

Report

	contigs
# contigs (≥ 0 bp)	626
# contigs (≥ 1000 bp)	544
# contigs (≥ 5000 bp)	317
# contigs (≥ 10000 bp)	157
# contigs (≥ 25000 bp)	23
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	4562505
Total length (≥ 1000 bp)	4523639
Total length (≥ 5000 bp)	3905694
Total length (≥ 10000 bp)	2753720
Total length (≥ 25000 bp)	753617
Total length (≥ 50000 bp)	0
# contigs	579
Largest contig	42373
Total length	4550318
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	12541
NG50	12032
N75	7117
NG75	6857
L50	114
LG50	118
L75	236
LG75	246
# misassemblies	8
# misassembled contigs	8
Misassembled contigs length	137106
# local misassemblies	9
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.738
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	180.35
# indels per 100 kbp	0.55
Largest alignment	42373
NA50	12041
NGA50	11871
NA75	7109
NGA75	6857
LA50	115
LGA50	119
LA75	239
LGA75	248

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

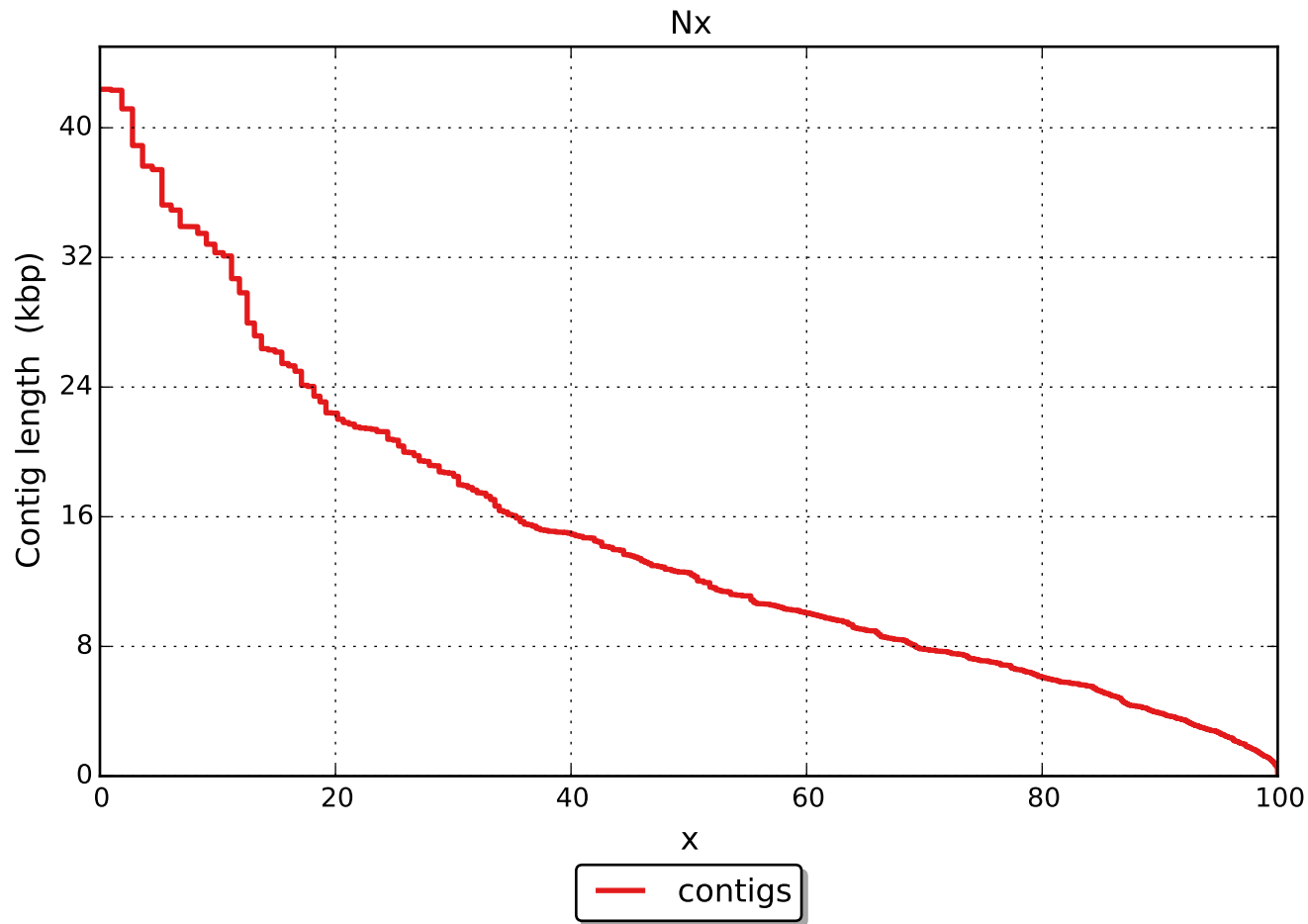
	contigs
# misassemblies	8
# relocations	8
# translocations	0
# inversions	0
# misassembled contigs	8
Misassembled contigs length	137106
# local misassemblies	9
# mismatches	8182
# indels	25
# short indels	22
# long indels	3
Indels length	190

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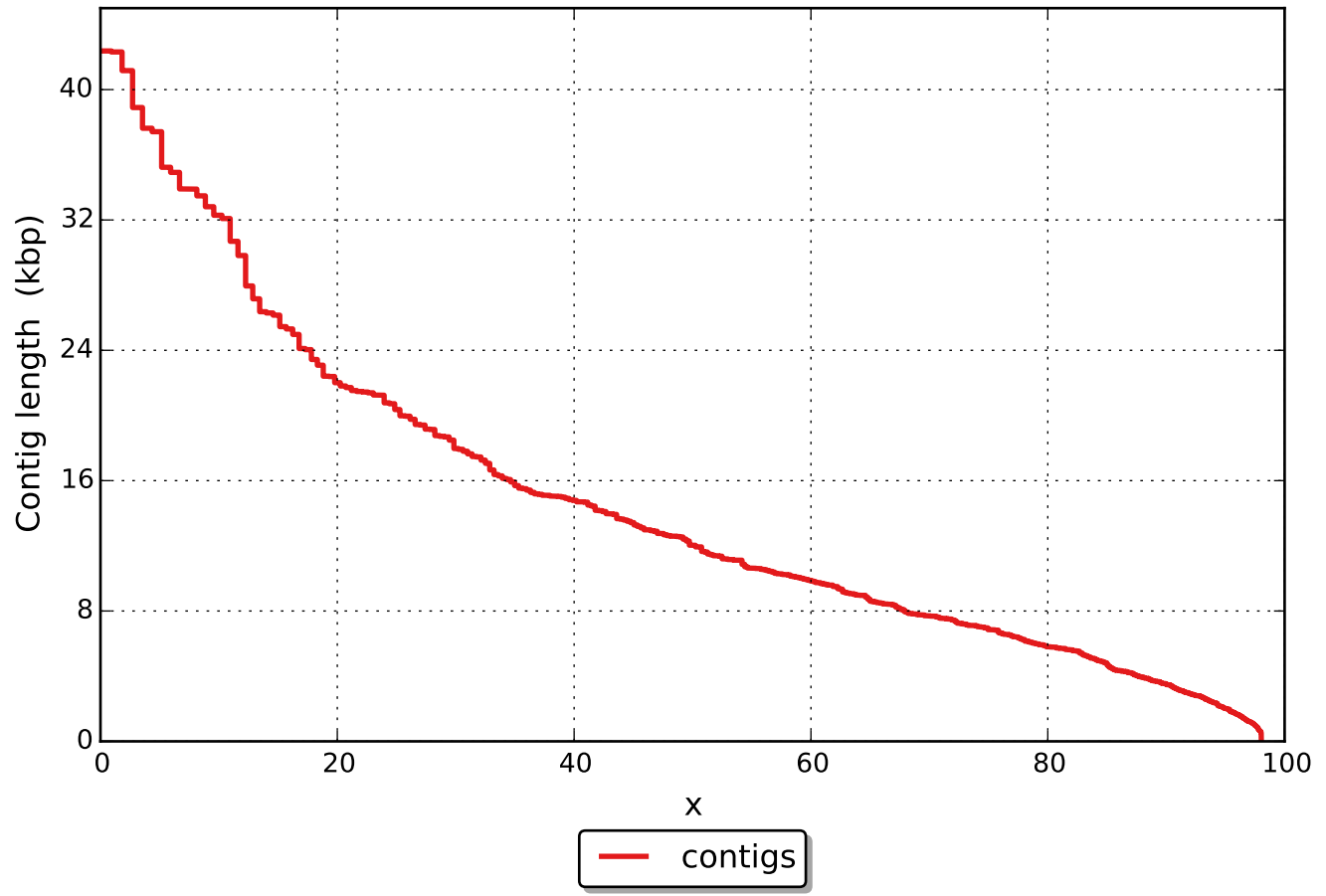
Unaligned report

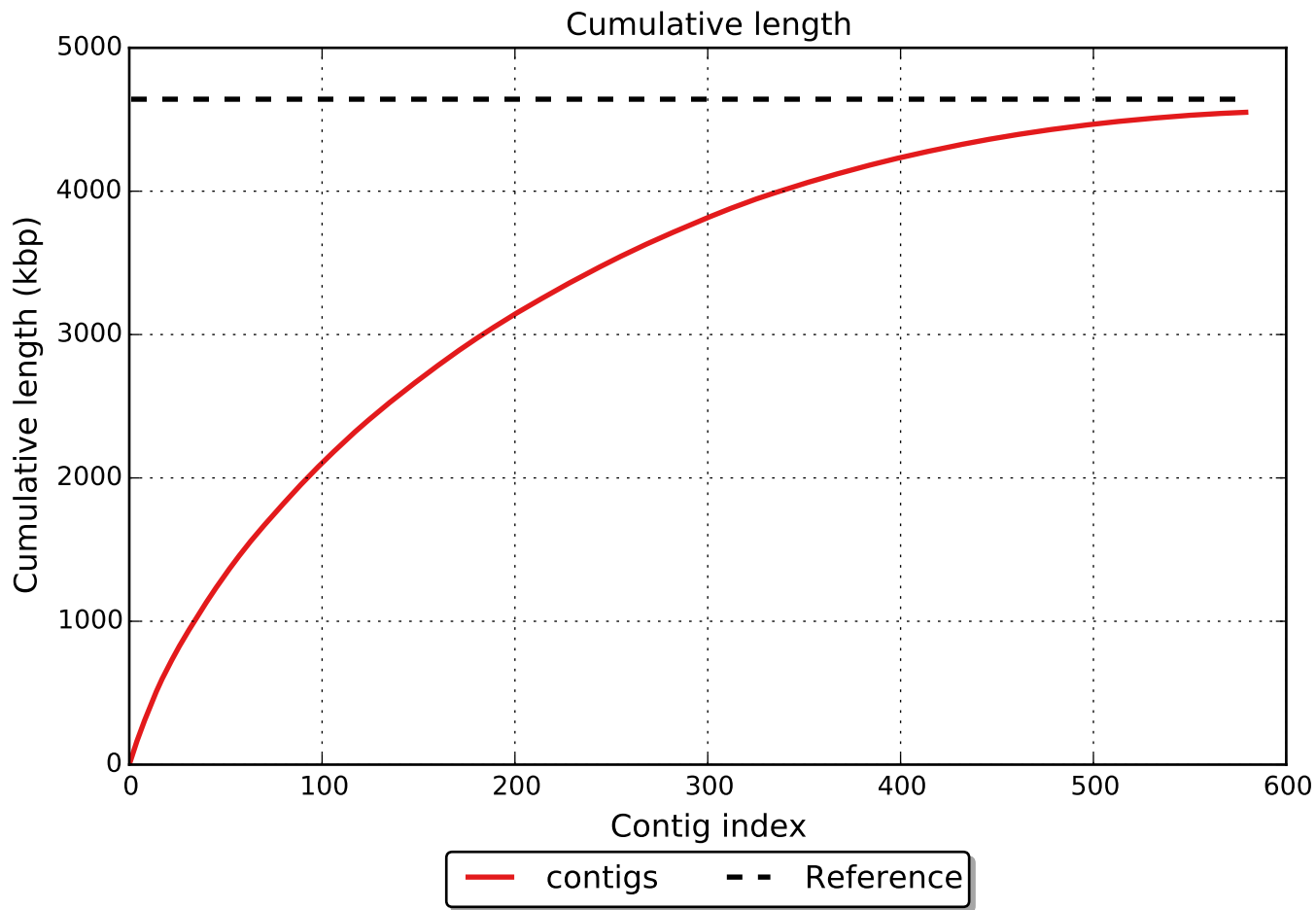
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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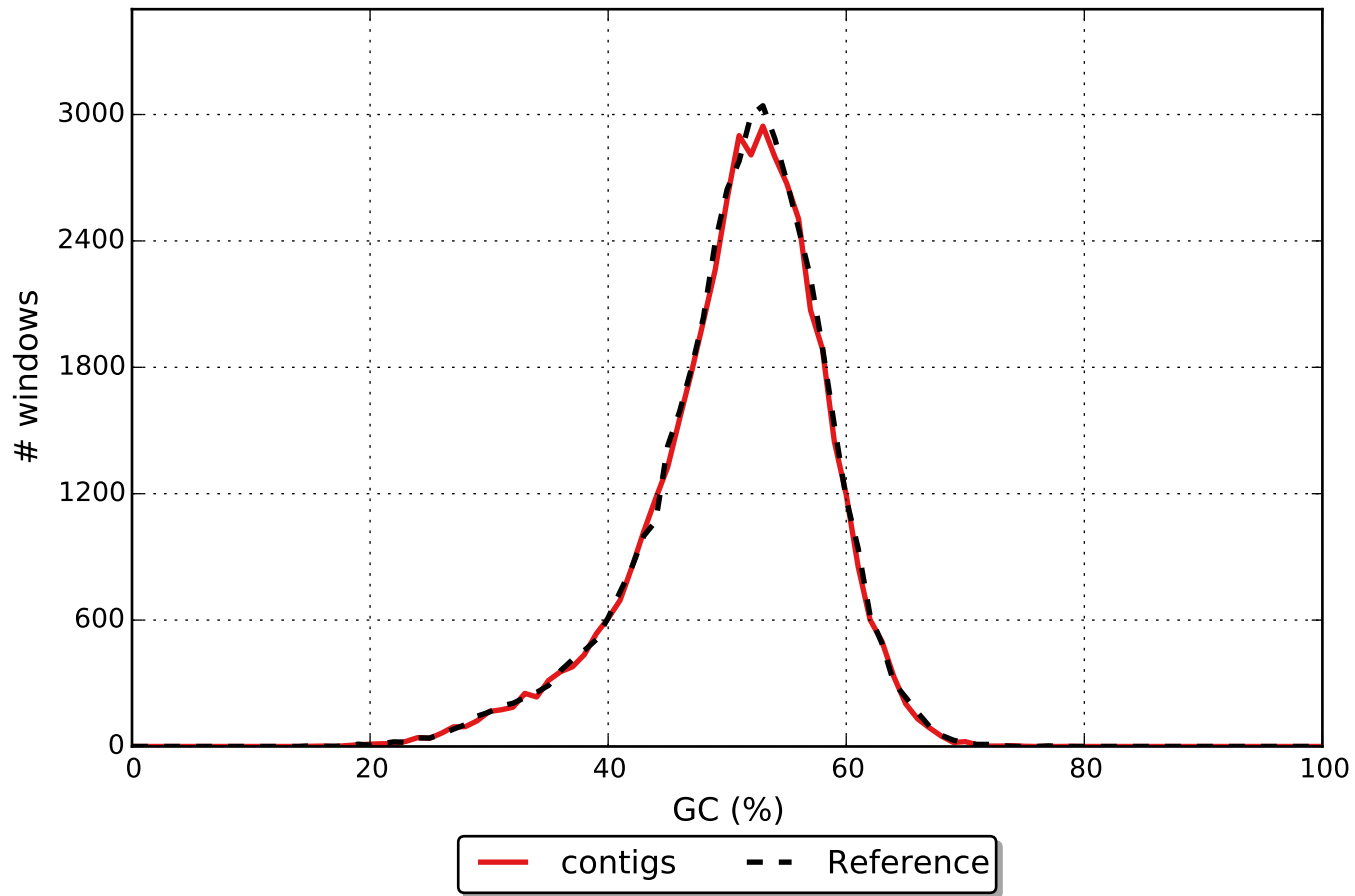


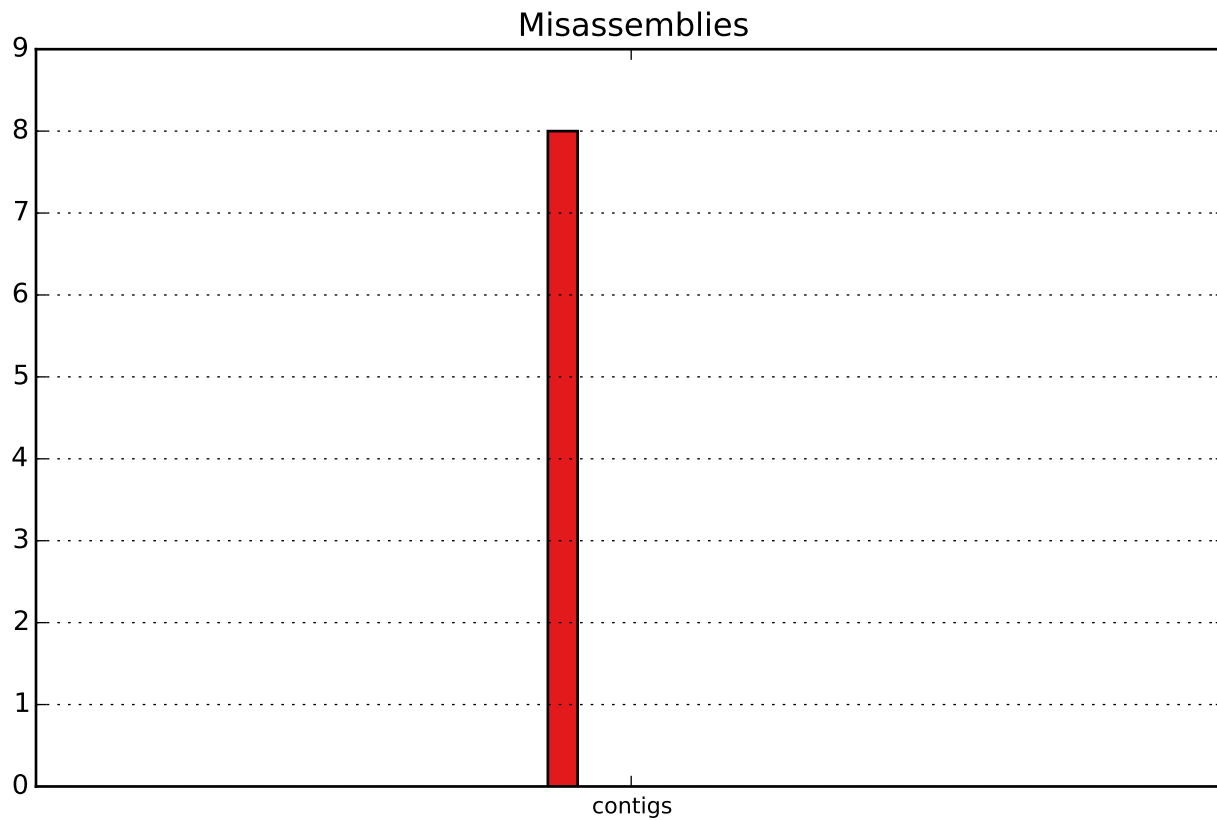
NGx



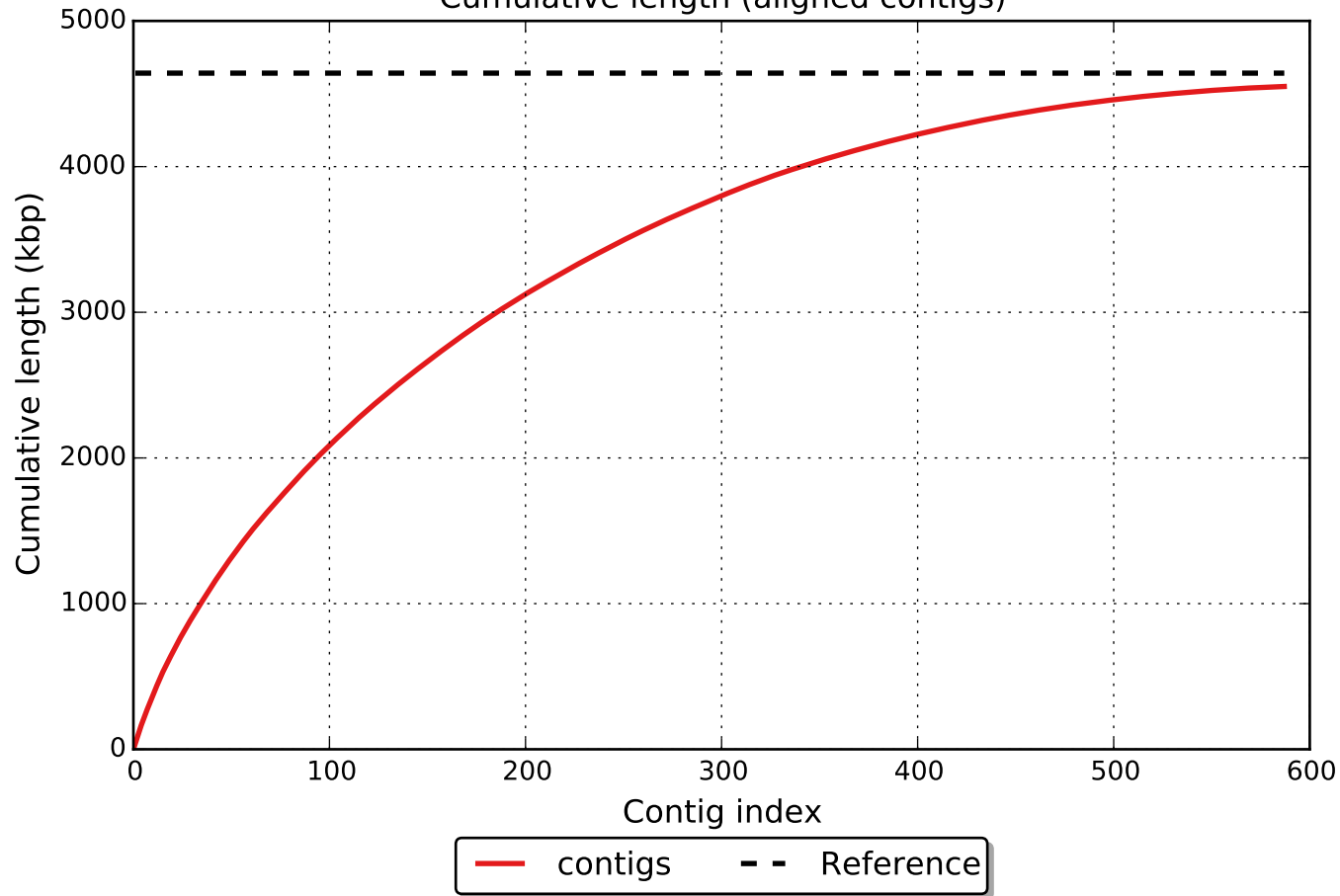


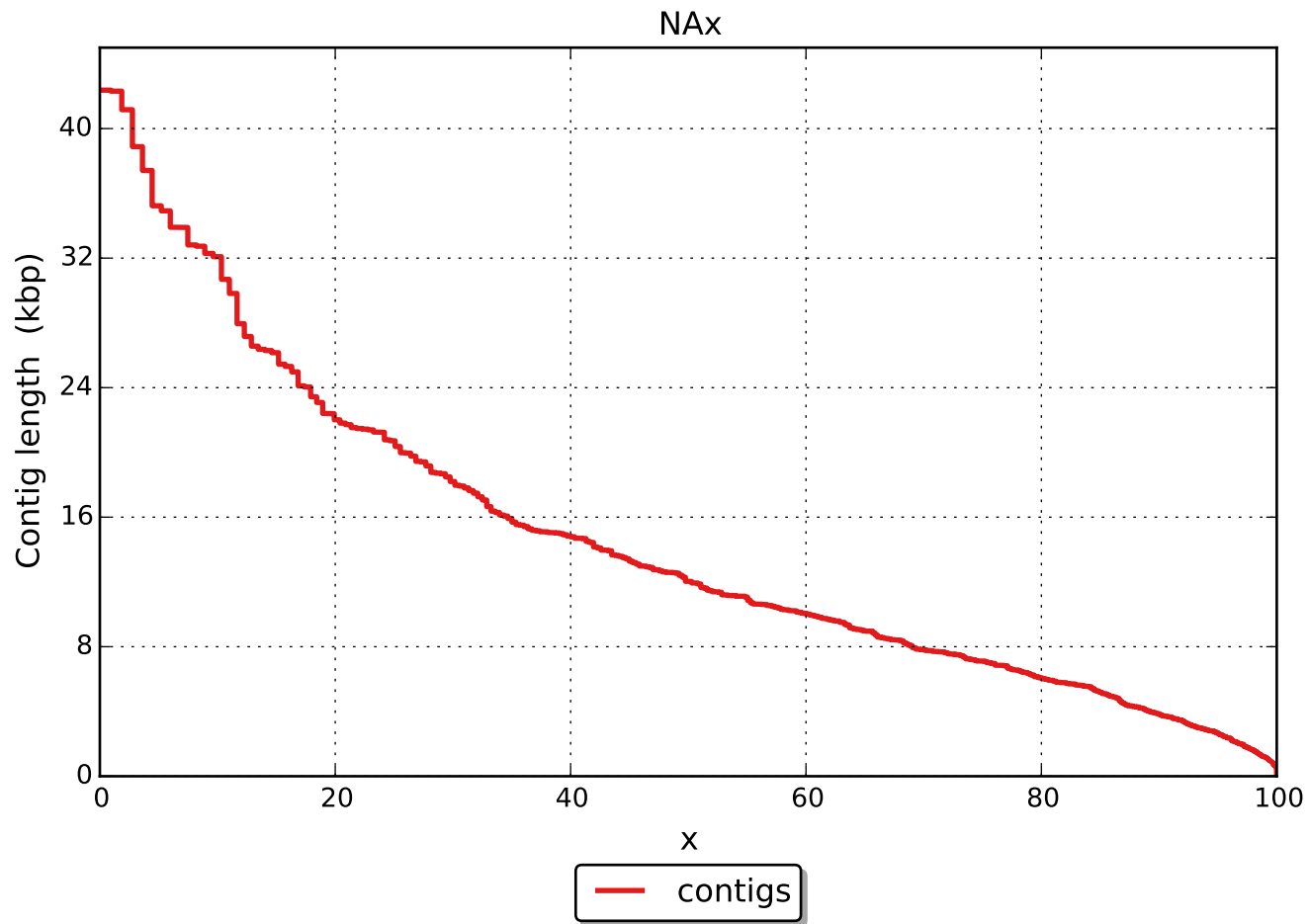
GC content





Cumulative length (aligned contigs)





NGAx

