

## Report

	contigs
# contigs (>= 0 bp)	138
# contigs (>= 1000 bp)	80
# contigs (>= 5000 bp)	61
# contigs (>= 10000 bp)	56
# contigs (>= 25000 bp)	45
# contigs (>= 50000 bp)	28
Total length (>= 0 bp)	4572132
Total length (>= 1000 bp)	4555867
Total length (>= 5000 bp)	4512976
Total length (>= 10000 bp)	4478122
Total length (>= 25000 bp)	4306415
Total length (>= 50000 bp)	3708905
# contigs	90
Largest contig	327173
Total length	4563056
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	132605
NG50	132605
N75	66175
NG75	60761
L50	12
LG50	12
L75	24
LG75	25
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.277
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2.19
# indels per 100 kbp	0.13
Largest alignment	327173
NA50	132605
NGA50	132605
NA75	66175
NGA75	60761
LA50	12
LGA50	12
LA75	24
LGA75	25

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

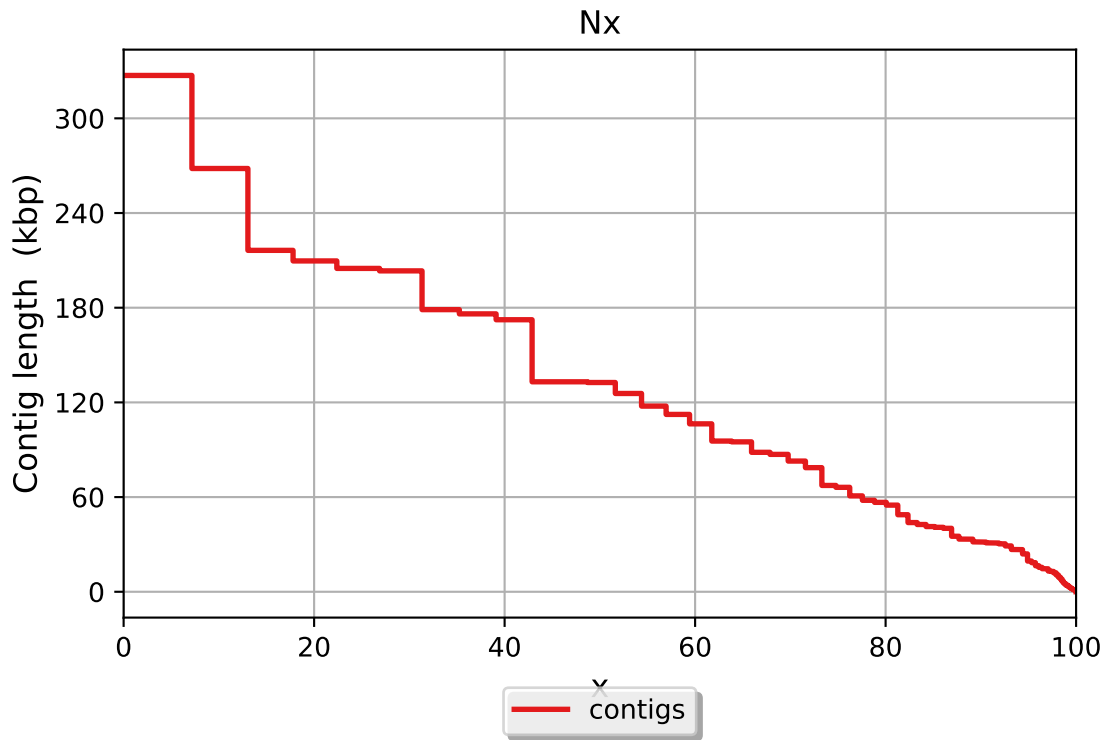
	contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	100
# indels	6
# short indels	6
# long indels	0
Indels length	7

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).

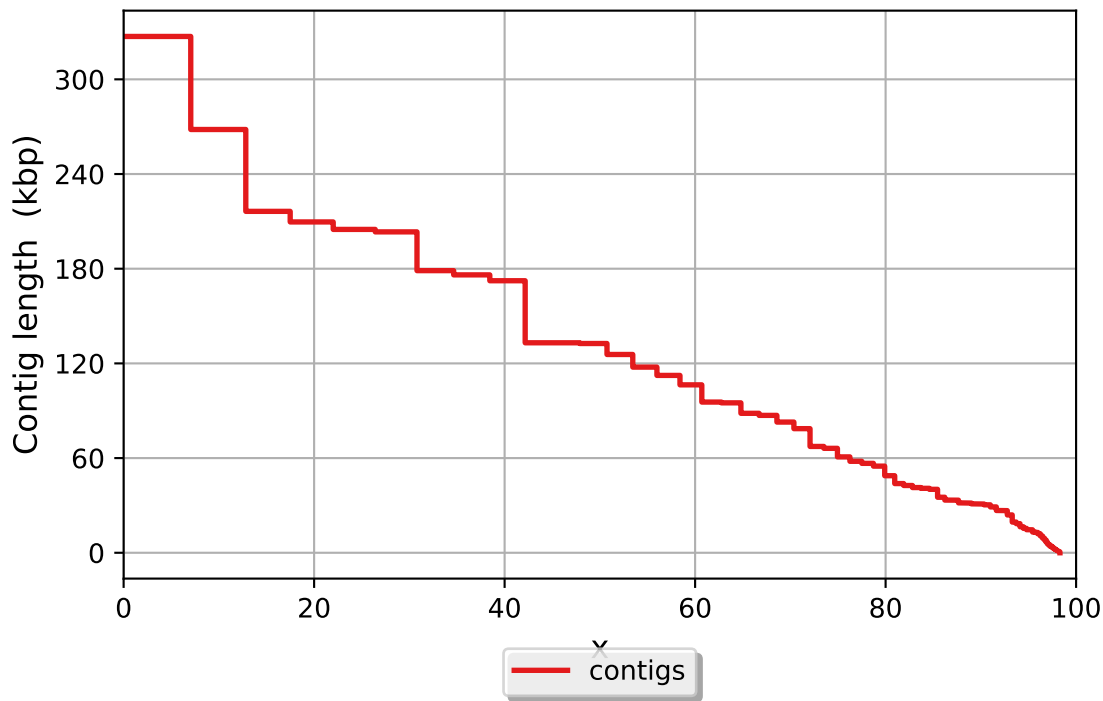
## Unaligned report

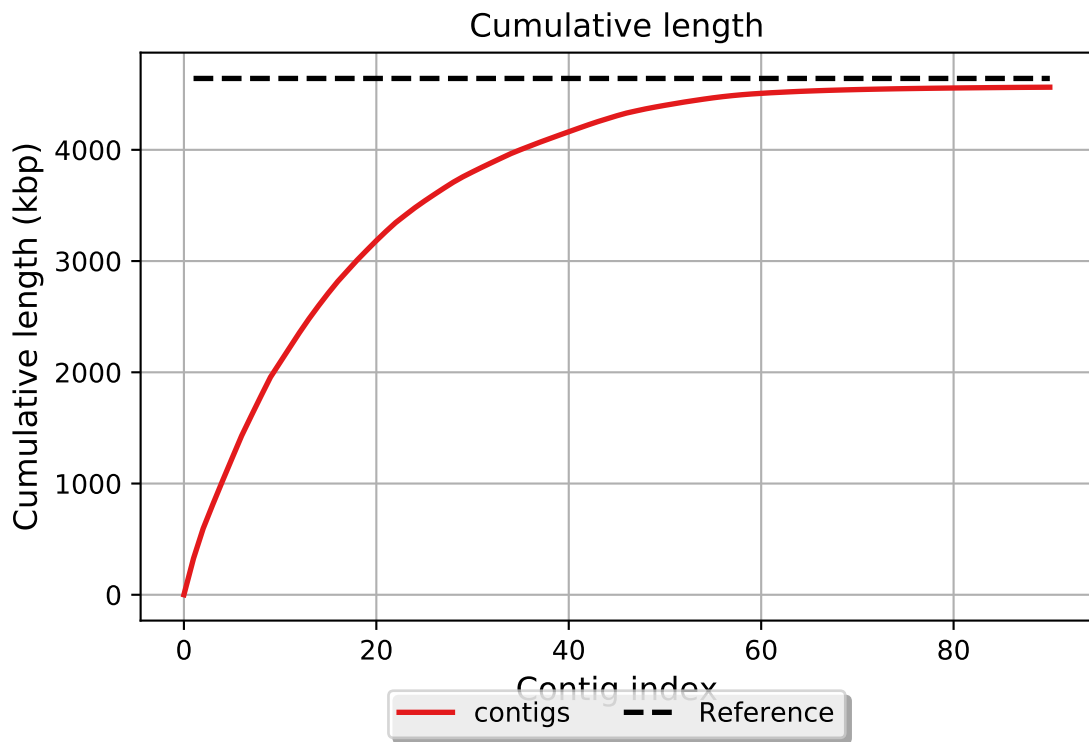
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

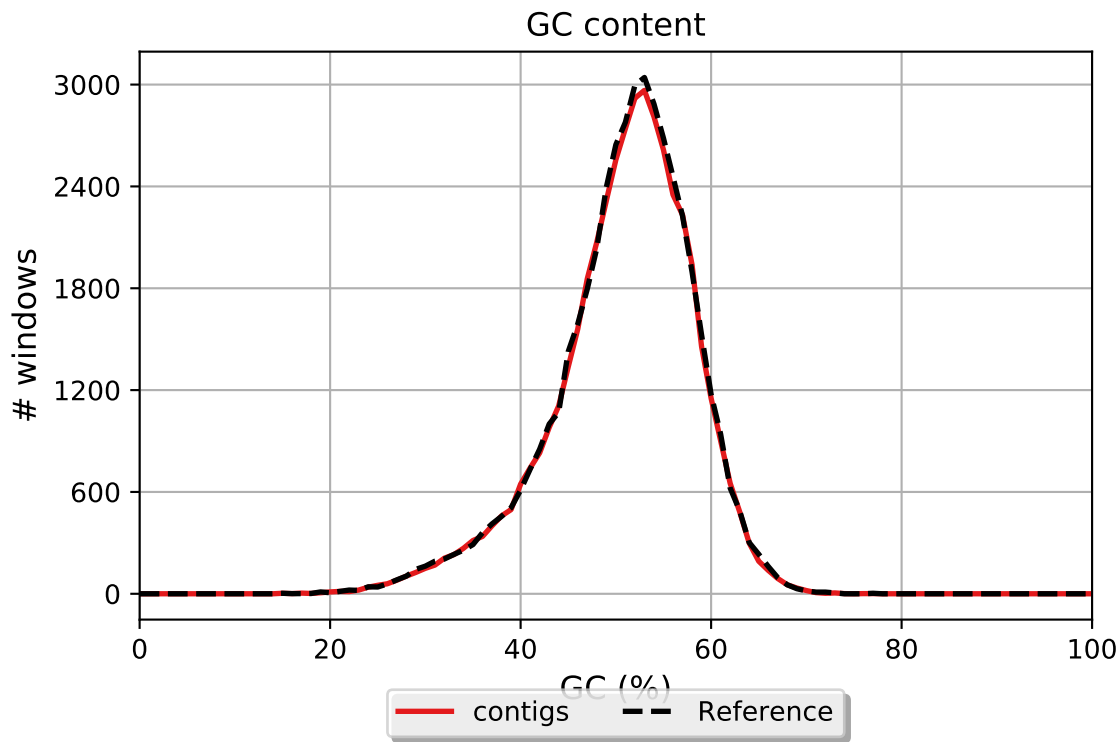
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



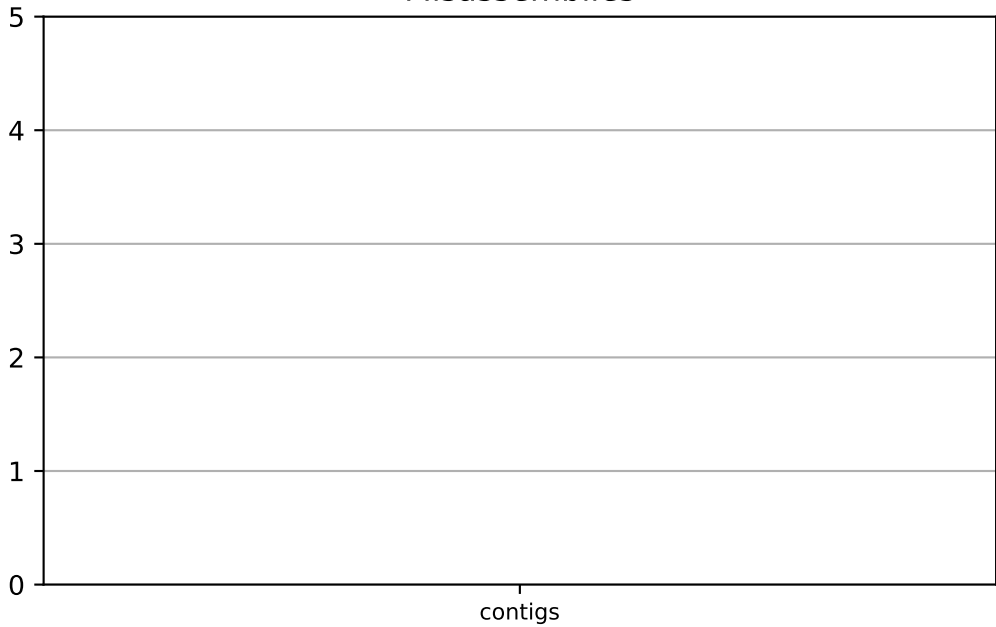
NGx





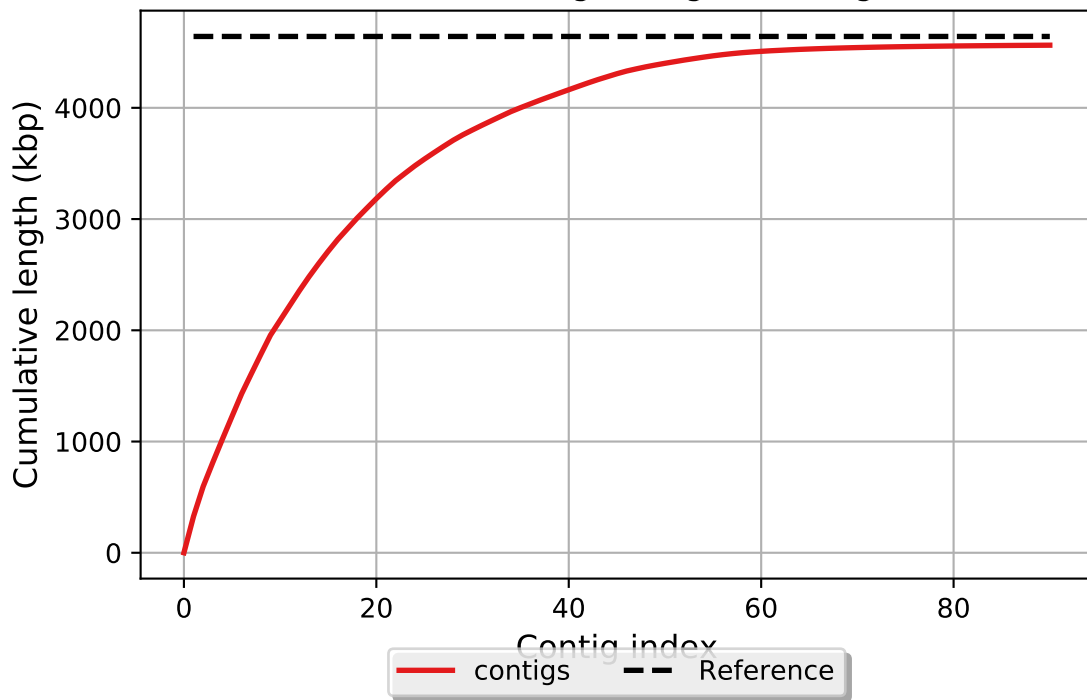


## Misassemblies

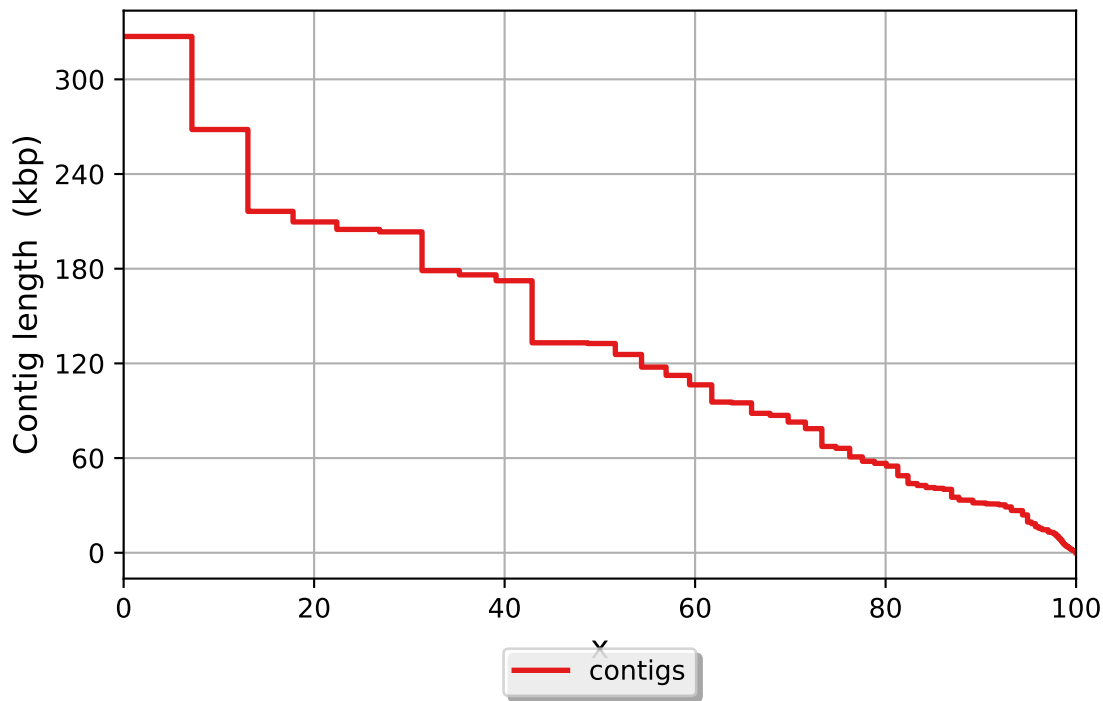




Cumulative length (aligned contigs)



NAx



# NGAx

