

Report

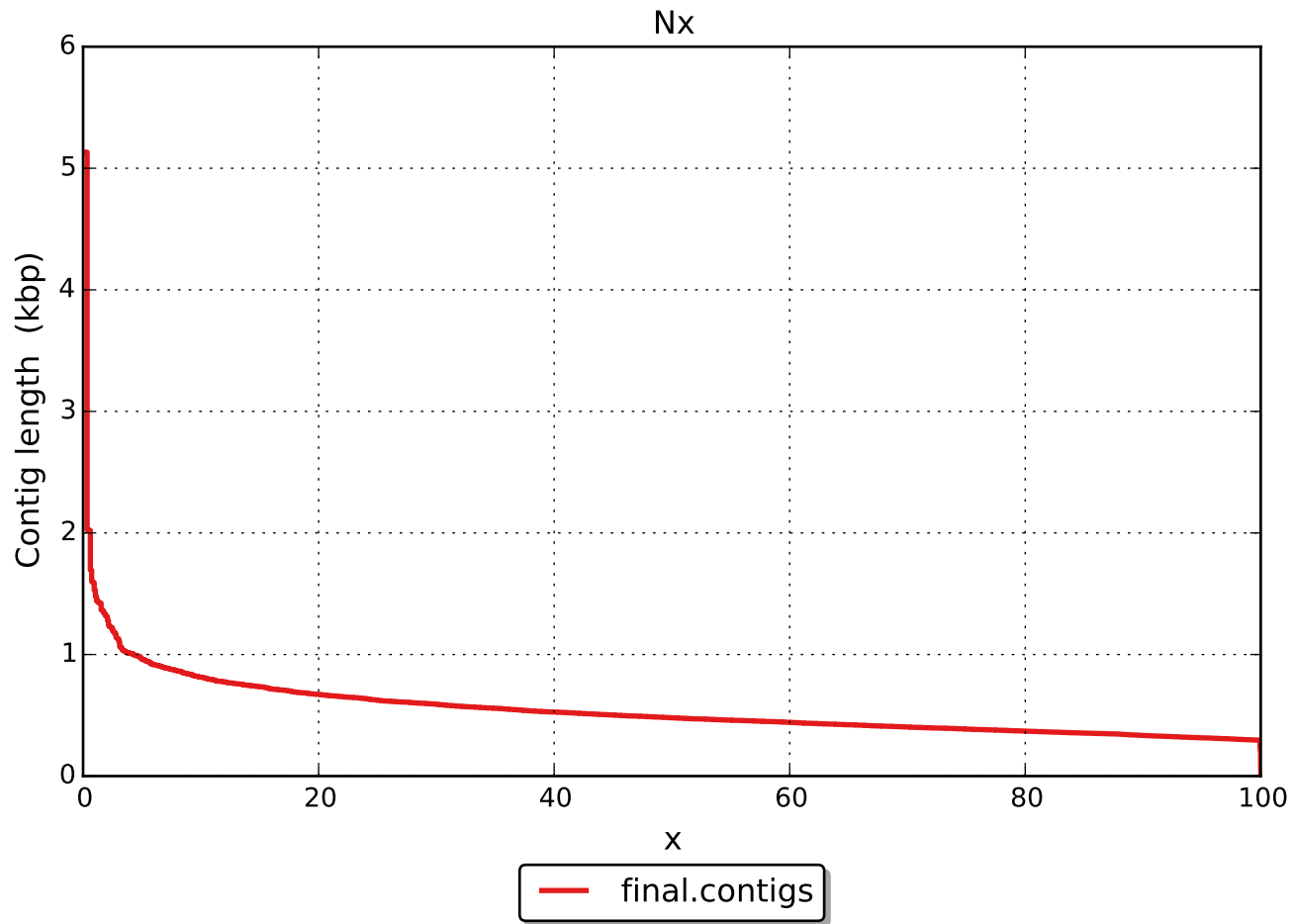
	final.contigs
# contigs (≥ 0 bp)	3109
# contigs (≥ 1000 bp)	48
# contigs (≥ 5000 bp)	1
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	1489995
Total length (≥ 1000 bp)	63684
Total length (≥ 5000 bp)	5132
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	3109
Largest contig	5132
Total length	1489995
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	480
N75	387
L50	1150
L75	2015
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	1694
# local misassemblies	0
# unaligned contigs	2216 + 14 part
Unaligned length	1070338
Genome fraction (%)	9.026
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	621.78
# indels per 100 kbp	0.48
Largest alignment	5132
NGA50	-

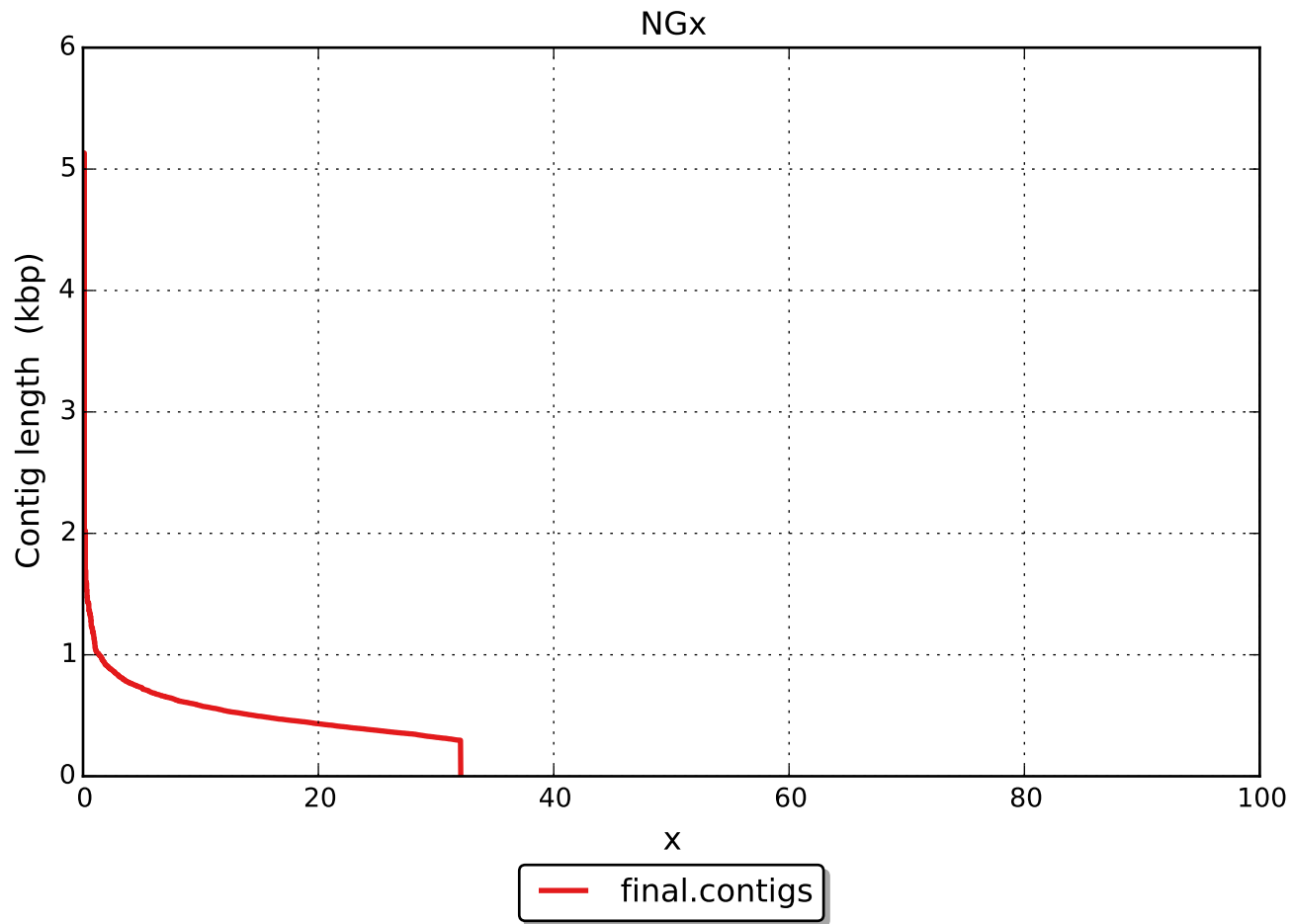
Misassemblies report

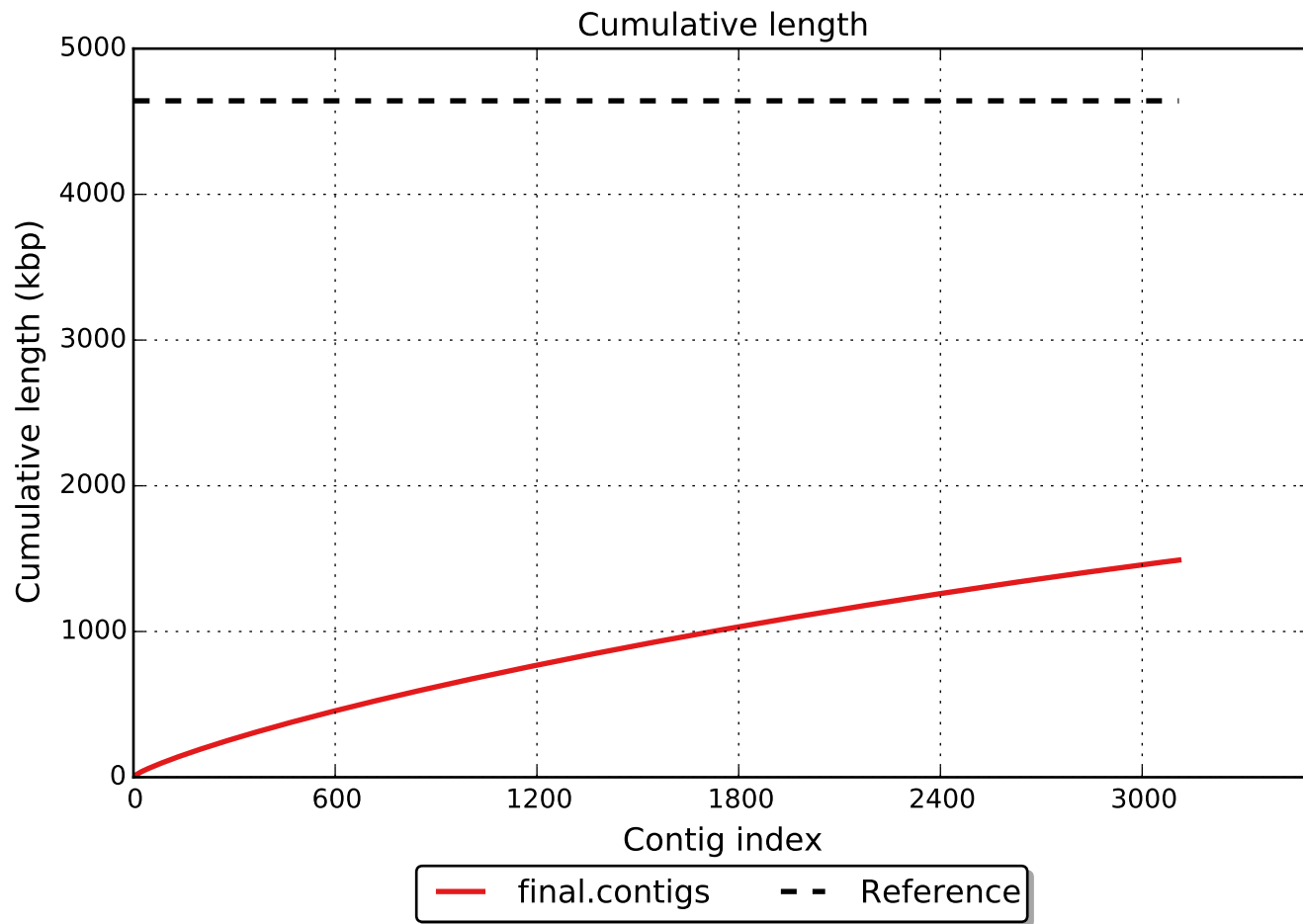
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# misassembled contigs	1
Misassembled contigs length	1694
# local misassemblies	0
# mismatches	2605
# indels	2
# short indels	2
# long indels	0
Indels length	2

Unaligned report

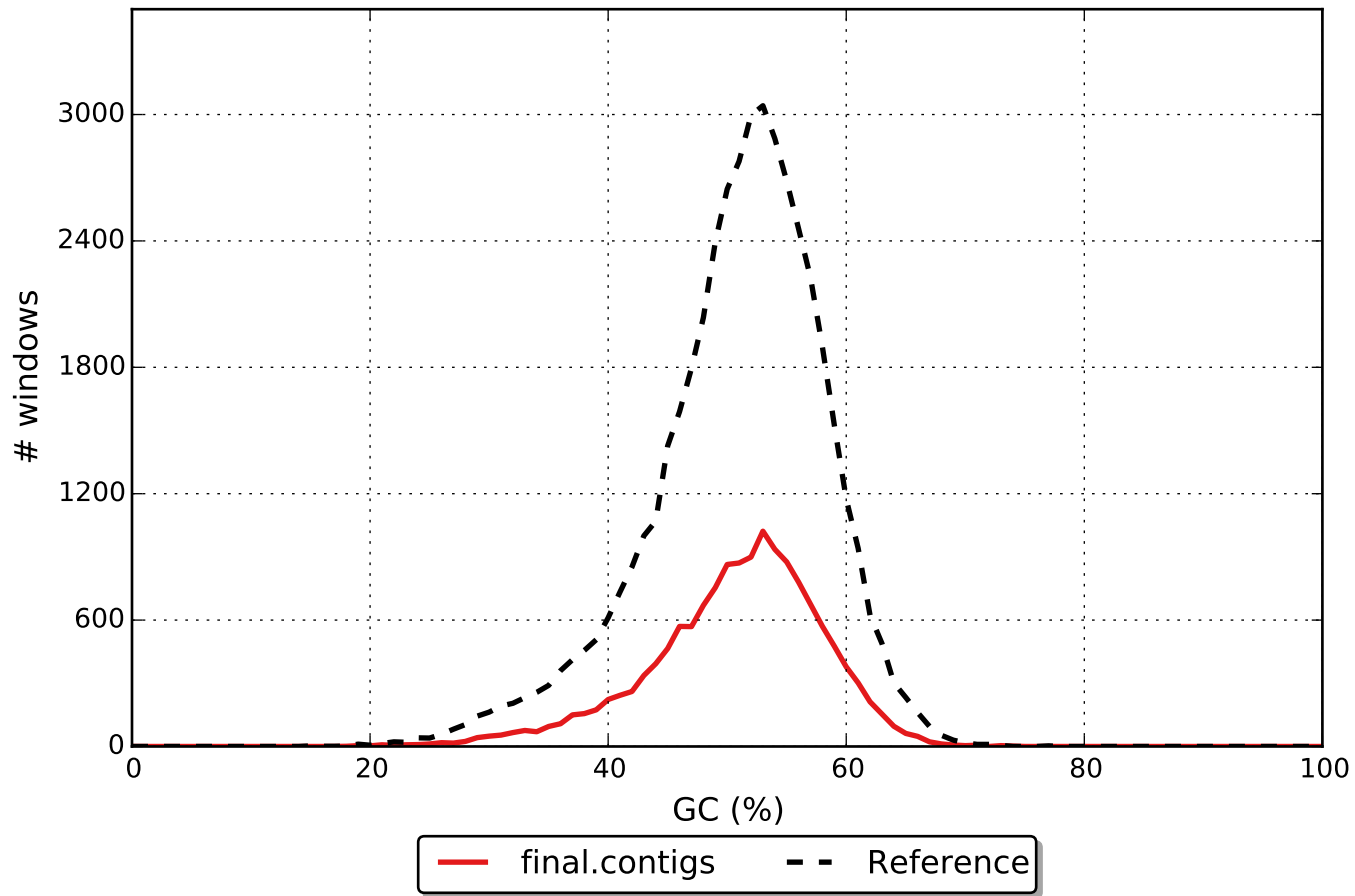
	final.contigs
# fully unaligned contigs	2216
Fully unaligned length	1066246
# partially unaligned contigs	14
# with misassembly	0
# both parts are significant	14
Partially unaligned length	4092
# N's	0

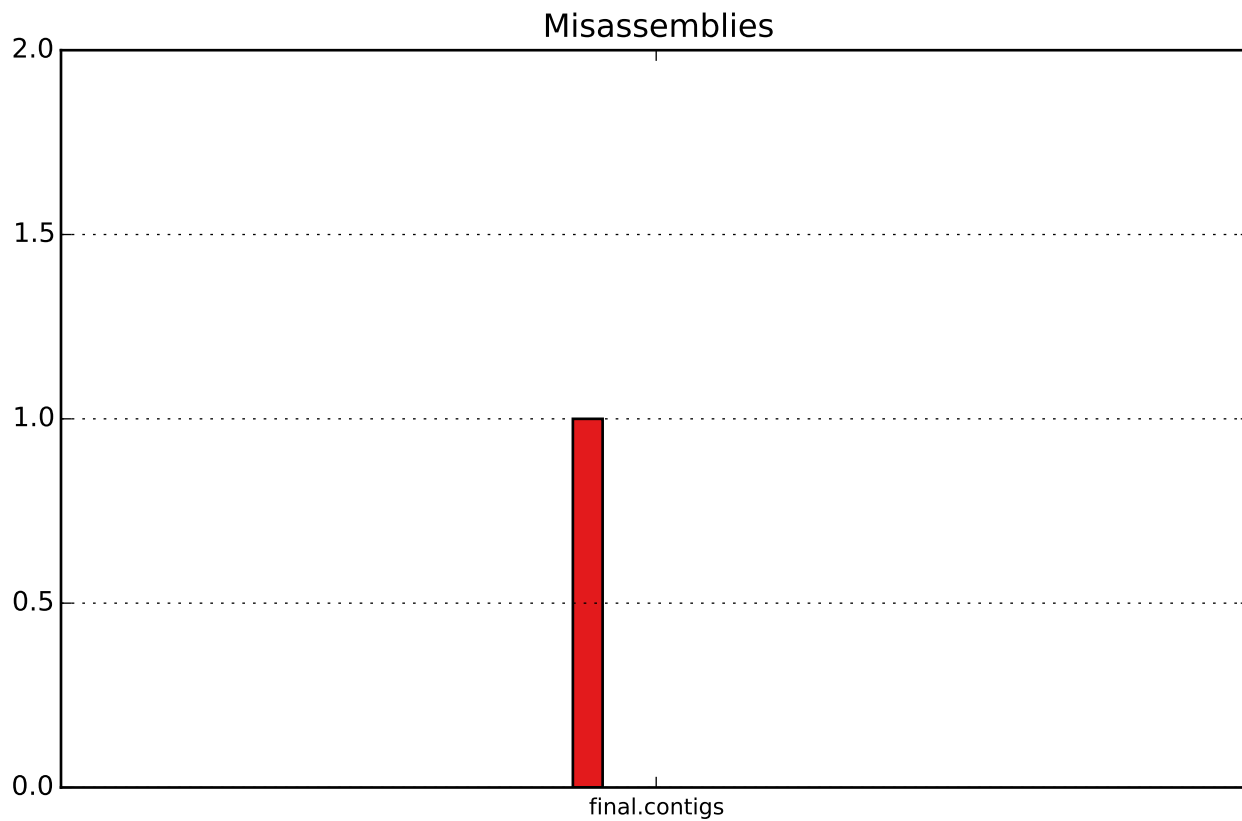






GC content





Cumulative length (aligned contigs)

