

Report

	contigs
# contigs (≥ 1000 bp)	32
# contigs (≥ 5000 bp)	28
# contigs (≥ 10000 bp)	27
# contigs (≥ 25000 bp)	26
# contigs (≥ 50000 bp)	23
Total length (≥ 1000 bp)	4696163
Total length (≥ 5000 bp)	4691474
Total length (≥ 10000 bp)	4686008
Total length (≥ 25000 bp)	4672841
Total length (≥ 50000 bp)	4576094
# contigs	40
Largest contig	529644
Total length	4701751
Reference length	4641652
GC (%)	50.82
Reference GC (%)	50.78
N50	305443
NG50	305443
N75	157347
NG75	157347
L50	6
LG50	6
L75	12
LG75	12
# misassemblies	3
# misassembled contigs	2
Misassembled contigs length	578950
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.119
Duplication ratio	1.022
# N's per 100 kbp	0.00
# mismatches per 100 kbp	374.98
# indels per 100 kbp	0.98
Largest alignment	529644
NA50	301763
NGA50	301763
NA75	126242
NGA75	126242
LA50	7
LGA50	7
LA75	13
LGA75	13

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	1
# misassembled contigs	2
Misassembled contigs length	578950
# local misassemblies	1
# mismatches	17252
# indels	45
# short indels	45
# long indels	0
Indels length	45

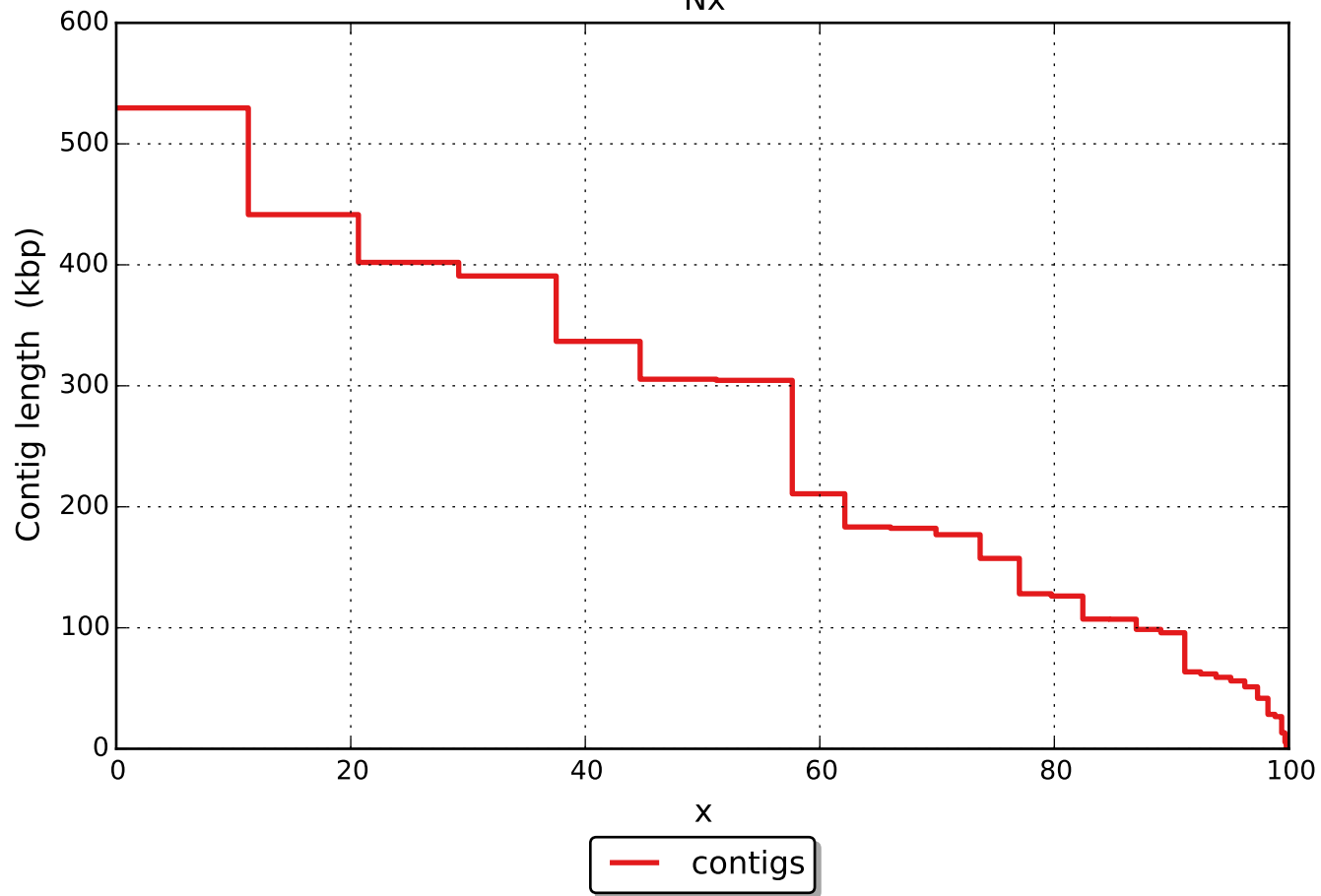
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

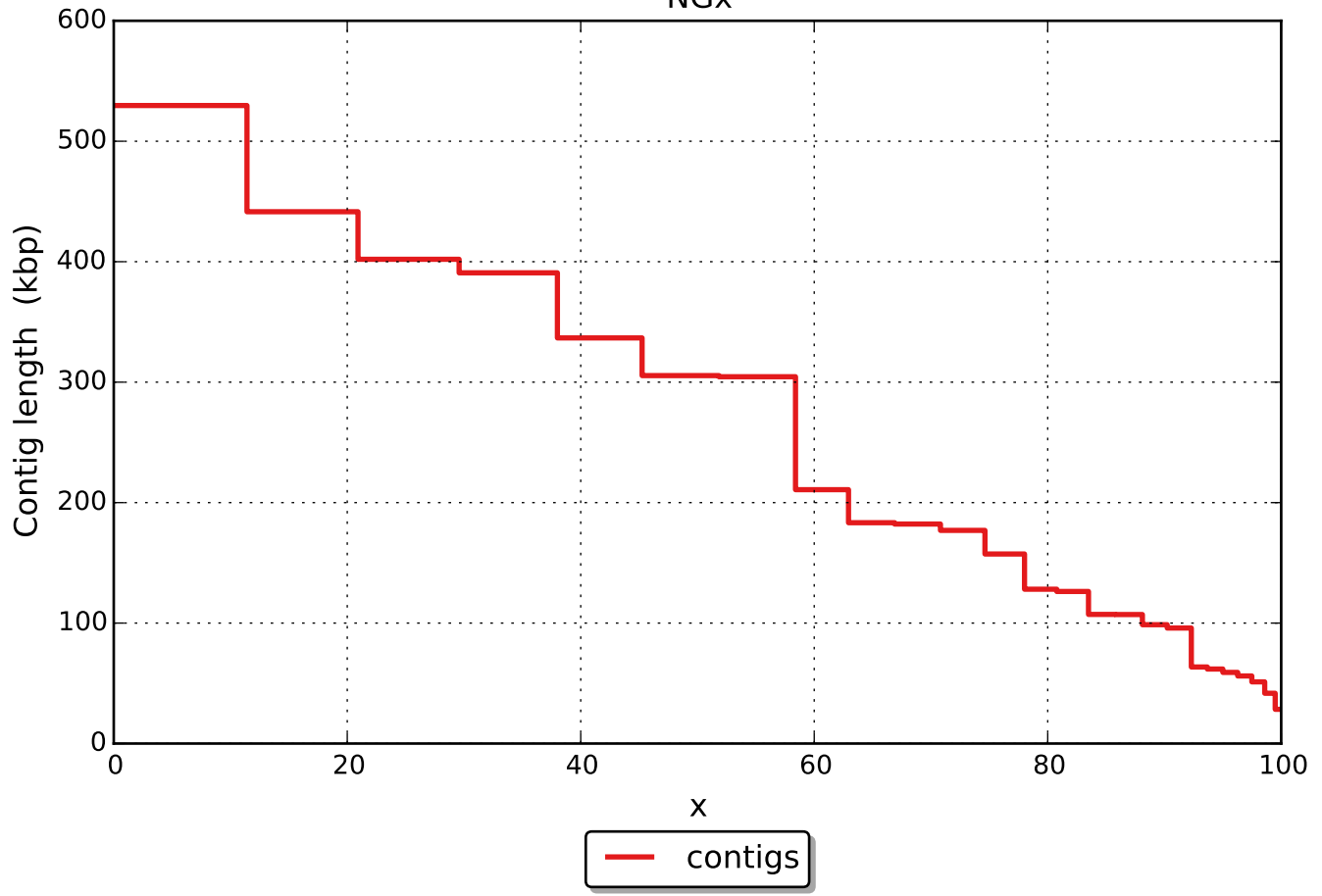
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

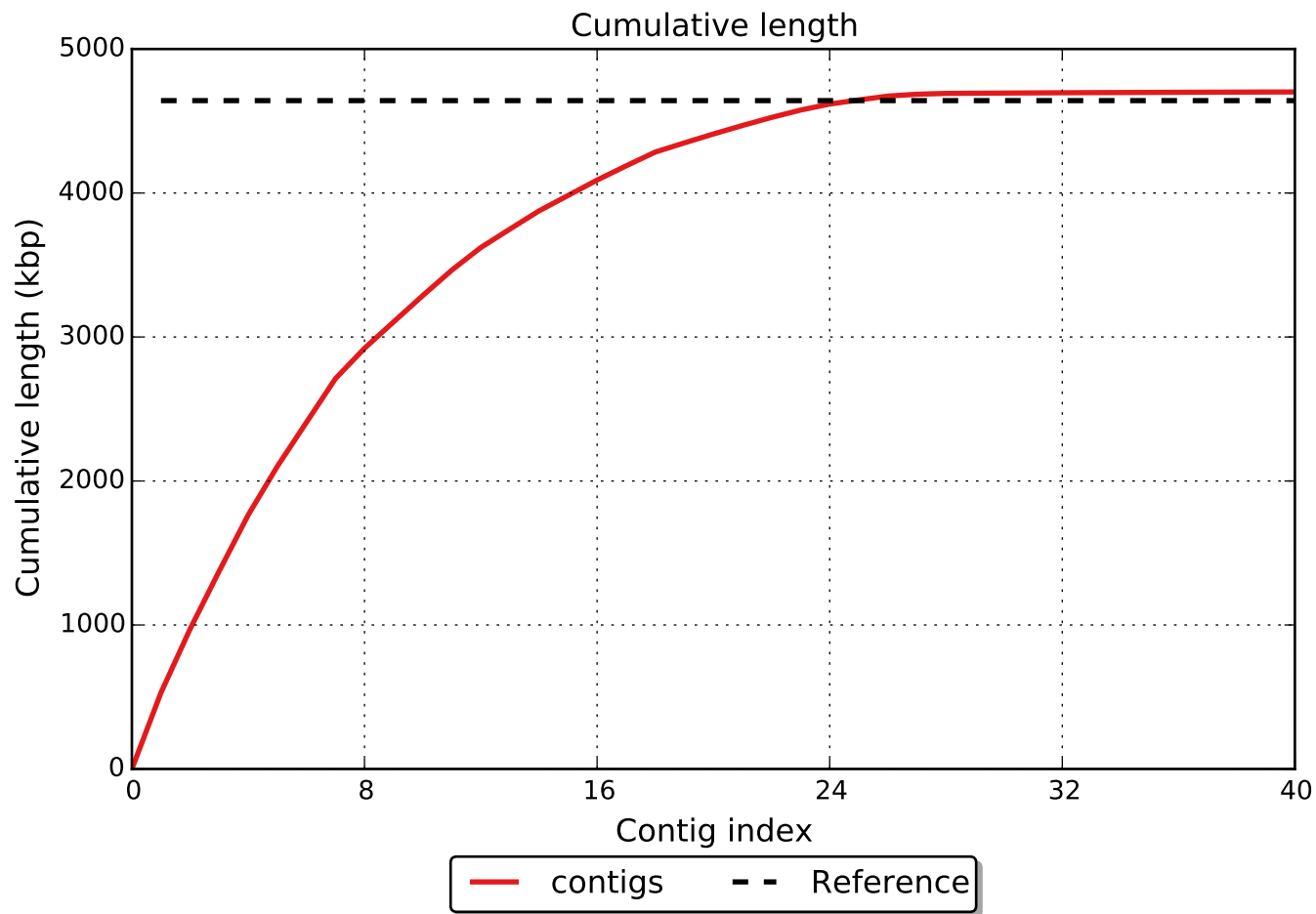
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

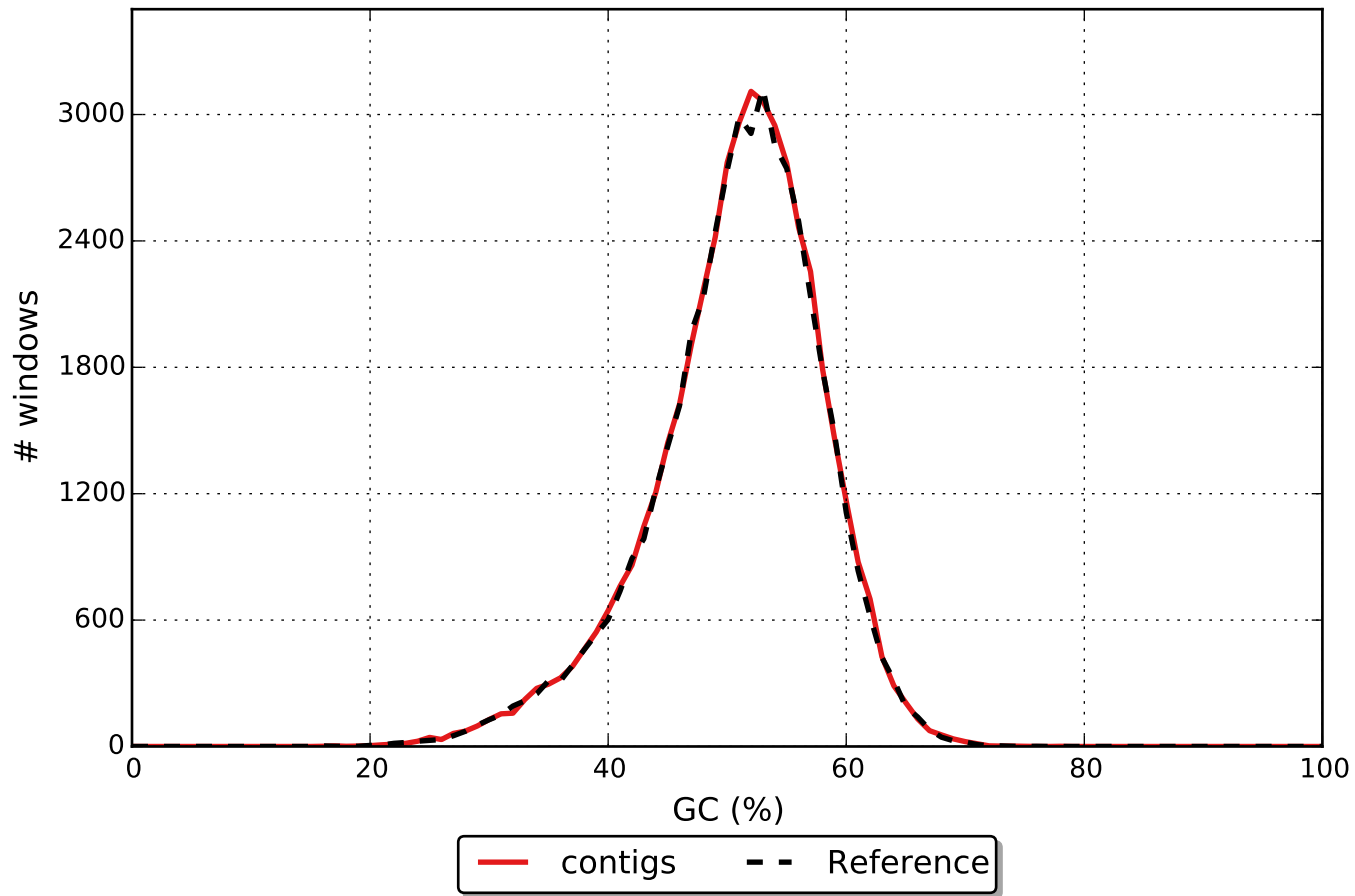


NGx

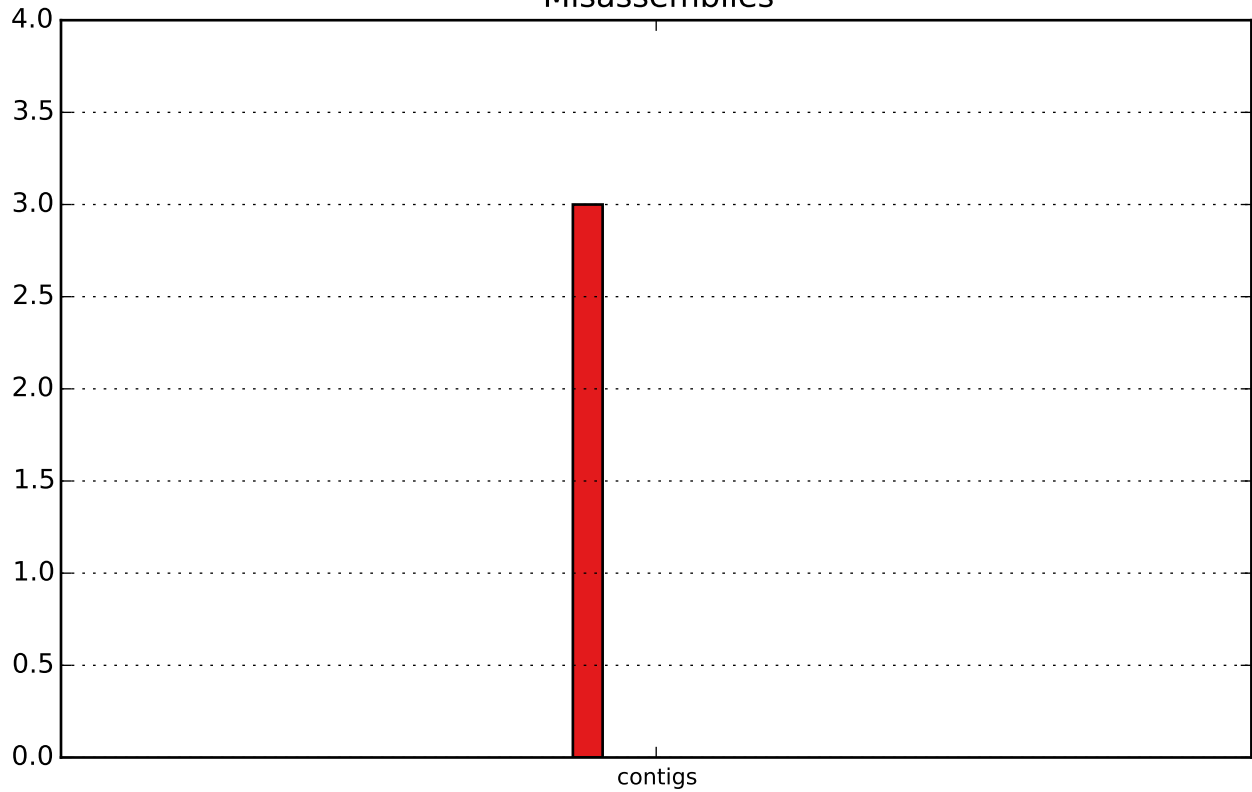




GC content

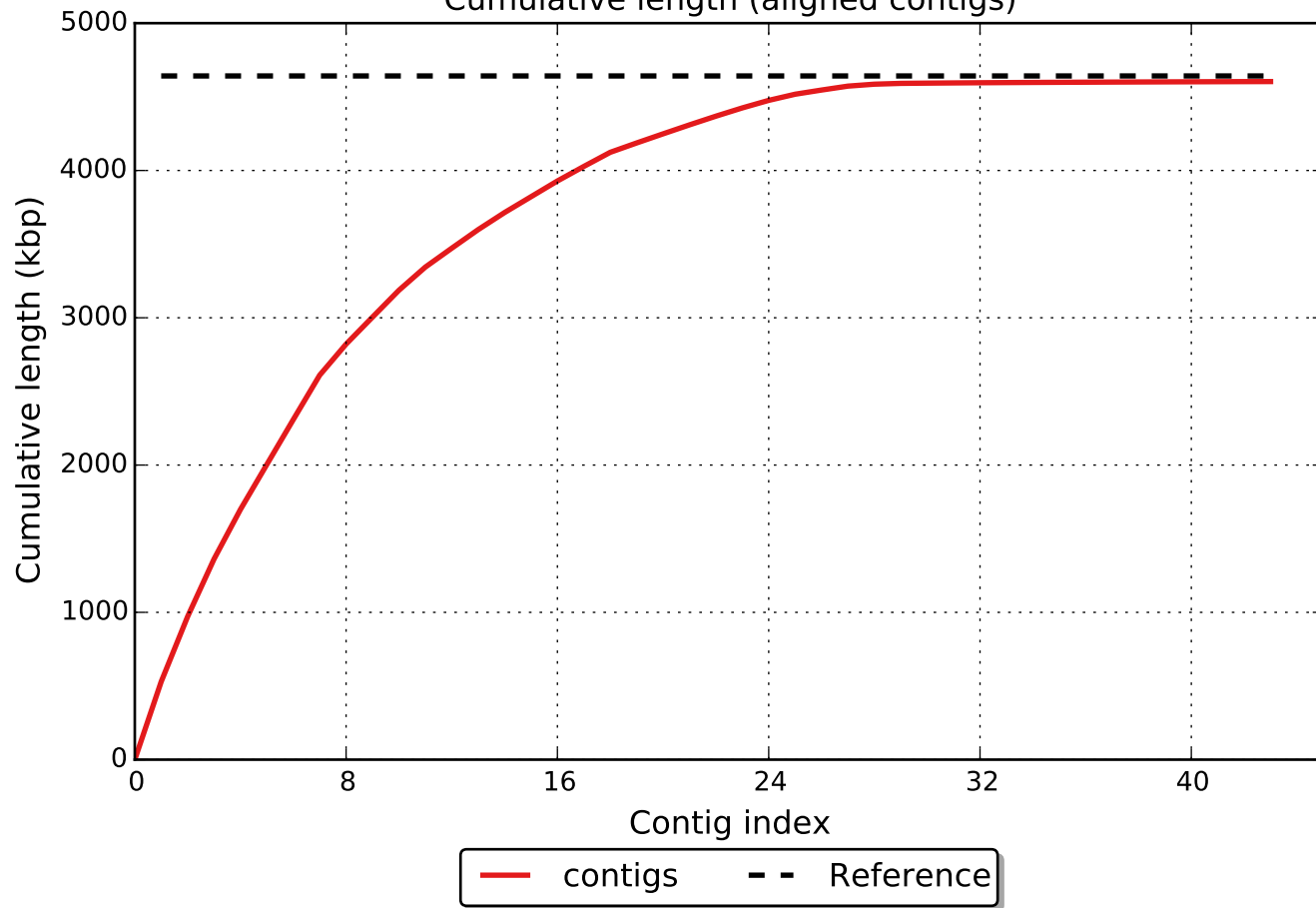


Misassemblies

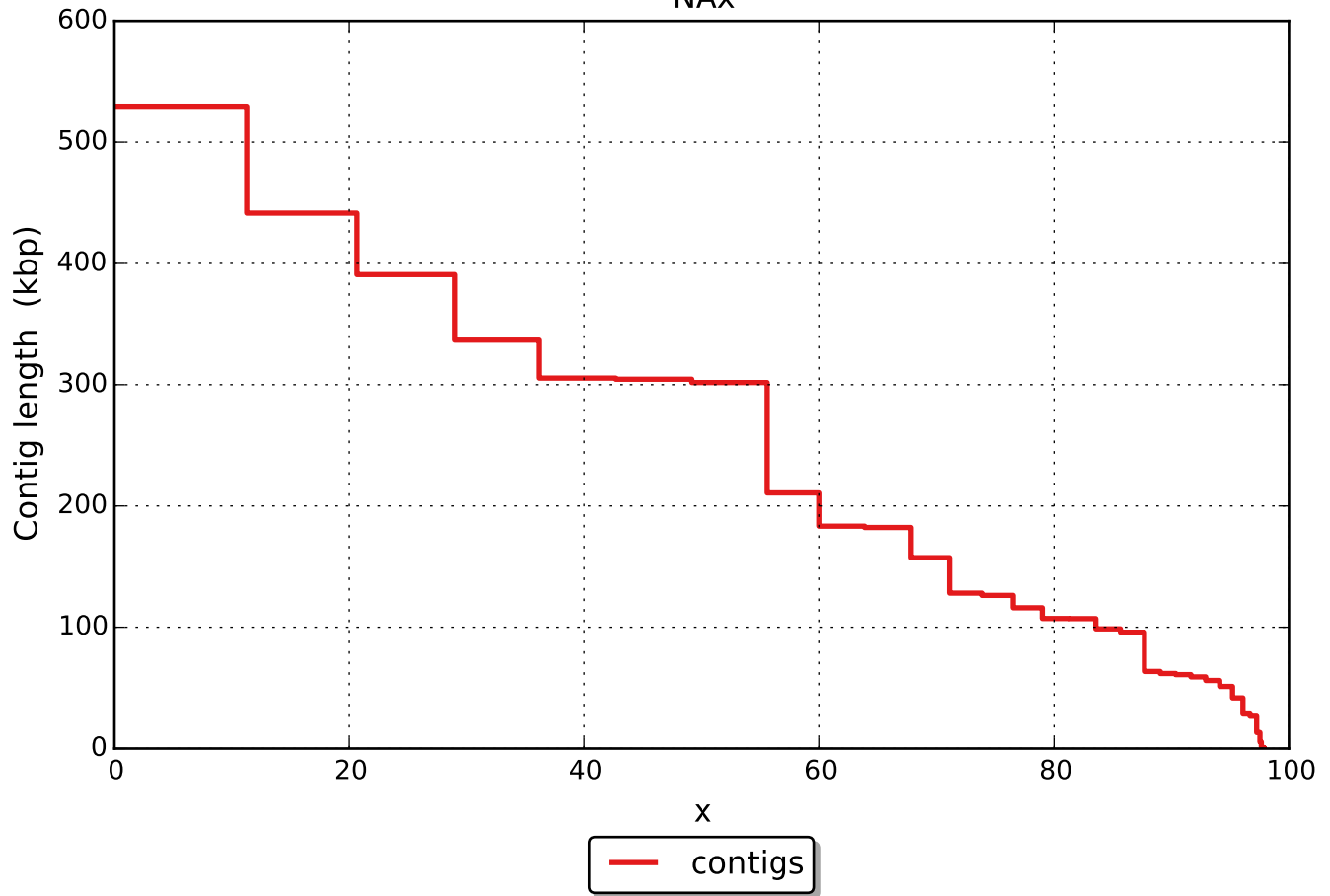


 # relocations

Cumulative length (aligned contigs)



NAx



NGAx

