

Report

	final.contigs
# contigs (≥ 0 bp)	4706
# contigs (≥ 1000 bp)	1260
Total length (≥ 0 bp)	4174850
Total length (≥ 1000 bp)	1760177
# contigs	4706
Largest contig	3544
Total length	4174850
Reference length	5547323
GC (%)	50.44
Reference GC (%)	50.48
N50	912
NG50	753
N75	684
NG75	502
L50	1603
LG50	2432
L75	2930
LG75	4678
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	788
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	36
Genome fraction (%)	71.835
Duplication ratio	1.048
# N's per 100 kbp	0.00
# mismatches per 100 kbp	121.41
# indels per 100 kbp	0.05
Largest alignment	3544
NA50	912
NGA50	753
NA75	683
NGA75	502
LA50	1603
LGA50	2432
LA75	2931
LGA75	4678

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

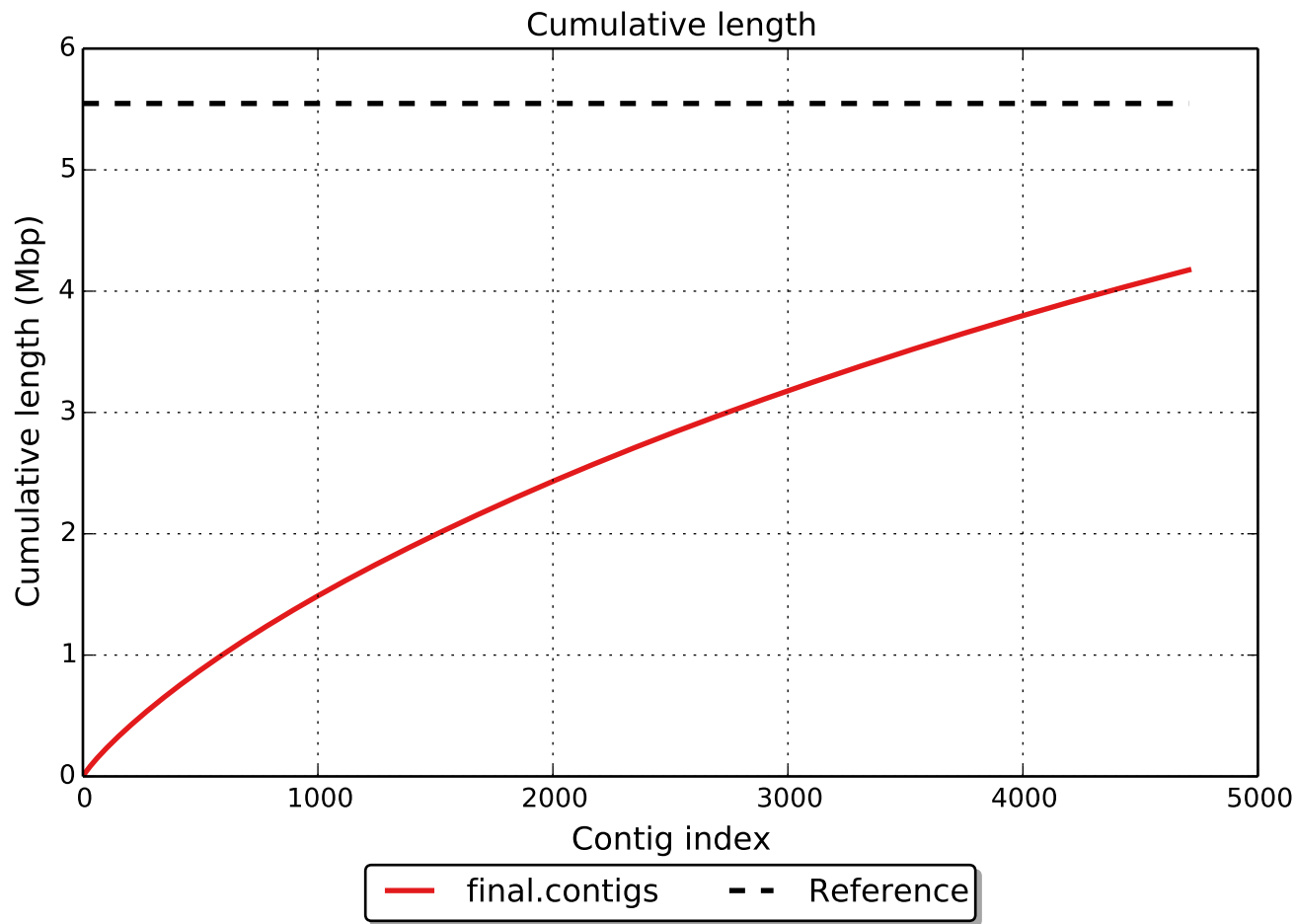
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	788
# local misassemblies	0
# mismatches	4838
# indels	2
# short indels	2
# long indels	0
Indels length	2

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).

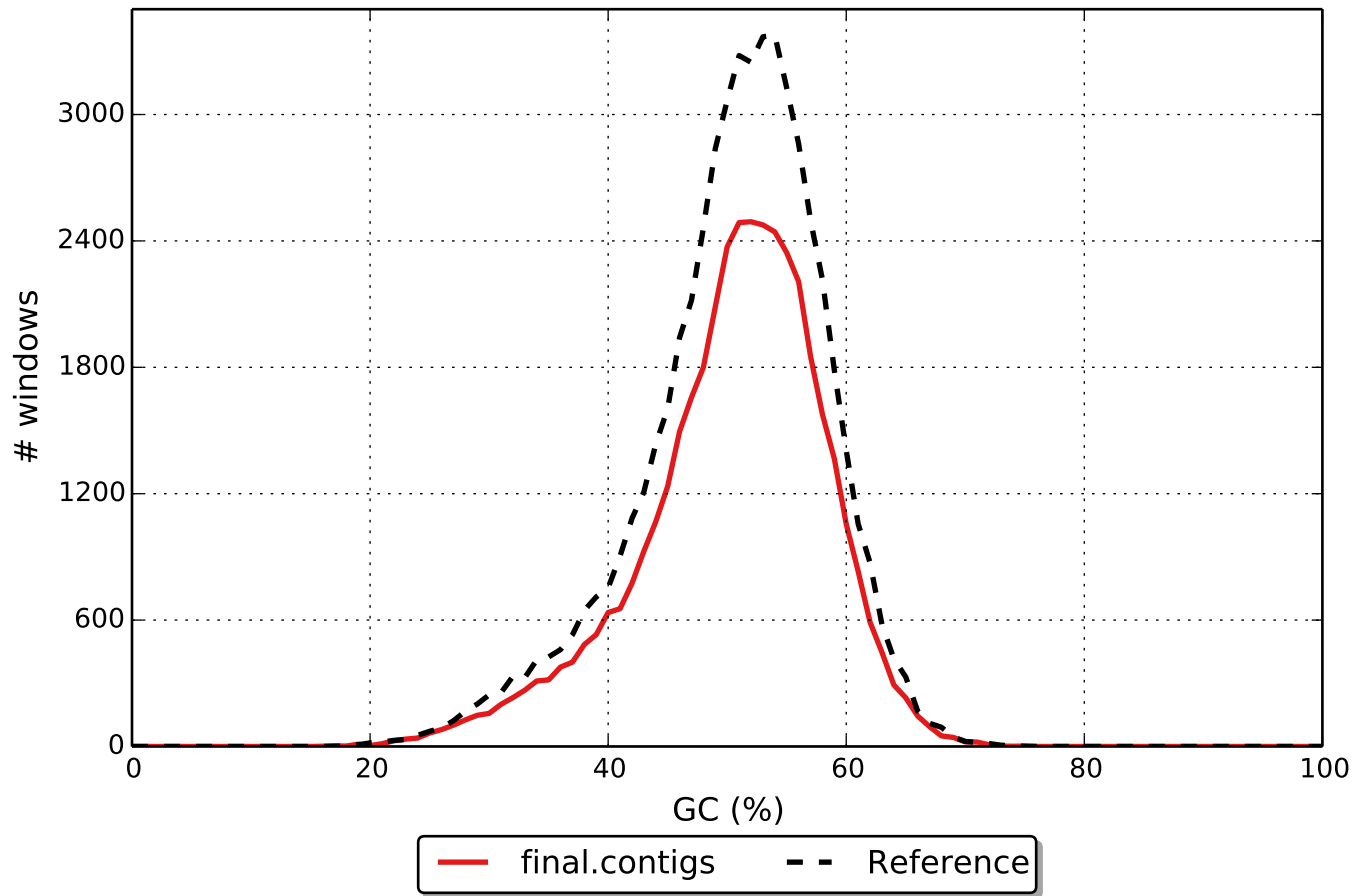
Unaligned report

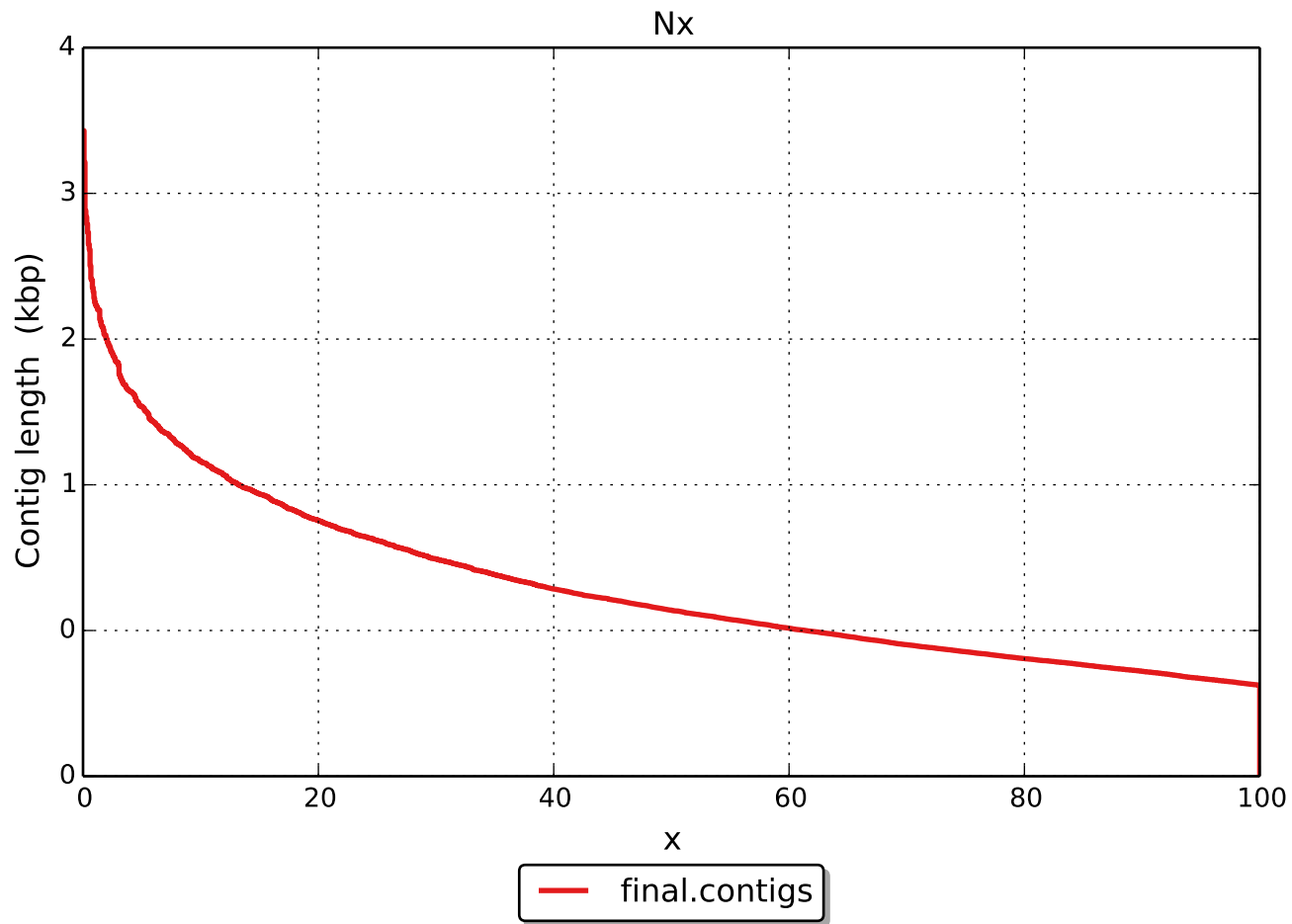
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	36
# N's	0

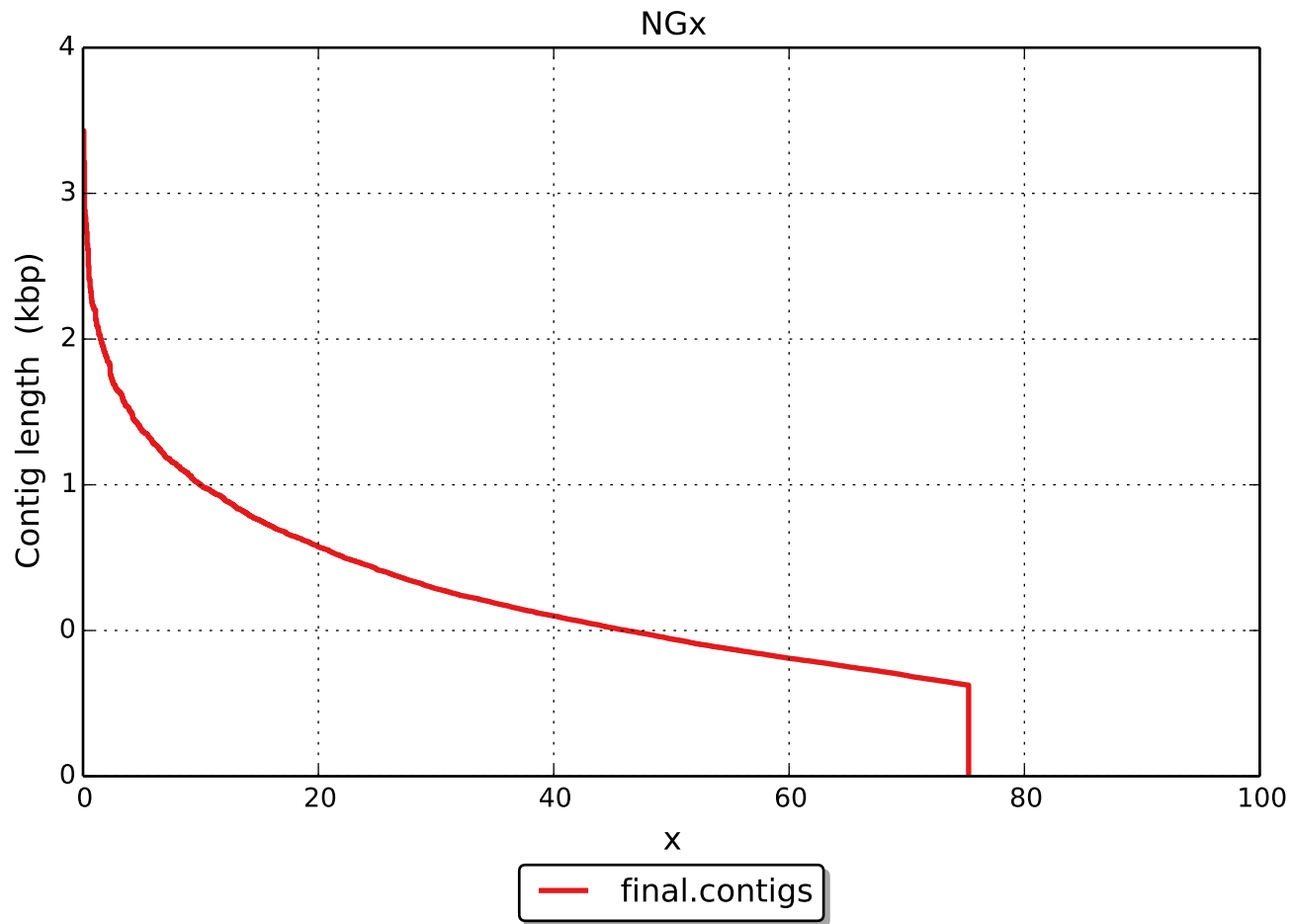
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



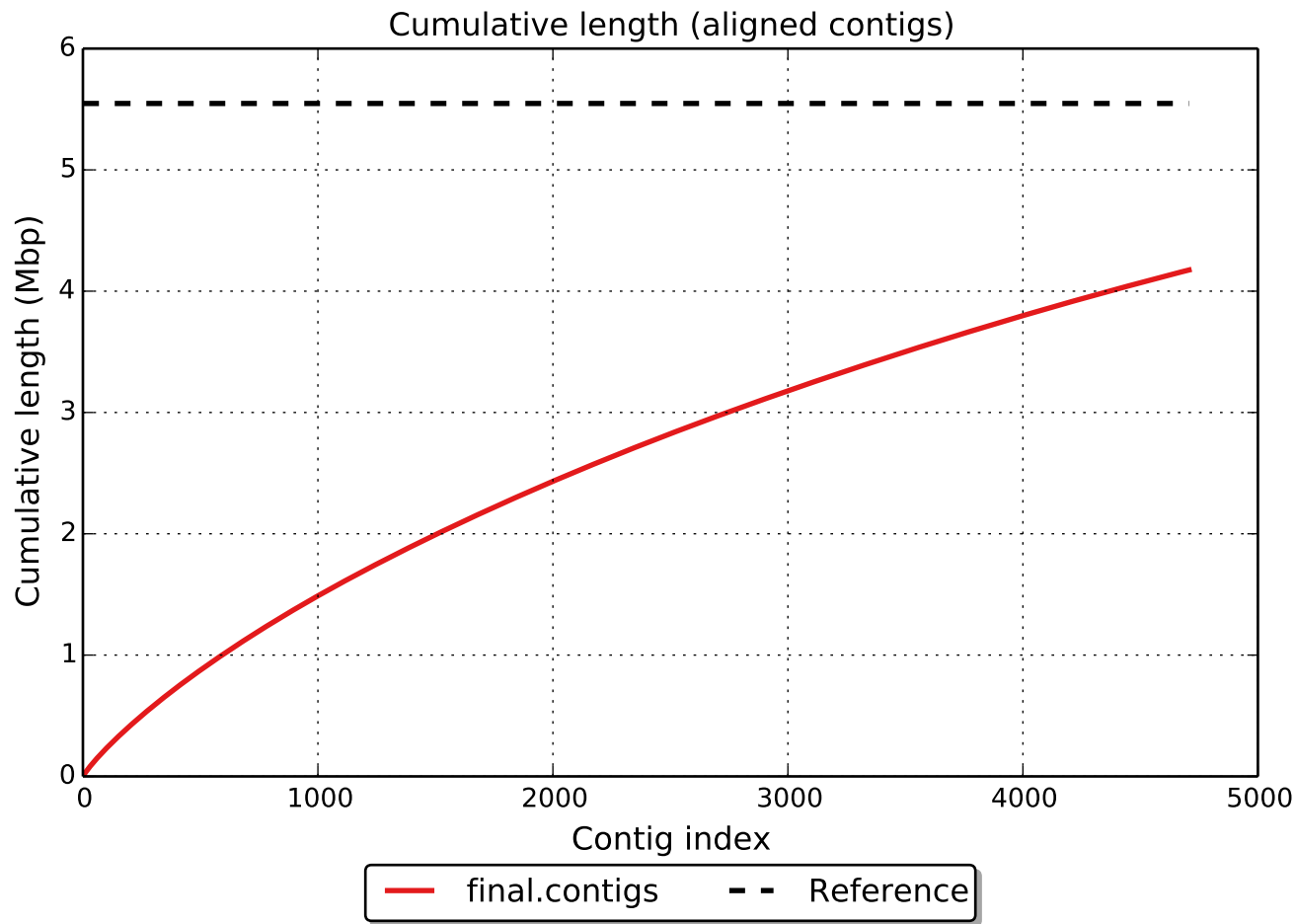
GC content

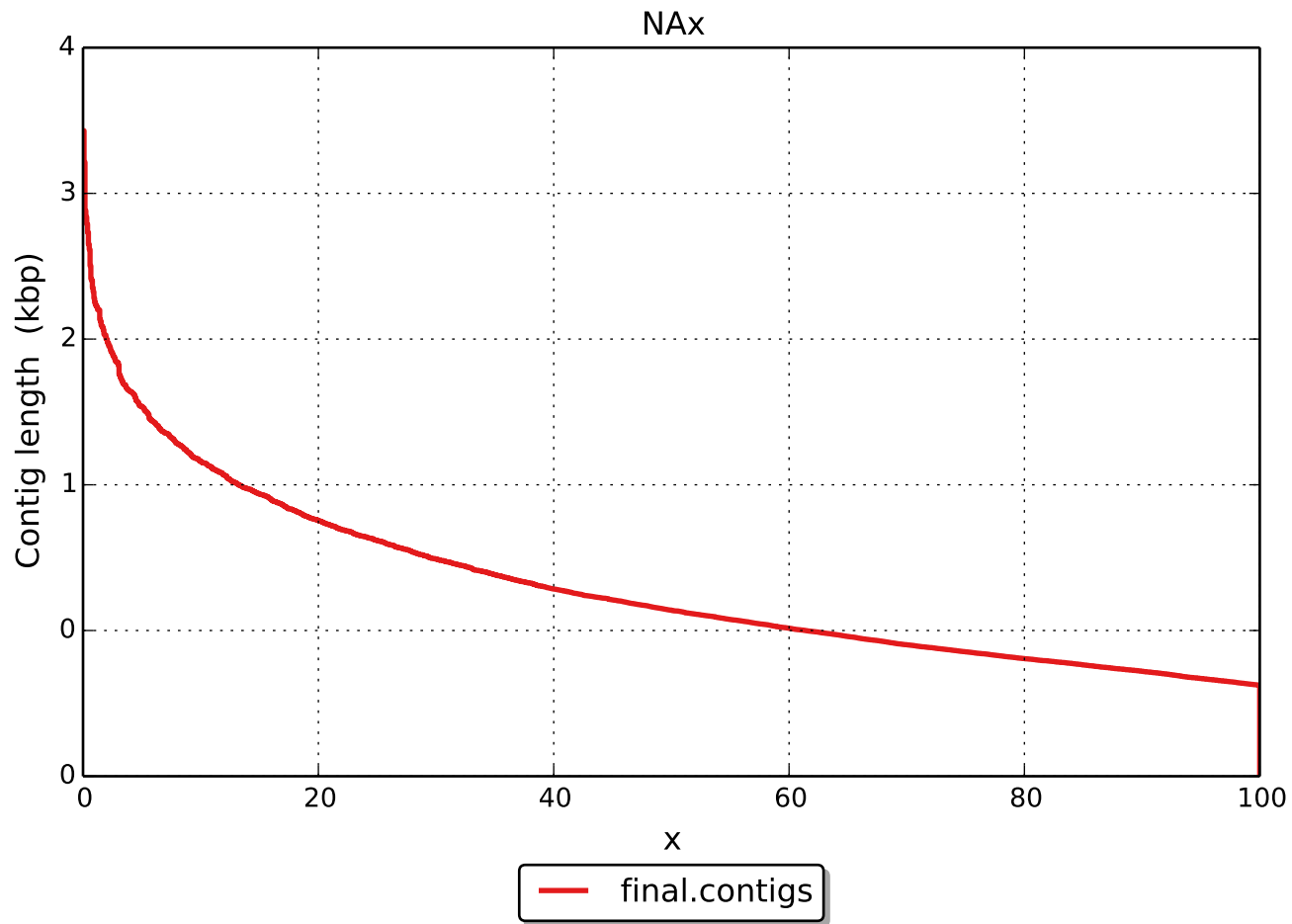




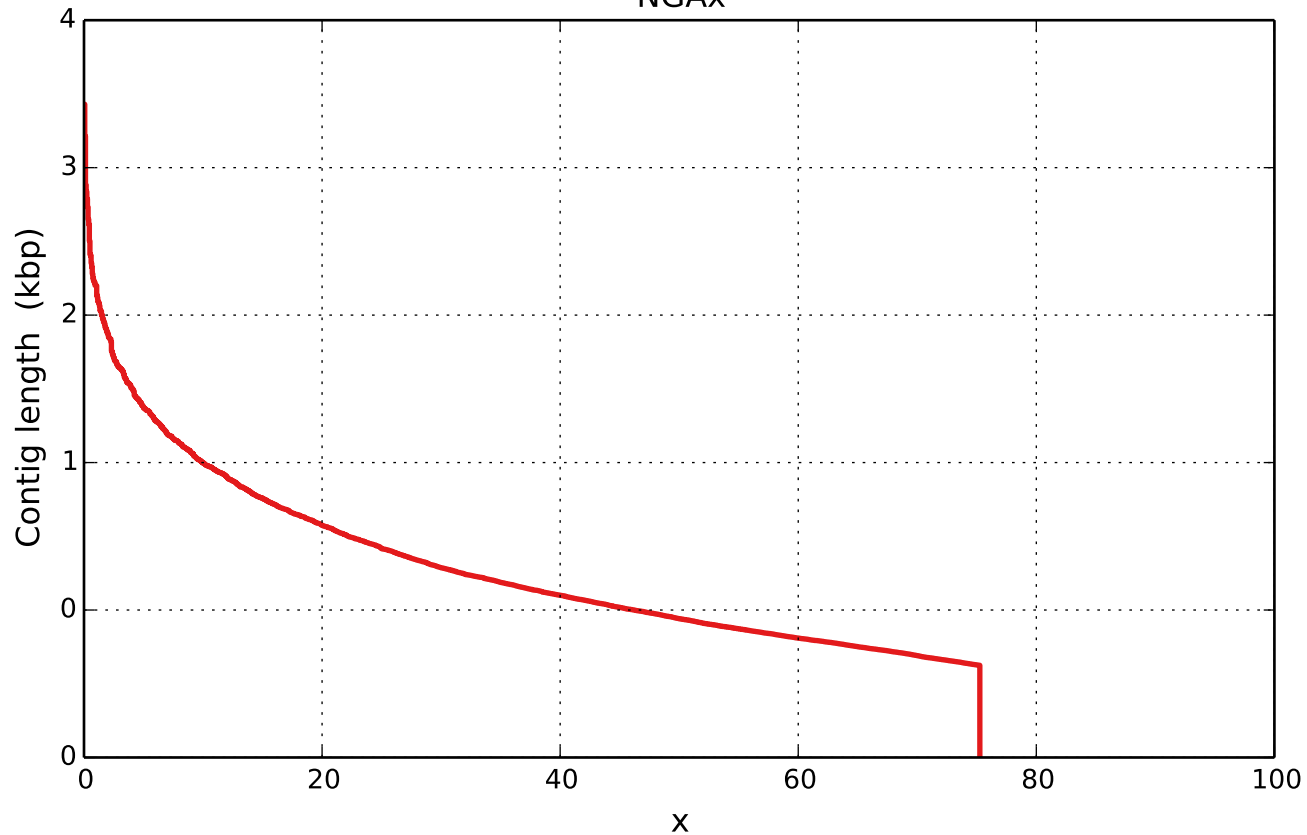








NGAx



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