

Report

	contigs
# contigs (≥ 0 bp)	260
# contigs (≥ 1000 bp)	211
# contigs (≥ 5000 bp)	167
# contigs (≥ 10000 bp)	137
# contigs (≥ 25000 bp)	64
# contigs (≥ 50000 bp)	20
Total length (≥ 0 bp)	4560371
Total length (≥ 1000 bp)	4544263
Total length (≥ 5000 bp)	4425997
Total length (≥ 10000 bp)	4199507
Total length (≥ 25000 bp)	2985931
Total length (≥ 50000 bp)	1430051
# contigs	223
Largest contig	118237
Total length	4553207
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	35236
NG50	35105
N75	20409
NG75	19577
L50	41
LG50	42
L75	84
LG75	87
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	2268
# local misassemblies	11
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.038
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	5.21
# indels per 100 kbp	0.44
Largest alignment	118237
NA50	35236
NGA50	35105
NA75	20409
NGA75	19577
LA50	41
LGA50	42
LA75	84
LGA75	87

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

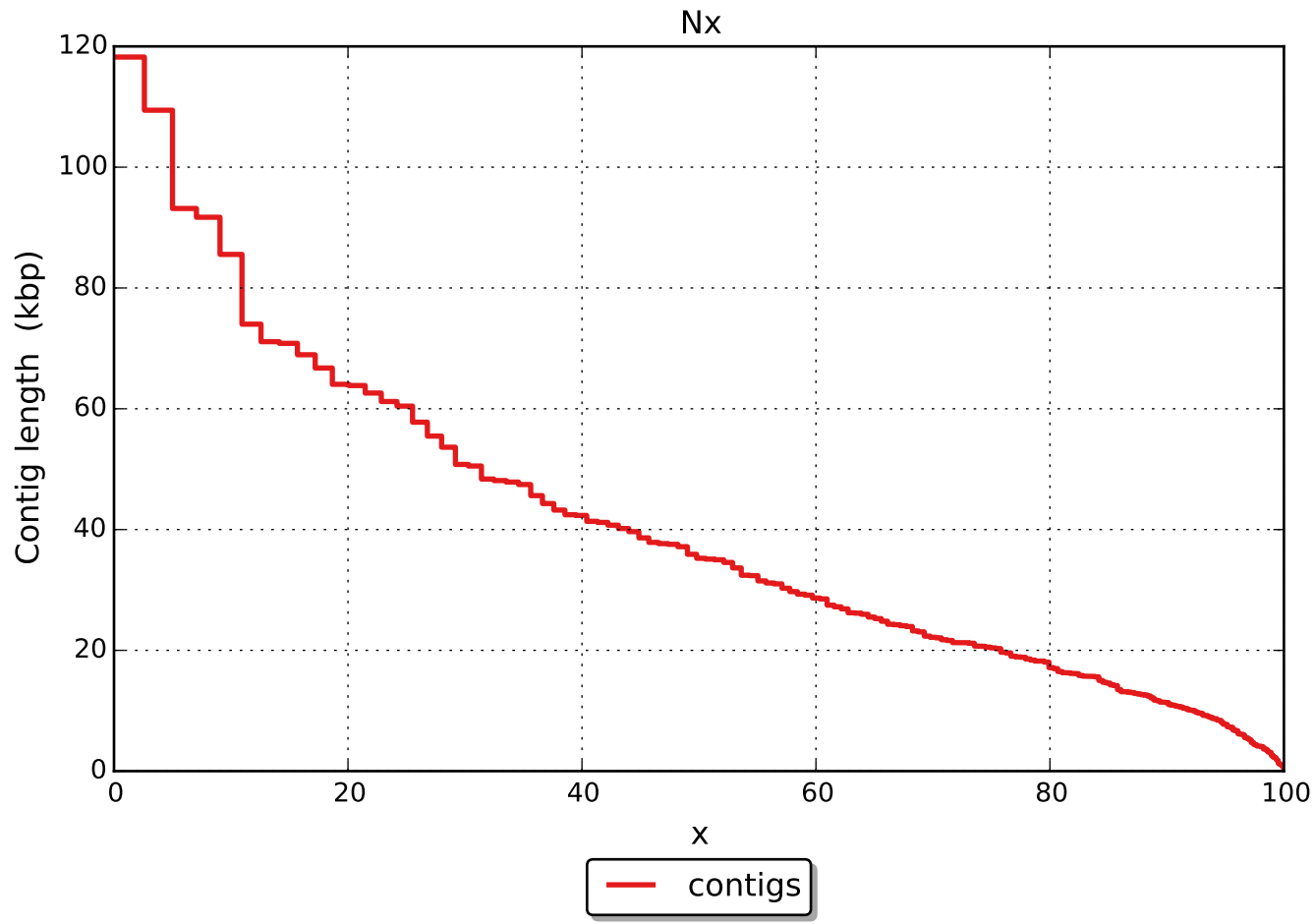
	contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# misassembled contigs	1
Misassembled contigs length	2268
# local misassemblies	11
# mismatches	237
# indels	20
# short indels	18
# long indels	2
Indels length	187

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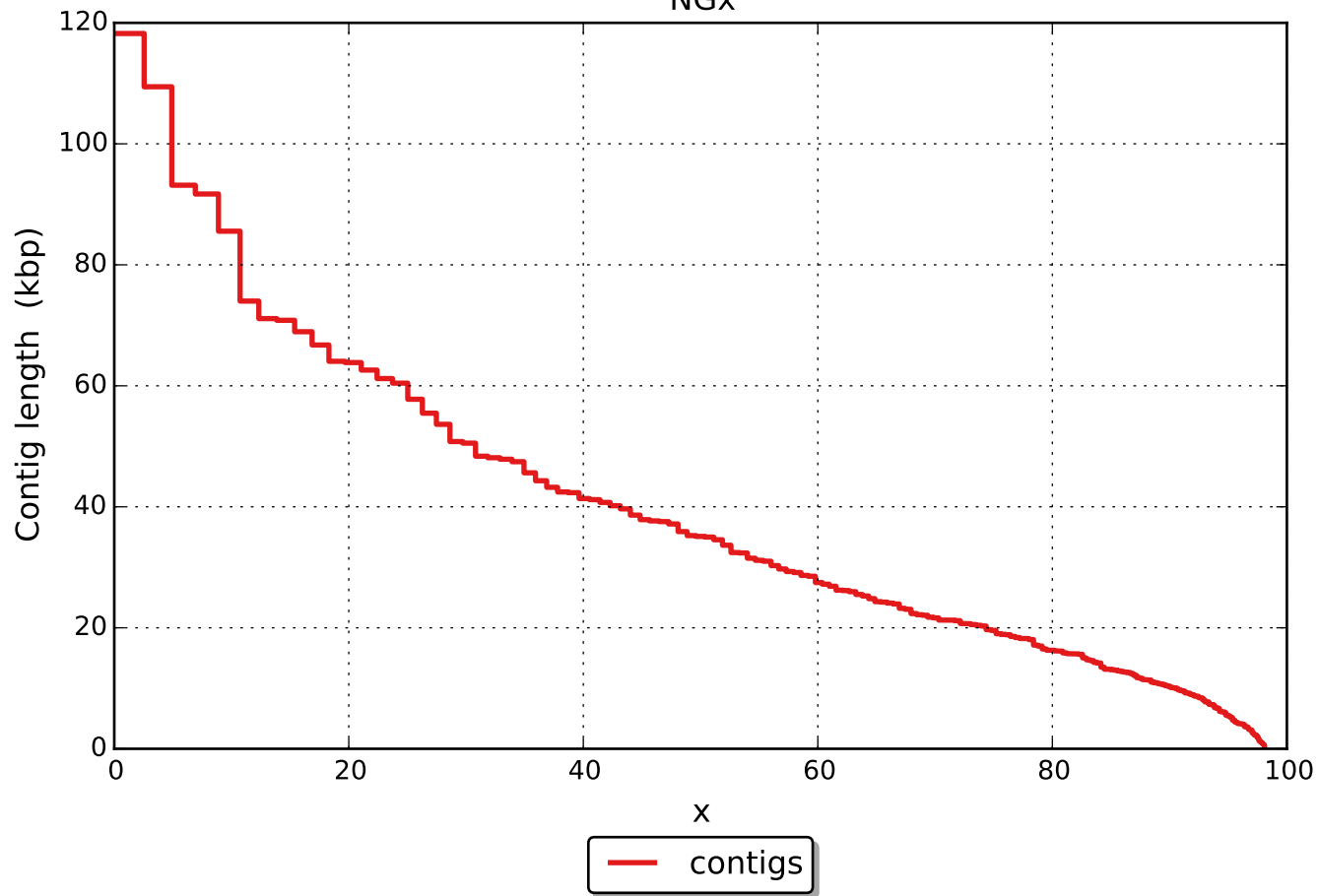
Unaligned report

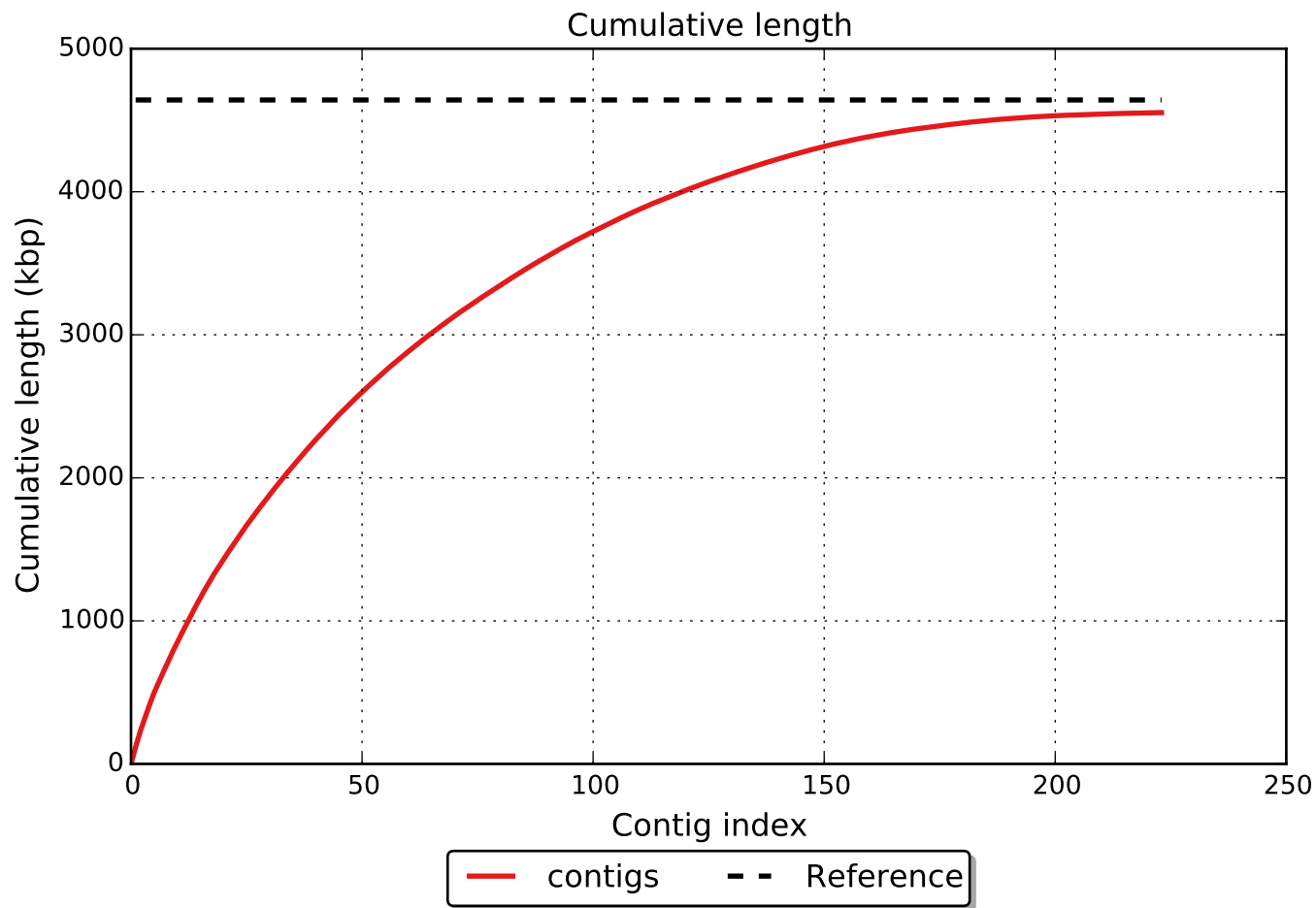
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

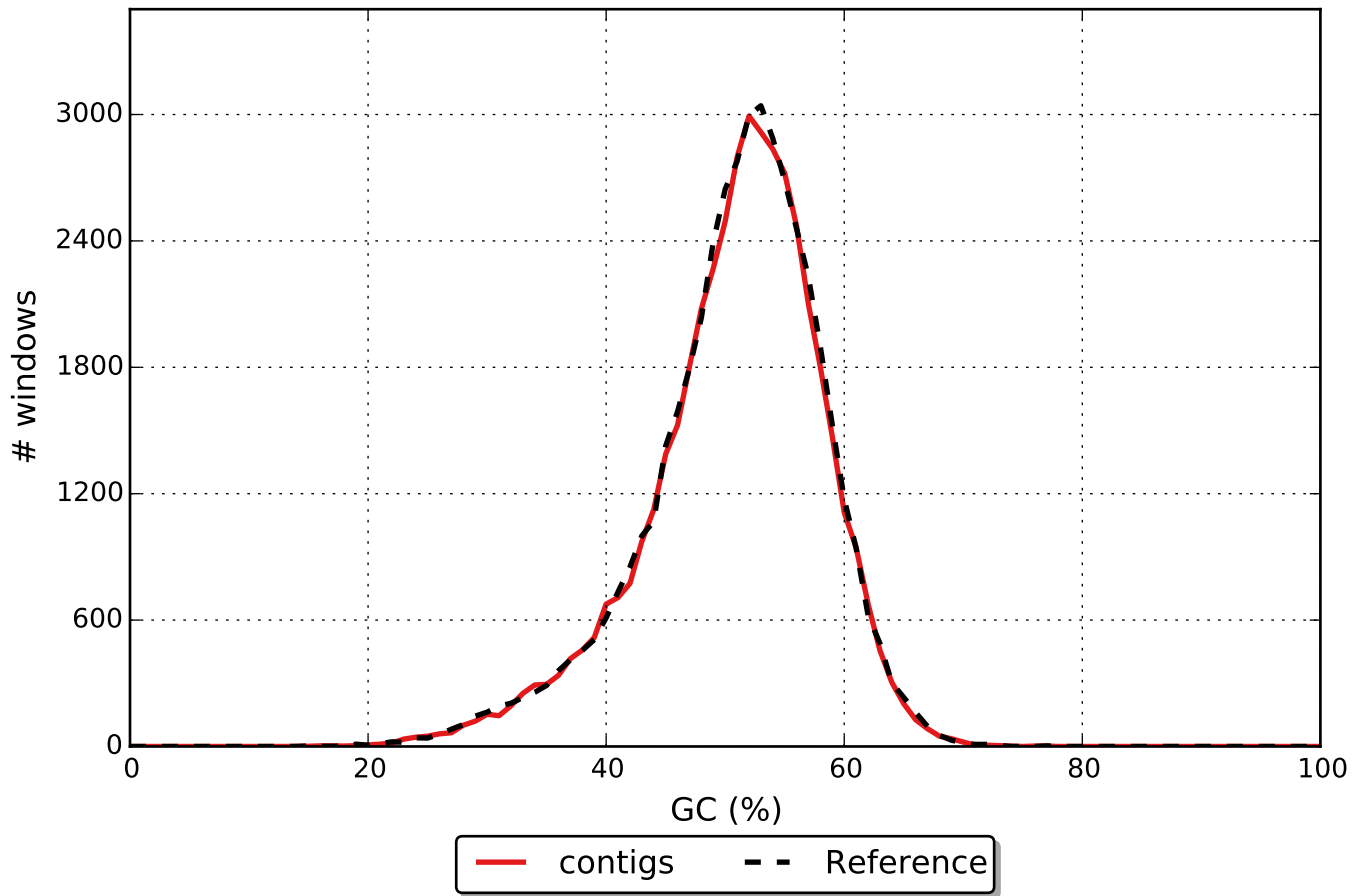


NGx





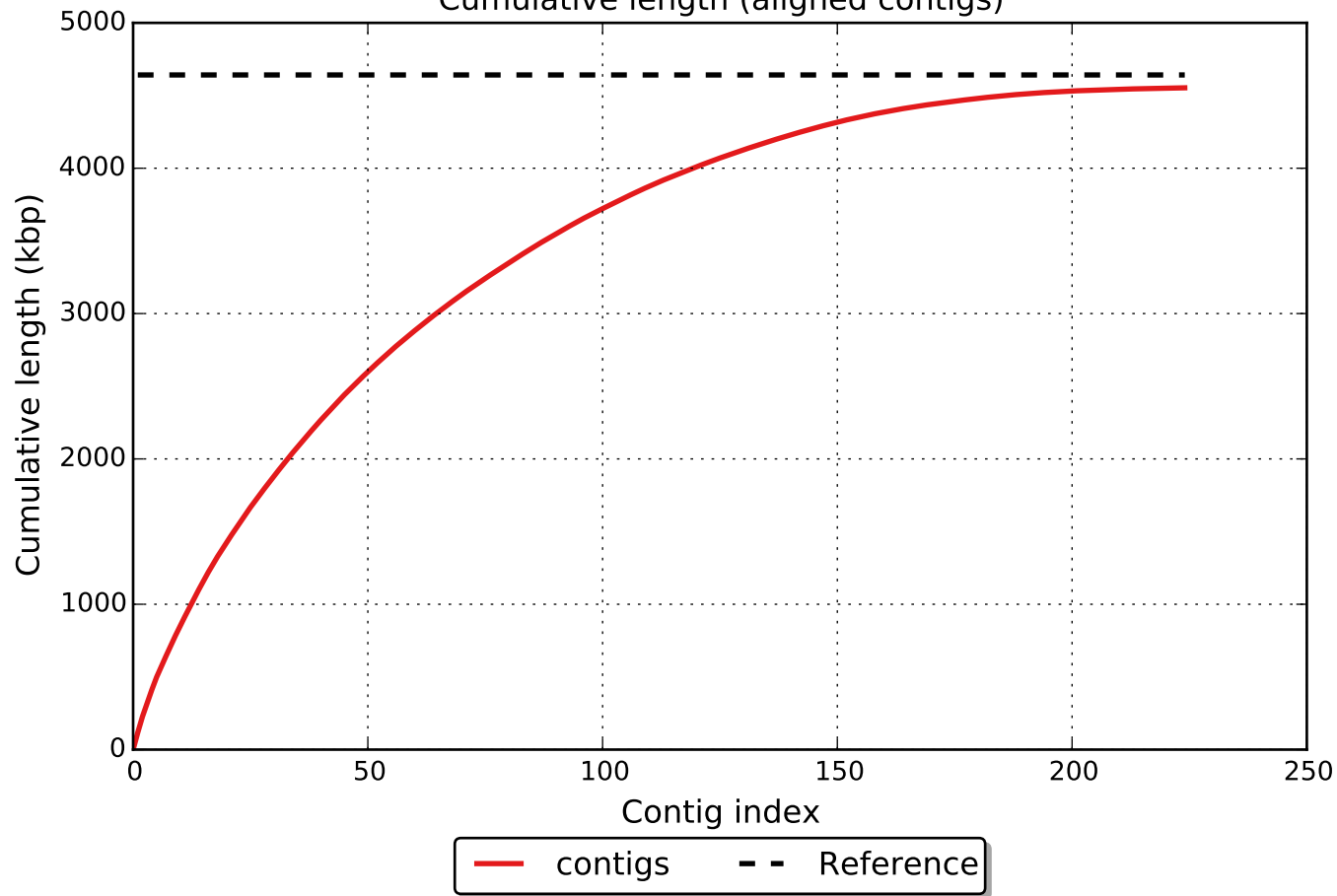
GC content



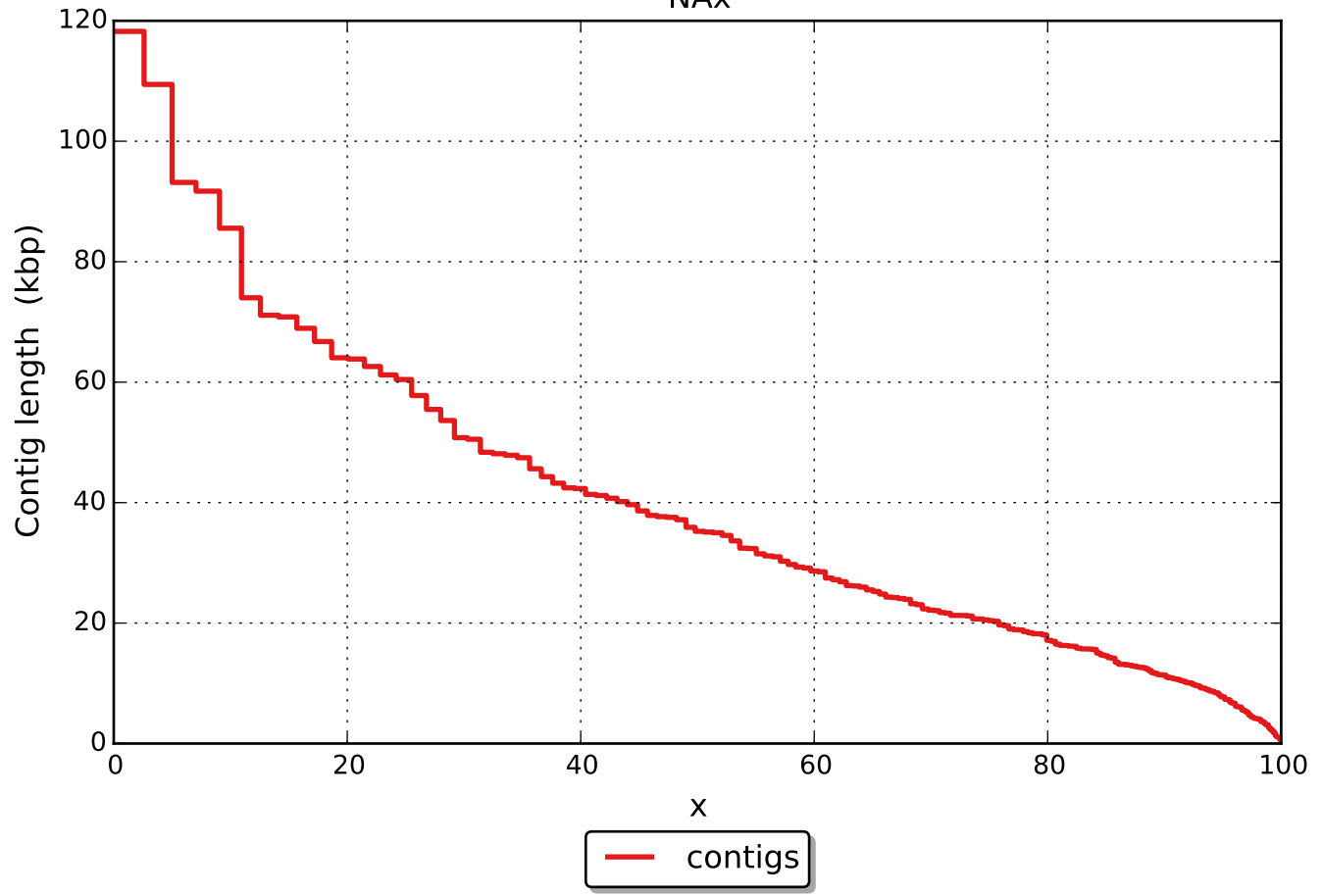
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

