

Report

	final.contigs
# contigs (≥ 0 bp)	248
# contigs (≥ 1000 bp)	125
# contigs (≥ 5000 bp)	96
# contigs (≥ 10000 bp)	80
# contigs (≥ 25000 bp)	59
# contigs (≥ 50000 bp)	30
Total length (≥ 0 bp)	4600560
Total length (≥ 1000 bp)	4556256
Total length (≥ 5000 bp)	4490129
Total length (≥ 10000 bp)	4368049
Total length (≥ 25000 bp)	4030828
Total length (≥ 50000 bp)	2995237
# contigs	248
Largest contig	238358
Total length	4600560
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	75638
NG50	75638
N75	40948
NG75	40948
L50	19
LG50	19
L75	41
LG75	41
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# unaligned contigs	52 + 6 part
Unaligned length	19969
Genome fraction (%)	98.435
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	7.81
# indels per 100 kbp	0.09
Largest alignment	238358
NA50	75638
NGA50	75638
NA75	40948
NGA75	40948
LA50	19
LGA50	19
LA75	41
LGA75	41

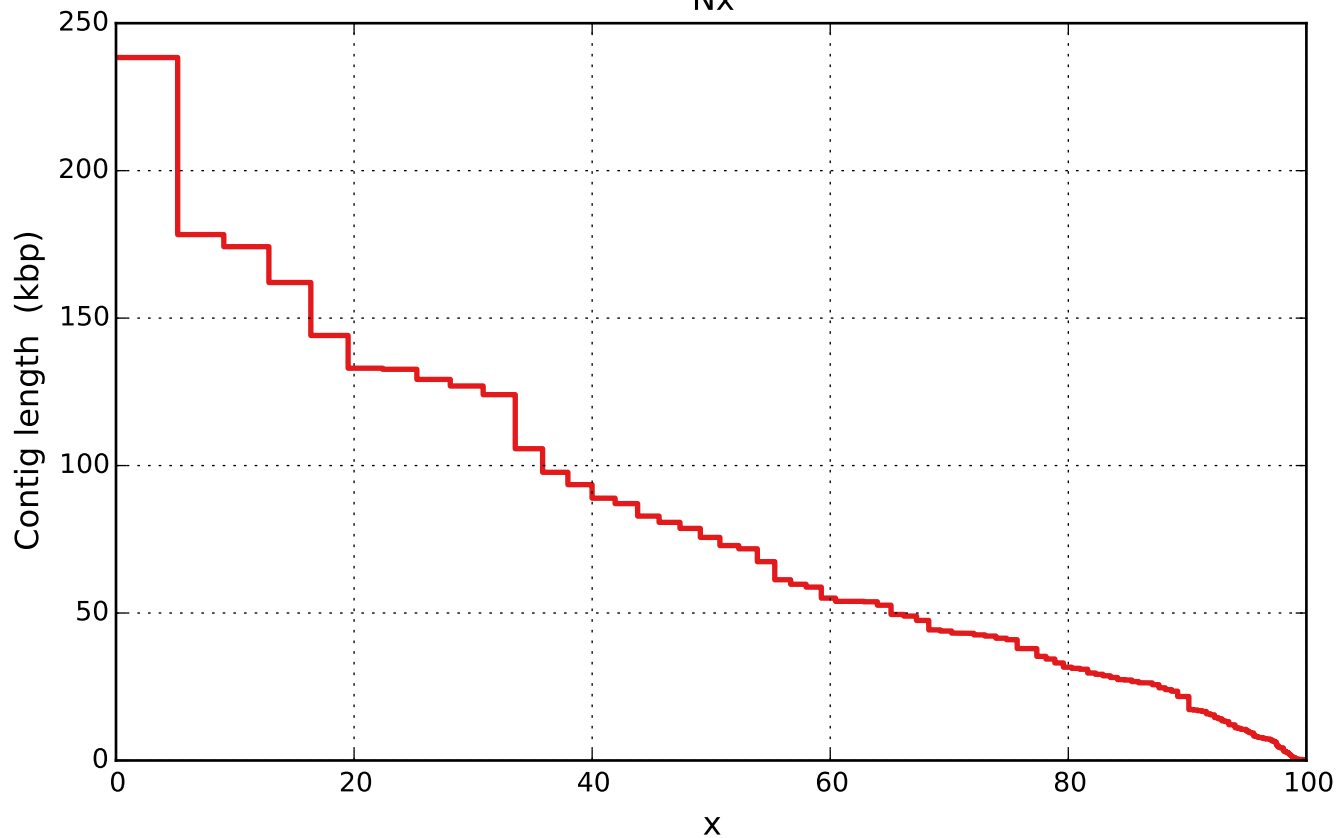
Misassemblies report

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# mismatches	357
# indels	4
# short indels	3
# long indels	1
Indels length	88

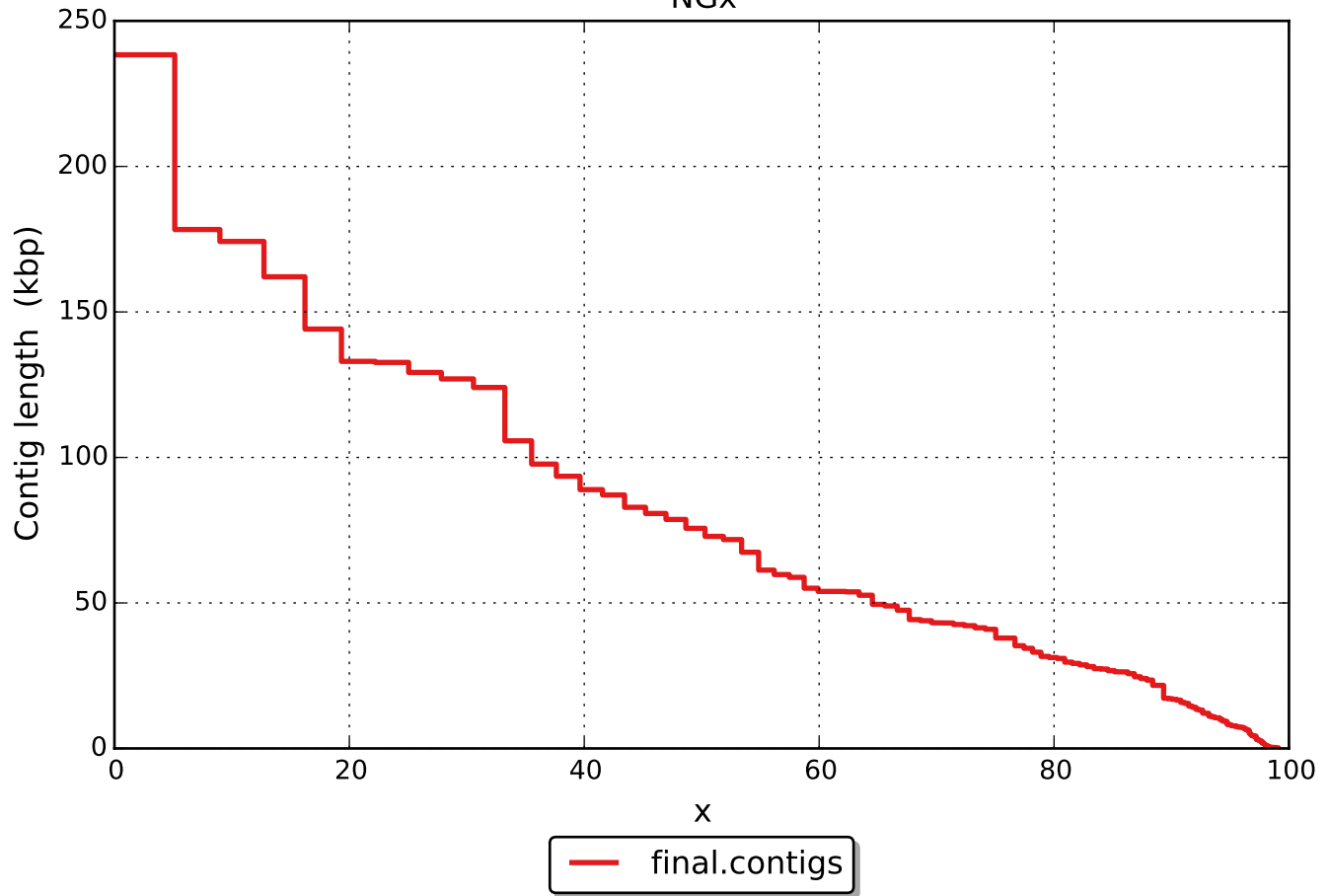
Unaligned report

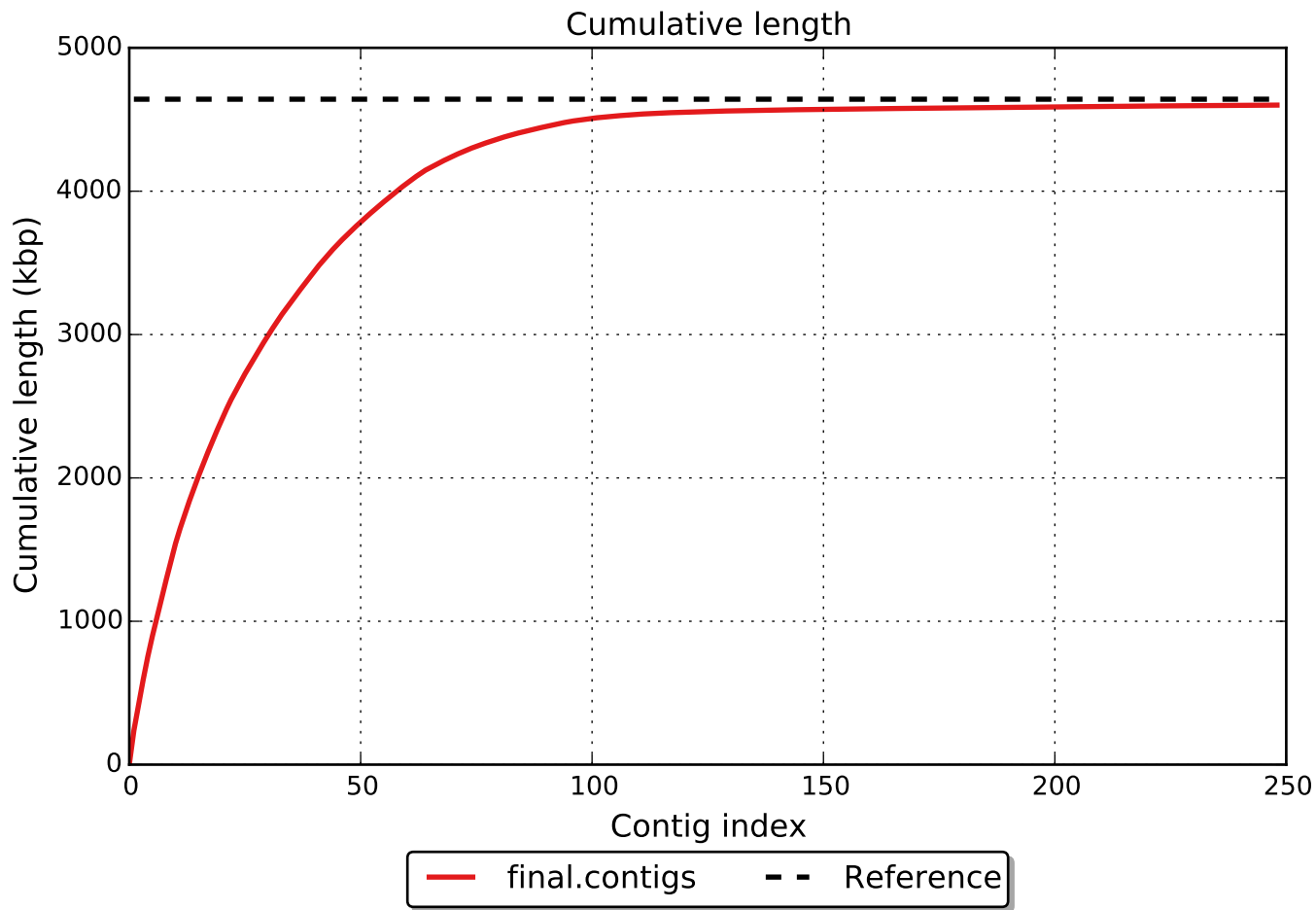
	final.contigs
# fully unaligned contigs	52
Fully unaligned length	17660
# partially unaligned contigs	6
# with misassembly	0
# both parts are significant	6
Partially unaligned length	2309
# N's	0

Nx

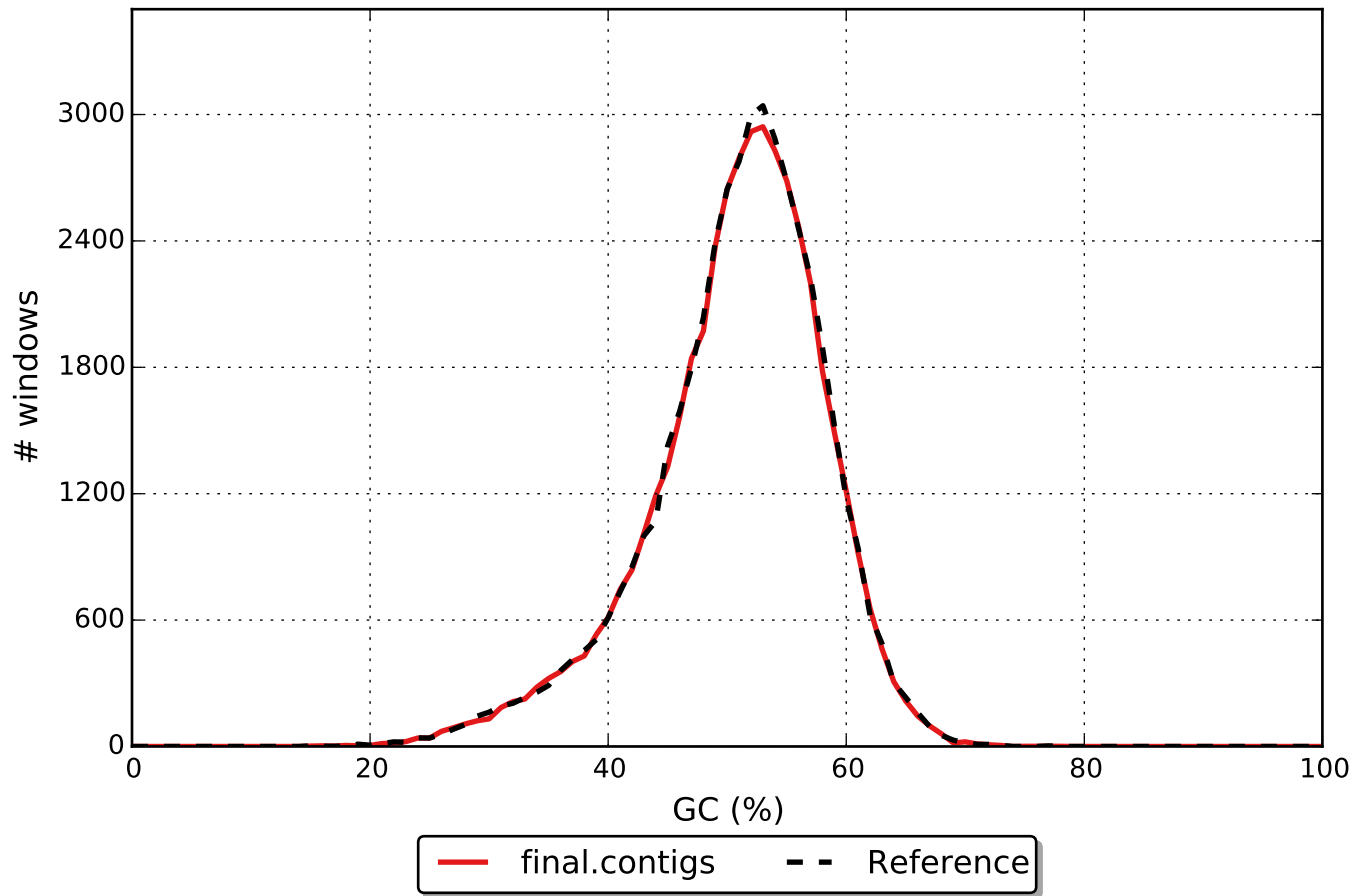


NGx





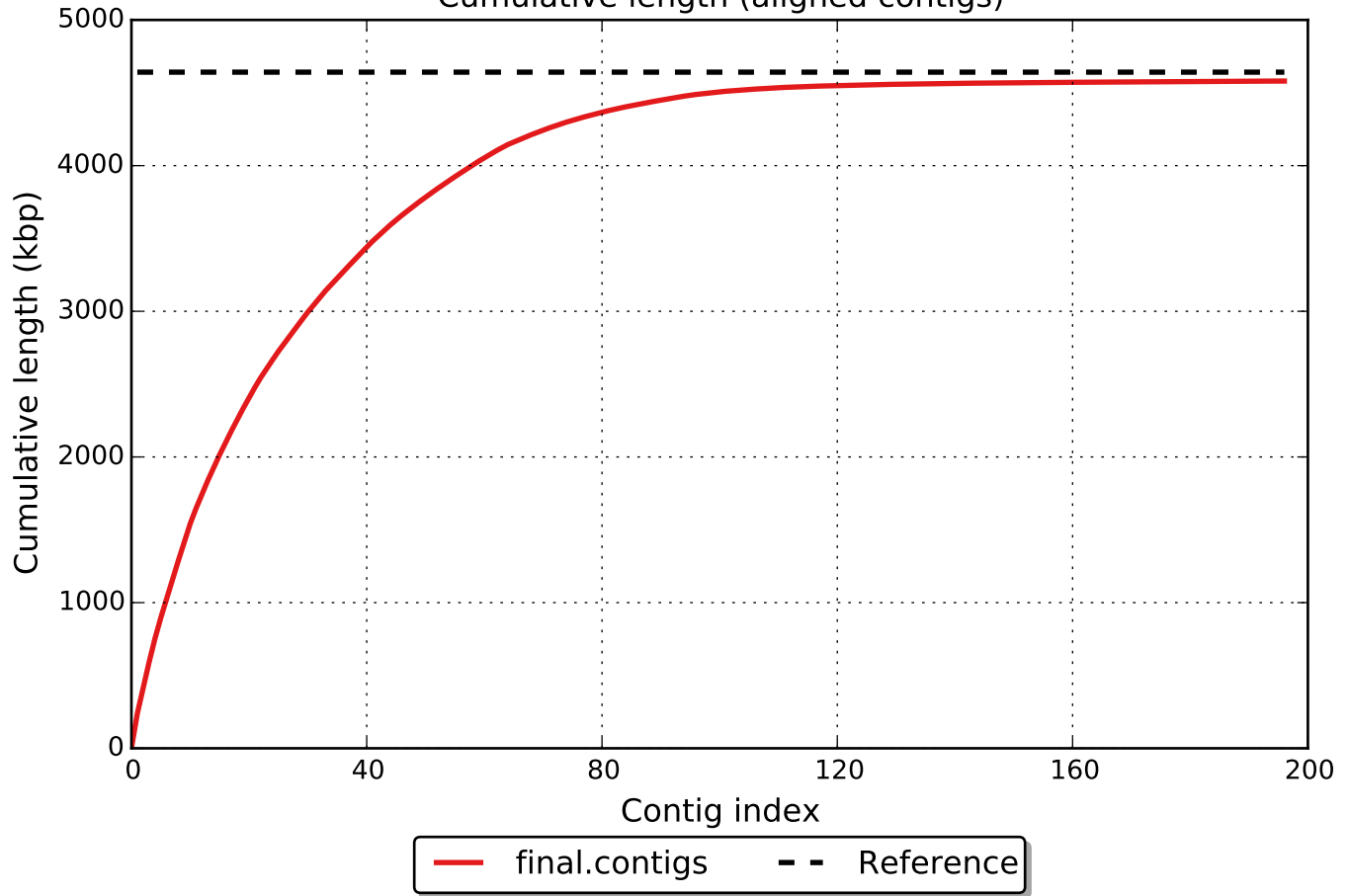
GC content



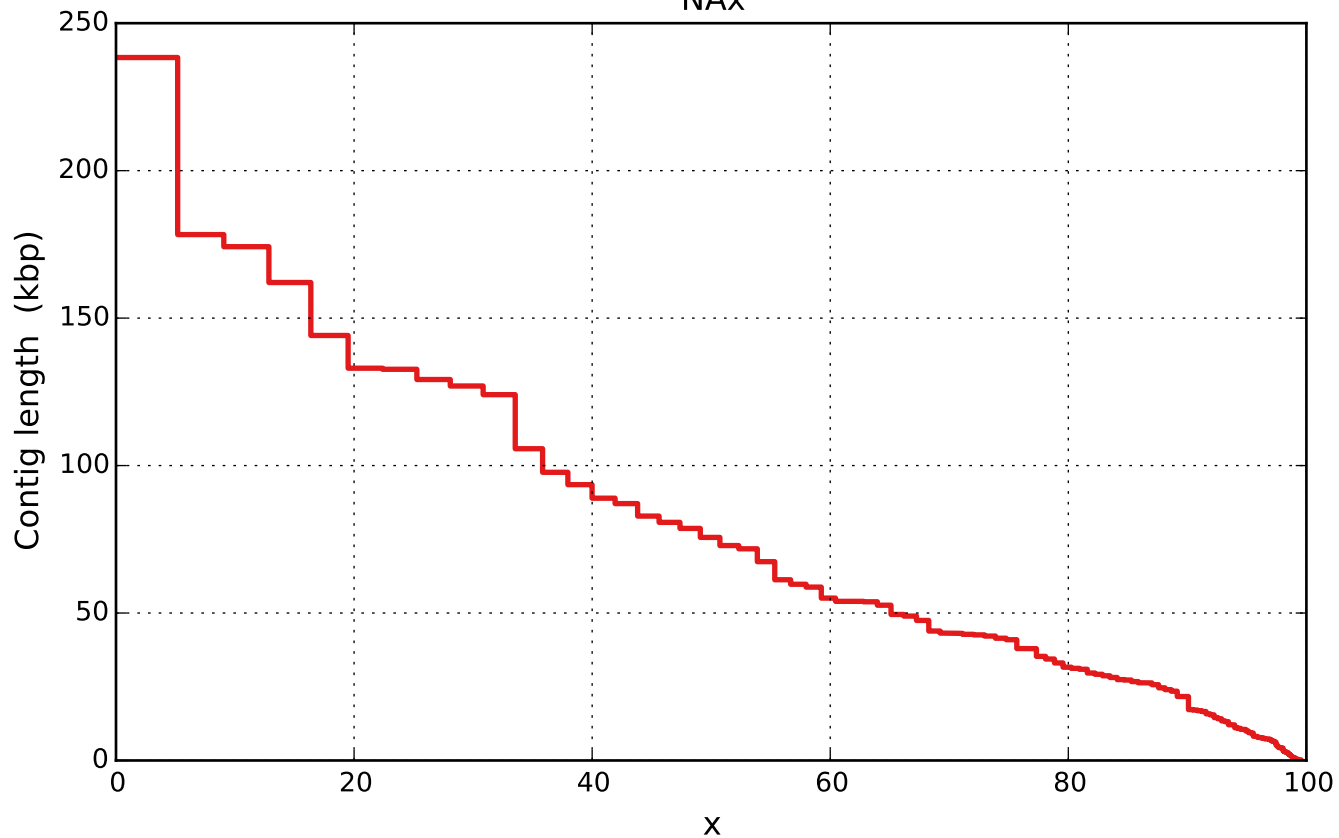
Misassemblies



Cumulative length (aligned contigs)



NAx



— final.contigs

NGAx

