

Report

	final.contigs
# contigs (>= 0 bp)	2635
# contigs (>= 1000 bp)	1647
# contigs (>= 5000 bp)	122
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	4745529
Total length (>= 1000 bp)	4152352
Total length (>= 5000 bp)	766717
Total length (>= 10000 bp)	11288
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2262
Largest contig	11288
Total length	4605006
Reference length	4641652
GC (%)	50.77
Reference GC (%)	50.79
N50	2648
NG50	2639
N75	1633
NG75	1616
L50	561
LG50	568
L75	1111
LG75	1128
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	7148
# local misassemblies	2
# unaligned contigs	320 + 11 part
Unaligned length	299050
Genome fraction (%)	90.331
Duplication ratio	1.027
# N's per 100 kbp	0.00
# mismatches per 100 kbp	374.85
# indels per 100 kbp	0.36
Largest alignment	11288
NA50	2638
NGA50	2618
NA75	1584
NGA75	1564
LA50	564
LGA50	571
LA75	1122
LGA75	1139

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

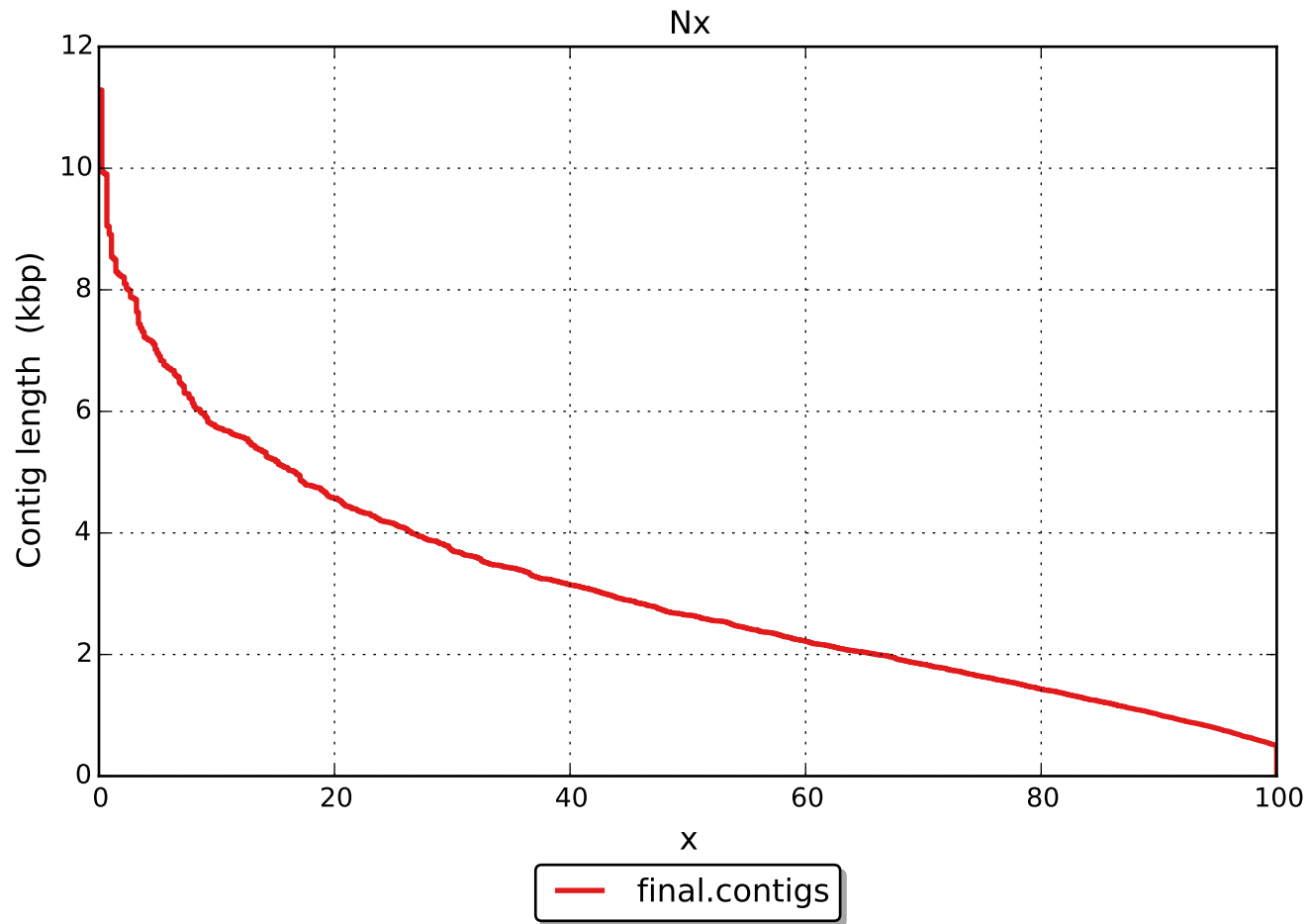
	final.contigs
# misassemblies	3
# relocations	3
# translocations	0
# inversions	0
# misassembled contigs	3
Misassembled contigs length	7148
# local misassemblies	2
# mismatches	15717
# indels	15
# short indels	14
# long indels	1
Indels length	98

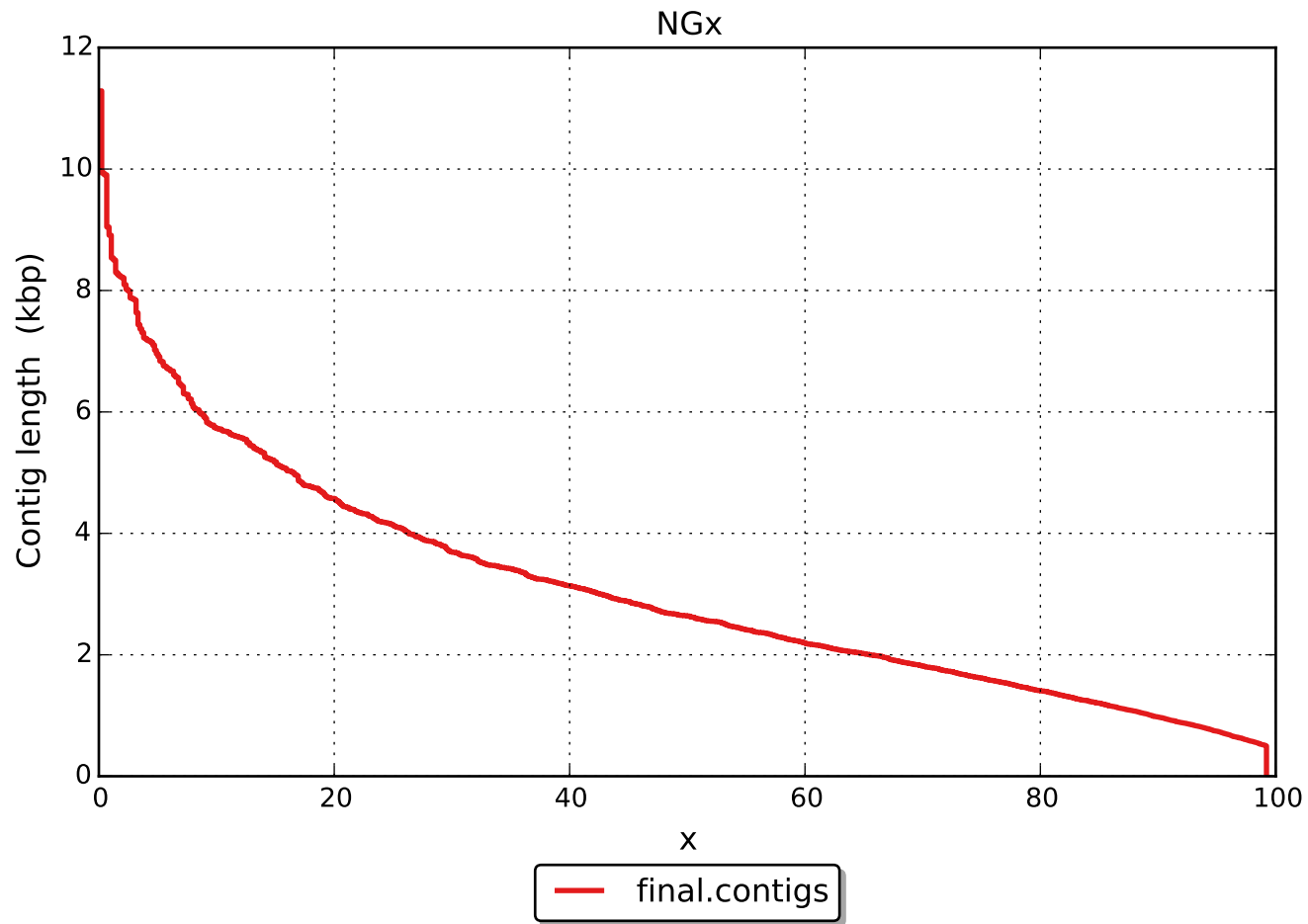
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

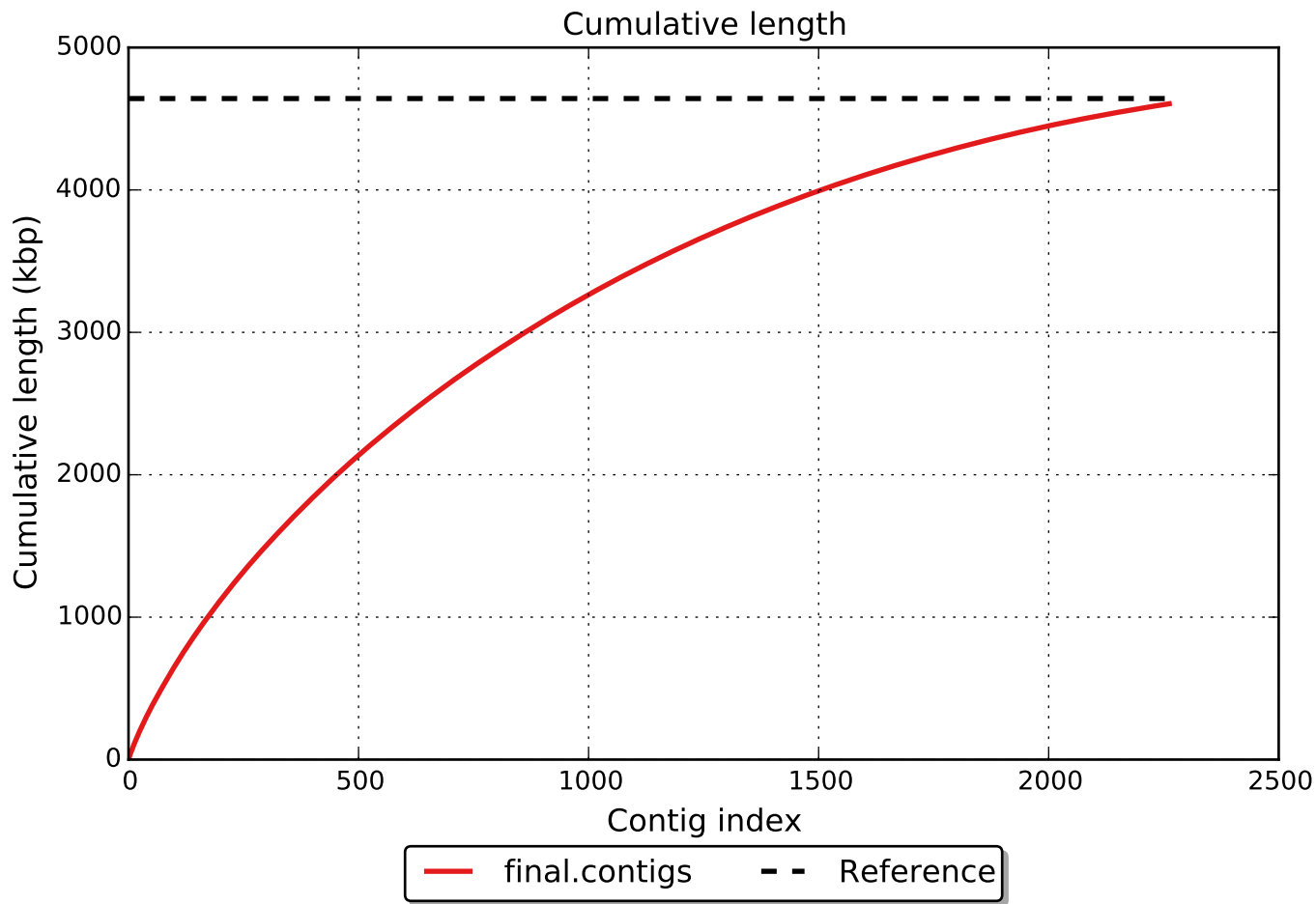
Unaligned report

	final.contigs
# fully unaligned contigs	320
Fully unaligned length	290837
# partially unaligned contigs	11
# with misassembly	0
# both parts are significant	3
Partially unaligned length	8213
# N's	0

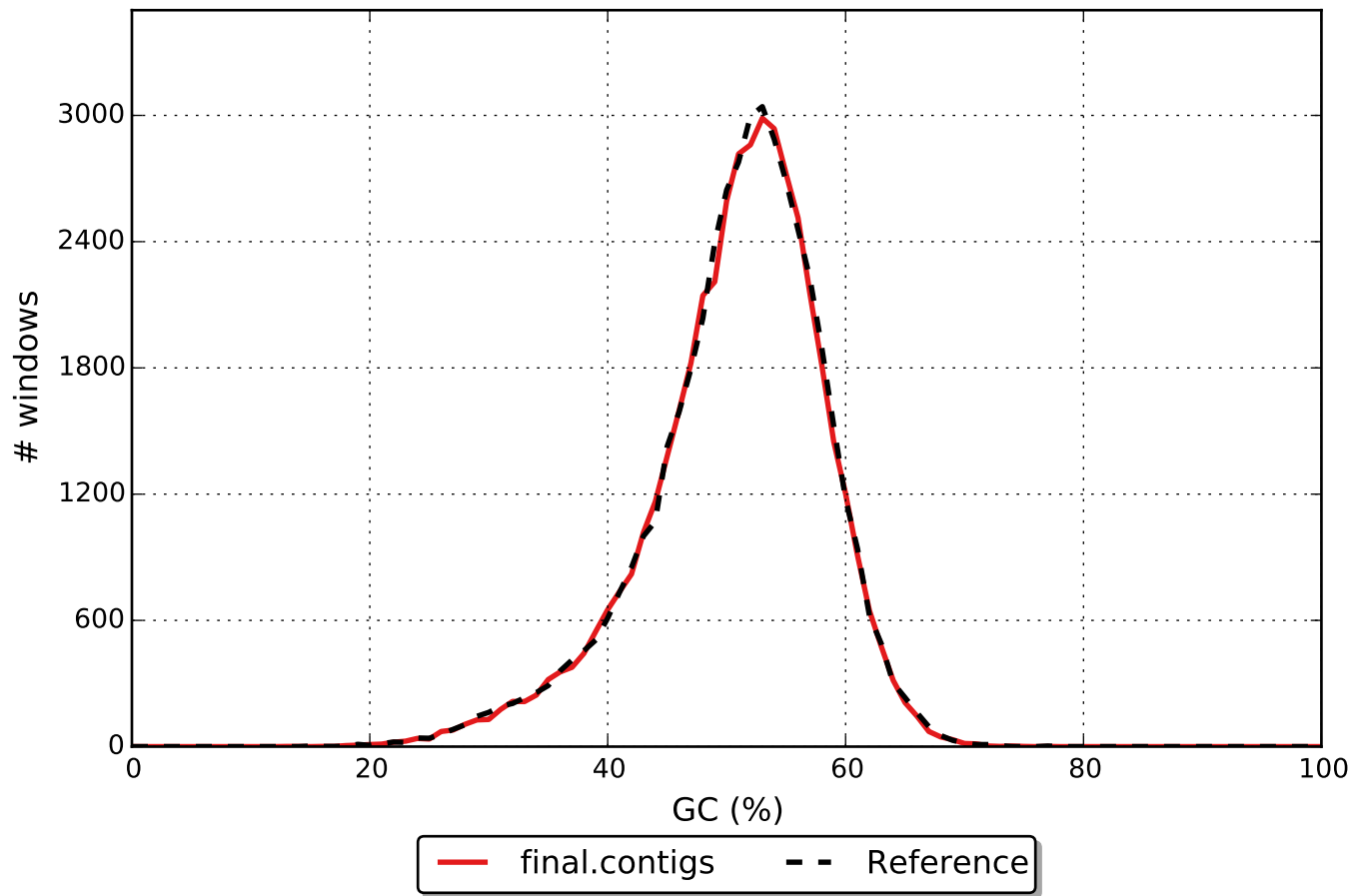
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

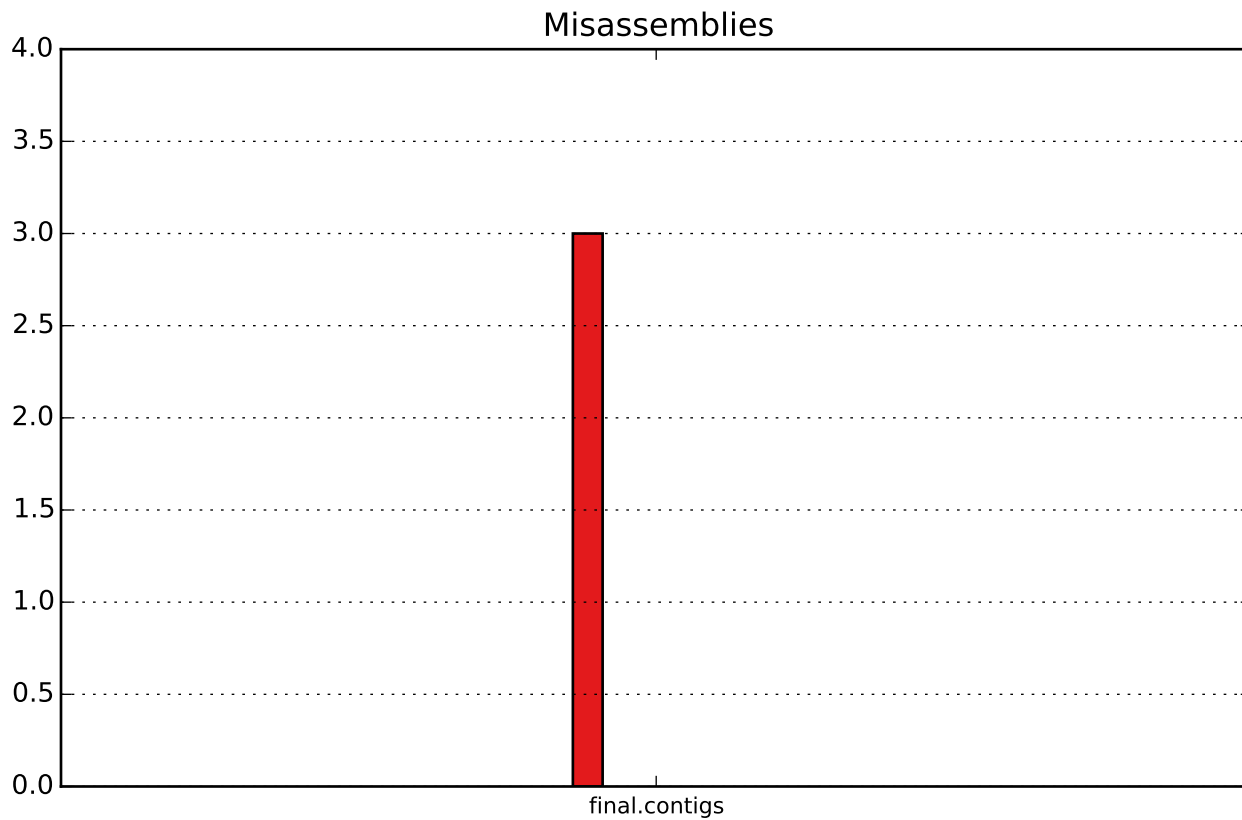




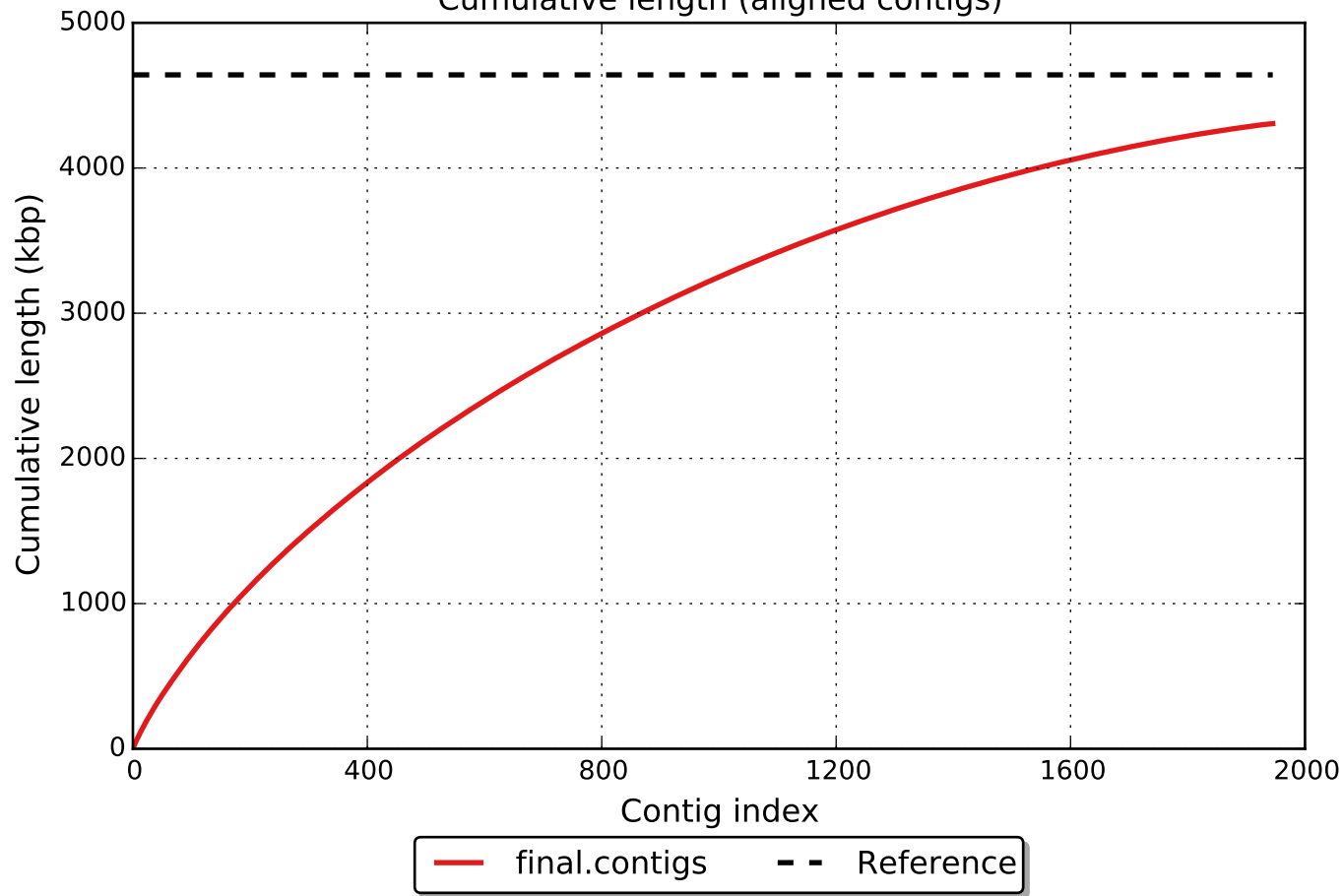


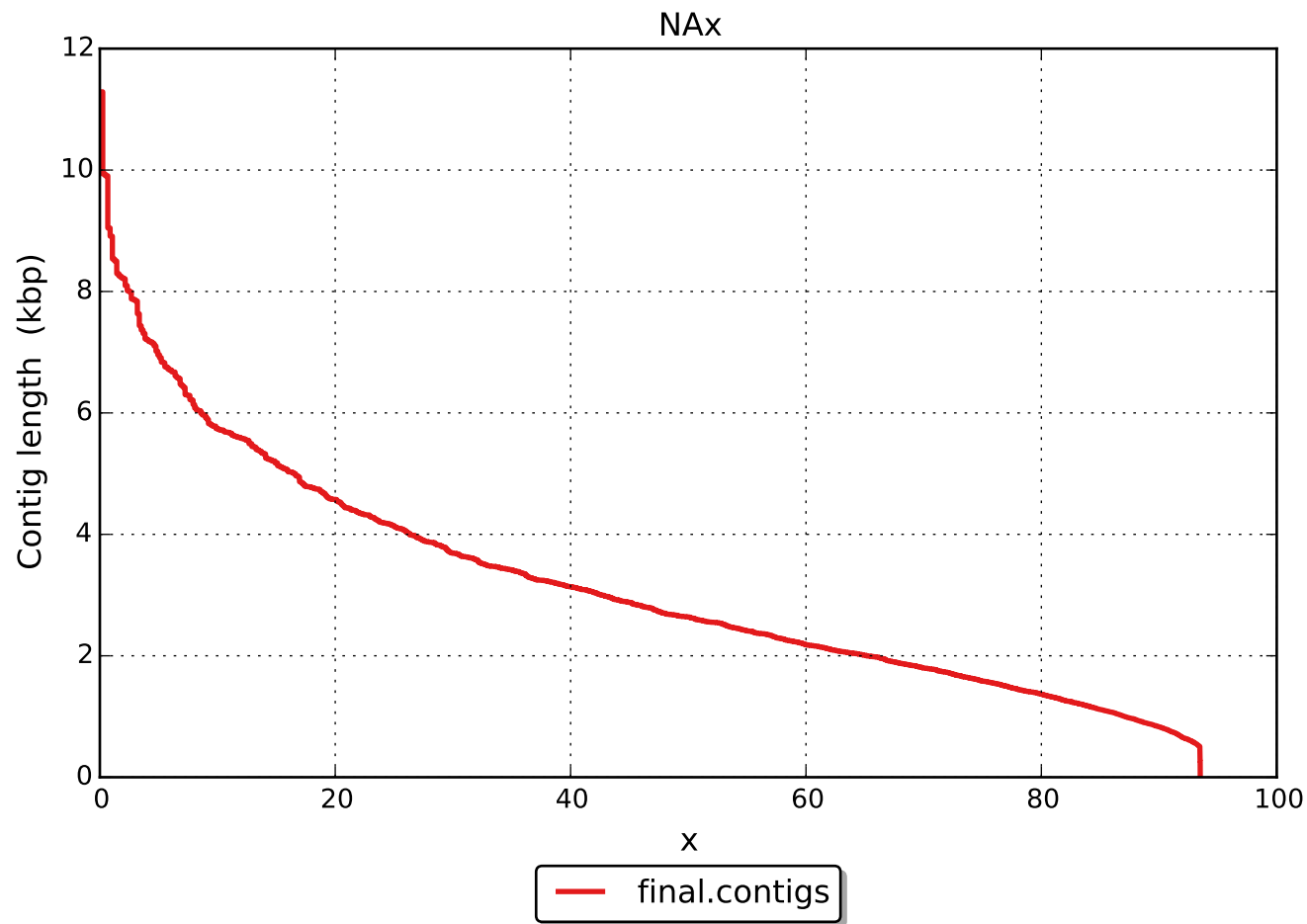
GC content





Cumulative length (aligned contigs)





NGAx

