

## Report

	contigs
# contigs ( $\geq 0$ bp)	4832
# contigs ( $\geq 1000$ bp)	1011
# contigs ( $\geq 5000$ bp)	3
# contigs ( $\geq 10000$ bp)	0
# contigs ( $\geq 25000$ bp)	0
# contigs ( $\geq 50000$ bp)	0
Total length ( $\geq 0$ bp)	3506228
Total length ( $\geq 1000$ bp)	1525120
Total length ( $\geq 5000$ bp)	18221
Total length ( $\geq 10000$ bp)	0
Total length ( $\geq 25000$ bp)	0
Total length ( $\geq 50000$ bp)	0
# contigs	2762
Largest contig	6520
Total length	2765545
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	1072
NG50	660
N75	764
L50	874
LG50	1989
L75	1643
# misassemblies	30
# misassembled contigs	30
Misassembled contigs length	58926
# local misassemblies	3
# unaligned contigs	1 + 13 part
Unaligned length	3749
Genome fraction (%)	59.379
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	773.65
# indels per 100 kbp	1.42
Largest alignment	6021
NA50	1064
NGA50	655
NA75	756
LA50	884
LGA50	2011
LA75	1661

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

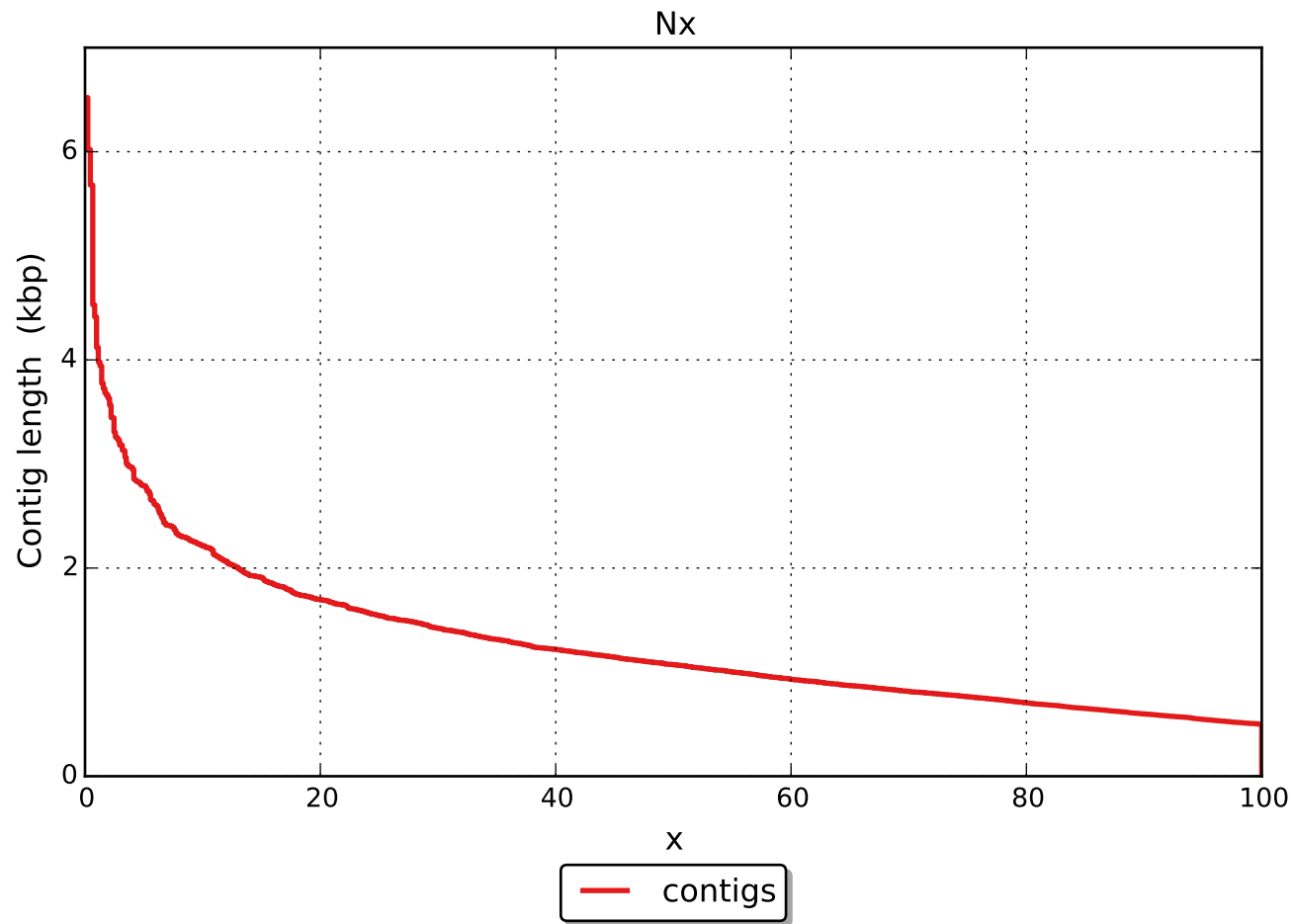
	contigs
# misassemblies	30
# relocations	30
# translocations	0
# inversions	0
# misassembled contigs	30
Misassembled contigs length	58926
# local misassemblies	3
# mismatches	21323
# indels	39
# short indels	38
# long indels	1
Indels length	135

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).

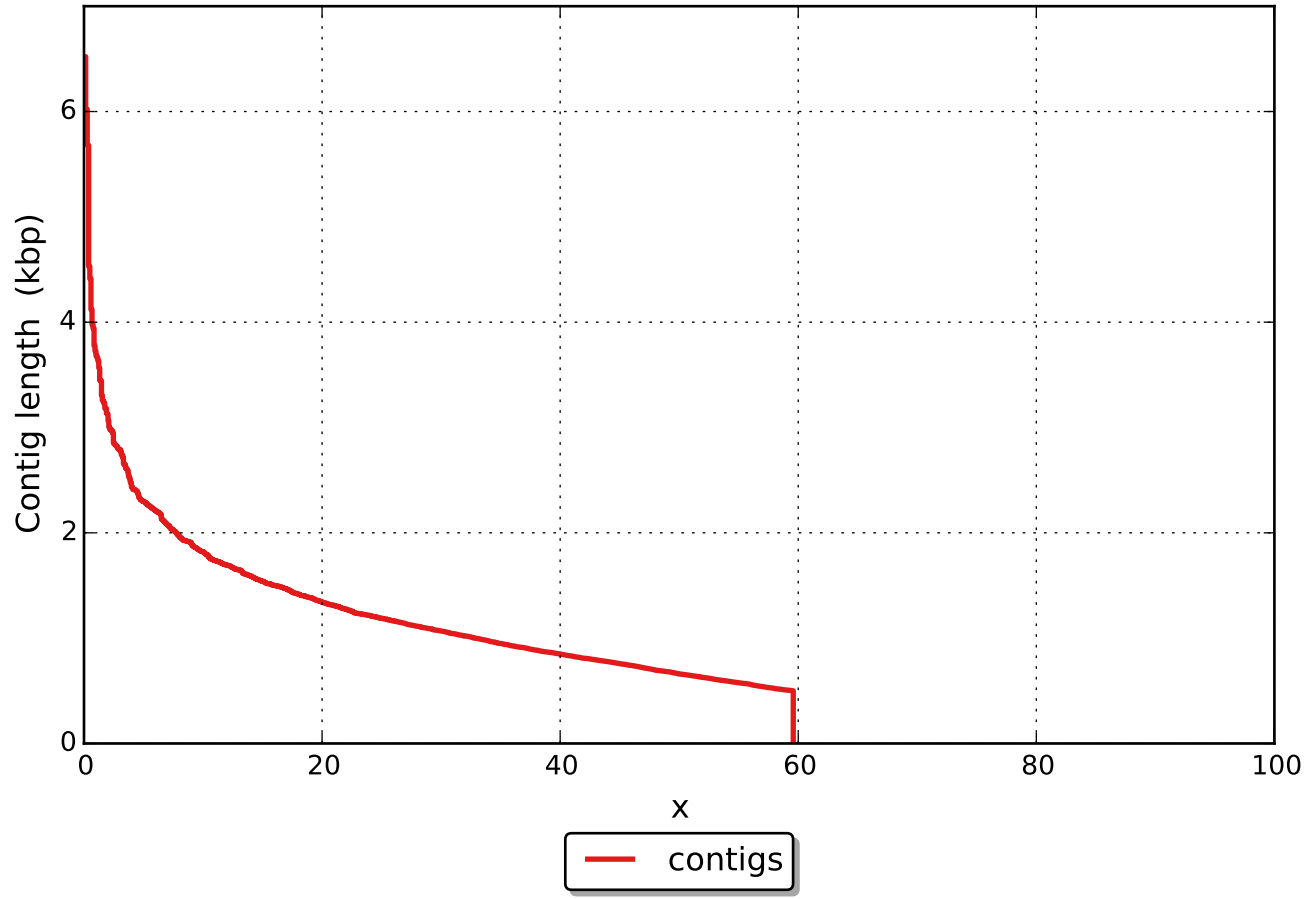
## Unaligned report

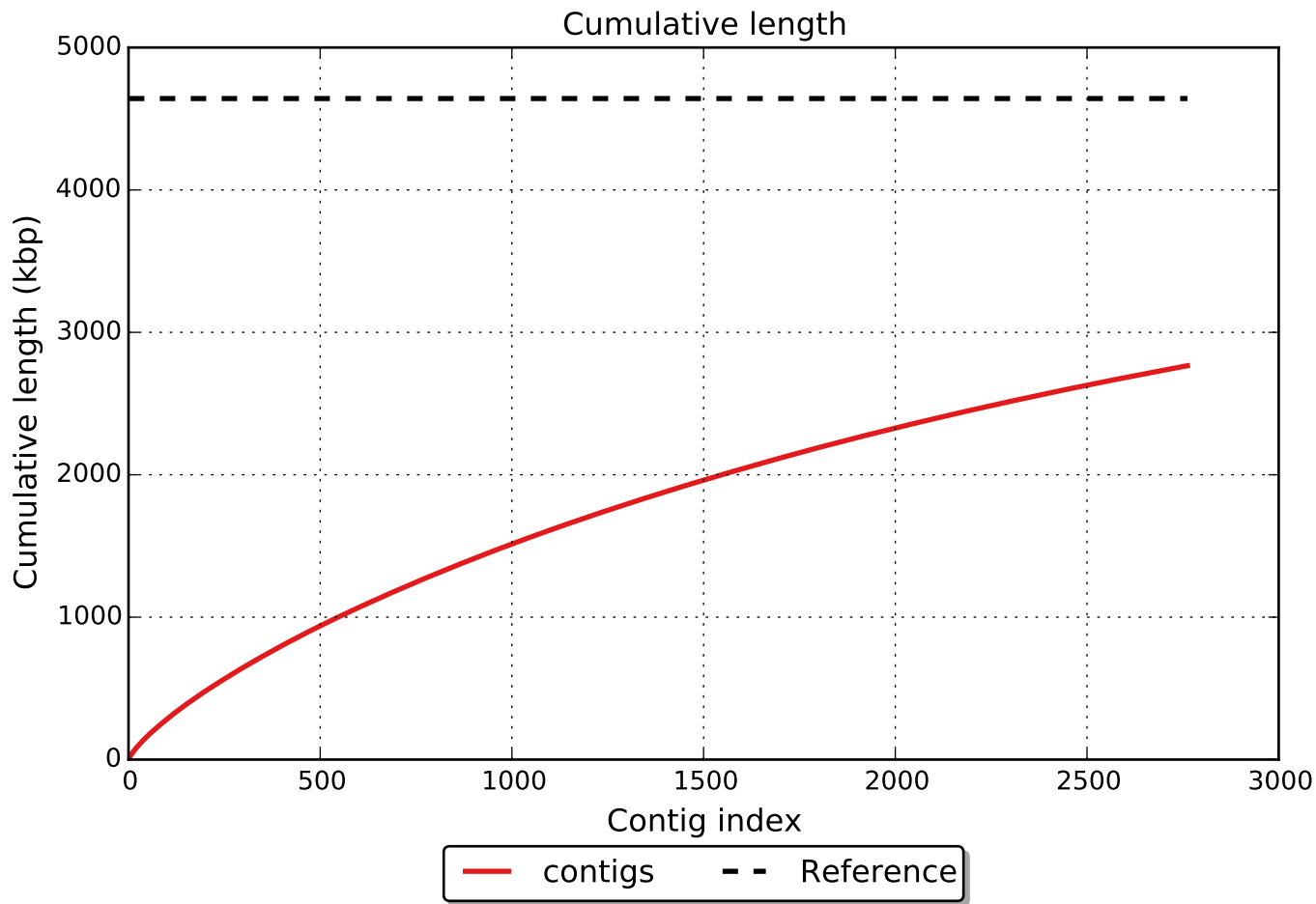
	contigs
# fully unaligned contigs	1
Fully unaligned length	989
# partially unaligned contigs	13
# with misassembly	0
# both parts are significant	1
Partially unaligned length	2760
# N's	0

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).

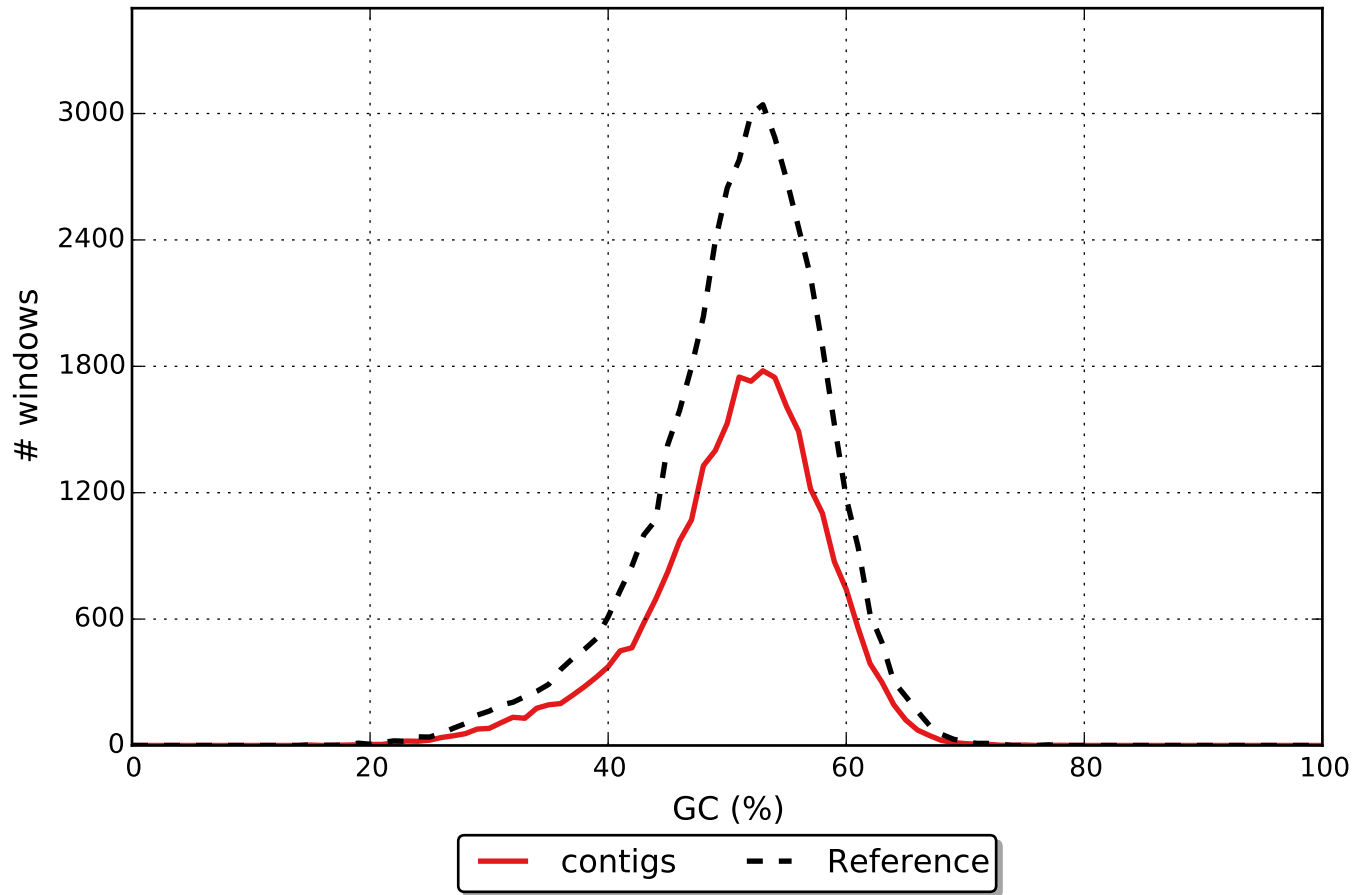


NGx

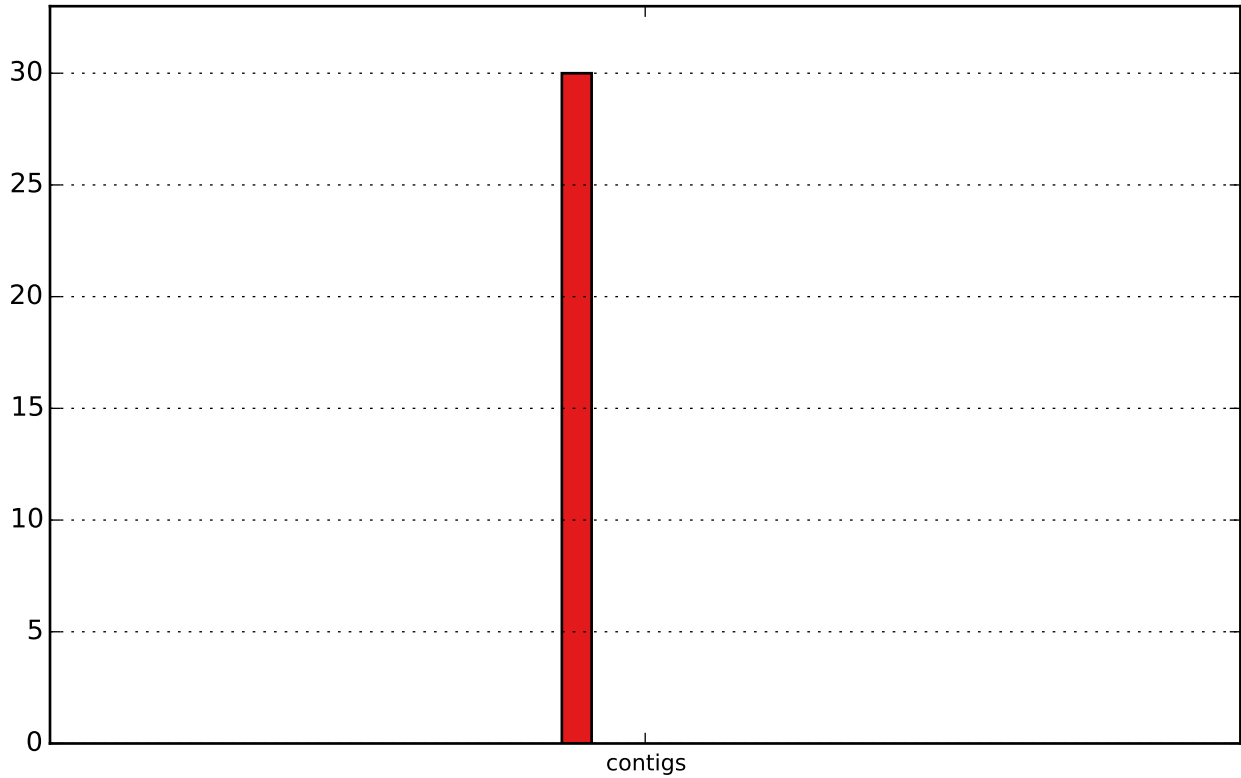




# GC content

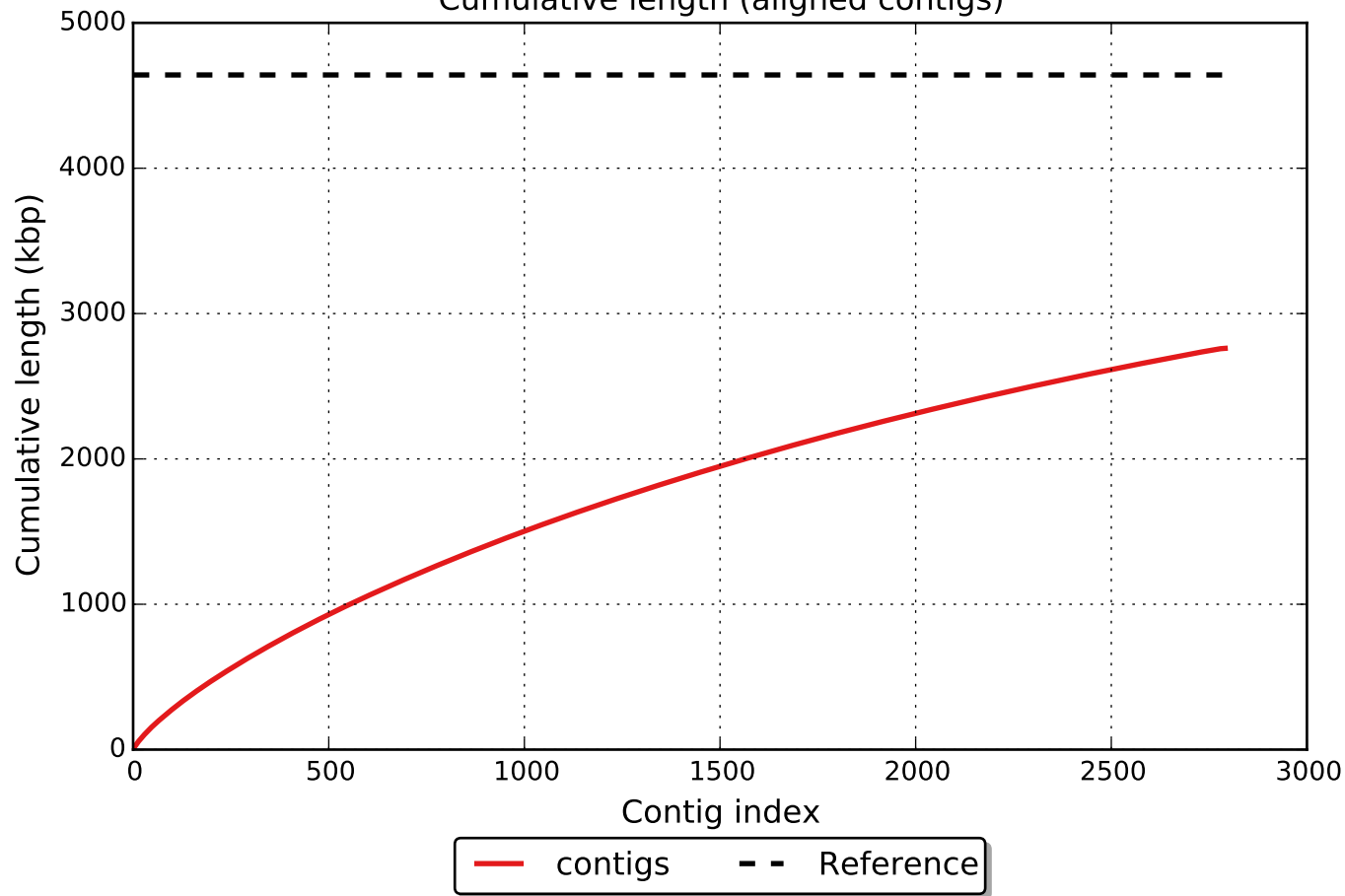


# Misassemblies

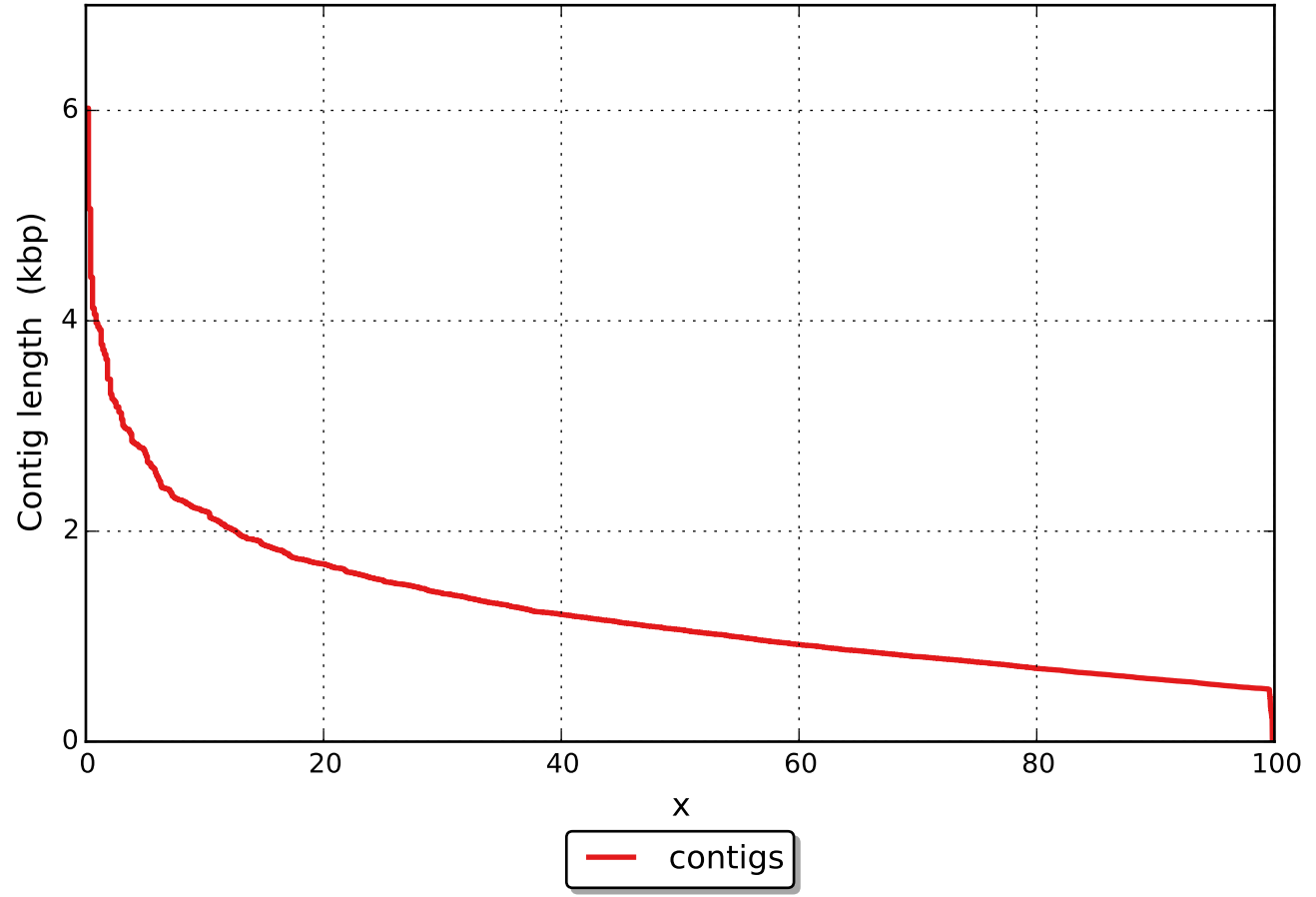




Cumulative length (aligned contigs)



NAx



NGAx

