

## Report

	contigs
# contigs ( $\geq 1000$ bp)	34
# contigs ( $\geq 5000$ bp)	29
# contigs ( $\geq 10000$ bp)	28
# contigs ( $\geq 25000$ bp)	26
# contigs ( $\geq 50000$ bp)	22
Total length ( $\geq 1000$ bp)	4849062
Total length ( $\geq 5000$ bp)	4836655
Total length ( $\geq 10000$ bp)	4828130
Total length ( $\geq 25000$ bp)	4800725
Total length ( $\geq 50000$ bp)	4638885
# contigs	46
Largest contig	472565
Total length	4857645
Reference length	4641652
GC (%)	50.70
Reference GC (%)	50.78
N50	305624
NG50	305624
N75	201240
NG75	214400
L50	7
LG50	7
L75	12
LG75	11
# misassemblies	15
# misassembled contigs	2
Misassembled contigs length	401494
# local misassemblies	3
# unaligned contigs	0 + 1 part
Unaligned length	222
Genome fraction (%)	98.837
Duplication ratio	1.059
# N's per 100 kbp	0.00
# mismatches per 100 kbp	526.87
# indels per 100 kbp	1.02
Largest alignment	472565
NA50	304586
NGA50	304586
NA75	156700
NGA75	183277
LA50	7
LGA50	7
LA75	13
LGA75	12

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	15
# relocations	15
# translocations	0
# inversions	0
# possibly misassembled contigs	2
# misassembled contigs	2
Misassembled contigs length	401494
# local misassemblies	3
# mismatches	24171
# indels	47
# short indels	47
# long indels	0
Indels length	47

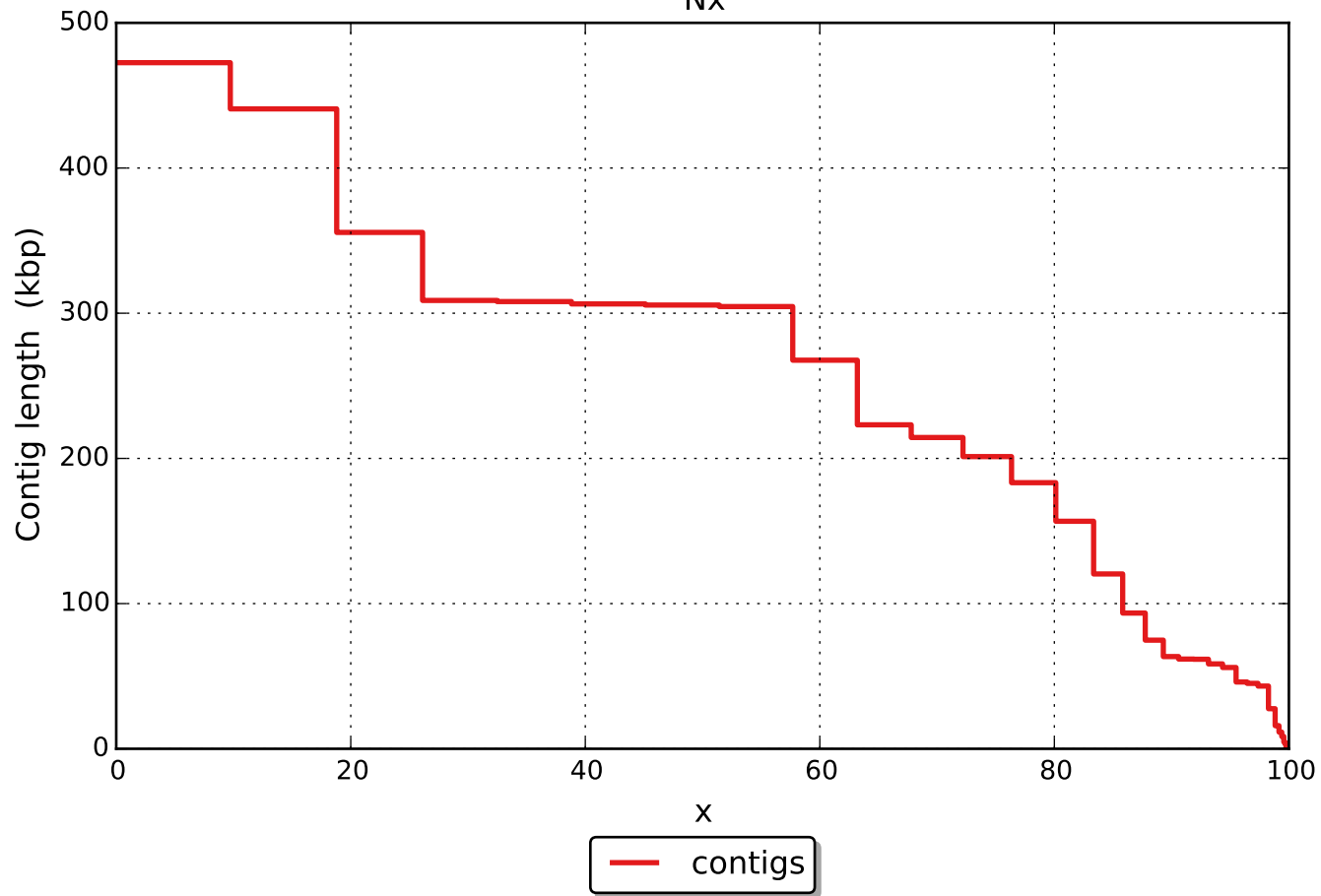
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

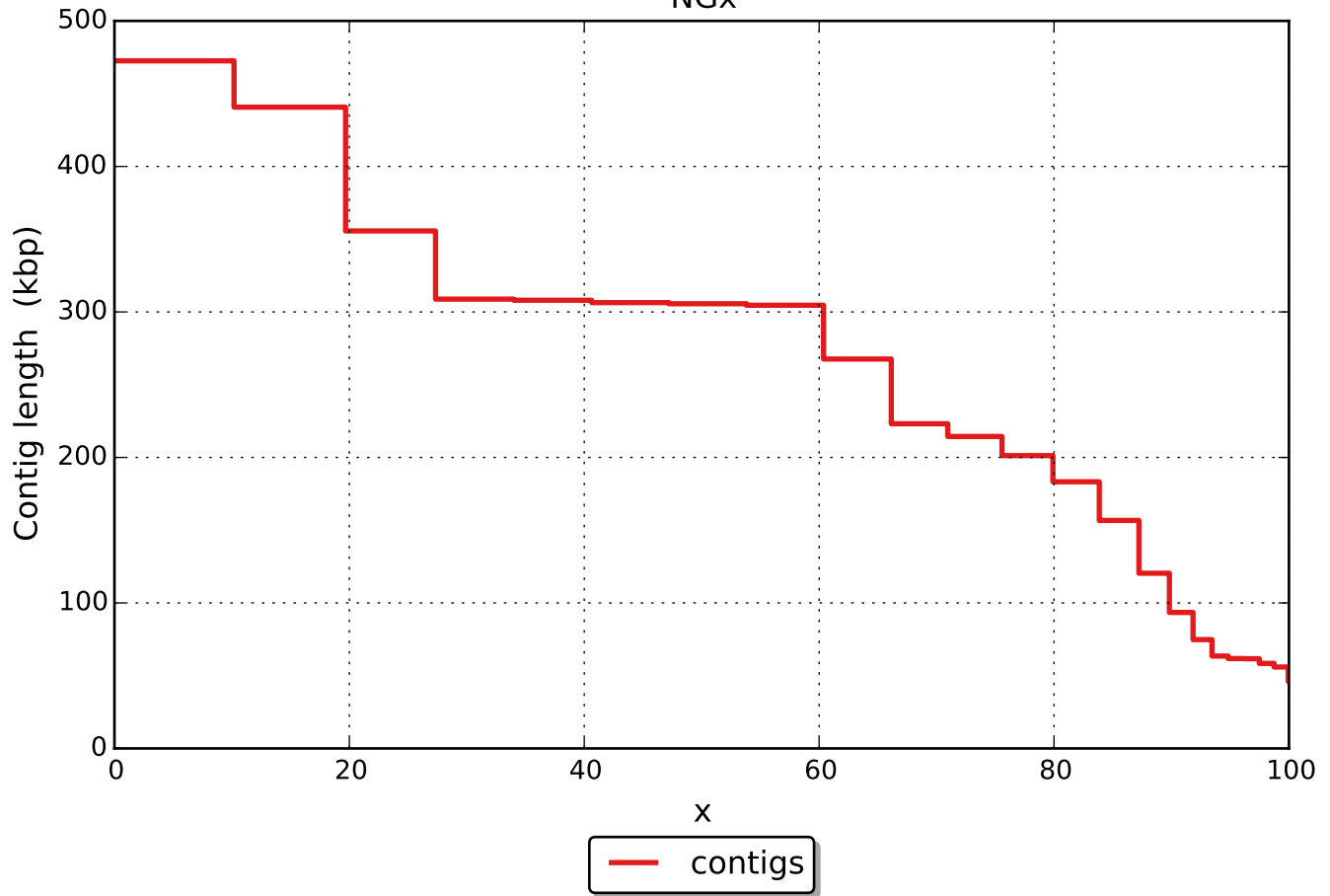
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	222
# N's	0

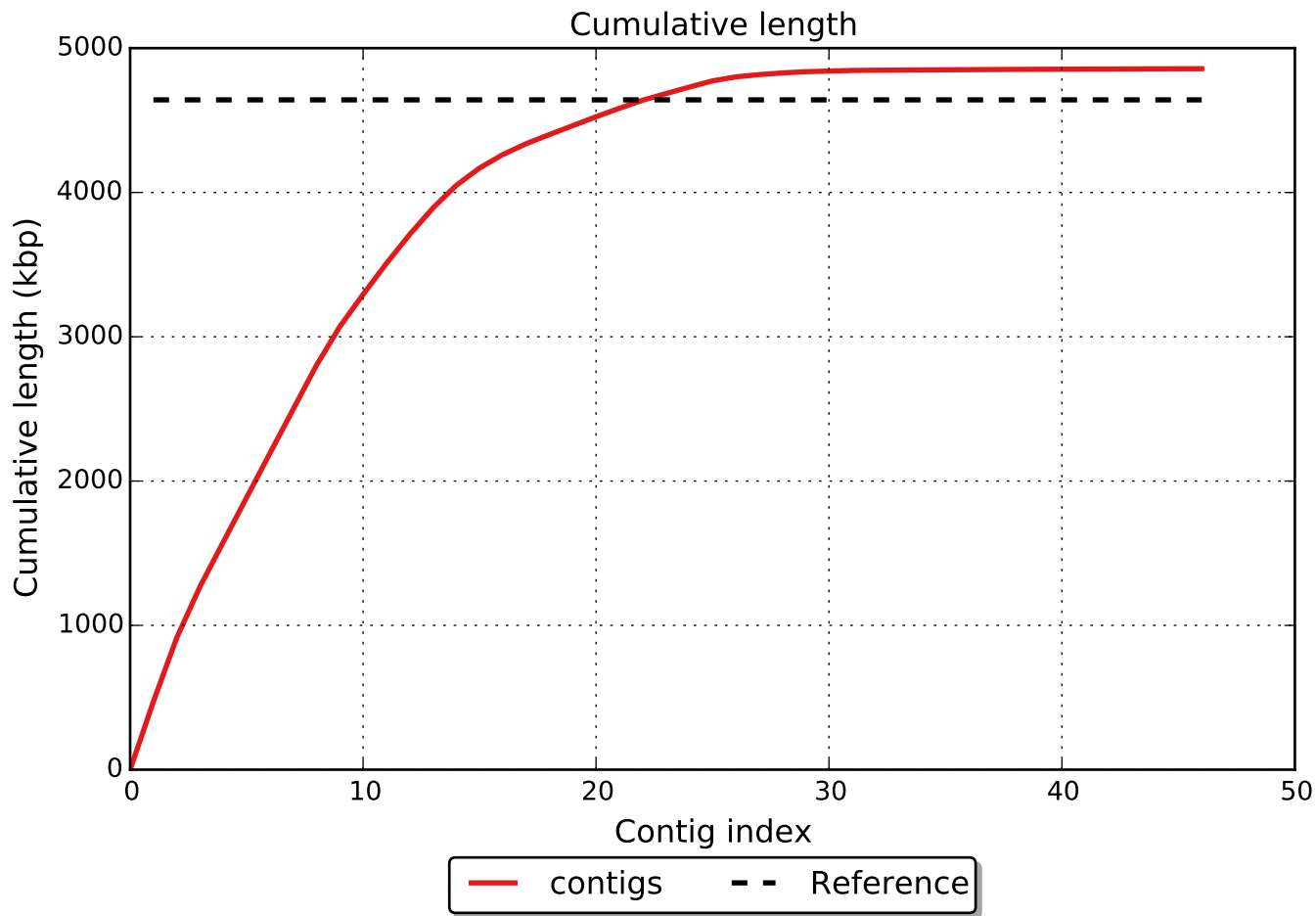
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

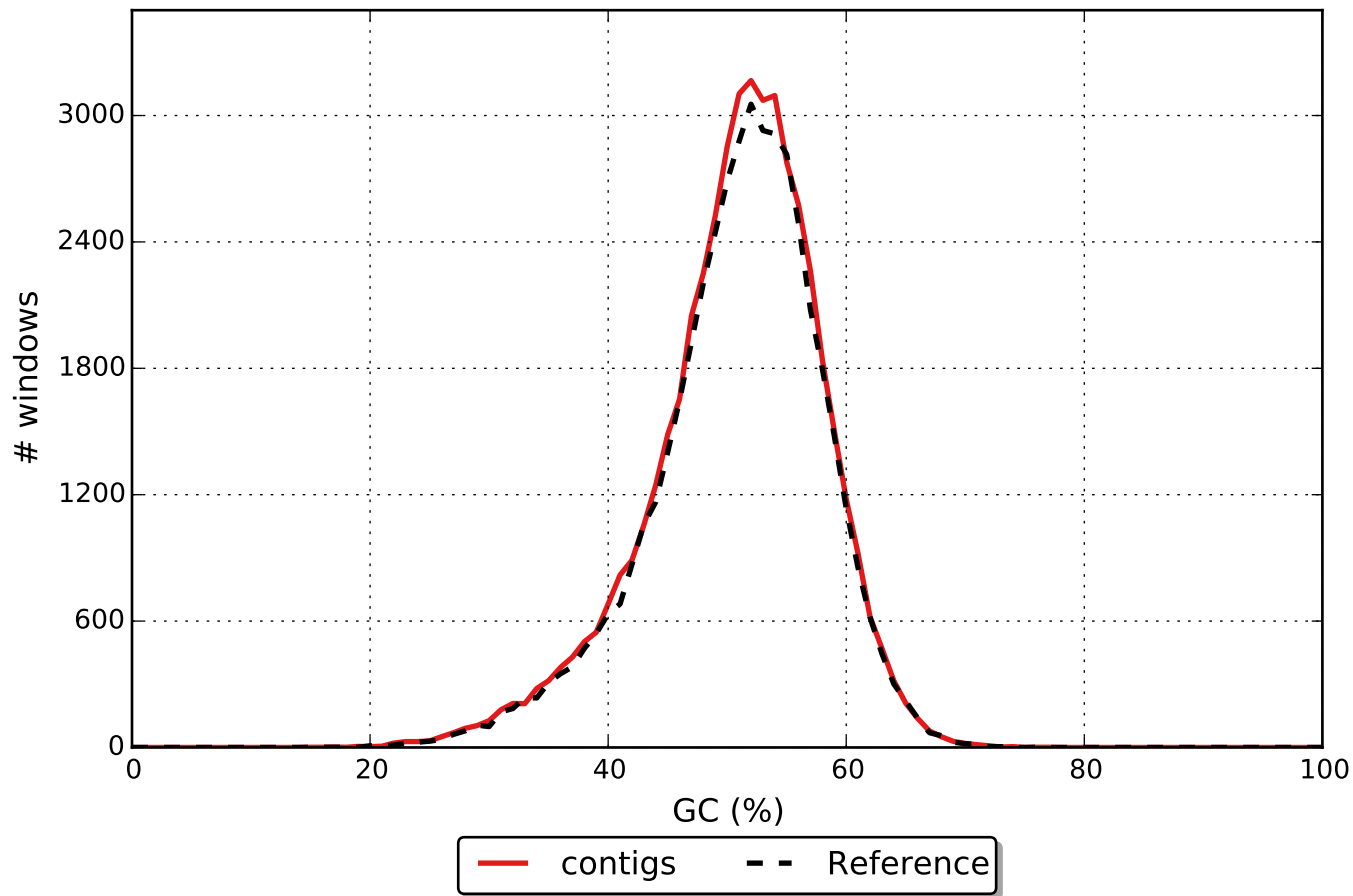


NGx

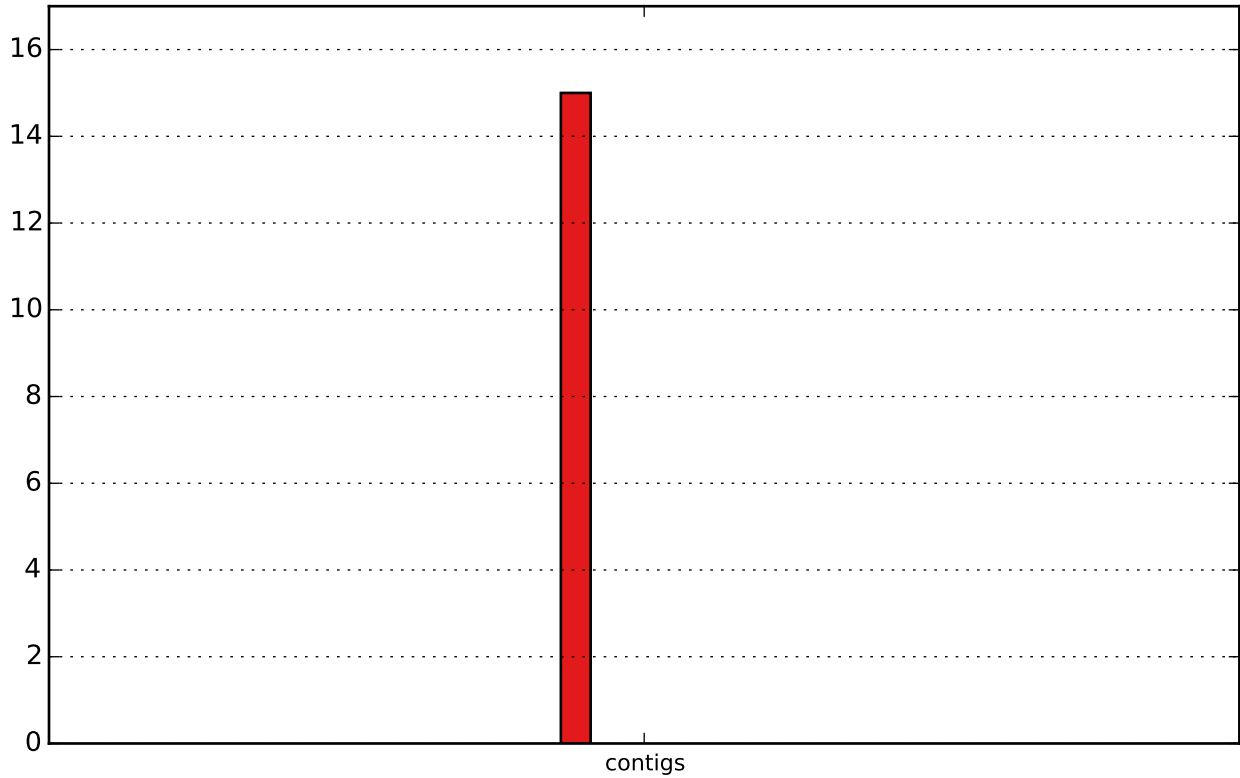




GC content

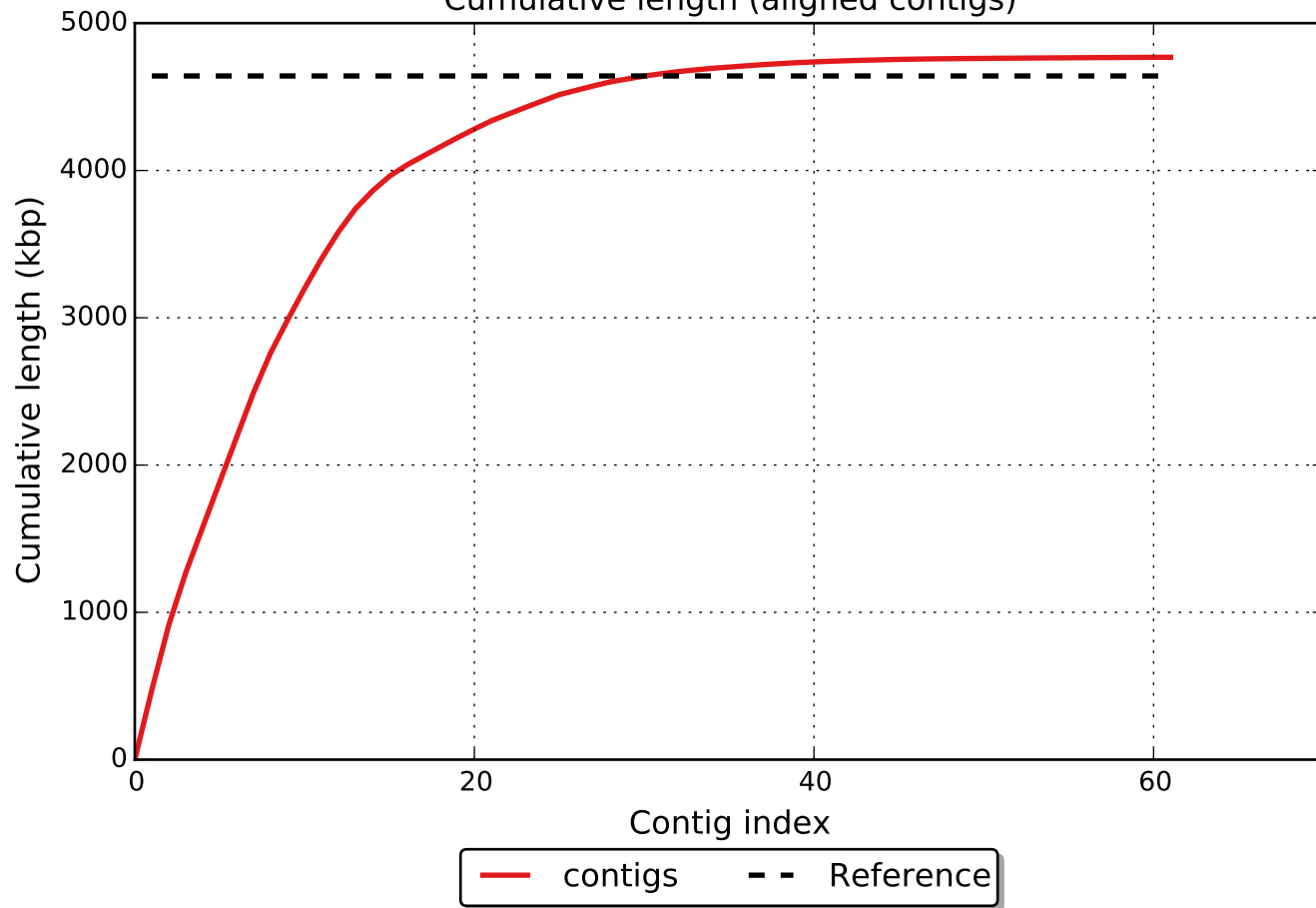


# Misassemblies

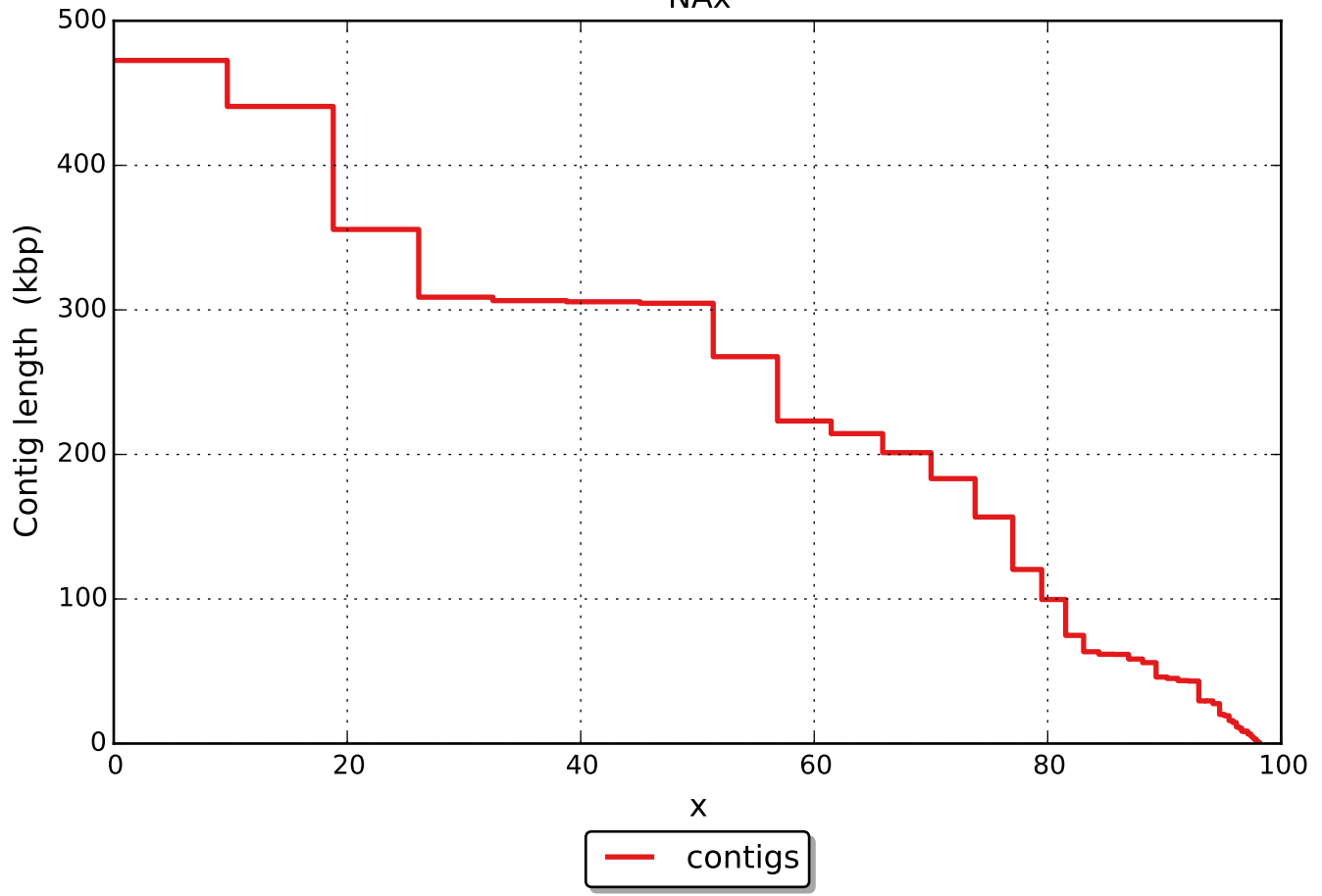




Cumulative length (aligned contigs)



NAx



NGAx

