

Report

	final.contigs
# contigs (≥ 0 bp)	5794
# contigs (≥ 1000 bp)	5
Total length (≥ 0 bp)	1480212
Total length (≥ 1000 bp)	43097
# contigs	8
Largest contig	23983
Total length	44953
Reference length	609578
GC (%)	44.65
Reference GC (%)	36.76
N50	23983
N75	4946
L50	1
L75	3
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	1 + 0 part
Unaligned length	520
Genome fraction (%)	7.349
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2.23
# indels per 100 kbp	0.00
Largest alignment	23983
NA50	23983
NA75	4946
LA50	1
LA75	3

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
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	1
# indels	0
# short indels	0
# long indels	0
Indels length	0

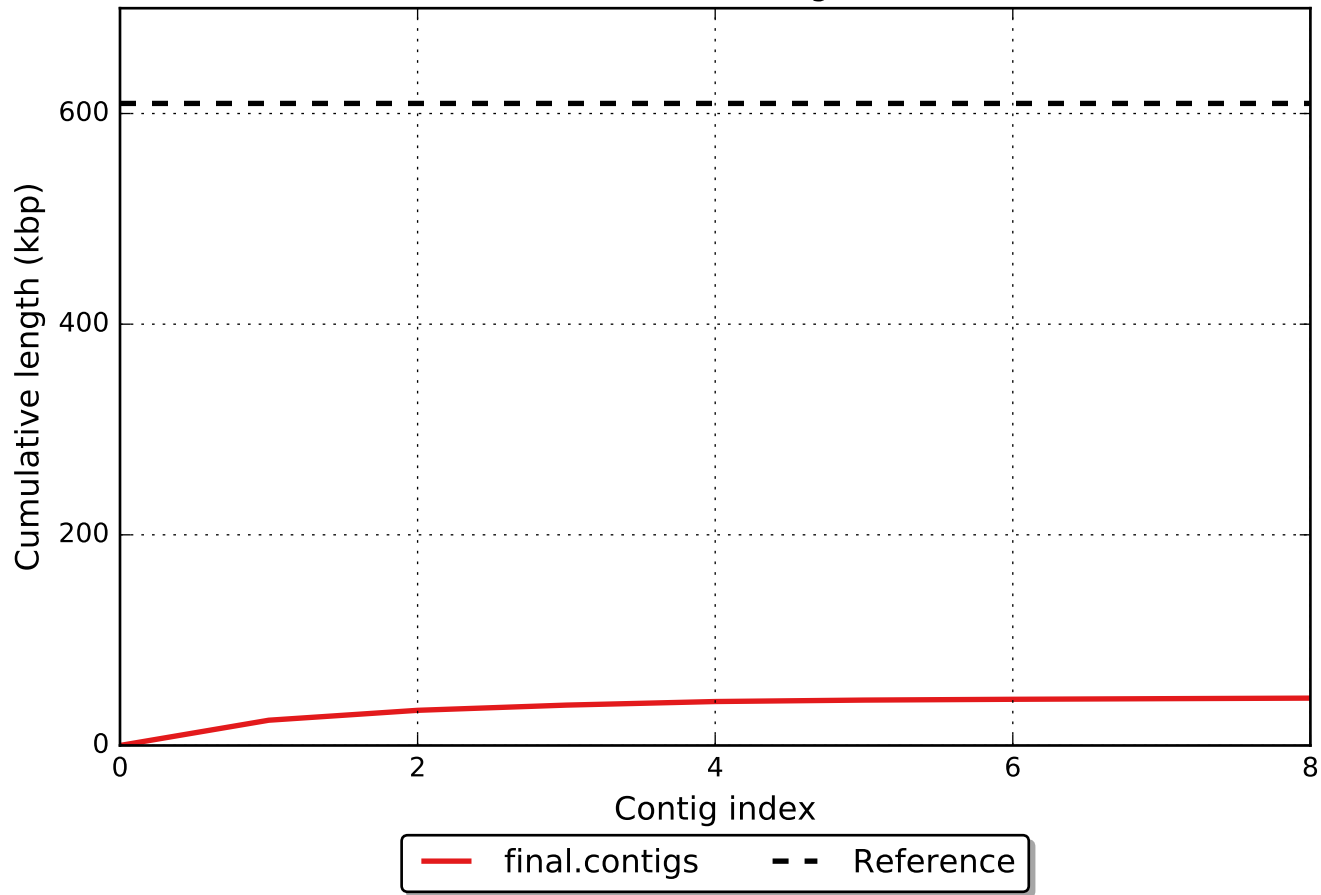
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

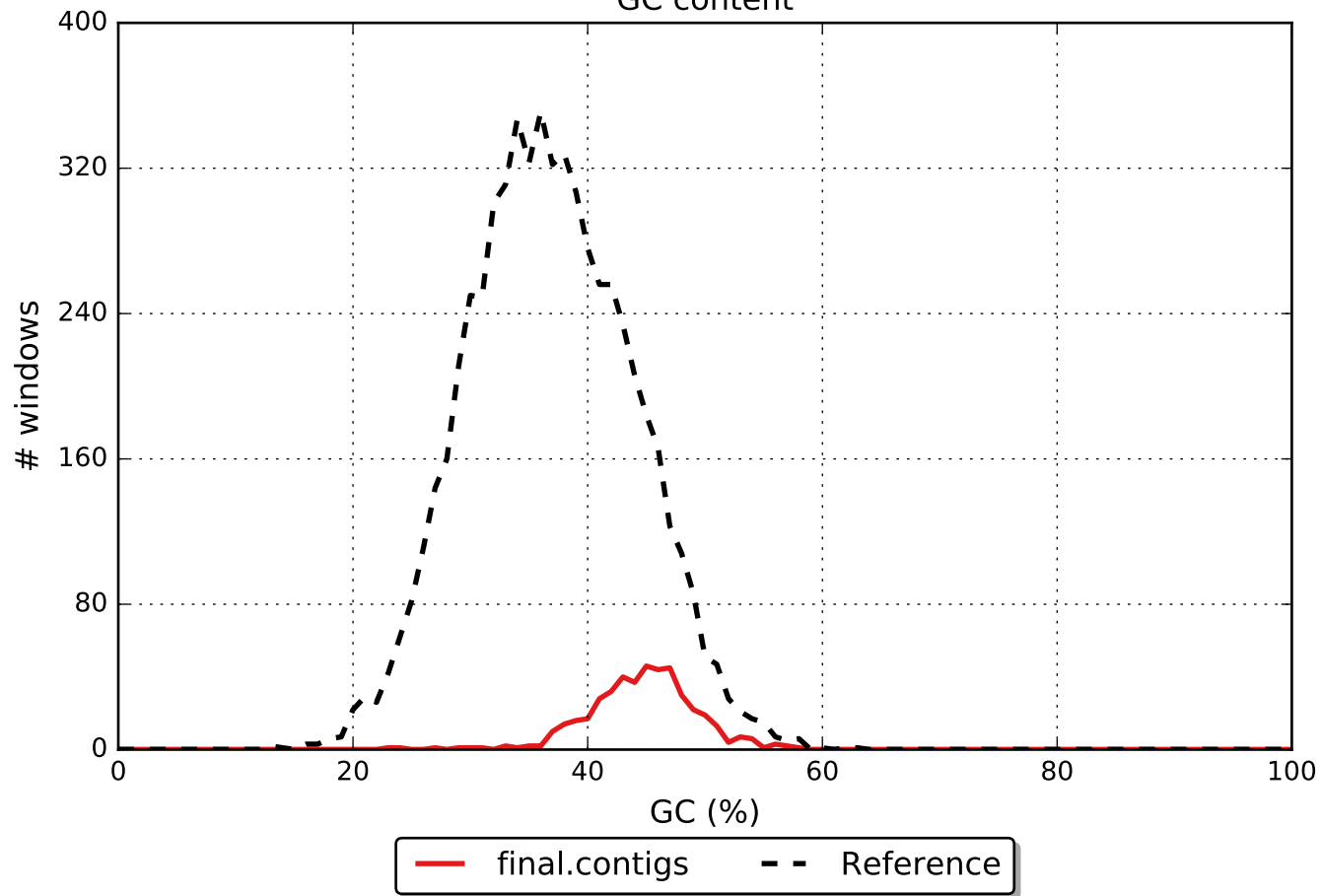
	final.contigs
# fully unaligned contigs	1
Fully unaligned length	520
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

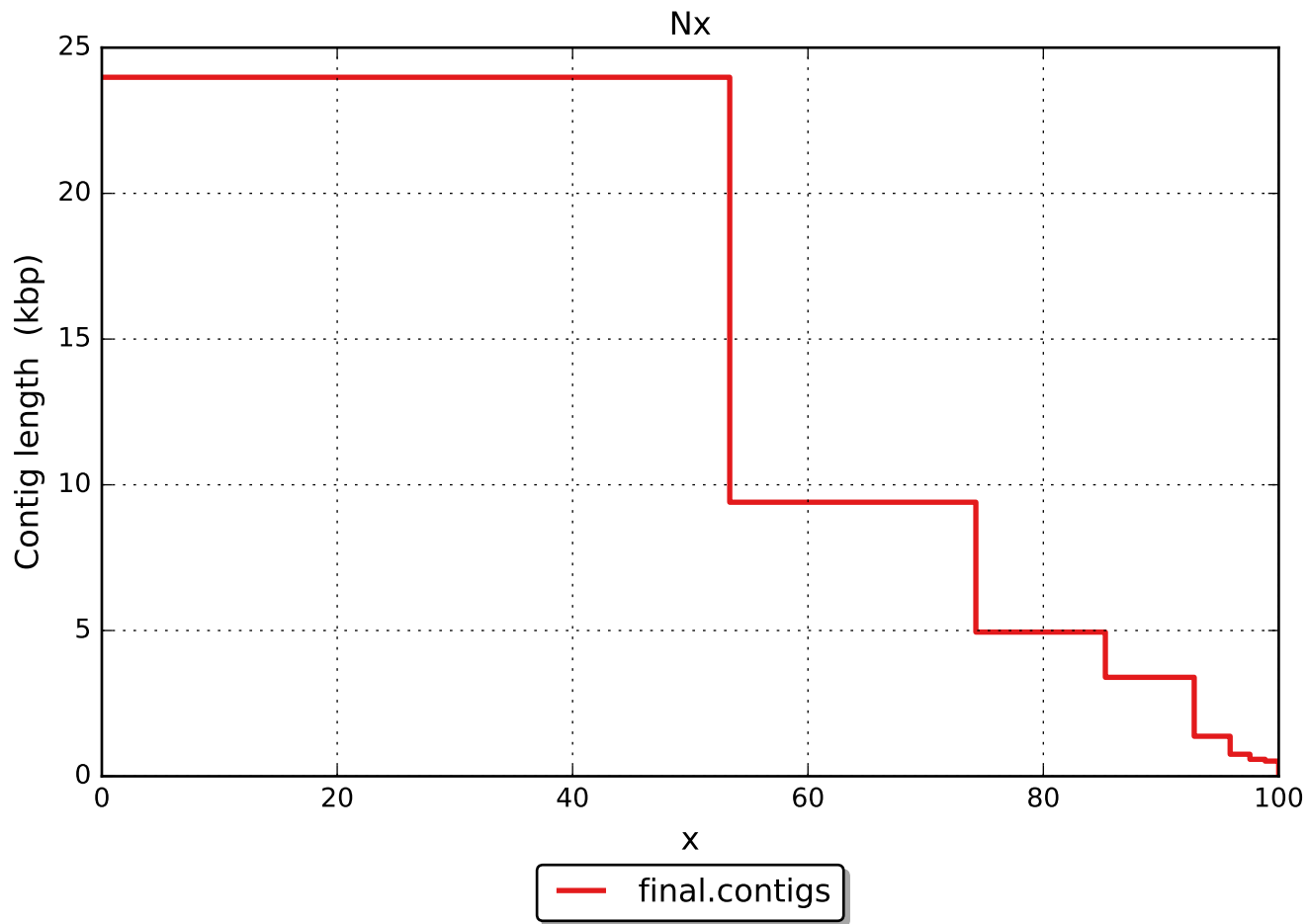
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Cumulative length

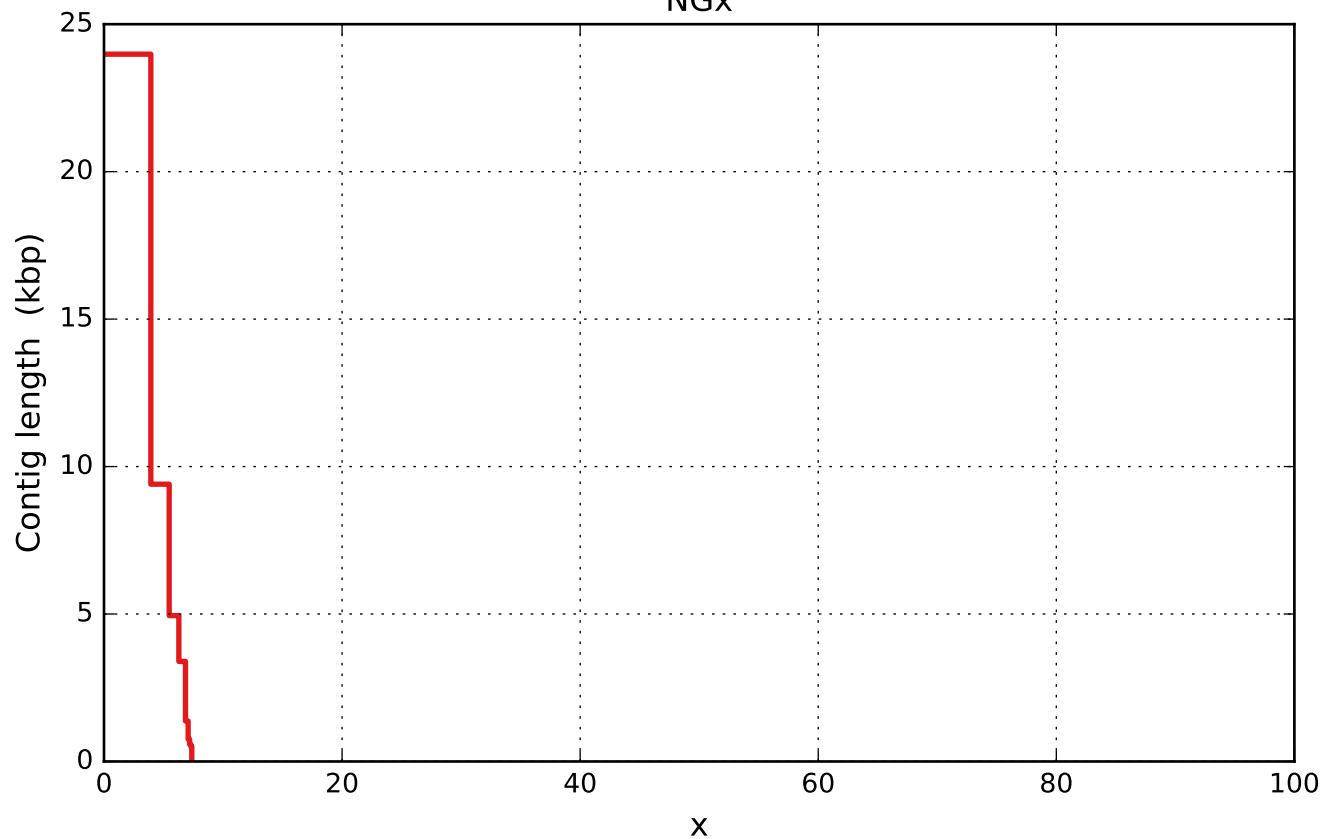


GC content

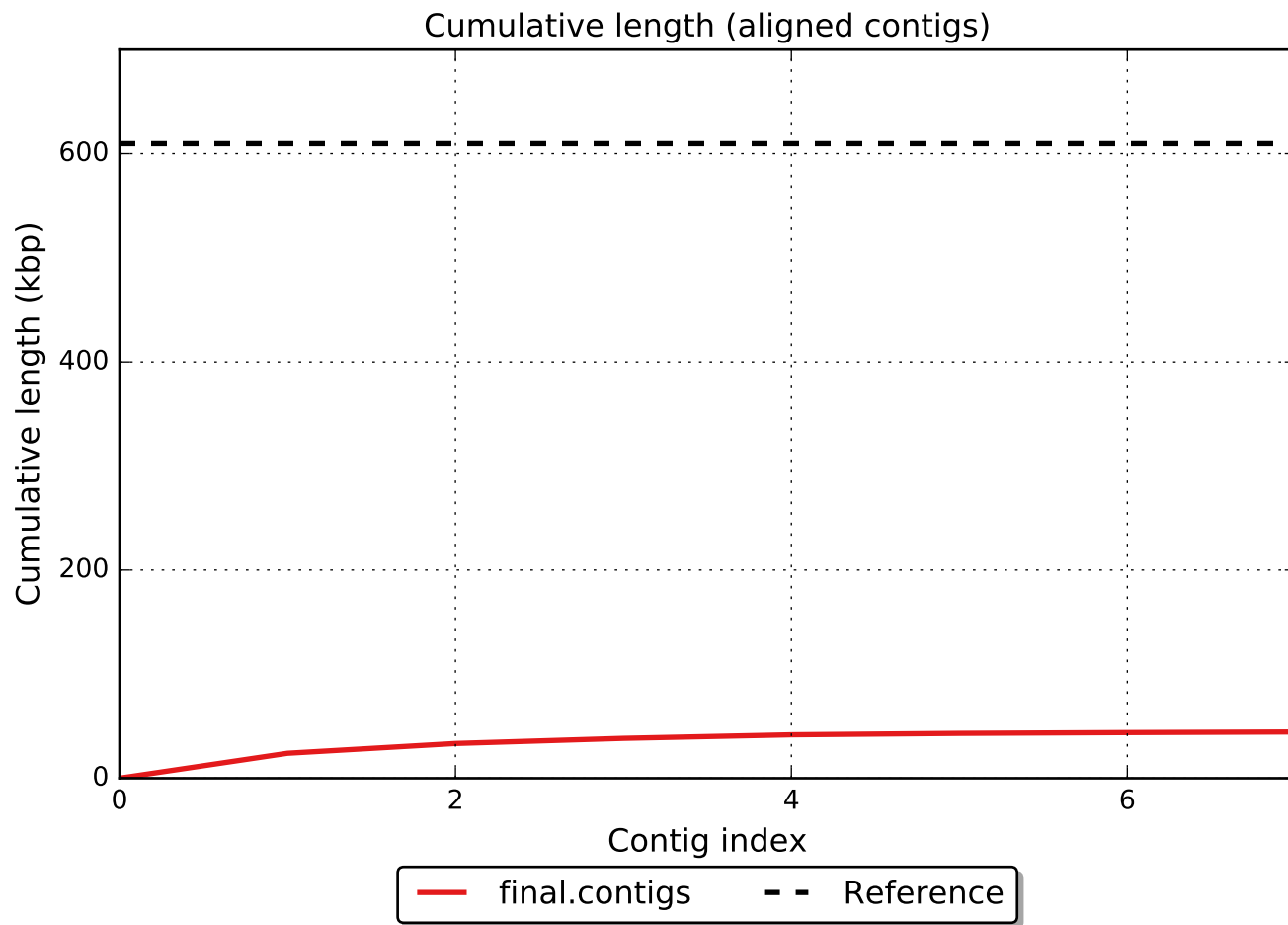


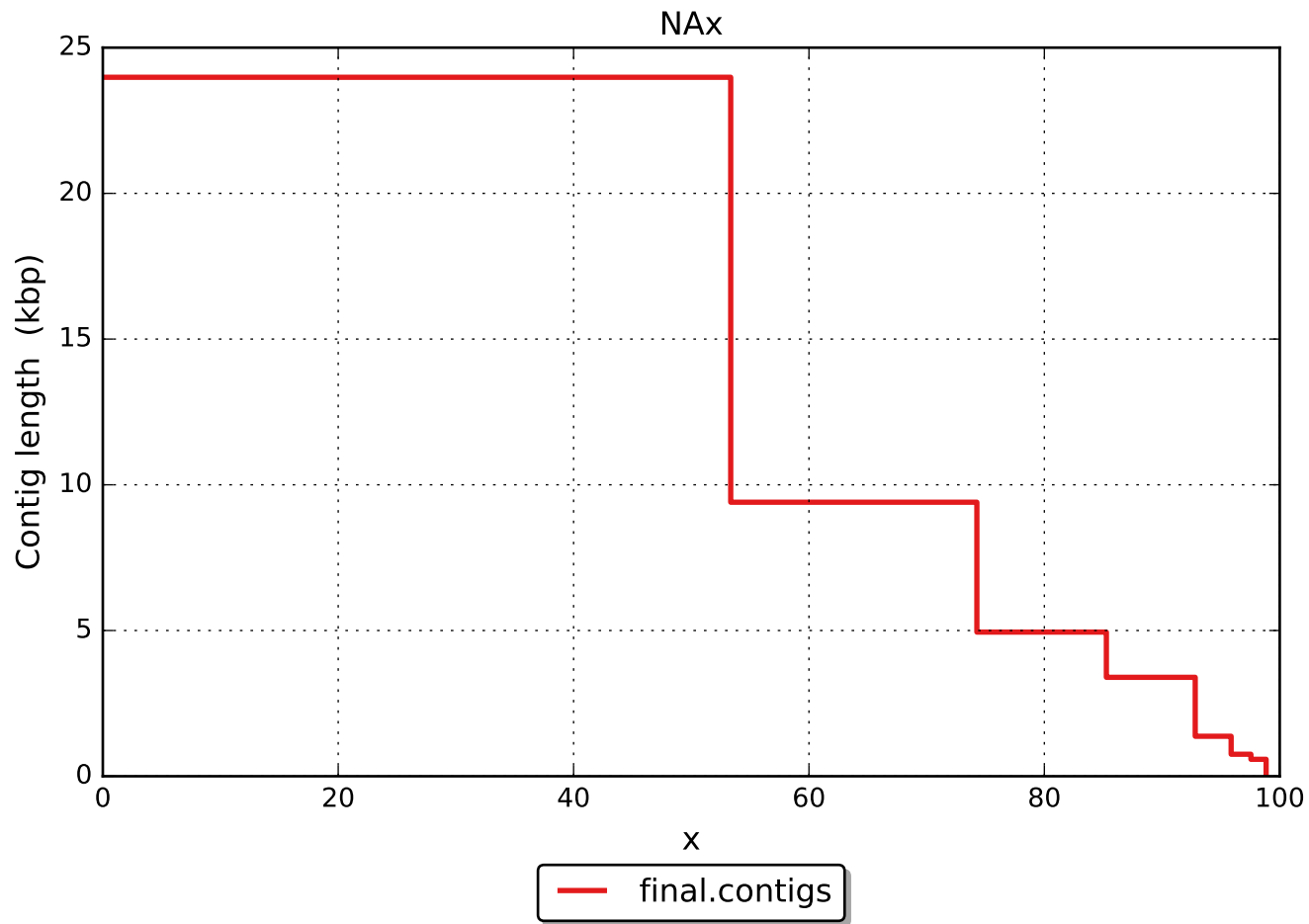


NGx

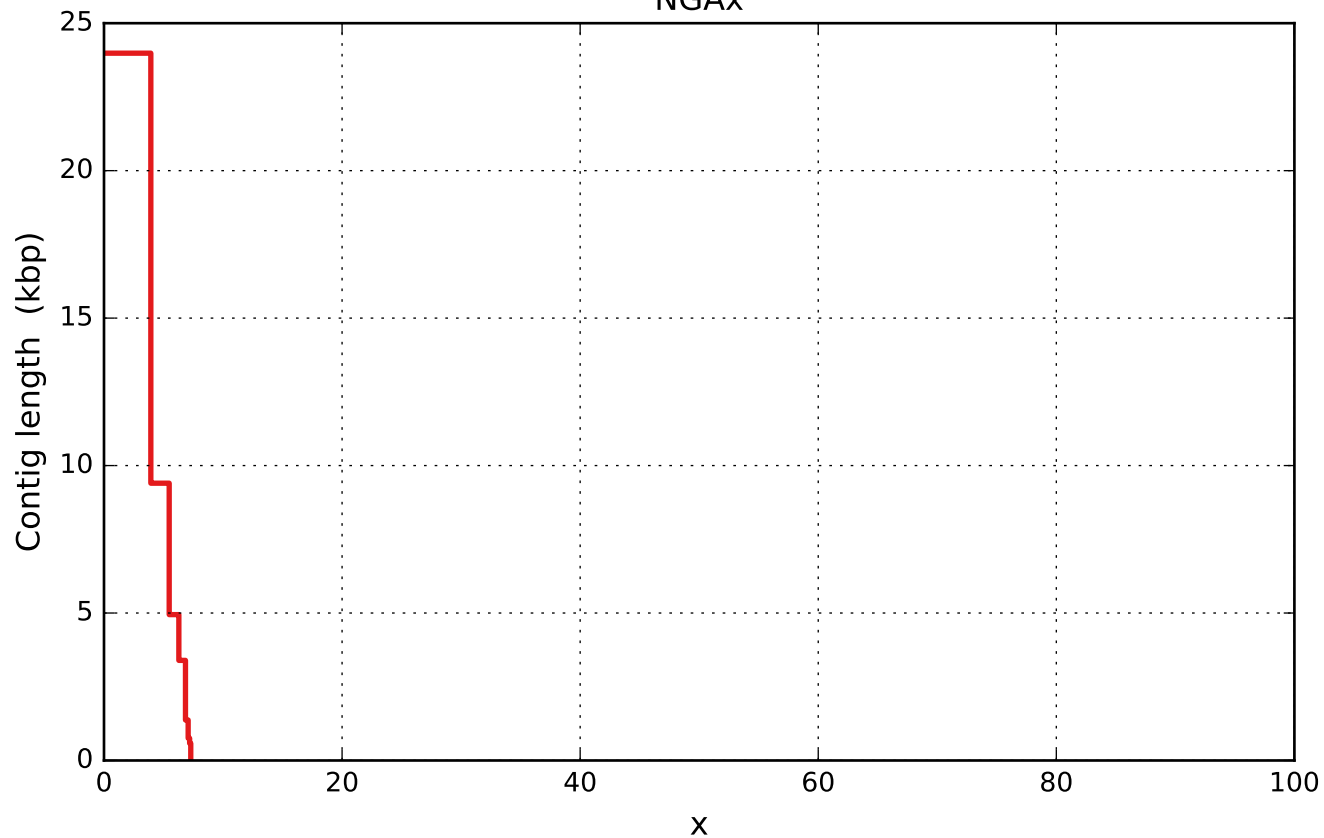


— final.contigs





NGAx



— final.contigs