Report

	final.contigs
# contigs (>= 1000 bp)	1668
# contigs (>= 5000 bp)	103
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4088721
Total length (>= 5000 bp)	653279
Total length (>= 10000 bp)	23602
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2362
Largest contig	13353
Total length	4603290
Reference length	4641652
GC (%)	50.73
Reference GC (%)	50.79
N50	2530
NG50	2507
N75	1537
NG75	1514
L50	581
LG50	589
L75	1158
LG75	1177
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	643
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	95.379
Duplication ratio	1.040
# N's per 100 kbp	0.00
# mismatches per 100 kbp	52.74
# indels per 100 kbp	0.07
Largest alignment	13353
NA50	2530
NGA50	2507
NA75	1537
NGA75	1514
LA50	581
LGA50	589
LA75	1158
LGA75	1177

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	643
# local misassemblies	2
# mismatches	2335
# 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
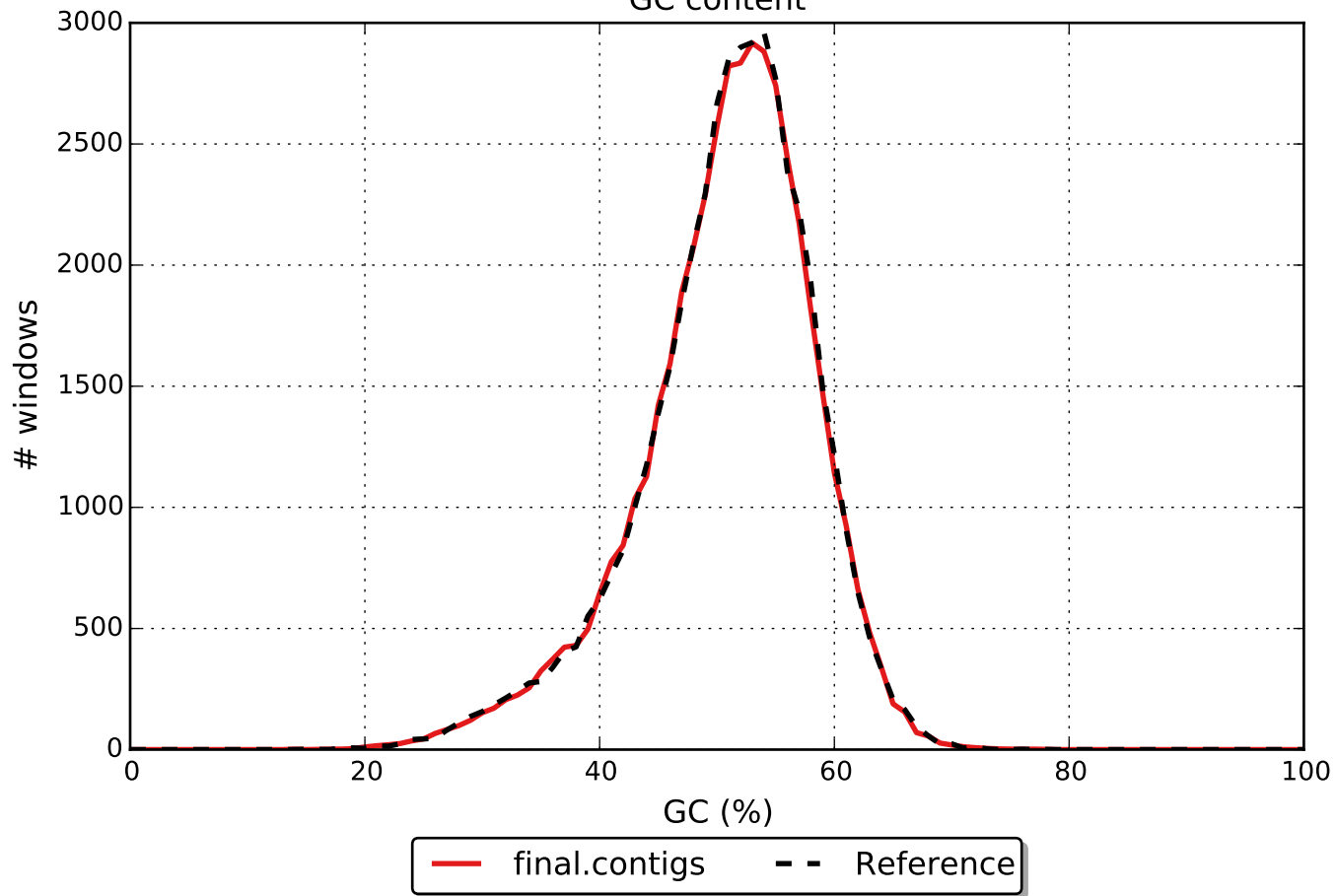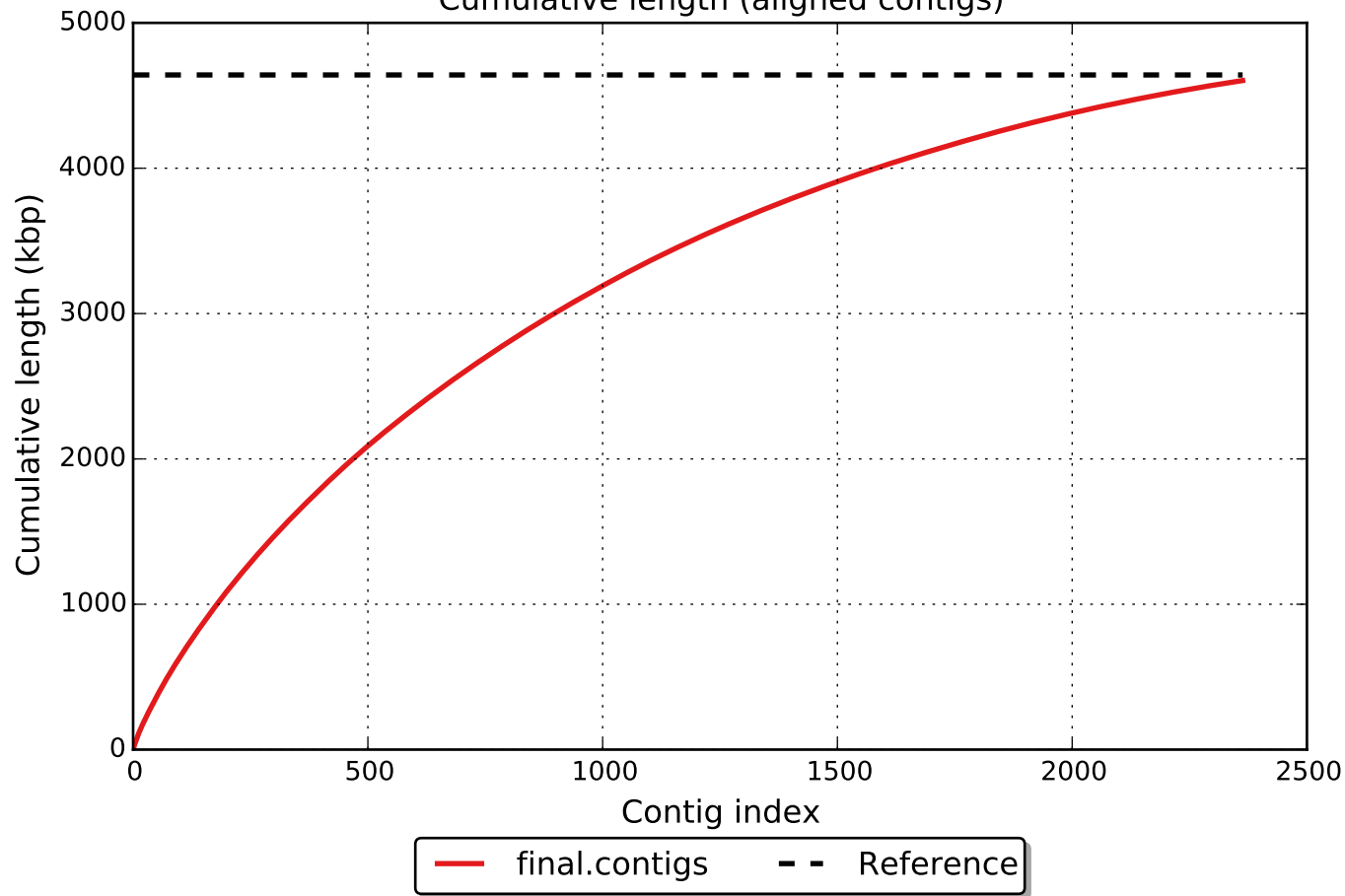(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

NGx

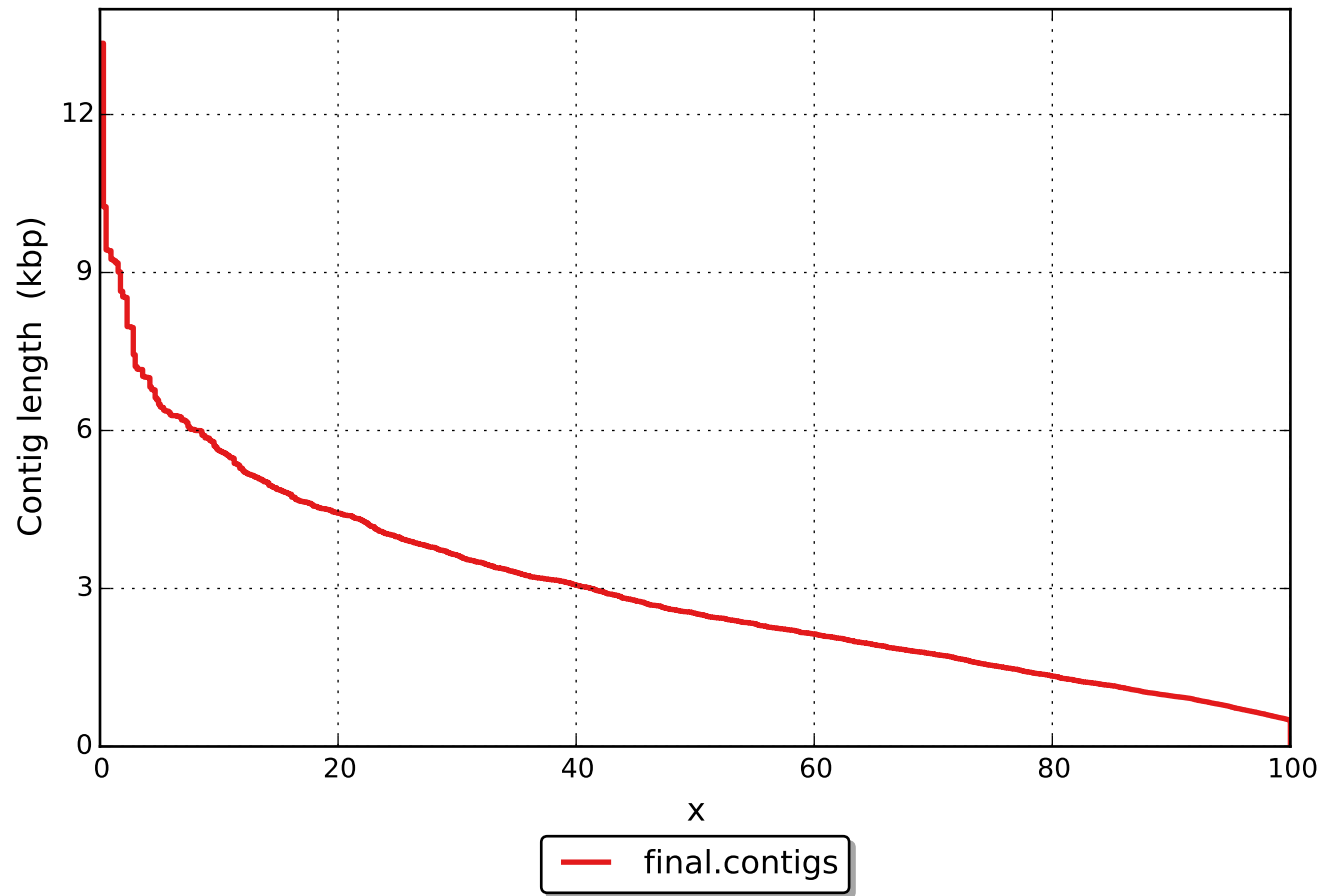Cumulative length

GC content

Misassemblies

final.contigs

relocations
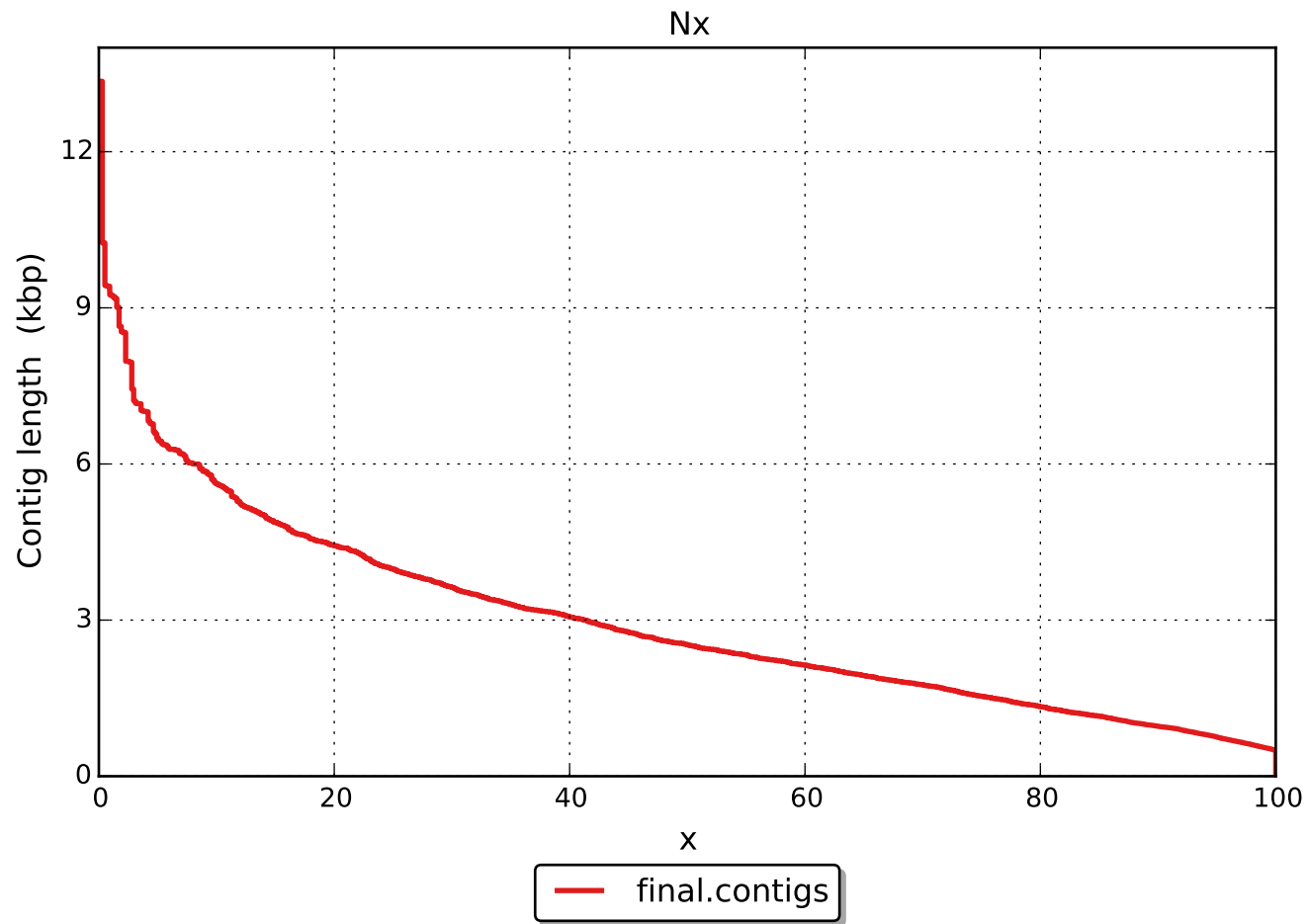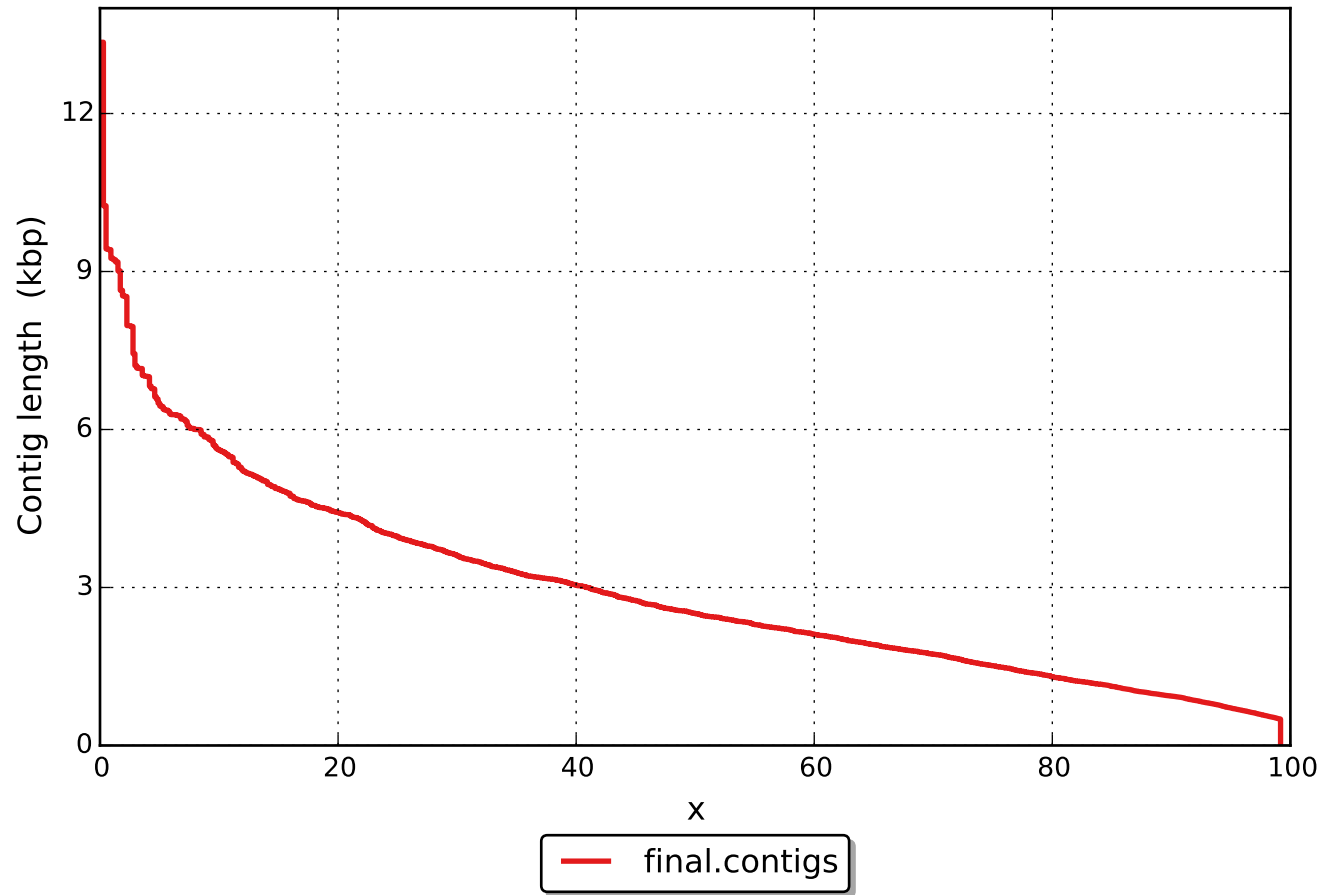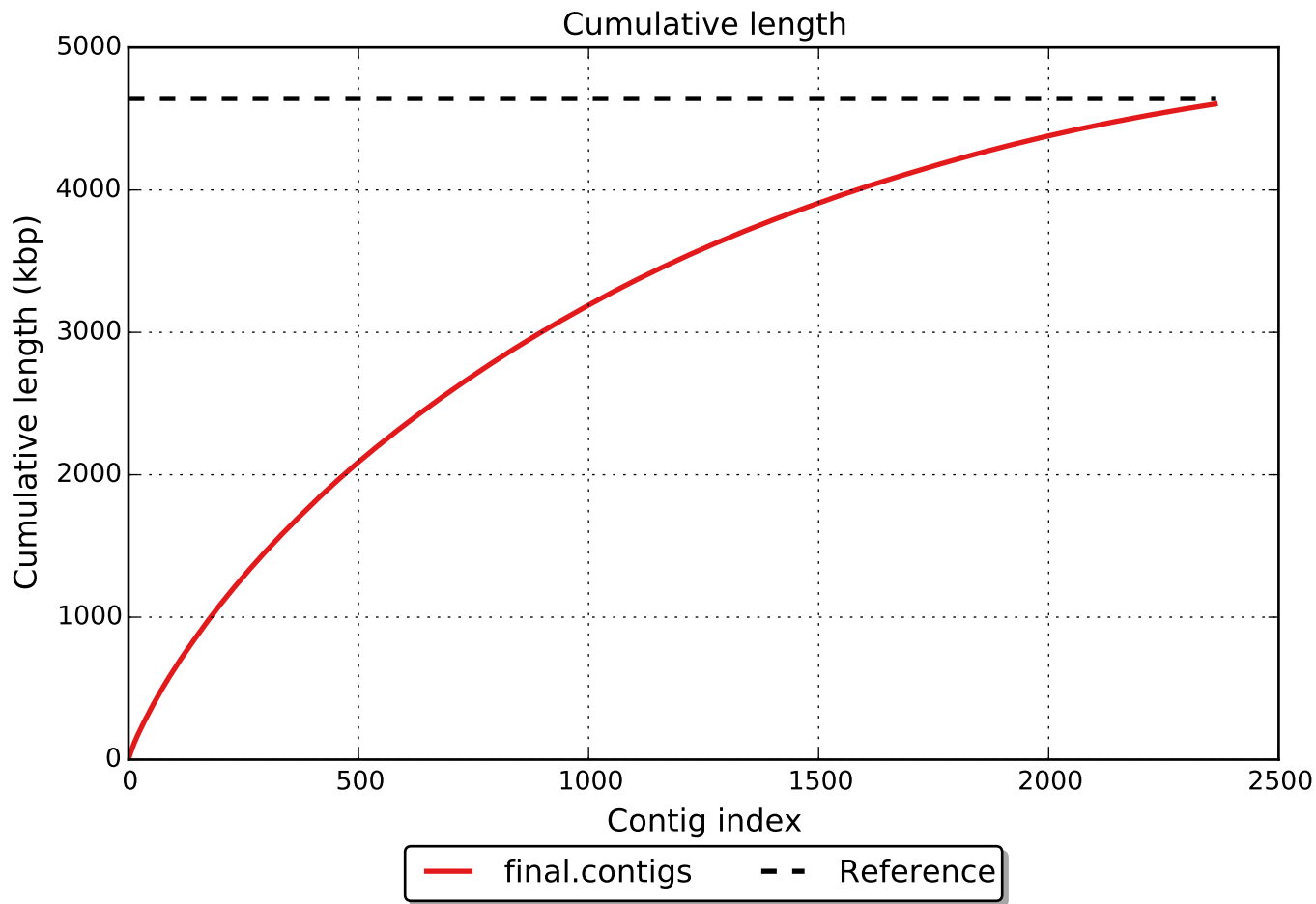
Cumulative length (aligned contigs)