

Report

	contigs
# contigs (≥ 0 bp)	129
# contigs (≥ 1000 bp)	70
# contigs (≥ 5000 bp)	53
# contigs (≥ 10000 bp)	48
# contigs (≥ 25000 bp)	42
# contigs (≥ 50000 bp)	27
Total length (≥ 0 bp)	4577834
Total length (≥ 1000 bp)	4558550
Total length (≥ 5000 bp)	4522512
Total length (≥ 10000 bp)	4487390
Total length (≥ 25000 bp)	4397600
Total length (≥ 50000 bp)	3870632
# contigs	81
Largest contig	327173
Total length	4566093
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	173566
NG50	133040
N75	87186
NG75	78649
L50	10
LG50	11
L75	20
LG75	21
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.304
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.07
# indels per 100 kbp	0.24
Largest alignment	327173
NA50	172028
NGA50	133040
NA75	87186
NGA75	78649
LA50	10
LGA50	11
LA75	20
LGA75	21

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	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	49
# indels	11
# short indels	11
# long indels	0
Indels length	12

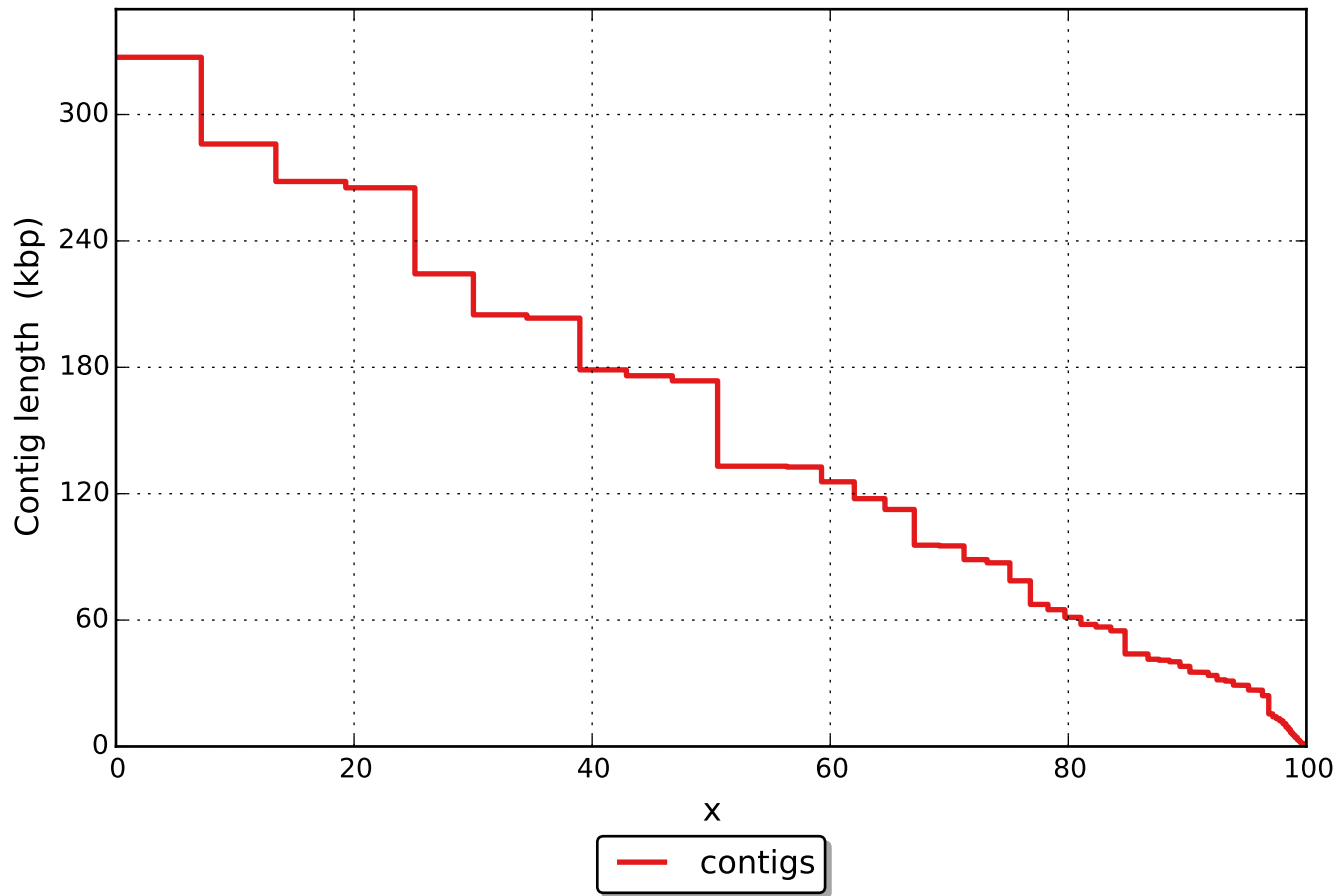
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

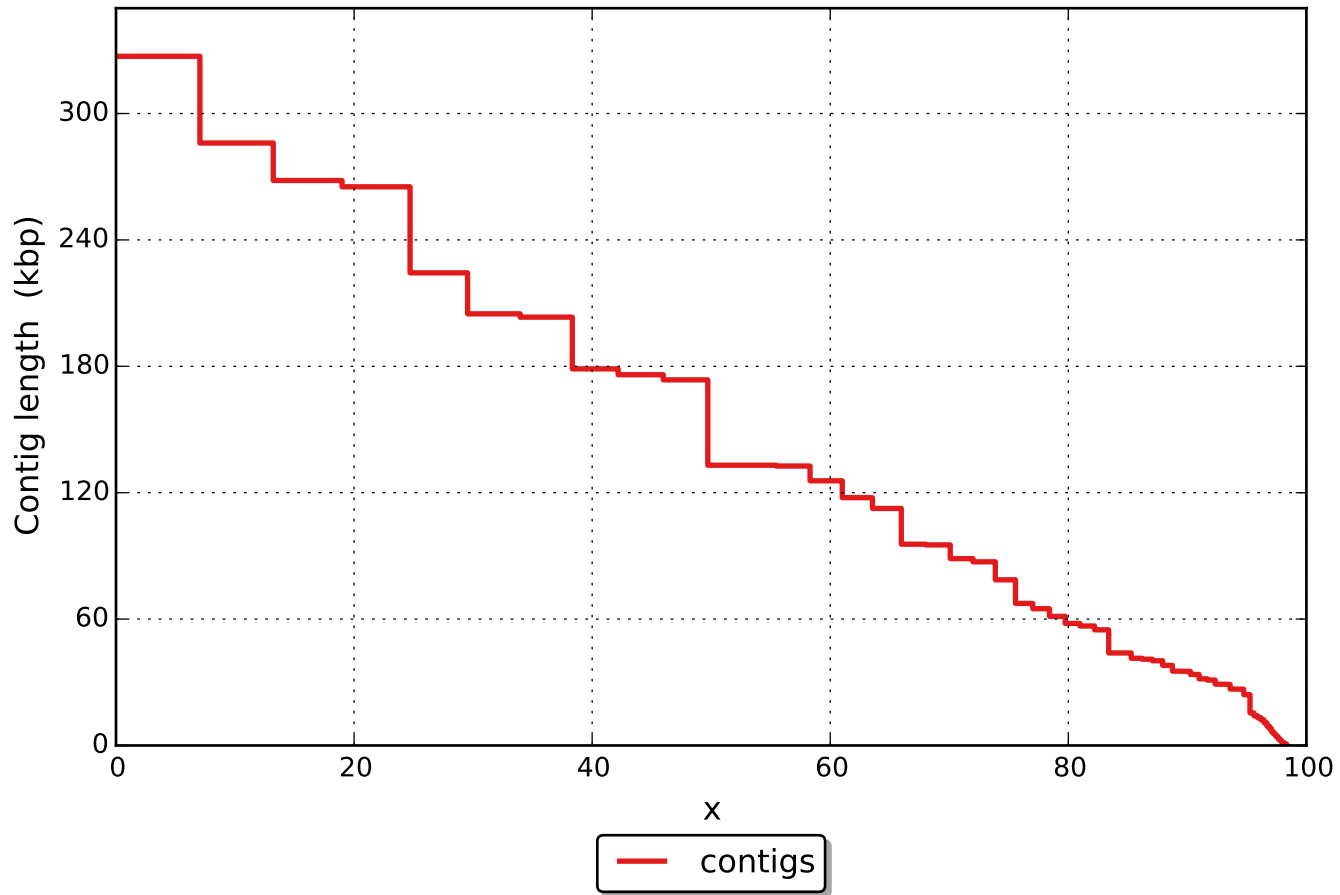
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

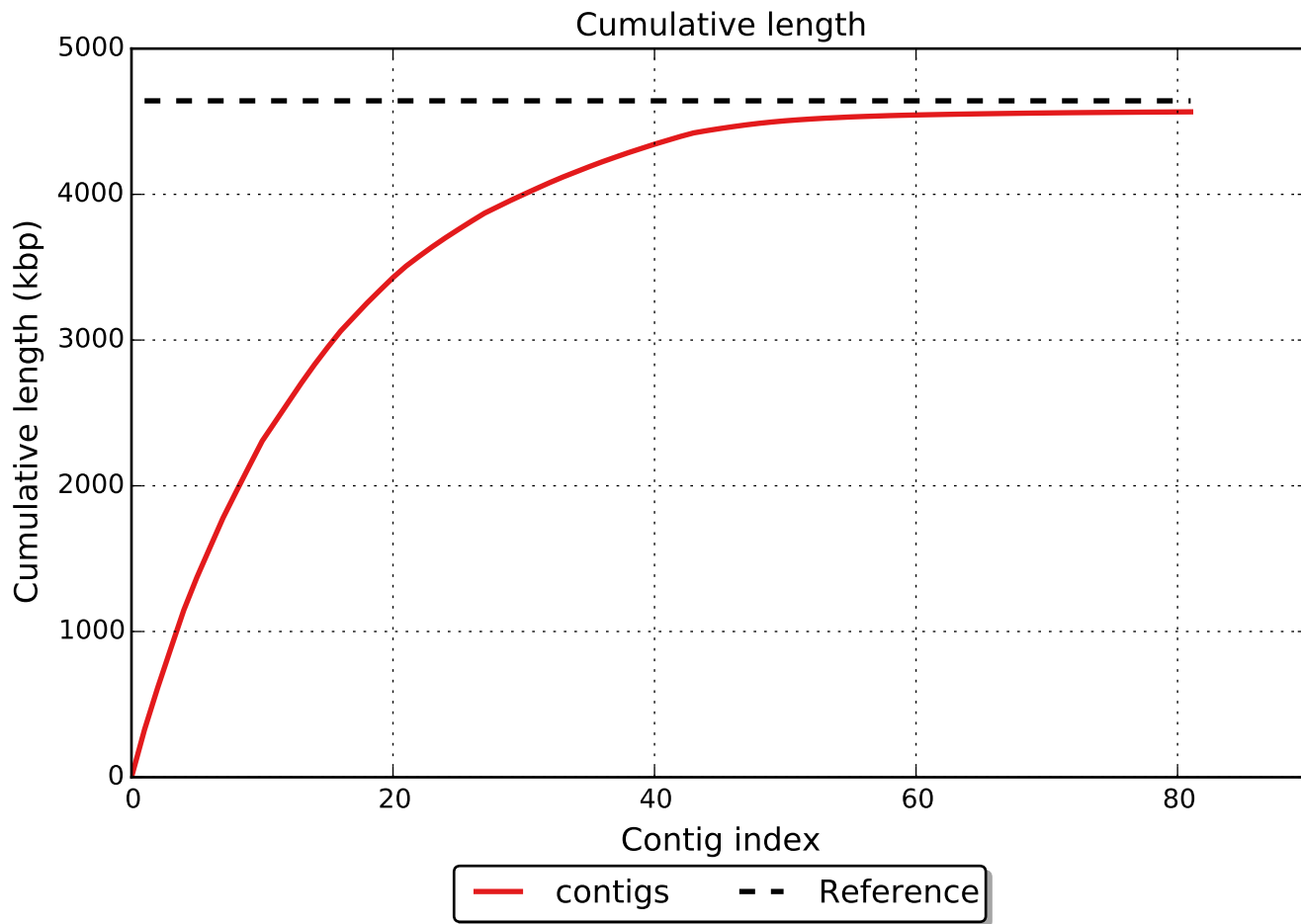
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

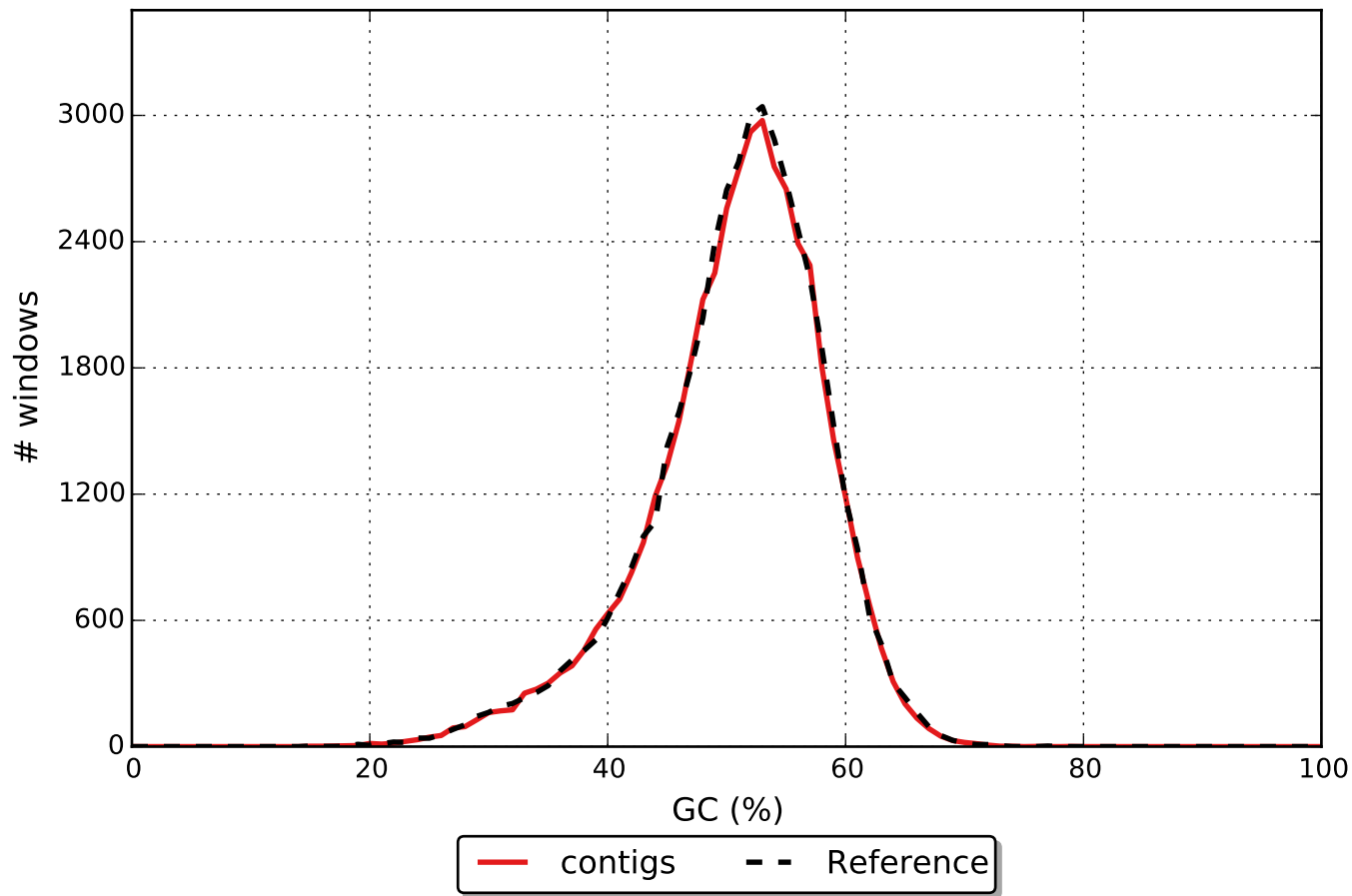


NGx

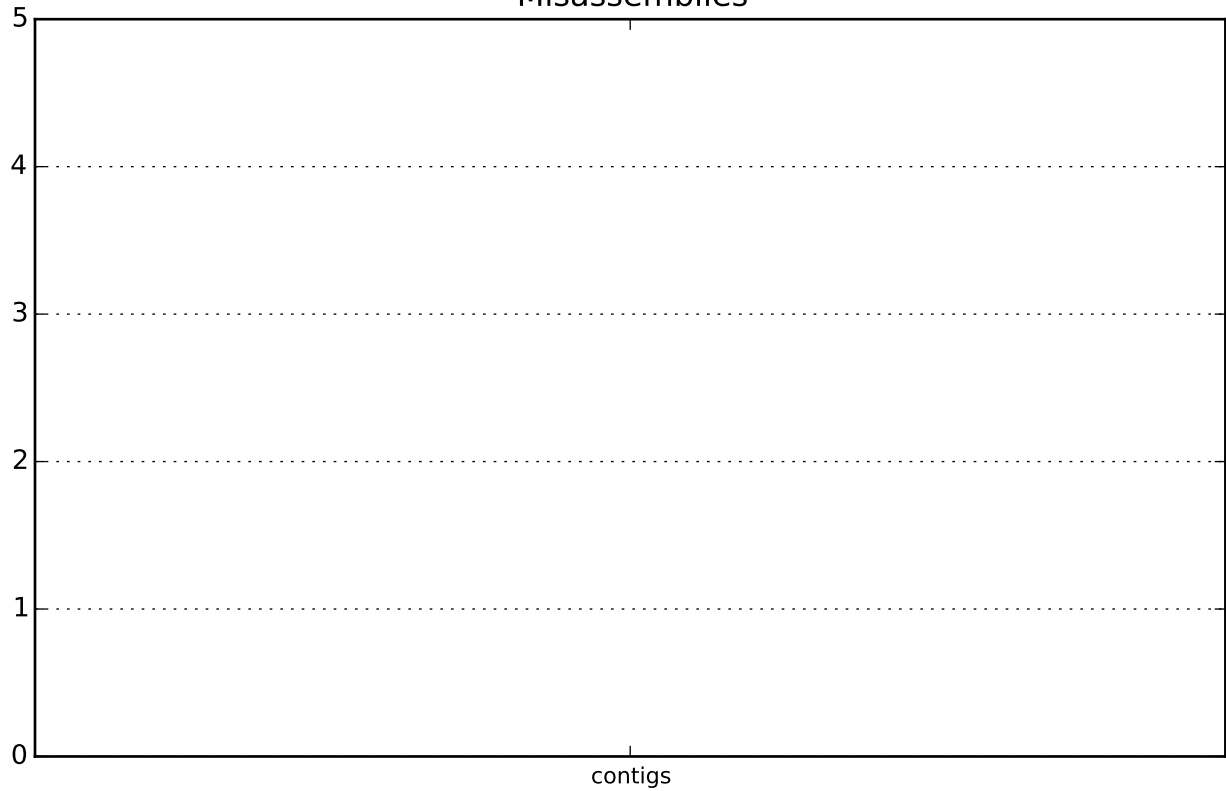




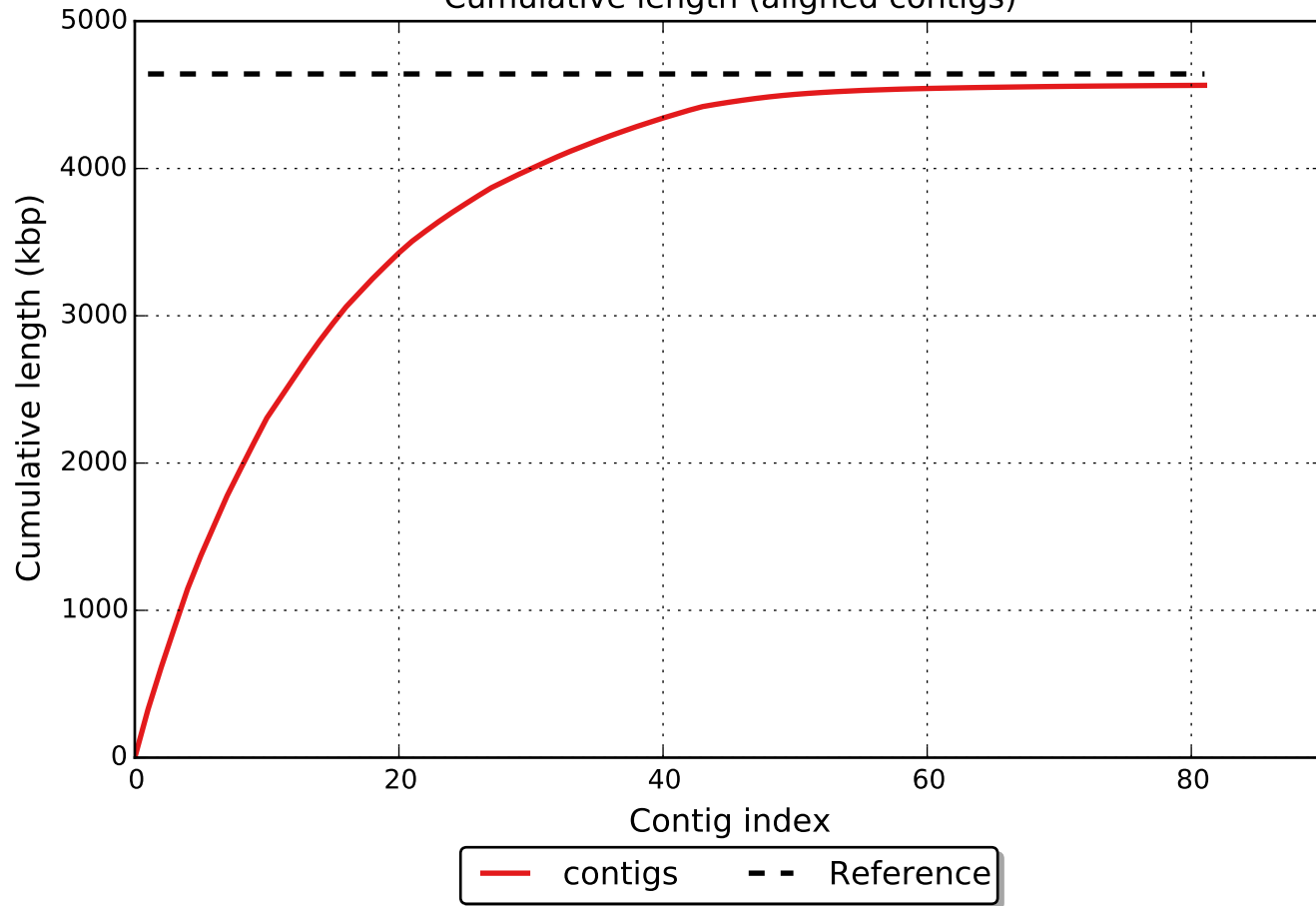
GC content



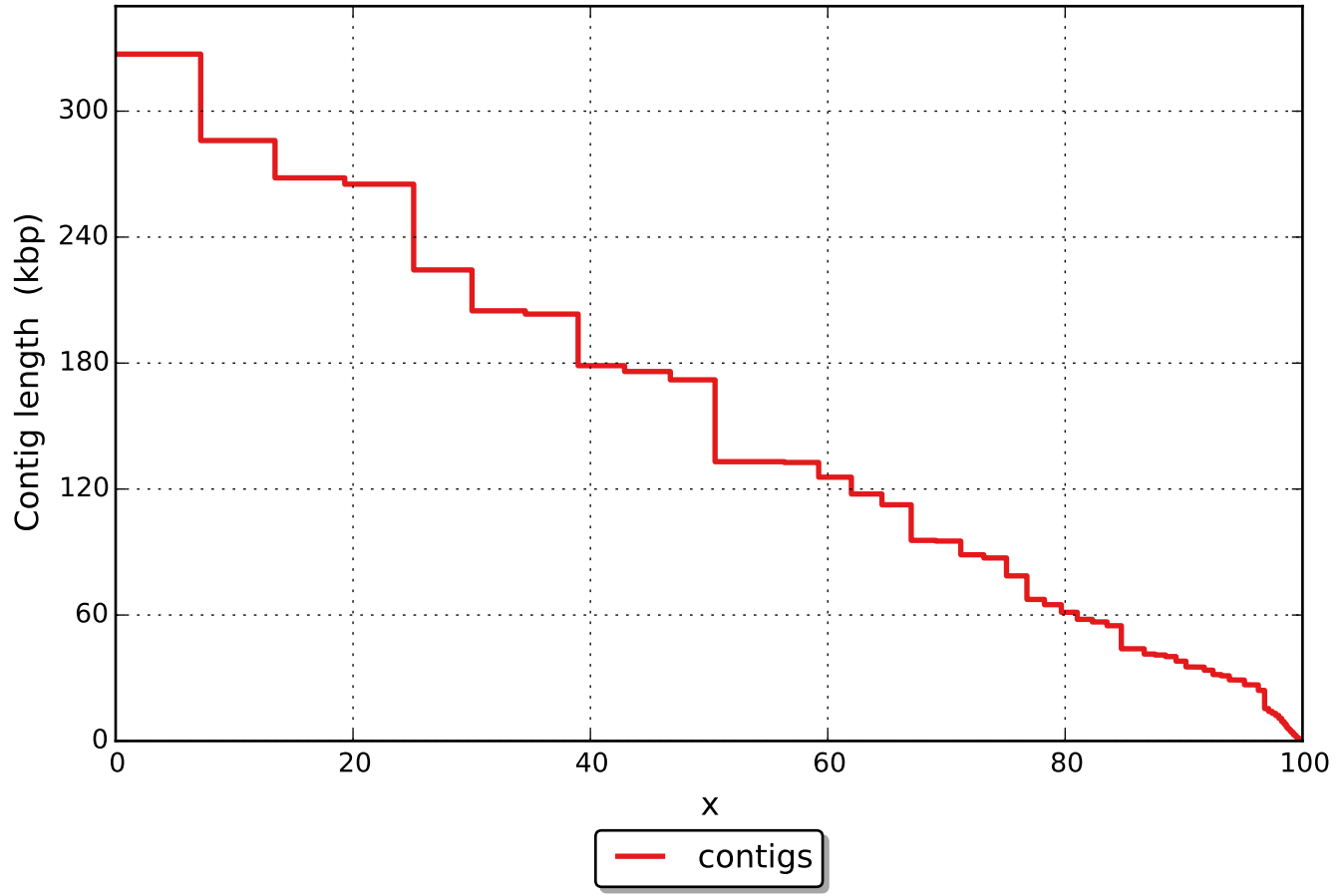
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

