

Report

	final.contigs
# contigs (>= 1000 bp)	1453
# contigs (>= 5000 bp)	9
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	2526846
Total length (>= 5000 bp)	54669
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3586
Largest contig	7423
Total length	4003534
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	1277
NG50	1110
N75	804
NG75	637
L50	990
LG50	1258
L75	1984
LG75	2658
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	521
# local misassemblies	0
# unaligned contigs	0 + 3 part
Unaligned length	155
Genome fraction (%)	79.686
Duplication ratio	1.082
# N's per 100 kbp	0.00
# mismatches per 100 kbp	549.32
# indels per 100 kbp	0.22
Largest alignment	7423
NA50	1277
NGA50	1110
NA75	803
NGA75	637
LA50	990
LGA50	1258
LA75	1984
LGA75	2658

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

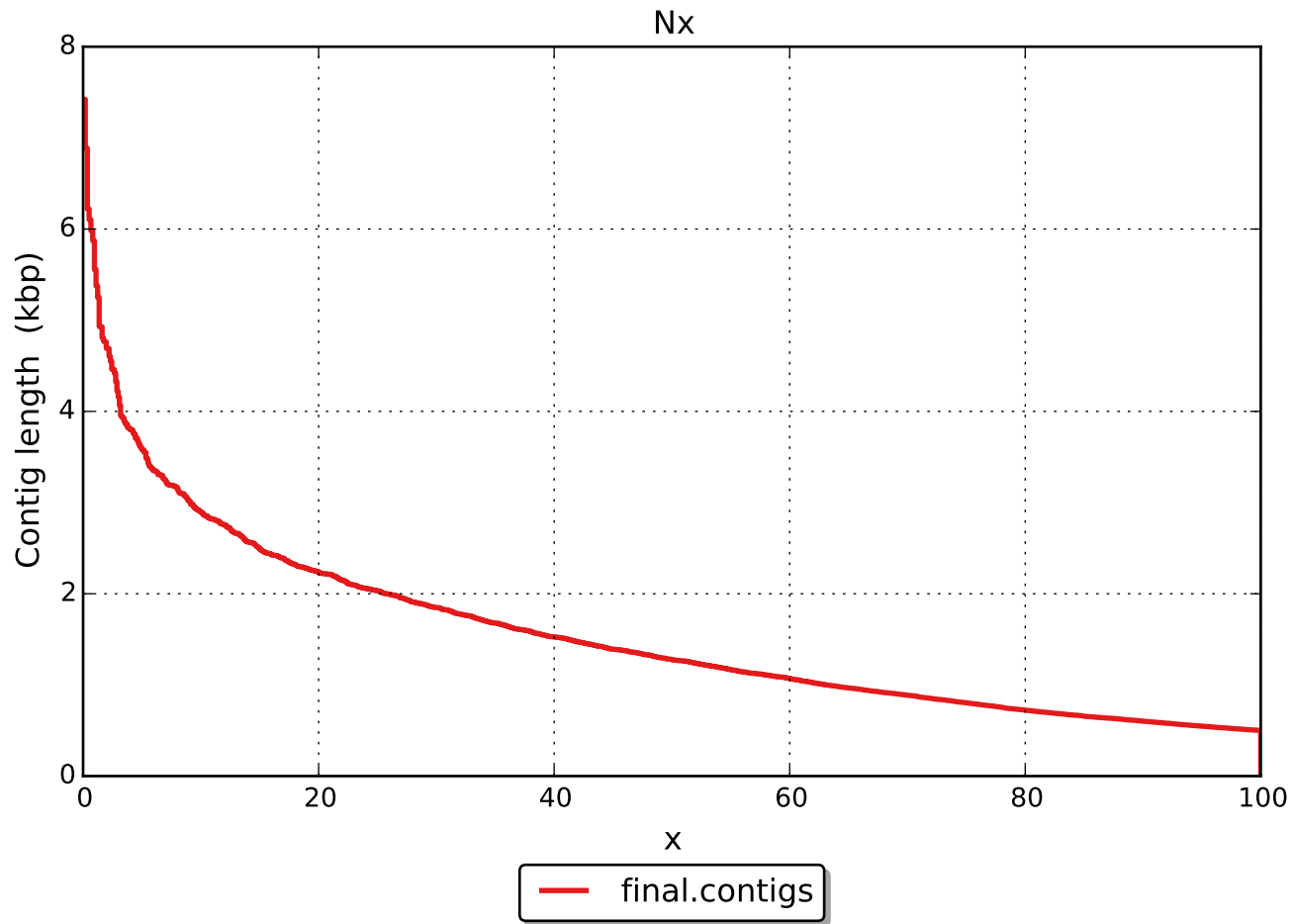
	final.contigs
# misassemblies	1
# relocations	0
# translocations	0
# inversions	1
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	521
# local misassemblies	0
# mismatches	20318
# indels	8
# short indels	8
# long indels	0
Indels length	8

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).

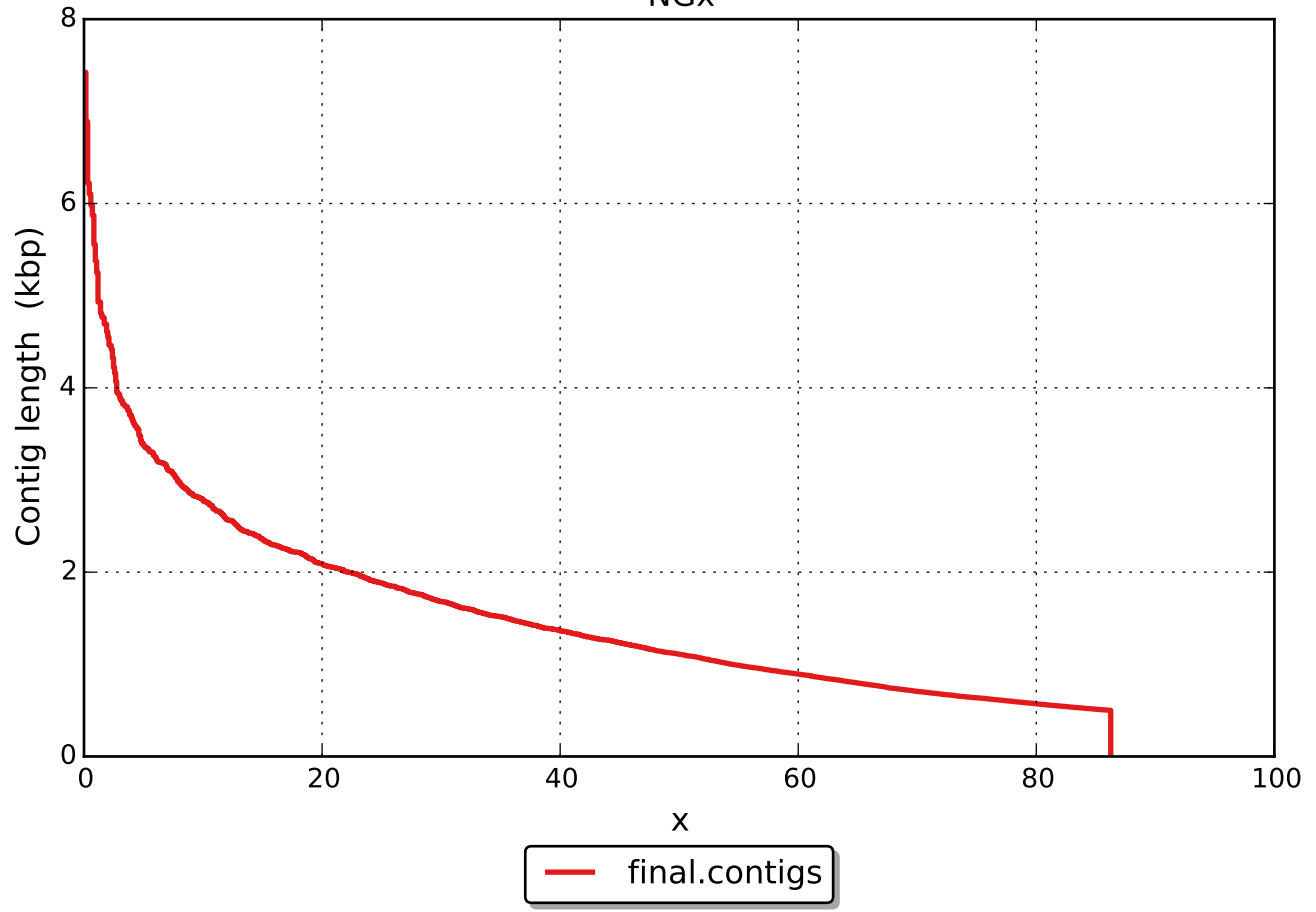
Unaligned report

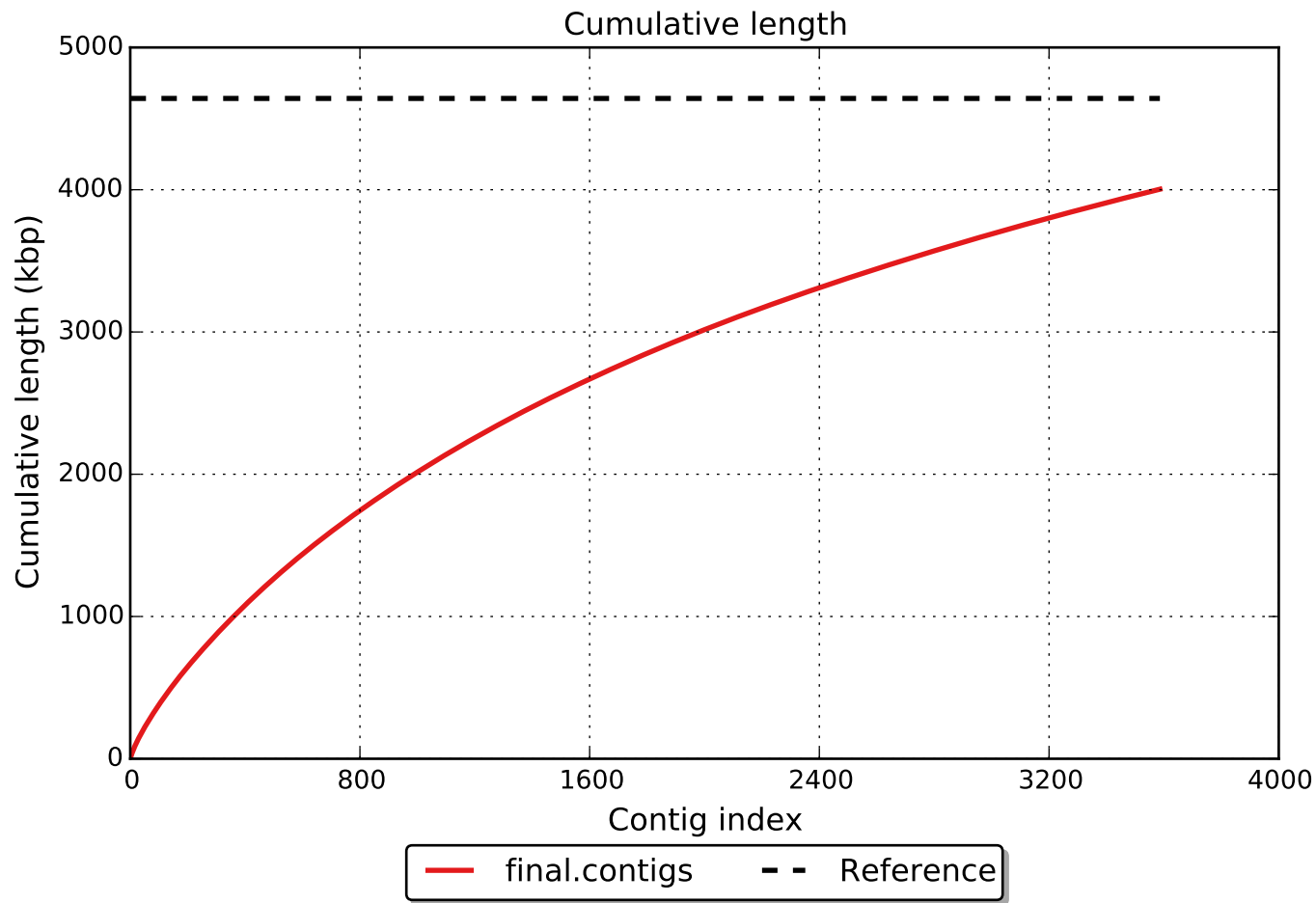
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
# with misassembly	0
# both parts are significant	0
Partially unaligned length	155
# N's	0

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).

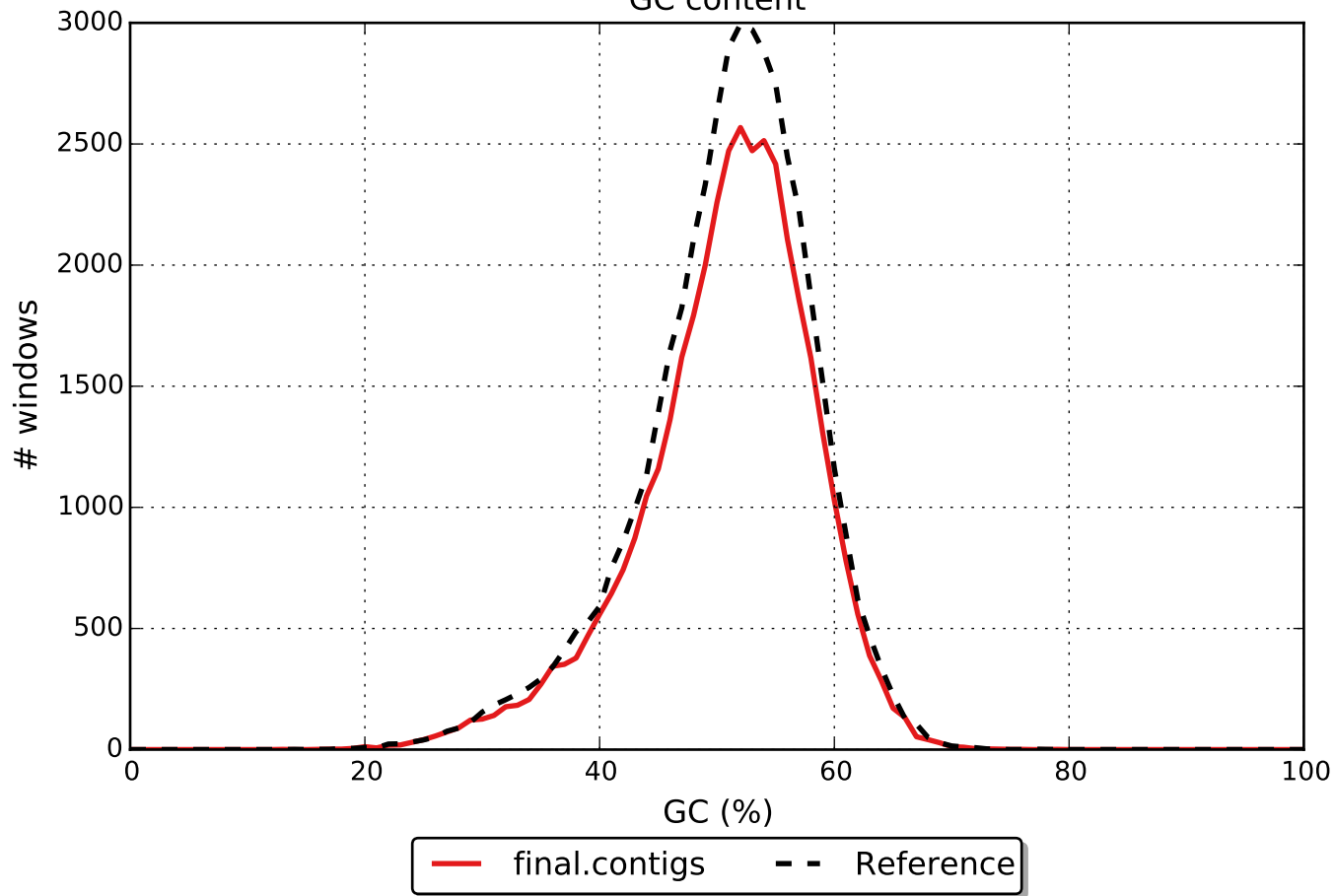


NGx

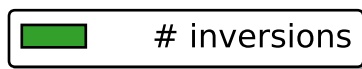
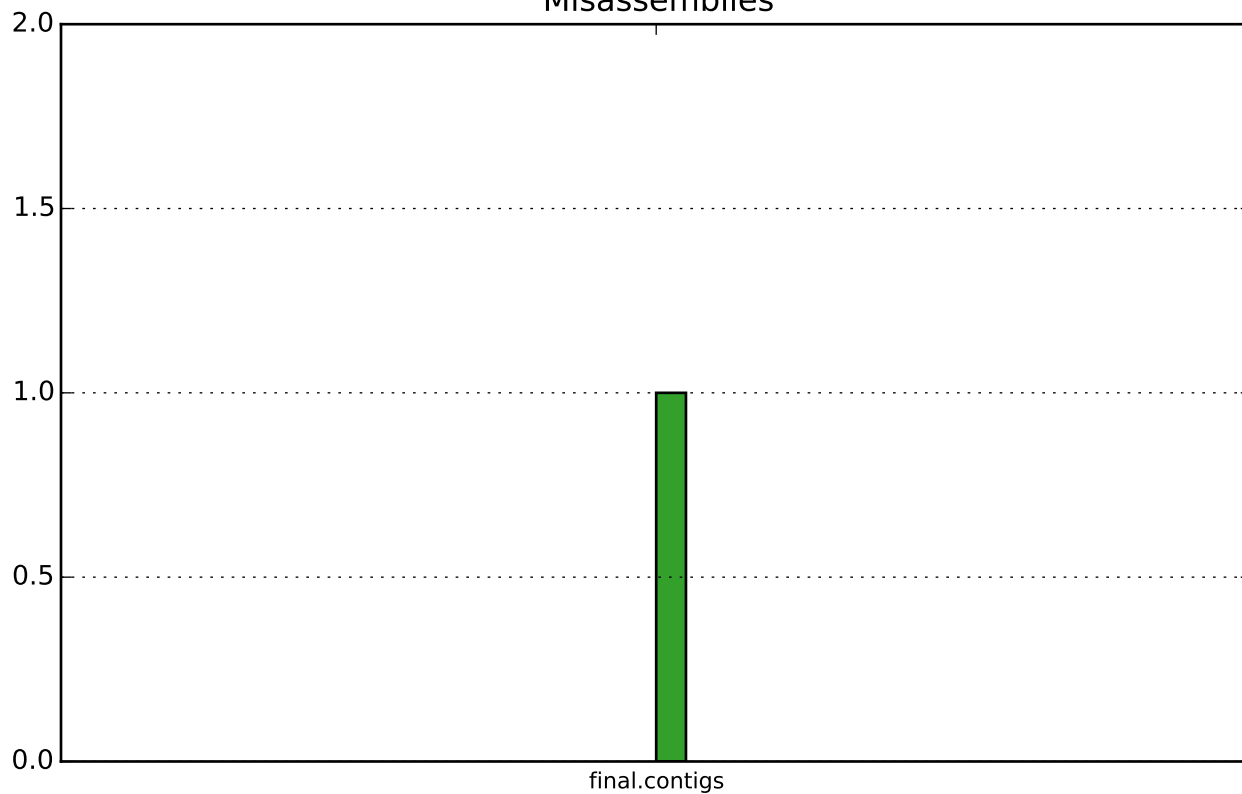




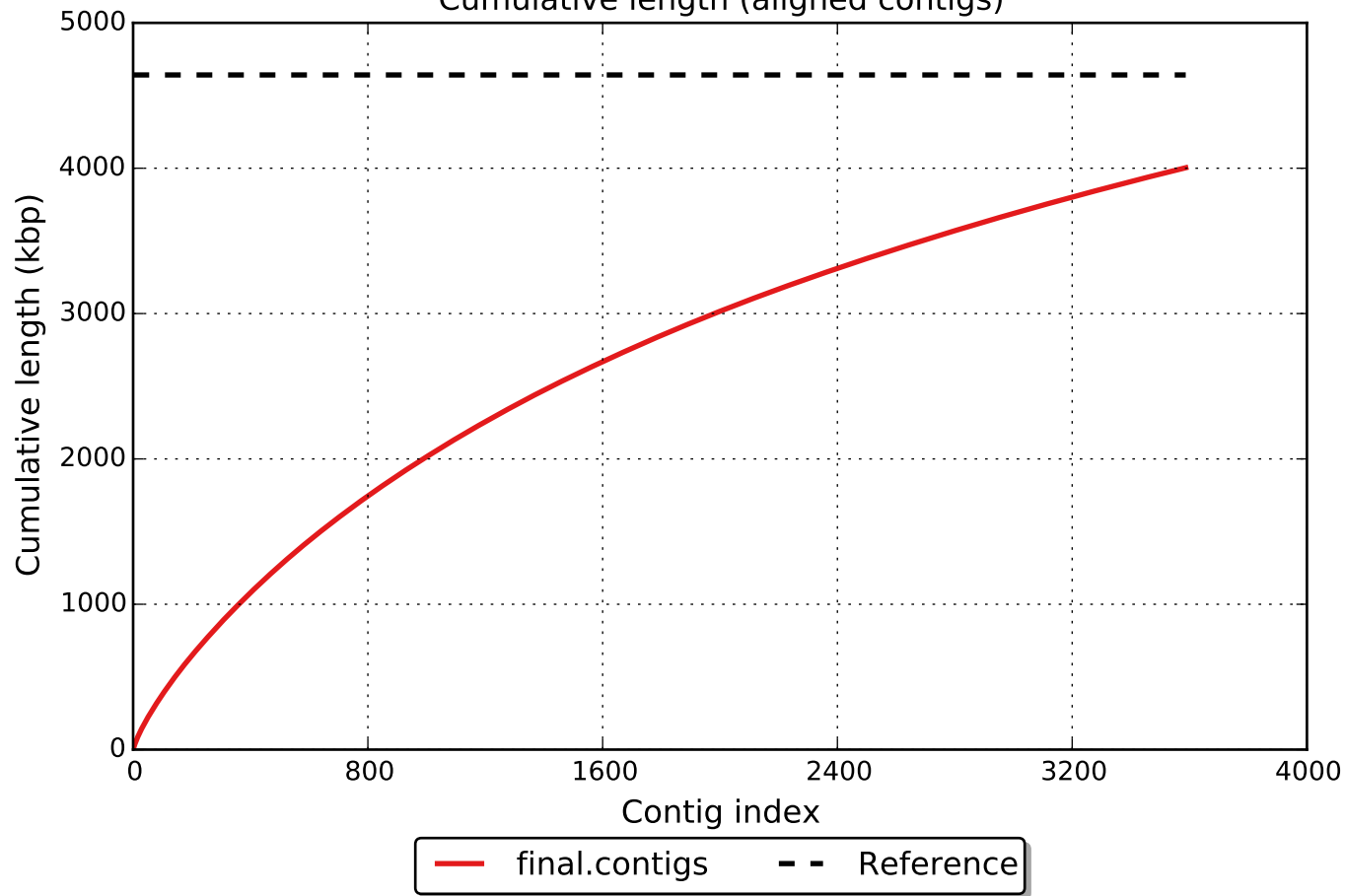
GC content

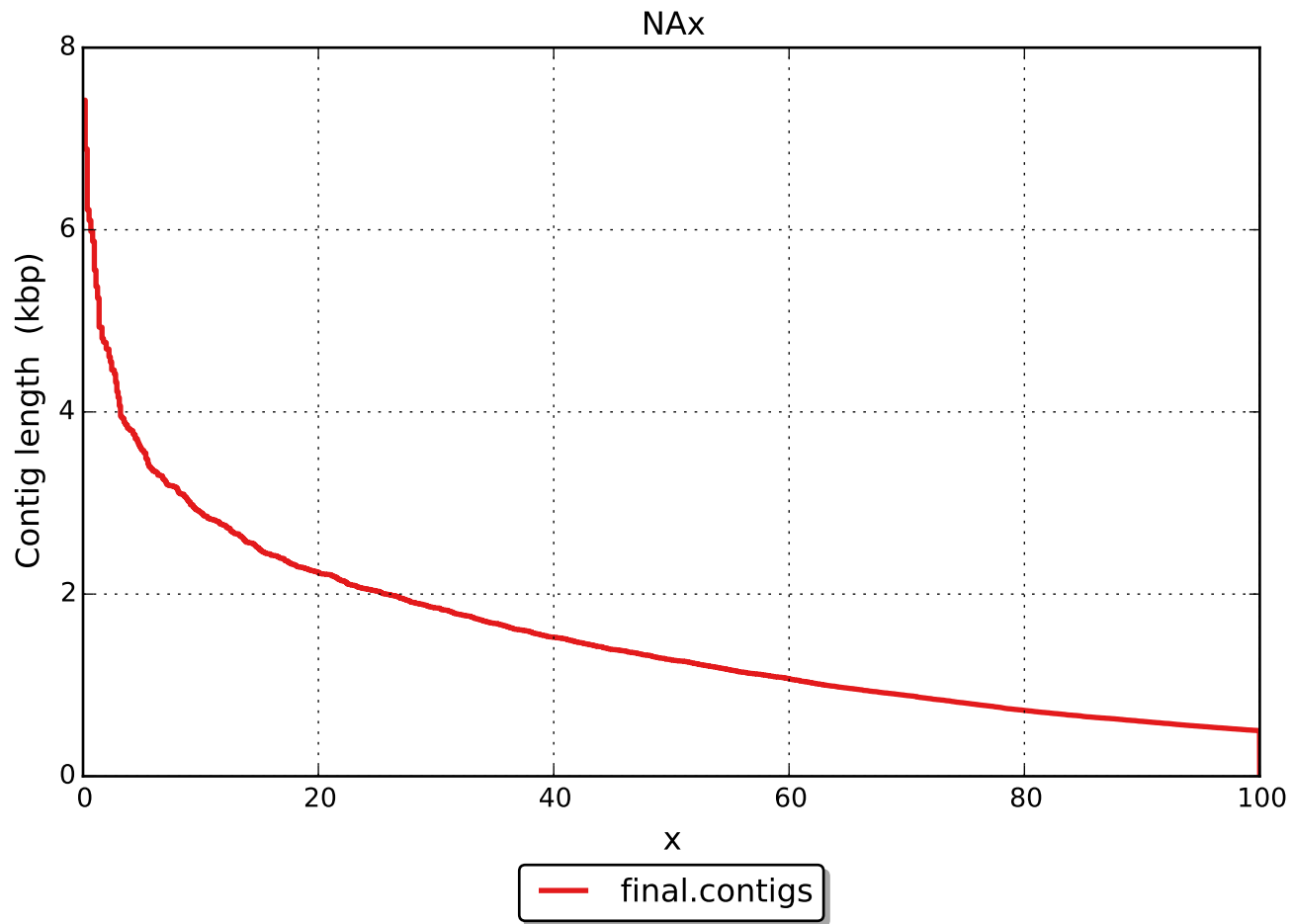


Misassemblies



Cumulative length (aligned contigs)





NGAx

