

Report

	contigs
# contigs (≥ 0 bp)	278
# contigs (≥ 1000 bp)	212
# contigs (≥ 5000 bp)	168
# contigs (≥ 10000 bp)	139
# contigs (≥ 25000 bp)	63
# contigs (≥ 50000 bp)	20
Total length (≥ 0 bp)	4572480
Total length (≥ 1000 bp)	4549646
Total length (≥ 5000 bp)	4429949
Total length (≥ 10000 bp)	4210450
Total length (≥ 25000 bp)	2929370
Total length (≥ 50000 bp)	1397111
# contigs	227
Largest contig	118259
Total length	4561005
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	35233
NG50	34996
N75	20292
NG75	19577
L50	42
LG50	43
L75	86
LG75	89
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	7
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.211
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3.27
# indels per 100 kbp	0.33
Largest alignment	118259
NA50	35233
NGA50	34996
NA75	20292
NGA75	19577
LA50	42
LGA50	43
LA75	86
LGA75	89

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

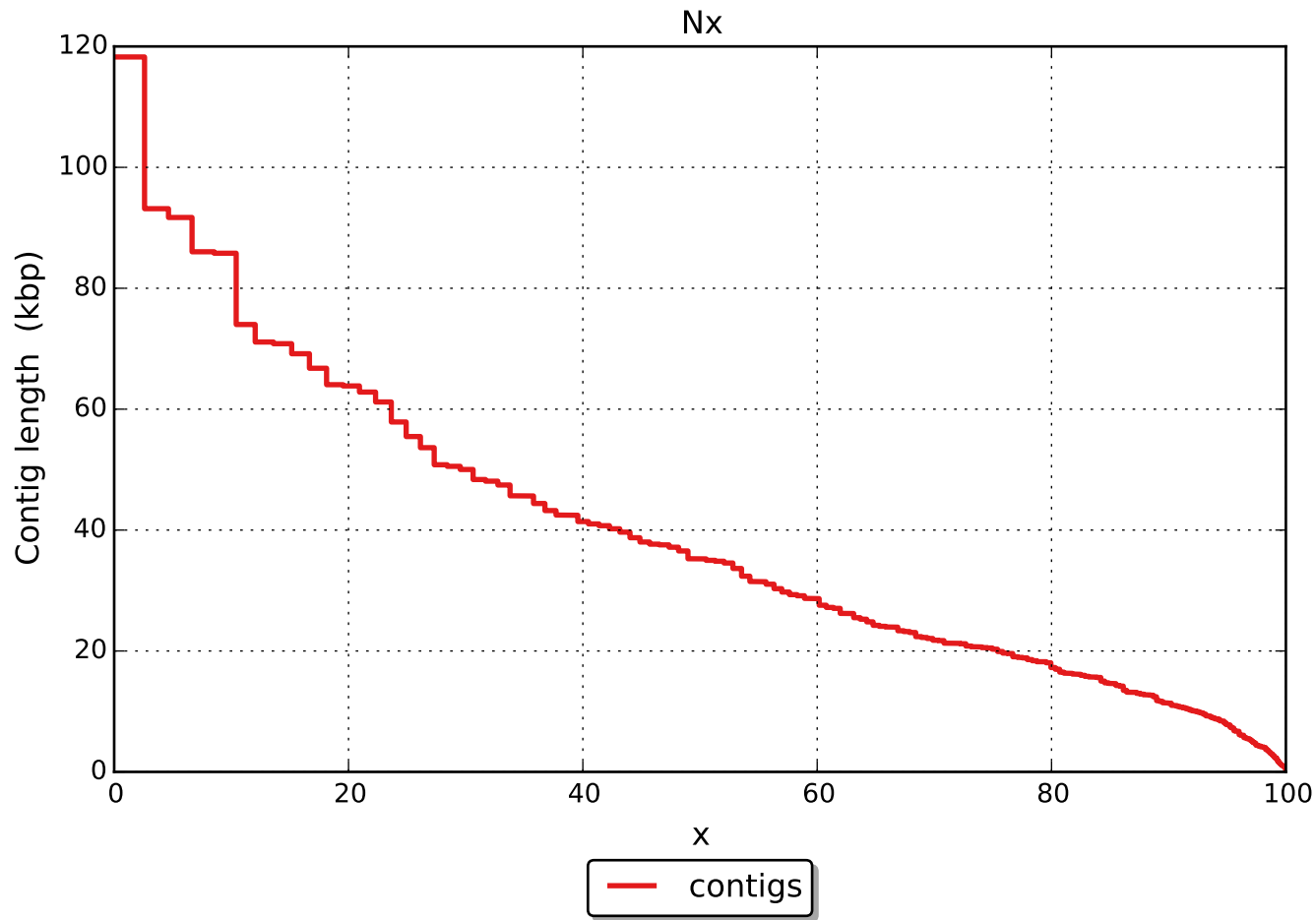
	contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	7
# mismatches	149
# indels	15
# short indels	13
# long indels	2
Indels length	180

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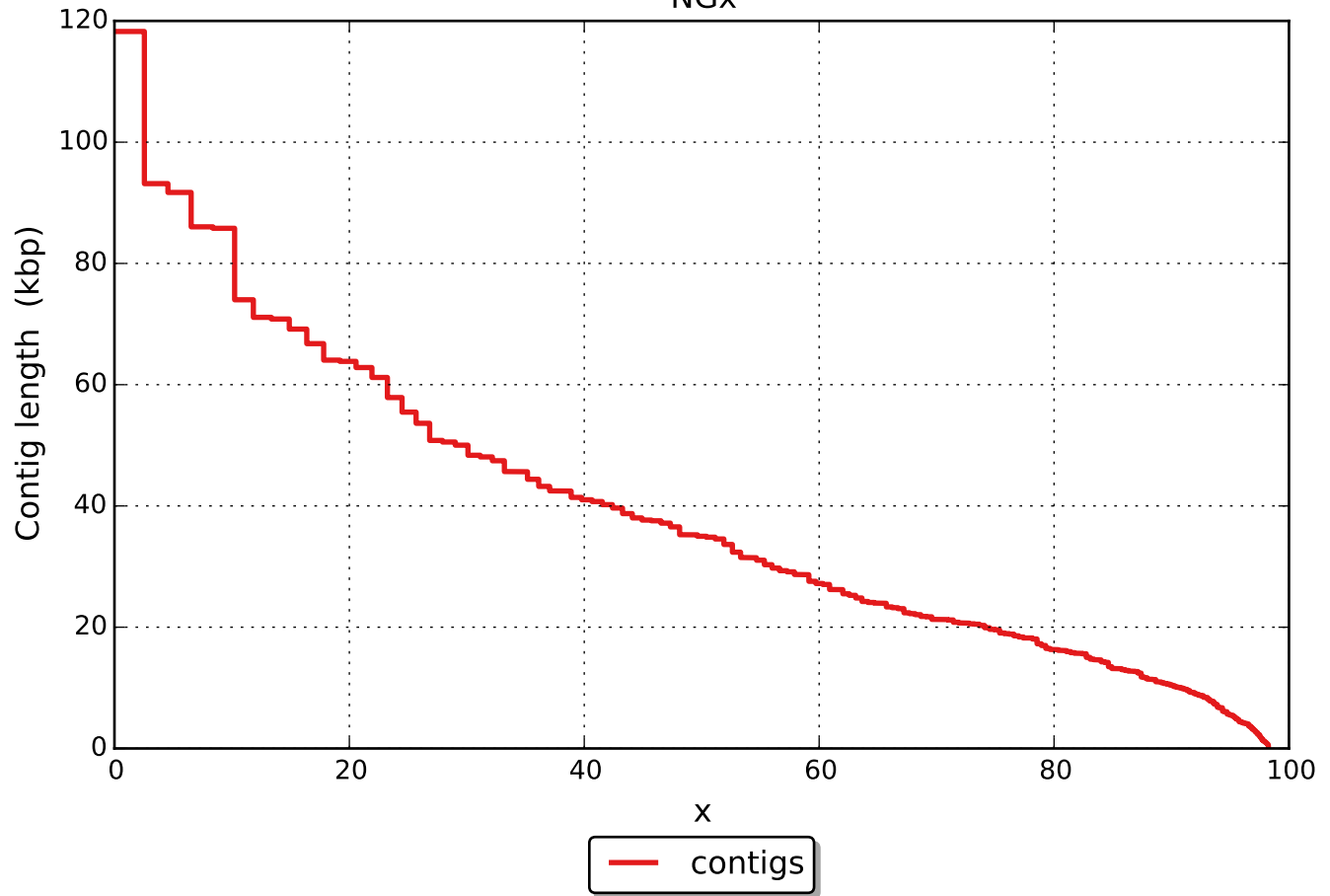
Unaligned report

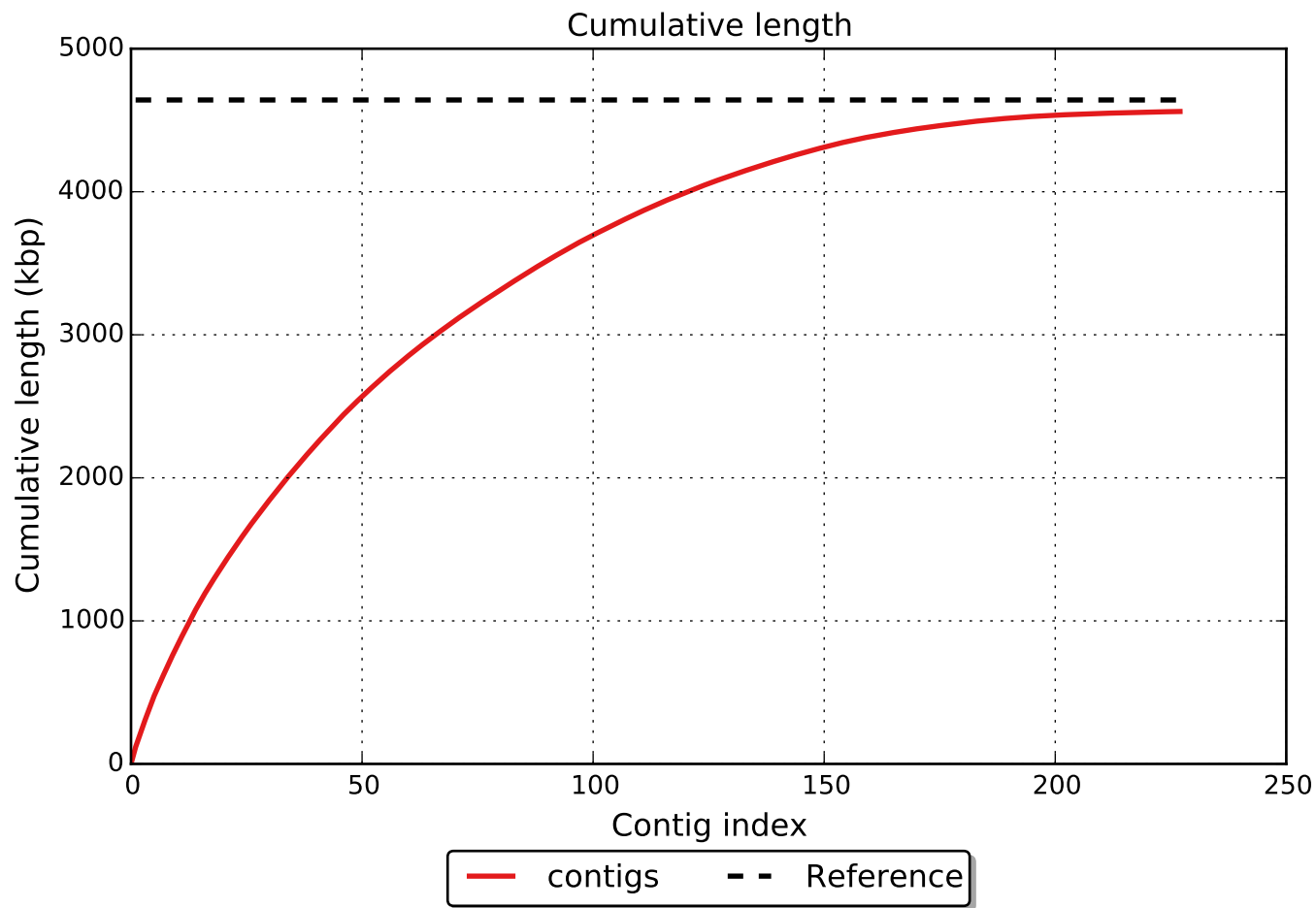
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

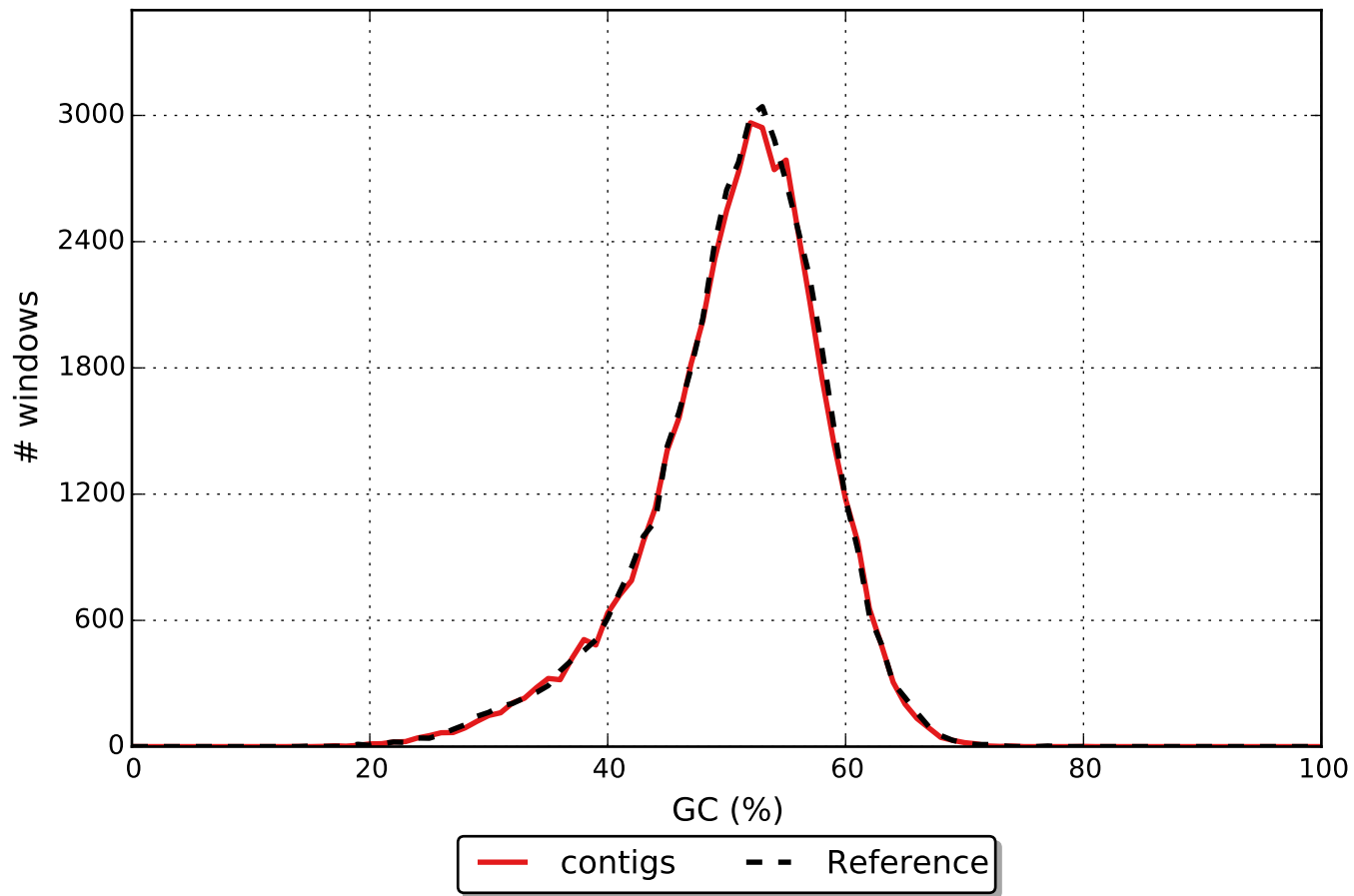


NGx





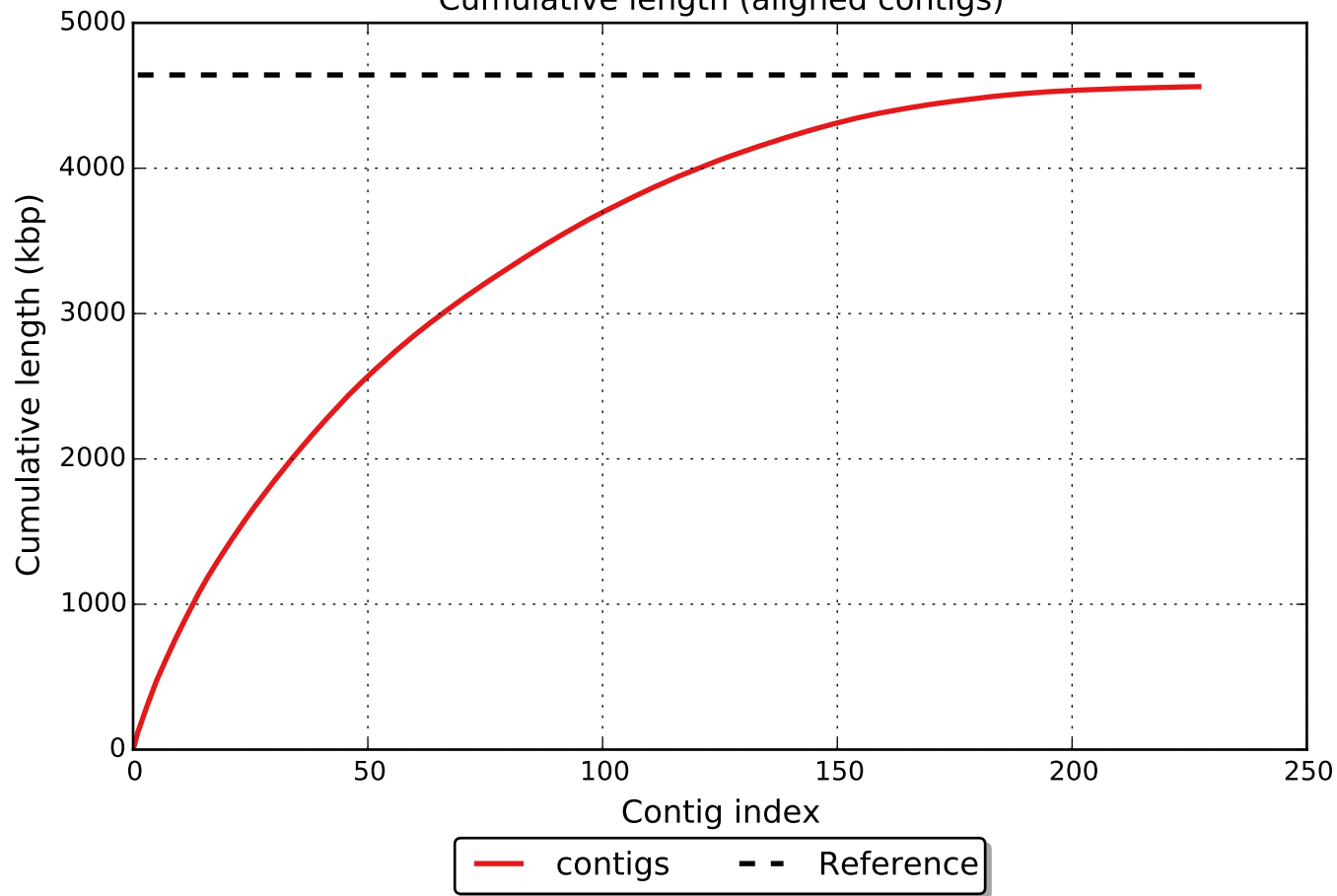
GC content



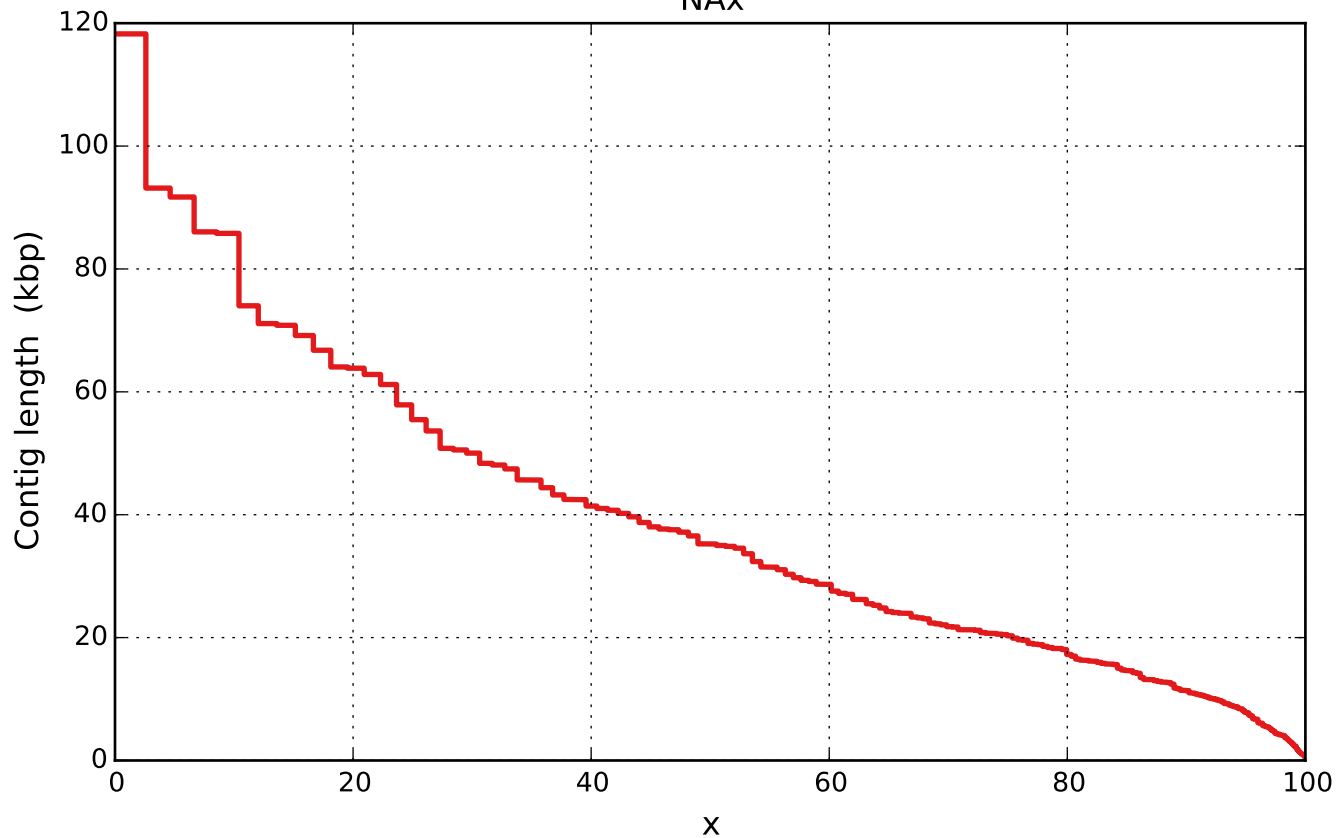
Misassemblies



Cumulative length (aligned contigs)



NAx



contigs

NGAx

