

Report

	contigs
# contigs (≥ 0 bp)	170
# contigs (≥ 1000 bp)	93
# contigs (≥ 5000 bp)	71
# contigs (≥ 10000 bp)	63
# contigs (≥ 25000 bp)	50
# contigs (≥ 50000 bp)	29
Total length (≥ 0 bp)	4572974
Total length (≥ 1000 bp)	4552301
Total length (≥ 5000 bp)	4504740
Total length (≥ 10000 bp)	4446064
Total length (≥ 25000 bp)	4260214
Total length (≥ 50000 bp)	3532679
# contigs	100
Largest contig	327012
Total length	4557112
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	112914
NG50	112267
N75	59600
NG75	54909
L50	14
LG50	15
L75	27
LG75	29
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	94109
# local misassemblies	8
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.118
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	15.39
# indels per 100 kbp	0.81
Largest alignment	327012
NA50	112914
NGA50	112267
NA75	54909
NGA75	46297
LA50	14
LGA50	15
LA75	28
LGA75	29

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
# misassembled contigs	3
Misassembled contigs length	94109
# local misassemblies	8
# mismatches	701
# indels	37
# short indels	37
# long indels	0
Indels length	45

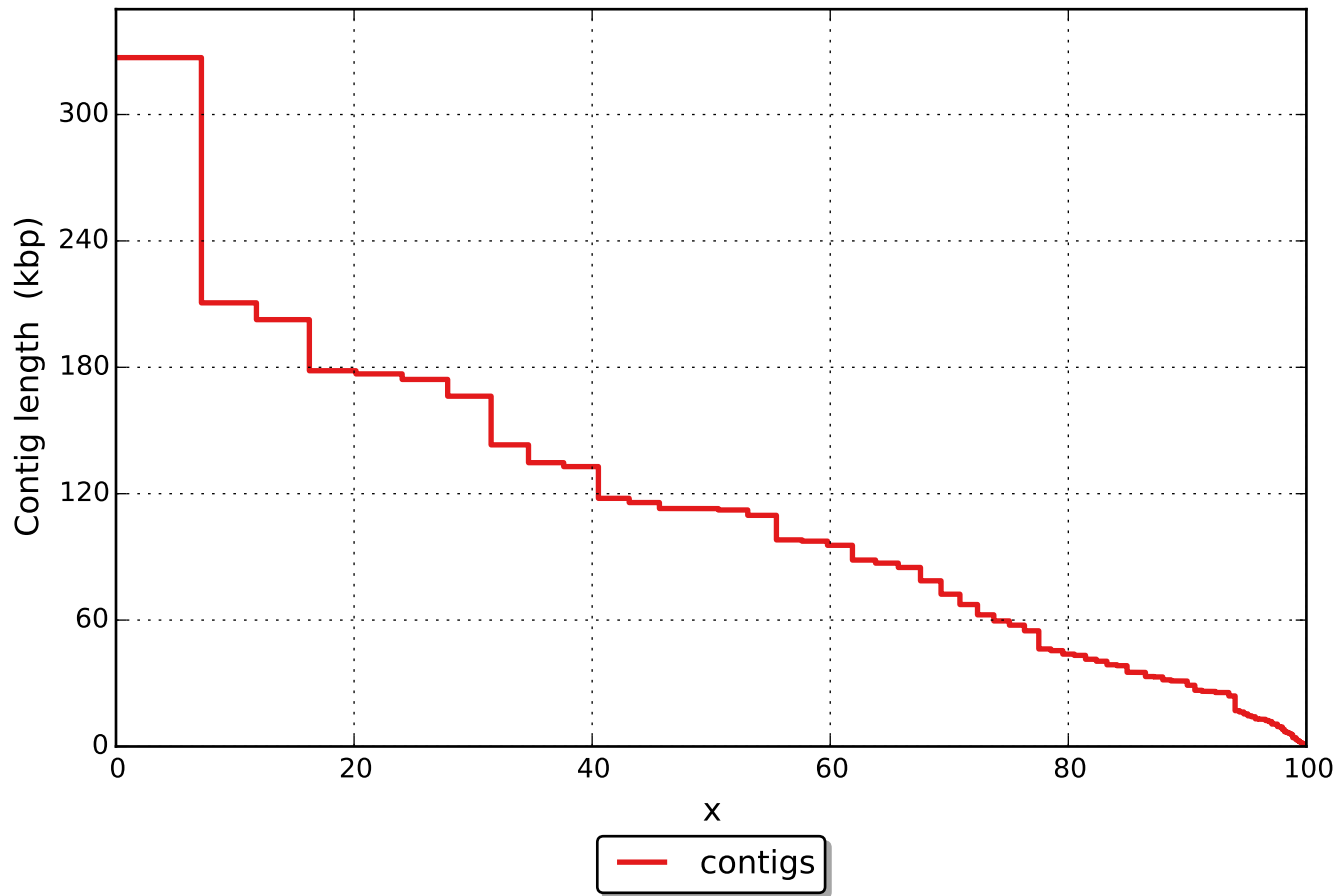
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

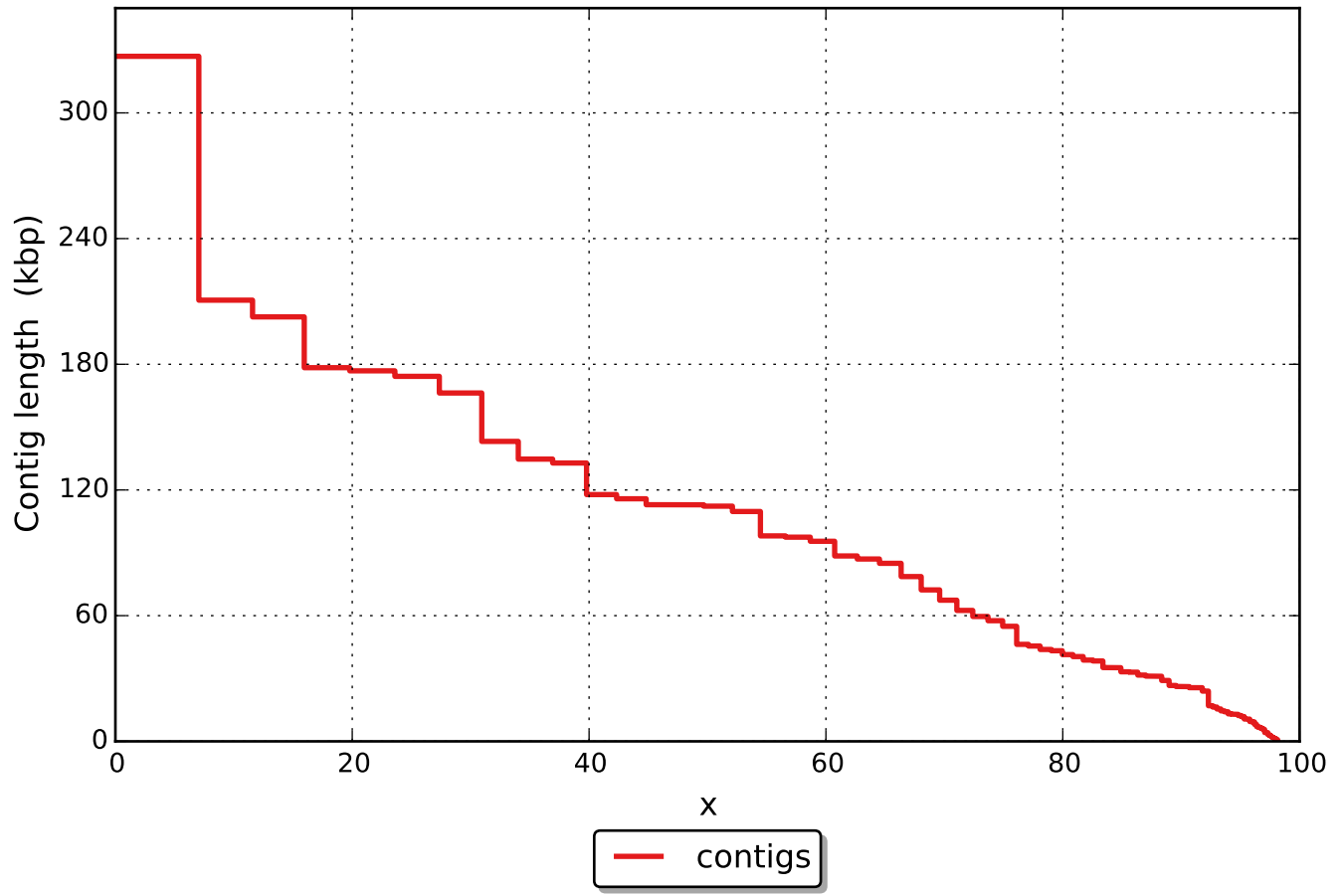
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

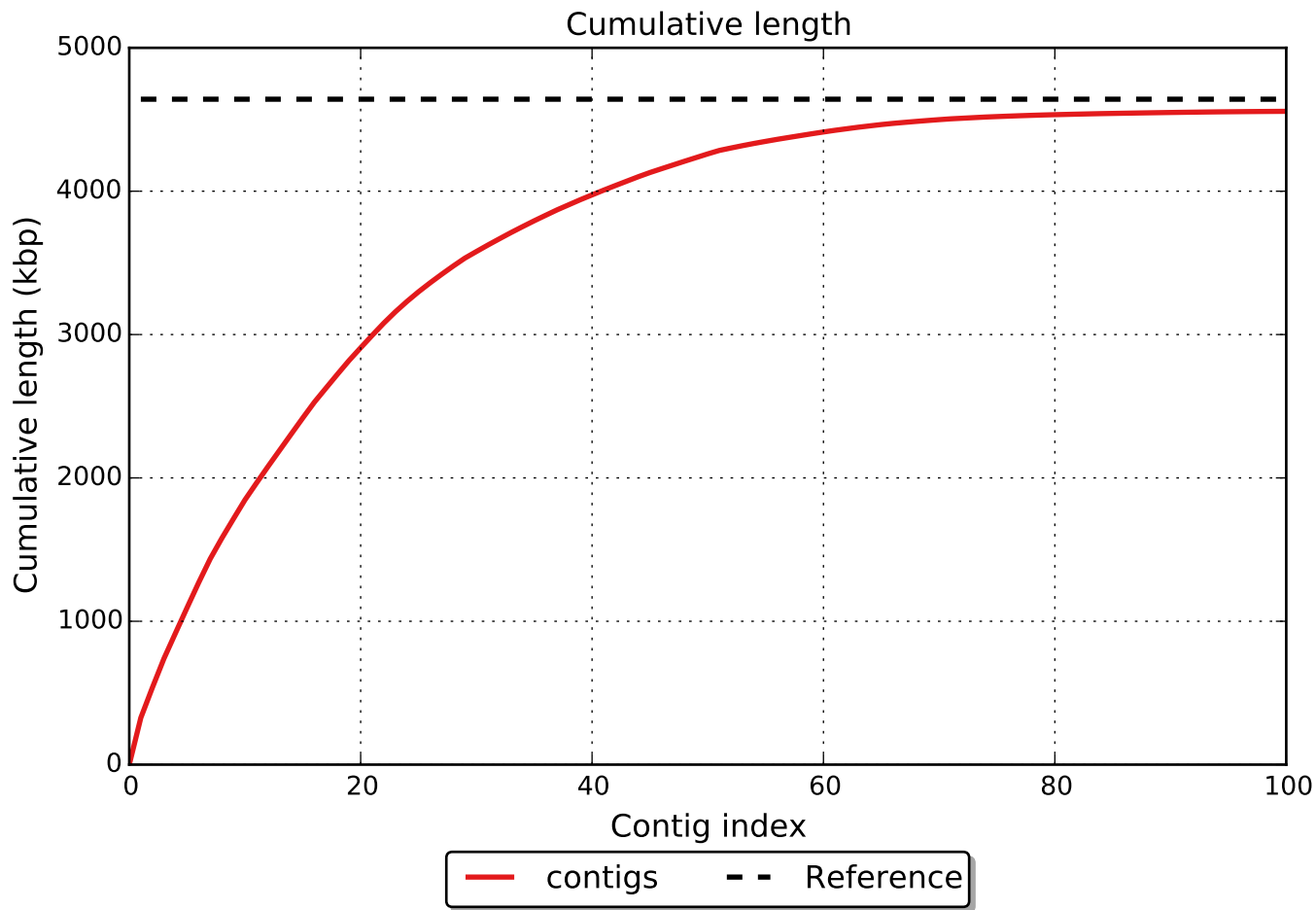
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

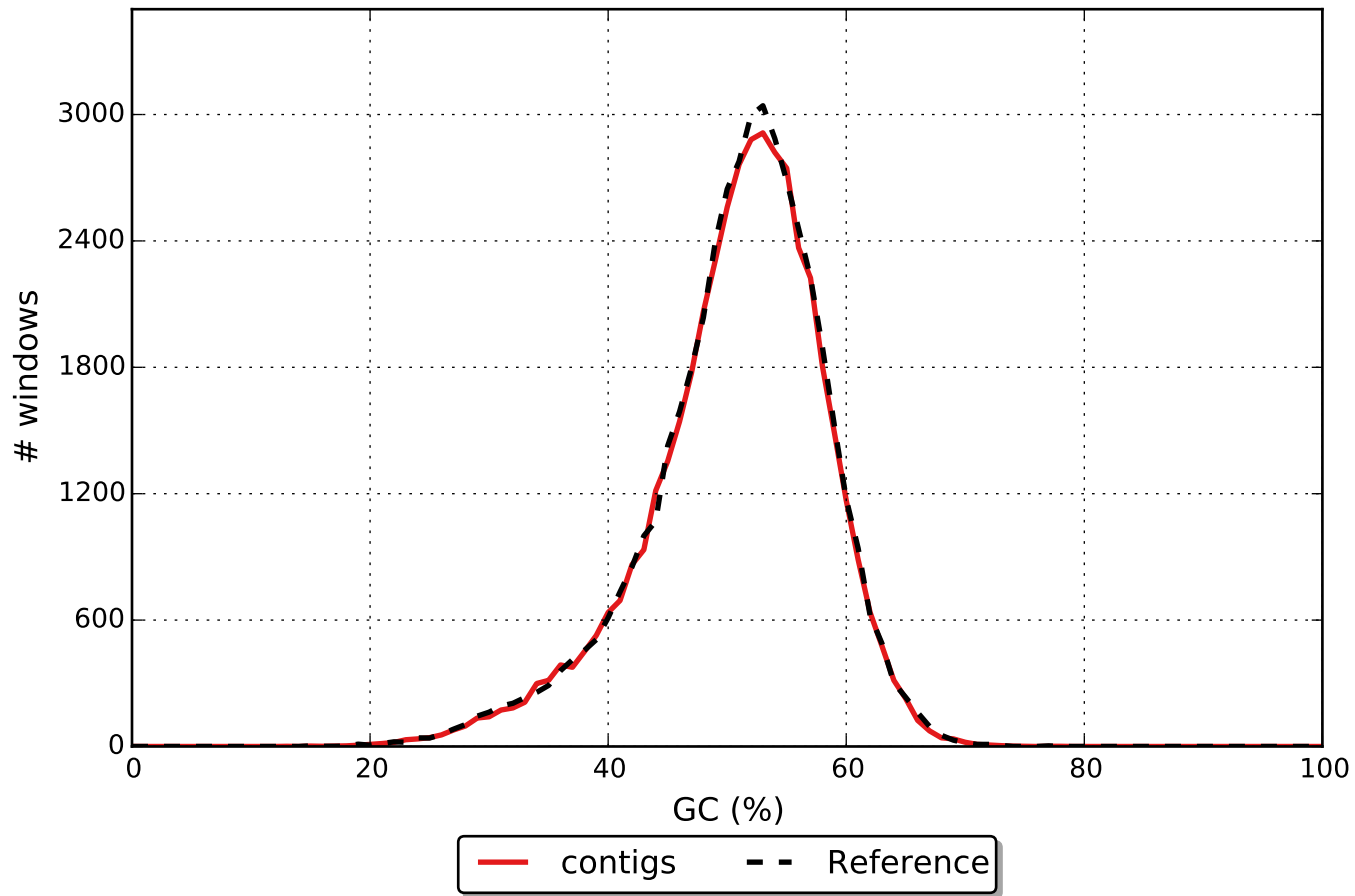


NGx

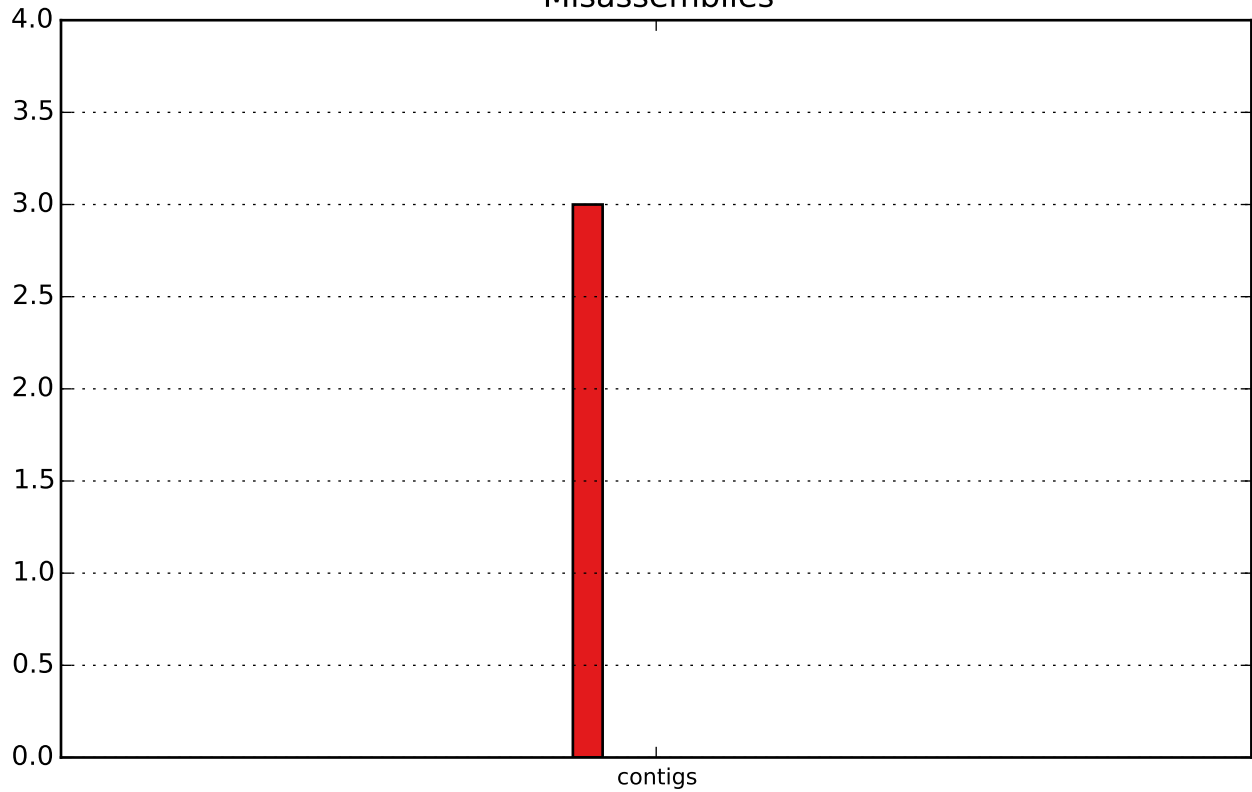




GC content

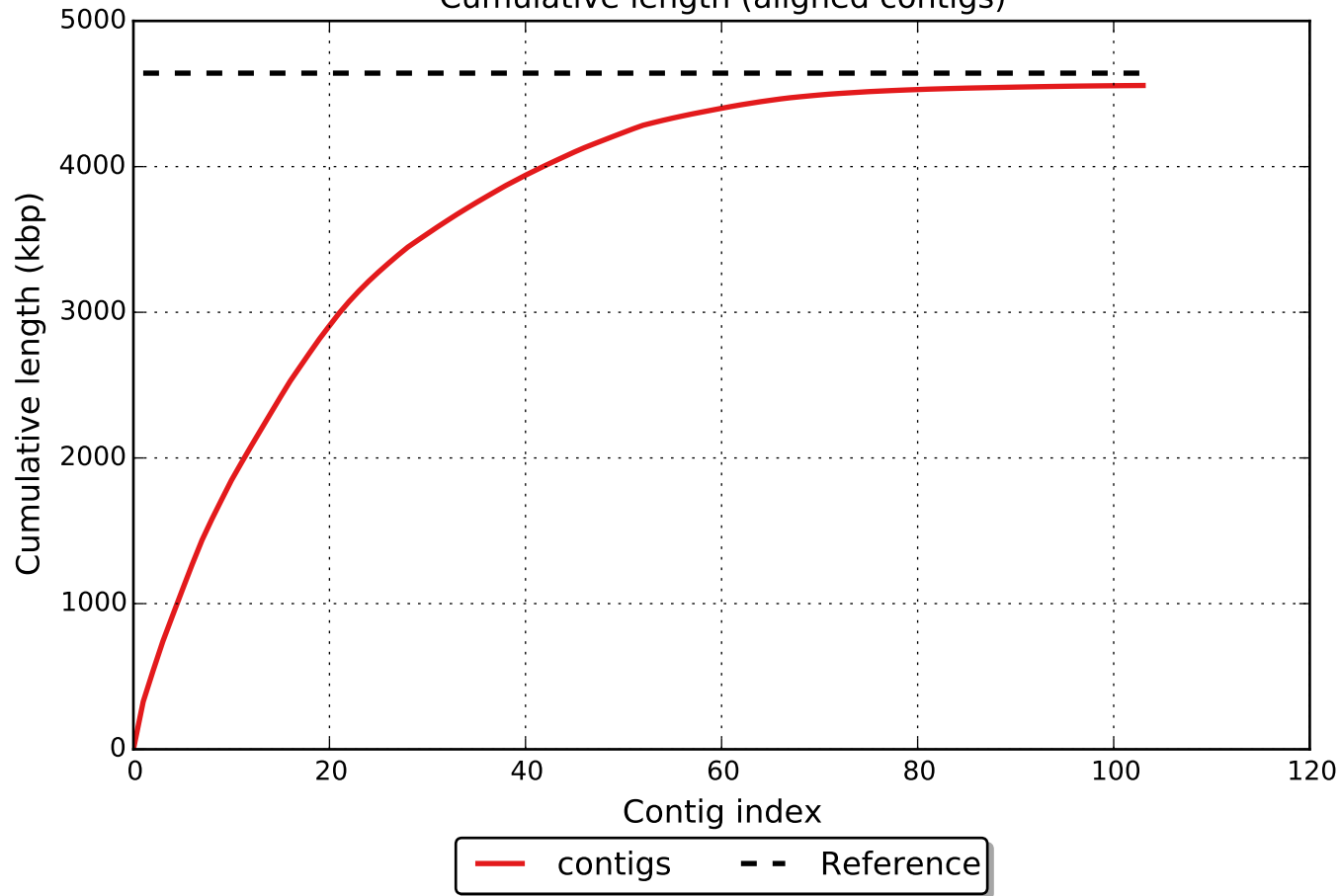


Misassemblies

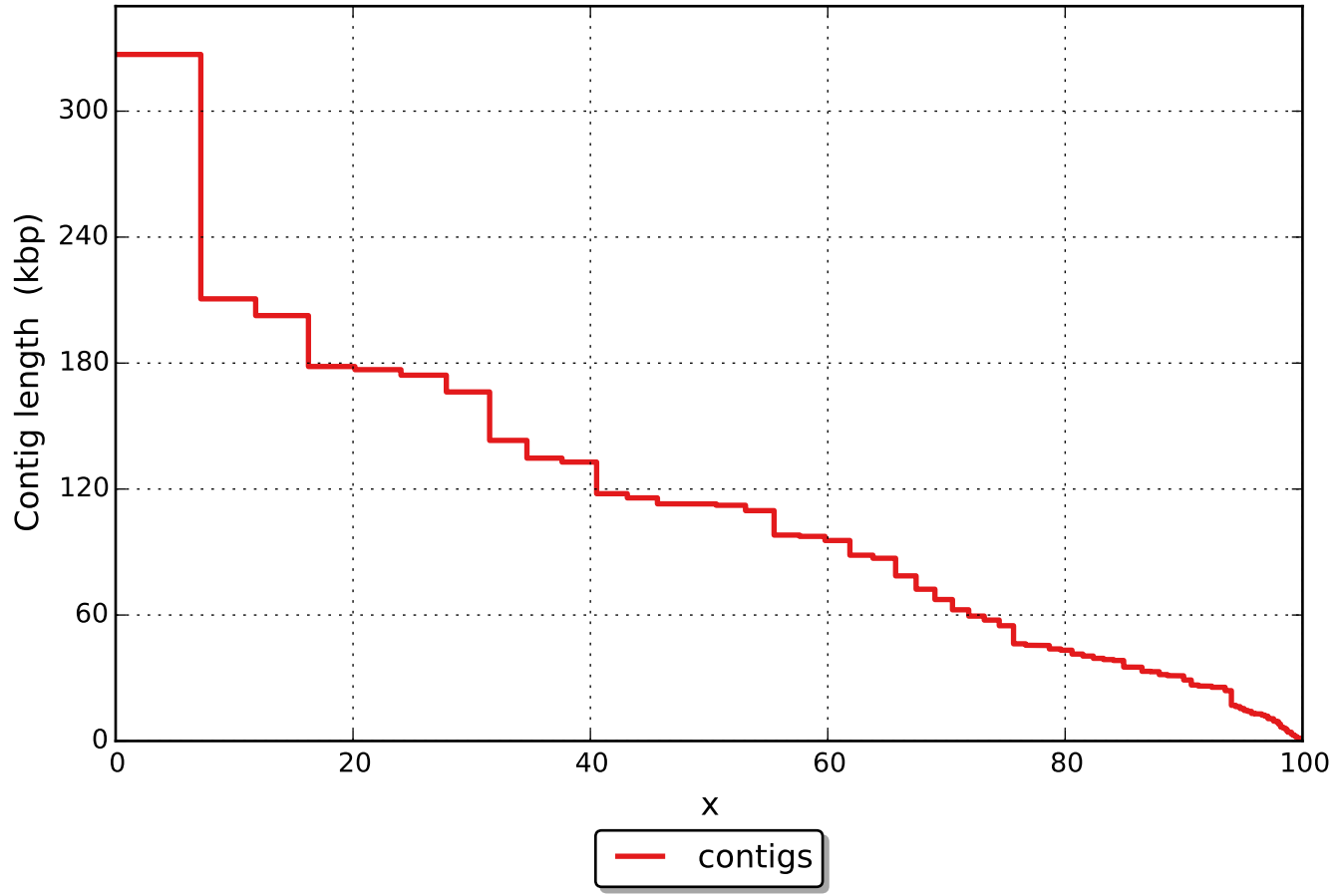


 # relocations

Cumulative length (aligned contigs)



NAx



NGAx

