

Report

	contigs
# contigs (≥ 0 bp)	6193
# contigs (≥ 1000 bp)	314
# contigs (≥ 5000 bp)	1
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	3041653
Total length (≥ 1000 bp)	414734
Total length (≥ 5000 bp)	7038
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	2142
Largest contig	7038
Total length	1652552
Reference length	4641652
GC (%)	50.73
Reference GC (%)	50.79
N50	764
N75	614
L50	792
L75	1396
# misassemblies	37
# misassembled contigs	37
Misassembled contigs length	53299
# local misassemblies	3
# unaligned contigs	5 + 11 part
Unaligned length	5457
Genome fraction (%)	35.366
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1462.09
# indels per 100 kbp	1.34
Largest alignment	6022
NA50	758
NGA50	-
NA75	607
LA50	807
LA75	1418

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

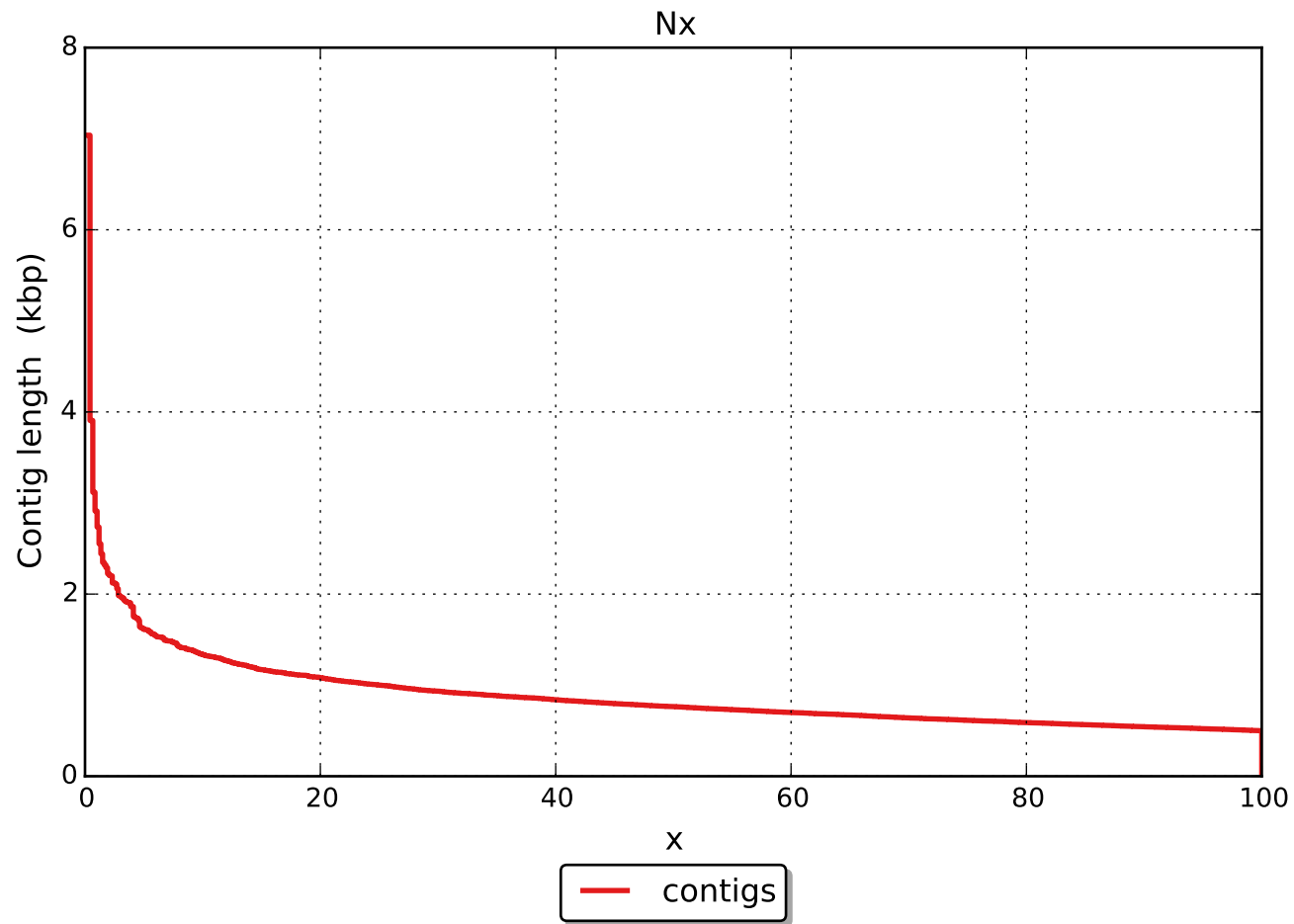
	contigs
# misassemblies	37
# relocations	37
# translocations	0
# inversions	0
# misassembled contigs	37
Misassembled contigs length	53299
# local misassemblies	3
# mismatches	24001
# indels	22
# short indels	21
# long indels	1
Indels length	28

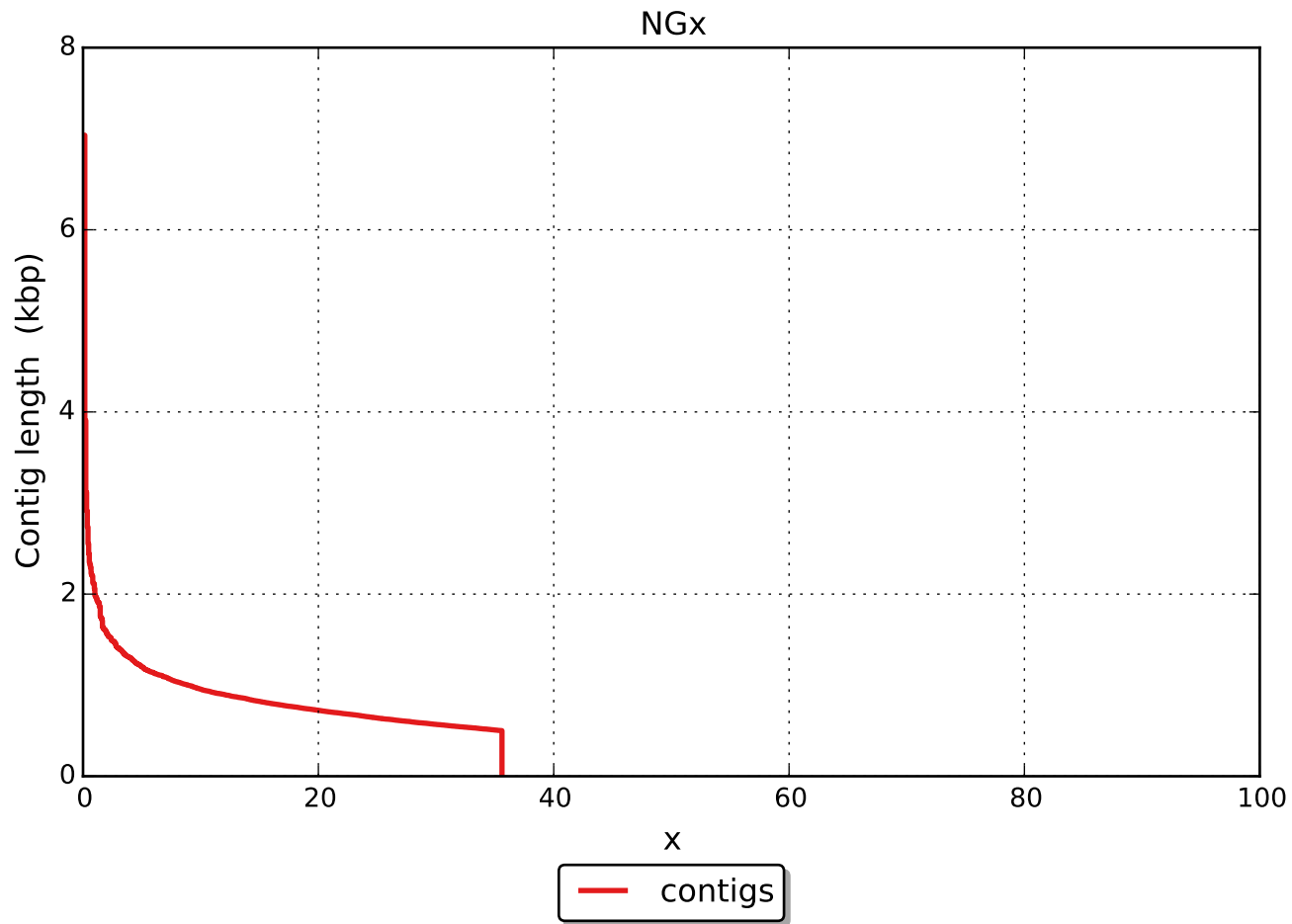
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

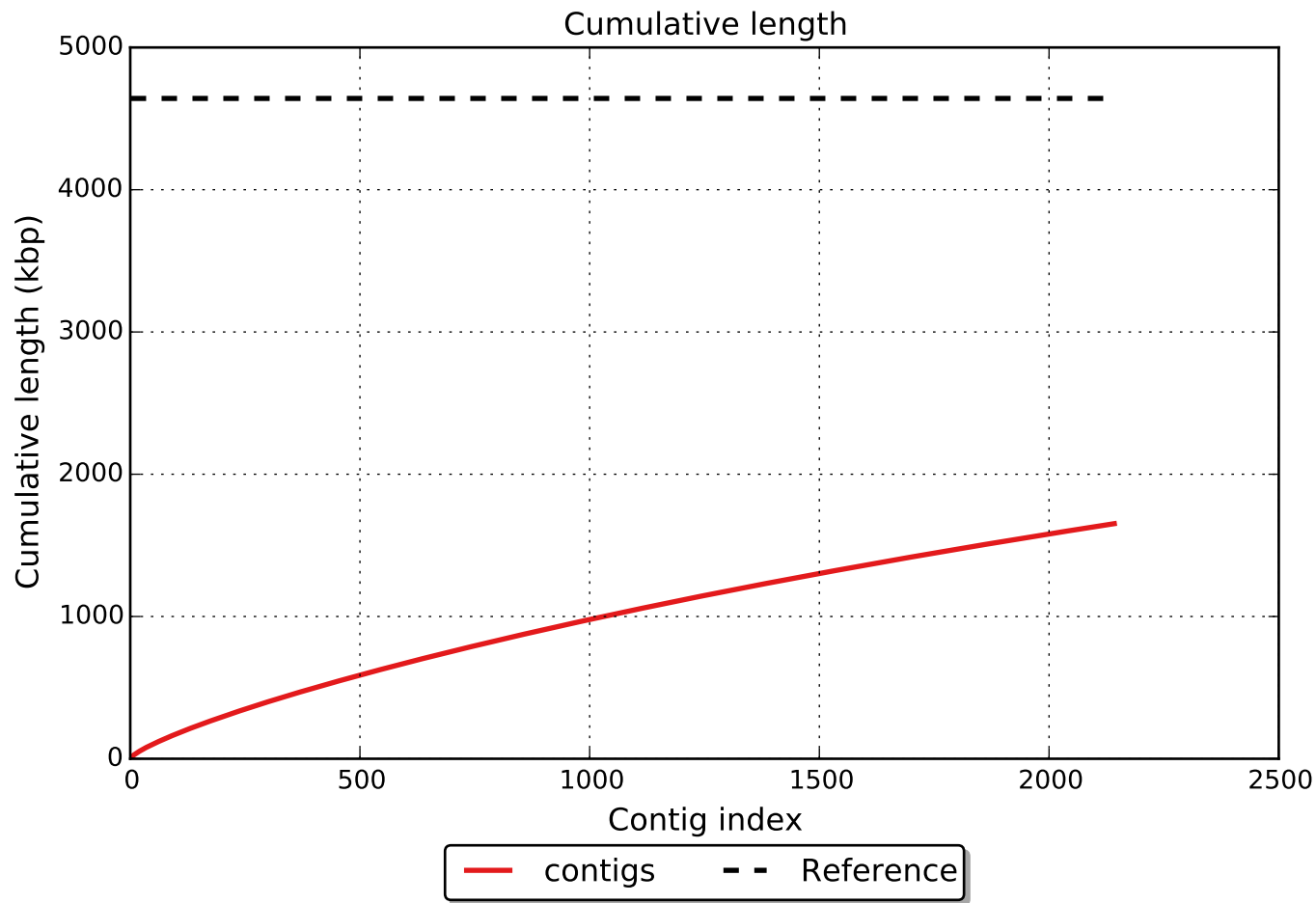
Unaligned report

	contigs
# fully unaligned contigs	5
Fully unaligned length	4251
# partially unaligned contigs	11
# with misassembly	0
# both parts are significant	0
Partially unaligned length	1206
# N's	0

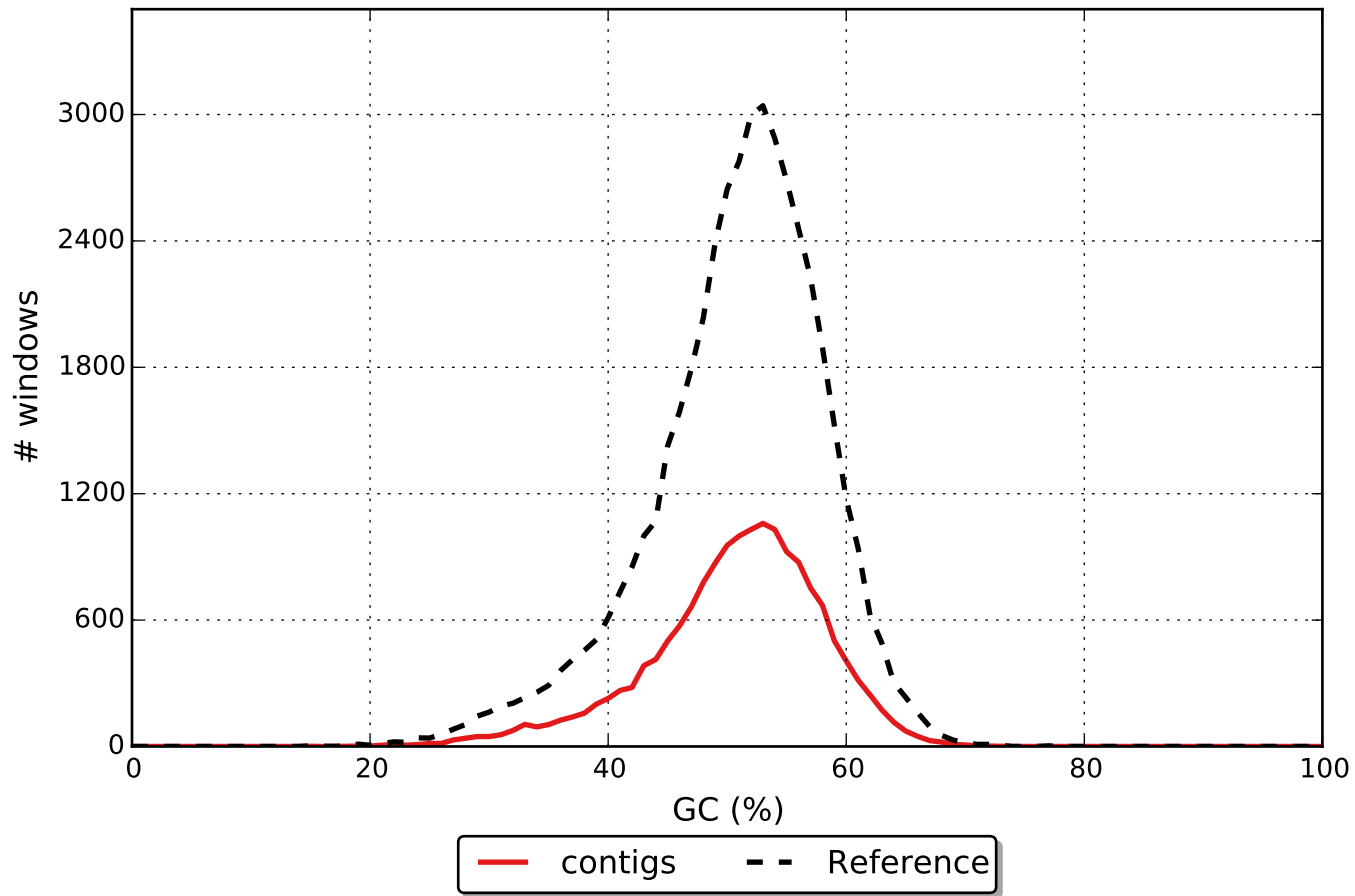
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



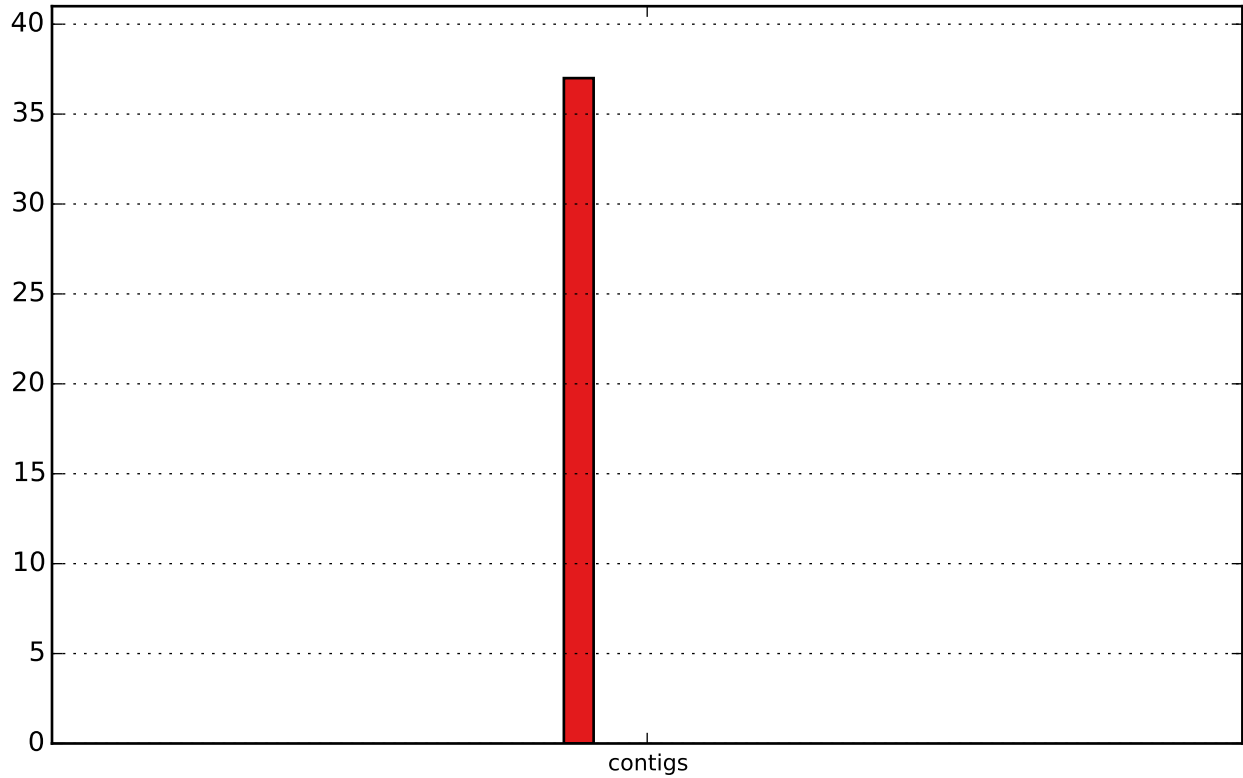




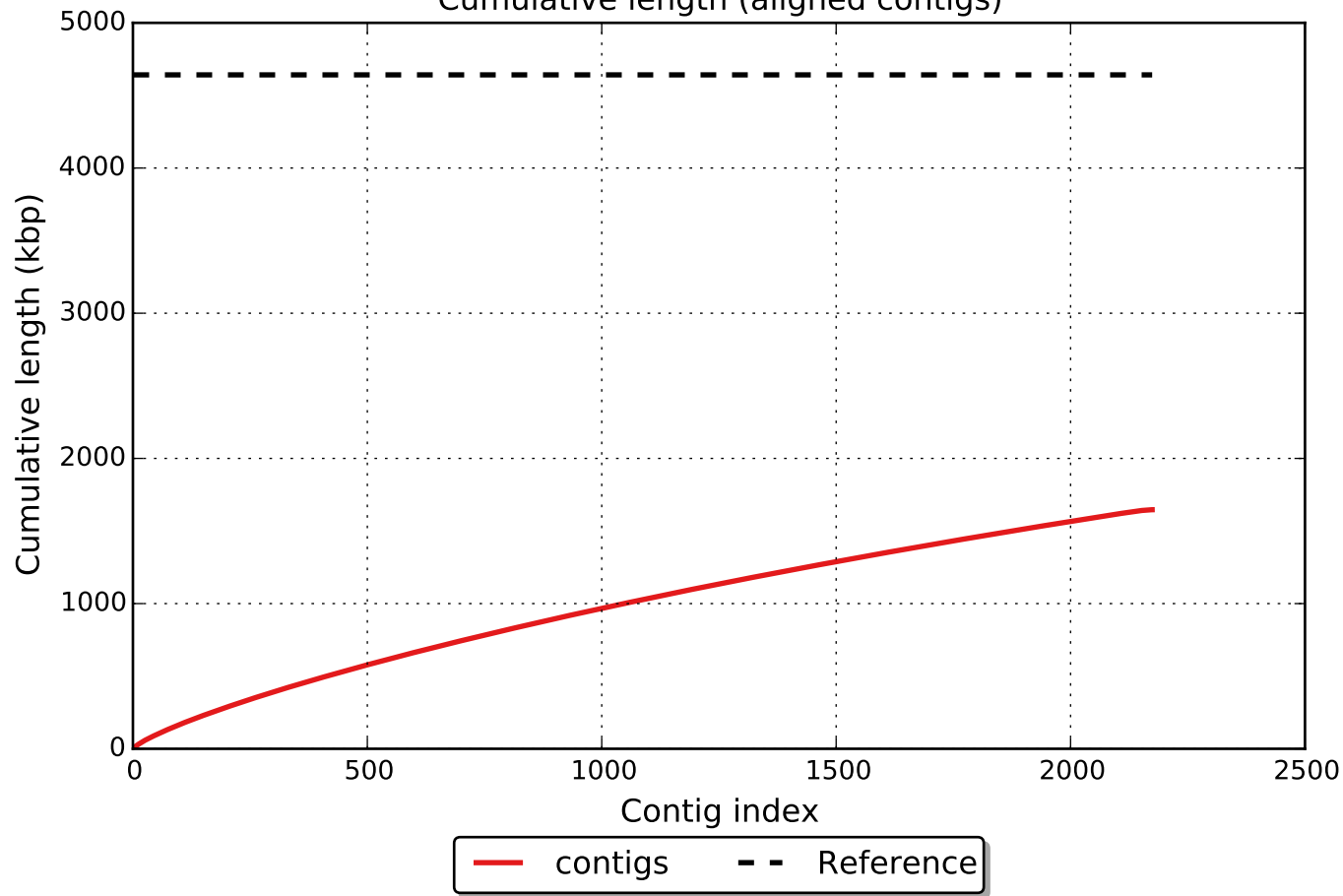
GC content



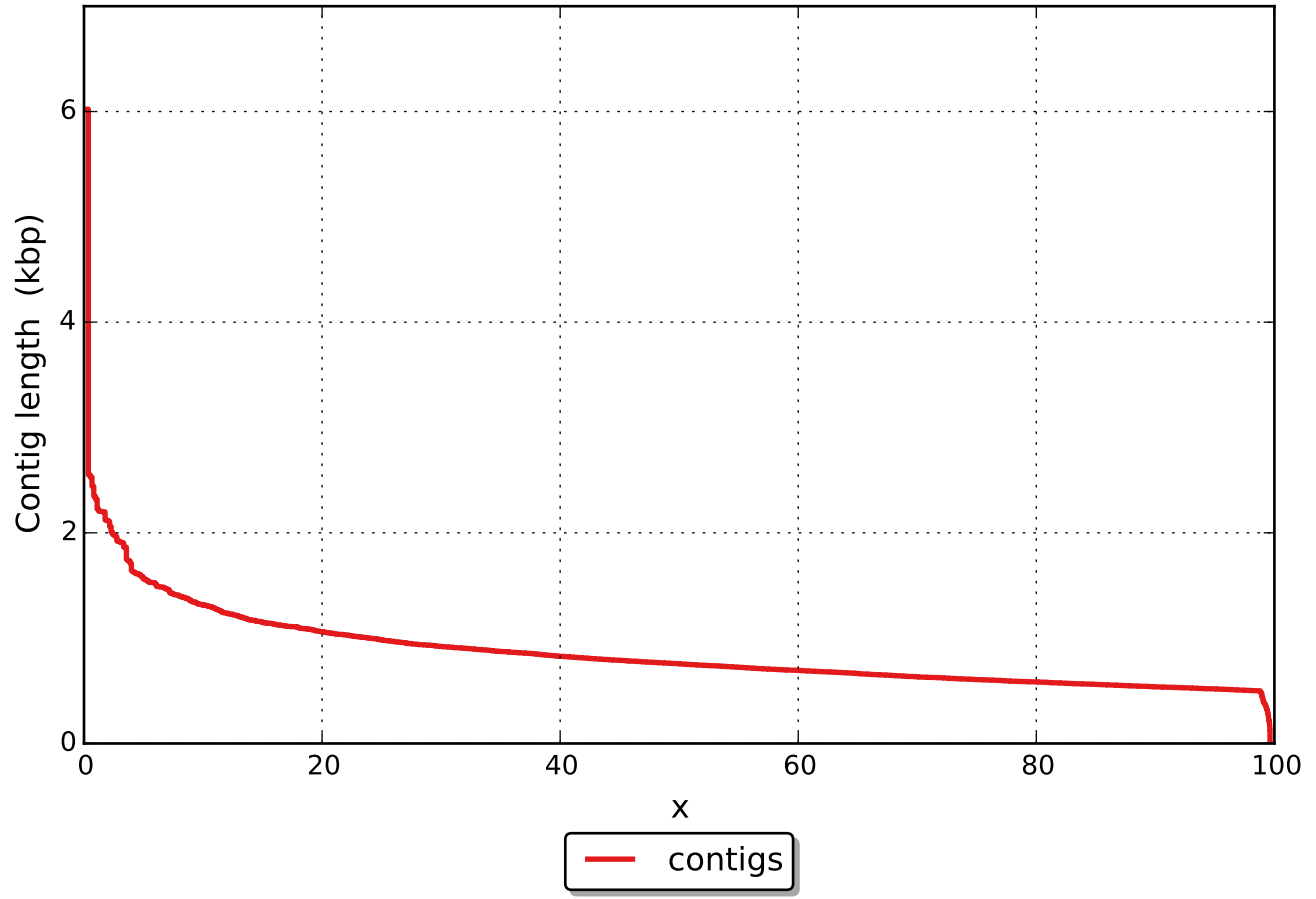
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

