

## Report

	contigs
# contigs ( $\geq 0$ bp)	12136
# contigs ( $\geq 1000$ bp)	1323
# contigs ( $\geq 5000$ bp)	1
# contigs ( $\geq 10000$ bp)	0
# contigs ( $\geq 25000$ bp)	0
# contigs ( $\geq 50000$ bp)	0
Total length ( $\geq 0$ bp)	6345835
Total length ( $\geq 1000$ bp)	1909138
Total length ( $\geq 5000$ bp)	5112
Total length ( $\geq 10000$ bp)	0
Total length ( $\geq 25000$ bp)	0
Total length ( $\geq 50000$ bp)	0
# contigs	4392
Largest contig	5112
Total length	4069569
Reference length	4641652
GC (%)	50.76
Reference GC (%)	50.79
N50	965
NG50	888
N75	706
NG75	618
L50	1452
LG50	1761
L75	2685
LG75	3334
# misassemblies	8
# misassembled contigs	8
Misassembled contigs length	18735
# local misassemblies	3
# unaligned contigs	3 + 25 part
Unaligned length	4390
Genome fraction (%)	81.116
Duplication ratio	1.080
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1301.66
# indels per 100 kbp	2.71
Largest alignment	4439
NA50	962
NGA50	885
NA75	704
NGA75	615
LA50	1458
LGA50	1768
LA75	2695
LGA75	3348

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

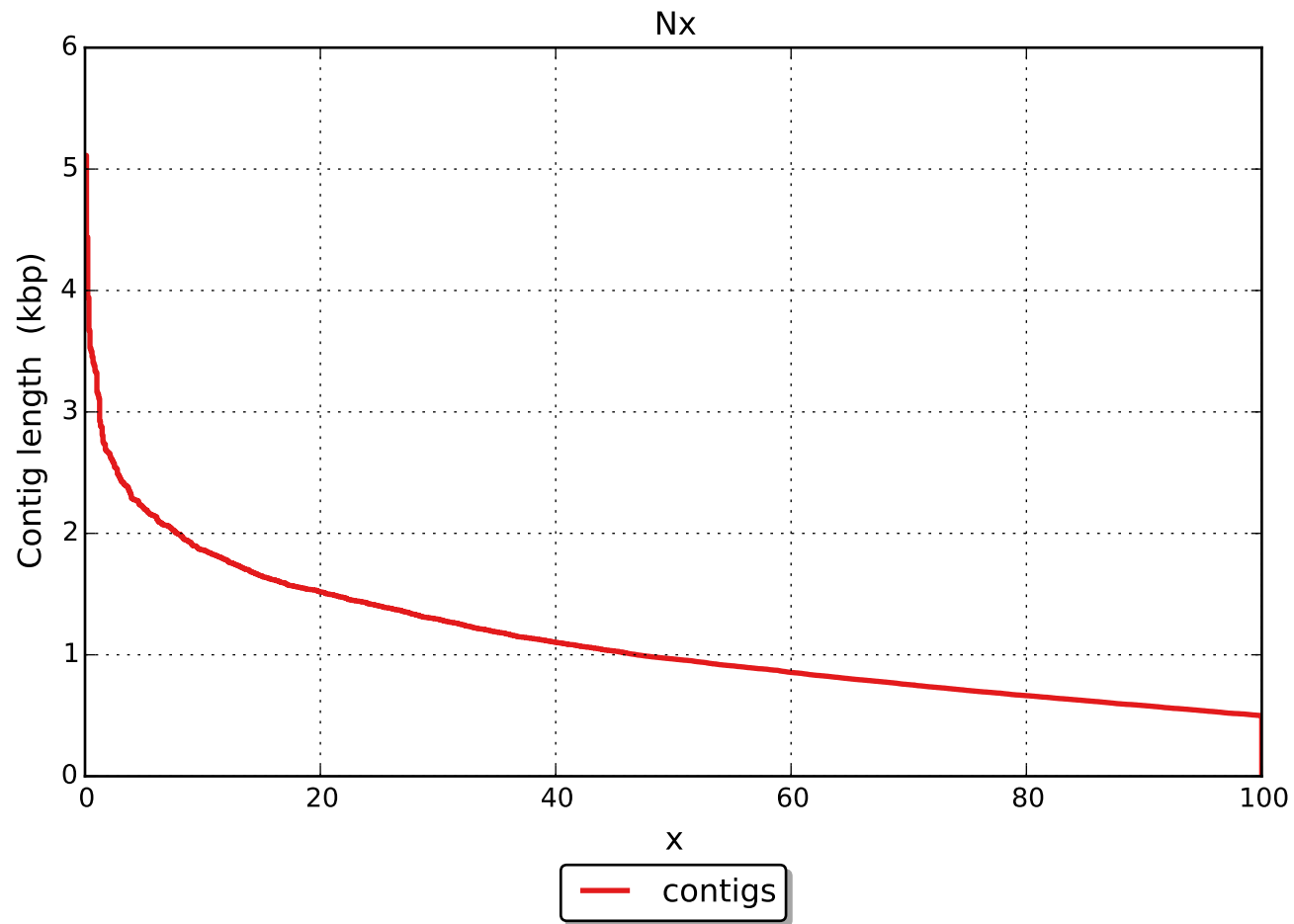
	contigs
# misassemblies	8
# relocations	8
# translocations	0
# inversions	0
# misassembled contigs	8
Misassembled contigs length	18735
# local misassemblies	3
# mismatches	49009
# indels	102
# short indels	102
# long indels	0
Indels length	113

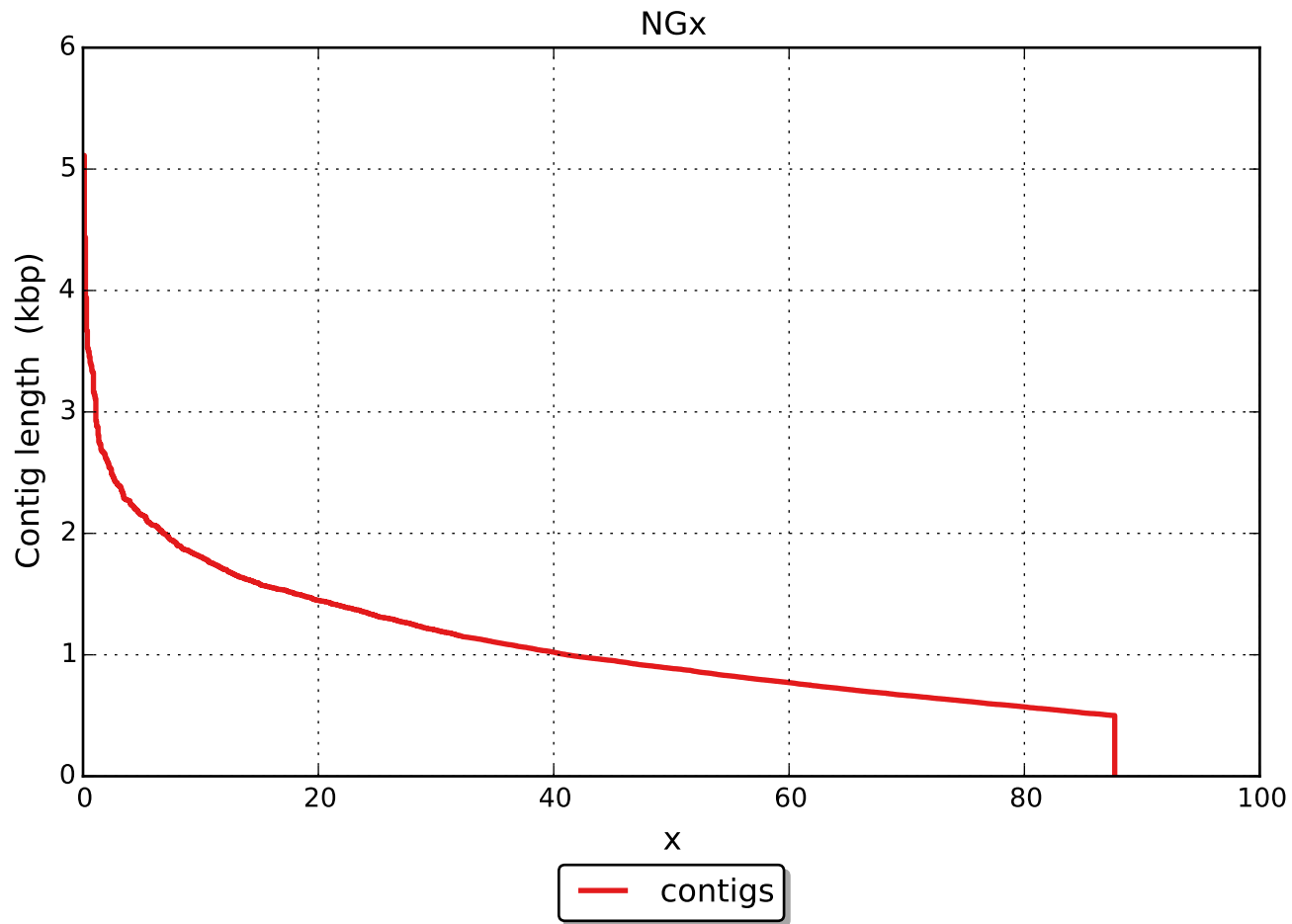
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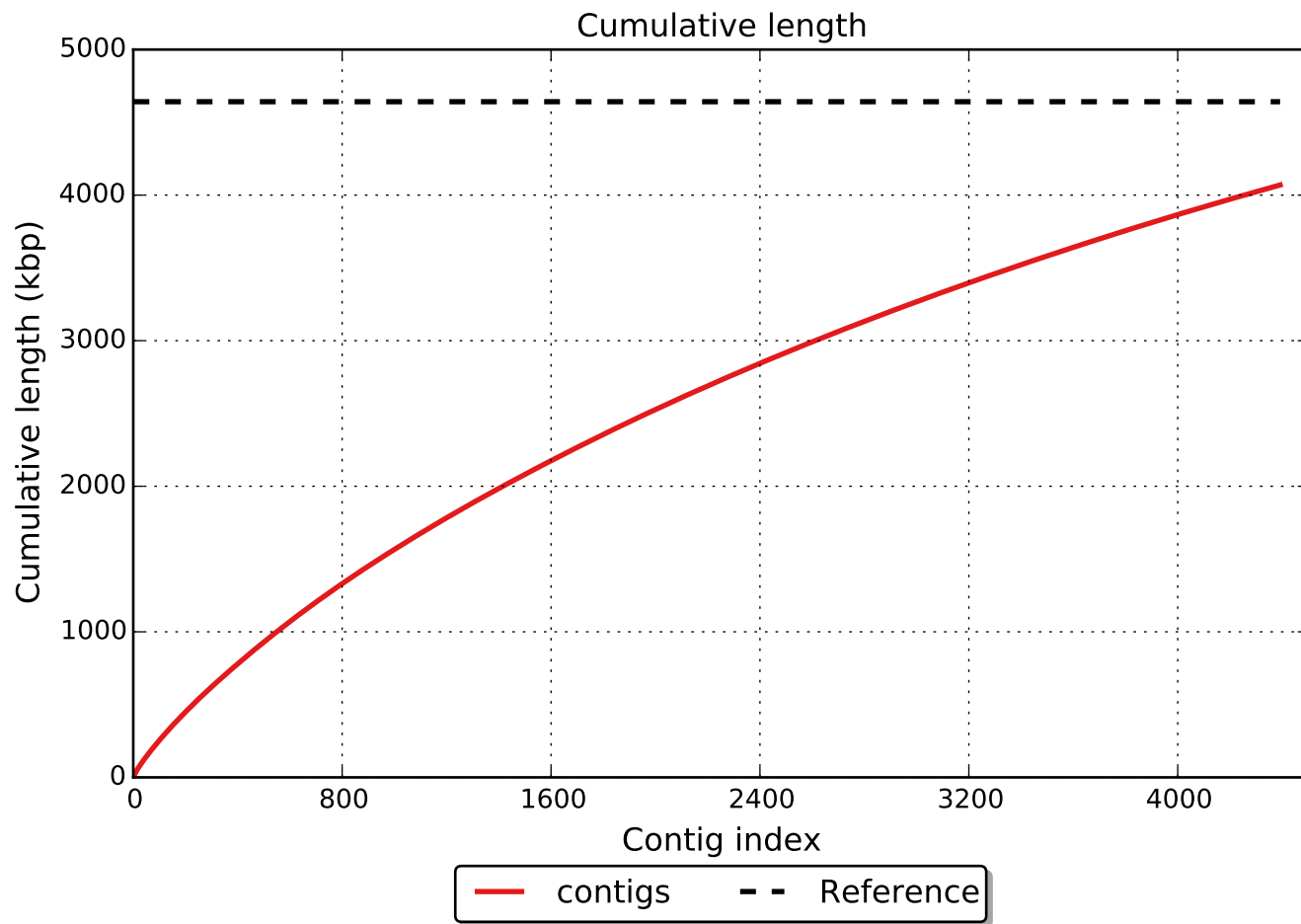
## Unaligned report

	contigs
# fully unaligned contigs	3
Fully unaligned length	2363
# partially unaligned contigs	25
# with misassembly	1
# both parts are significant	1
Partially unaligned length	2027
# N's	0

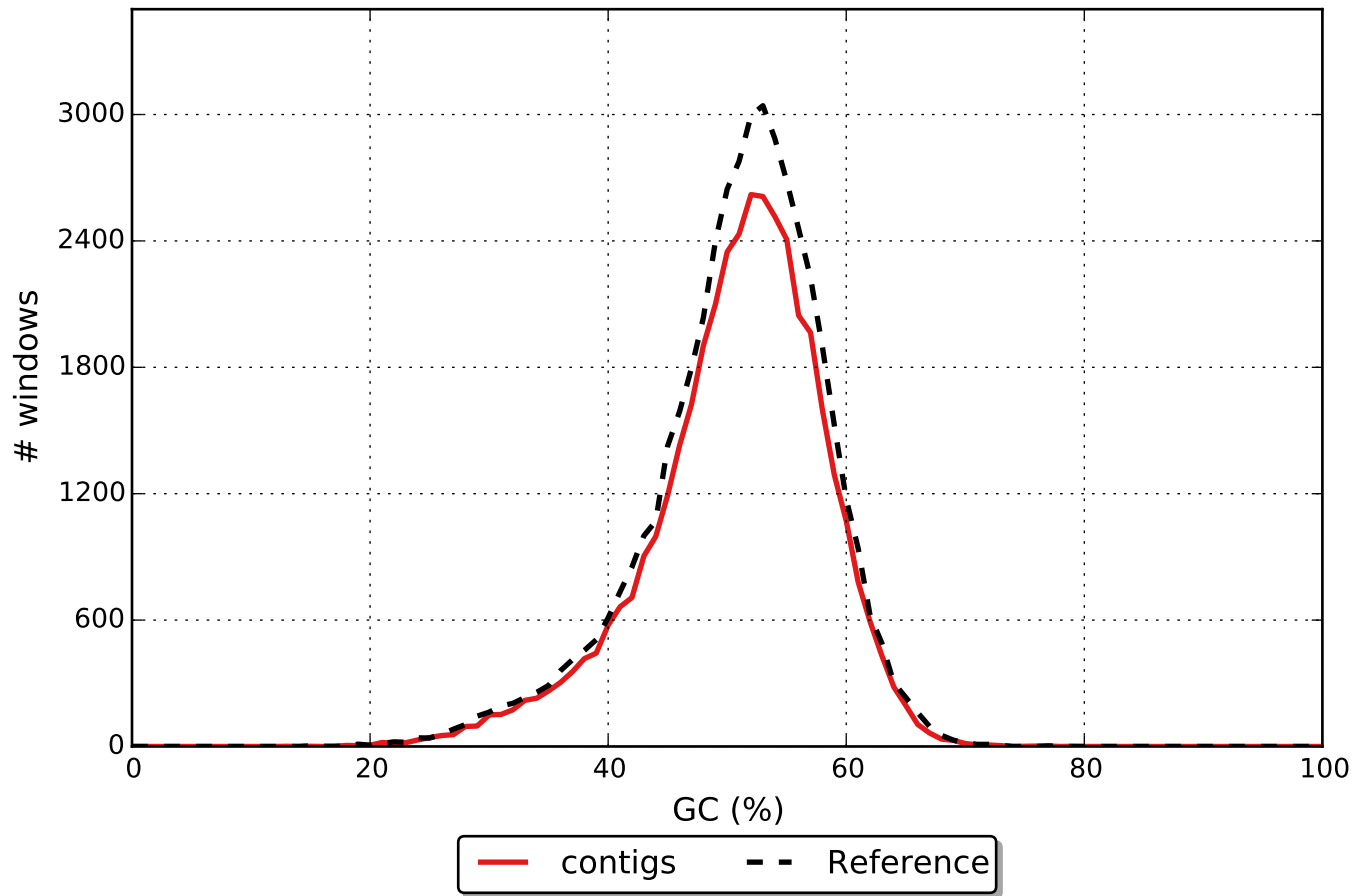
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

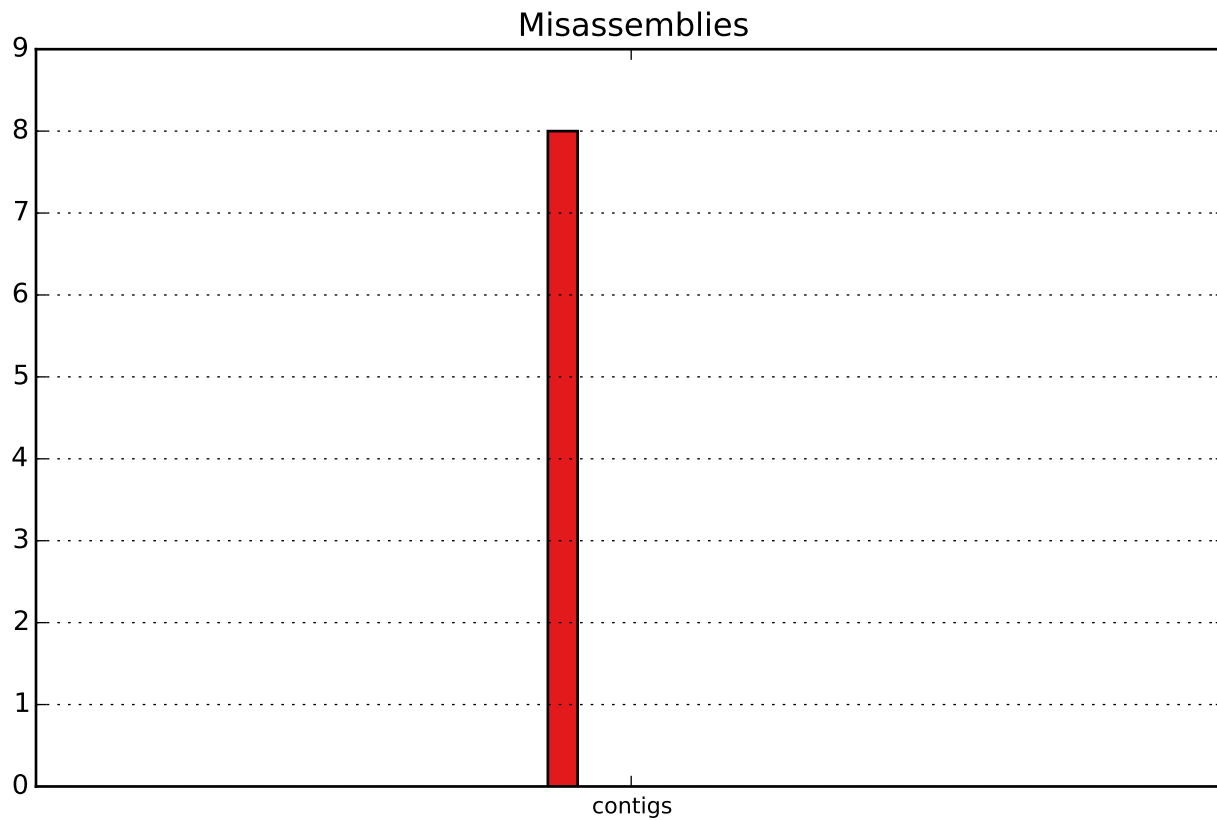






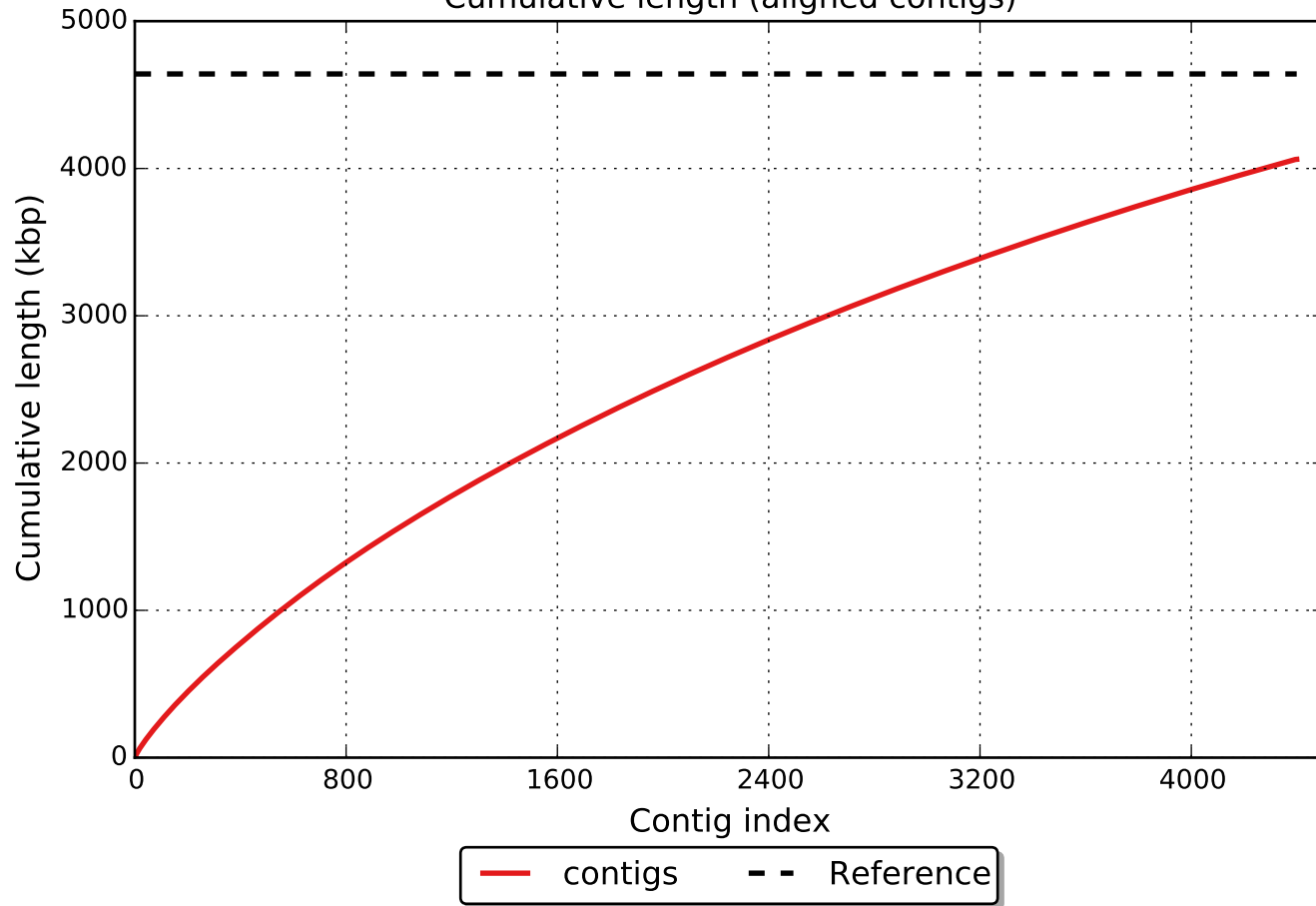
# GC content



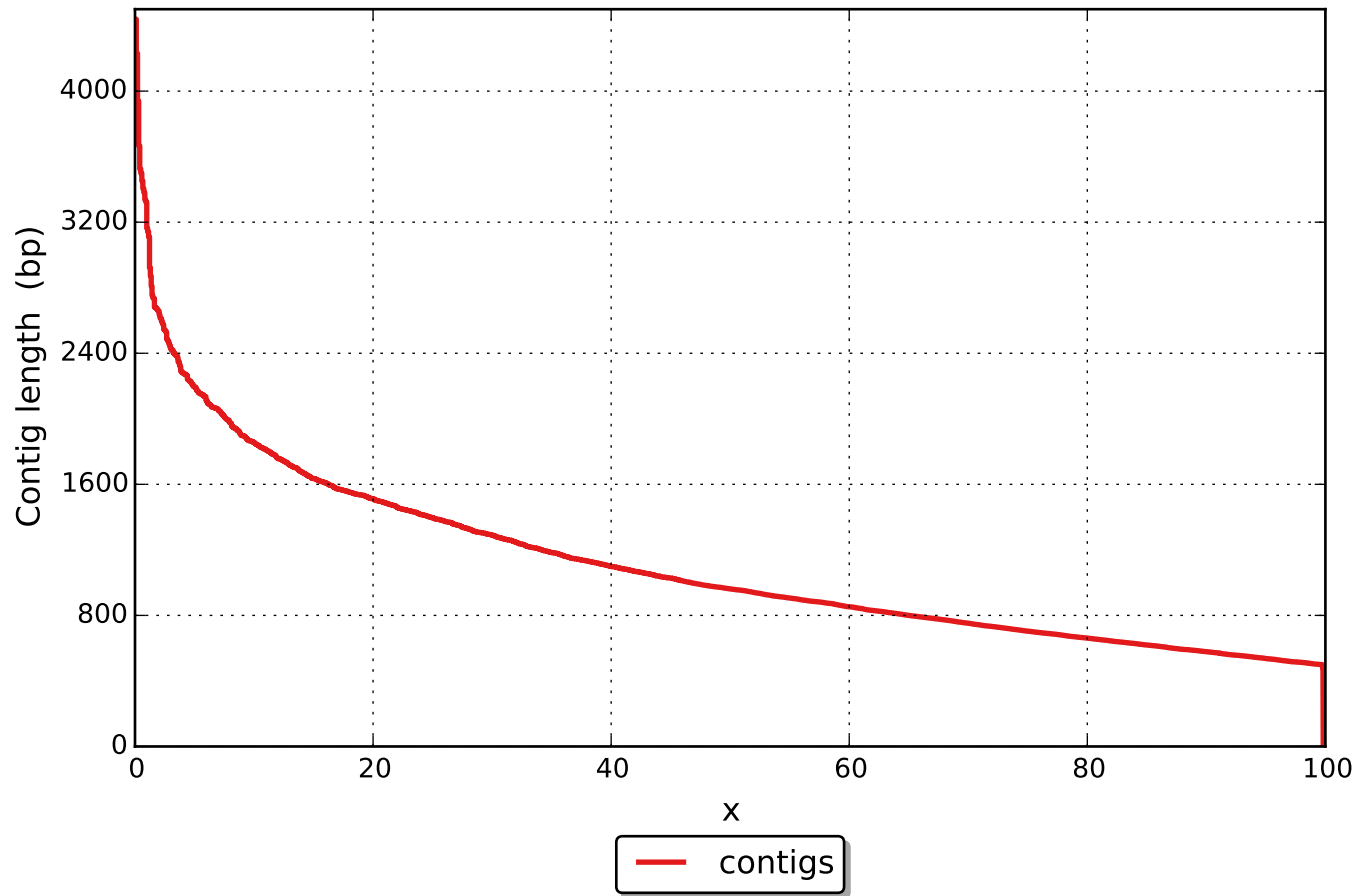




Cumulative length (aligned contigs)



NAx



NGAx

