

Report

	scaffolds
# contigs (>= 1000 bp)	56
# contigs (>= 5000 bp)	42
# contigs (>= 10000 bp)	41
# contigs (>= 25000 bp)	35
# contigs (>= 50000 bp)	30
Total length (>= 1000 bp)	4597846
Total length (>= 5000 bp)	4574350
Total length (>= 10000 bp)	4567854
Total length (>= 25000 bp)	4459002
Total length (>= 50000 bp)	4284789
# contigs	69
Largest contig	527156
Total length	4606111
Reference length	4641652
GC (%)	50.73
Reference GC (%)	50.78
N50	197358
NG50	197358
N75	101046
NG75	86132
L50	8
LG50	8
L75	18
LG75	19
# misassemblies	6
# misassembled contigs	1
Misassembled contigs length	82061
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.922
Duplication ratio	1.013
# N's per 100 kbp	0.00
# mismatches per 100 kbp	676.93
# indels per 100 kbp	0.95
Largest alignment	527156
NA50	197358
NGA50	197358
NA75	101046
NGA75	86132
LA50	8
LGA50	8
LA75	18
LGA75	19

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

	scaffolds
# misassemblies	6
# relocations	4
# translocations	0
# inversions	2
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	82061
# local misassemblies	0
# mismatches	30768
# indels	43
# short indels	43
# long indels	0
Indels length	43

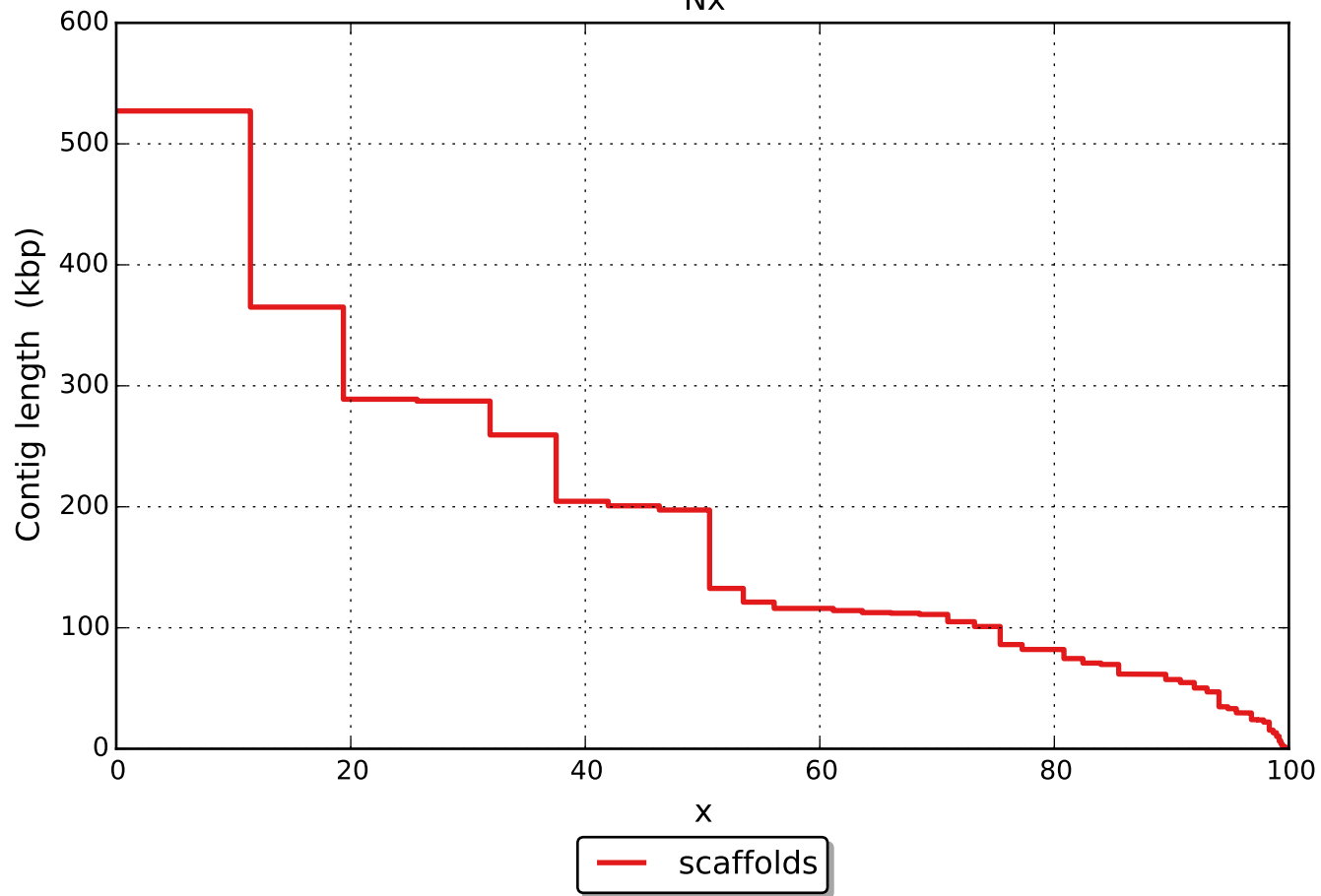
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

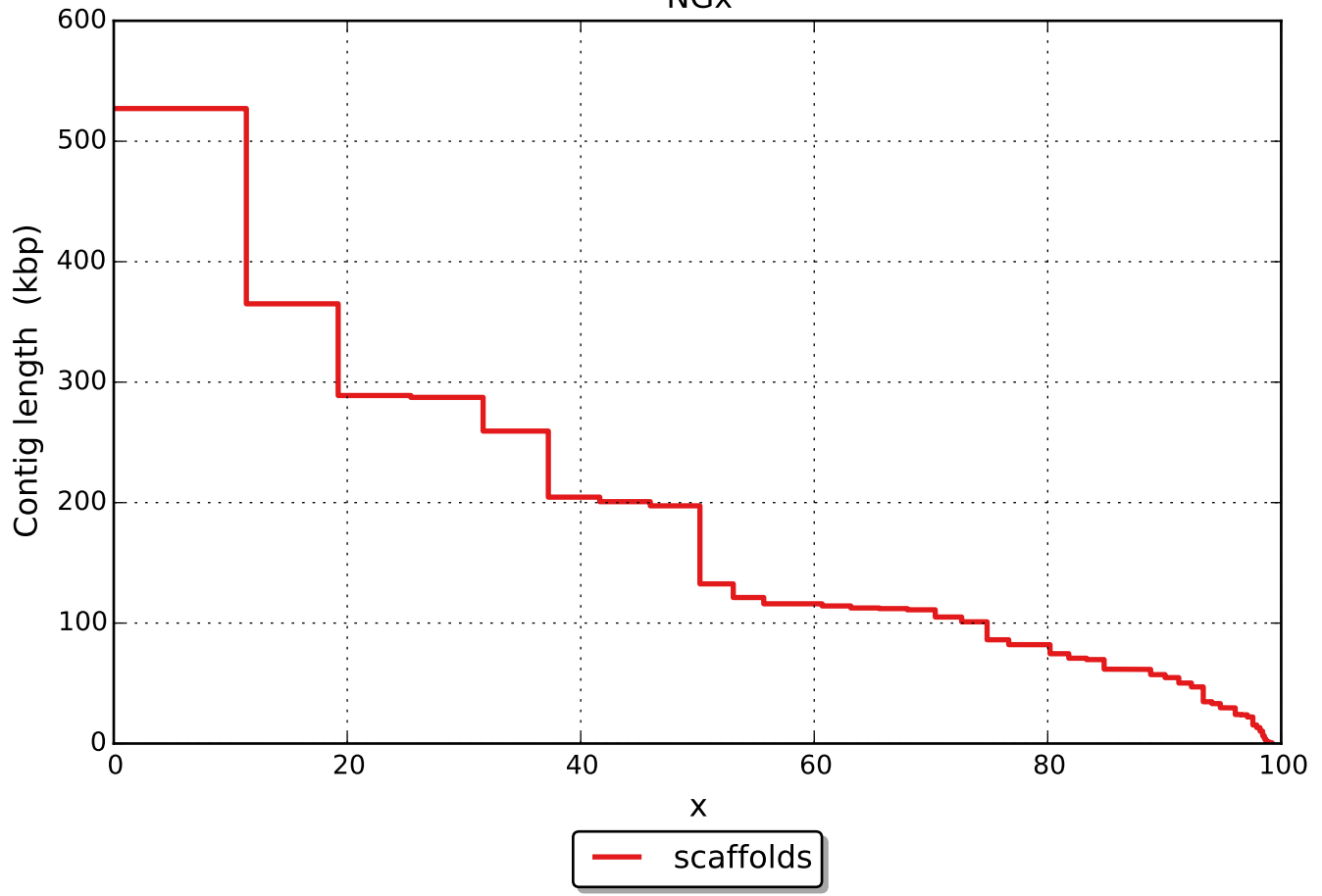
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

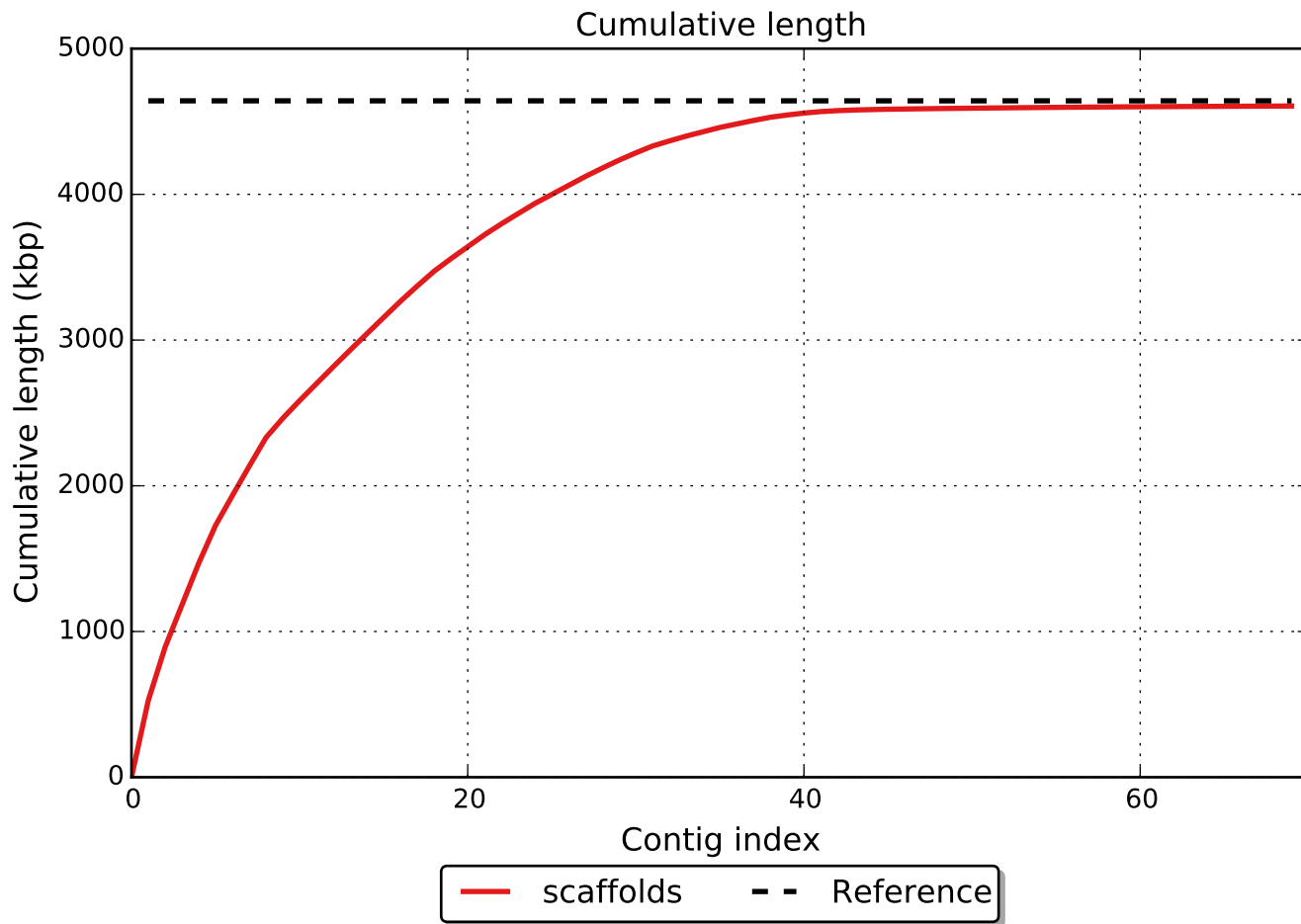
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

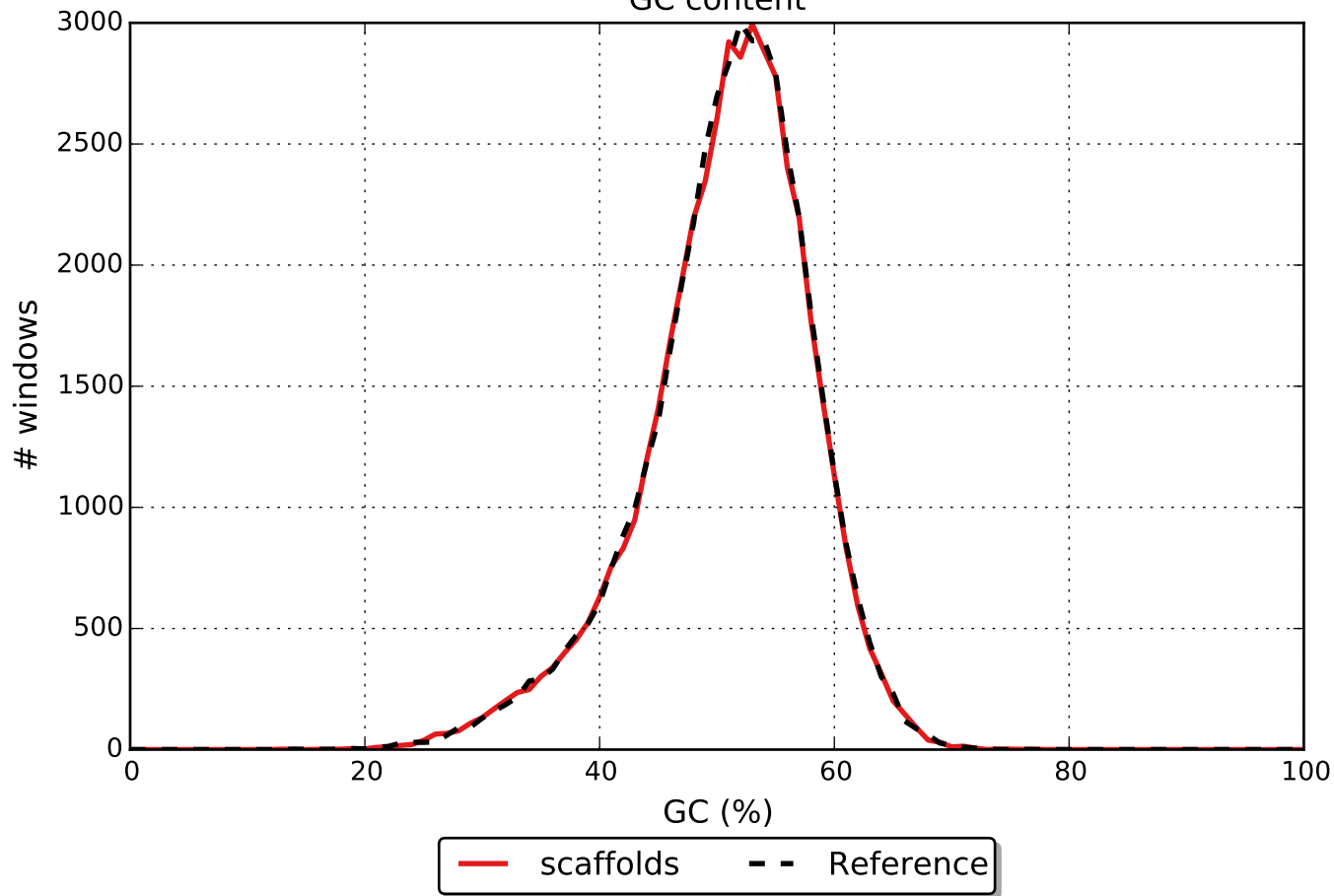


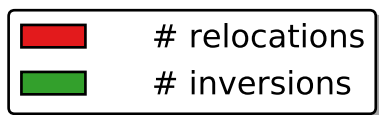
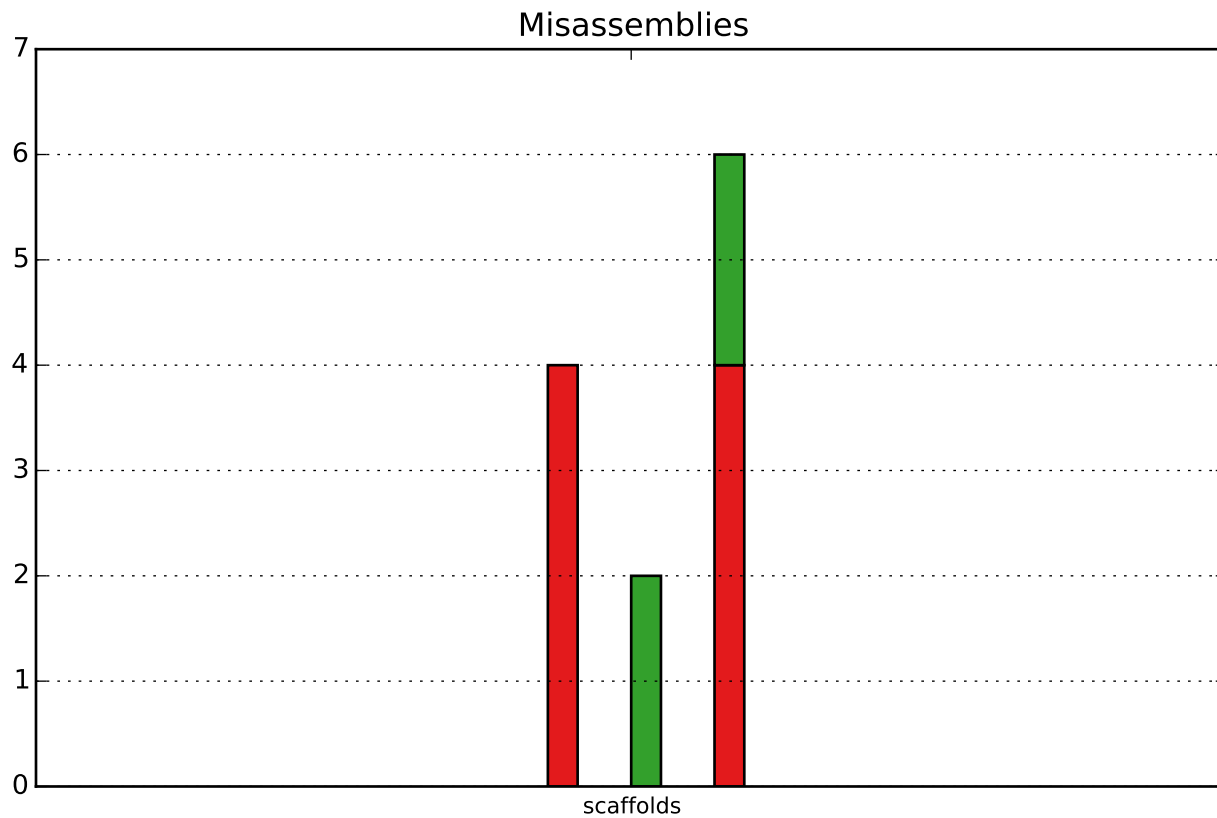
NGx



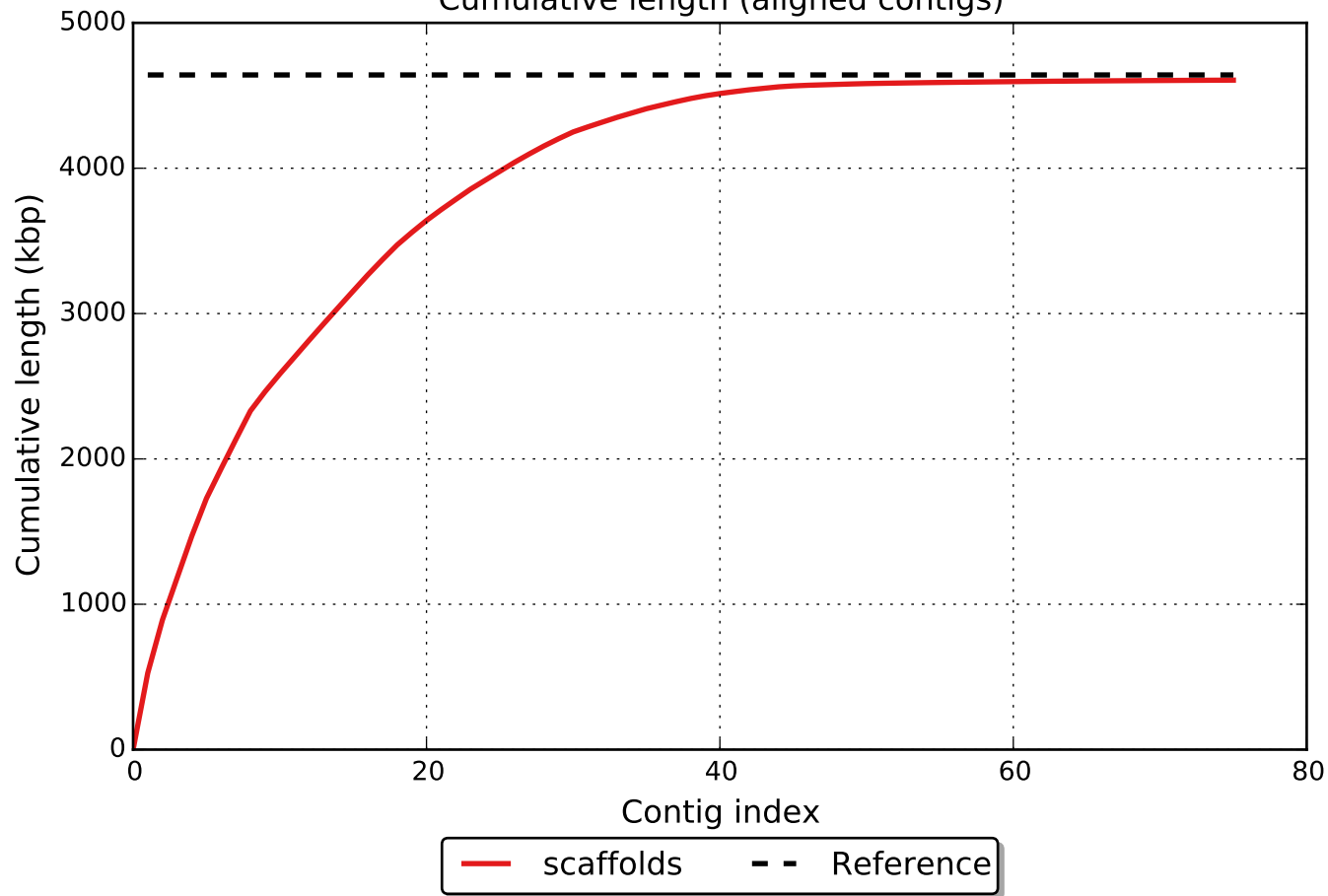


GC content

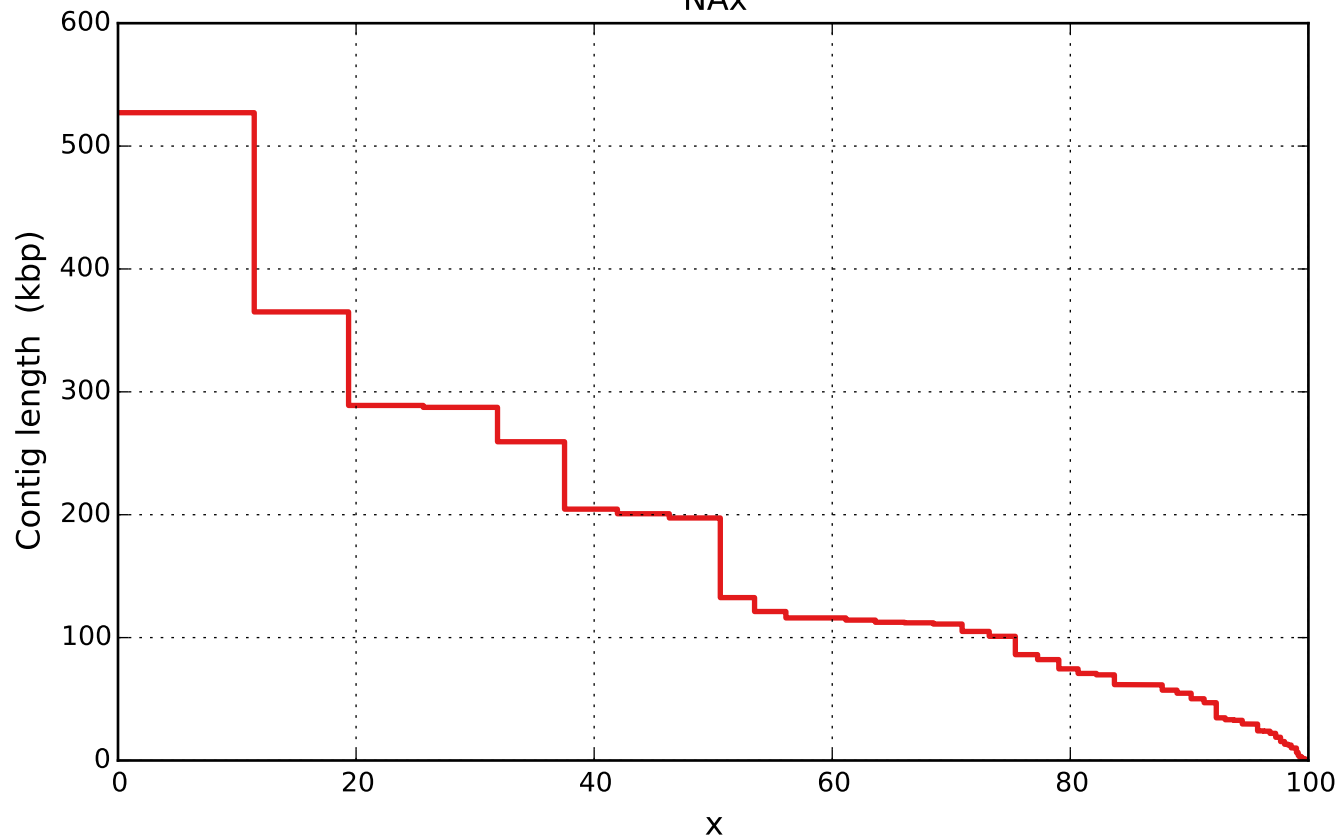




Cumulative length (aligned contigs)



NAx



— scaffolds

NGAx

