Report

|	final.contigs
# contigs (>= 1000 bp)	1786
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	2898070
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	4044
Largest contig	4855
Total length	4511616
Reference length	4857432
GC (%)	52.22
Reference GC (%)	52.23
N50	1234
NG50	1161
N75	836
NG75	763
L50	1205
LG50	1350
L75	2319
LG75	2644
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	3673
# local misassemblies	0
# unaligned contigs	0 + 2 part
Unaligned length	172
Genome fraction (%)	88.151
Duplication ratio	1.054
# N's per 100 kbp	0.00
# mismatches per 100 kbp	93.56
# indels per 100 kbp	0.07
Largest alignment	4855
NA50	1234
NGA50	1161
NA75	836
NGA75	763
LA50	1206
LGA50	1351
LA75	2320
LGA75	2645

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	3673
# local misassemblies	0
# mismatches	4006
# 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	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	172
# N's	0

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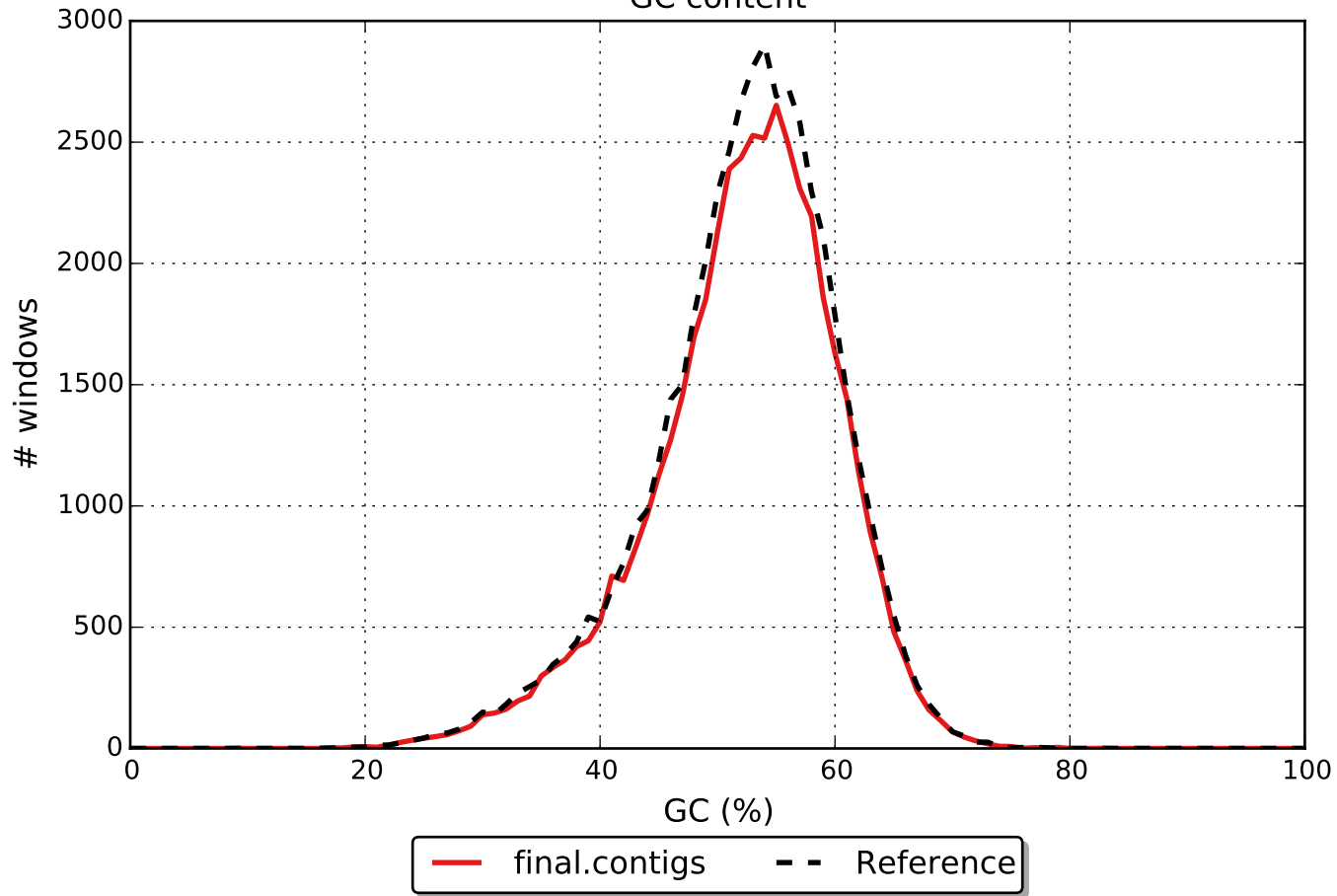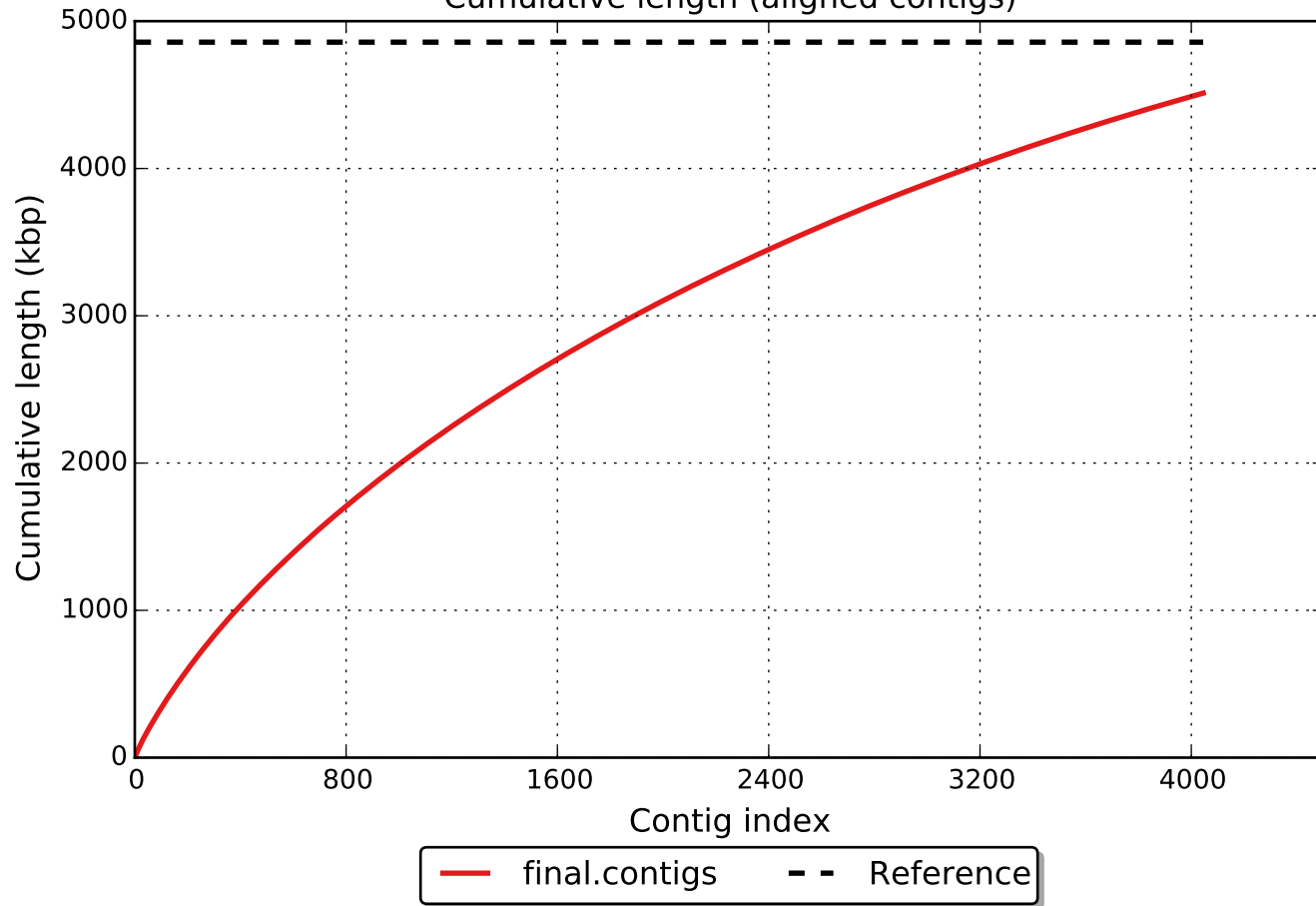(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

NGx

Cumulative length
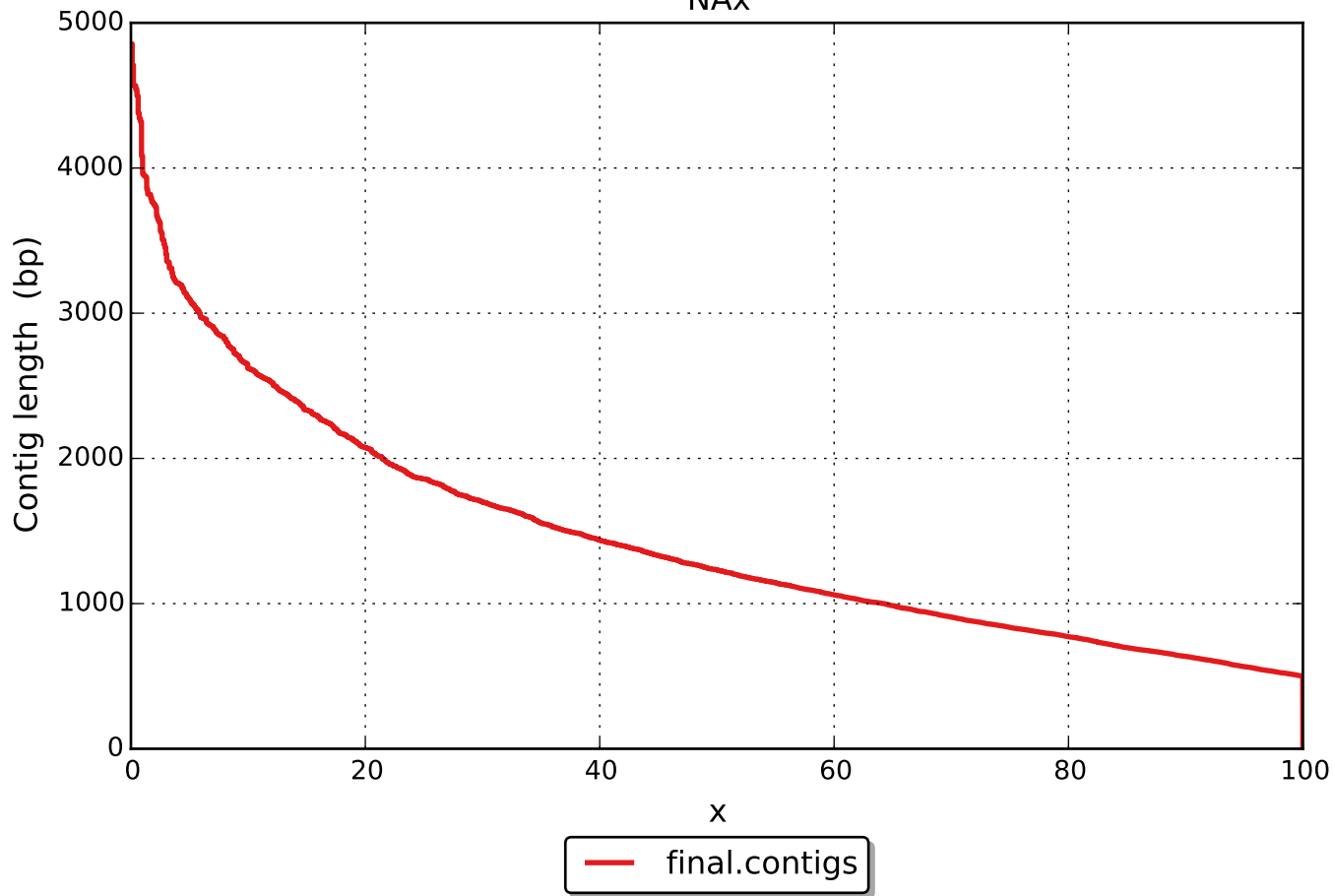
GC content

windows

GC (%)

final.contigs   - - - Reference
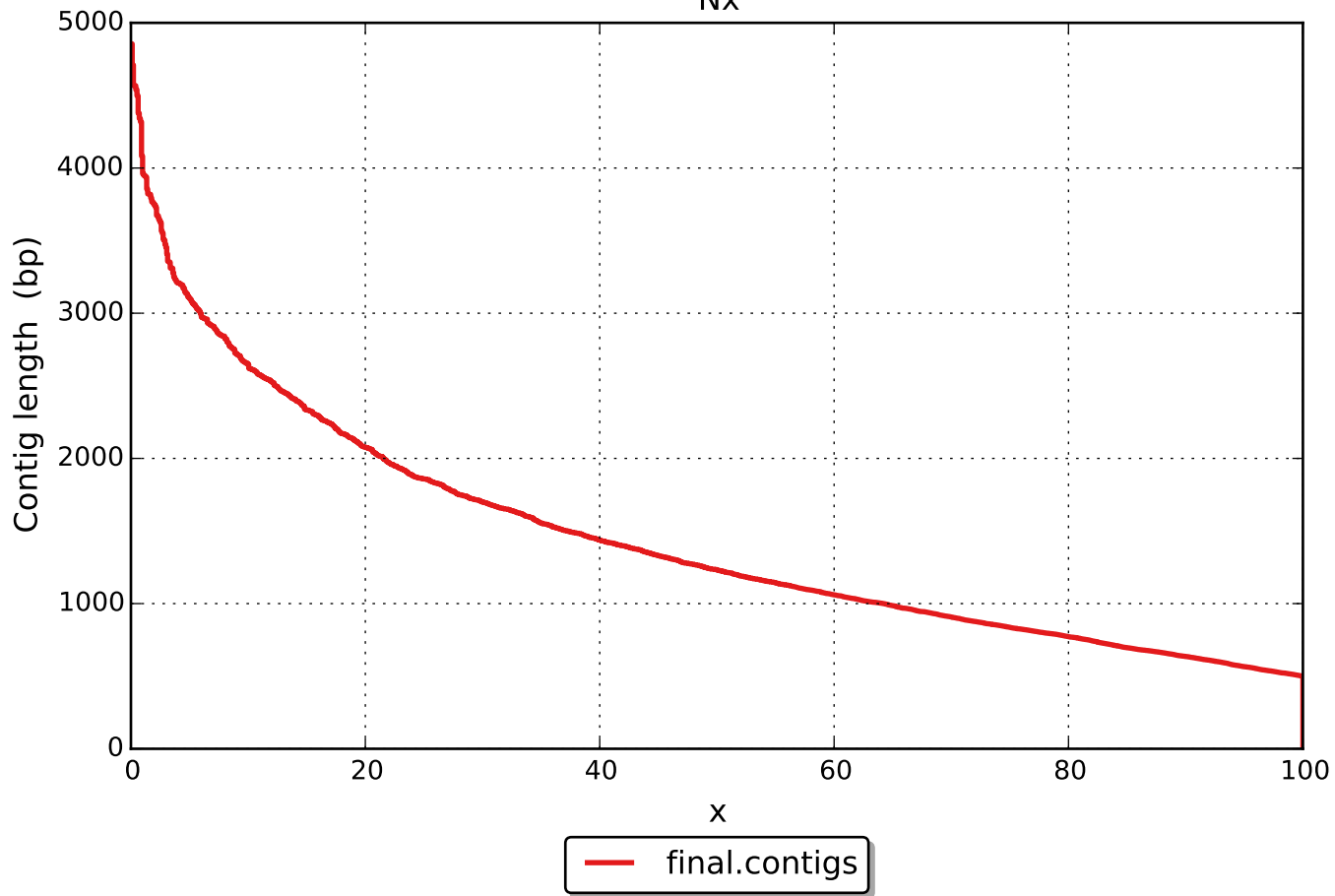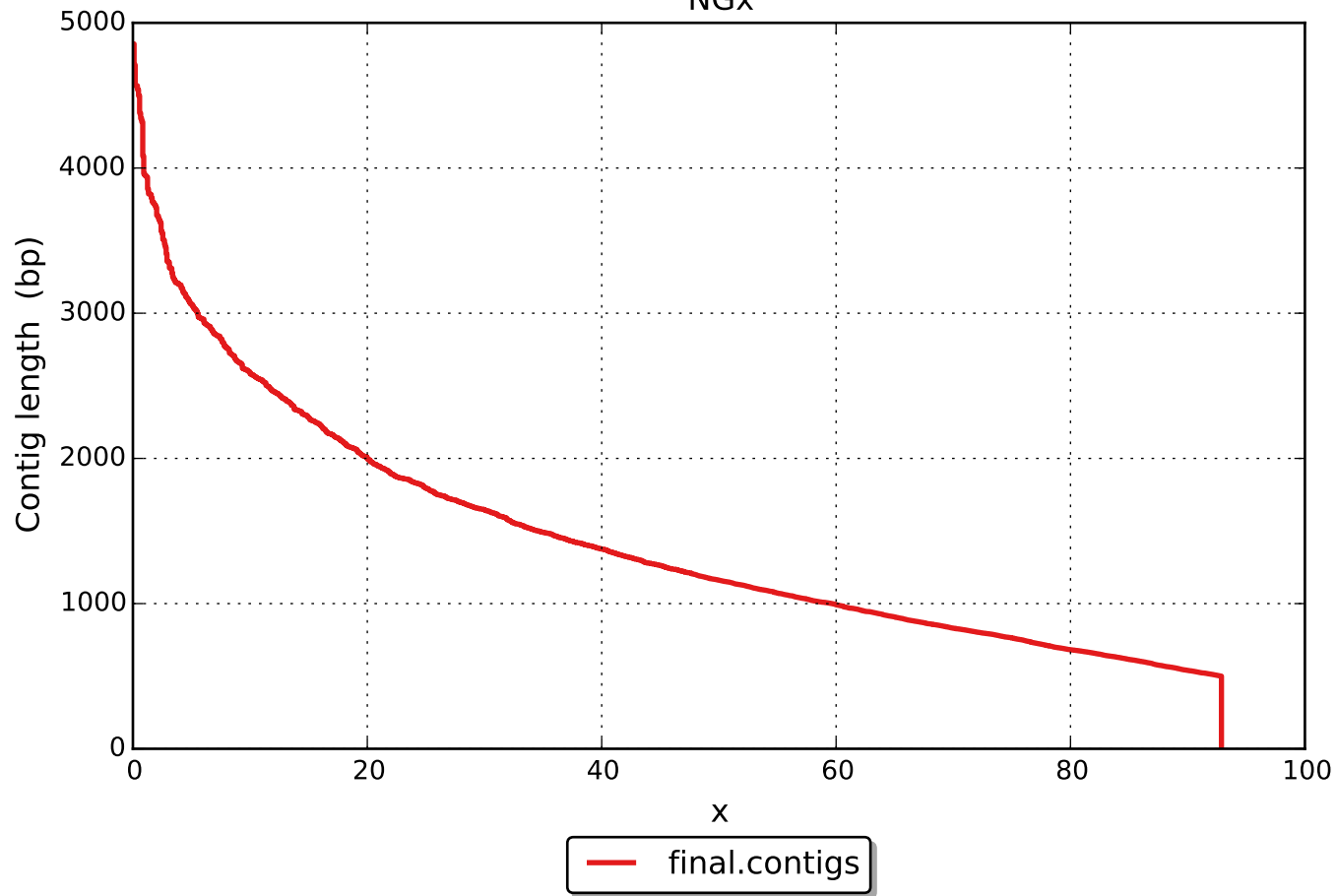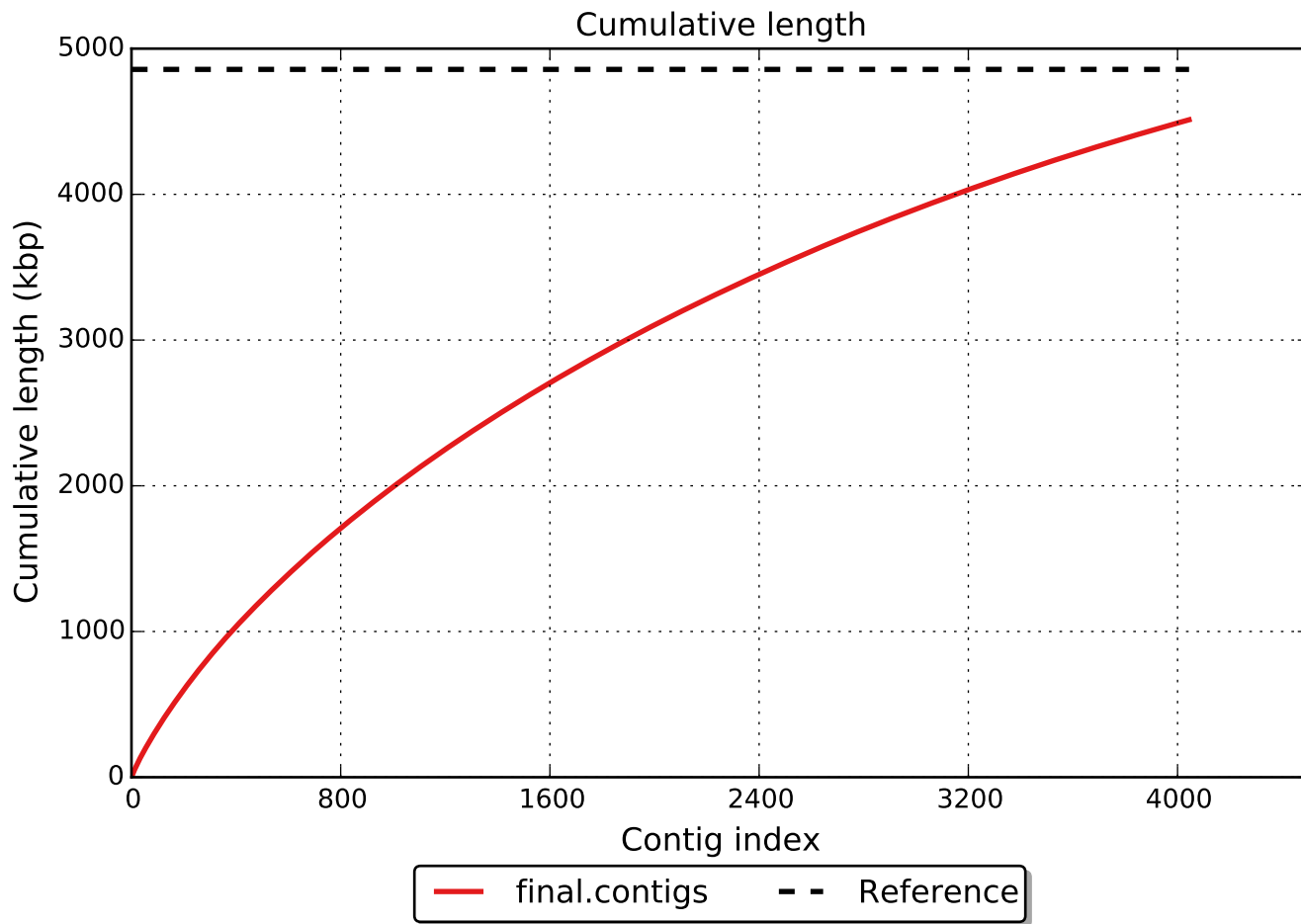
Cumulative length (aligned contigs)