

Report

	final.contigs
# contigs (>= 1000 bp)	1429
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	2055609
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	4523
Largest contig	3778
Total length	4243543
Reference length	4857432
GC (℥)	52.21
Reference GC (℥)	52.22
N50	977
NG50	898
N75	718
NG75	623
L50	1497
LG50	1824
L75	2765
LG75	3451
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	81.968
Duplication ratio	1.066
# N's per 100 kbp	0.00
# mismatches per 100 kbp	182.42
# indels per 100 kbp	0.05
Largest alignment	3778
NA50	977
NGA50	898
NA75	718
NGA75	623
LA50	1497
LGA50	1824
LA75	2765
LGA75	3452

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	7263
# indels	2
# short indels	2
# long indels	0
Indels length	2

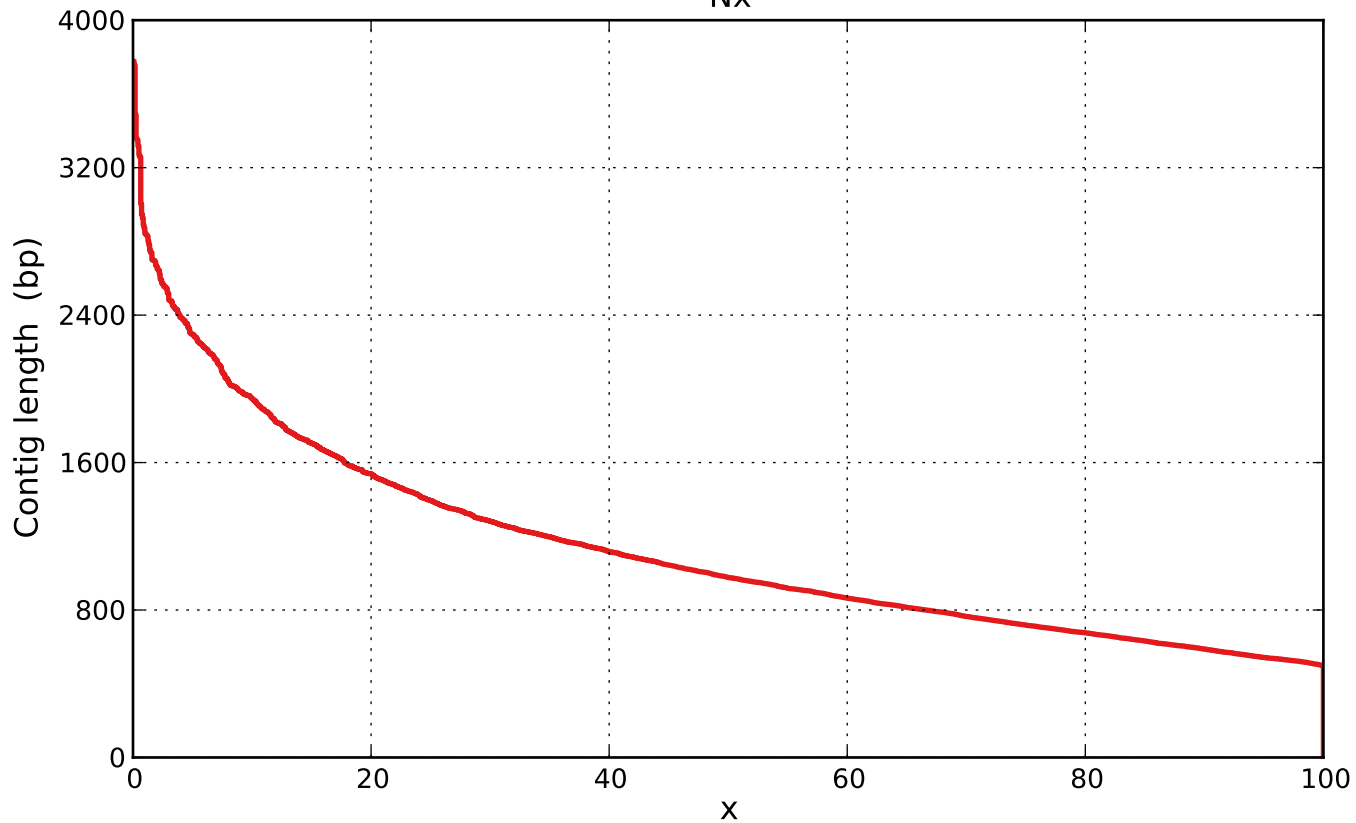
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

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).

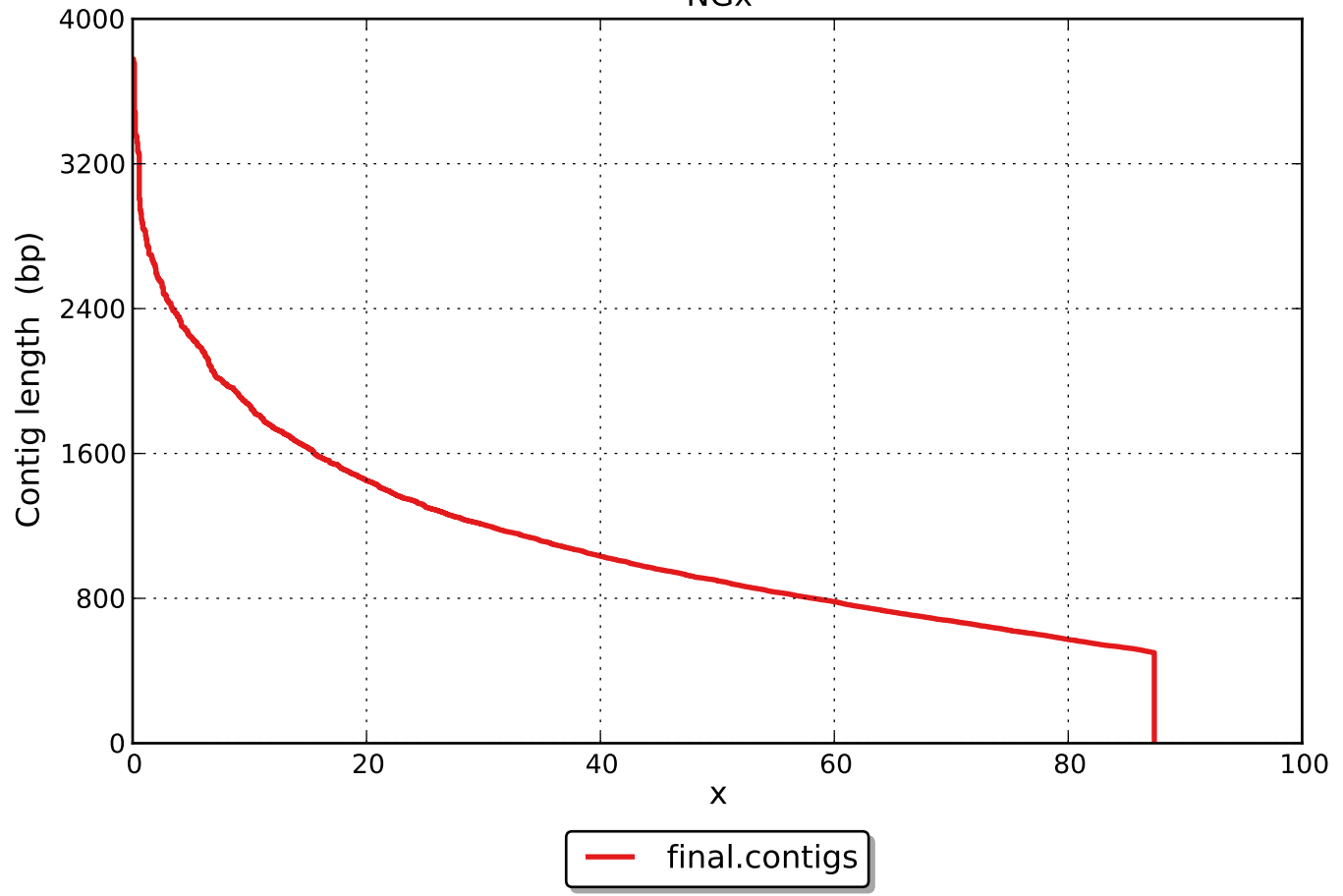
Nx

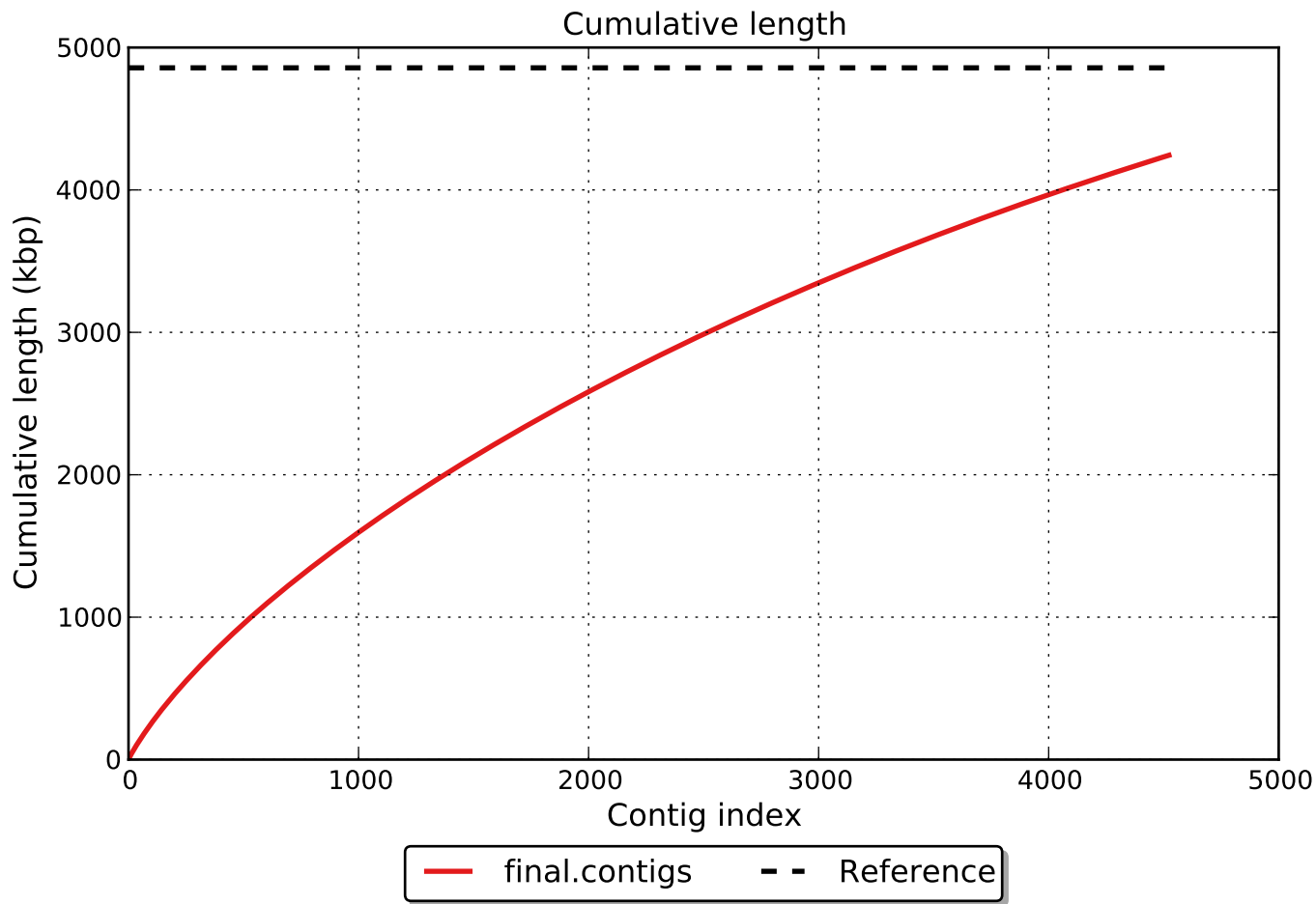


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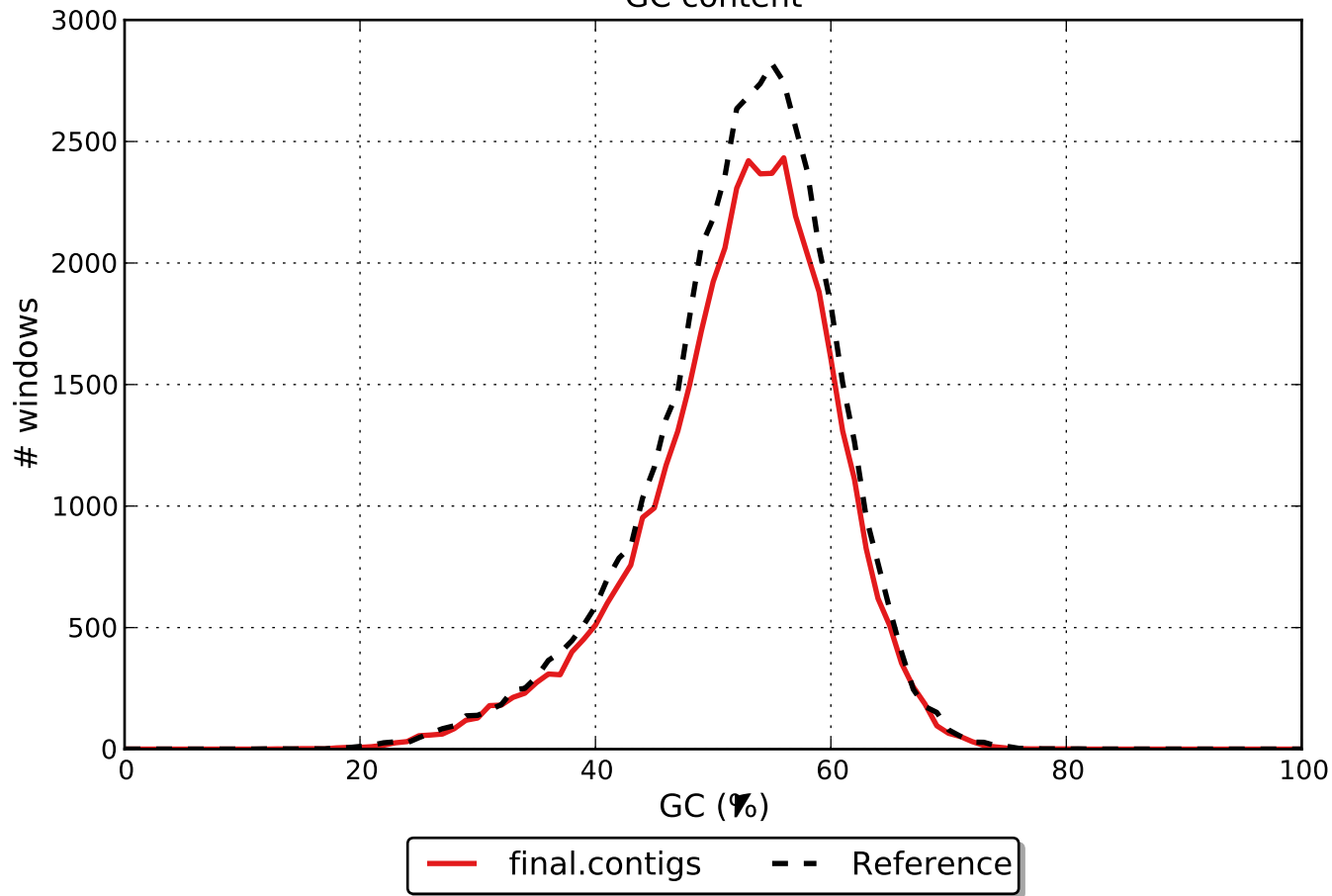
final.contigs

NGx





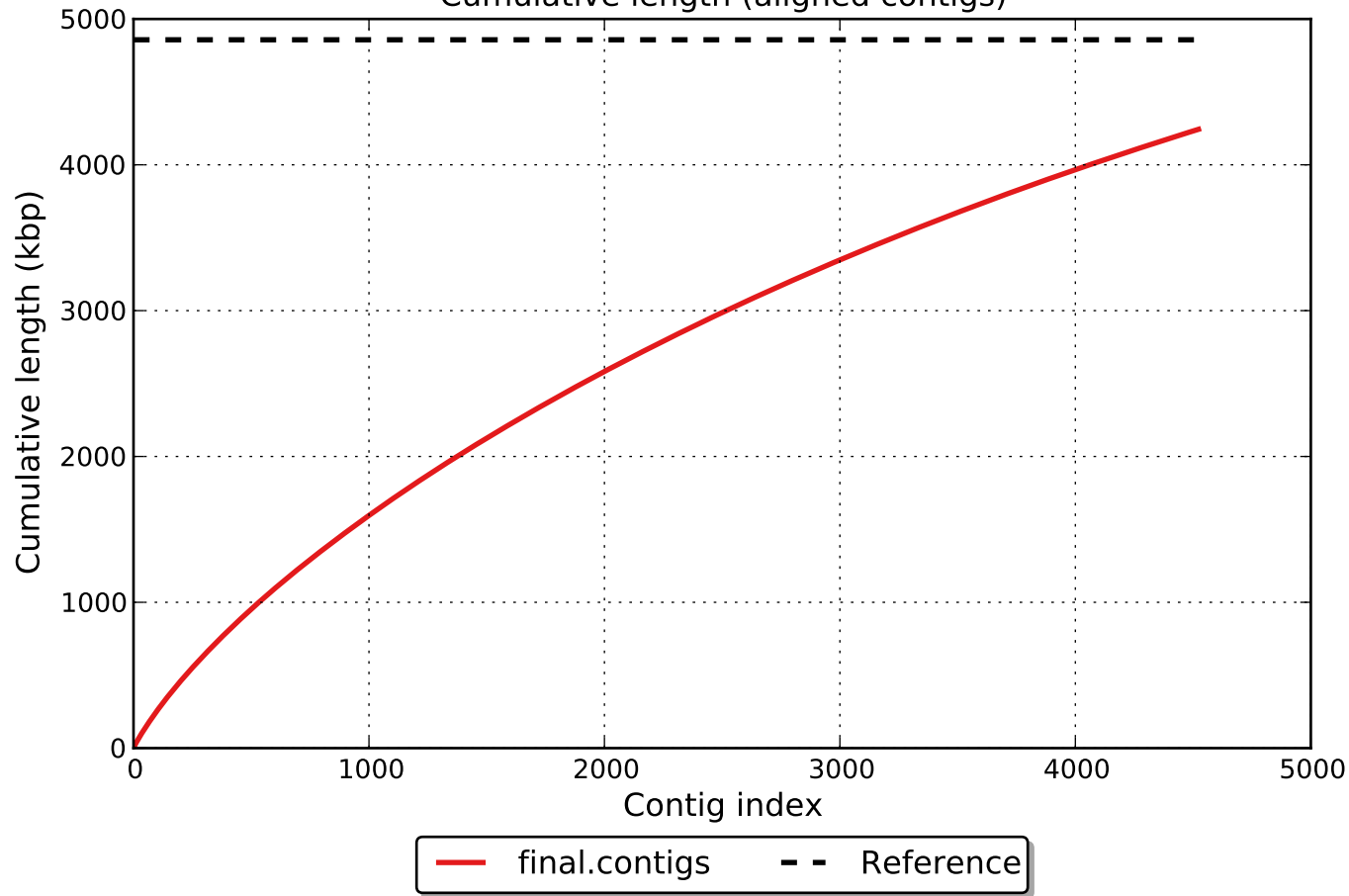
GC content



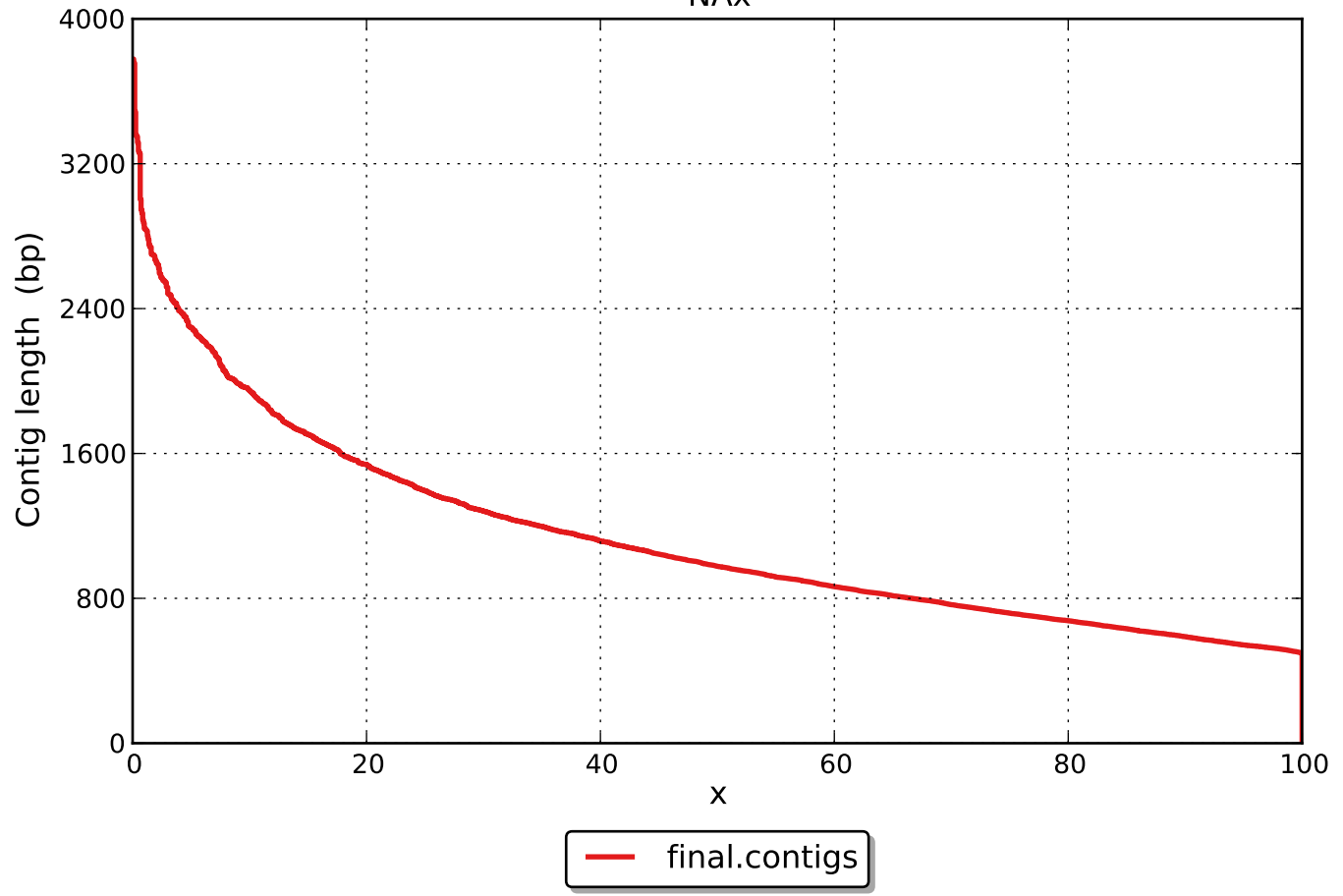
Misassemblies



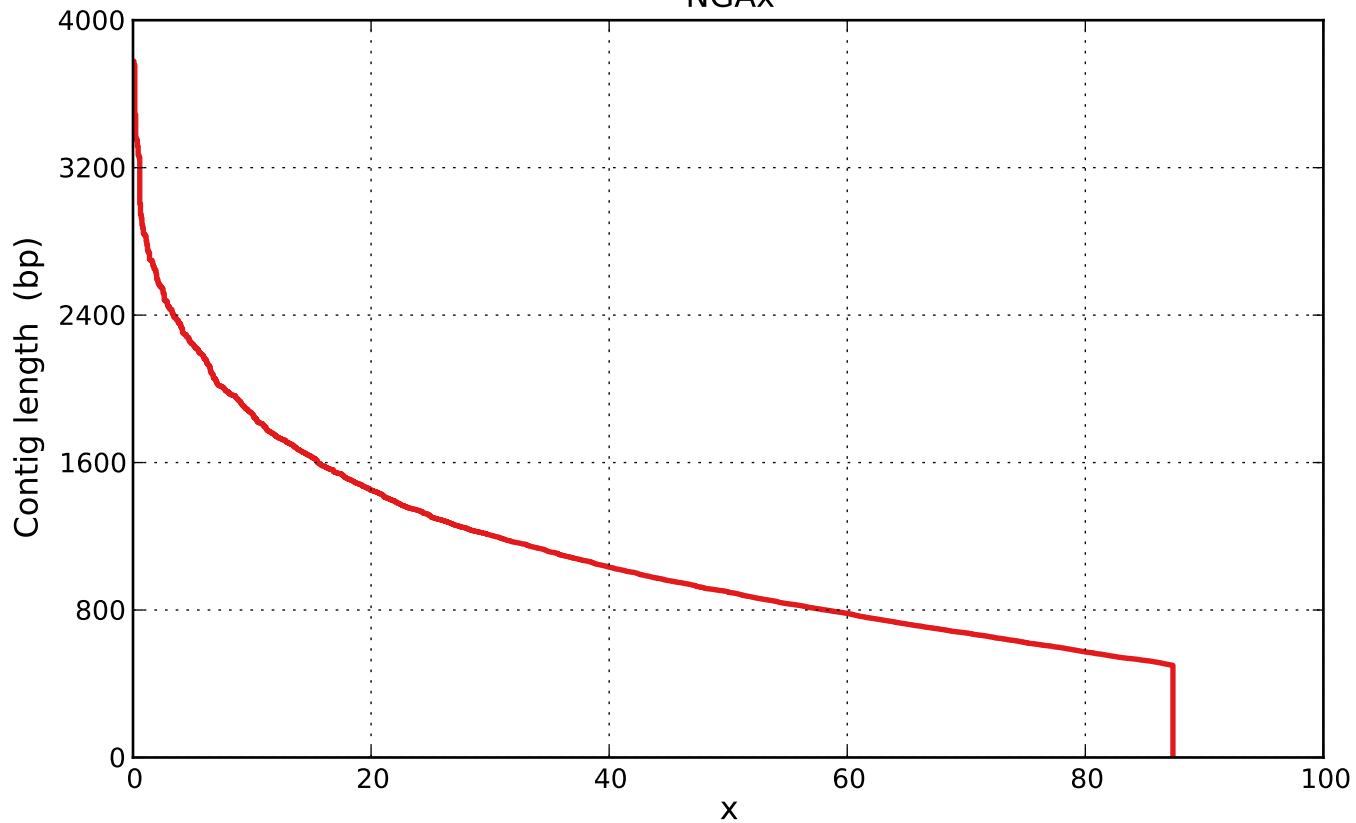
Cumulative length (aligned contigs)



NAx



NGAx



— final.contigs