

Report

	final.contigs
# contigs (>= 0 bp)	2102
# contigs (>= 1000 bp)	1683
Total length (>= 0 bp)	5560799
Total length (>= 1000 bp)	5251635
# contigs	2102
Largest contig	19900
Total length	5560799
Reference length	5478683
GC (%)	50.48
Reference GC (%)	50.49
N50	3636
NG50	3677
N75	2141
NG75	2208
L50	477
LG50	466
L75	968
LG75	939
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	9427
# local misassemblies	0
# unaligned contigs	0 + 2 part
Unaligned length	116
Genome fraction (%)	98.202
Duplication ratio	1.034
# N's per 100 kbp	0.00
# mismatches per 100 kbp	35.78
# indels per 100 kbp	0.00
Largest alignment	19900
NA50	3628
NGA50	3677
NA75	2139
NGA75	2207
LA50	478
LGA50	466
LA75	969
LGA75	940

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

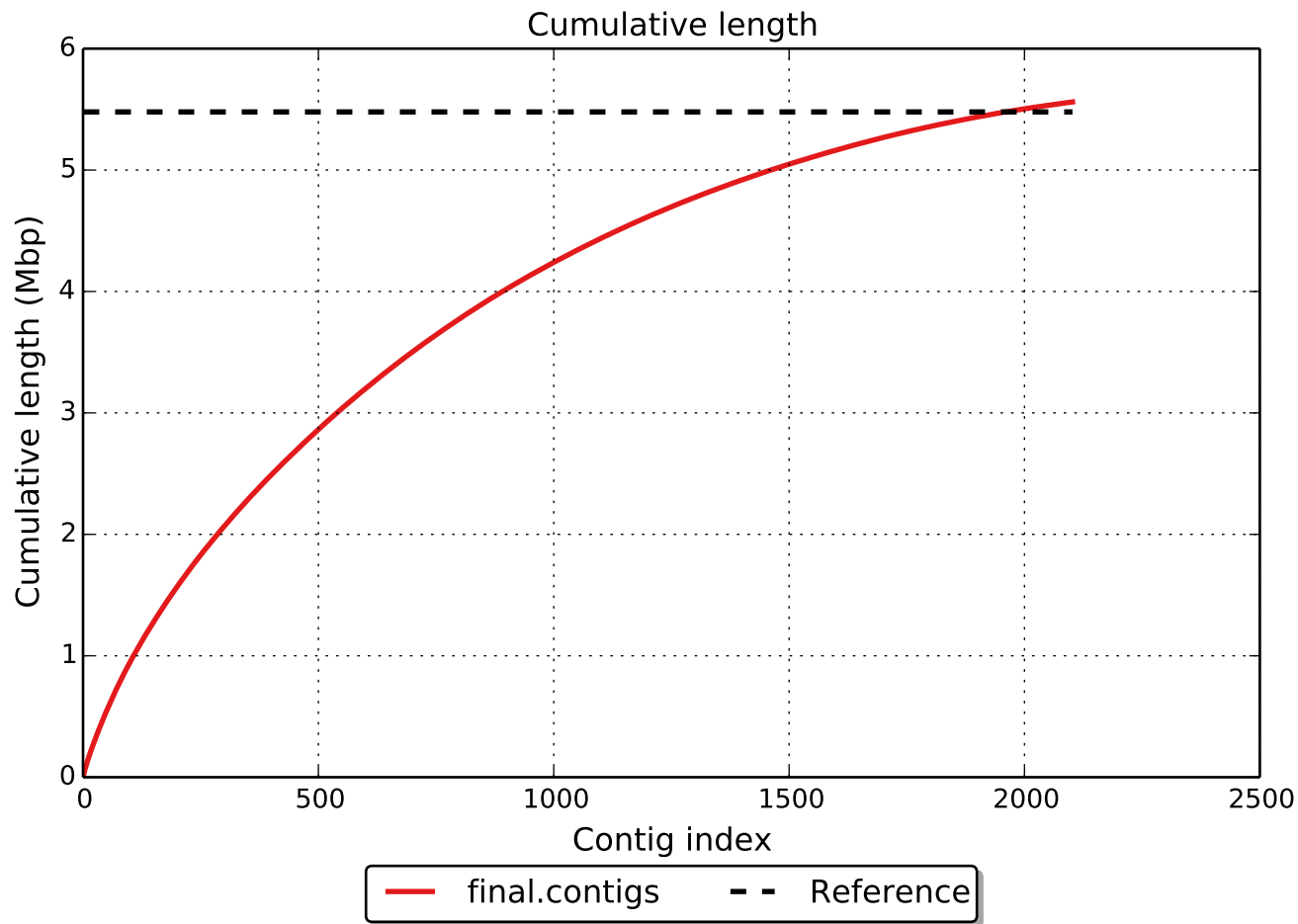
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	9427
# local misassemblies	0
# mismatches	1925
# indels	0
# short indels	0
# long indels	0
Indels length	0

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).

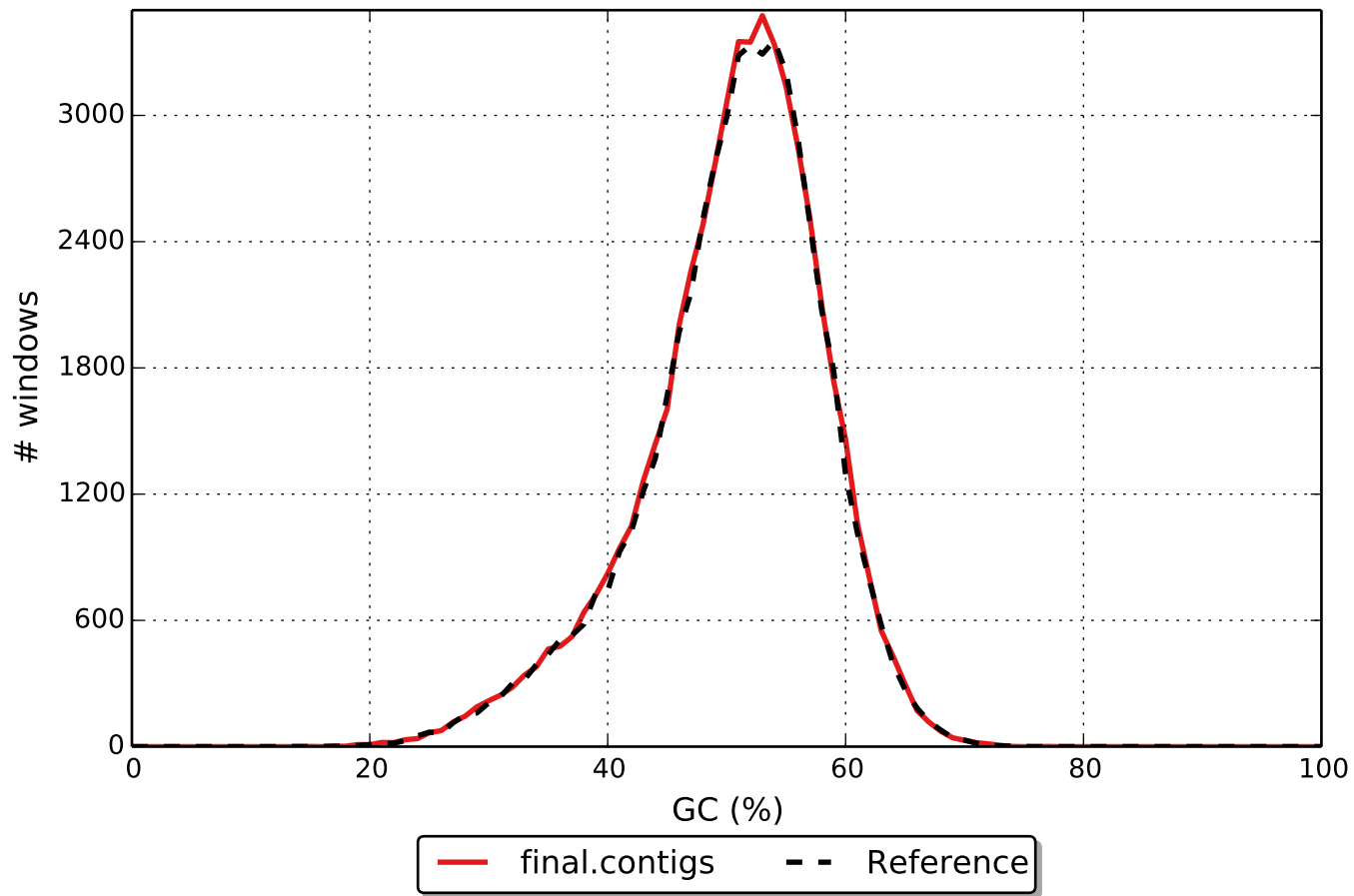
Unaligned report

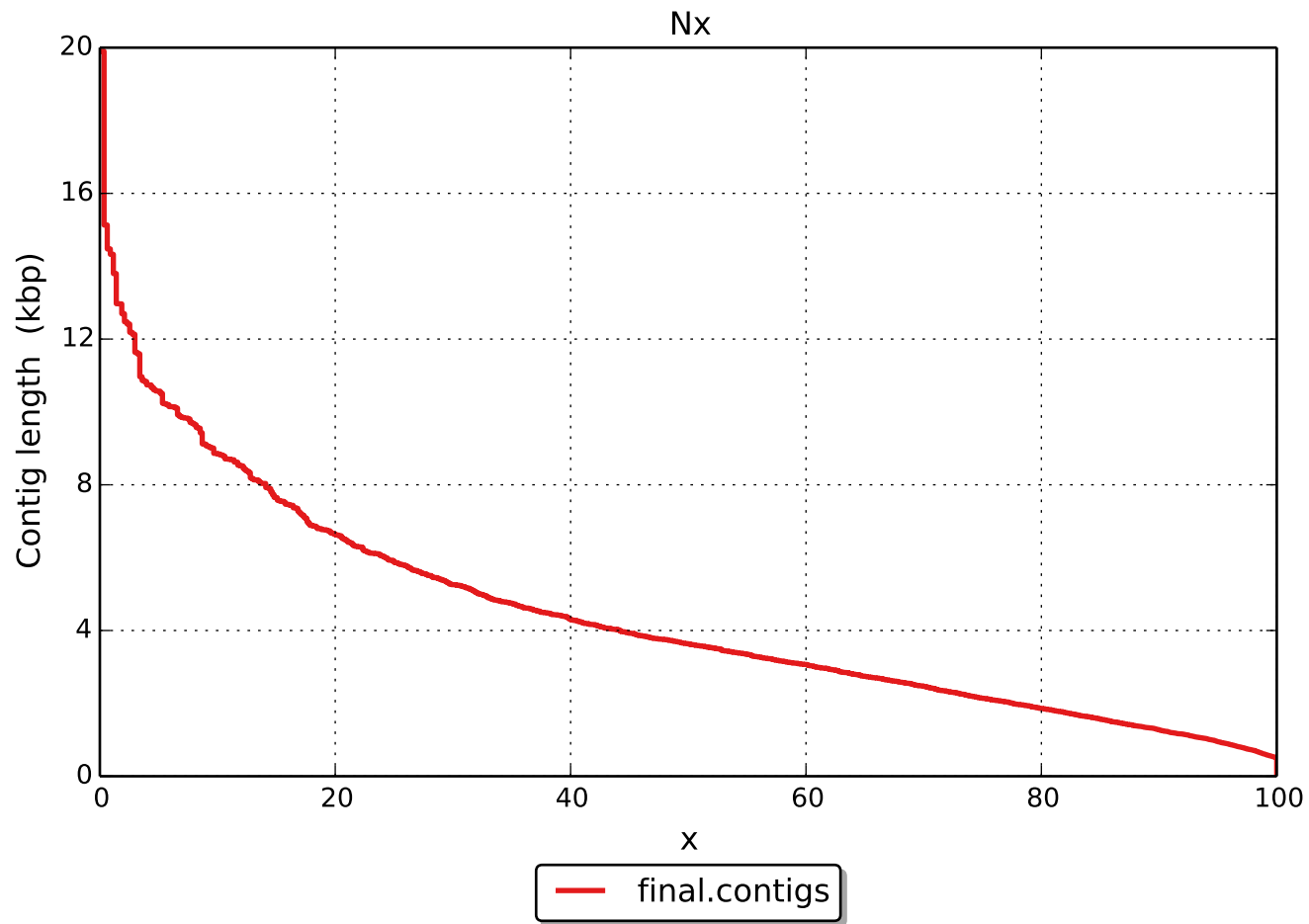
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	116
# N's	0

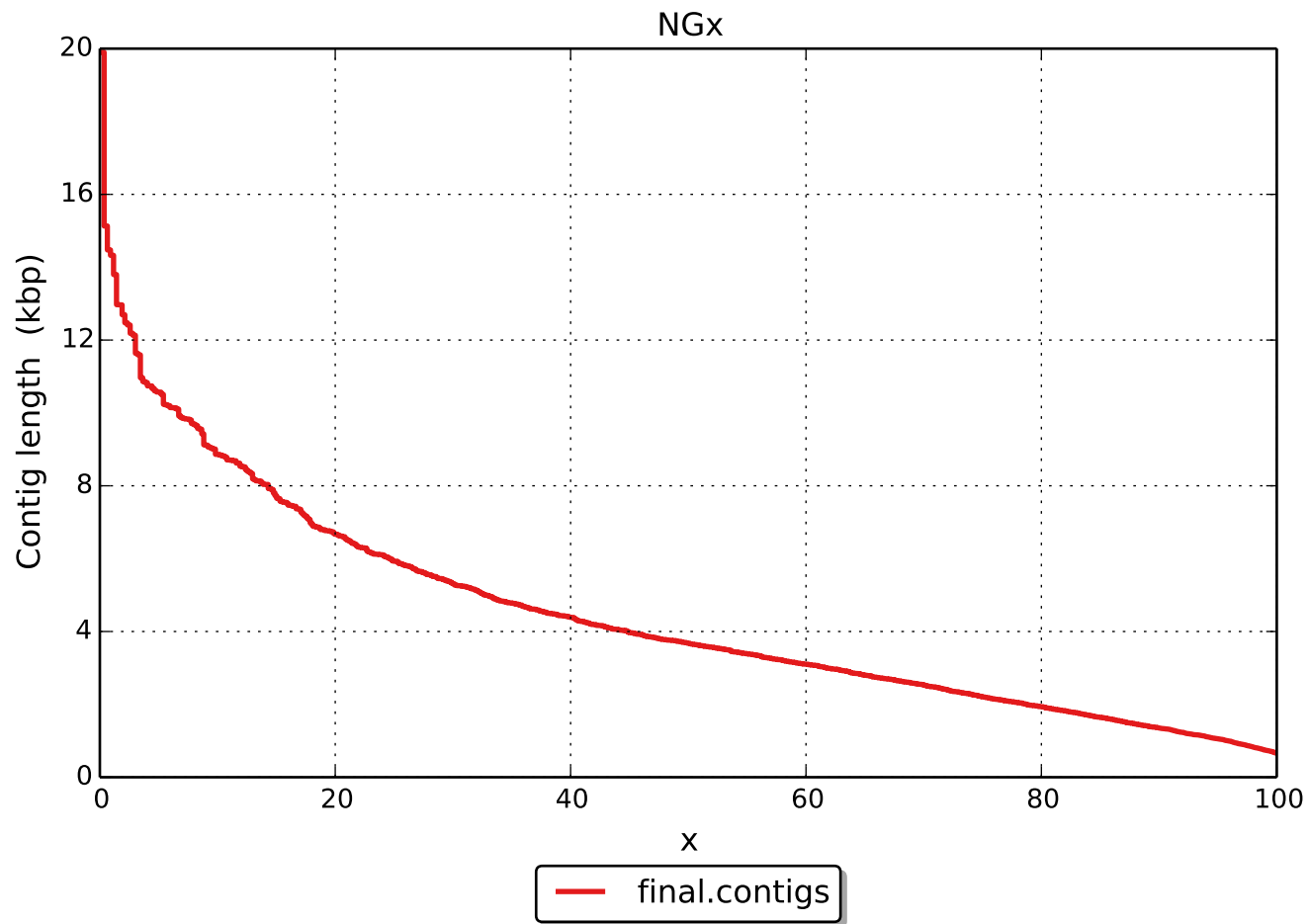
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



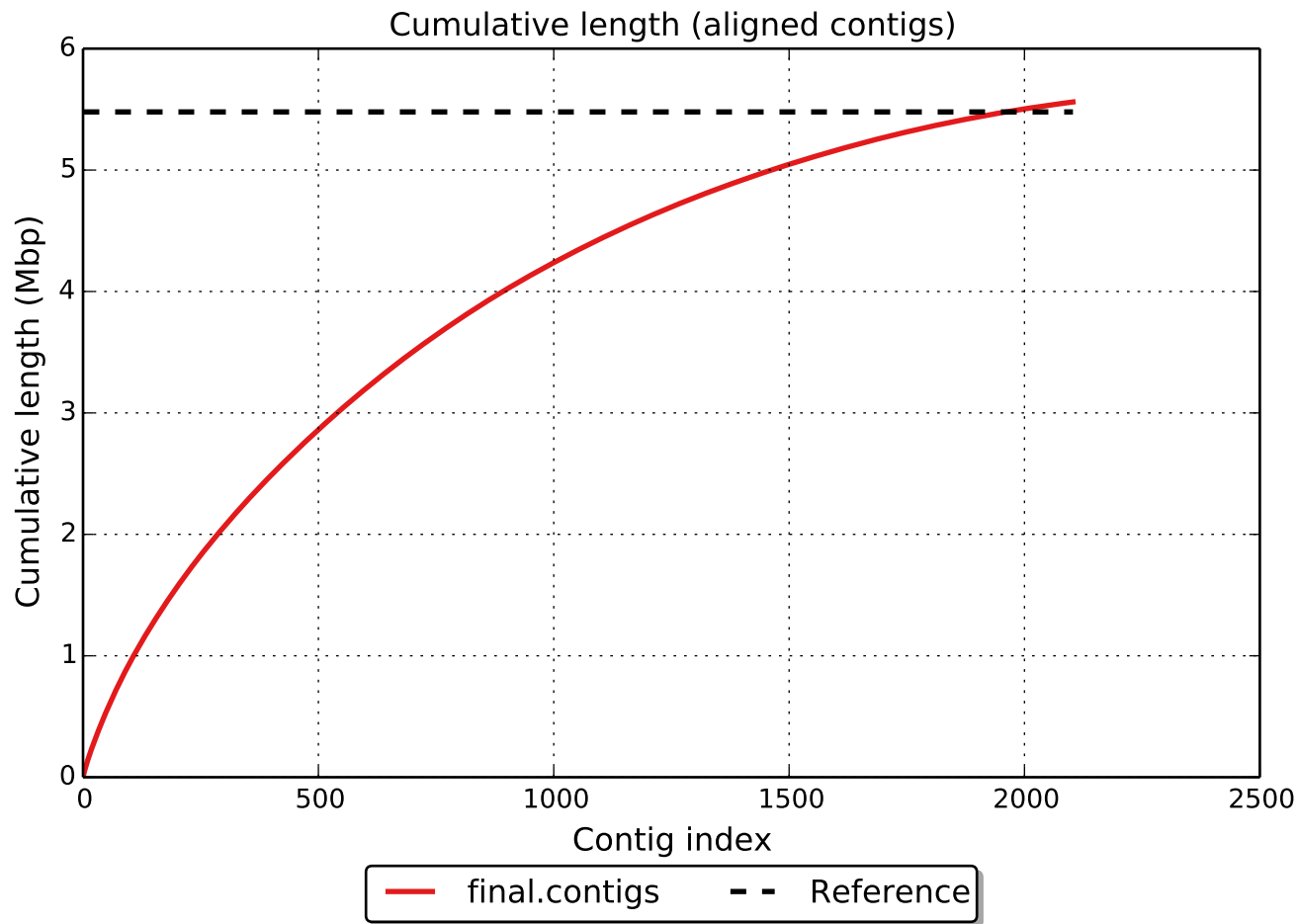
GC content

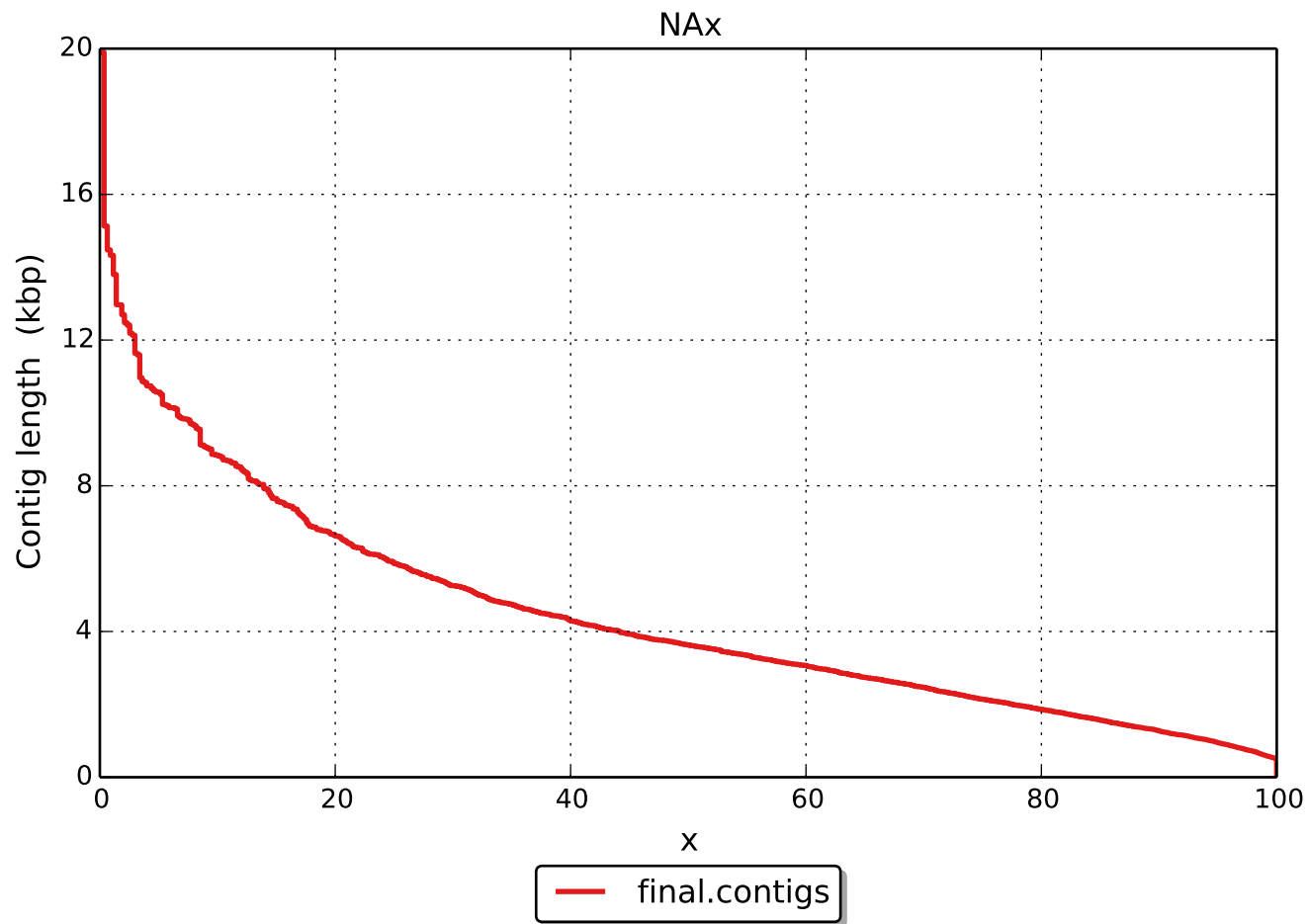












NGAx

