

Report

	final.contigs
# contigs (>= 0 bp)	520
# contigs (>= 1000 bp)	364
# contigs (>= 5000 bp)	241
# contigs (>= 10000 bp)	160
# contigs (>= 25000 bp)	52
# contigs (>= 50000 bp)	5
Total length (>= 0 bp)	4655654
Total length (>= 1000 bp)	4594340
Total length (>= 5000 bp)	4266773
Total length (>= 10000 bp)	3679268
Total length (>= 25000 bp)	1936808
Total length (>= 50000 bp)	317938
# contigs	394
Largest contig	85460
Total length	4615600
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	21600
NG50	21600
N75	12033
NG75	11932
L50	69
LG50	69
L75	141
LG75	142
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	111486
# local misassemblies	2
# unaligned contigs	9 + 4 part
Unaligned length	14056
Genome fraction (%)	98.052
Duplication ratio	1.011
# N's per 100 kbp	0.00
# mismatches per 100 kbp	57.65
# indels per 100 kbp	0.20
Largest alignment	85460
NA50	21513
NGA50	21513
NA75	11661
NGA75	11546
LA50	70
LGA50	70
LA75	143
LGA75	144

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

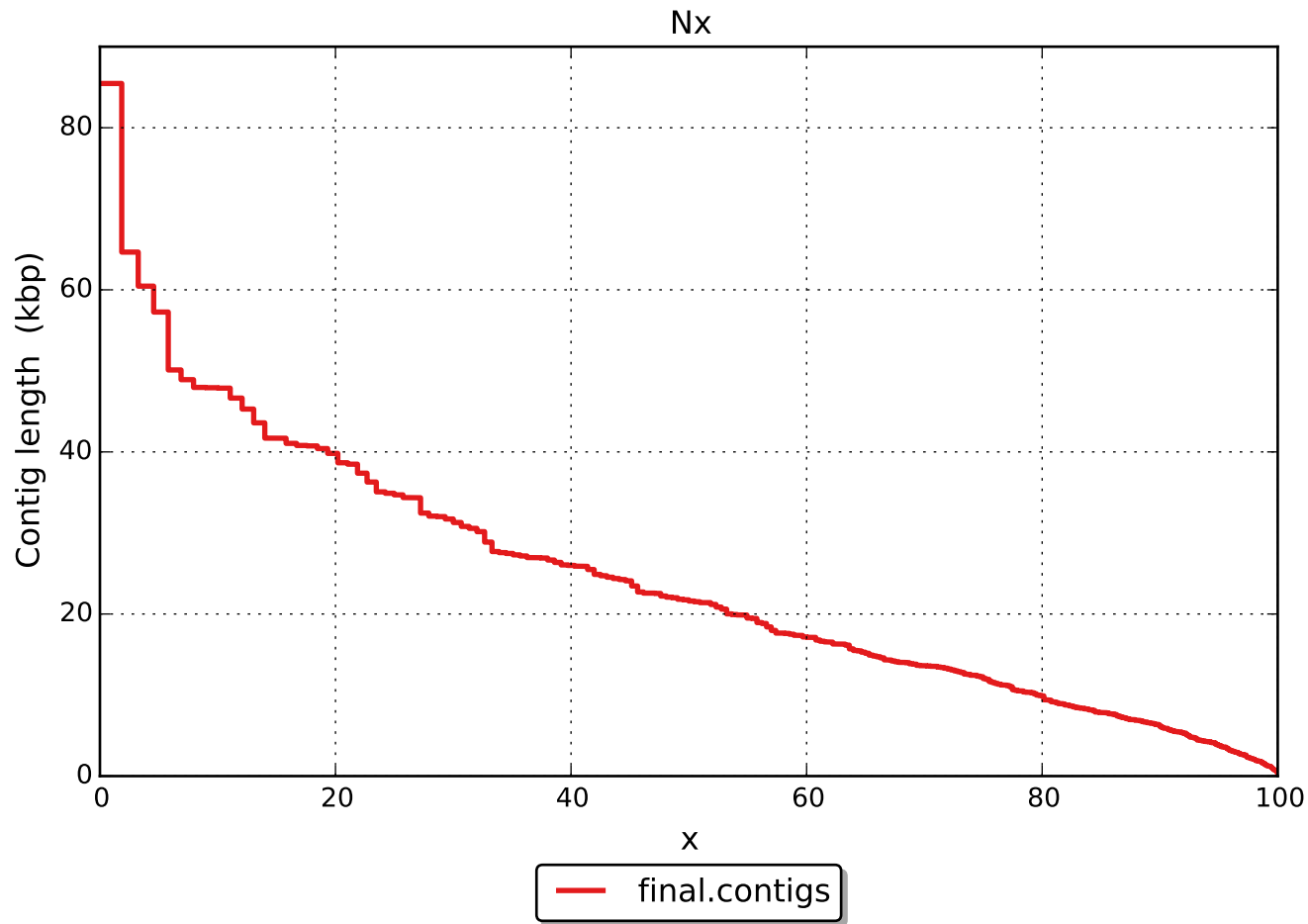
	final.contigs
# misassemblies	3
# relocations	3
# translocations	0
# inversions	0
# misassembled contigs	3
Misassembled contigs length	111486
# local misassemblies	2
# mismatches	2624
# indels	9
# short indels	8
# long indels	1
Indels length	90

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).

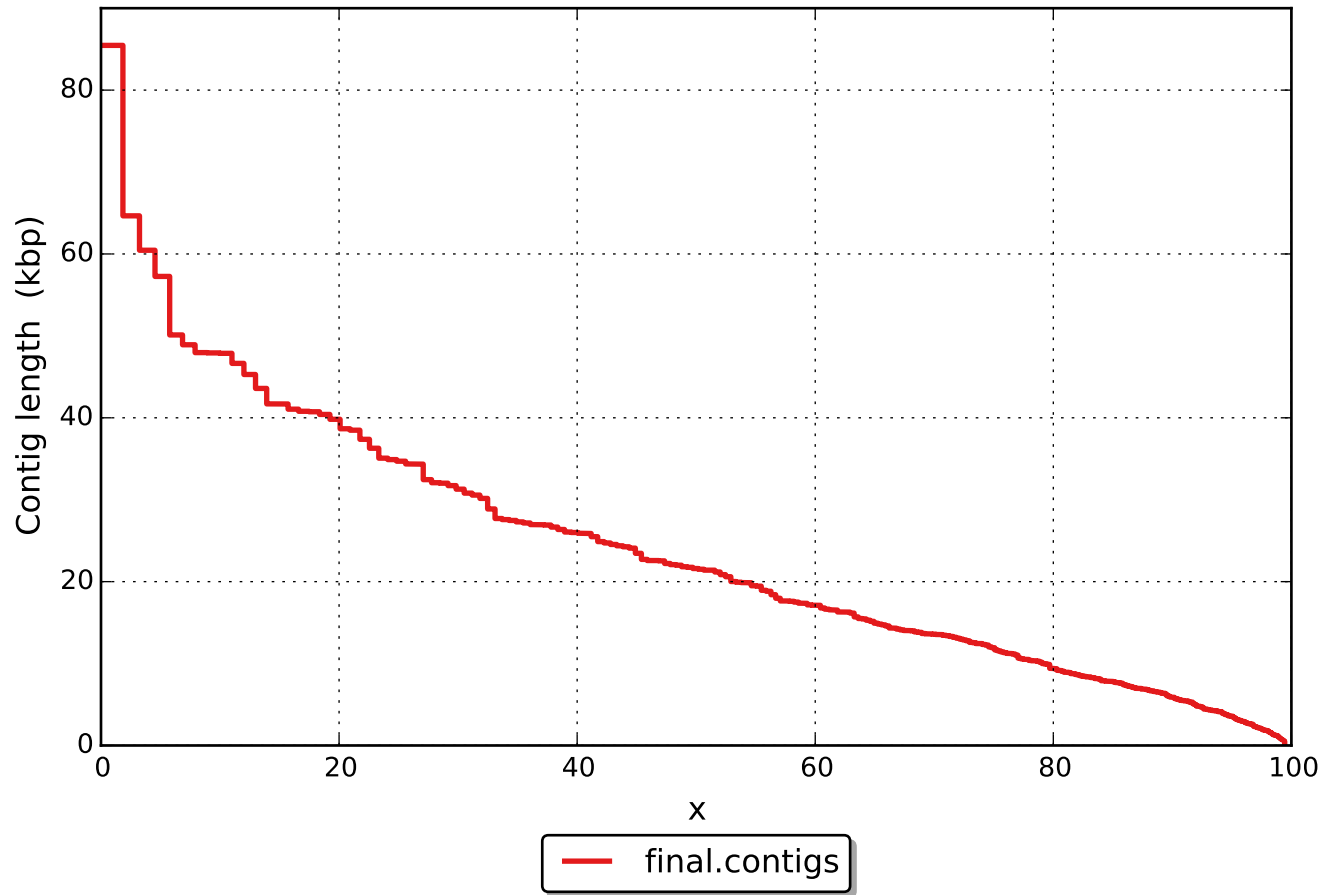
Unaligned report

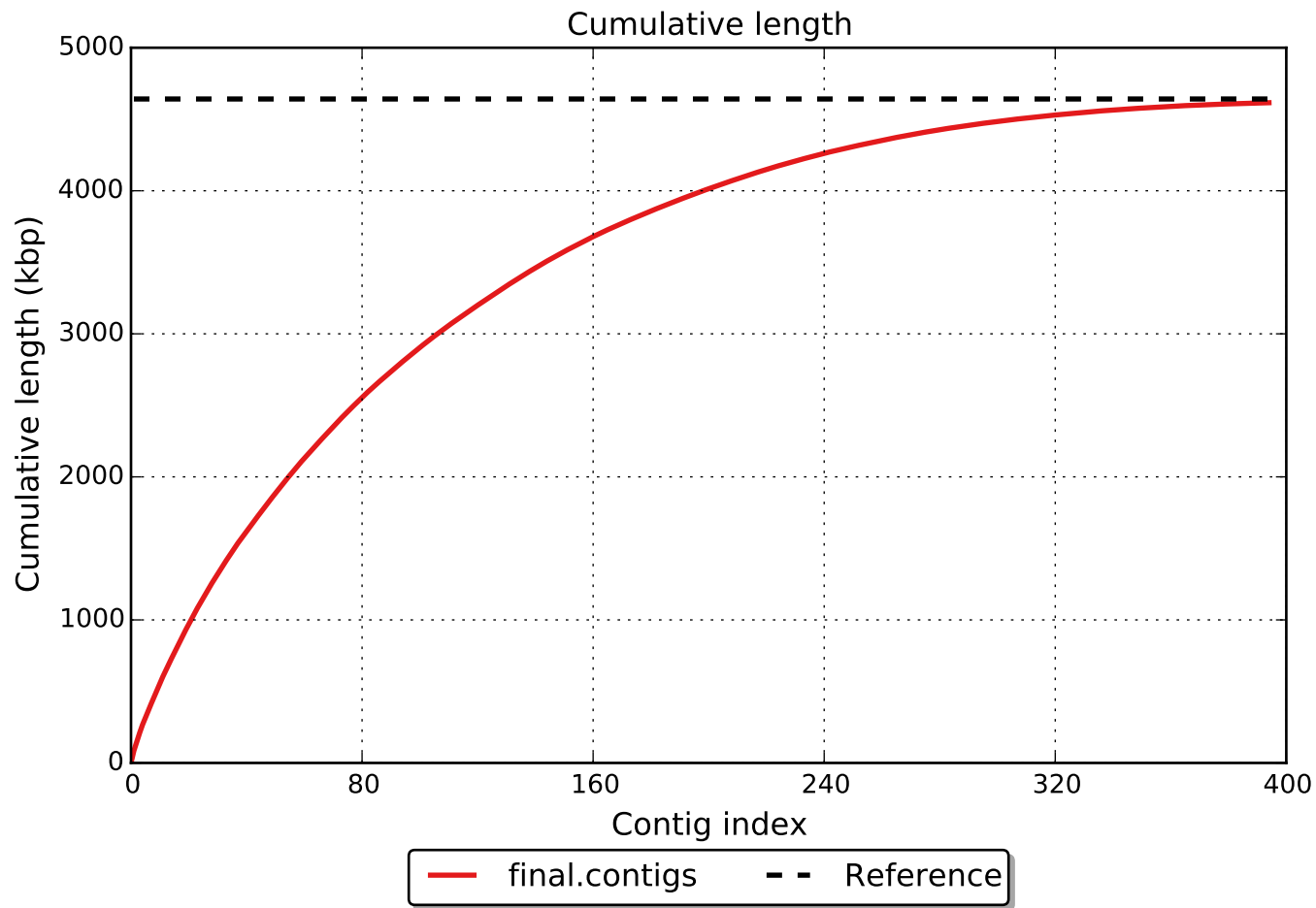
	final.contigs
# fully unaligned contigs	9
Fully unaligned length	6369
# partially unaligned contigs	4
# with misassembly	0
# both parts are significant	2
Partially unaligned length	7687
# N's	0

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).

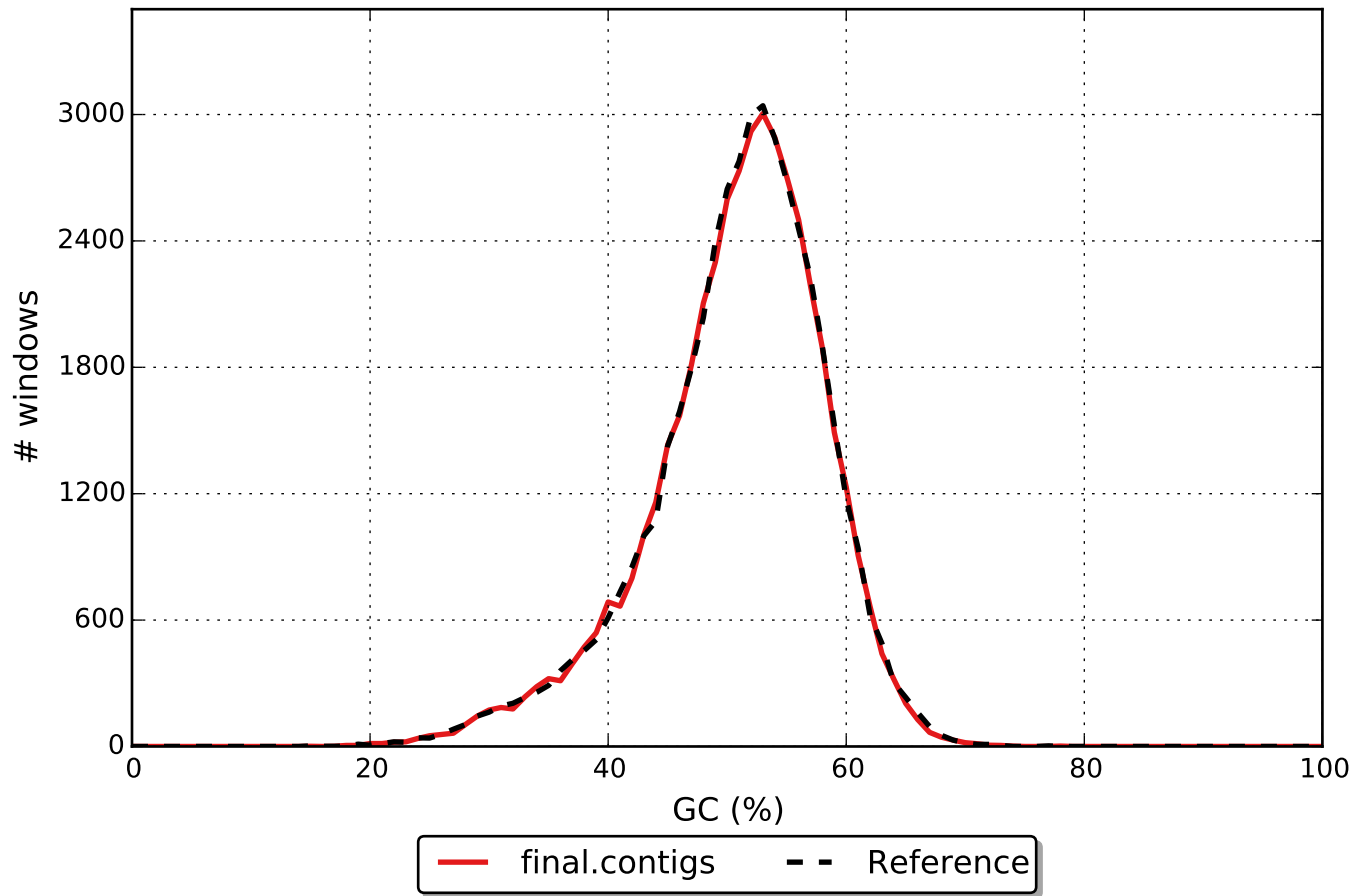


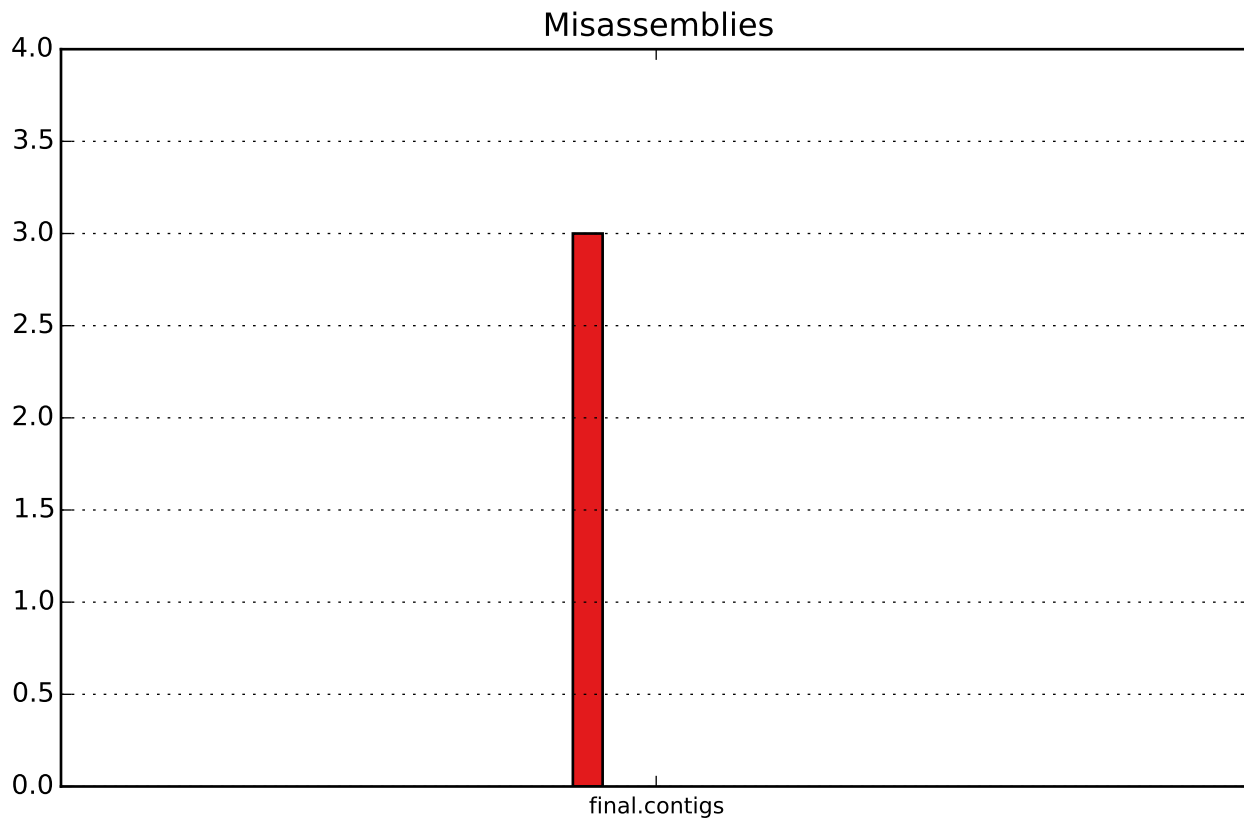
NGx



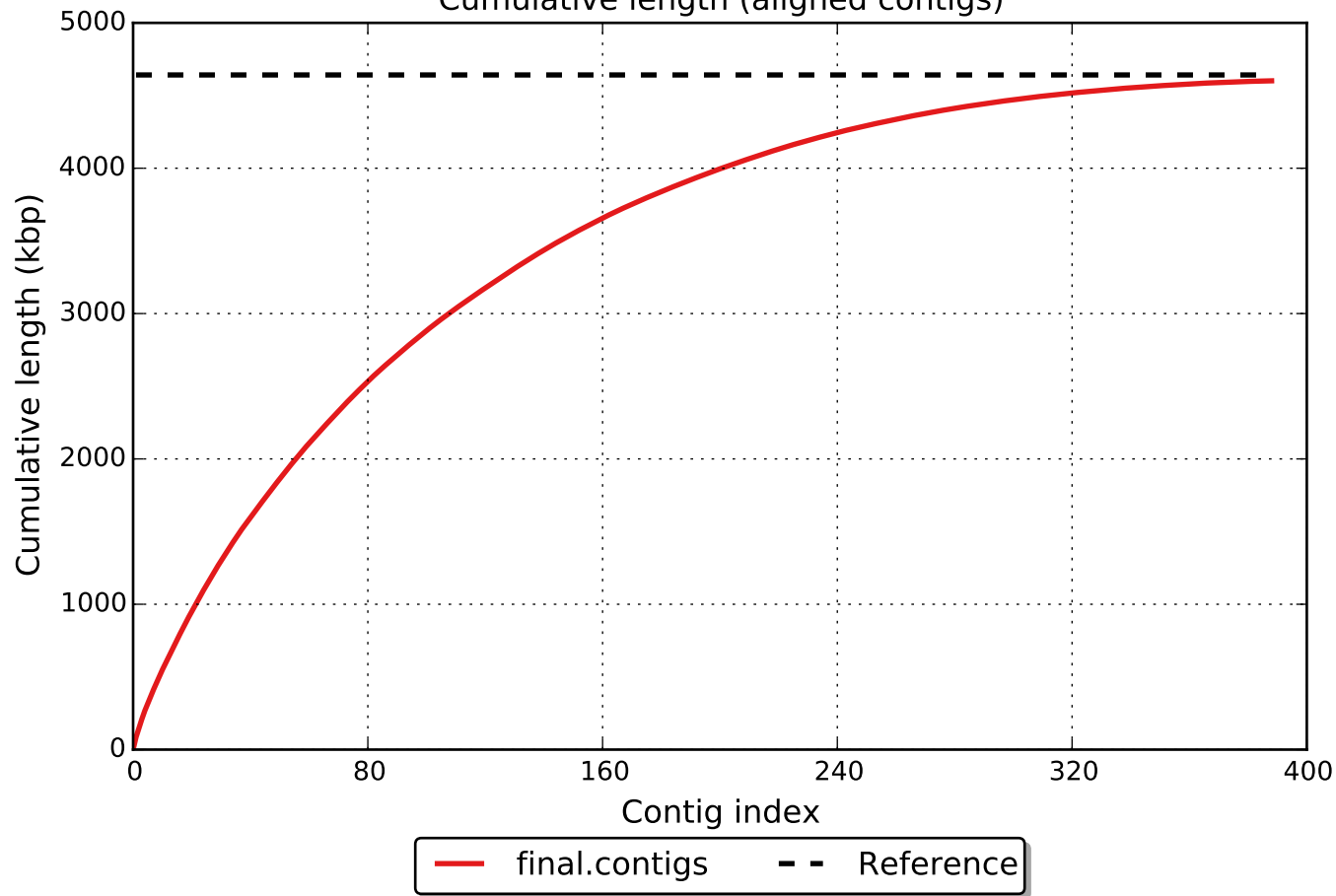


GC content

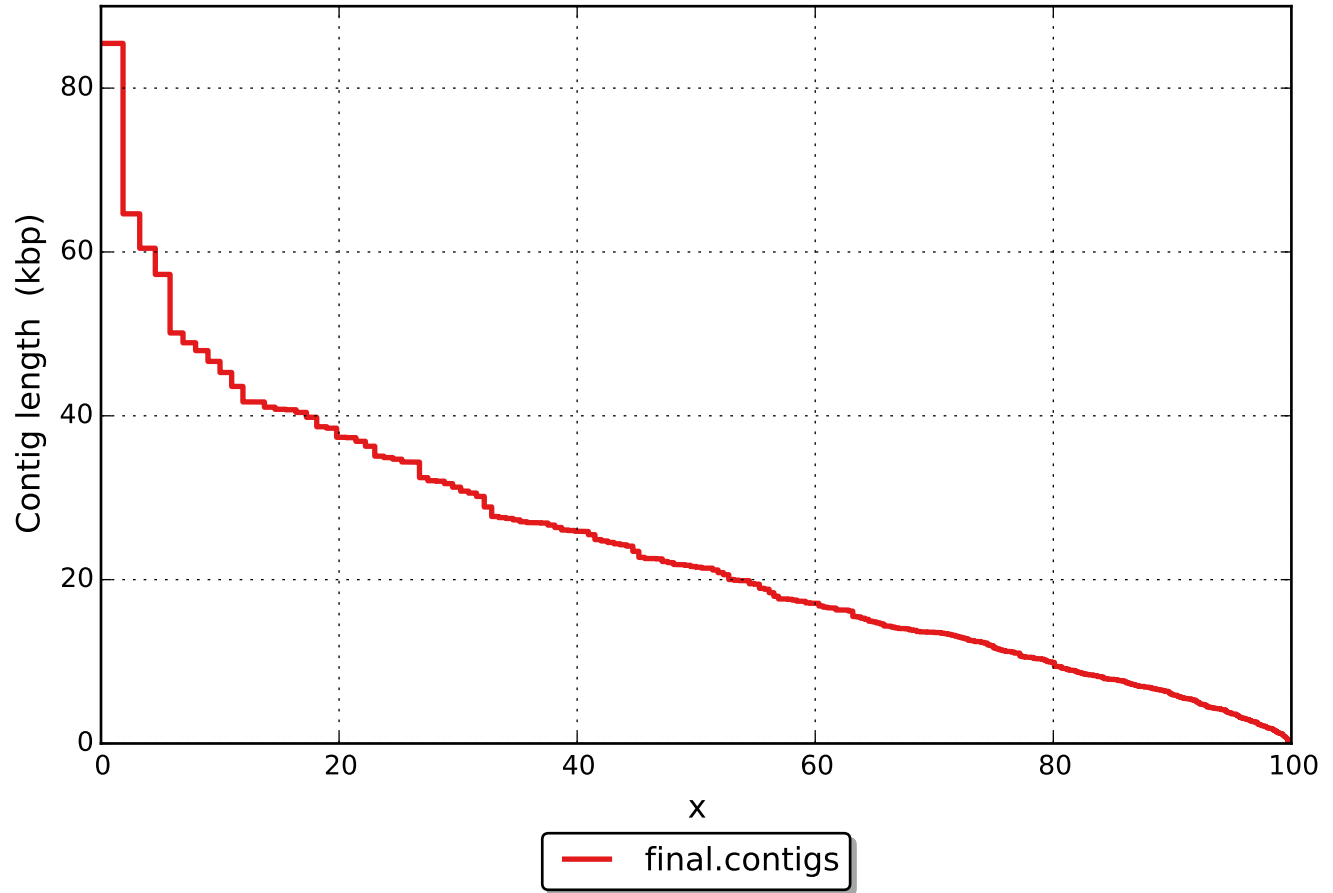




Cumulative length (aligned contigs)



NAx



NGAx

