

Report

	final.contigs
# contigs (≥ 0 bp)	265
# contigs (≥ 1000 bp)	227
# contigs (≥ 5000 bp)	185
# contigs (≥ 10000 bp)	146
# contigs (≥ 25000 bp)	57
# contigs (≥ 50000 bp)	17
Total length (≥ 0 bp)	4566014
Total length (≥ 1000 bp)	4548797
Total length (≥ 5000 bp)	4425559
Total length (≥ 10000 bp)	4128091
Total length (≥ 25000 bp)	2649706
Total length (≥ 50000 bp)	1252351
# contigs	238
Largest contig	101514
Total length	4556499
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	31074
NG50	29777
N75	17989
NG75	17429
L50	44
LG50	46
L75	94
LG75	98
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	135627
# local misassemblies	7
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.094
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4.35
# indels per 100 kbp	0.90
Largest alignment	101514
NA50	31074
NGA50	29777
NA75	17460
NGA75	17319
LA50	45
LGA50	47
LA75	96
LGA75	99

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

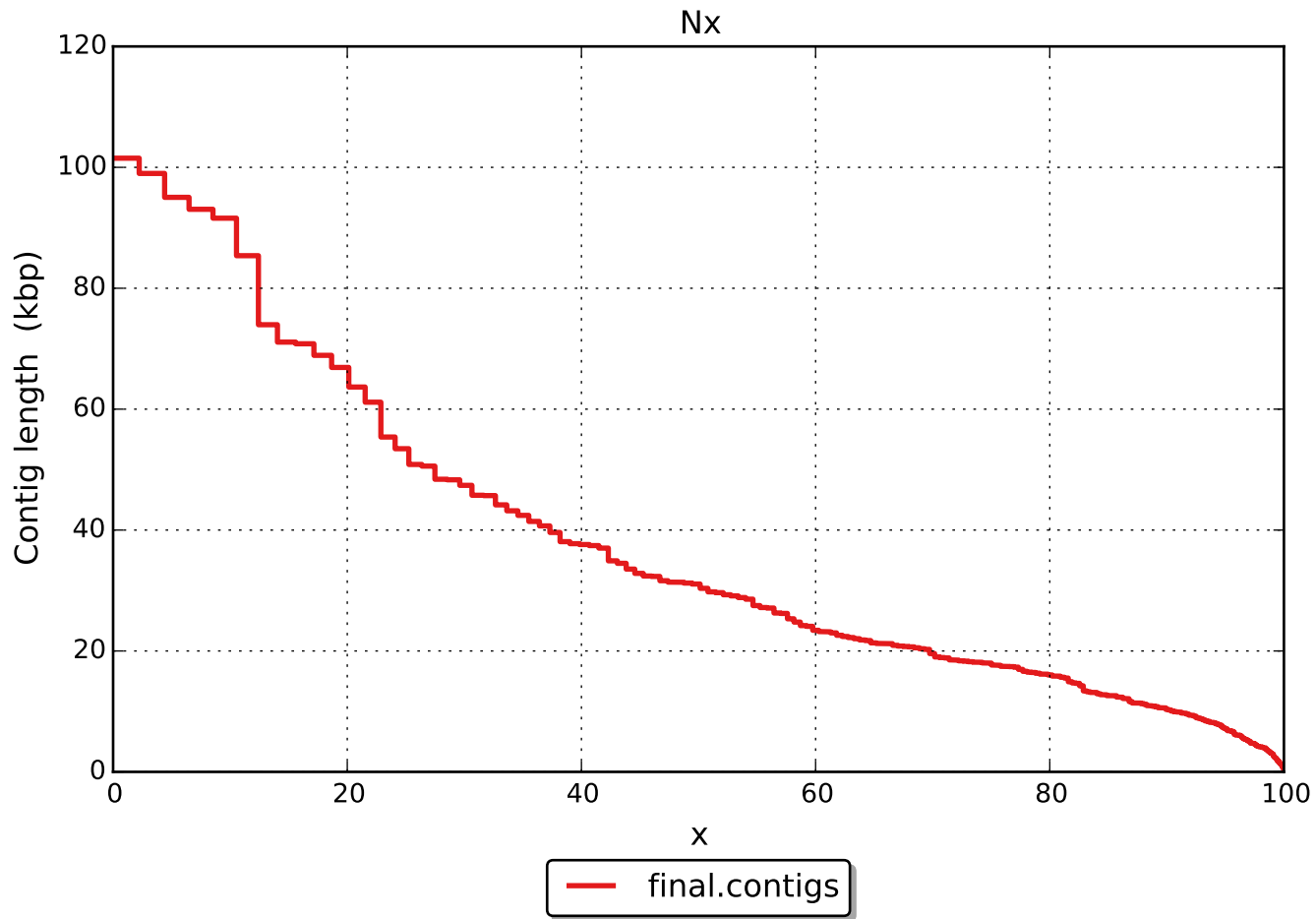
	final.contigs
# misassemblies	3
# relocations	3
# translocations	0
# inversions	0
# misassembled contigs	3
Misassembled contigs length	135627
# local misassemblies	7
# mismatches	198
# indels	41
# short indels	35
# long indels	6
Indels length	216

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).

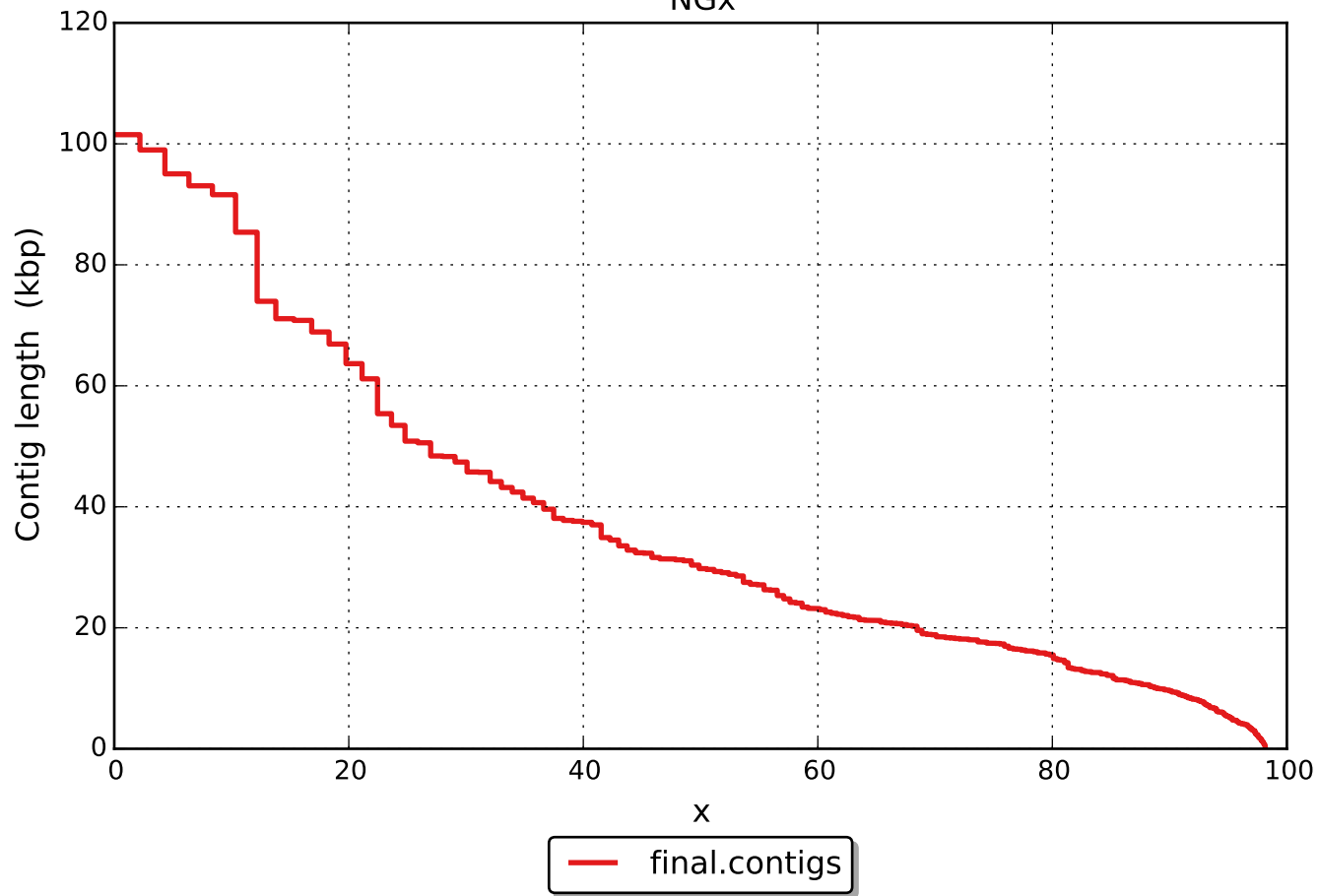
Unaligned report

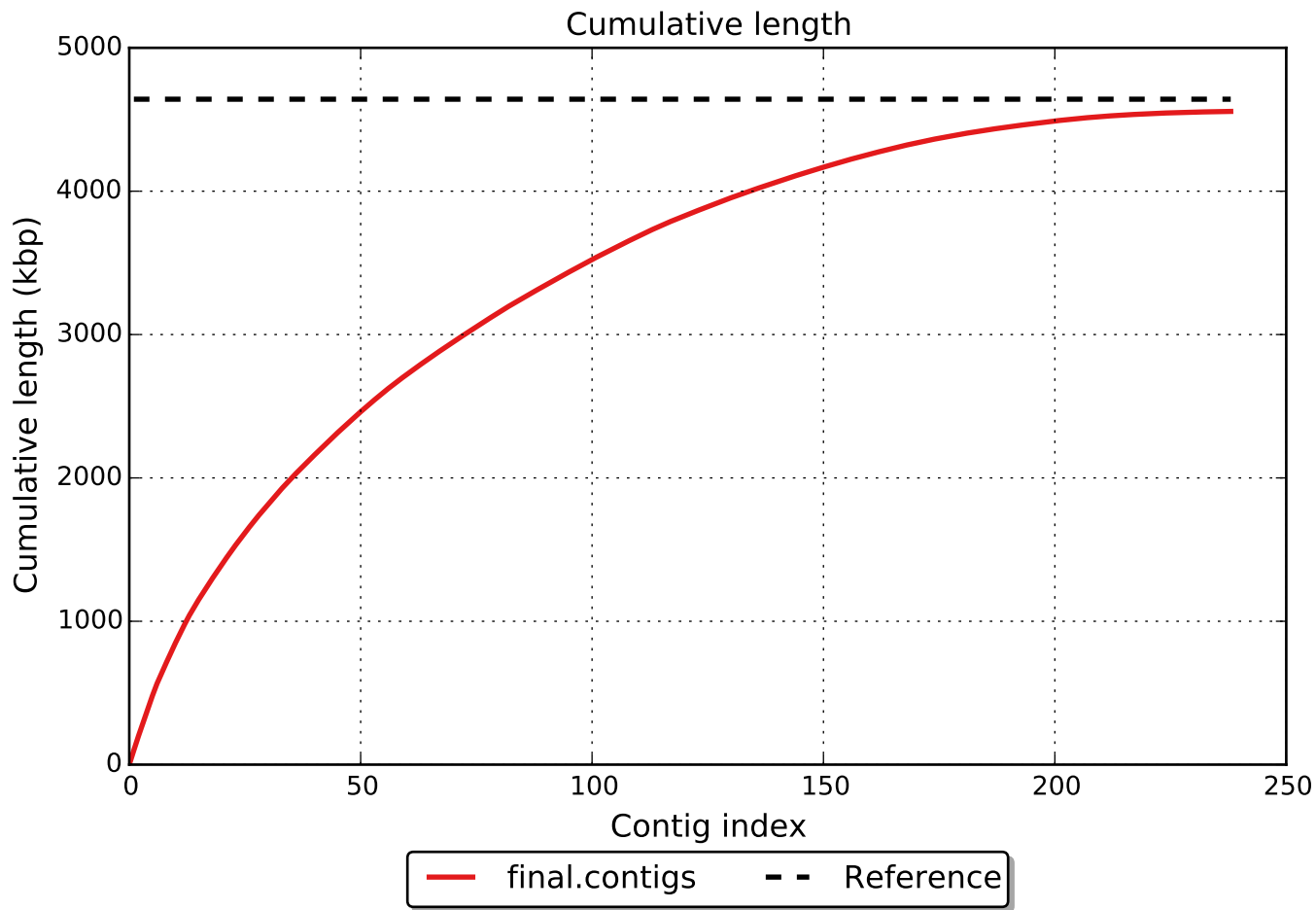
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

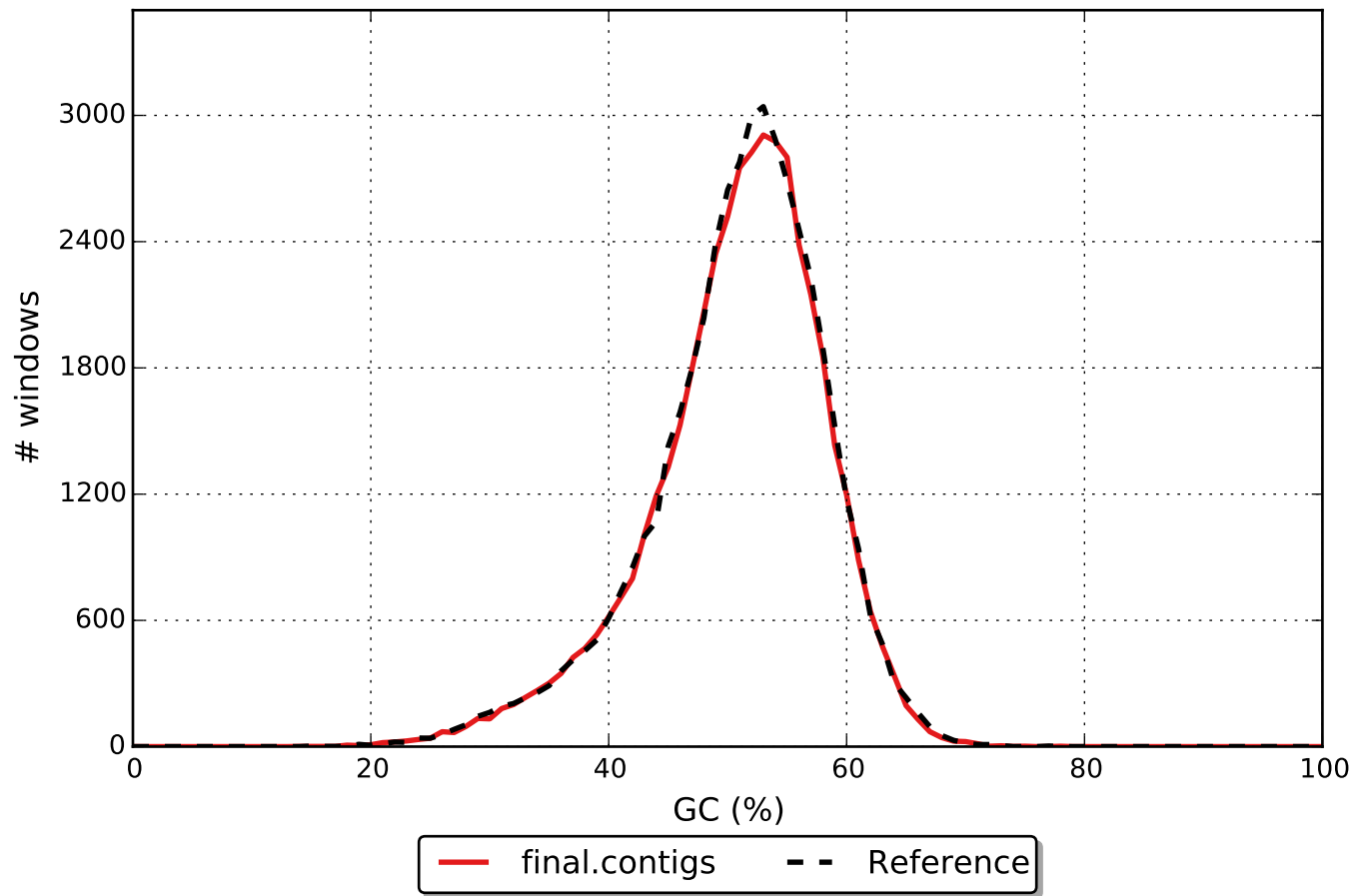


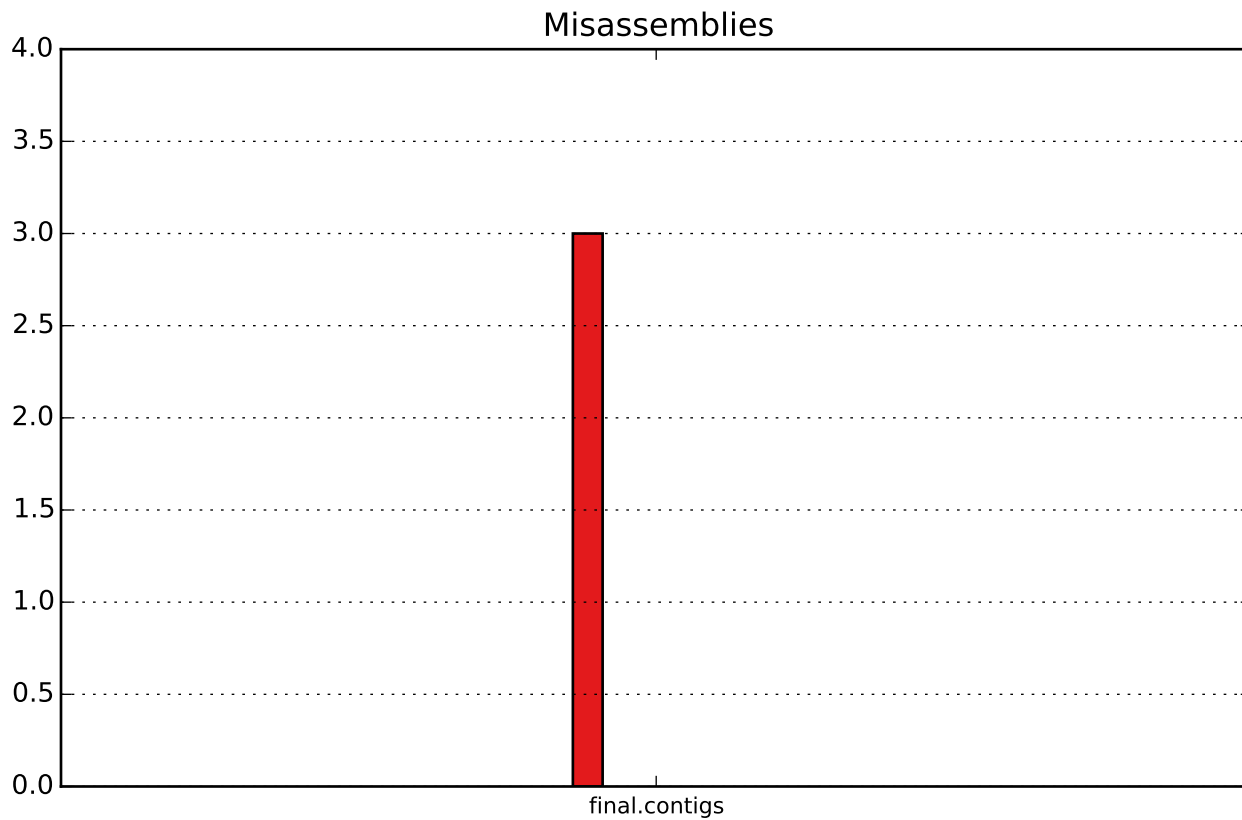
NGx



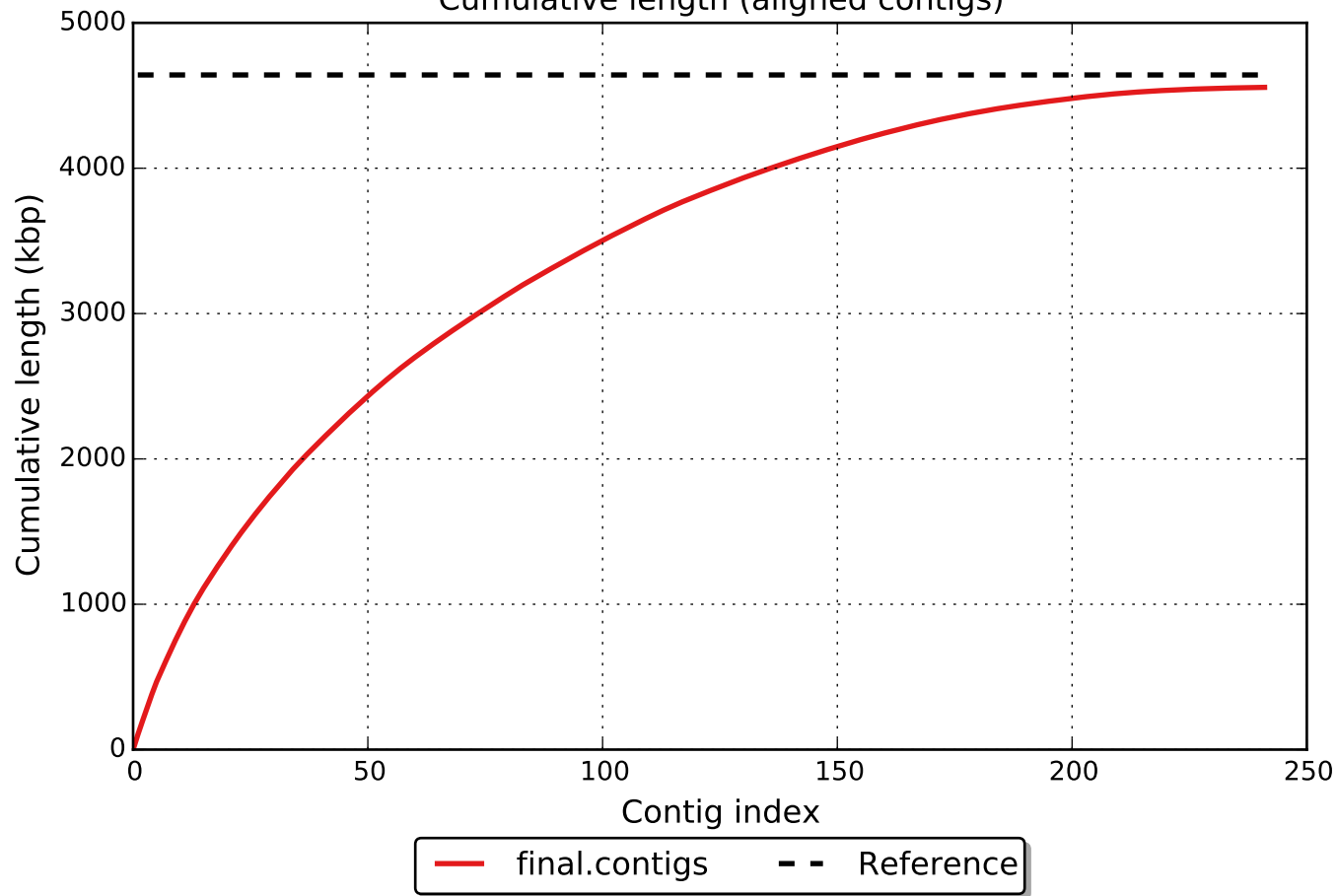


GC content

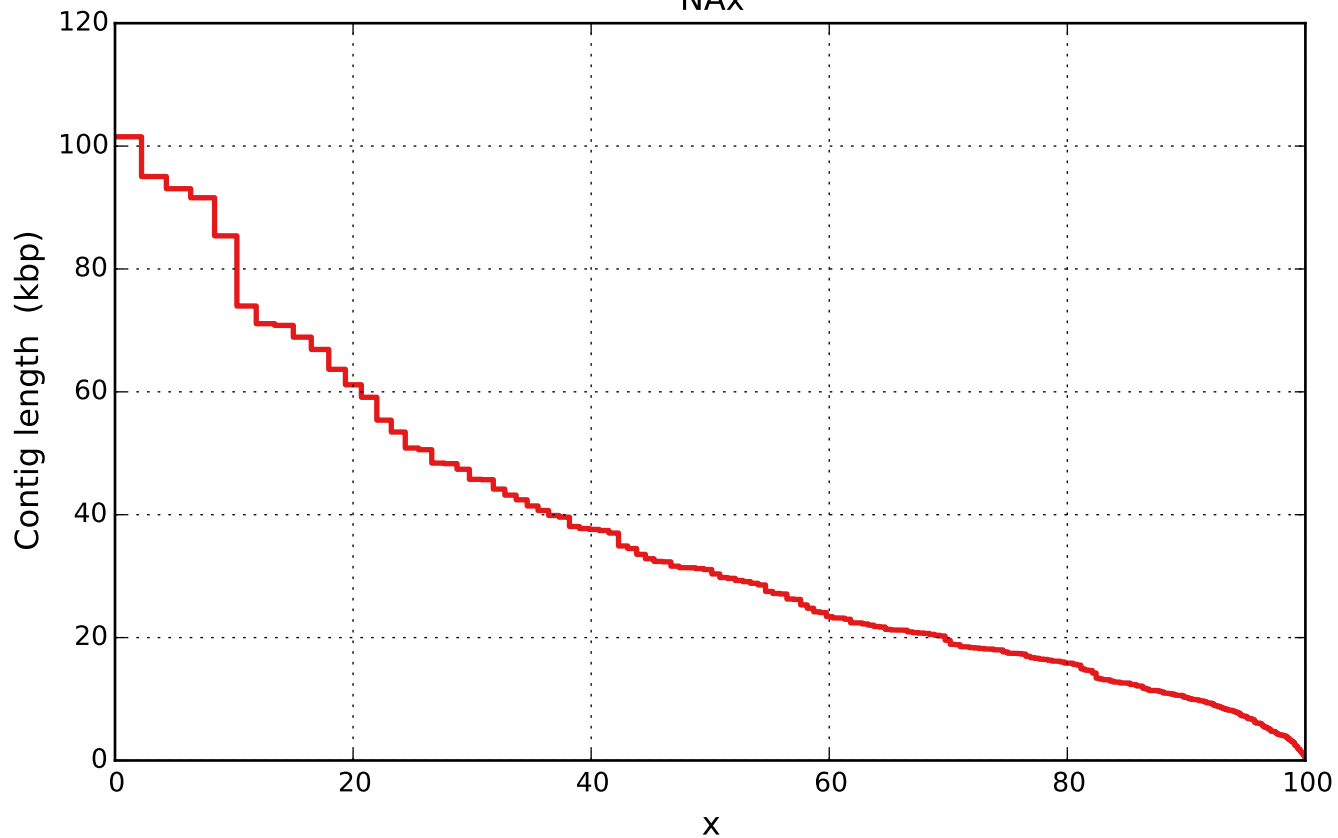




Cumulative length (aligned contigs)



NAx



— final.contigs

NGAx

