

Report

	final.contigs
# contigs (>= 0 bp)	2366
# contigs (>= 1000 bp)	1339
Total length (>= 0 bp)	4995475
Total length (>= 1000 bp)	4296594
# contigs	2366
Largest contig	18257
Total length	4995475
Reference length	5547323
GC (%)	50.33
Reference GC (%)	50.48
N50	3493
NG50	3029
N75	1726
NG75	1170
L50	422
LG50	507
L75	926
LG75	1214
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	11
Genome fraction (%)	87.211
Duplication ratio	1.033
# N's per 100 kbp	0.00
# mismatches per 100 kbp	617.49
# indels per 100 kbp	0.25
Largest alignment	18257
NA50	3493
NGA50	3029
NA75	1726
NGA75	1170
LA50	422
LGA50	507
LA75	926
LGA75	1214

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

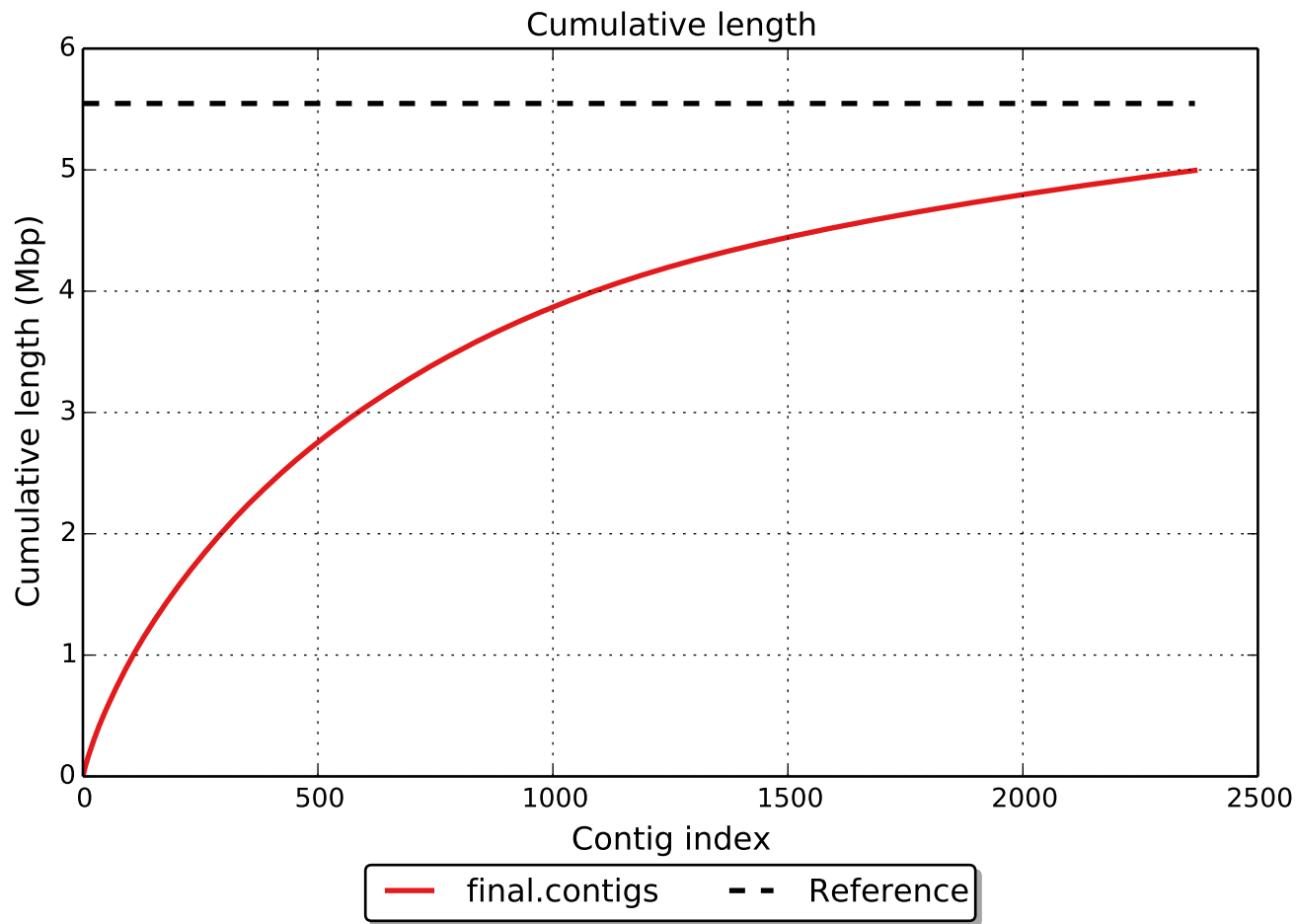
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	29873
# indels	12
# short indels	12
# long indels	0
Indels length	12

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).

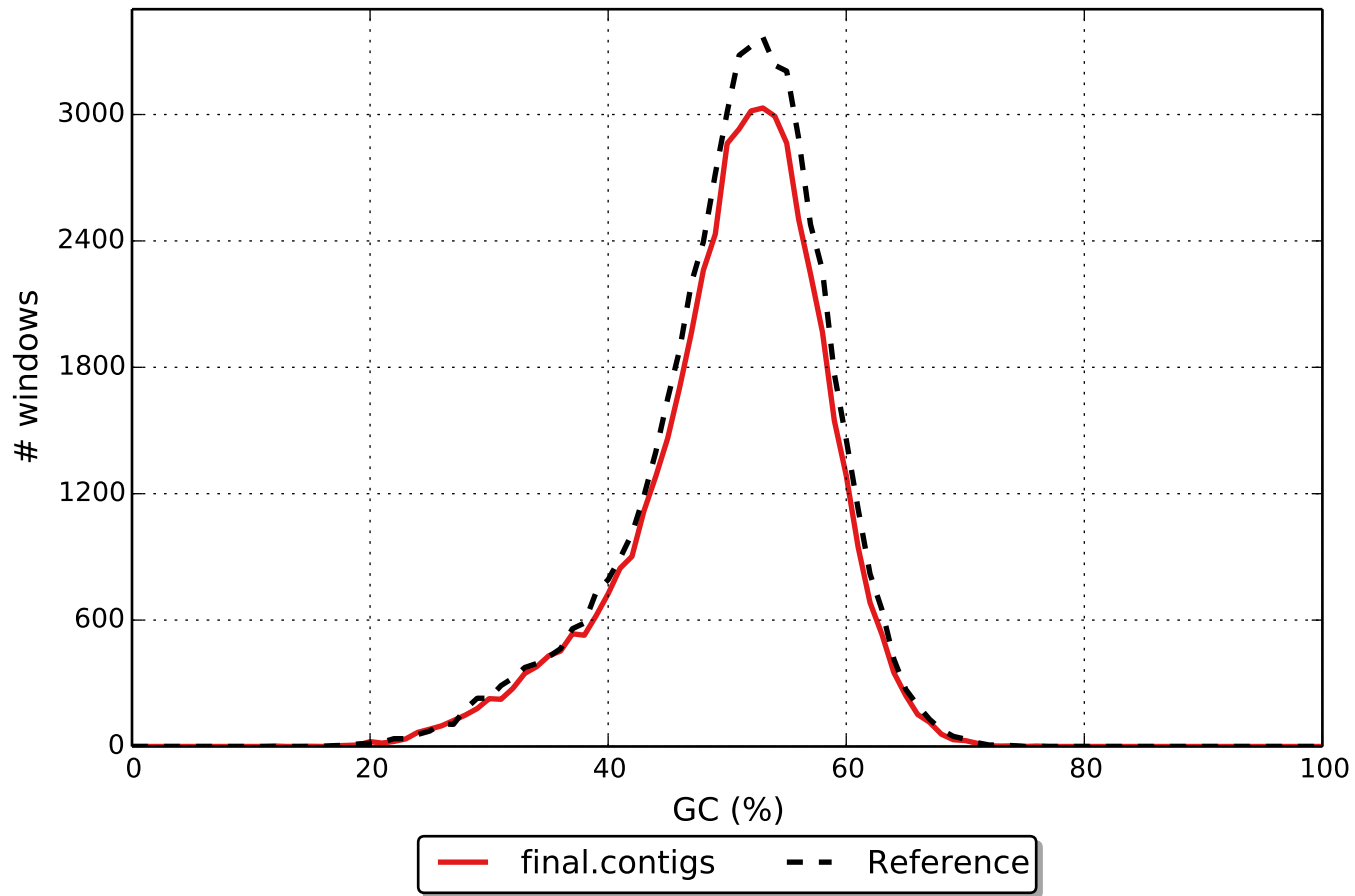
Unaligned report

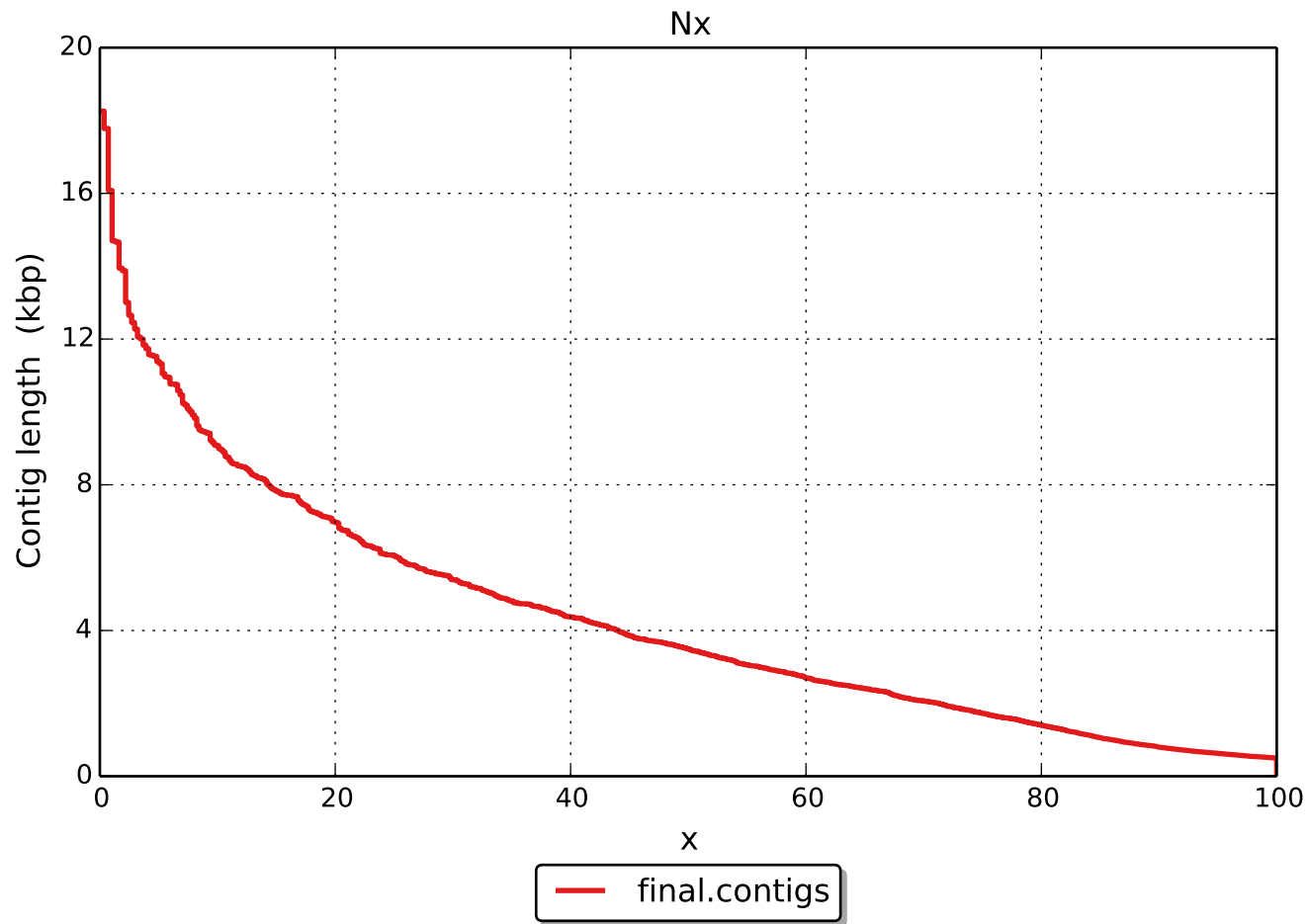
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	11
# N's	0

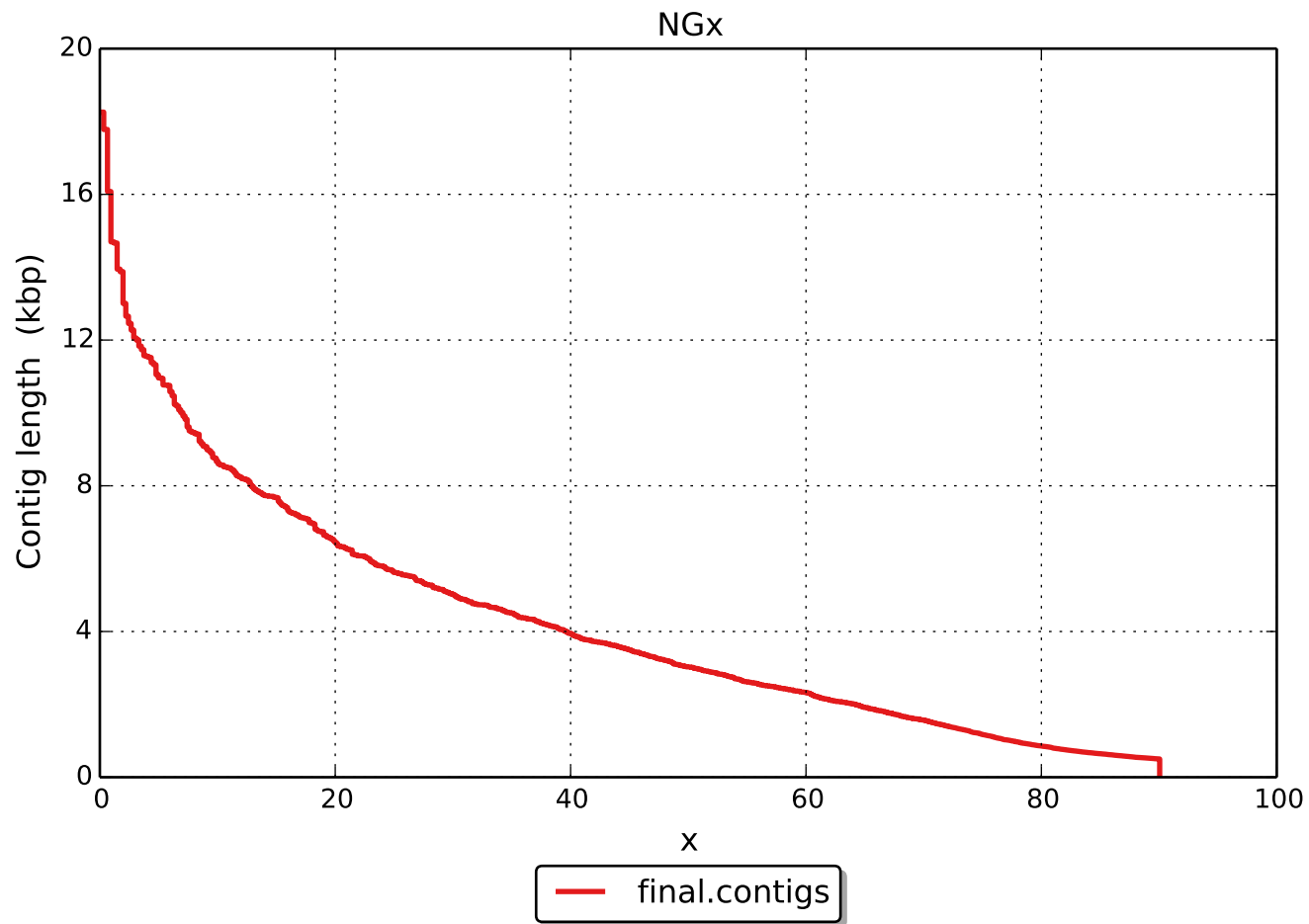
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



GC content







Misassemblies



