

Report

	contigs
# contigs (≥ 1000 bp)	306
# contigs (≥ 5000 bp)	186
# contigs (≥ 10000 bp)	116
# contigs (≥ 25000 bp)	53
# contigs (≥ 50000 bp)	23
Total length (≥ 1000 bp)	4854429
Total length (≥ 5000 bp)	4533544
Total length (≥ 10000 bp)	4039165
Total length (≥ 25000 bp)	3041270
Total length (≥ 50000 bp)	1956185
# contigs	351
Largest contig	186891
Total length	4883608
Reference length	4641652
GC (%)	50.73
Reference GC (%)	50.79
N50	36519
NG50	41626
N75	15187
NG75	17101
L50	35
LG50	32
L75	87
LG75	75
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	66116
# local misassemblies	3
# unaligned contigs	0 + 1 part
Unaligned length	54
Genome fraction (%)	90.193
Duplication ratio	1.167
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1127.86
# indels per 100 kbp	0.79
Largest alignment	186891
NA50	36519
NGA50	41626
NA75	14917
NGA75	16867
LA50	35
LGA50	32
LA75	88
LGA75	76

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

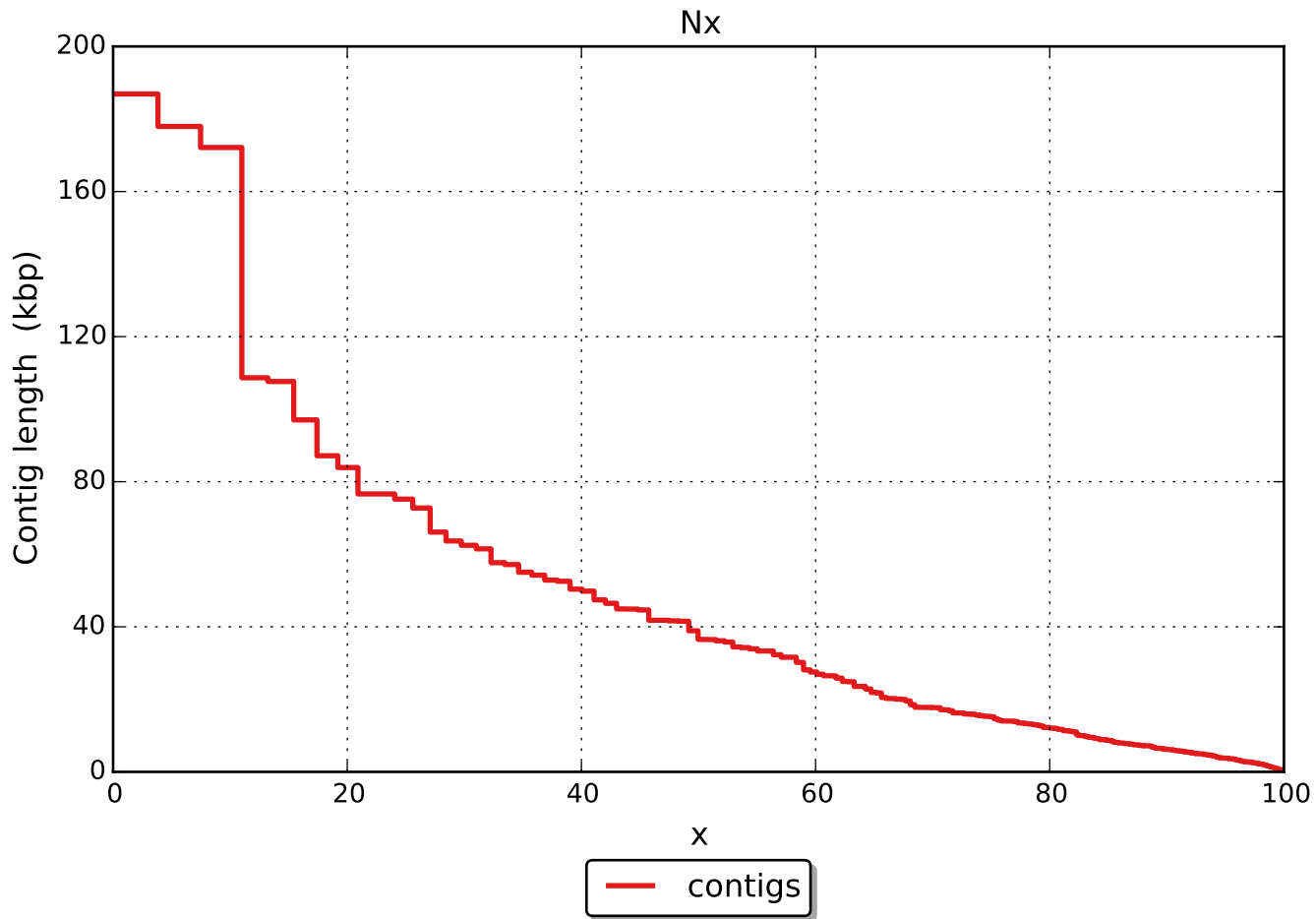
	contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	66116
# local misassemblies	3
# mismatches	47217
# indels	33
# short indels	33
# long indels	0
Indels length	39

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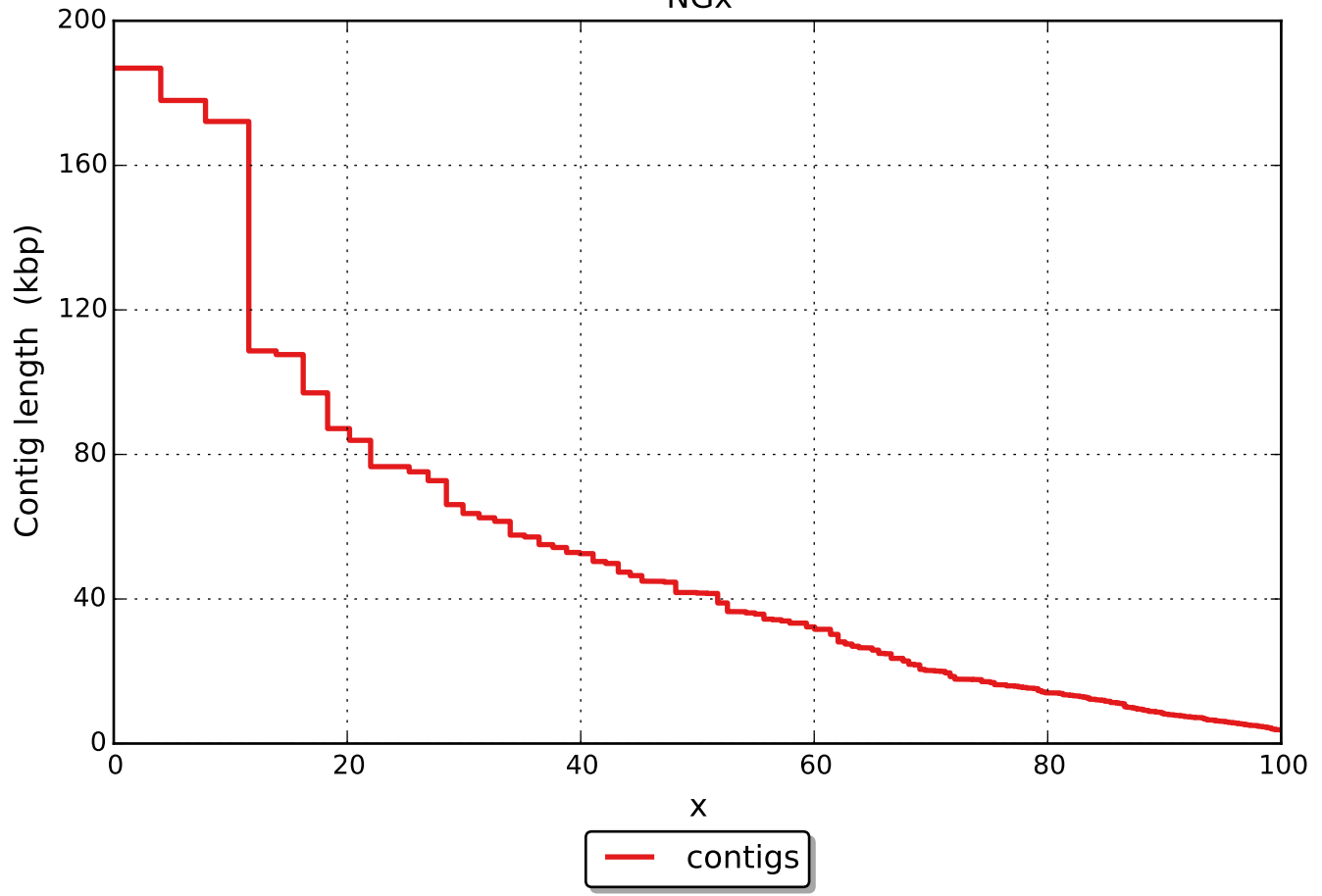
Unaligned report

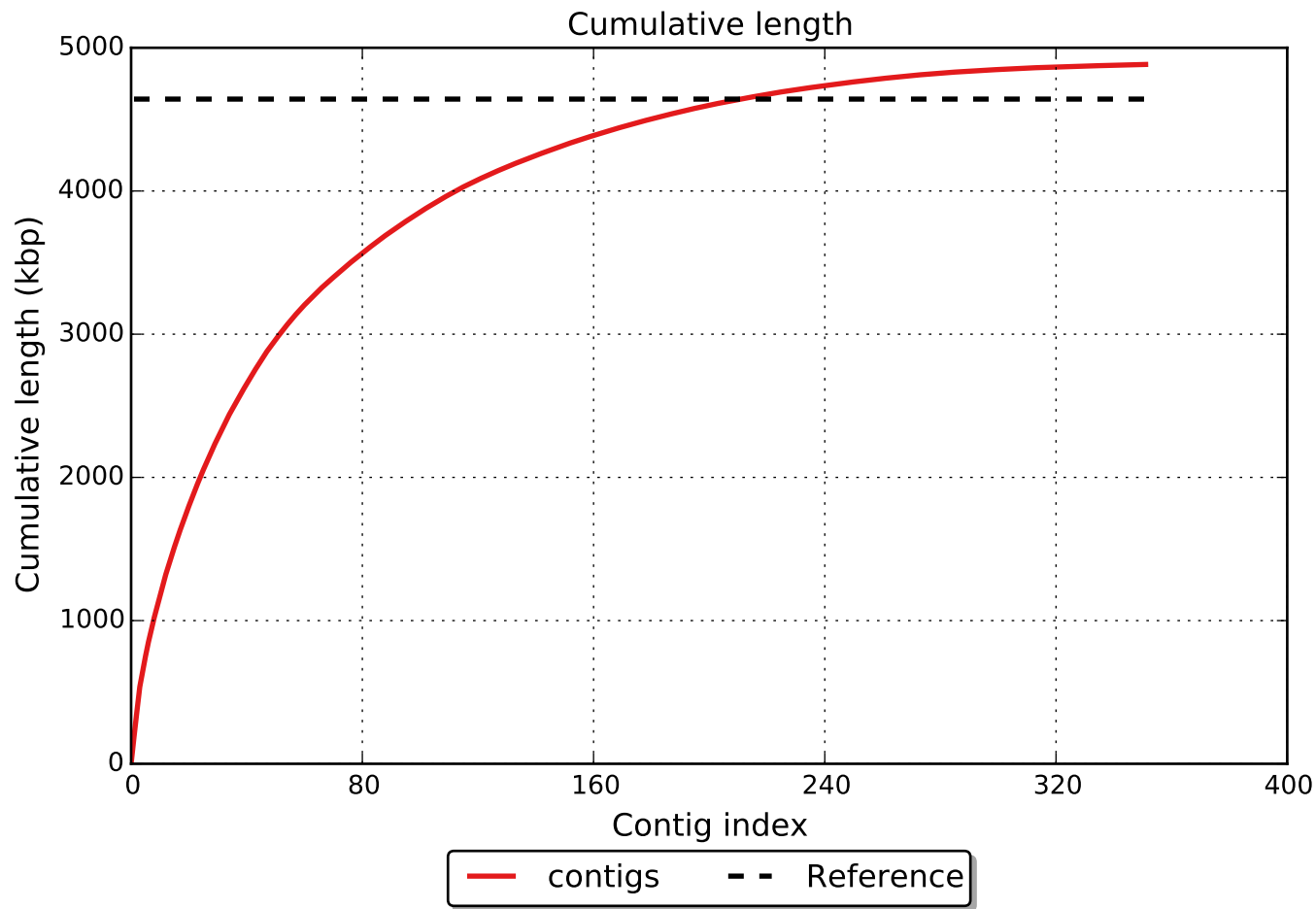
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	54
# N's	0

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).

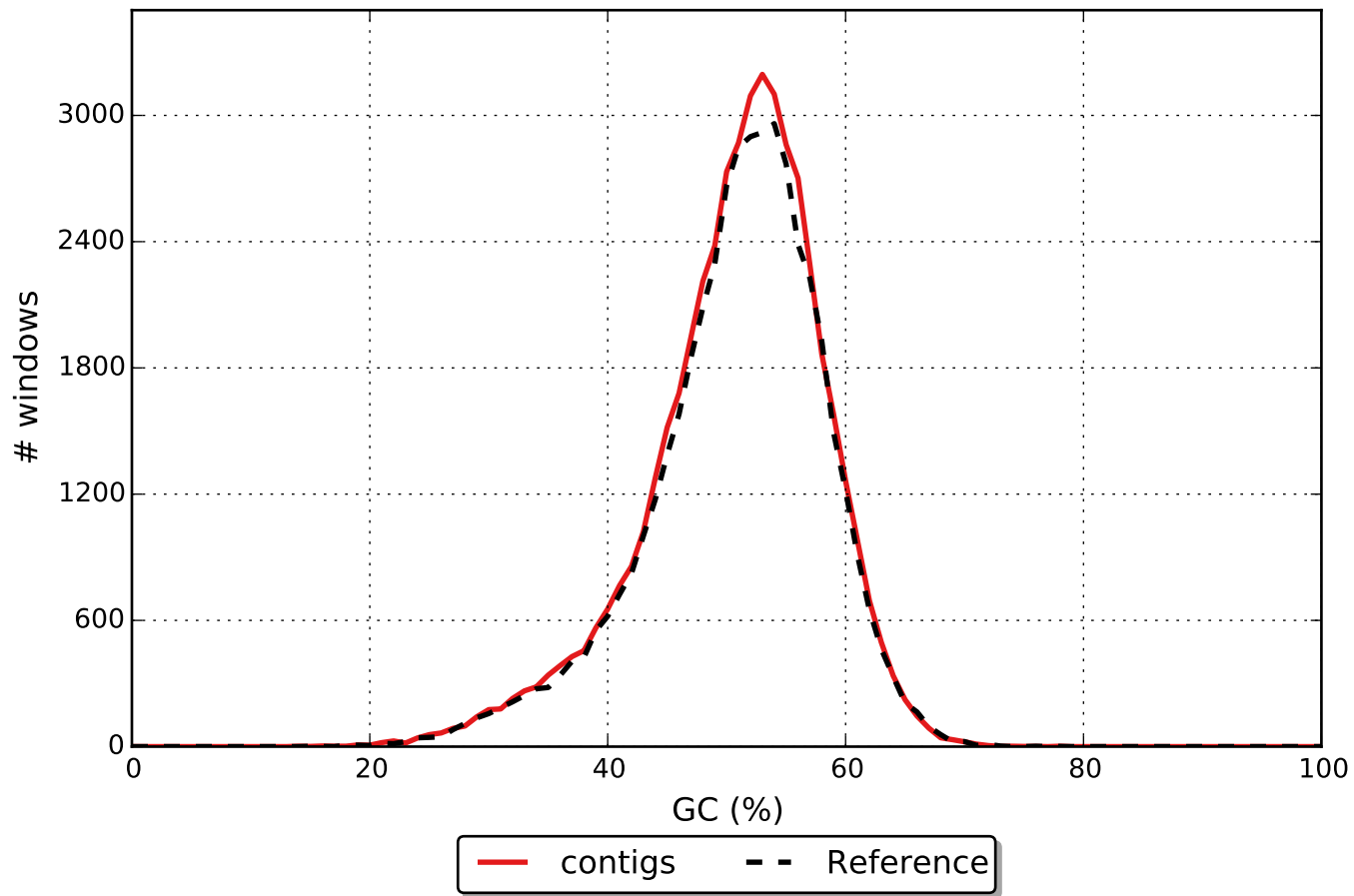


NGx





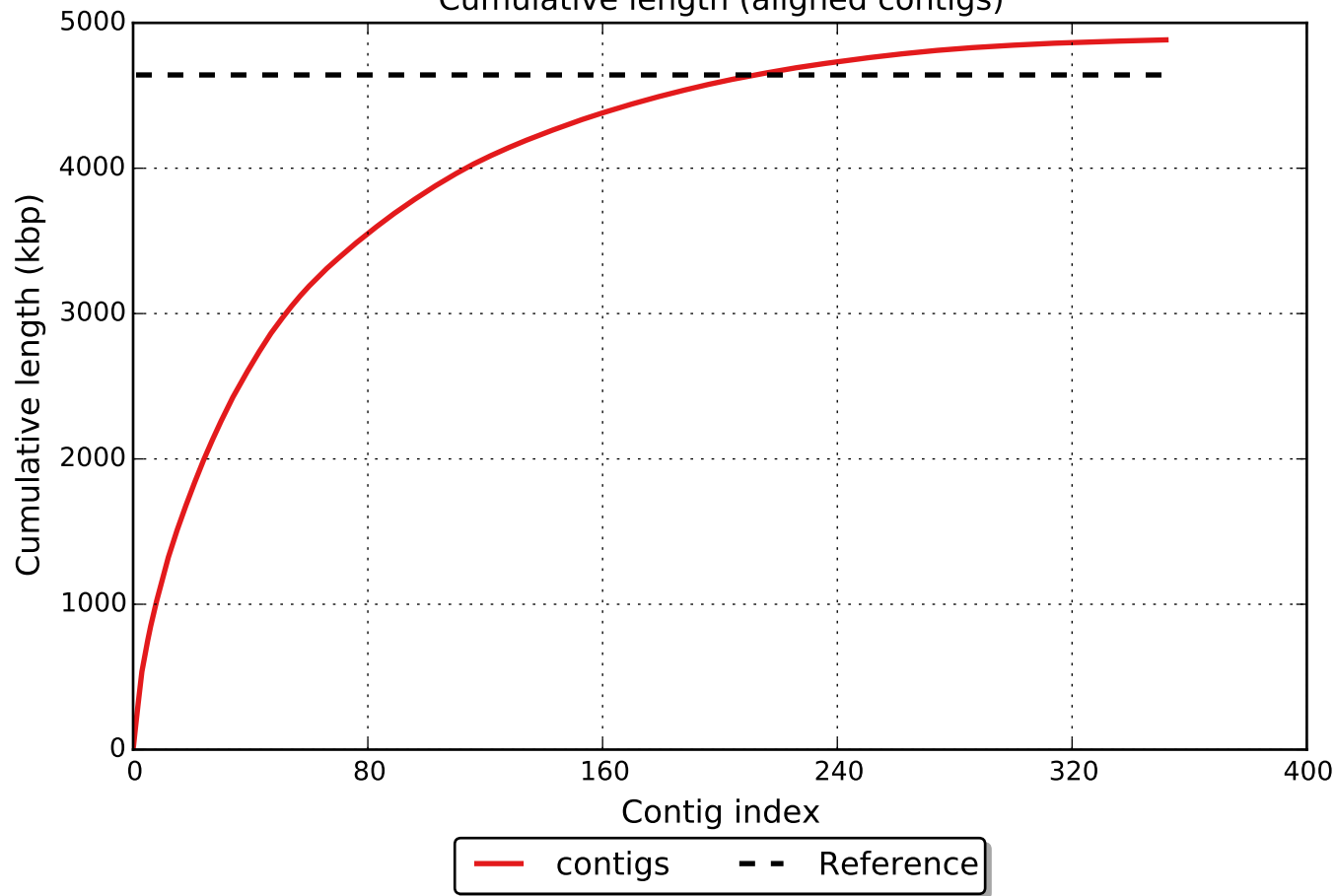
GC content



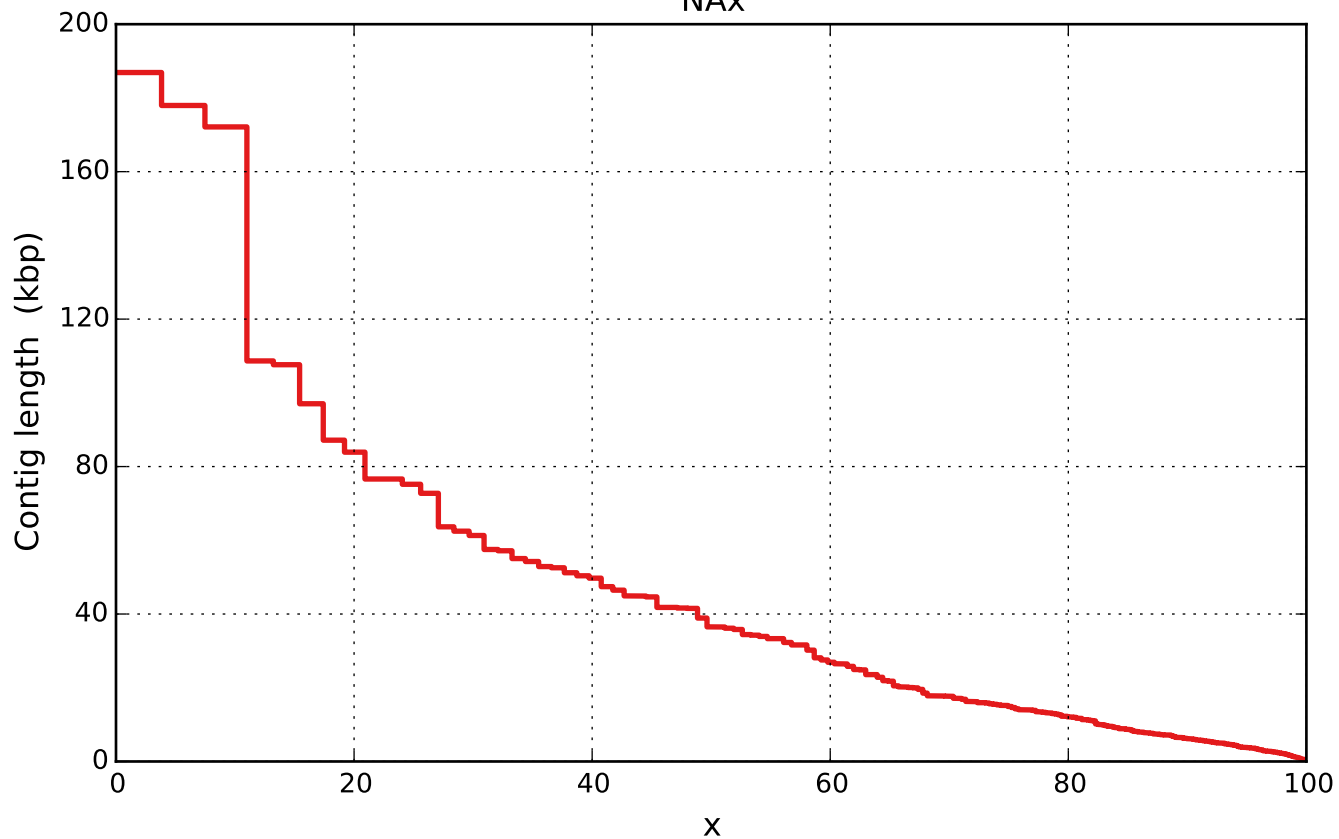
Misassemblies



Cumulative length (aligned contigs)



NAx



contigs

NGAx

