

Report

	final.contigs
# contigs (>= 1000 bp)	1390
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	1985480
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	4328
Largest contig	4826
Total length	4065023
Reference length	4641652
GC (℥)	50.76
Reference GC (℥)	50.78
N50	986
NG50	902
N75	722
NG75	628
L50	1438
LG50	1742
L75	2647
LG75	3290
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	82.244
Duplication ratio	1.065
# N's per 100 kbp	0.00
# mismatches per 100 kbp	184.81
# indels per 100 kbp	0.16
Largest alignment	4826
NA50	986
NGA50	902
NA75	722
NGA75	628
LA50	1438
LGA50	1742
LA75	2647
LGA75	3290

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	7055
# indels	6
# short indels	6
# long indels	0
Indels length	6

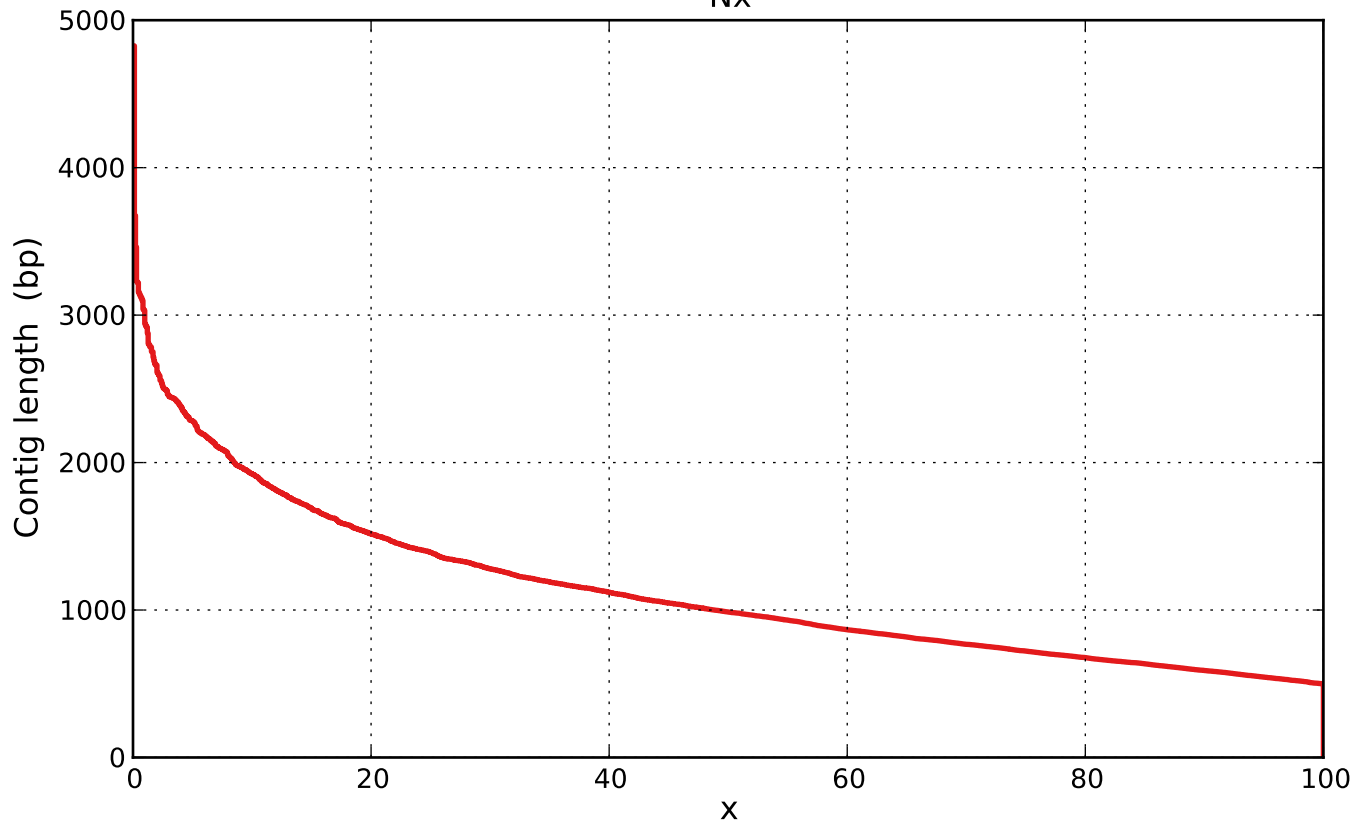
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

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).

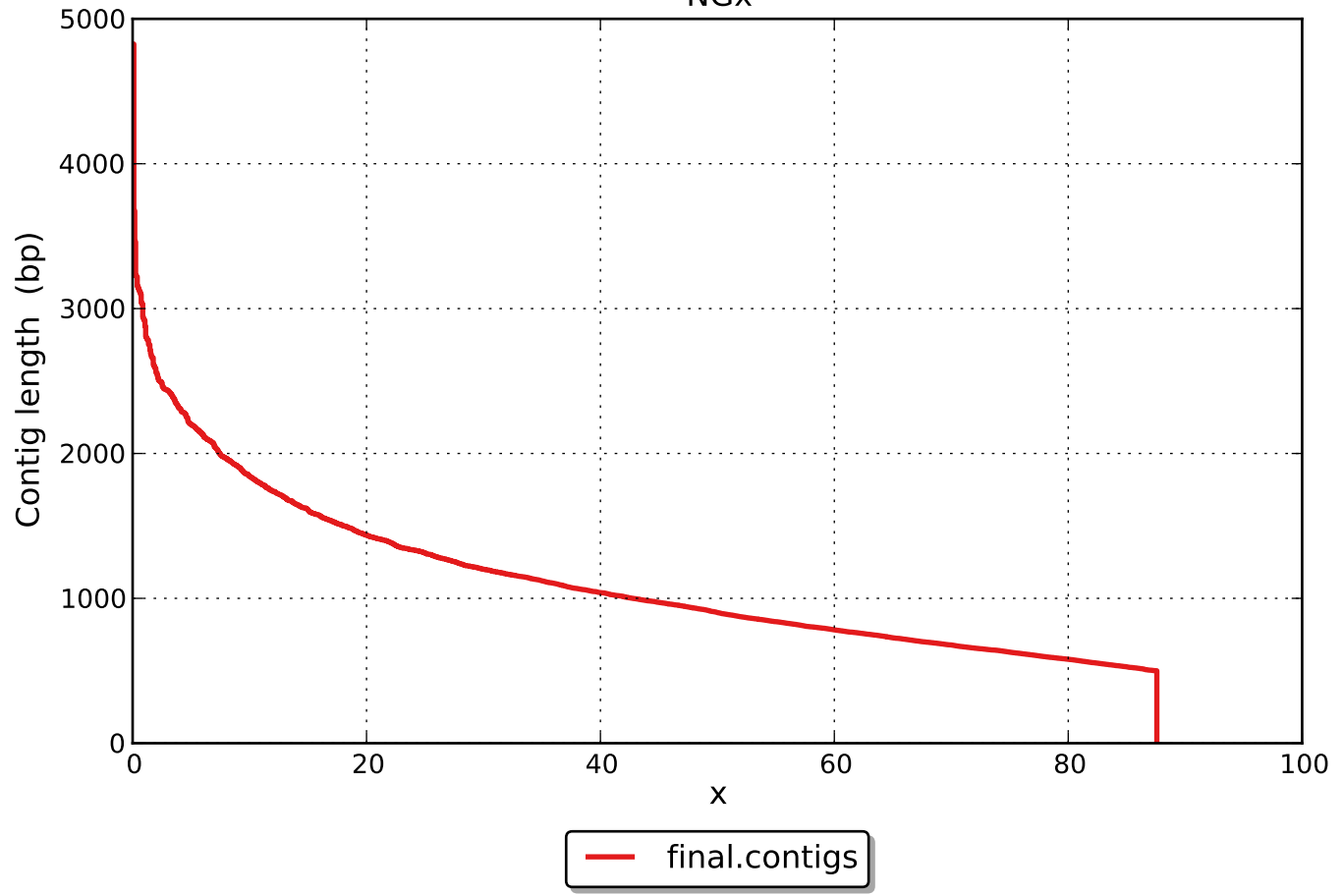
Nx

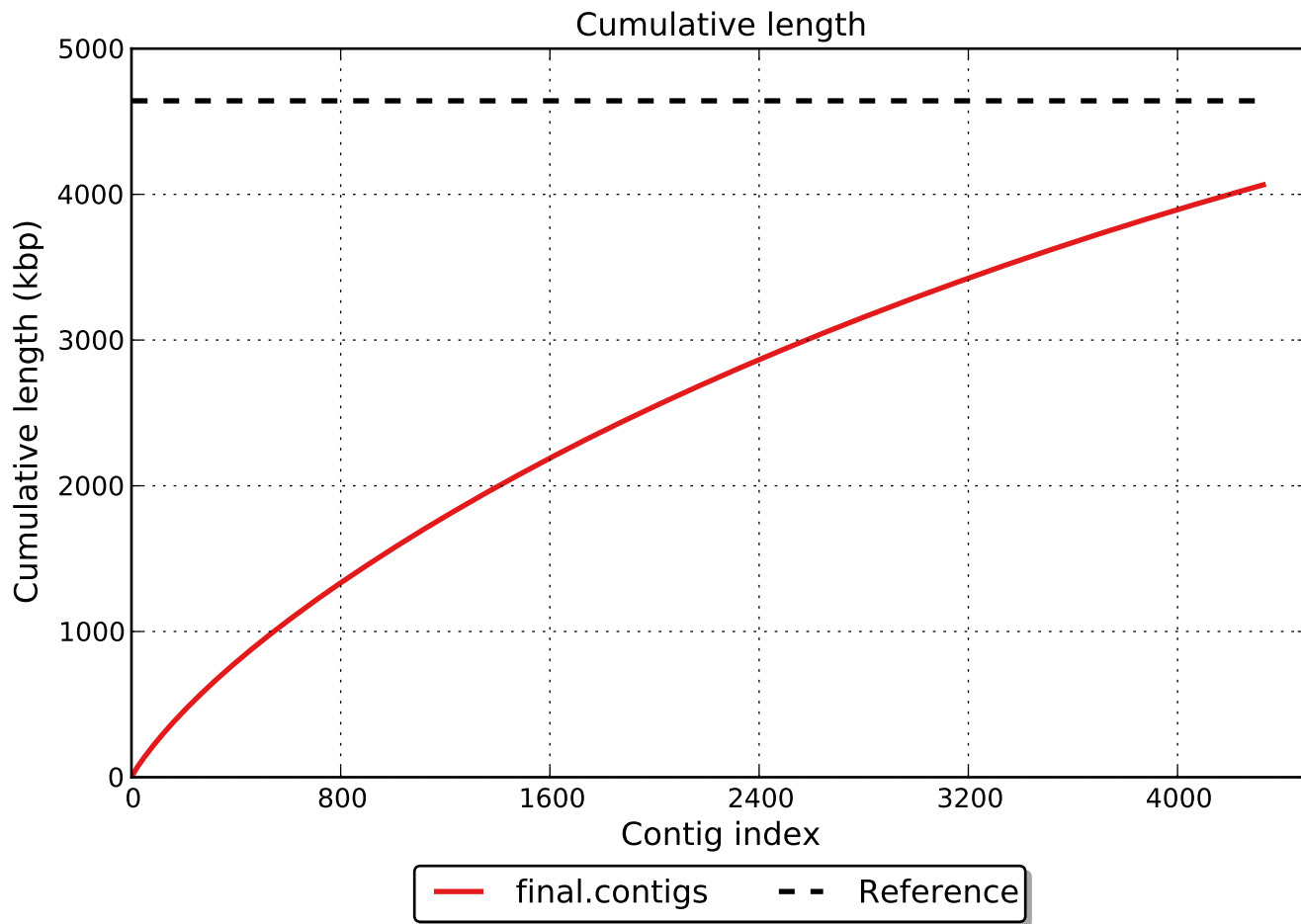


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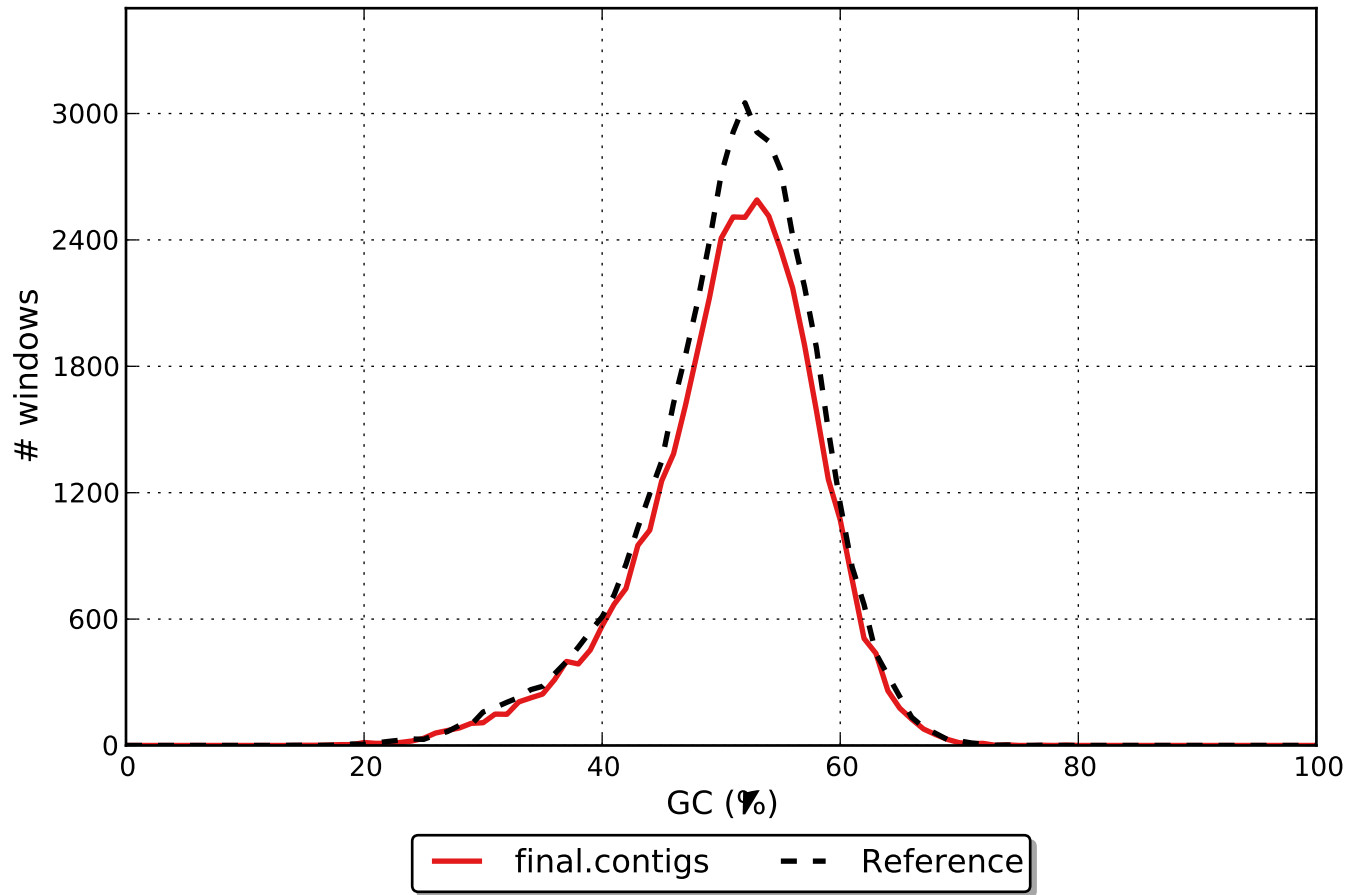
final.contigs

NGx

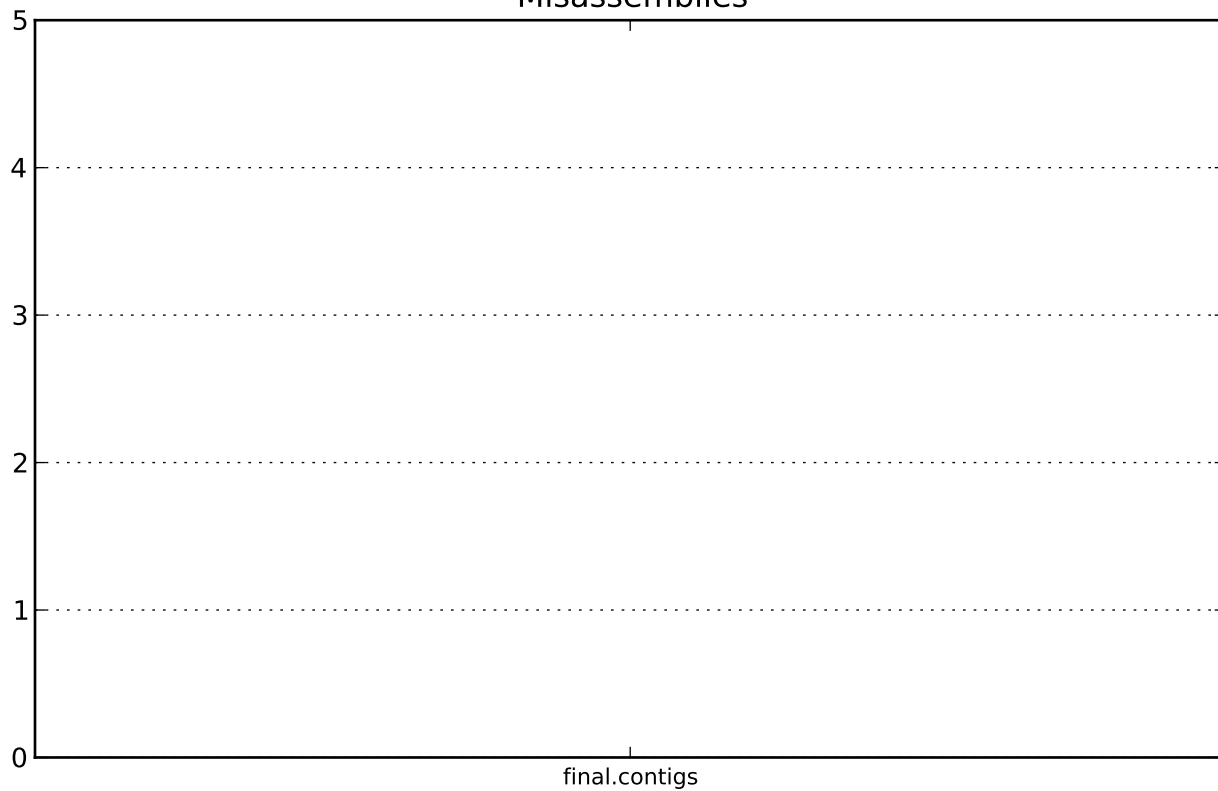




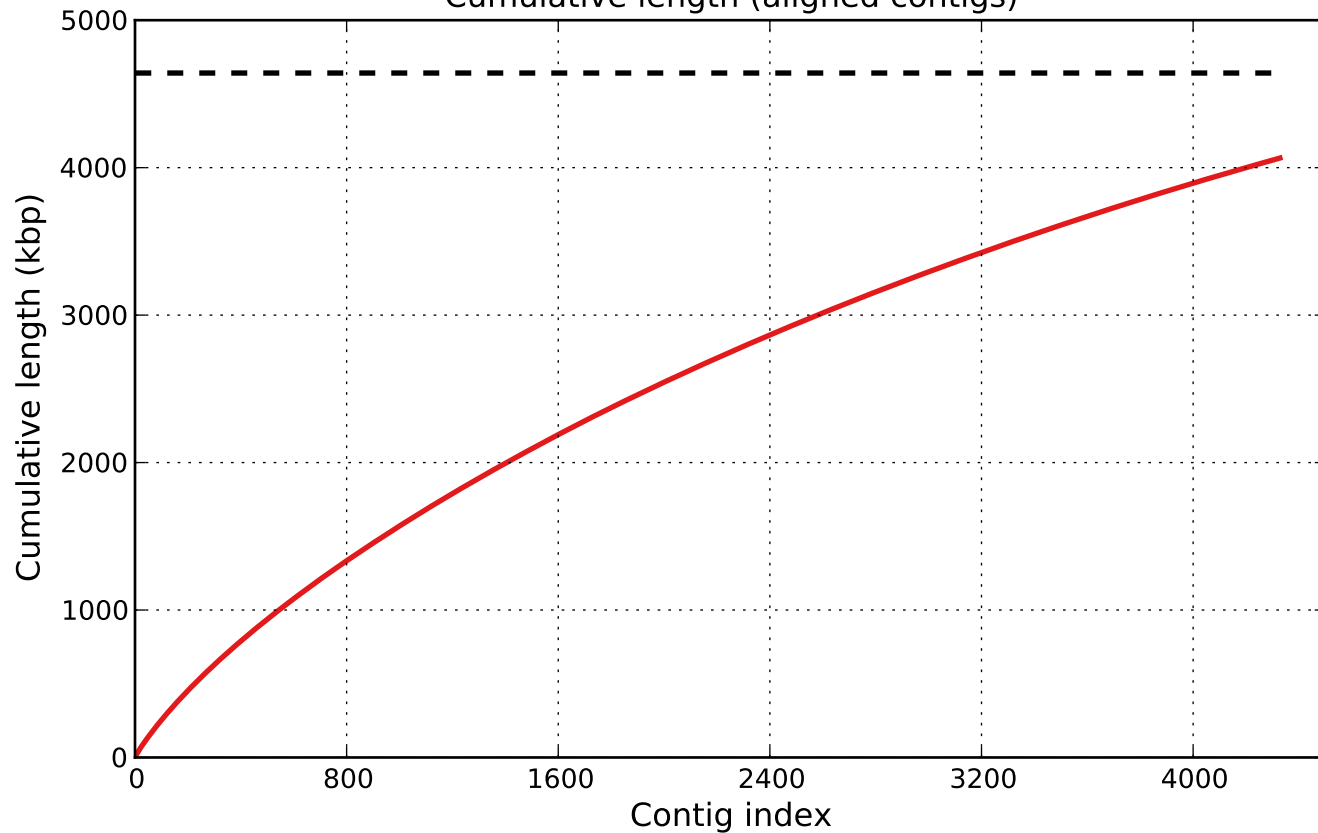
GC content



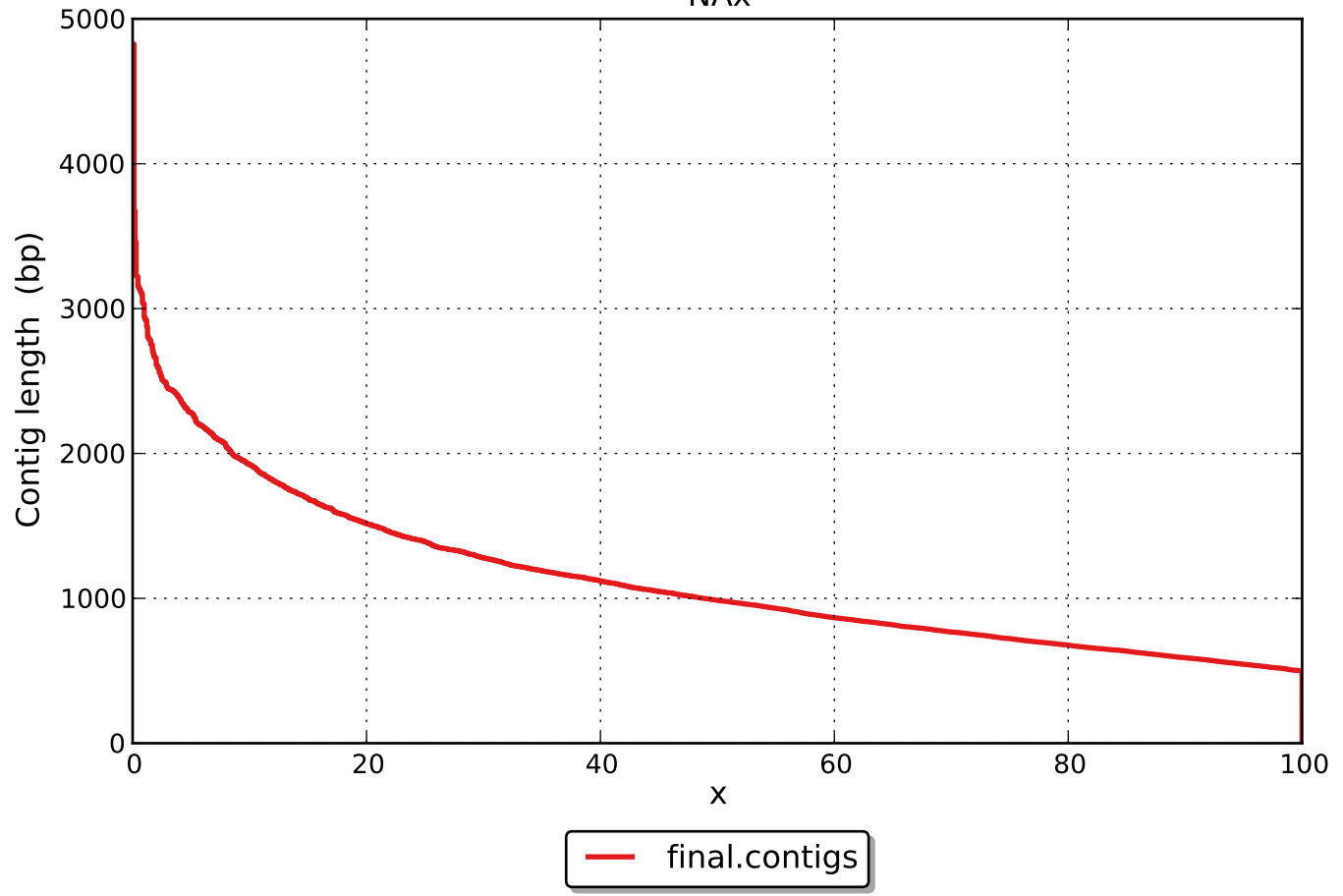
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

