

Report

	final.contigs
# contigs (>= 1000 bp)	1561
# contigs (>= 5000 bp)	55
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	3488041
Total length (>= 5000 bp)	332705
Total length (>= 10000 bp)	12848
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2695
Largest contig	12848
Total length	4261274
Reference length	4641652
GC (%)	50.76
Reference GC (%)	50.78
N50	2135
NG50	1939
N75	1219
NG75	1005
L50	639
LG50	732
L75	1296
LG75	1555
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	3619
# local misassemblies	2
# unaligned contigs	0 + 6 part
Unaligned length	783
Genome fraction (%)	86.338
Duplication ratio	1.063
# N's per 100 kbp	0.00
# mismatches per 100 kbp	600.02
# indels per 100 kbp	0.20
Largest alignment	12848
NA50	2134
NGA50	1939
NA75	1219
NGA75	1005
LA50	639
LGA50	732
LA75	1296
LGA75	1555

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

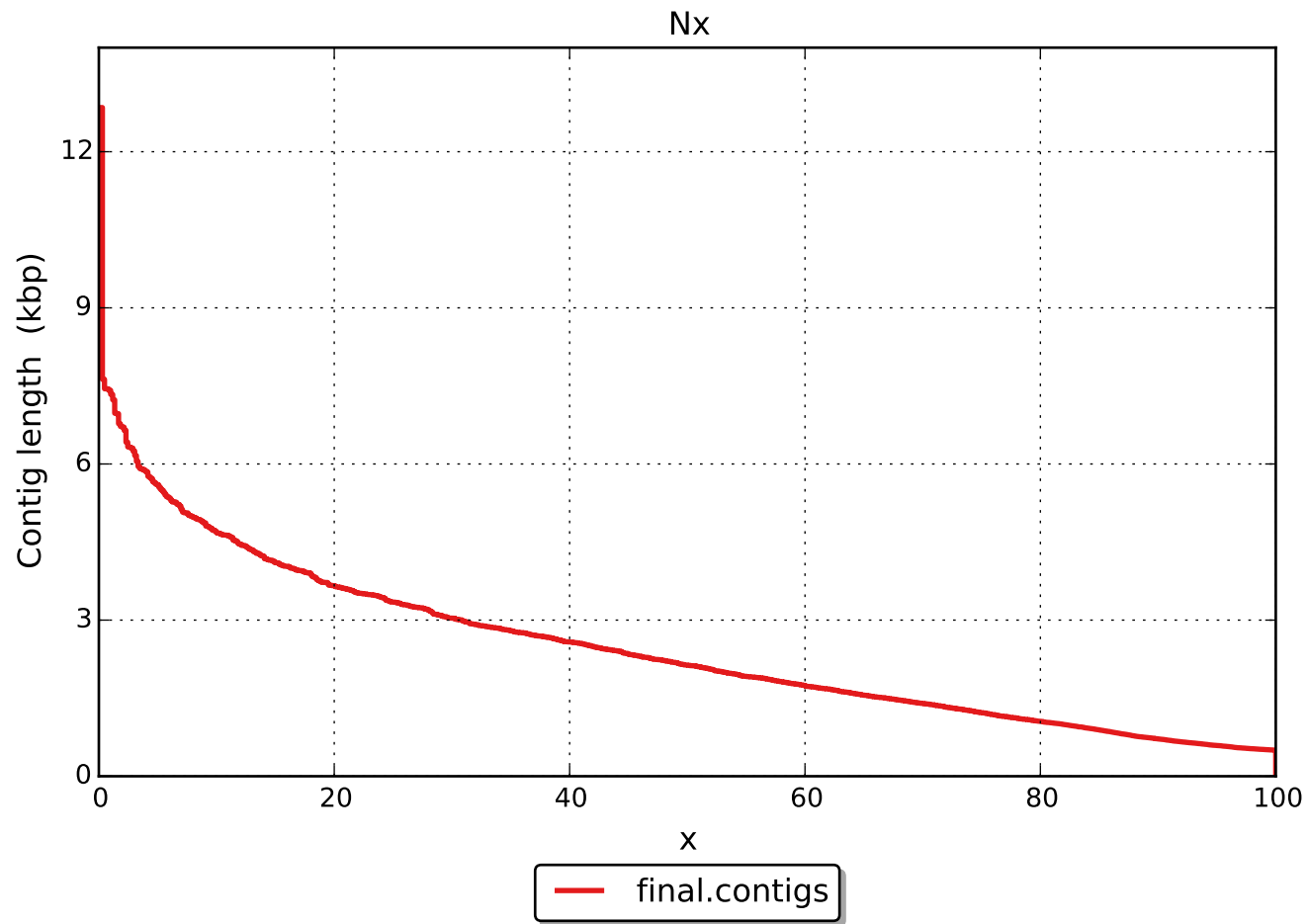
	final.contigs
# misassemblies	3
# relocations	2
# translocations	0
# inversions	1
# possibly misassembled contigs	0
# misassembled contigs	3
Misassembled contigs length	3619
# local misassemblies	2
# mismatches	24046
# indels	8
# short indels	8
# long indels	0
Indels length	8

All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

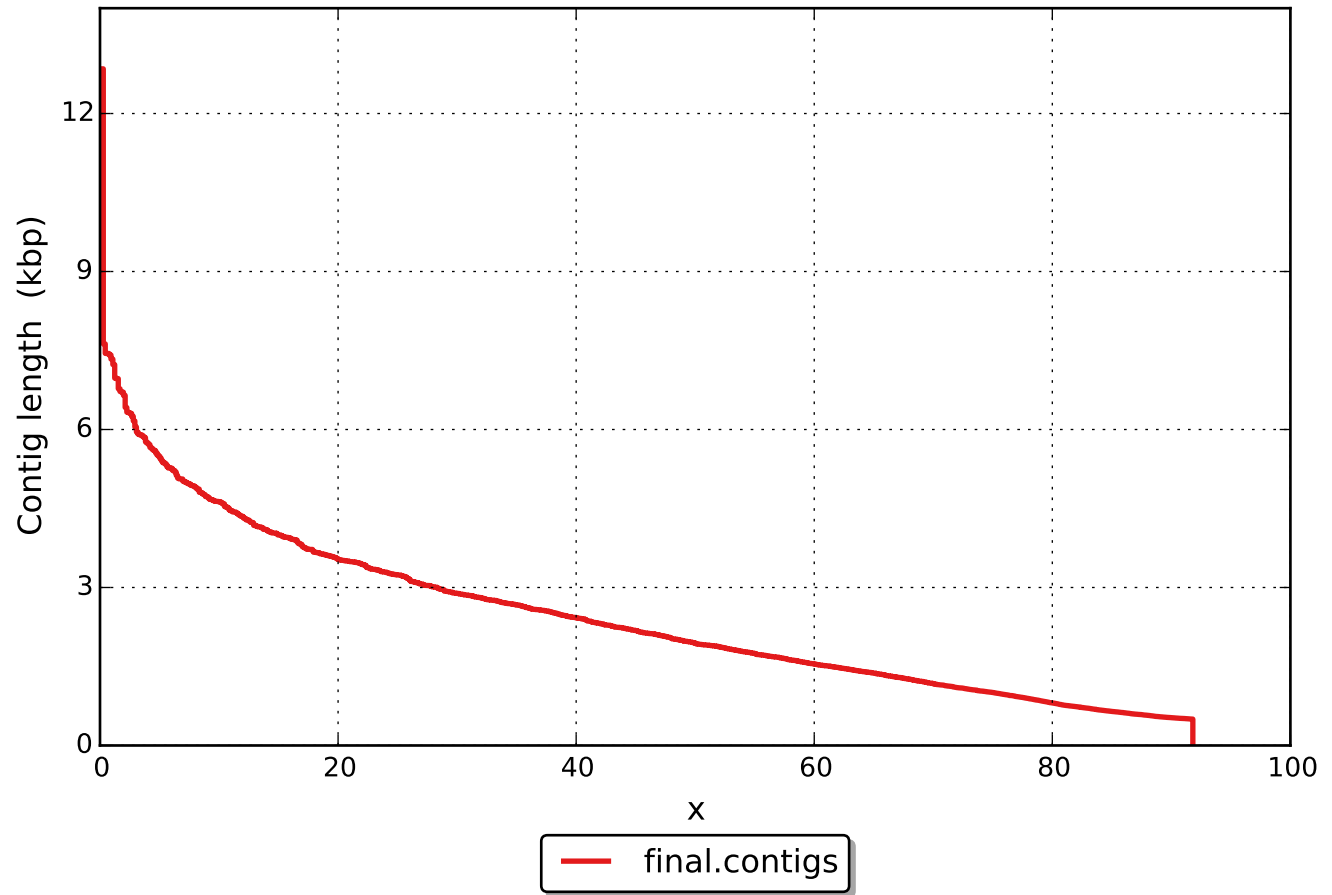
Unaligned report

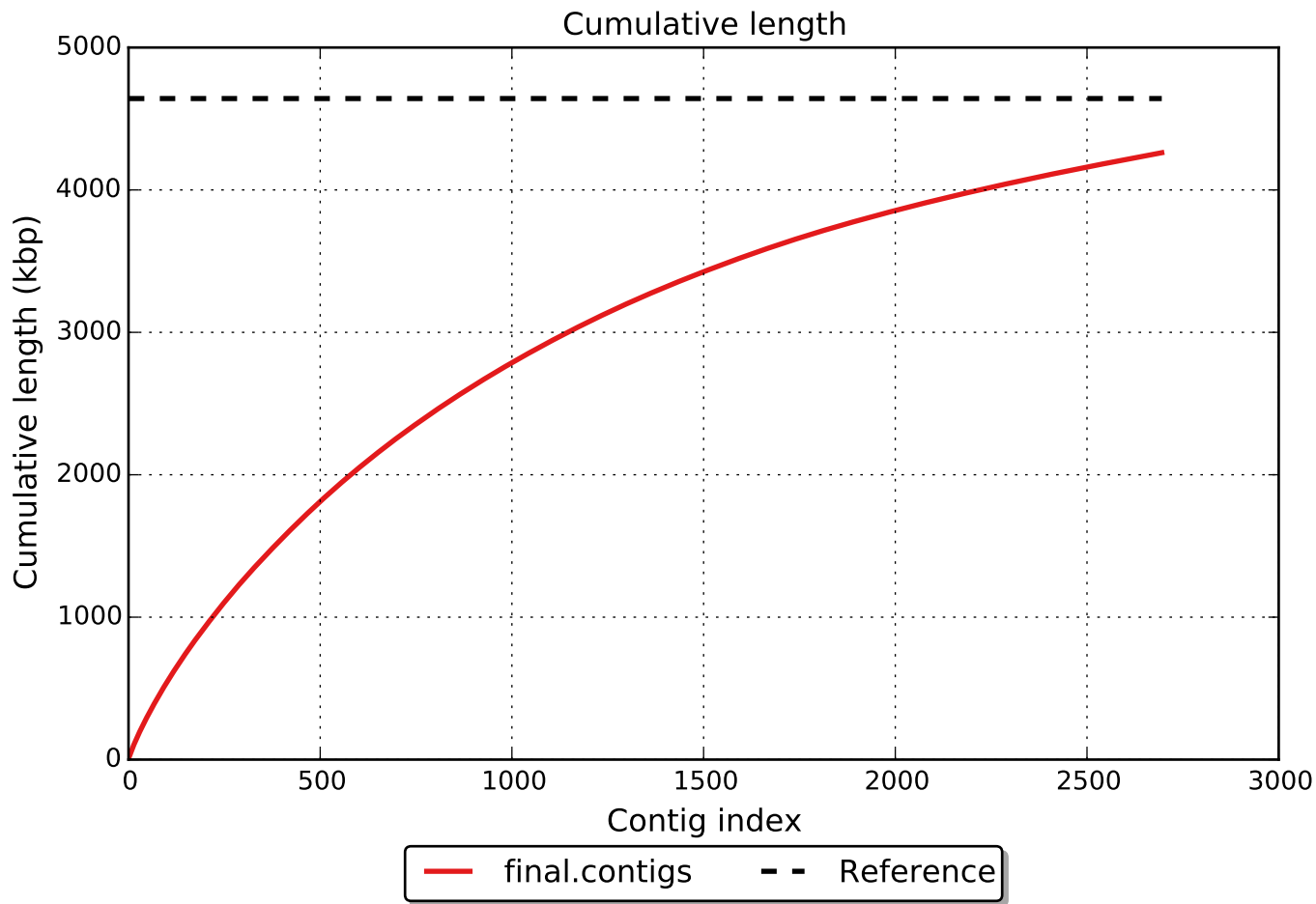
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	6
# with misassembly	0
# both parts are significant	0
Partially unaligned length	783
# N's	0

All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

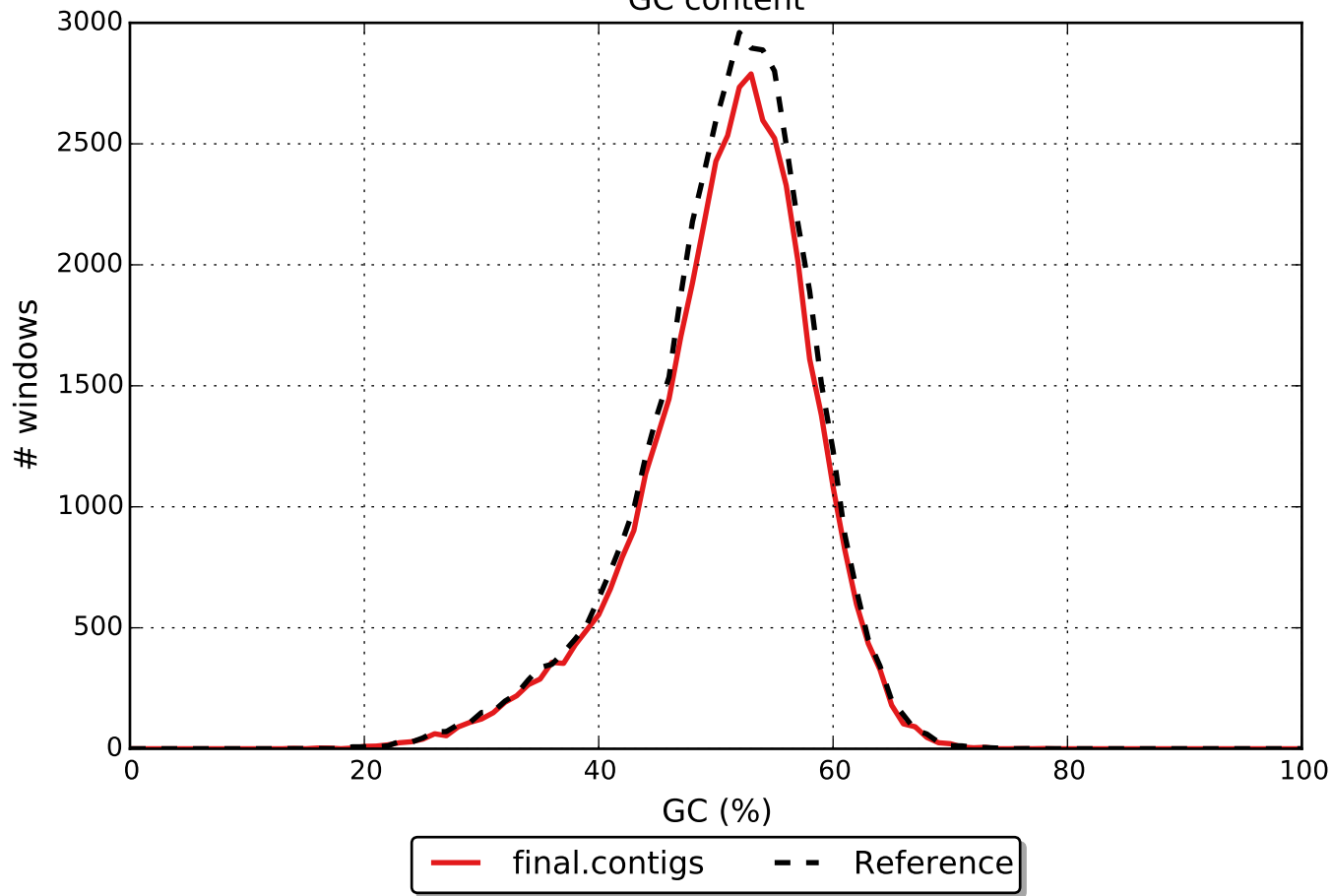


NGx

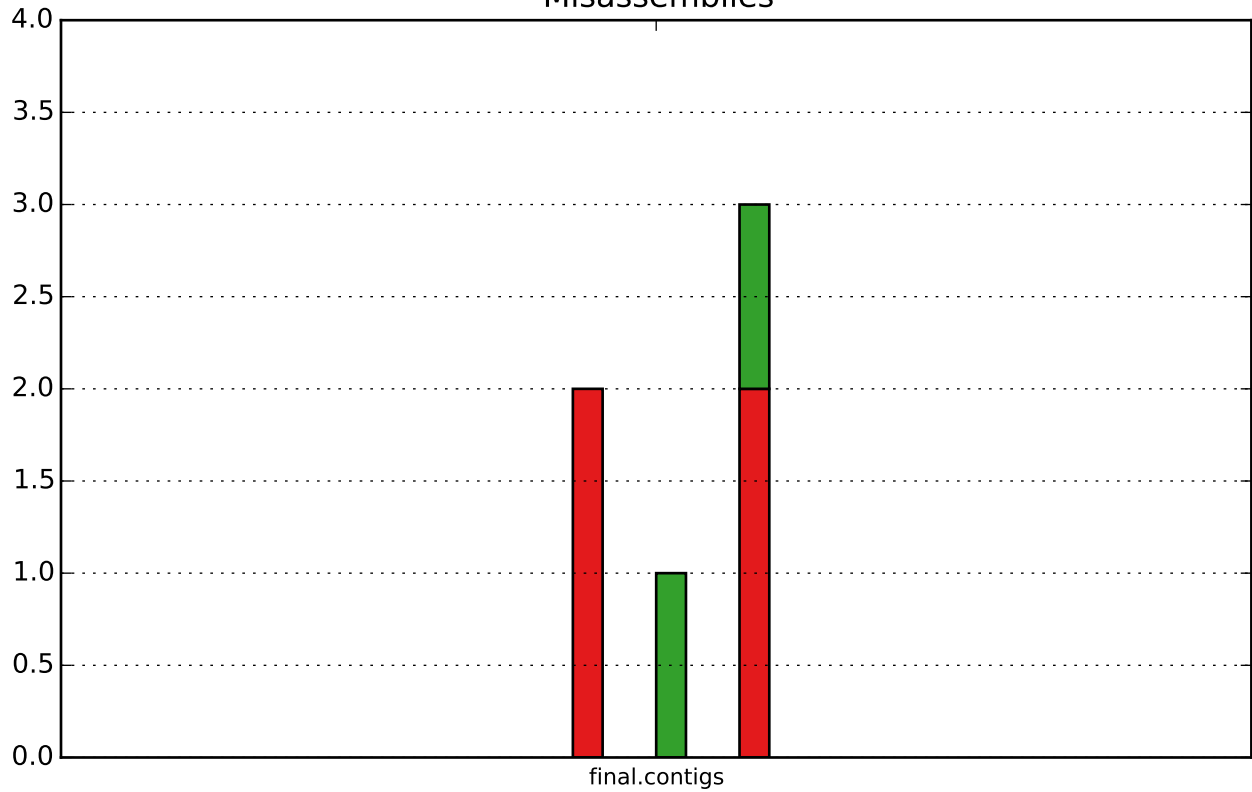




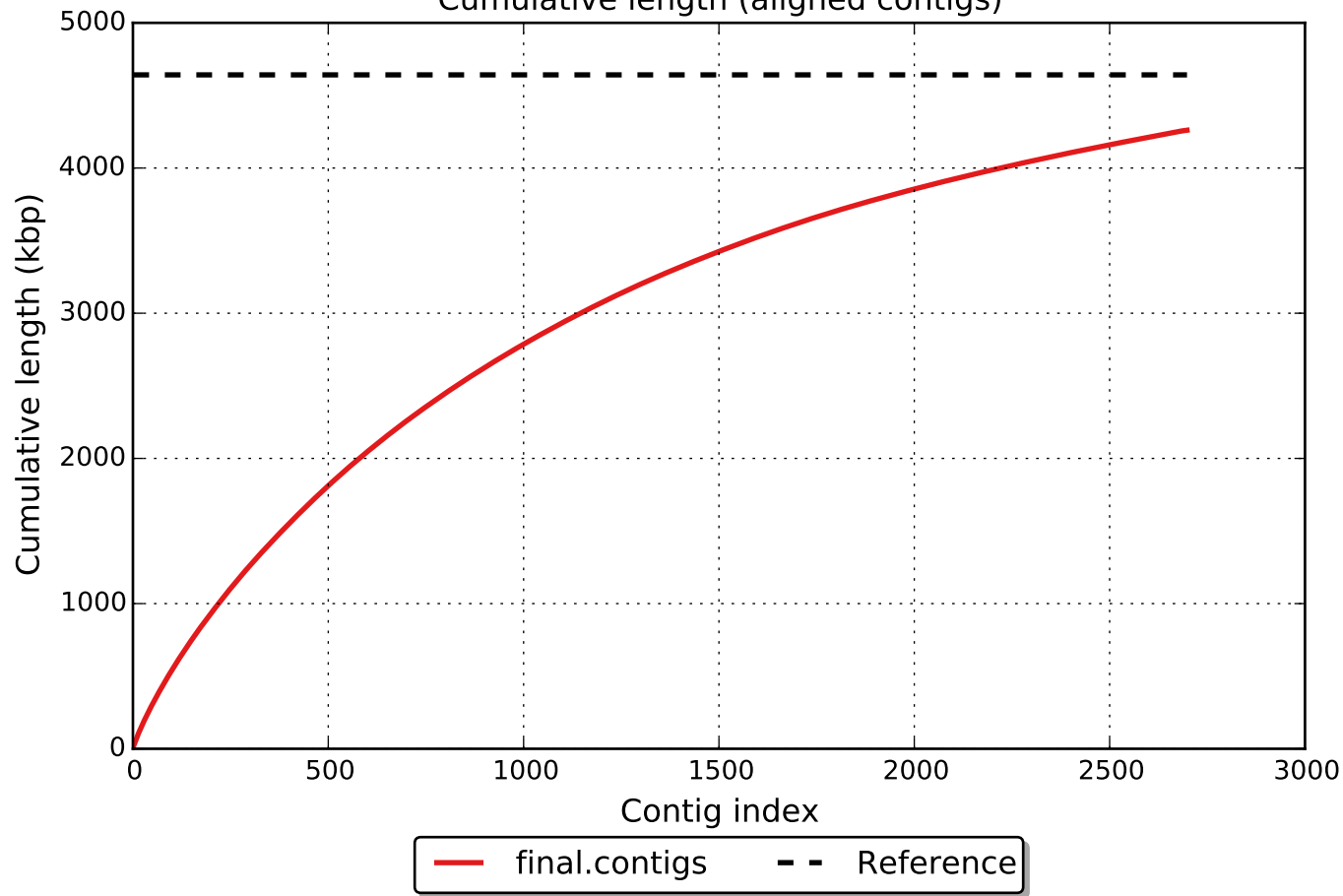
GC content

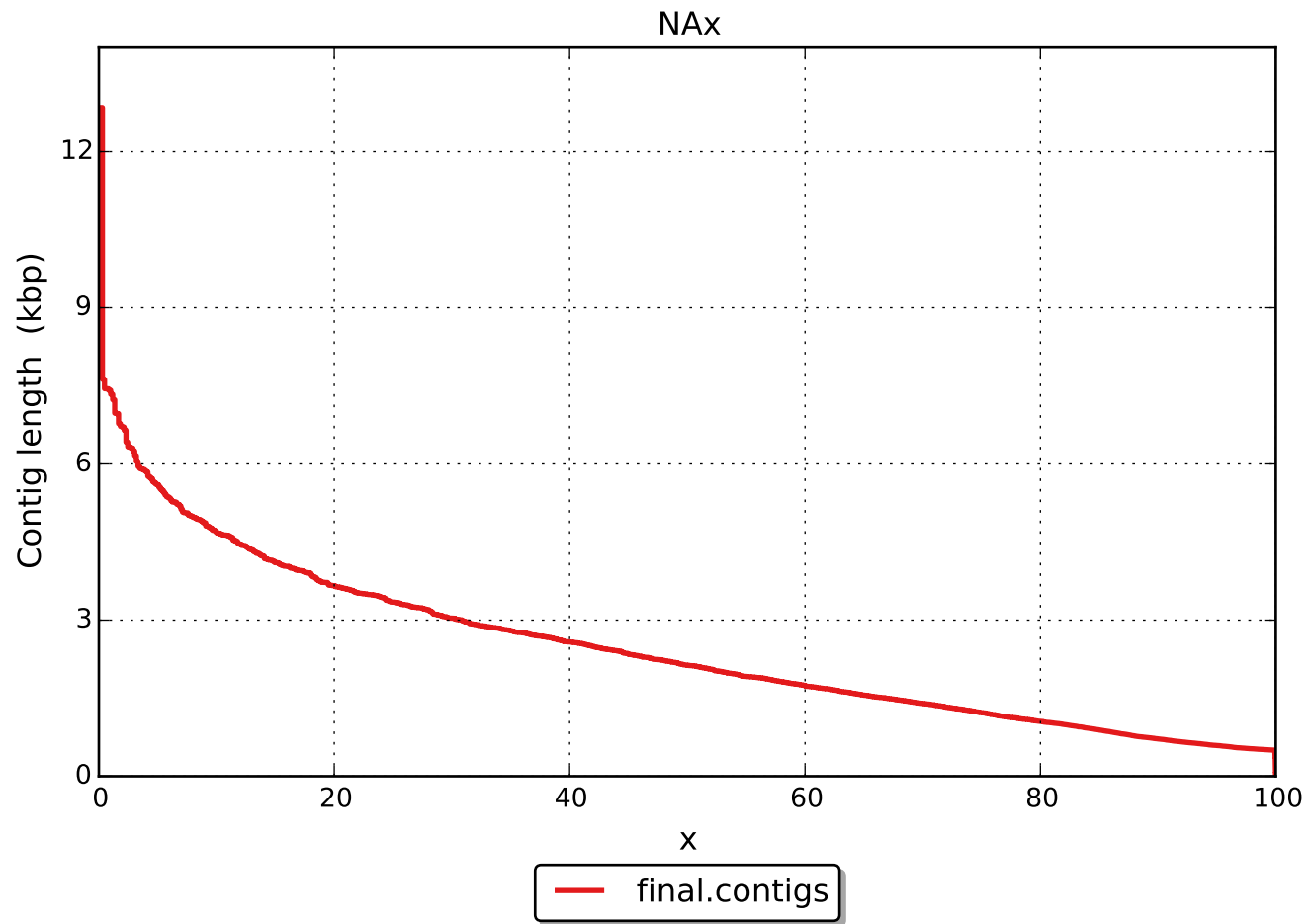


Misassemblies



Cumulative length (aligned contigs)





NGAx

