

Report

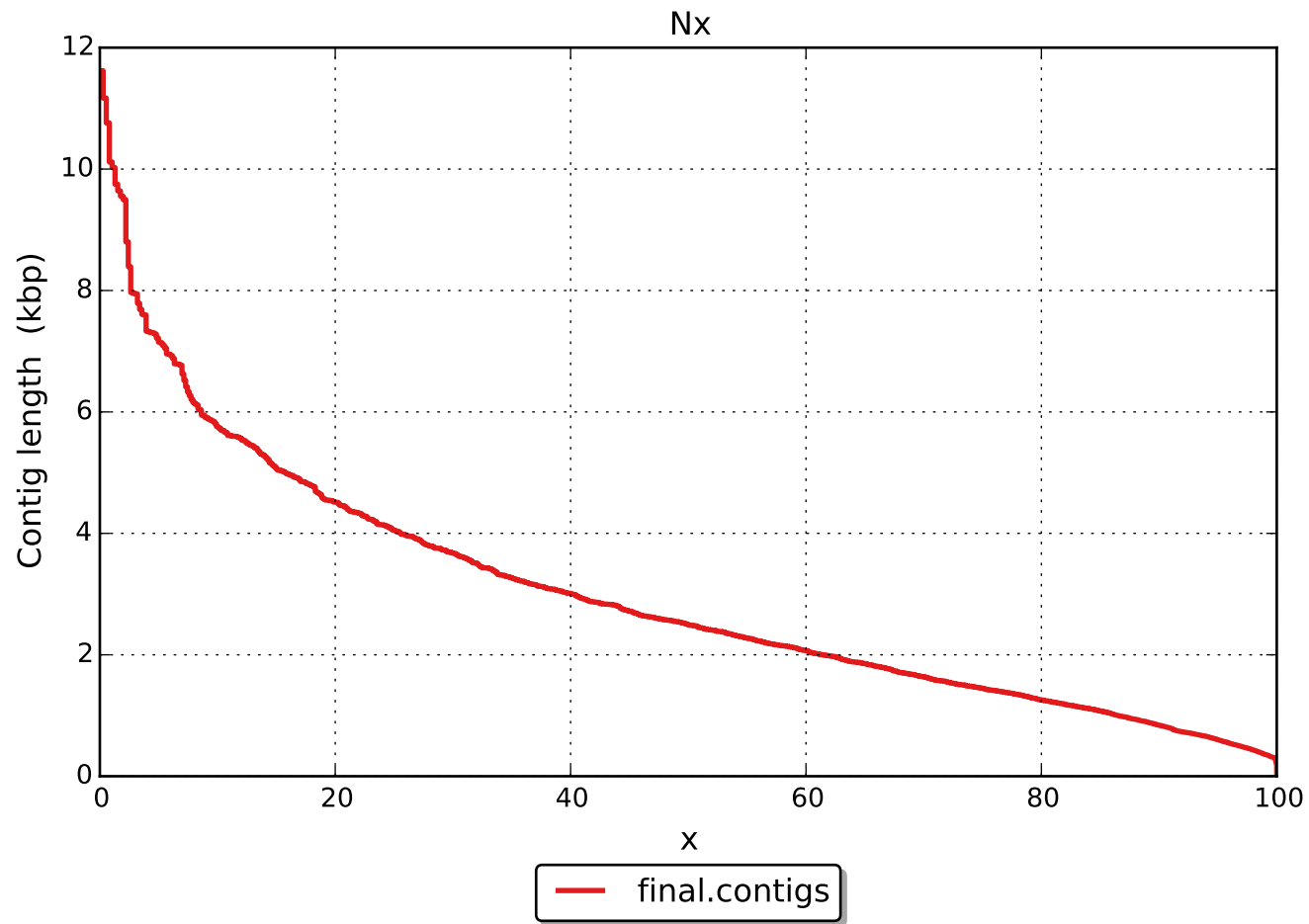
	final.contigs
# contigs (≥ 0 bp)	2394
# contigs (≥ 1000 bp)	1462
# contigs (≥ 5000 bp)	101
# contigs (≥ 10000 bp)	5
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	4169554
Total length (≥ 1000 bp)	3608376
Total length (≥ 5000 bp)	655840
Total length (≥ 10000 bp)	53689
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	2394
Largest contig	11619
Total length	4169554
Reference length	4641652
GC (%)	50.77
Reference GC (%)	50.79
N50	2494
NG50	2243
N75	1449
NG75	1132
L50	522
LG50	622
L75	1068
LG75	1344
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	11265
# local misassemblies	2
# unaligned contigs	0 + 5 part
Unaligned length	801
Genome fraction (%)	89.693
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.56
# indels per 100 kbp	0.05
Largest alignment	11619
NA50	2486
NGA50	2235
NA75	1444
NGA75	1127
LA50	523
LGA50	623
LA75	1071
LGA75	1347

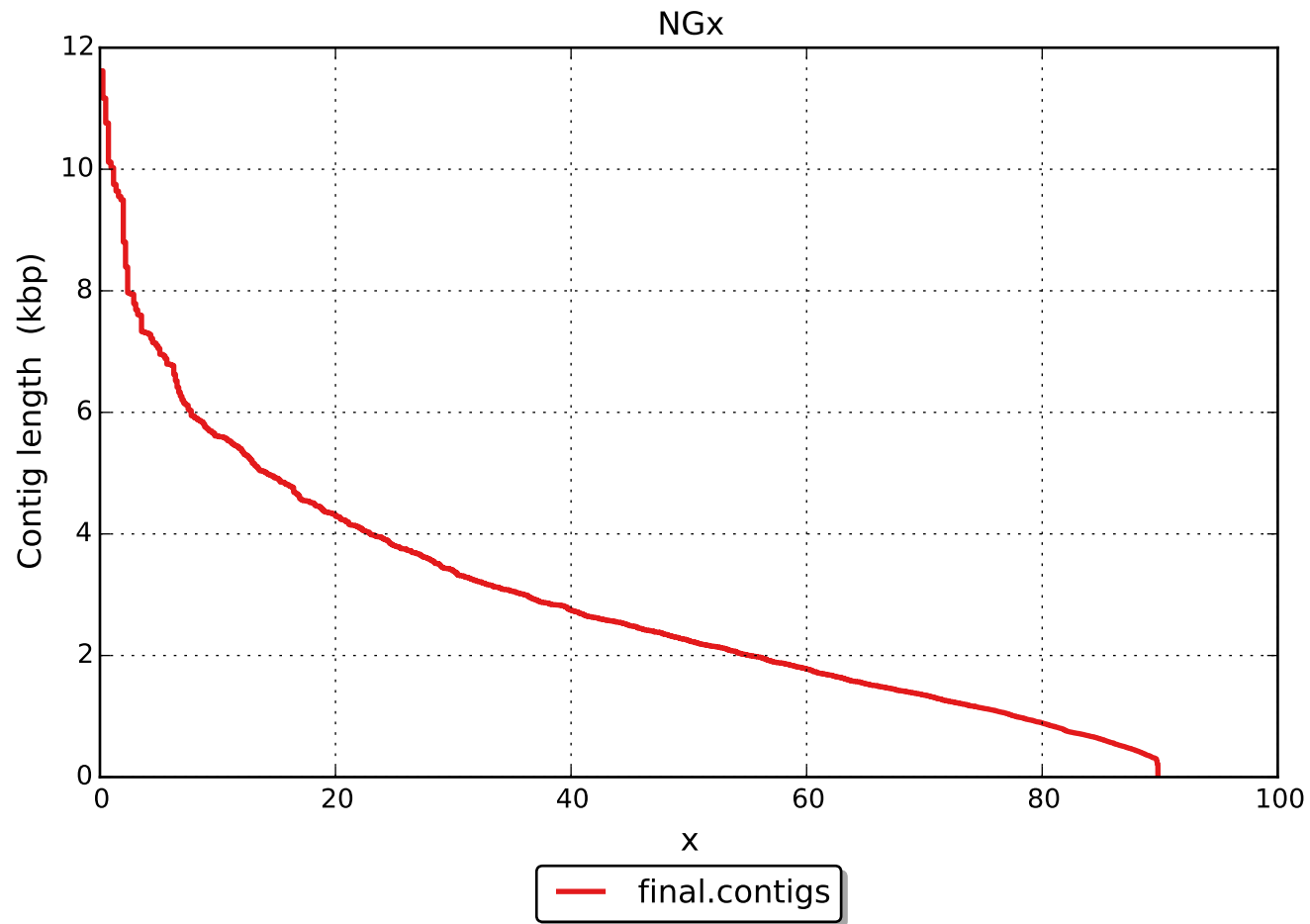
Misassemblies report

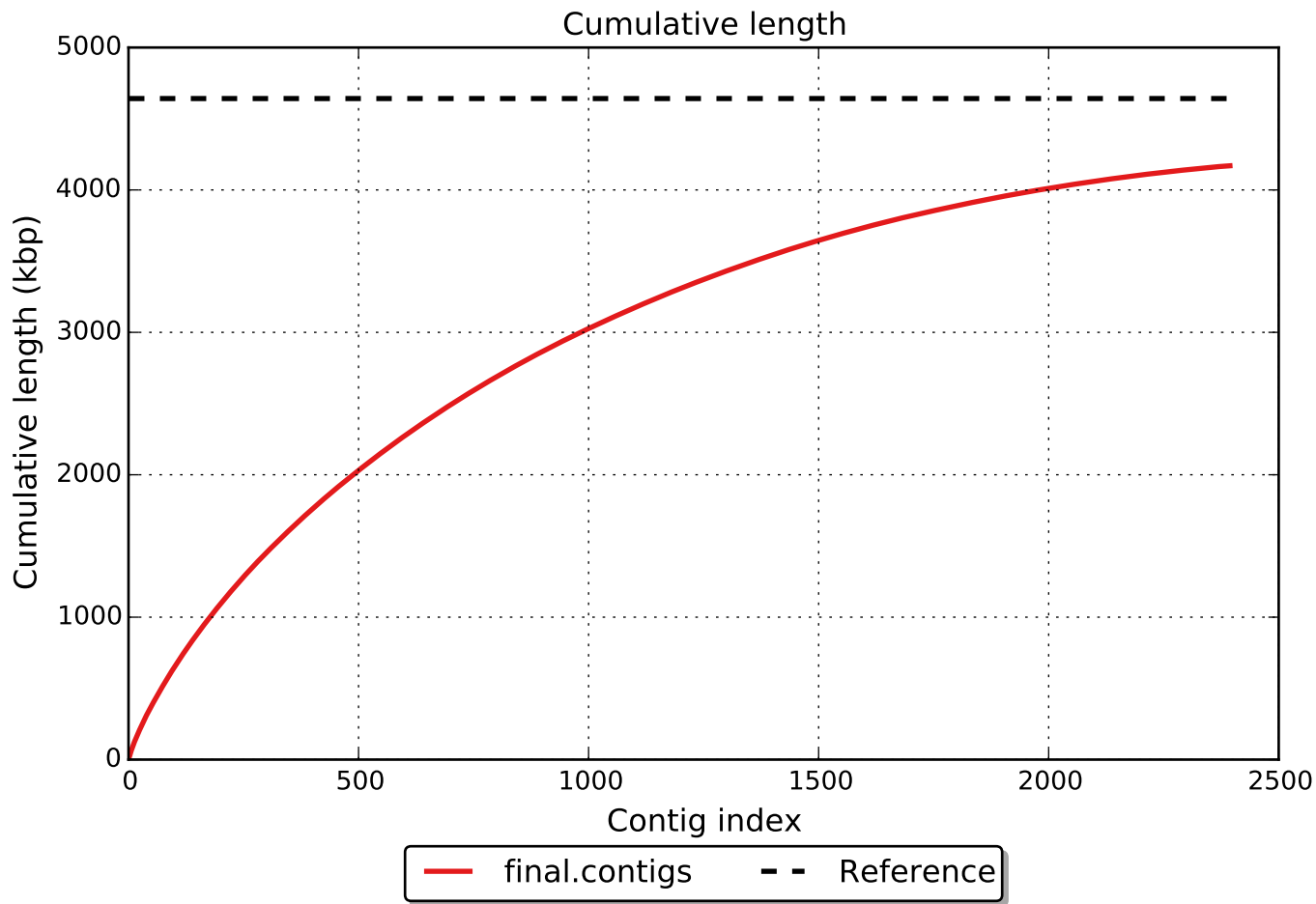
	final.contigs
# misassemblies	3
# relocations	3
# translocations	0
# inversions	0
# misassembled contigs	3
Misassembled contigs length	11265
# local misassemblies	2
# mismatches	65
# indels	2
# short indels	2
# long indels	0
Indels length	2

Unaligned report

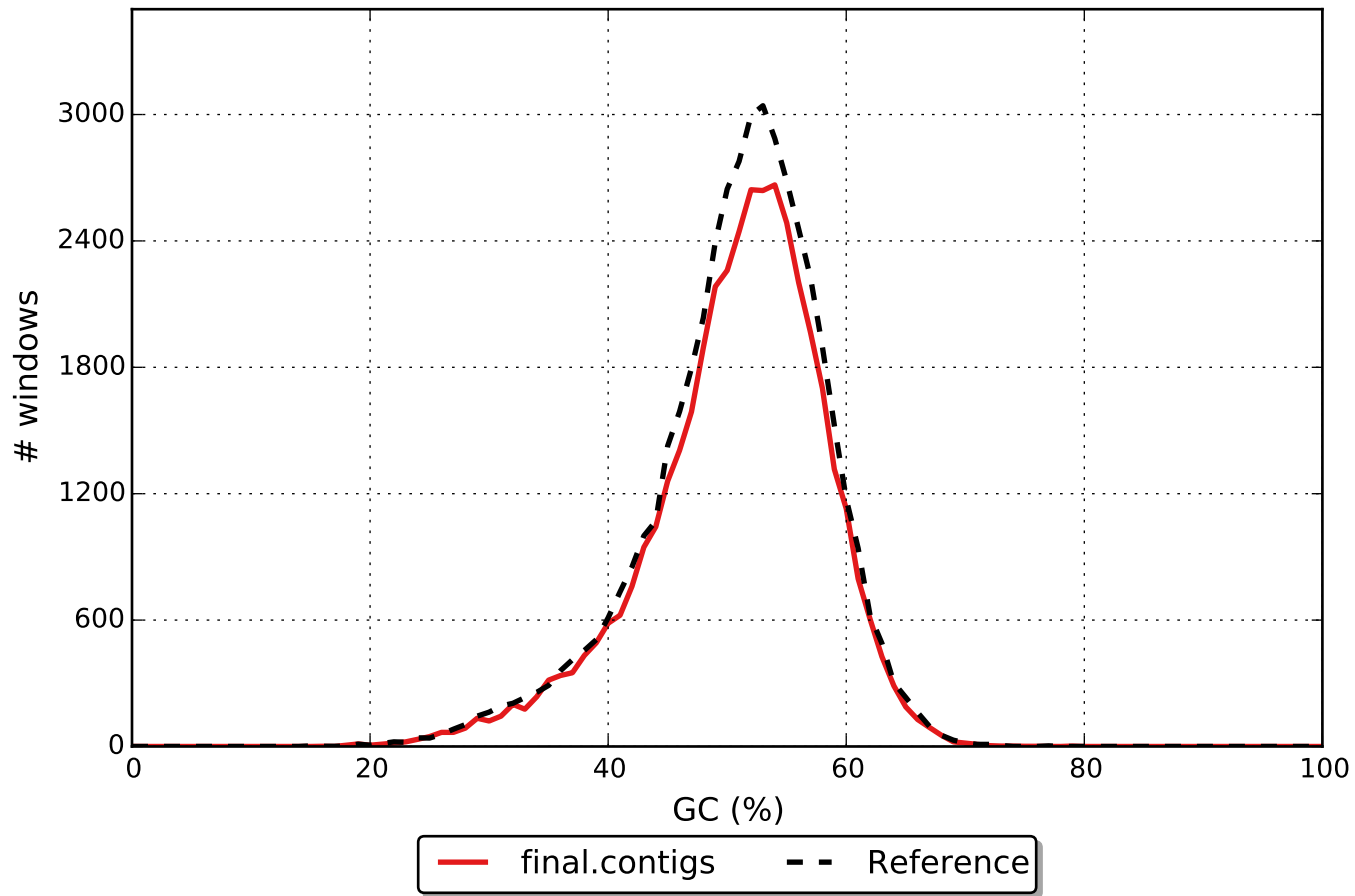
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	5
# with misassembly	0
# both parts are significant	5
Partially unaligned length	801
# N's	0



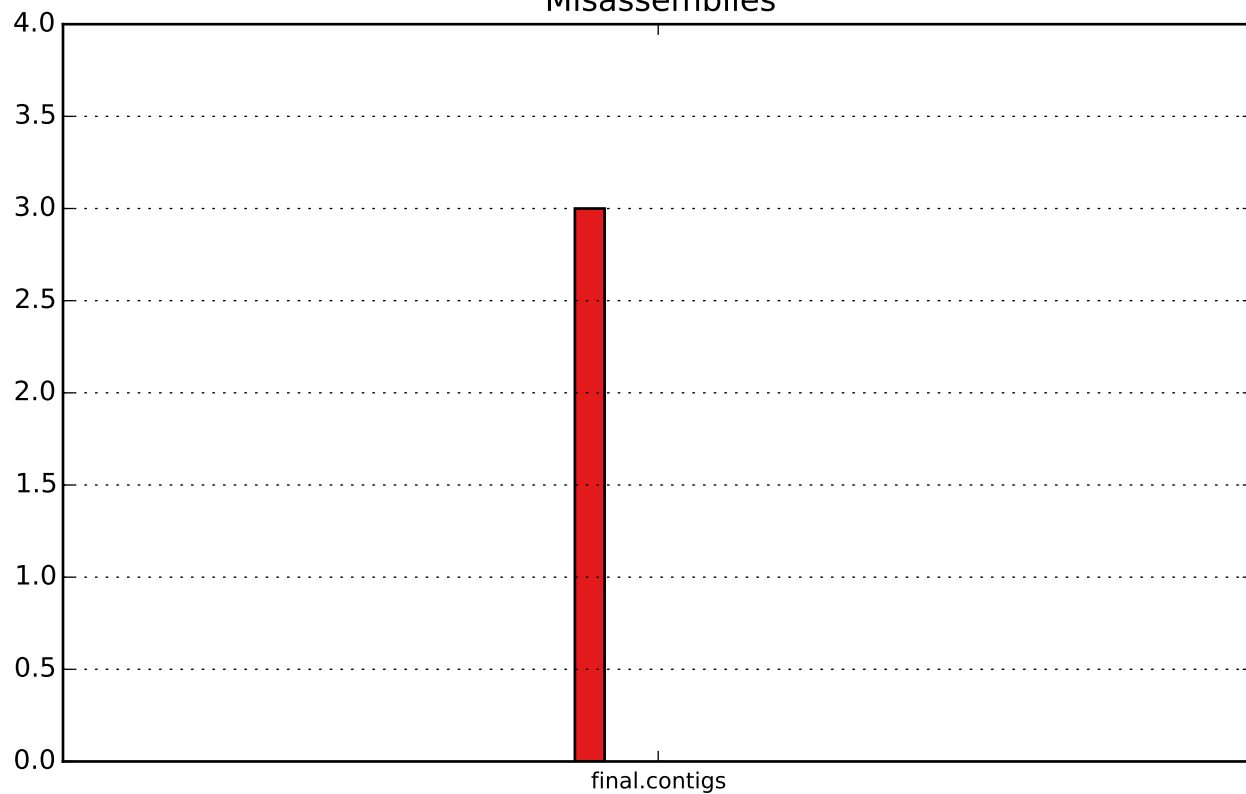




GC content



Misassemblies



Cumulative length (aligned contigs)

