

Report

	final.contigs
# contigs (>= 1000 bp)	133
# contigs (>= 5000 bp)	105
# contigs (>= 10000 bp)	93
# contigs (>= 25000 bp)	62
# contigs (>= 50000 bp)	34
Total length (>= 1000 bp)	4547220
Total length (>= 5000 bp)	4487299
Total length (>= 10000 bp)	4395413
Total length (>= 25000 bp)	3903398
Total length (>= 50000 bp)	2908019
# contigs	153
Largest contig	275855
Total length	4560832
Reference length	4641652
GC (℥)	50.74
Reference GC (℥)	50.79
N50	57159
NG50	57159
N75	37529
NG75	36334
L50	23
LG50	23
L75	47
LG75	48
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	9
# unaligned contigs	0 + 2 part
Unaligned length	117
Genome fraction (℥)	98.189
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	58.03
# indels per 100 kbp	9.33
Largest alignment	275855
NA50	57159
NGA50	57159
NA75	37529
NGA75	36331
LA50	23
LGA50	23
LA75	47
LGA75	48

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	9
# mismatches	2645
# indels	425
# short indels	425
# long indels	0
Indels length	597

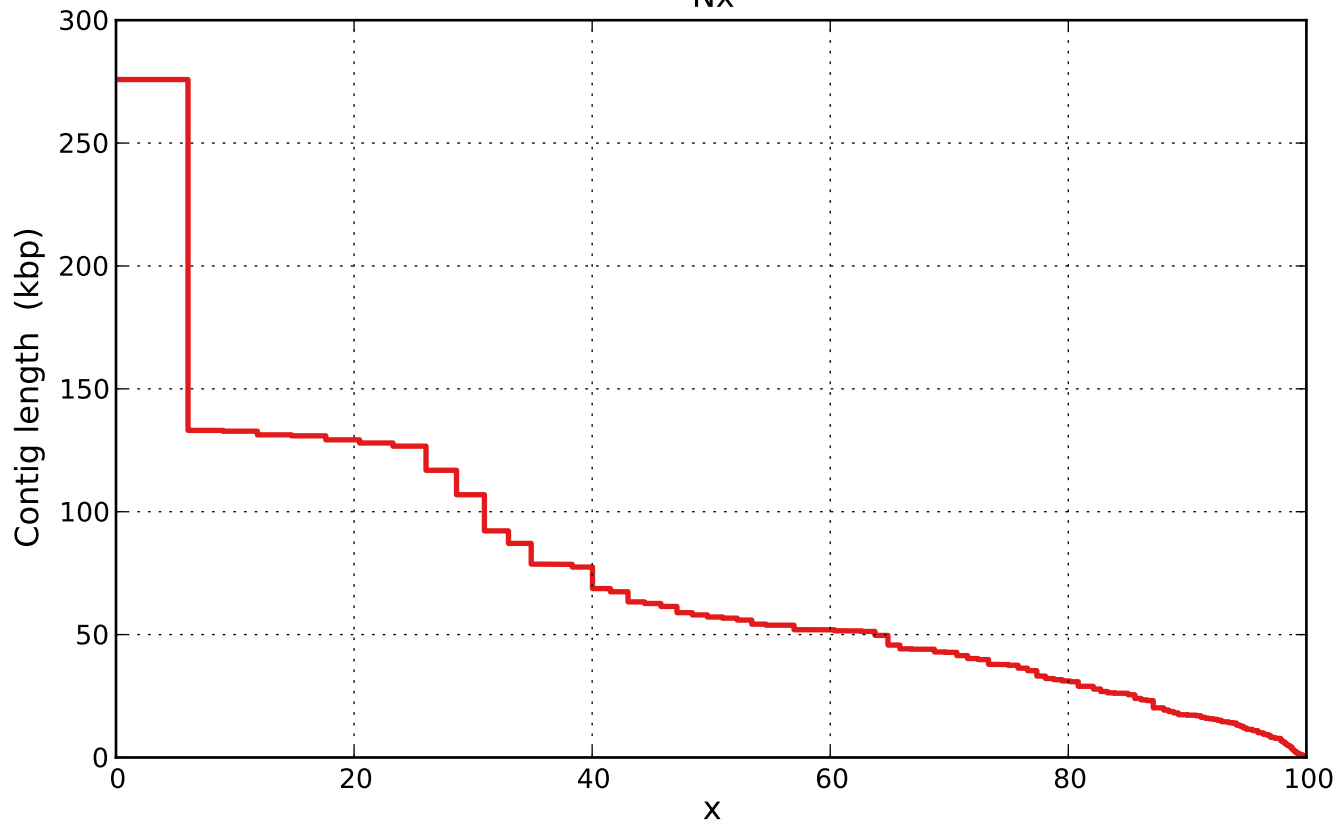
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	117
# N's	0

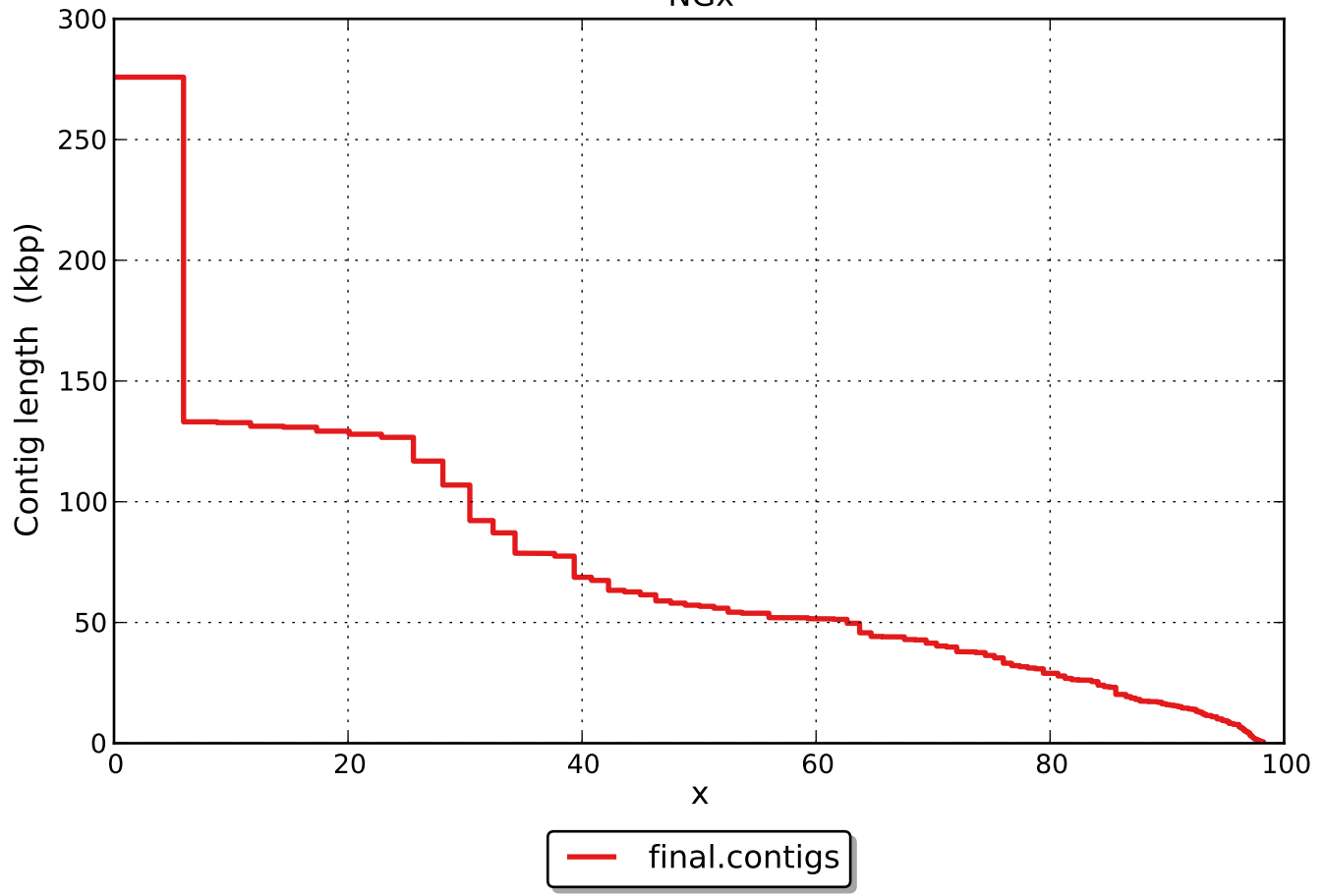
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

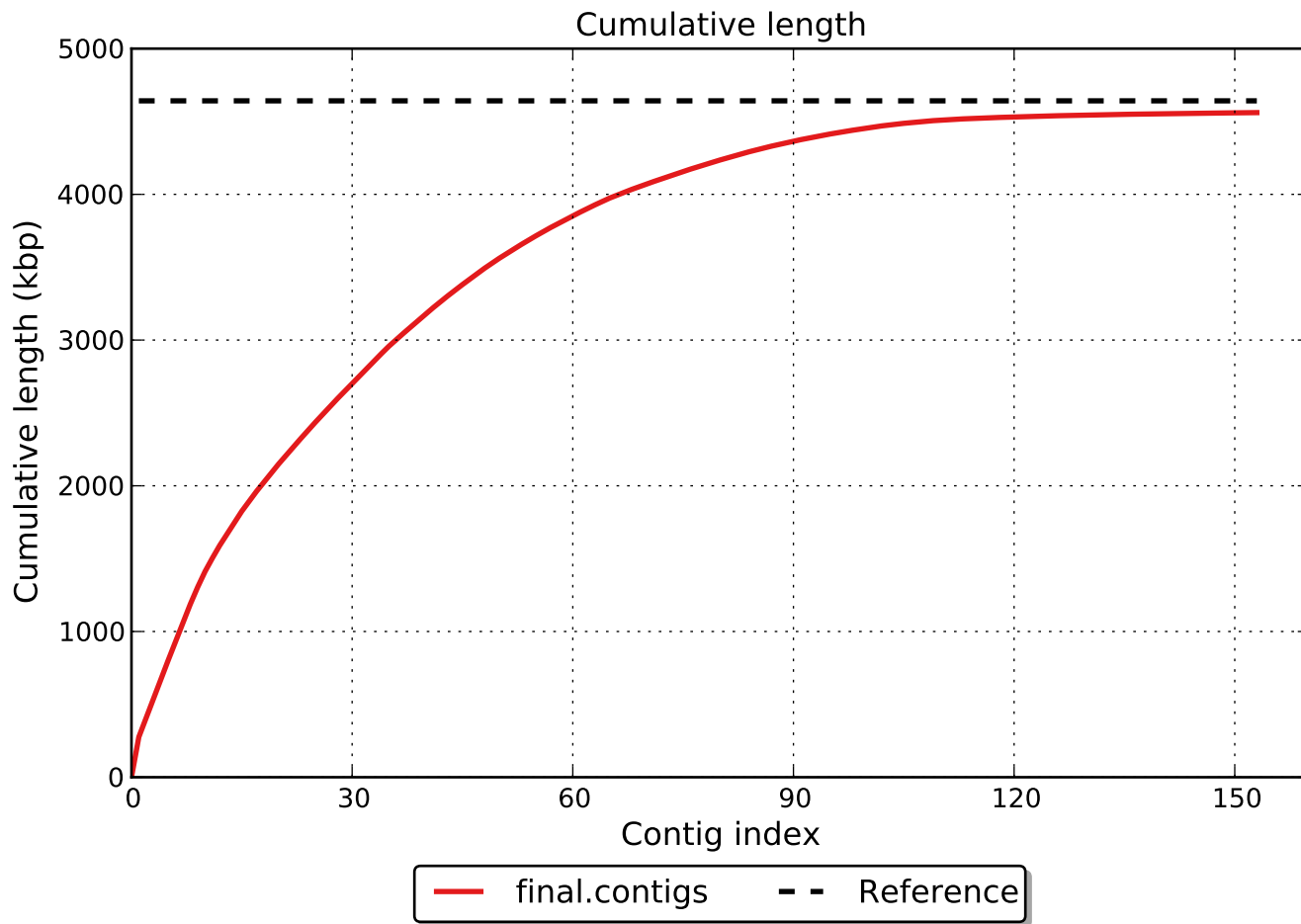
Nx



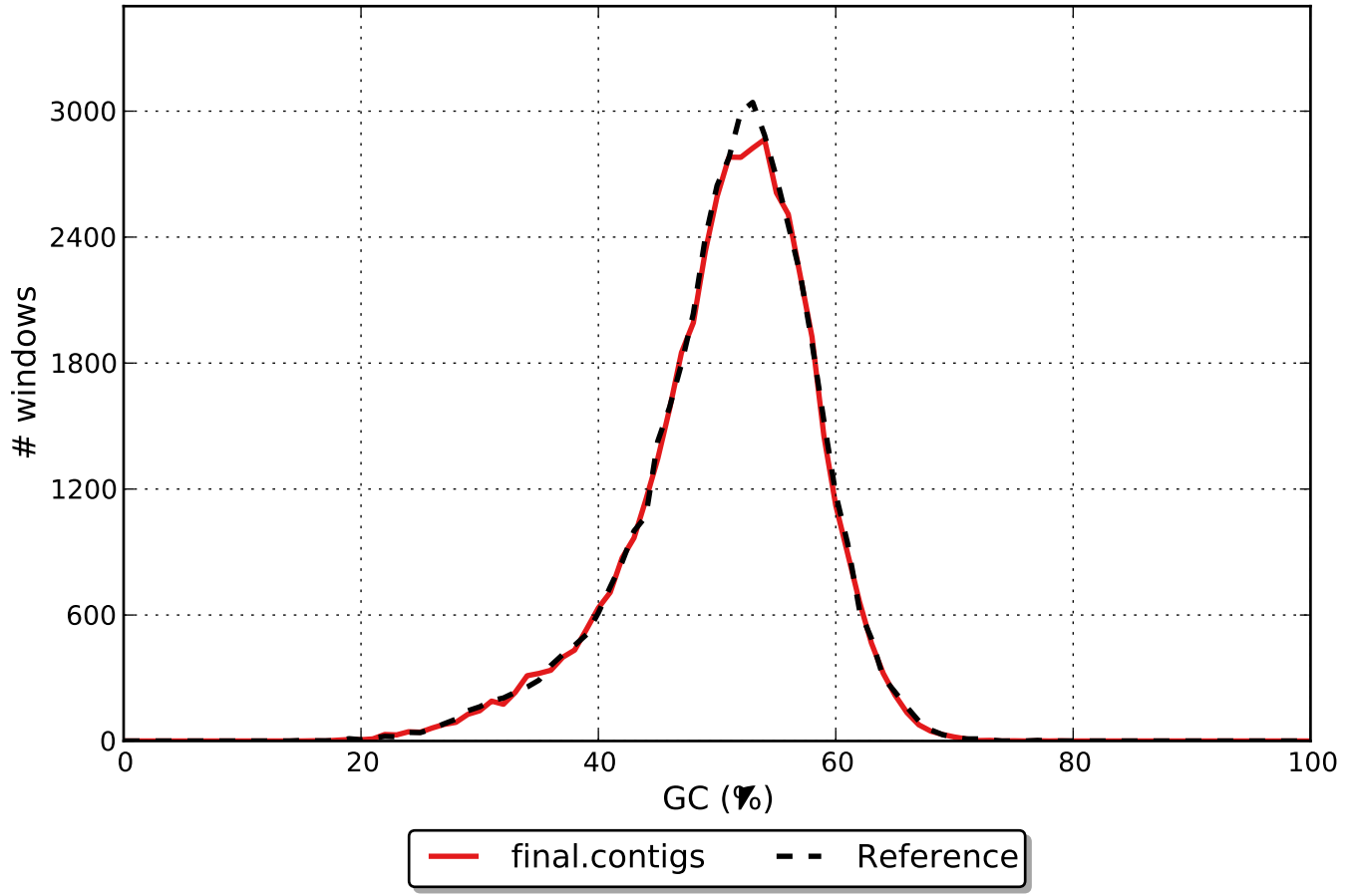
— final.contigs

NGx





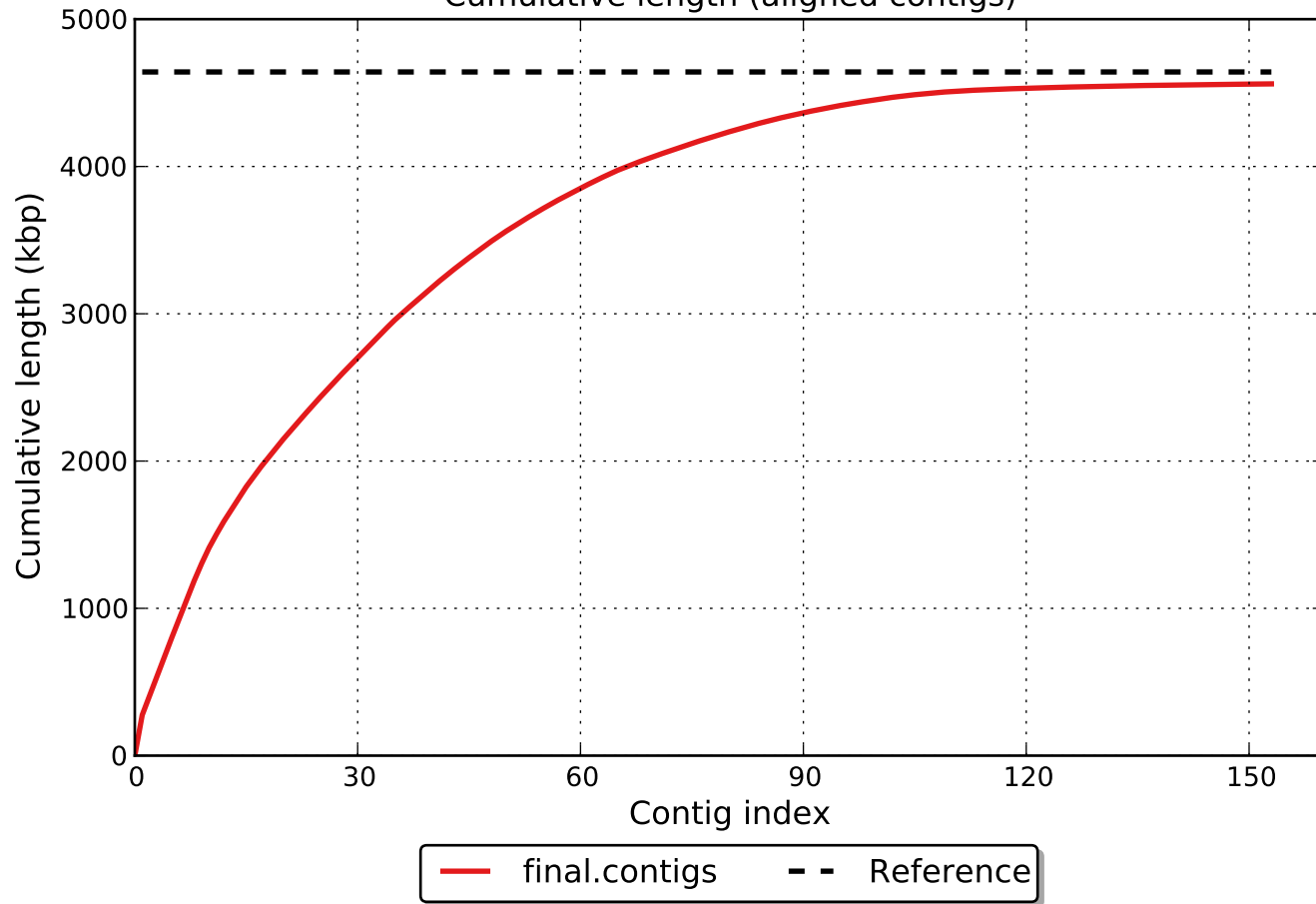
GC content



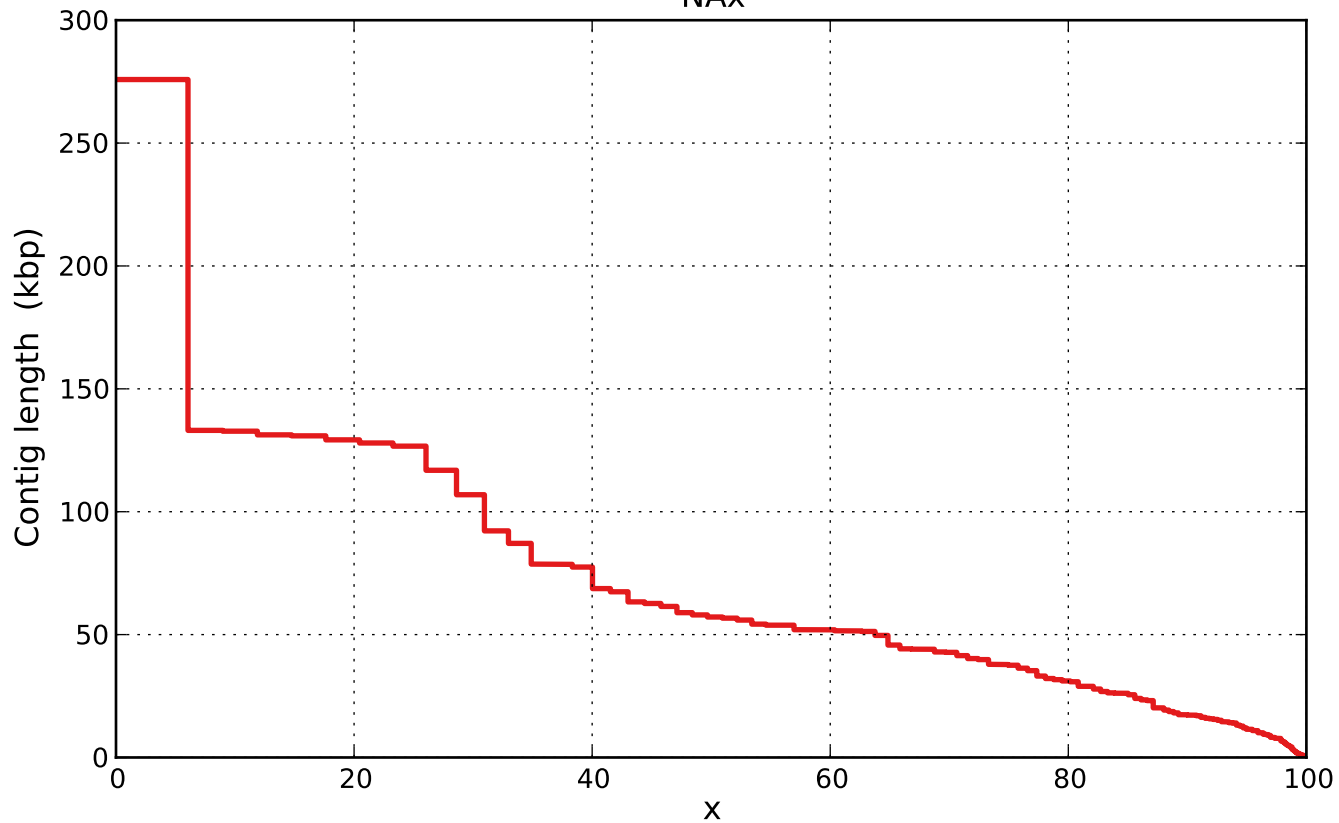
Misassemblies



Cumulative length (aligned contigs)

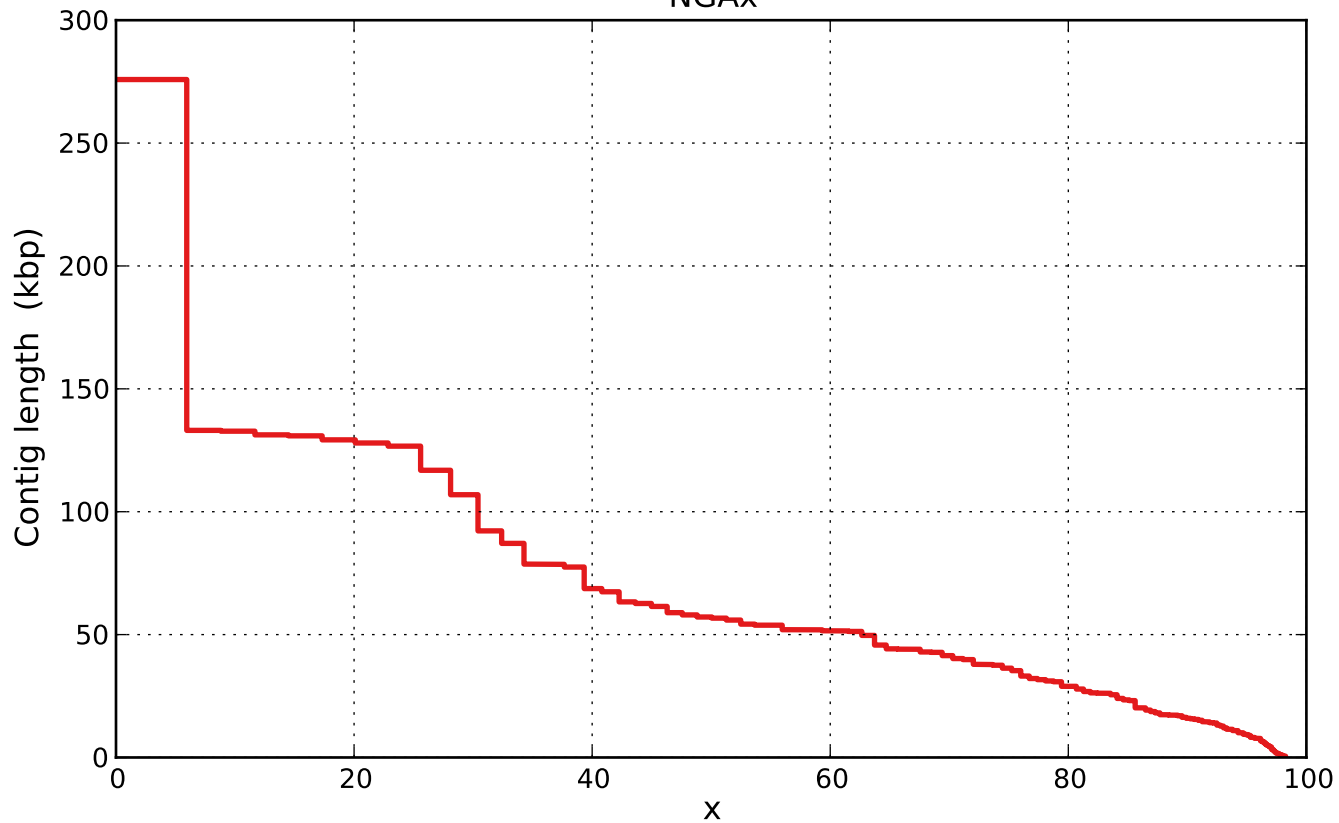


NAx



— final.contigs

NGAx



— final.contigs