

Report

	contigs
# contigs (≥ 1000 bp)	108
# contigs (≥ 5000 bp)	80
# contigs (≥ 10000 bp)	53
# contigs (≥ 25000 bp)	25
# contigs (≥ 50000 bp)	13
Total length (≥ 1000 bp)	2147463
Total length (≥ 5000 bp)	2060481
Total length (≥ 10000 bp)	1856831
Total length (≥ 25000 bp)	1443351
Total length (≥ 50000 bp)	1010886
# contigs	115
Largest contig	130415
Total length	2152378
Reference length	4641652
GC (%)	50.60
Reference GC (%)	50.78
N50	42832
N75	15611
L50	15
L75	34
# misassemblies	5
# misassembled contigs	4
Misassembled contigs length	339551
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	45.569
Duplication ratio	1.018
# N's per 100 kbp	0.00
# mismatches per 100 kbp	704.95
# indels per 100 kbp	0.47
Largest alignment	122264
NA50	39253
NGA50	-
NA75	13877
LA50	17
LA75	38

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	5
# relocations	5
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	4
Misassembled contigs length	339551
# local misassemblies	3
# mismatches	14911
# indels	10
# short indels	10
# long indels	0
Indels length	16

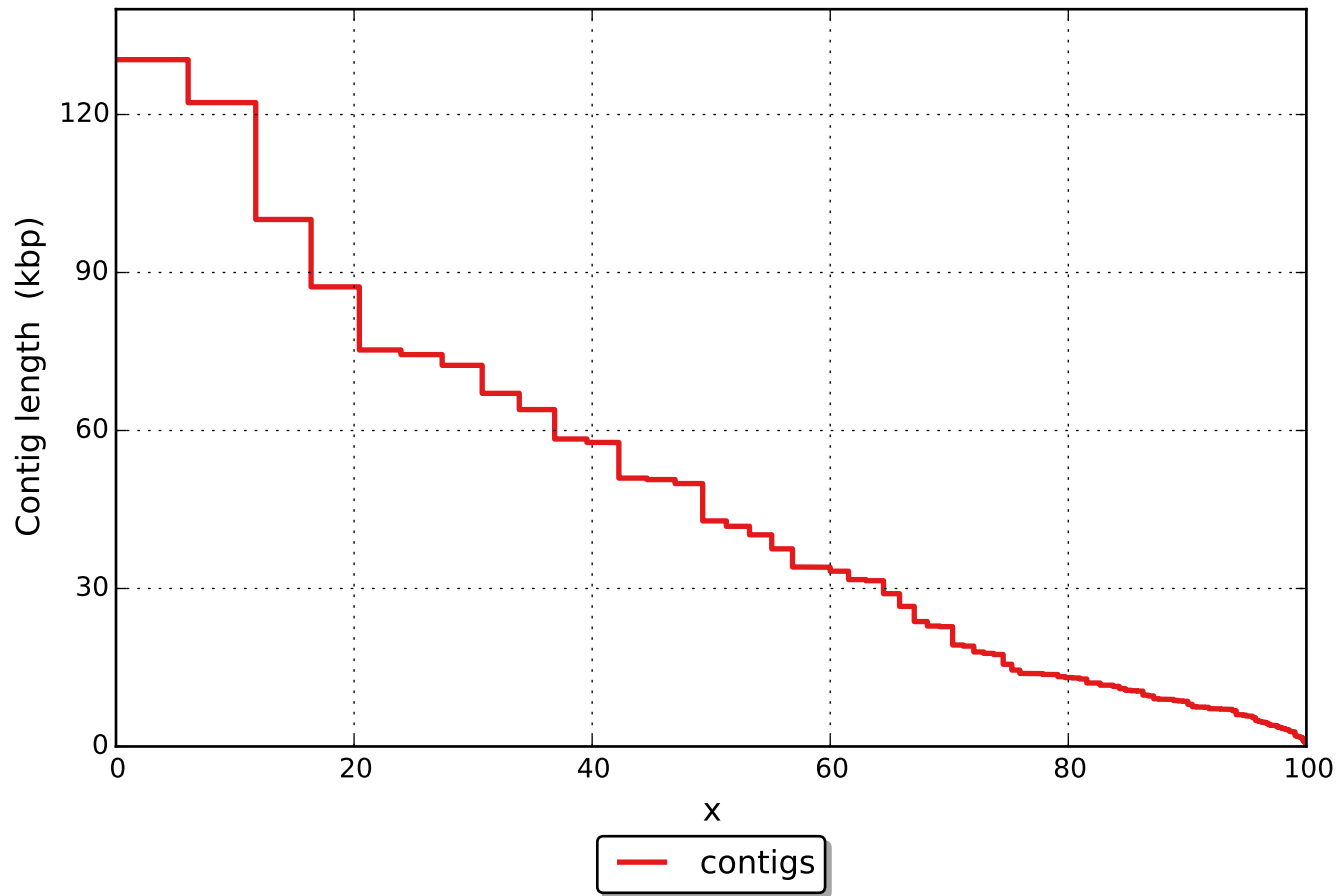
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

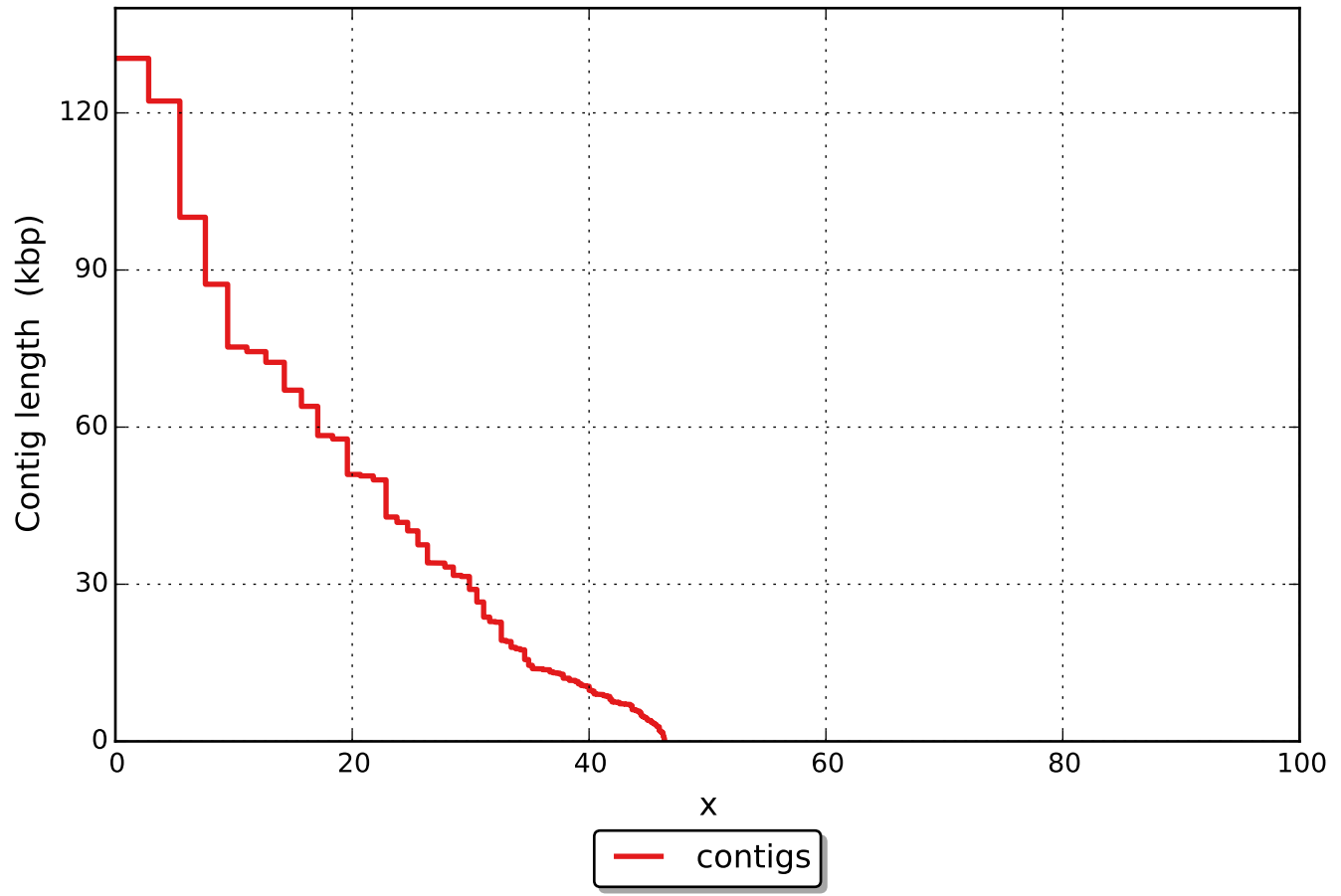
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

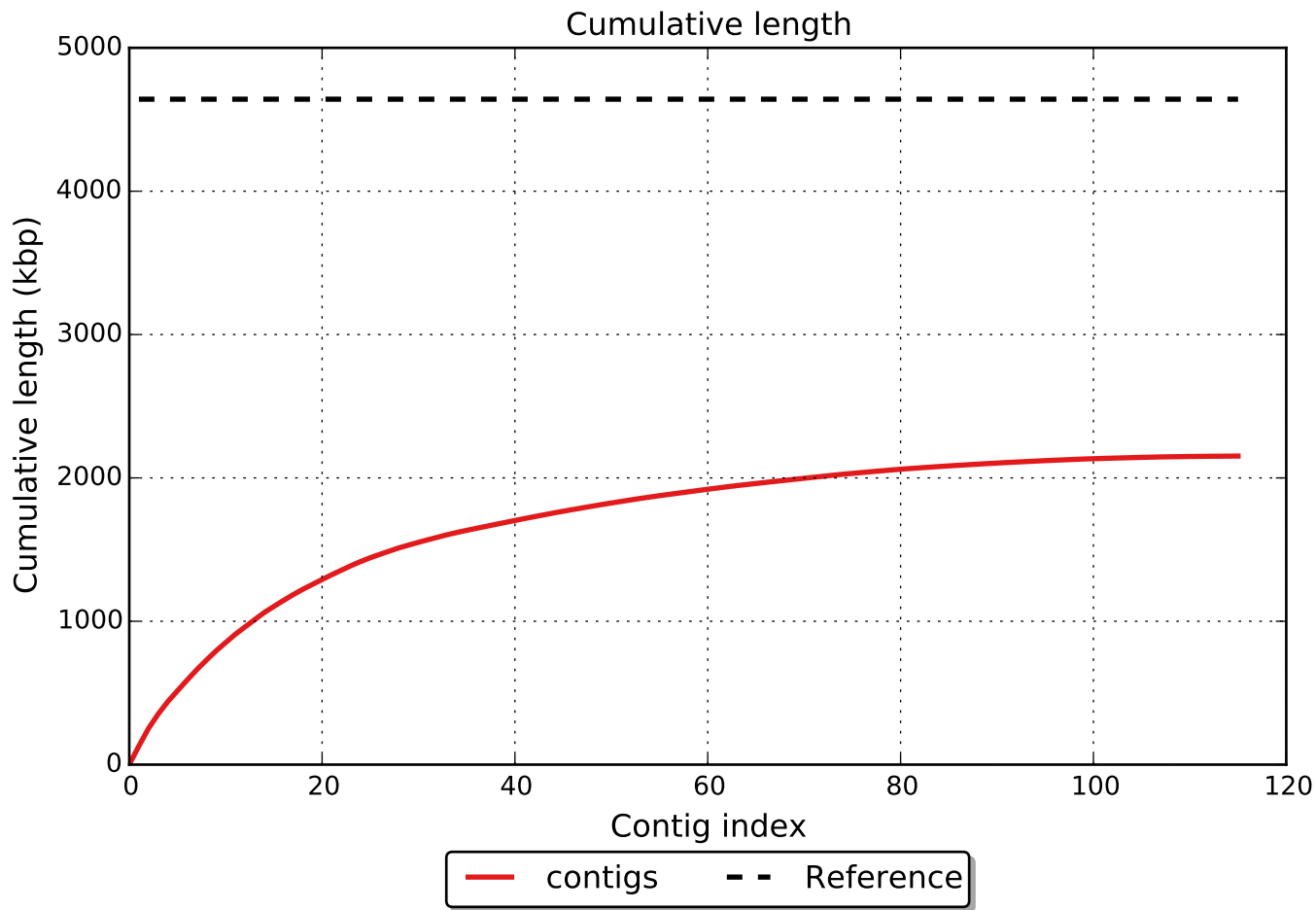
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

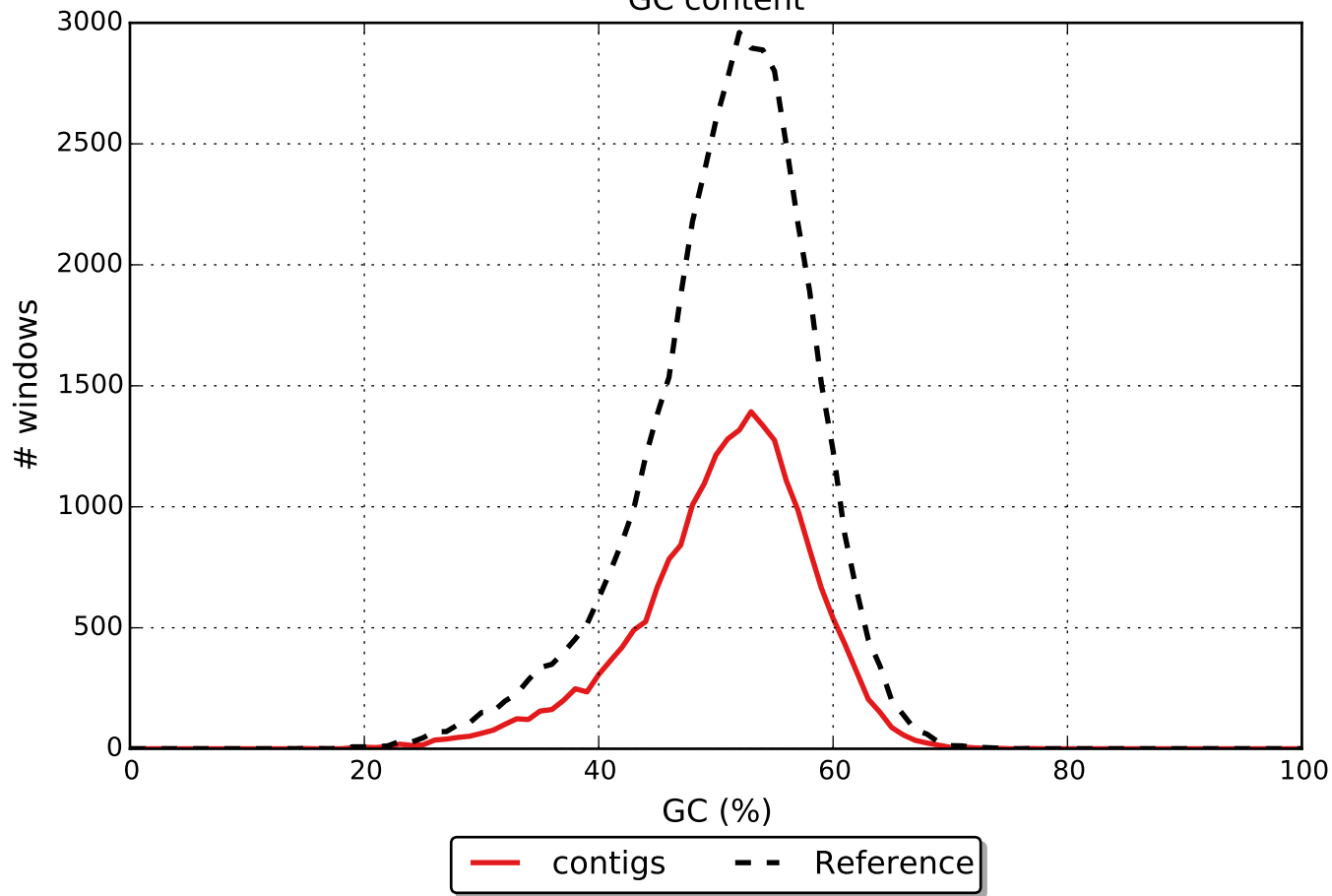


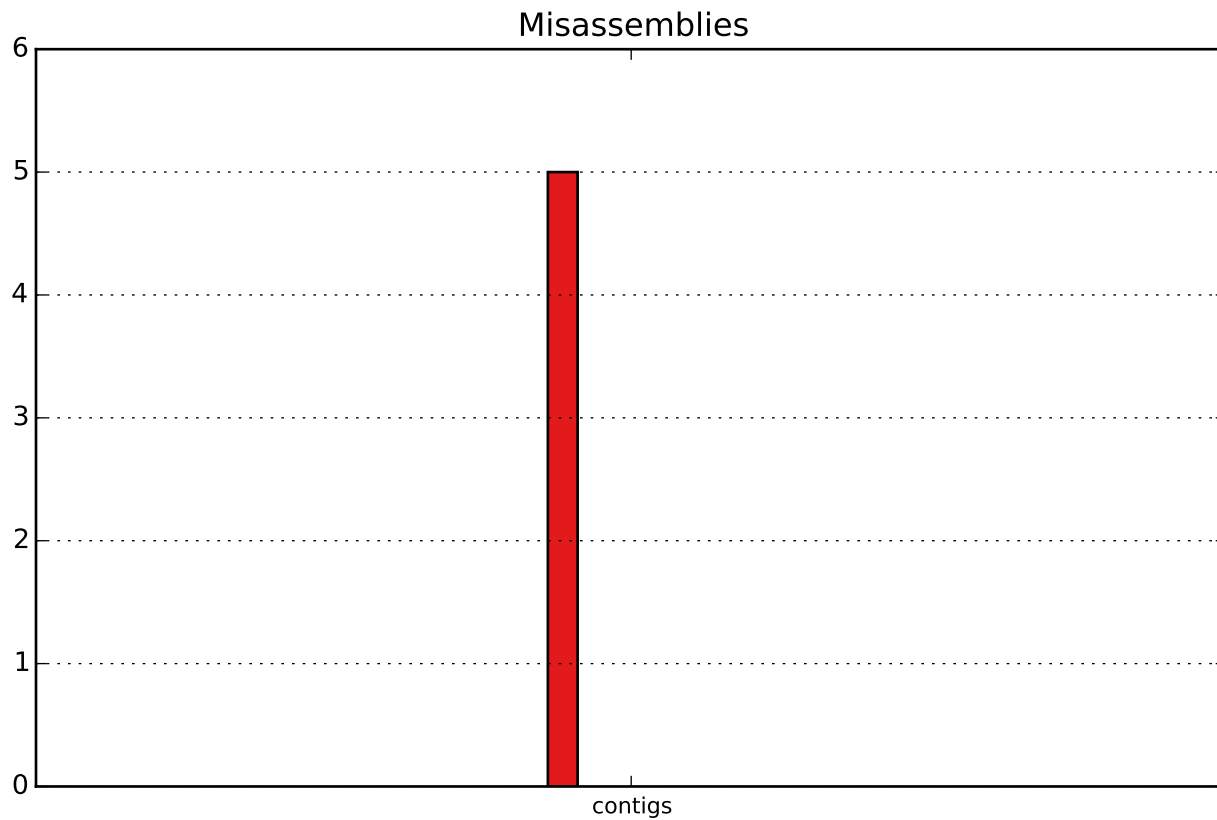
NGx



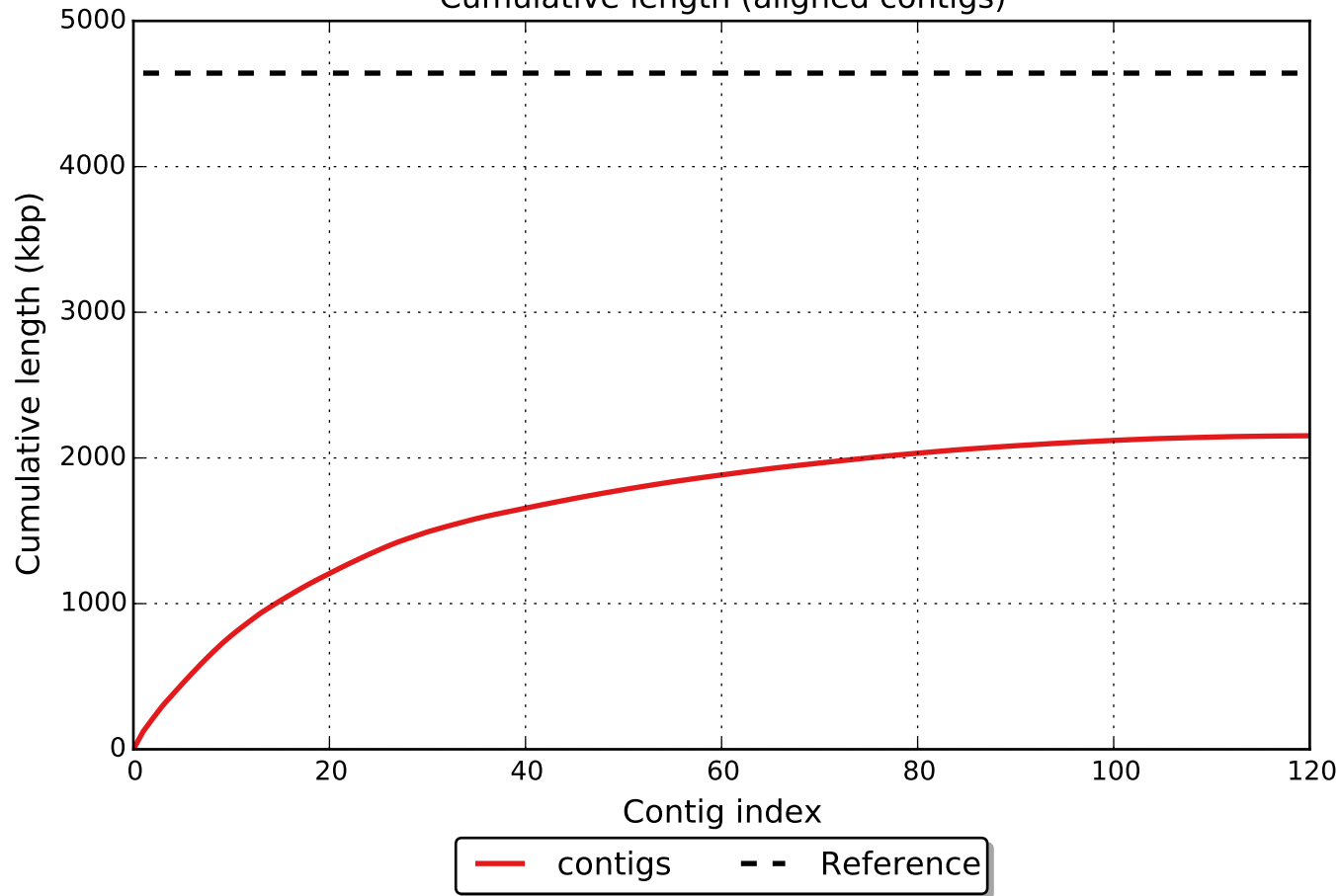


GC content

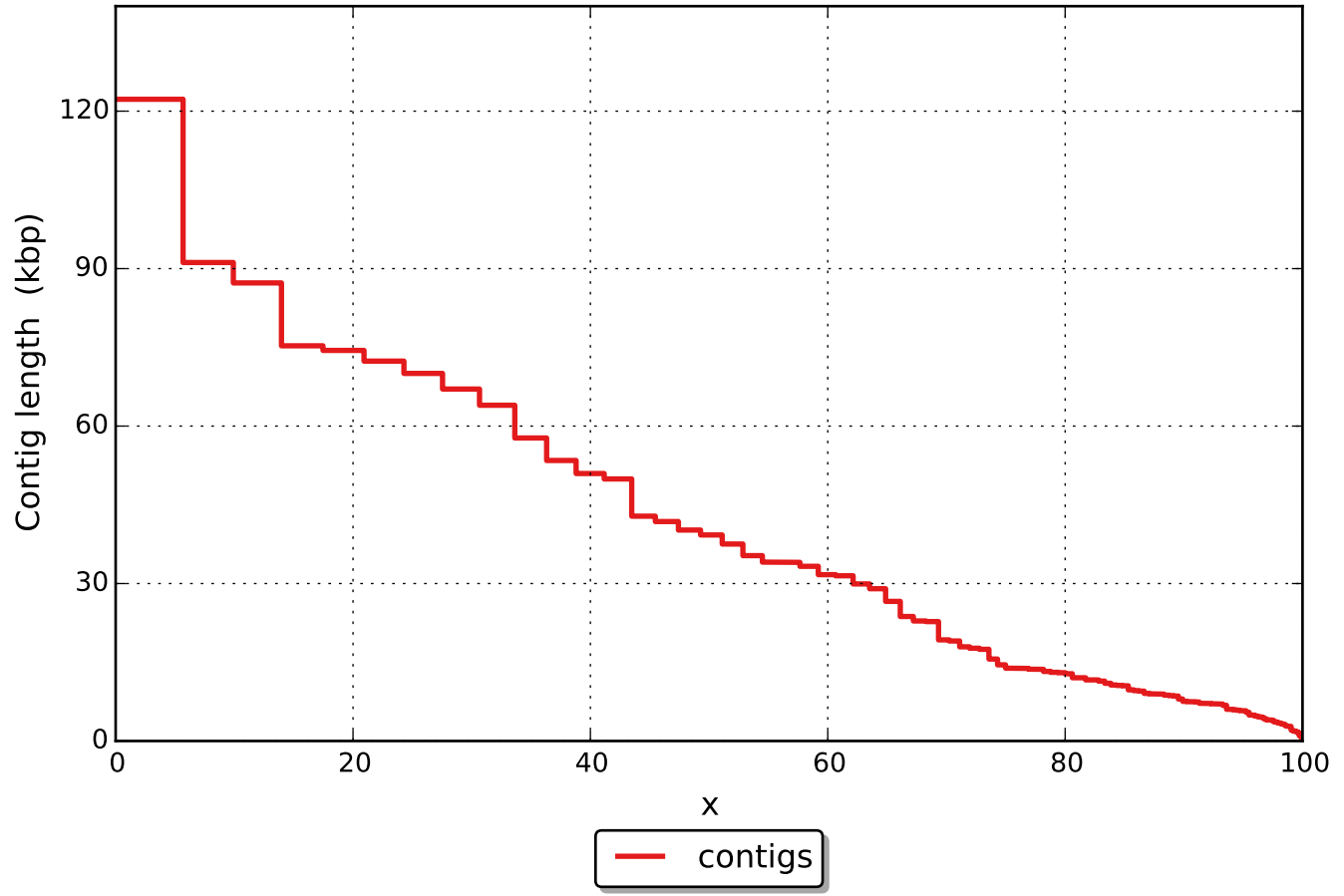




Cumulative length (aligned contigs)



NAx



NGAx

