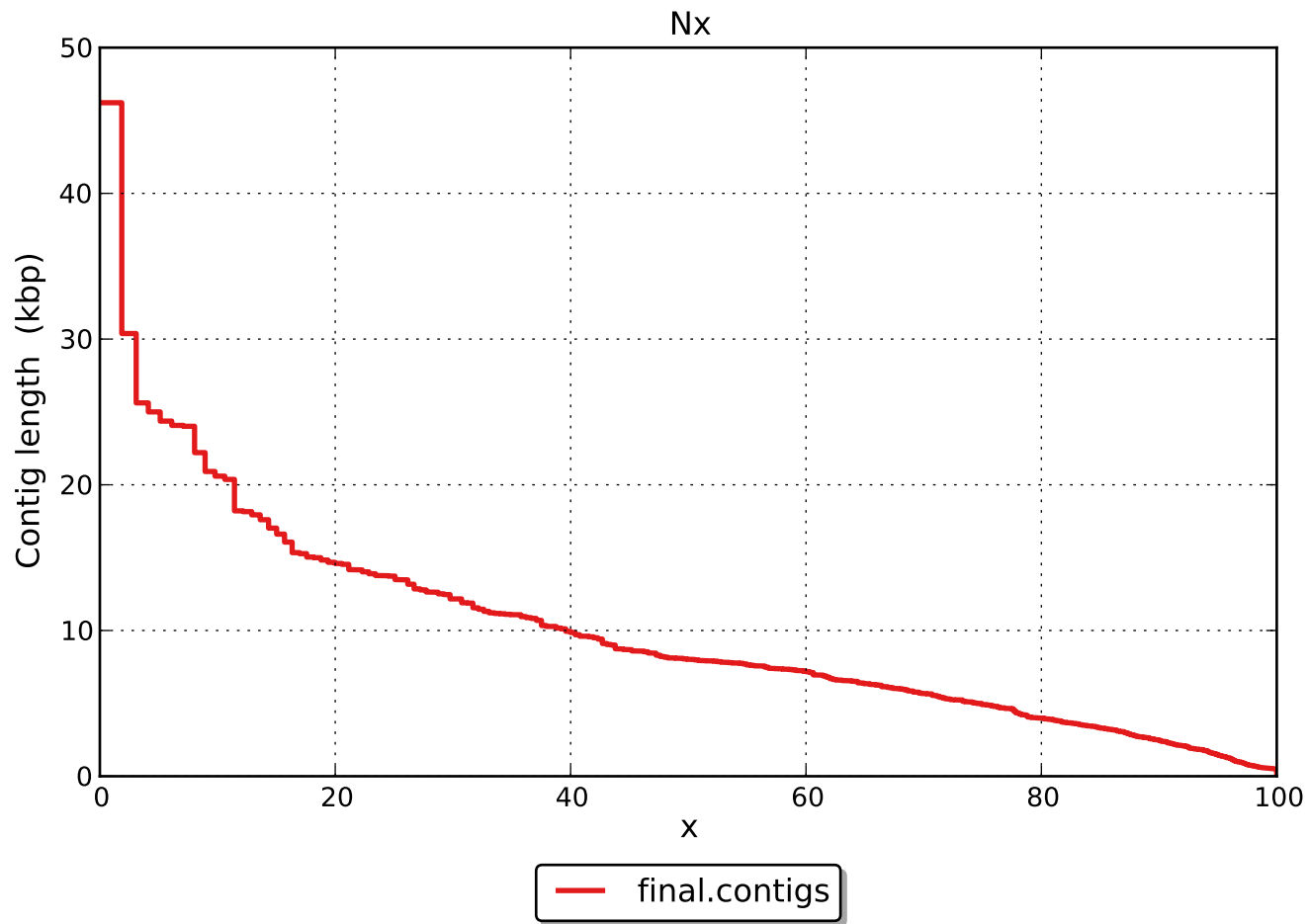
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	10684
# indels	0
# short indels	0
# long indels	0
Indels length	0

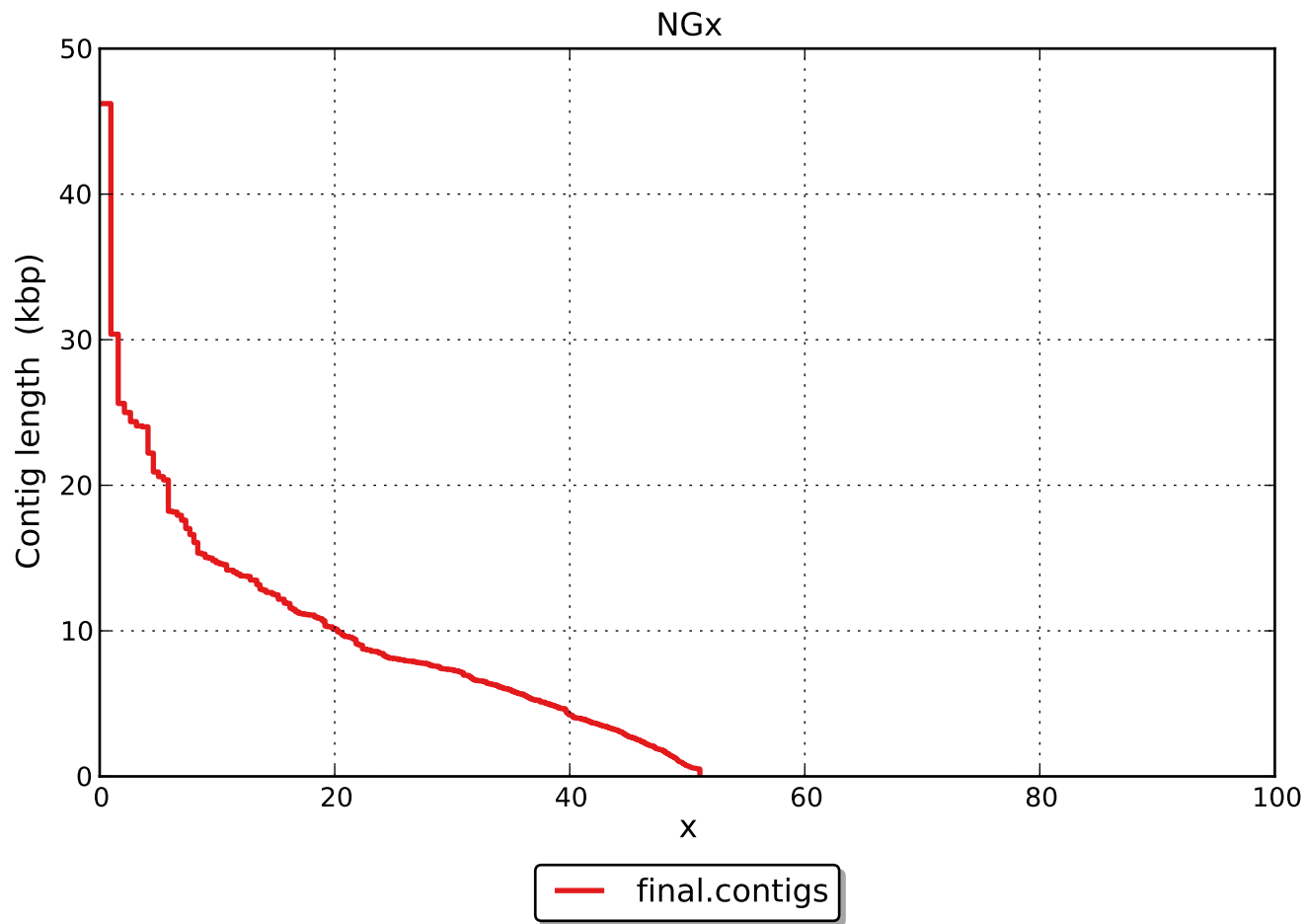
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

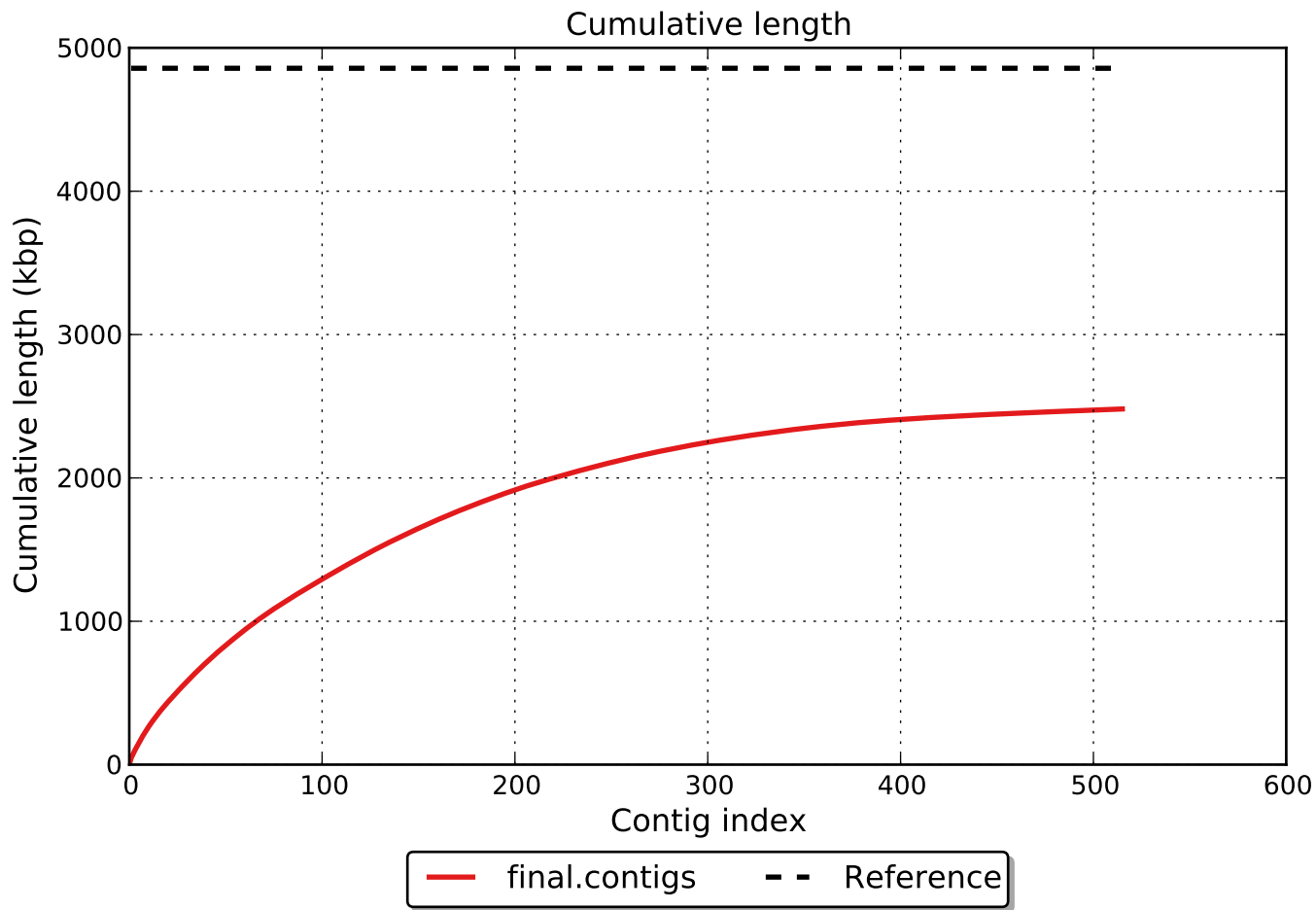
Unaligned report

	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

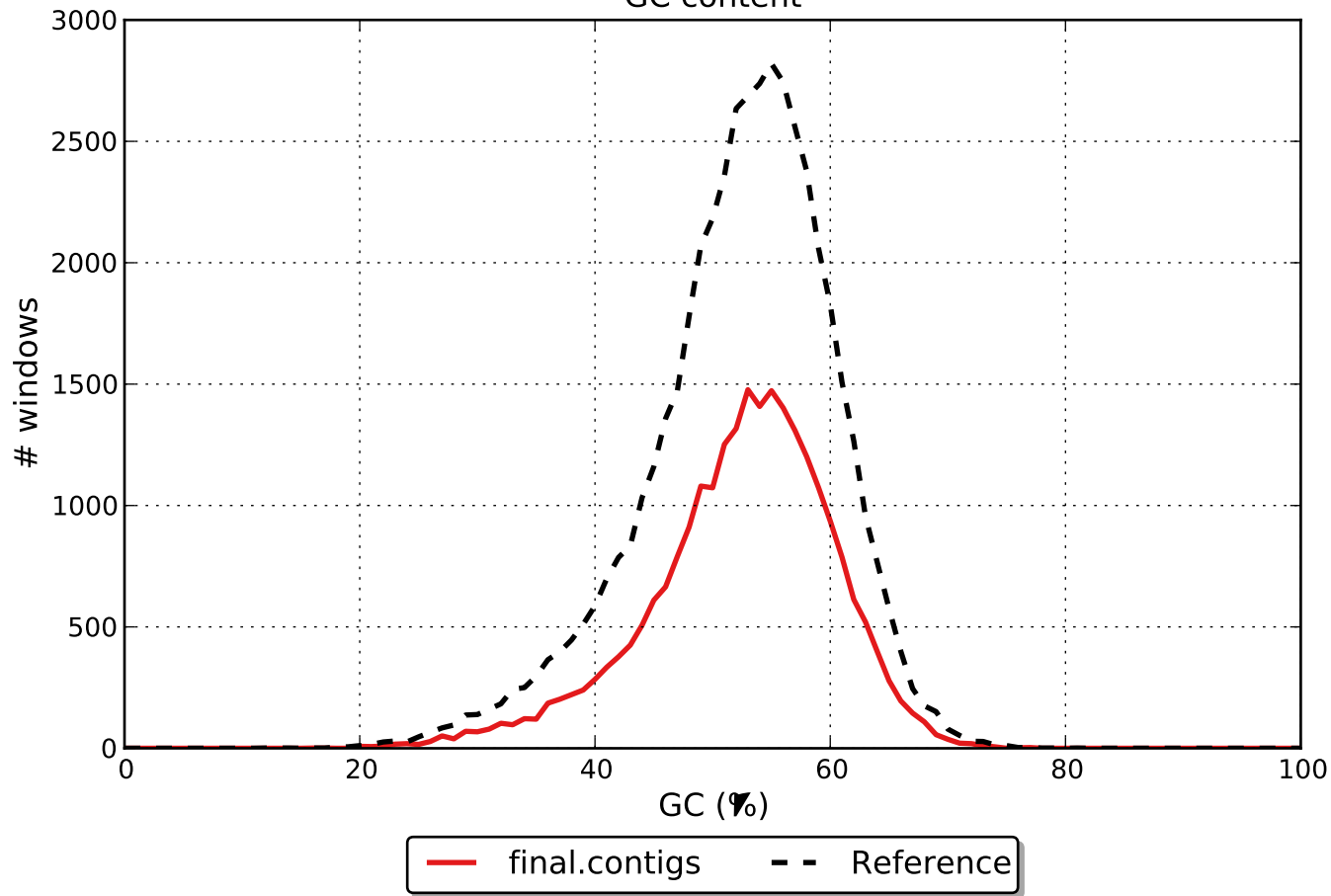
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).







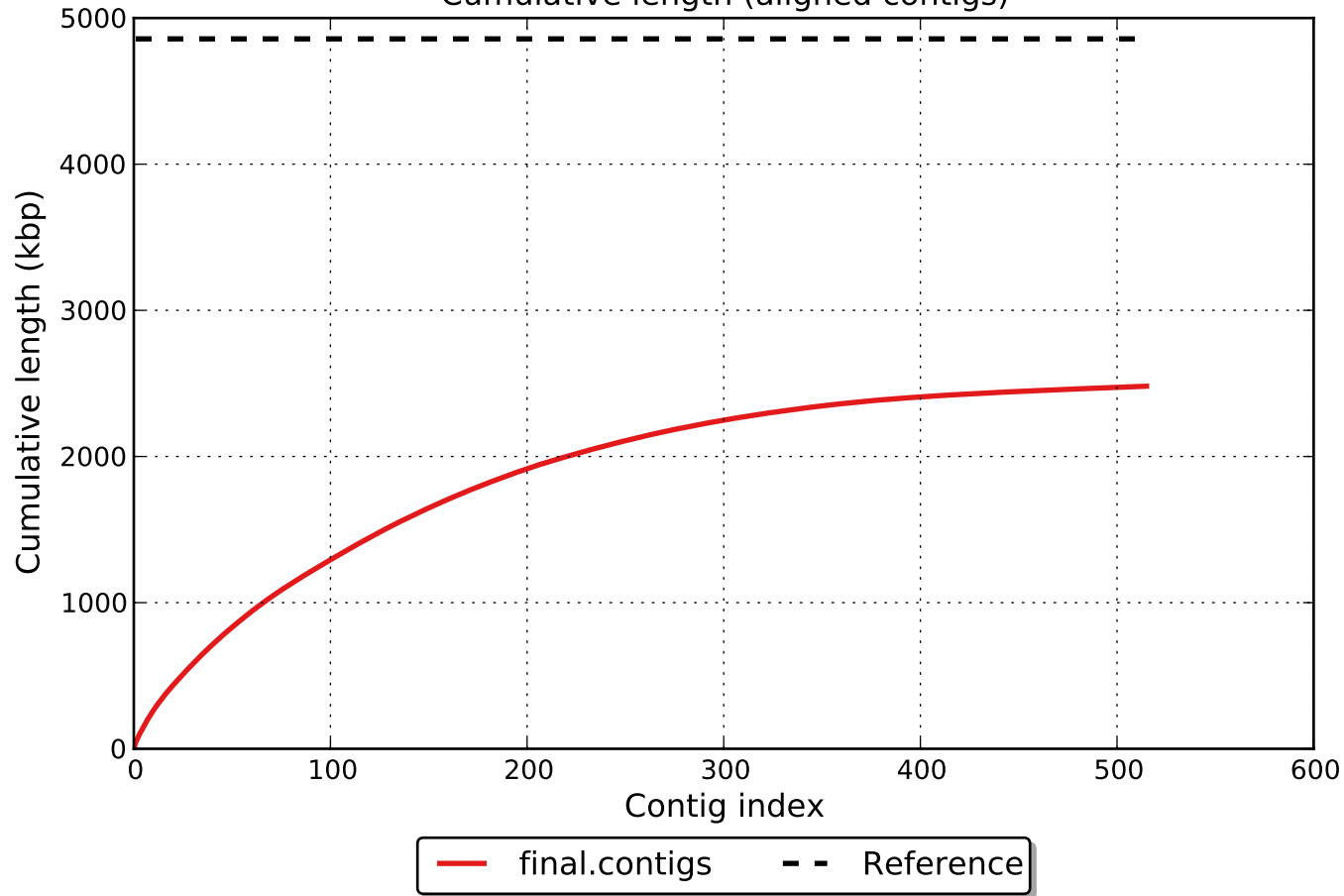
GC content



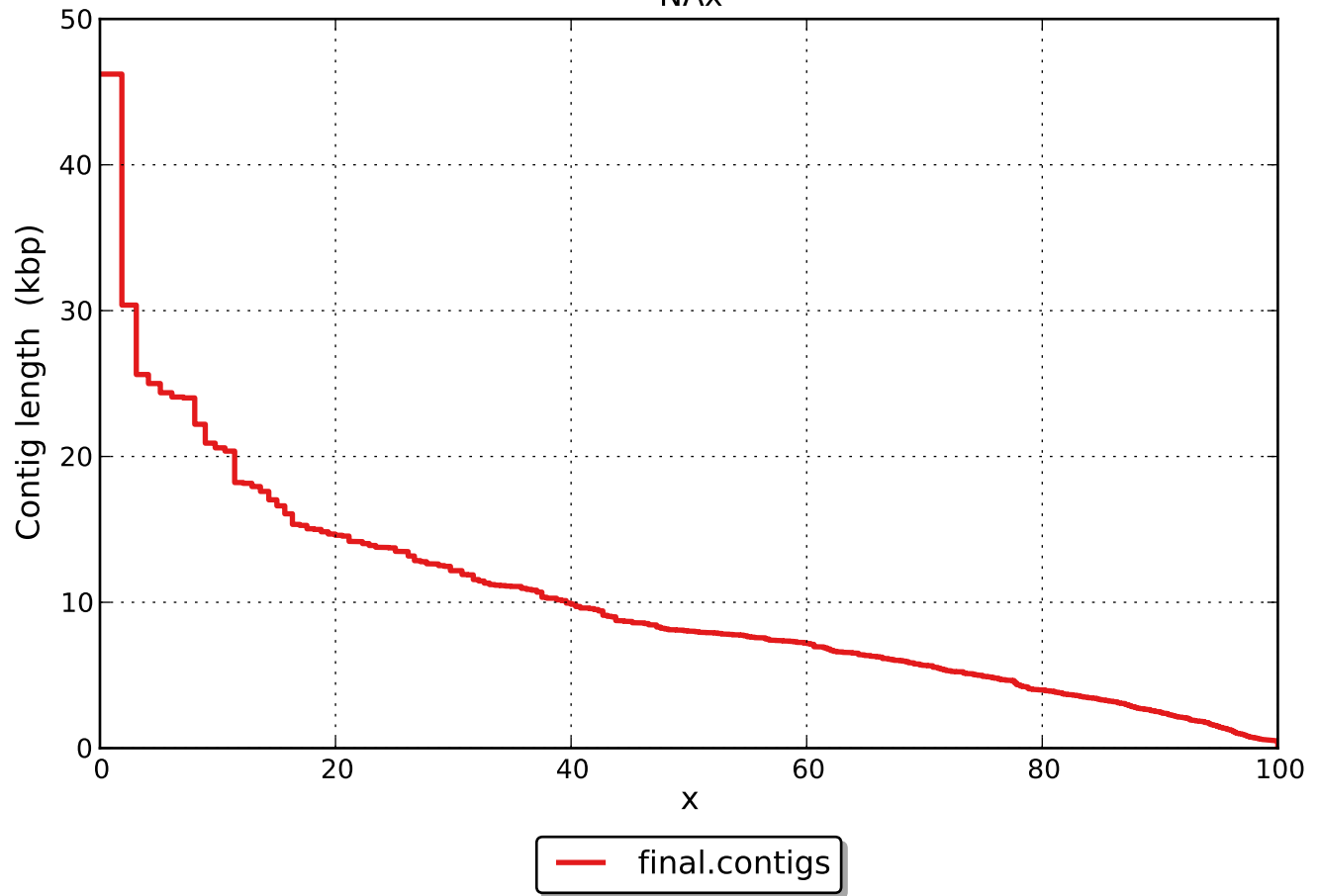
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

