

Report

	scaffolds
# contigs (≥ 1000 bp)	232
# contigs (≥ 5000 bp)	1
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 1000 bp)	313361
Total length (≥ 5000 bp)	5609
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	1261
Largest contig	5609
Total length	1007735
Reference length	4641652
GC (▼)	50.79
Reference GC (▼)	50.79
N50	802
N75	614
L50	447
L75	806
# misassemblies	8
# misassembled contigs	8
Misassembled contigs length	12509
# local misassemblies	3
# unaligned contigs	0 + 15 part
Unaligned length	5768
Genome fraction (▼)	21.527
Duplication ratio	1.003
# N's per 100 kbp	753.37
# mismatches per 100 kbp	368.10
# indels per 100 kbp	46.64
Largest alignment	5592
NA50	792
NGA50	-
NA75	607
LA50	454
LA75	819

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

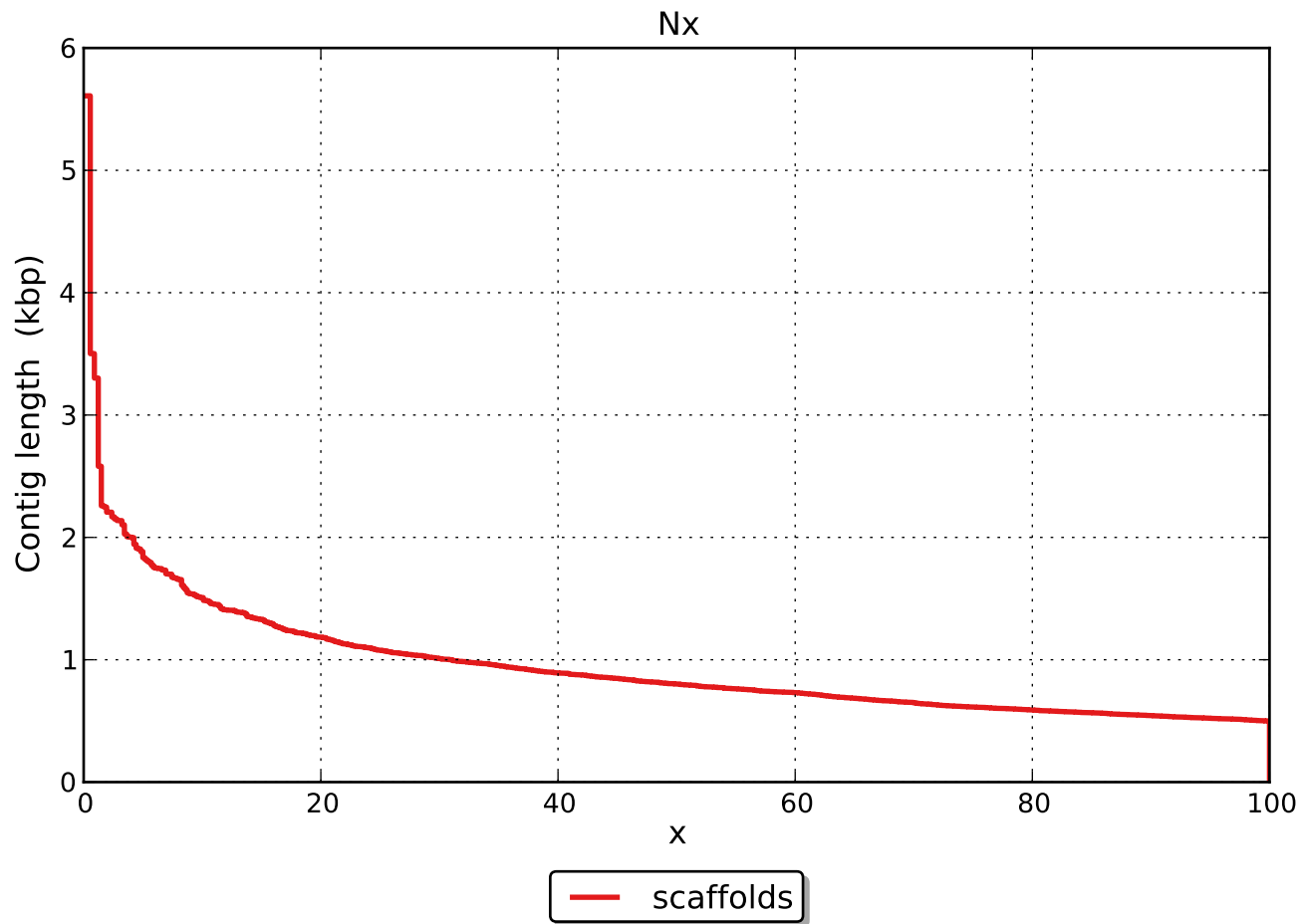
	scaffolds
# misassemblies	8
# relocations	8
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	8
Misassembled contigs length	12509
# local misassemblies	3
# mismatches	3678
# indels	466
# short indels	221
# long indels	245
Indels length	4110

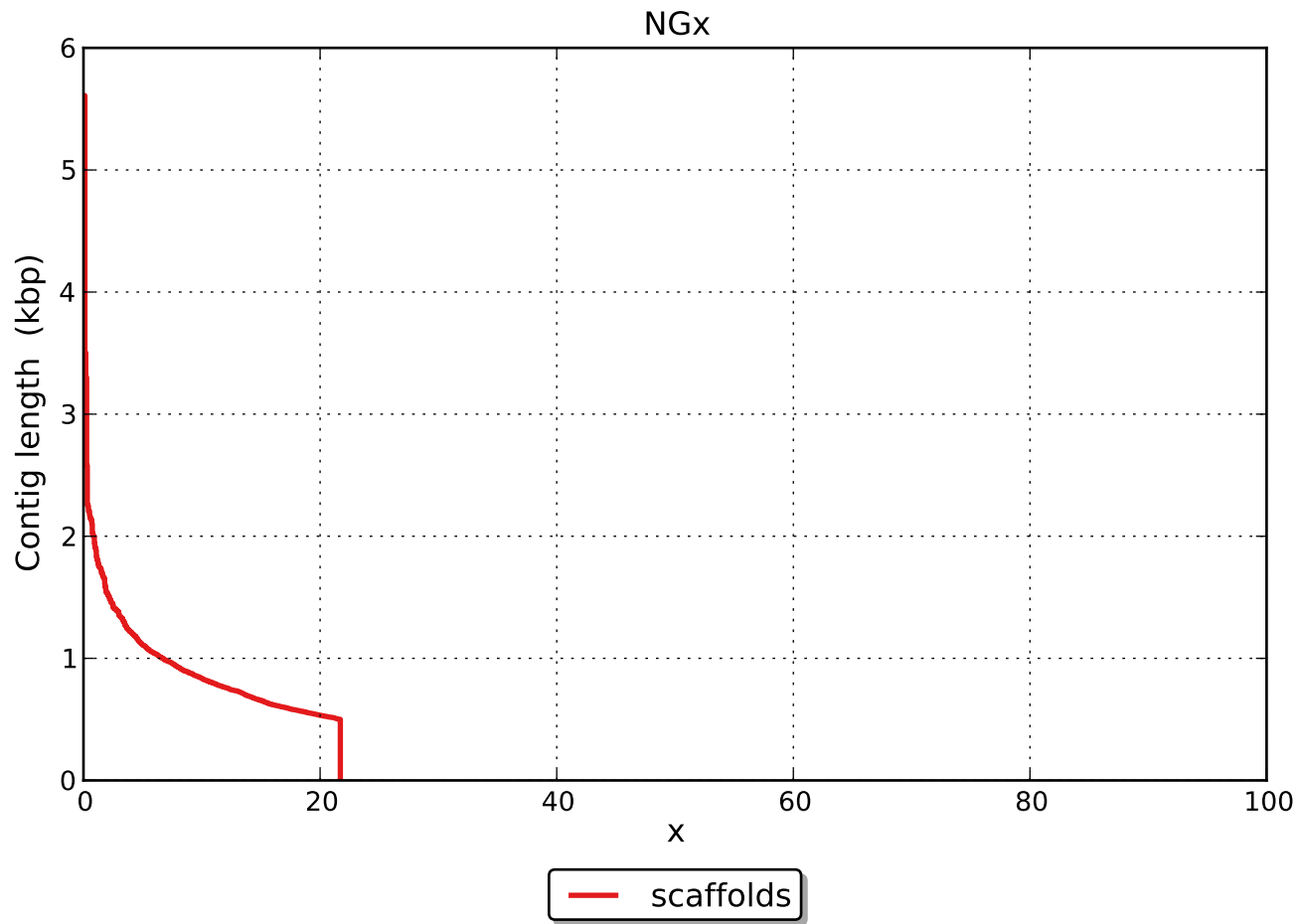
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

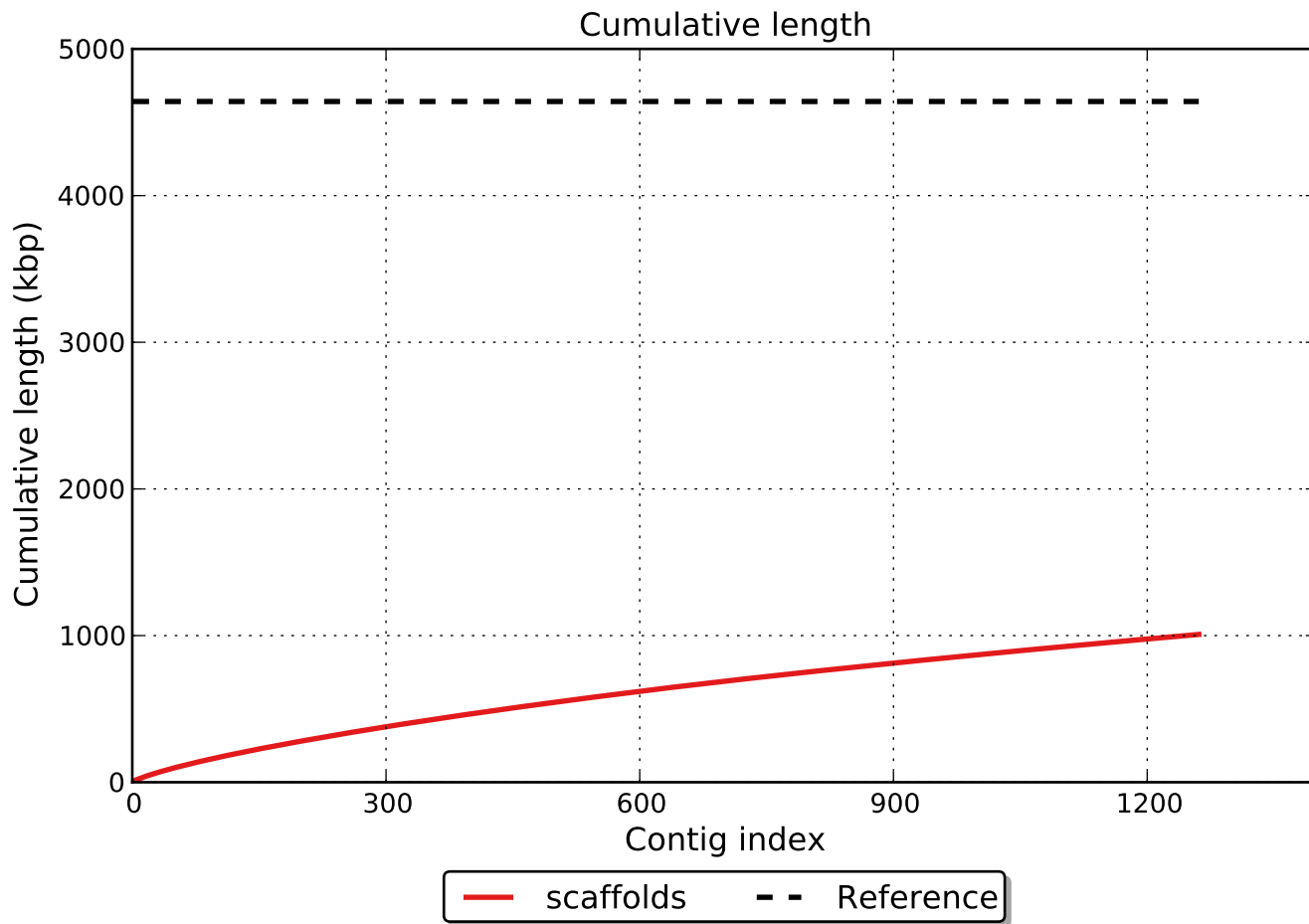
Unaligned report

	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	15
# with misassembly	0
# both parts are significant	0
Partially unaligned length	5768
# N's	7592

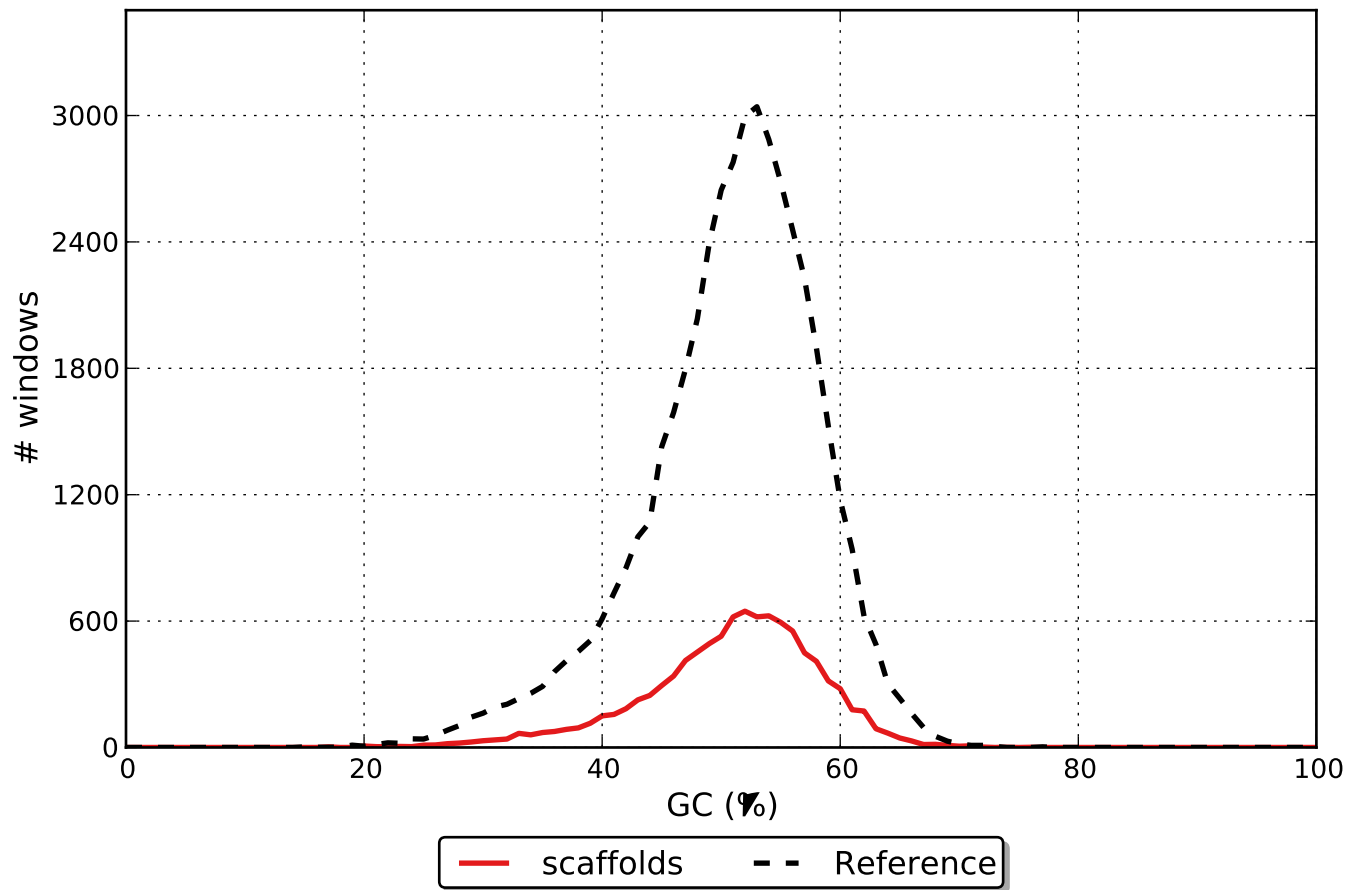
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

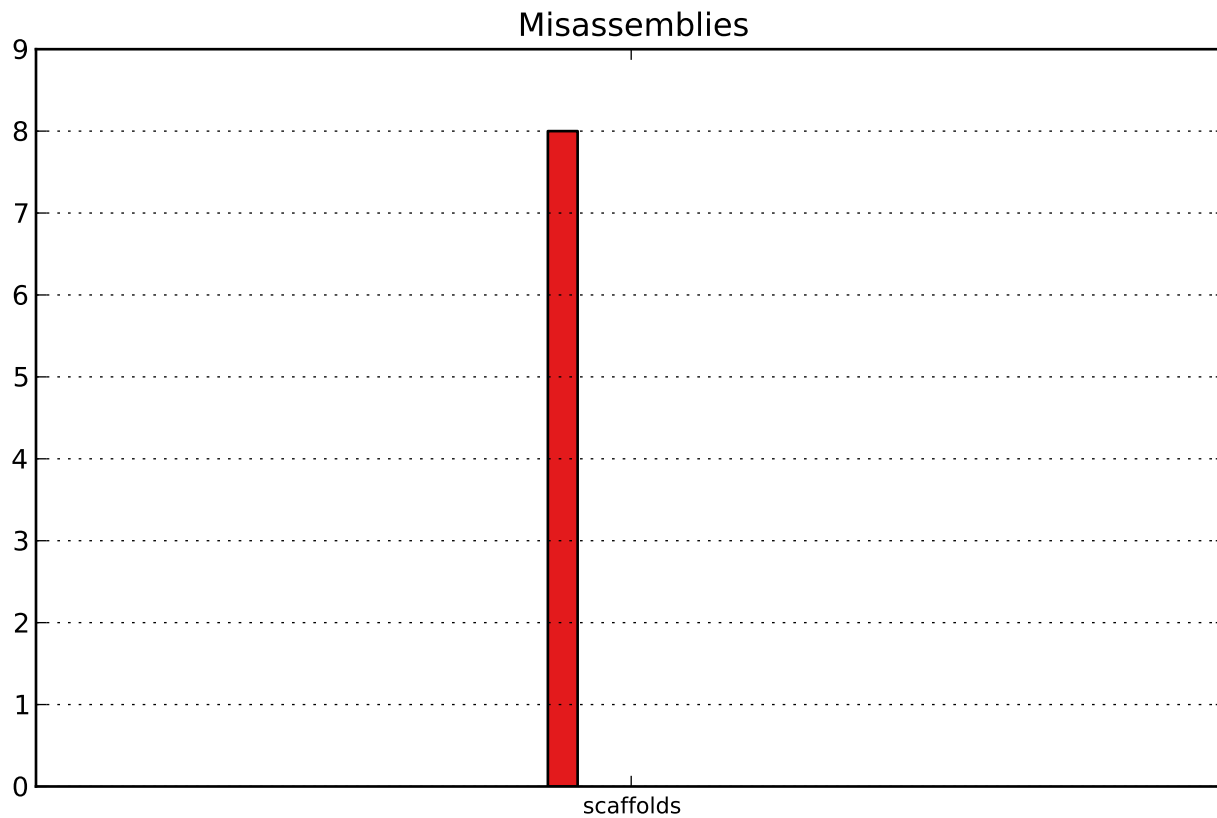




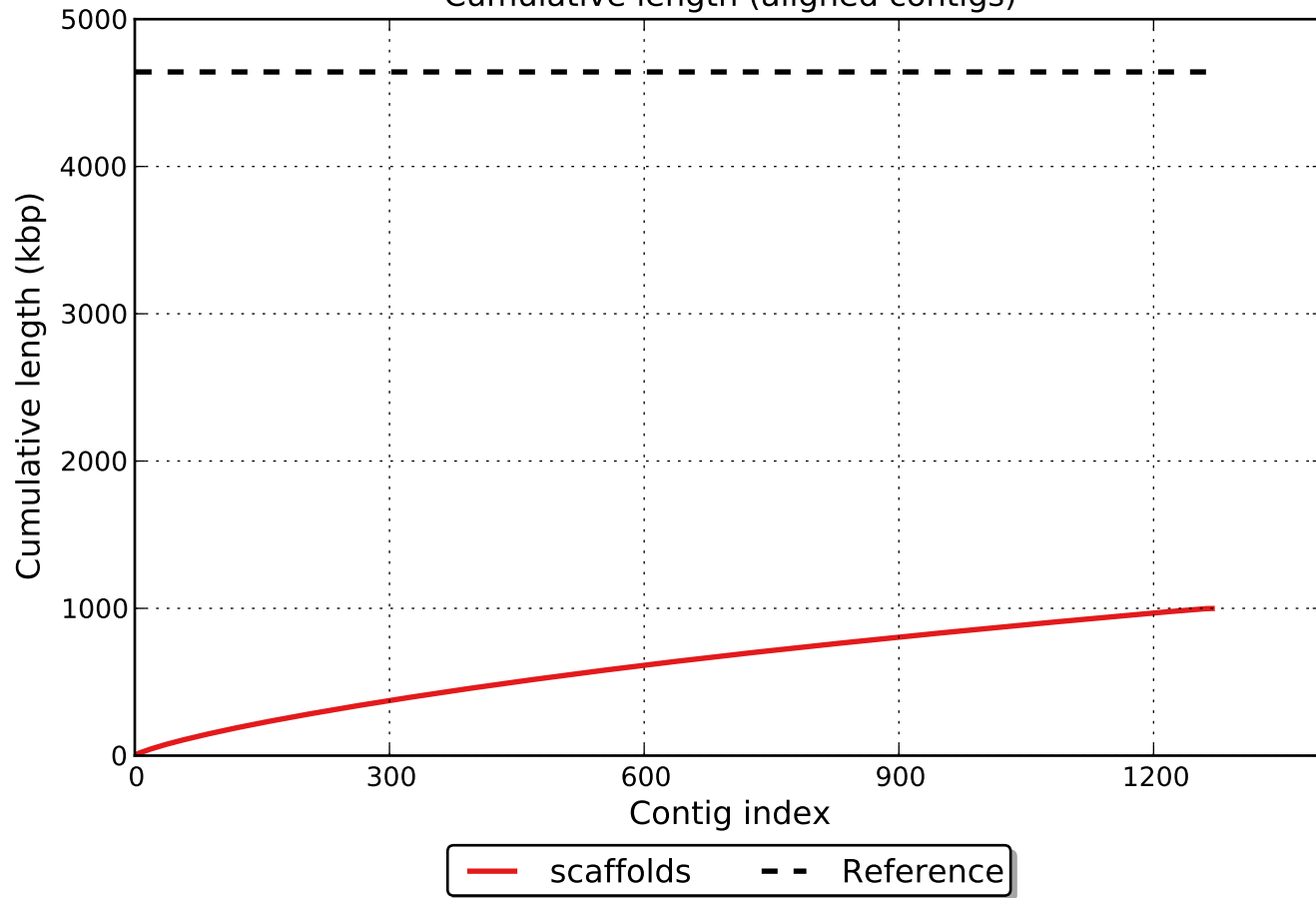


GC content

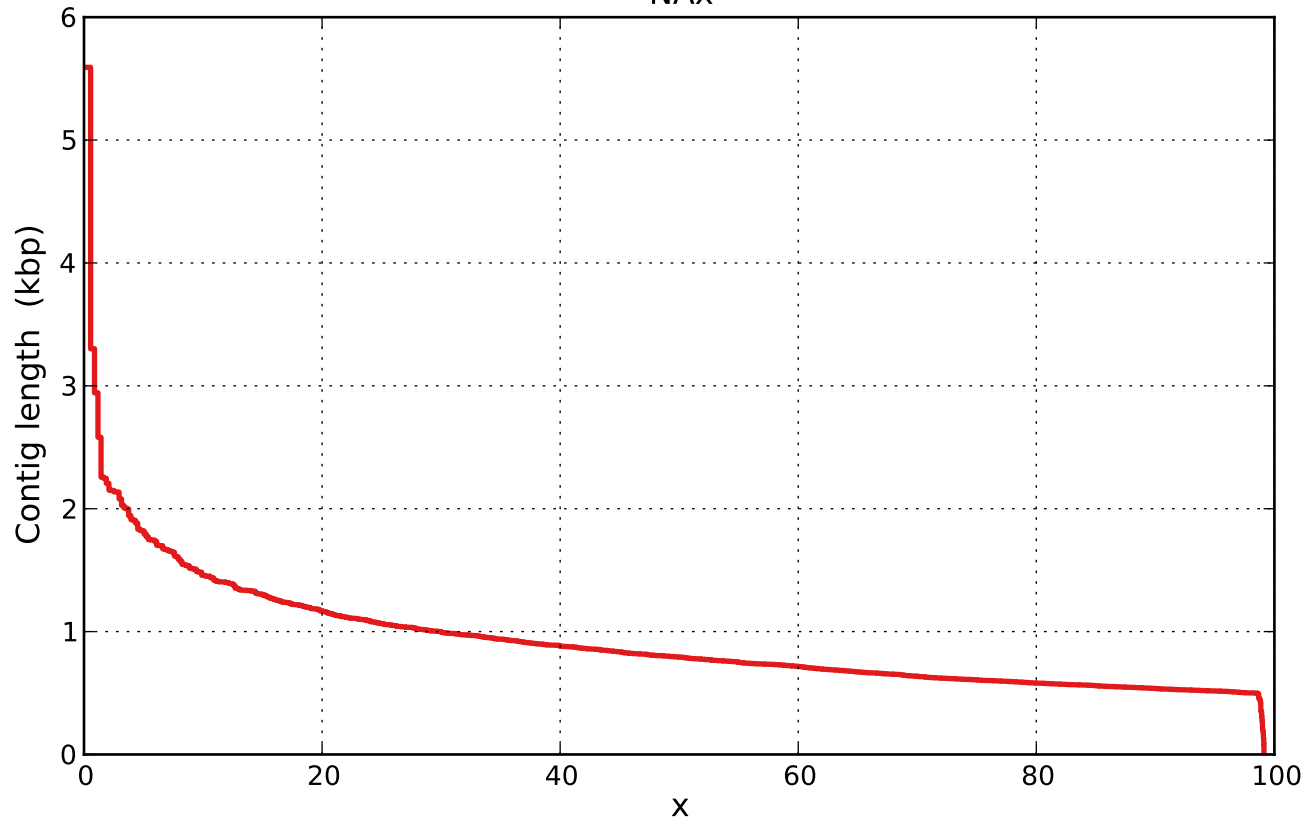




Cumulative length (aligned contigs)

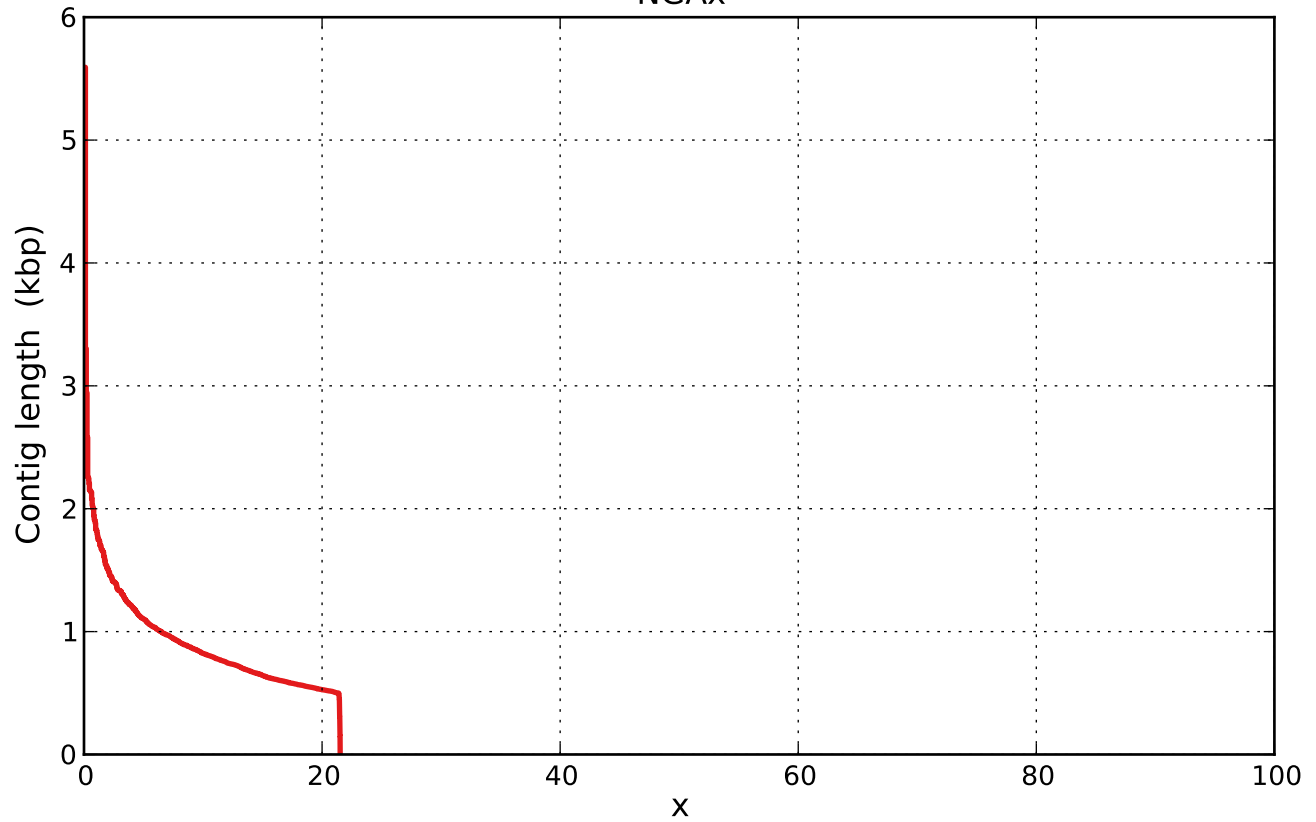


NAx



— scaffolds

NGAx



— scaffolds