

Report

	final.contigs
# contigs (≥ 0 bp)	3657
# contigs (≥ 1000 bp)	575
# contigs (≥ 5000 bp)	0
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	2482272
Total length (≥ 1000 bp)	804538
Total length (≥ 5000 bp)	0
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	2153
Largest contig	3631
Total length	1902131
Reference length	4641652
GC (%)	50.87
Reference GC (%)	50.79
N50	909
N75	683
L50	729
L75	1335
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	5007
# local misassemblies	1
# unaligned contigs	7 + 10 part
Unaligned length	9244
Genome fraction (%)	40.768
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2.96
# indels per 100 kbp	0.26
Largest alignment	3631
NA50	900
NGA50	-
NA75	678
LA50	733
LA75	1342

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

	final.contigs
# misassemblies	2
# relocations	2
# translocations	0
# inversions	0
# misassembled contigs	2
Misassembled contigs length	5007
# local misassemblies	1
# mismatches	56
# indels	5
# short indels	5
# long indels	0
Indels length	5

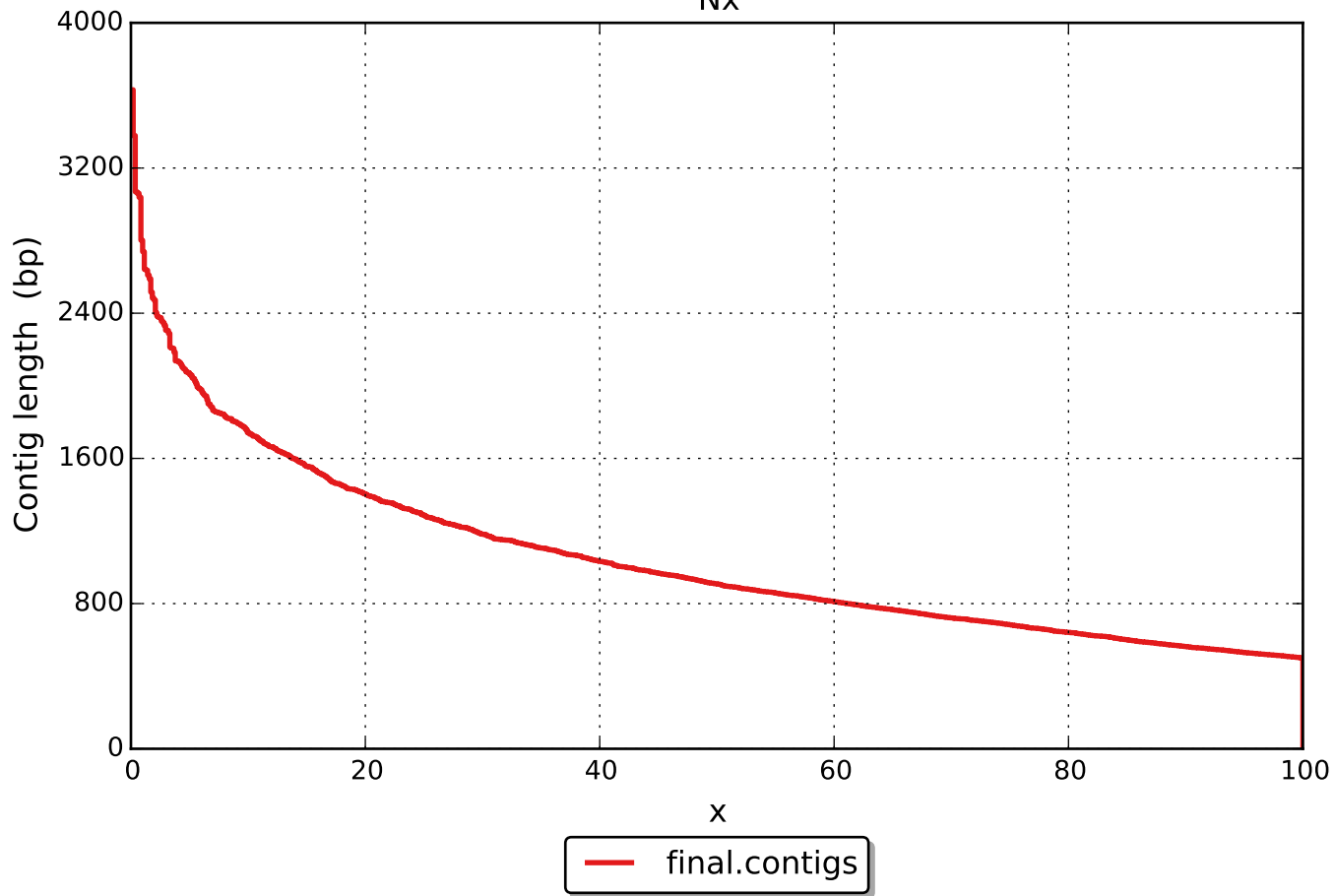
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

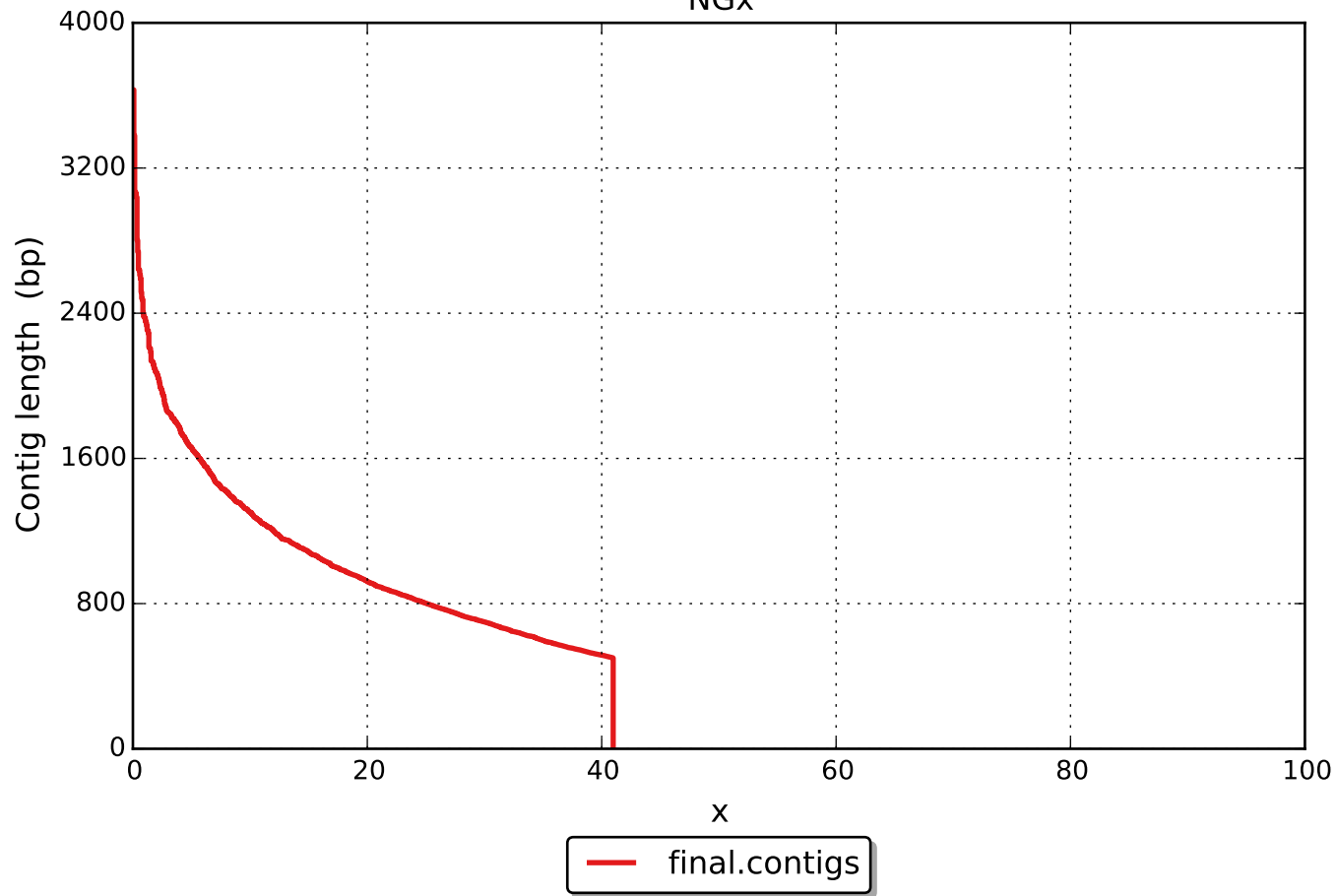
	final.contigs
# fully unaligned contigs	7
Fully unaligned length	6244
# partially unaligned contigs	10
# with misassembly	0
# both parts are significant	1
Partially unaligned length	3000
# N's	0

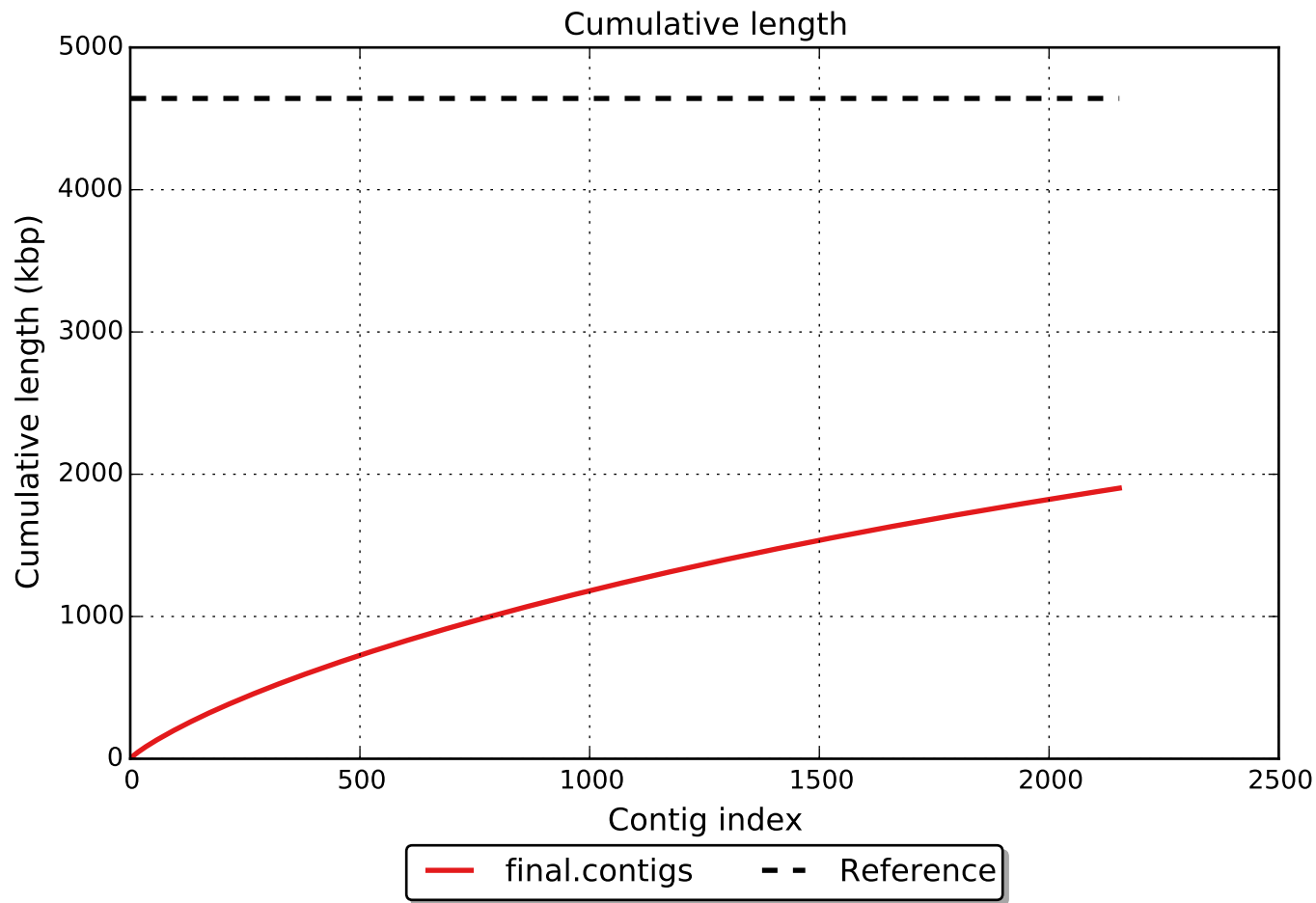
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

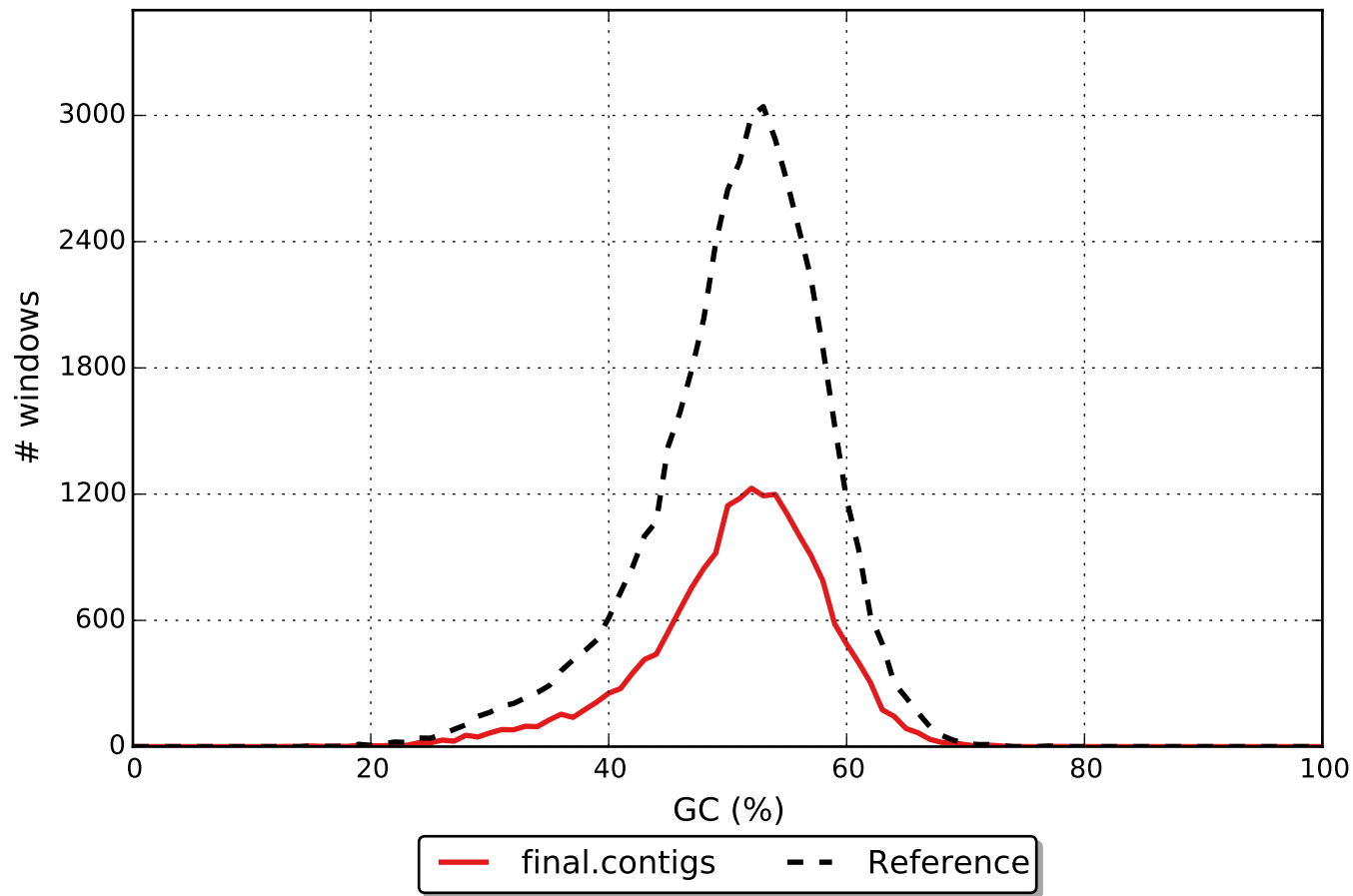


NGx



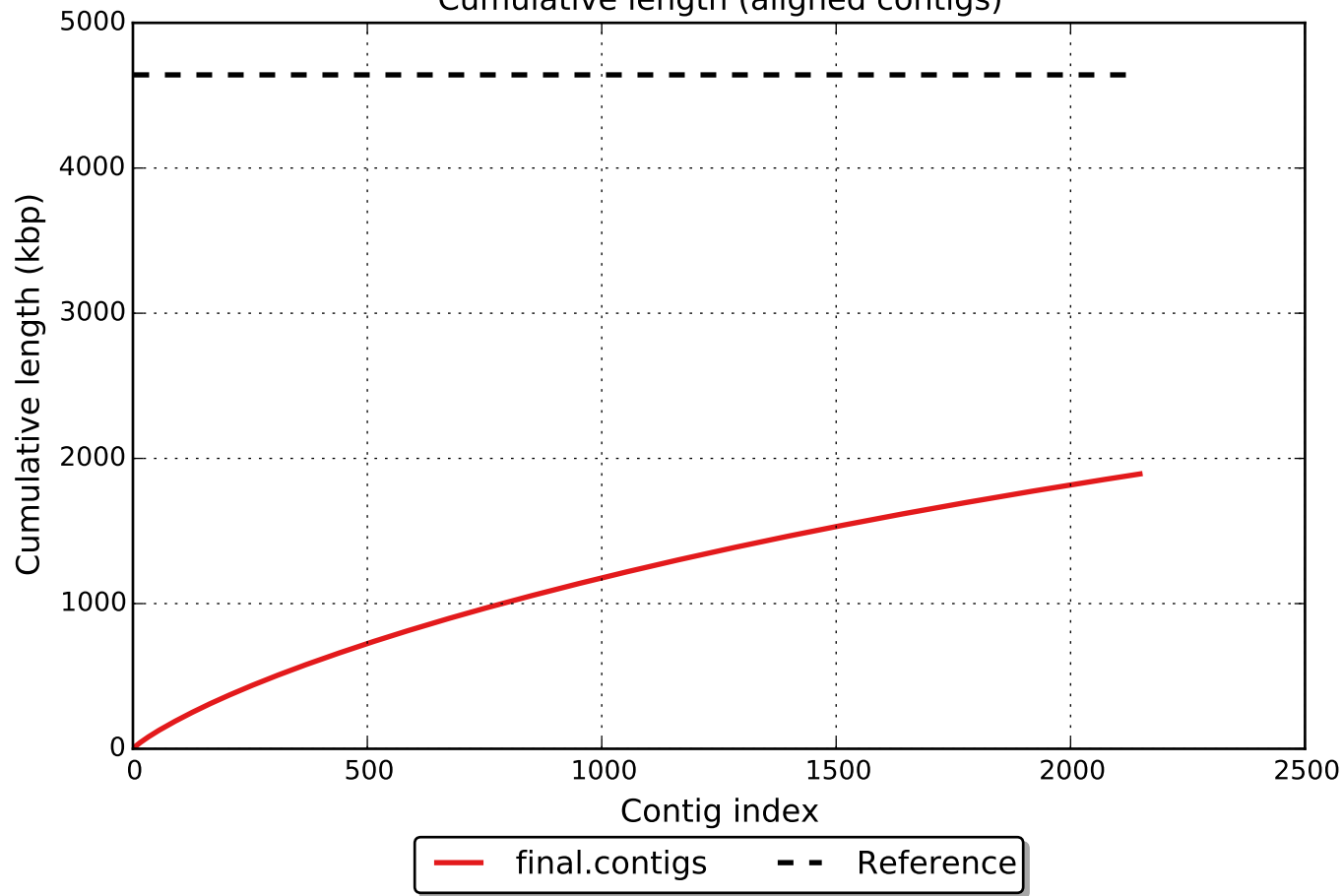


GC content

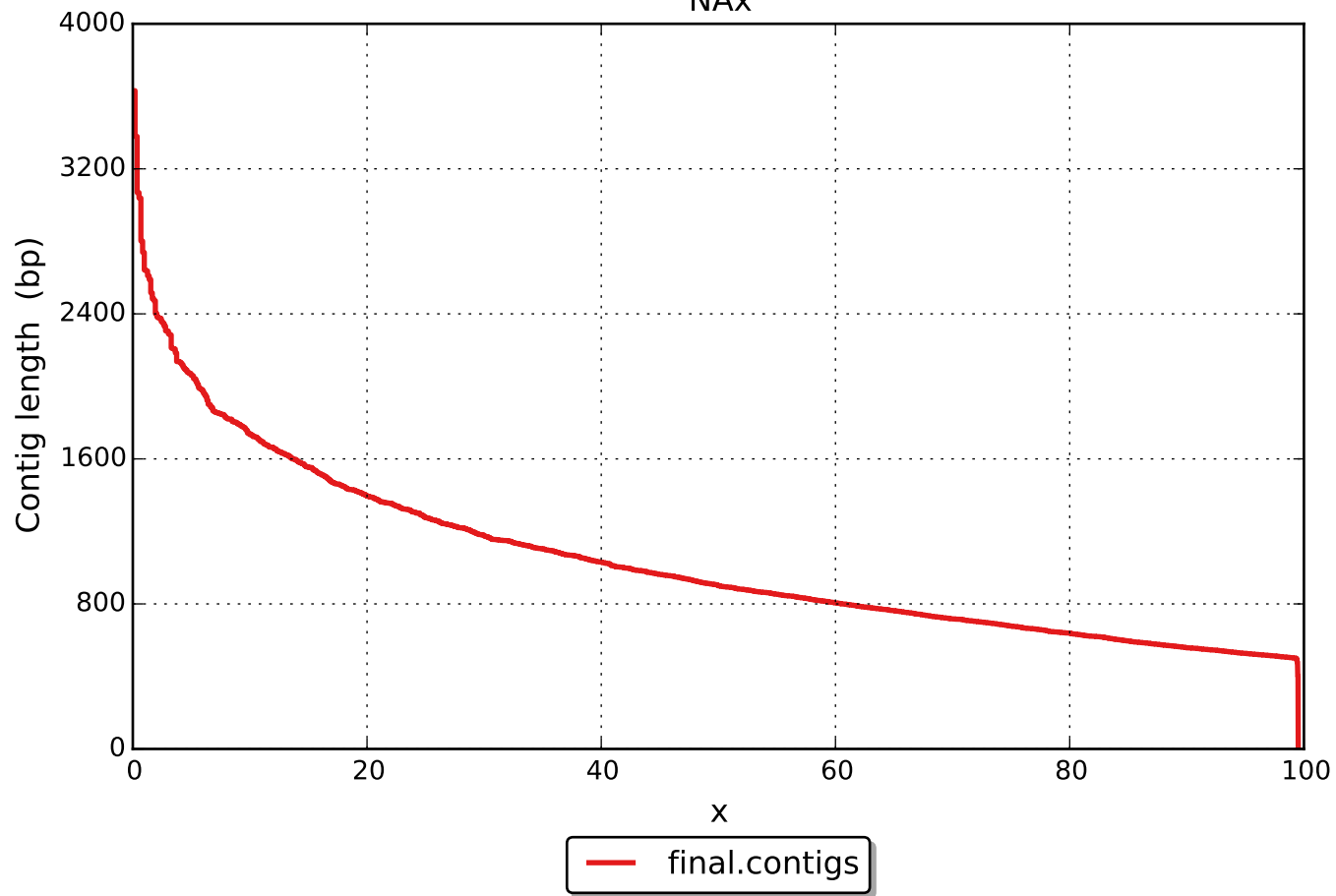




Cumulative length (aligned contigs)



NAx



NGAx

