Report

	final.contigs
# contigs (>= 1000 bp)	1842
# contigs (>= 5000 bp)	14
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	3345008
Total length (>= 5000 bp)	84664
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3420
Largest contig	8764
Total length	4494523
Reference length	4641652
GC (%)	50.78
Reference GC (%)	50.78
N50	1531
NG50	1490
N75	986
NG75	942
L50	959
LG50	1008
L75	1869
LG75	1983
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	3248
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	92.304
Duplication ratio	1.049
# N's per 100 kbp	0.00
# mismatches per 100 kbp	73.90
# indels per 100 kbp	0.07
Largest alignment	8764
NA50	1529
NGA50	1490
NA75	986
NGA75	942
LA50	960
LGA50	1008
LA75	1870
LGA75	1984

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
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	3248
# local misassemblies	0
# mismatches	3166
# indels	3
# short indels	3
# long indels	0
Indels length	3

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).
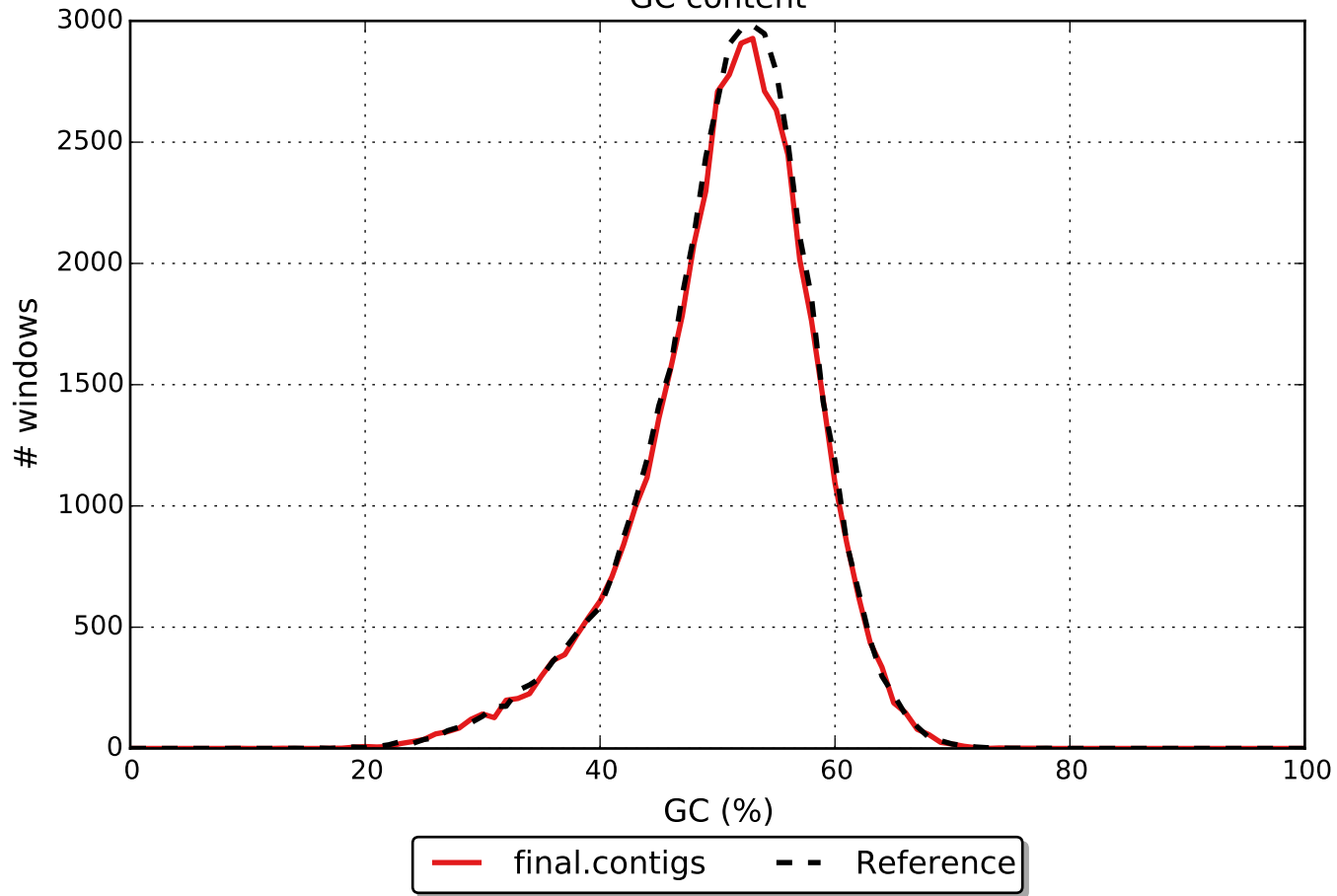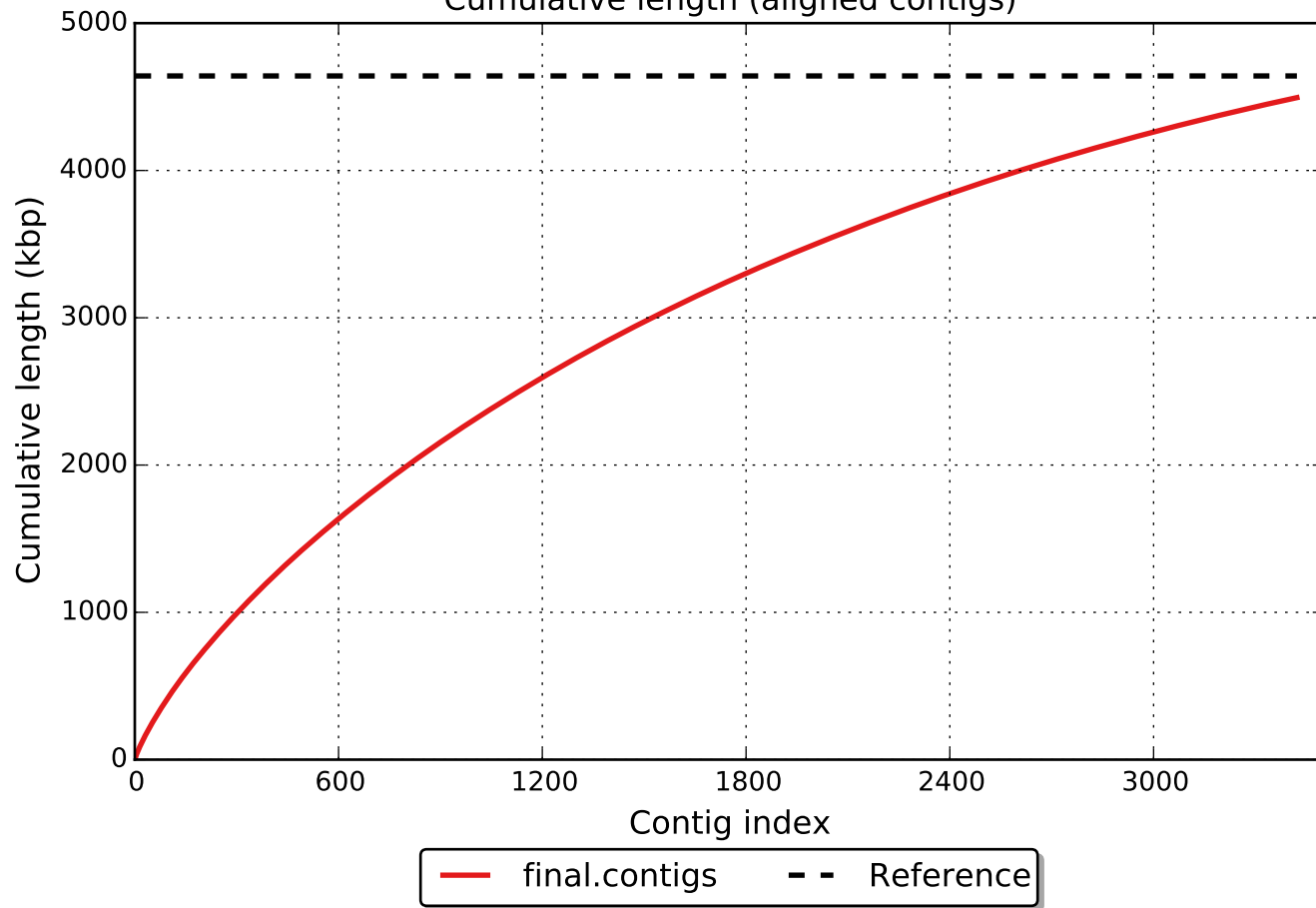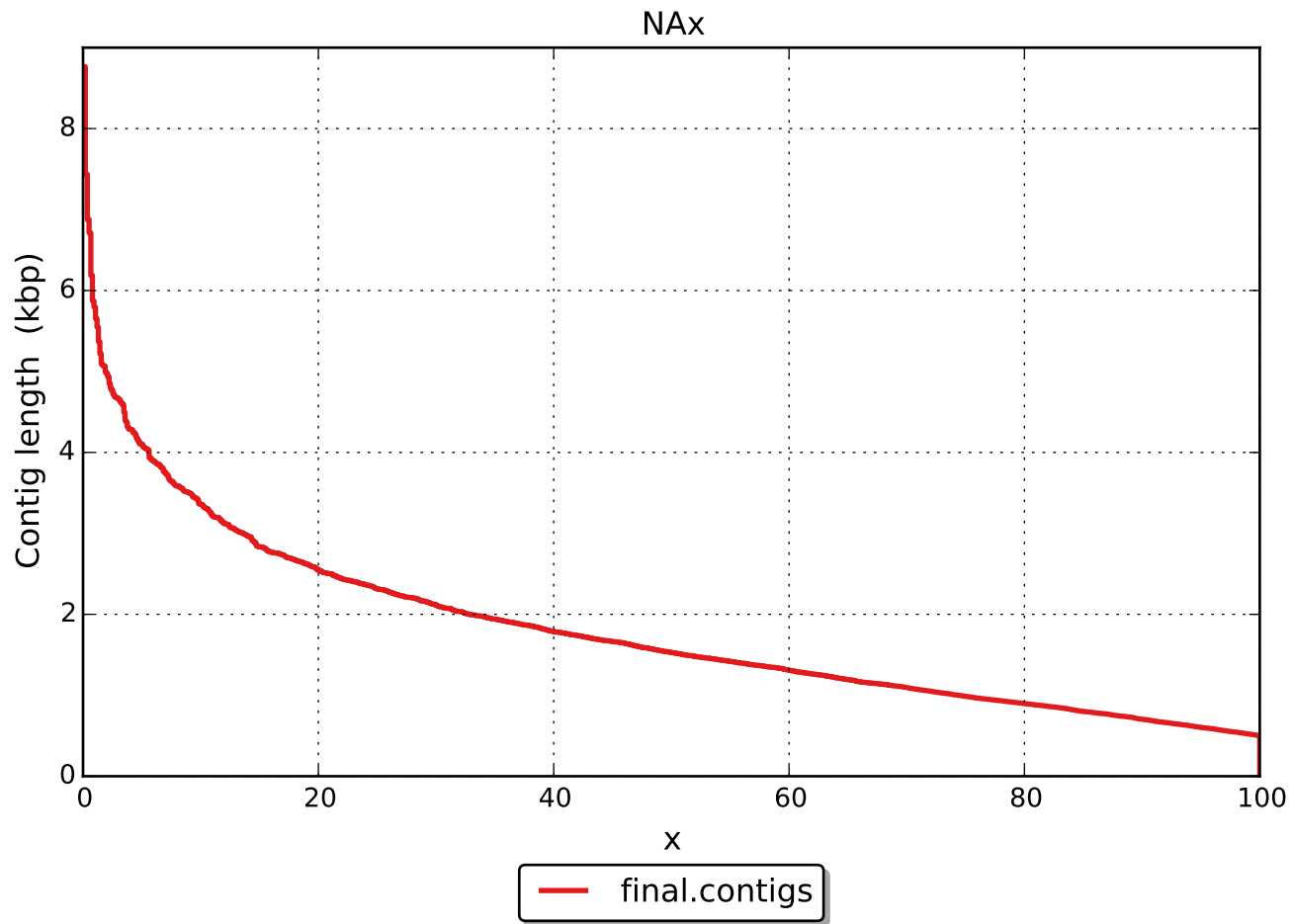
Cumulative length

GC content

Misassemblies

relocations
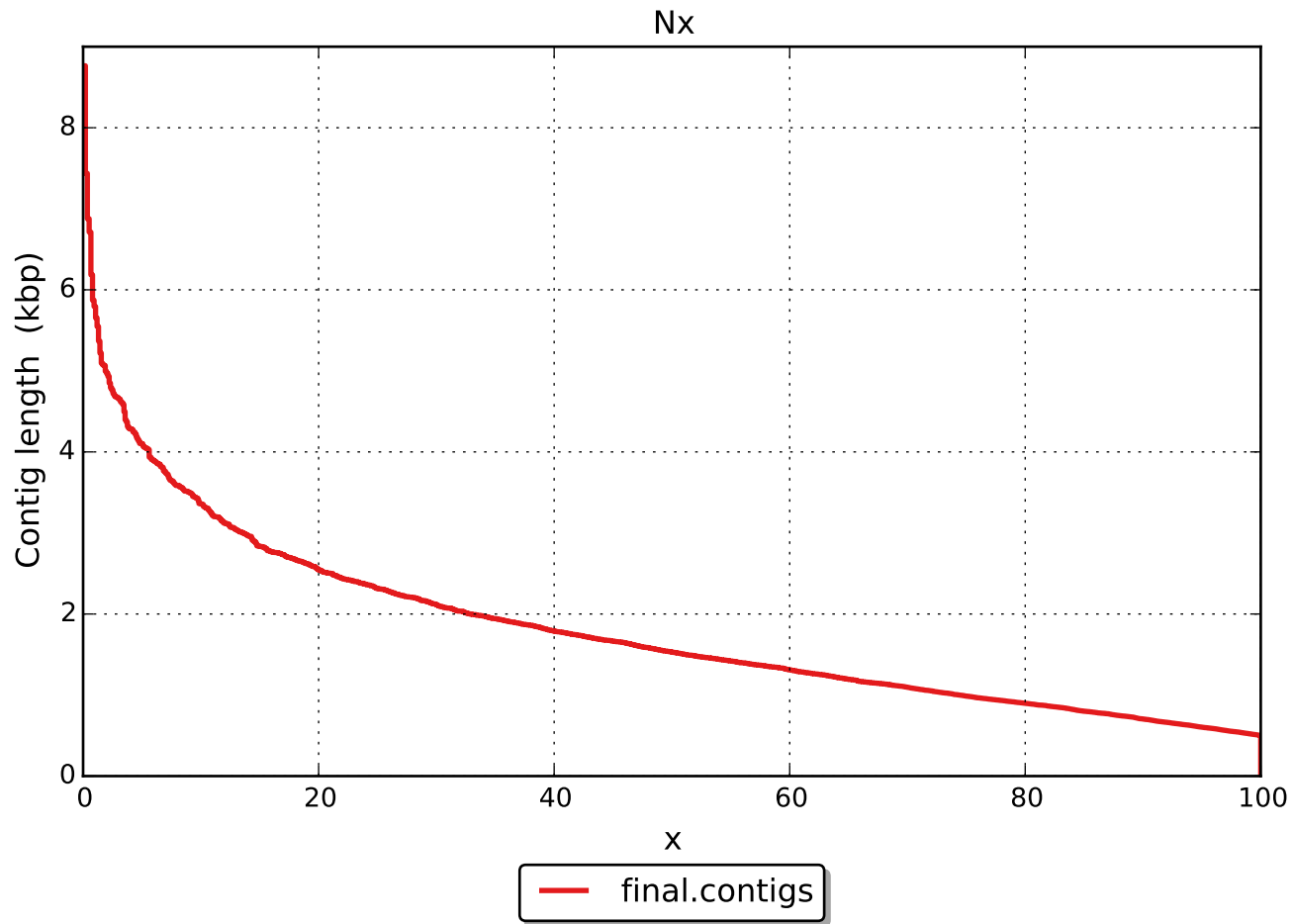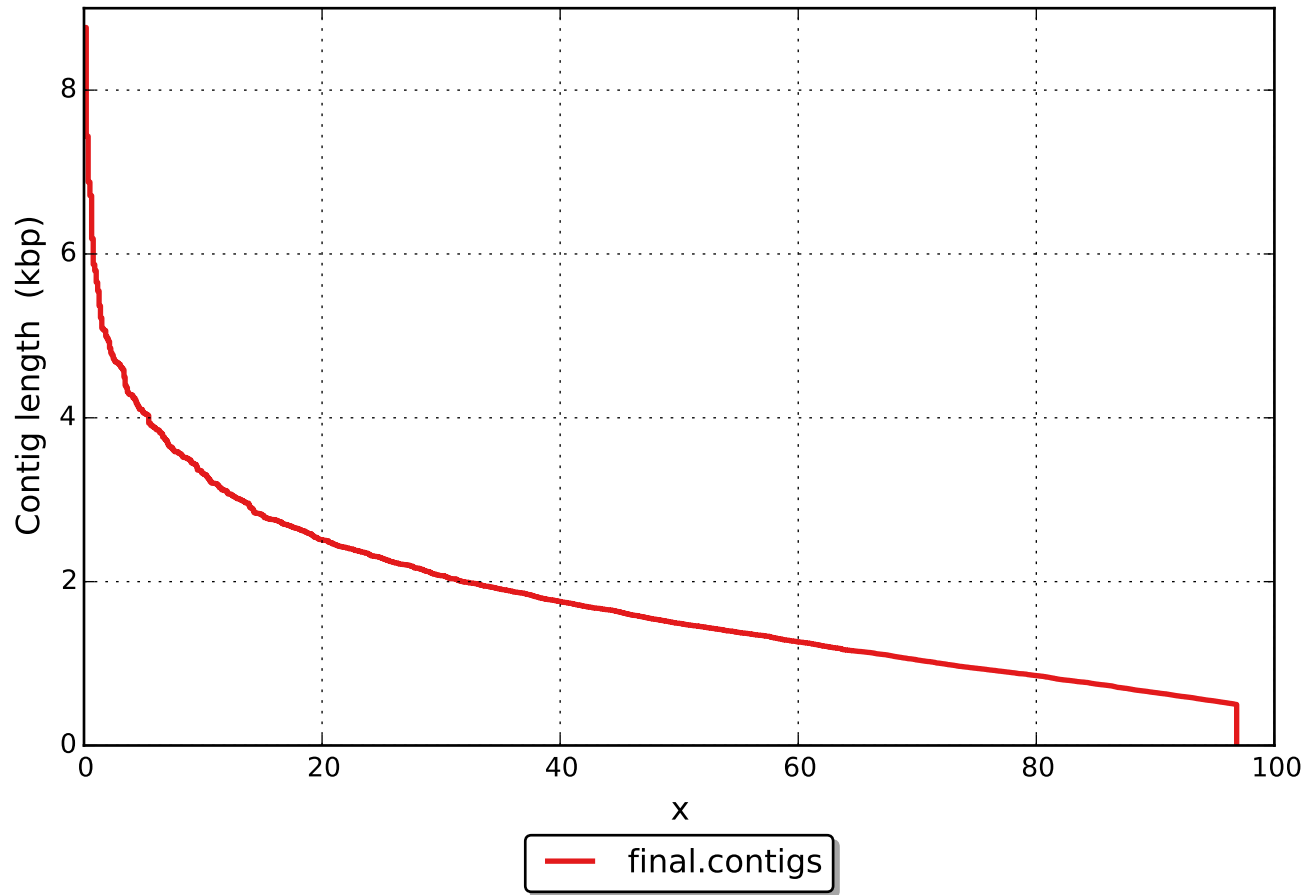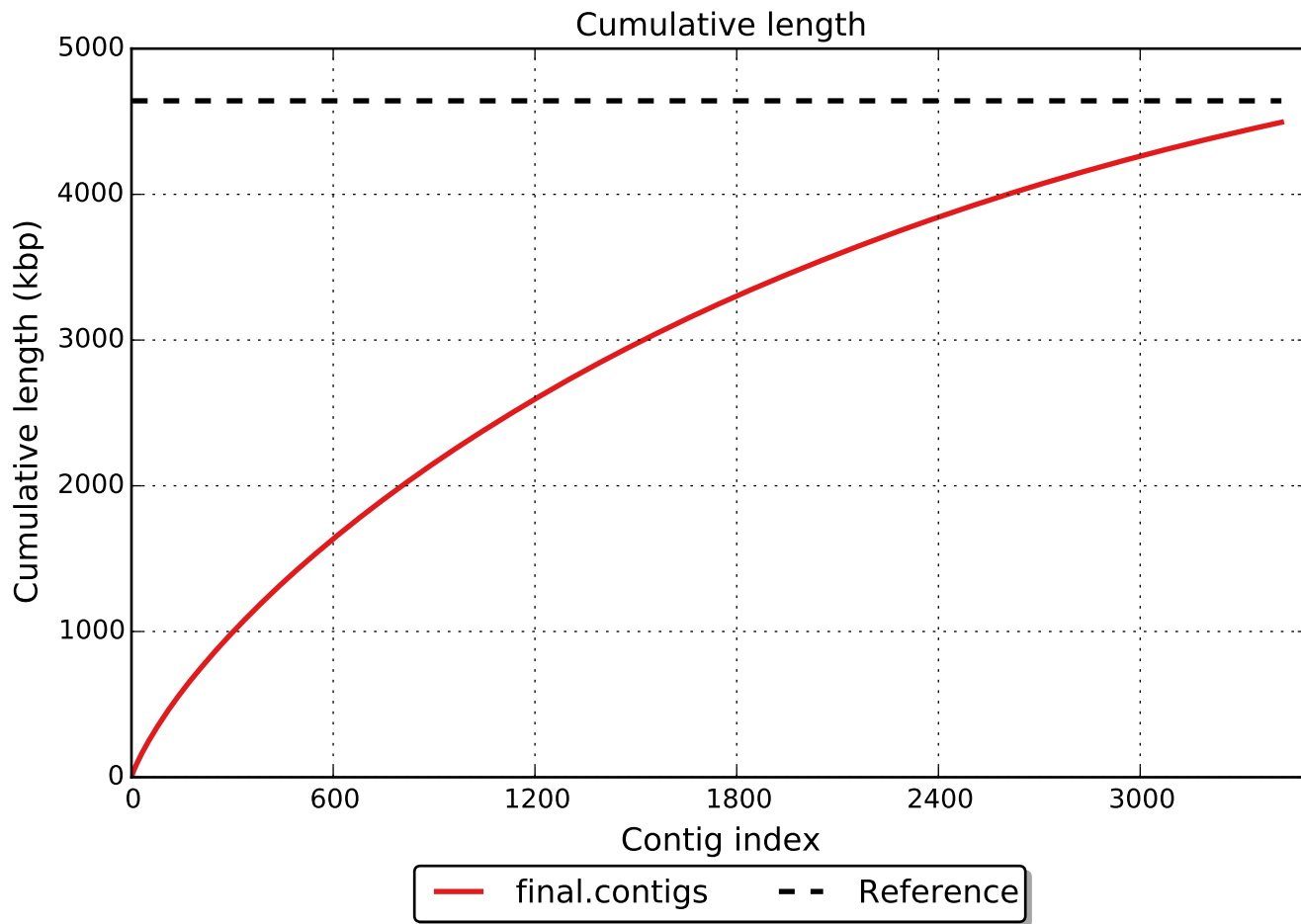
Cumulative length (aligned contigs)