

## Report

	contigs
# contigs ( $\geq 0$ bp)	2506
# contigs ( $\geq 1000$ bp)	1513
# contigs ( $\geq 5000$ bp)	124
# contigs ( $\geq 10000$ bp)	6
# contigs ( $\geq 25000$ bp)	0
# contigs ( $\geq 50000$ bp)	0
Total length ( $\geq 0$ bp)	4431186
Total length ( $\geq 1000$ bp)	3862221
Total length ( $\geq 5000$ bp)	801169
Total length ( $\geq 10000$ bp)	64962
Total length ( $\geq 25000$ bp)	0
Total length ( $\geq 50000$ bp)	0
# contigs	2090
Largest contig	11817
Total length	4286021
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	2702
NG50	2524
N75	1586
NG75	1357
L50	499
LG50	567
L75	1009
LG75	1190
# misassemblies	7
# misassembled contigs	7
Misassembled contigs length	30151
# local misassemblies	7
# unaligned contigs	0 + 1 part
Unaligned length	178
Genome fraction (%)	92.141
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	5.89
# indels per 100 kbp	0.23
Largest alignment	11817
NA50	2697
NGA50	2514
NA75	1584
NGA75	1355
LA50	502
LGA50	570
LA75	1014
LGA75	1195

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

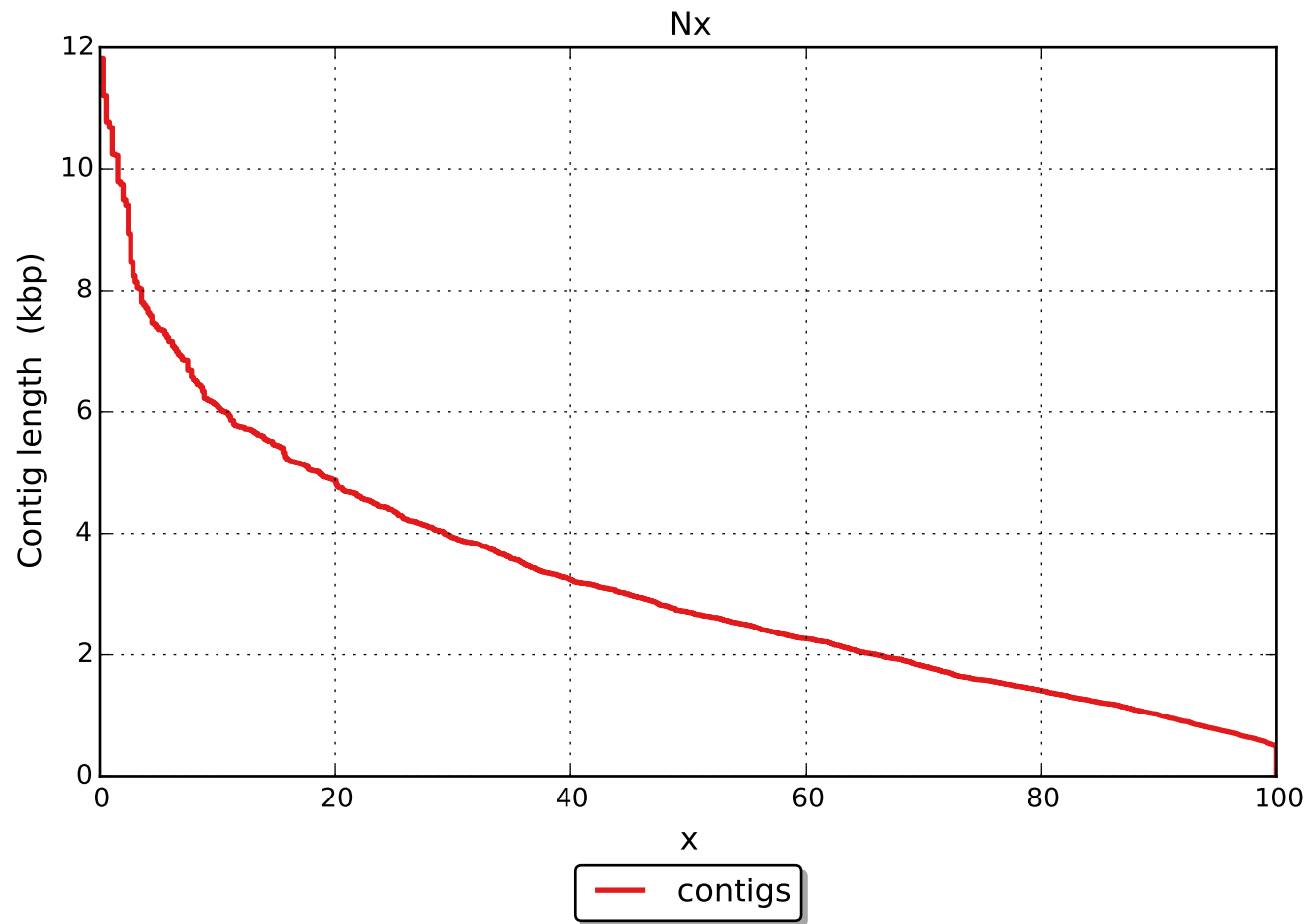
	contigs
# misassemblies	7
# relocations	7
# translocations	0
# inversions	0
# misassembled contigs	7
Misassembled contigs length	30151
# local misassemblies	7
# mismatches	252
# indels	10
# short indels	9
# long indels	1
Indels length	95

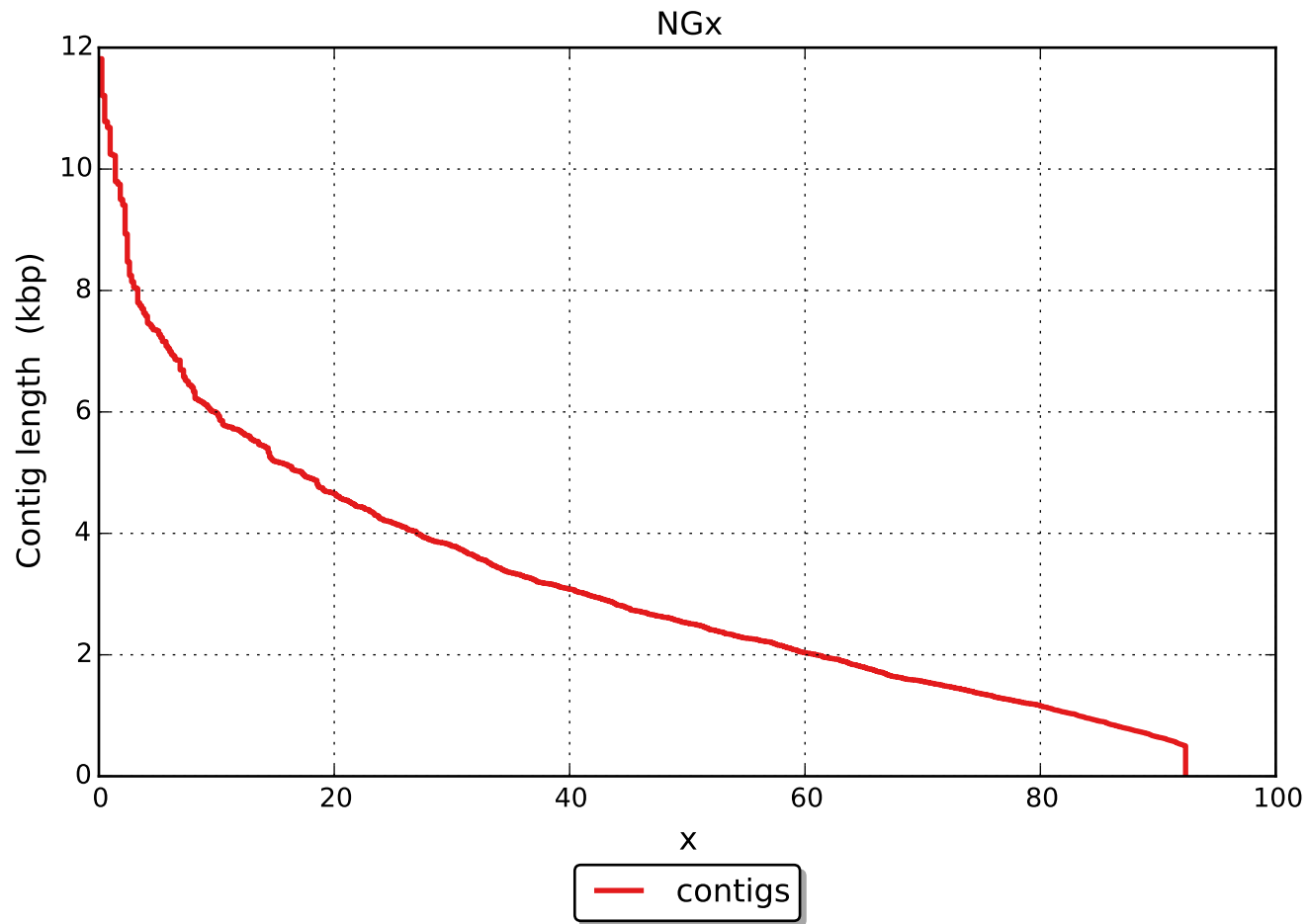
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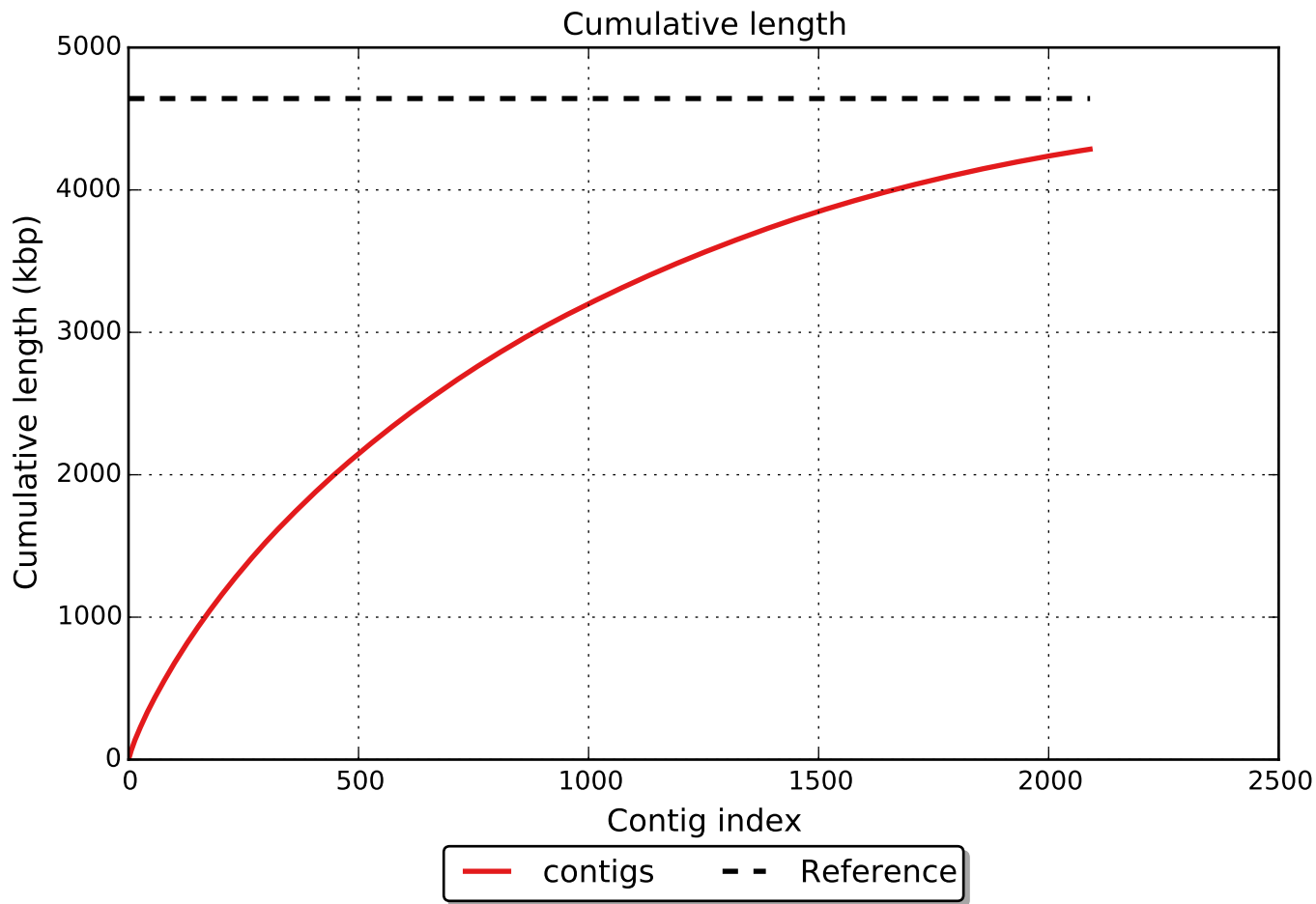
## Unaligned report

	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	178
# N's	0

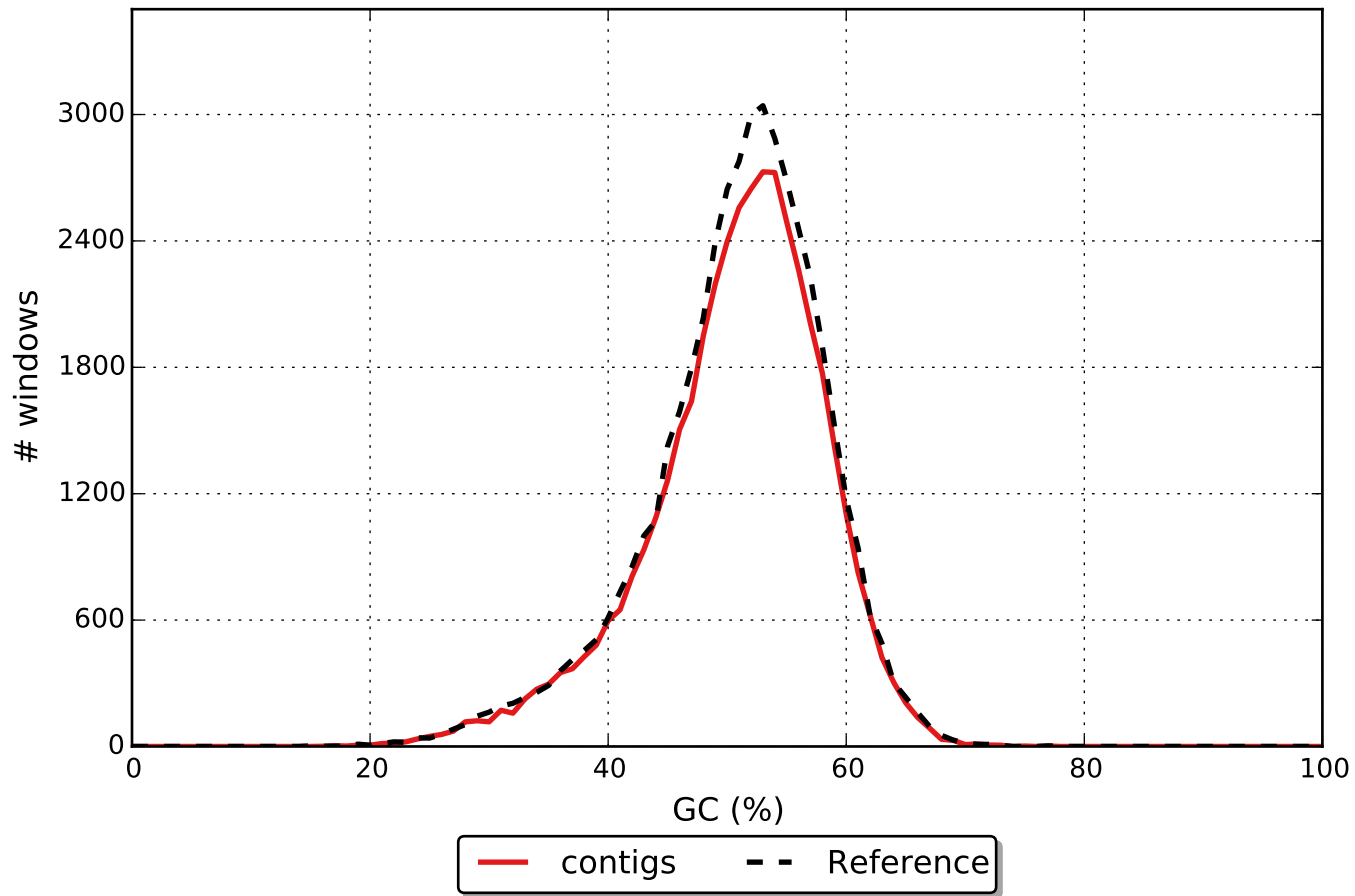
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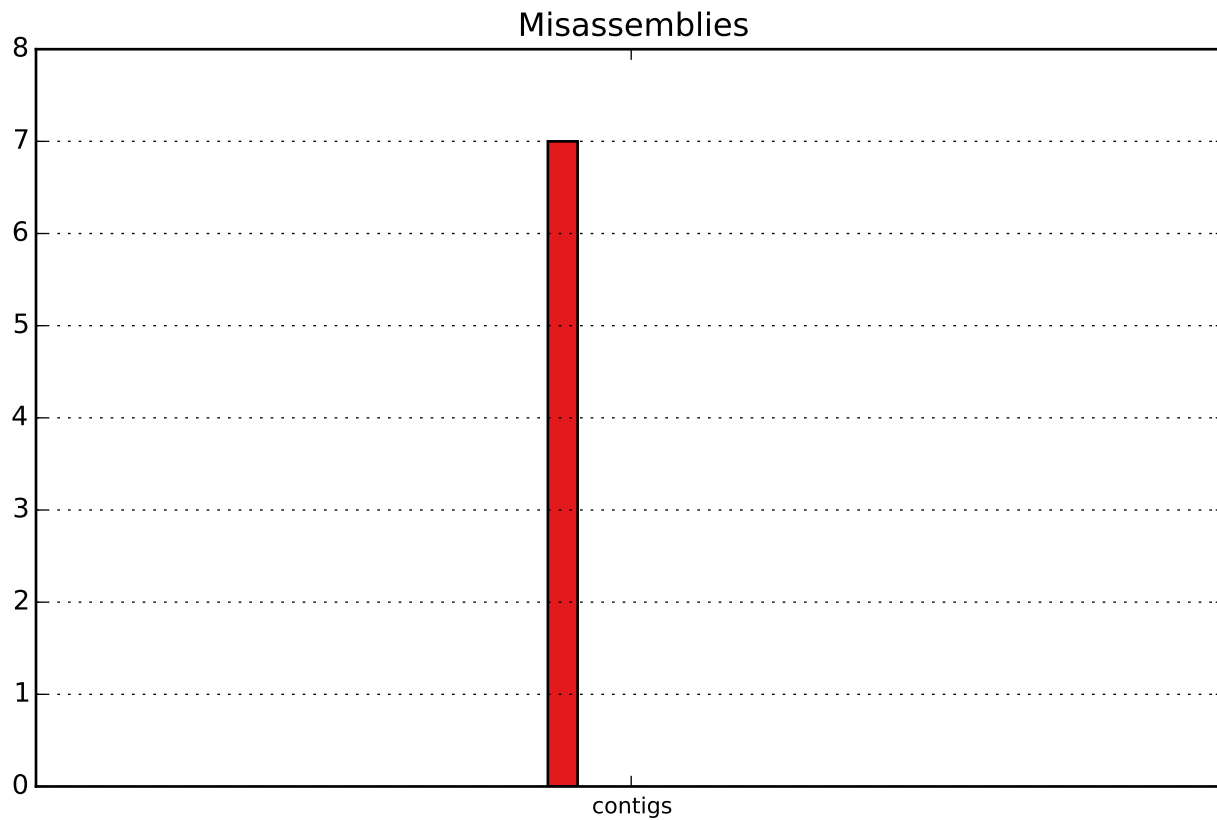






# GC content







Cumulative length (aligned contigs)

