

Report

	final.contigs
# contigs (≥ 0 bp)	288
# contigs (≥ 1000 bp)	244
Total length (≥ 0 bp)	1244192
Total length (≥ 1000 bp)	1210316
# contigs	288
Largest contig	18968
Total length	1244192
Reference length	615980
GC (%)	25.36
Reference GC (%)	25.32
N50	7100
NG50	10455
N75	3778
NG75	8739
L50	59
LG50	23
L75	118
LG75	39
# misassemblies	6
# misassembled contigs	6
Misassembled contigs length	26690
# local misassemblies	0
# unaligned contigs	78 + 15 part
Unaligned length	480908
Genome fraction (%)	99.574
Duplication ratio	1.244
# N's per 100 kbp	0.00
# mismatches per 100 kbp	522.86
# indels per 100 kbp	1.63
Largest alignment	16137
NA50	2512
NGA50	7613
NGA75	5004
LA50	101
LGA50	29
LGA75	53

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	6
# relocations	6
# translocations	0
# inversions	0
# possibly misassembled contigs	9
# misassembled contigs	6
Misassembled contigs length	26690
# local misassemblies	0
# mismatches	3207
# indels	10
# short indels	10
# long indels	0
Indels length	10

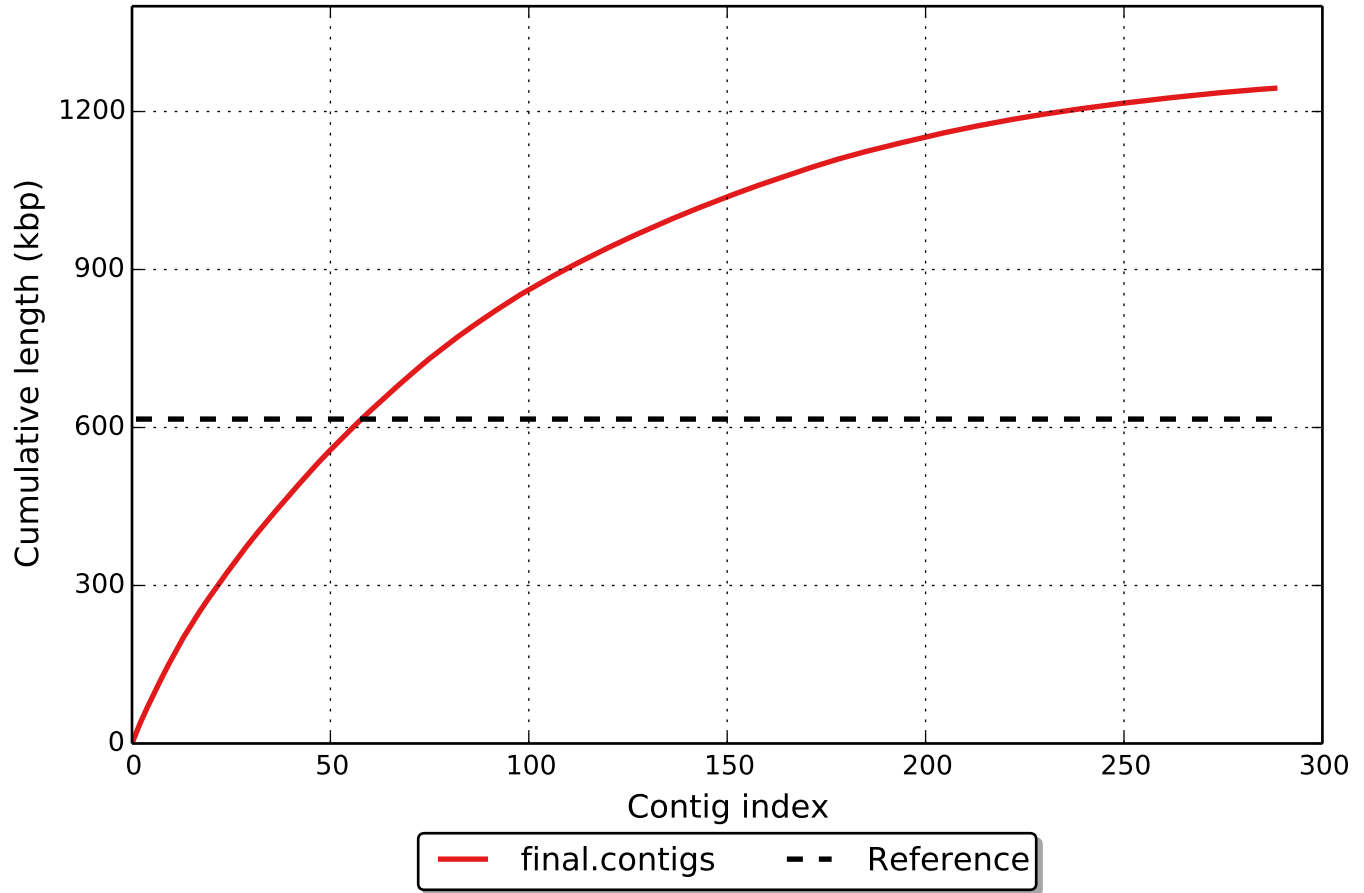
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

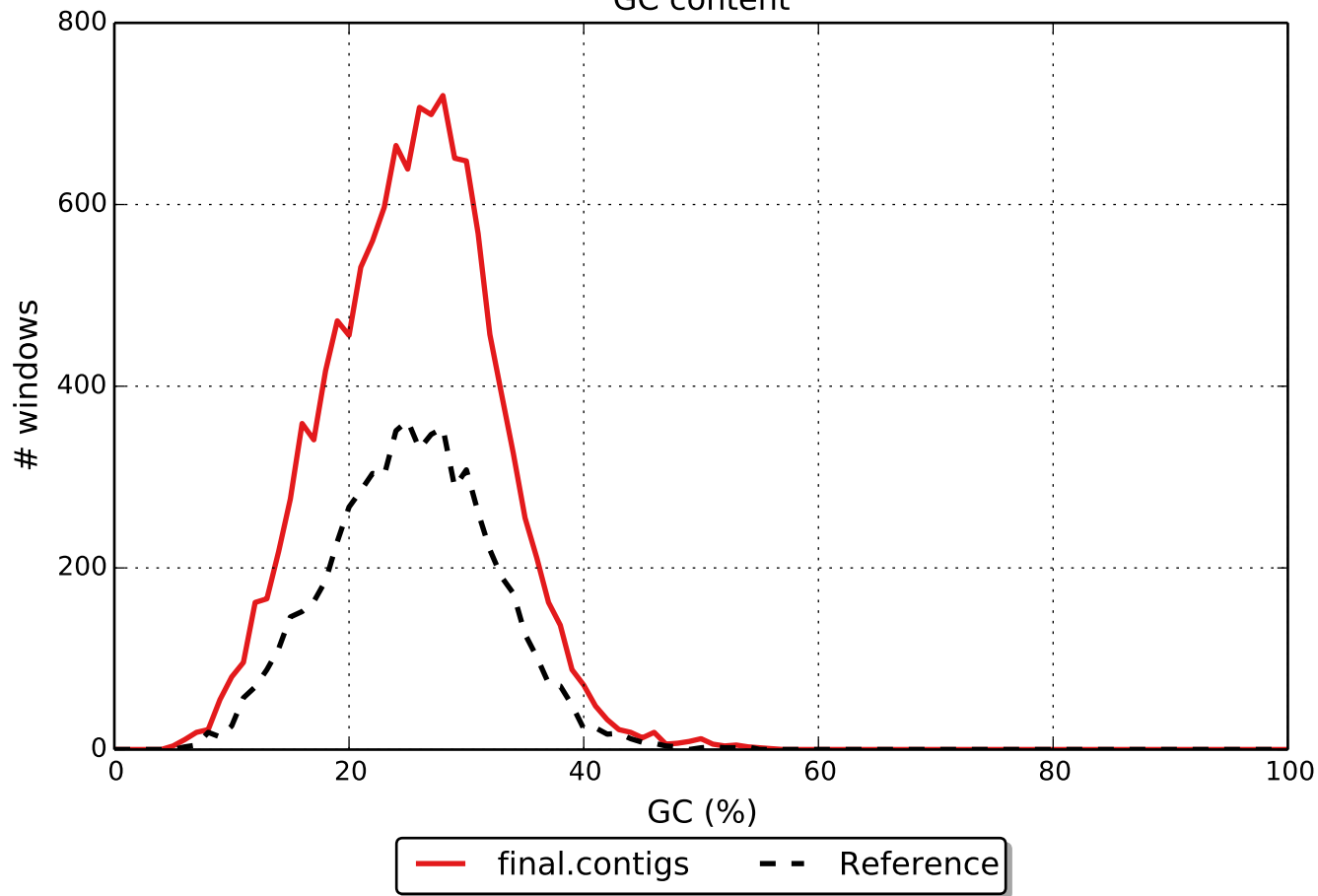
	final.contigs
# fully unaligned contigs	78
Fully unaligned length	406936
# partially unaligned contigs	15
# with misassembly	1
# both parts are significant	9
Partially unaligned length	73972
# N's	0

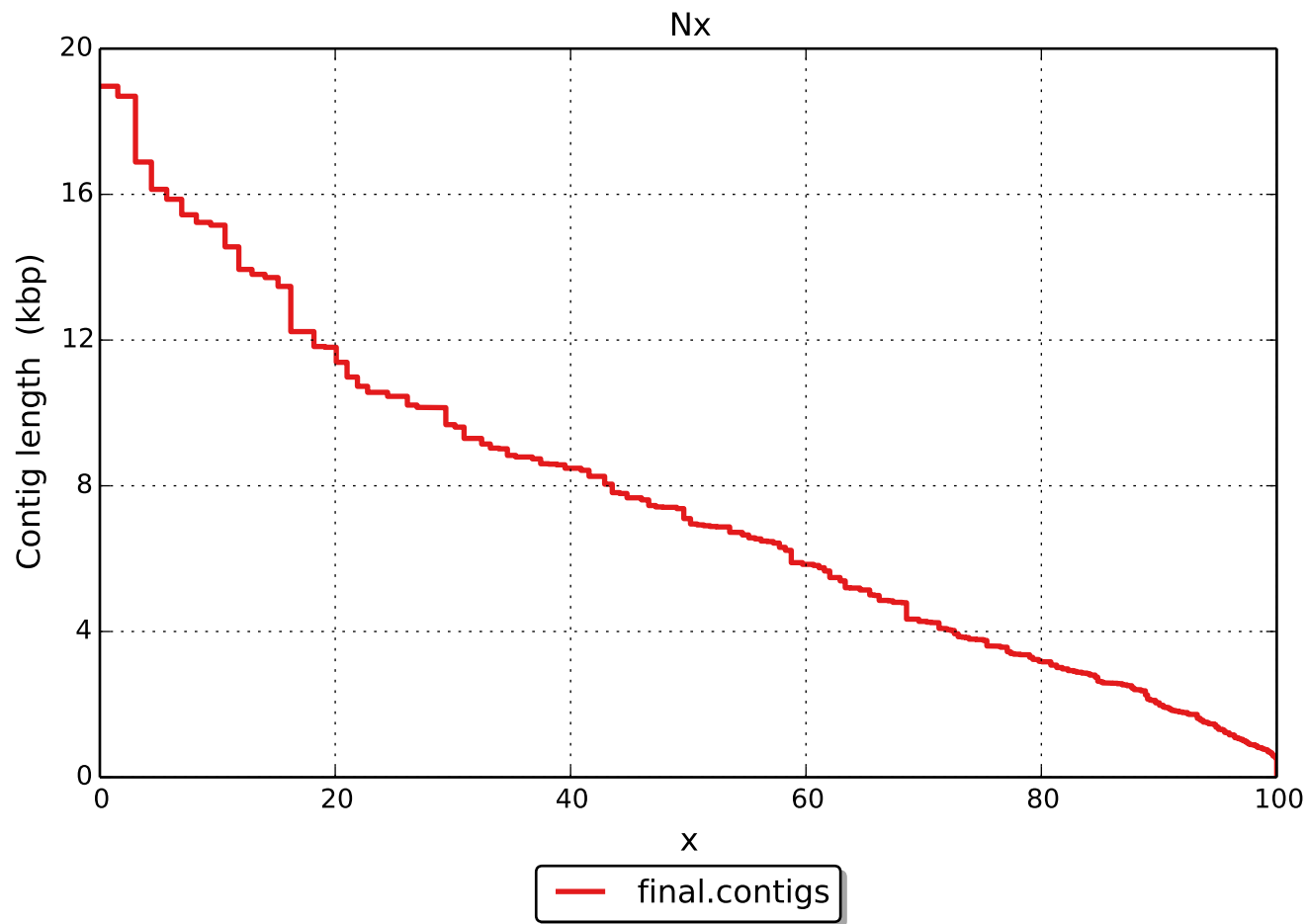
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

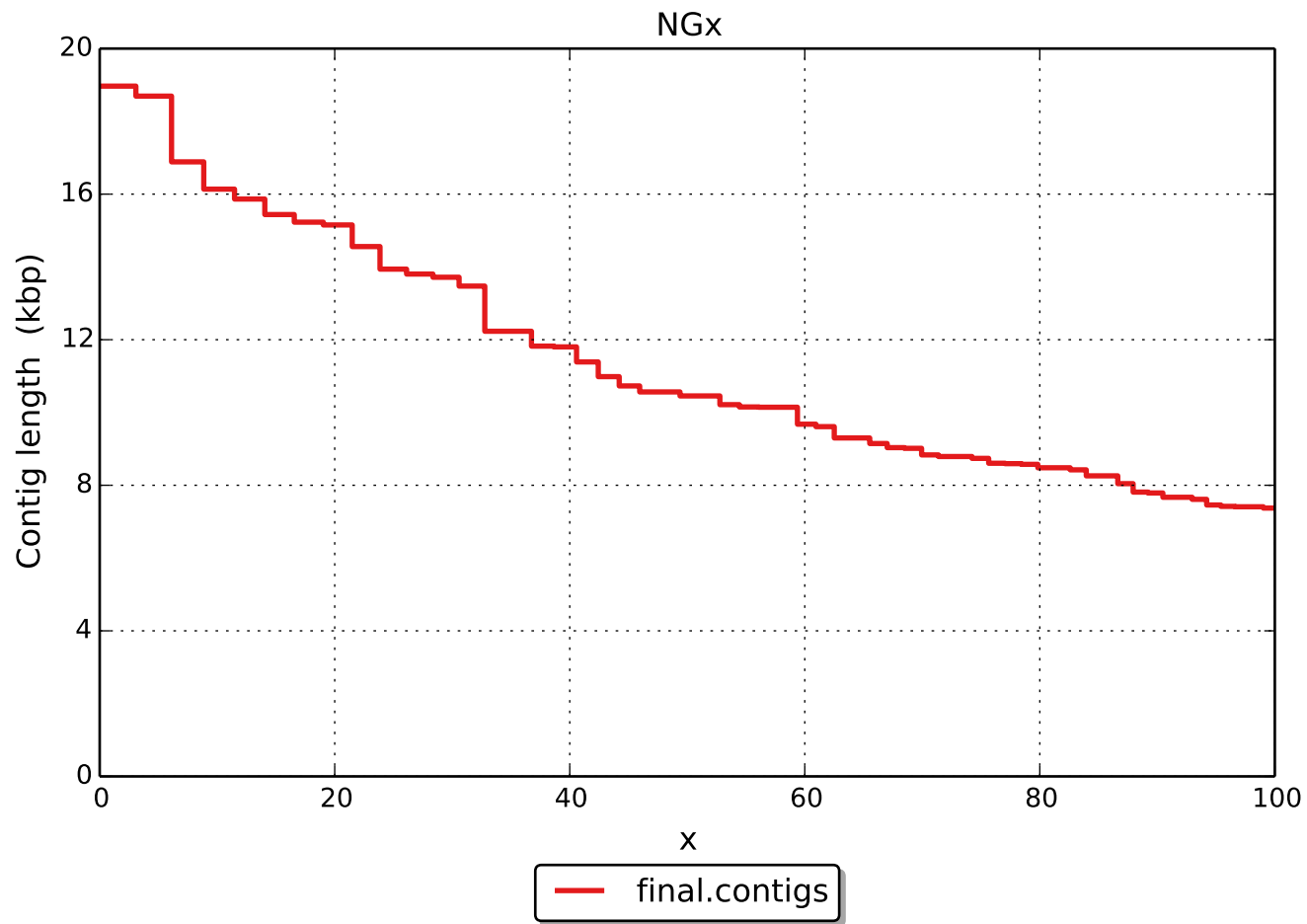
Cumulative length

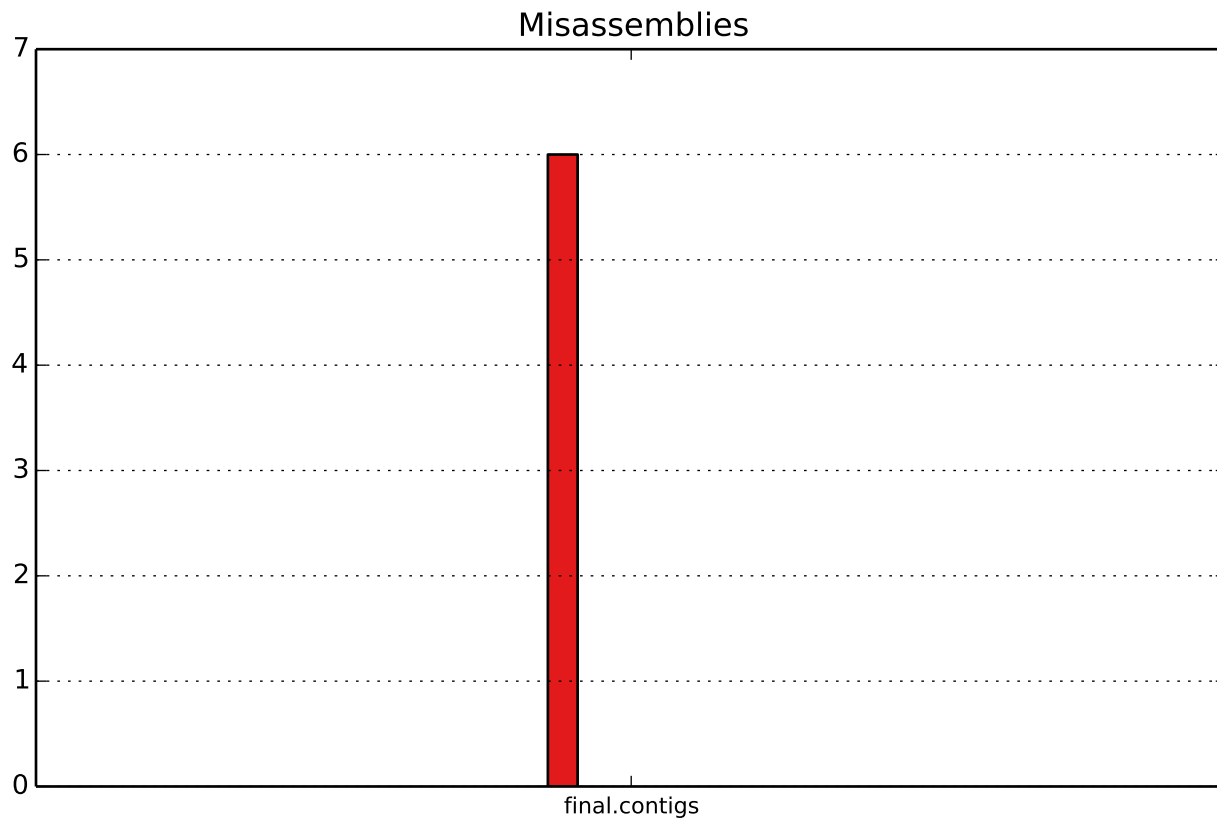


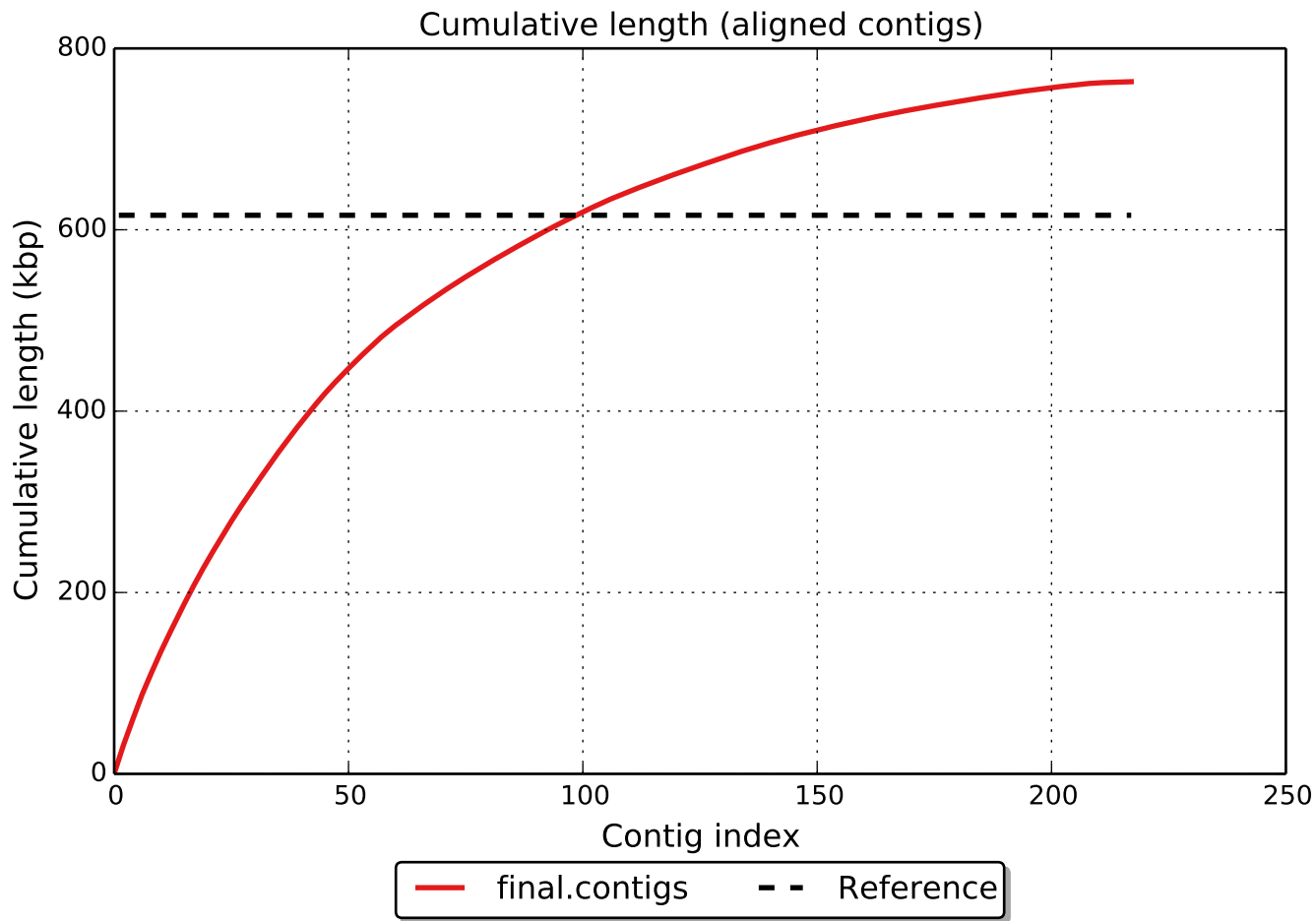
GC content

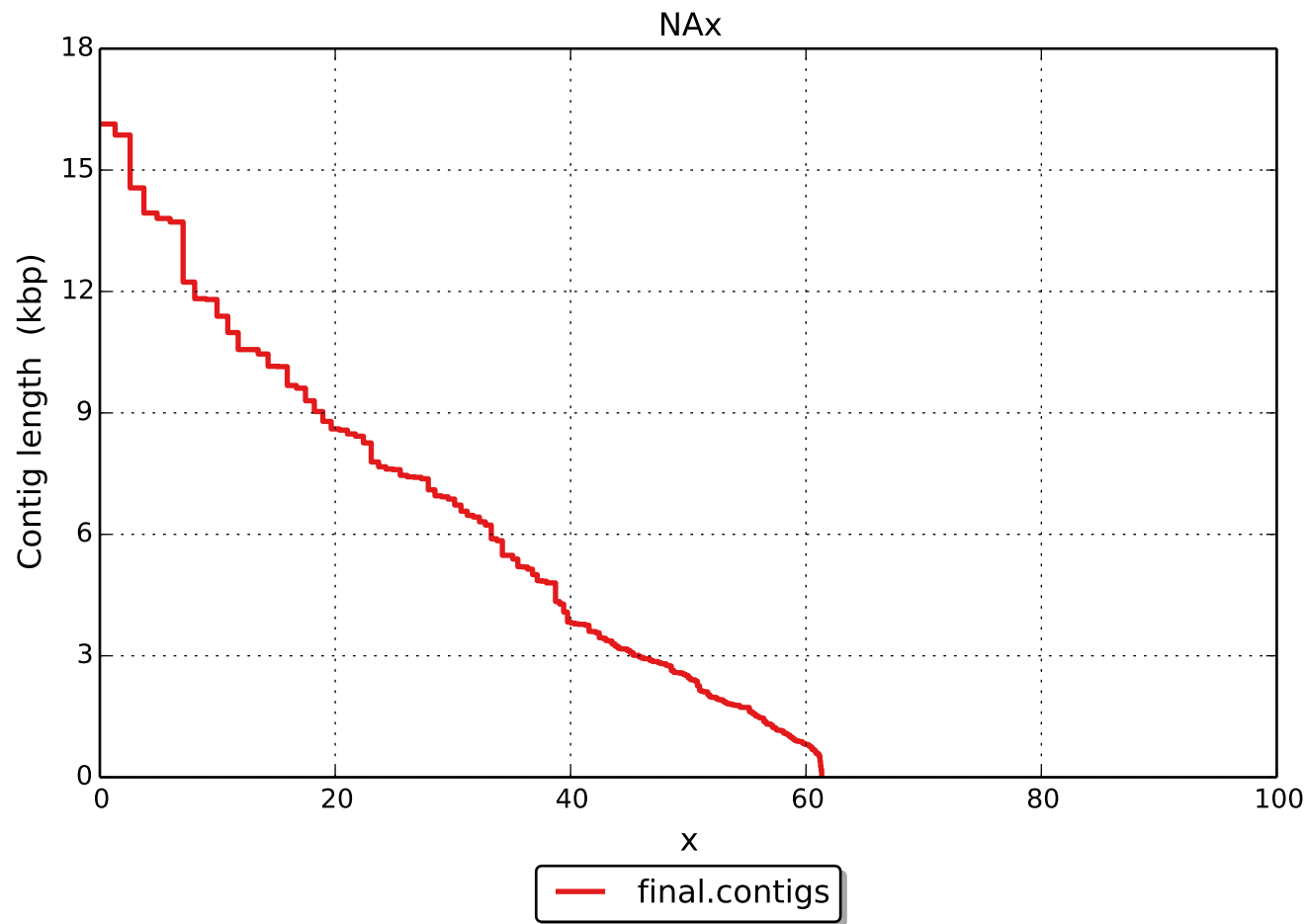




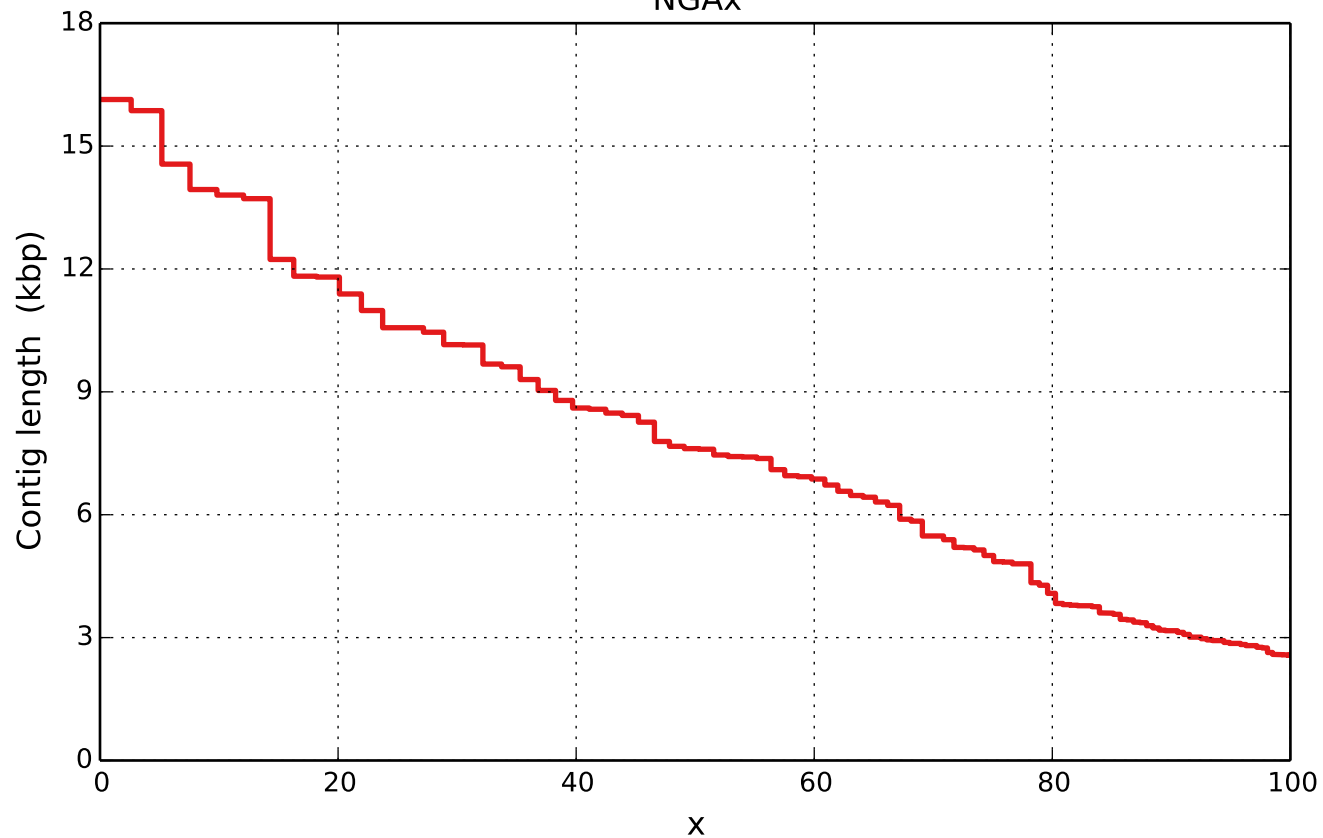








NGAx



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