Report

	final.contigs
# contigs (>= 1000 bp)	1942
# contigs (>= 5000 bp)	18
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	3531774
Total length (>= 5000 bp)	99232
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3604
Largest contig	6648
Total length	4737469
Reference length	4857432
GC (%)	52.23
Reference GC (%)	52.23
N50	1525
NG50	1498
N75	987
NG75	949
L50	1003
LG50	1042
L75	1964
LG75	2057
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	1359
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	59
Genome fraction (%)	92.776
Duplication ratio	1.051
# N's per 100 kbp	0.00
# mismatches per 100 kbp	76.95
# indels per 100 kbp	0.02
Largest alignment	6648
NA50	1525
NGA50	1497
NA75	987
NGA75	949
LA50	1003
LGA50	1043
LA75	1964
LGA75	2057

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	1359
# local misassemblies	0
# mismatches	3468
# indels	1
# short indels	1
# 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	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	59
# N's	0

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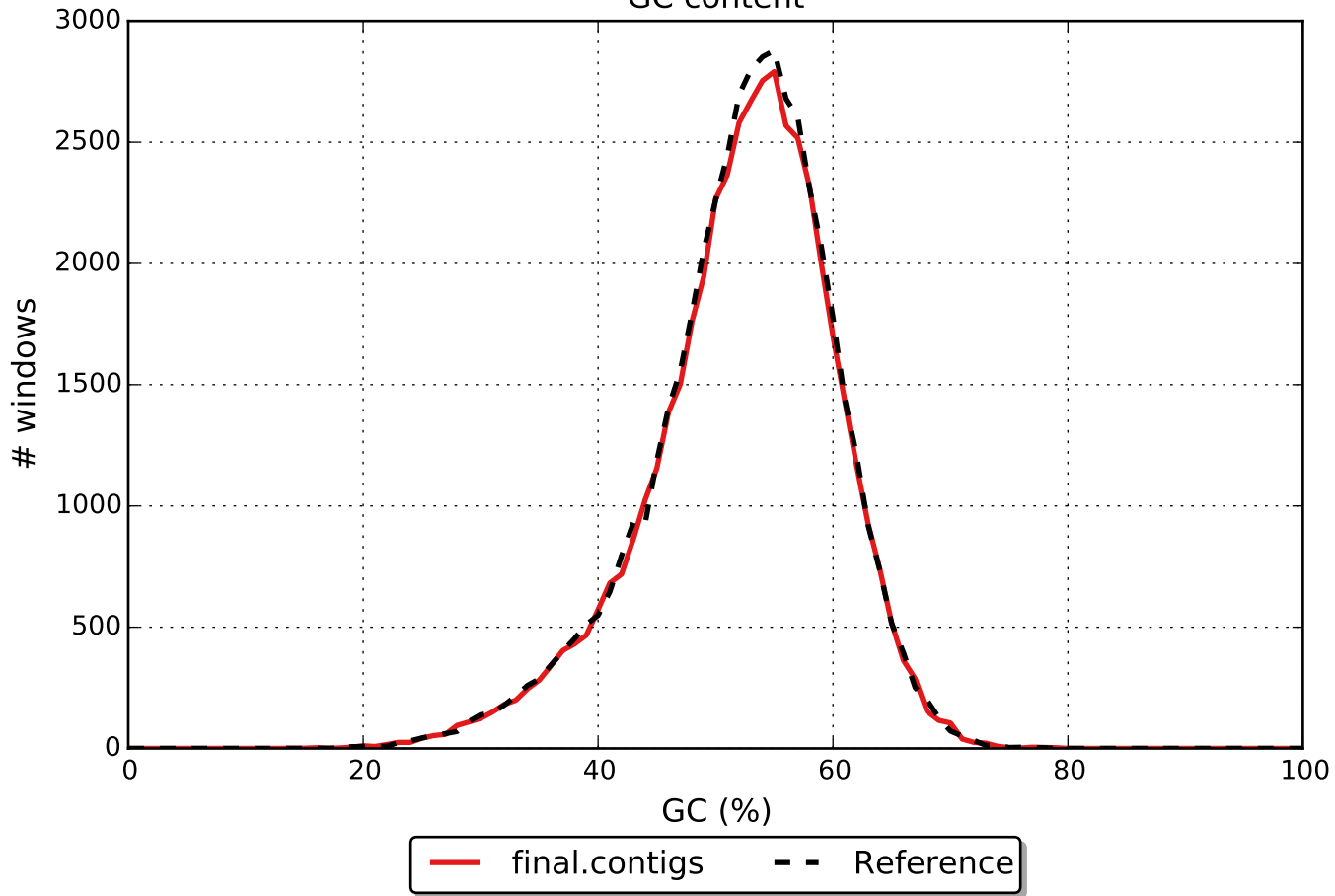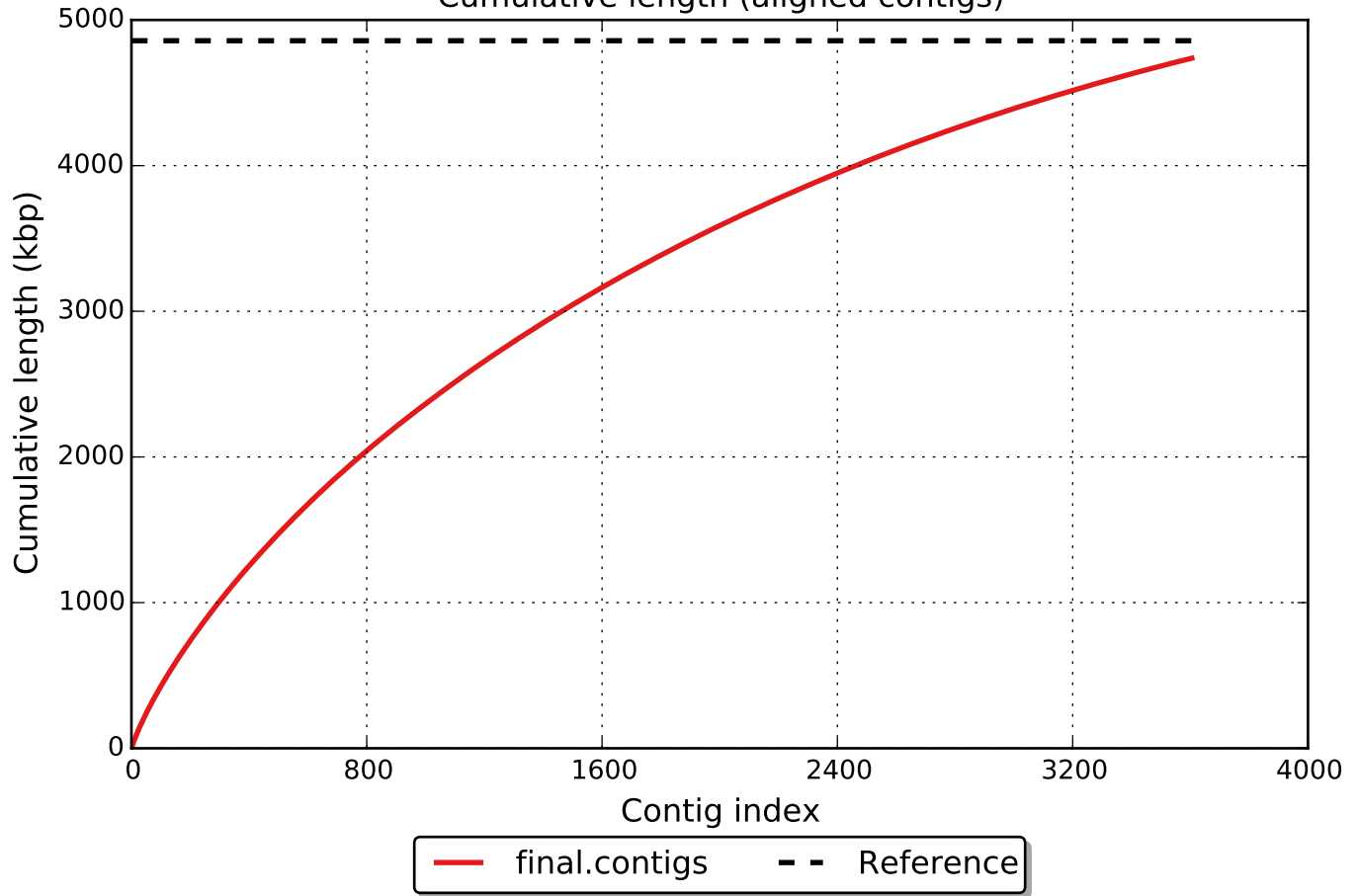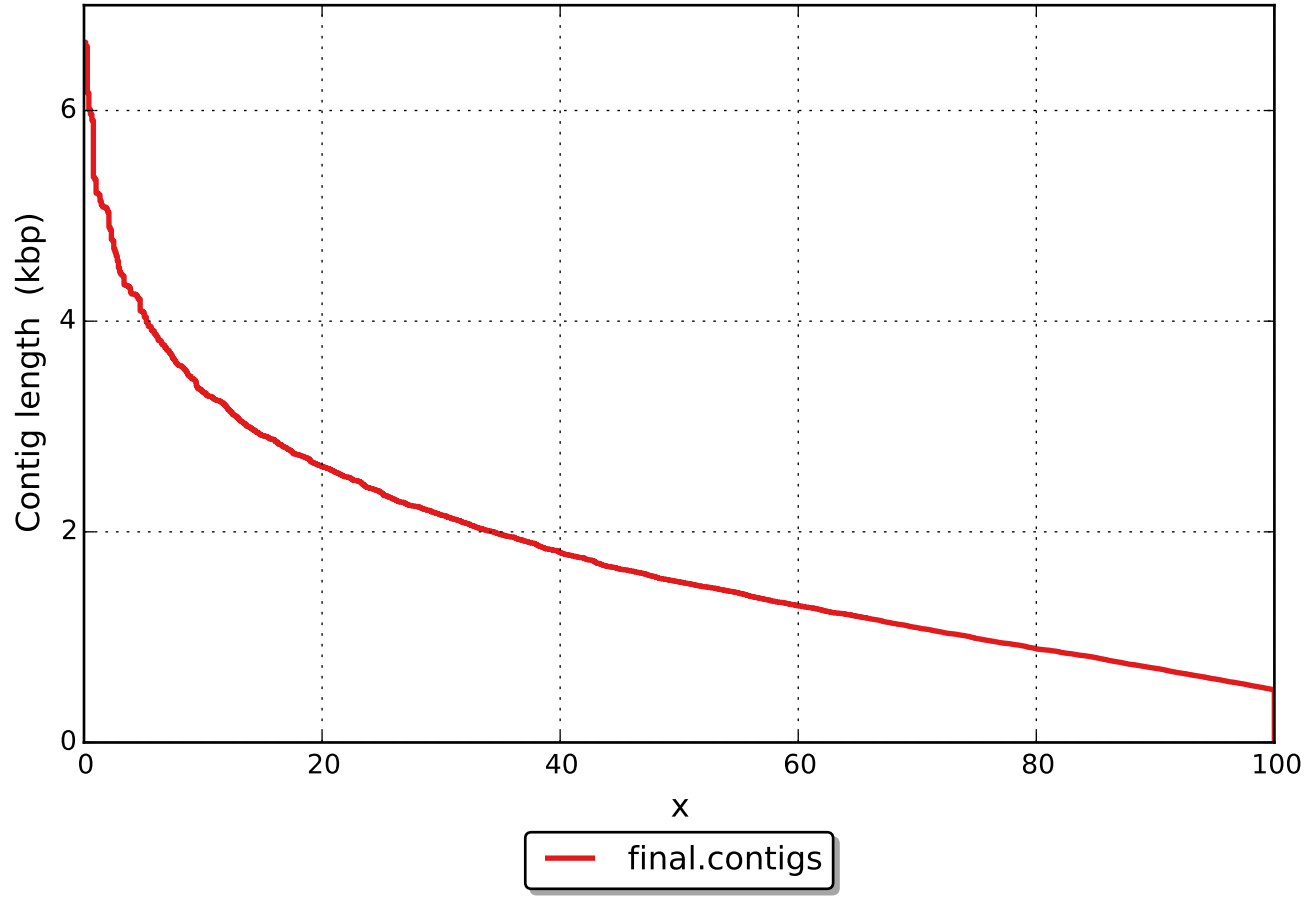(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Nx

NGx

Cumulative length

GC content

Misassemblies
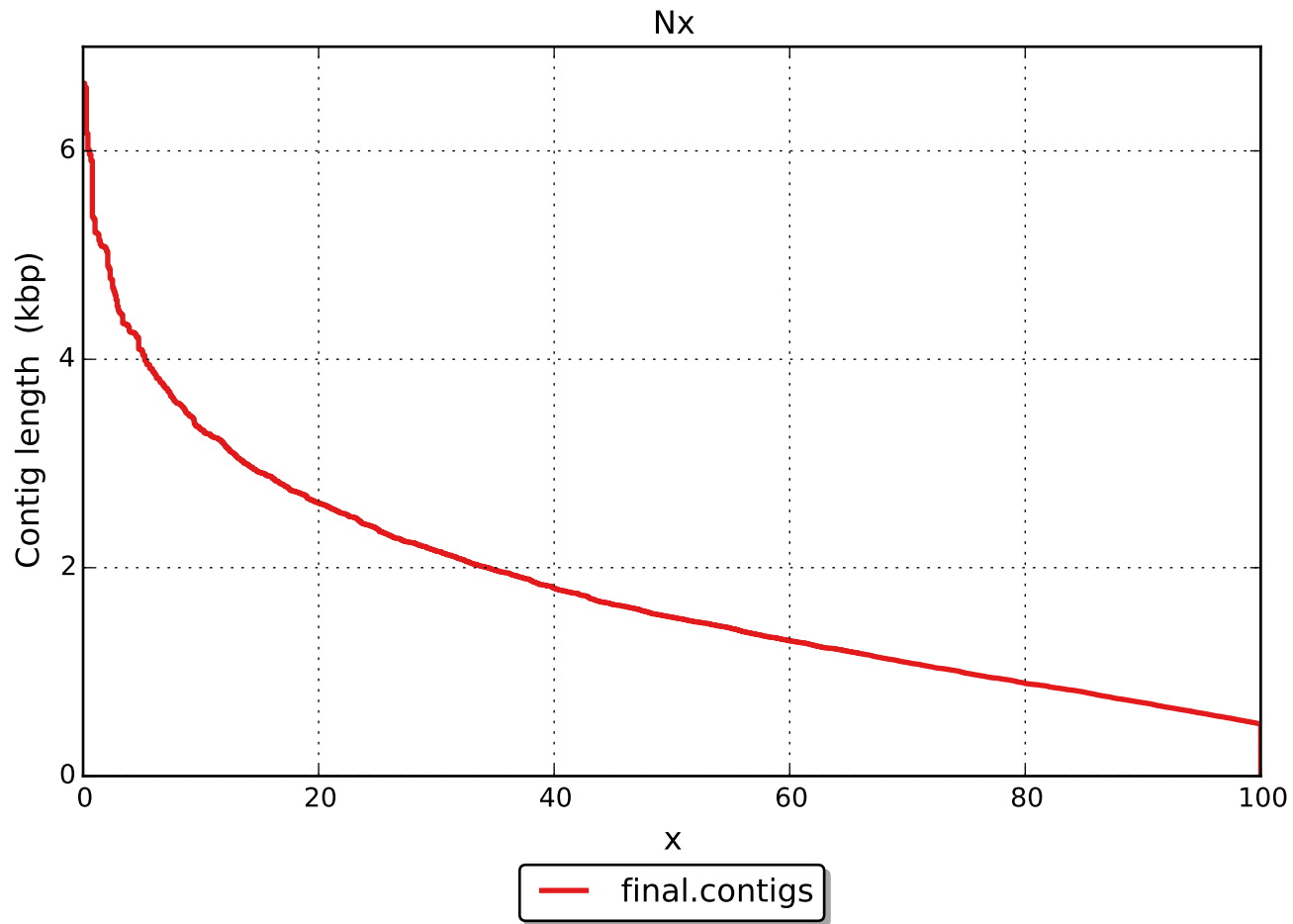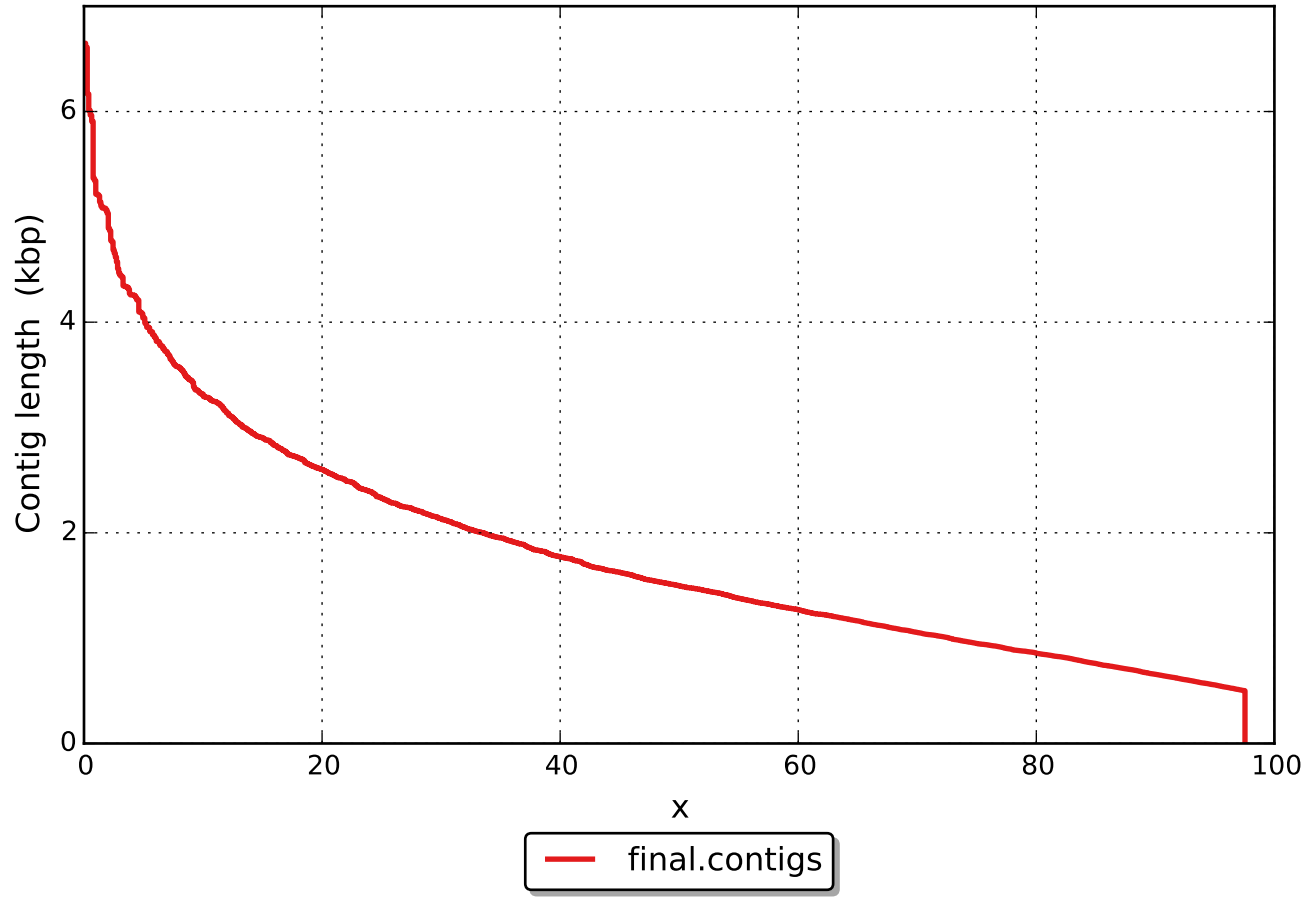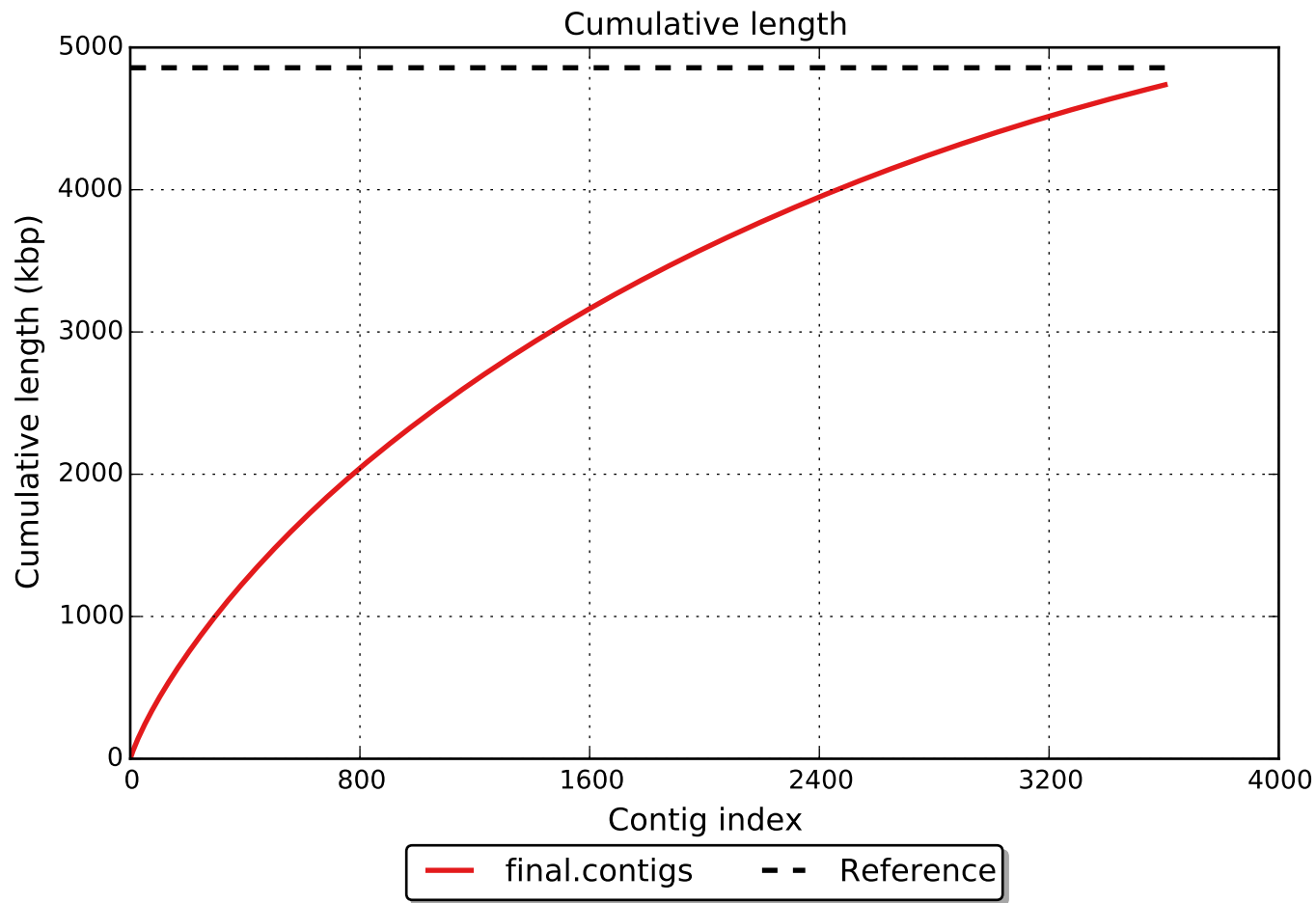
Cumulative length (aligned contigs)