

Report

	final.contigs
# contigs (>= 1000 bp)	230
# contigs (>= 5000 bp)	175
# contigs (>= 10000 bp)	132
# contigs (>= 25000 bp)	68
# contigs (>= 50000 bp)	18
Total length (>= 1000 bp)	4559428
Total length (>= 5000 bp)	4402689
Total length (>= 10000 bp)	4083869
Total length (>= 25000 bp)	2978058
Total length (>= 50000 bp)	1233984
# contigs	245
Largest contig	111876
Total length	4570955
Reference length	4641652
GC (℥)	50.74
Reference GC (℥)	50.79
N50	33574
NG50	33519
N75	19585
NG75	19123
L50	44
LG50	45
L75	89
LG75	91
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	98.164
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.53
# indels per 100 kbp	0.00
Largest alignment	111876
NA50	33574
NGA50	33519
NA75	19585
NGA75	19123
LA50	44
LGA50	45
LA75	89
LGA75	91

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

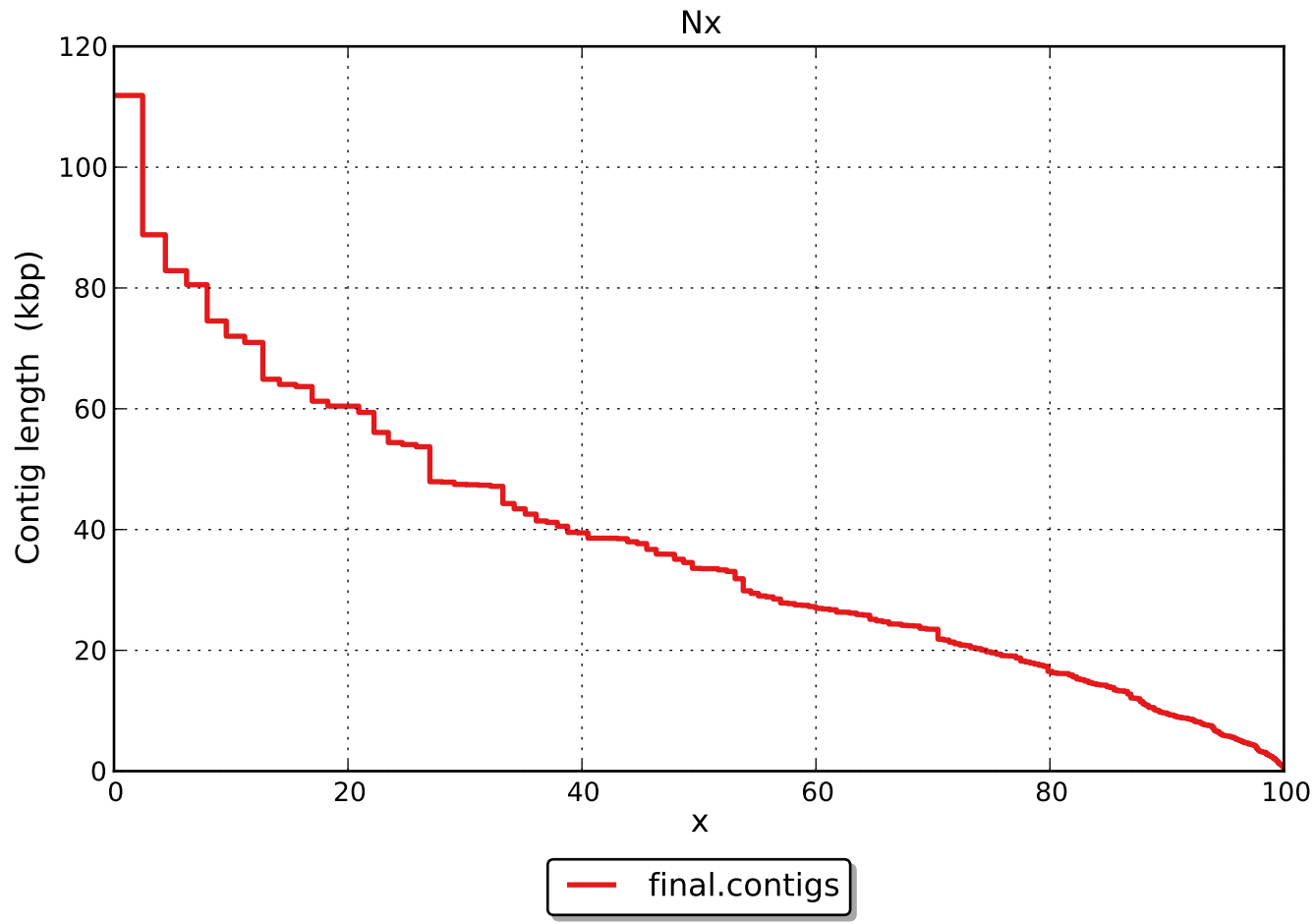
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	24
# indels	0
# short indels	0
# long indels	0
Indels length	0

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).

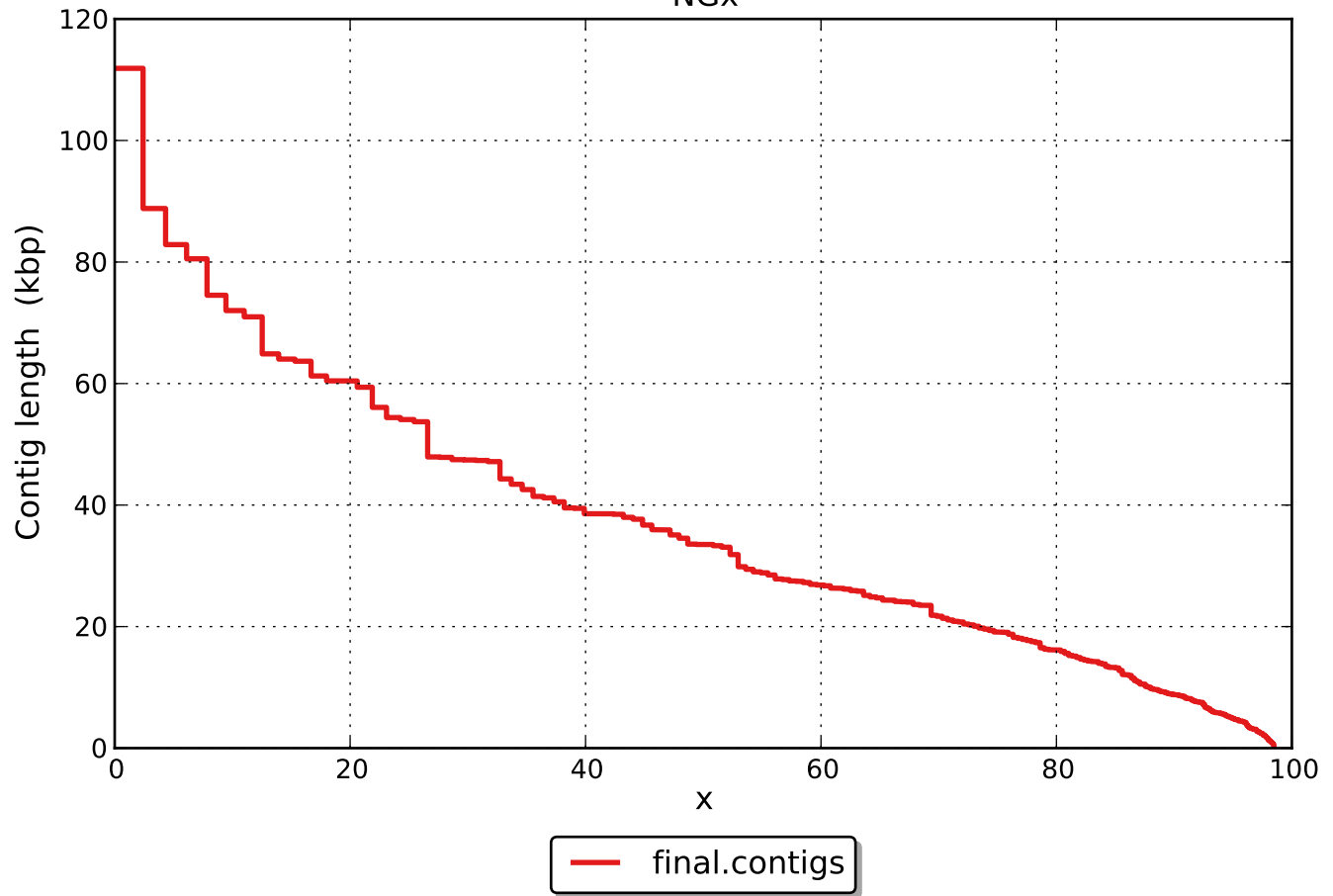
Unaligned report

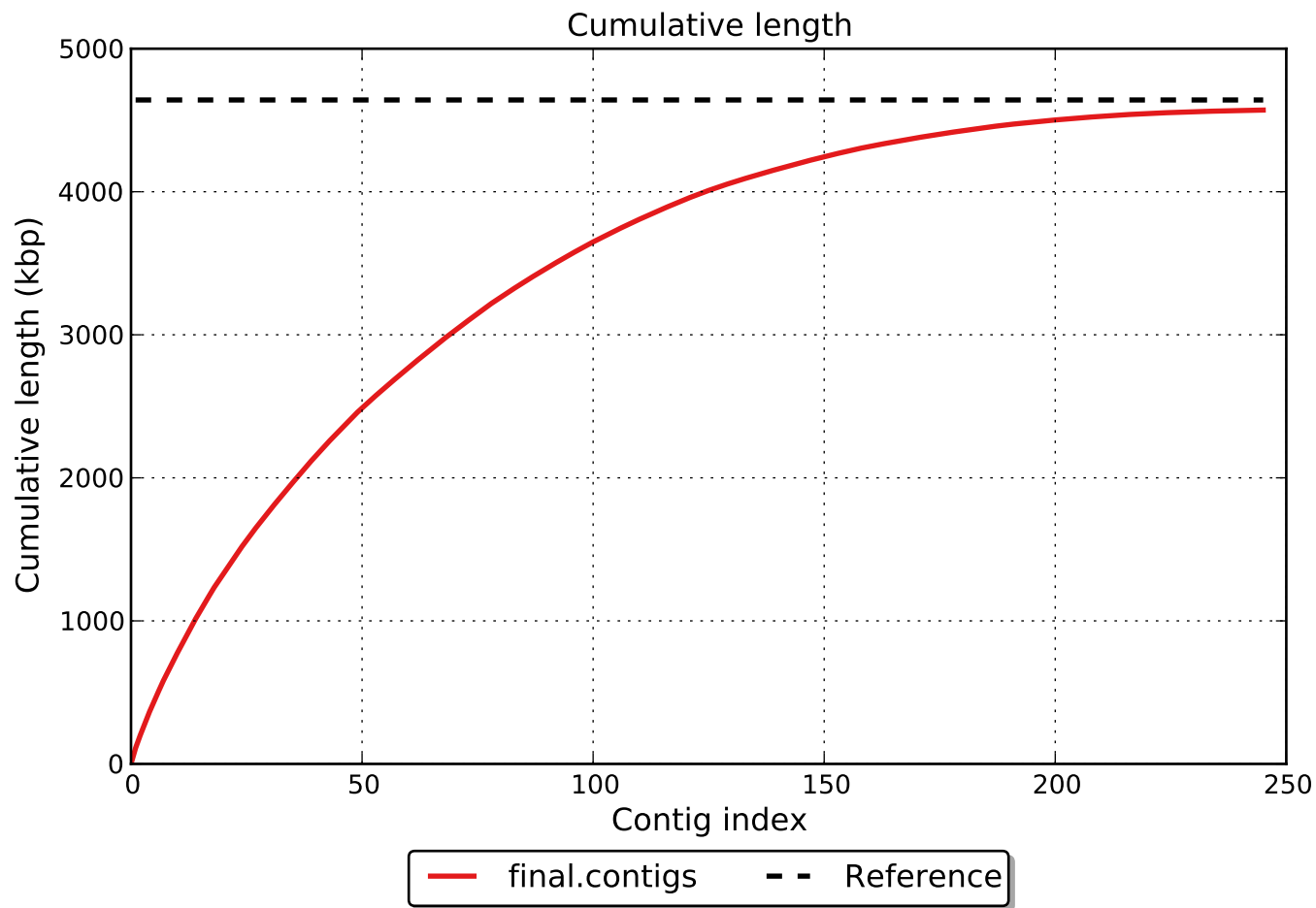
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

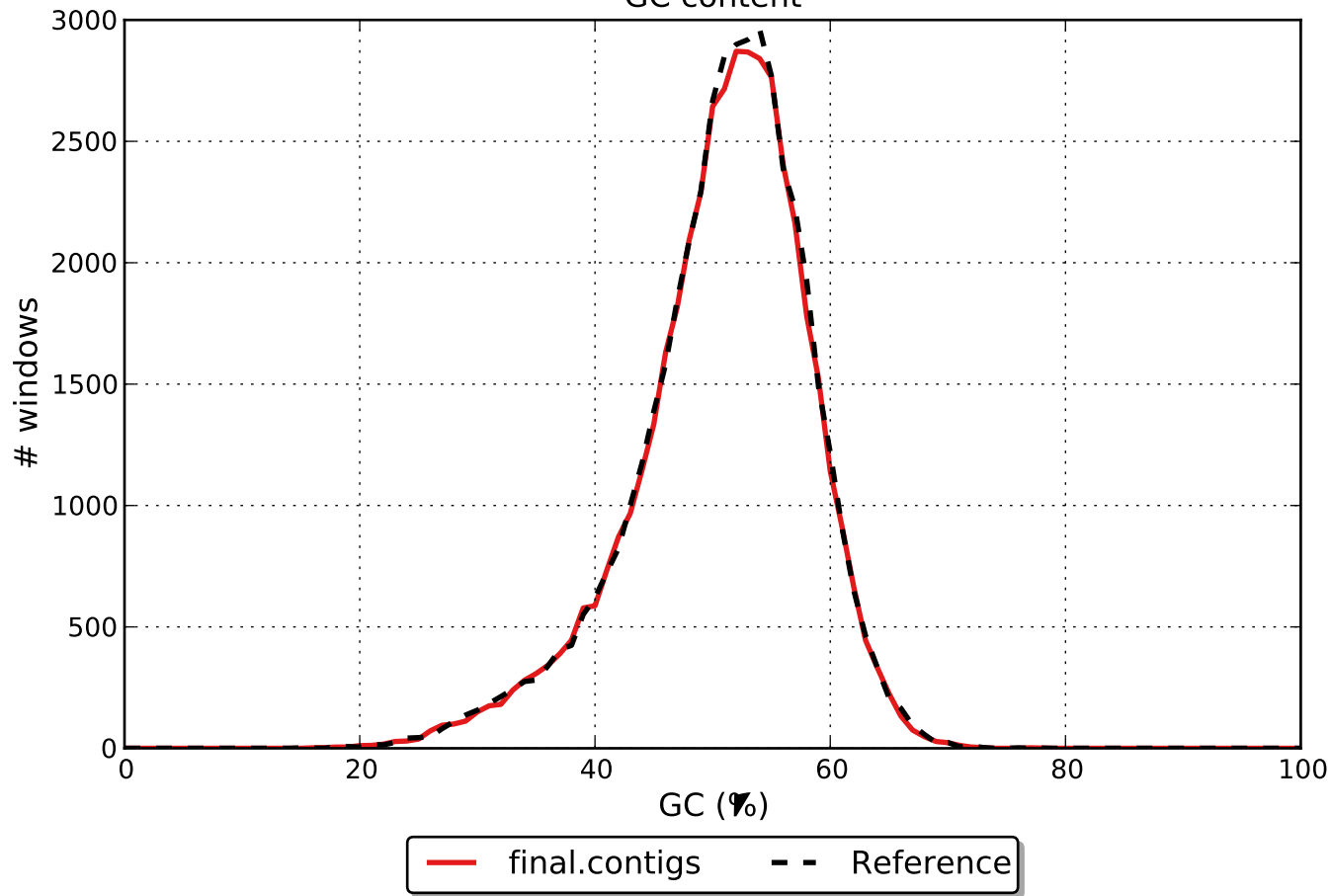


NGx

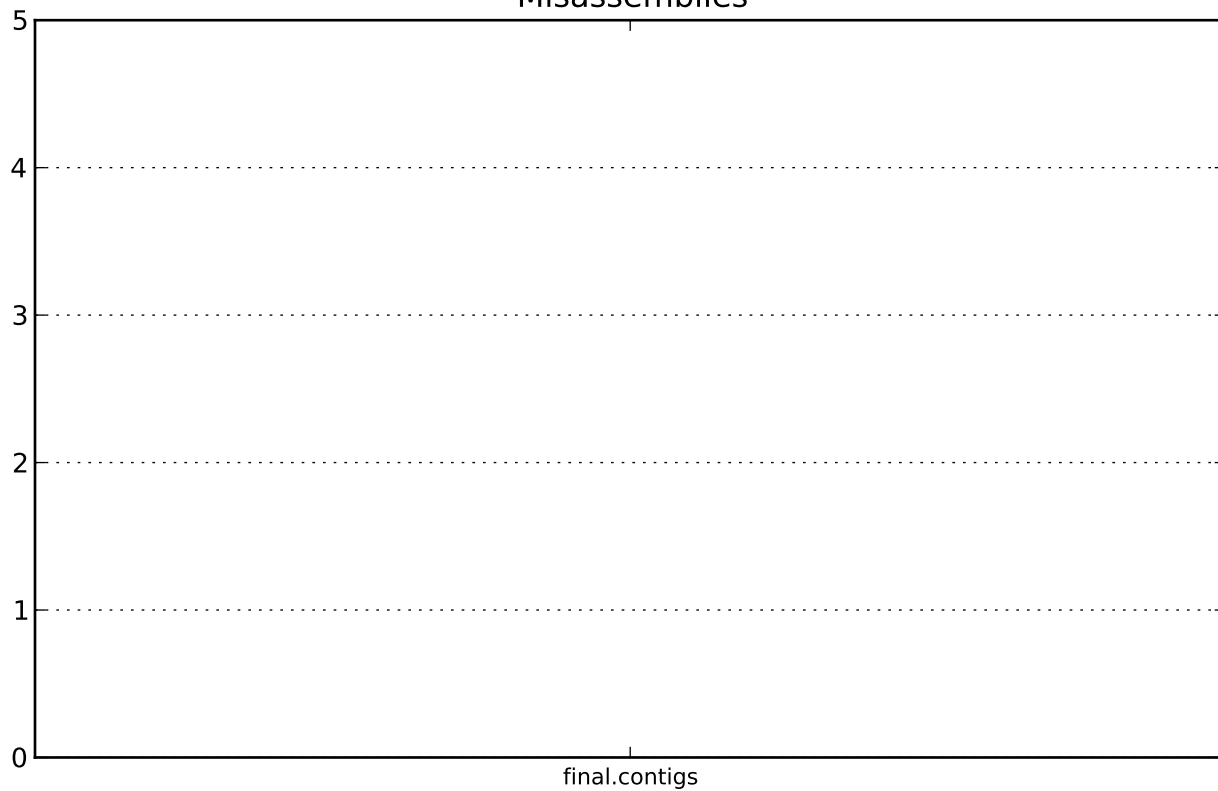




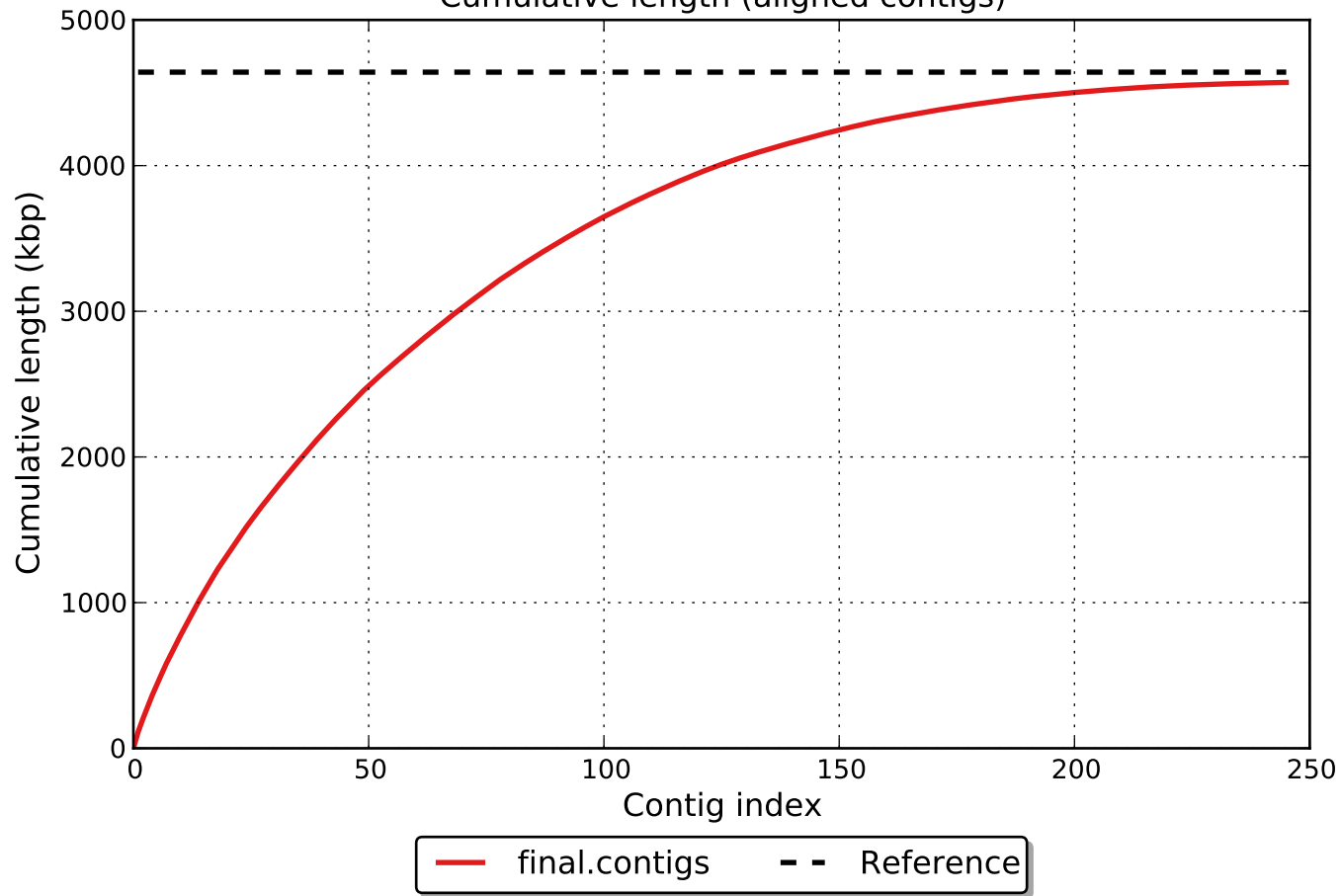
GC content



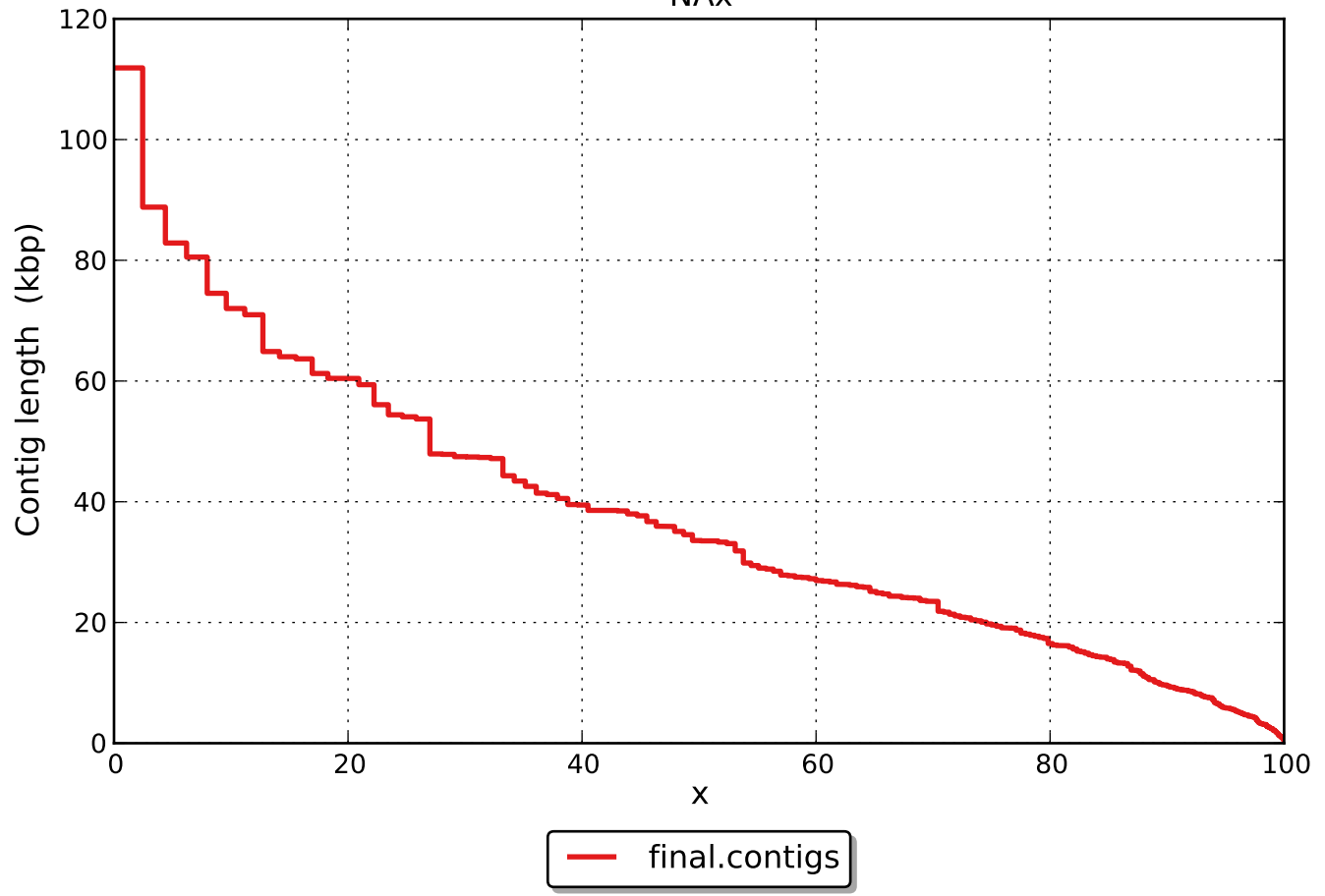
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

