

## Report

	contigs
# contigs ( $\geq 0$ bp)	731
# contigs ( $\geq 1000$ bp)	246
# contigs ( $\geq 5000$ bp)	190
# contigs ( $\geq 10000$ bp)	148
# contigs ( $\geq 25000$ bp)	64
# contigs ( $\geq 50000$ bp)	12
Total length ( $\geq 0$ bp)	4654686
Total length ( $\geq 1000$ bp)	4554565
Total length ( $\geq 5000$ bp)	4411218
Total length ( $\geq 10000$ bp)	4105821
Total length ( $\geq 25000$ bp)	2717679
Total length ( $\geq 50000$ bp)	898297
# contigs	261
Largest contig	119129
Total length	4564334
Reference length	4641652
GC (%)	50.73
Reference GC (%)	50.79
N50	29580
NG50	28528
N75	17465
NG75	16351
L50	48
LG50	50
L75	97
LG75	101
# misassemblies	9
# misassembled contigs	9
Misassembled contigs length	249605
# local misassemblies	11
# unaligned contigs	0 + 3 part
Unaligned length	130
Genome fraction (%)	97.871
Duplication ratio	1.005
# N's per 100 kbp	0.00
# mismatches per 100 kbp	135.20
# indels per 100 kbp	1.67
Largest alignment	119129
NA50	28083
NGA50	27932
NA75	16351
NGA75	15721
LA50	50
LGA50	52
LA75	101
LGA75	104

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

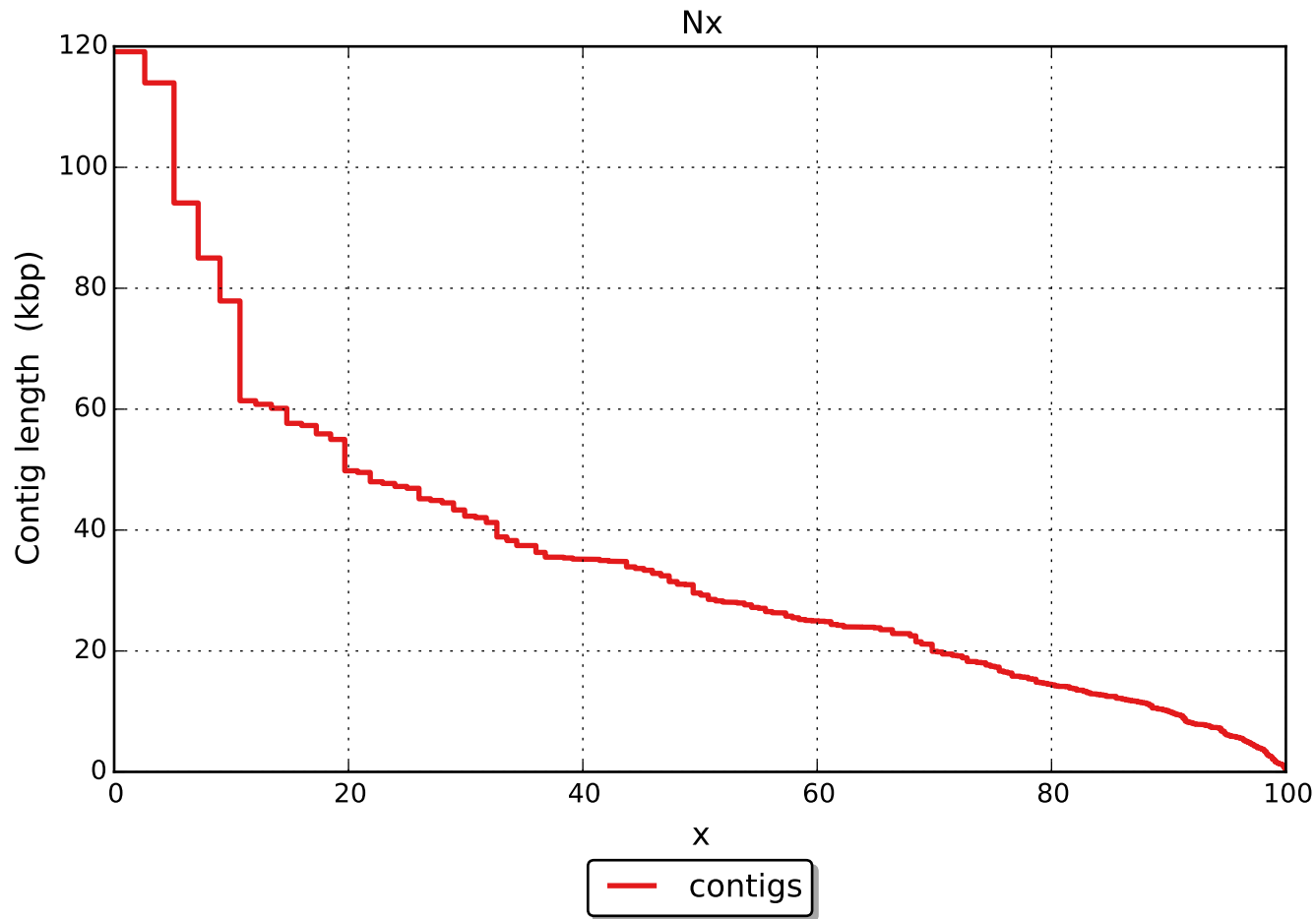
	contigs
# misassemblies	9
# relocations	9
# translocations	0
# inversions	0
# misassembled contigs	9
Misassembled contigs length	249605
# local misassemblies	11
# mismatches	6142
# indels	76
# short indels	75
# long indels	1
Indels length	103

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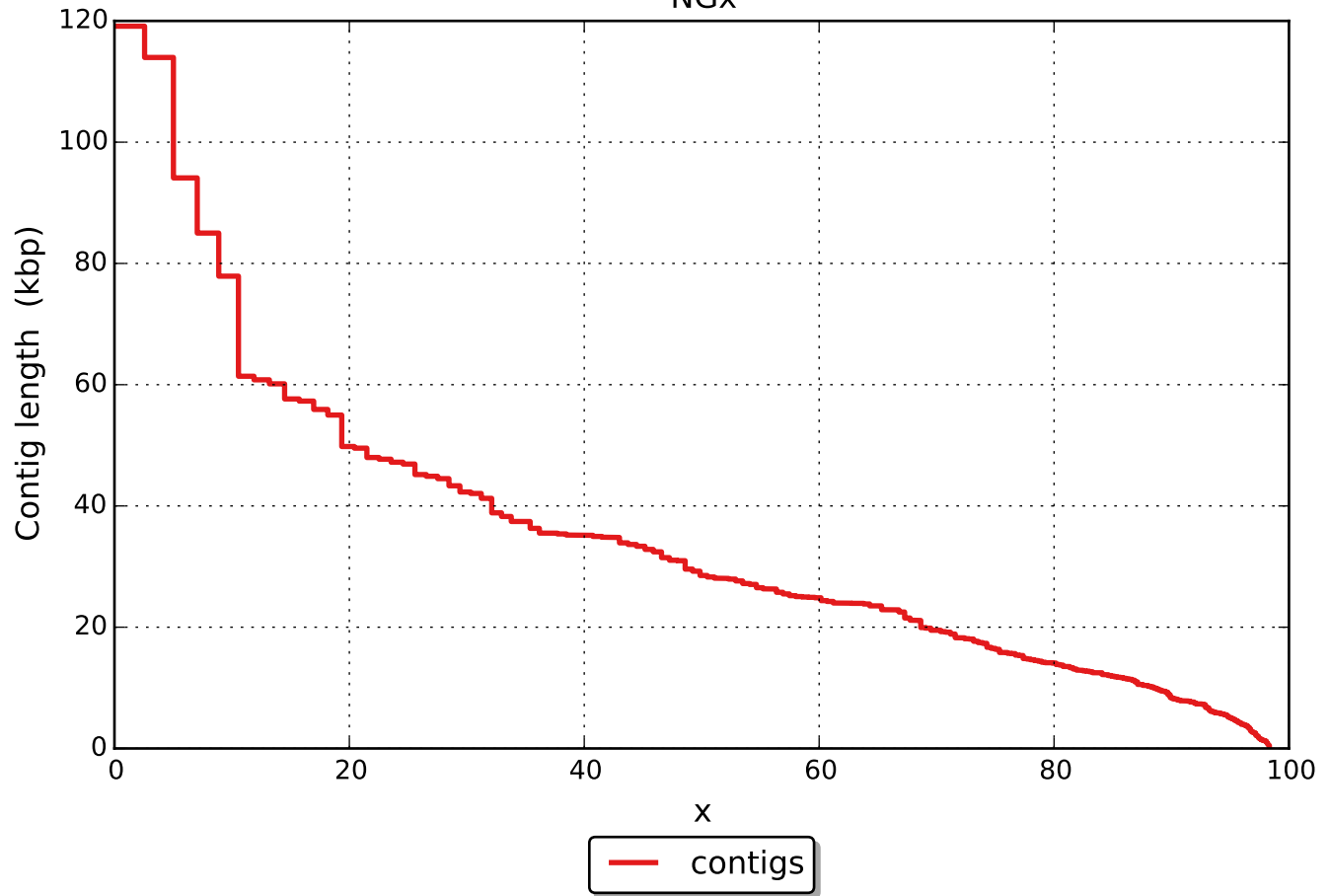
## Unaligned report

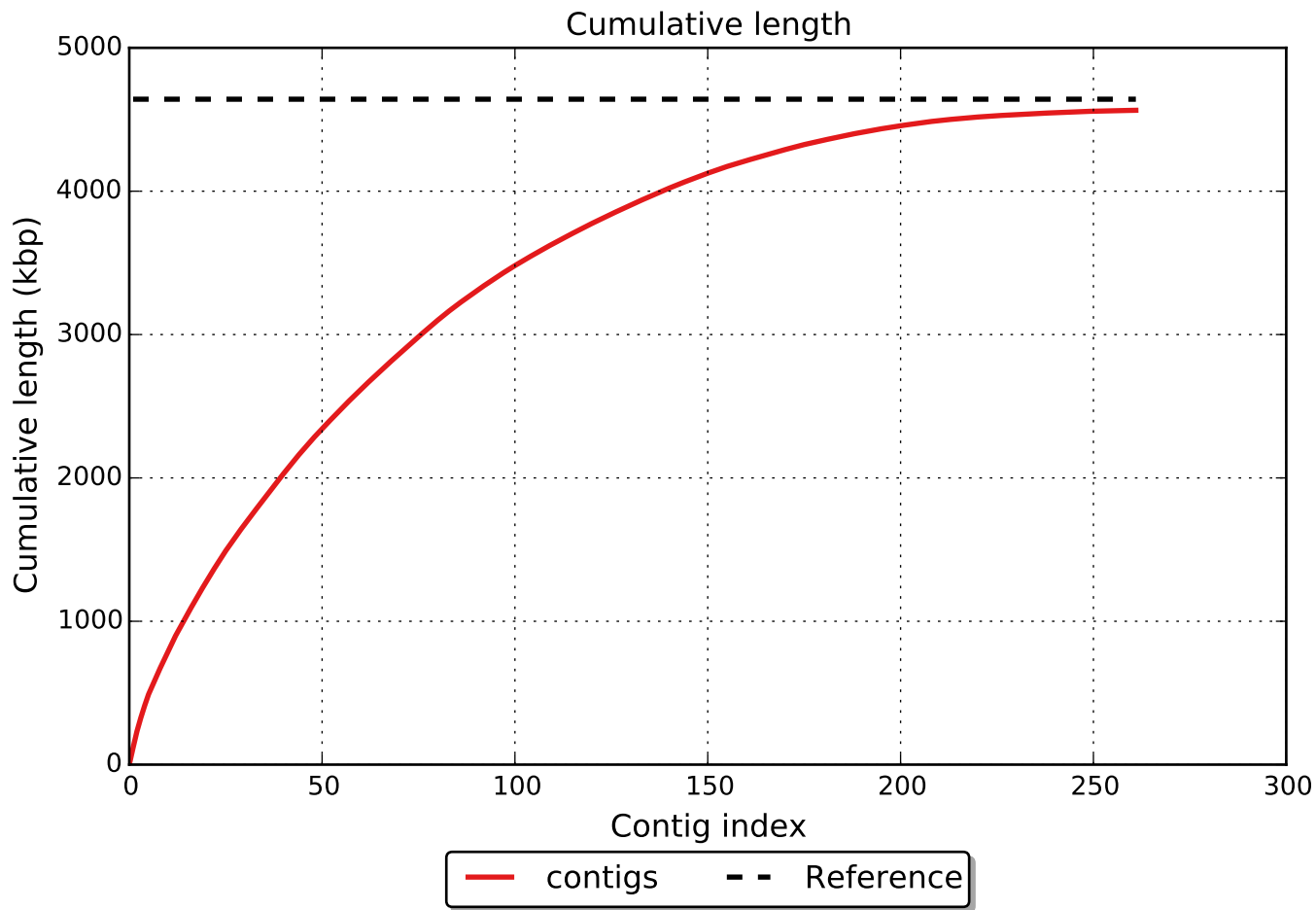
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
# with misassembly	0
# both parts are significant	0
Partially unaligned length	130
# N's	0

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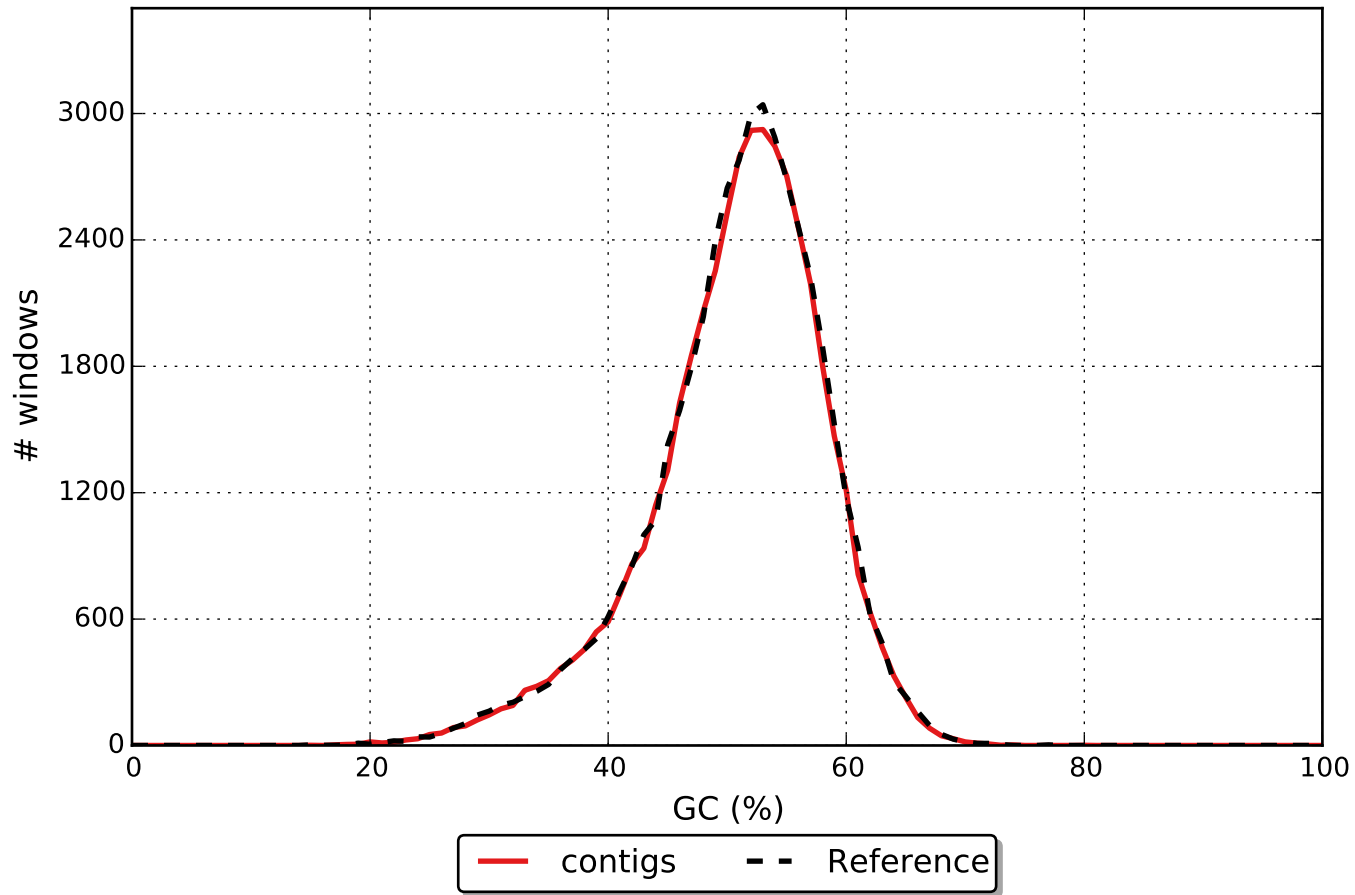


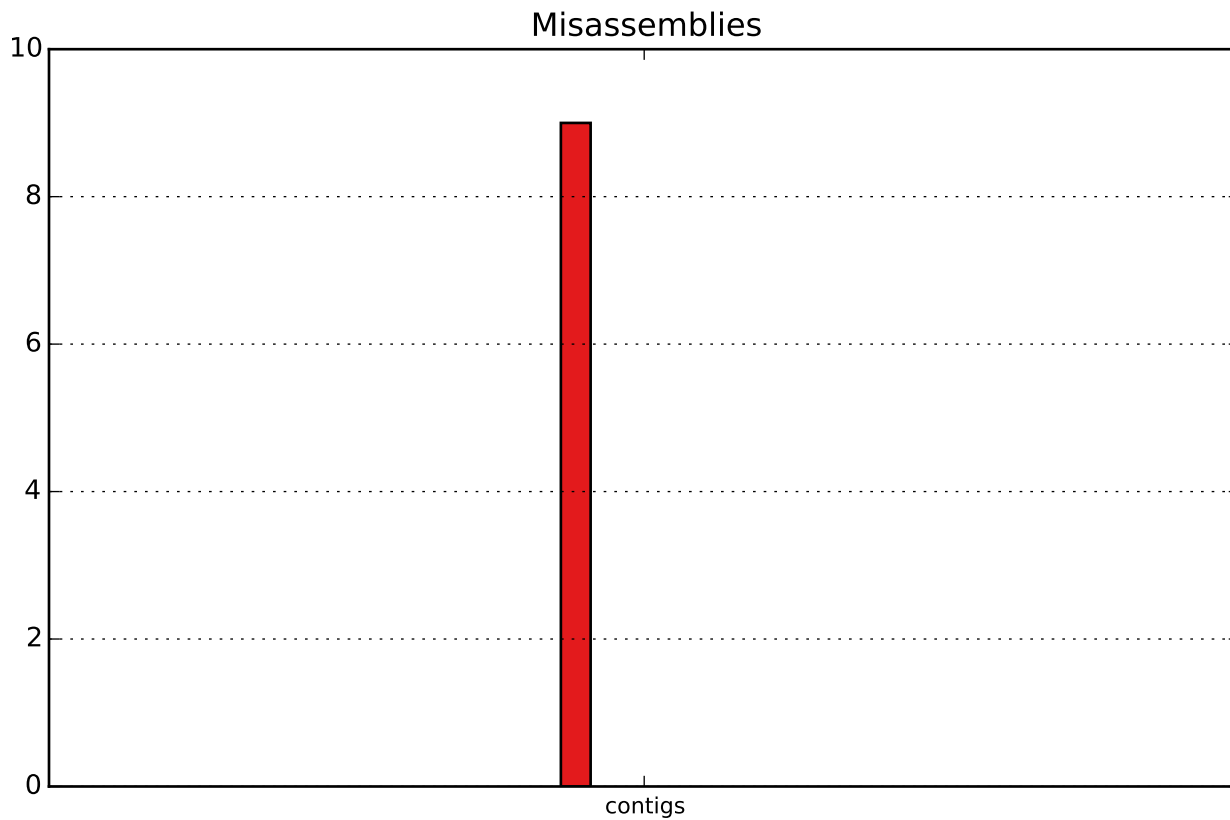
NGx





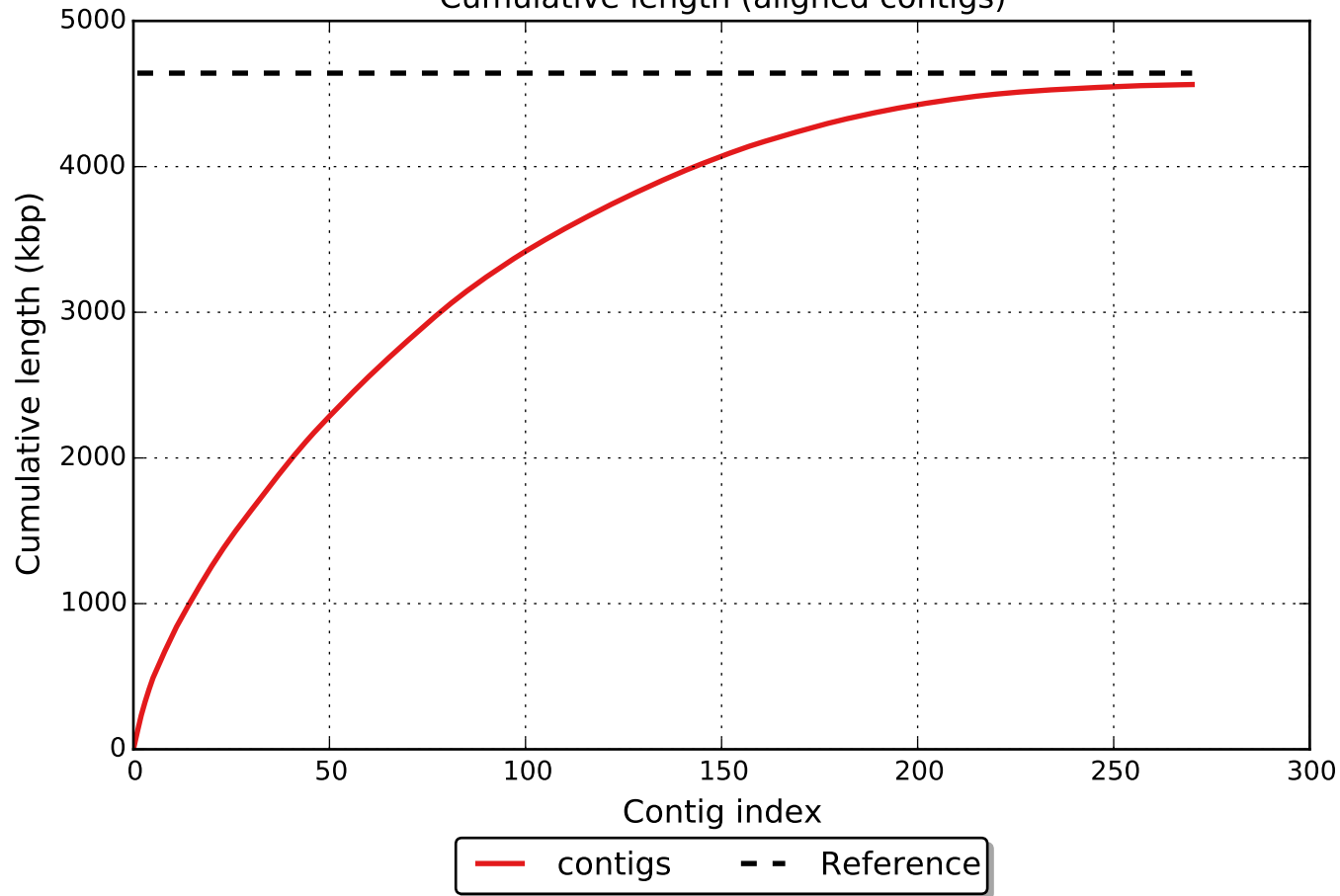
# GC content



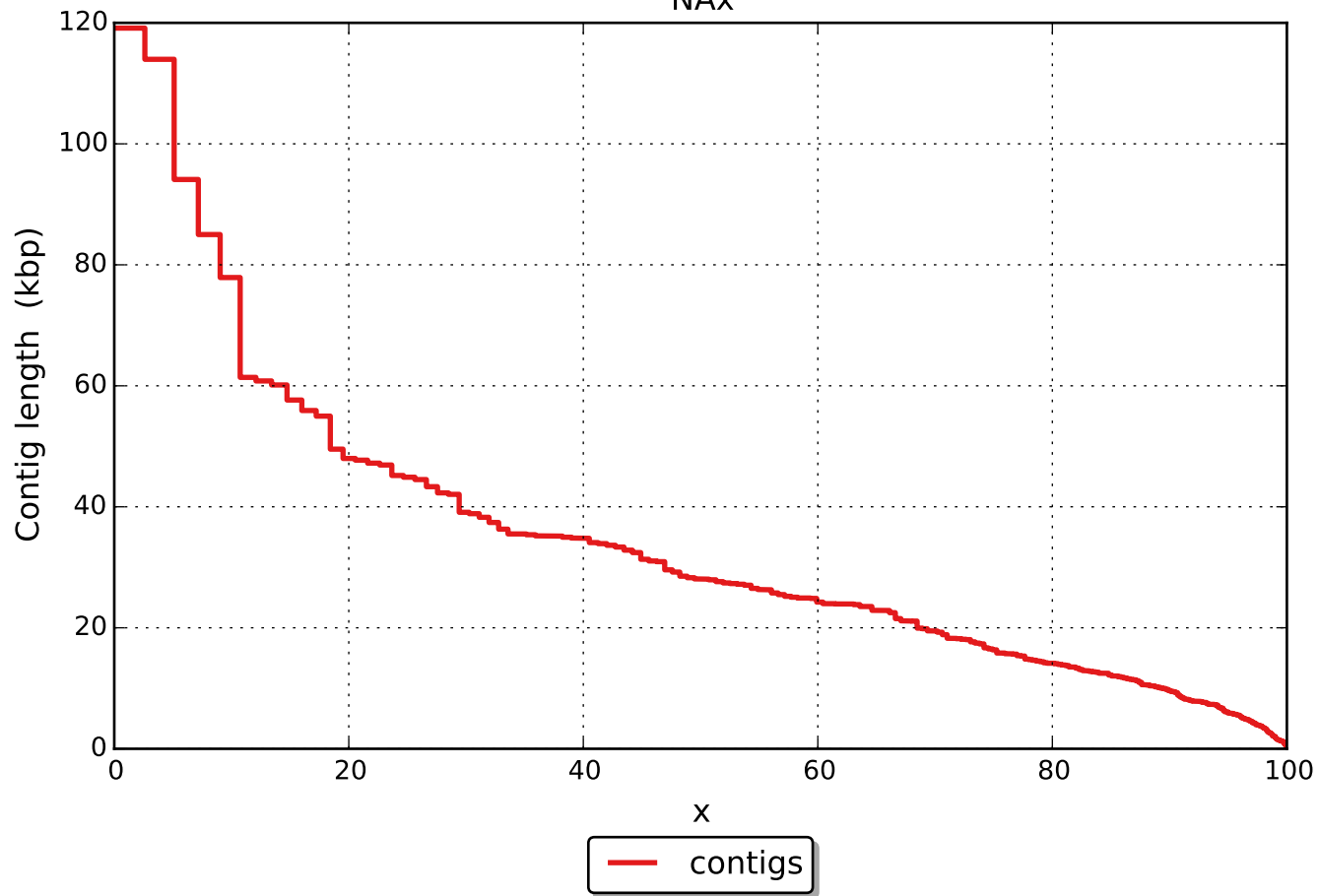




Cumulative length (aligned contigs)



NAx



NGAx

