

Report

	final.contigs
# contigs (>= 0 bp)	167
# contigs (>= 1000 bp)	136
# contigs (>= 5000 bp)	113
# contigs (>= 10000 bp)	96
# contigs (>= 25000 bp)	67
# contigs (>= 50000 bp)	31
Total length (>= 0 bp)	4590177
Total length (>= 1000 bp)	4574633
Total length (>= 5000 bp)	4513731
Total length (>= 10000 bp)	4378048
Total length (>= 25000 bp)	3899194
Total length (>= 50000 bp)	2653753
# contigs	150
Largest contig	203782
Total length	4584254
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	55771
NG50	55771
N75	32926
NG75	32748
L50	25
LG50	25
L75	51
LG75	52
# misassemblies	7
# misassembled contigs	7
Misassembled contigs length	378190
# local misassemblies	4
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.465
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	21.40
# indels per 100 kbp	0.33
Largest alignment	203782
NA50	55641
NGA50	55641
NA75	31775
NGA75	31267
LA50	26
LGA50	26
LA75	53
LGA75	54

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	7
# relocations	7
# translocations	0
# inversions	0
# misassembled contigs	7
Misassembled contigs length	378190
# local misassemblies	4
# mismatches	978
# indels	15
# short indels	10
# long indels	5
Indels length	92

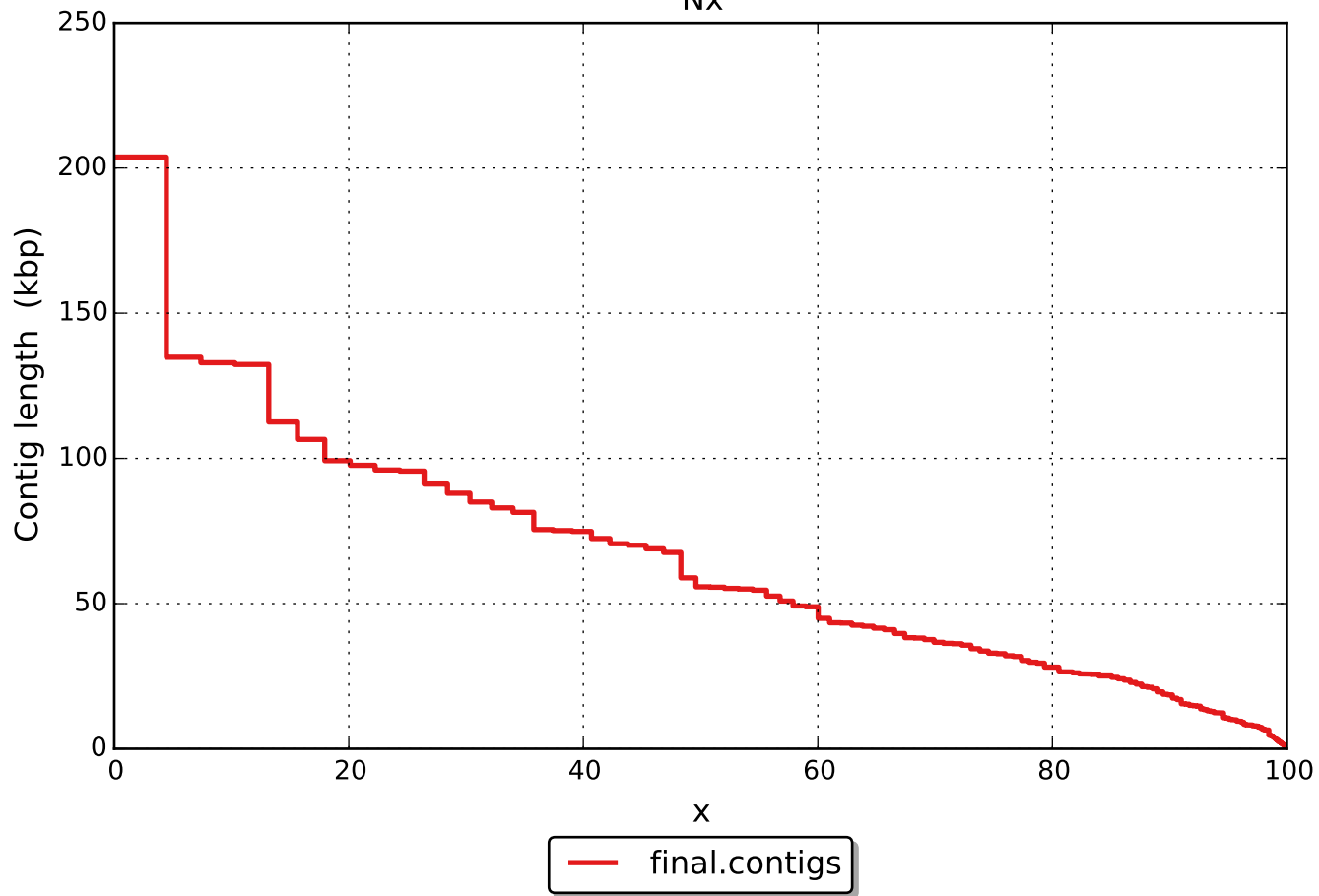
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

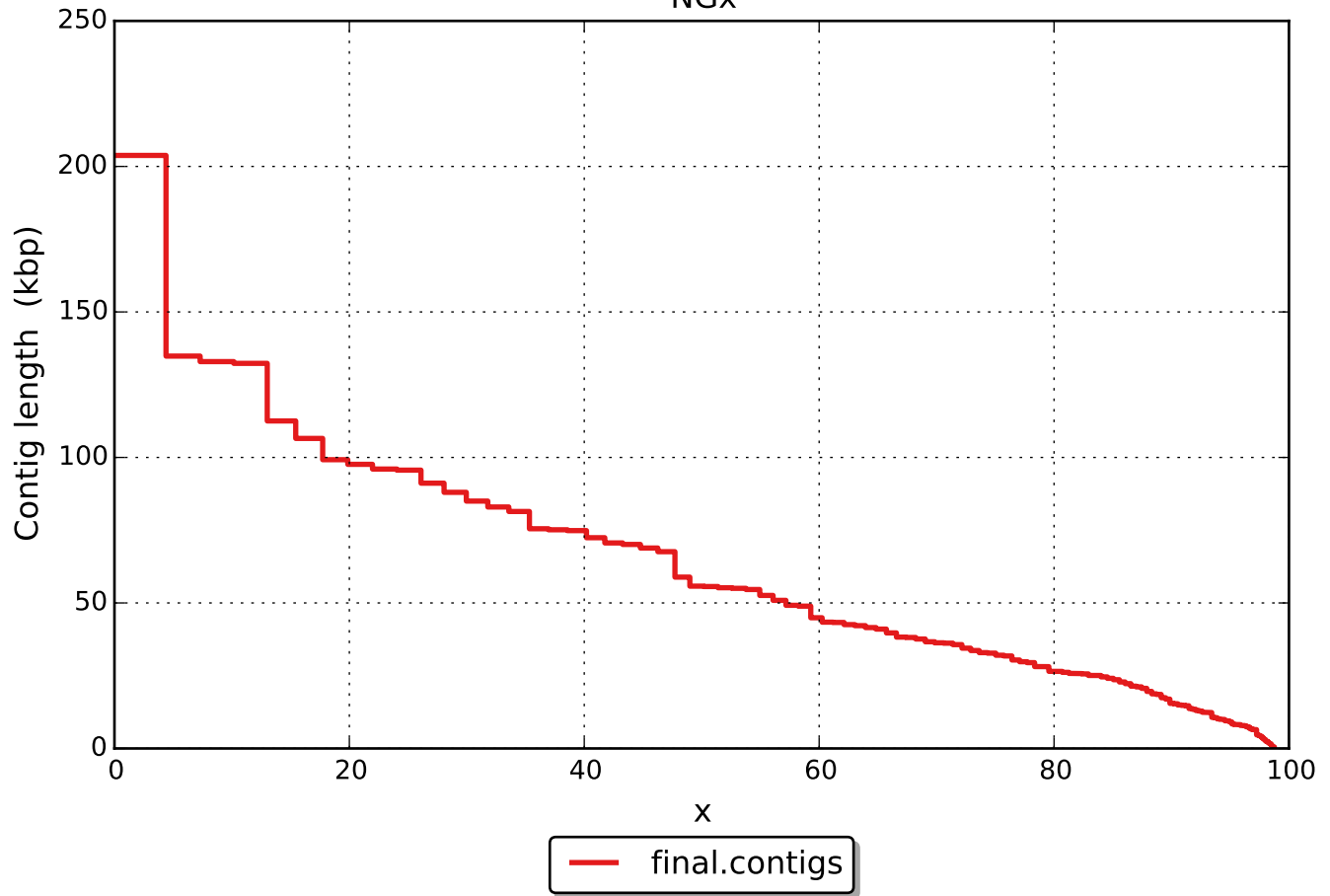
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

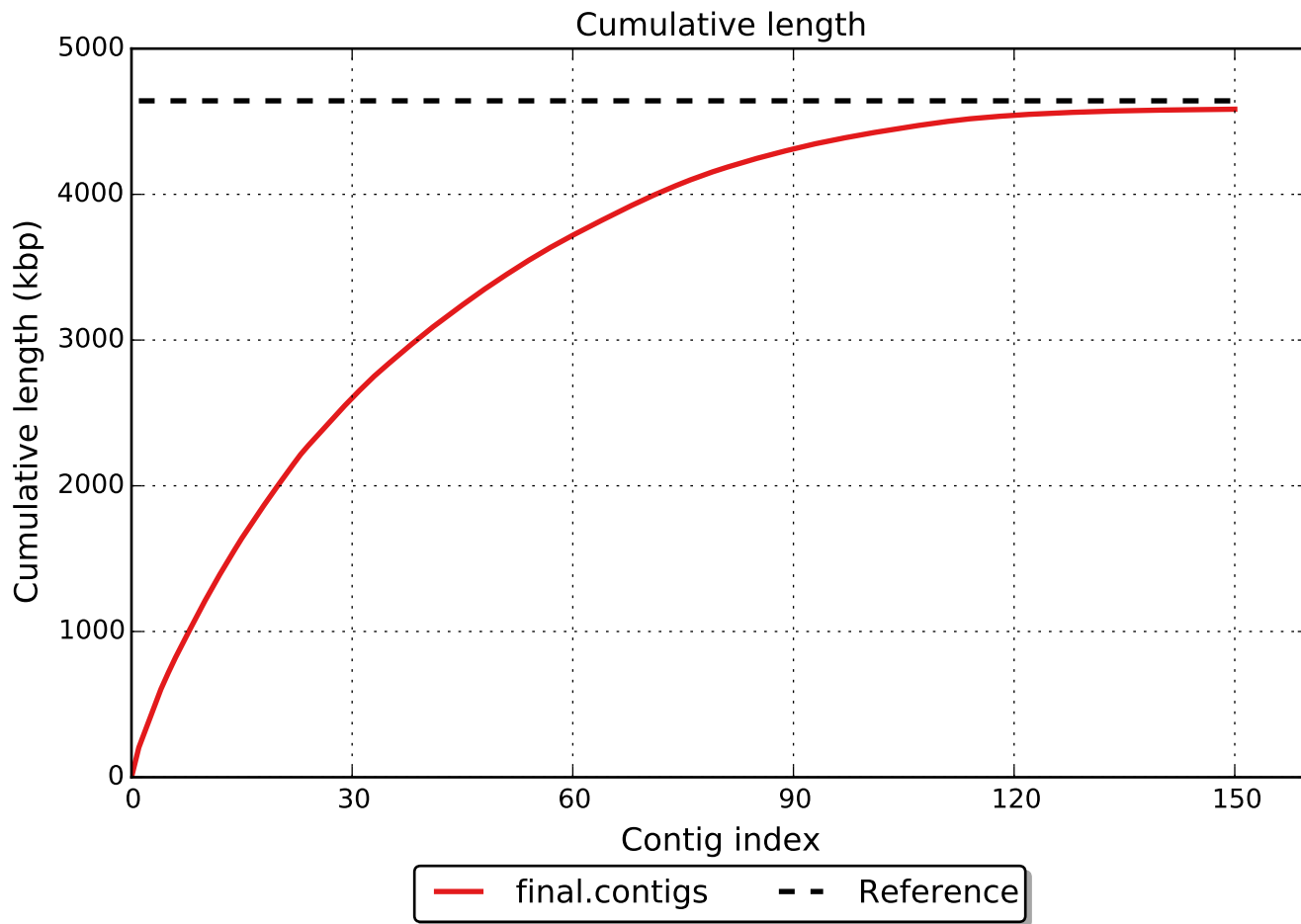
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

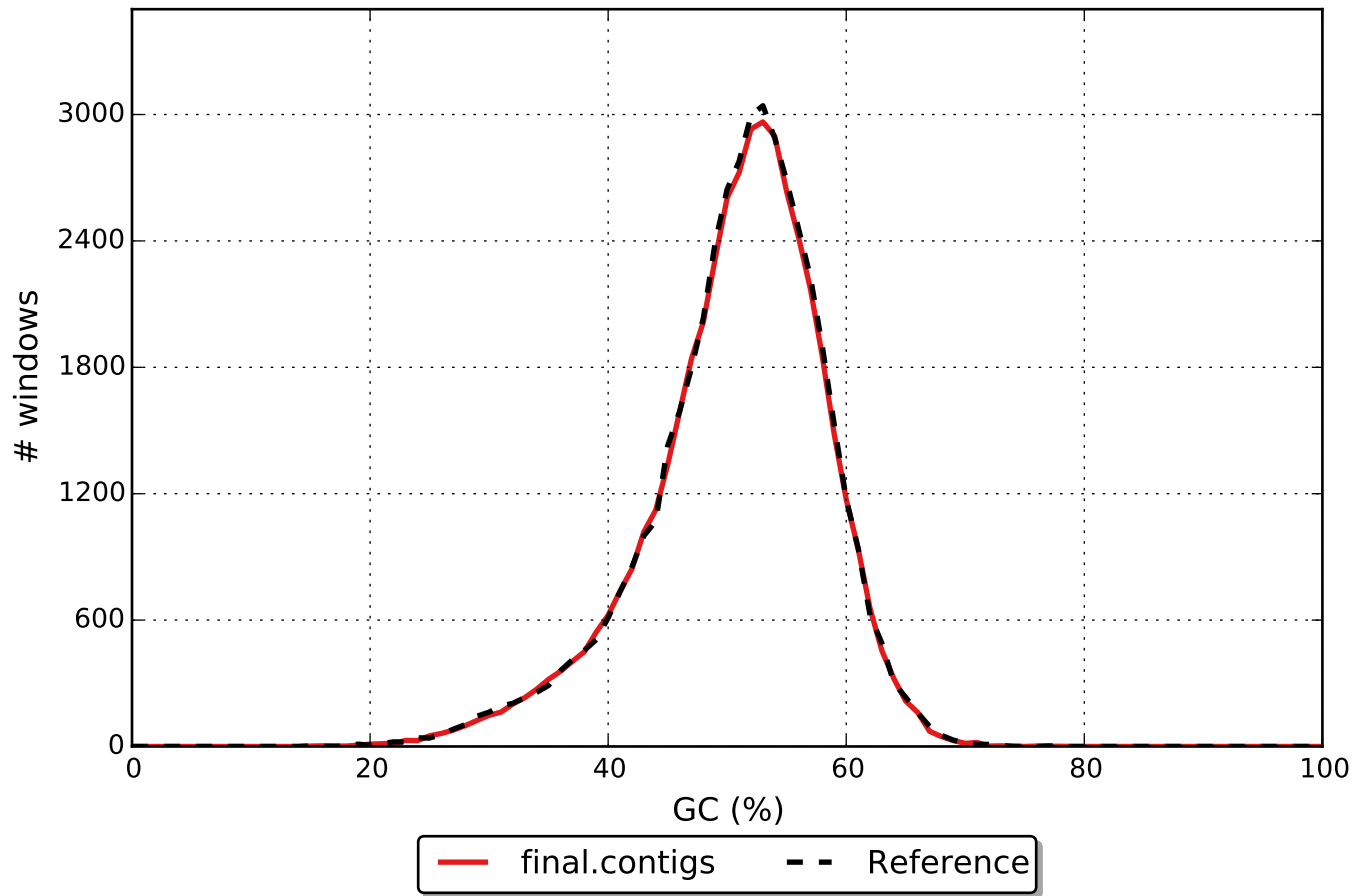


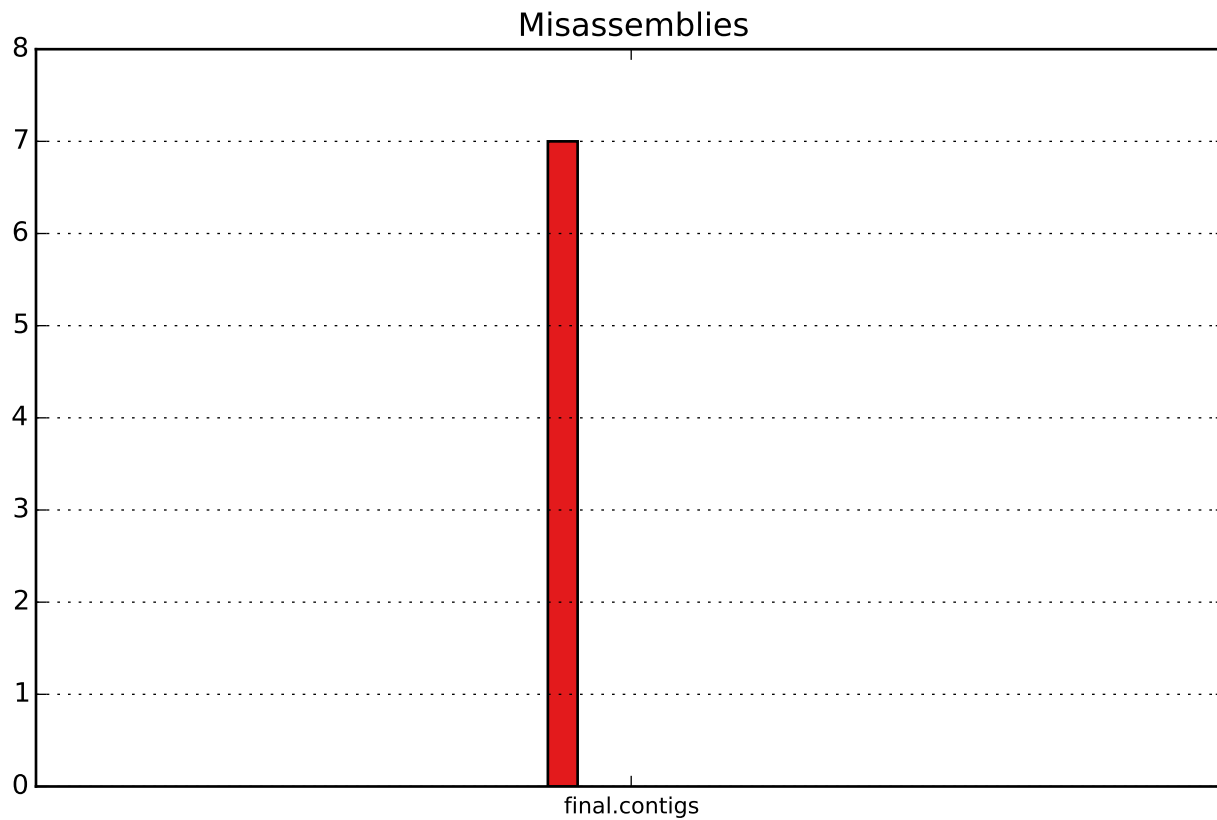
NGx



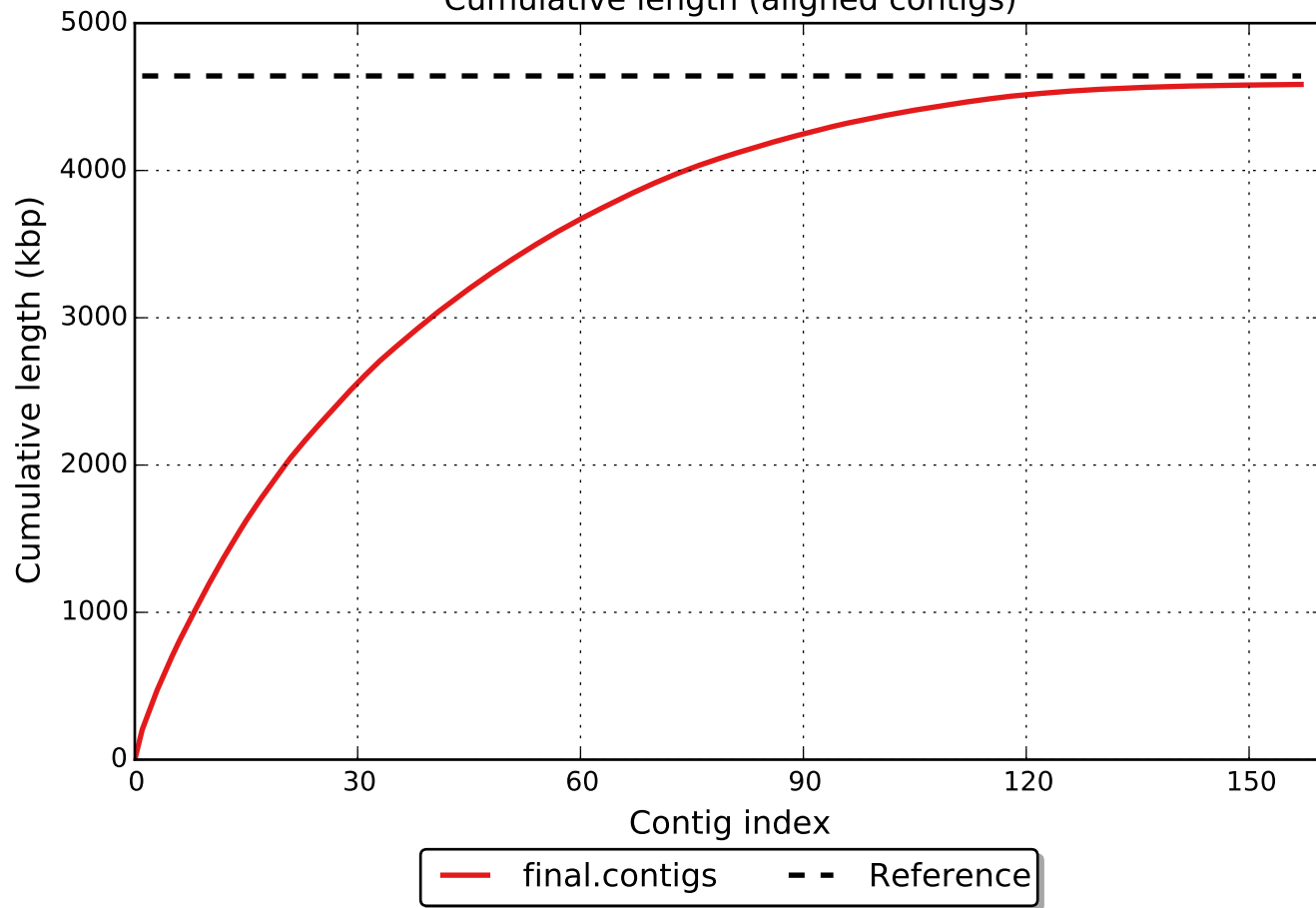


GC content

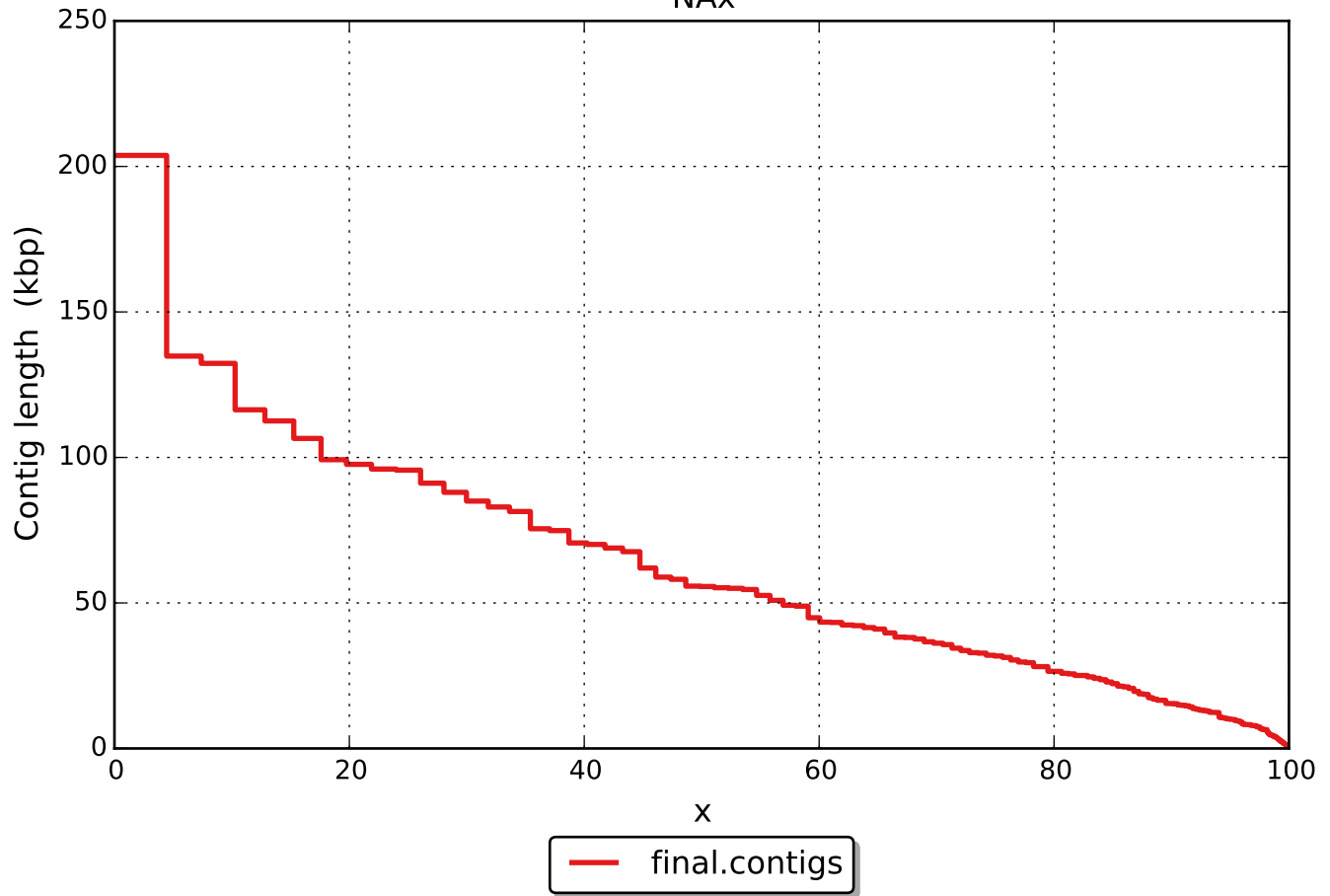




Cumulative length (aligned contigs)



NAx



NGAx

