

Report

	final.contigs
# contigs (≥ 0 bp)	1428
# contigs (≥ 1000 bp)	917
Total length (≥ 0 bp)	3466761
Total length (≥ 1000 bp)	3117078
# contigs	1428
Largest contig	21352
Total length	3466761
Reference length	1892775
GC (%)	32.28
Reference GC (%)	32.26
N50	3894
NG50	6047
N75	2129
NG75	4583
L50	272
LG50	110
L75	572
LG75	198
# misassemblies	6
# misassembled contigs	6
Misassembled contigs length	6031
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	91.301
Duplication ratio	2.006
# N's per 100 kbp	0.00
# mismatches per 100 kbp	683.87
# indels per 100 kbp	0.17
Largest alignment	21352
NA50	677
NGA50	3571
NGA75	1697
LA50	654
LGA50	157
LGA75	347

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

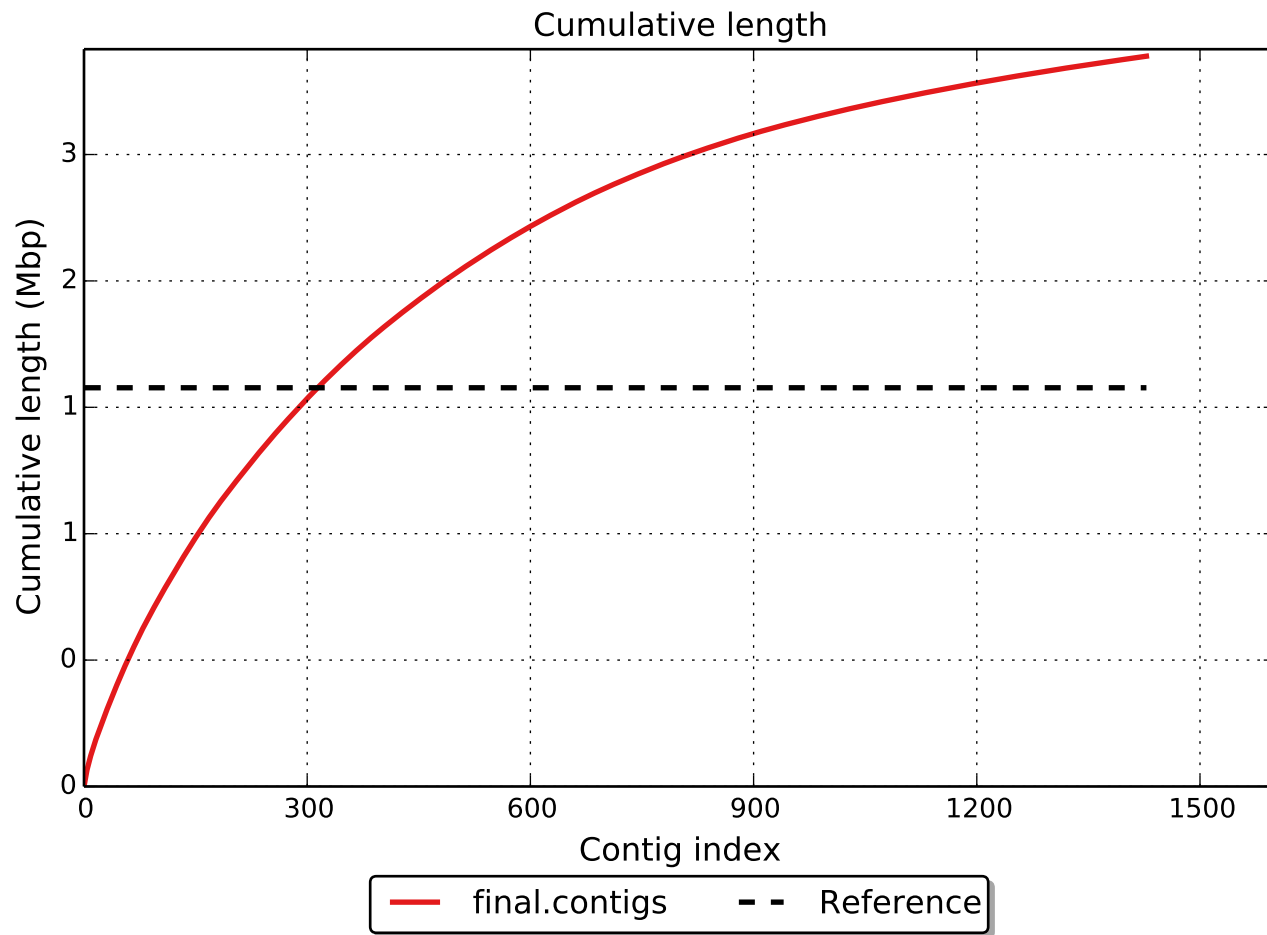
	final.contigs
# misassemblies	6
# relocations	6
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	6
Misassembled contigs length	6031
# local misassemblies	0
# mismatches	11818
# indels	3
# short indels	2
# long indels	1
Indels length	29

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).

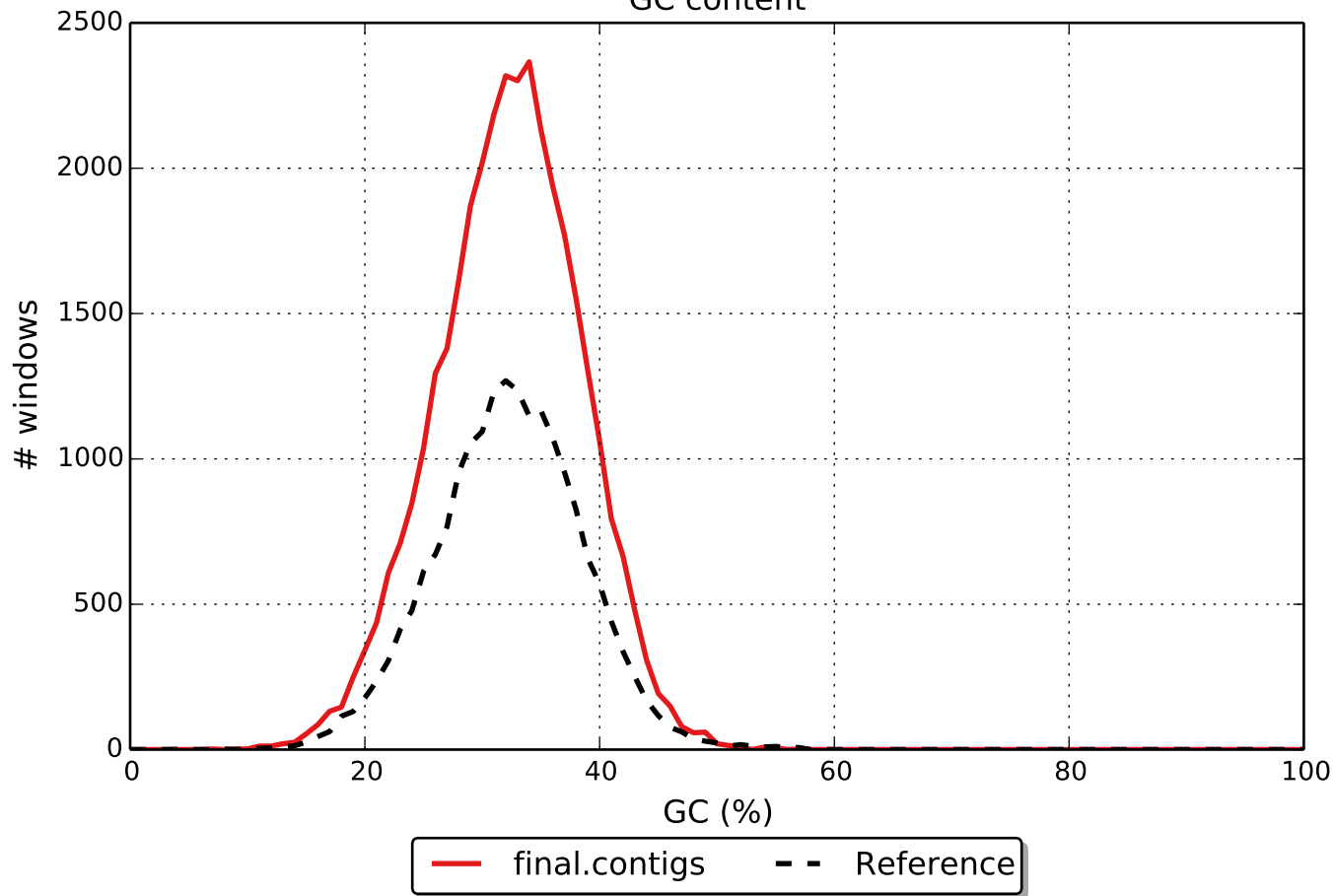
Unaligned report

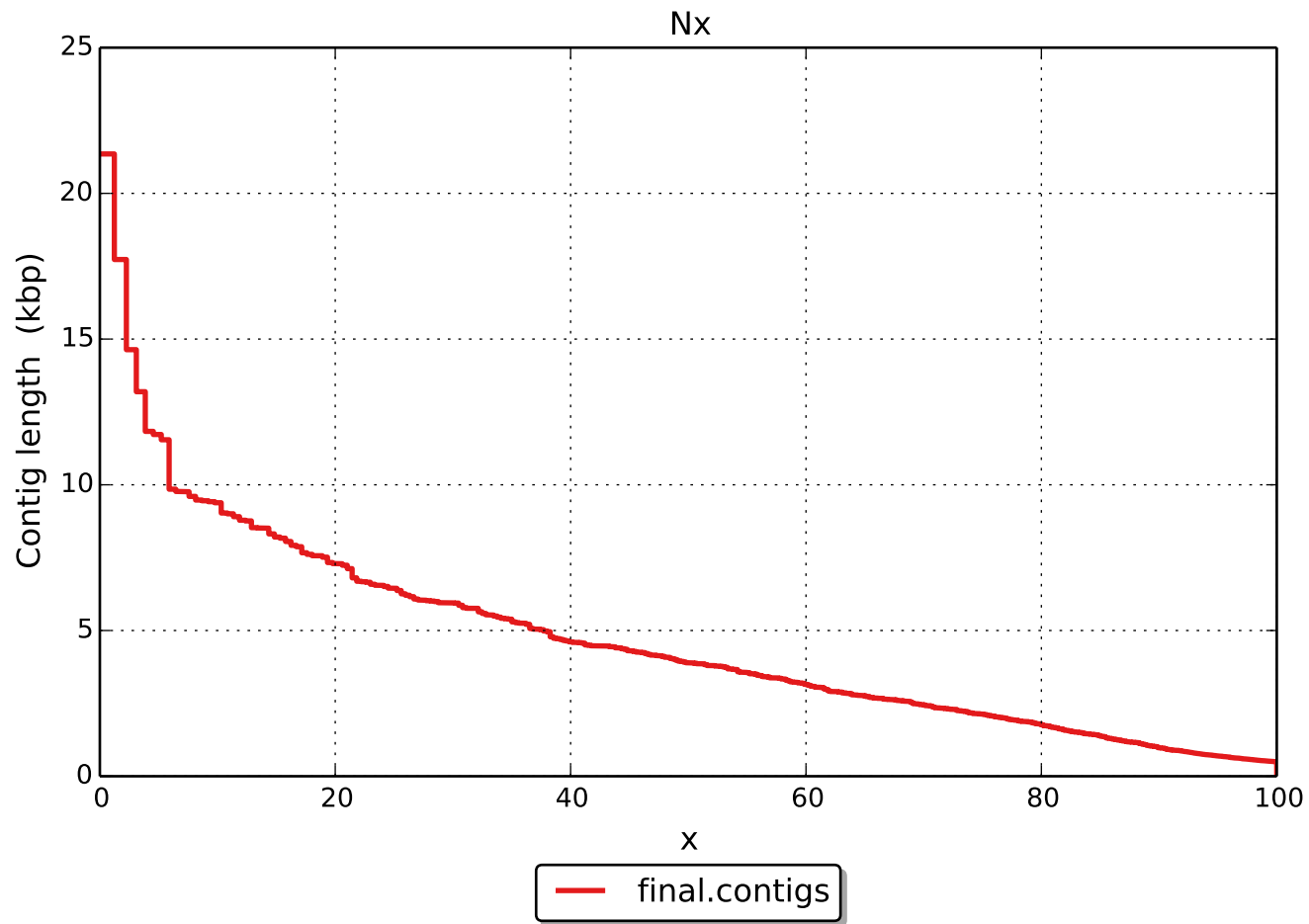
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

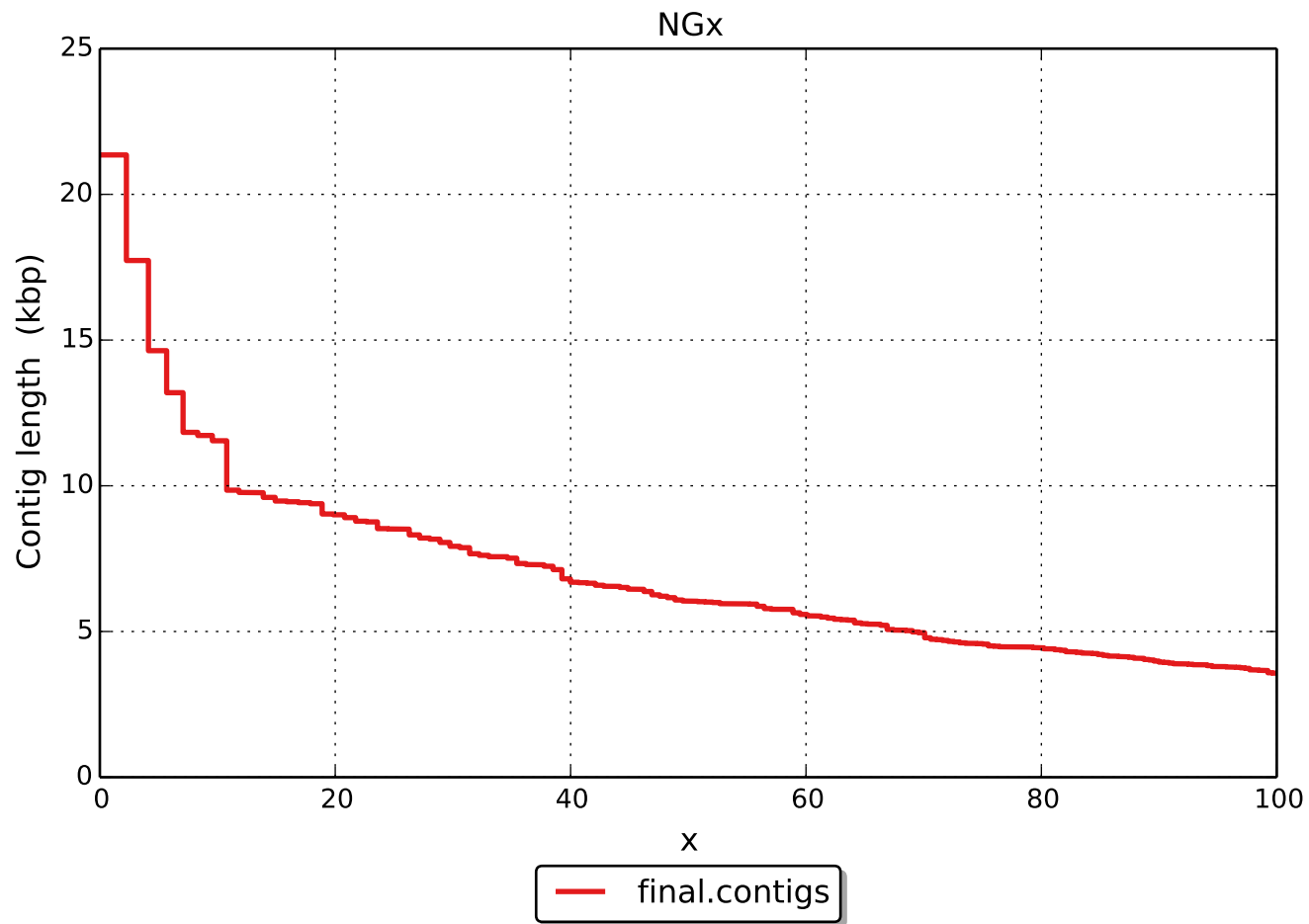
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

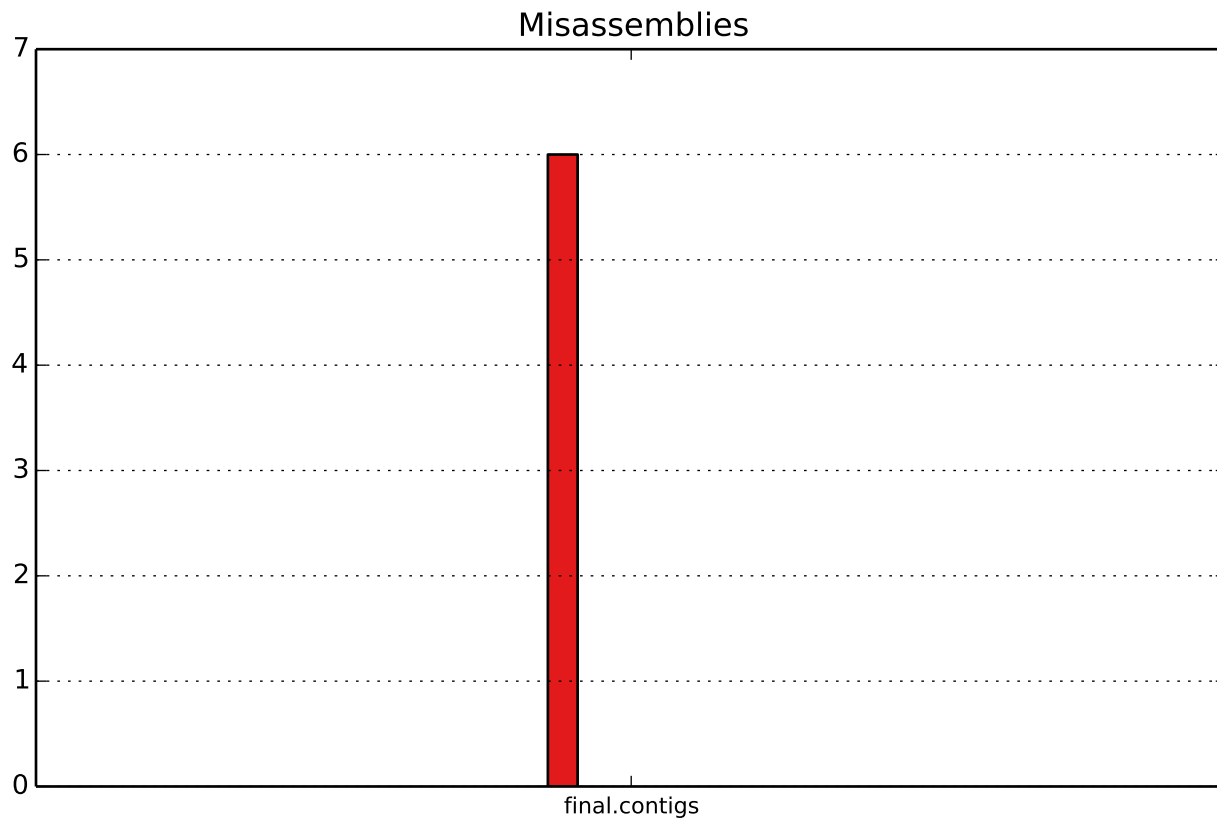


GC content

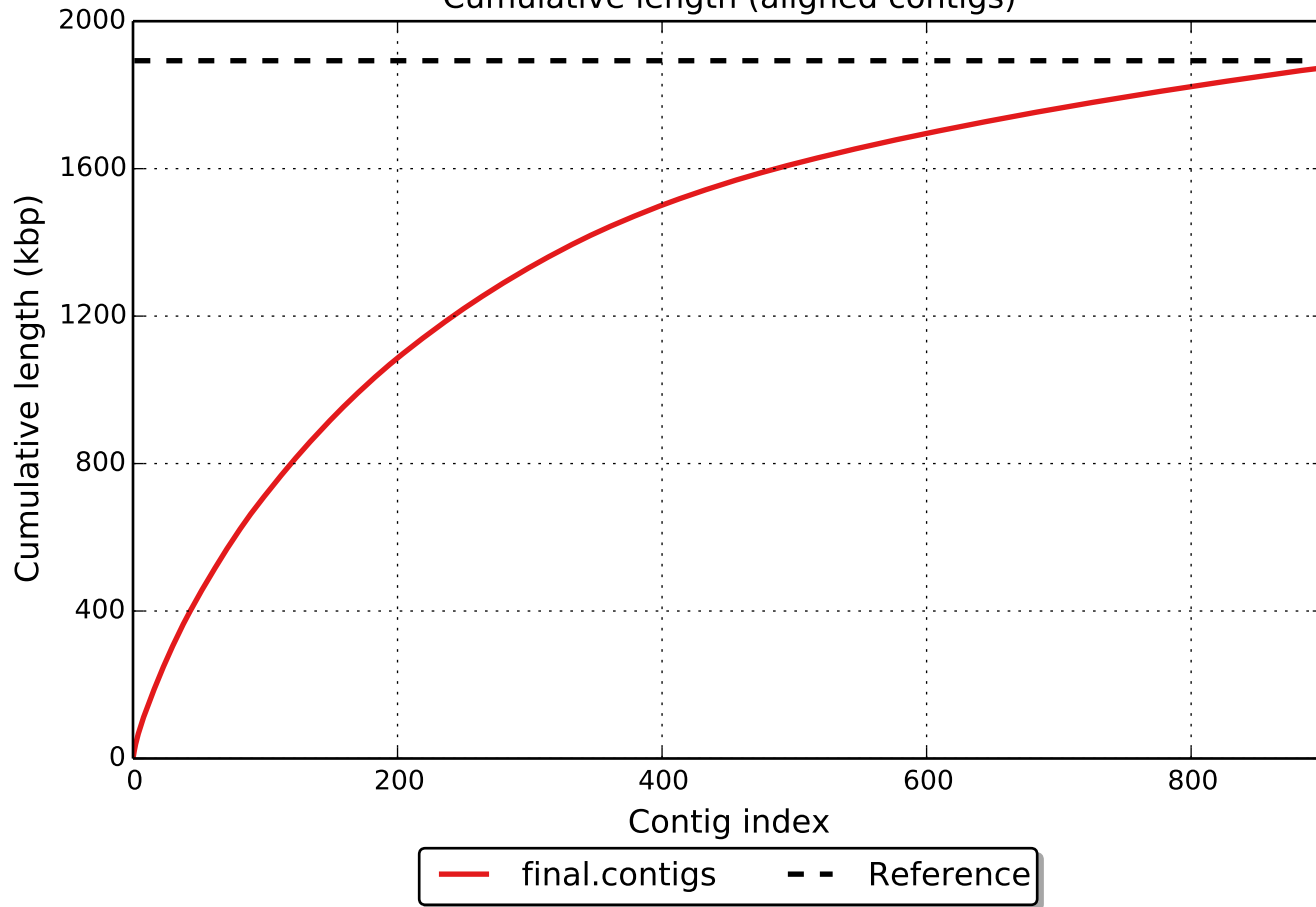


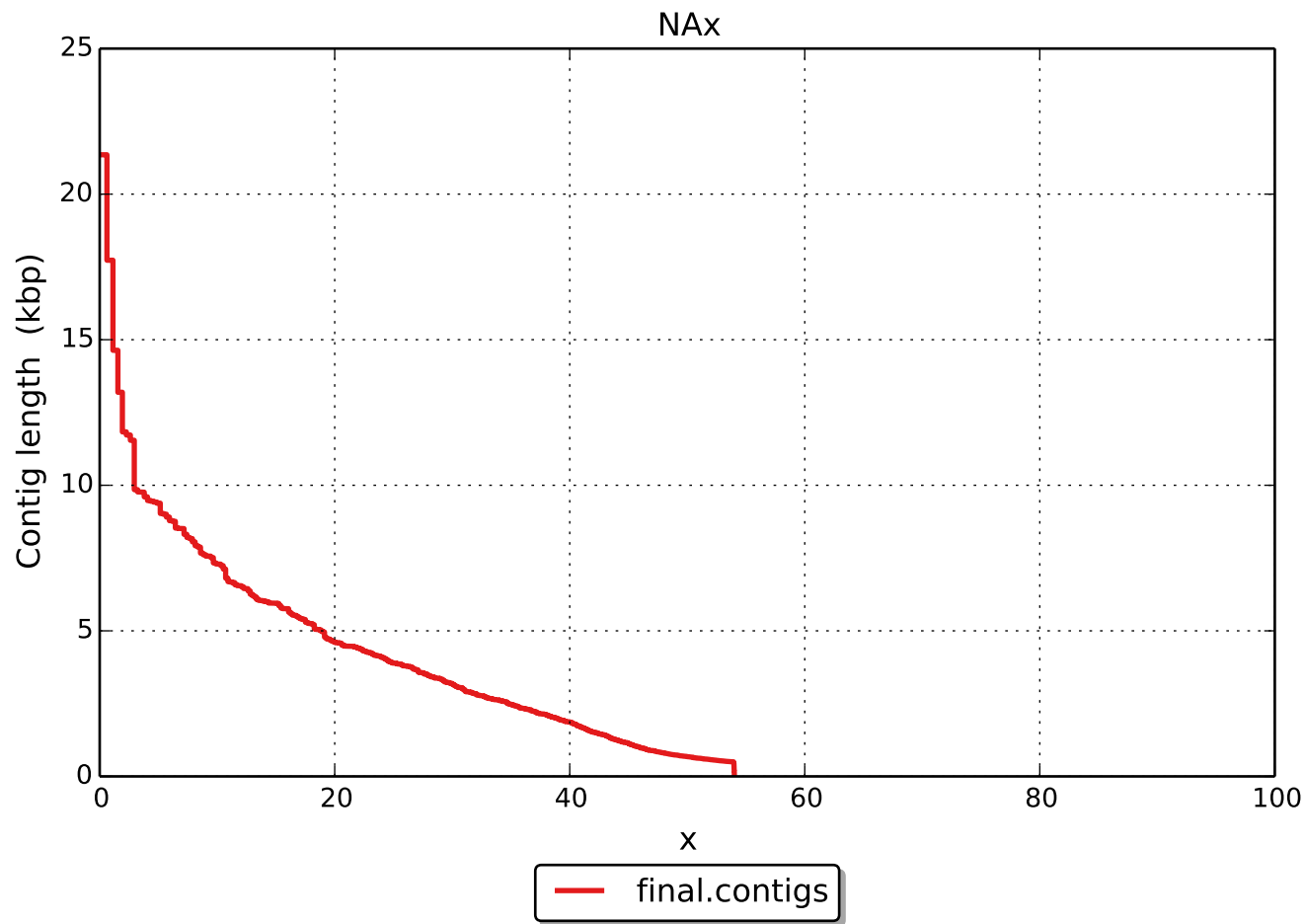






Cumulative length (aligned contigs)





NGAx

