

Report

	scaffolds
# contigs (>= 1000 bp)	87
# contigs (>= 5000 bp)	66
# contigs (>= 10000 bp)	57
# contigs (>= 25000 bp)	48
# contigs (>= 50000 bp)	28
Total length (>= 1000 bp)	4547503
Total length (>= 5000 bp)	4497765
Total length (>= 10000 bp)	4428326
Total length (>= 25000 bp)	4282915
Total length (>= 50000 bp)	3594211
# contigs	94
Largest contig	284701
Total length	4553225
Reference length	4641652
GC (▼)	50.75
Reference GC (▼)	50.79
N50	172142
NG50	117600
N75	57777
NG75	57309
L50	11
LG50	12
L75	25
LG75	26
# misassemblies	7
# misassembled contigs	5
Misassembled contigs length	422276
# local misassemblies	15
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (▼)	98.032
Duplication ratio	1.001
# N's per 100 kbp	3.73
# mismatches per 100 kbp	7.25
# indels per 100 kbp	0.66
Largest alignment	284701
NA50	112272
NGA50	110200
NA75	57309
NGA75	56777
LA50	12
LGA50	13
LA75	27
LGA75	28

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	7
# relocations	7
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	5
Misassembled contigs length	422276
# local misassemblies	15
# mismatches	330
# indels	30
# short indels	28
# long indels	2
Indels length	129

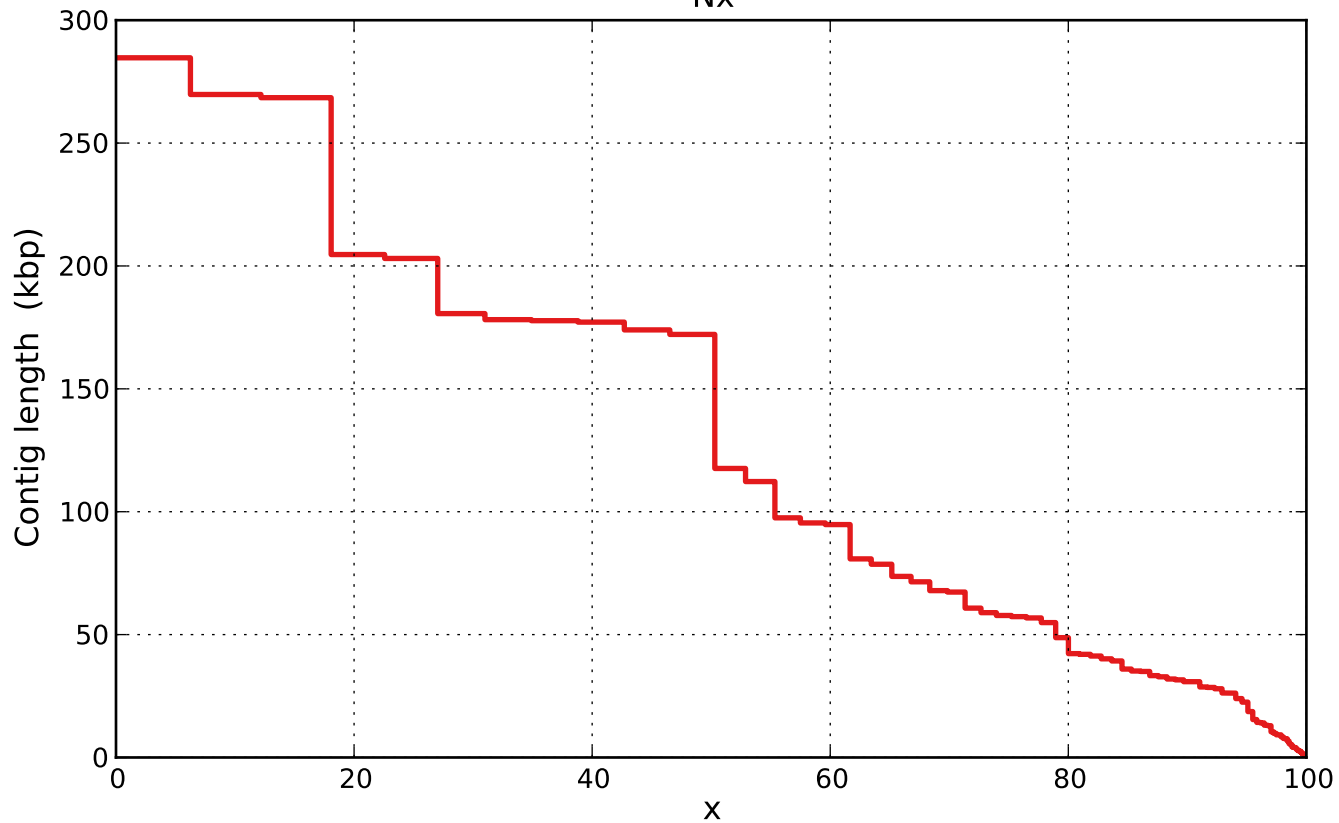
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

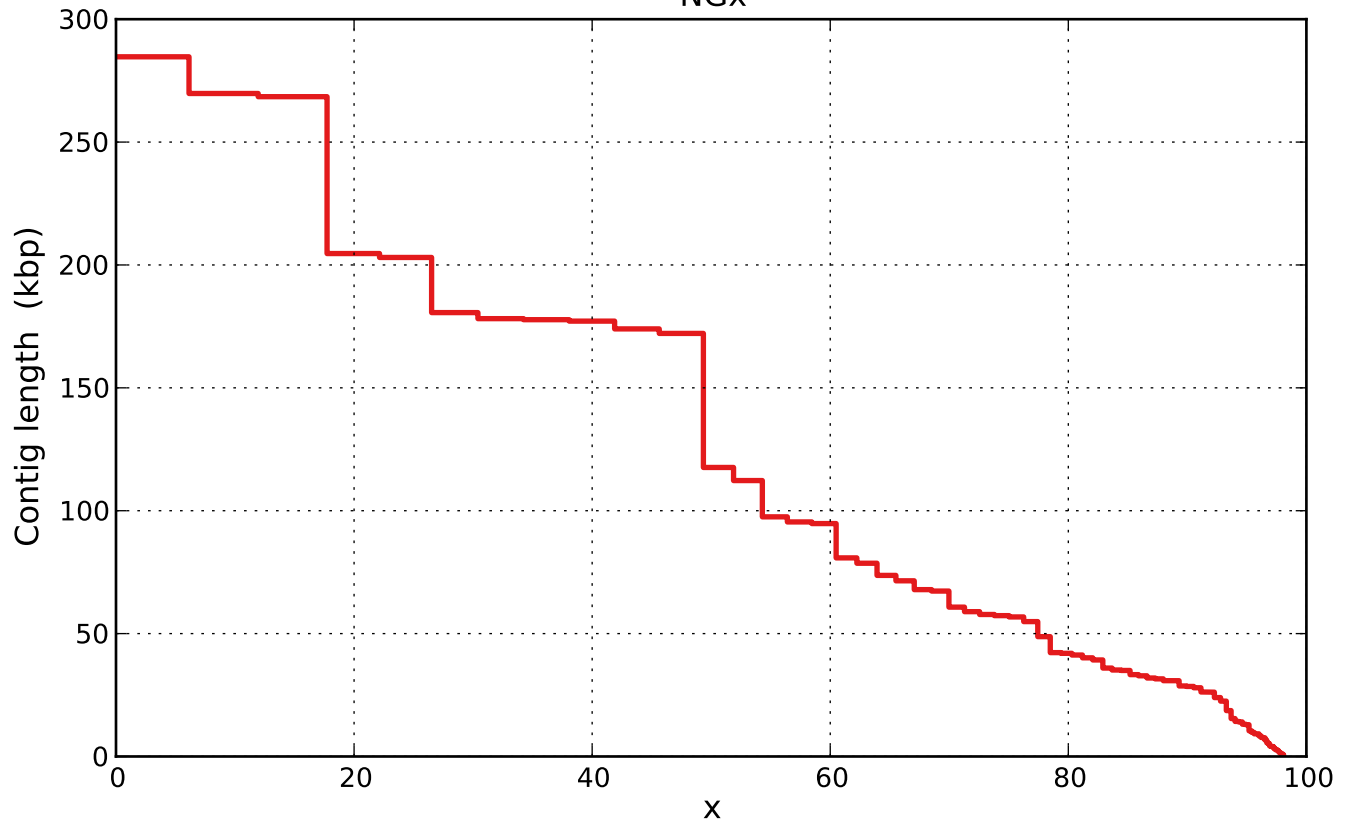
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	170

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).

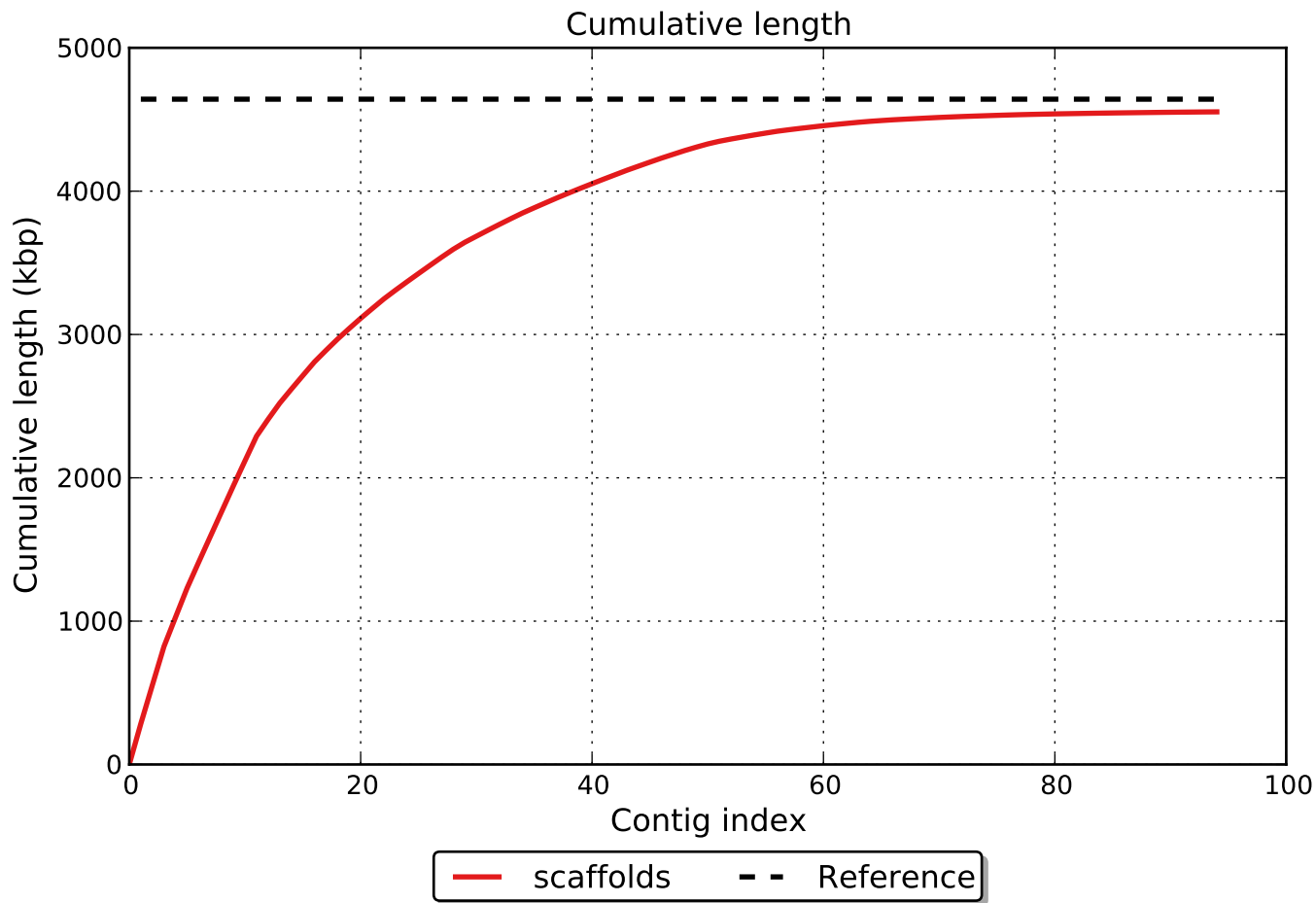
Nx



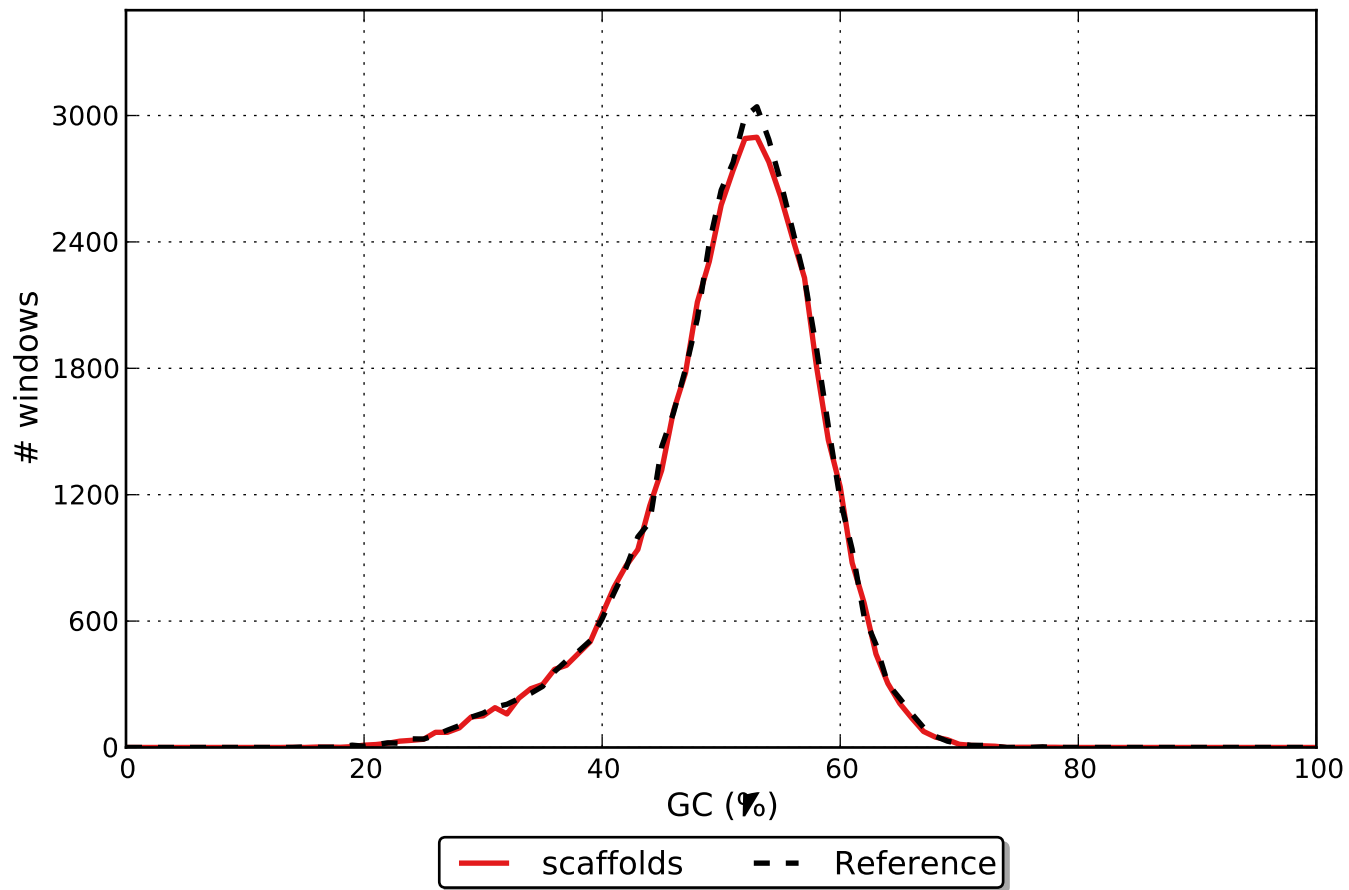
NGx

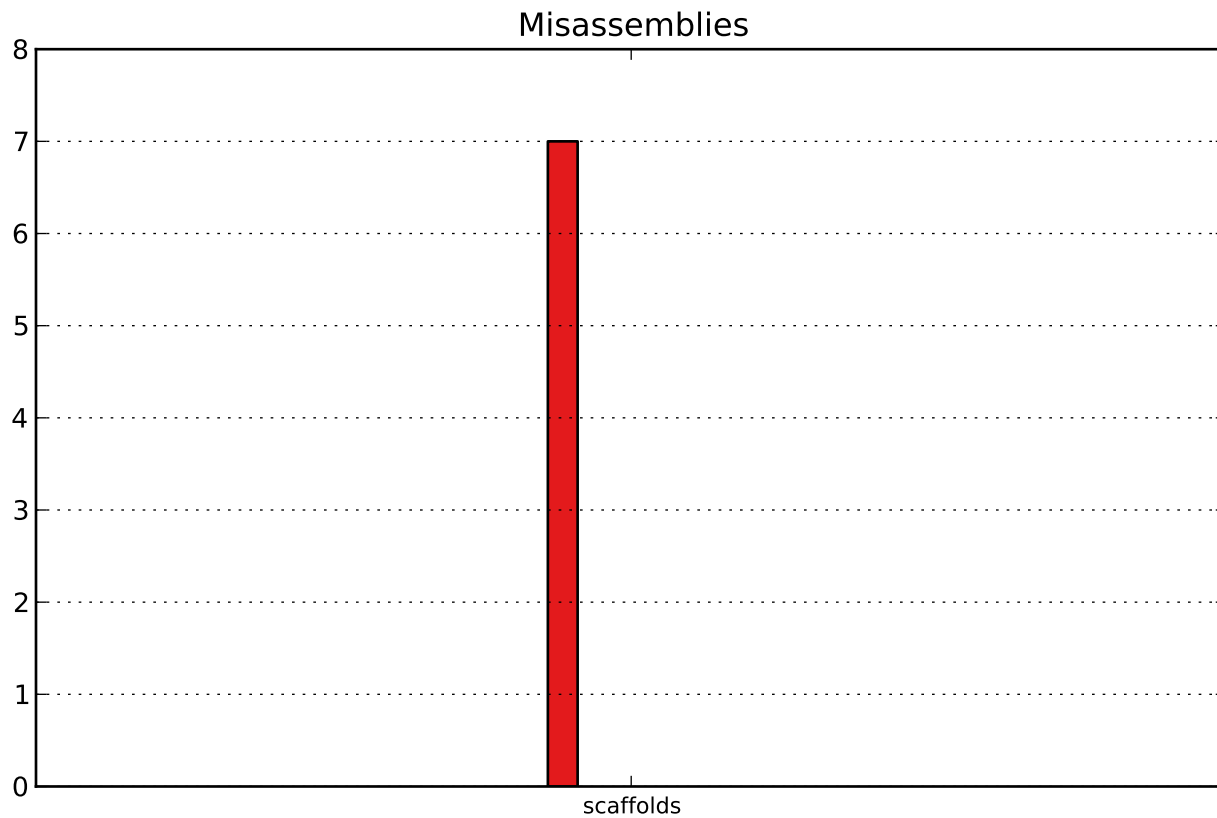


— scaffolds

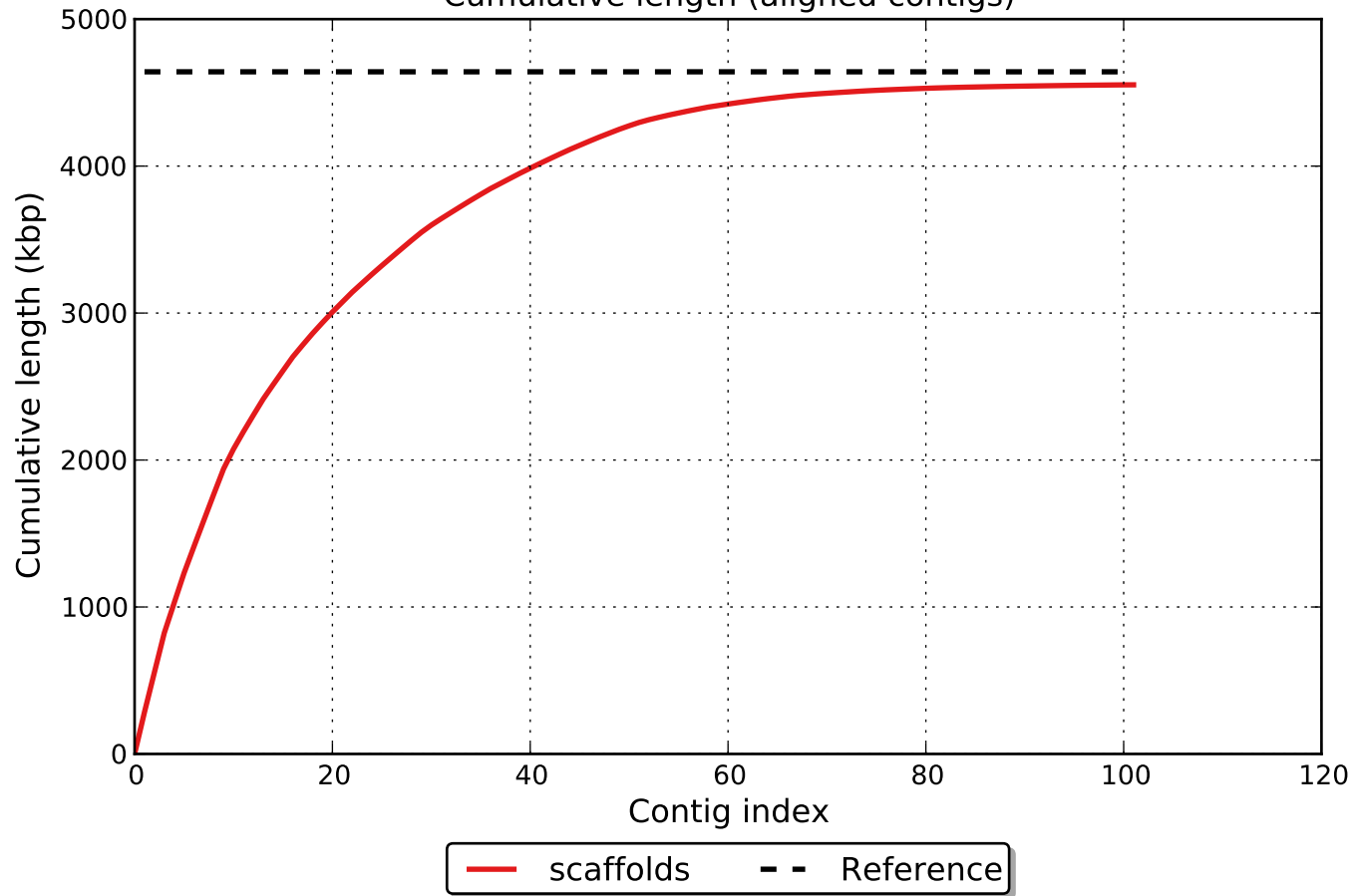


GC content

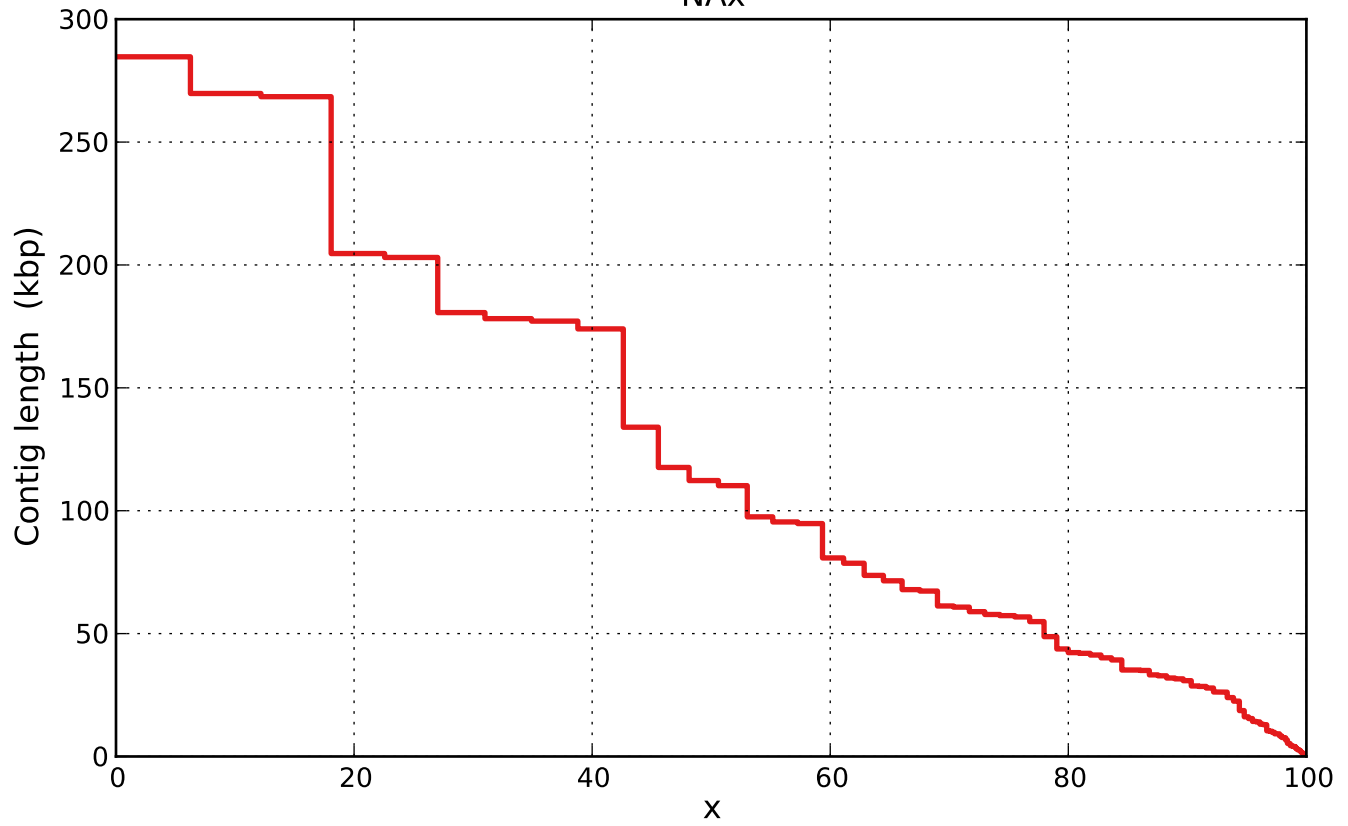




Cumulative length (aligned contigs)

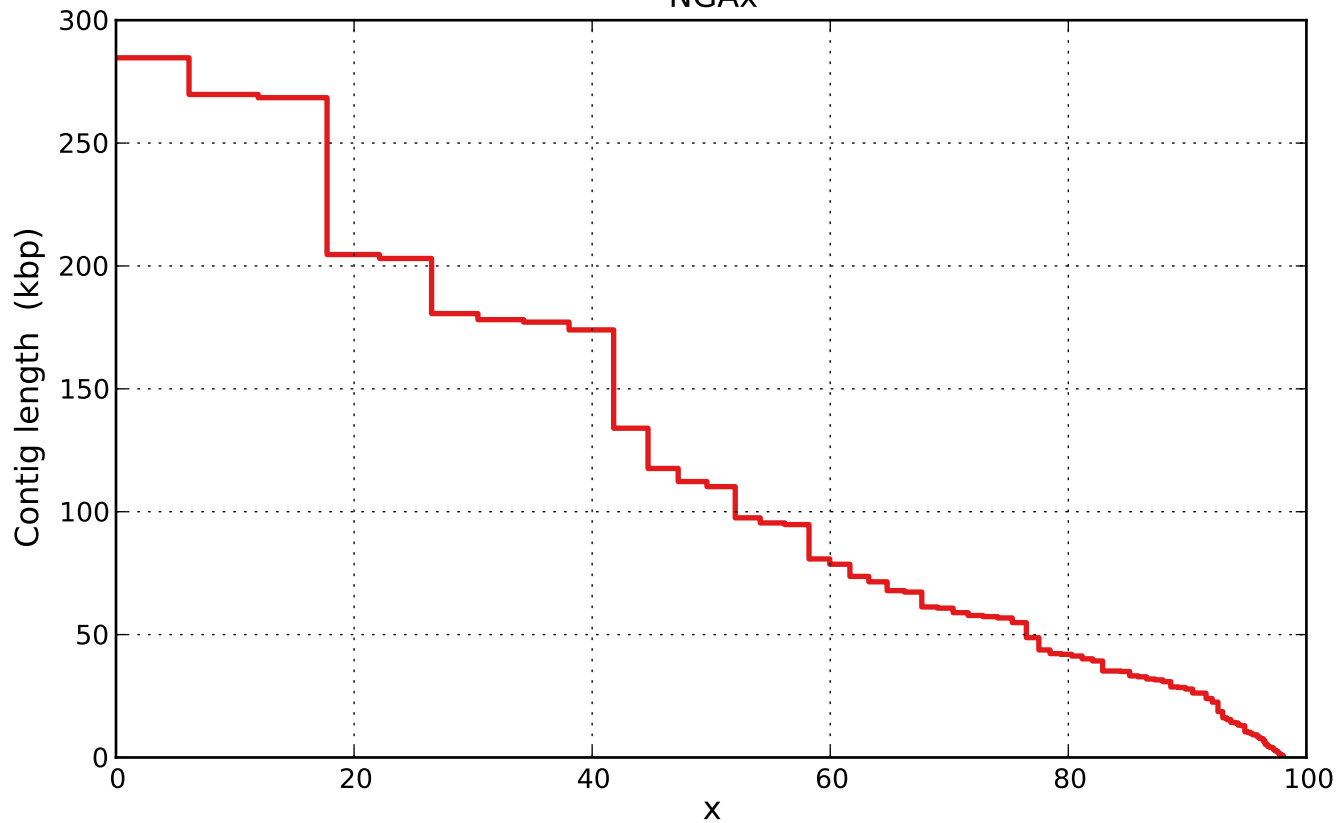


NAx



— scaffolds

NGAx



— scaffolds