

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	3280
# contigs ( $\geq 1000$ bp)	2237
Total length ( $\geq 0$ bp)	10998794
Total length ( $\geq 1000$ bp)	10499566
# contigs	2646
Largest contig	31841
Total length	10795490
Reference length	10957366
GC (%)	50.38
Reference GC (%)	50.49
N50	6333
NG50	6121
N75	3532
NG75	3414
L50	527
LG50	540
L75	1099
LG75	1134
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	29757
# local misassemblies	2
# unaligned contigs	0 + 1 part
Unaligned length	13
Genome fraction (%)	97.158
Duplication ratio	1.022
# N's per 100 kbp	0.00
# mismatches per 100 kbp	28.43
# indels per 100 kbp	0.08
Largest alignment	31841
NA50	6330
NGA50	6106
NA75	3532
NGA75	3414
LA50	528
LGA50	541
LA75	1100
LGA75	1135

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

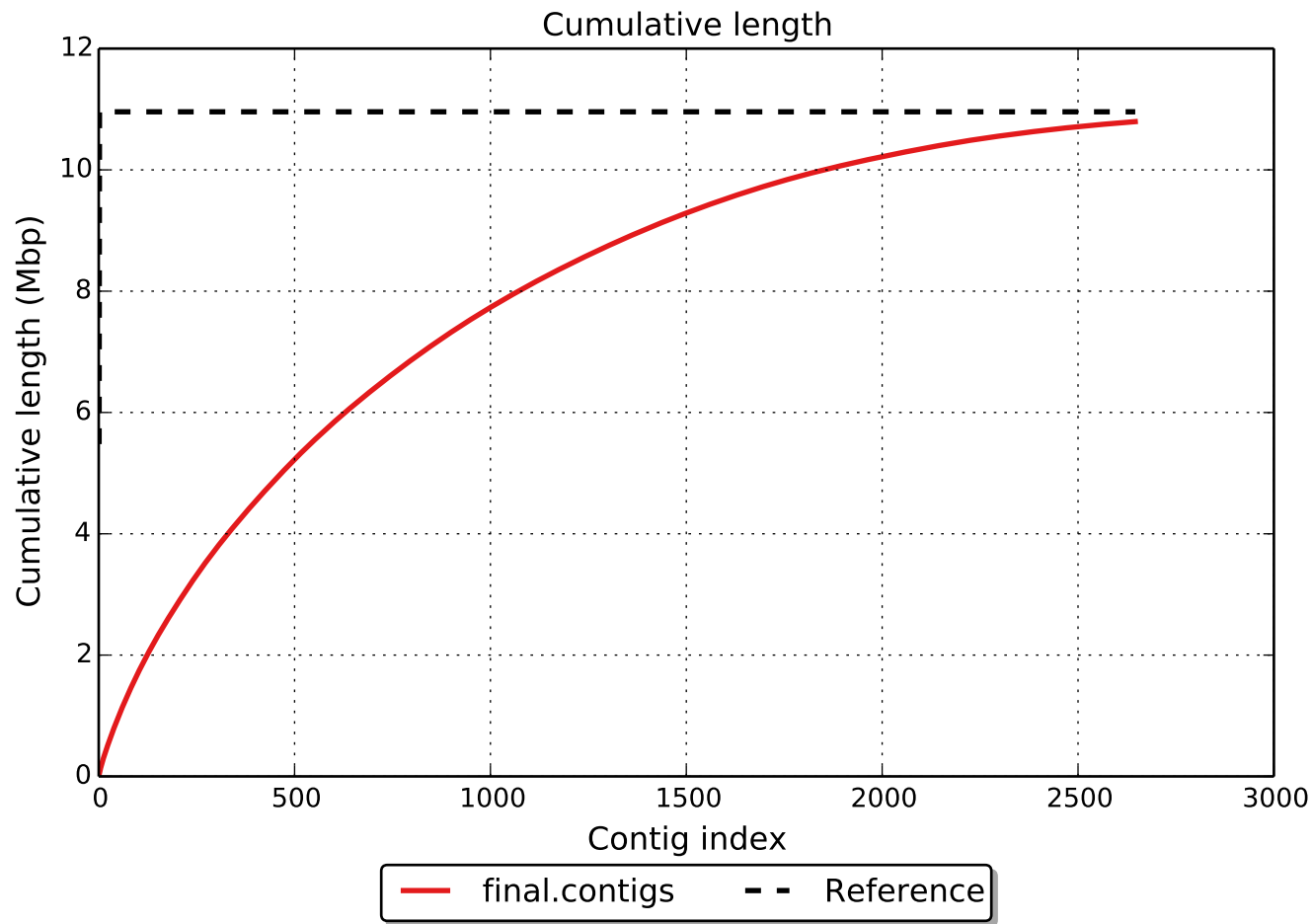
	final.contigs
# misassemblies	1
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	29757
# local misassemblies	2
# mismatches	3027
# indels	8
# short indels	6
# long indels	2
Indels length	40

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).

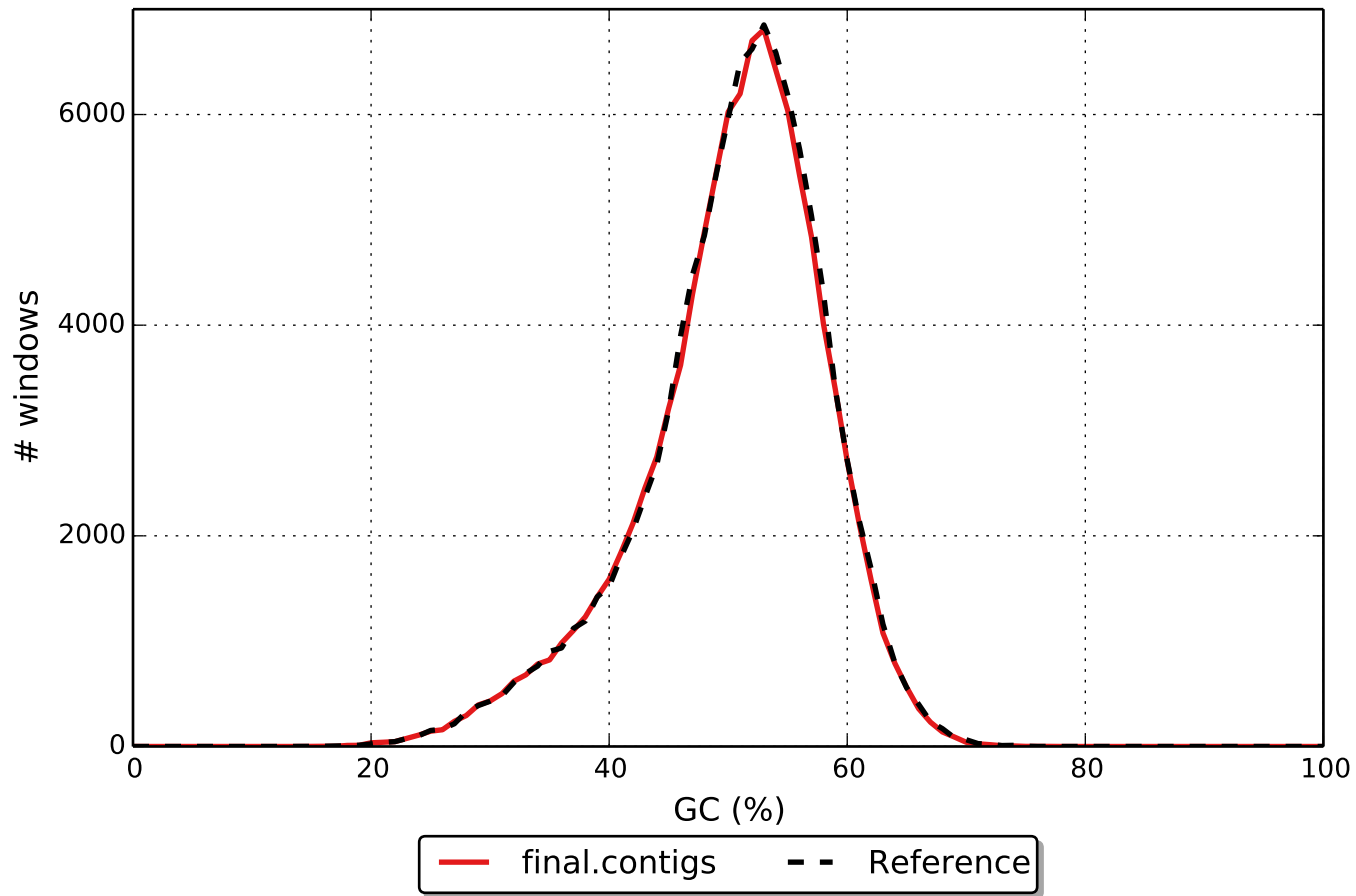
## Unaligned report

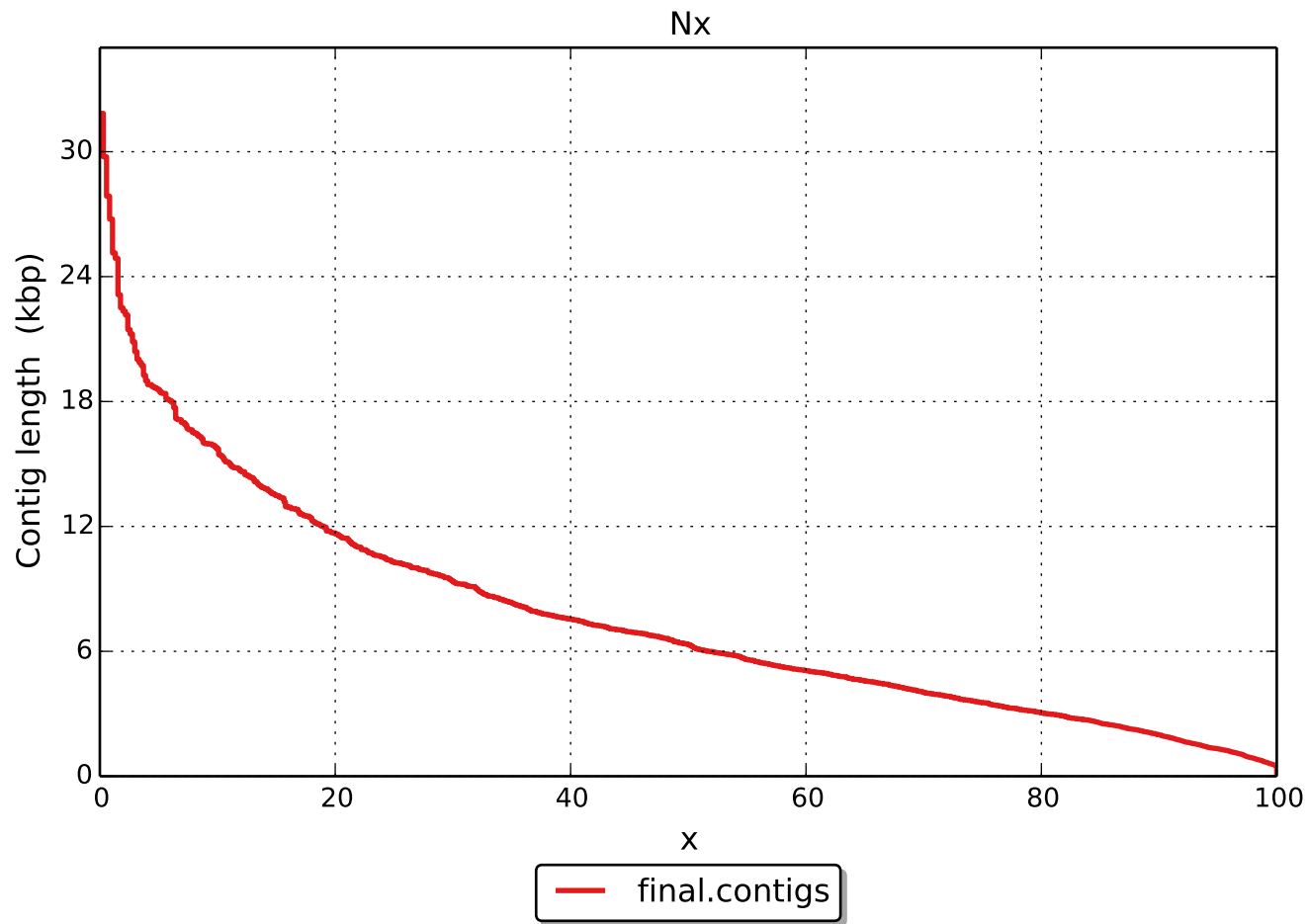
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	13
# N's	0

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).

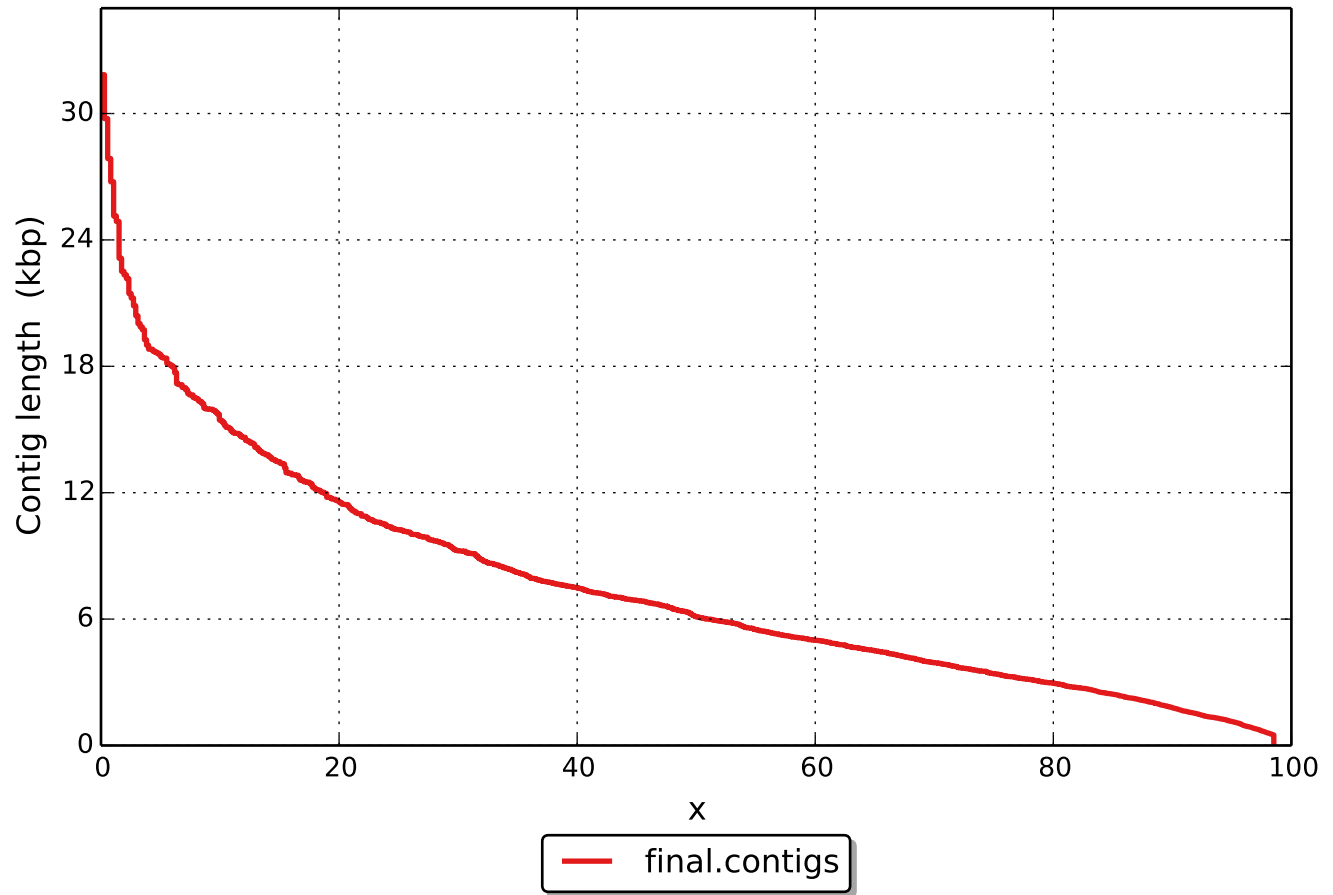


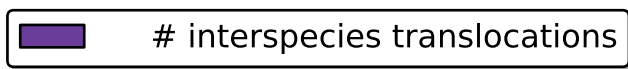
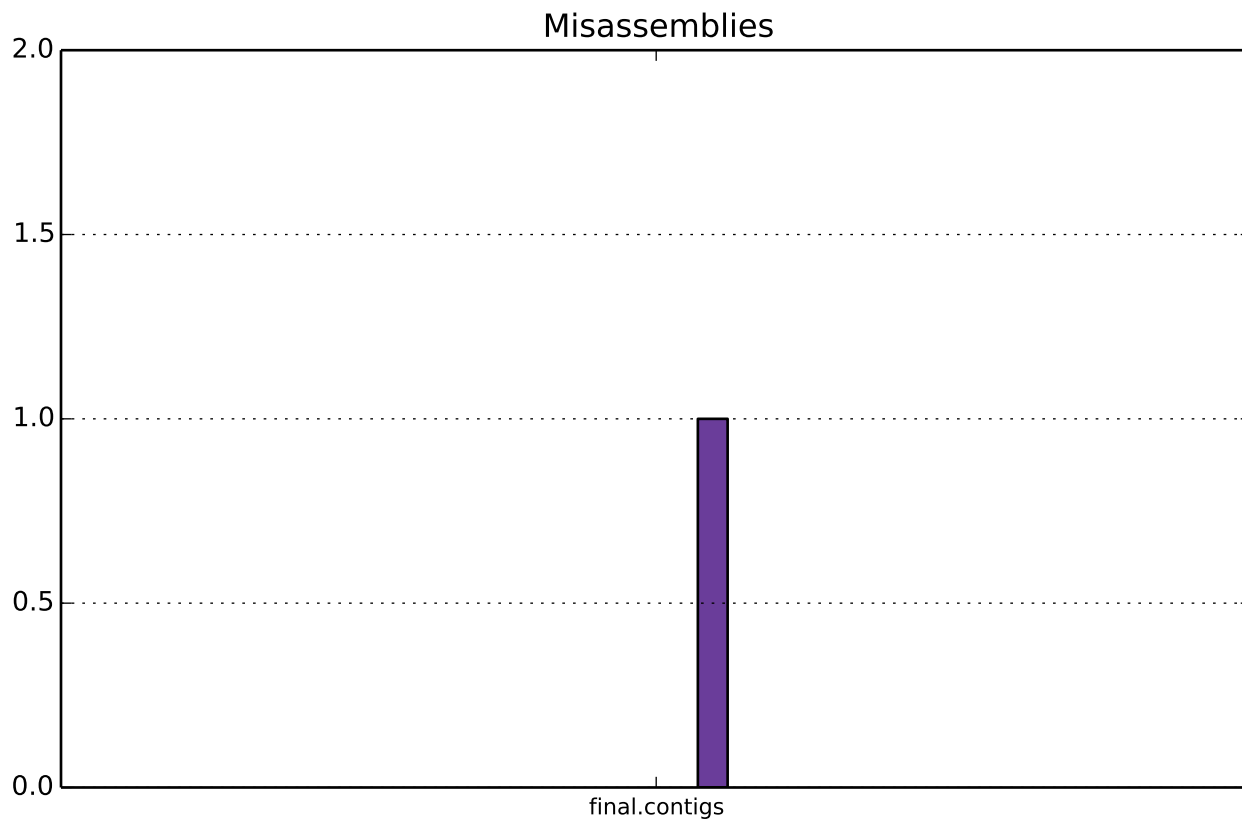
GC content



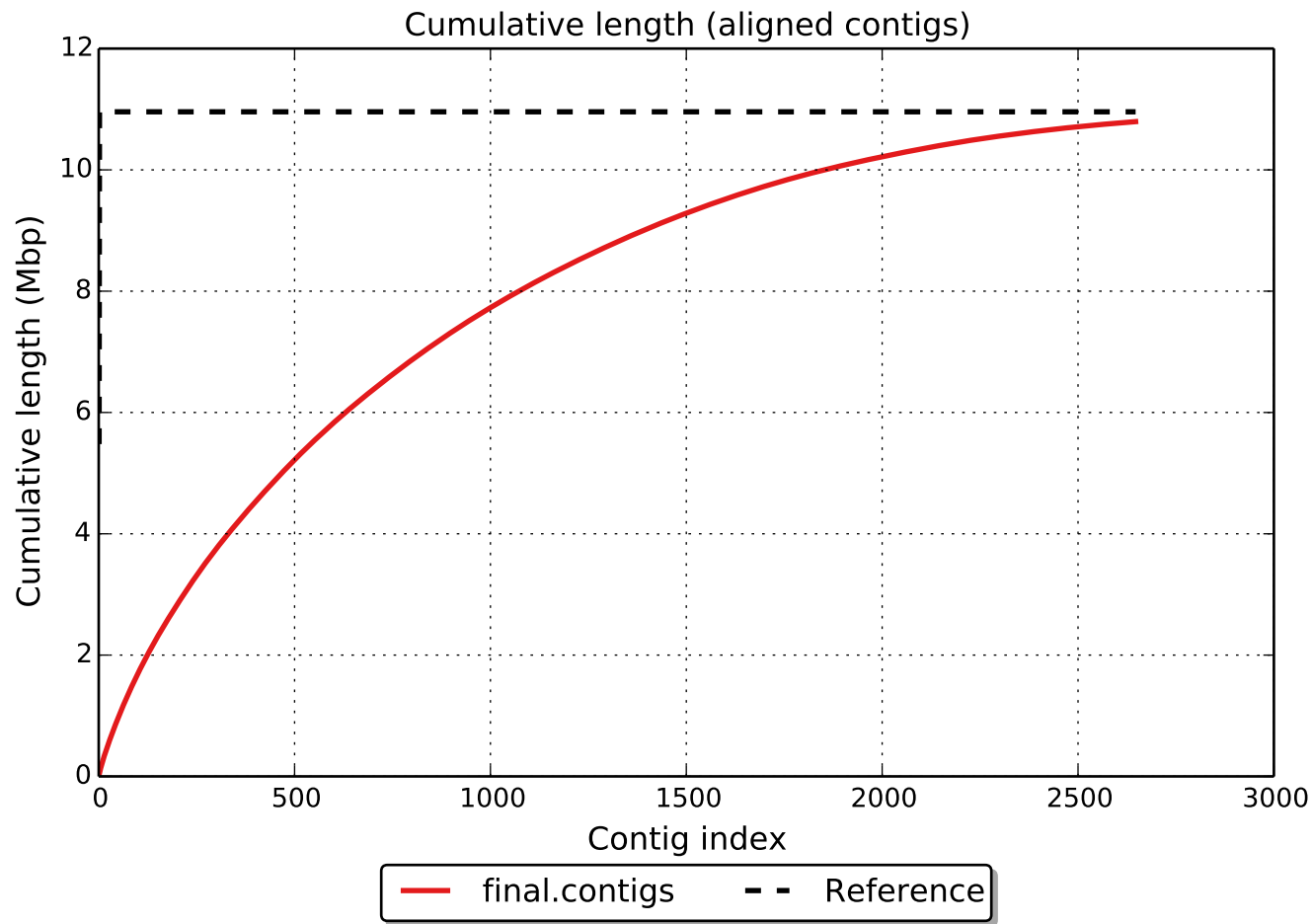


NGx

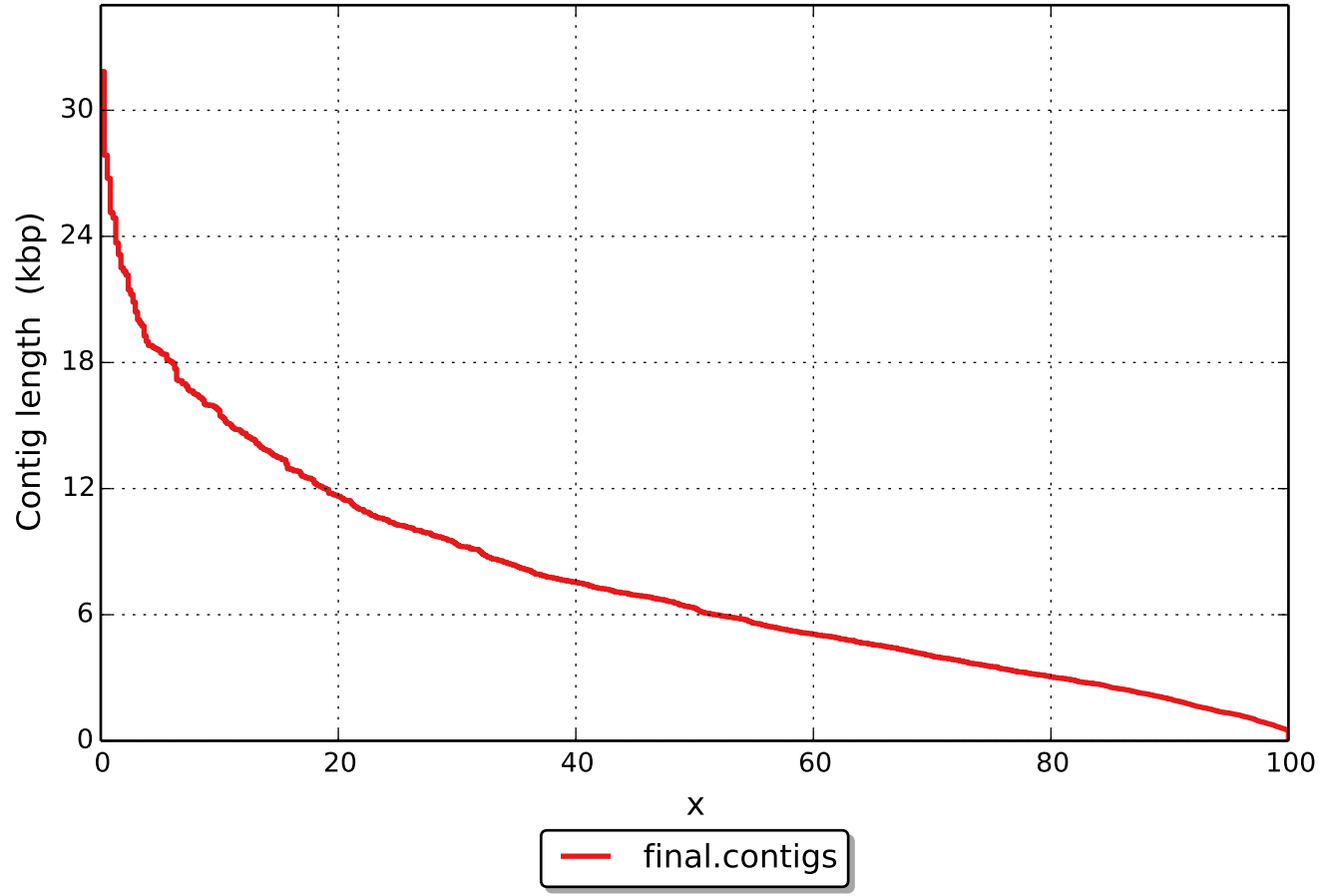








NAx



NGAx

