

Report

	final.contigs
# contigs (>= 1000 bp)	220
# contigs (>= 5000 bp)	179
# contigs (>= 10000 bp)	141
# contigs (>= 25000 bp)	66
# contigs (>= 50000 bp)	17
Total length (>= 1000 bp)	4558247
Total length (>= 5000 bp)	4448128
Total length (>= 10000 bp)	4170159
Total length (>= 25000 bp)	2844381
Total length (>= 50000 bp)	1149839
# contigs	237
Largest contig	99838
Total length	4570899
Reference length	4641652
GC (℥)	50.74
Reference GC (℥)	50.79
N50	31594
NG50	31121
N75	19932
NG75	19321
L50	46
LG50	48
L75	92
LG75	95
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	36763
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	98.171
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.48
# indels per 100 kbp	0.00
Largest alignment	99838
NA50	31433
NGA50	31121
NA75	19932
NGA75	19321
LA50	47
LGA50	48
LA75	92
LGA75	95

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	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	36763
# local misassemblies	0
# mismatches	22
# indels	0
# short indels	0
# long indels	0
Indels length	0

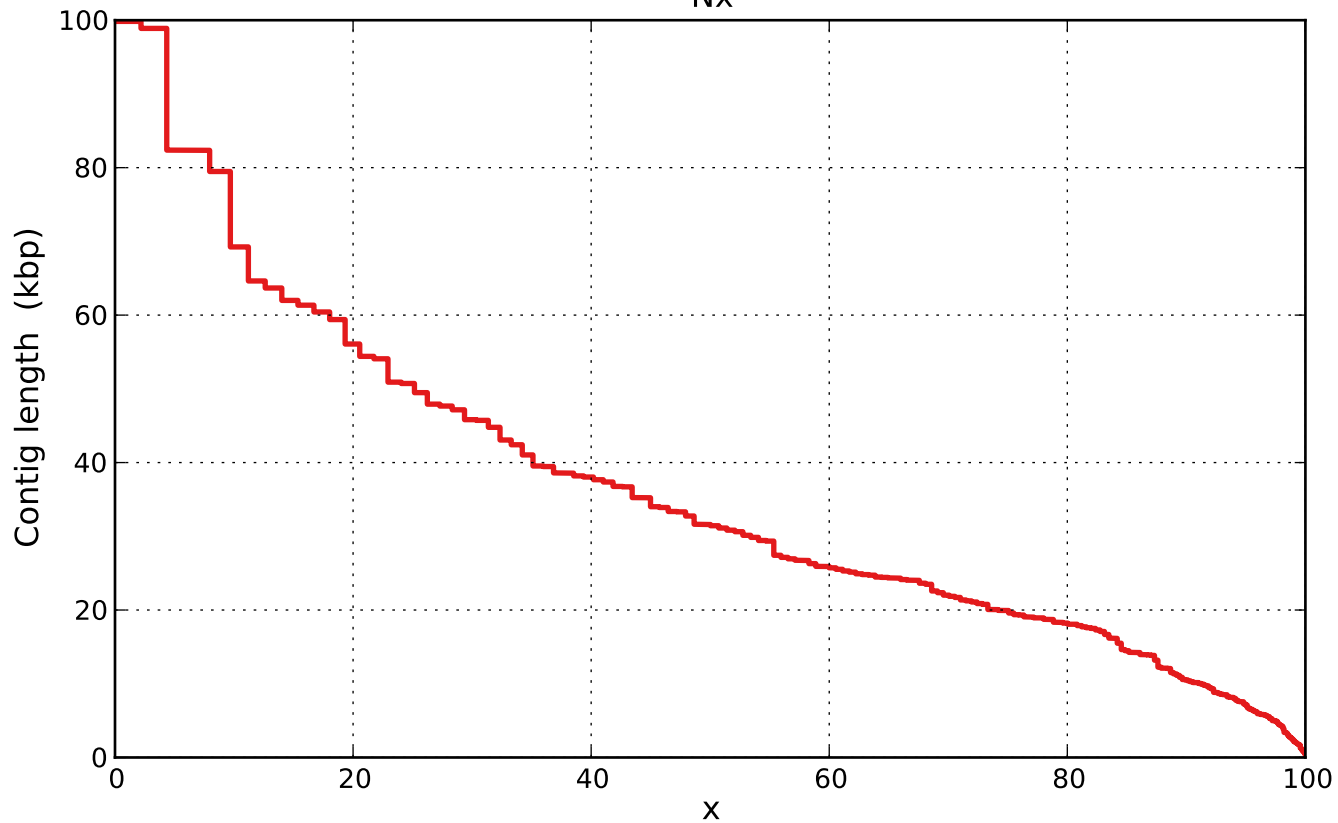
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

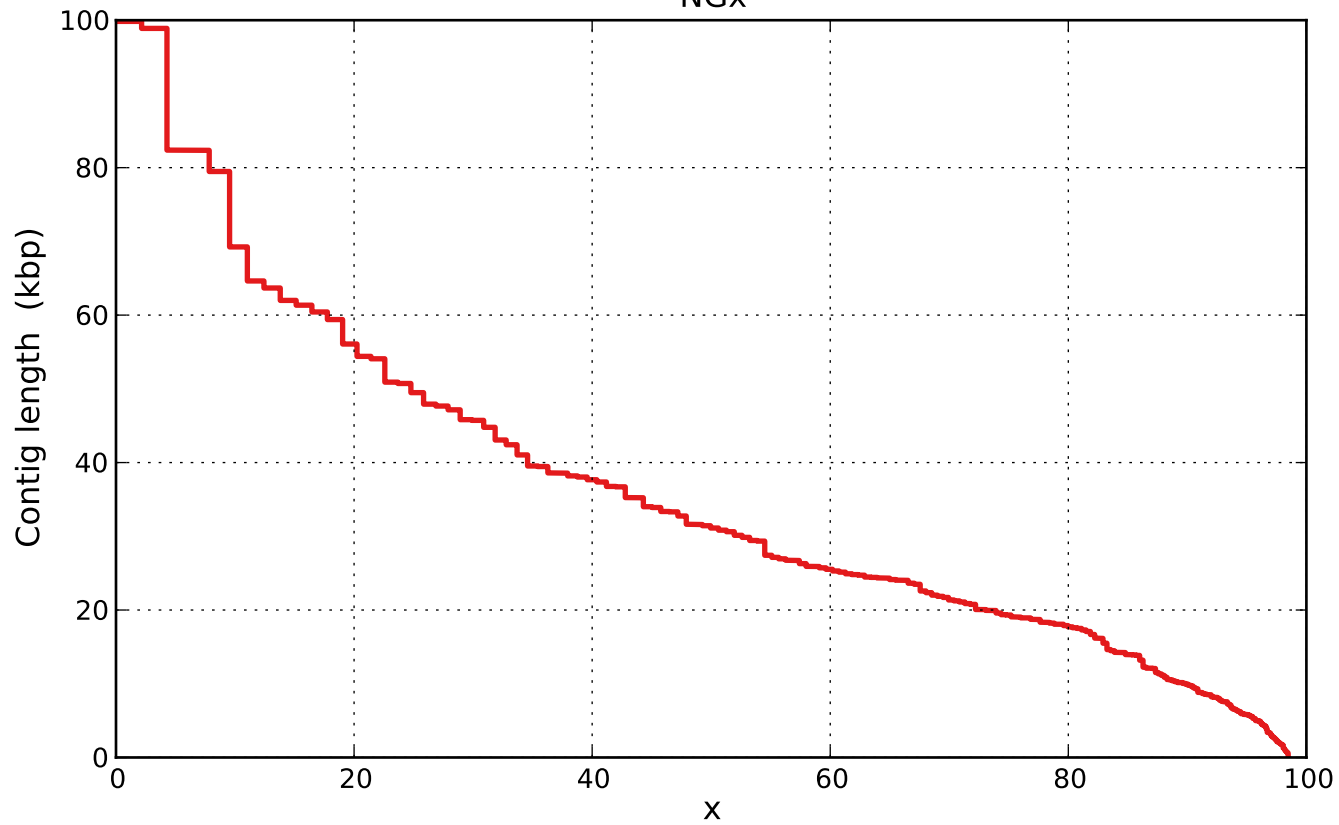
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

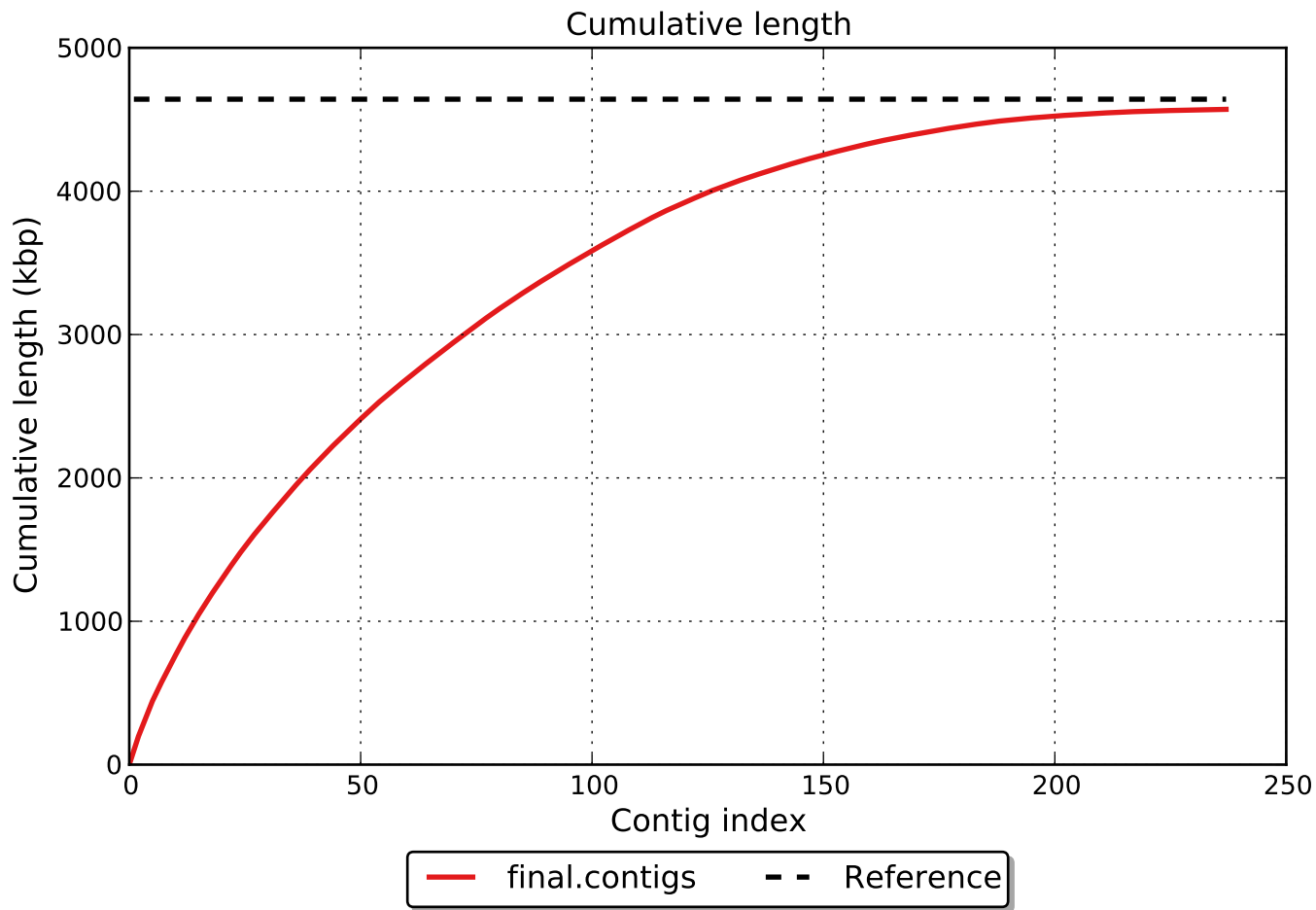
Nx



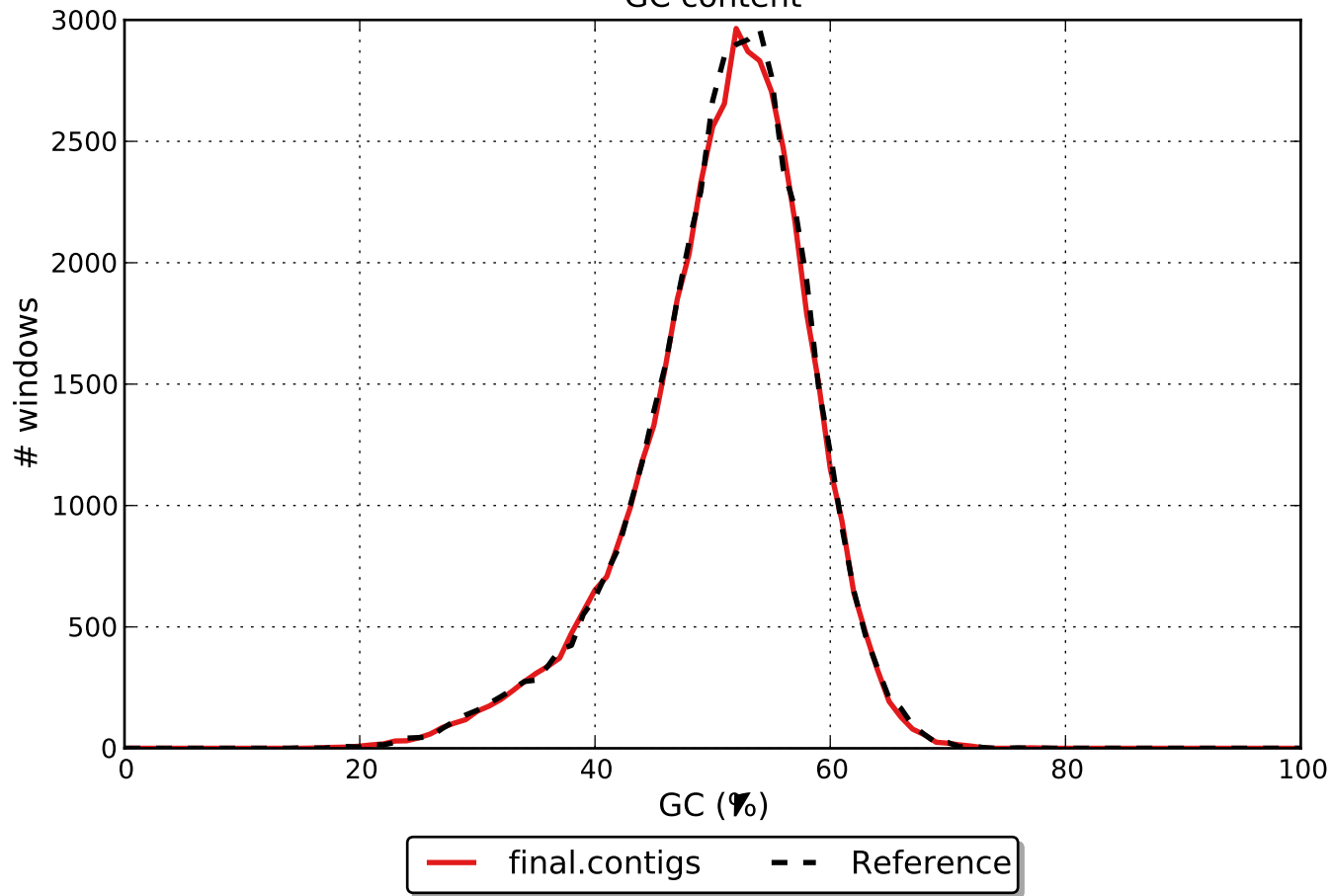
NGx



— final.contigs

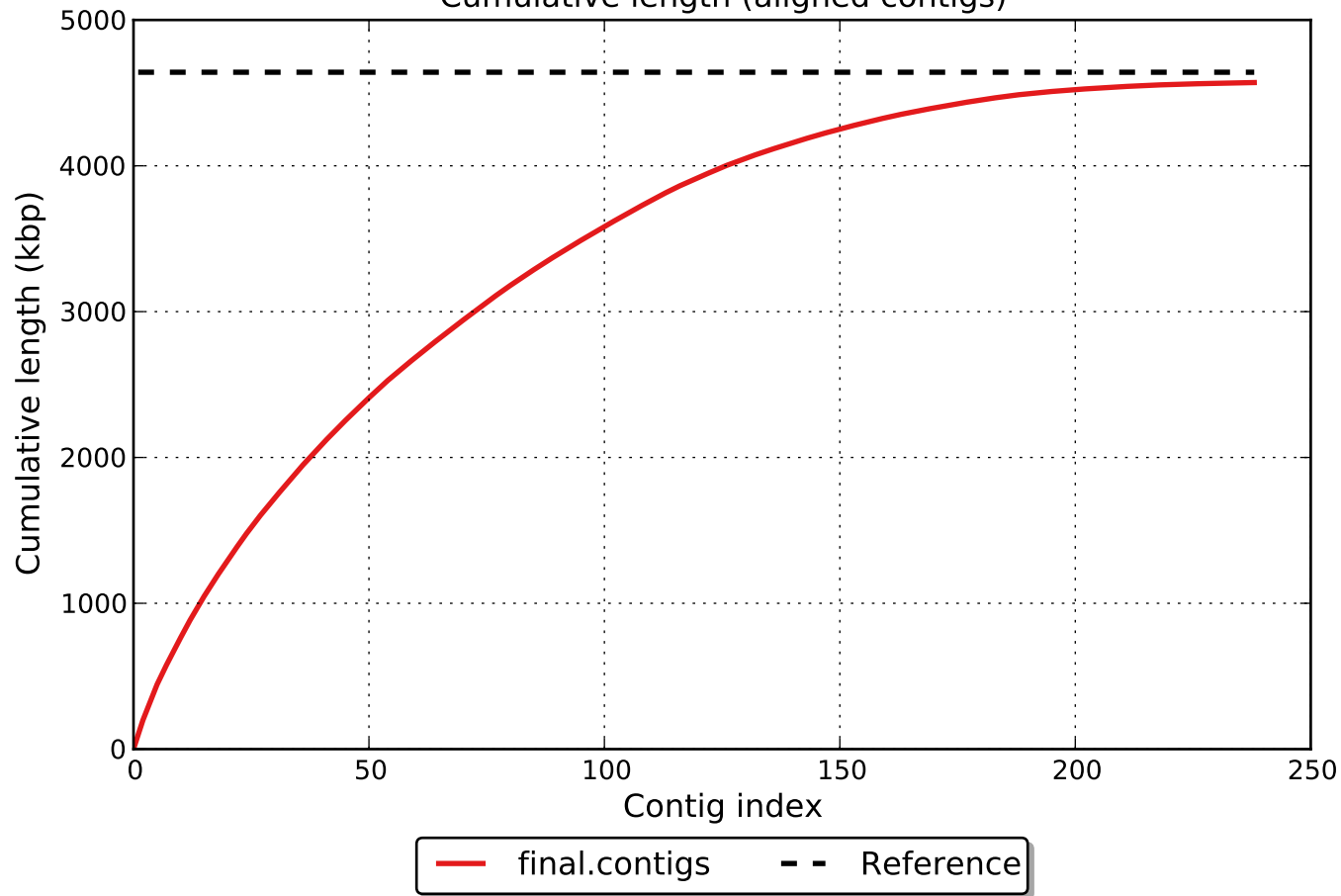


GC content

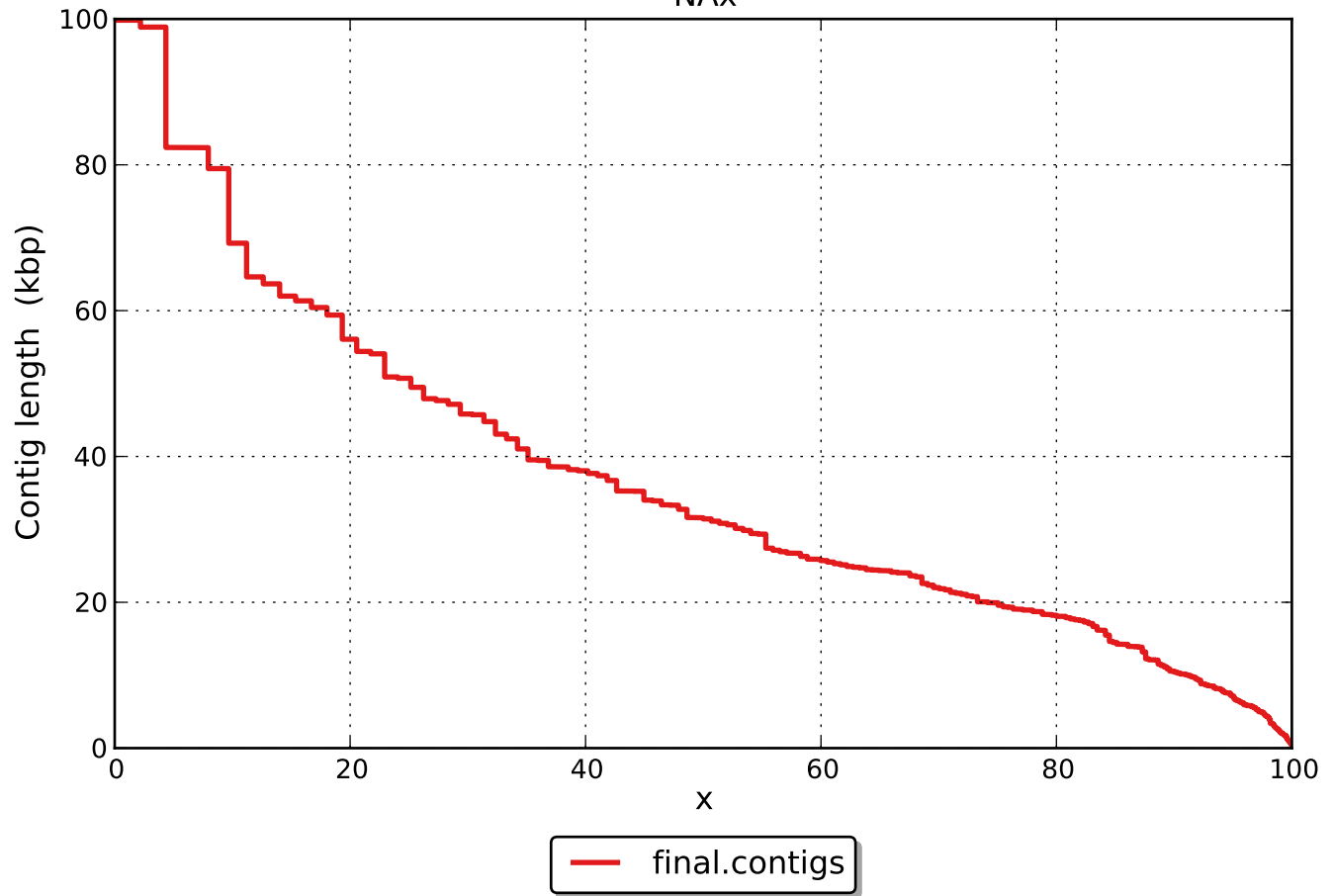




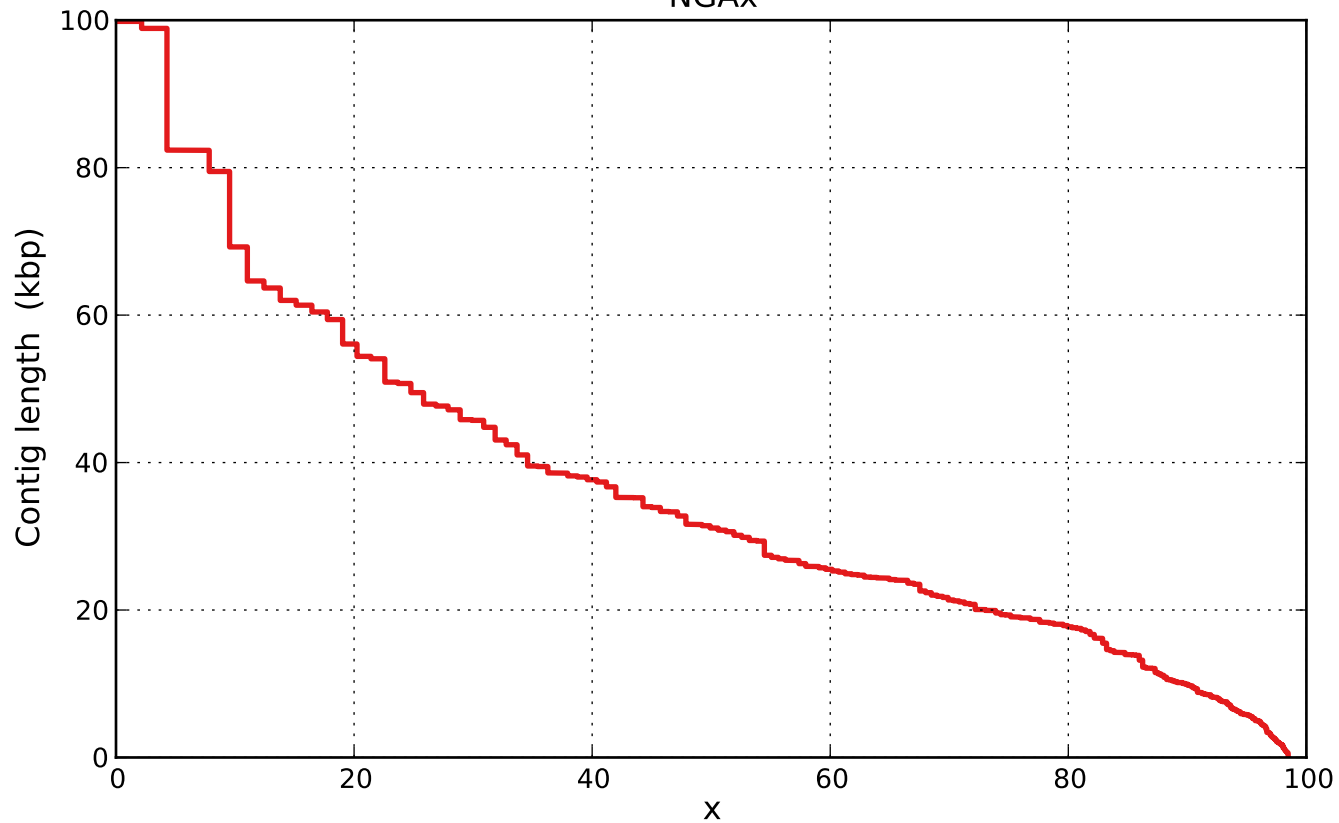
Cumulative length (aligned contigs)



NAx



NGAx



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