

Report

	contigs
# contigs (≥ 1000 bp)	301
# contigs (≥ 5000 bp)	184
# contigs (≥ 10000 bp)	113
# contigs (≥ 25000 bp)	50
# contigs (≥ 50000 bp)	24
Total length (≥ 1000 bp)	4881575
Total length (≥ 5000 bp)	4556020
Total length (≥ 10000 bp)	4055002
Total length (≥ 25000 bp)	3082199
Total length (≥ 50000 bp)	2167762
# contigs	337
Largest contig	189810
Total length	4905252
Reference length	4641652
GC (%)	50.67
Reference GC (%)	50.78
N50	39330
NG50	41789
N75	14280
NG75	16238
L50	31
LG50	28
L75	83
LG75	70
# misassemblies	3
# misassembled contigs	2
Misassembled contigs length	129141
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	87.157
Duplication ratio	1.213
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1087.38
# indels per 100 kbp	0.44
Largest alignment	189810
NA50	38903
NGA50	40925
NA75	14041
NGA75	15950
LA50	32
LGA50	29
LA75	86
LGA75	73

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

Misassemblies report

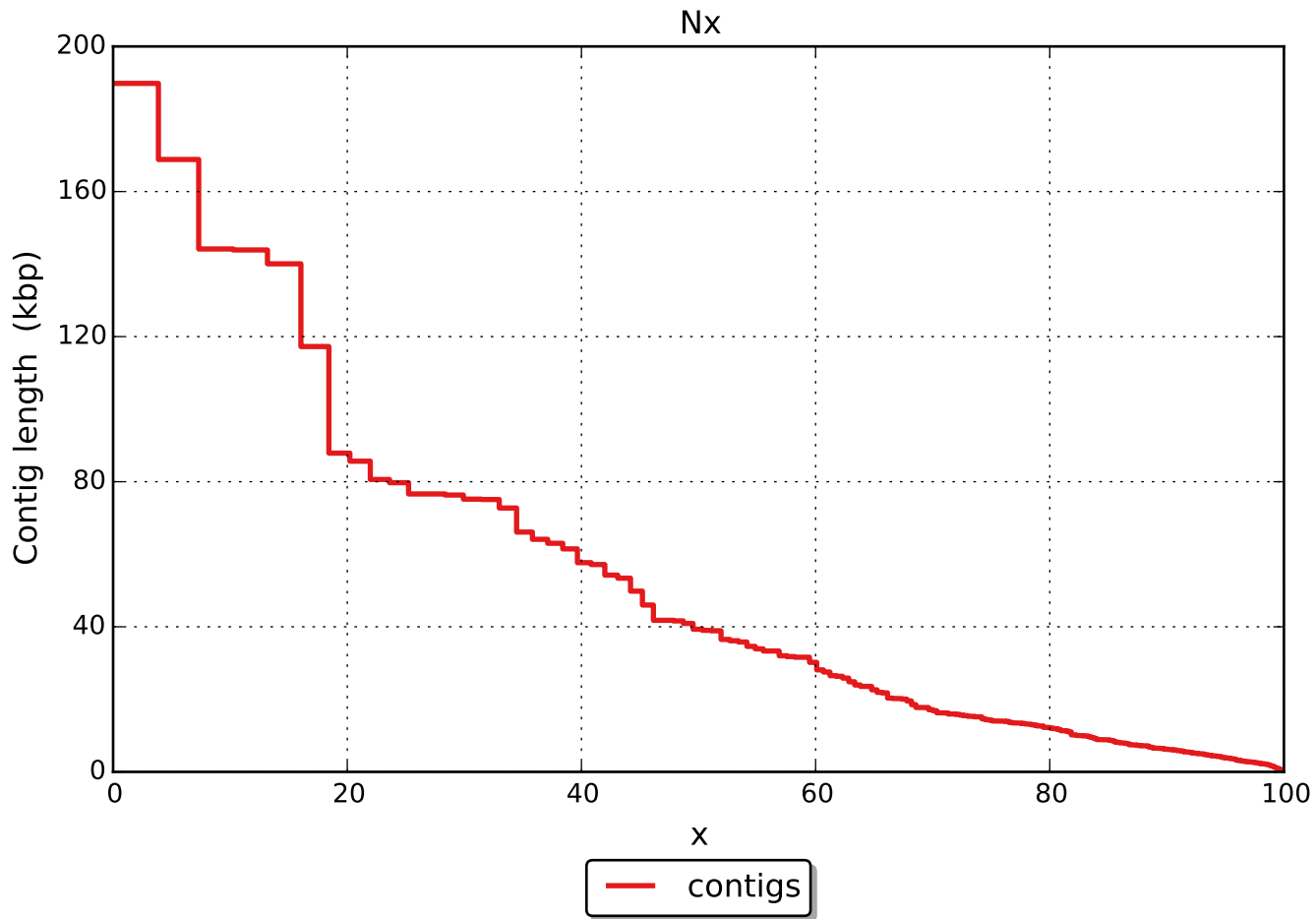
	contigs
# misassemblies	3
# relocations	3
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	129141
# local misassemblies	3
# mismatches	43990
# indels	18
# short indels	18
# long indels	0
Indels length	18

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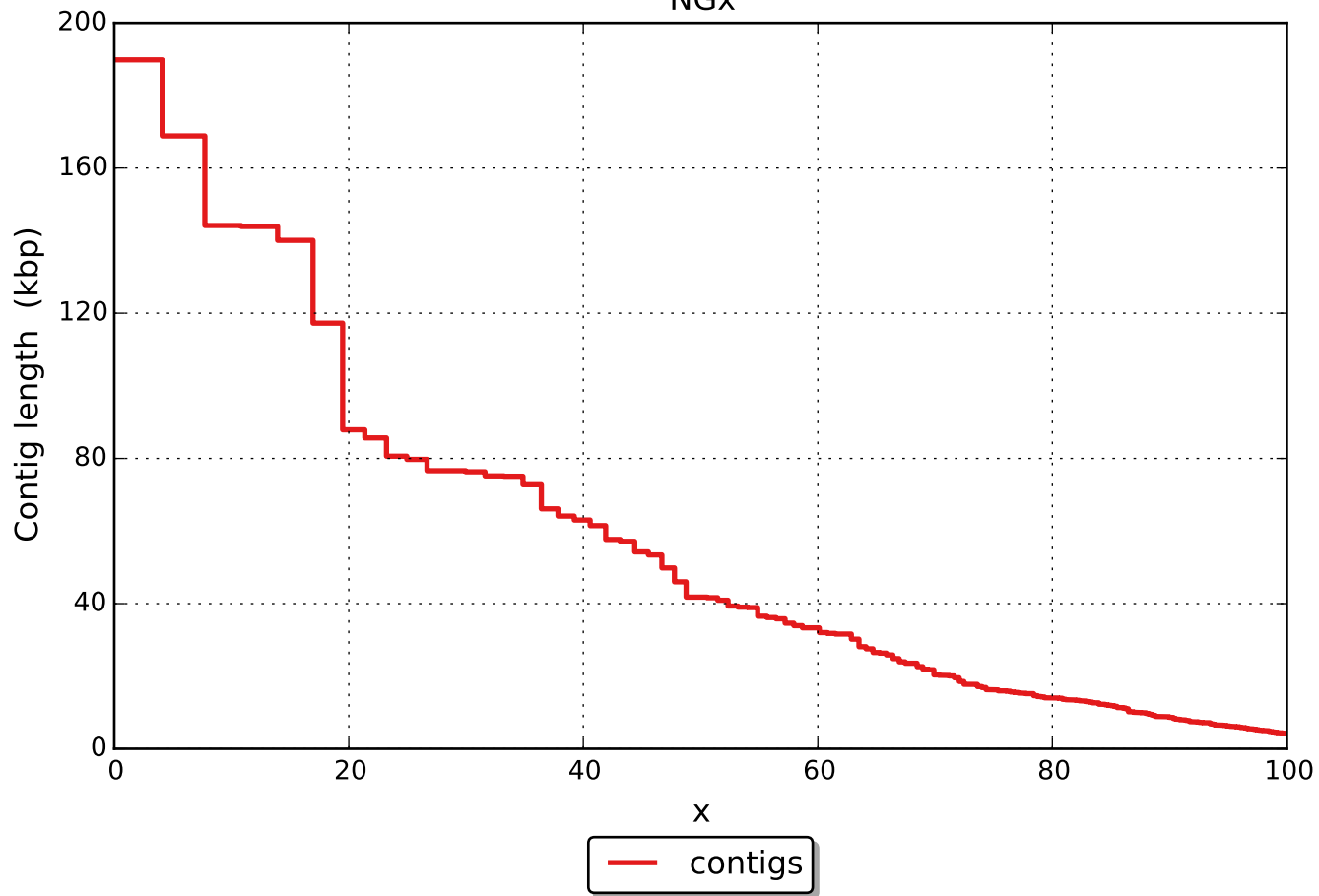
Unaligned report

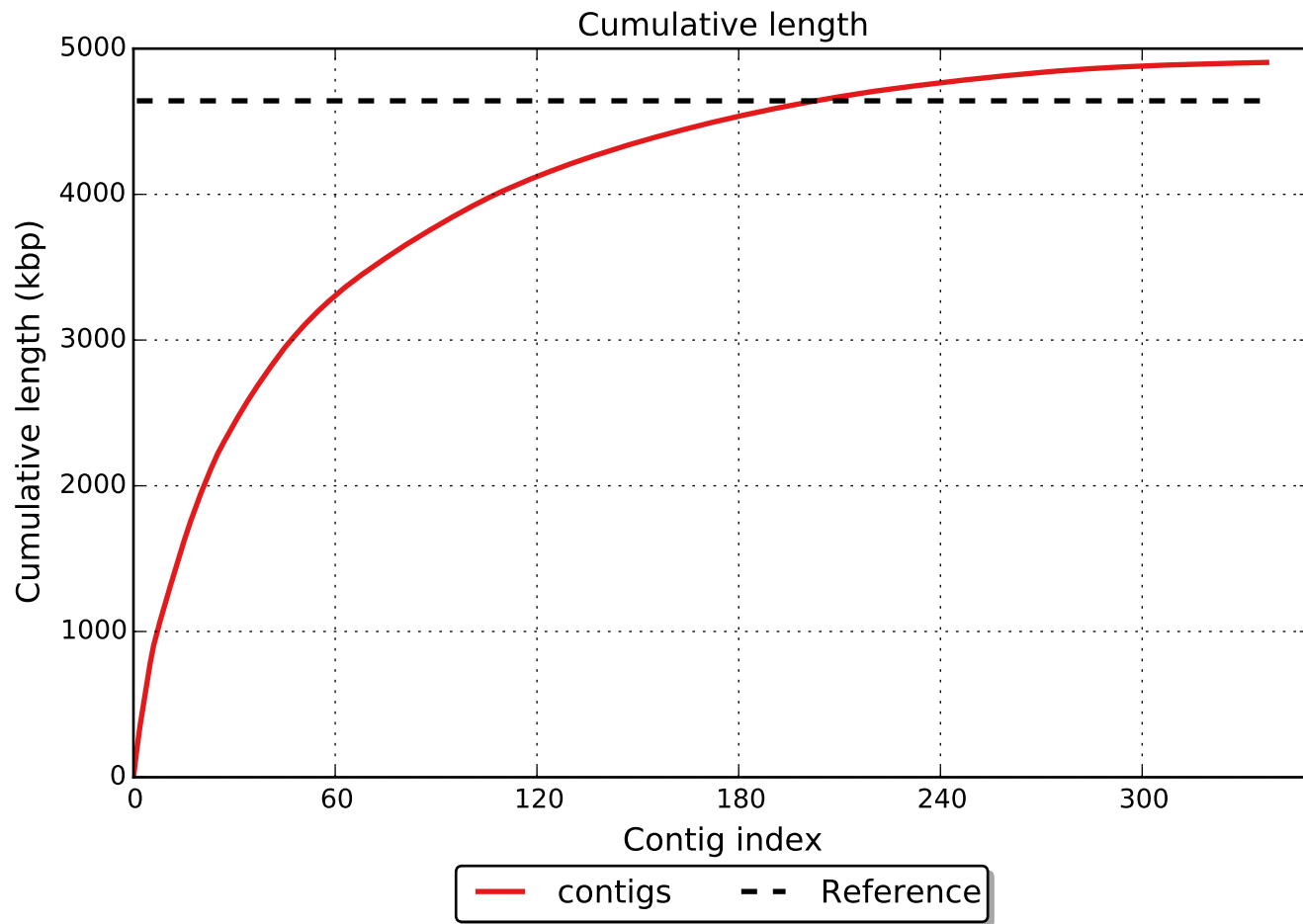
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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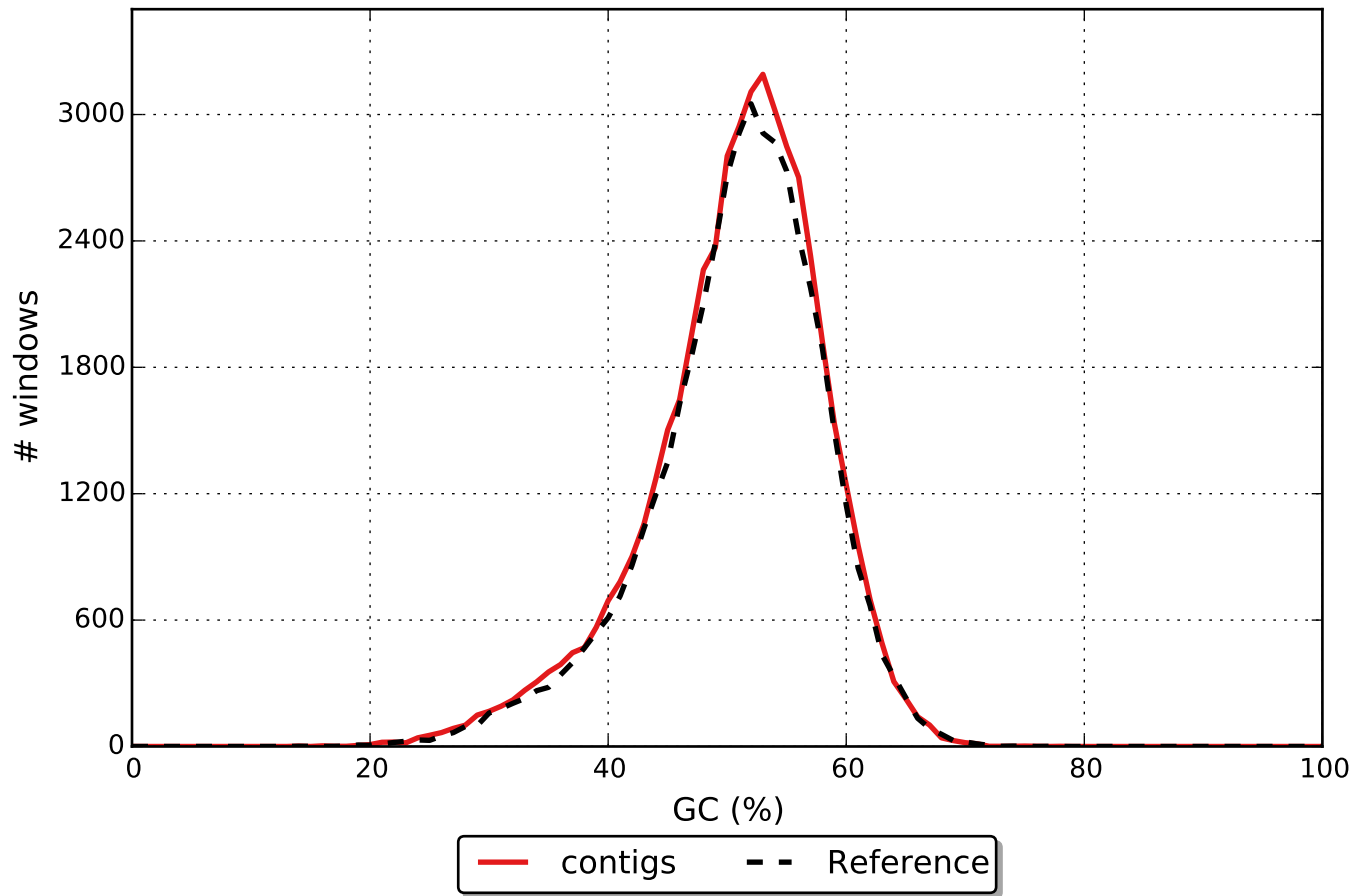


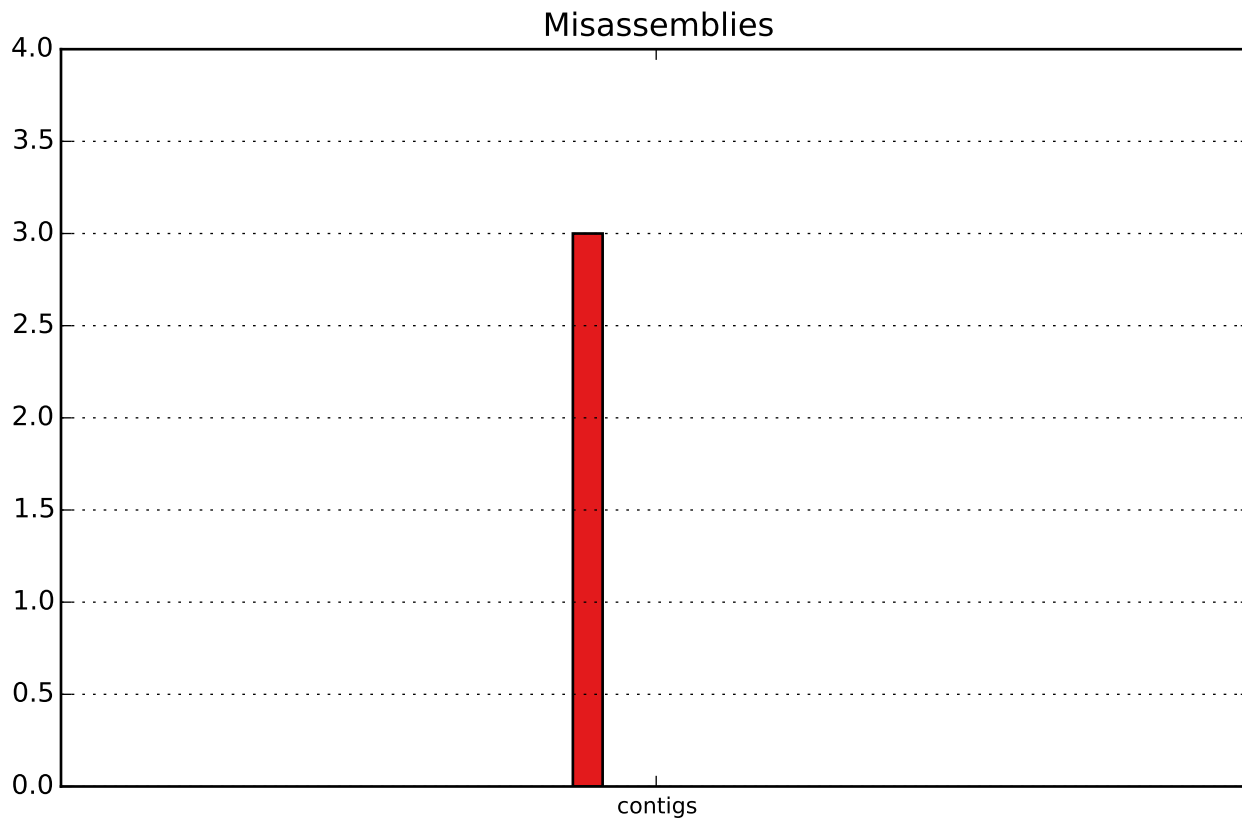
NGx



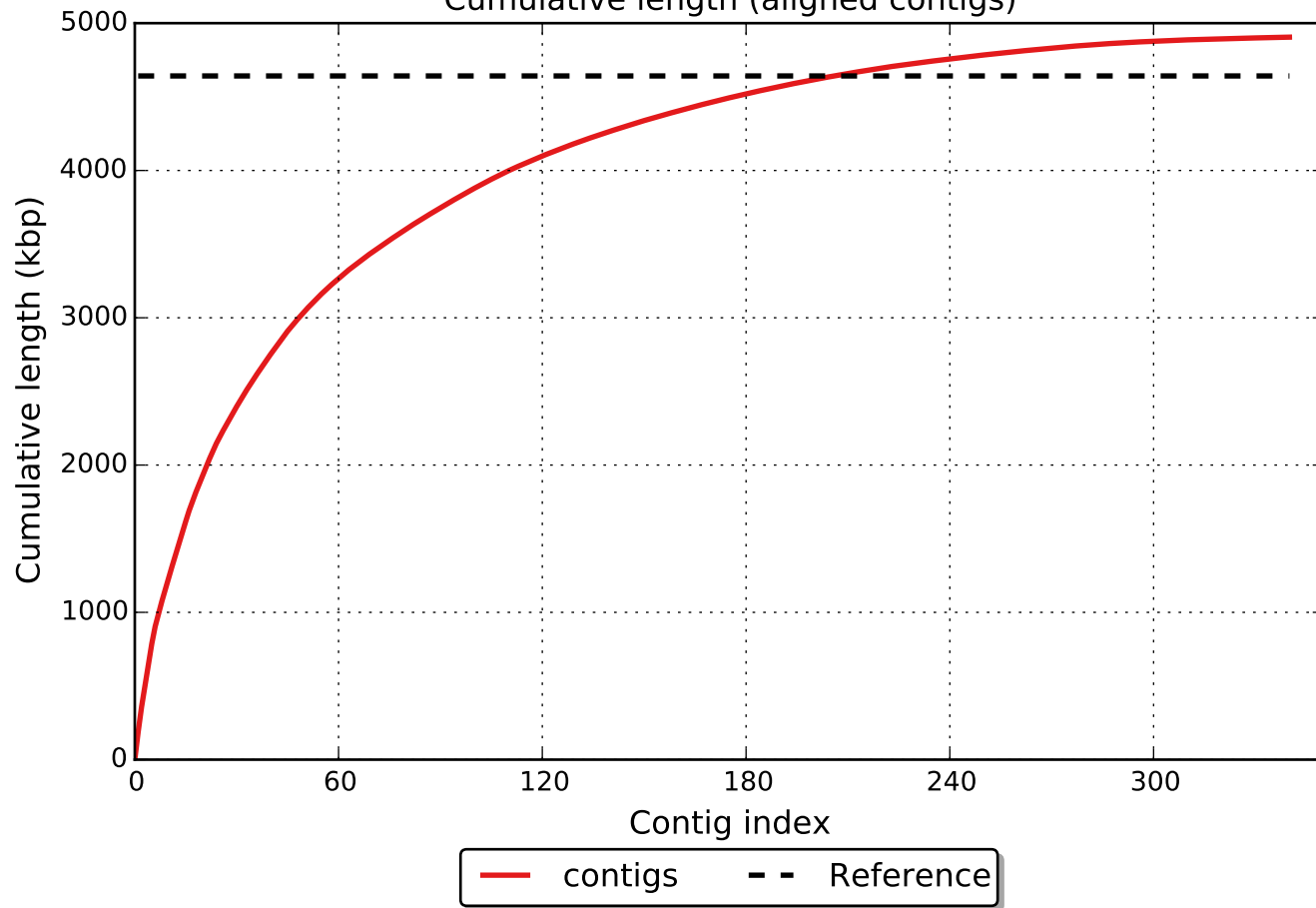


GC content

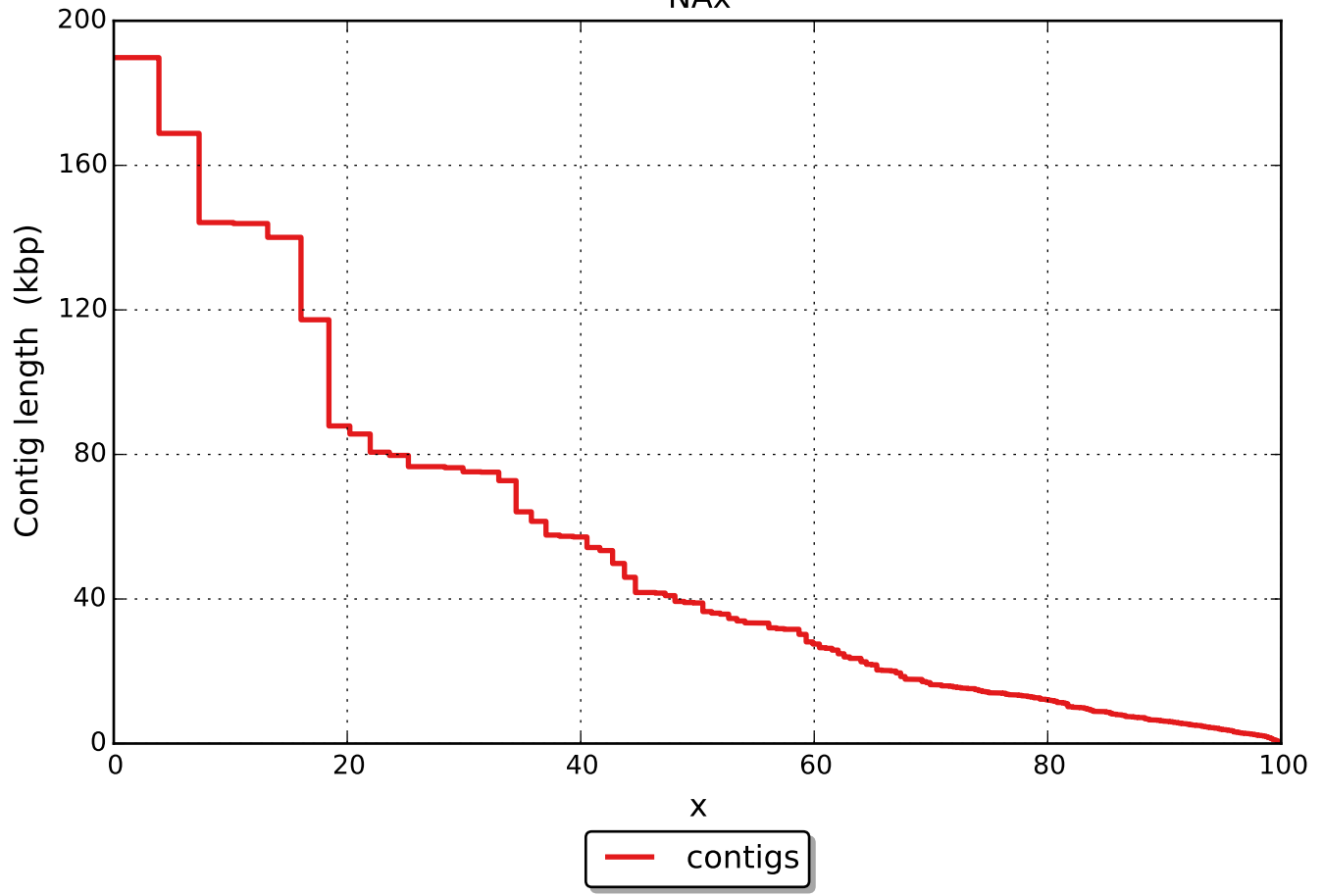




Cumulative length (aligned contigs)



NAx



NGAx

