

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	9
# misassembled contigs	9
Misassembled contigs length	18977
# local misassemblies	8
# unaligned contigs	0 + 3 part
Unaligned length	116
Genome fraction (%)	95.399
Duplication ratio	1.040
# N's per 100 kbp	0.00
# mismatches per 100 kbp	416.68
# indels per 100 kbp	0.47
Largest alignment	11288
NA50	2647
NGA50	2638
NA75	1632
NGA75	1613
LA50	562
LGA50	569
LA75	1113
LGA75	1130

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

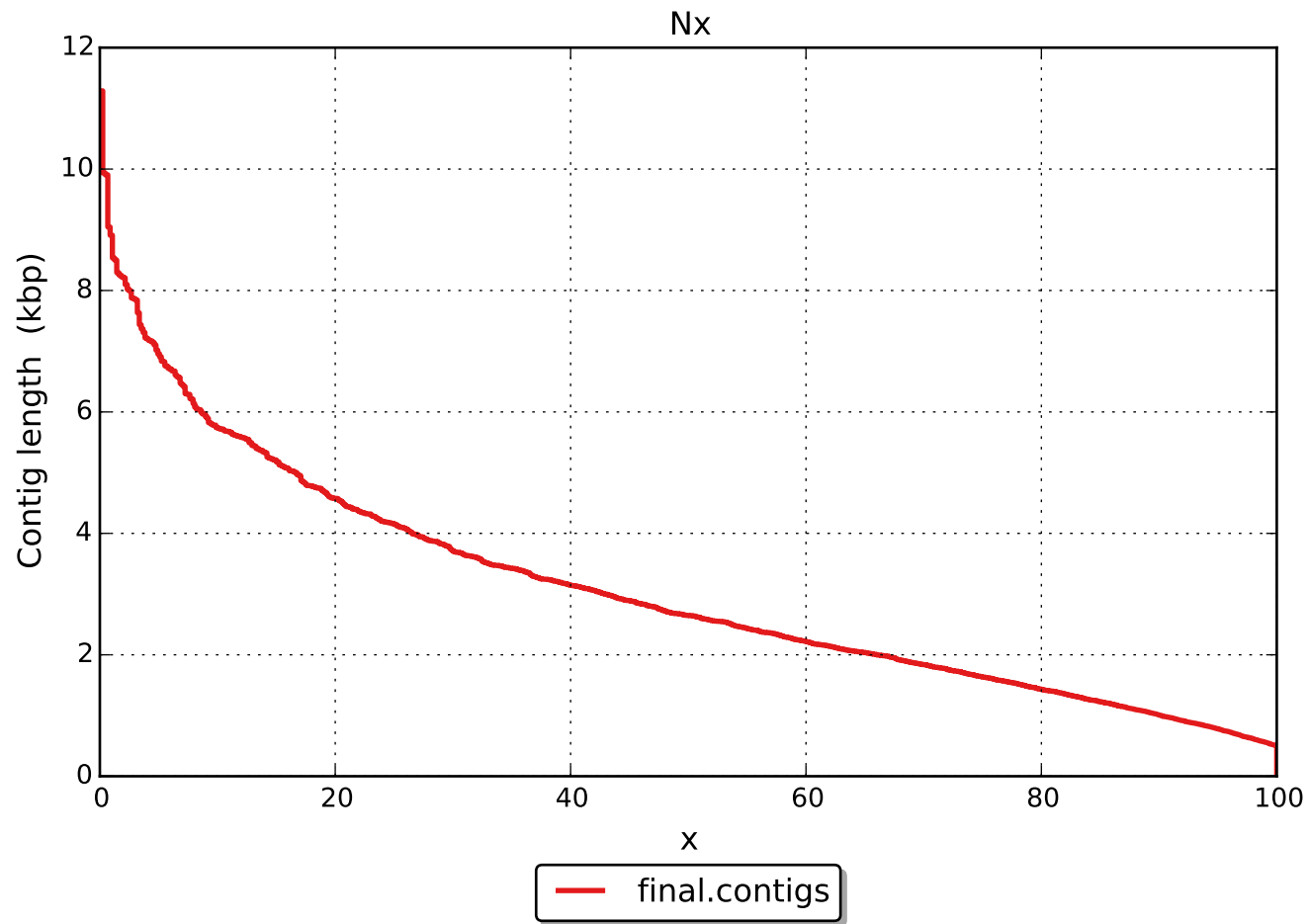
	final.contigs
# misassemblies	9
# relocations	9
# translocations	0
# inversions	0
# misassembled contigs	9
Misassembled contigs length	18977
# local misassemblies	8
# mismatches	18451
# indels	21
# short indels	20
# long indels	1
Indels length	108

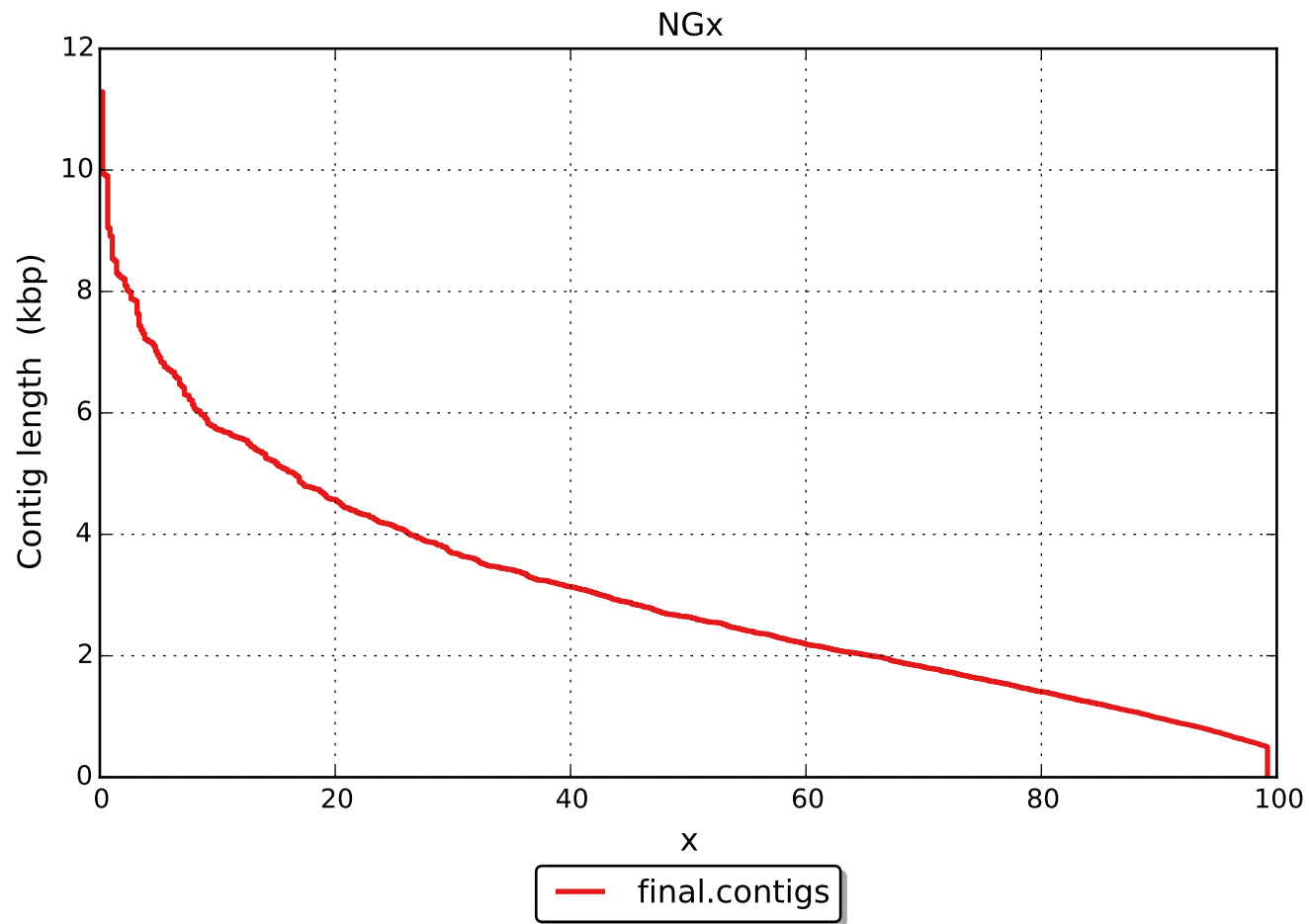
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

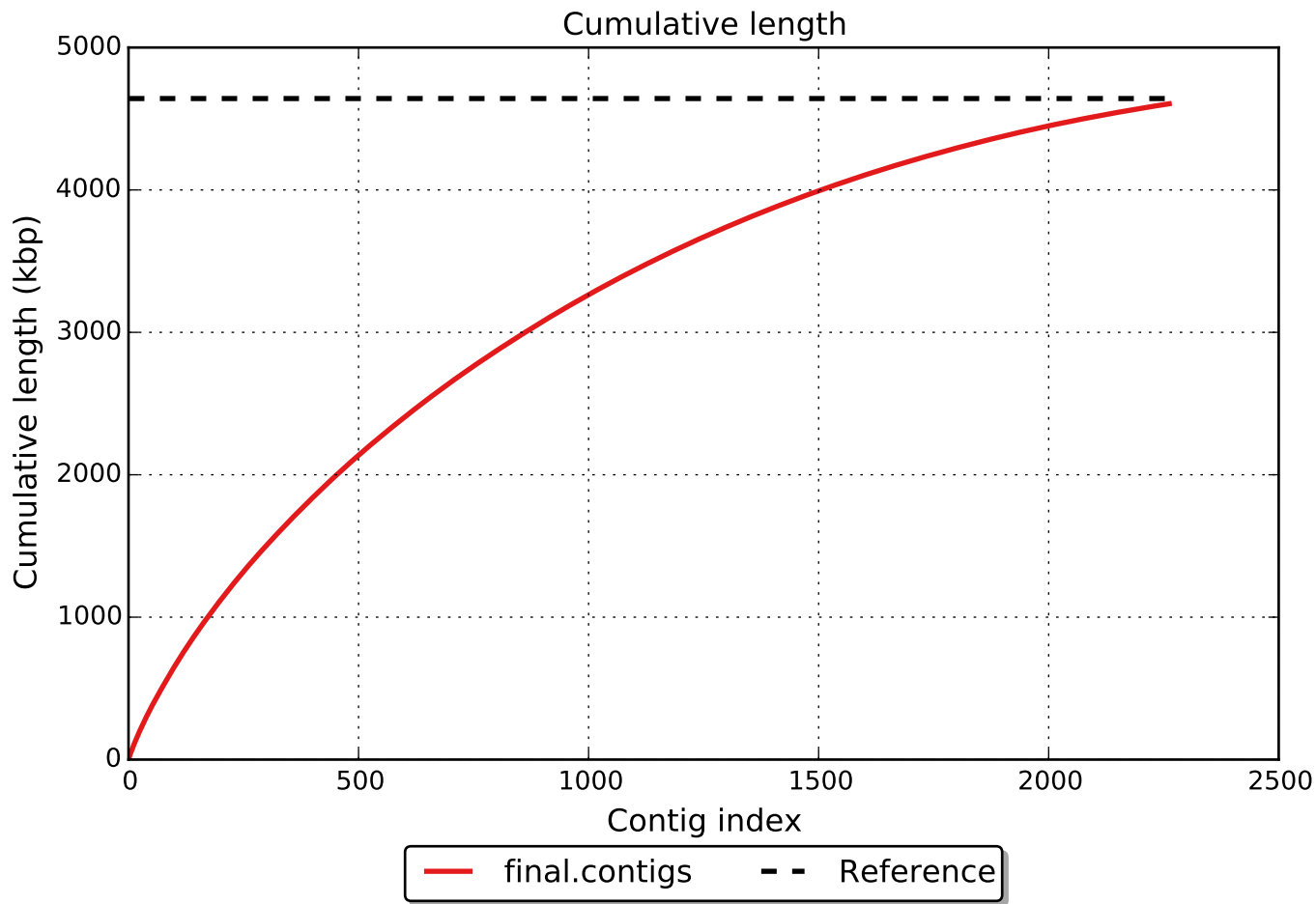
Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
# with misassembly	0
# both parts are significant	0
Partially unaligned length	116
# N's	0

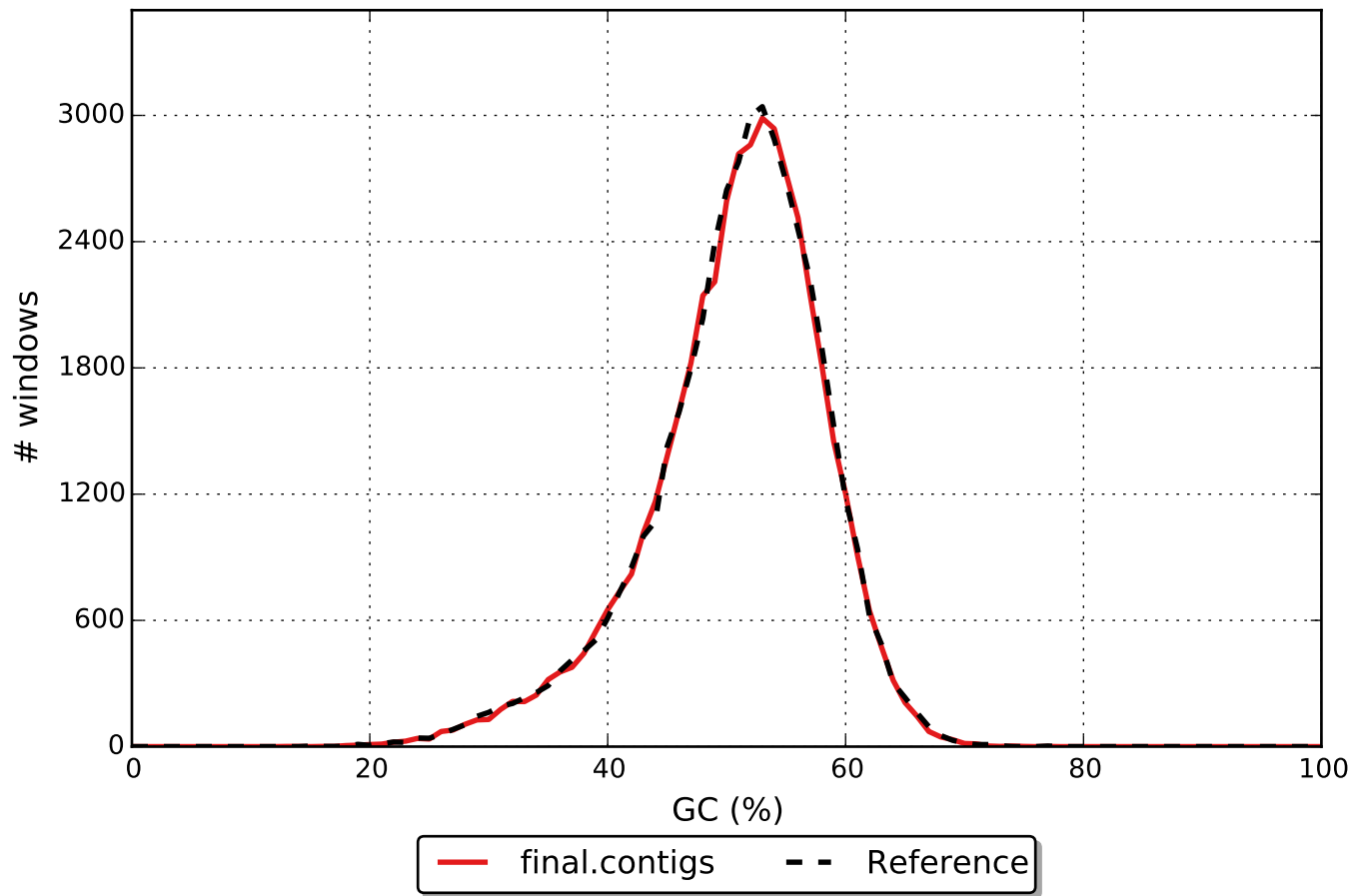
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

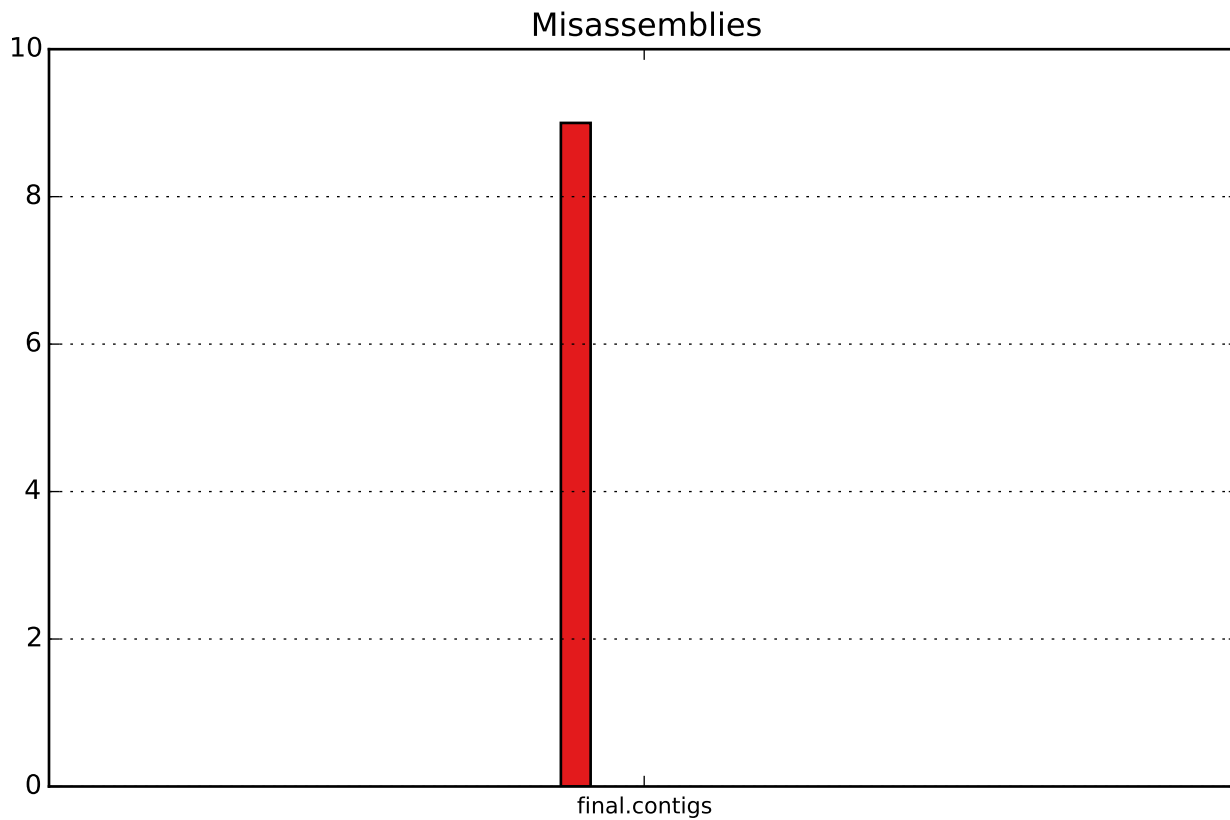




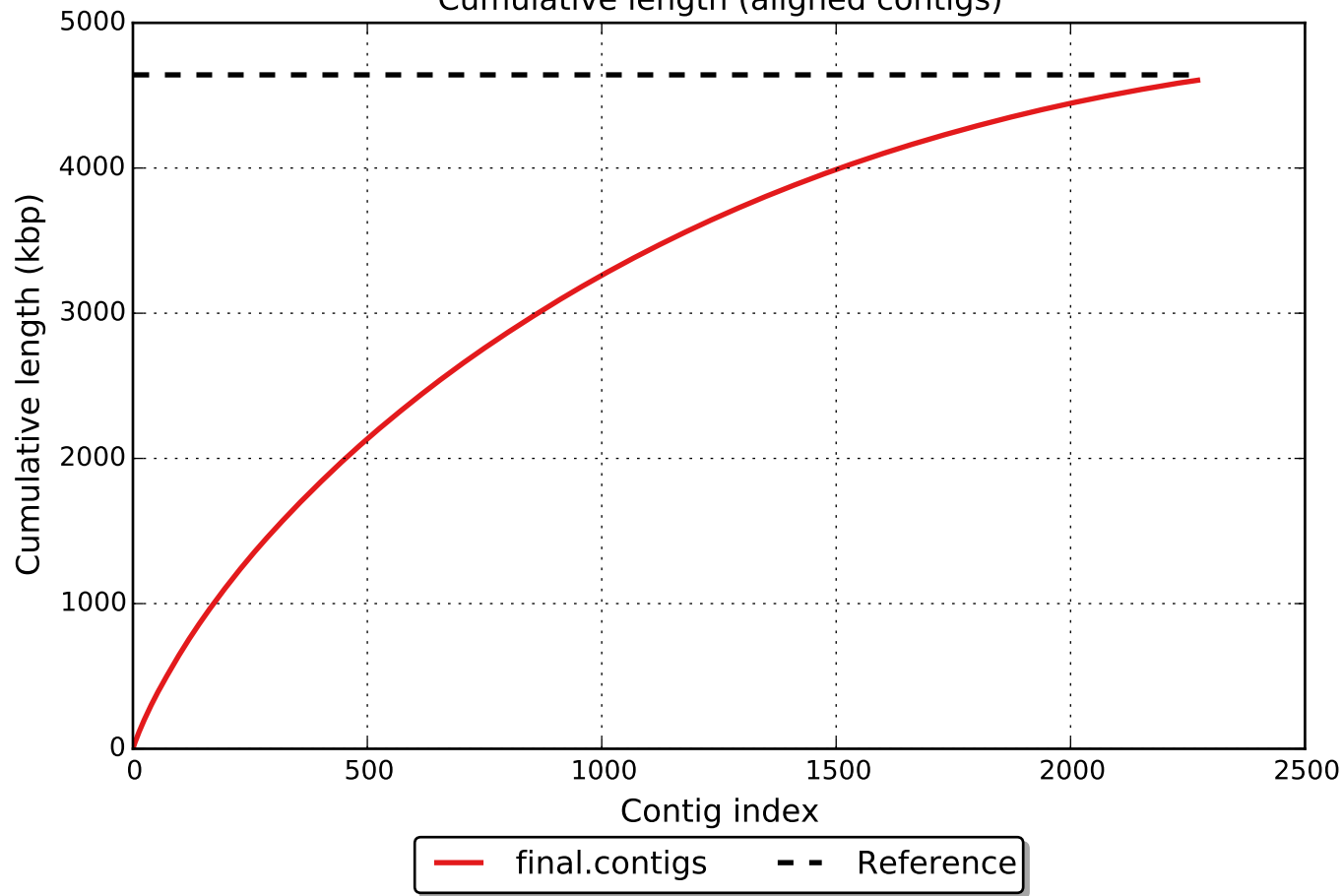


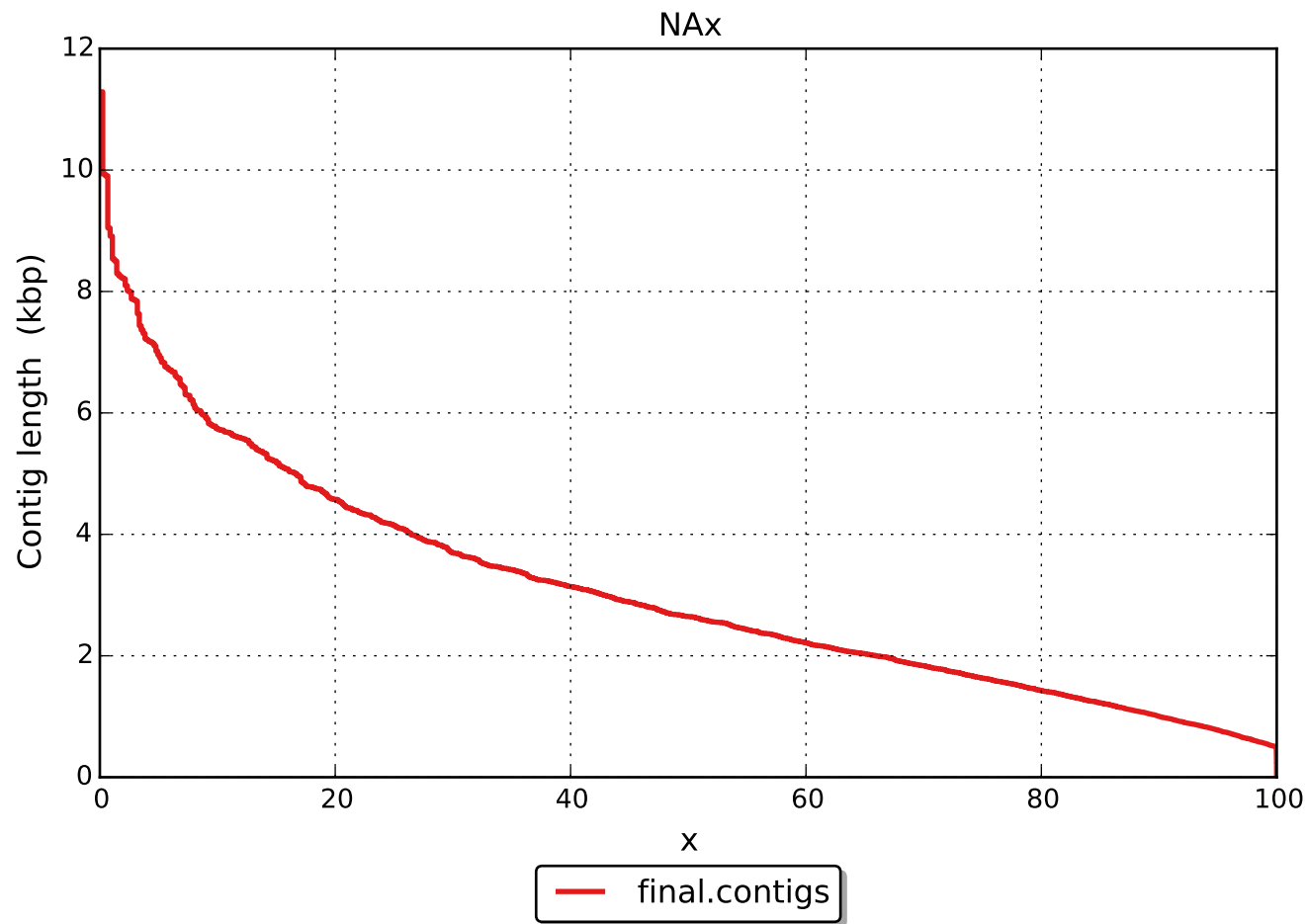
GC content





Cumulative length (aligned contigs)





NGAx

