

Report

	contigs
# contigs (≥ 1000 bp)	102
# contigs (≥ 5000 bp)	55
# contigs (≥ 10000 bp)	50
# contigs (≥ 25000 bp)	47
# contigs (≥ 50000 bp)	33
Total length (≥ 1000 bp)	4590072
Total length (≥ 5000 bp)	4493857
Total length (≥ 10000 bp)	4458336
Total length (≥ 25000 bp)	4400770
Total length (≥ 50000 bp)	3937426
# contigs	137
Largest contig	330092
Total length	4614346
Reference length	4641652
GC (%)	50.81
Reference GC (%)	50.79
N50	105688
NG50	105688
N75	78911
NG75	78911
L50	13
LG50	13
L75	26
LG75	26
# misassemblies	3
# misassembled contigs	2
Misassembled contigs length	198850
# local misassemblies	5
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	96.780
Duplication ratio	1.027
# N's per 100 kbp	0.00
# mismatches per 100 kbp	929.90
# indels per 100 kbp	0.89
Largest alignment	330092
NA50	102895
NGA50	102895
NA75	65960
NGA75	65960
LA50	13
LGA50	13
LA75	27
LGA75	27

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	3
# relocations	3
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	198850
# local misassemblies	5
# mismatches	41773
# indels	40
# short indels	40
# long indels	0
Indels length	49

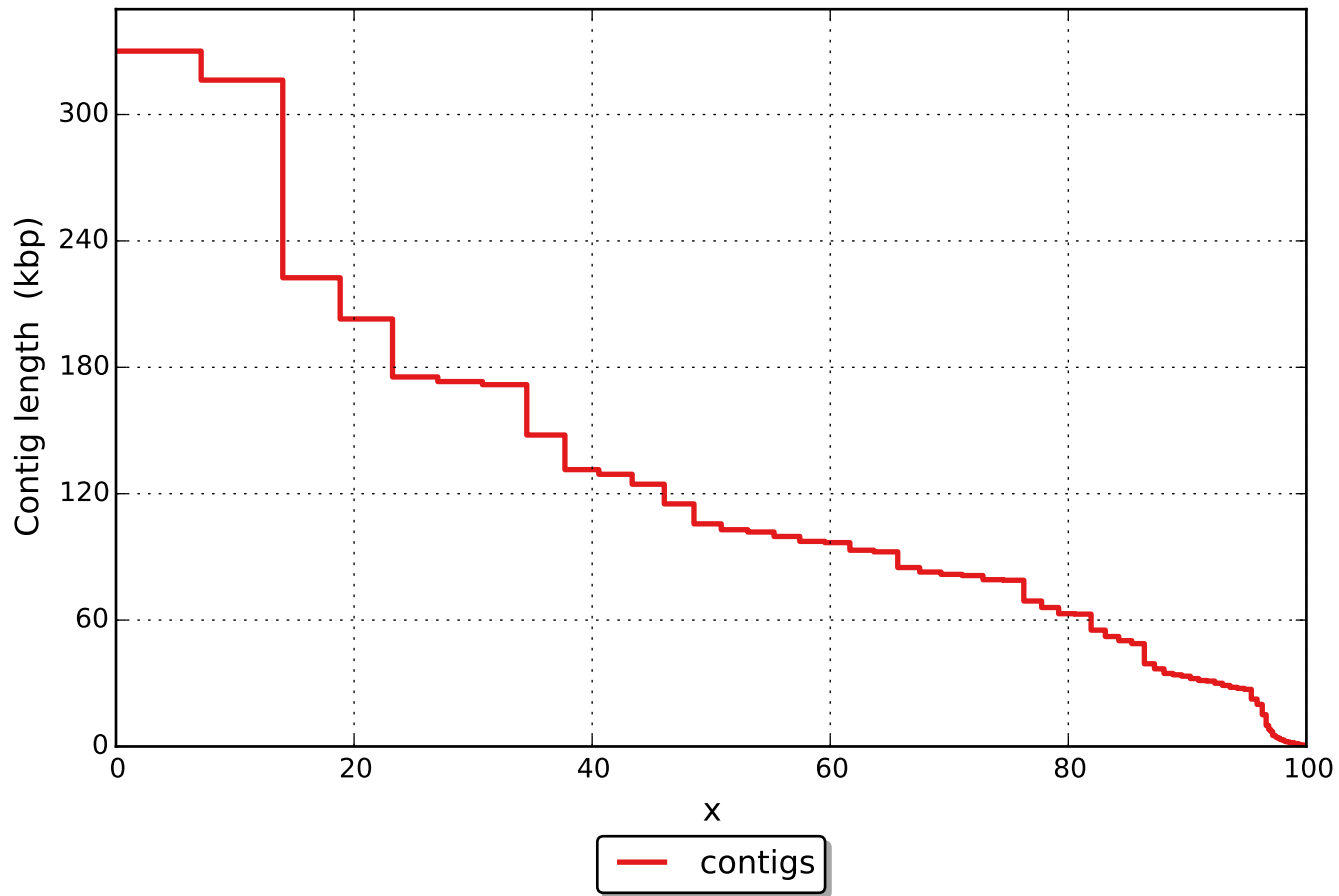
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

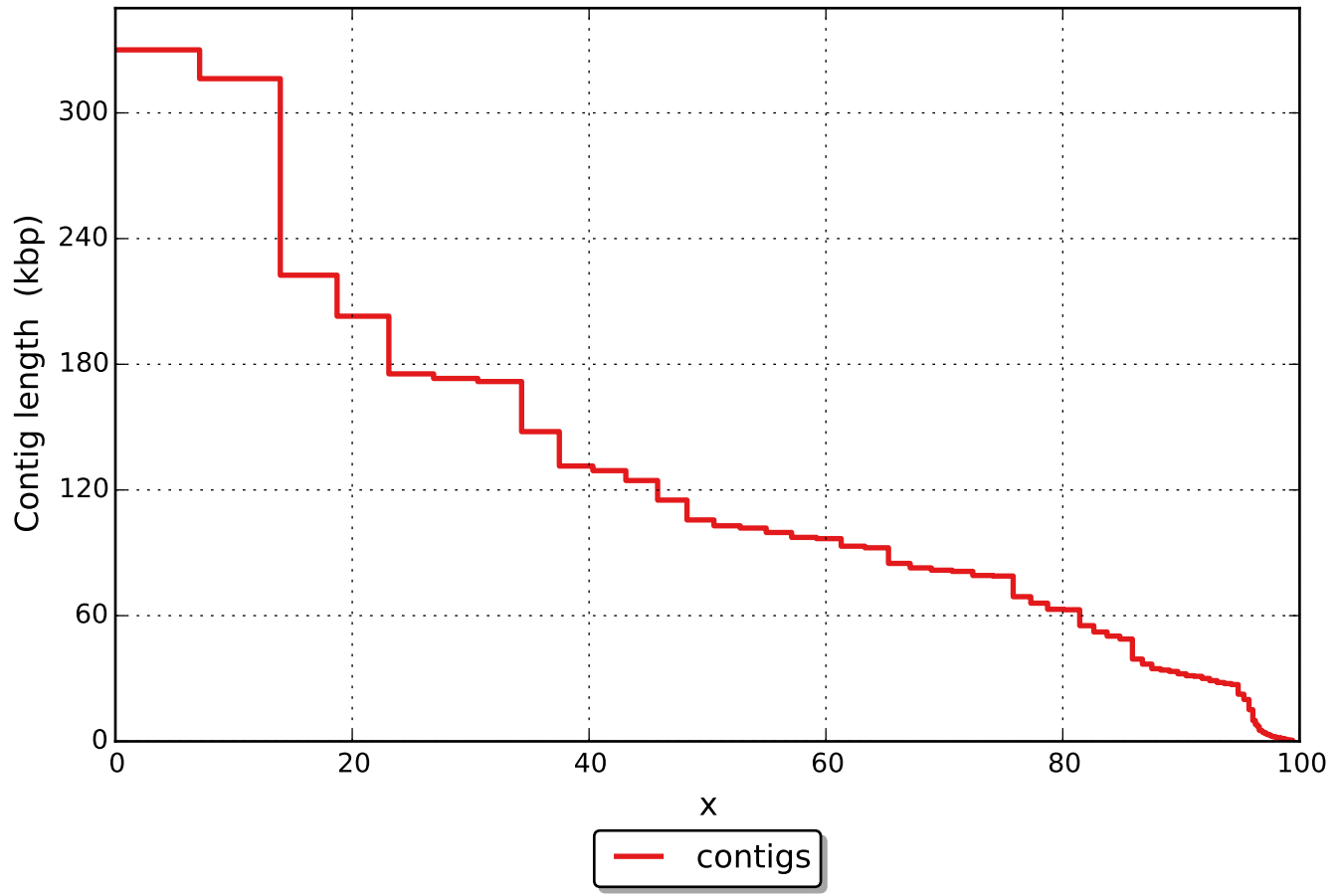
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

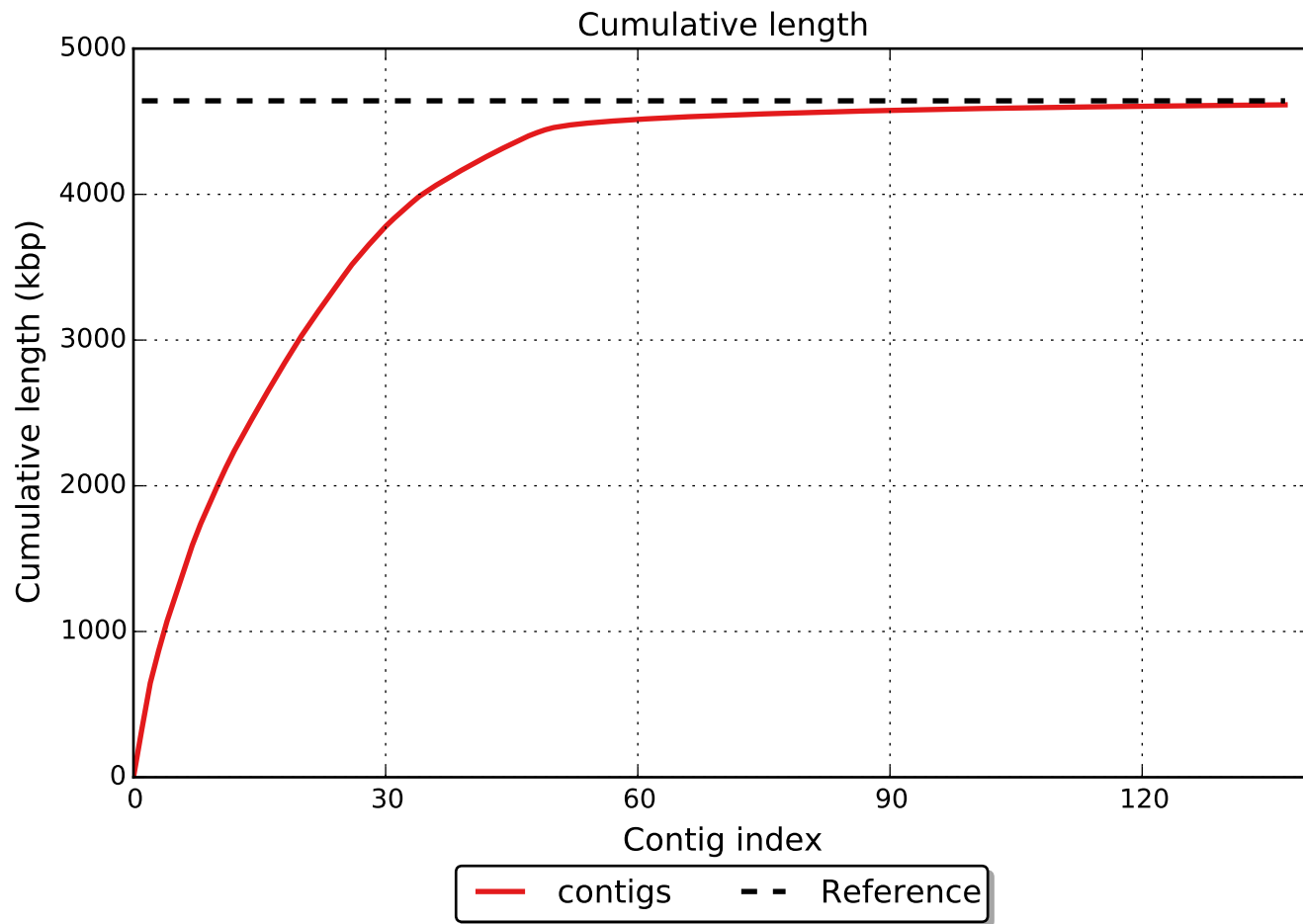
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

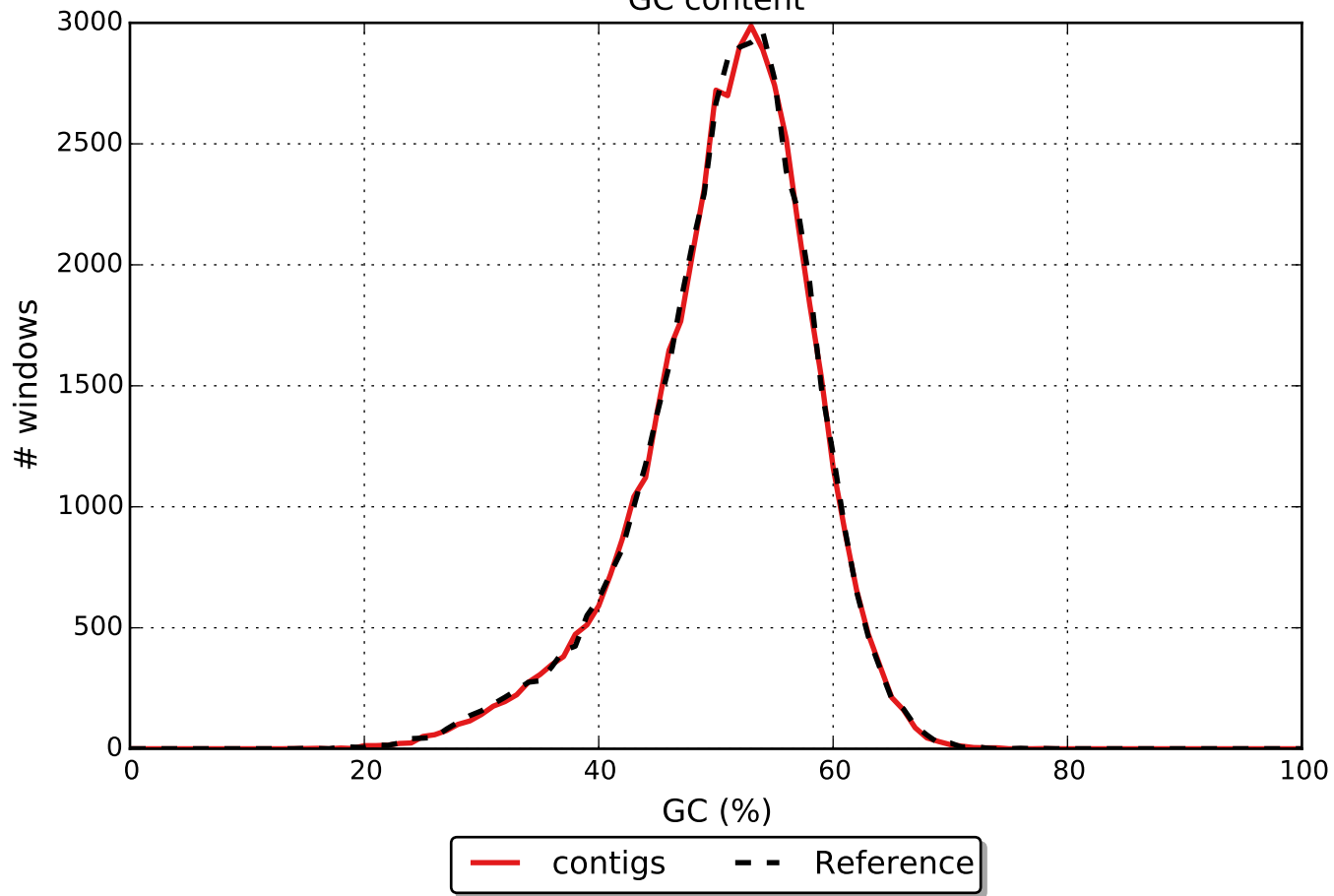


NGx

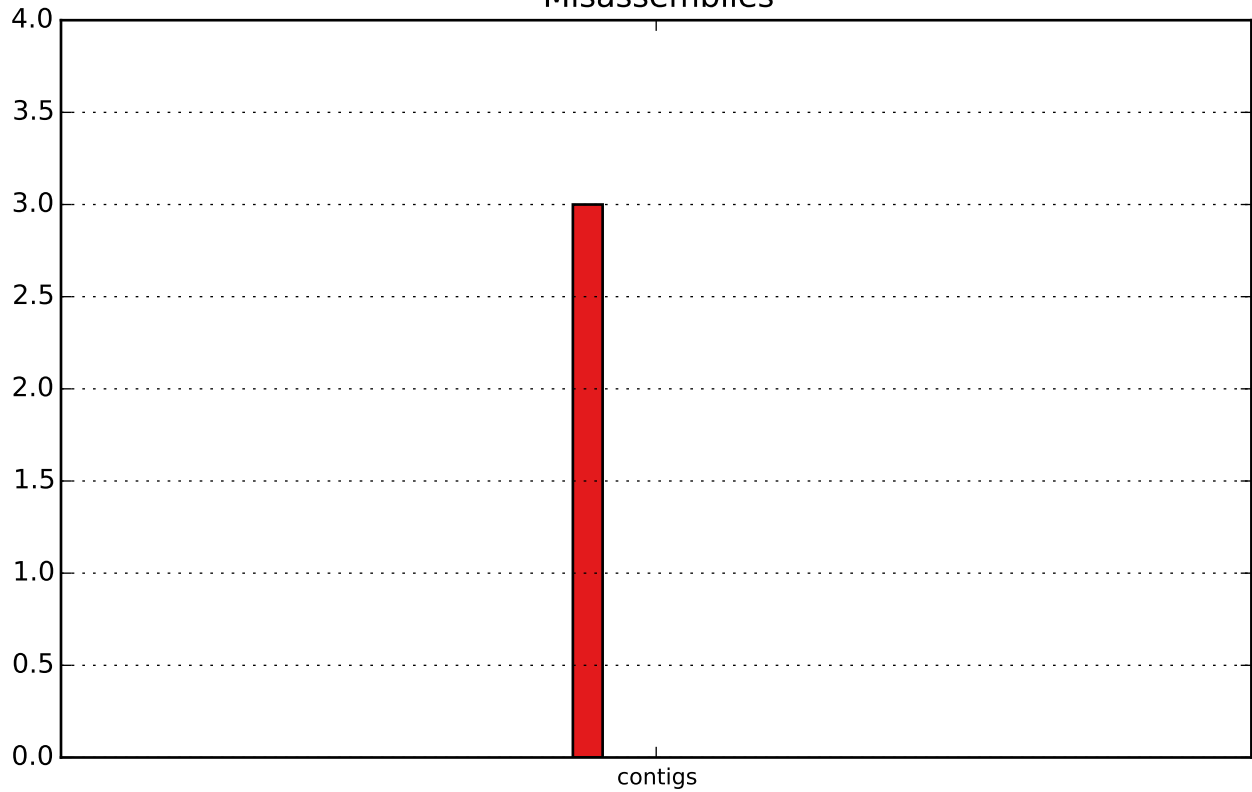




GC content

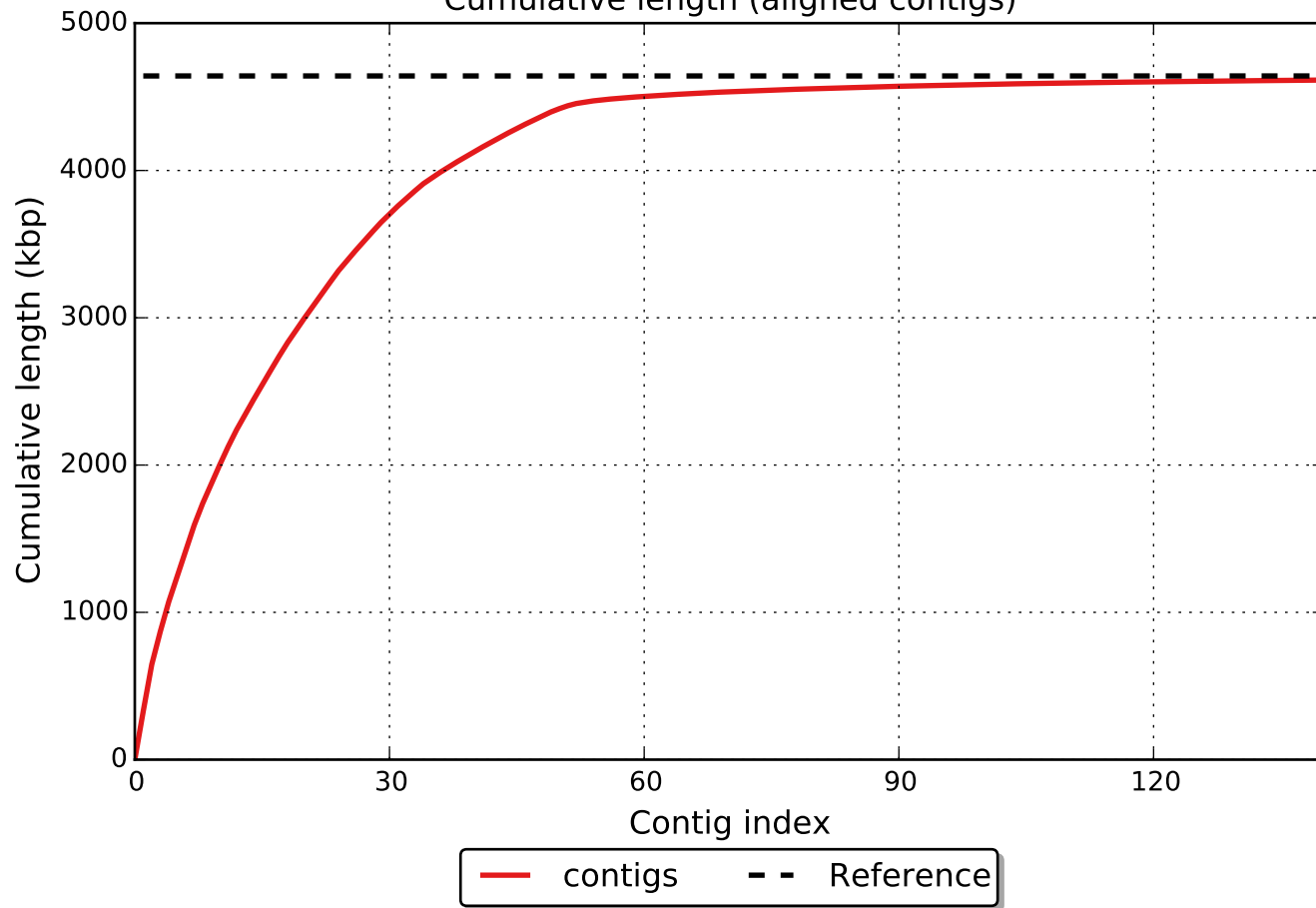


Misassemblies

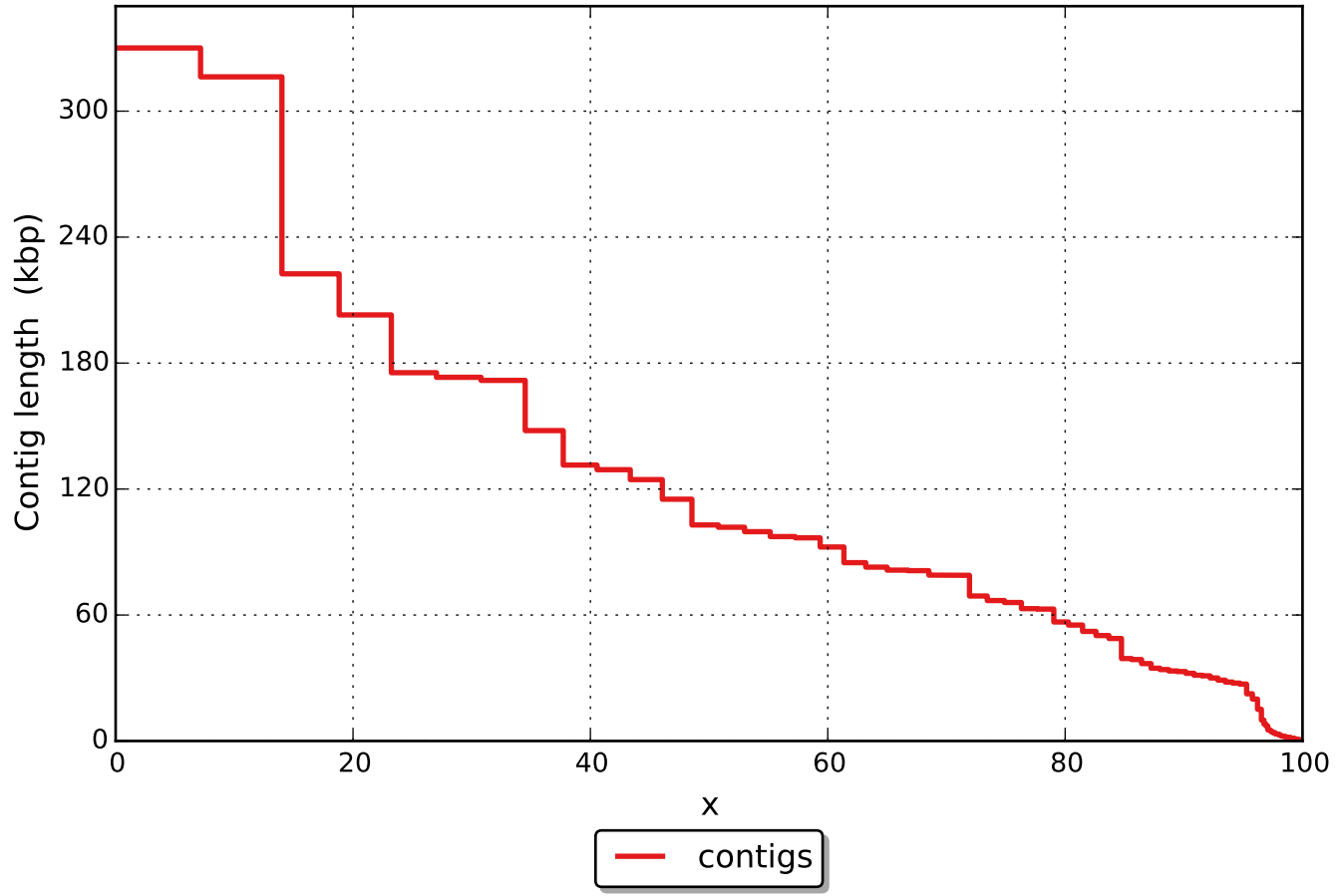


 # relocations

Cumulative length (aligned contigs)



NAx



NGAx

