

Report

	final.contigs
# contigs (>= 0 bp)	3238
# contigs (>= 1000 bp)	1986
Total length (>= 0 bp)	5123175
Total length (>= 1000 bp)	4215379
# contigs	3238
Largest contig	10098
Total length	5123175
Reference length	5478683
GC (%)	50.26
Reference GC (%)	50.49
N50	1977
NG50	1859
N75	1218
NG75	1058
L50	828
LG50	920
L75	1648
LG75	1883
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	3732
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	89.891
Duplication ratio	1.040
# N's per 100 kbp	0.00
# mismatches per 100 kbp	34.52
# indels per 100 kbp	0.22
Largest alignment	10098
NA50	1977
NGA50	1859
NA75	1217
NGA75	1058
LA50	828
LGA50	920
LA75	1649
LGA75	1884

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

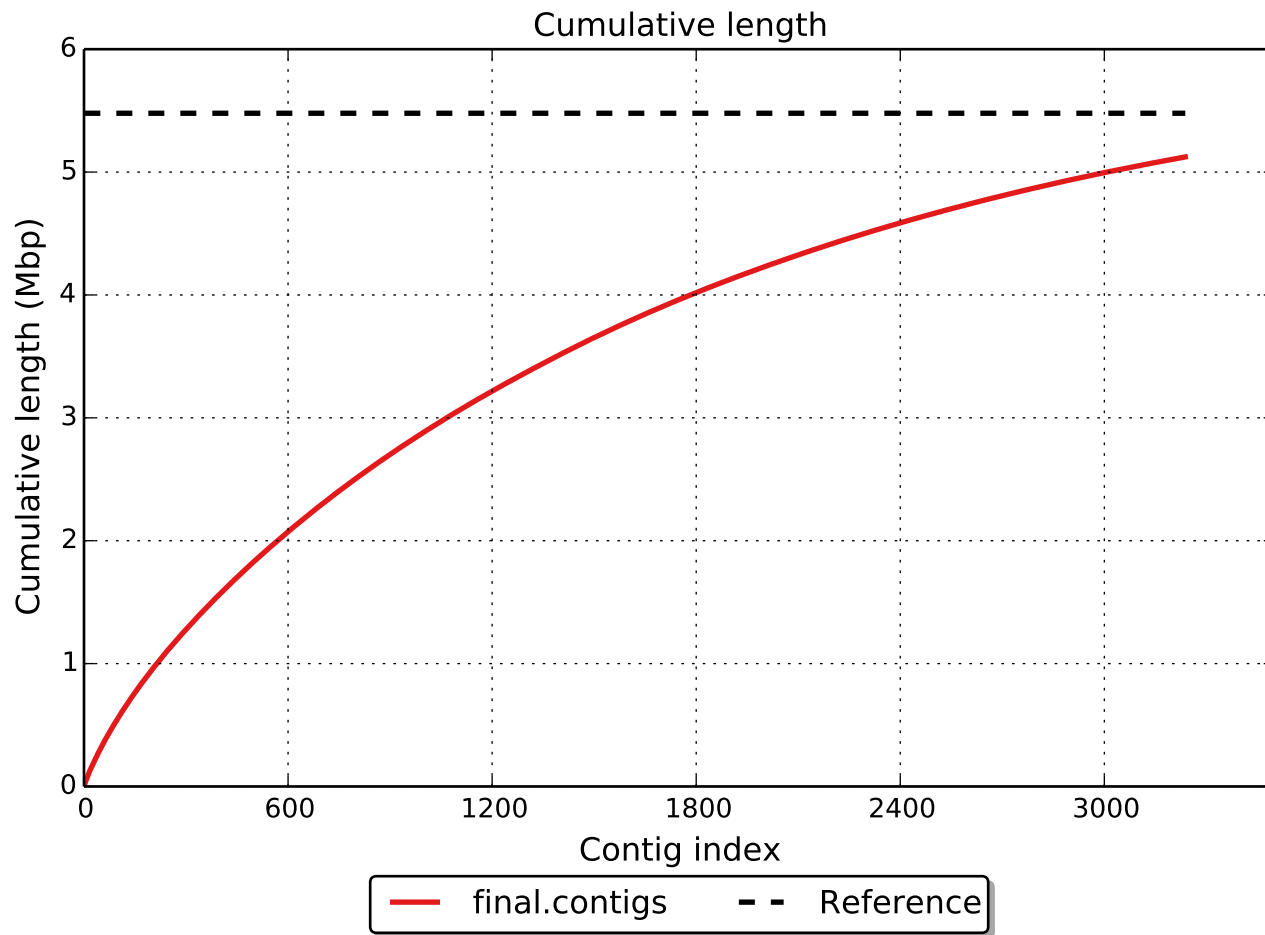
	final.contigs
# misassemblies	2
# relocations	2
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	3732
# local misassemblies	1
# mismatches	1700
# indels	11
# short indels	11
# long indels	0
Indels length	17

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).

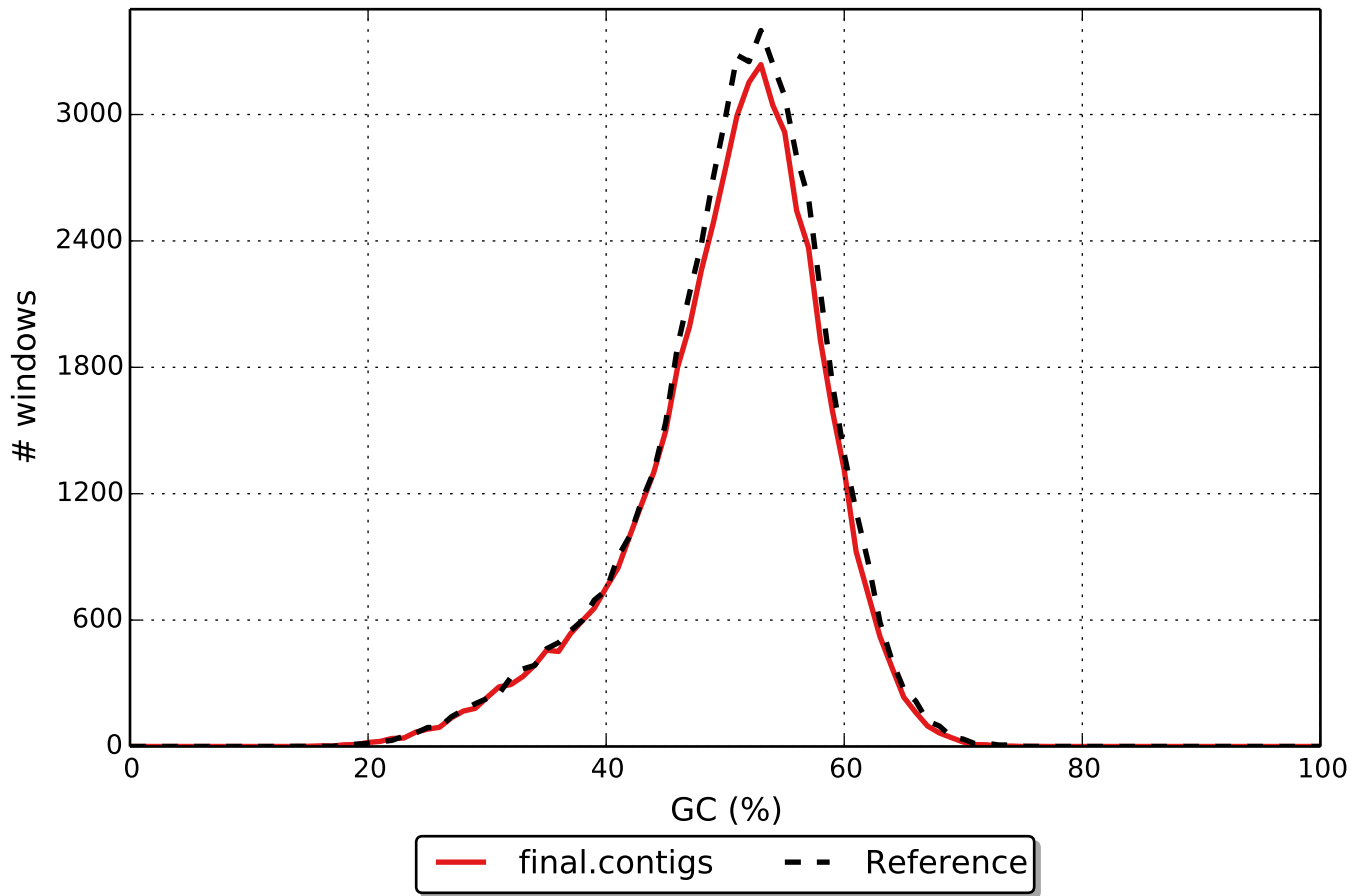
Unaligned report

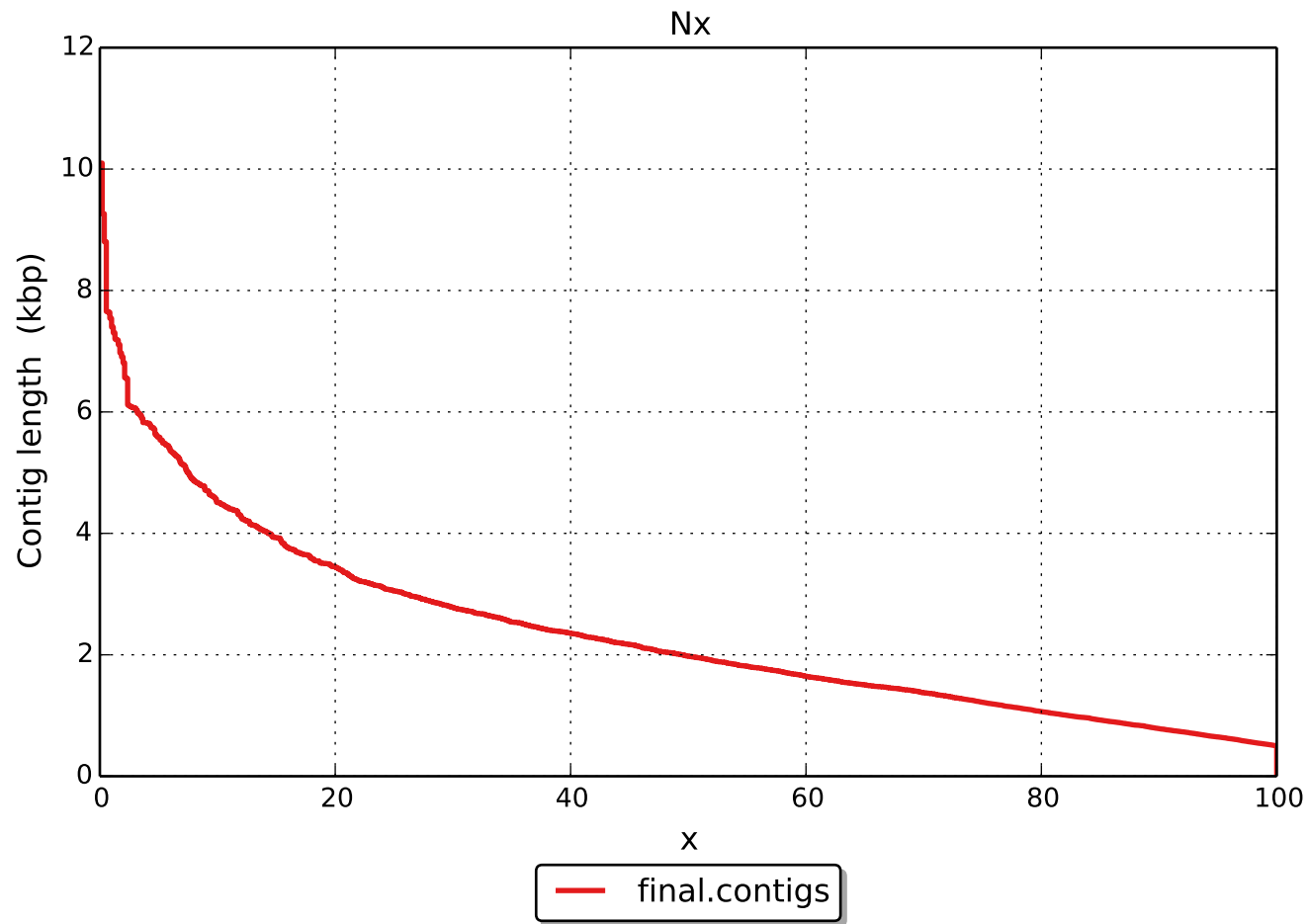
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

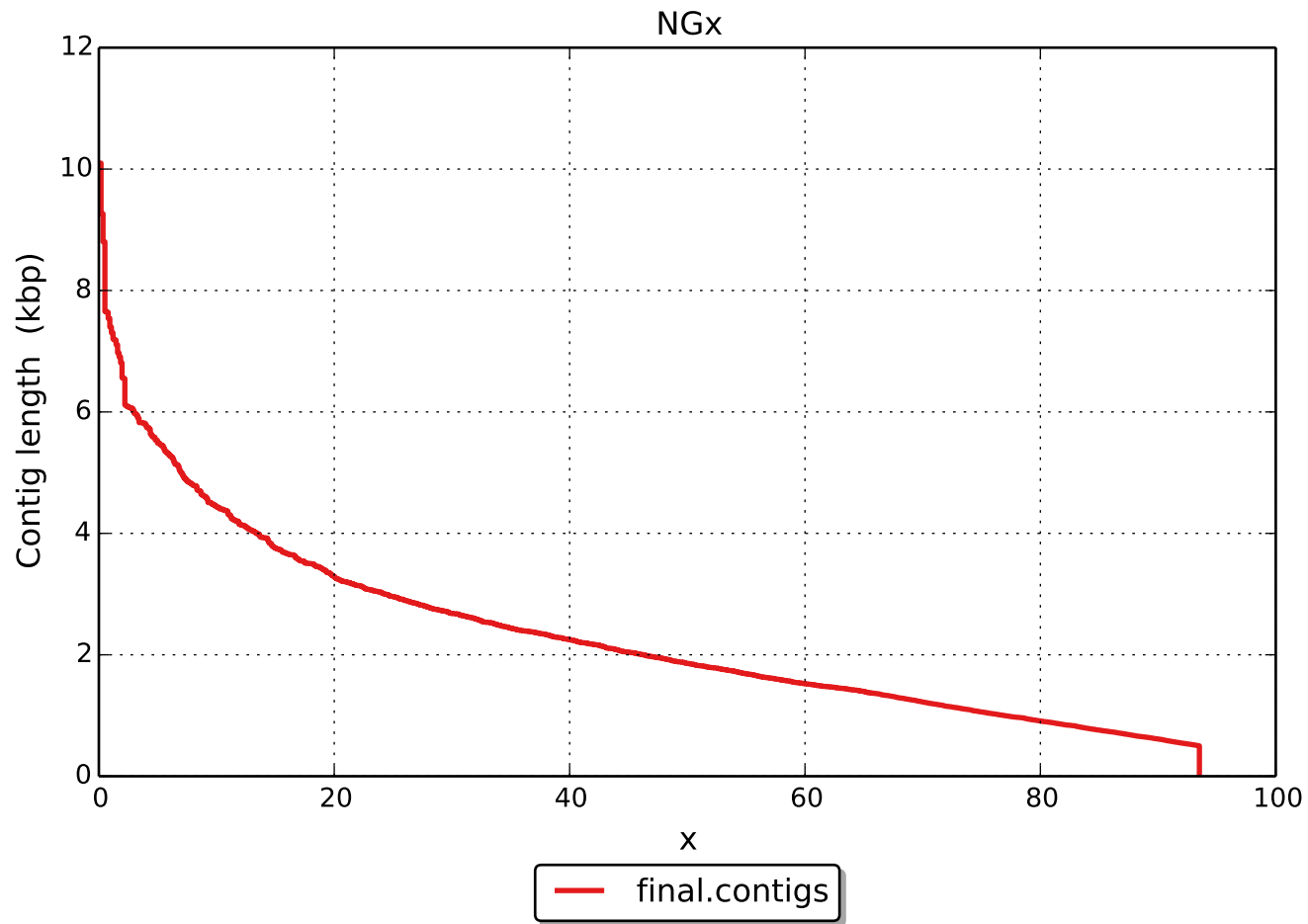
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



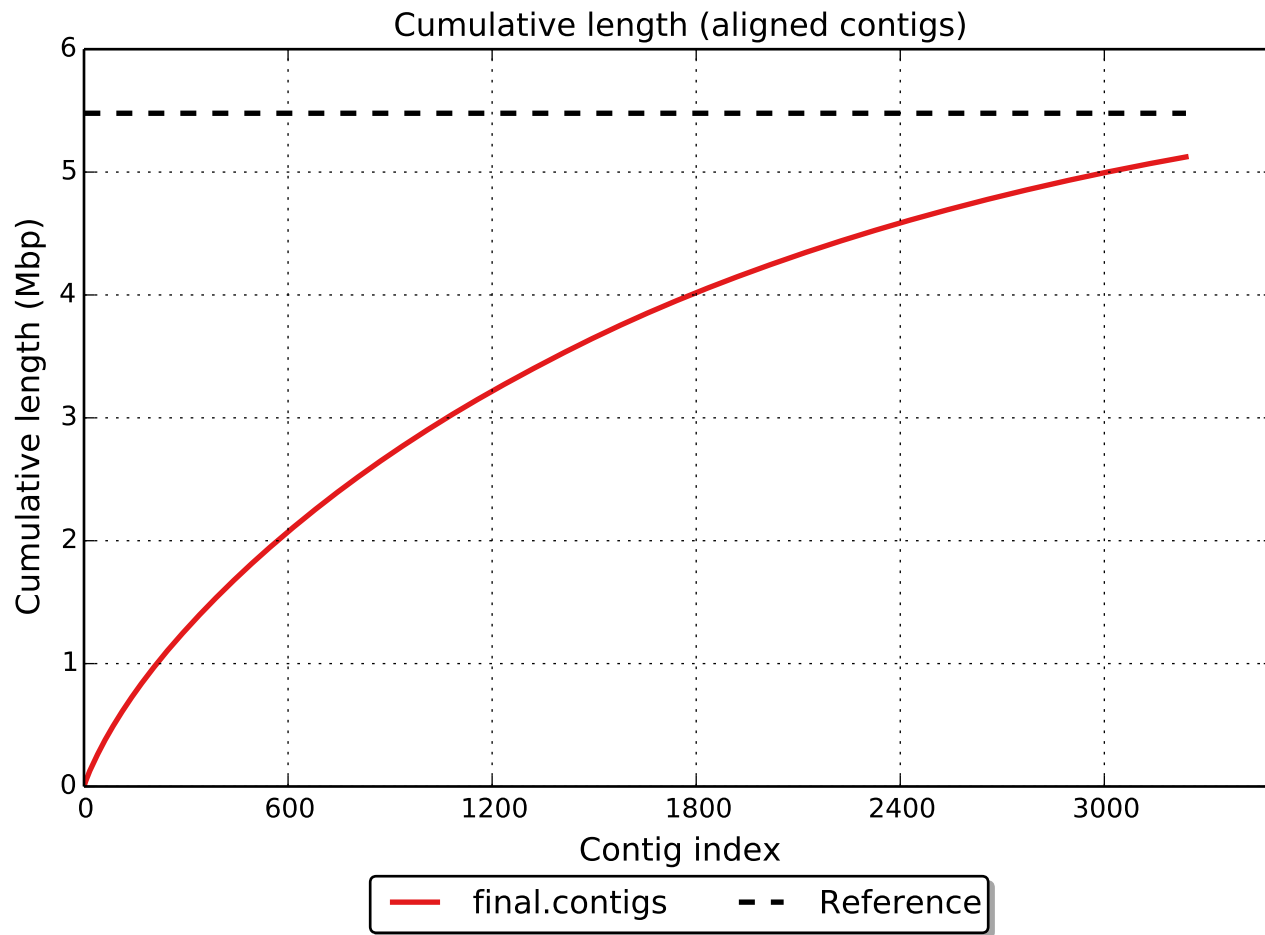
GC content

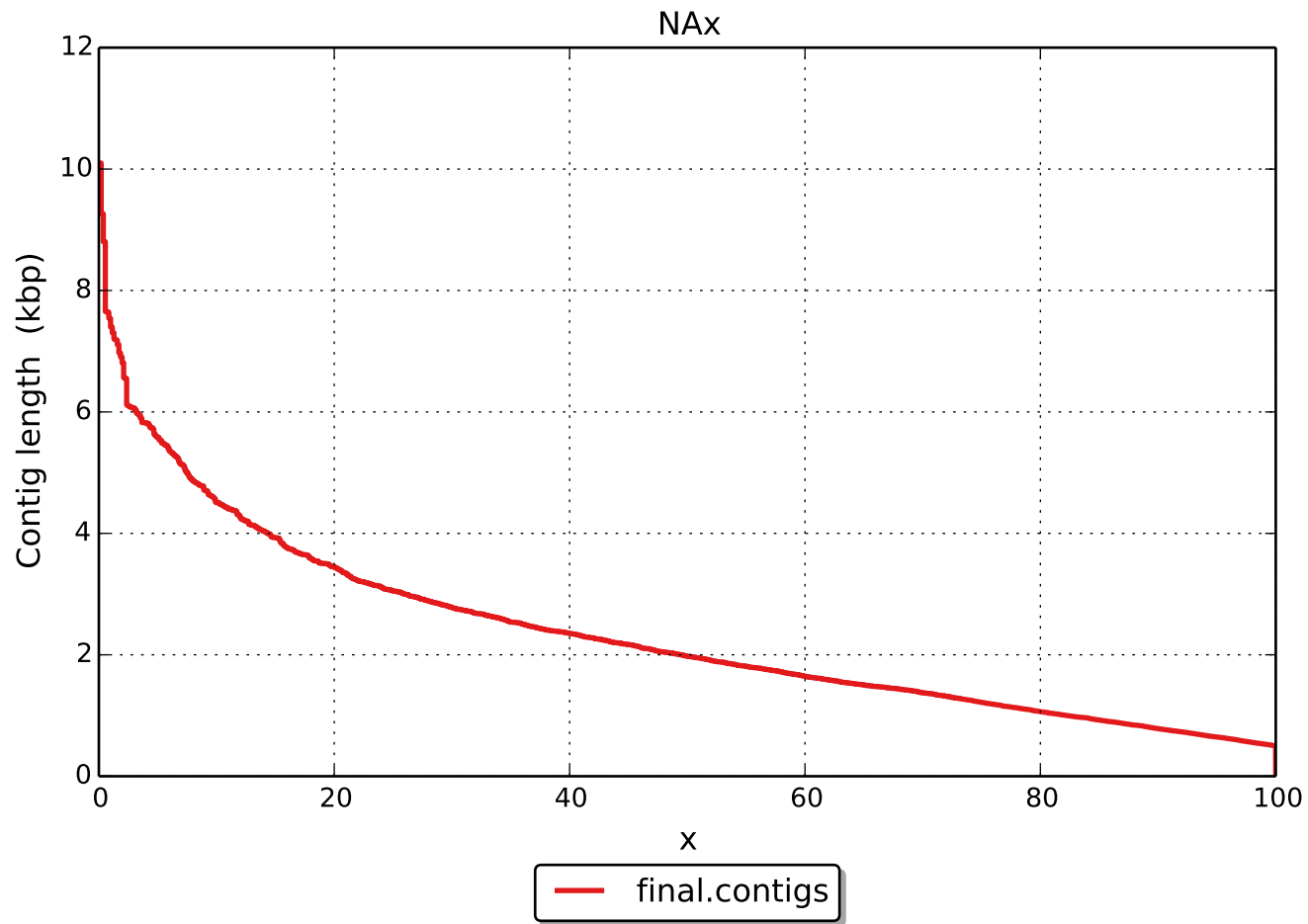












NGAx

