

Report

	contigs
# contigs (≥ 0 bp)	780
# contigs (≥ 1000 bp)	134
# contigs (≥ 5000 bp)	91
# contigs (≥ 10000 bp)	74
# contigs (≥ 25000 bp)	57
# contigs (≥ 50000 bp)	29
Total length (≥ 0 bp)	4621983
Total length (≥ 1000 bp)	4555717
Total length (≥ 5000 bp)	4440080
Total length (≥ 10000 bp)	4310611
Total length (≥ 25000 bp)	4026686
Total length (≥ 50000 bp)	2992466
# contigs	145
Largest contig	236743
Total length	4562833
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	78609
NG50	78609
N75	38671
NG75	37846
L50	18
LG50	18
L75	39
LG75	41
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	454654
# local misassemblies	5
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.110
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	19.28
# indels per 100 kbp	1.12
Largest alignment	210558
NA50	77801
NGA50	77801
NA75	38671
NGA75	37846
LA50	20
LGA50	20
LA75	41
LGA75	43

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	454654
# local misassemblies	5
# mismatches	878
# indels	51
# short indels	49
# long indels	2
Indels length	143

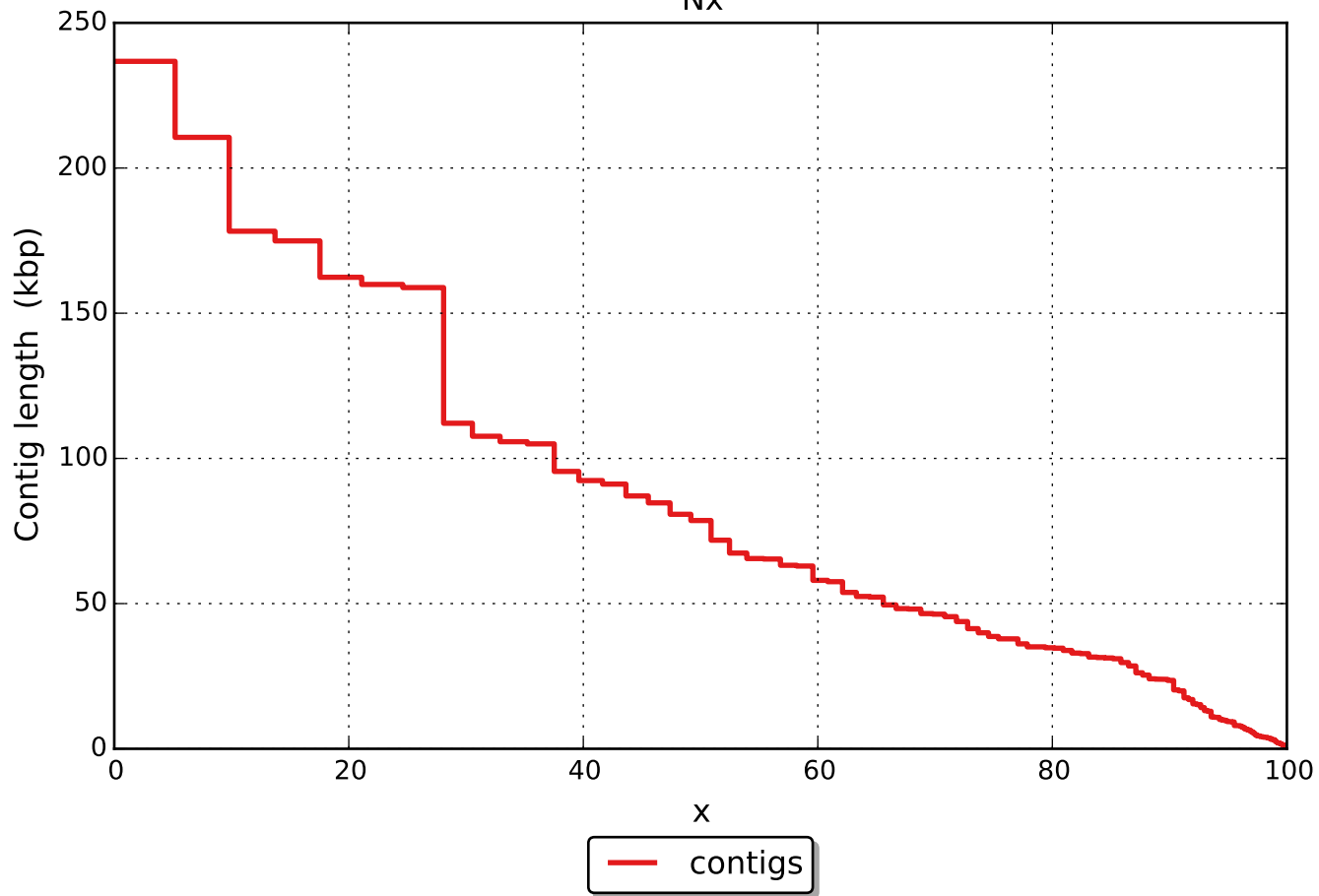
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

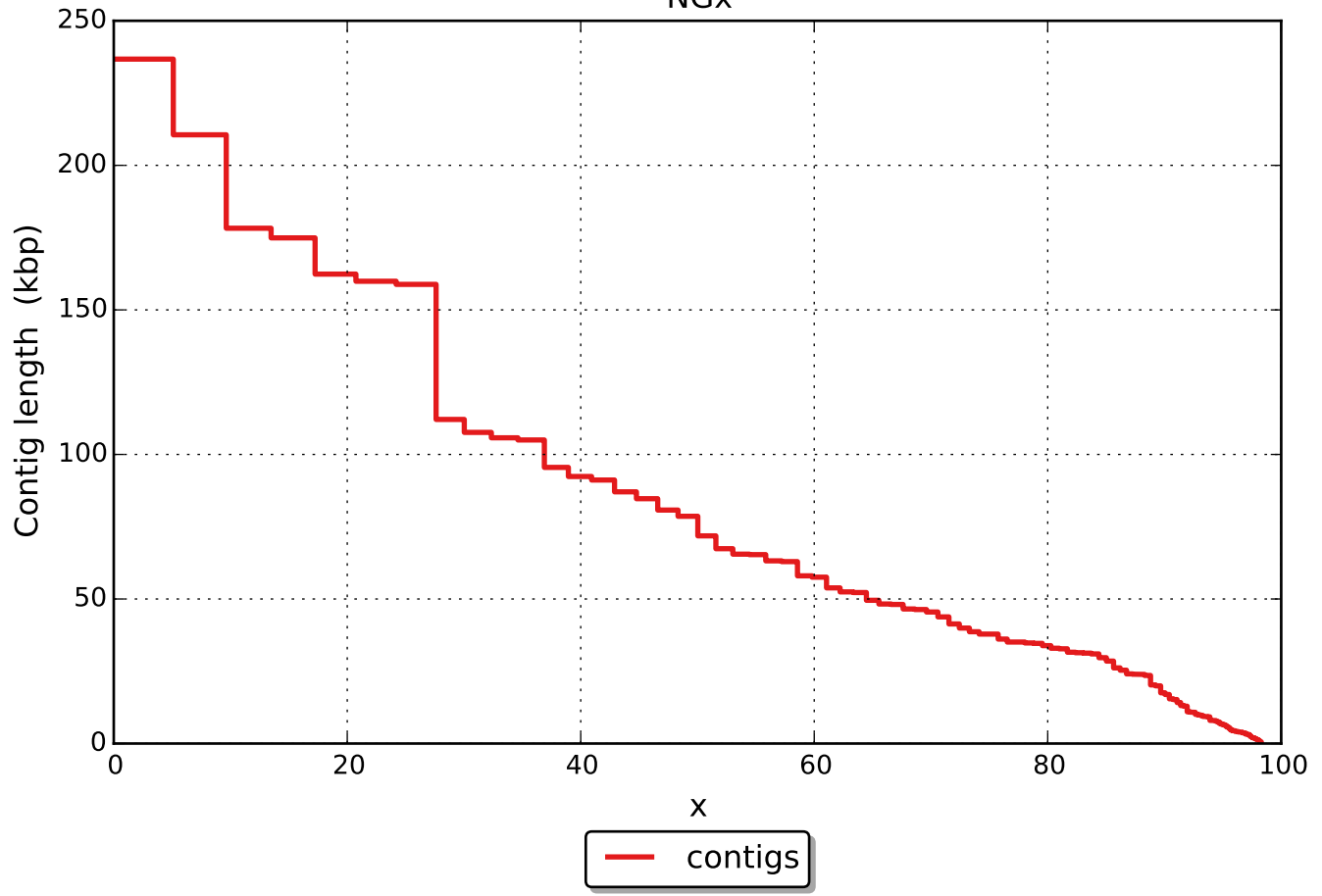
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

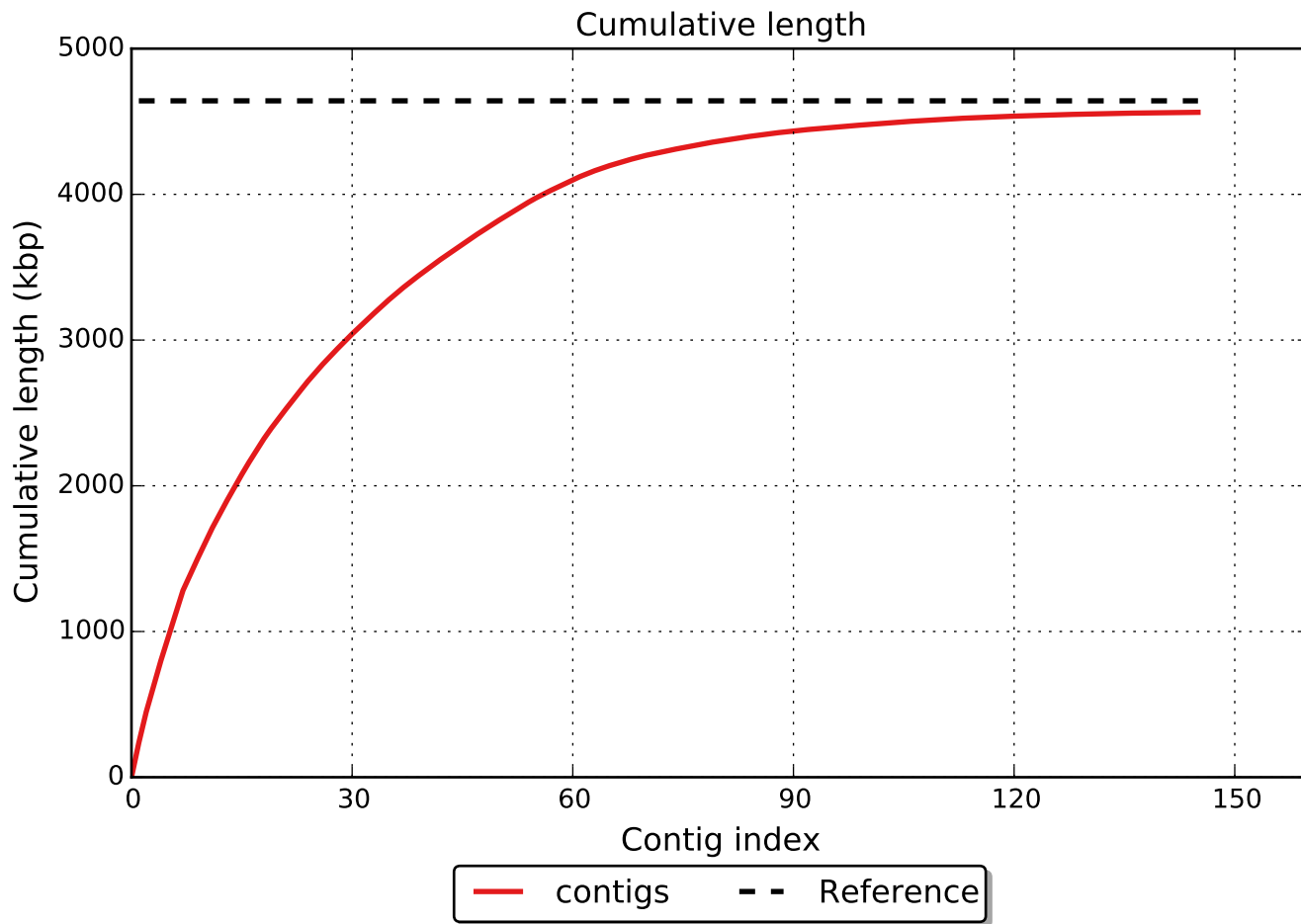
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

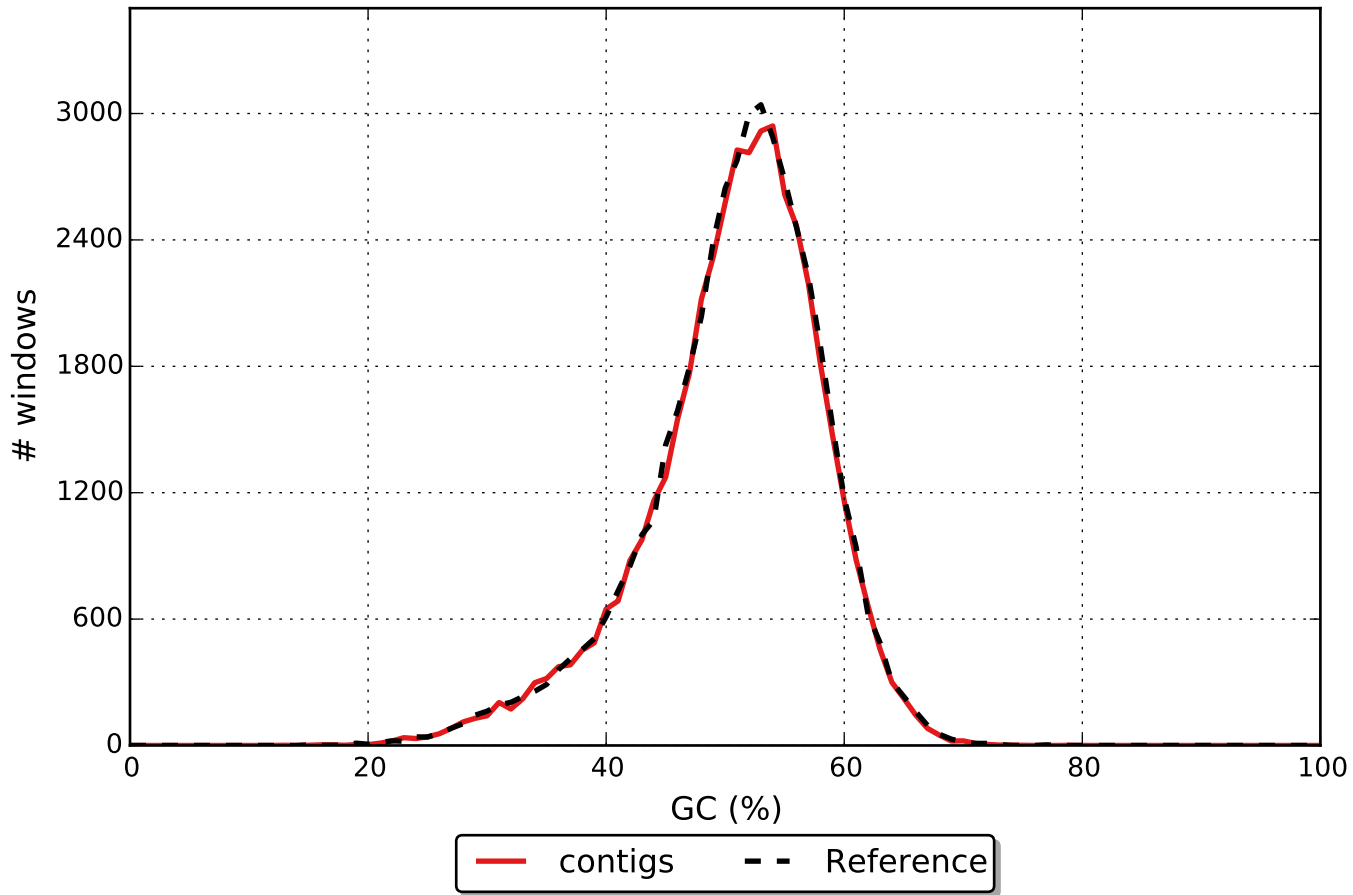


NGx

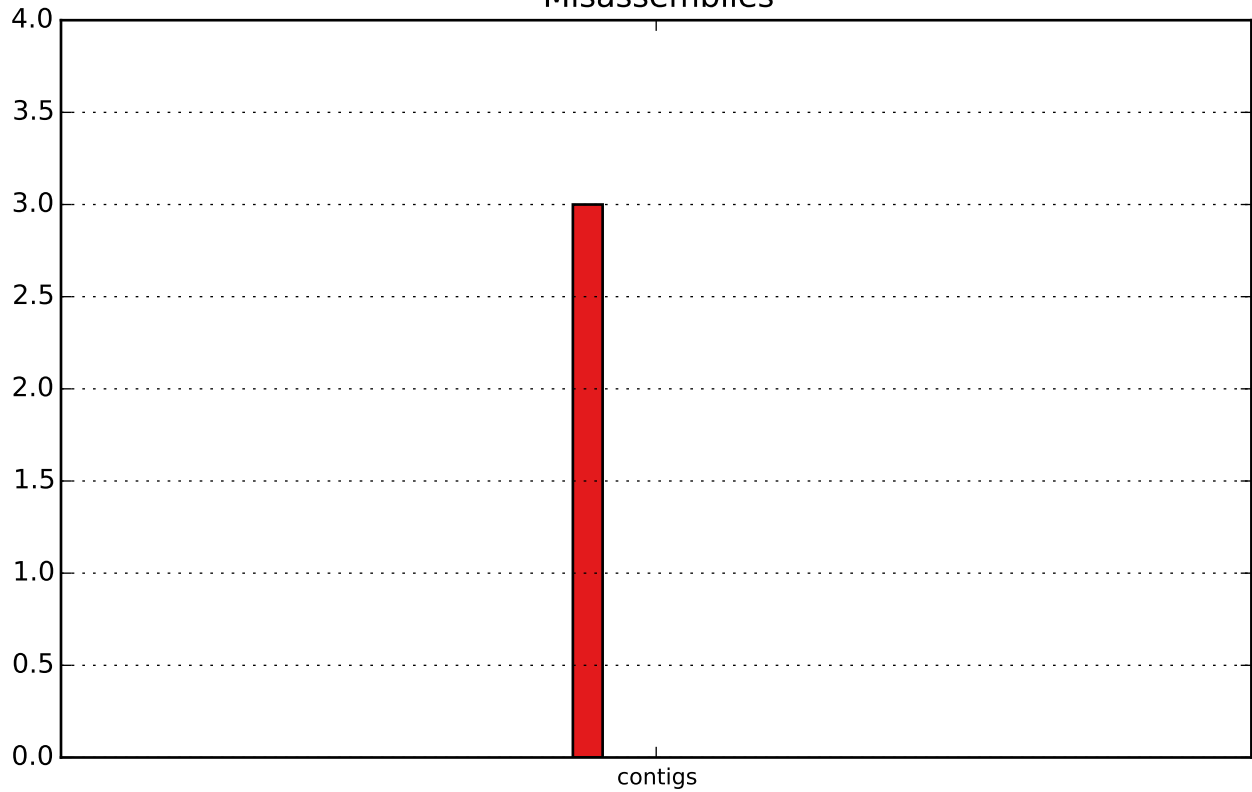




GC content

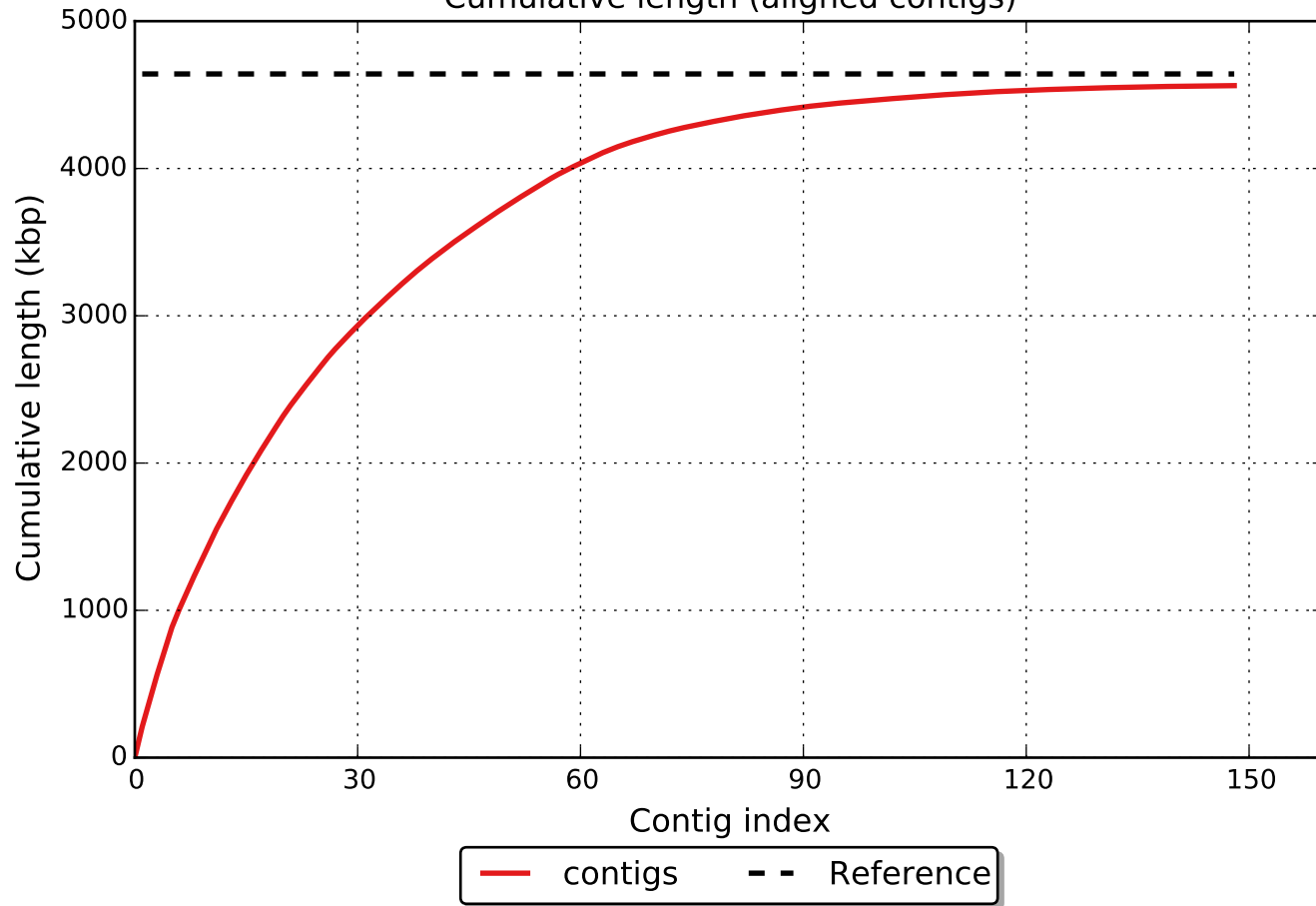


Misassemblies

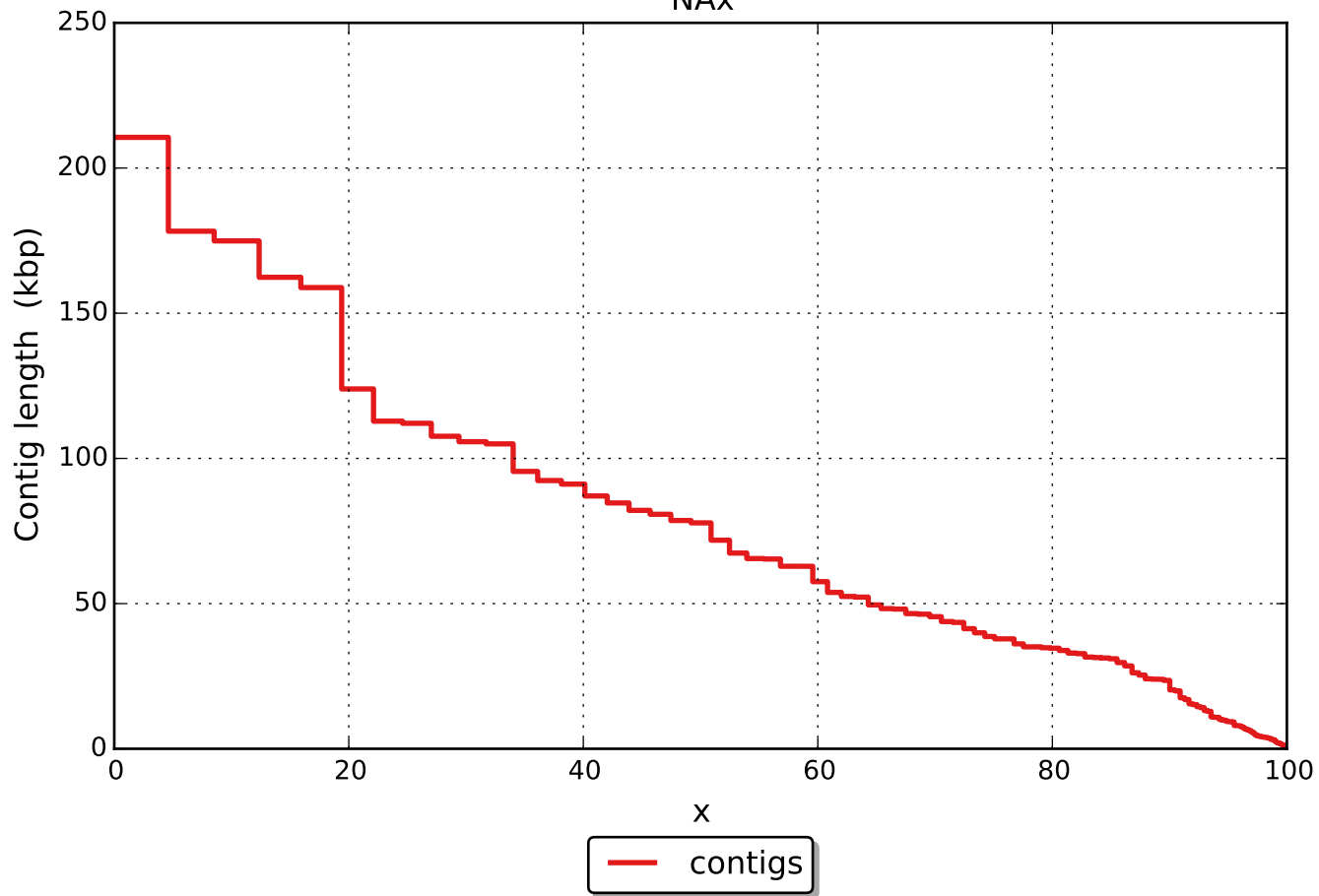


 # relocations

Cumulative length (aligned contigs)



NAx



NGAx

