

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	1433
# contigs ( $\geq 1000$ bp)	843
Total length ( $\geq 0$ bp)	10926316
Total length ( $\geq 1000$ bp)	10700074
# contigs	976
Largest contig	83434
Total length	10789178
Reference length	11094646
GC (%)	50.39
Reference GC (%)	50.48
N50	20236
NG50	19557
N75	11059
NG75	10461
L50	168
LG50	175
L75	346
LG75	367
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	48702
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.677
Duplication ratio	1.008
# N's per 100 kbp	0.00
# mismatches per 100 kbp	12.67
# indels per 100 kbp	0.26
Largest alignment	83434
NA50	20236
NGA50	19550
NA75	11056
NGA75	10401
LA50	168
LGA50	176
LA75	347
LGA75	368

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

## Misassemblies report

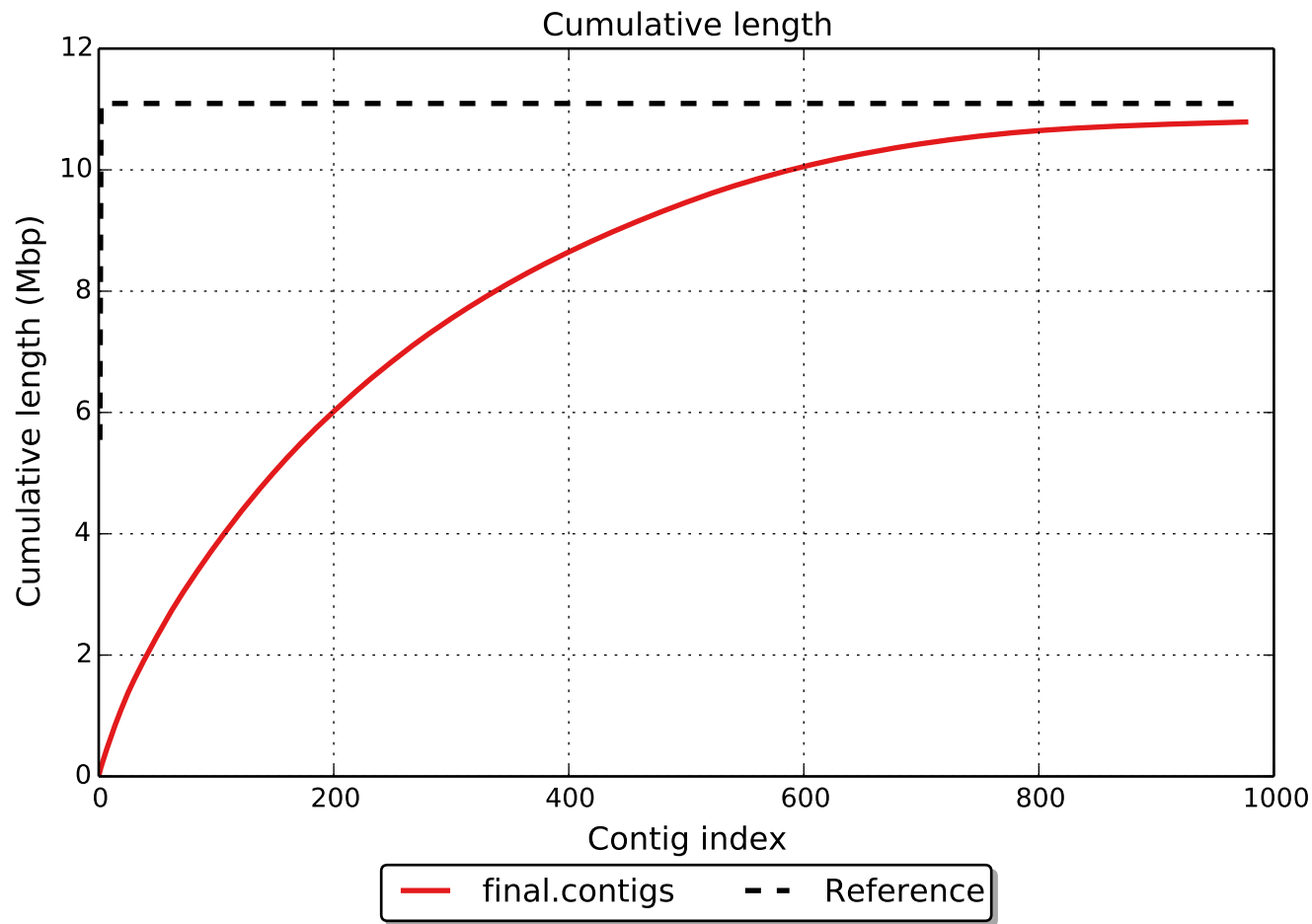
	final.contigs
# misassemblies	1
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	48702
# local misassemblies	2
# mismatches	1373
# indels	28
# short indels	26
# long indels	2
Indels length	94

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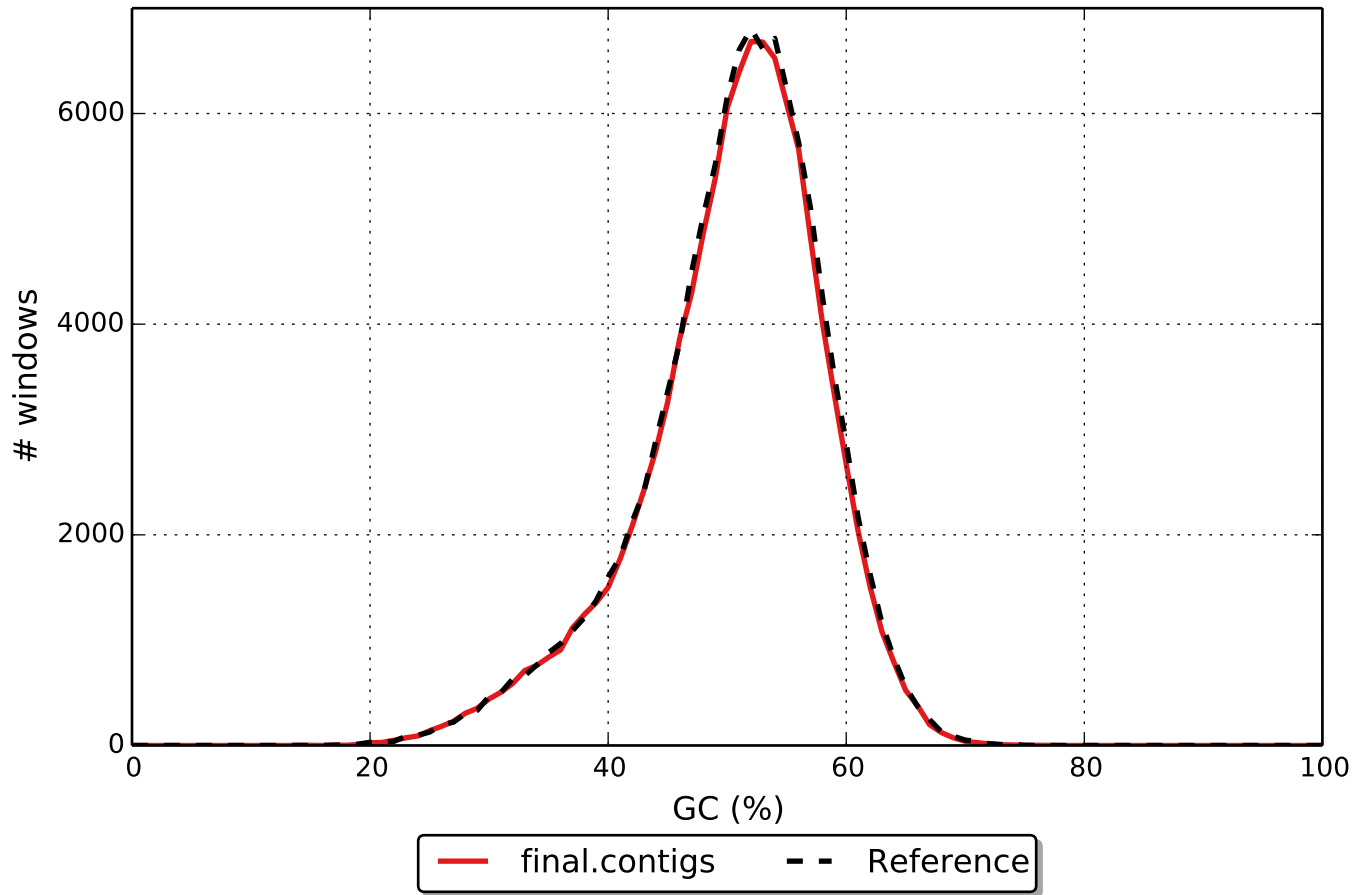
## Unaligned report

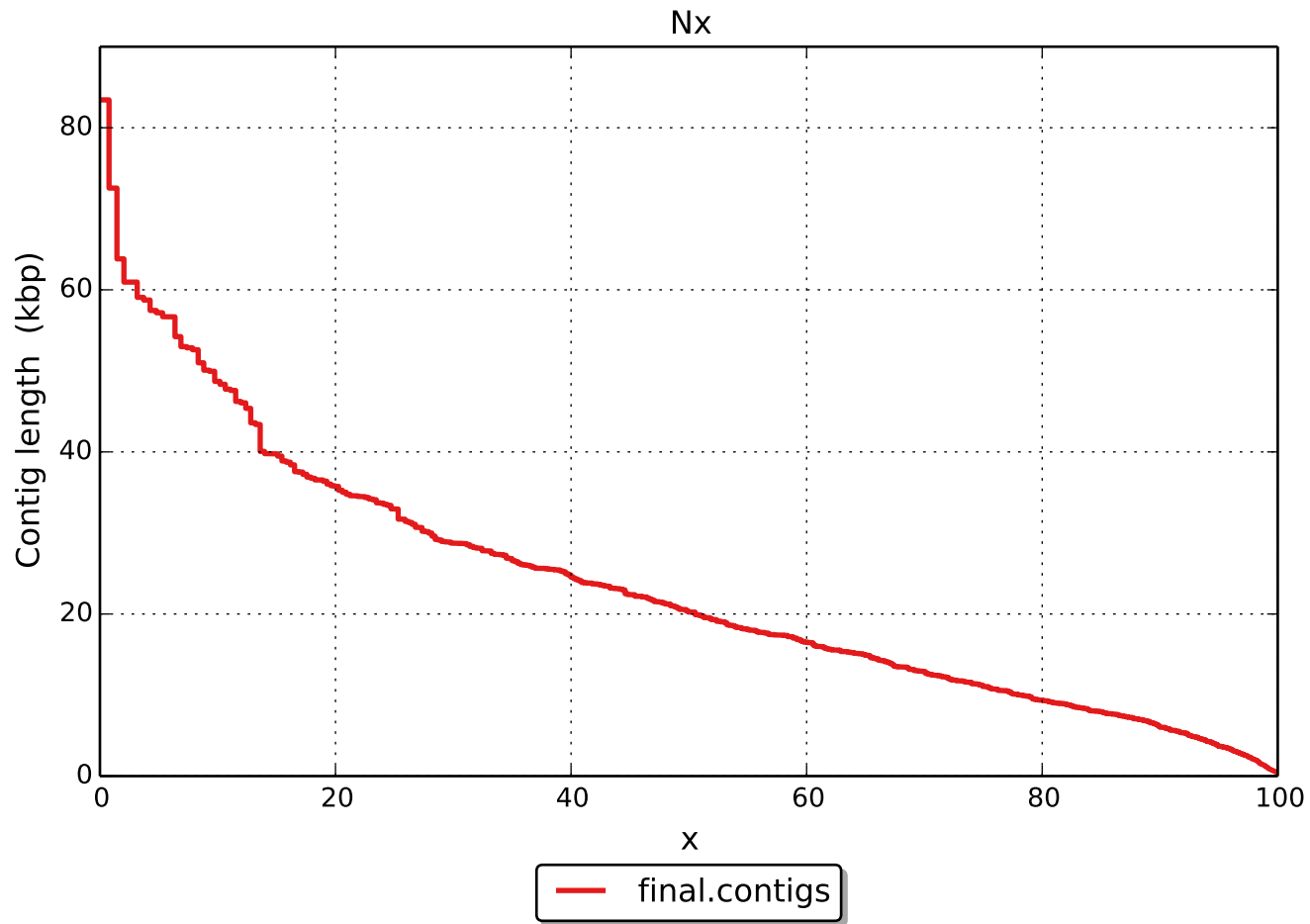
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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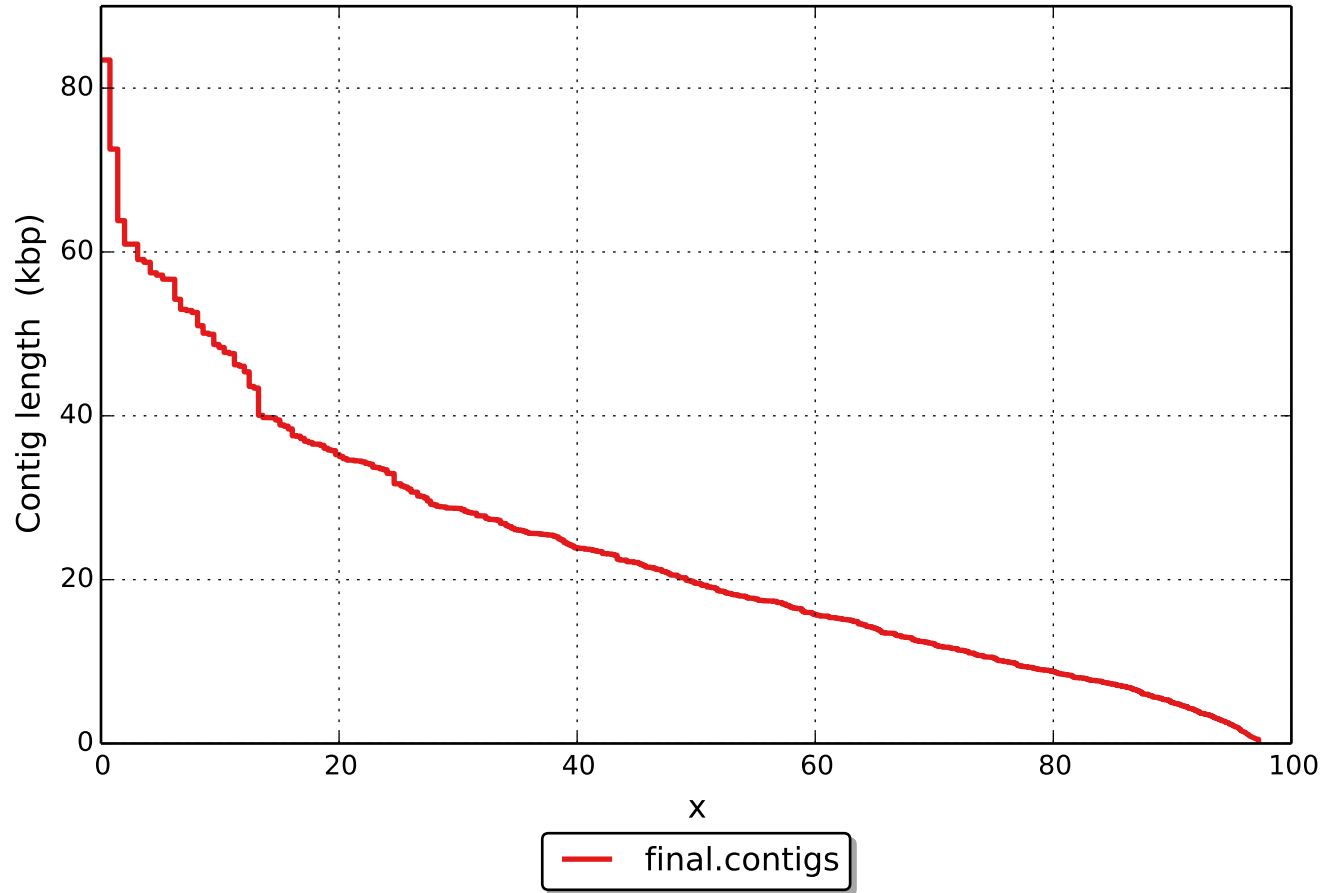


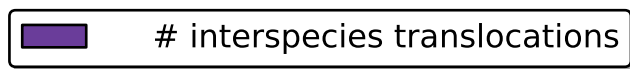
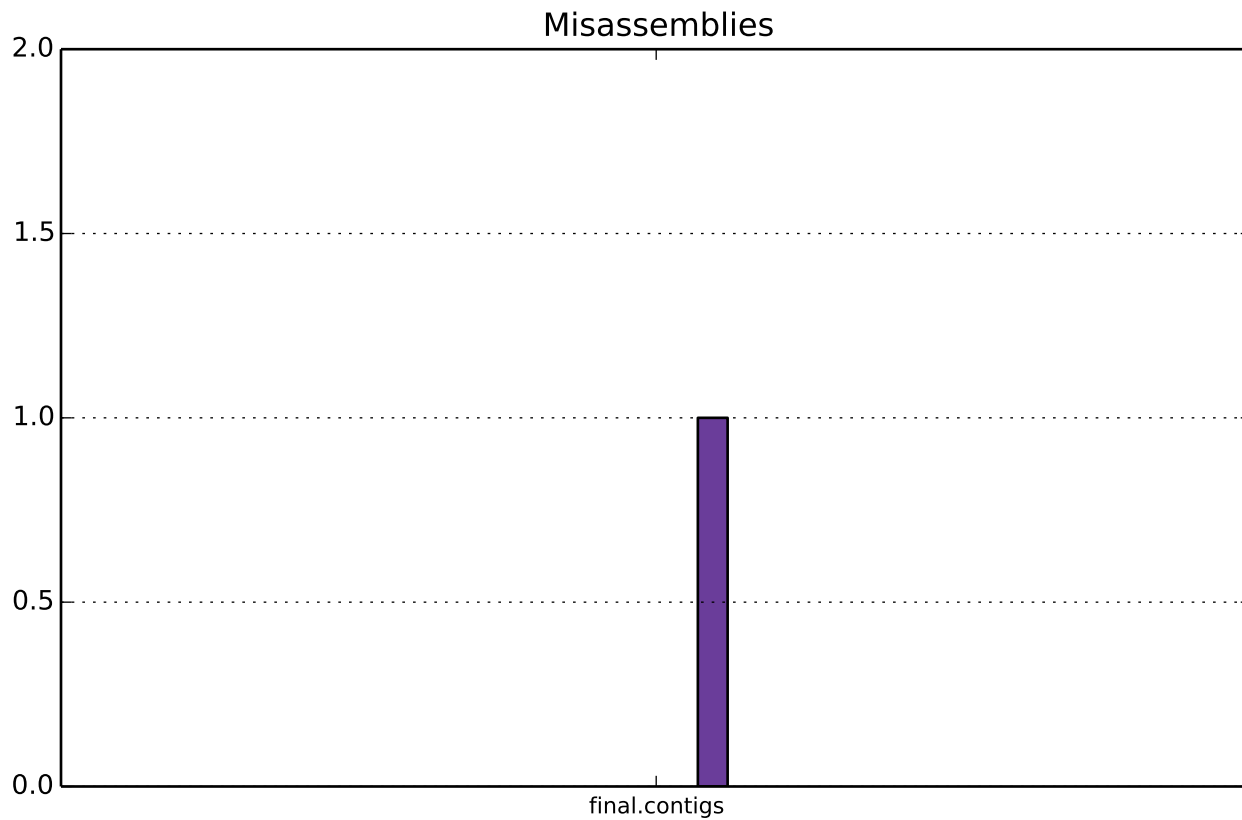
# GC content



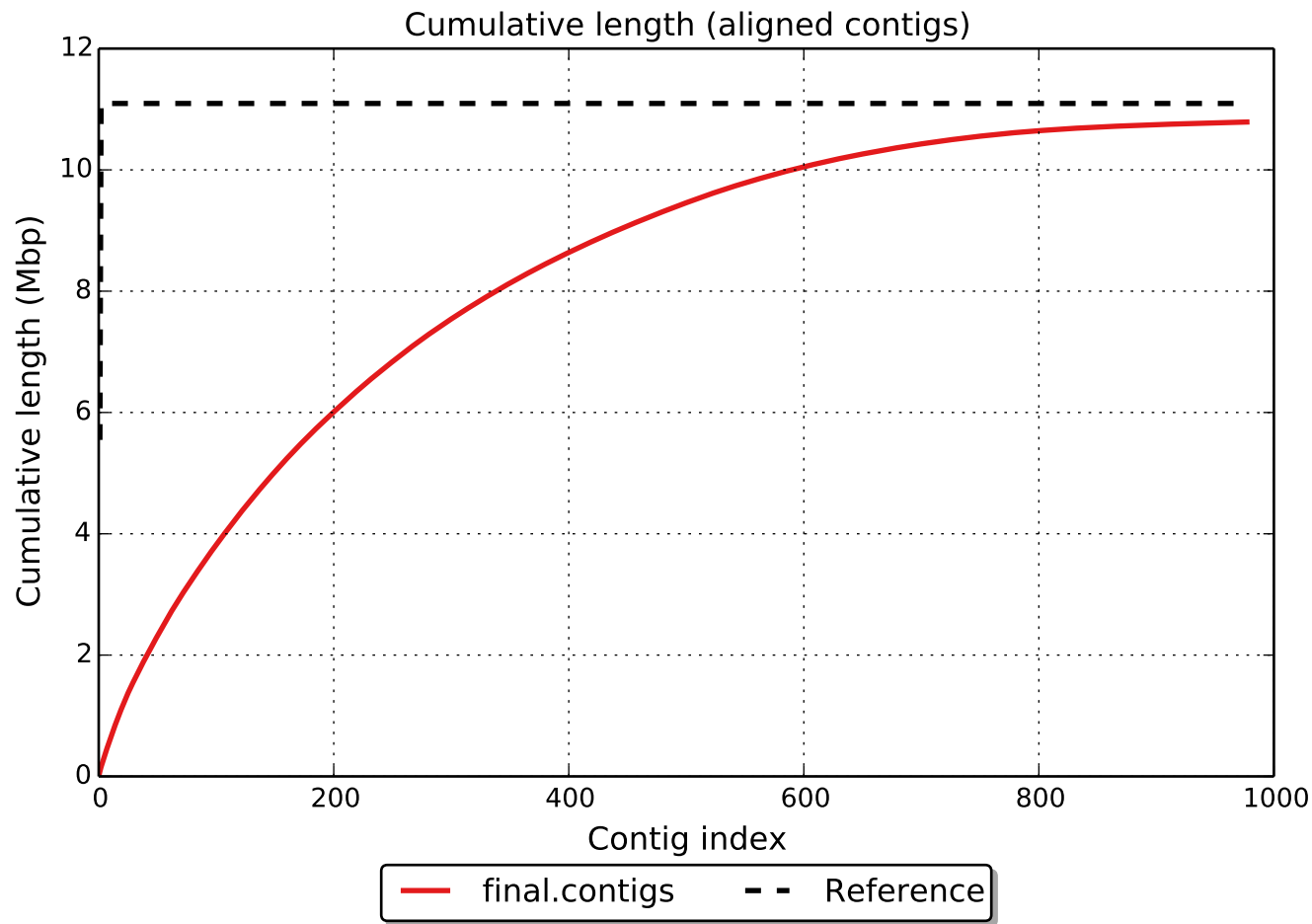


NGx

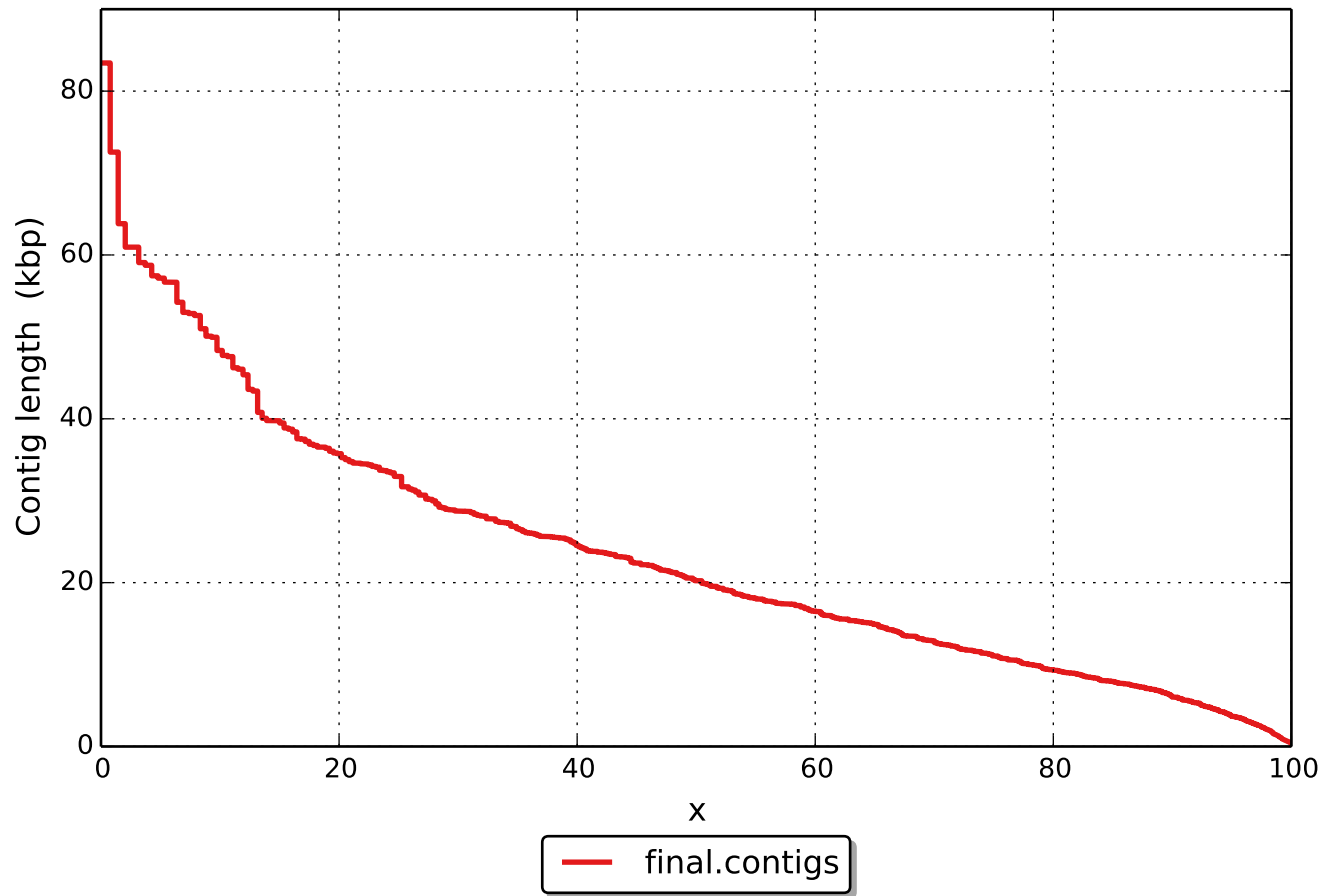








NAx



# NGAx

