

Report

	final.contigs
# contigs (>= 1000 bp)	1407
# contigs (>= 5000 bp)	201
# contigs (>= 10000 bp)	18
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4282104
Total length (>= 5000 bp)	1393577
Total length (>= 10000 bp)	203284
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1946
Largest contig	15182
Total length	4661253
Reference length	4857432
GC (%)	52.17
Reference GC (%)	52.22
N50	3410
NG50	3257
N75	2000
NG75	1829
L50	431
LG50	461
L75	872
LG75	949
# misassemblies	3
# misassembled contigs	2
Misassembled contigs length	8223
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	92.586
Duplication ratio	1.036
# N's per 100 kbp	0.00
# mismatches per 100 kbp	521.71
# indels per 100 kbp	0.07
Largest alignment	15182
NA50	3410
NGA50	3257
NA75	1997
NGA75	1828
LA50	431
LGA50	461
LA75	873
LGA75	950

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

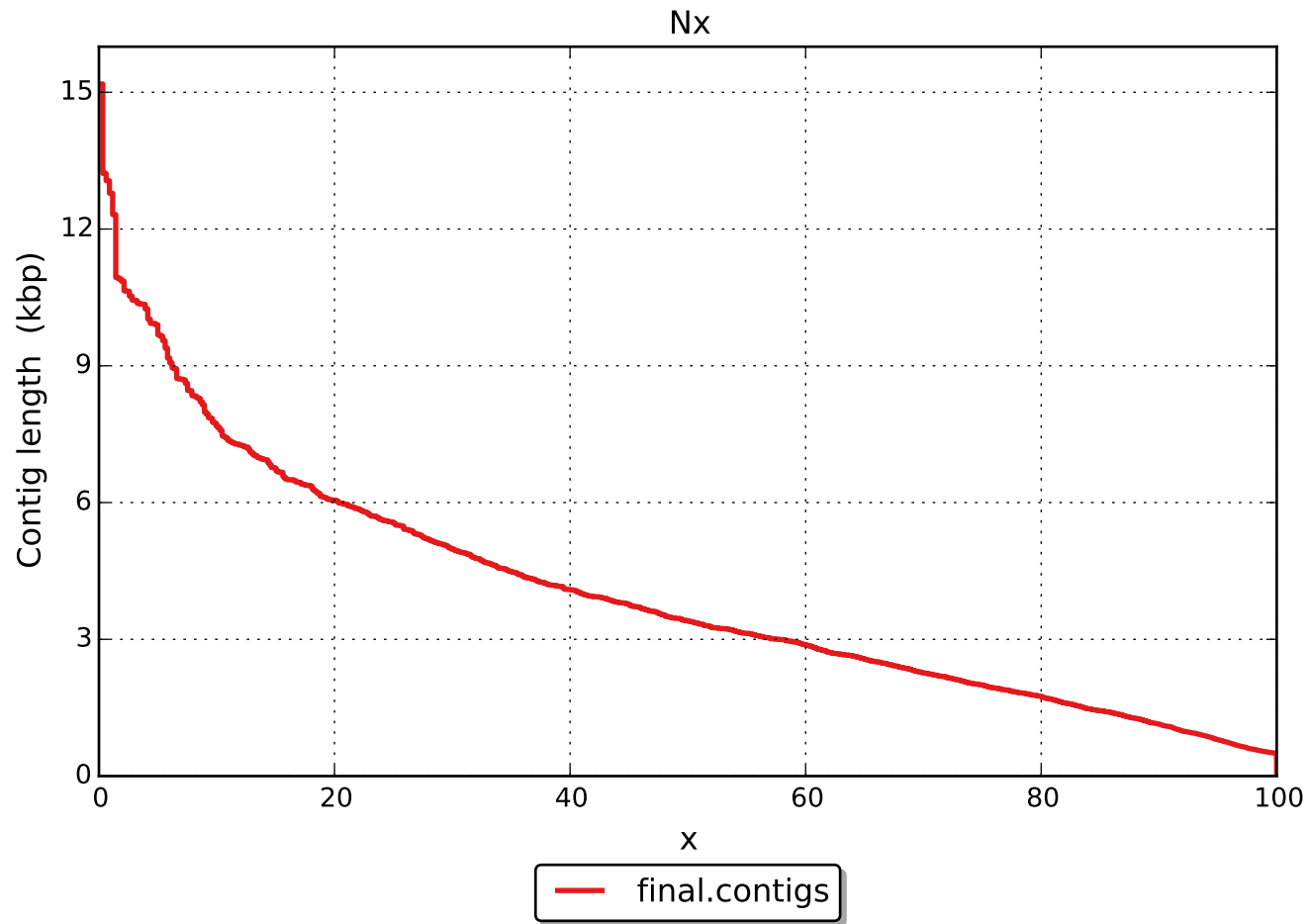
	final.contigs
# misassemblies	3
# relocations	3
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	8223
# local misassemblies	2
# mismatches	23463
# indels	3
# short indels	3
# long indels	0
Indels length	3

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).

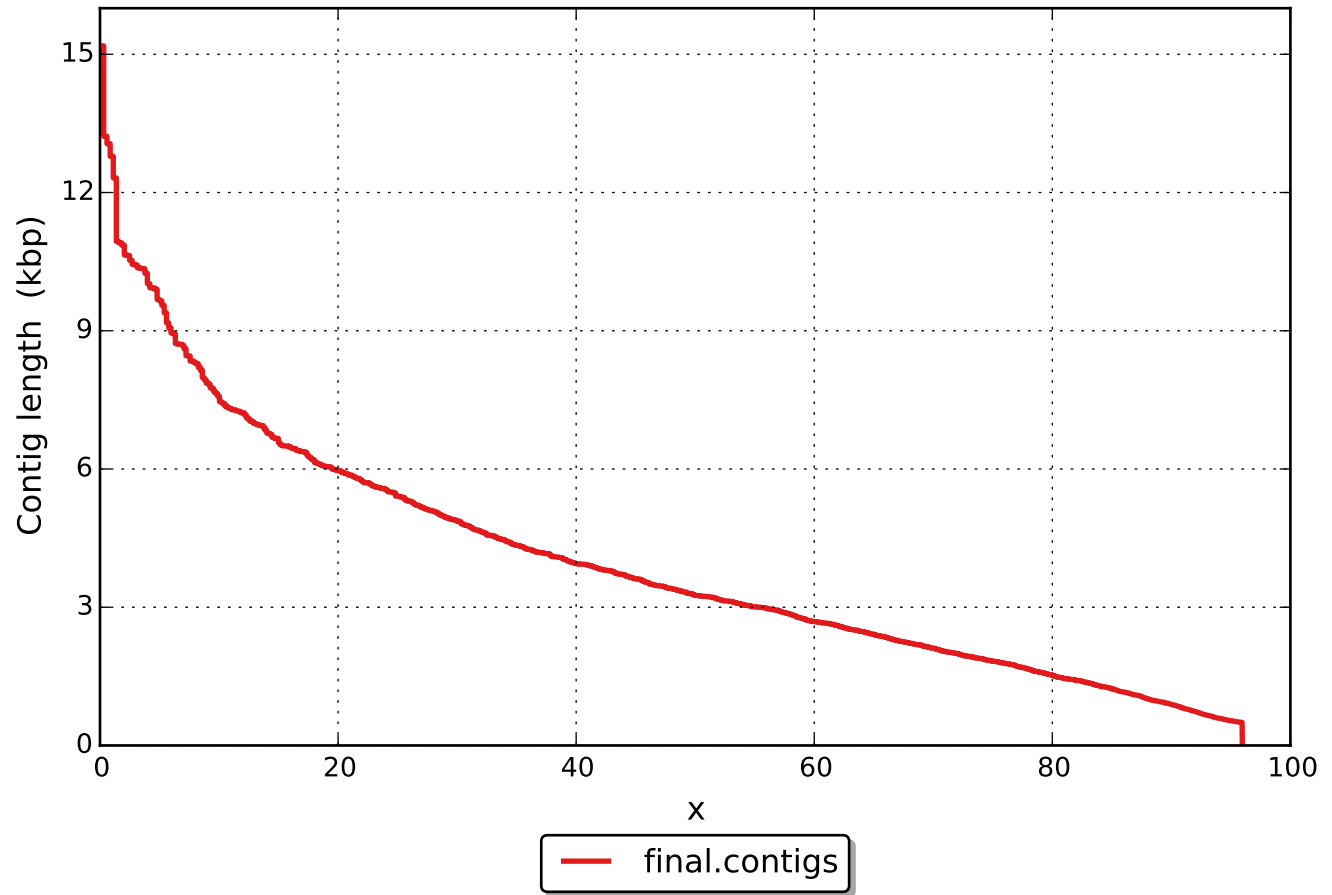
Unaligned report

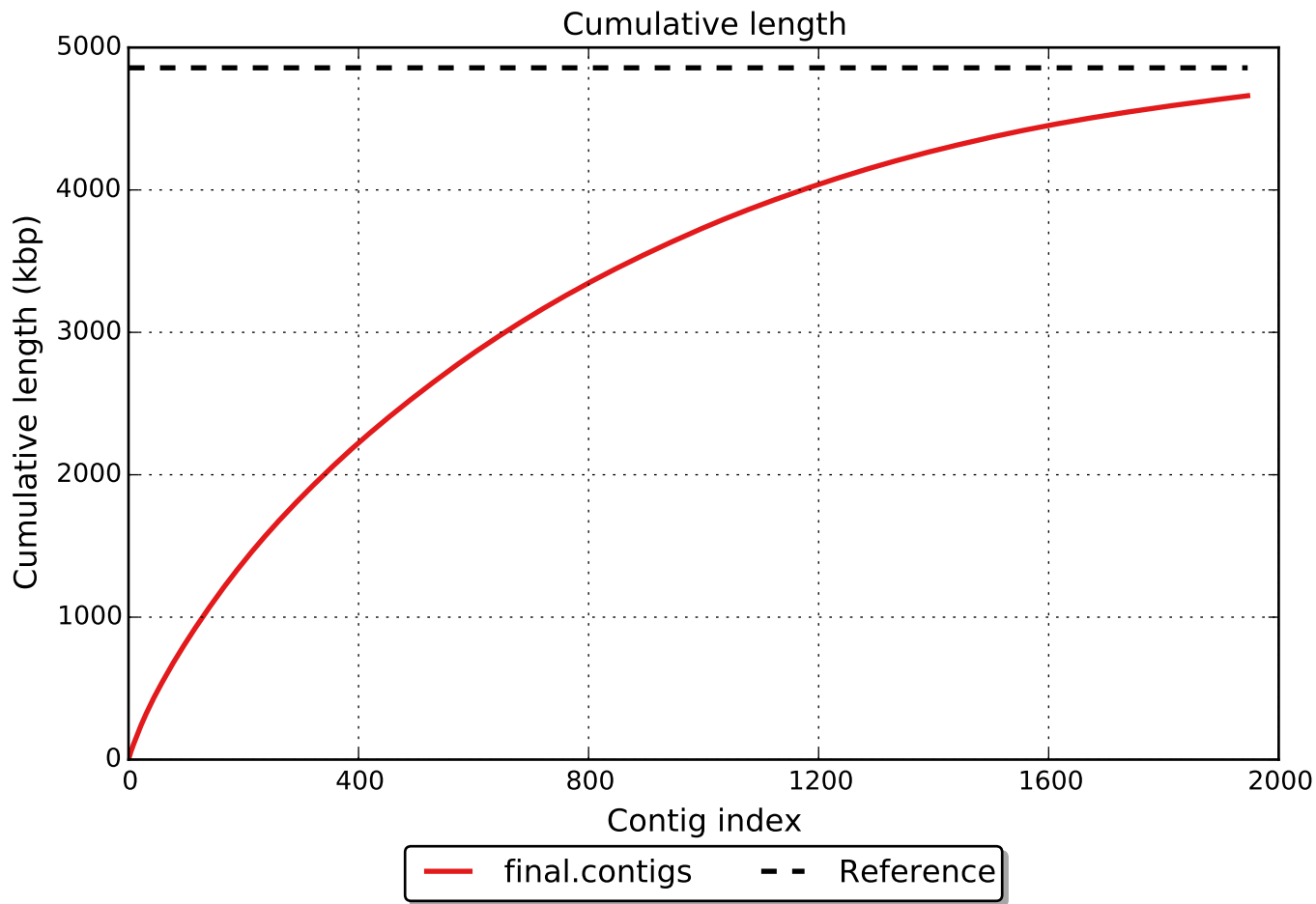
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

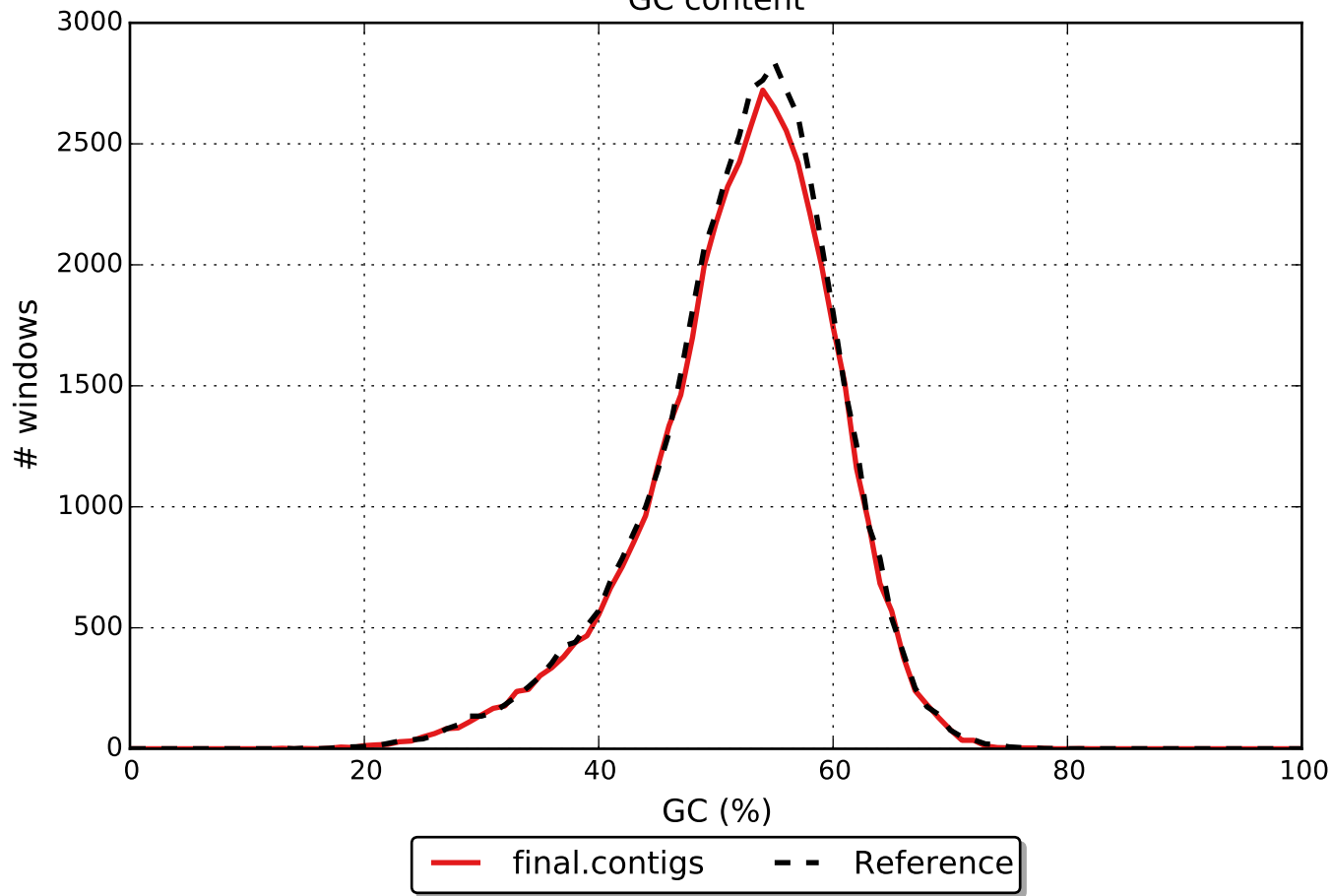


NGx

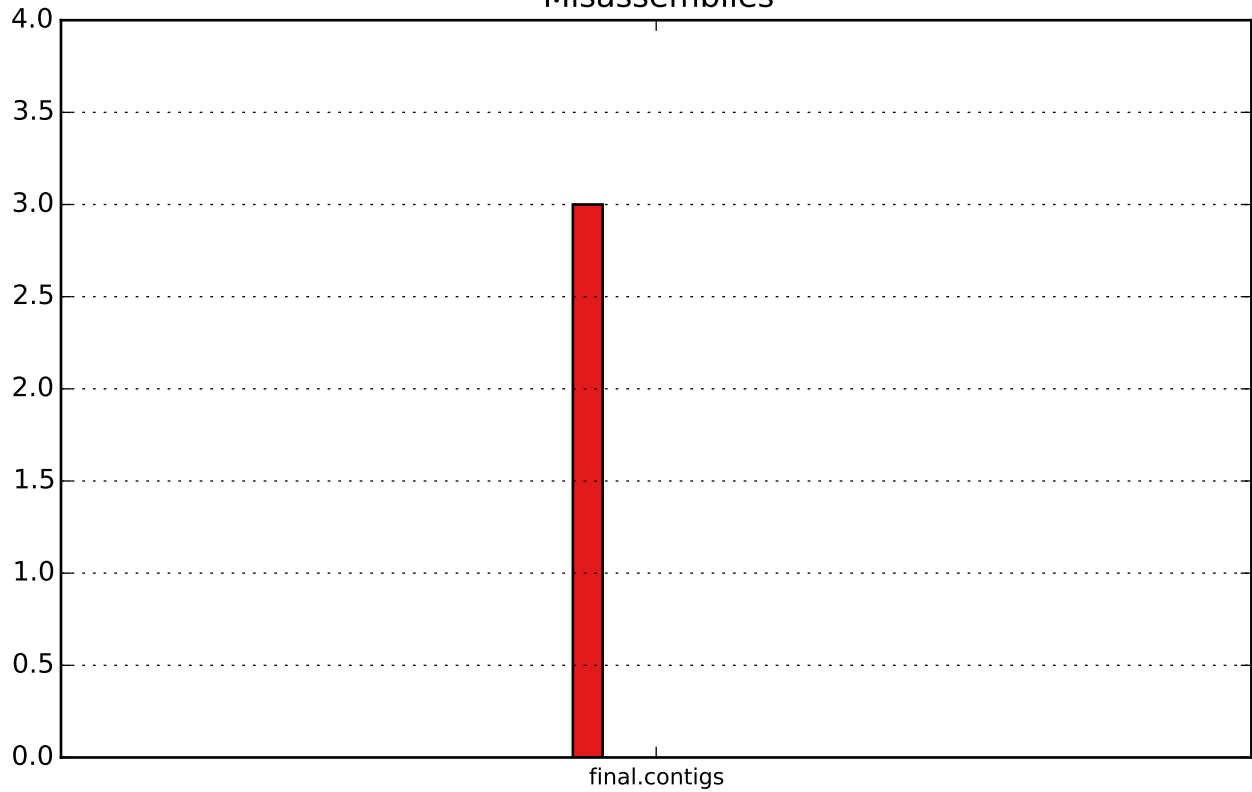




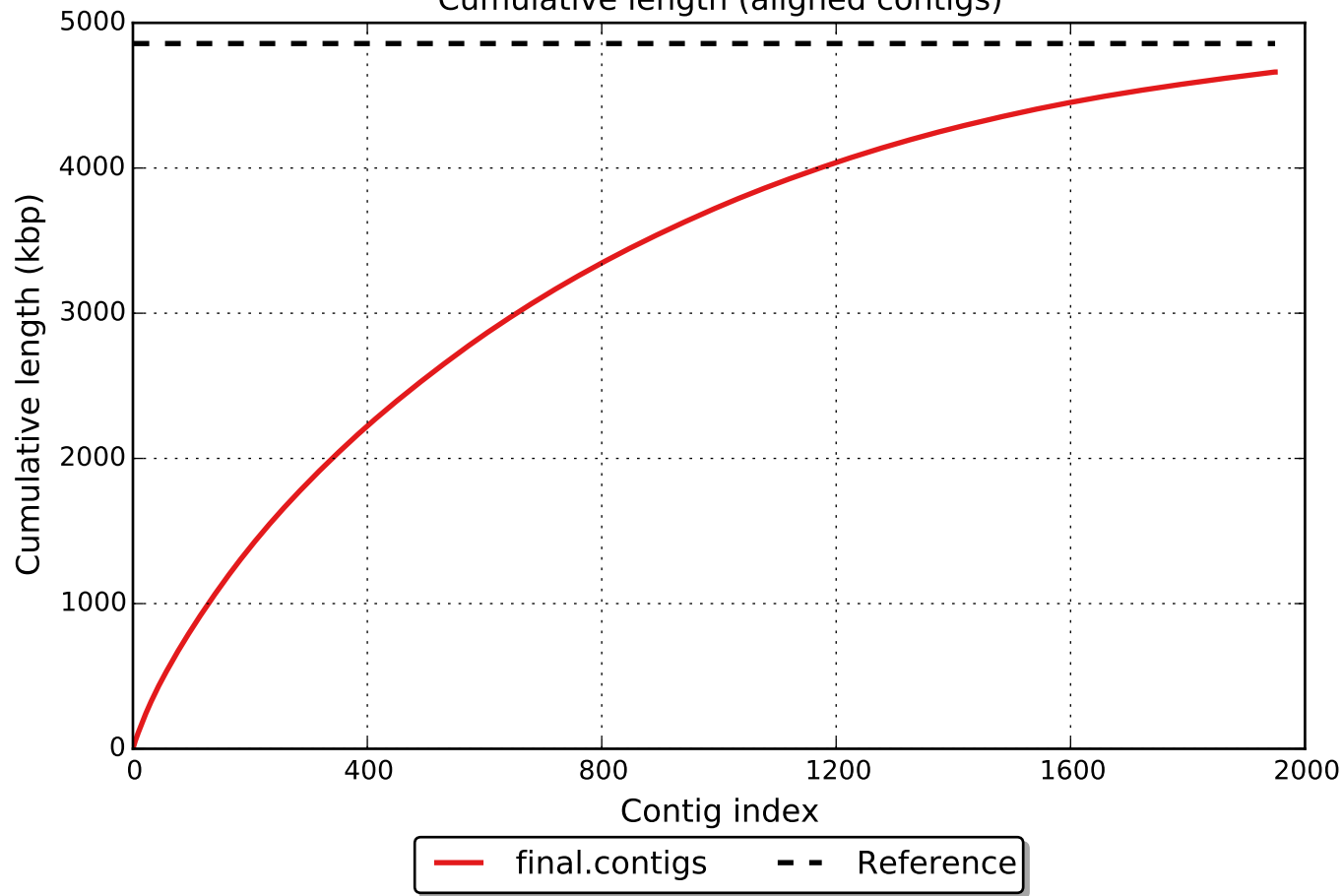
GC content

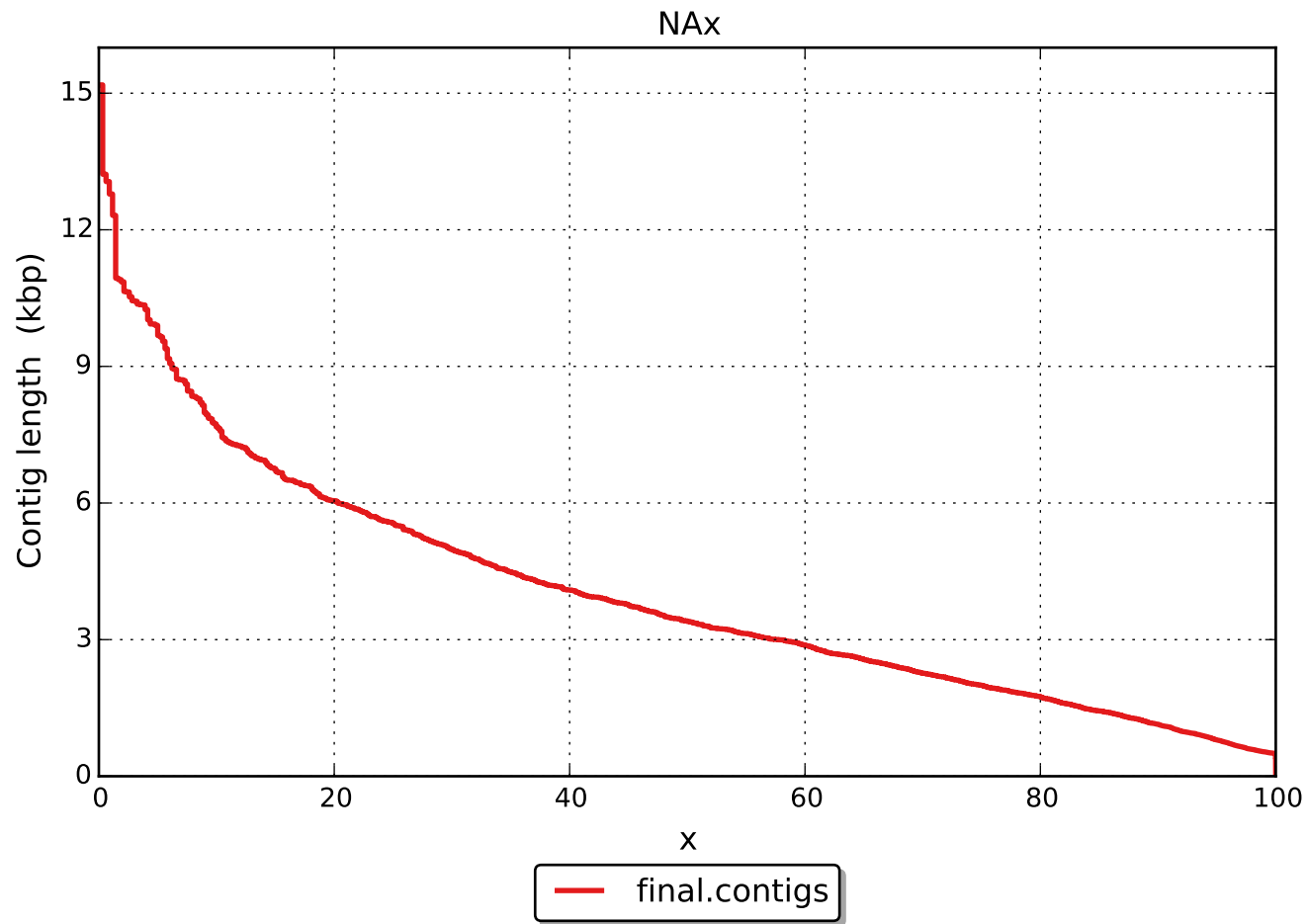


Misassemblies



Cumulative length (aligned contigs)





NGAx

