Report

|	final.contigs
# contigs (>= 0 bp)	175
# contigs (>= 1000 bp)	92
# contigs (>= 5000 bp)	68
# contigs (>= 10000 bp)	62
# contigs (>= 25000 bp)	48
# contigs (>= 50000 bp)	29
Total length (>= 0 bp)	4581153
Total length (>= 1000 bp)	4551639
Total length (>= 5000 bp)	4499021
Total length (>= 10000 bp)	4453408
Total length (>= 25000 bp)	4228516
Total length (>= 50000 bp)	3587629
# contigs	108
Largest contig	327151
Total length	4562700
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	125651
NG50	125651
N75	58008
NG75	54946
L50	13
LG50	13
L75	27
LG75	28
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.246
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.48
# indels per 100 kbp	0.00
Largest alignment	327151
NA50	125651
NGA50	125651
NA75	58008
NGA75	54946
LA50	13
LGA50	13
LA75	27
LGA75	28

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
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	22
# indels	0
# short indels	0
# long indels	0
Indels length	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).

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).
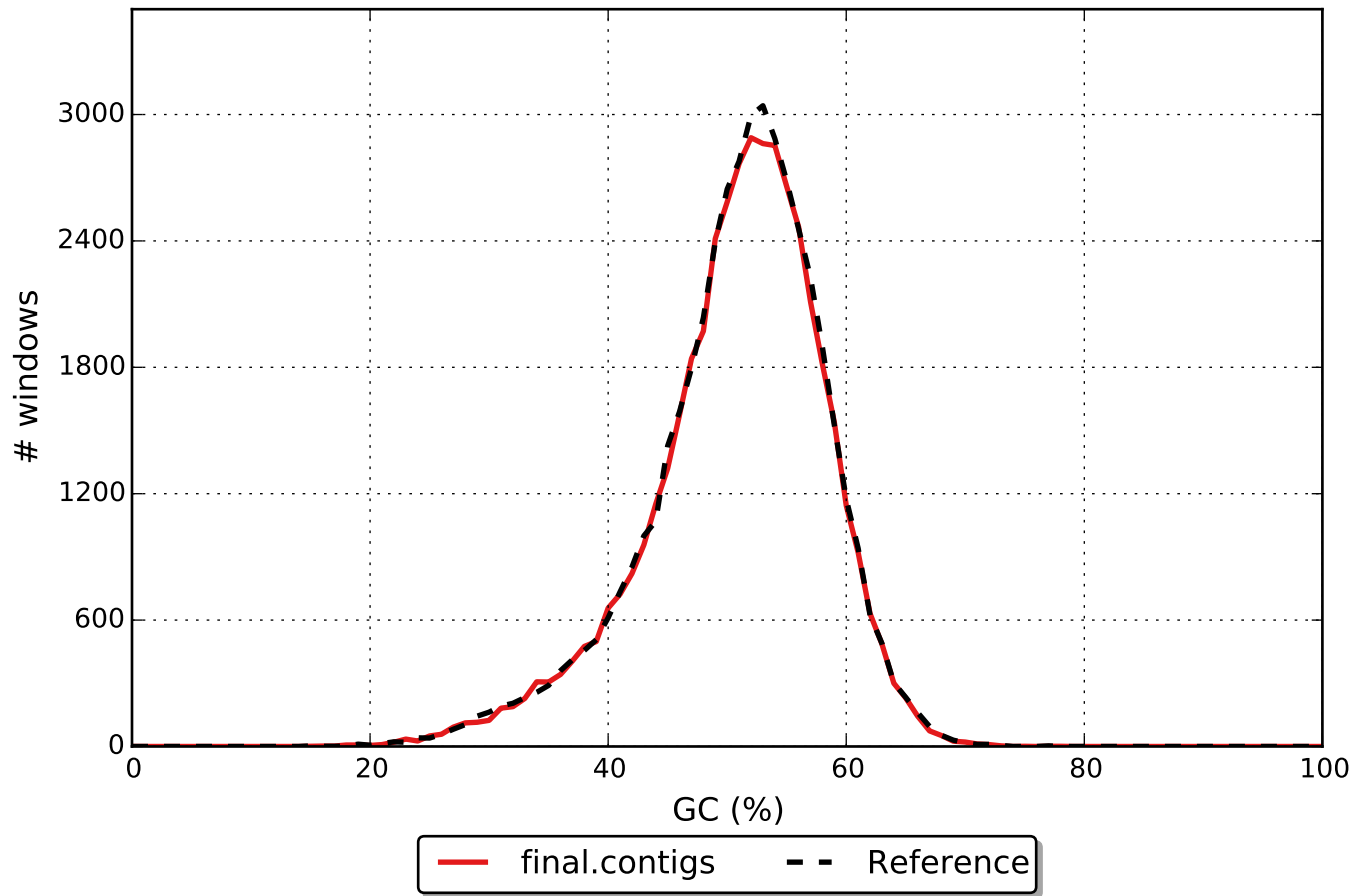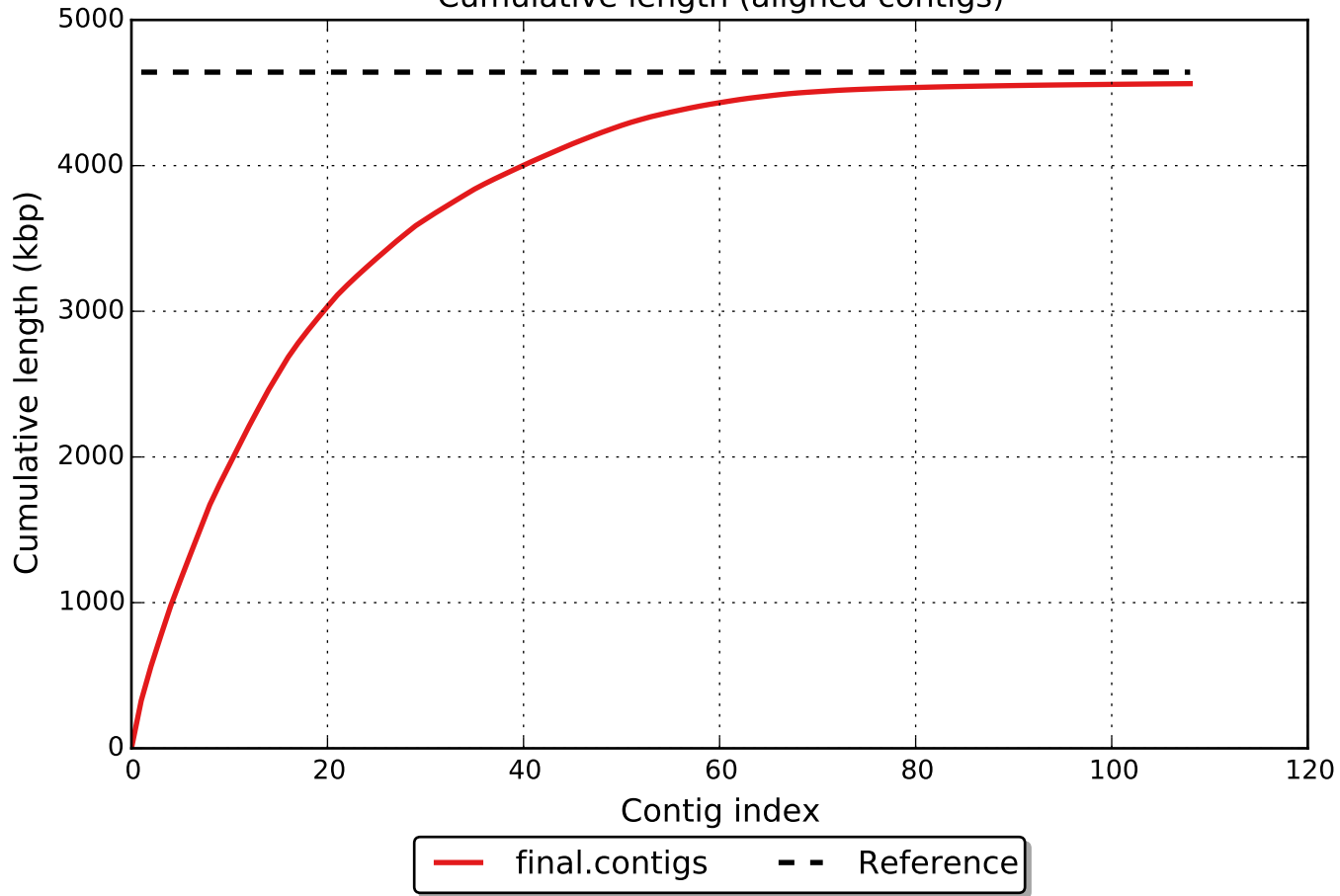
Cumulative length
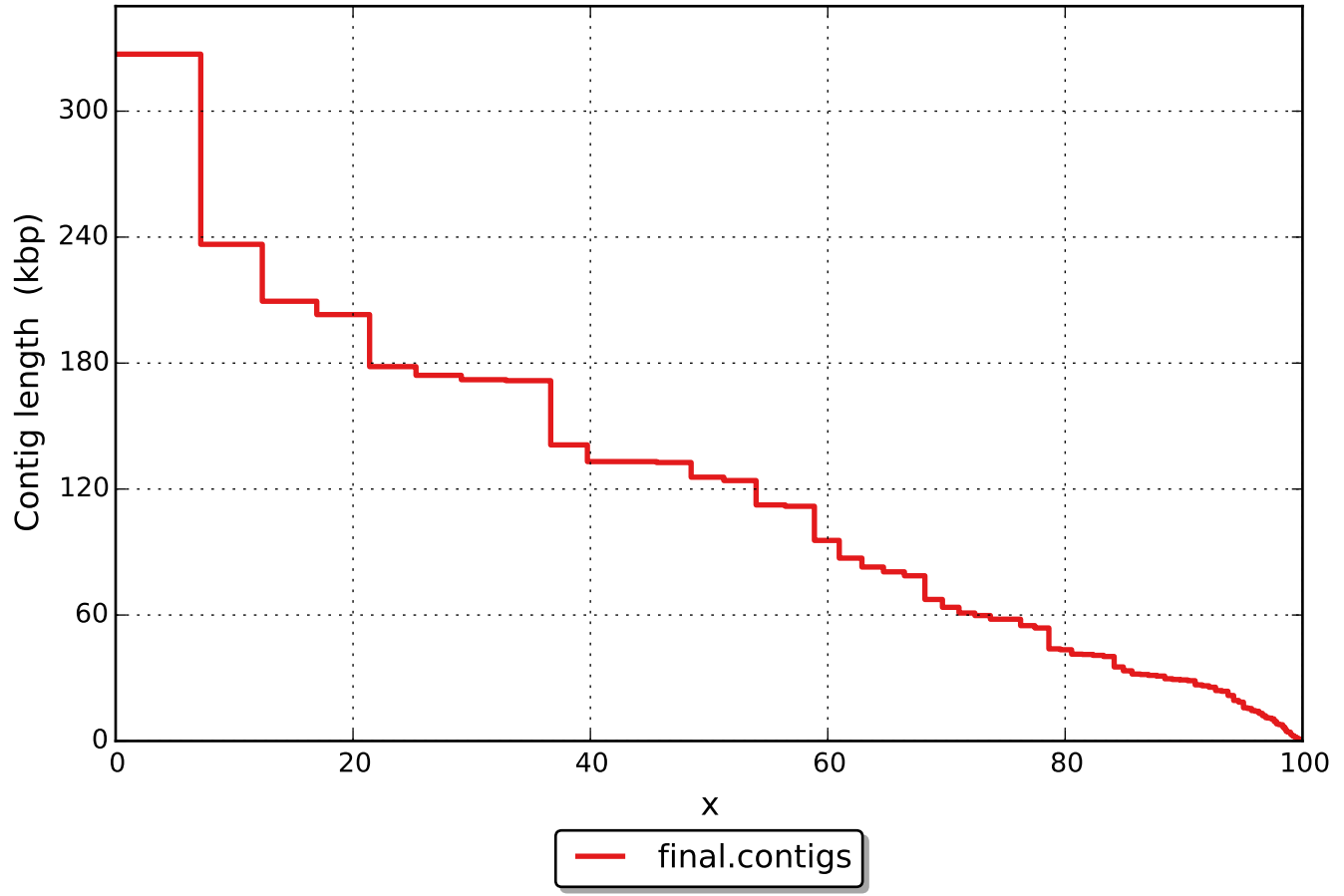
Misassemblies

final.contigs
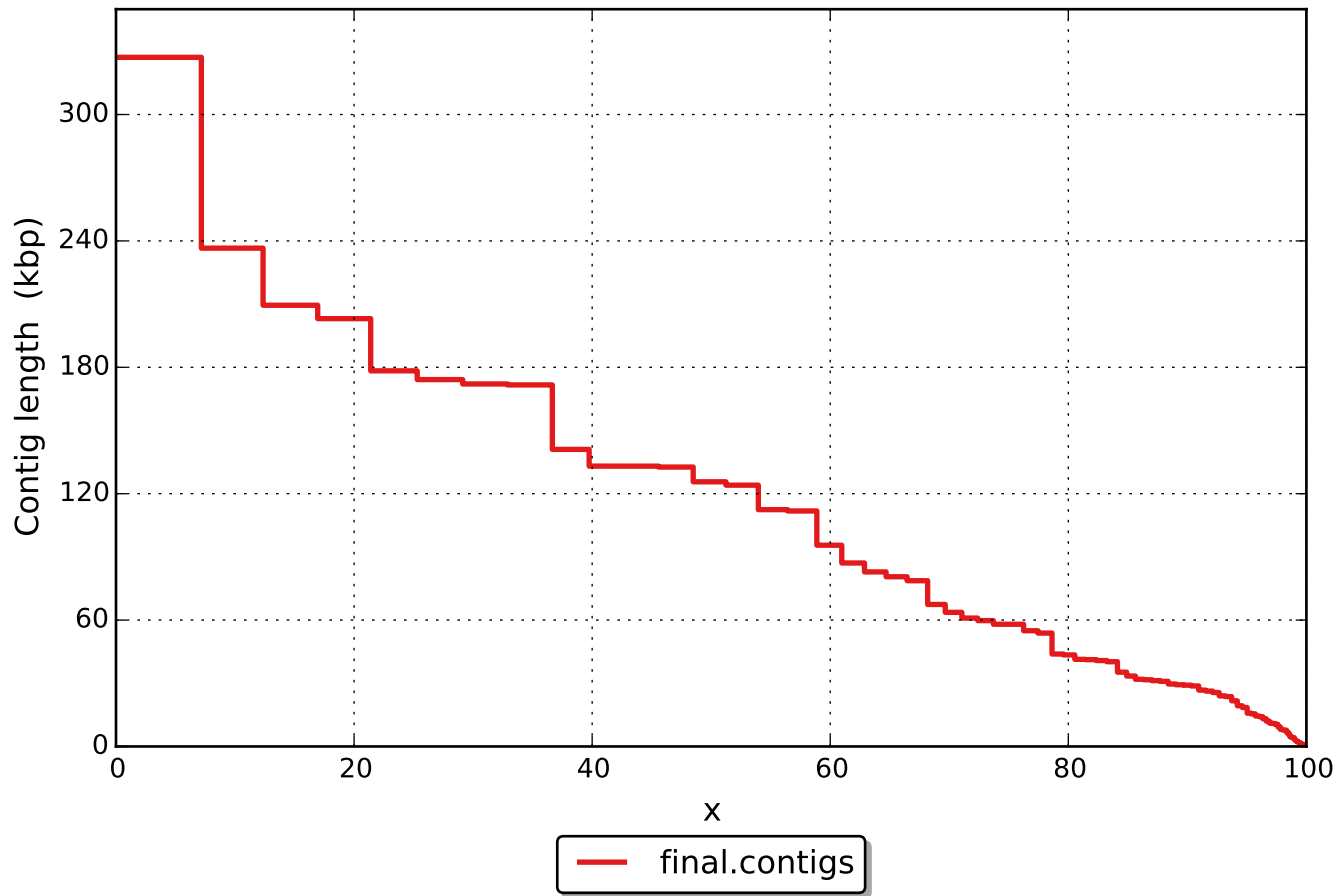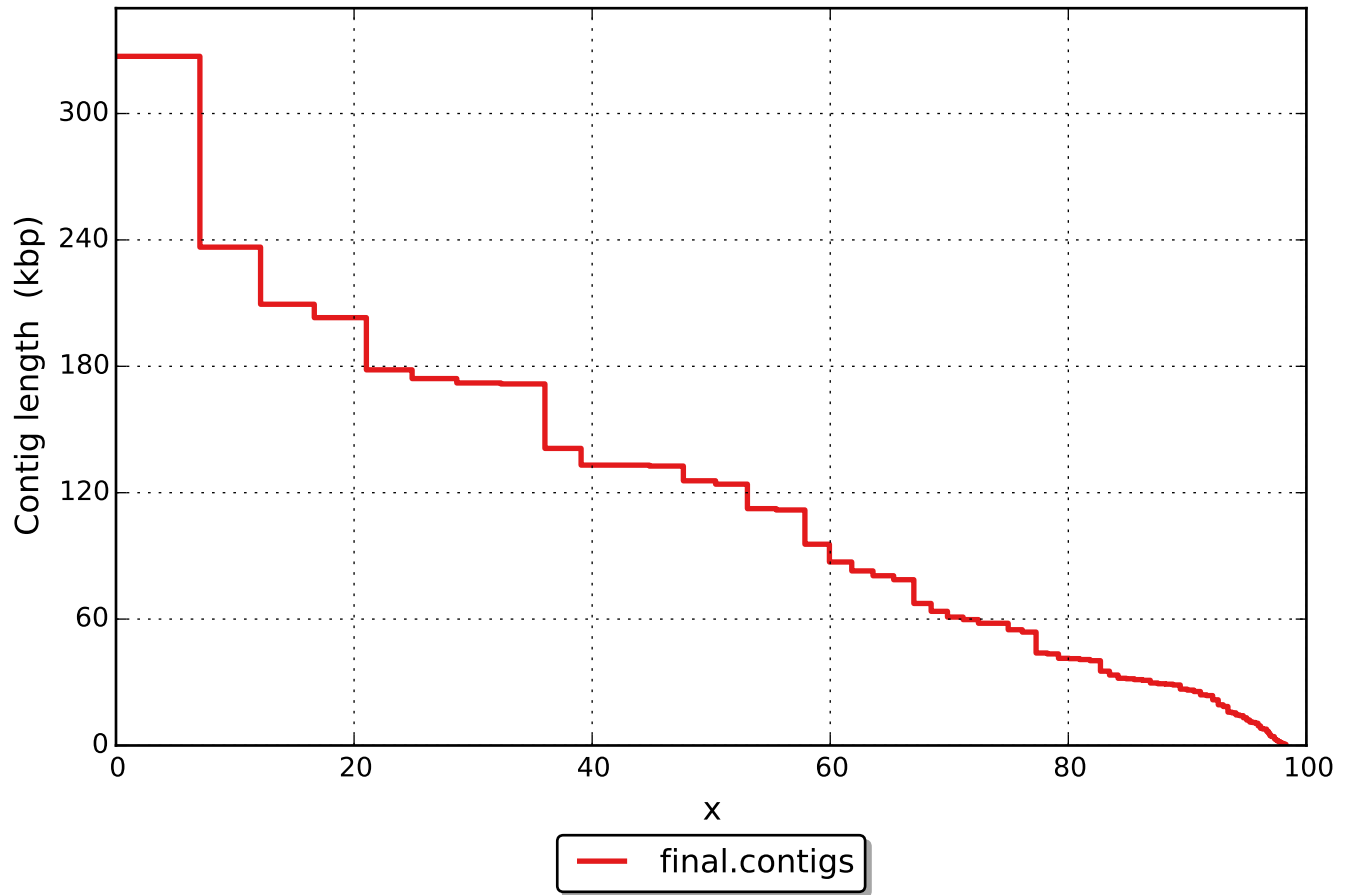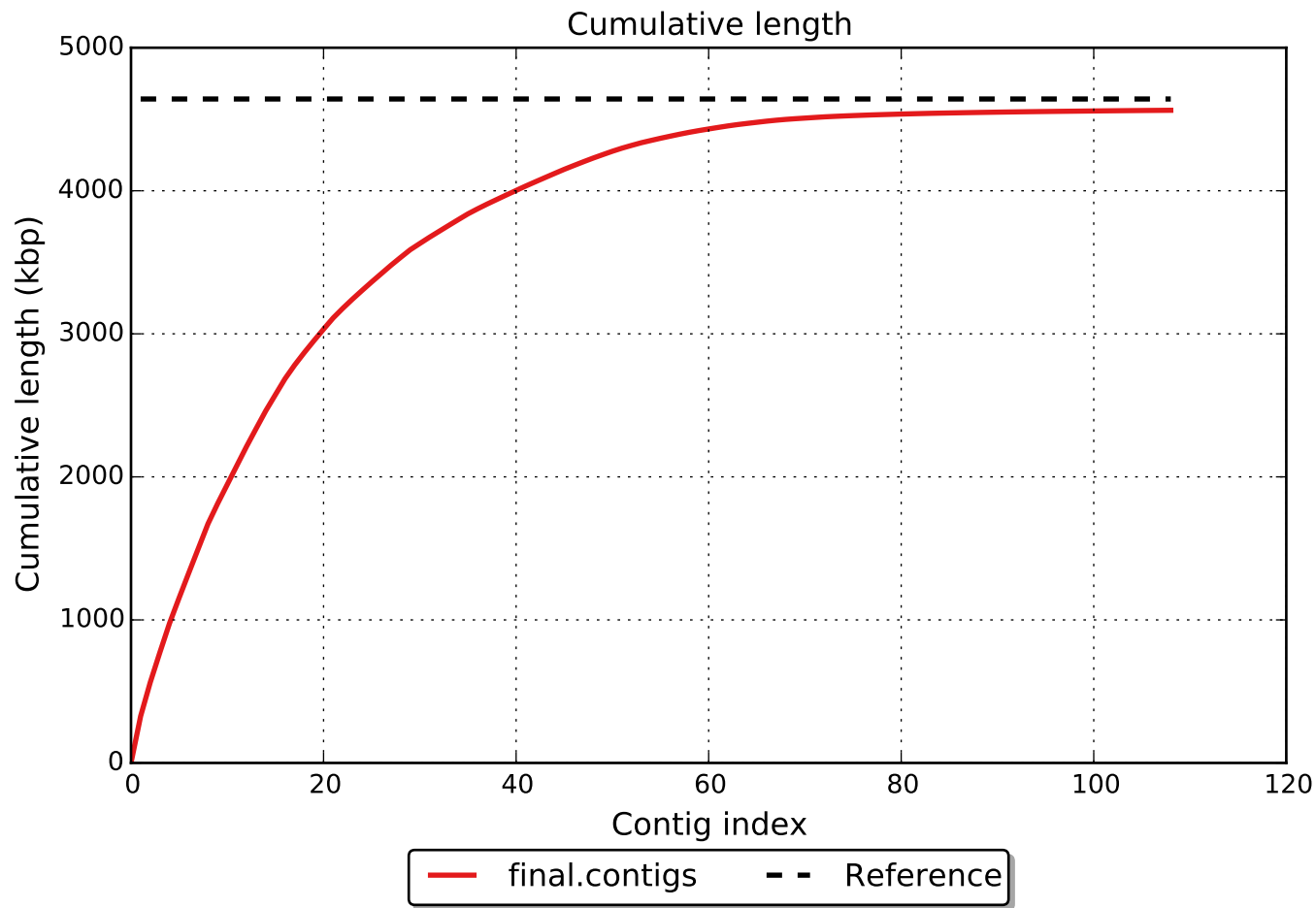
Cumulative length (aligned contigs)

NAx