Report

	final.contigs
# contigs (>= 0 bp)	12122
# contigs (>= 1000 bp)	1560
# contigs (>= 5000 bp)	14
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	6709677
Total length (>= 1000 bp)	2972934
Total length (>= 5000 bp)	88998
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	12122
Largest contig	9644
Total length	6709677
Reference length	4641652
GC (%)	50.73
Reference GC (%)	50.79
N50	802
NG50	1390
N75	322
NG75	724
L50	1988
LG50	1005
L75	5909
LG75	2153
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	5325 + 32 part
Unaligned length	1748678
Genome fraction (%)	95.618
Duplication ratio	1.118
# N's per 100 kbp	0.00
# mismatches per 100 kbp	53.62
# indels per 100 kbp	0.00
Largest alignment	9644
NA50	802
NGA50	1390
NGA75	724
LA50	1988
LGA50	1005
LGA75	2153

Misassemblies report

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	2380
# indels	0
# short indels	0
# long indels	0
Indels length	0

Unaligned report

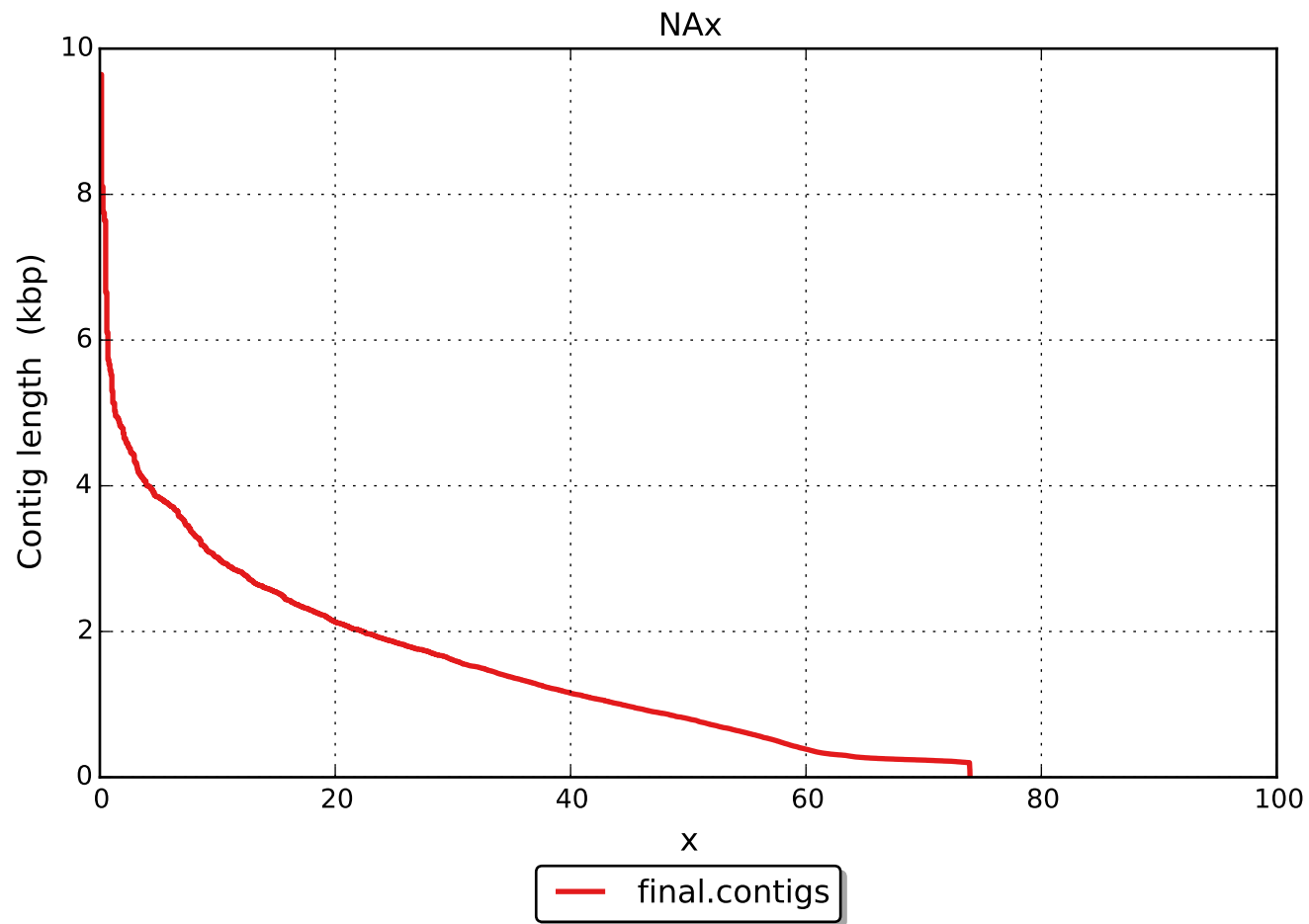|	final.contigs
# fully unaligned contigs	5325
Fully unaligned length	1741811
# partially unaligned contigs	32
# with misassembly	0
# both parts are significant	32
Partially unaligned length	6867
# N's	0

Nx

NGx
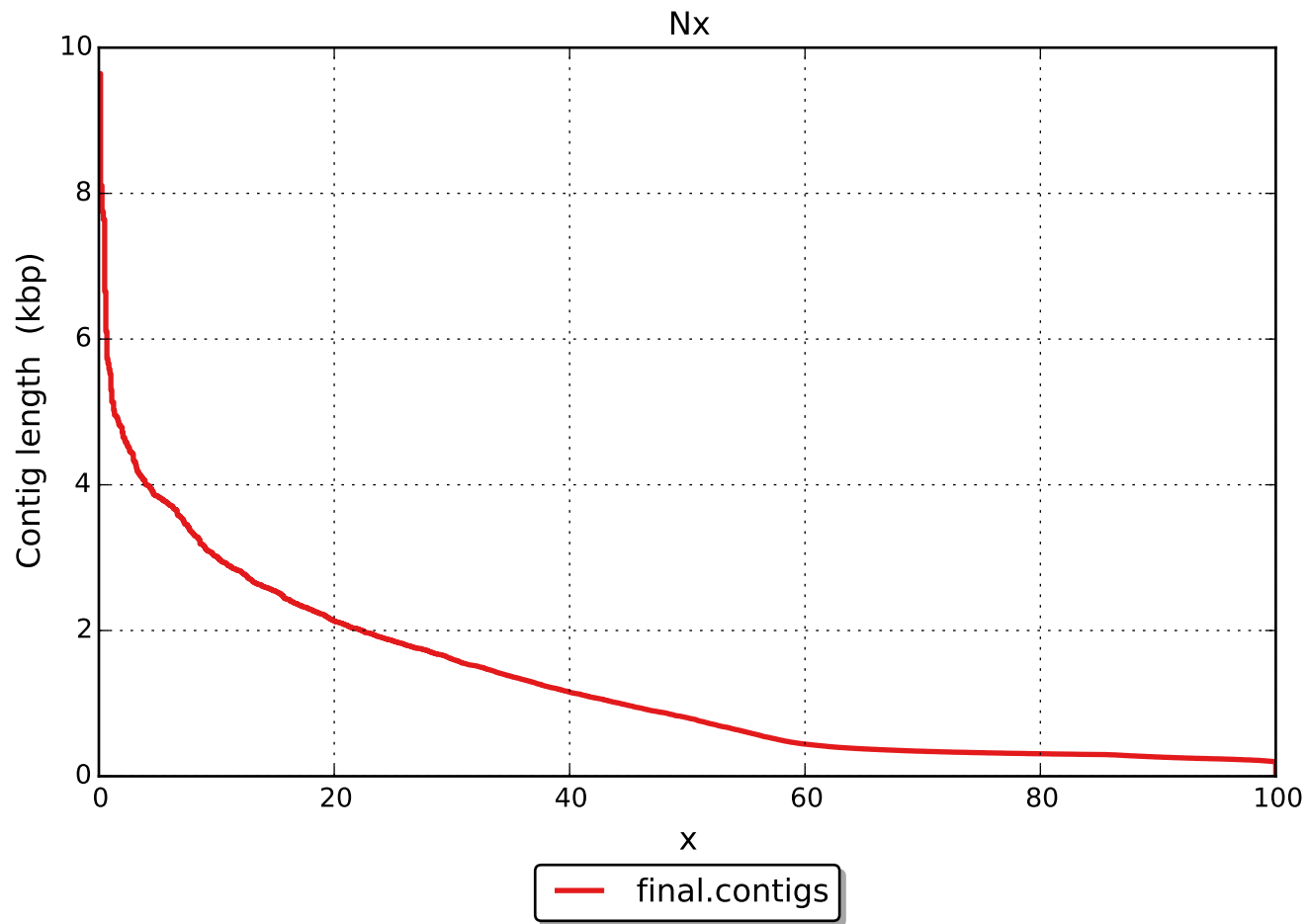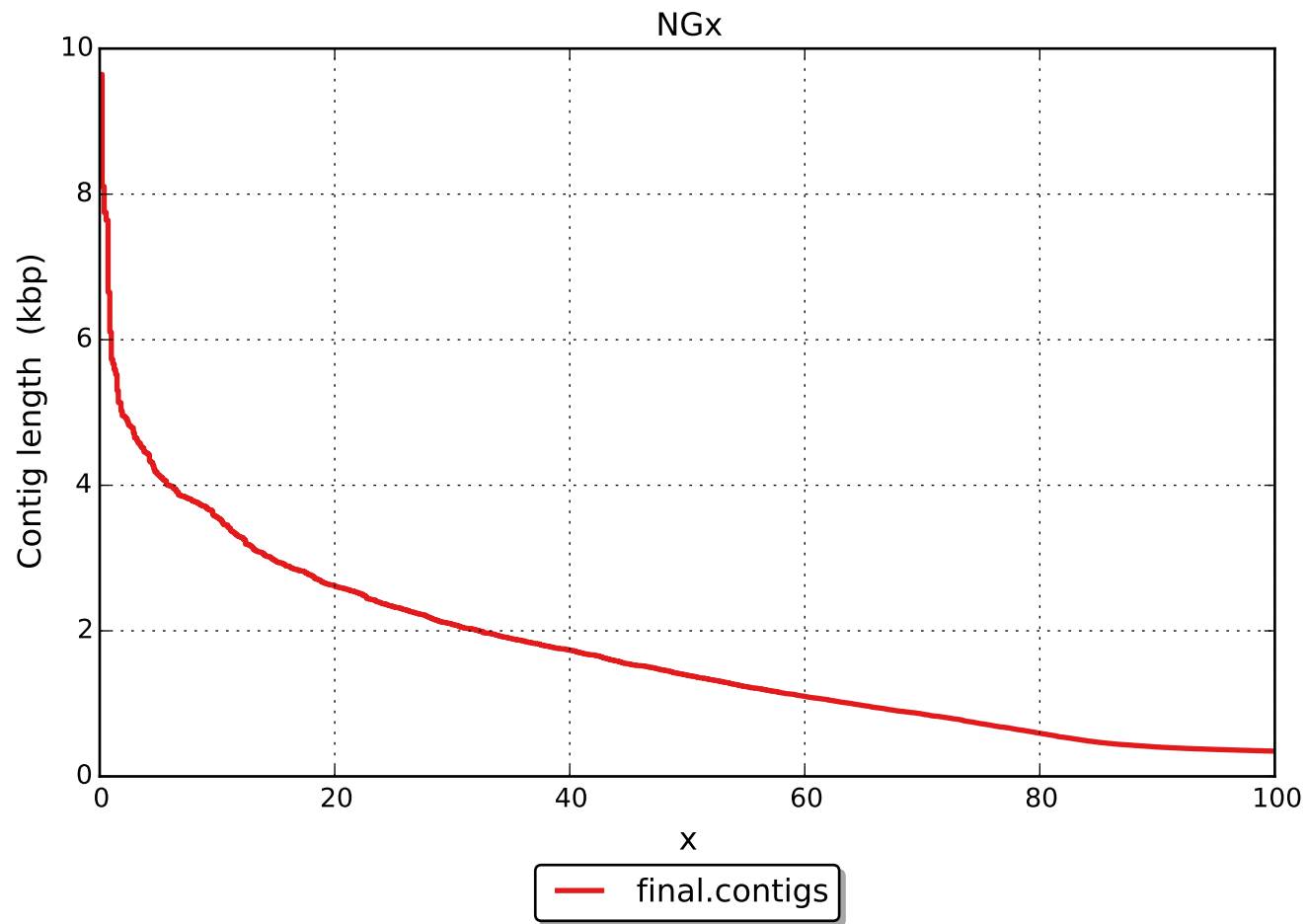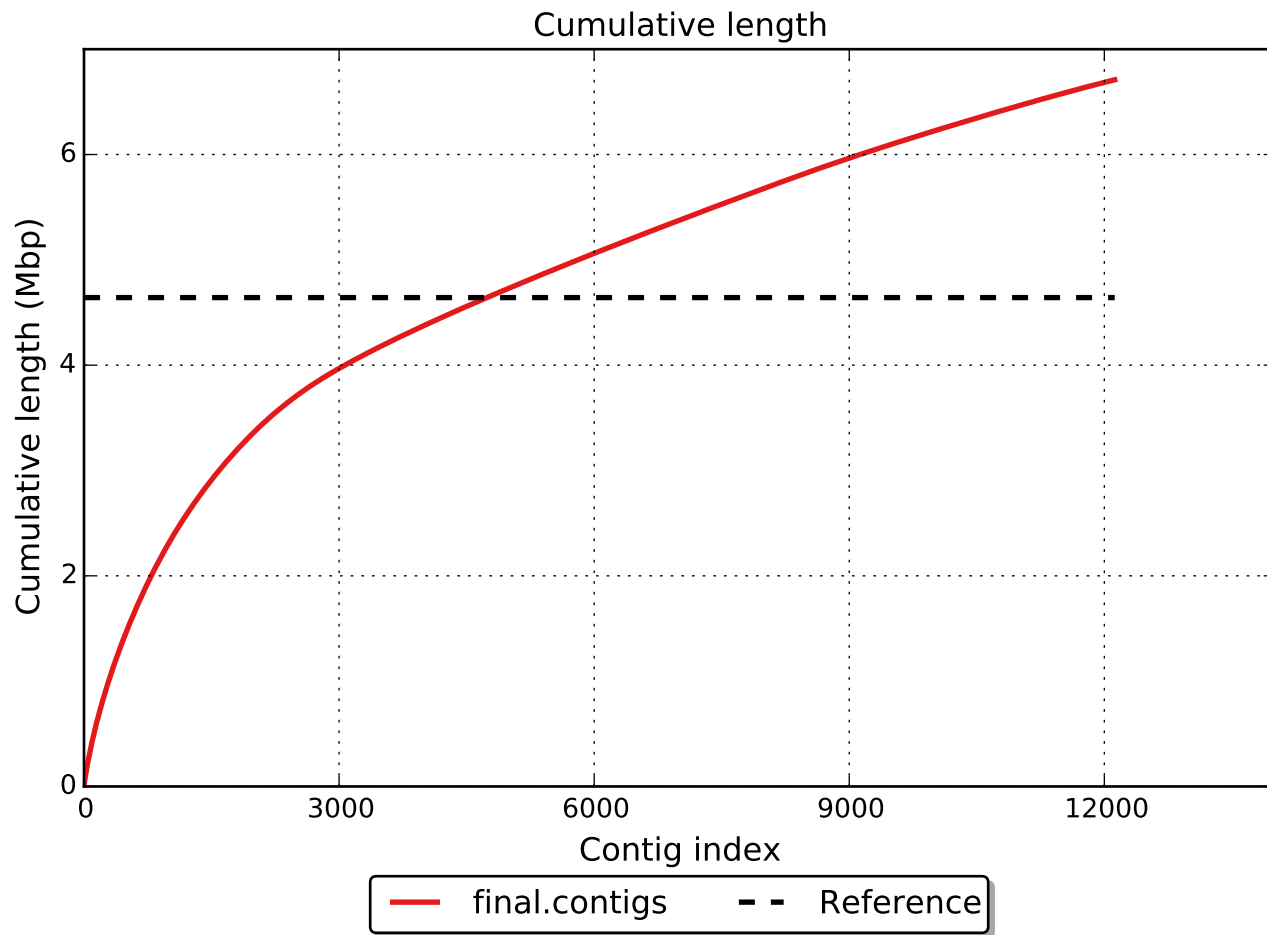
Cumulative length

GC content
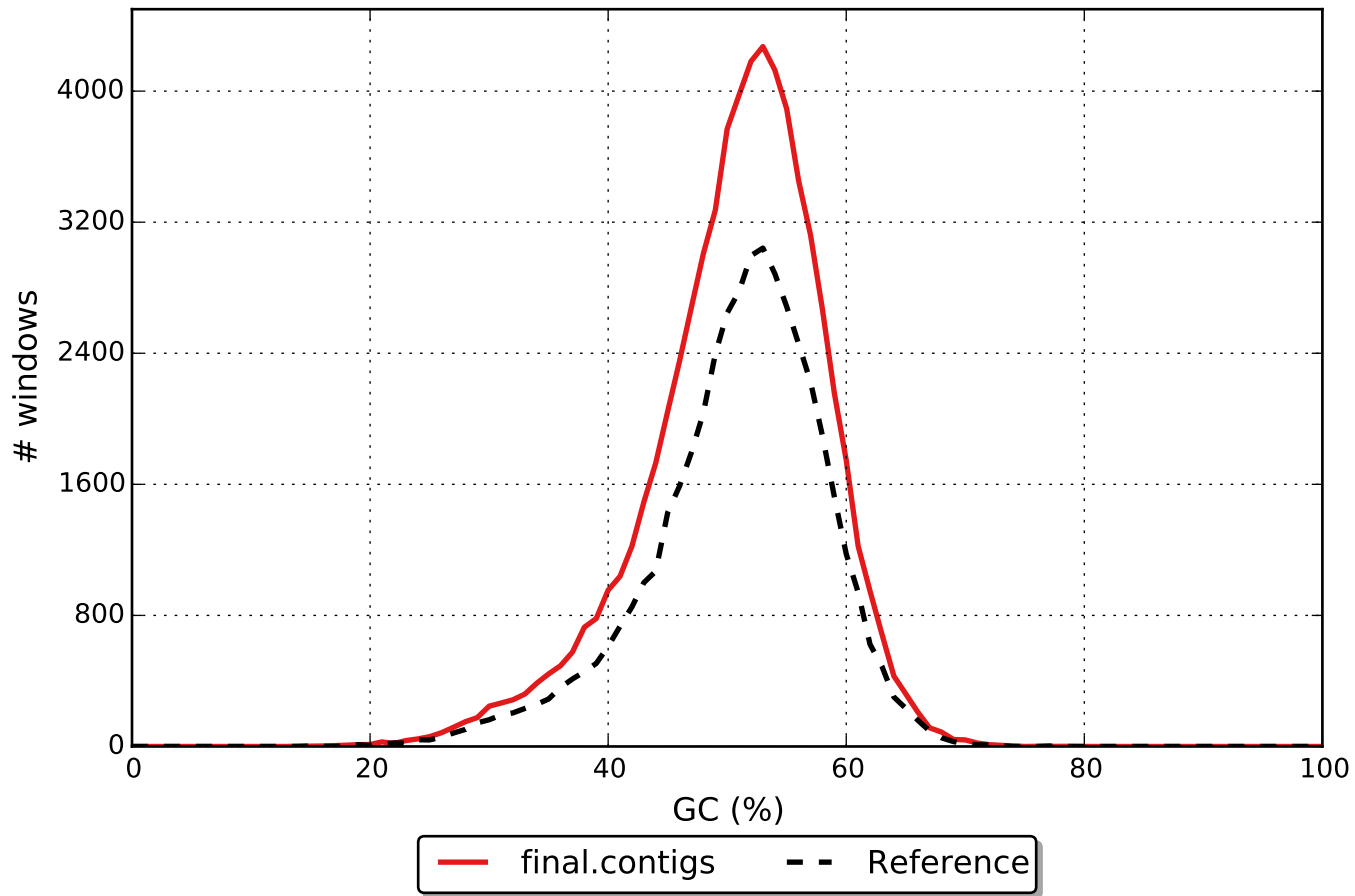
Misassemblies

final.contigs

Cumulative length (aligned contigs)

NAx

NGAx