

Report

	contigs
# contigs (≥ 0 bp)	45
# contigs (≥ 1000 bp)	5
# contigs (≥ 5000 bp)	0
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	21281
Total length (≥ 1000 bp)	8050
Total length (≥ 5000 bp)	0
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	10
Largest contig	2951
Total length	11595
Reference length	4641652
GC (%)	51.92
Reference GC (%)	50.79
N50	1416
N75	795
L50	3
L75	6
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	2419
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	0.250
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	940.79
# indels per 100 kbp	17.26
Largest alignment	2951
NA50	1322
NGA50	-
NA75	764
LA50	3
LA75	7

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	2
# relocations	2
# translocations	0
# inversions	0
# misassembled contigs	2
Misassembled contigs length	2419
# local misassemblies	0
# mismatches	109
# indels	2
# short indels	2
# long indels	0
Indels length	2

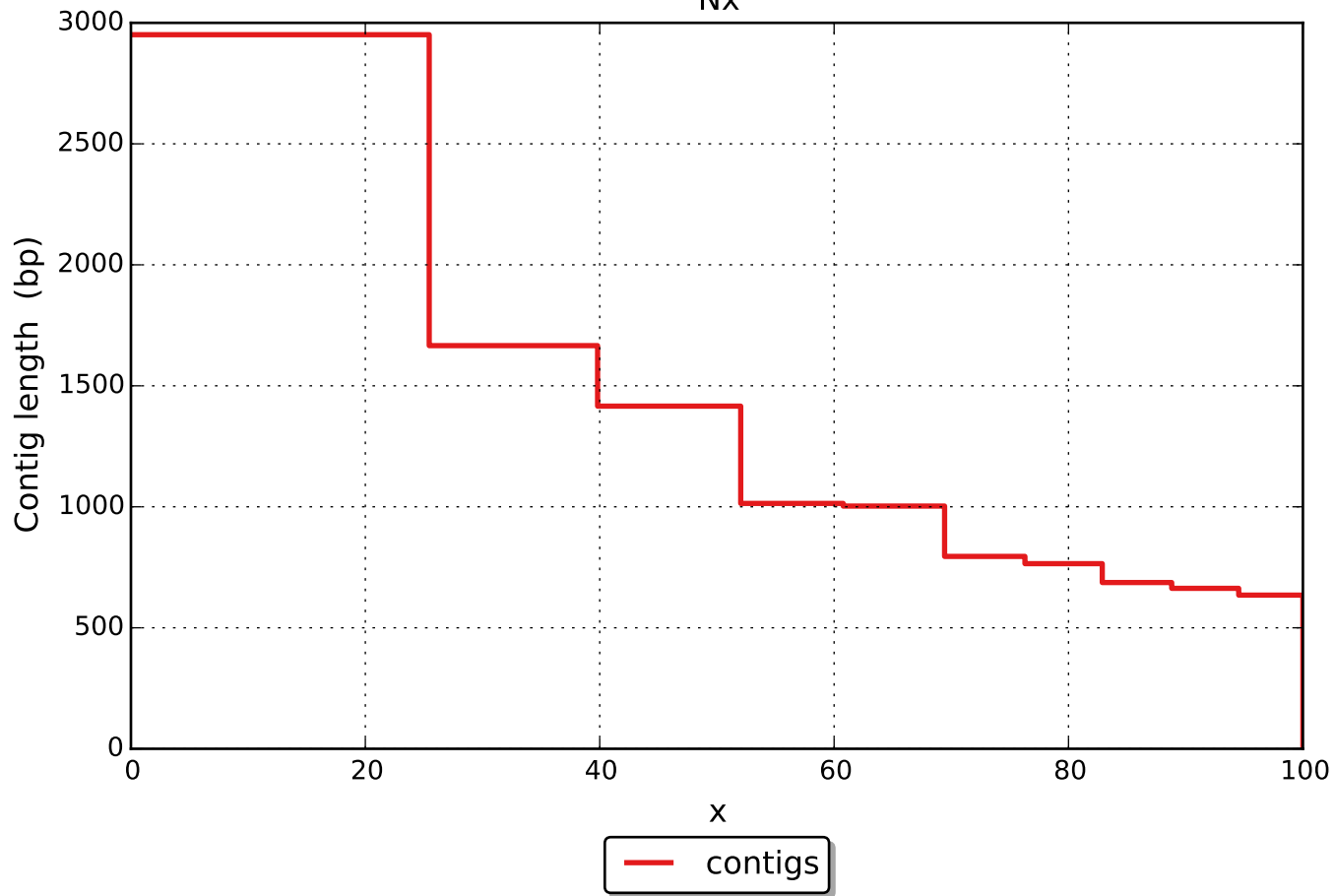
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

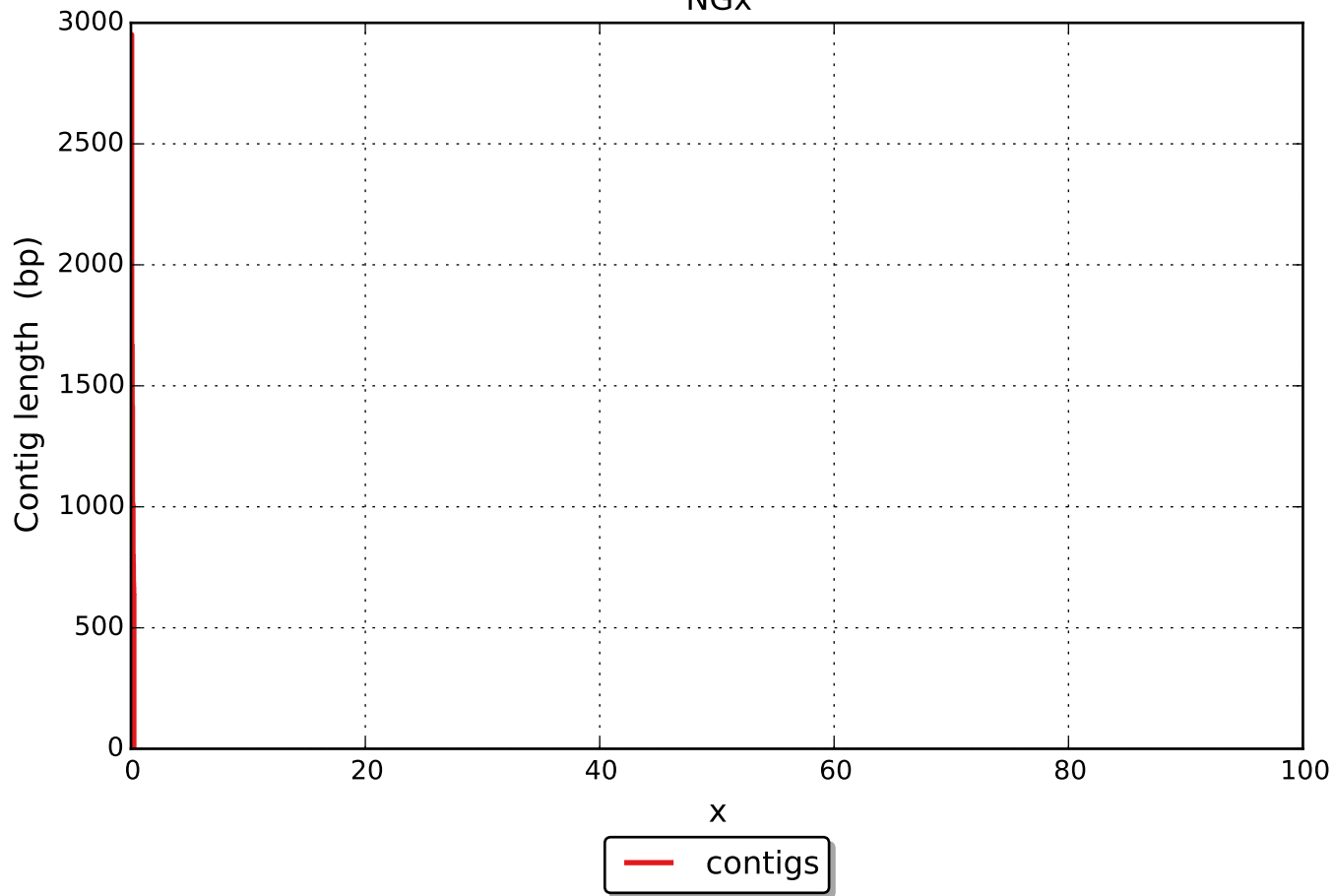
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

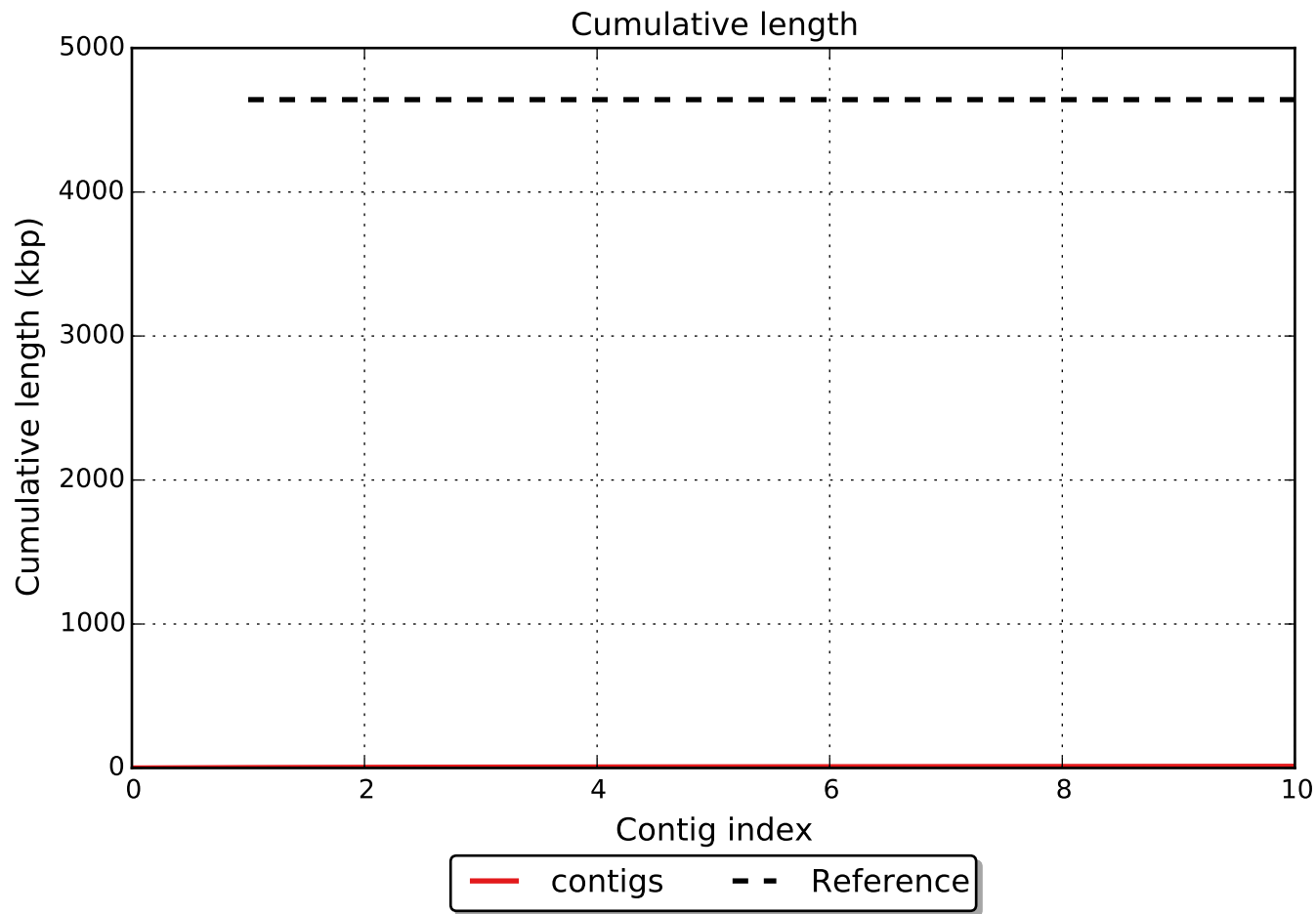
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

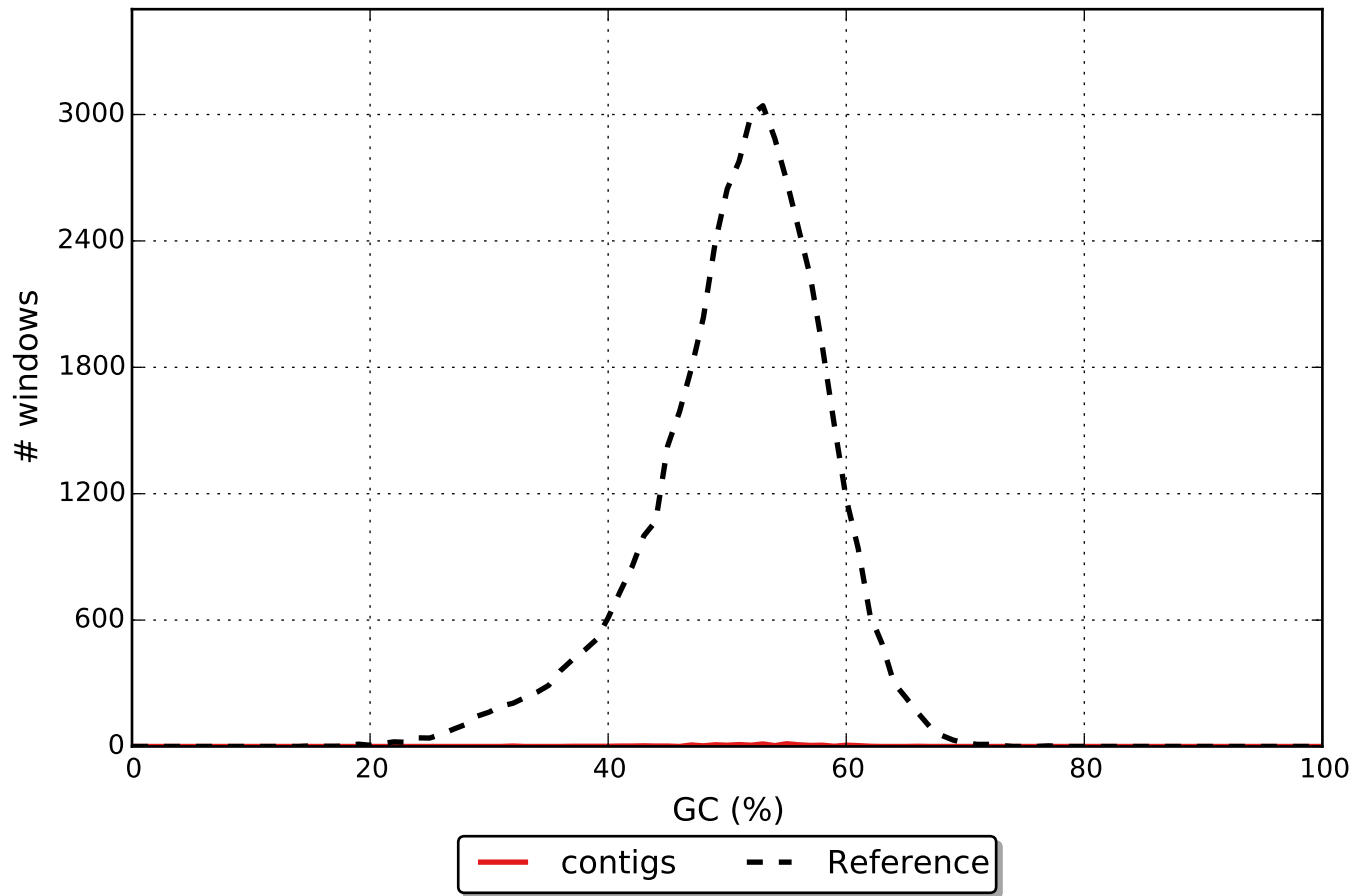


NGx



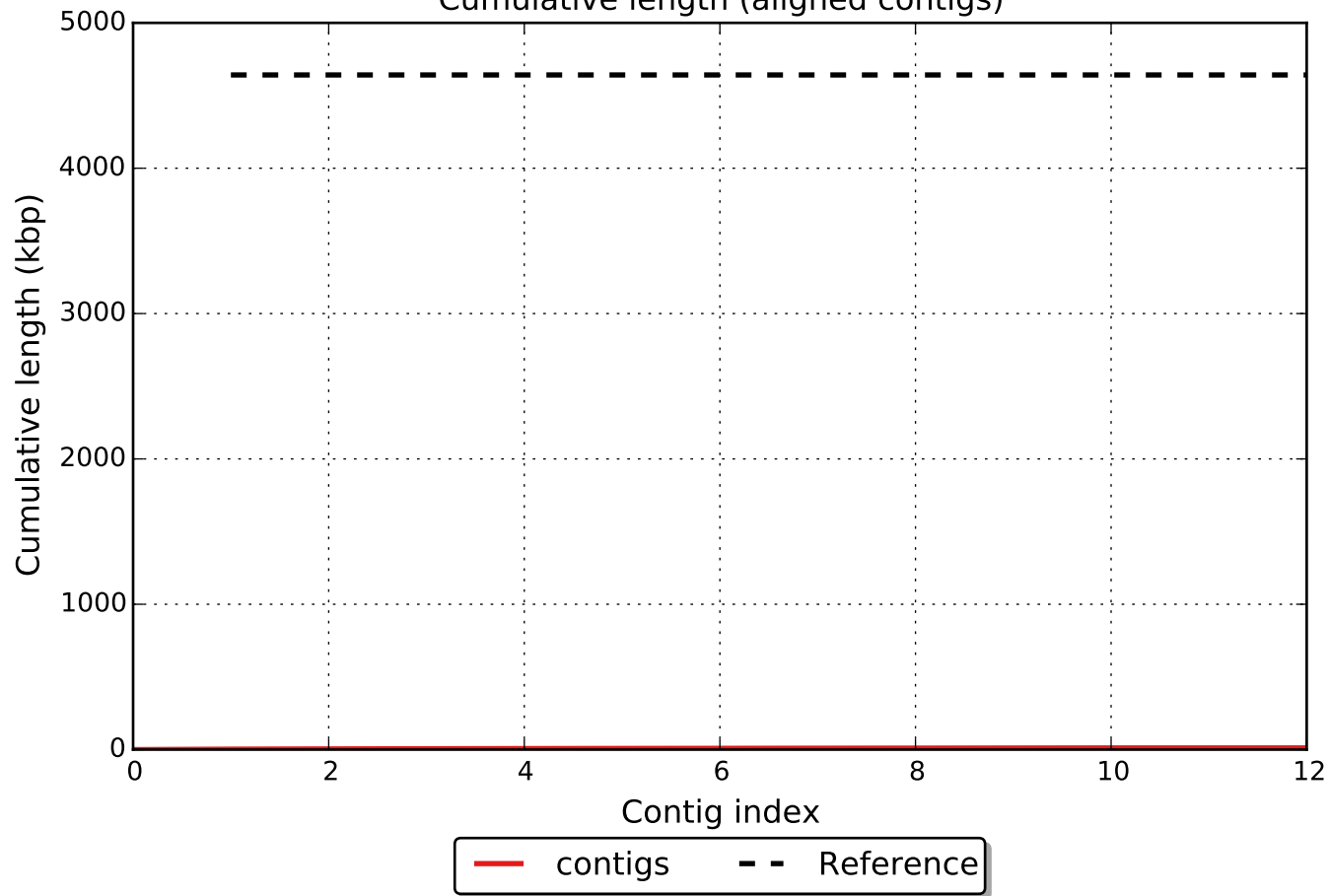


GC content

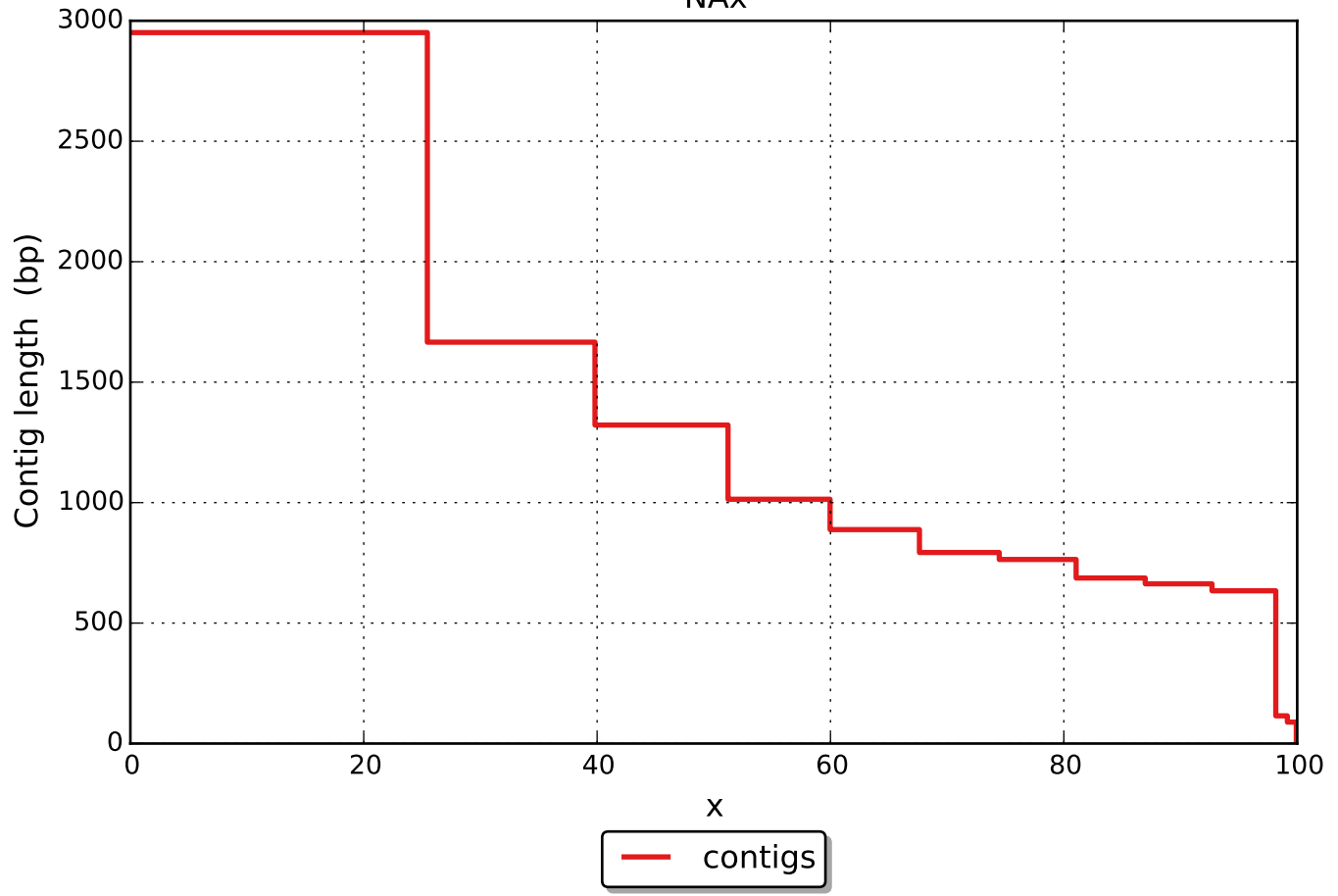




Cumulative length (aligned contigs)



NAx



NGAx

