

Report

	final.contigs
# contigs (>= 0 bp)	725
# contigs (>= 1000 bp)	473
Total length (>= 0 bp)	1238100
Total length (>= 1000 bp)	1052065
# contigs	725
Largest contig	11393
Total length	1238100
Reference length	615980
GC (%)	25.36
Reference GC (%)	25.35
N50	2209
NG50	3342
N75	1304
NG75	2683
L50	186
LG50	70
L75	365
LG75	122
# misassemblies	36
# misassembled contigs	35
Misassembled contigs length	114660
# local misassemblies	0
# unaligned contigs	1 + 3 part
Unaligned length	1801
Genome fraction (%)	97.708
Duplication ratio	2.054
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1663.35
# indels per 100 kbp	2.66
Largest alignment	11393
NA50	2035
NGA50	3054
NA75	1250
NGA75	2553
LA50	198
LGA50	75
LA75	387
LGA75	130

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	36
# relocations	36
# translocations	0
# inversions	0
# possibly misassembled contigs	2
# misassembled contigs	35
Misassembled contigs length	114660
# local misassemblies	0
# mismatches	10011
# indels	16
# short indels	16
# long indels	0
Indels length	16

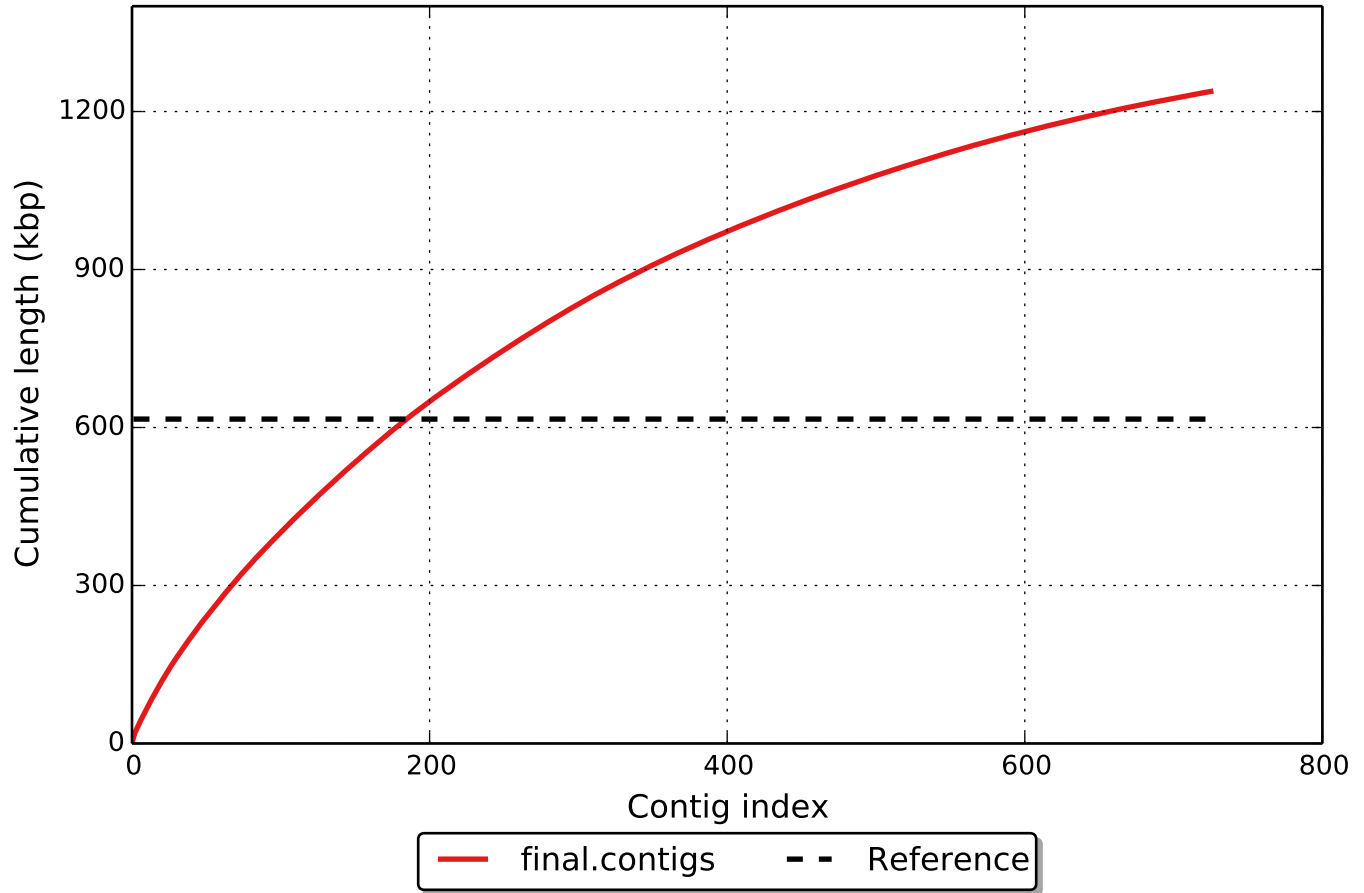
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

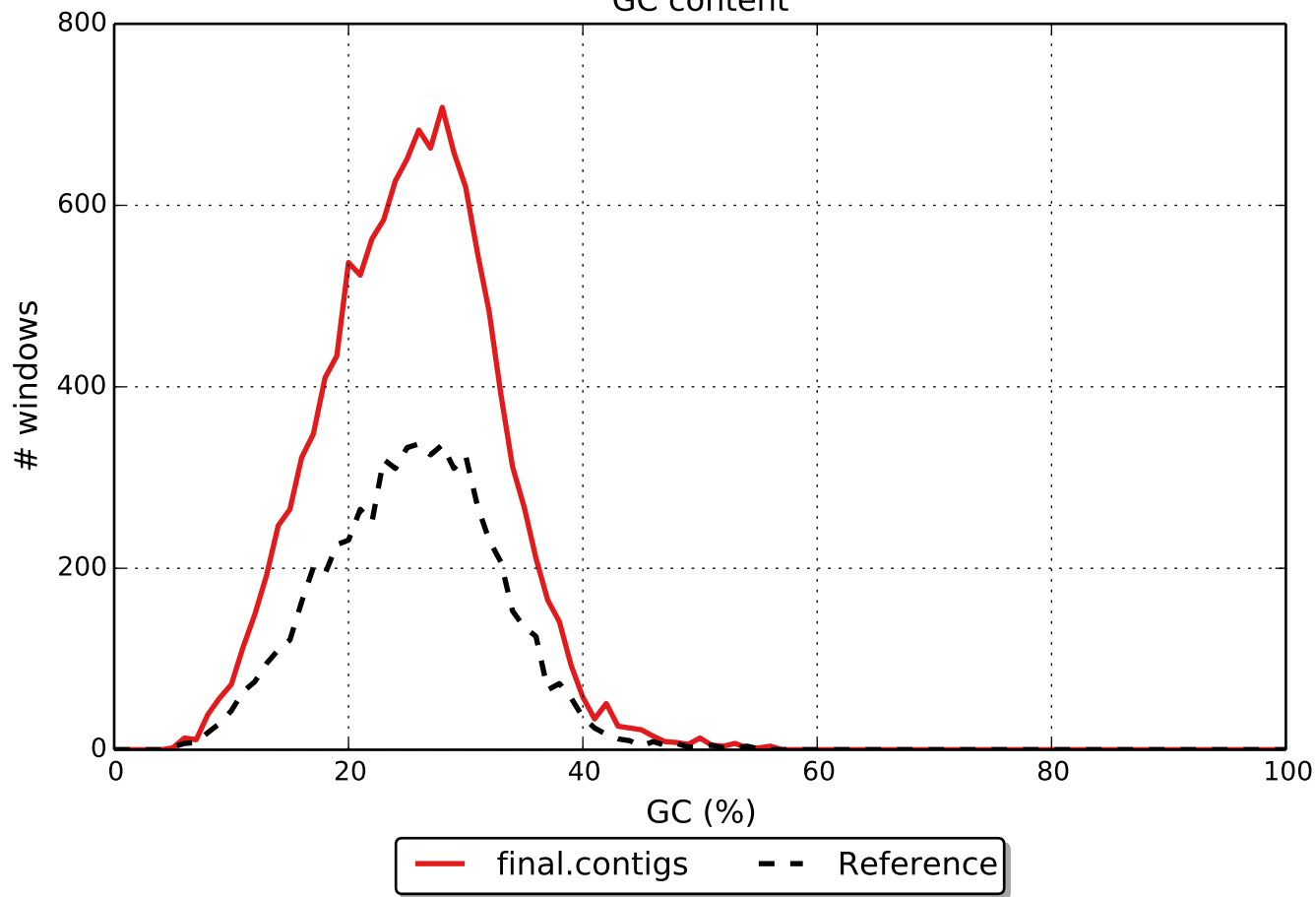
	final.contigs
# fully unaligned contigs	1
Fully unaligned length	599
# partially unaligned contigs	3
# with misassembly	0
# both parts are significant	1
Partially unaligned length	1202
# N's	0

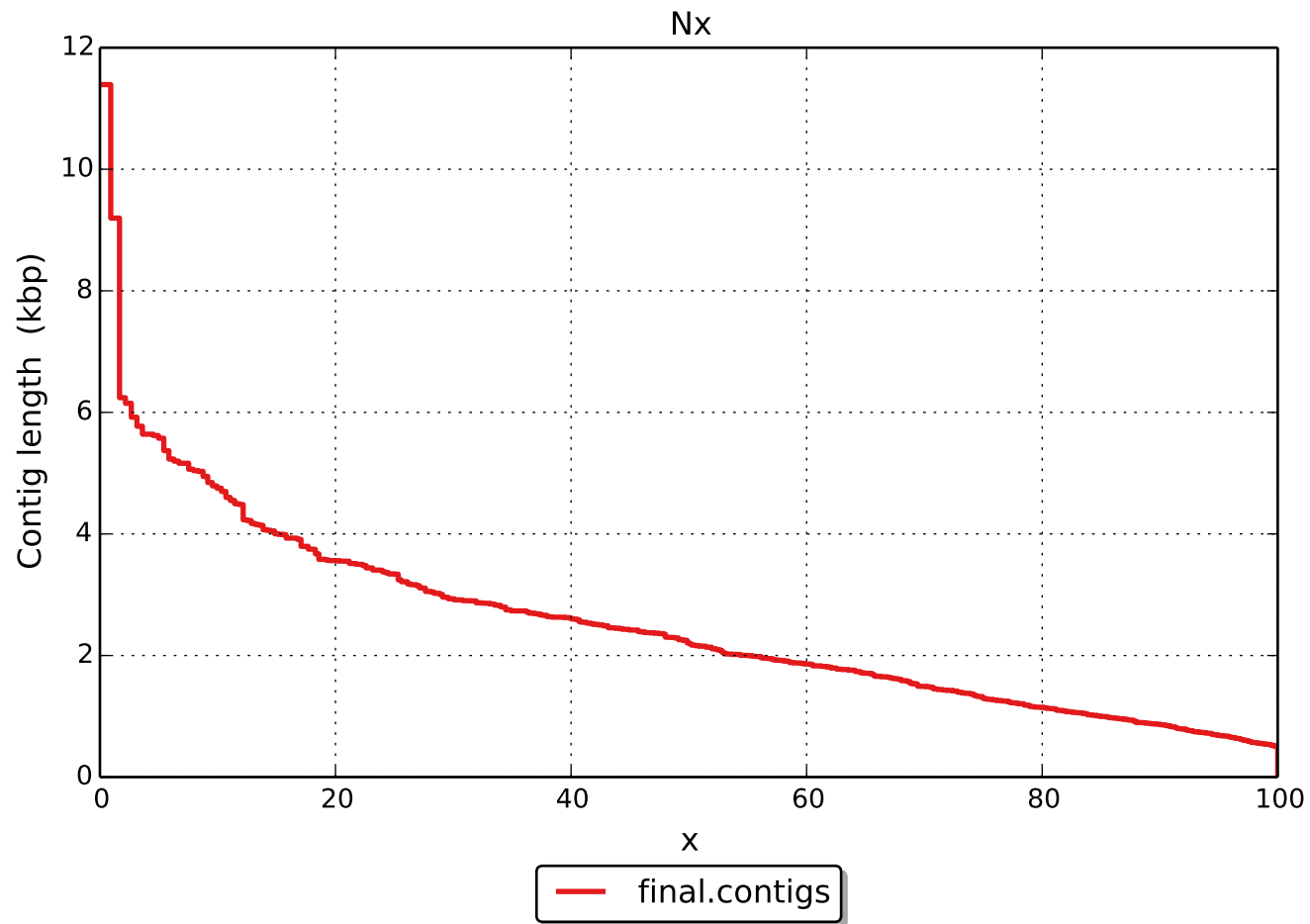
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

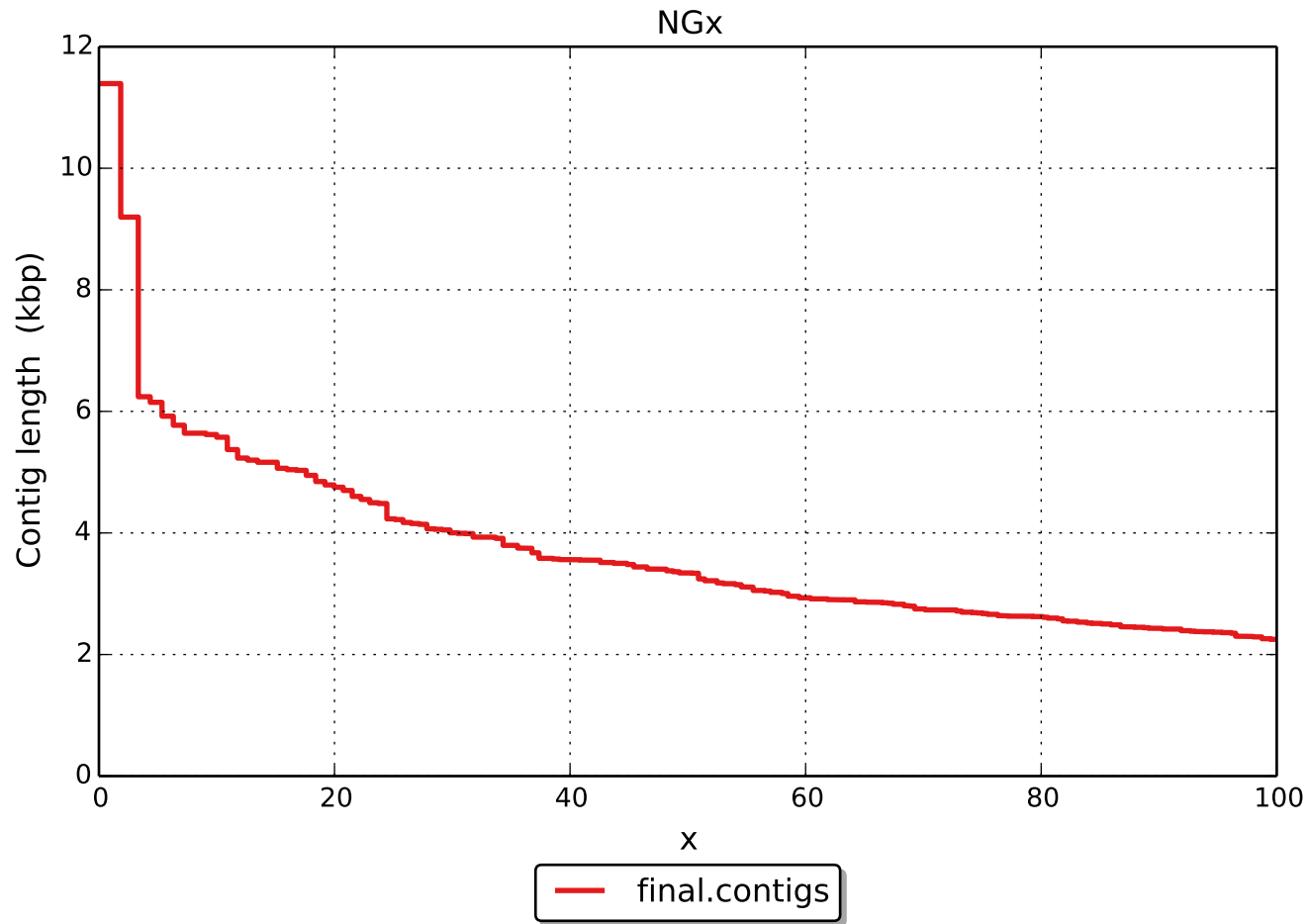
Cumulative length

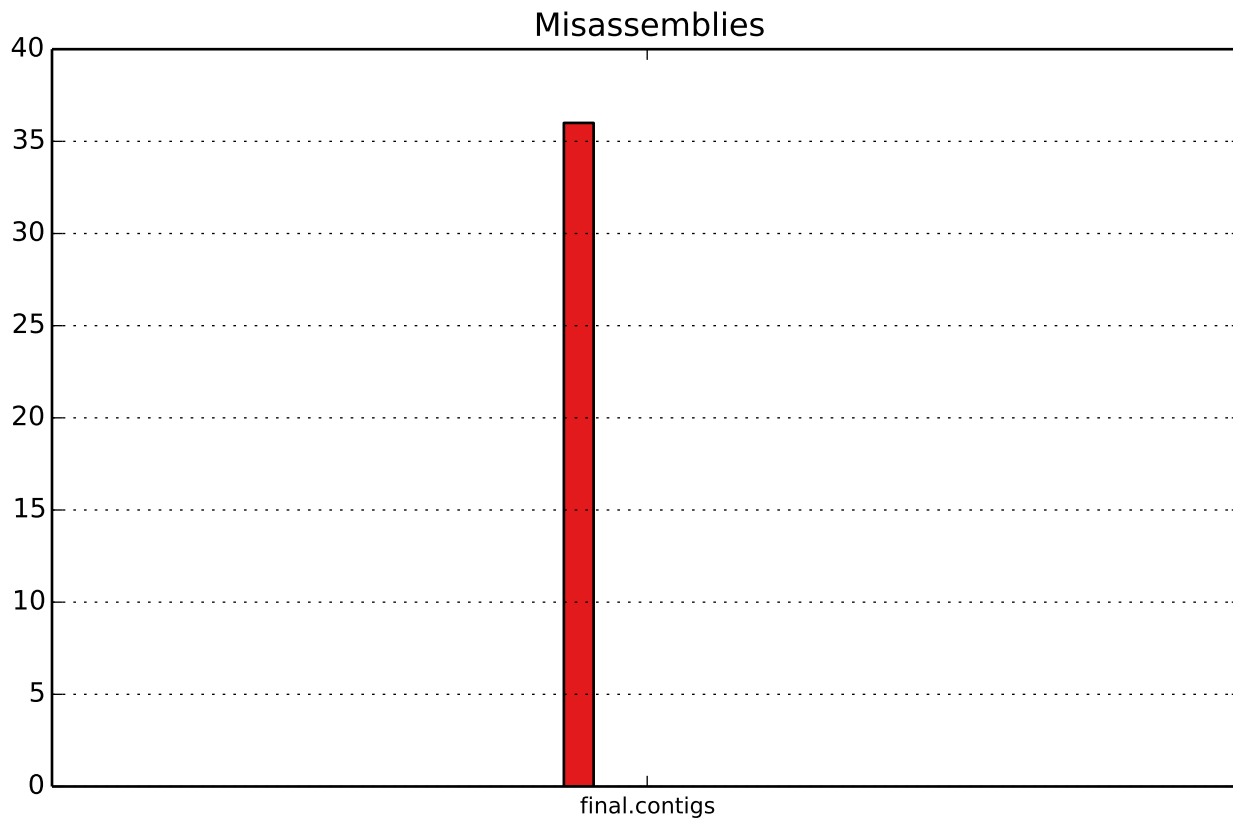


GC content

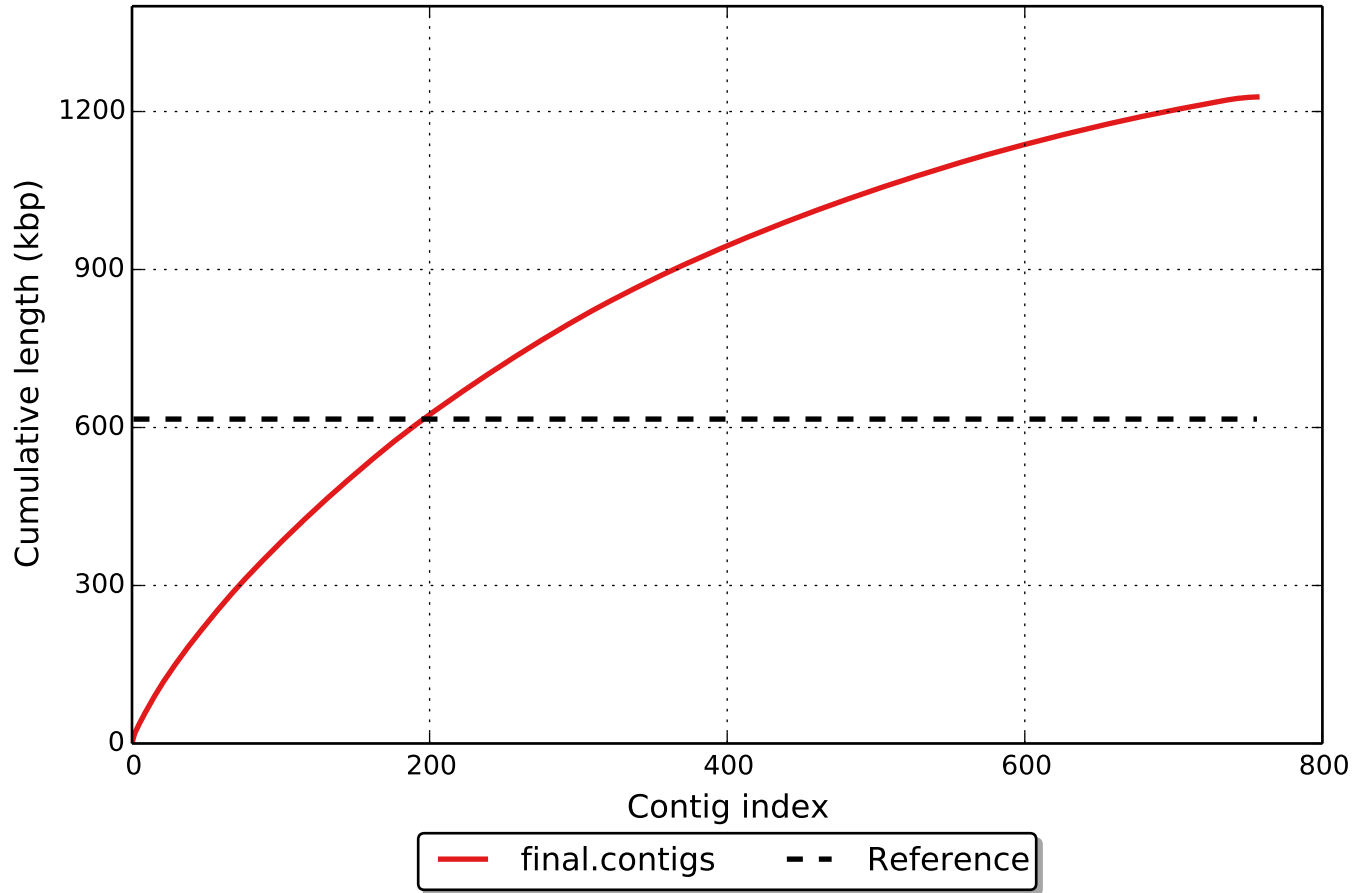


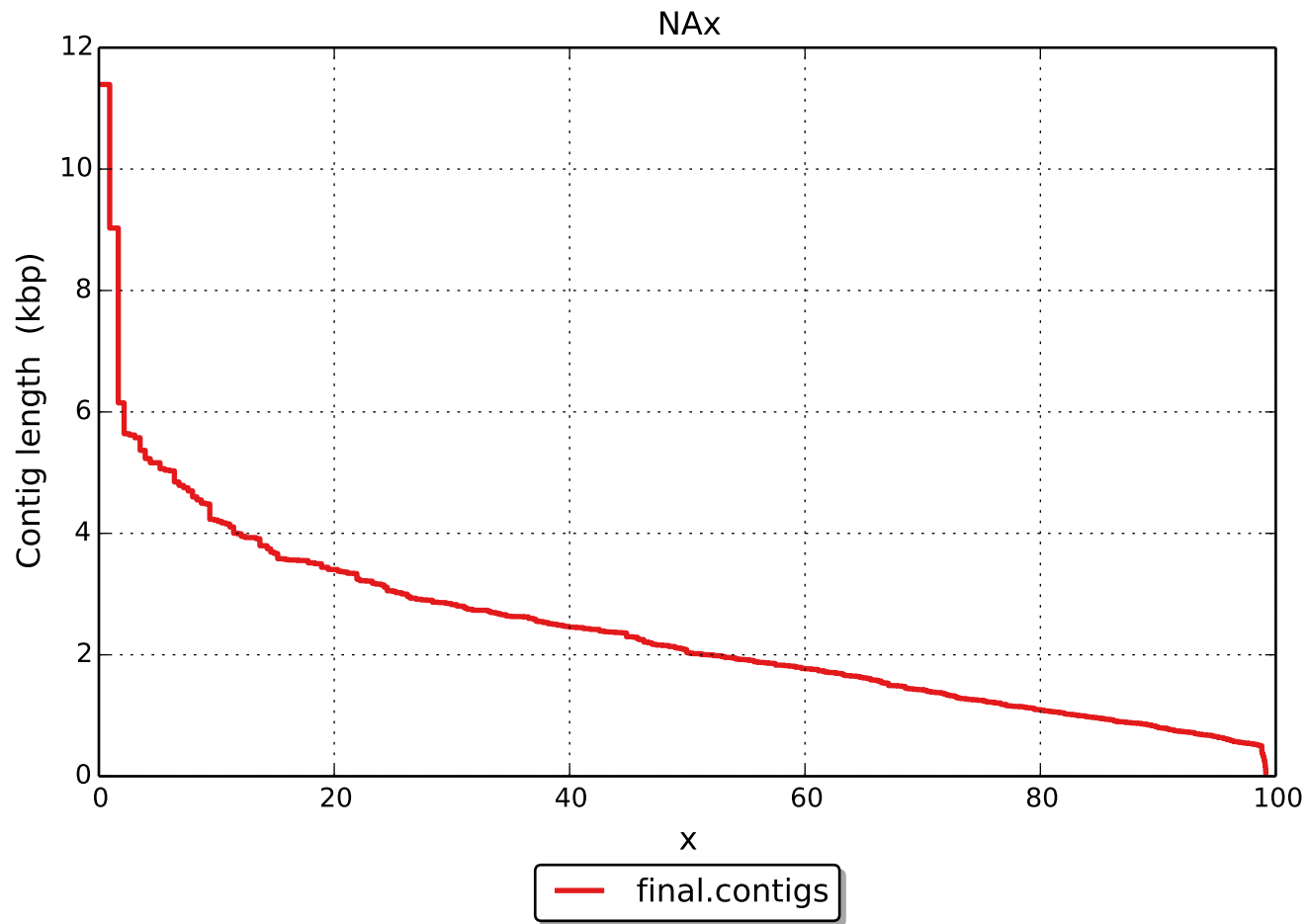






Cumulative length (aligned contigs)





NGAx

