

## Report

	contigs
# contigs ( $\geq 1000$ bp)	197
# contigs ( $\geq 5000$ bp)	111
# contigs ( $\geq 10000$ bp)	77
# contigs ( $\geq 25000$ bp)	50
# contigs ( $\geq 50000$ bp)	29
Total length ( $\geq 1000$ bp)	4720176
Total length ( $\geq 5000$ bp)	4495997
Total length ( $\geq 10000$ bp)	4262691
Total length ( $\geq 25000$ bp)	3801827
Total length ( $\geq 50000$ bp)	3082893
# contigs	242
Largest contig	276573
Total length	4750449
Reference length	4641652
GC (%)	50.84
Reference GC (%)	50.79
N50	71499
NG50	71499
N75	30248
NG75	33490
L50	17
LG50	17
L75	42
LG75	39
# misassemblies	3
# misassembled contigs	2
Misassembled contigs length	139104
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	90.363
Duplication ratio	1.133
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1111.06
# indels per 100 kbp	0.69
Largest alignment	276573
NA50	71087
NGA50	71087
NA75	30198
NGA75	32072
LA50	17
LGA50	17
LA75	43
LGA75	40

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	3
# relocations	3
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	139104
# local misassemblies	2
# mismatches	46602
# indels	29
# short indels	29
# long indels	0
Indels length	36

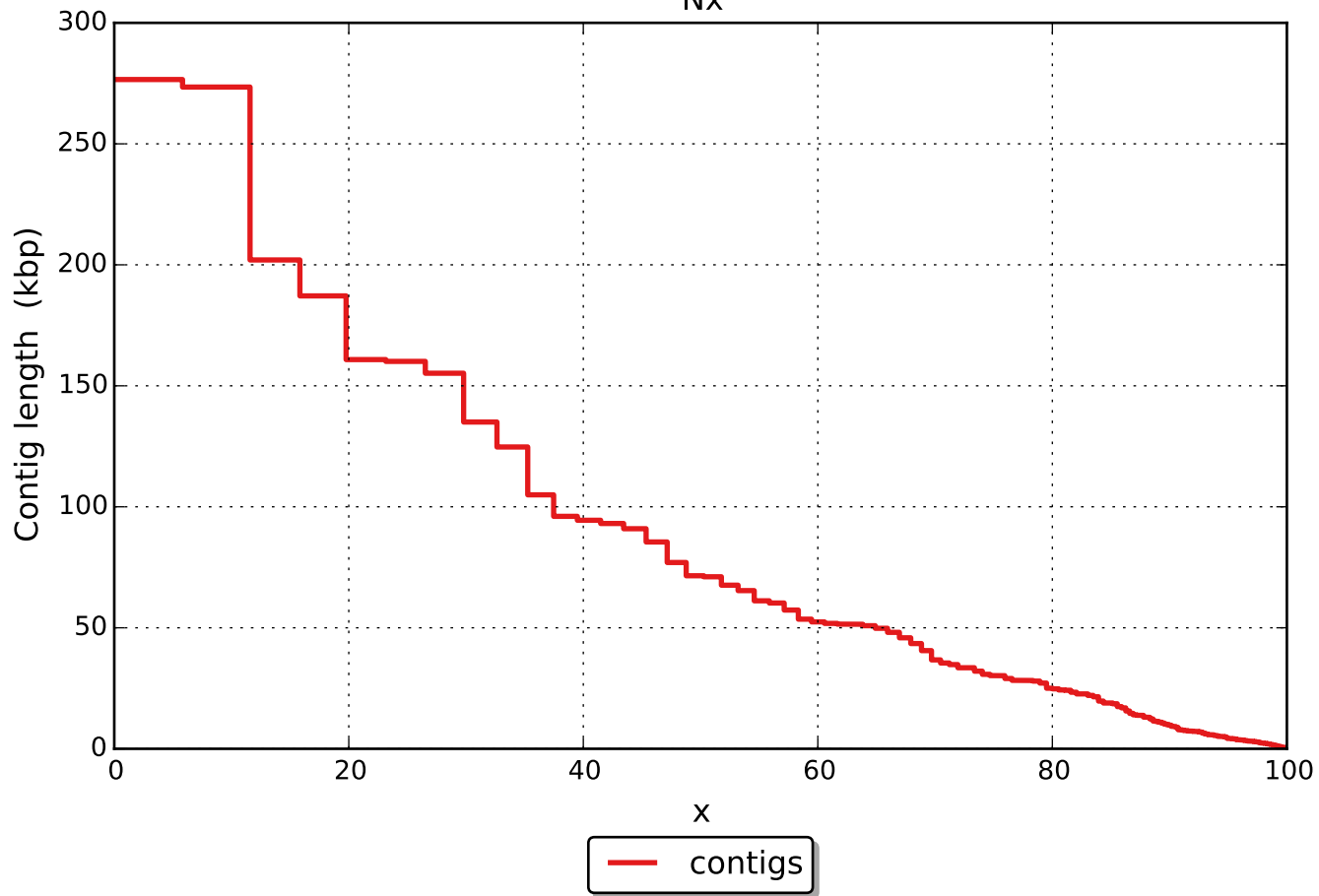
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

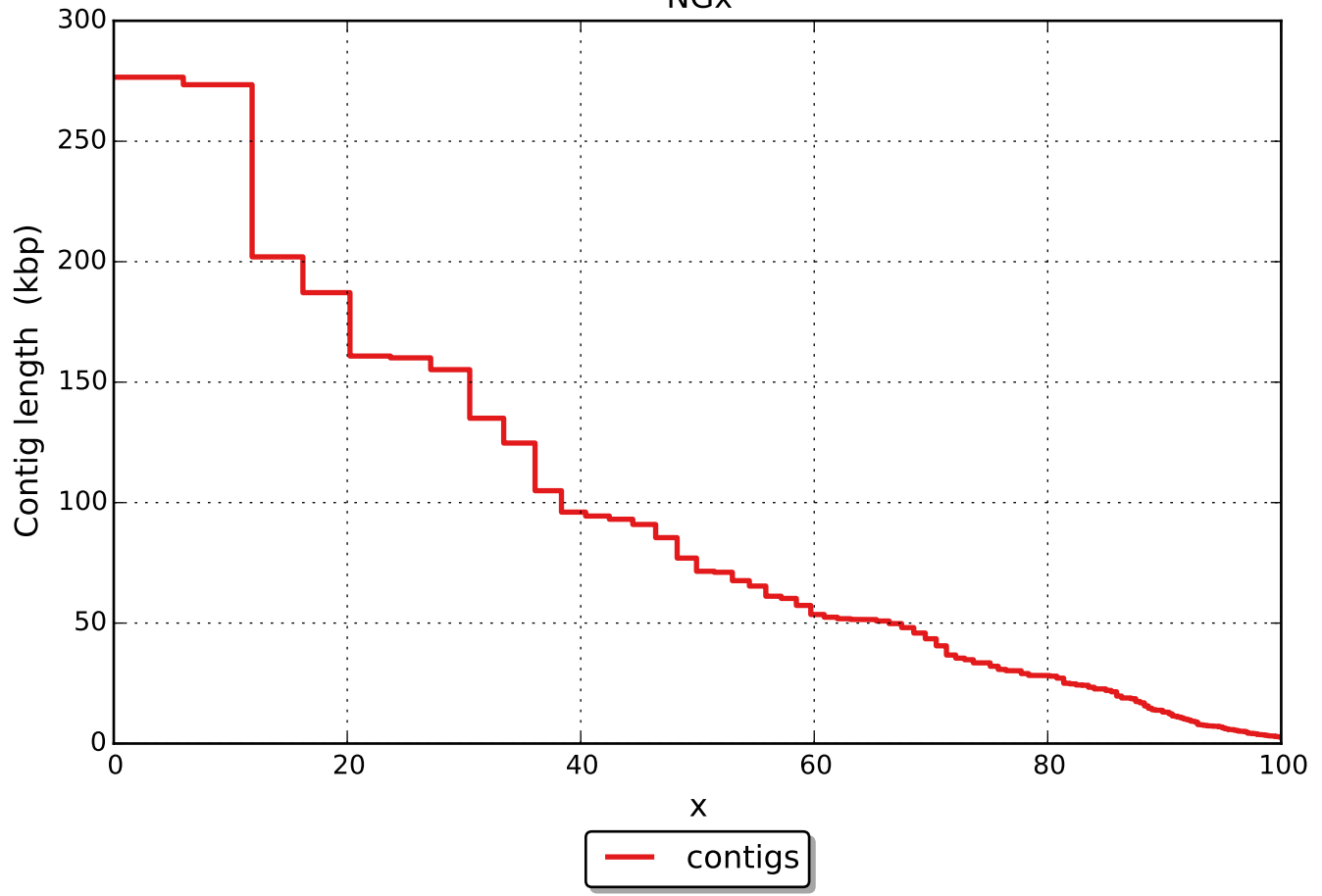
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

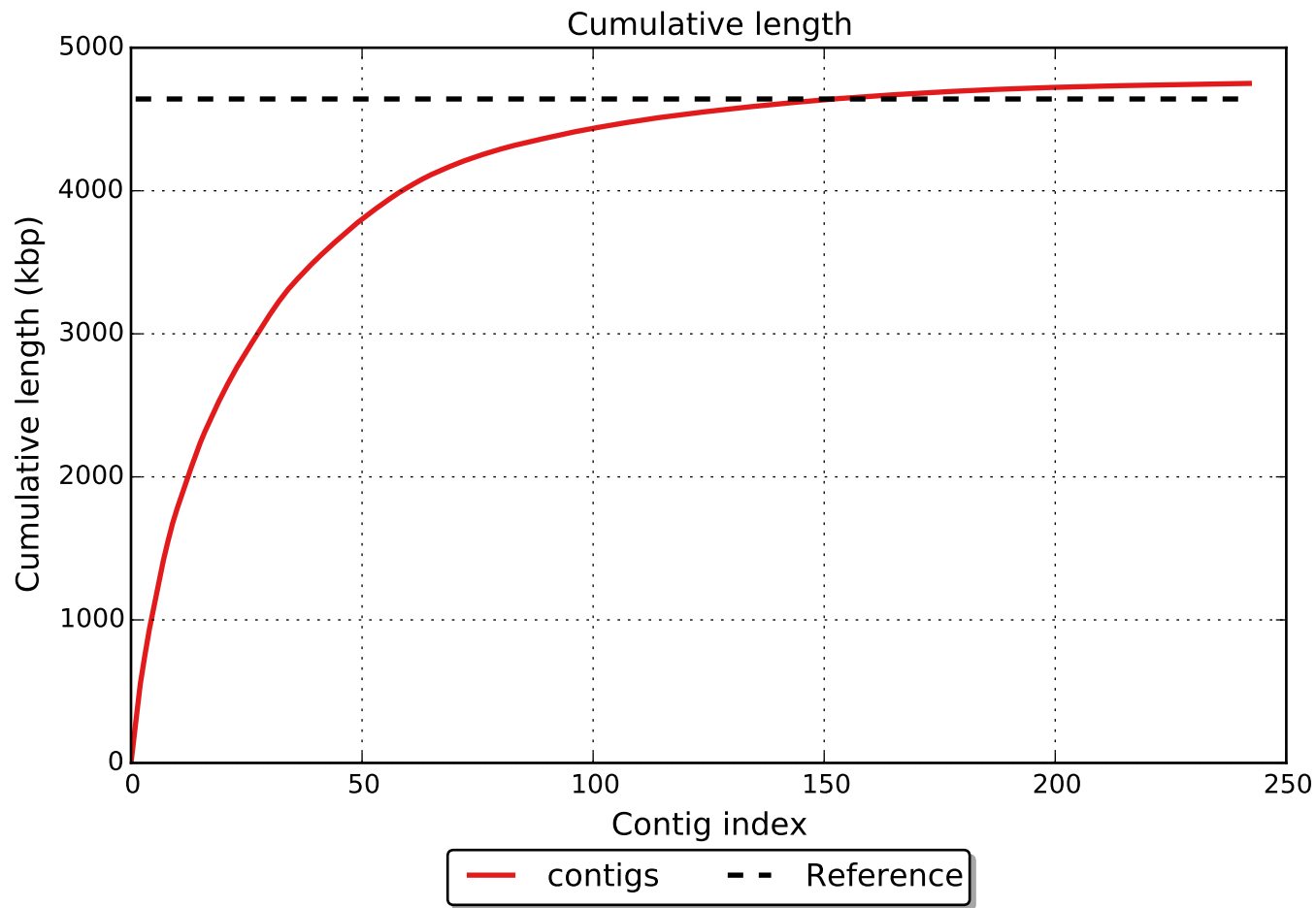
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

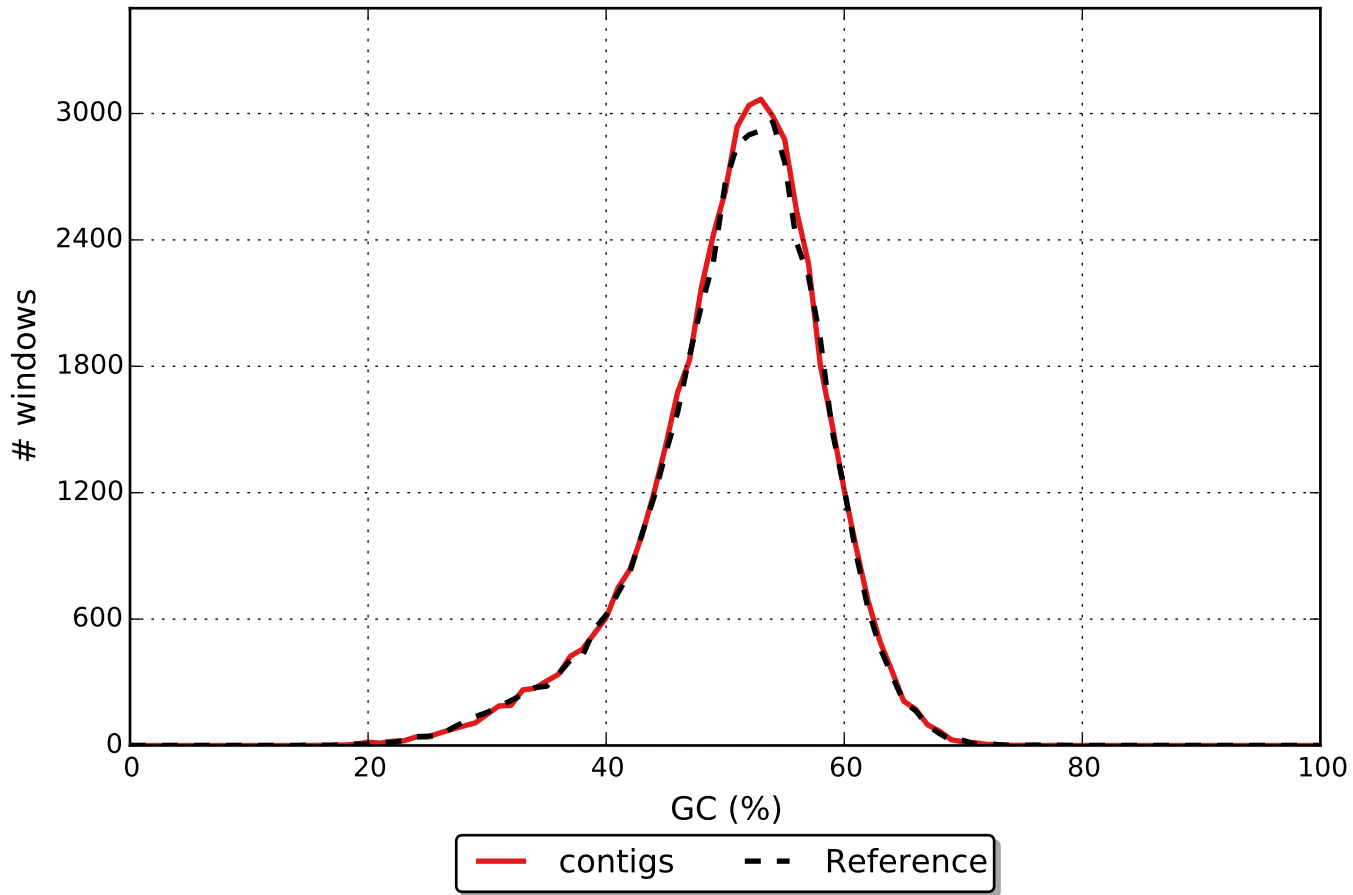


NGx

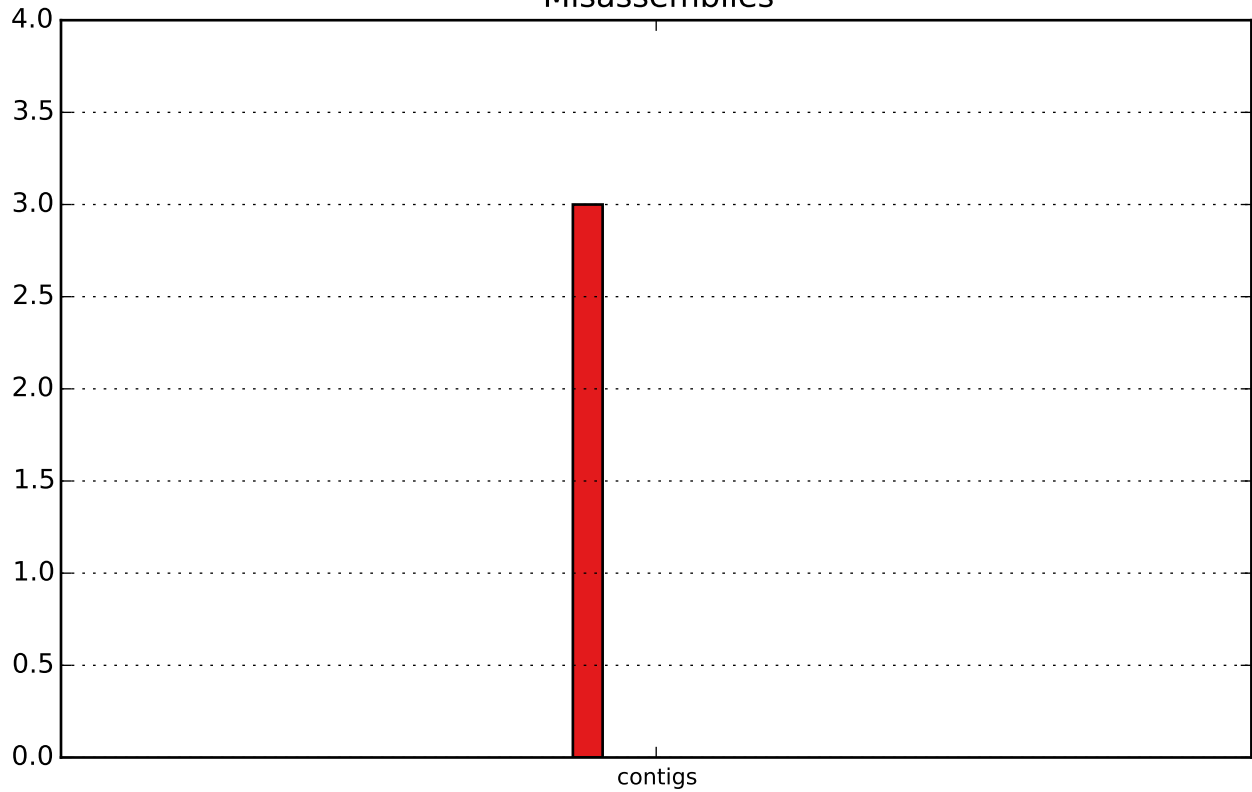




# GC content

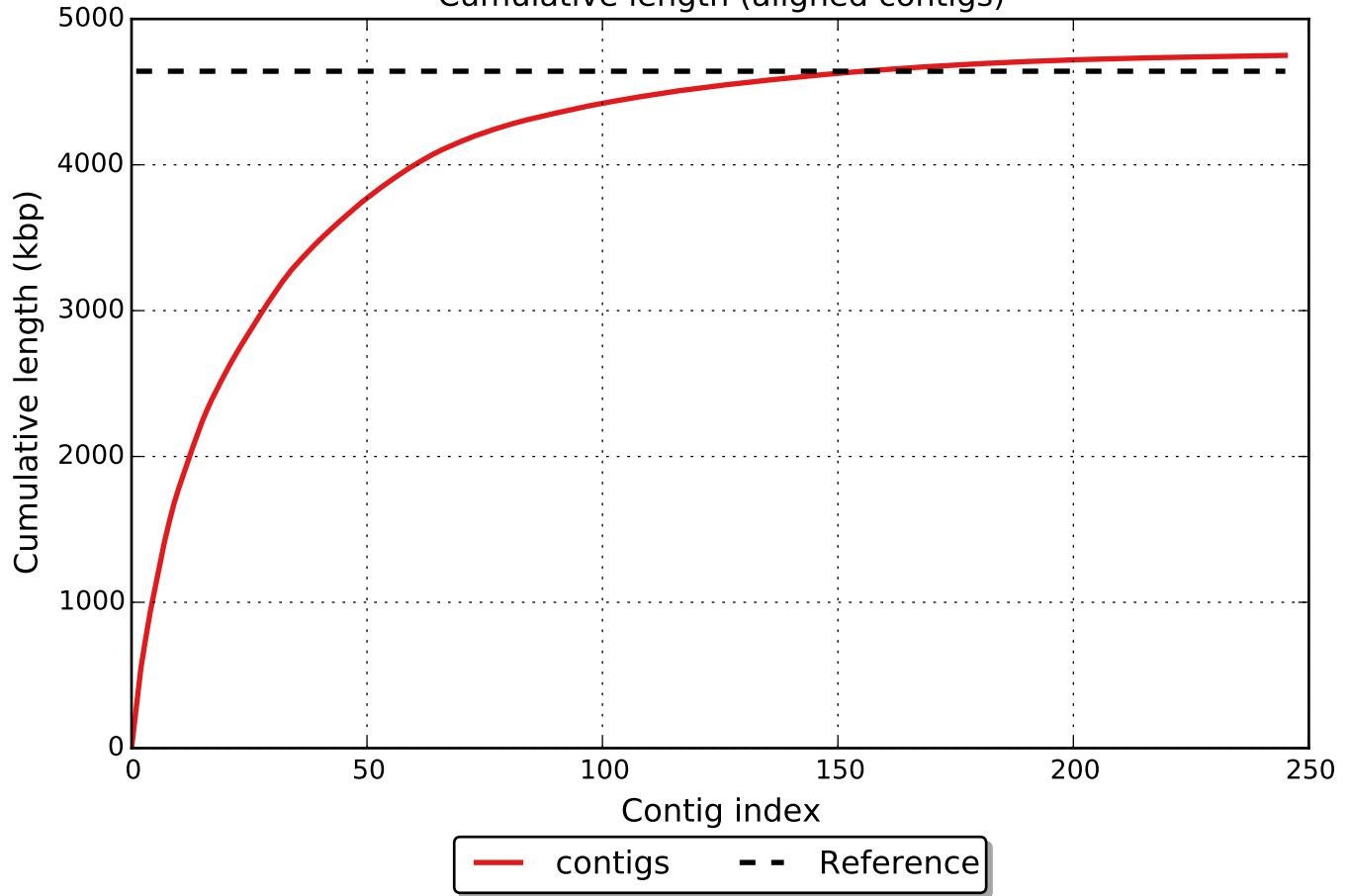


# Misassemblies

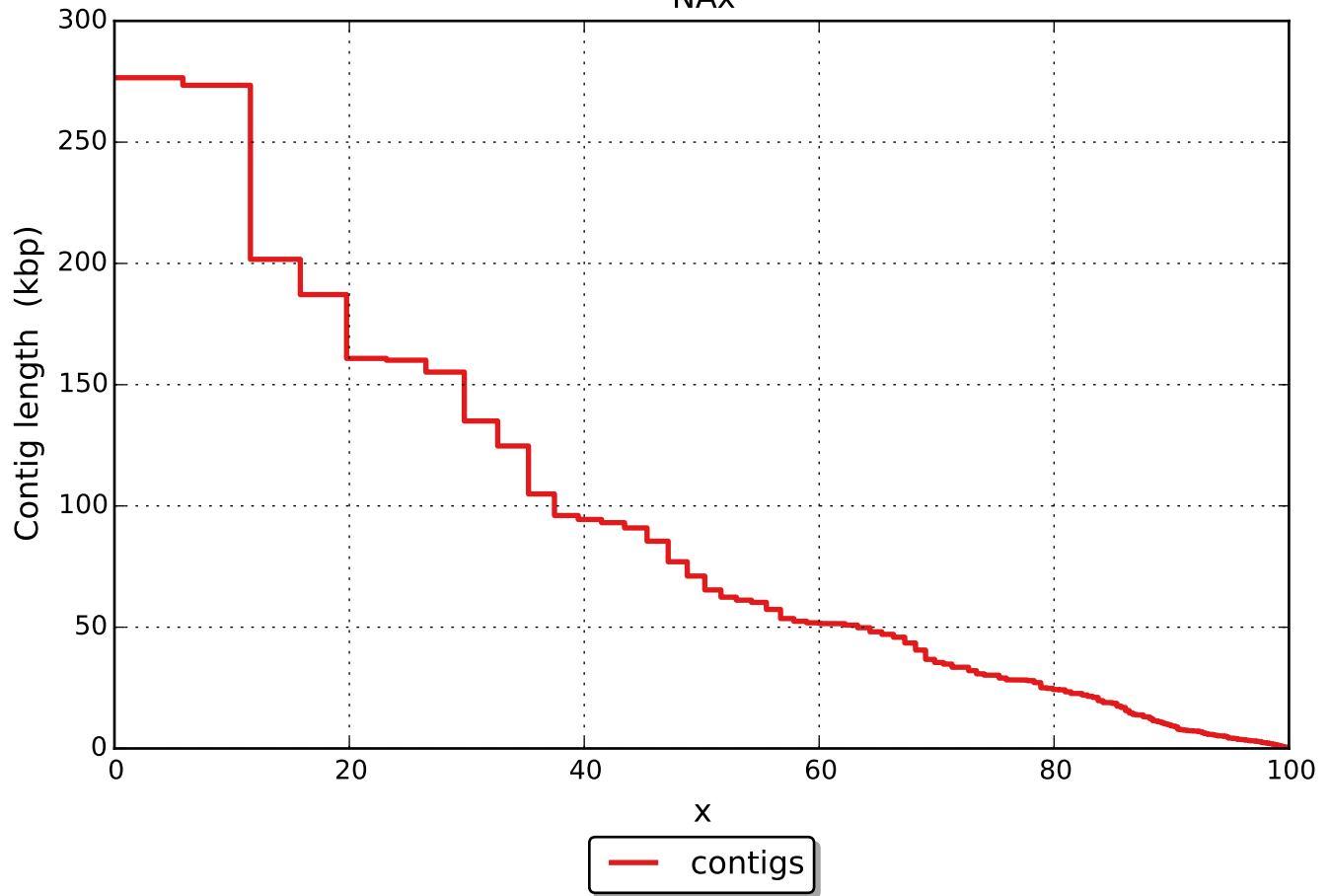




Cumulative length (aligned contigs)



NAx



# NGAx

