Report

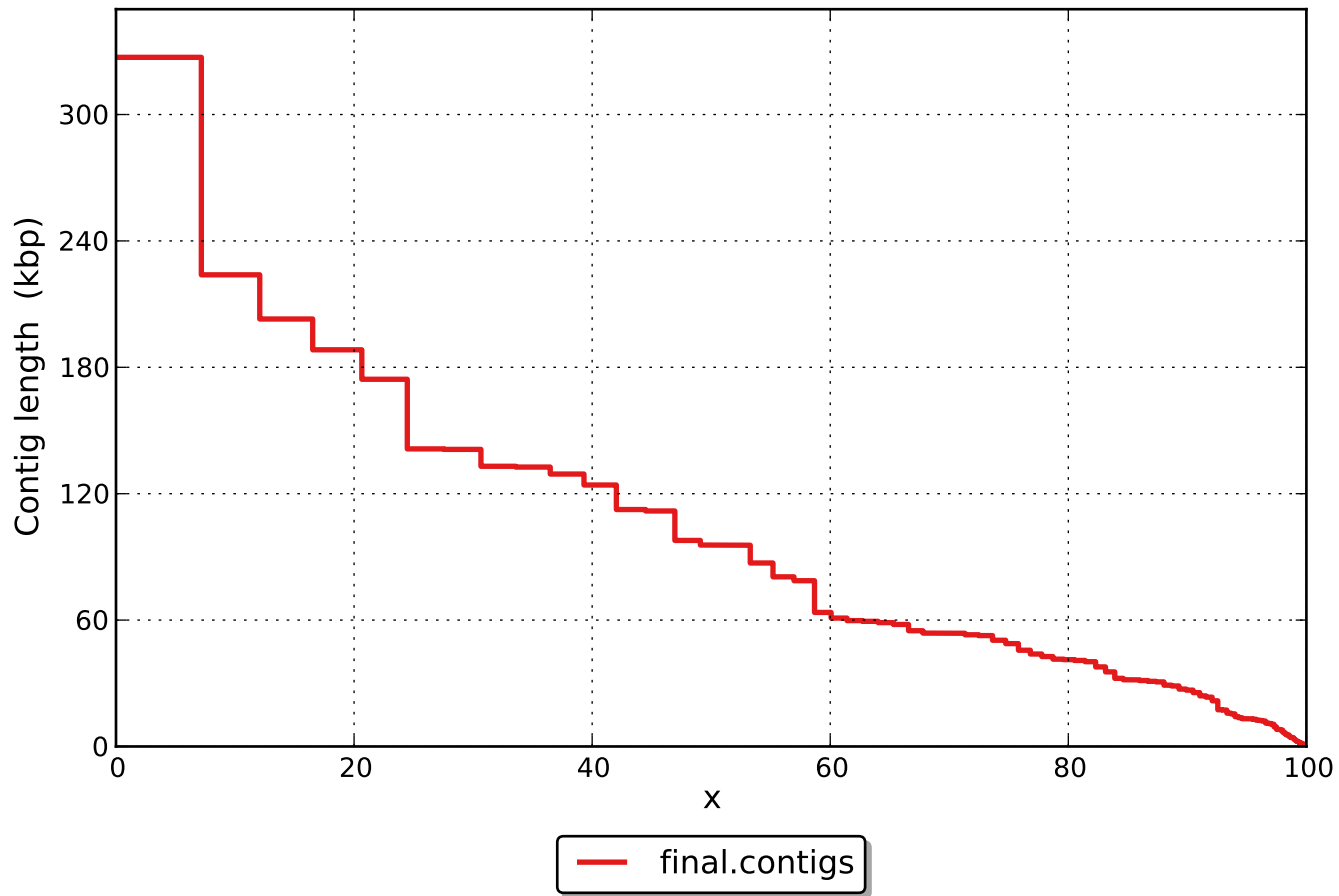|	final.contigs
# contigs (>= 1000 bp)	107
# contigs (>= 5000 bp)	80
# contigs (>= 10000 bp)	72
# contigs (>= 25000 bp)	53
# contigs (>= 50000 bp)	32
Total length (>= 1000 bp)	4556492
Total length (>= 5000 bp)	4496334
Total length (>= 10000 bp)	4439145
Total length (>= 25000 bp)	4154402
Total length (>= 50000 bp)	3410468
# contigs	117
Largest contig	327151
Total length	4563137
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	95630
NG50	95630
N75	48825
NG75	45686
L50	15
LG50	15
L75	33
LG75	34
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	188309
# local misassemblies	8
# unaligned contigs	0 + 1 part
Unaligned length	53
Genome fraction (%)	98.243
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2.04
# indels per 100 kbp	0.22
Largest alignment	327151
NA50	95630
NGA50	95537
NA75	48825
NGA75	45686
LA50	15
LGA50	16
LA75	33
LGA75	34

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	188309
# local misassemblies	8
# mismatches	93
# indels	10
# short indels	8
# long indels	2
Indels length	57

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	53
# N's	0

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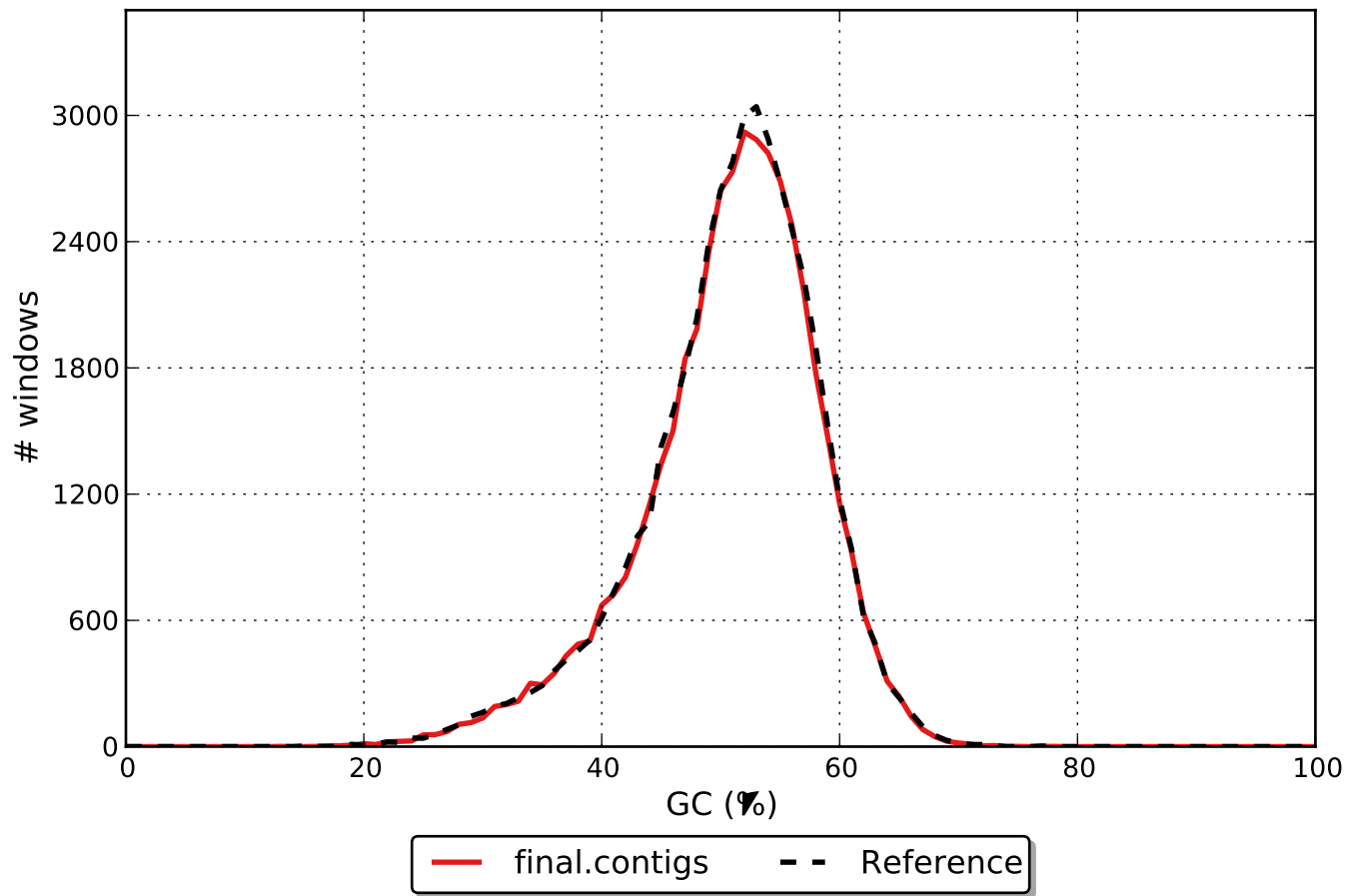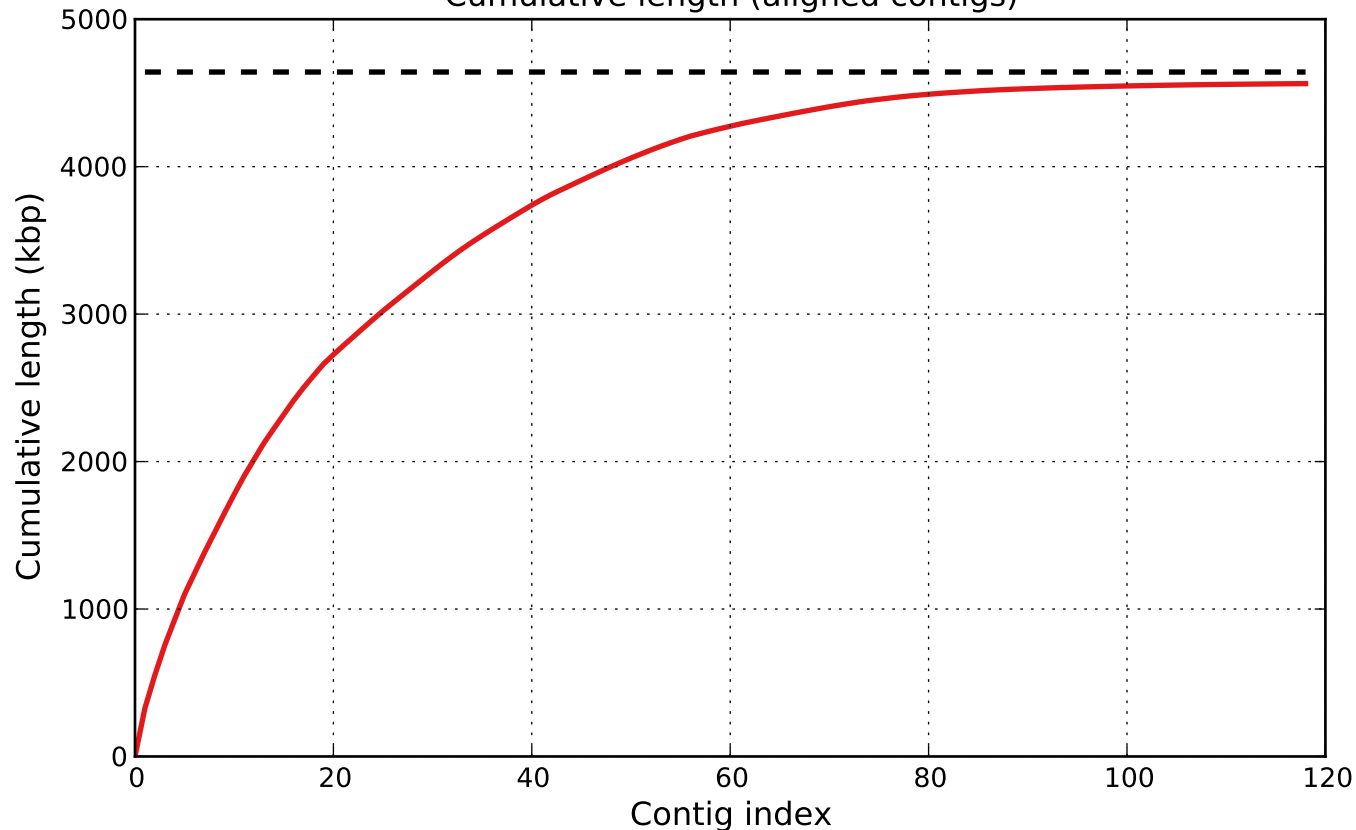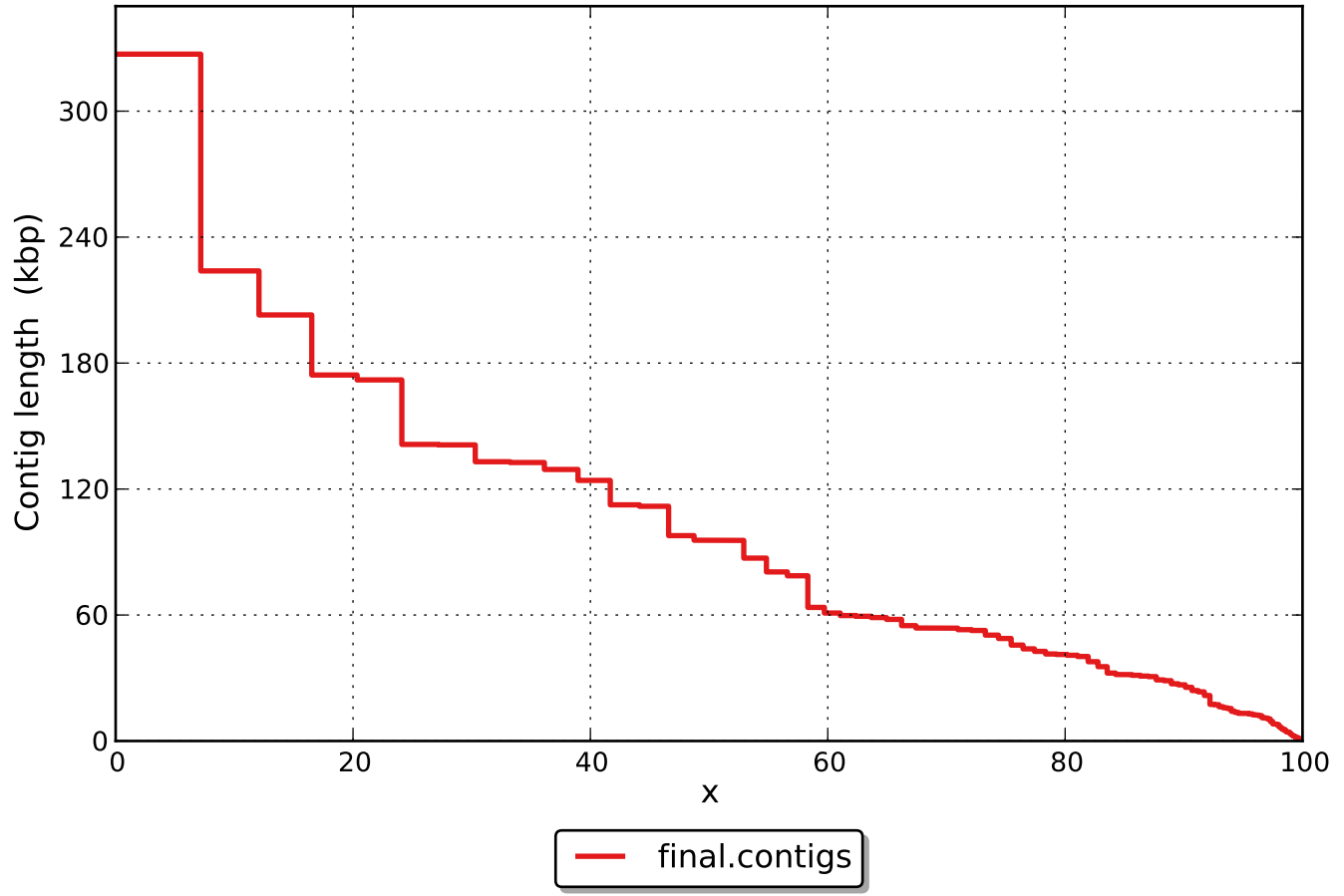(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Cumulative length

GC content

Misassemblies

final.contigs

relocations
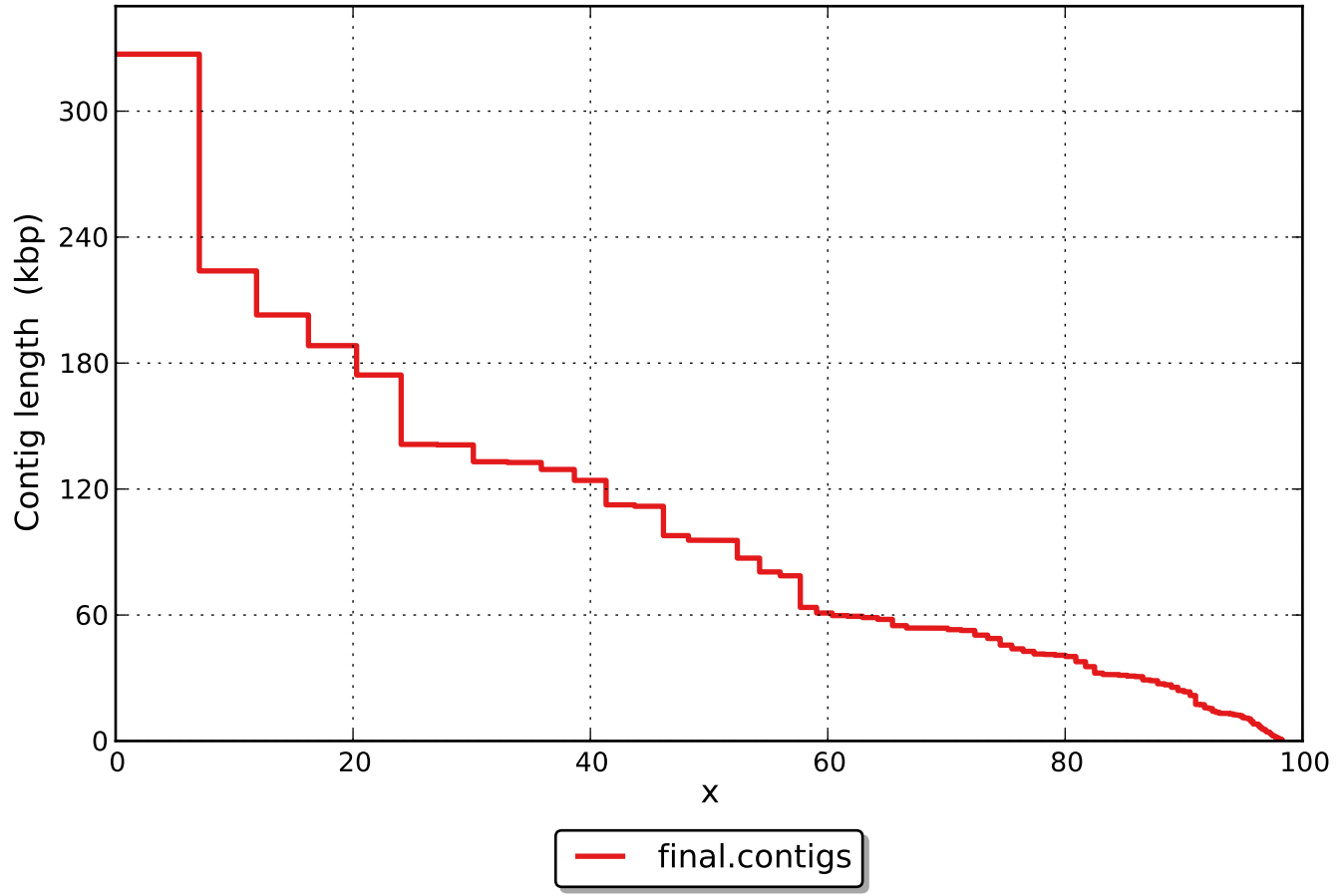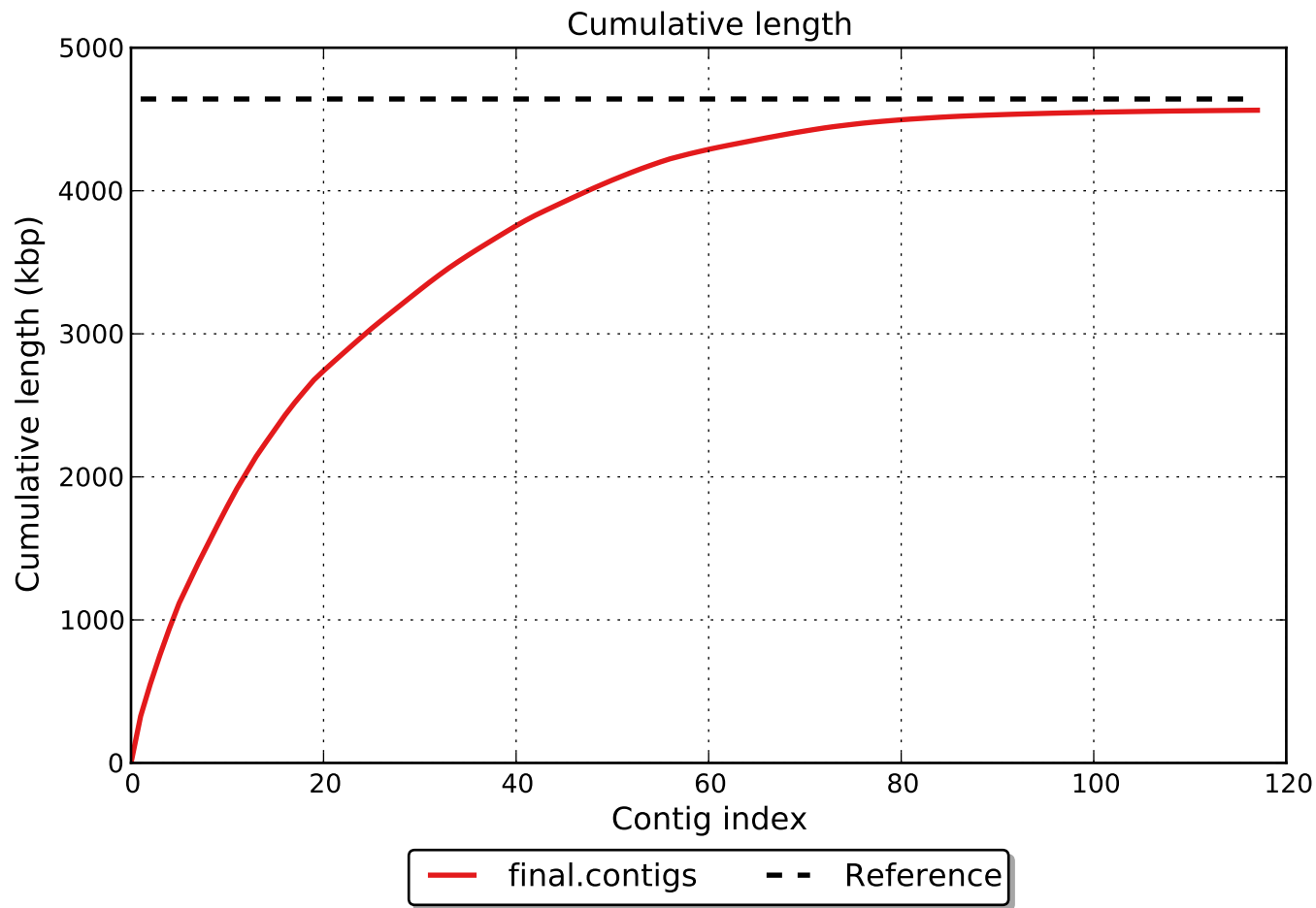
Cumulative length (aligned contigs)