Report

	final.contigs
# contigs (>= 0 bp)	10411
# contigs (>= 1000 bp)	1839
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	7076166
Total length (>= 1000 bp)	2660324
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	10411
Largest contig	4077
Total length	7076166
Reference length	4641652
GC (%)	50.71
Reference GC (%)	50.79
N50	806
NG50	1091
N75	492
NG75	819
L50	2816
LG50	1515
L75	5617
LG75	2746
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	9367 + 25 part
Unaligned length	5679890
Genome fraction (%)	29.590
Duplication ratio	1.017
# N's per 100 kbp	0.00
# mismatches per 100 kbp	692.99
# indels per 100 kbp	0.95
Largest alignment	4077
NGA50	-

Misassemblies report

|	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	9518
# indels	13
# short indels	13
# long indels	0
Indels length	13

Unaligned report

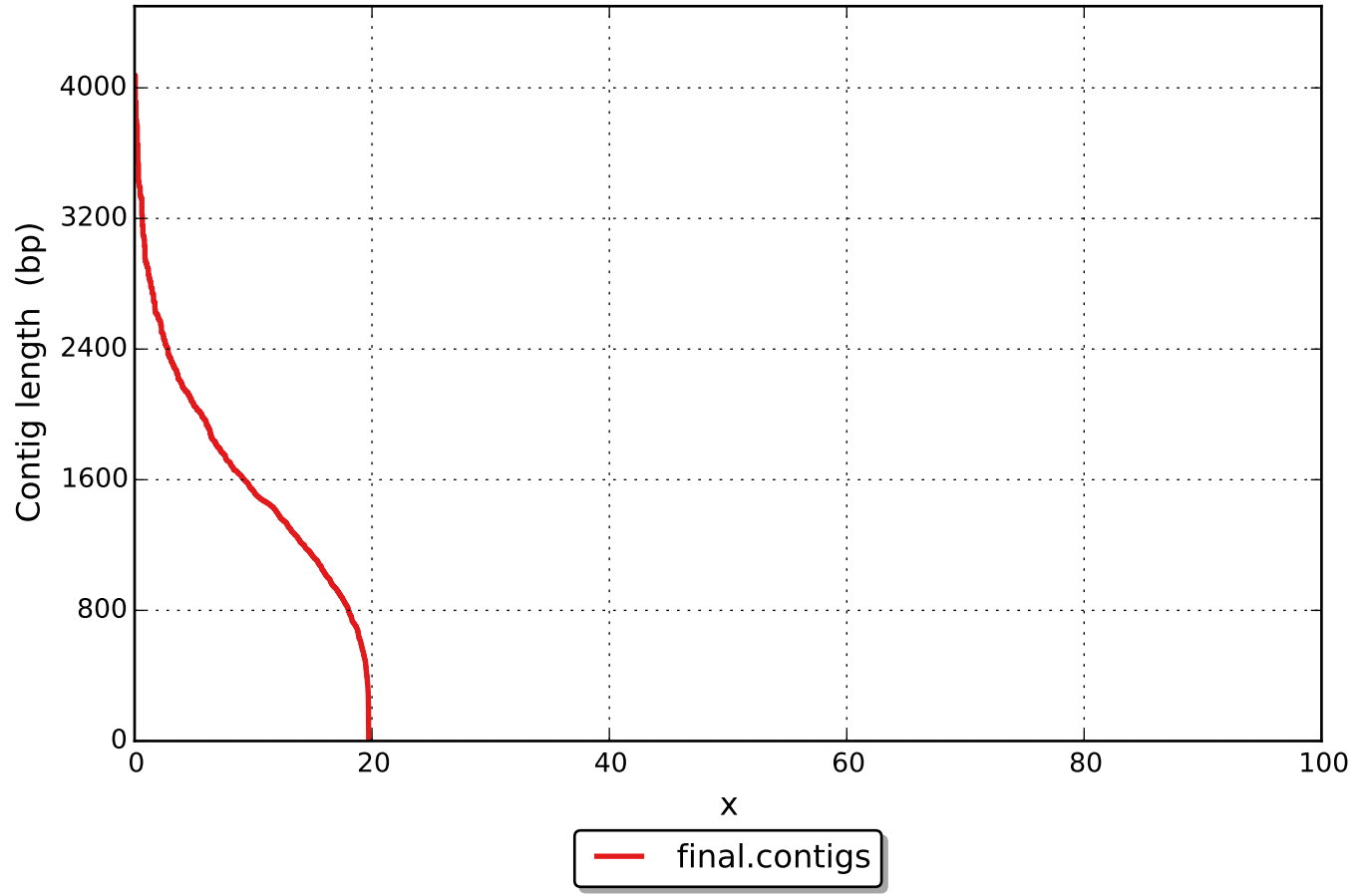|	final.contigs
# fully unaligned contigs	9367
Fully unaligned length	5671385
# partially unaligned contigs	25
# with misassembly	0
# both parts are significant	25
Partially unaligned length	8505
# N's	0
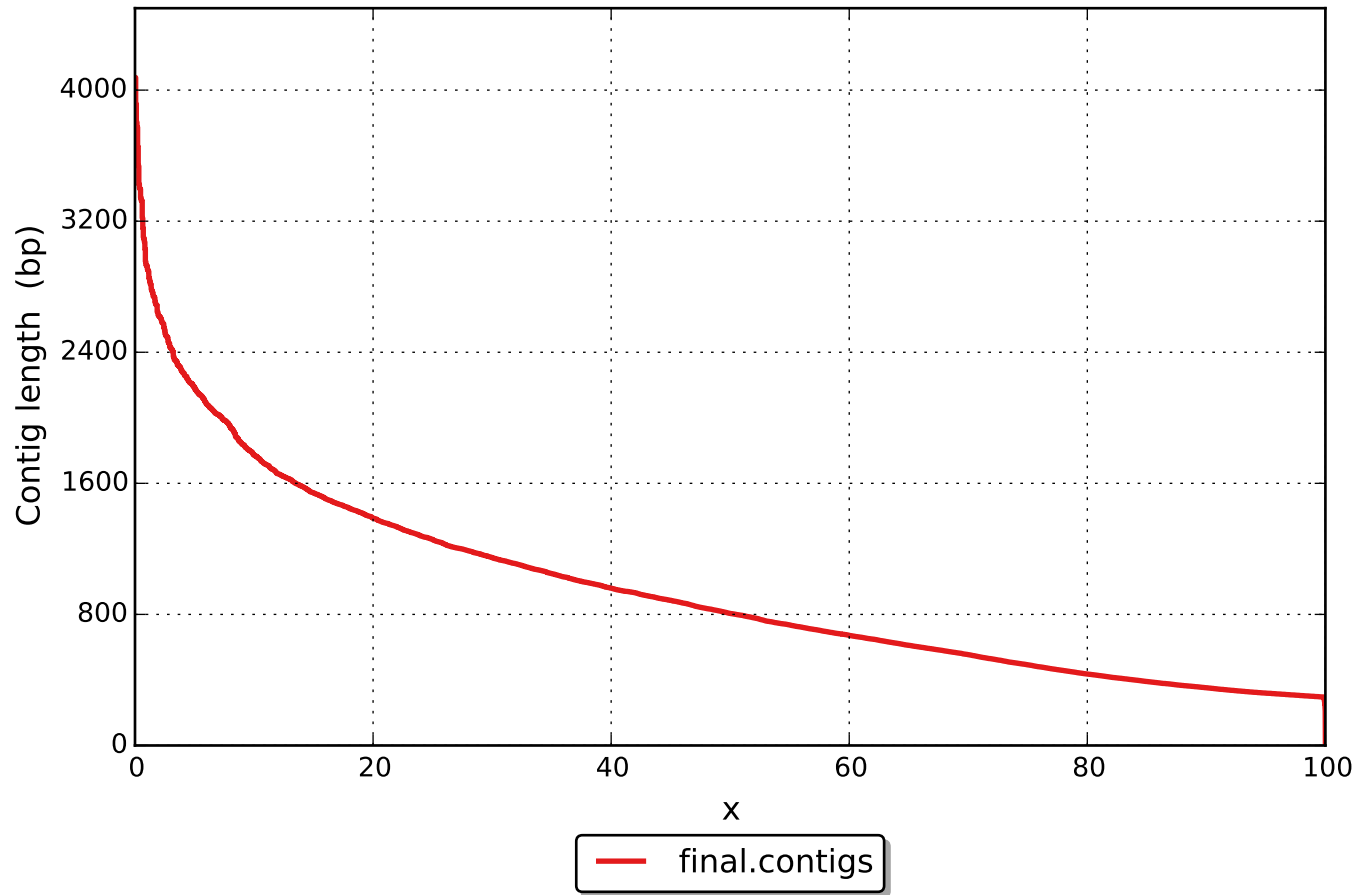
Cumulative length
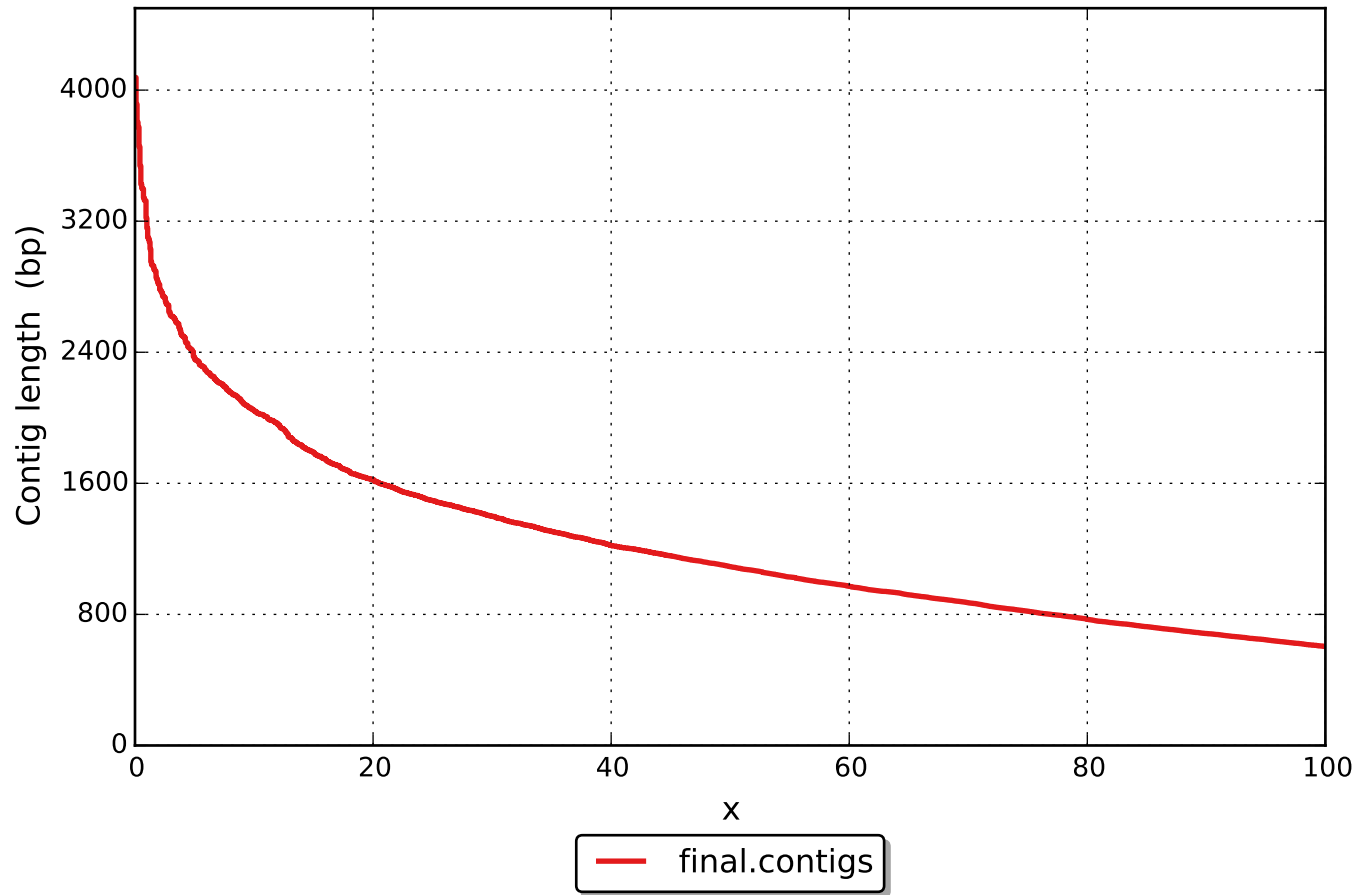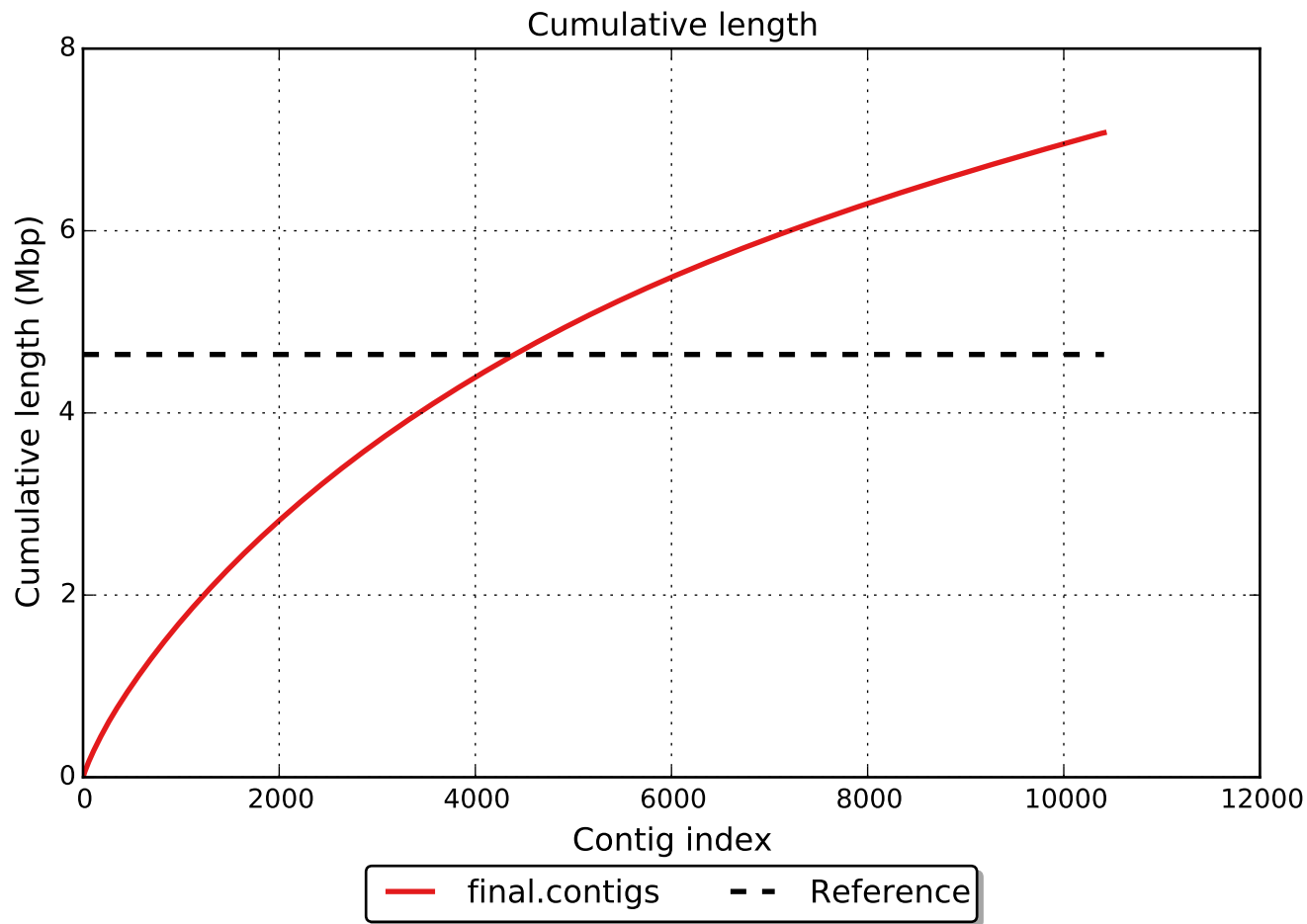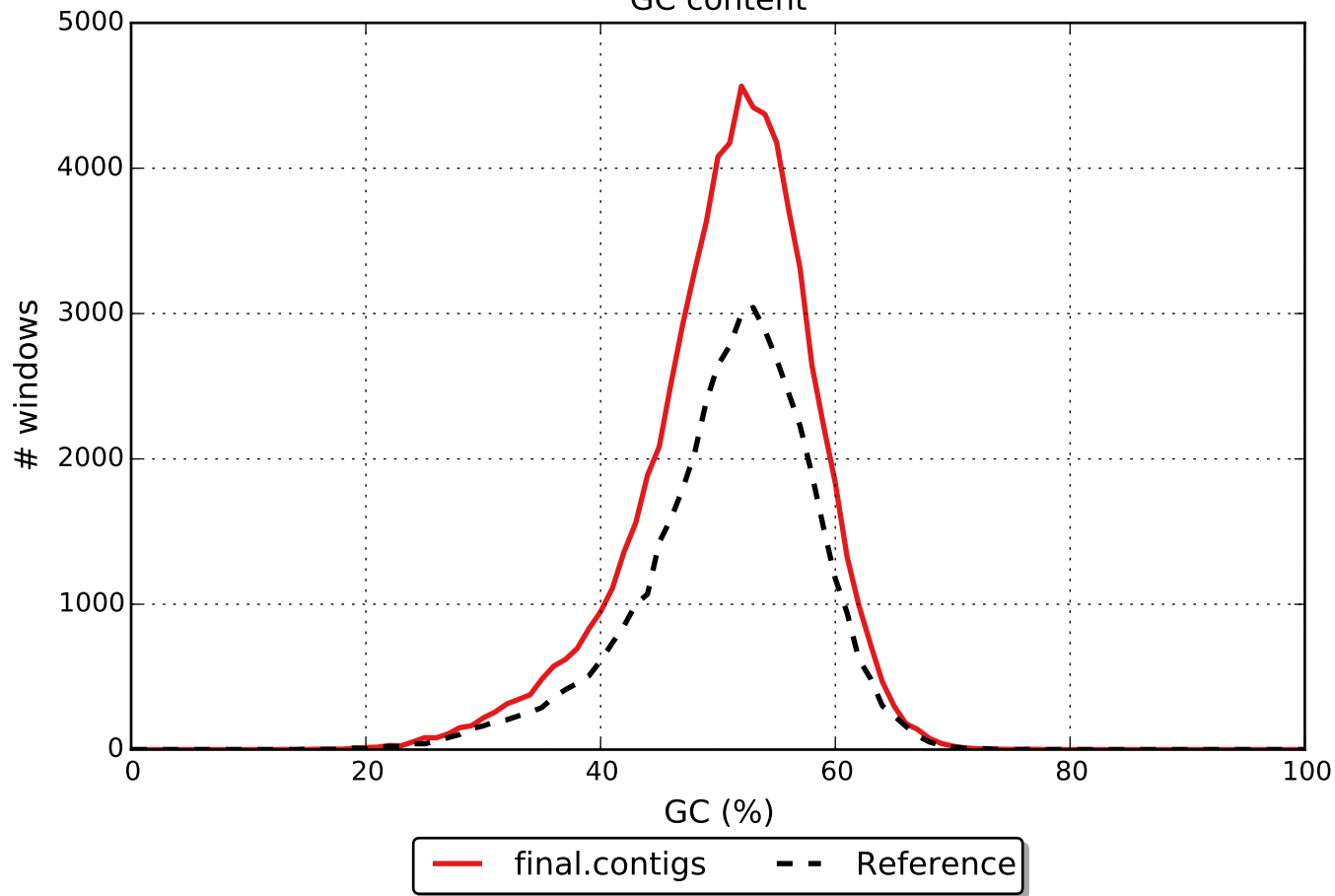
Misassemblies

final.contigs

Cumulative length (aligned contigs)

NGAx