Report

	final.contigs
# contigs (>= 1000 bp)	334
# contigs (>= 5000 bp)	233
# contigs (>= 10000 bp)	164
# contigs (>= 25000 bp)	57
# contigs (>= 50000 bp)	9
Total length (>= 1000 bp)	4801422
Total length (>= 5000 bp)	4519136
Total length (>= 10000 bp)	3999437
Total length (>= 25000 bp)	2321798
Total length (>= 50000 bp)	683424
# contigs	361
Largest contig	110430
Total length	4820113
Reference length	4857432
GC (%)	52.20
Reference GC (%)	52.22
N50	24280
NG50	24256
N75	12369
NG75	12302
L50	61
LG50	62
L75	131
LG75	133
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.585
Duplication ratio	1.007
# N's per 100 kbp	0.00
# mismatches per 100 kbp	10.75
# indels per 100 kbp	0.02
Largest alignment	110430
NA50	24280
NGA50	24256
NA75	12369
NGA75	12302
LA50	61
LGA50	62
LA75	131
LGA75	133

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).
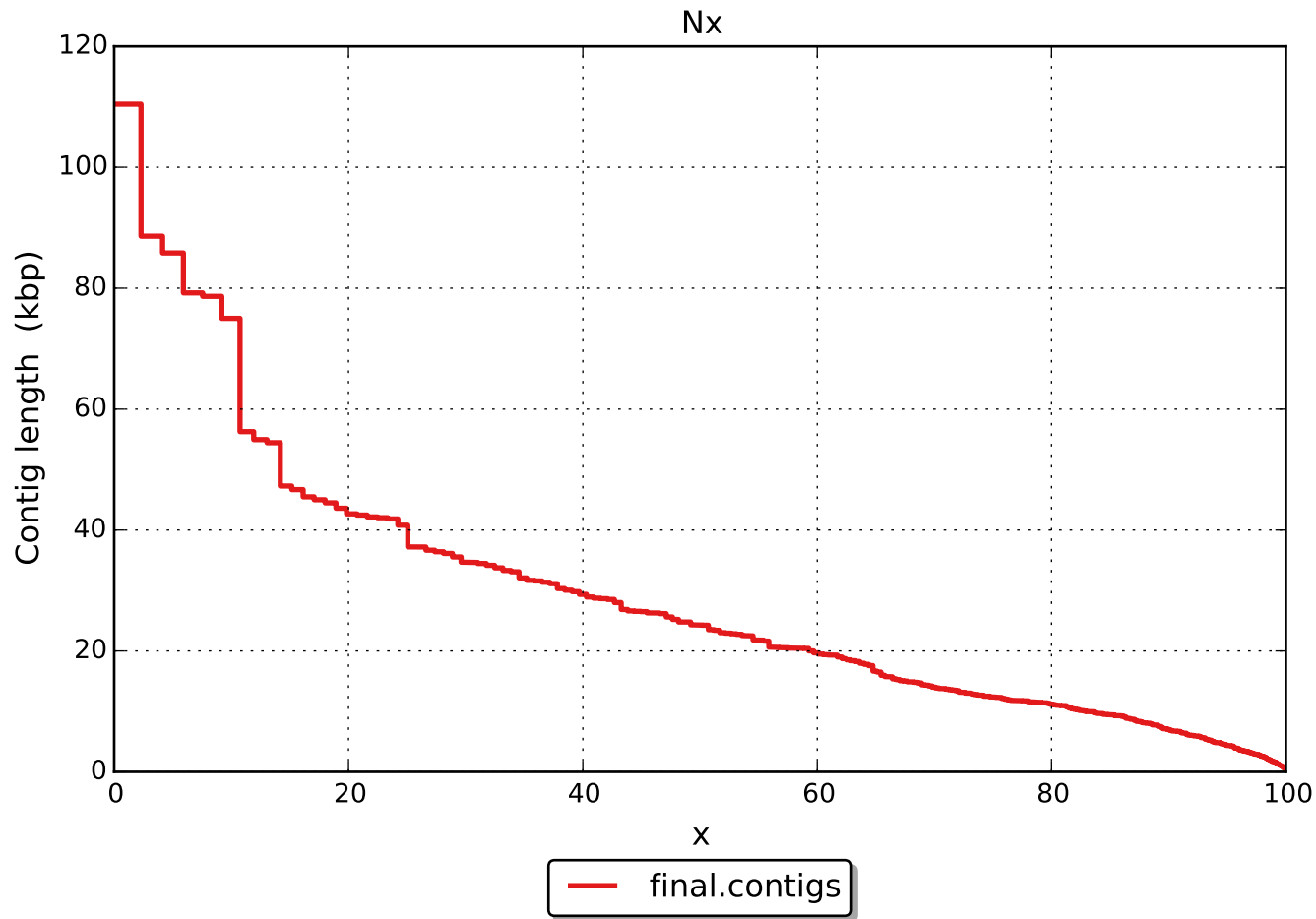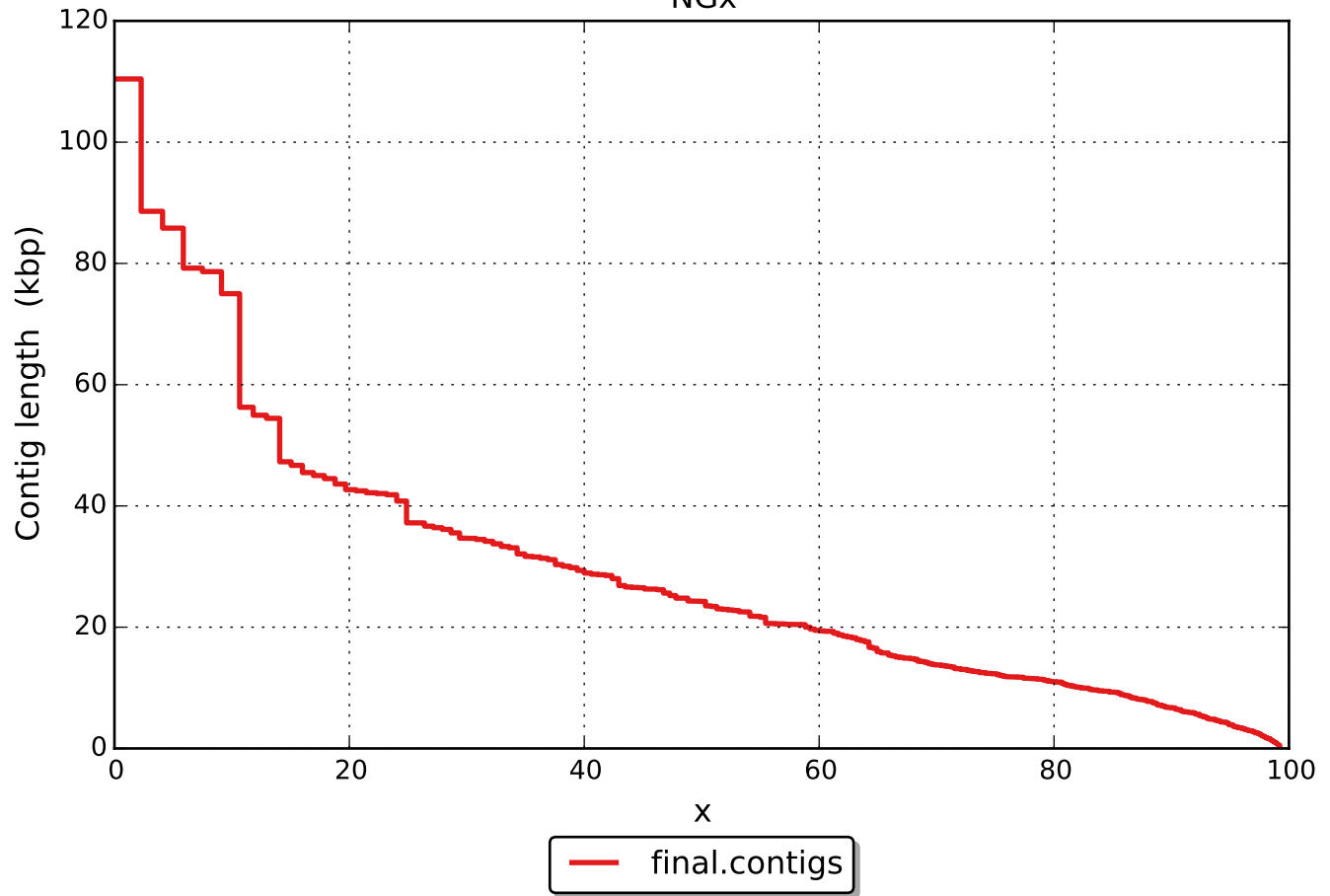
Misassemblies report

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	515
# indels	1
# short indels	1
# long indels	0
Indels length	1

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).
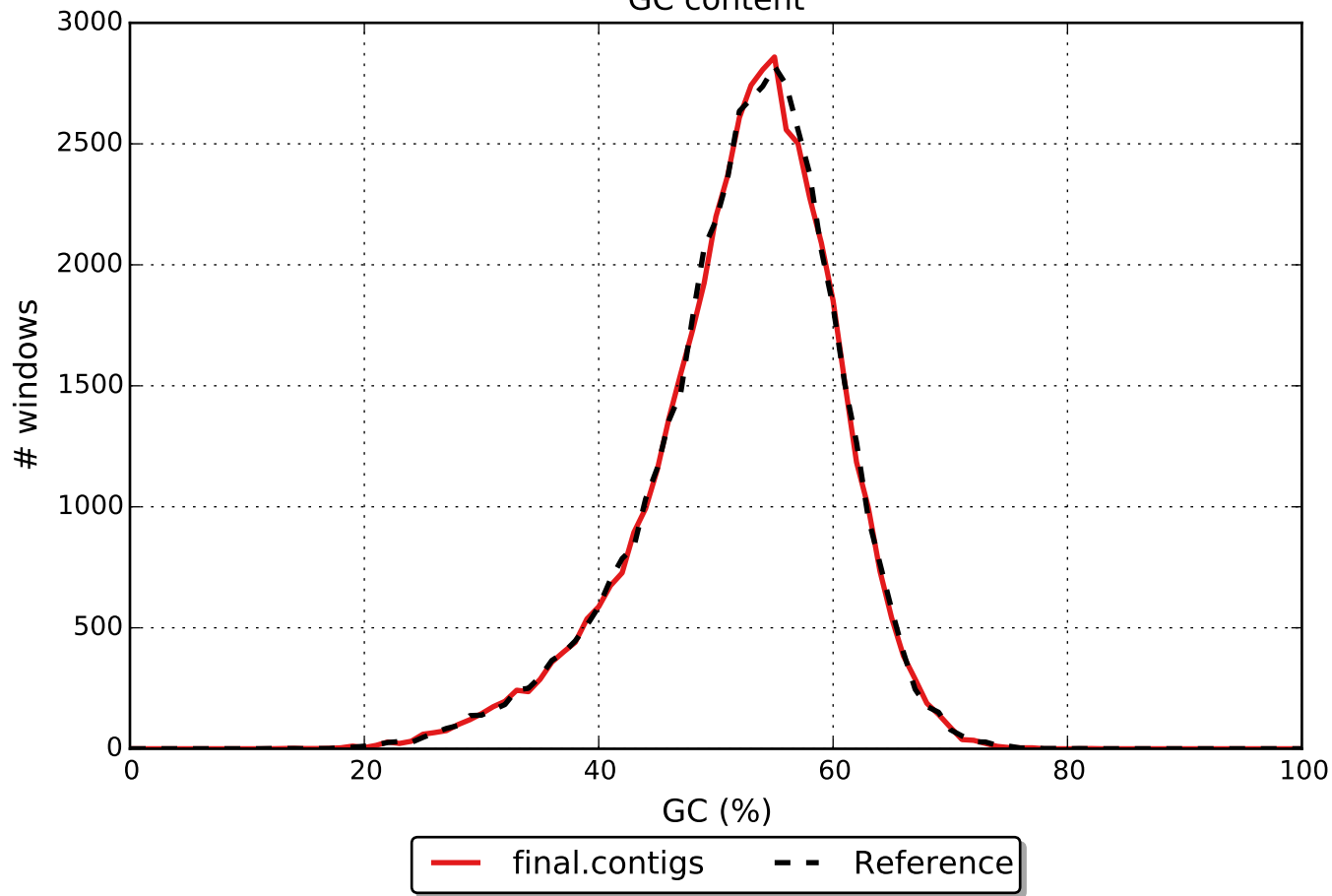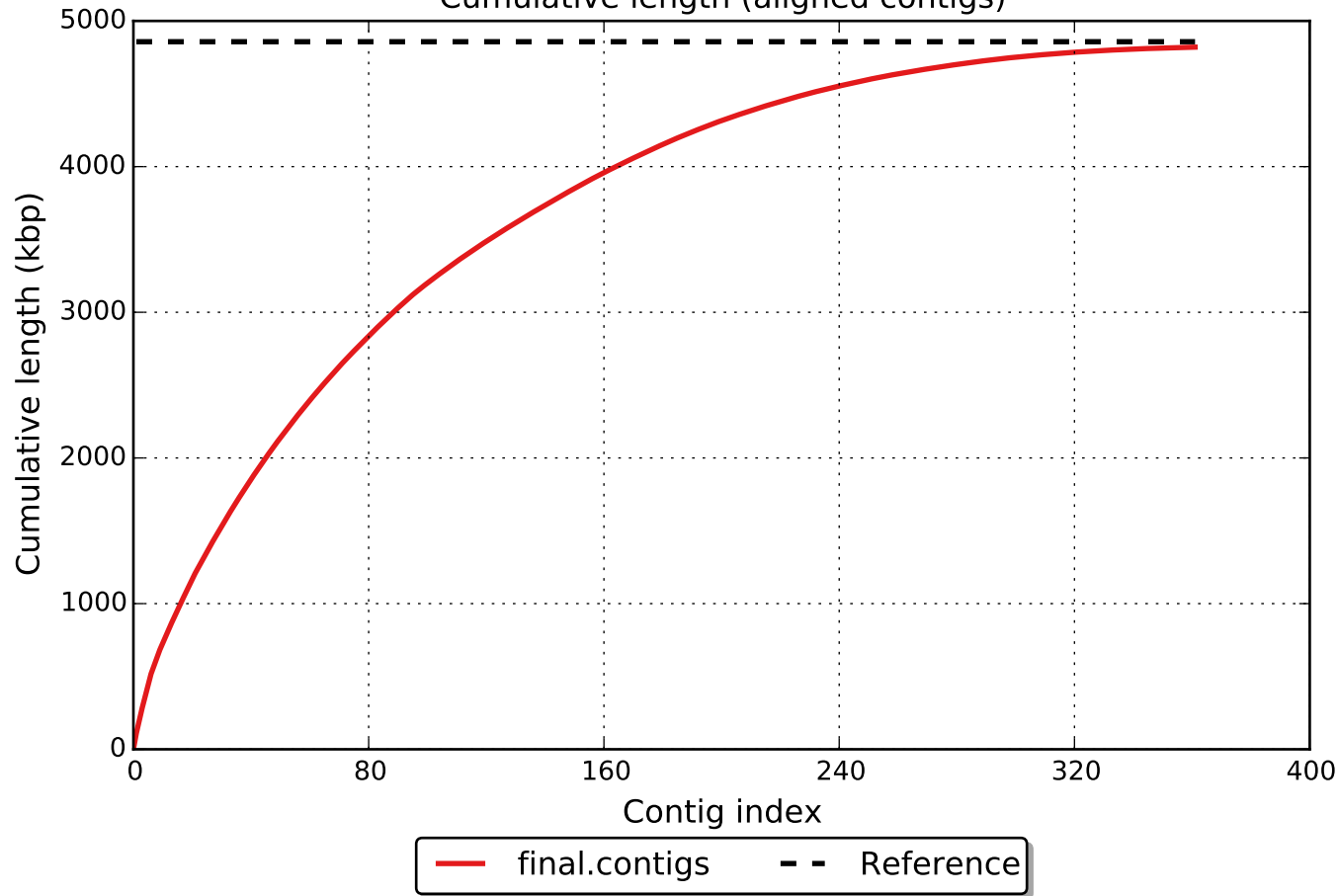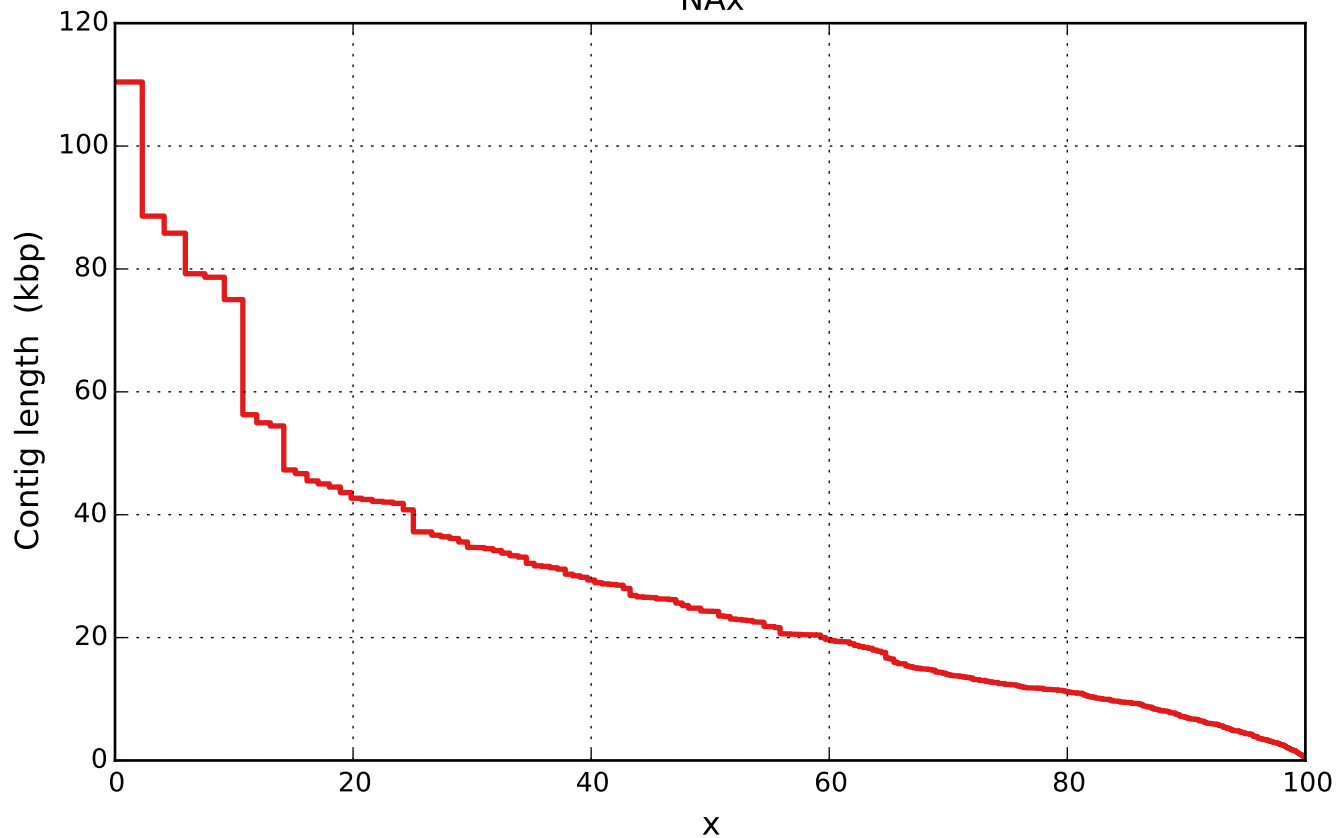
NGx

Contig length (kbp) vs x

final.contigs
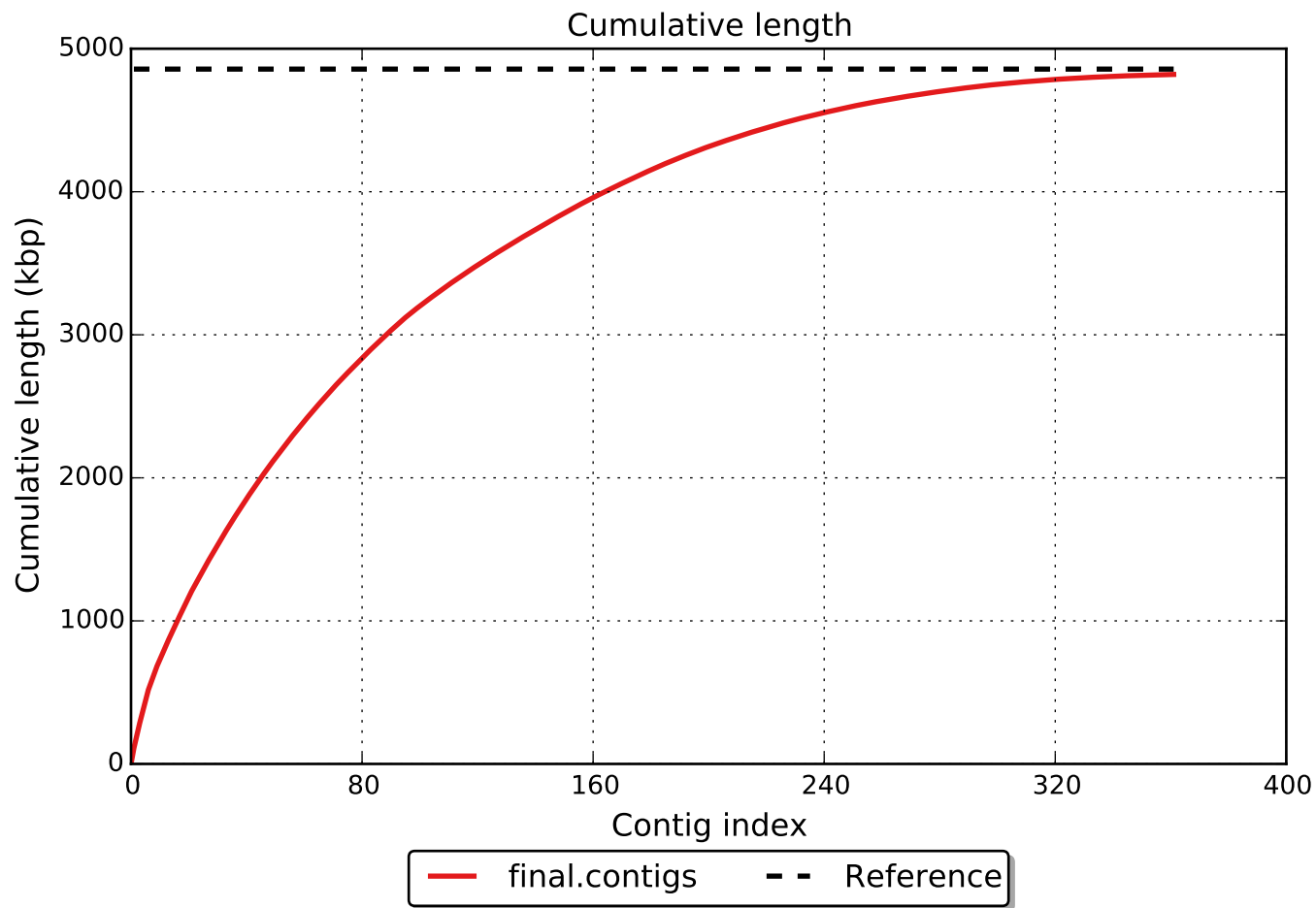
Cumulative length

GC content

Misassemblies

final.contigs

Cumulative length (aligned contigs)

NGAx