

Report

	final.contigs
# contigs (>= 0 bp)	432
# contigs (>= 1000 bp)	322
Total length (>= 0 bp)	5286639
Total length (>= 1000 bp)	5208802
# contigs	432
Largest contig	194428
Total length	5286639
Reference length	5478683
GC (%)	50.29
Reference GC (%)	50.49
N50	34639
NG50	33958
N75	20245
NG75	18435
L50	45
LG50	48
L75	95
LG75	102
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 2 part
Unaligned length	52404
Genome fraction (%)	94.912
Duplication ratio	1.007
# N's per 100 kbp	0.00
# mismatches per 100 kbp	11.83
# indels per 100 kbp	0.12
Largest alignment	180345
NA50	33958
NGA50	33535
NA75	19880
NGA75	17639
LA50	47
LGA50	49
LA75	97
LGA75	105

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

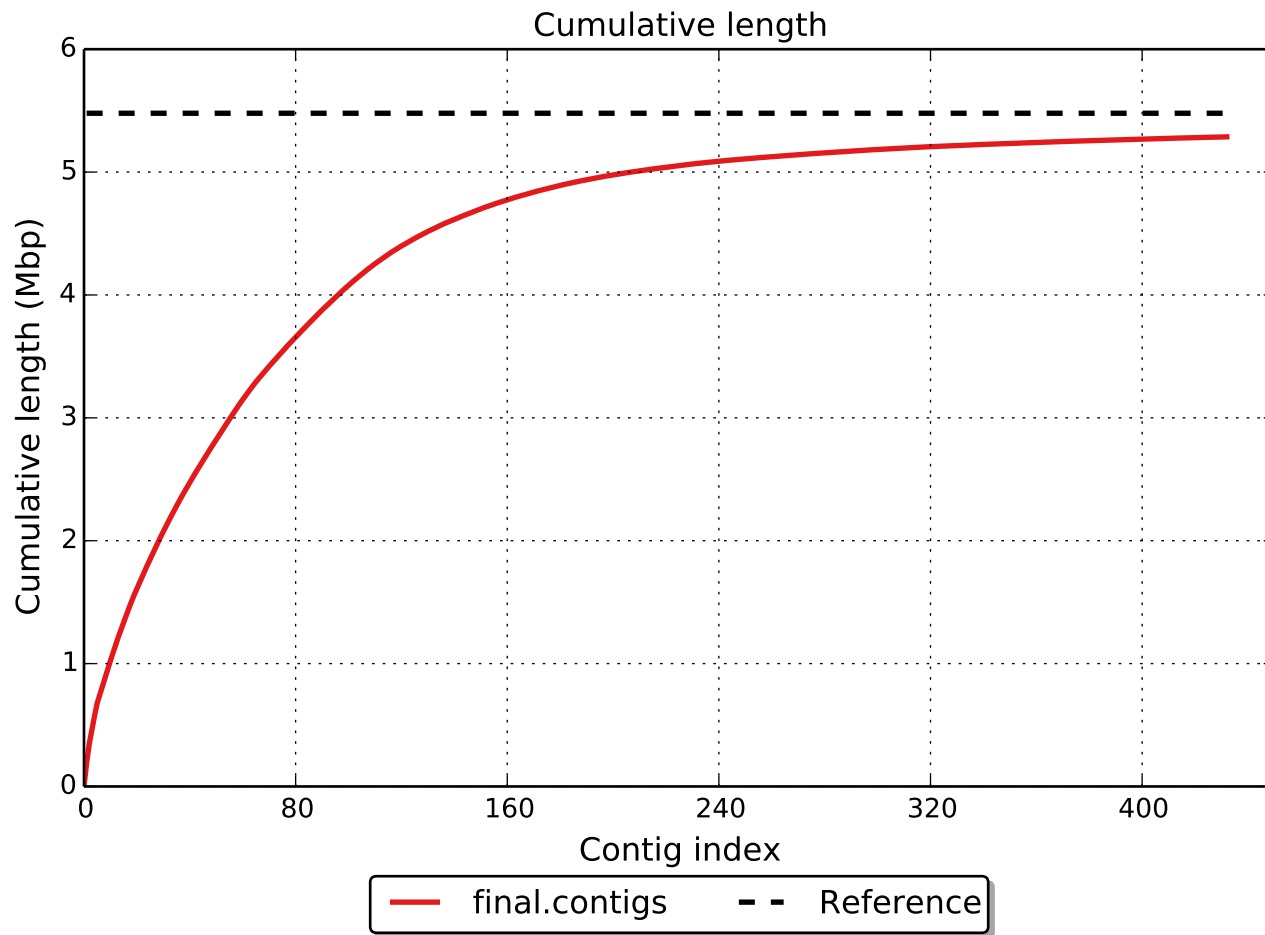
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	2
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	615
# indels	6
# short indels	4
# long indels	2
Indels length	30

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).

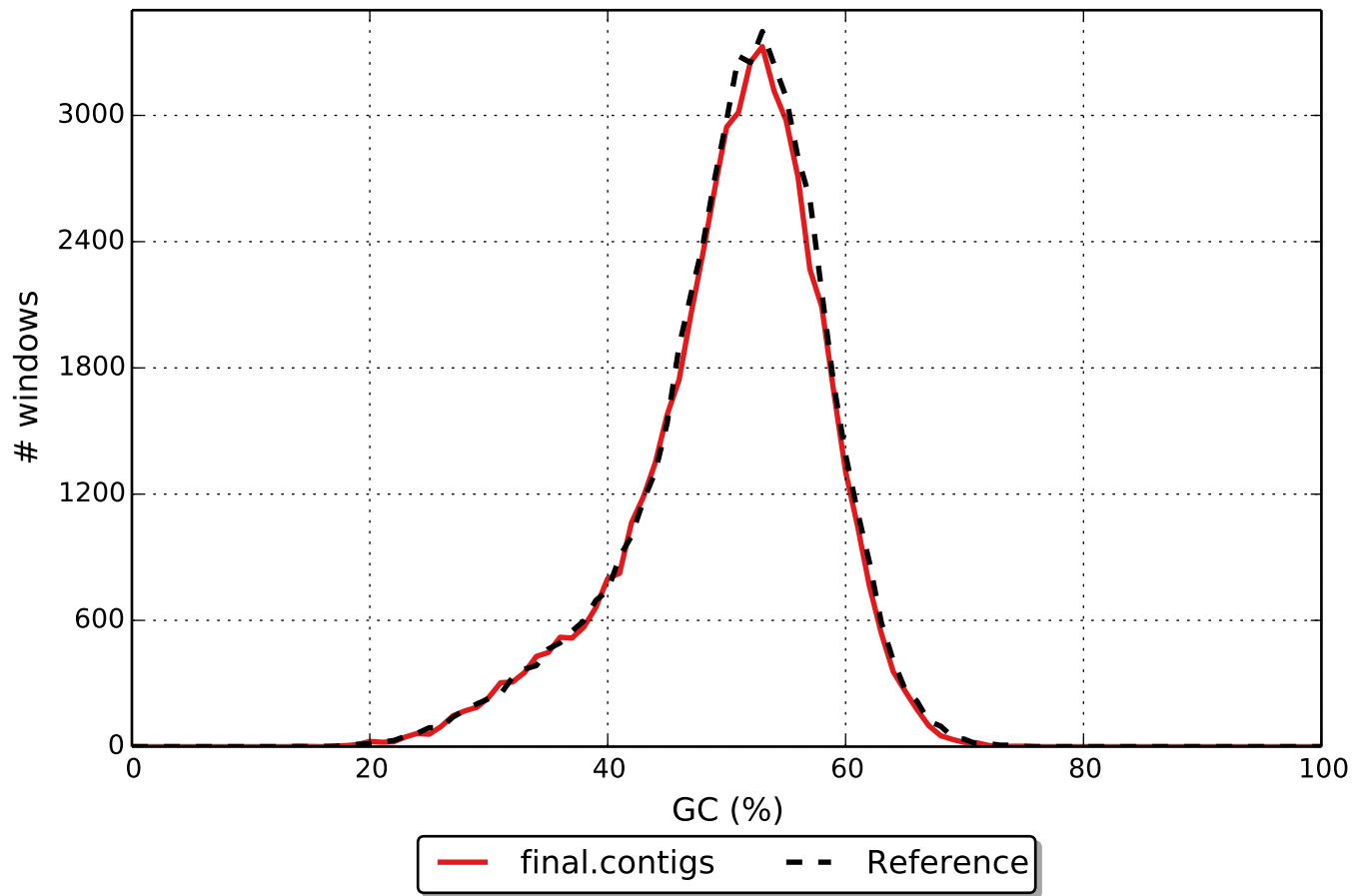
Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	2
Partially unaligned length	52404
# N's	0

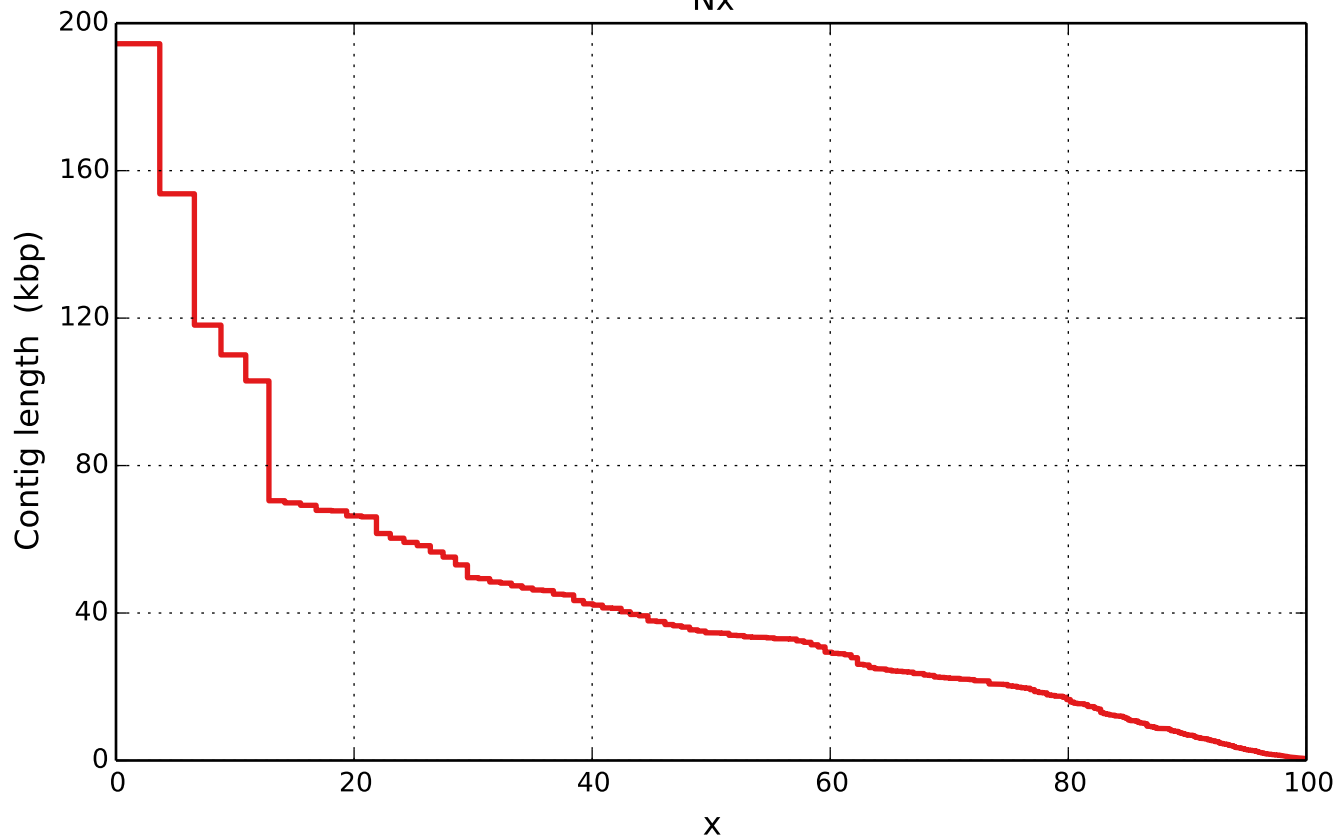
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



GC content

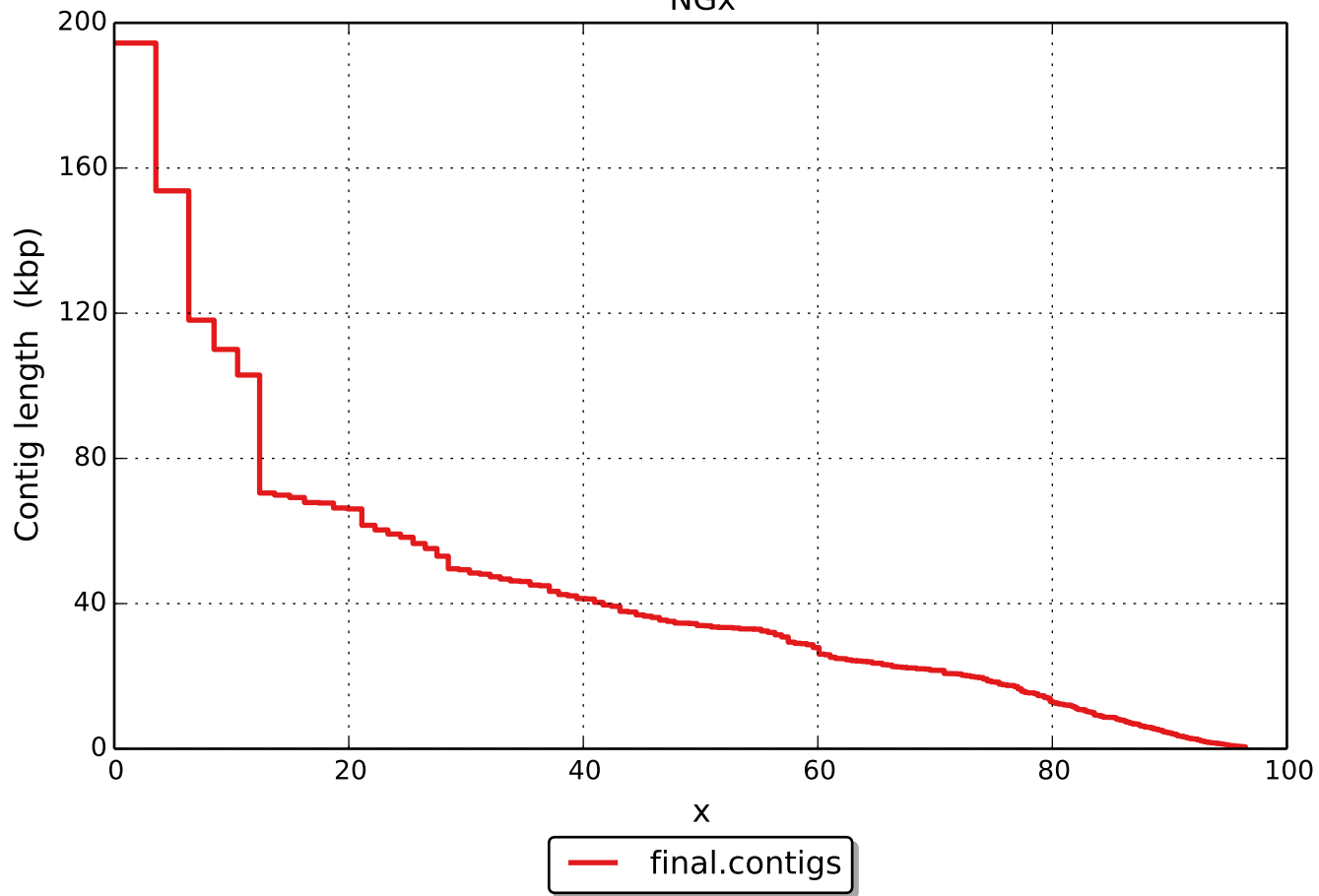


Nx



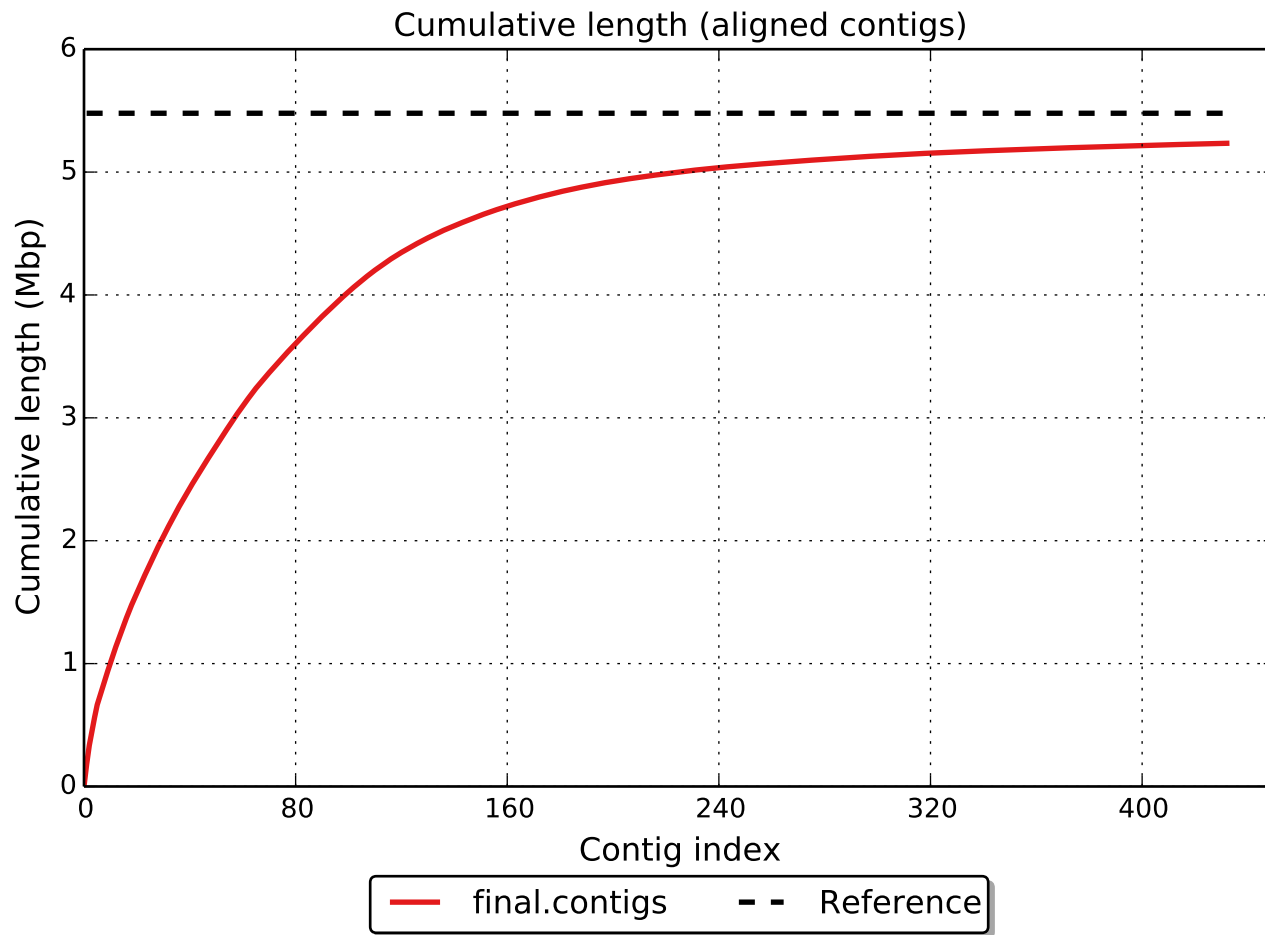
— final.contigs

NGx

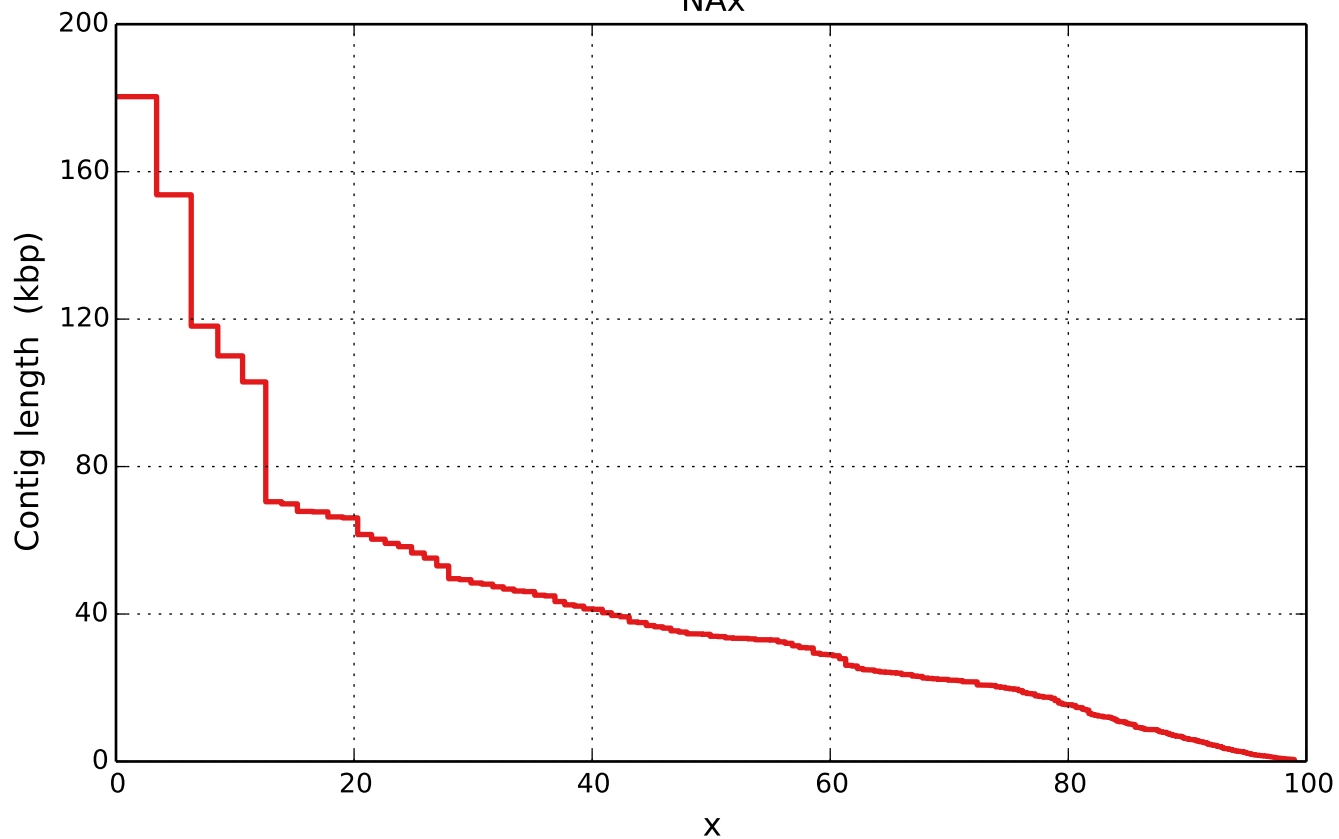


Misassemblies





NAx



— final.contigs

NGAx

