

Report

	final.contigs
# contigs (>= 1000 bp)	1565
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	2339057
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	4362
Largest contig	4818
Total length	4316375
Reference length	4857432
GC (%)	52.18
Reference GC (%)	52.22
N50	1052
NG50	976
N75	750
NG75	650
L50	1389
LG50	1656
L75	2601
LG75	3182
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	1050
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	83.286
Duplication ratio	1.067
# N's per 100 kbp	0.00
# mismatches per 100 kbp	181.90
# indels per 100 kbp	0.15
Largest alignment	4818
NA50	1052
NGA50	975
NA75	750
NGA75	650
LA50	1389
LGA50	1656
LA75	2602
LGA75	3182

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	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	1050
# local misassemblies	0
# mismatches	7359
# indels	6
# short indels	6
# long indels	0
Indels length	6

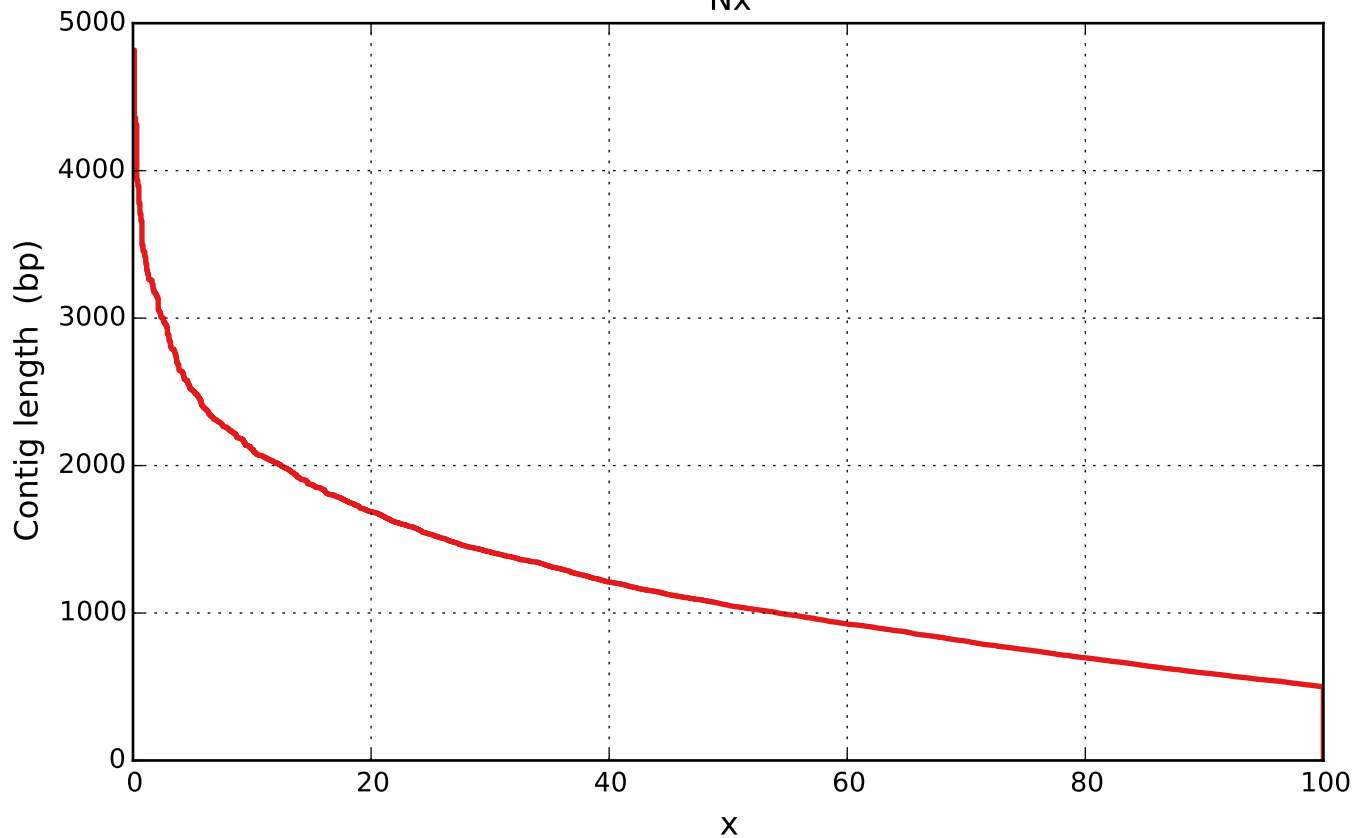
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	final.contigs
# fully unaligned contigs	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).

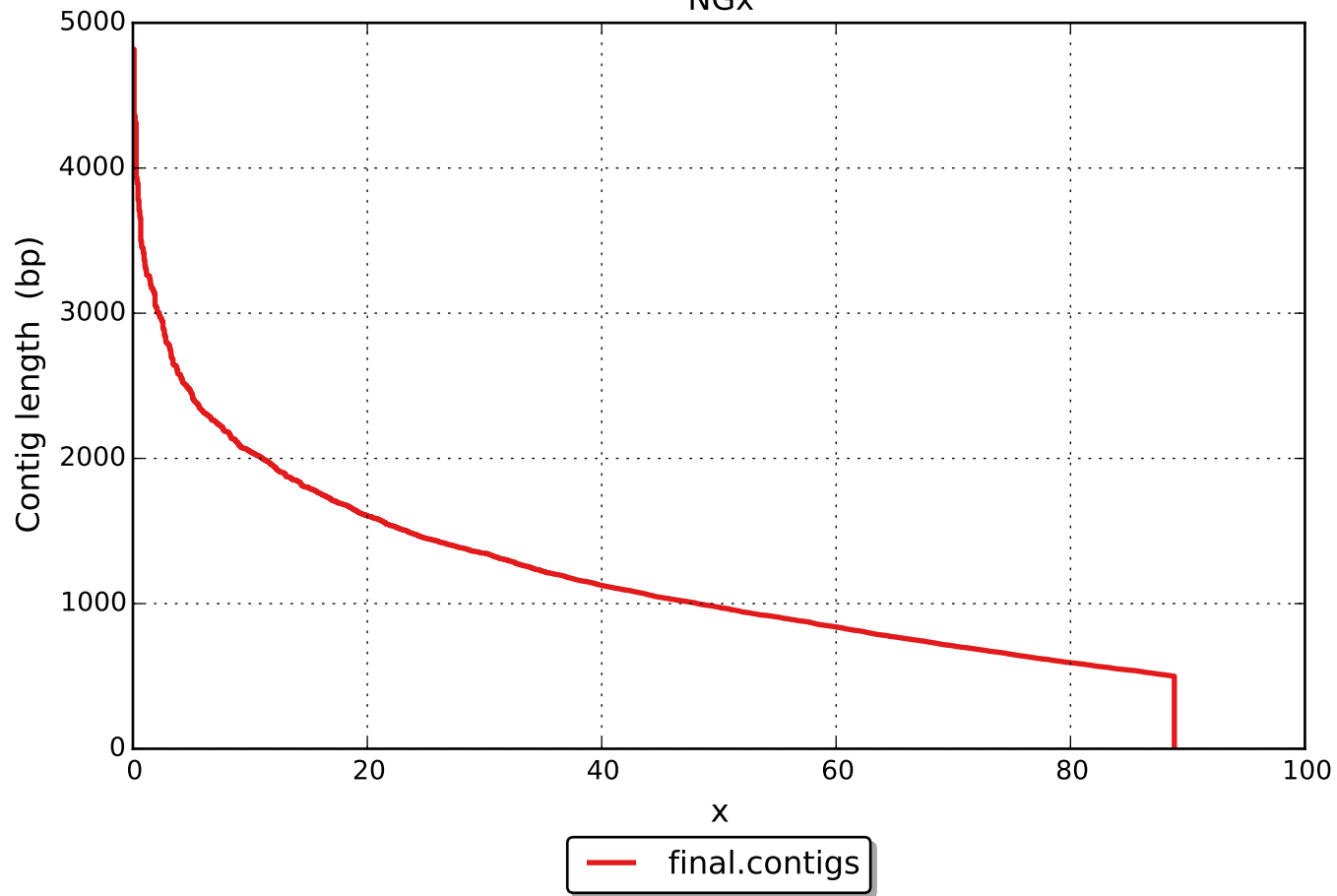
Nx

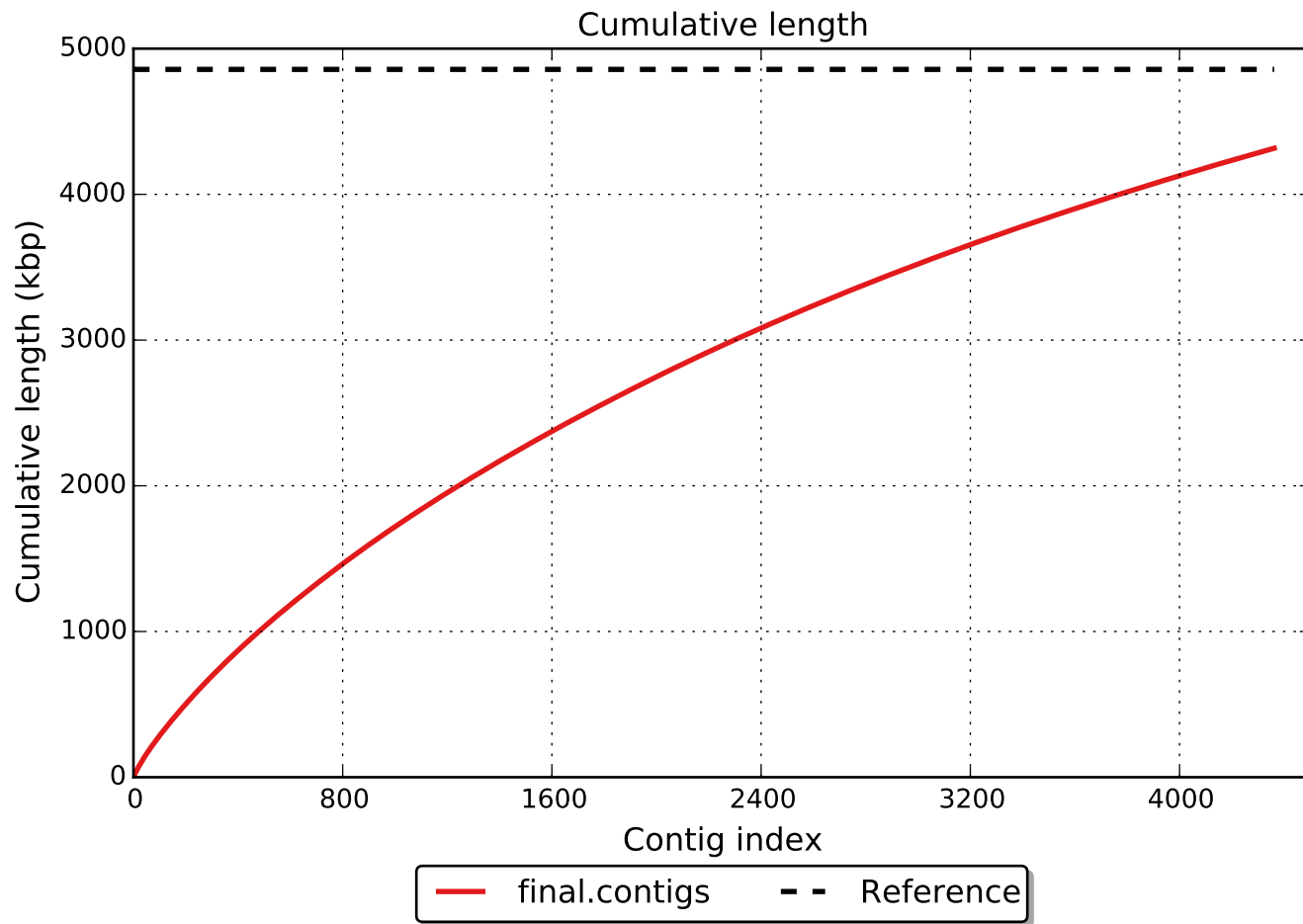


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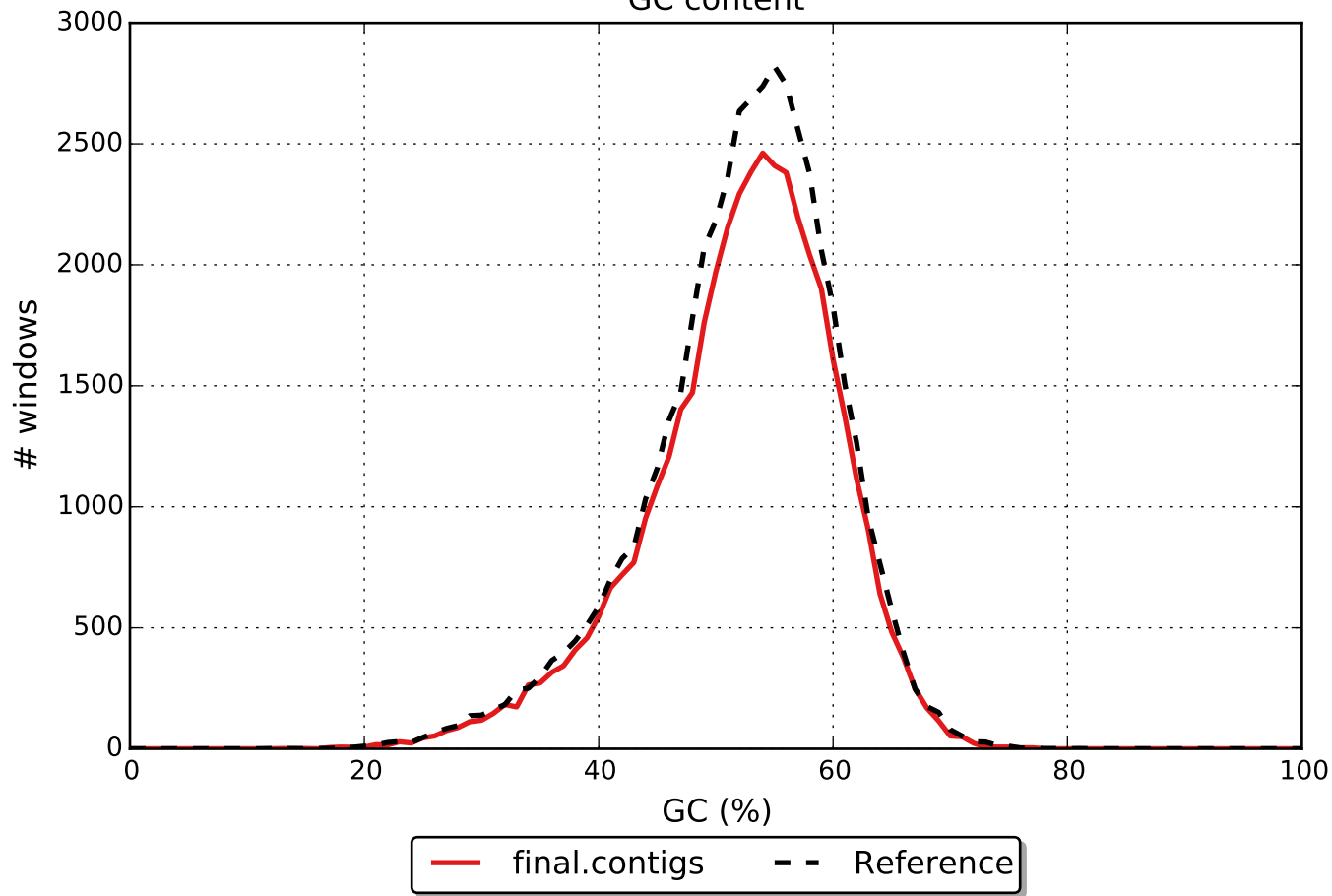
final.contigs

NGx



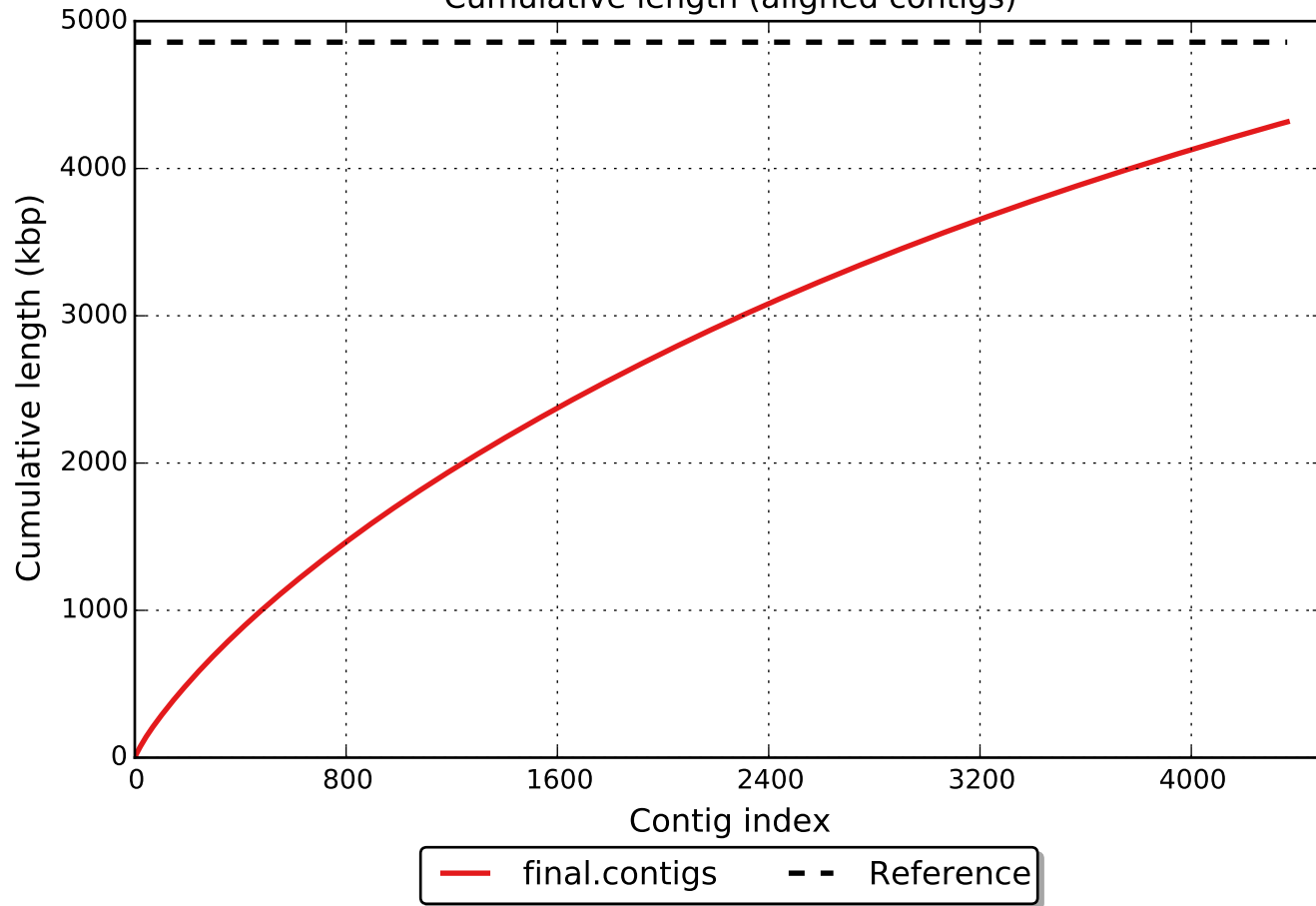


GC content

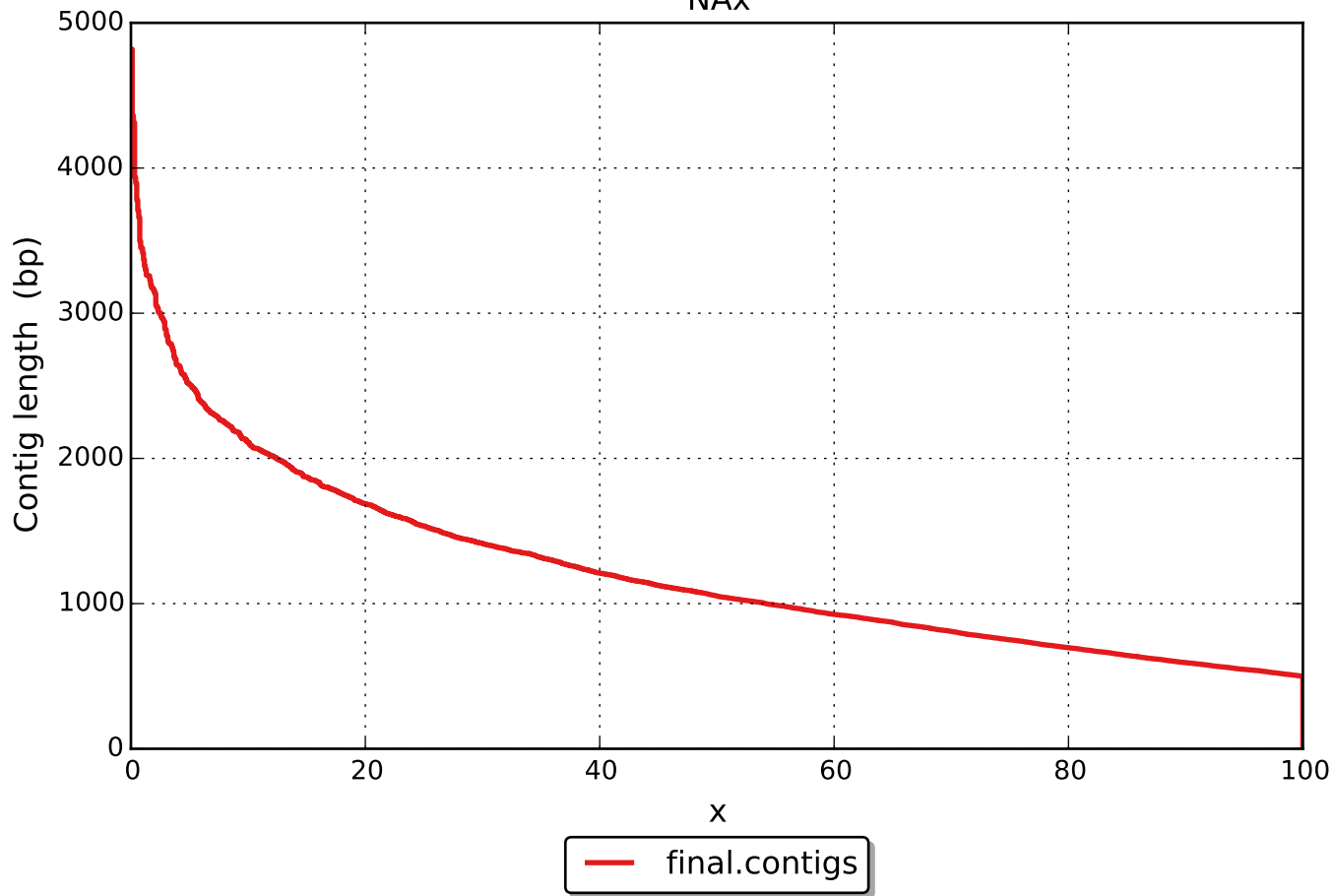




Cumulative length (aligned contigs)



NAx



NGAx

