

Report

	final.contigs
# contigs (>= 0 bp)	71838
# contigs (>= 1000 bp)	1462
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	29195863
Total length (>= 1000 bp)	2036512
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	8312
Largest contig	4275
Total length	6384066
Reference length	4641652
GC (%)	50.69
Reference GC (%)	50.79
N50	751
NG50	929
N75	567
NG75	705
L50	2803
LG50	1757
L75	5290
LG75	3201
# misassemblies	12
# misassembled contigs	12
Misassembled contigs length	10609
# local misassemblies	16
# unaligned contigs	1162 + 133 part
Unaligned length	656044
Genome fraction (%)	89.735
Duplication ratio	1.375
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1218.00
# indels per 100 kbp	1.37
Largest alignment	4275
NA50	747
NGA50	927
NA75	550
NGA75	697
LA50	2812
LGA50	1762
LA75	5341
LGA75	3213

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	12
# relocations	4
# translocations	0
# inversions	8
# misassembled contigs	12
Misassembled contigs length	10609
# local misassemblies	16
# mismatches	50732
# indels	57
# short indels	57
# long indels	0
Indels length	58

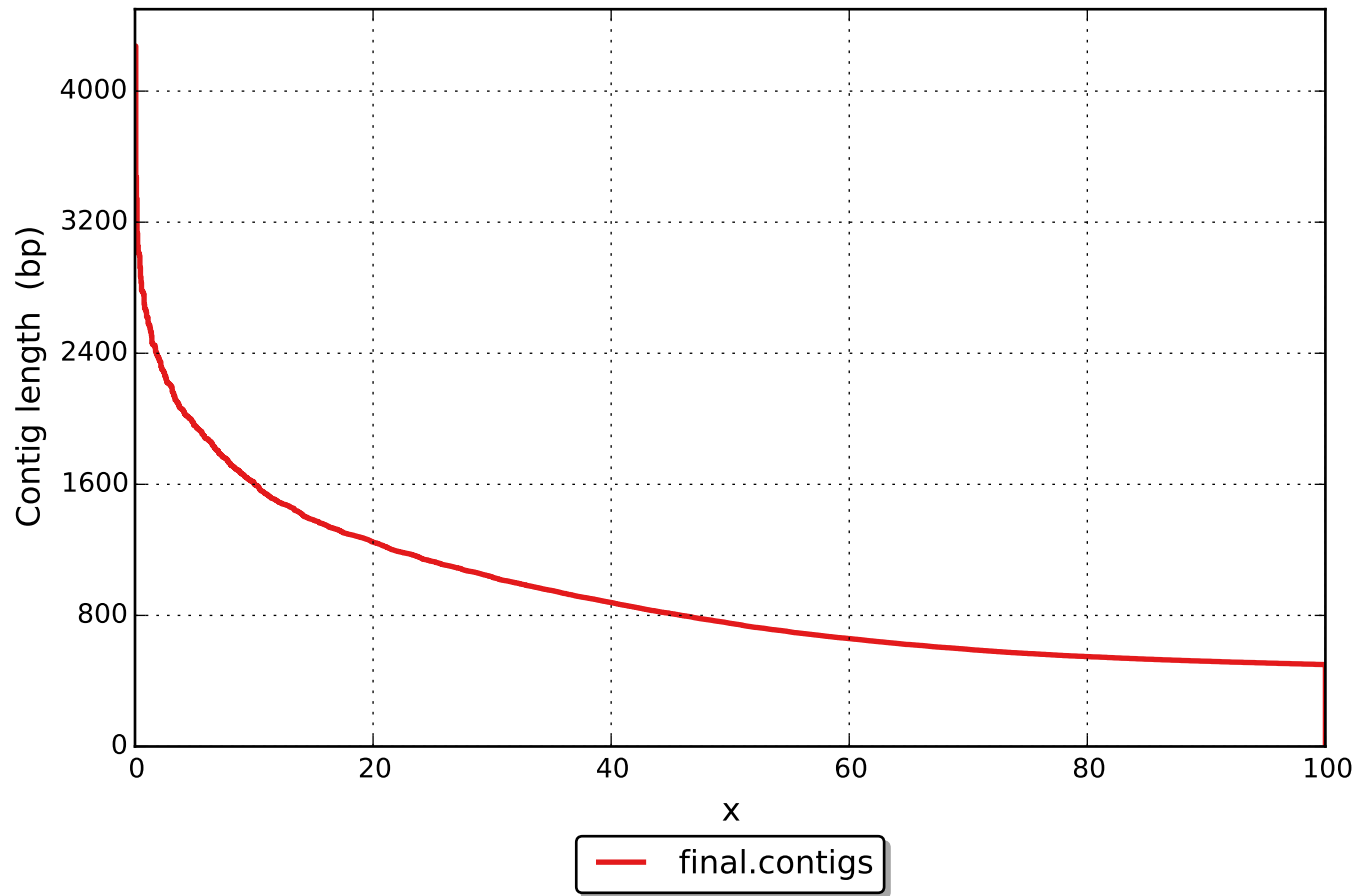
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

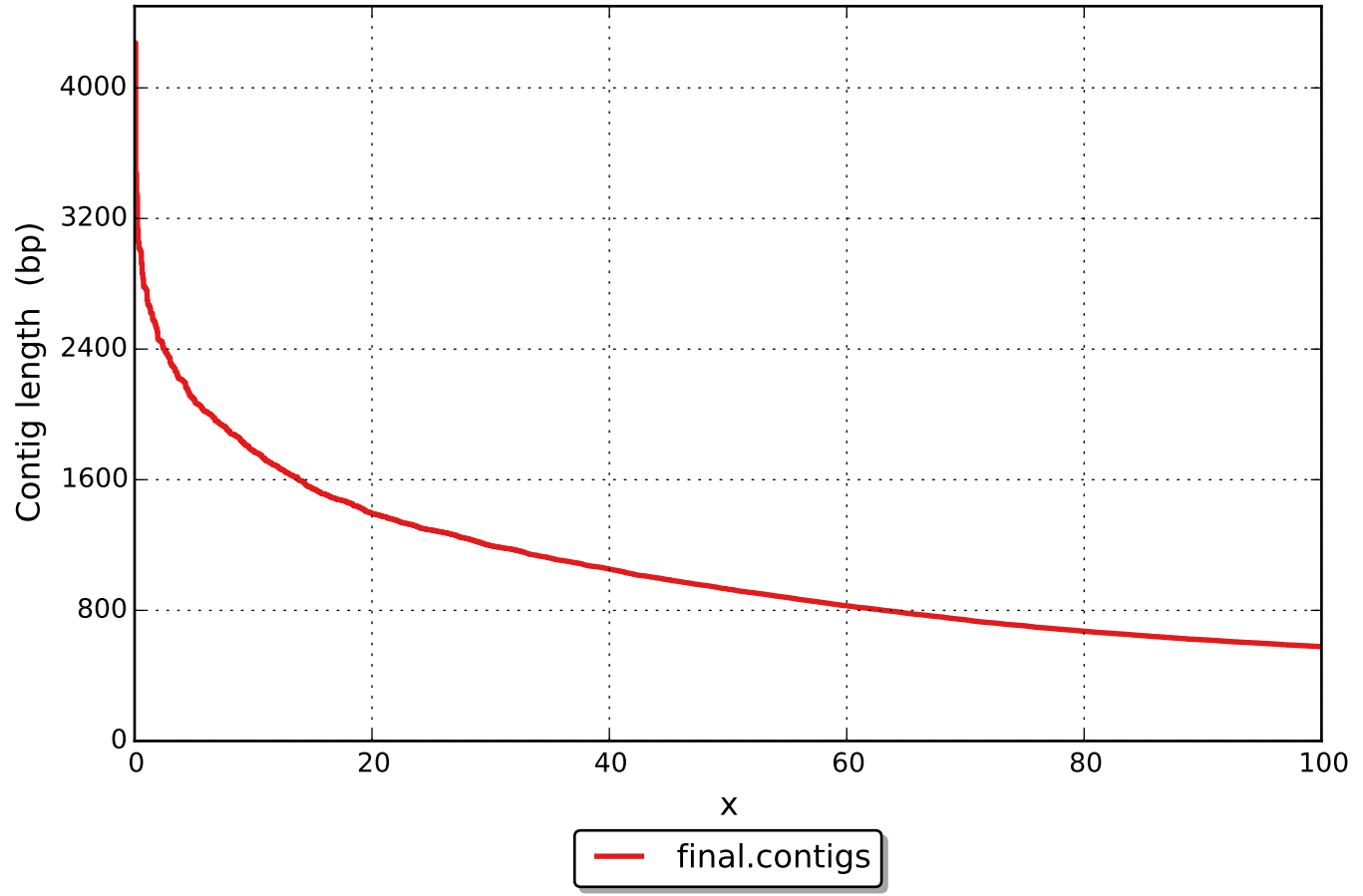
	final.contigs
# fully unaligned contigs	1162
Fully unaligned length	636246
# partially unaligned contigs	133
# with misassembly	0
# both parts are significant	0
Partially unaligned length	19798
# N's	0

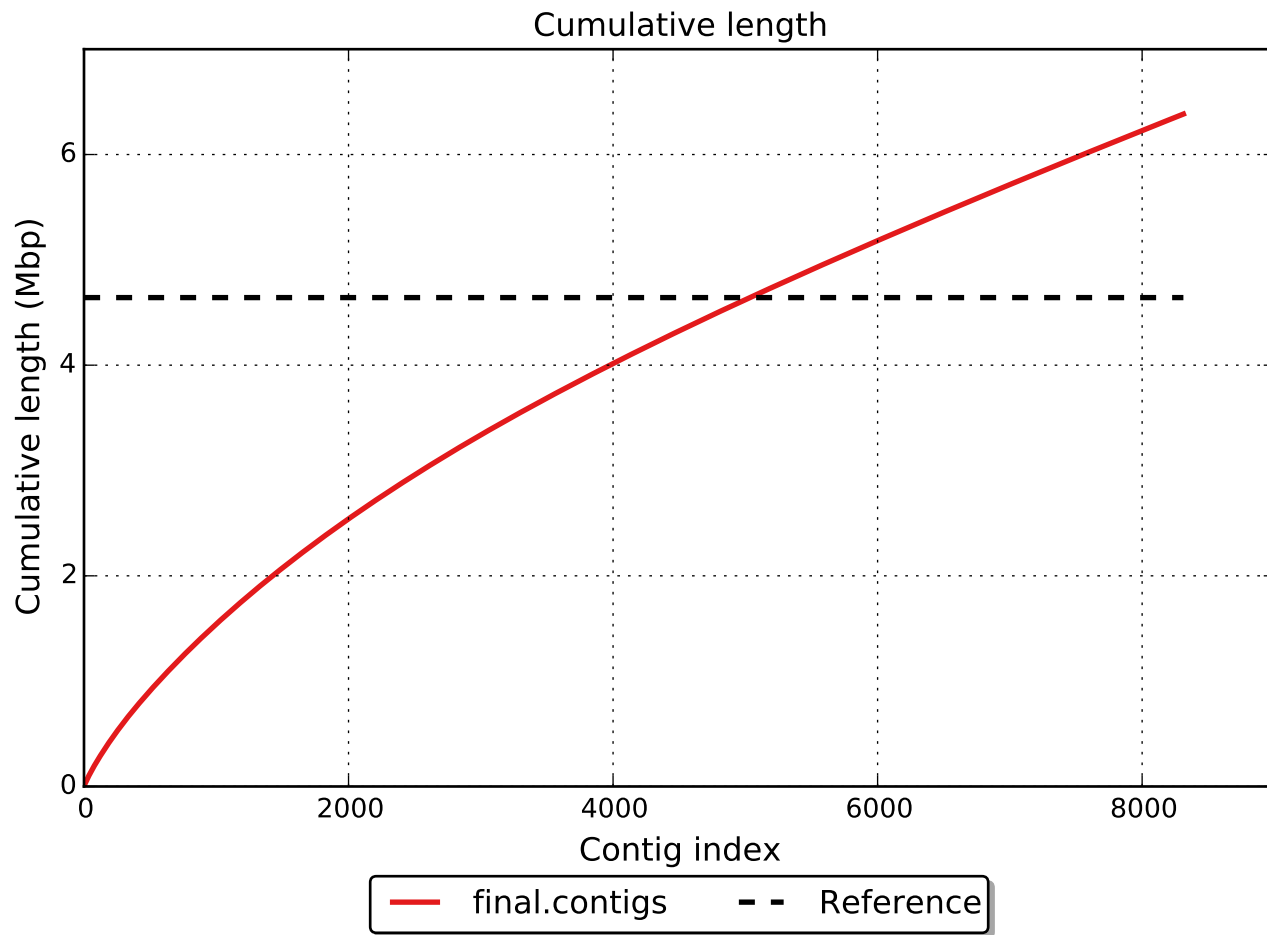
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

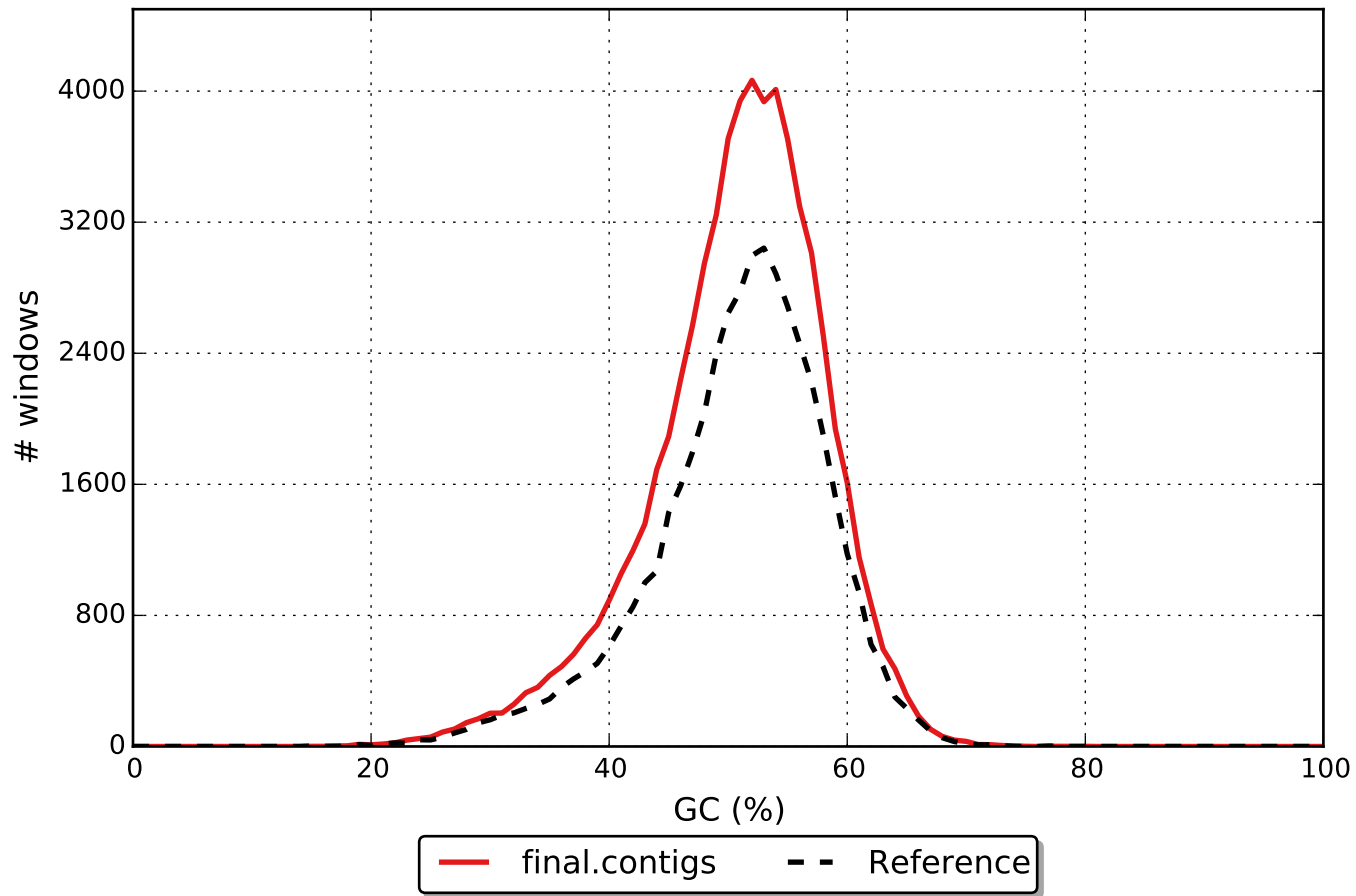


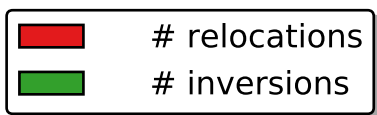
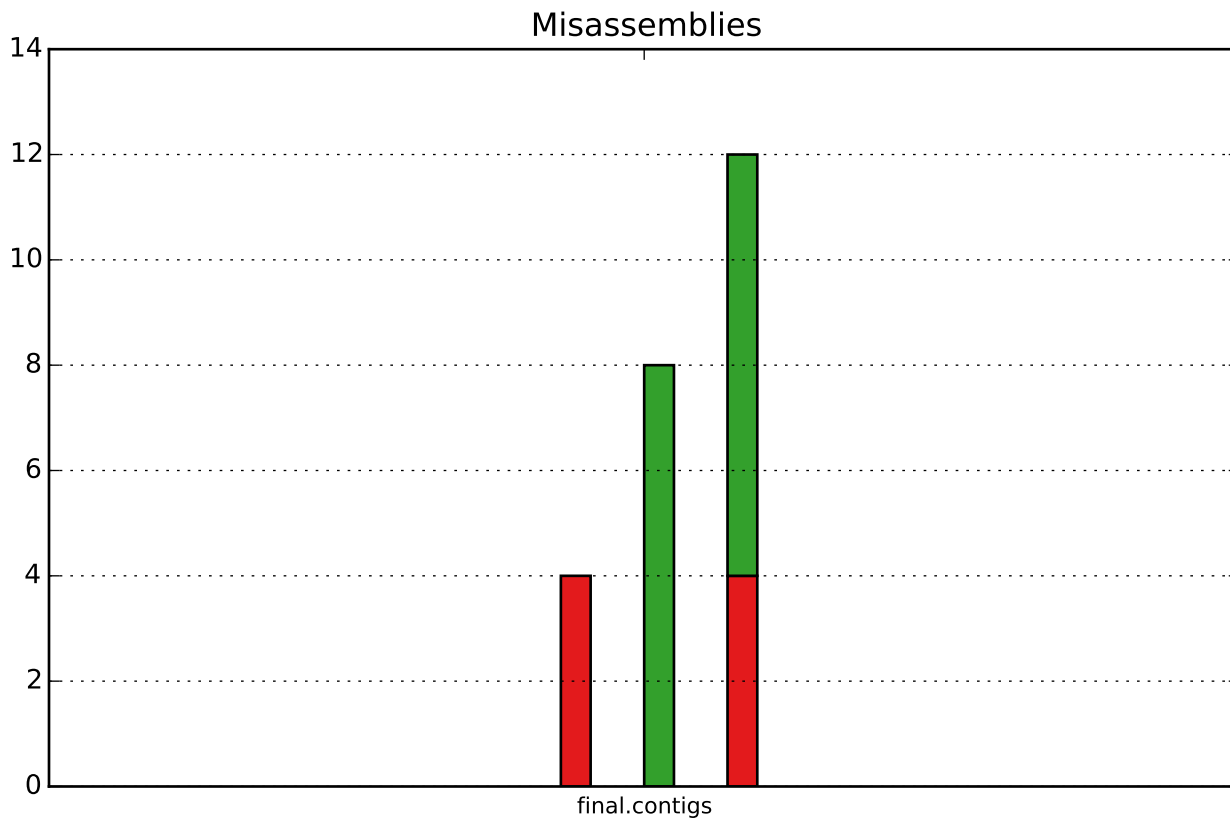
NGx

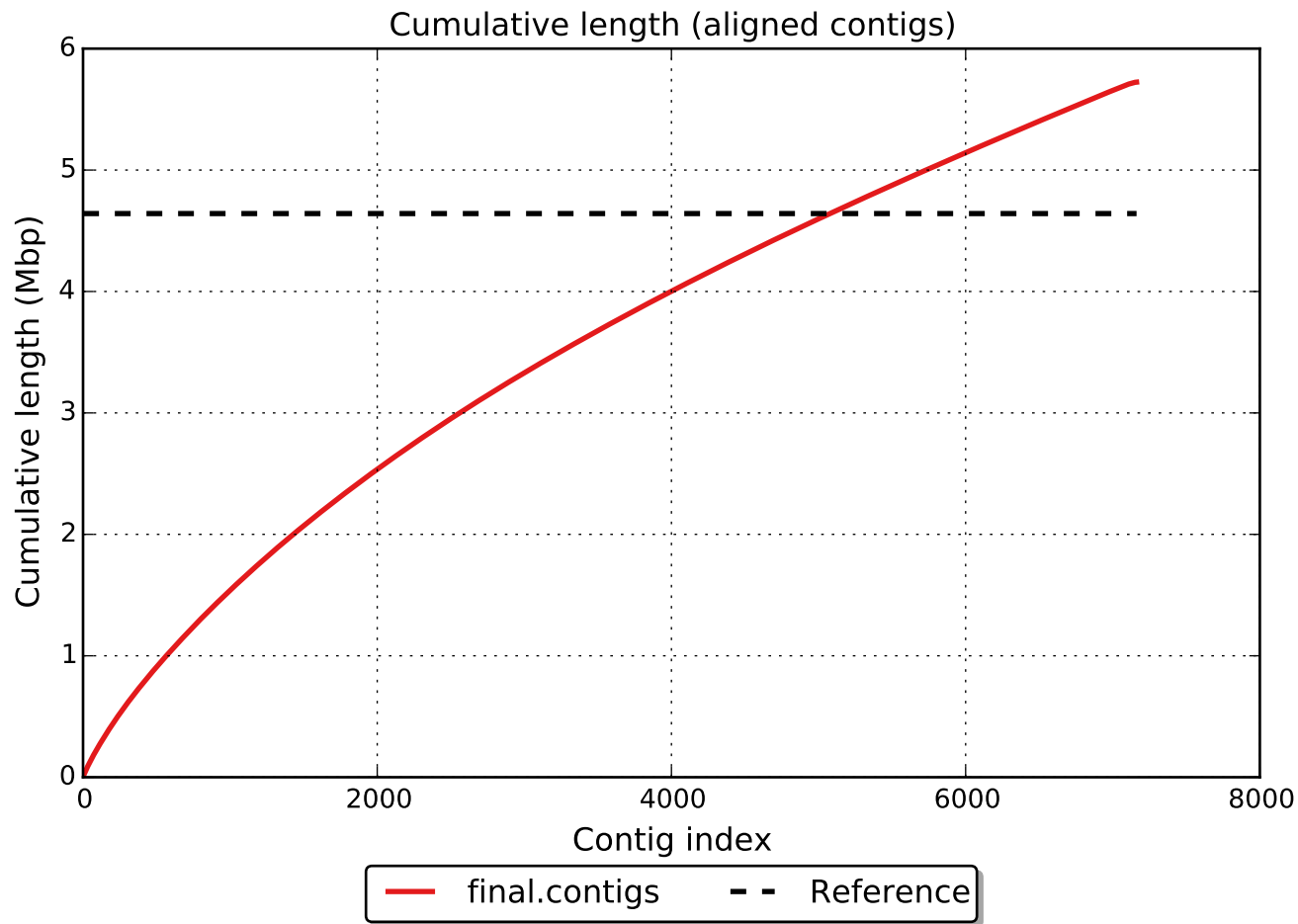




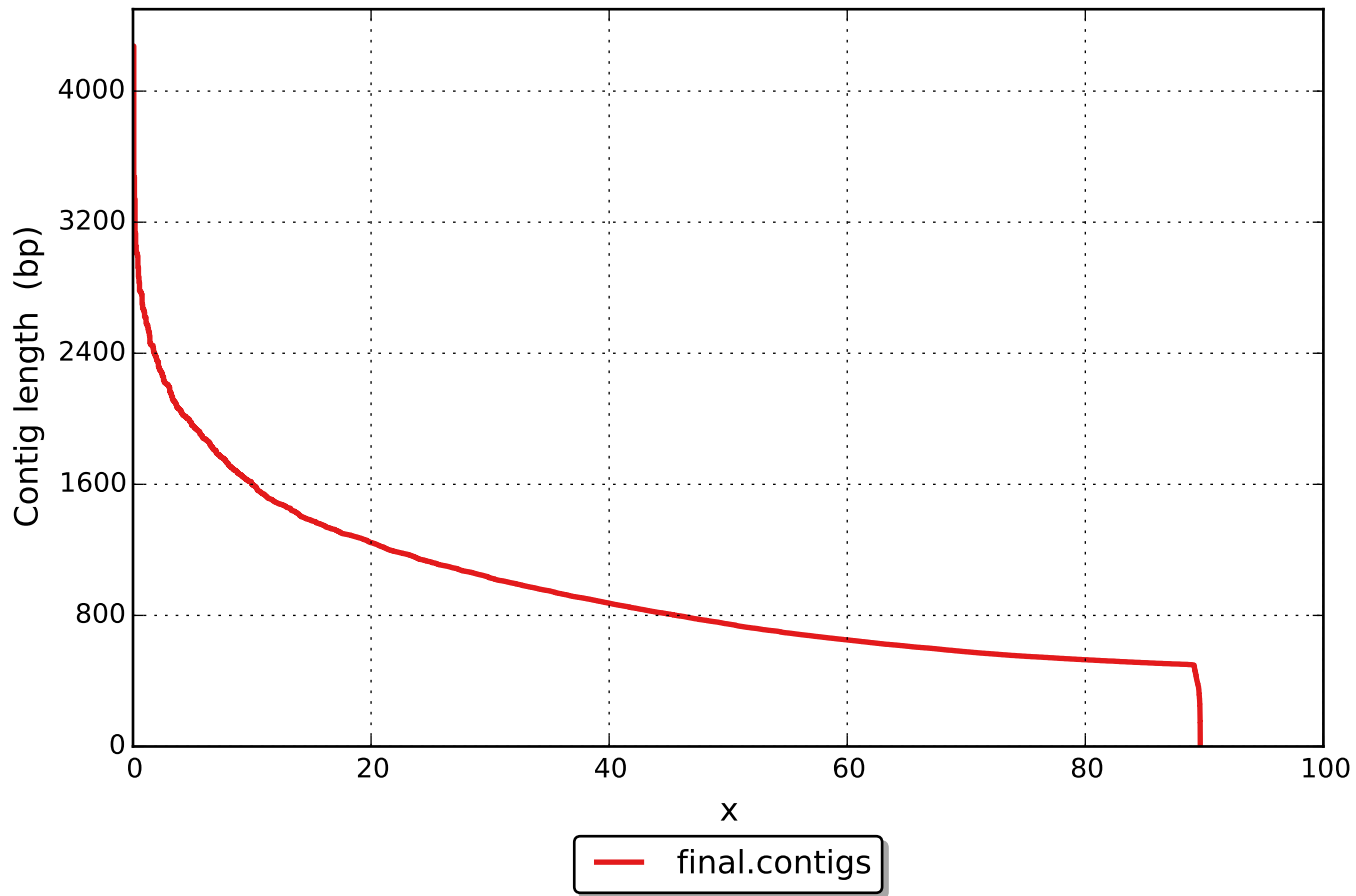
GC content







NAx



NGAx

