

Report

	final.contigs
# contigs (>= 0 bp)	1608
# contigs (>= 1000 bp)	189
# contigs (>= 5000 bp)	152
# contigs (>= 10000 bp)	125
# contigs (>= 25000 bp)	67
# contigs (>= 50000 bp)	27
Total length (>= 0 bp)	5176976
Total length (>= 1000 bp)	4596775
Total length (>= 5000 bp)	4494879
Total length (>= 10000 bp)	4287756
Total length (>= 25000 bp)	3346787
Total length (>= 50000 bp)	1913055
# contigs	408
Largest contig	151001
Total length	4726159
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	41834
NG50	42719
N75	21748
NG75	22234
L50	38
LG50	37
L75	76
LG75	73
# misassemblies	12
# misassembled contigs	12
Misassembled contigs length	224612
# local misassemblies	7
# unaligned contigs	112 + 21 part
Unaligned length	69921
Genome fraction (%)	98.678
Duplication ratio	1.017
# N's per 100 kbp	0.00
# mismatches per 100 kbp	67.14
# indels per 100 kbp	0.33
Largest alignment	151001
NA50	41563
NGA50	41828
NA75	20233
NGA75	21808
LA50	38
LGA50	37
LA75	78
LGA75	75

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

	final.contigs
# misassemblies	12
# relocations	12
# translocations	0
# inversions	0
# misassembled contigs	12
Misassembled contigs length	224612
# local misassemblies	7
# mismatches	3075
# indels	15
# short indels	15
# long indels	0
Indels length	16

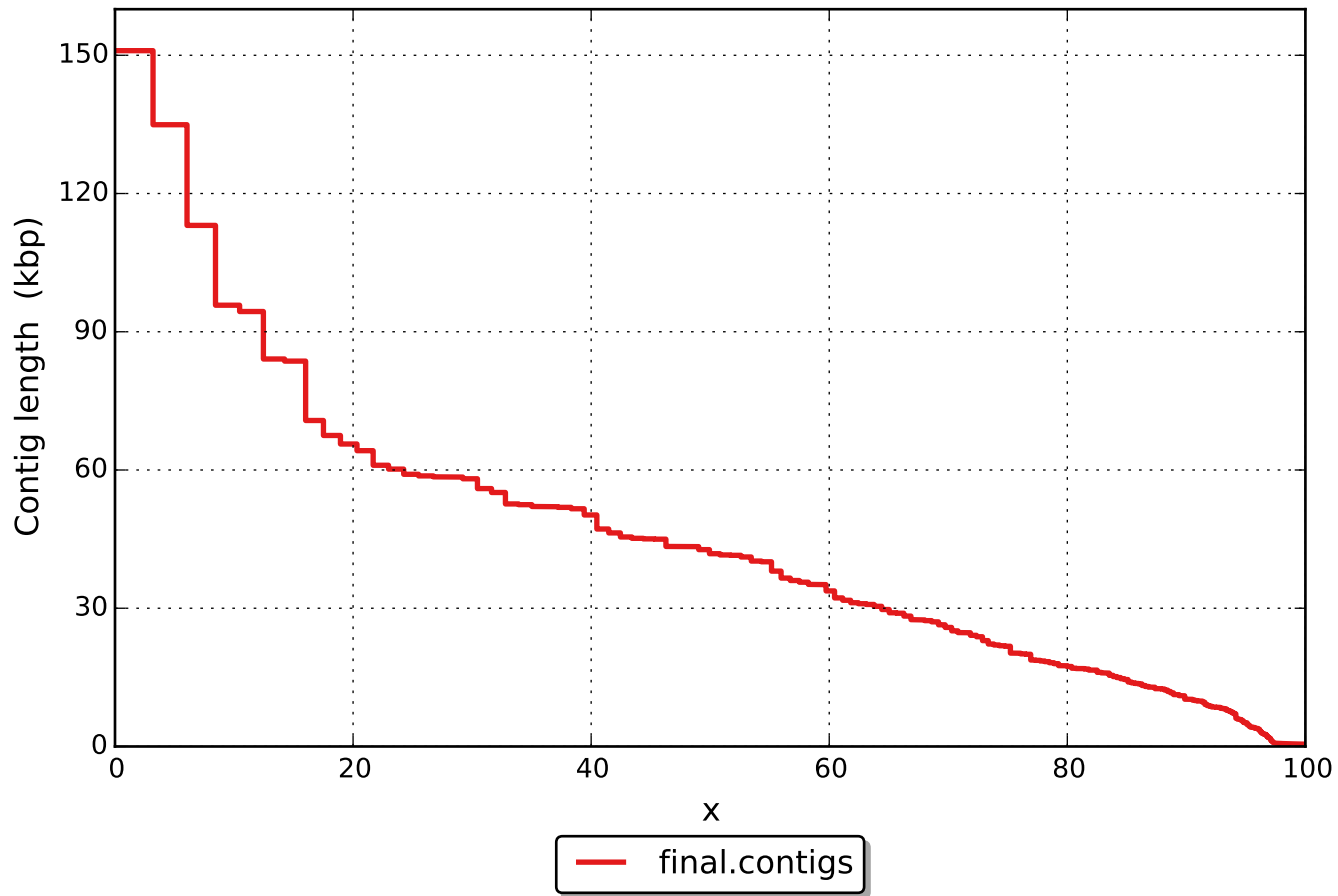
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

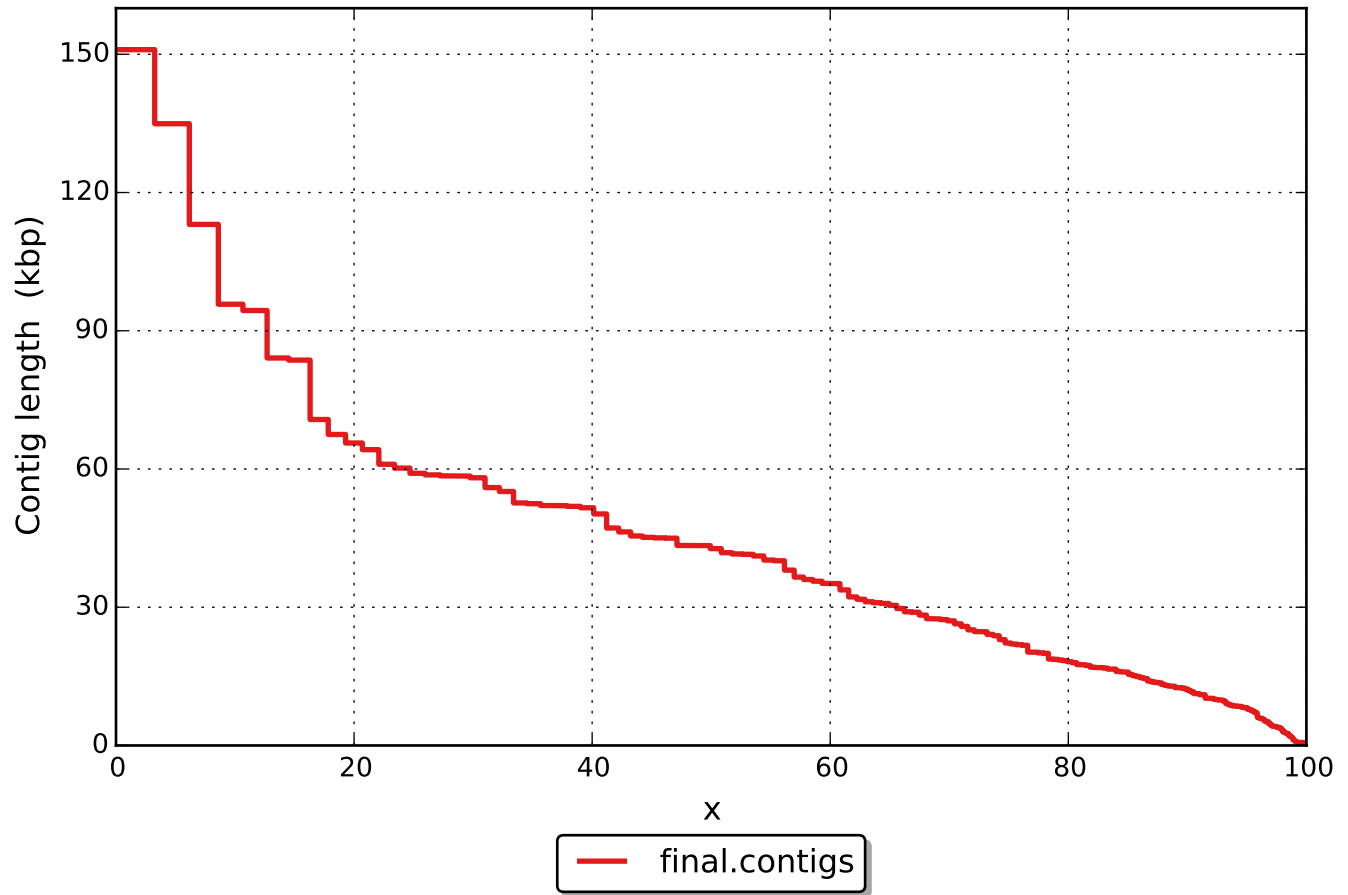
	final.contigs
# fully unaligned contigs	112
Fully unaligned length	65712
# partially unaligned contigs	21
# with misassembly	0
# both parts are significant	0
Partially unaligned length	4209
# N's	0

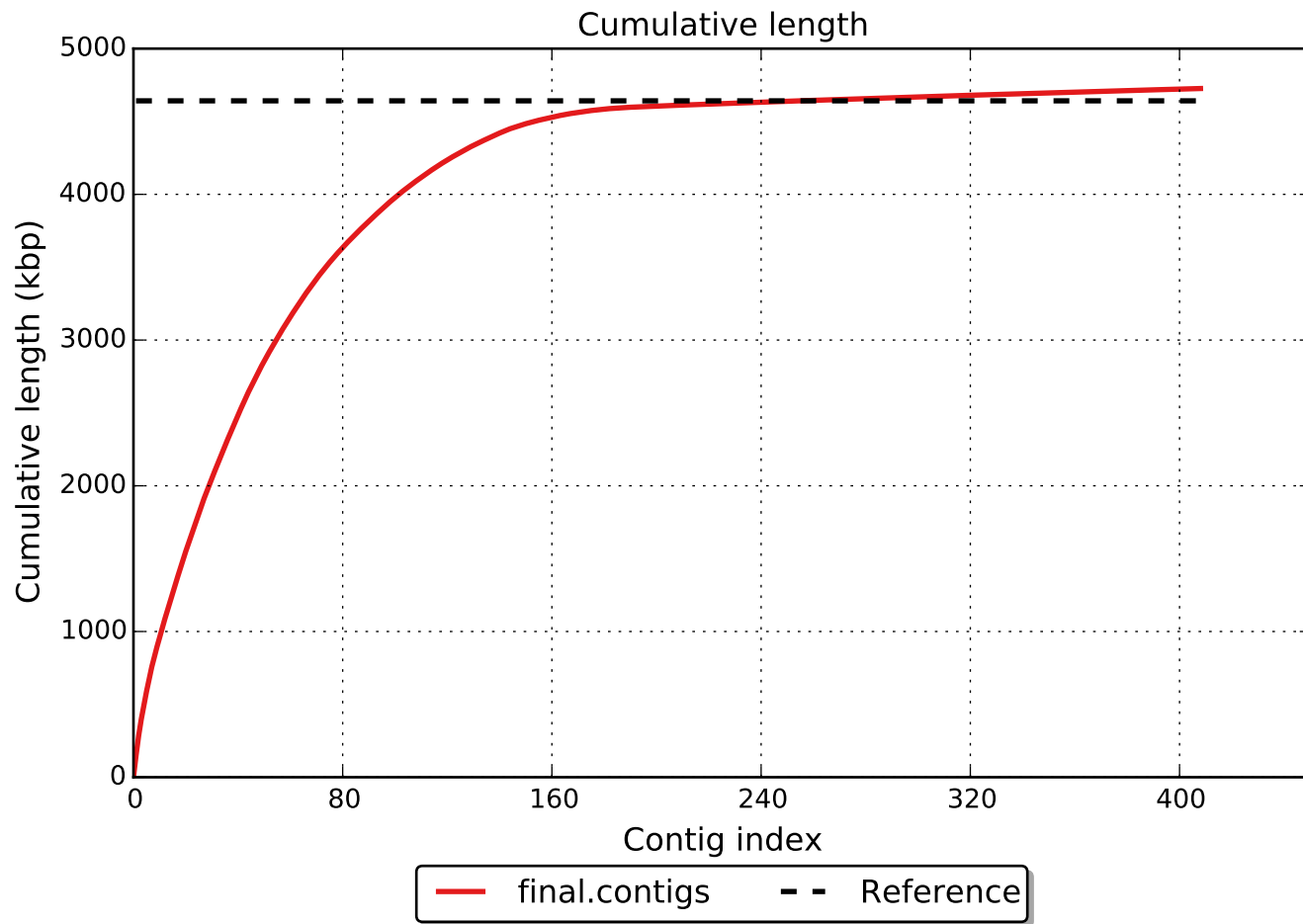
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

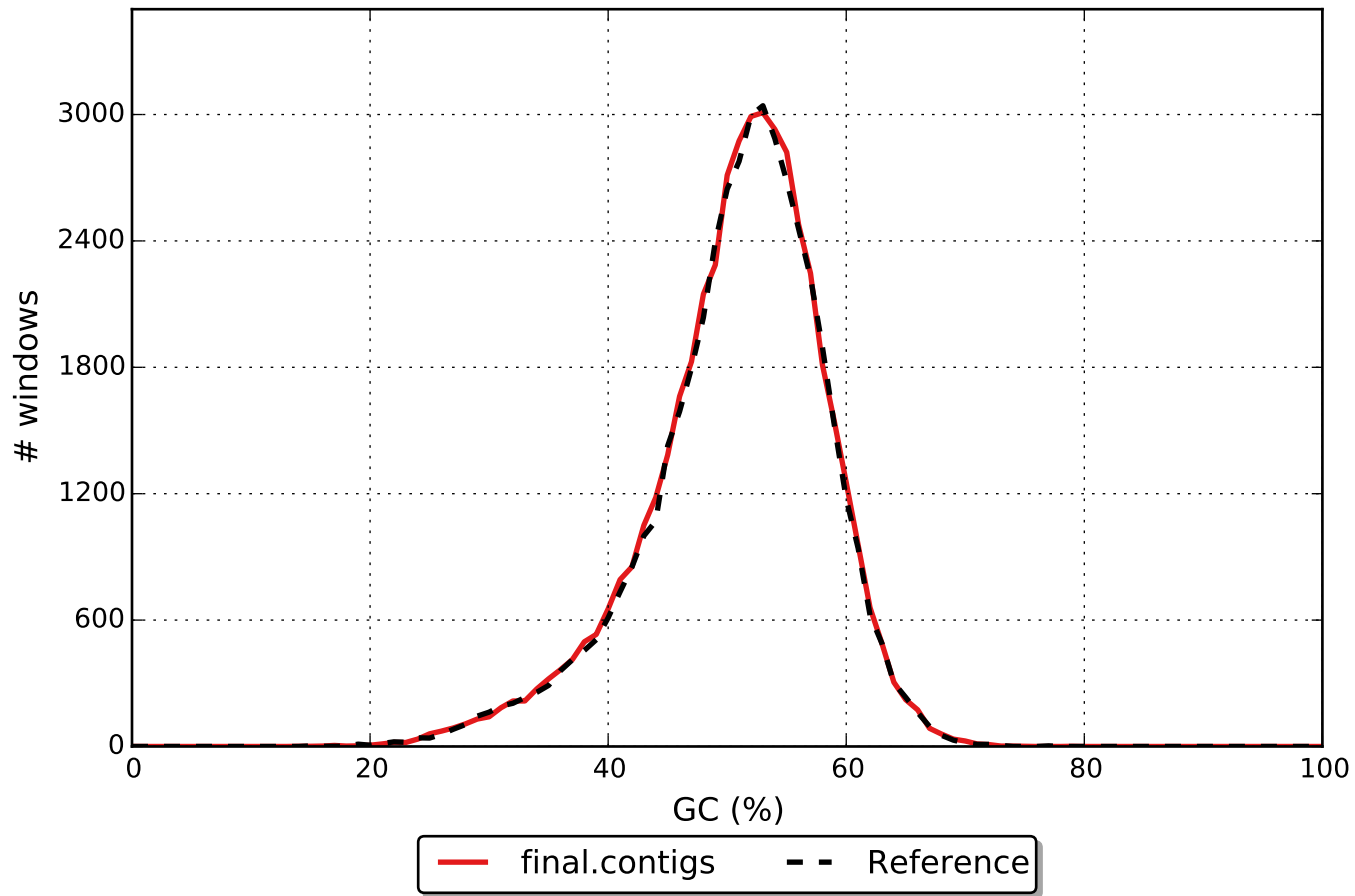


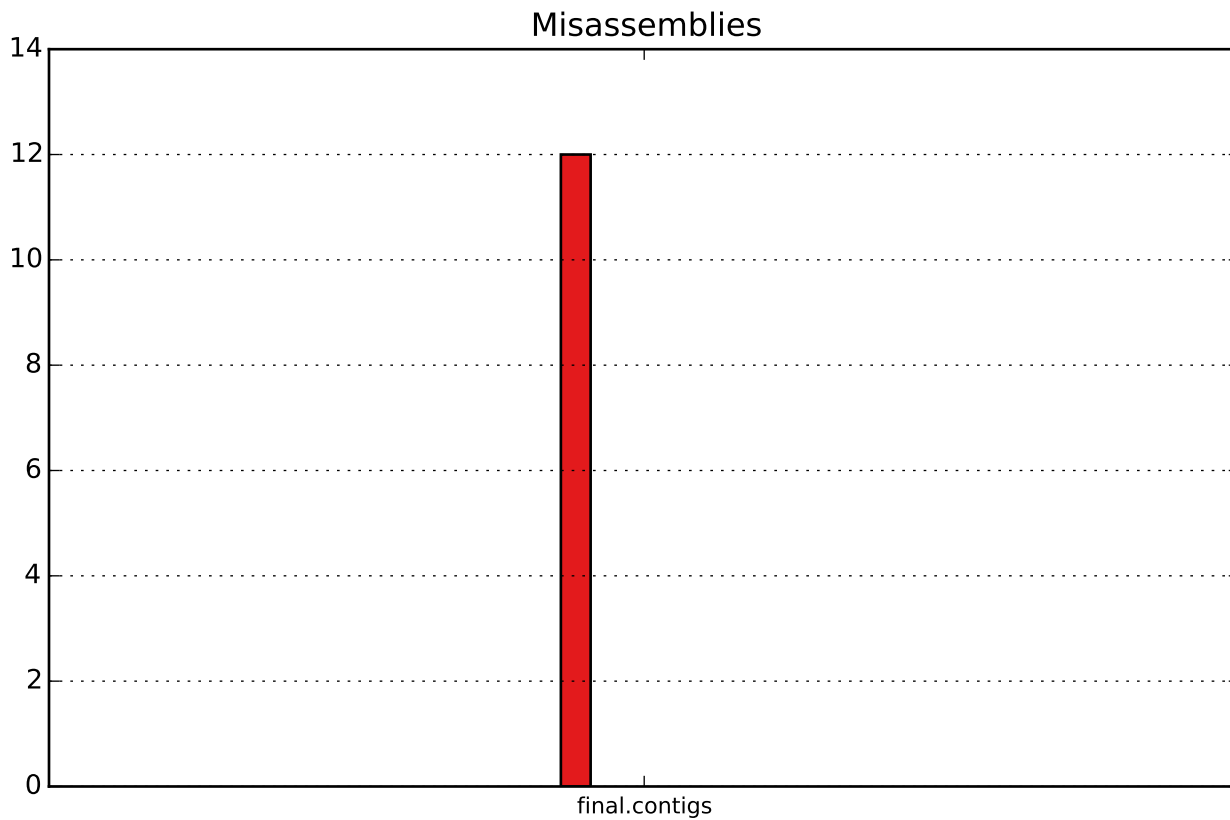
NGx



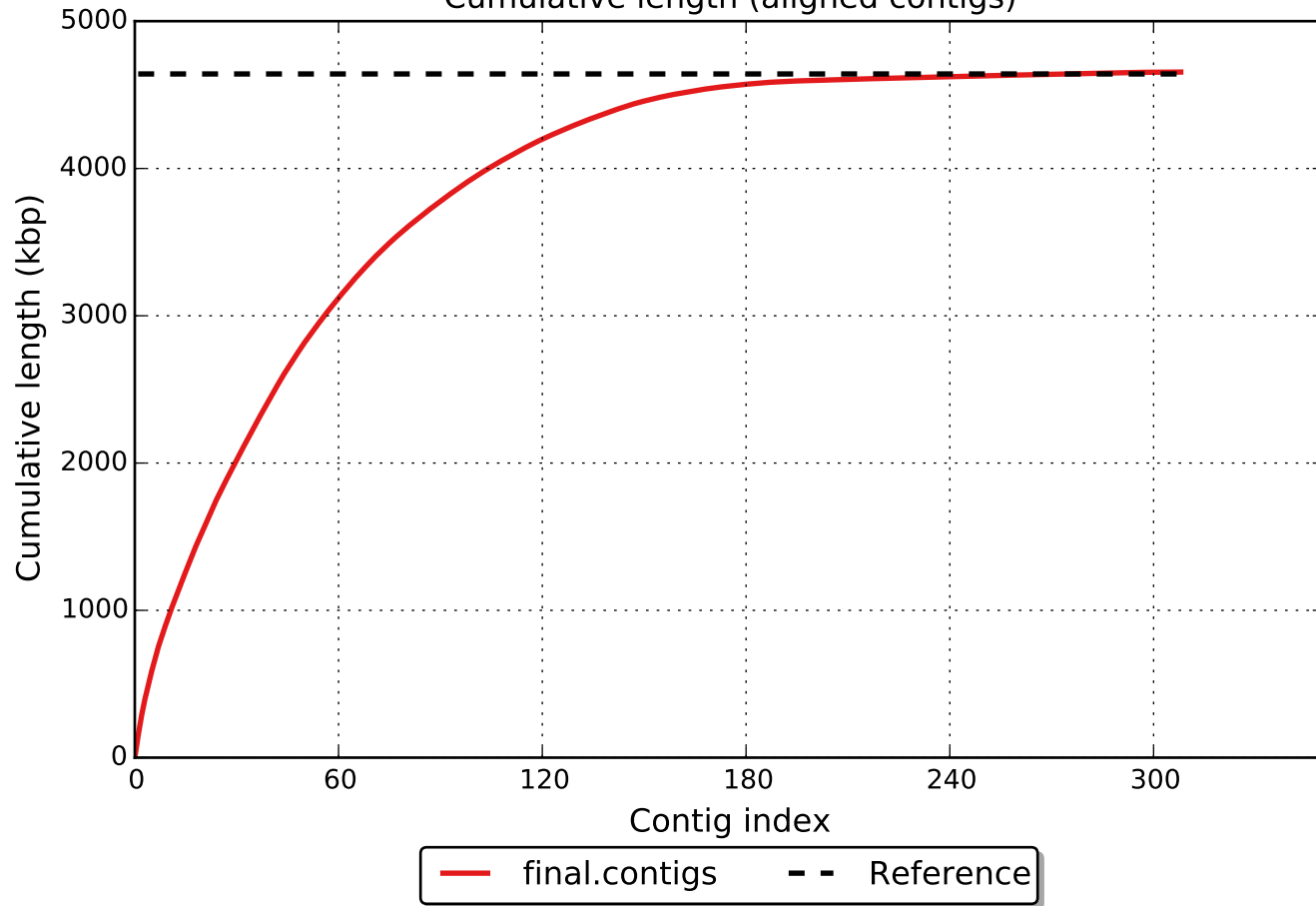


GC content

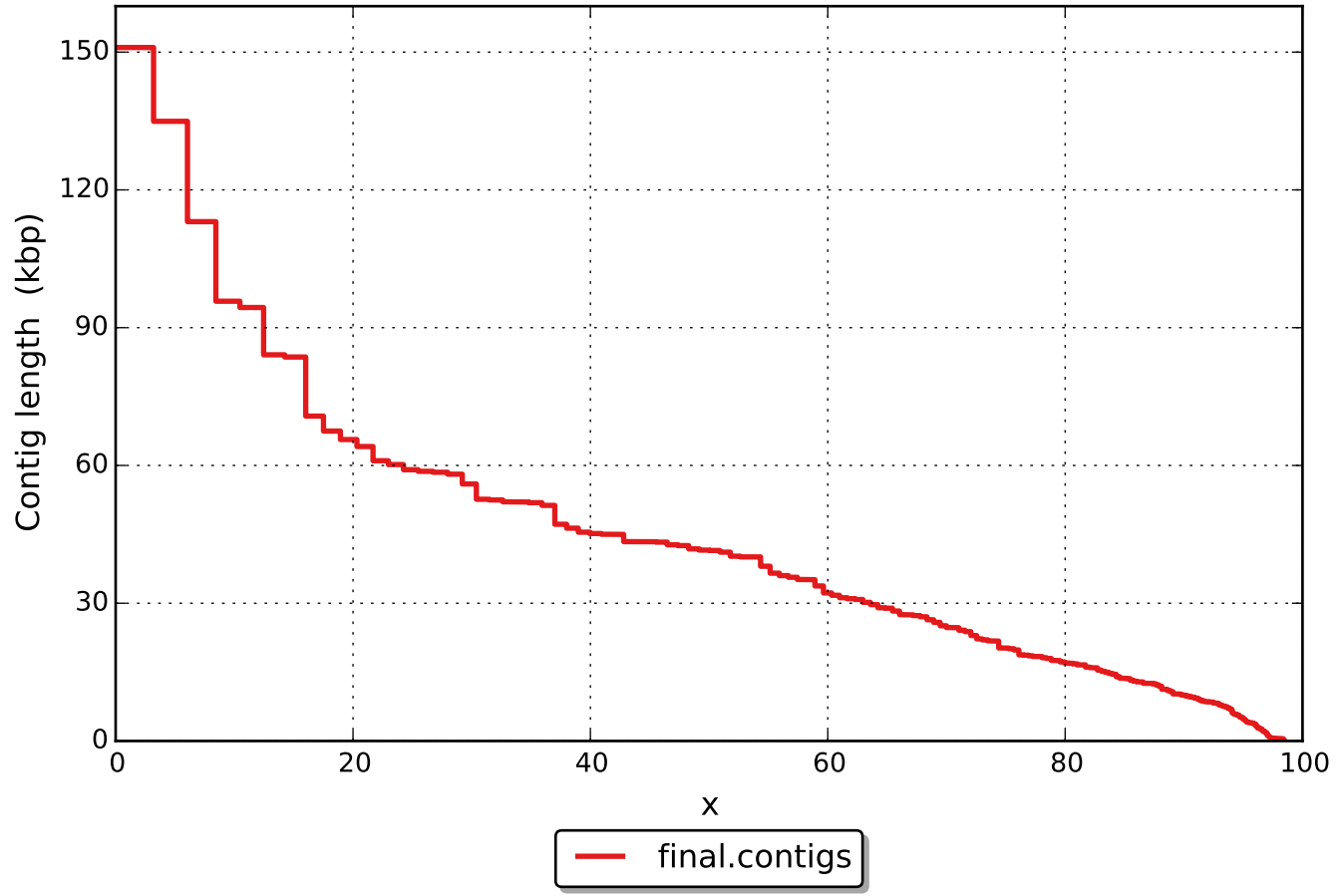




Cumulative length (aligned contigs)



NAx



NGAx

