

## Report

	final.contigs
# contigs (>= 0 bp)	4223
# contigs (>= 1000 bp)	1417
# contigs (>= 5000 bp)	5
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	3997179
Total length (>= 1000 bp)	2339195
Total length (>= 5000 bp)	27250
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3095
Largest contig	5714
Total length	3545357
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	1286
NG50	1009
N75	859
NG75	528
L50	915
LG50	1399
L75	1763
LG75	2971
# misassemblies	14
# misassembled contigs	14
Misassembled contigs length	25546
# local misassemblies	5
# unaligned contigs	0 + 5 part
Unaligned length	135
Genome fraction (%)	75.391
Duplication ratio	1.013
# N's per 100 kbp	0.00
# mismatches per 100 kbp	699.92
# indels per 100 kbp	0.66
Largest alignment	5714
NA50	1283
NGA50	1007
NA75	859
NGA75	525
LA50	917
LGA50	1403
LA75	1767
LGA75	2979

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

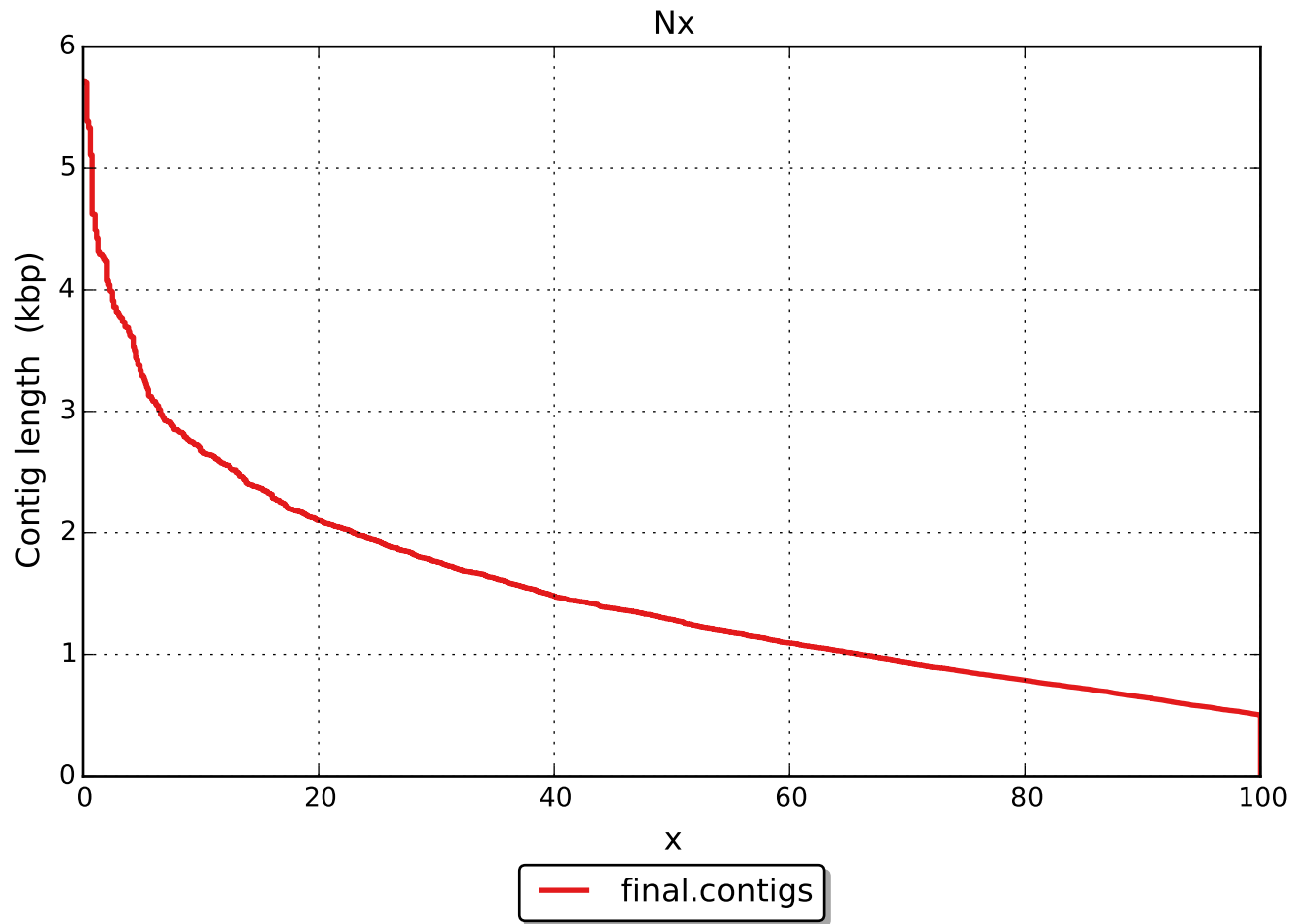
	final.contigs
# misassemblies	14
# relocations	14
# translocations	0
# inversions	0
# misassembled contigs	14
Misassembled contigs length	25546
# local misassemblies	5
# mismatches	24493
# indels	23
# short indels	20
# long indels	3
Indels length	143

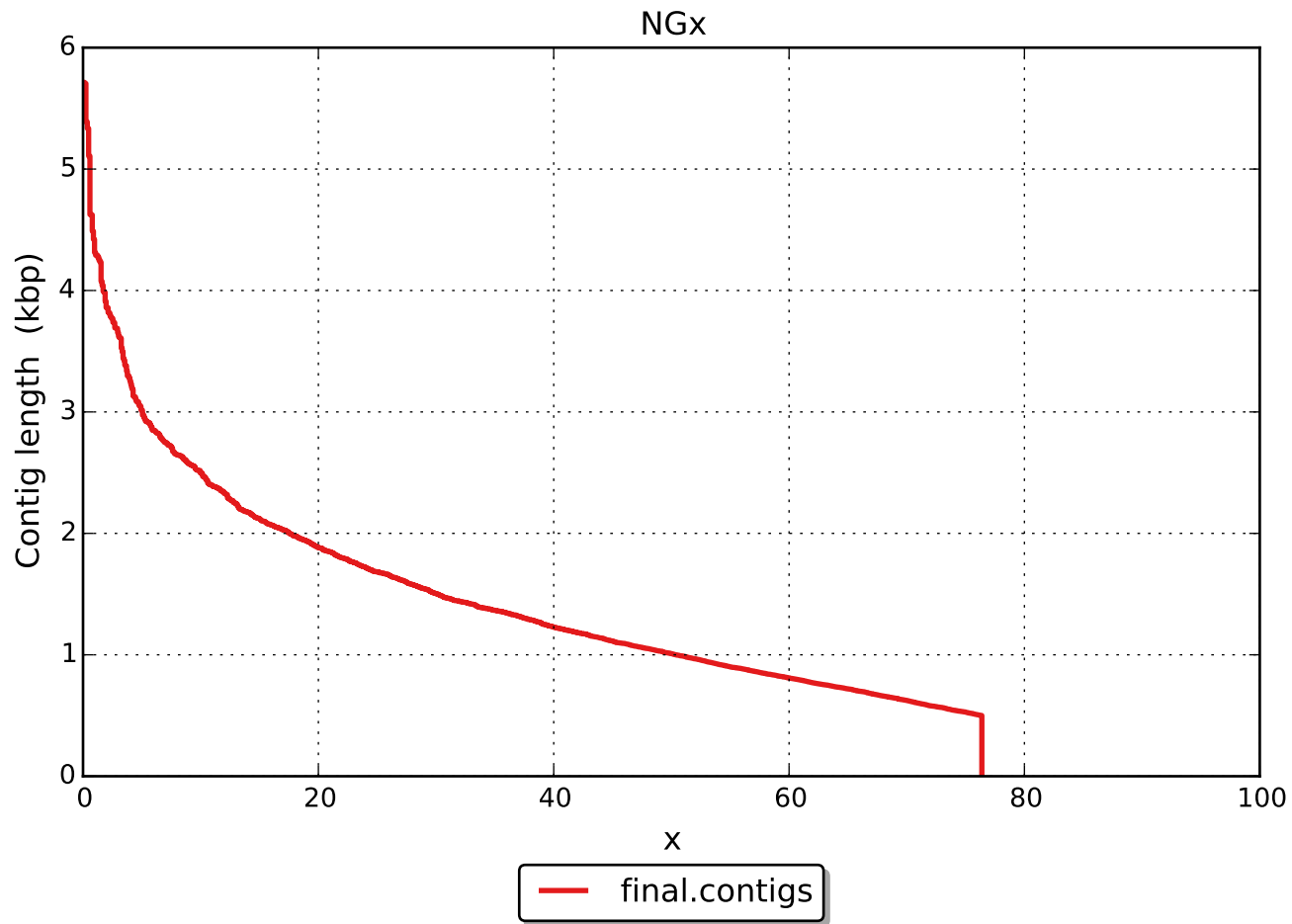
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

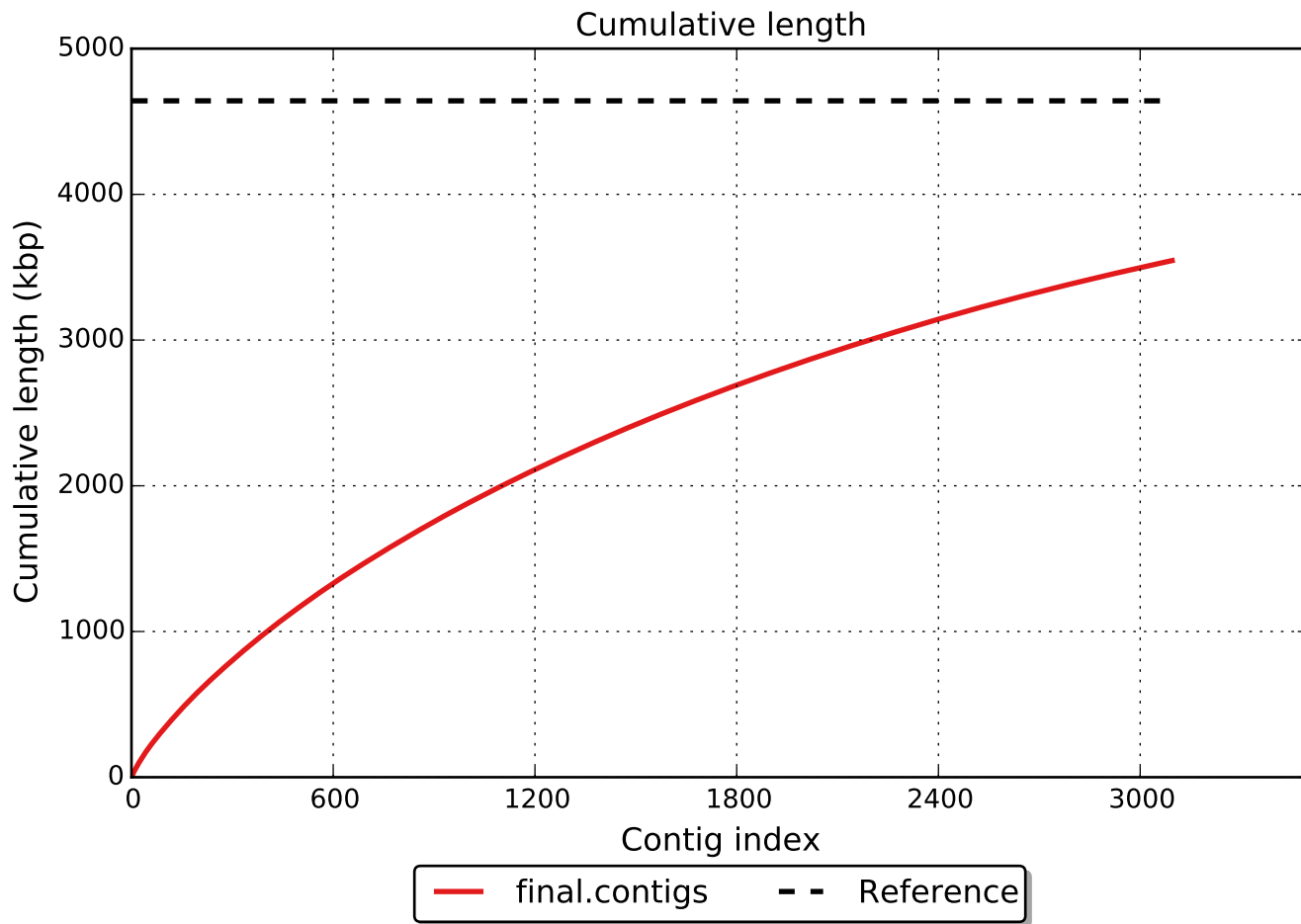
## Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	5
# with misassembly	0
# both parts are significant	0
Partially unaligned length	135
# N's	0

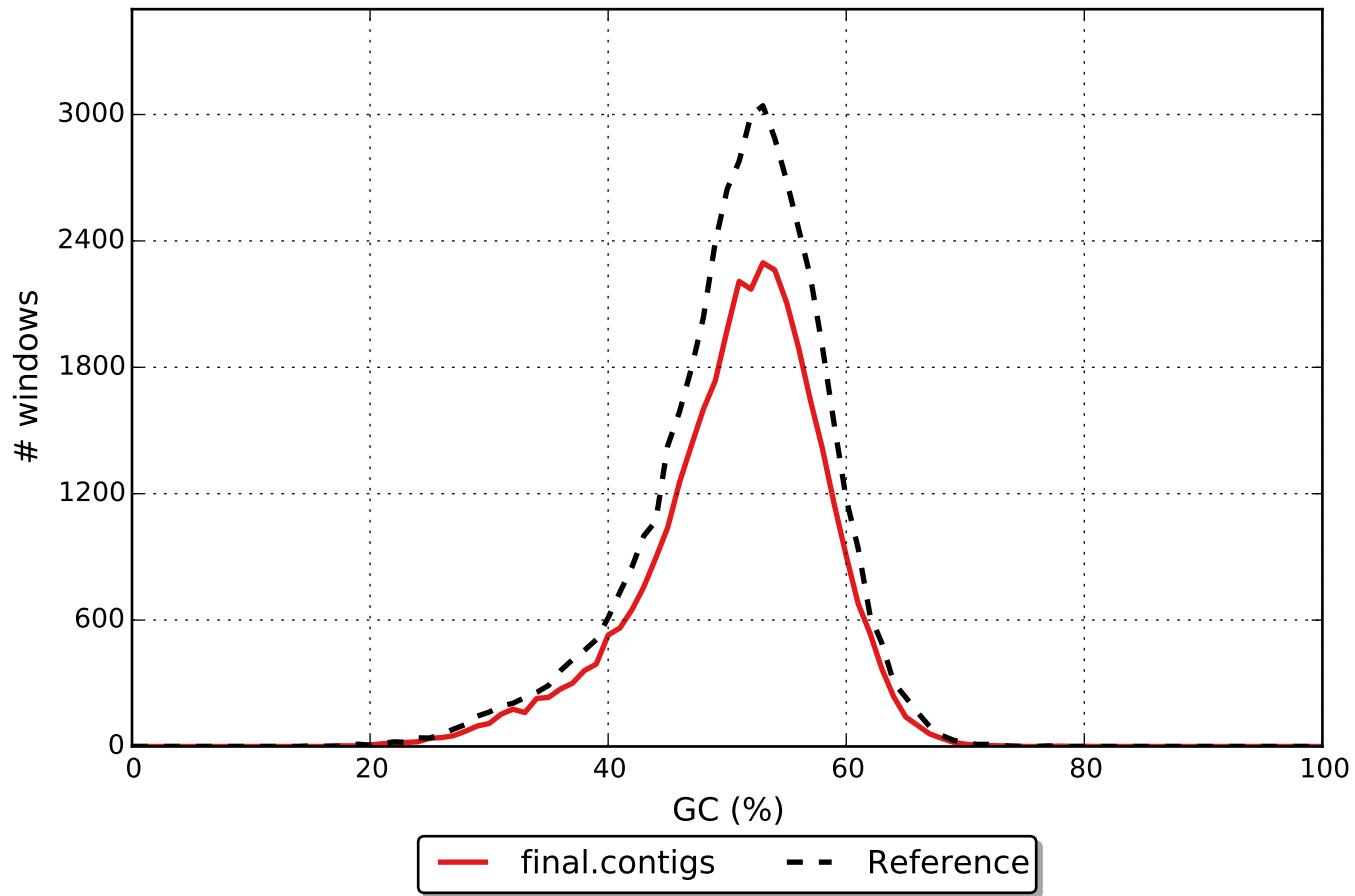
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

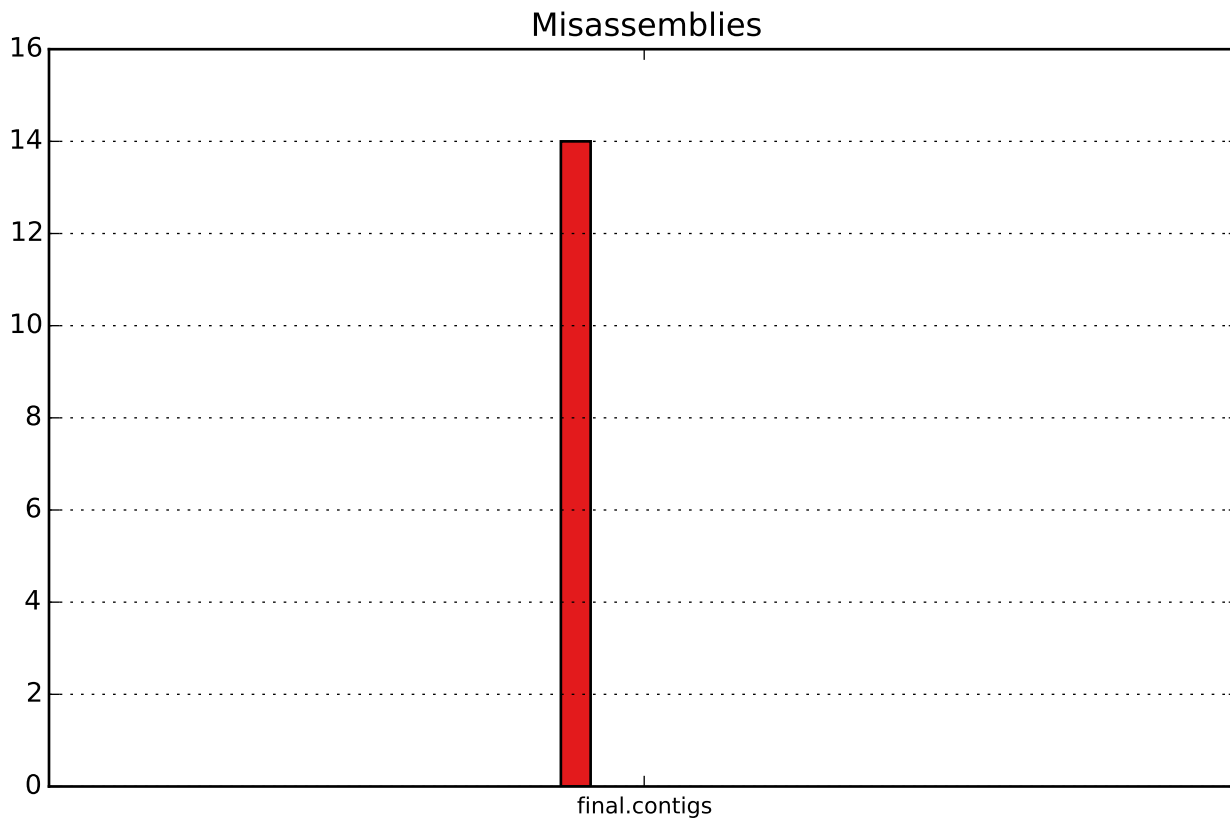






# GC content







Cumulative length (aligned contigs)

