

# Report

	contigs
# contigs ( $\geq 0$ bp)	3580
# contigs ( $\geq 1000$ bp)	27
# contigs ( $\geq 5000$ bp)	1
# contigs ( $\geq 10000$ bp)	0
# contigs ( $\geq 25000$ bp)	0
# contigs ( $\geq 50000$ bp)	0
Total length ( $\geq 0$ bp)	1368025
Total length ( $\geq 1000$ bp)	42738
Total length ( $\geq 5000$ bp)	6131
Total length ( $\geq 10000$ bp)	0
Total length ( $\geq 25000$ bp)	0
Total length ( $\geq 50000$ bp)	0
# contigs	564
Largest contig	6131
Total length	383603
Reference length	4641652
GC (%)	50.97
Reference GC (%)	50.79
N50	641
N75	555
L50	222
L75	383
# misassemblies	17
# misassembled contigs	17
Misassembled contigs length	23200
# local misassemblies	1
# unaligned contigs	2 + 6 part
Unaligned length	2167
Genome fraction (%)	8.214
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1052.54
# indels per 100 kbp	4.20
Largest alignment	5916
NA50	631
NGA50	-
NA75	549
LA50	227
LA75	391

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

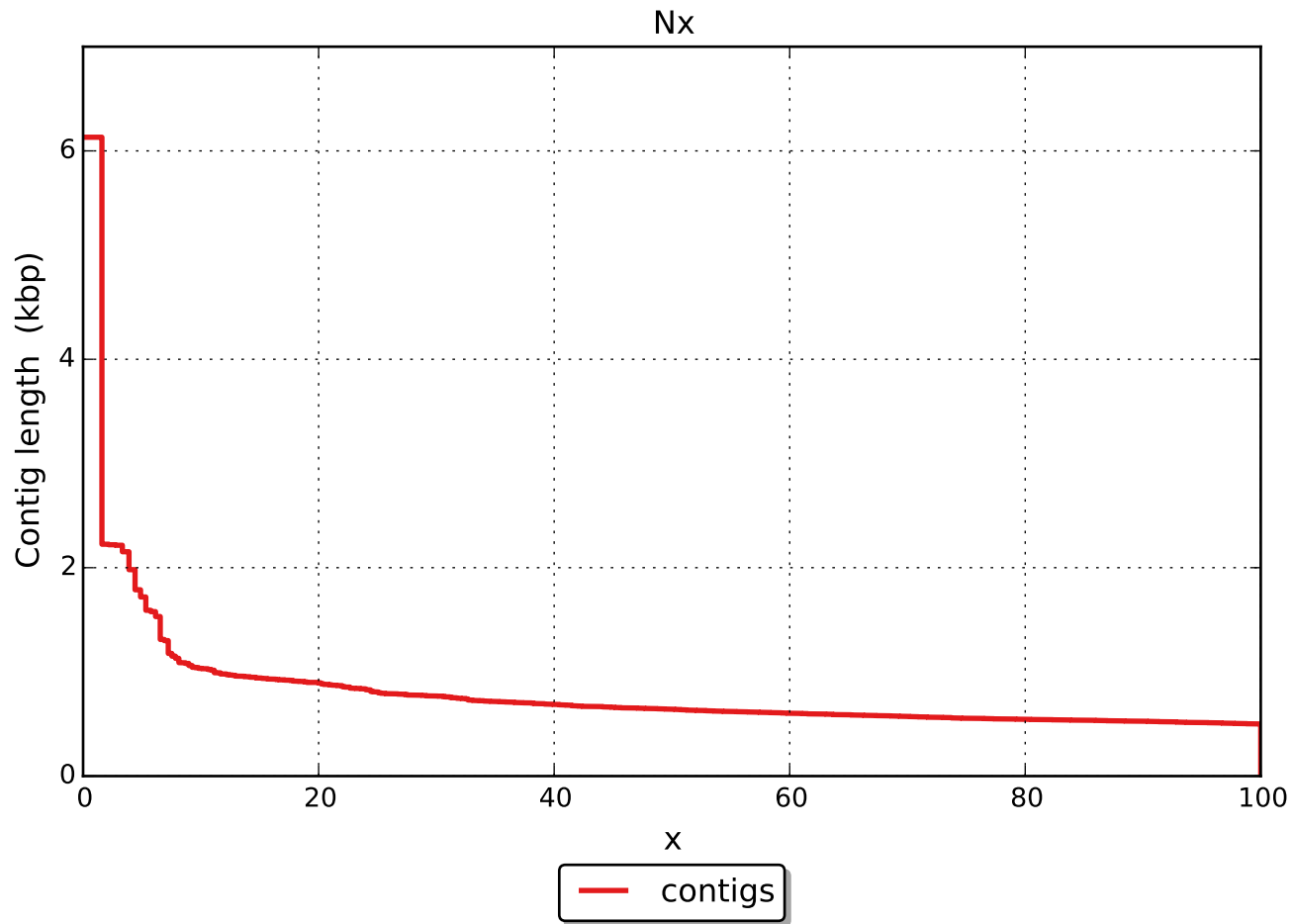
	contigs
# misassemblies	17
# relocations	17
# translocations	0
# inversions	0
# misassembled contigs	17
Misassembled contigs length	23200
# local misassemblies	1
# mismatches	4013
# indels	16
# short indels	16
# long indels	0
Indels length	20

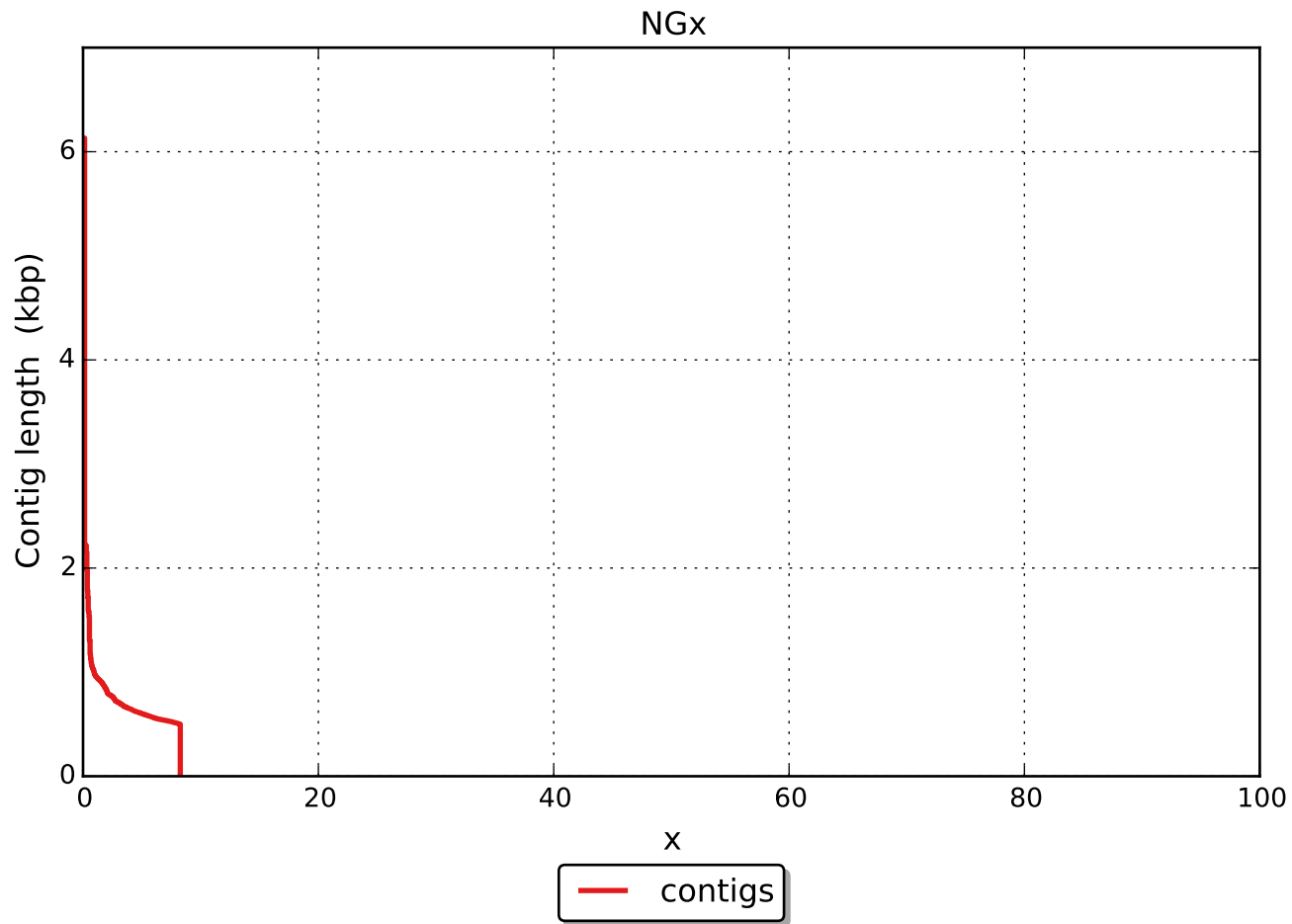
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

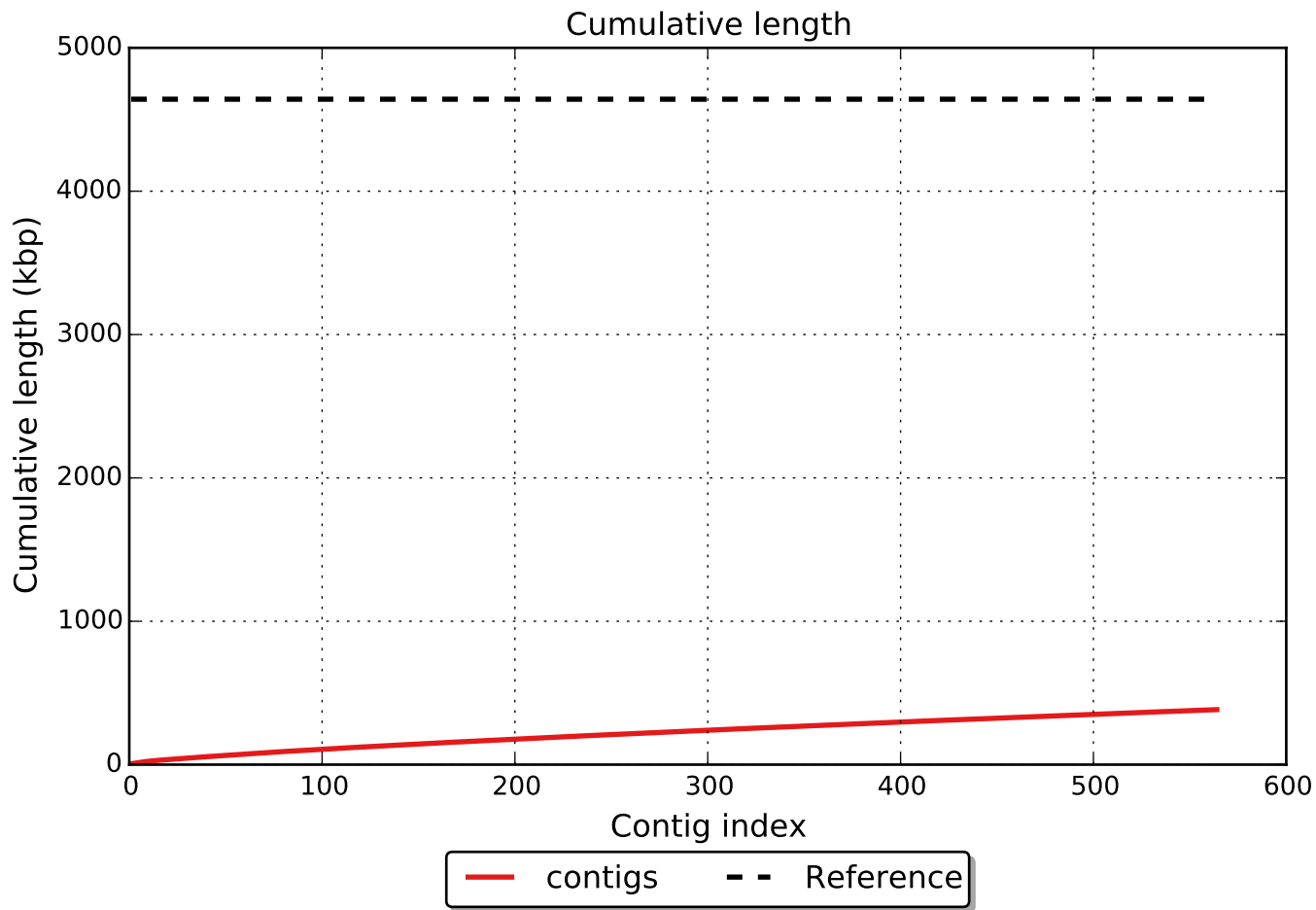
## Unaligned report

	contigs
# fully unaligned contigs	2
Fully unaligned length	1556
# partially unaligned contigs	6
# with misassembly	0
# both parts are significant	0
Partially unaligned length	611
# N's	0

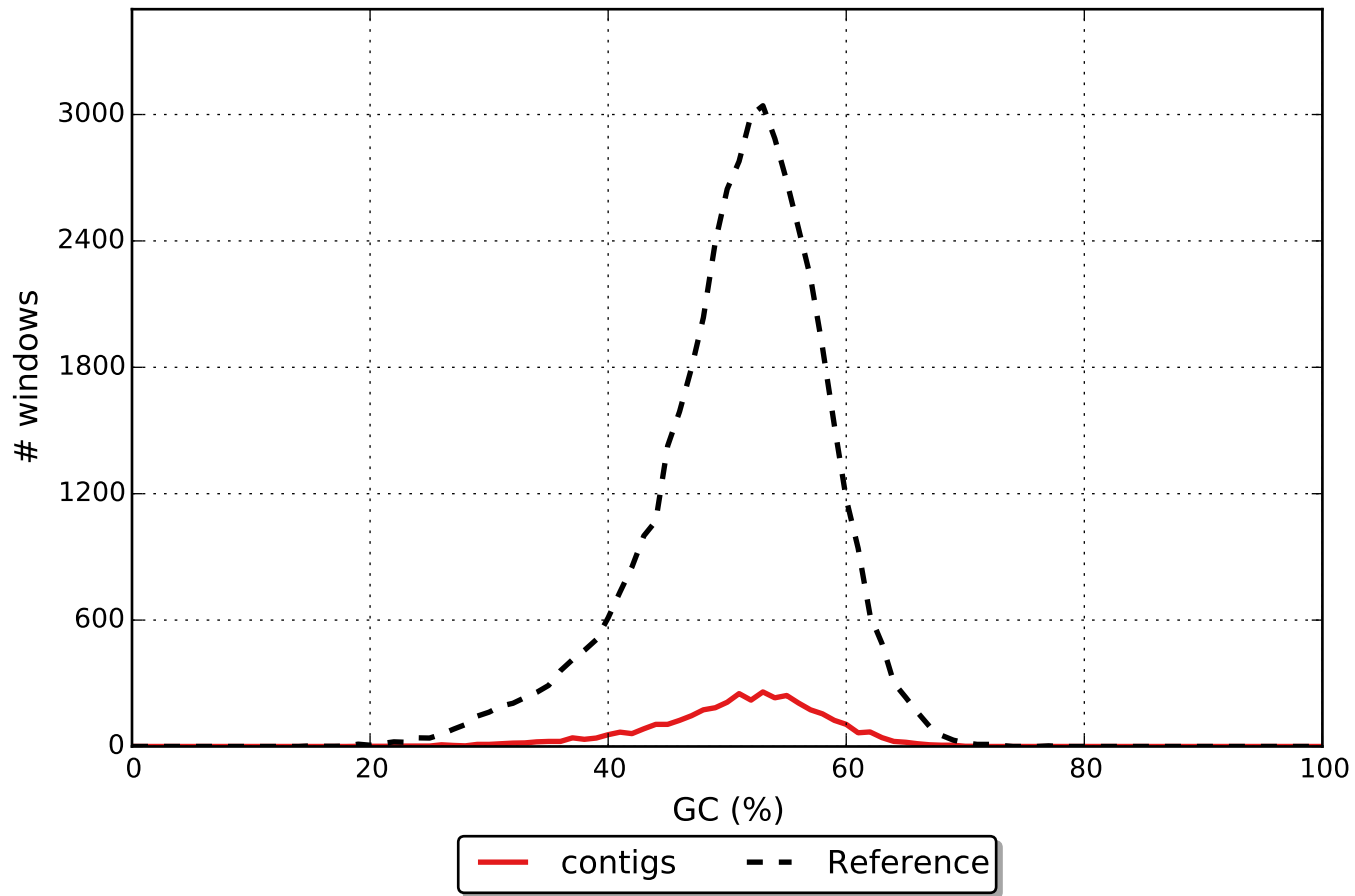
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



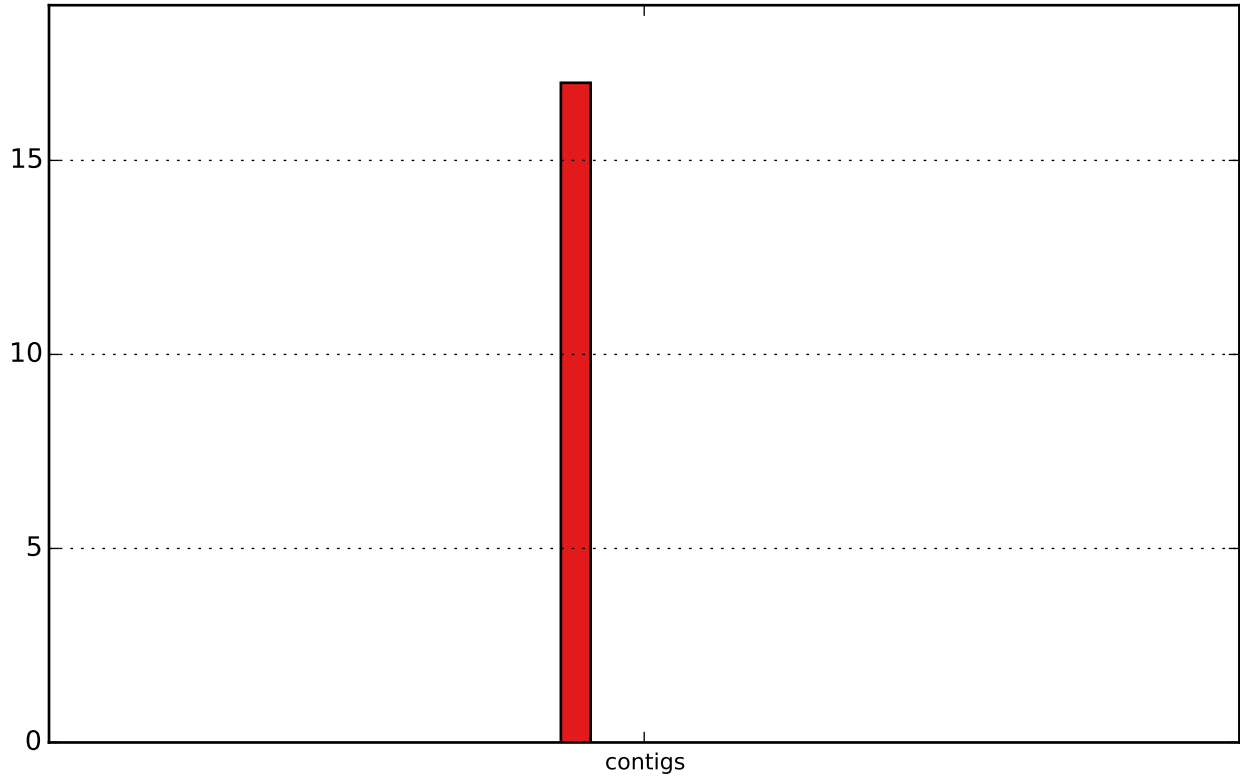




GC content



# Misassemblies



 # relocations



Cumulative length (aligned contigs)

