

## Report

	final.contigs
# contigs (>= 0 bp)	5326
# contigs (>= 1000 bp)	809
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	3611011
Total length (>= 1000 bp)	1111056
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3188
Largest contig	4425
Total length	2765777
Reference length	4641652
GC (%)	50.71
Reference GC (%)	50.79
N50	891
NG50	606
N75	674
L50	1098
LG50	2377
L75	1991
# misassemblies	11
# misassembled contigs	11
Misassembled contigs length	18198
# local misassemblies	3
# unaligned contigs	2 + 7 part
Unaligned length	2111
Genome fraction (%)	58.161
Duplication ratio	1.024
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1015.10
# indels per 100 kbp	1.19
Largest alignment	3996
NA50	890
NGA50	605
NA75	672
LA50	1101
LGA50	2384
LA75	1997

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	11
# relocations	11
# translocations	0
# inversions	0
# misassembled contigs	11
Misassembled contigs length	18198
# local misassemblies	3
# mismatches	27404
# indels	32
# short indels	31
# long indels	1
Indels length	79

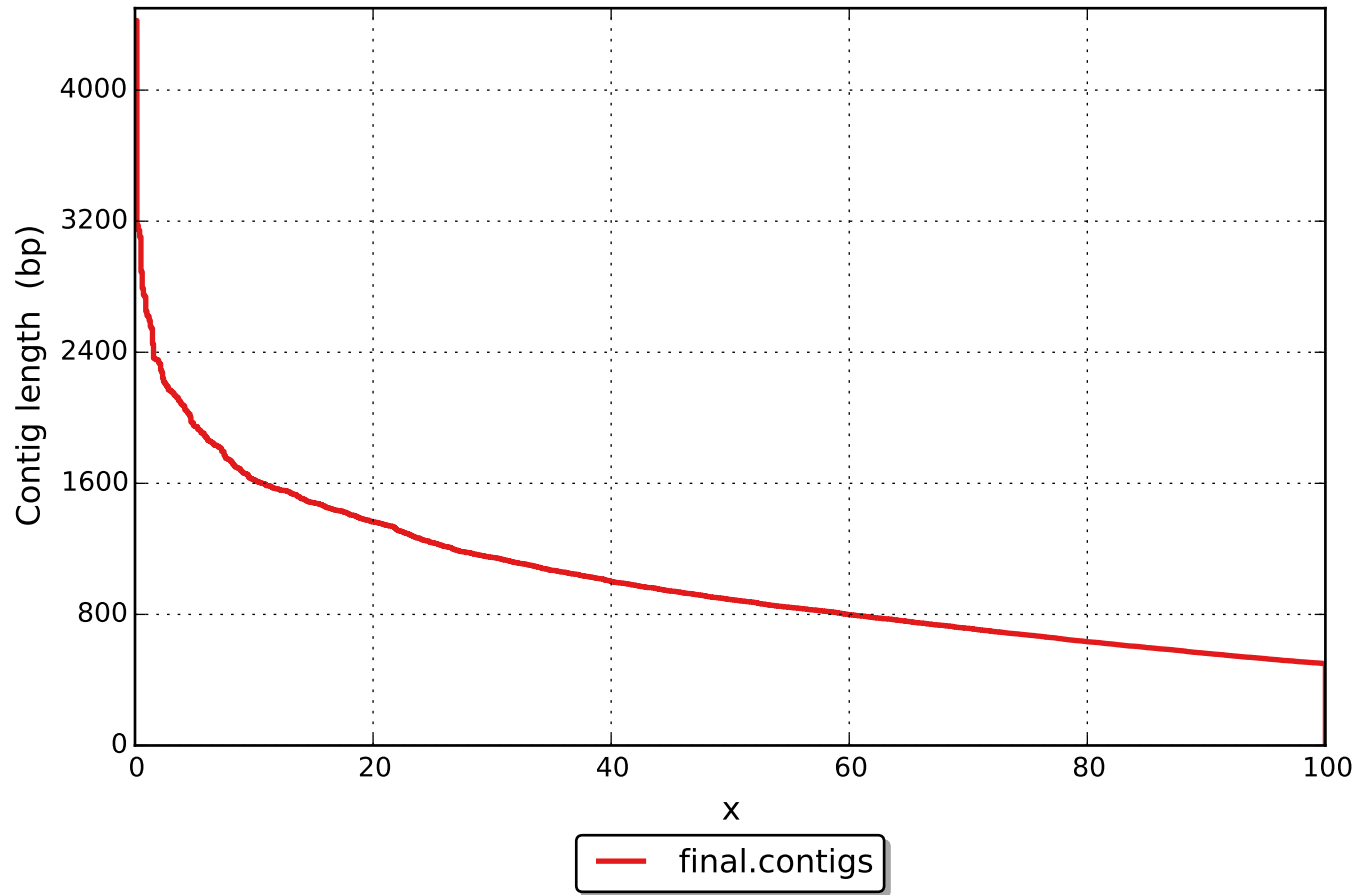
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

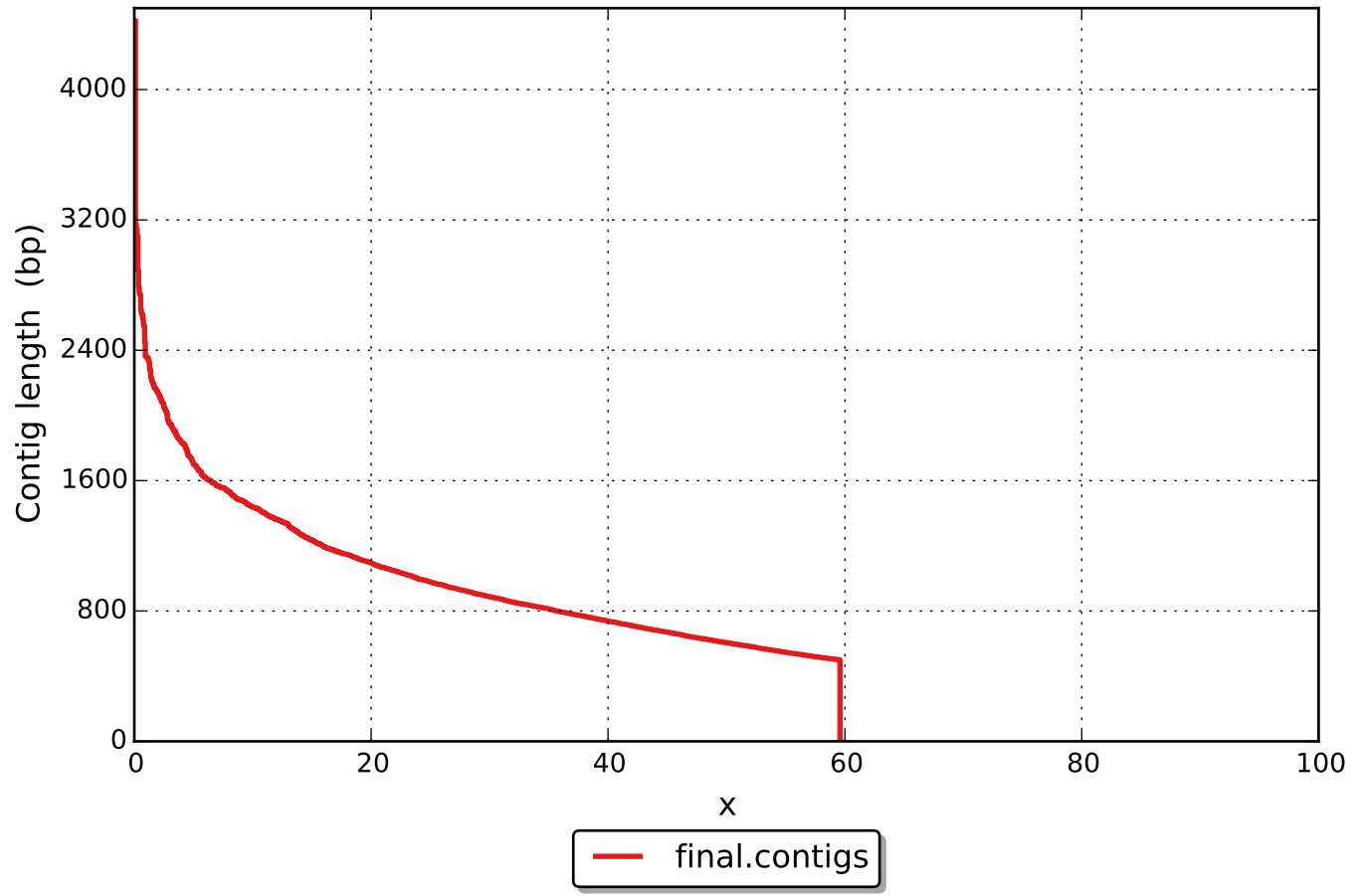
	final.contigs
# fully unaligned contigs	2
Fully unaligned length	1791
# partially unaligned contigs	7
# with misassembly	0
# both parts are significant	0
Partially unaligned length	320
# N's	0

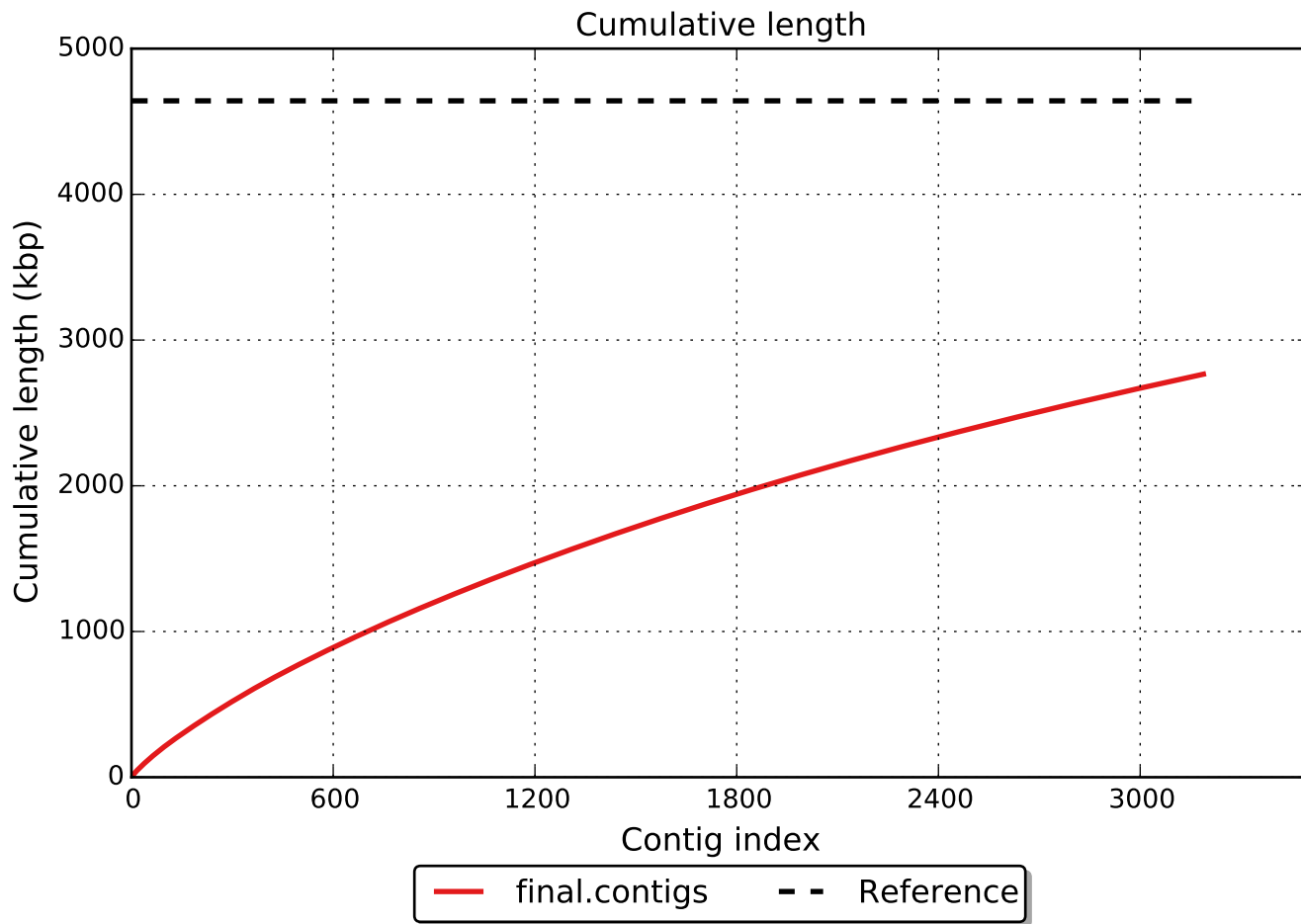
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

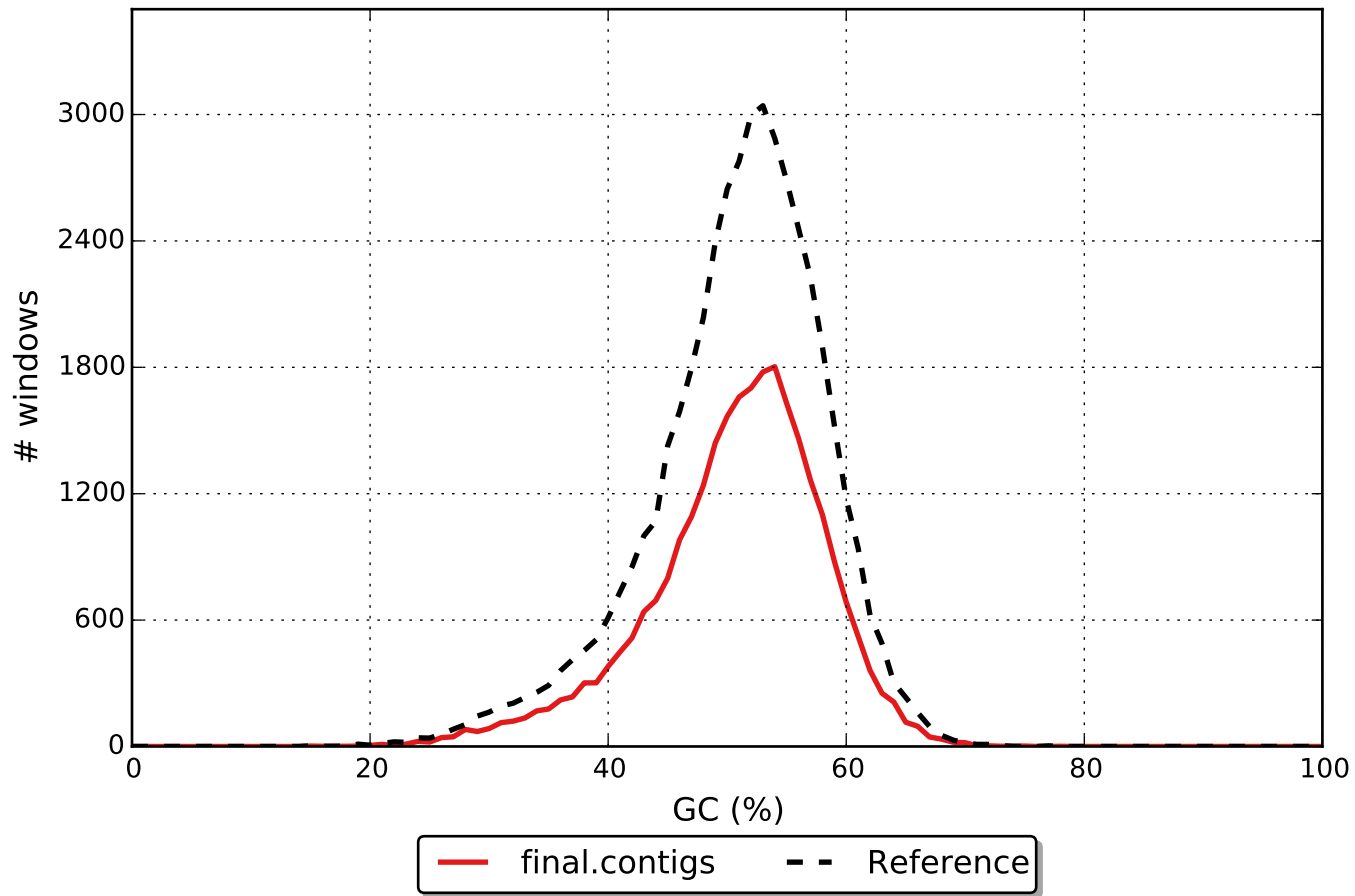


NGx

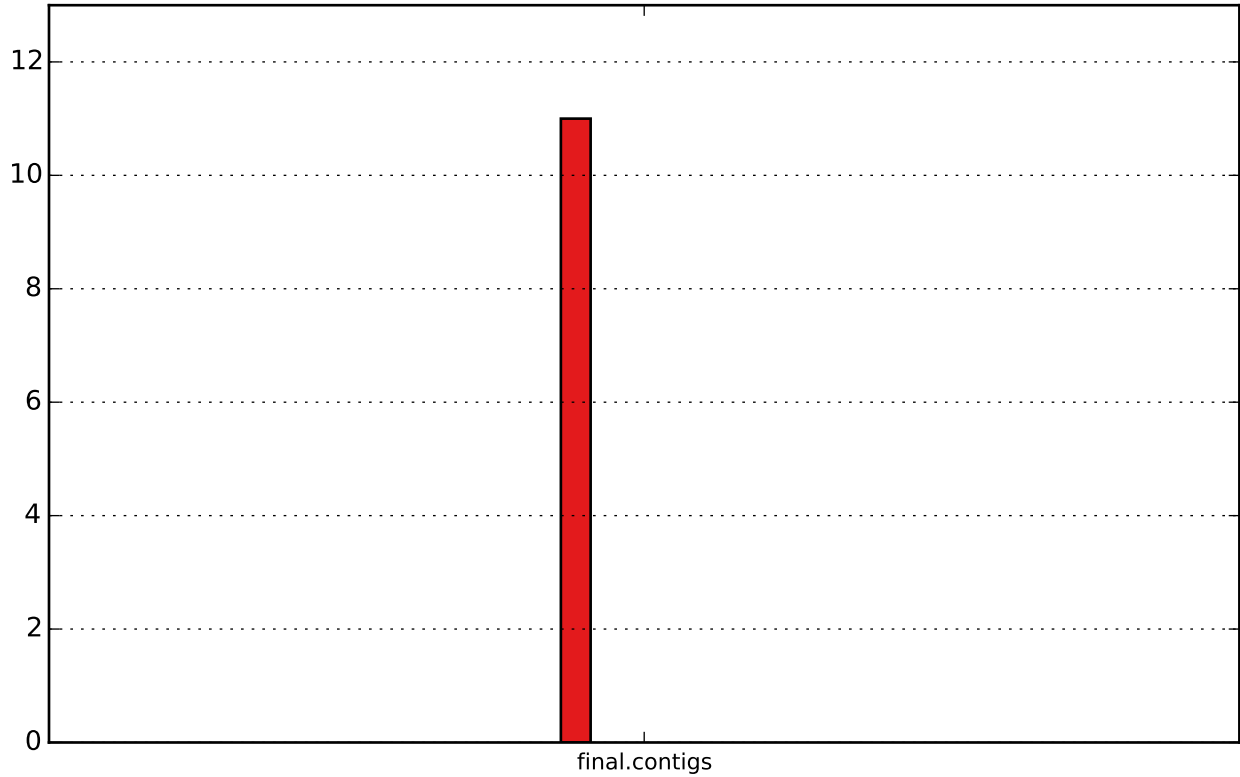




GC content



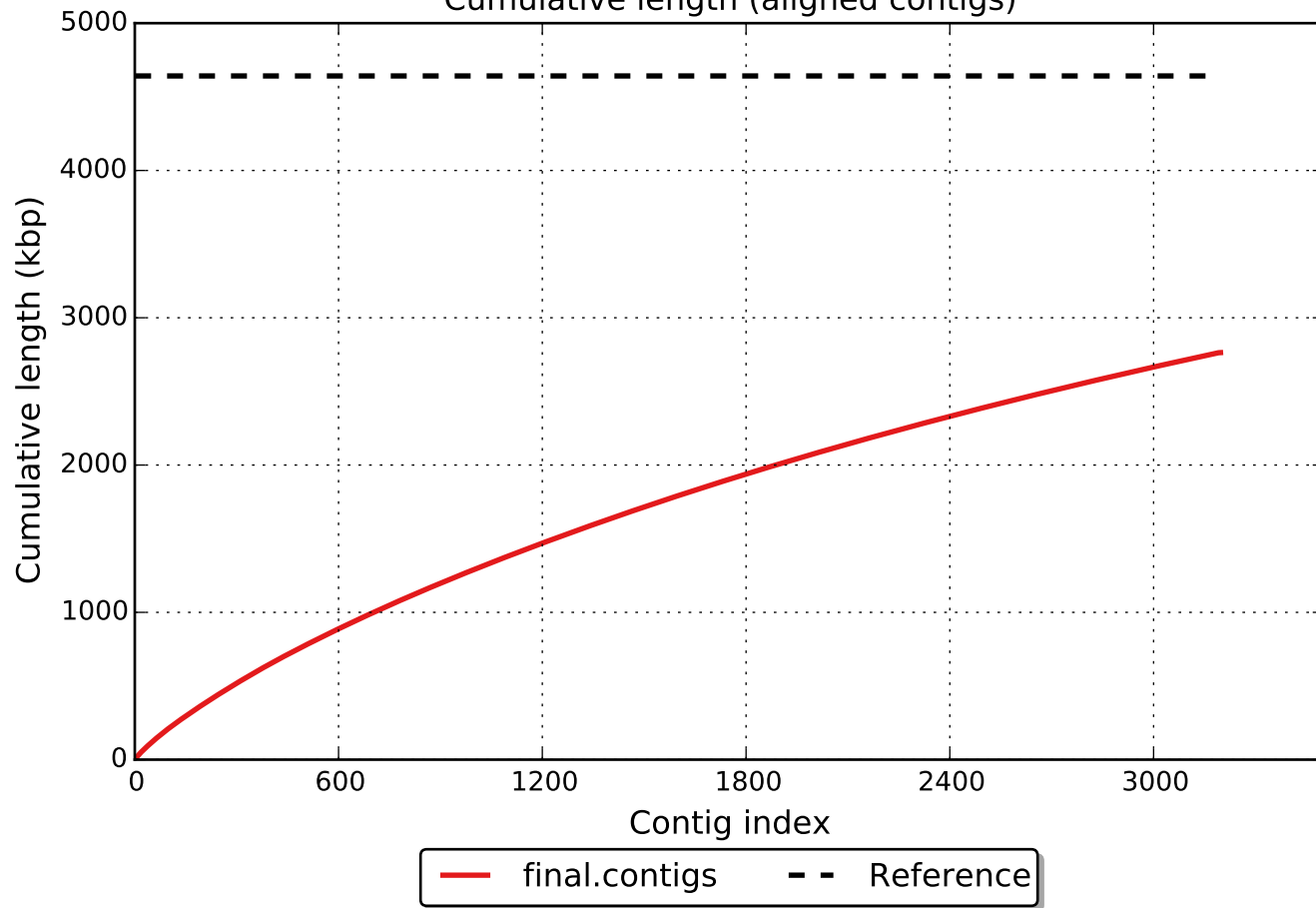
# Misassemblies



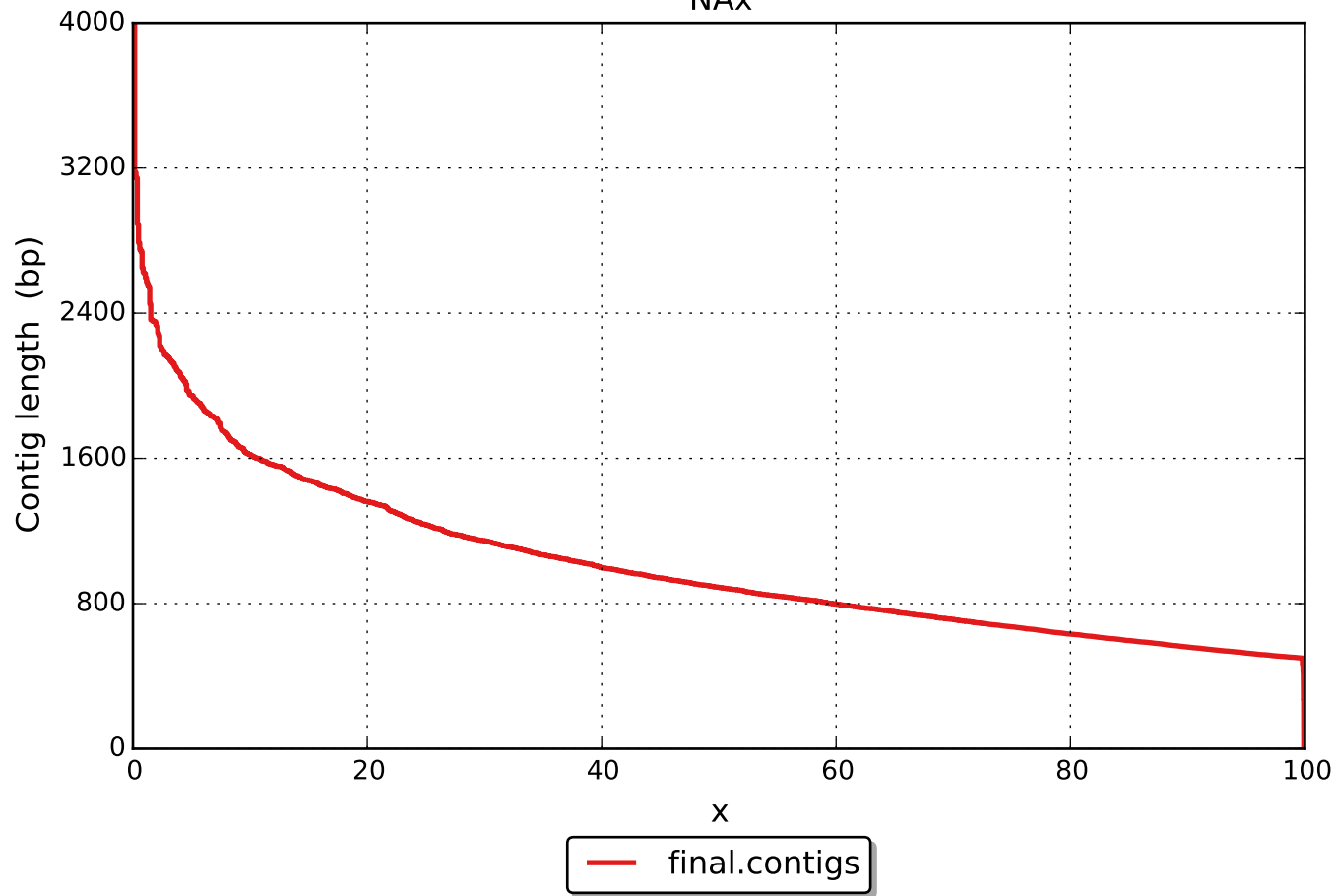
 # relocations



Cumulative length (aligned contigs)



NAx



NGAx

