

Report

	final.contigs
# contigs (>= 0 bp)	4598
# contigs (>= 1000 bp)	244
# contigs (>= 5000 bp)	171
# contigs (>= 10000 bp)	133
# contigs (>= 25000 bp)	65
# contigs (>= 50000 bp)	19
Total length (>= 0 bp)	6452829
Total length (>= 1000 bp)	4612374
Total length (>= 5000 bp)	4427670
Total length (>= 10000 bp)	4136328
Total length (>= 25000 bp)	3044938
Total length (>= 50000 bp)	1370424
# contigs	1074
Largest contig	138569
Total length	5104824
Reference length	4641652
GC (%)	50.78
Reference GC (%)	50.79
N50	31783
NG50	36738
N75	14143
NG75	18125
L50	49
LG50	42
L75	108
LG75	86
# misassemblies	14
# misassembled contigs	14
Misassembled contigs length	309015
# local misassemblies	7
# unaligned contigs	476 + 63 part
Unaligned length	290282
Genome fraction (%)	99.212
Duplication ratio	1.045
# N's per 100 kbp	0.00
# mismatches per 100 kbp	117.65
# indels per 100 kbp	0.35
Largest alignment	138569
NA50	31322
NGA50	35424
NA75	13791
NGA75	17728
LA50	50
LGA50	43
LA75	111
LGA75	88

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

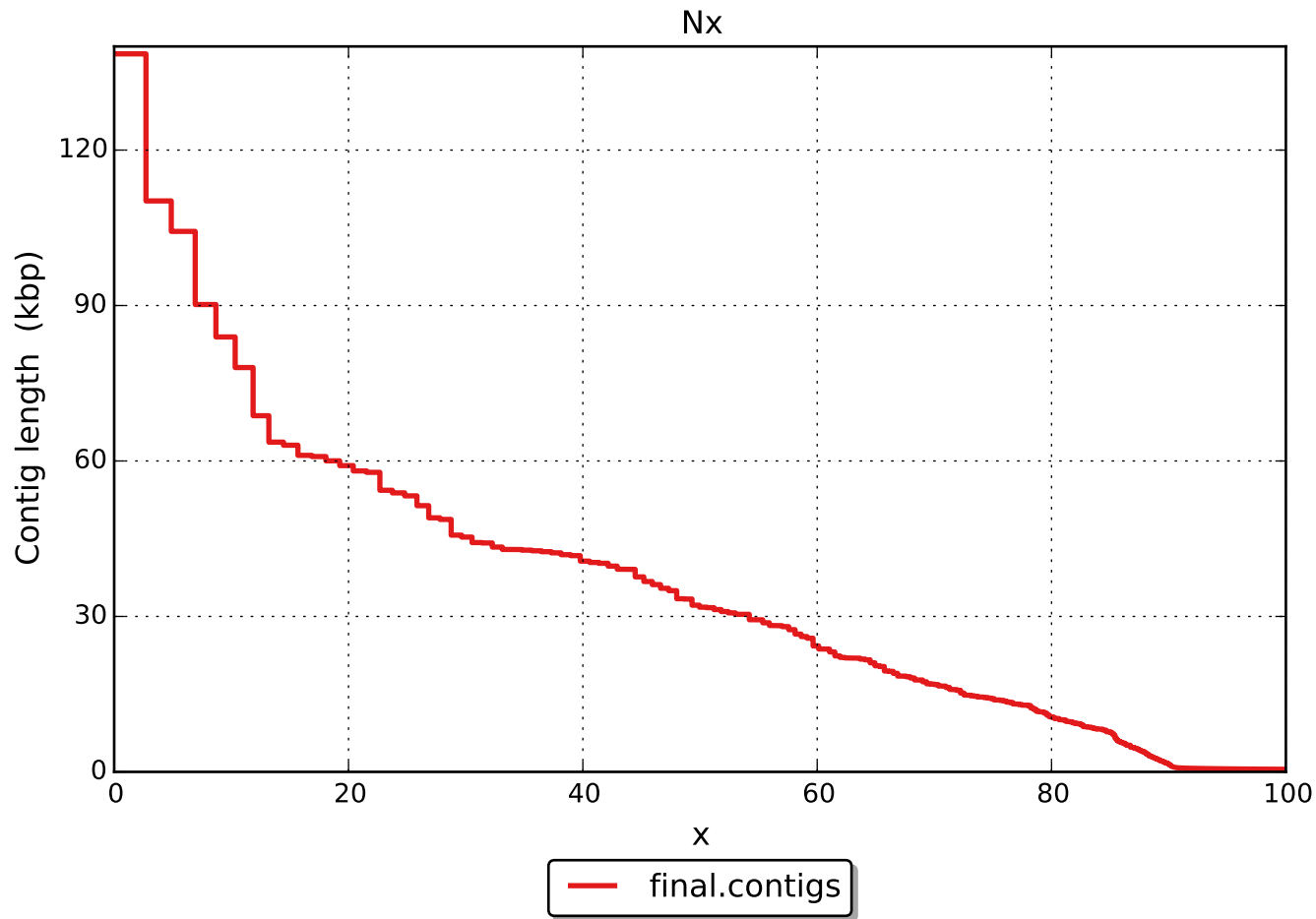
	final.contigs
# misassemblies	14
# relocations	13
# translocations	0
# inversions	1
# misassembled contigs	14
Misassembled contigs length	309015
# local misassemblies	7
# mismatches	5418
# indels	16
# short indels	16
# long indels	0
Indels length	19

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).

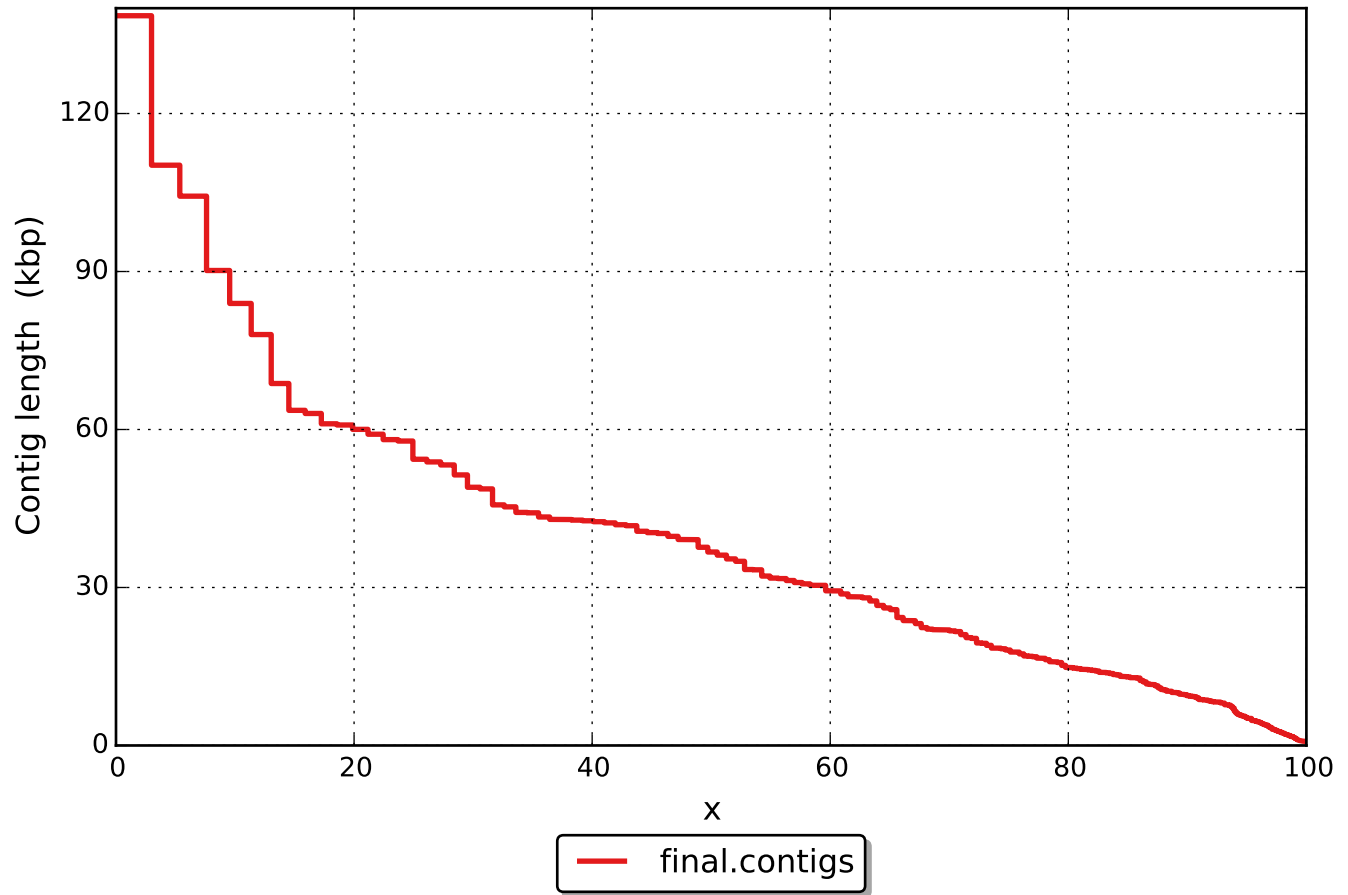
Unaligned report

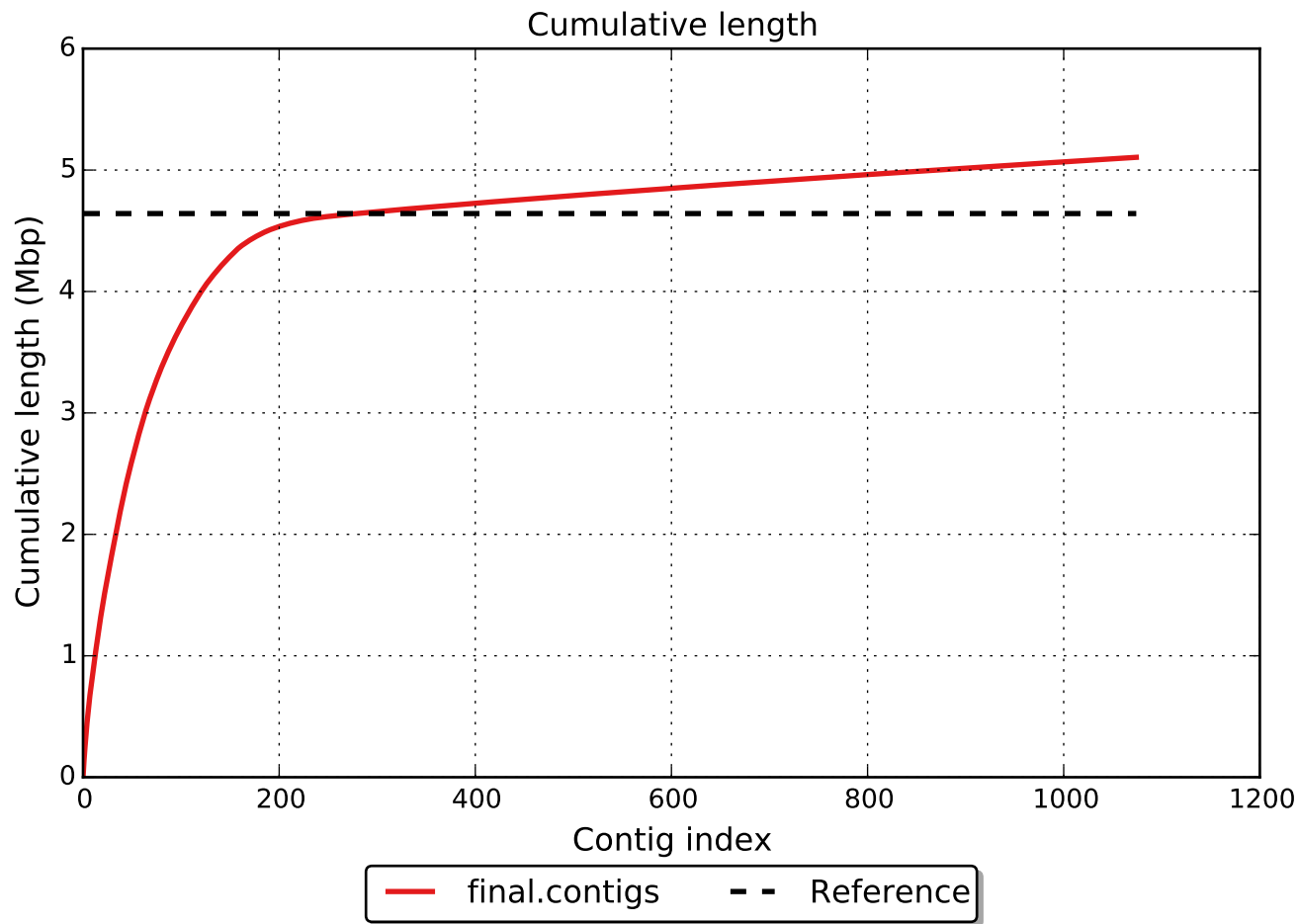
	final.contigs
# fully unaligned contigs	476
Fully unaligned length	276881
# partially unaligned contigs	63
# with misassembly	0
# both parts are significant	0
Partially unaligned length	13401
# N's	0

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).

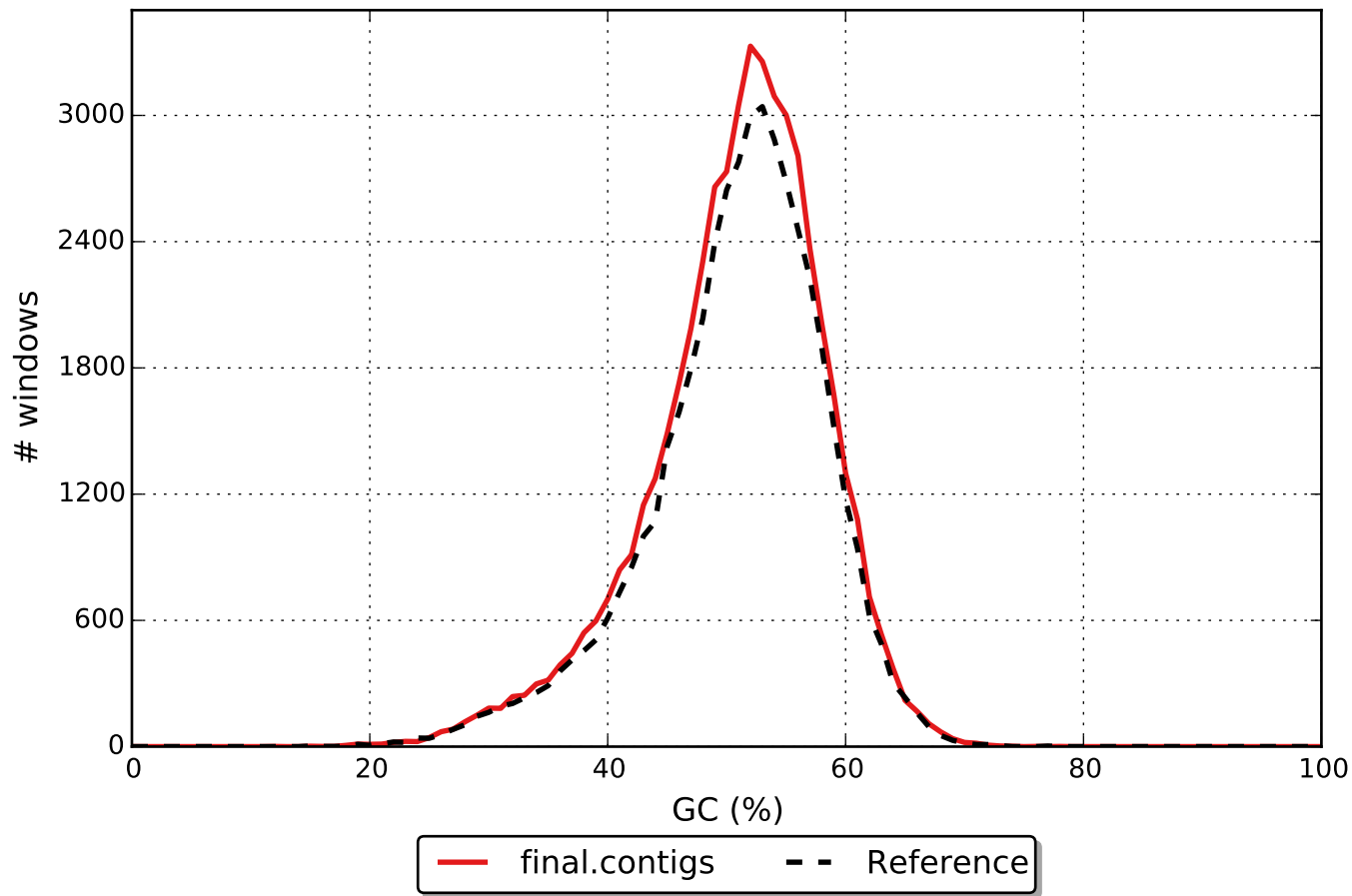


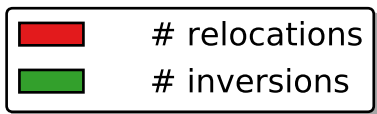
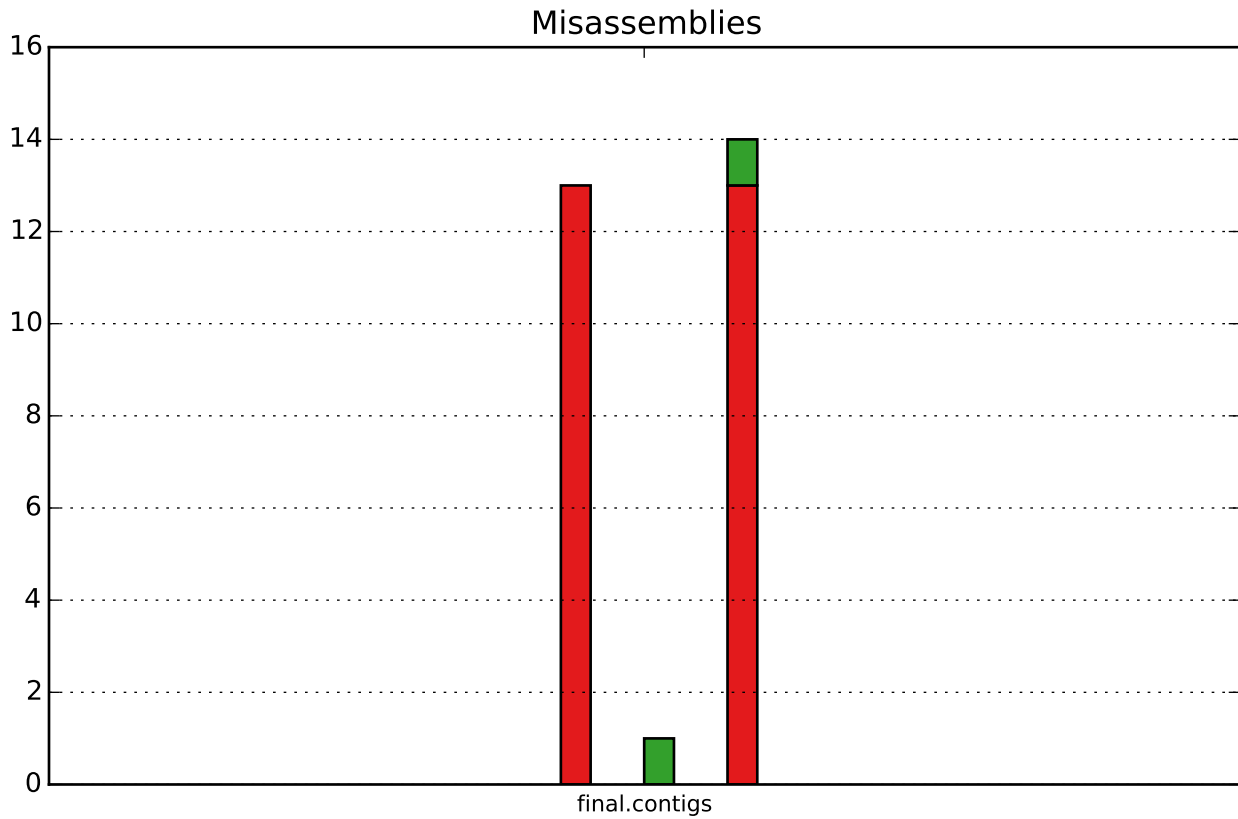
NGx



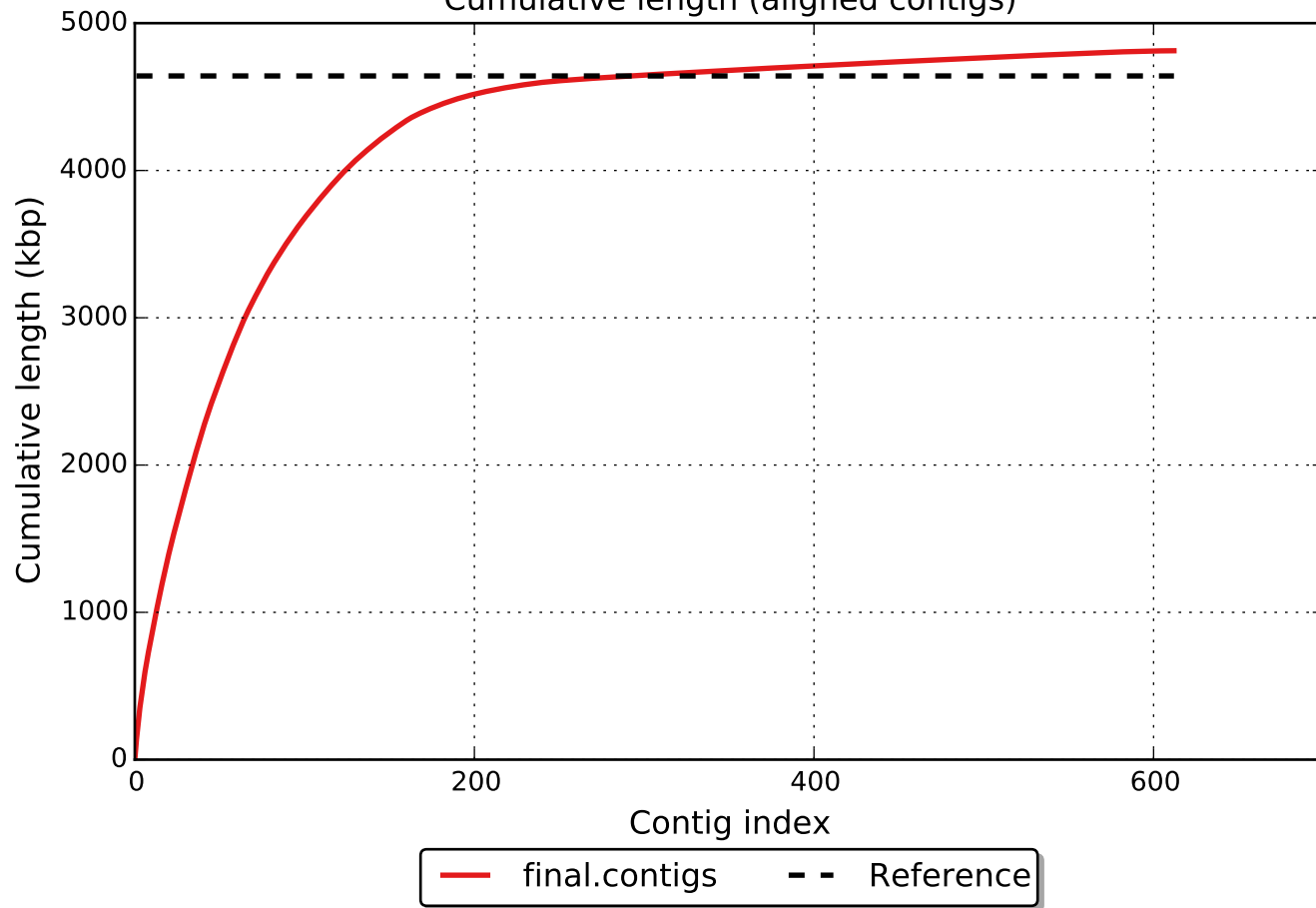


GC content

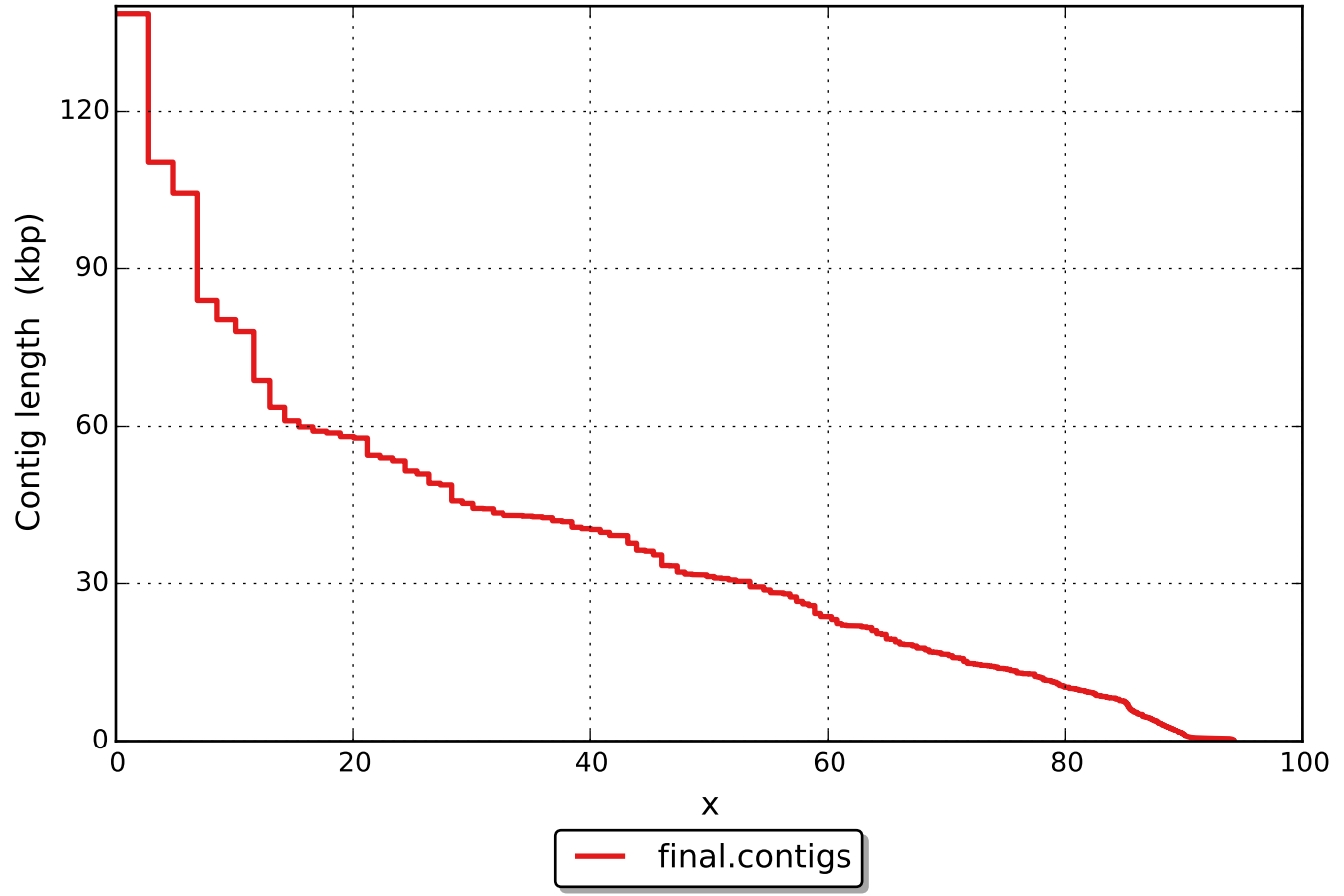




Cumulative length (aligned contigs)



NAx



NGAx

