

Report

	contigs
# contigs (≥ 0 bp)	12534
# contigs (≥ 1000 bp)	9
# contigs (≥ 5000 bp)	0
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	3356364
Total length (≥ 1000 bp)	19577
Total length (≥ 5000 bp)	0
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	117
Largest contig	4442
Total length	83219
Reference length	4641652
GC (%)	50.81
Reference GC (%)	50.79
N50	611
N75	538
L50	41
L75	77
# misassemblies	6
# misassembled contigs	6
Misassembled contigs length	8723
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	1.778
Duplication ratio	1.008
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1974.73
# indels per 100 kbp	1.21
Largest alignment	4442
NA50	605
NGA50	-
NA75	535
LA50	43
LA75	79

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

	contigs
# misassemblies	6
# relocations	6
# translocations	0
# inversions	0
# misassembled contigs	6
Misassembled contigs length	8723
# local misassemblies	0
# mismatches	1630
# indels	1
# short indels	1
# long indels	0
Indels length	1

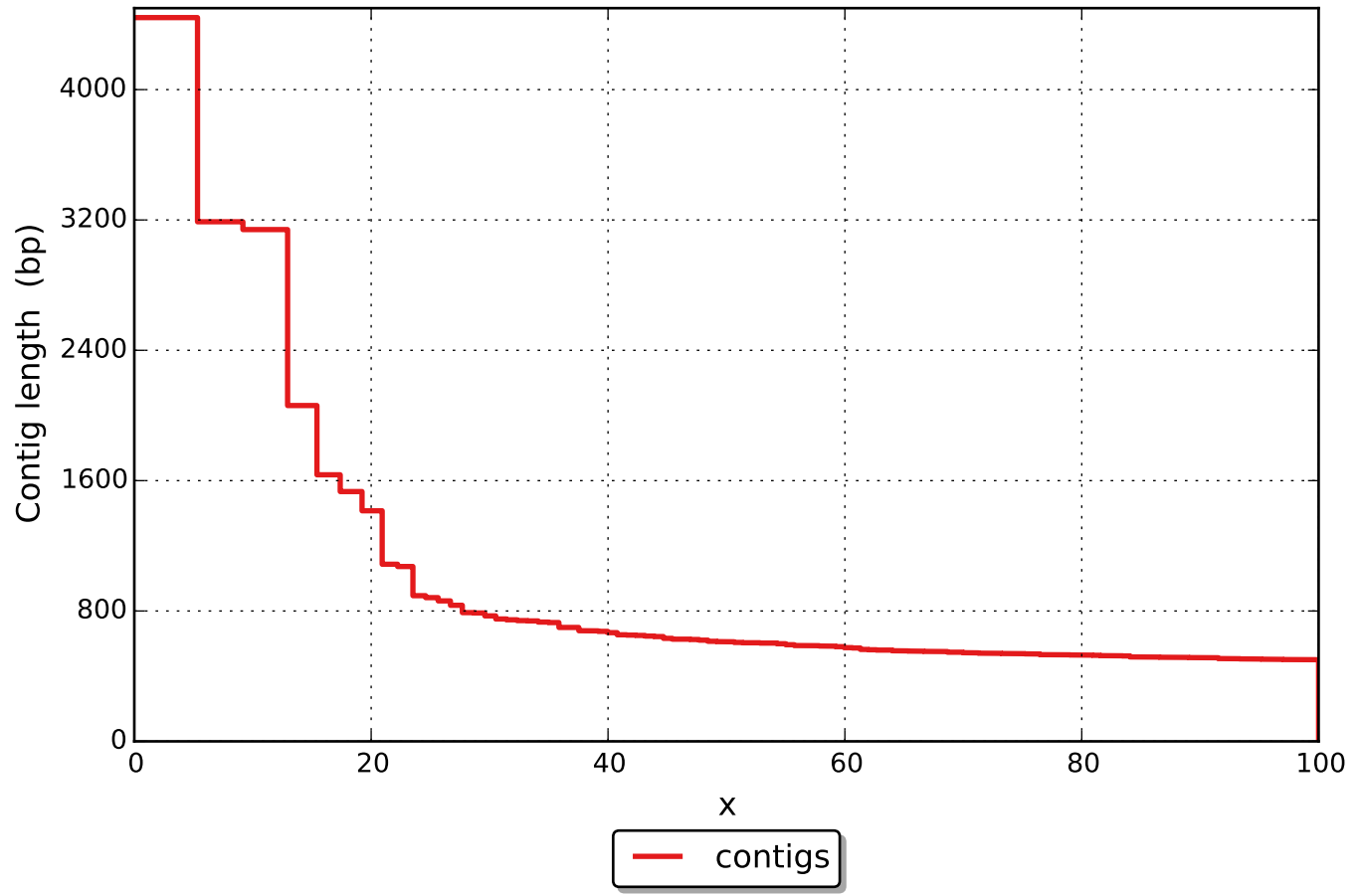
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

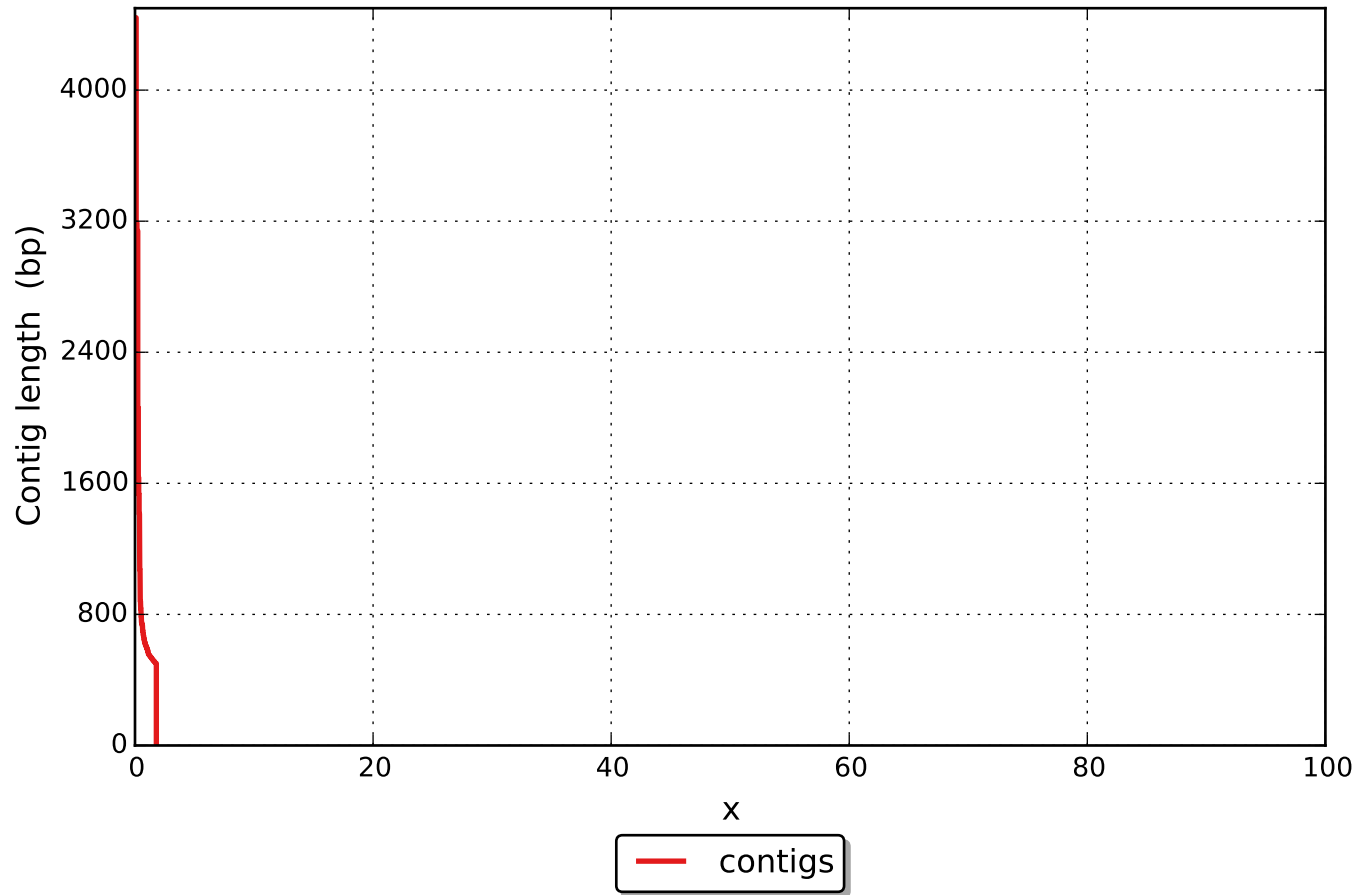
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

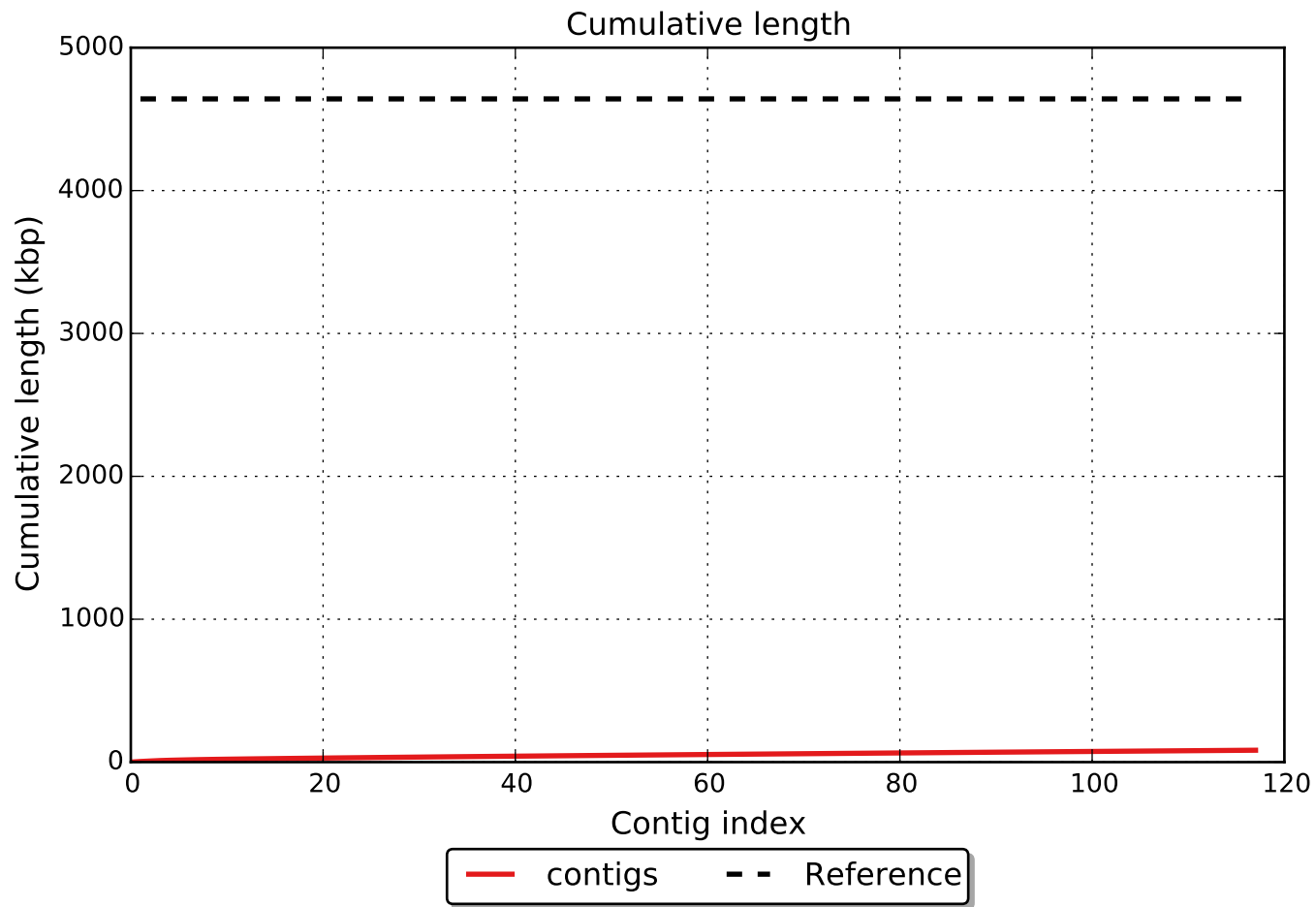
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

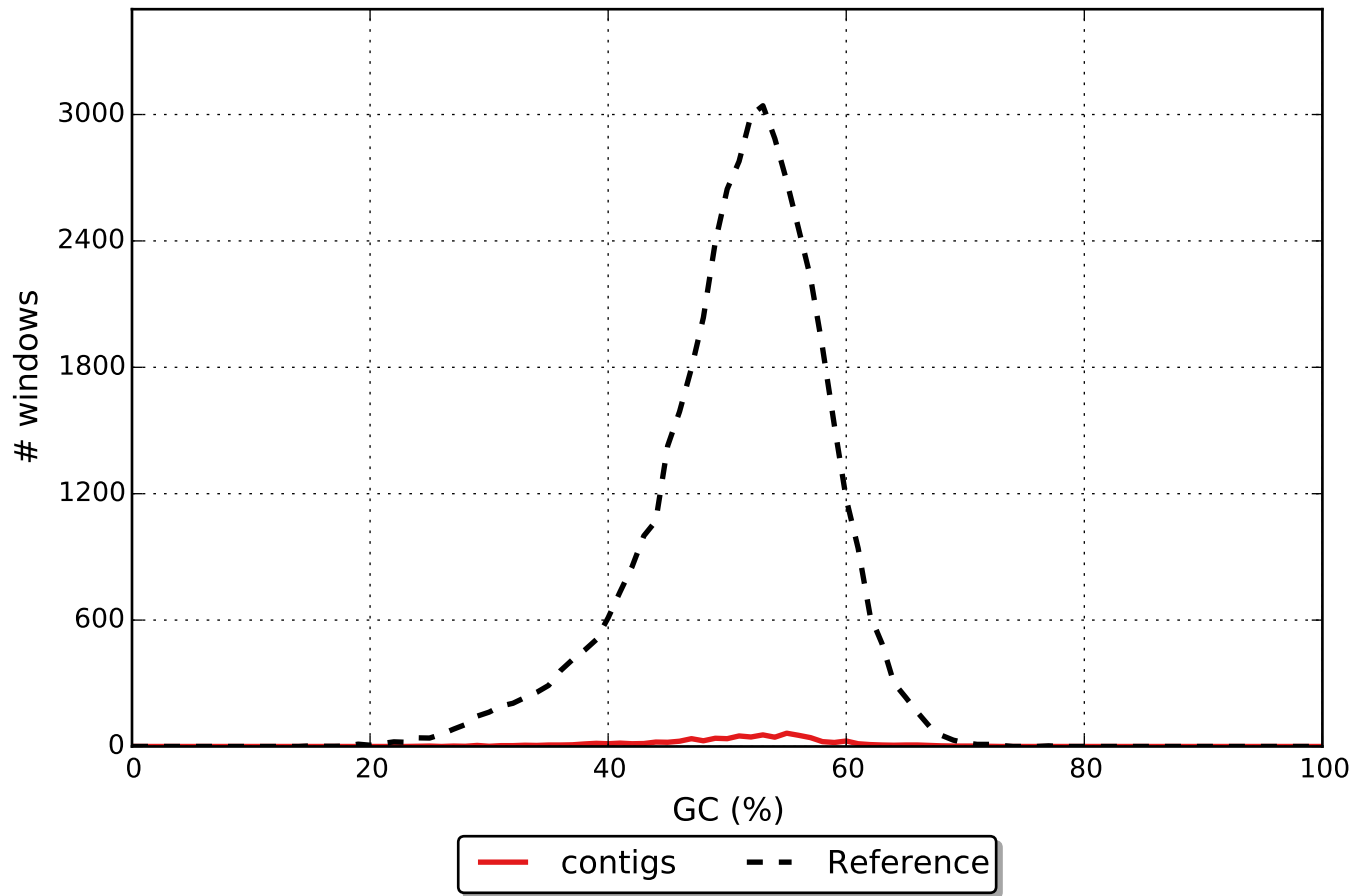


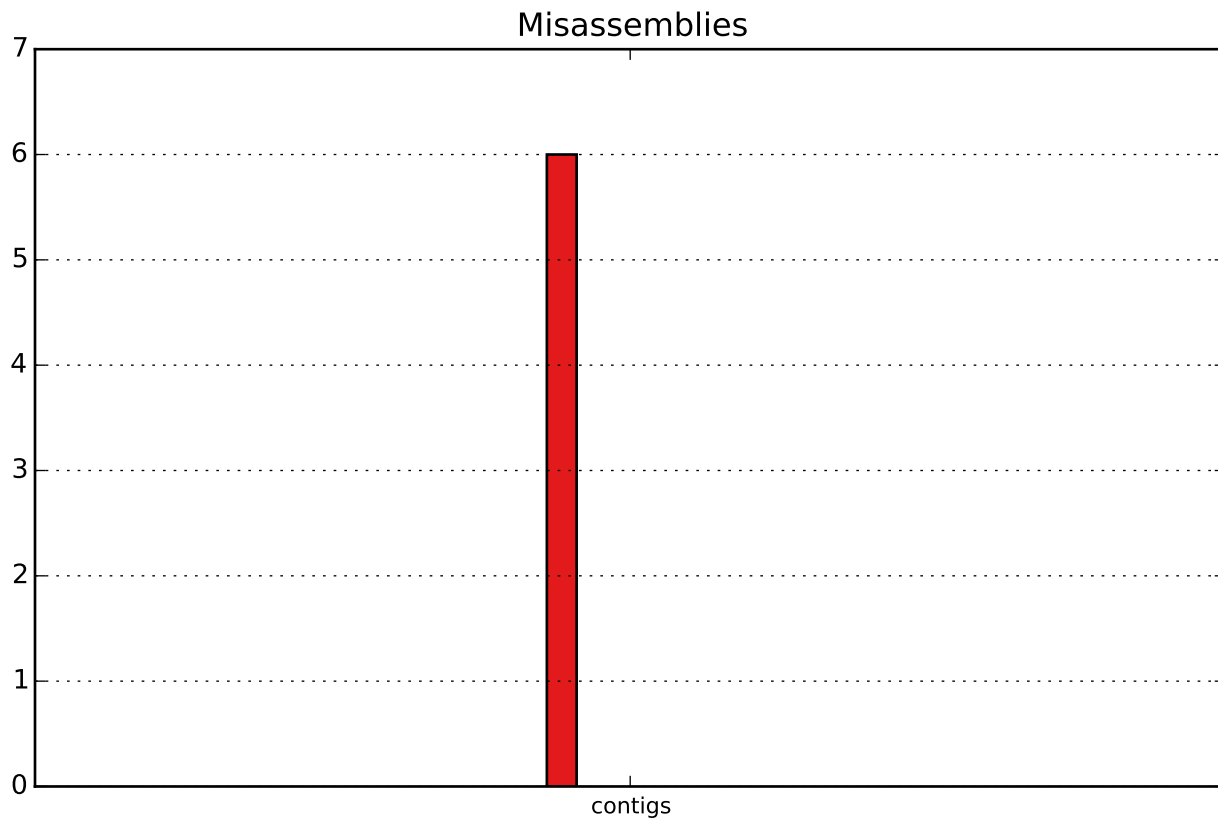
NGx



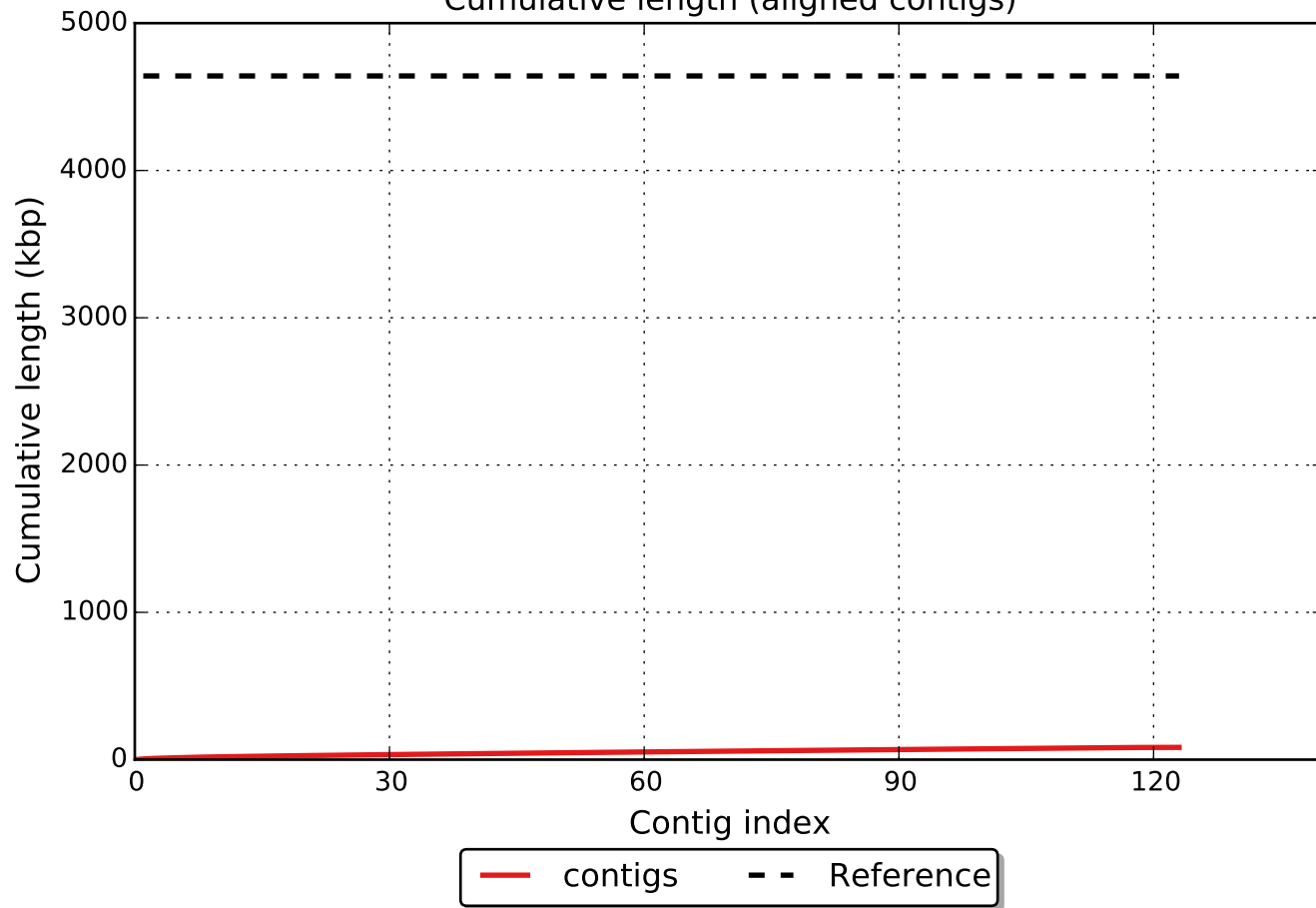


GC content

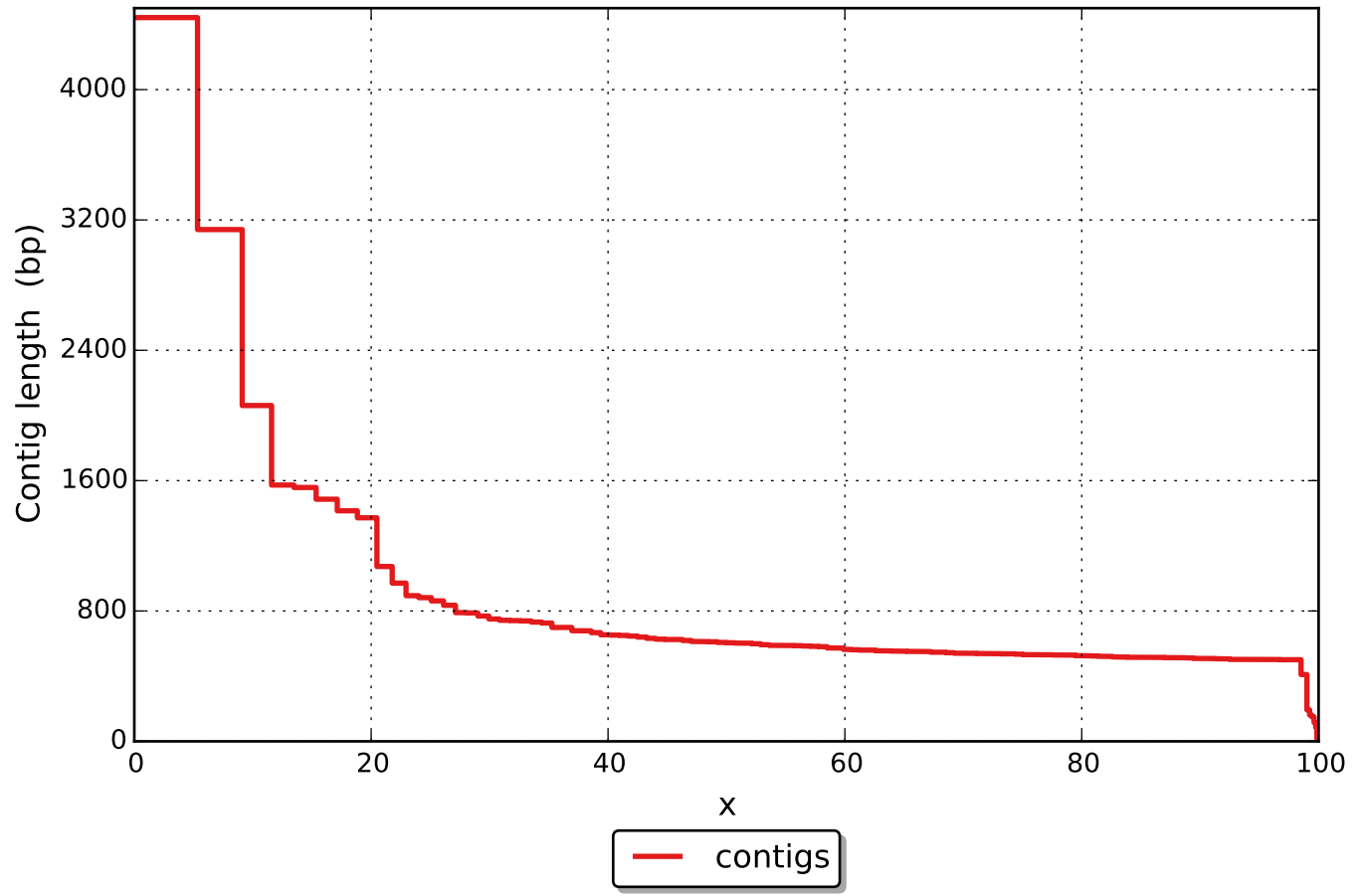




Cumulative length (aligned contigs)



NAx



NGAx

