

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	4499
# contigs ( $\geq 1000$ bp)	2007
Total length ( $\geq 0$ bp)	5057591
Total length ( $\geq 1000$ bp)	3266903
# contigs	4499
Largest contig	5549
Total length	5057591
Reference length	5547323
GC (%)	50.44
Reference GC (%)	50.49
N50	1246
NG50	1161
N75	848
NG75	742
L50	1346
LG50	1550
L75	2579
LG75	3041
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	135
Genome fraction (%)	87.167
Duplication ratio	1.046
# N's per 100 kbp	0.00
# mismatches per 100 kbp	50.52
# indels per 100 kbp	0.00
Largest alignment	5549
NA50	1246
NGA50	1161
NA75	848
NGA75	741
LA50	1346
LGA50	1550
LA75	2579
LGA75	3042

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

## Misassemblies report

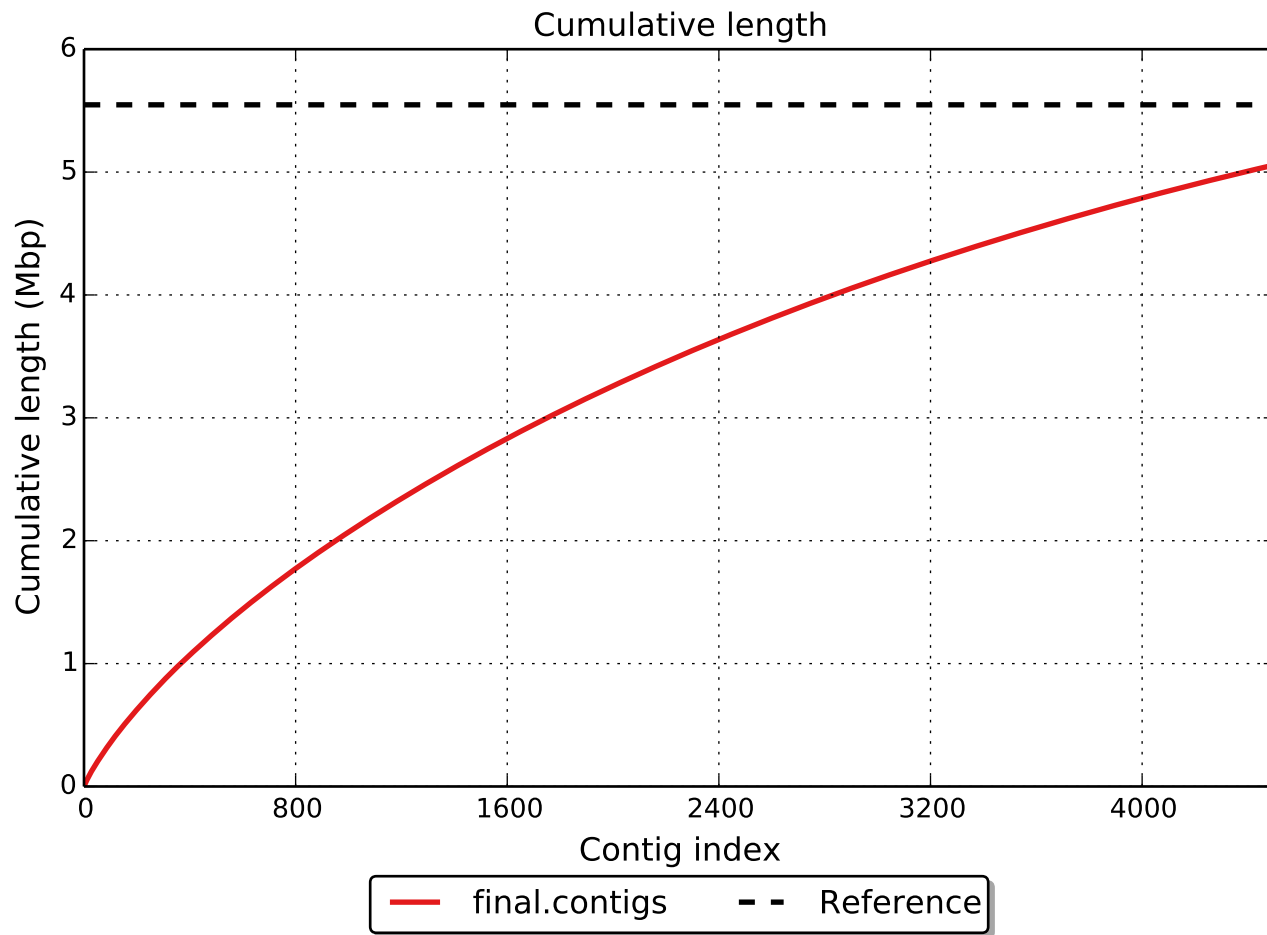
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	2443
# indels	0
# short indels	0
# long indels	0
Indels length	0

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

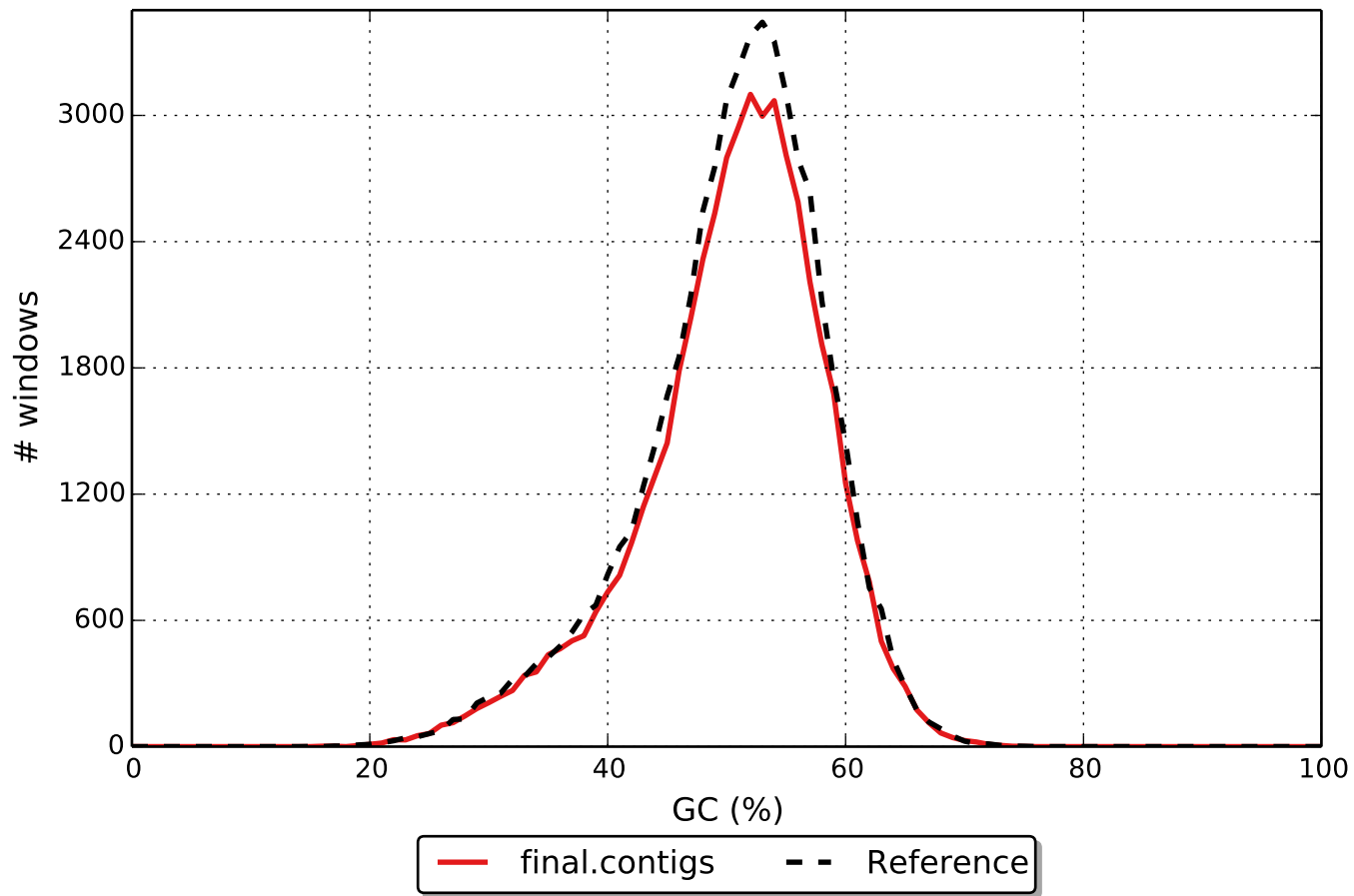
## Unaligned report

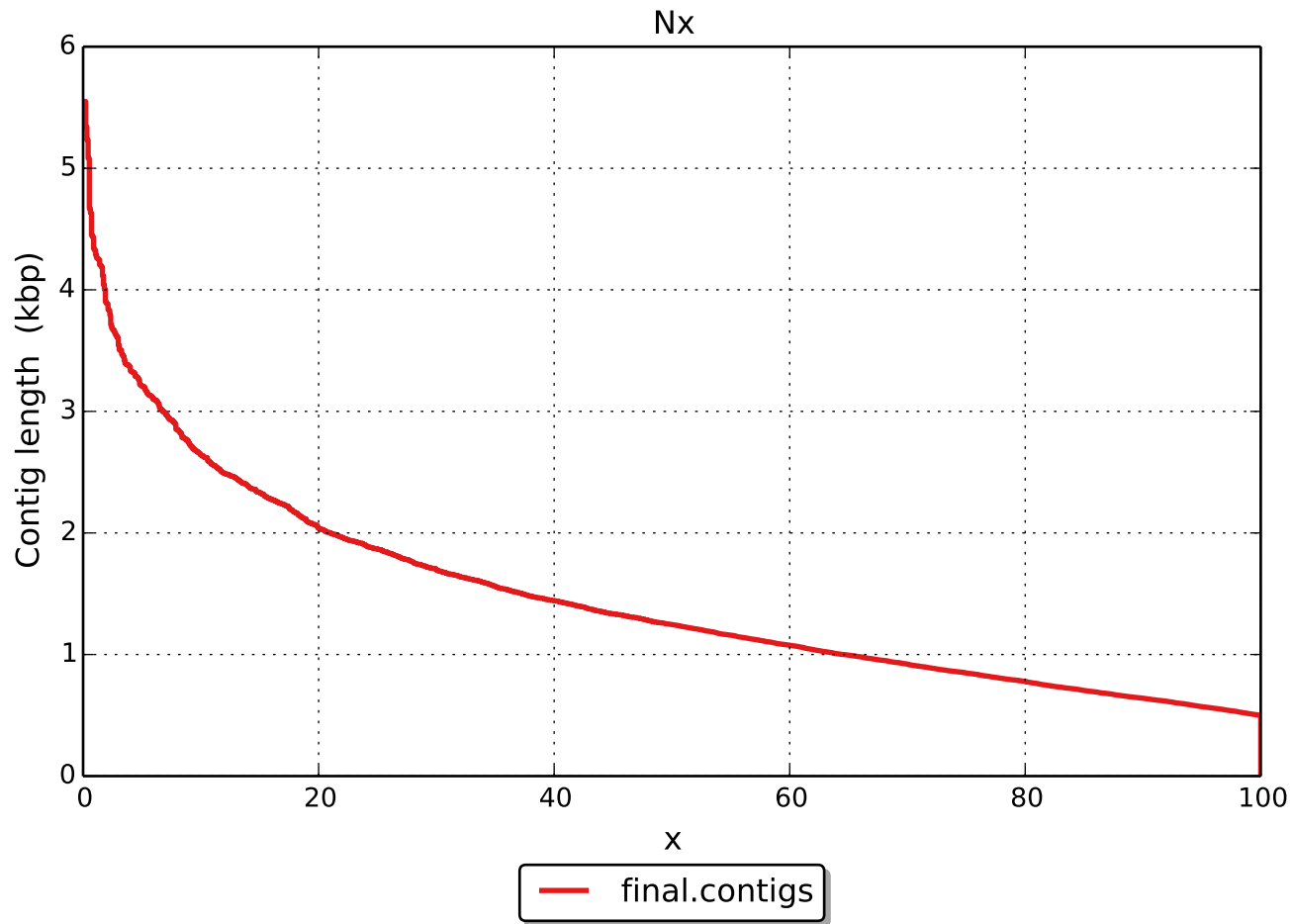
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	135
# N's	0

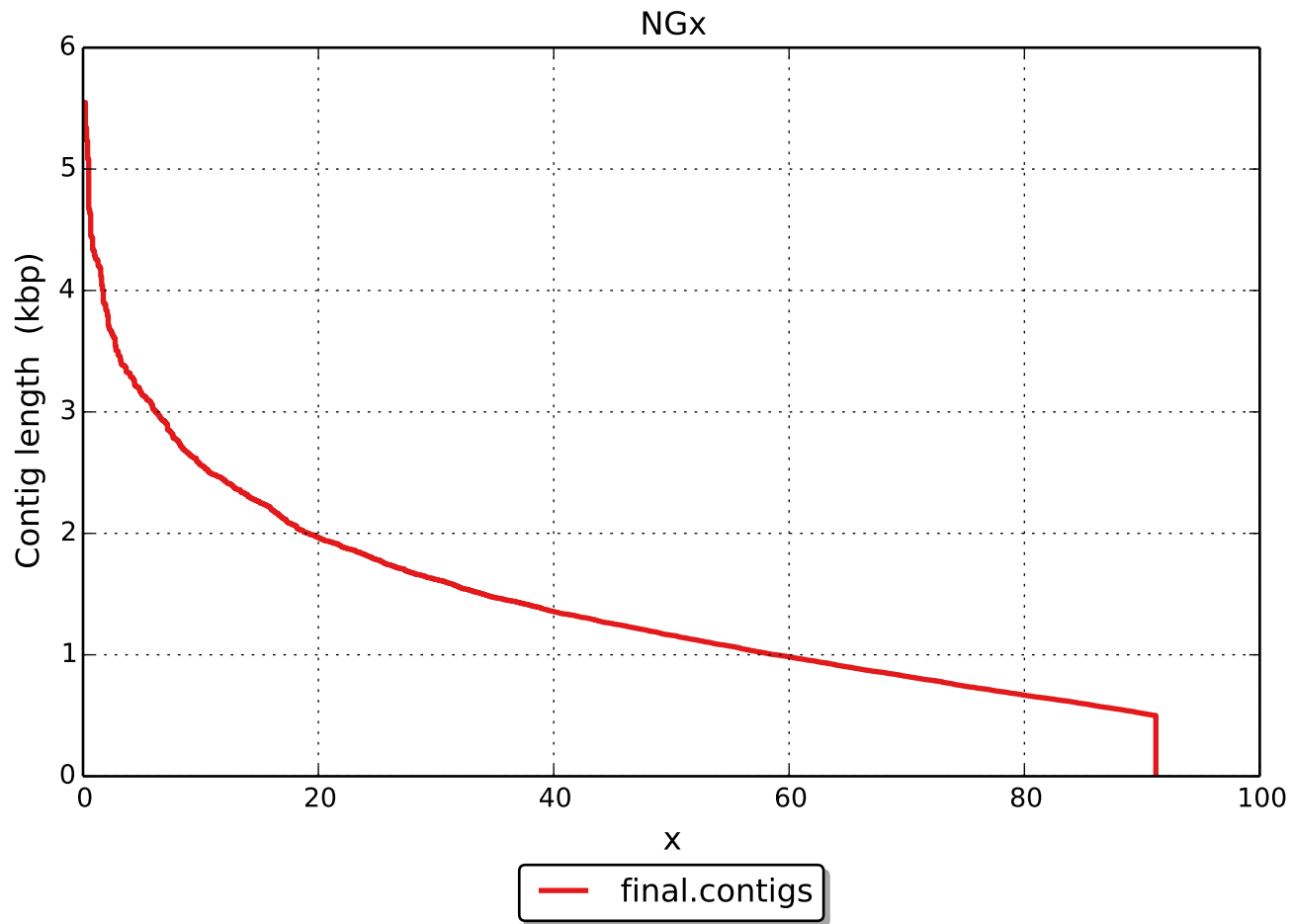
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



GC content







# Misassemblies





