

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	1757
# contigs ( $\geq 1000$ bp)	1404
Total length ( $\geq 0$ bp)	5290040
Total length ( $\geq 1000$ bp)	5034917
# contigs	1757
Largest contig	20525
Total length	5290040
Reference length	5478683
GC (%)	50.28
Reference GC (%)	50.49
N50	4420
NG50	4239
N75	2524
NG75	2341
L50	369
LG50	391
L75	757
LG75	815
# misassemblies	5
# misassembled contigs	4
Misassembled contigs length	26942
# local misassemblies	1
# unaligned contigs	0 + 2 part
Unaligned length	9710
Genome fraction (%)	93.630
Duplication ratio	1.029
# N's per 100 kbp	0.00
# mismatches per 100 kbp	34.51
# indels per 100 kbp	0.14
Largest alignment	20525
NA50	4405
NGA50	4219
NA75	2504
NGA75	2303
LA50	373
LGA50	394
LA75	764
LGA75	822

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

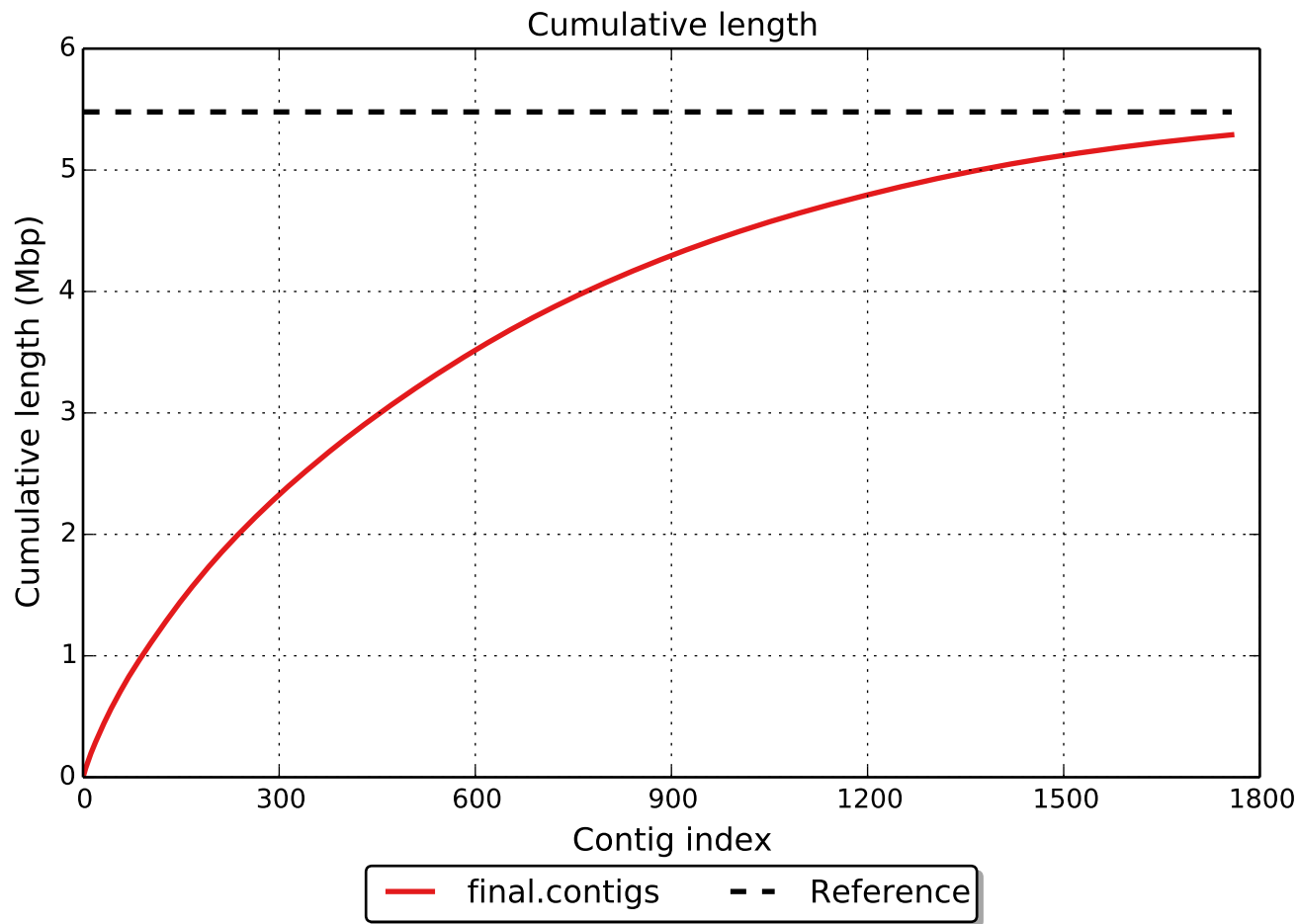
	final.contigs
# misassemblies	5
# relocations	5
# translocations	0
# inversions	0
# possibly misassembled contigs	2
# misassembled contigs	4
Misassembled contigs length	26942
# local misassemblies	1
# mismatches	1770
# indels	7
# short indels	6
# long indels	1
Indels length	14

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).

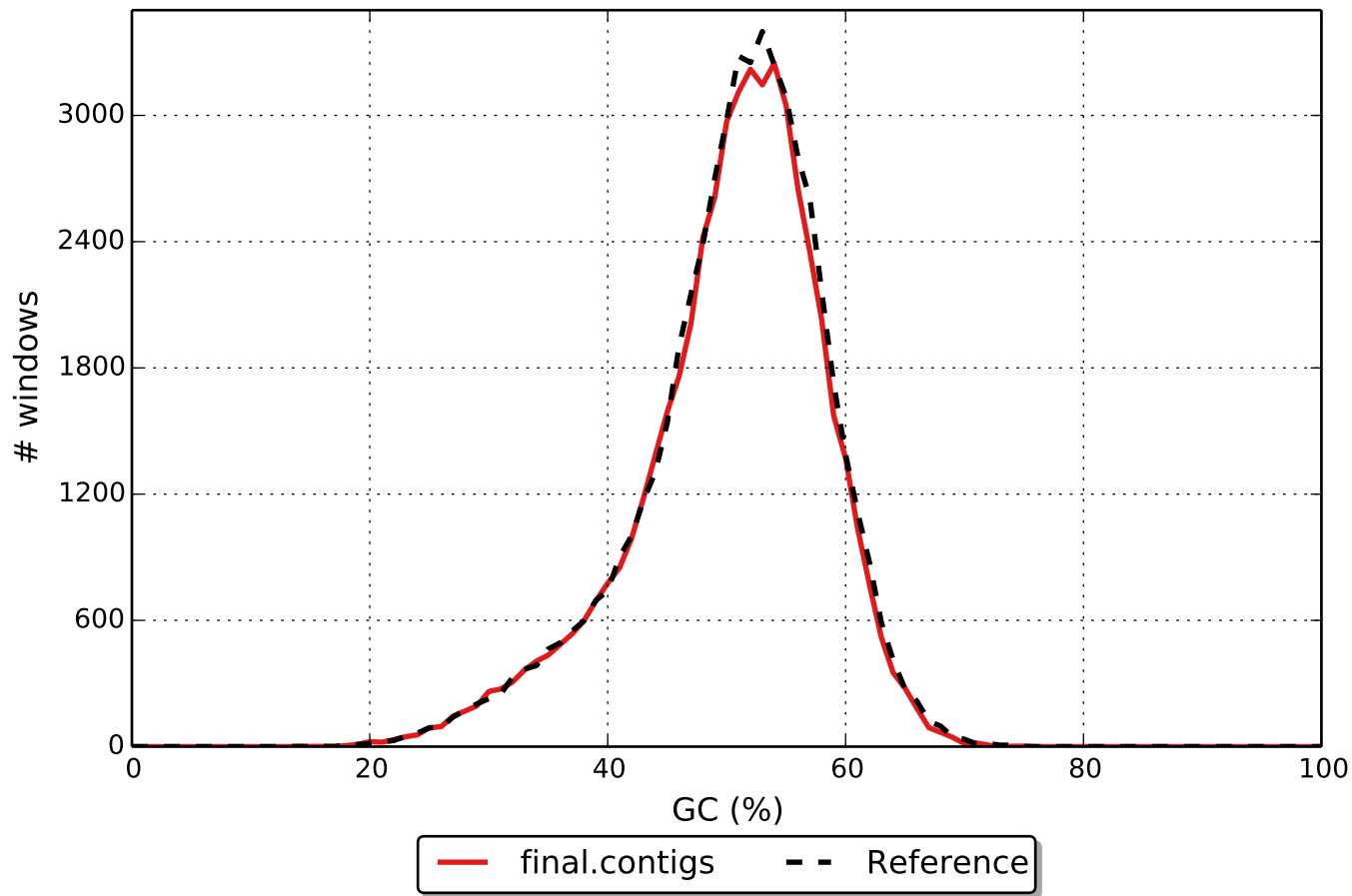
## Unaligned report

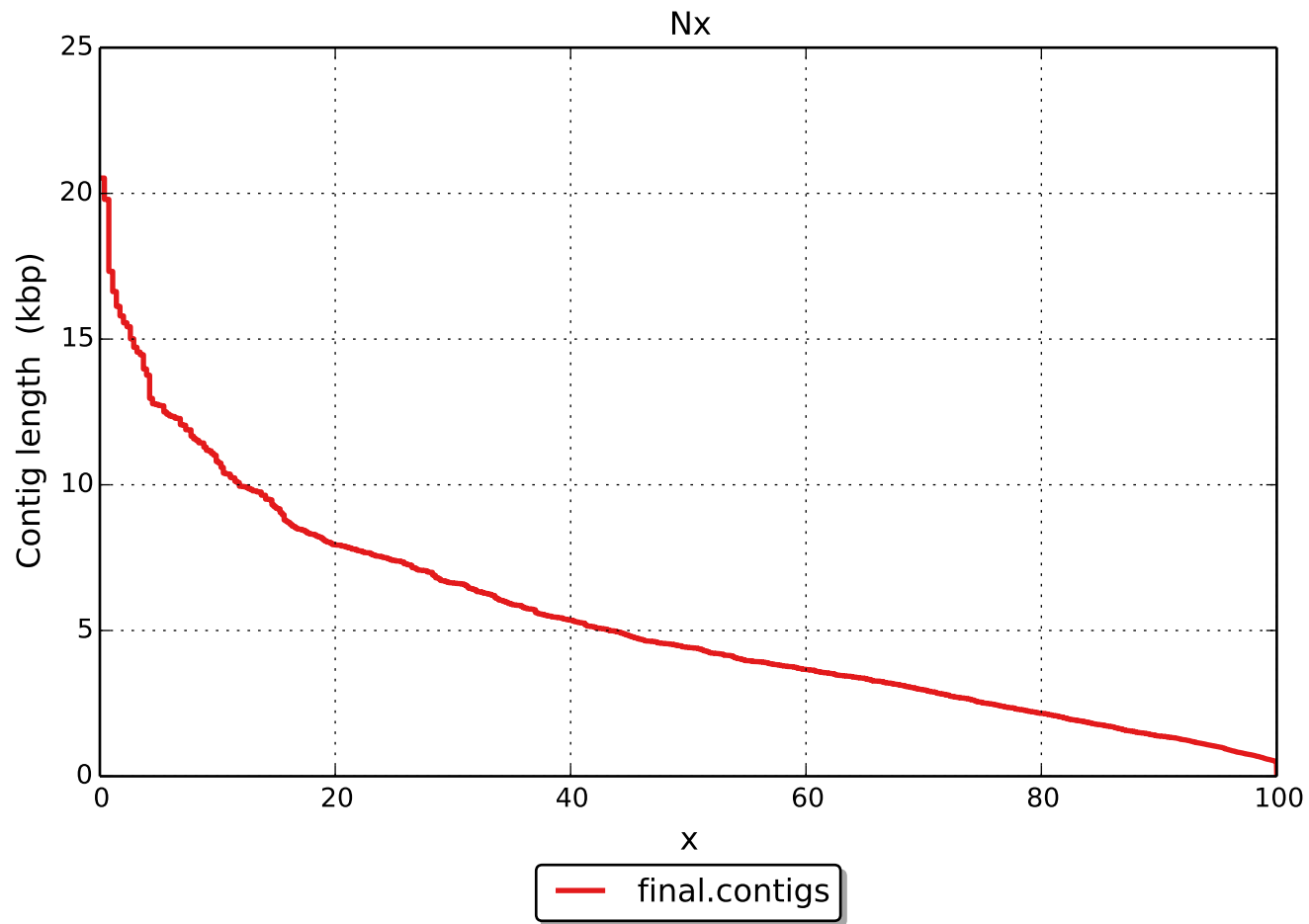
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	2
Partially unaligned length	9710
# N's	0

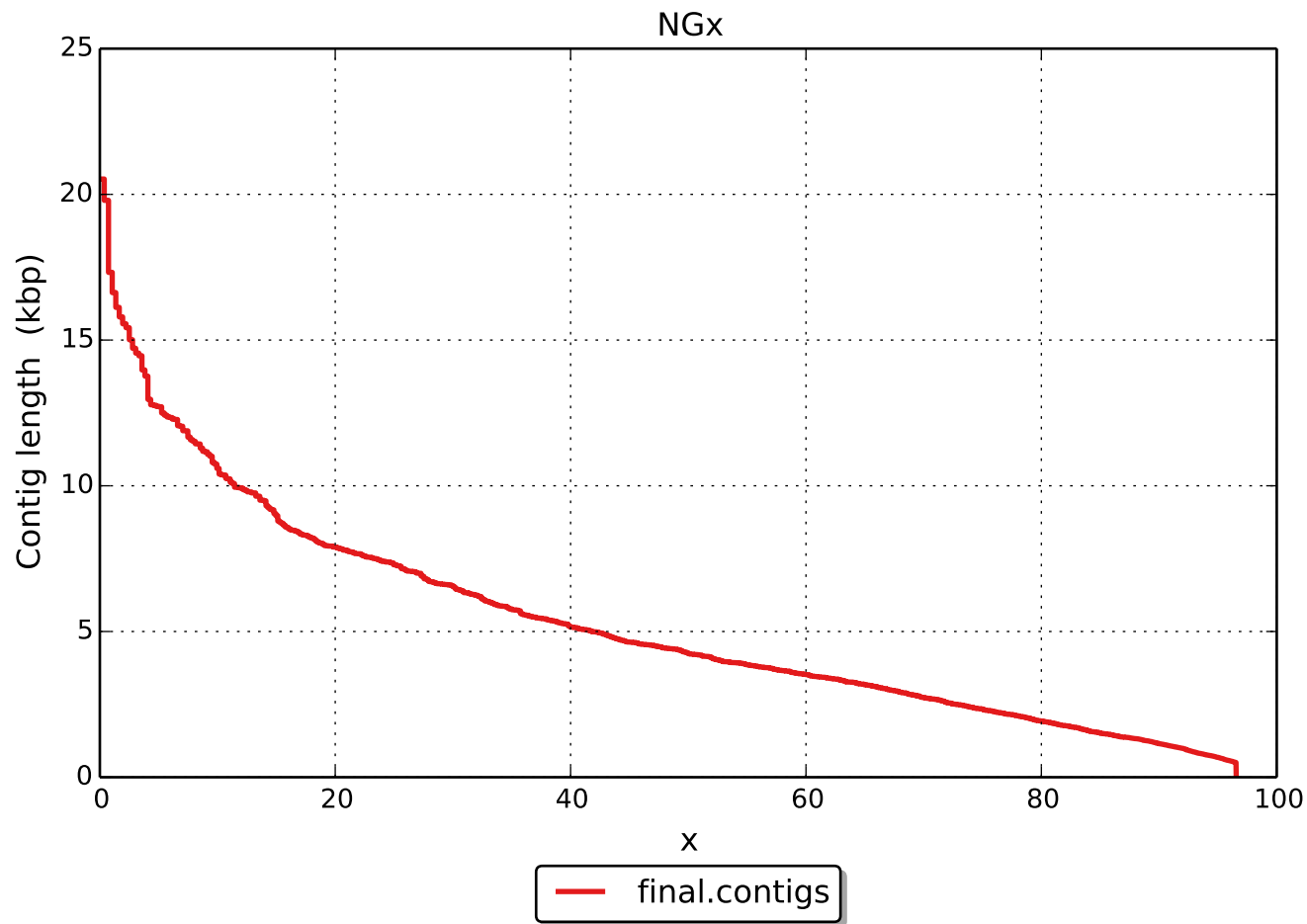
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

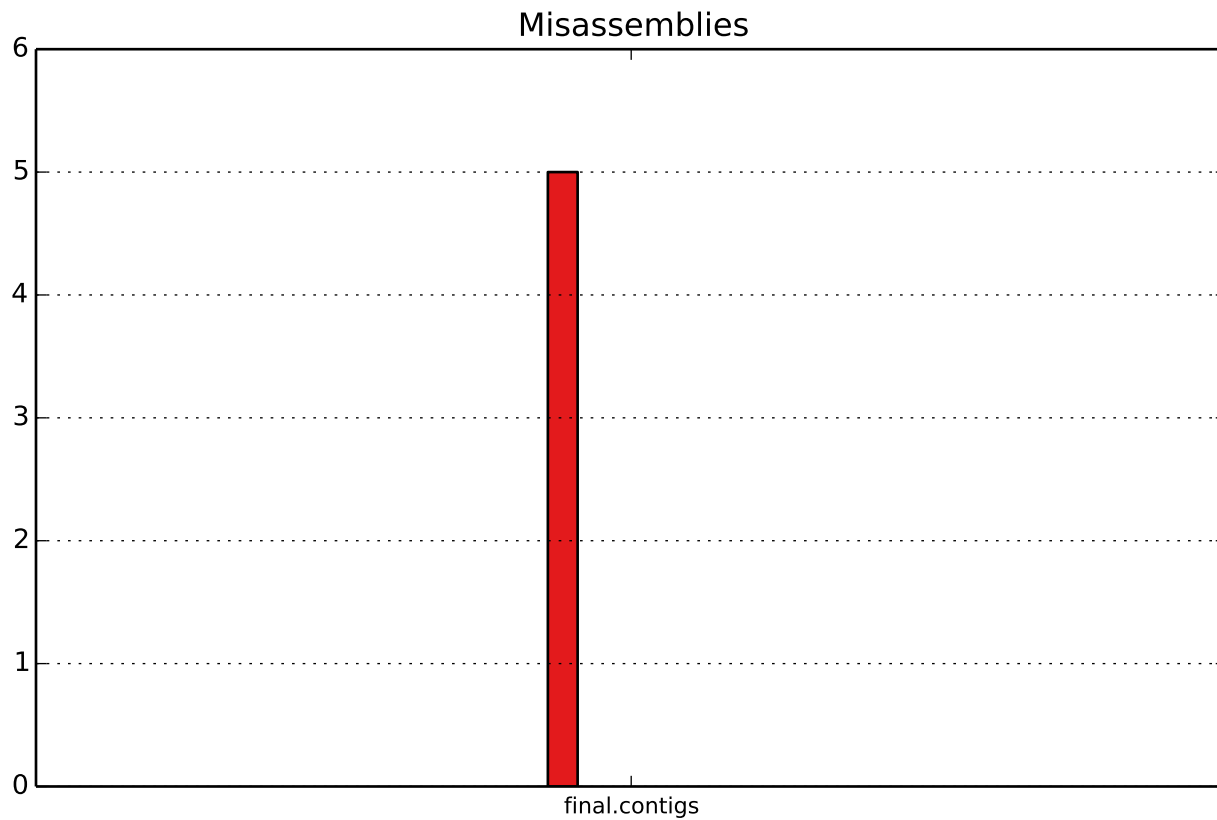


GC content

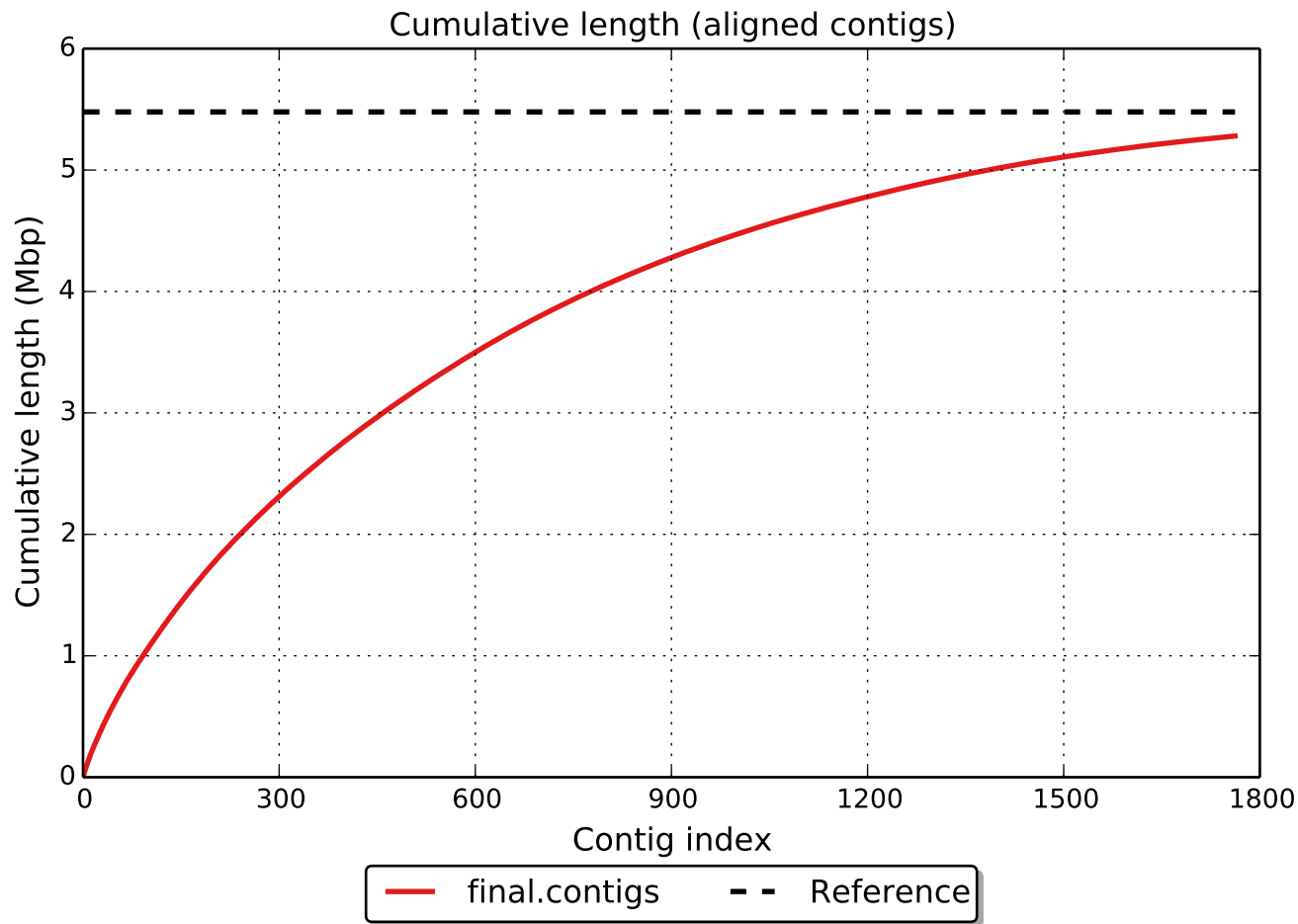


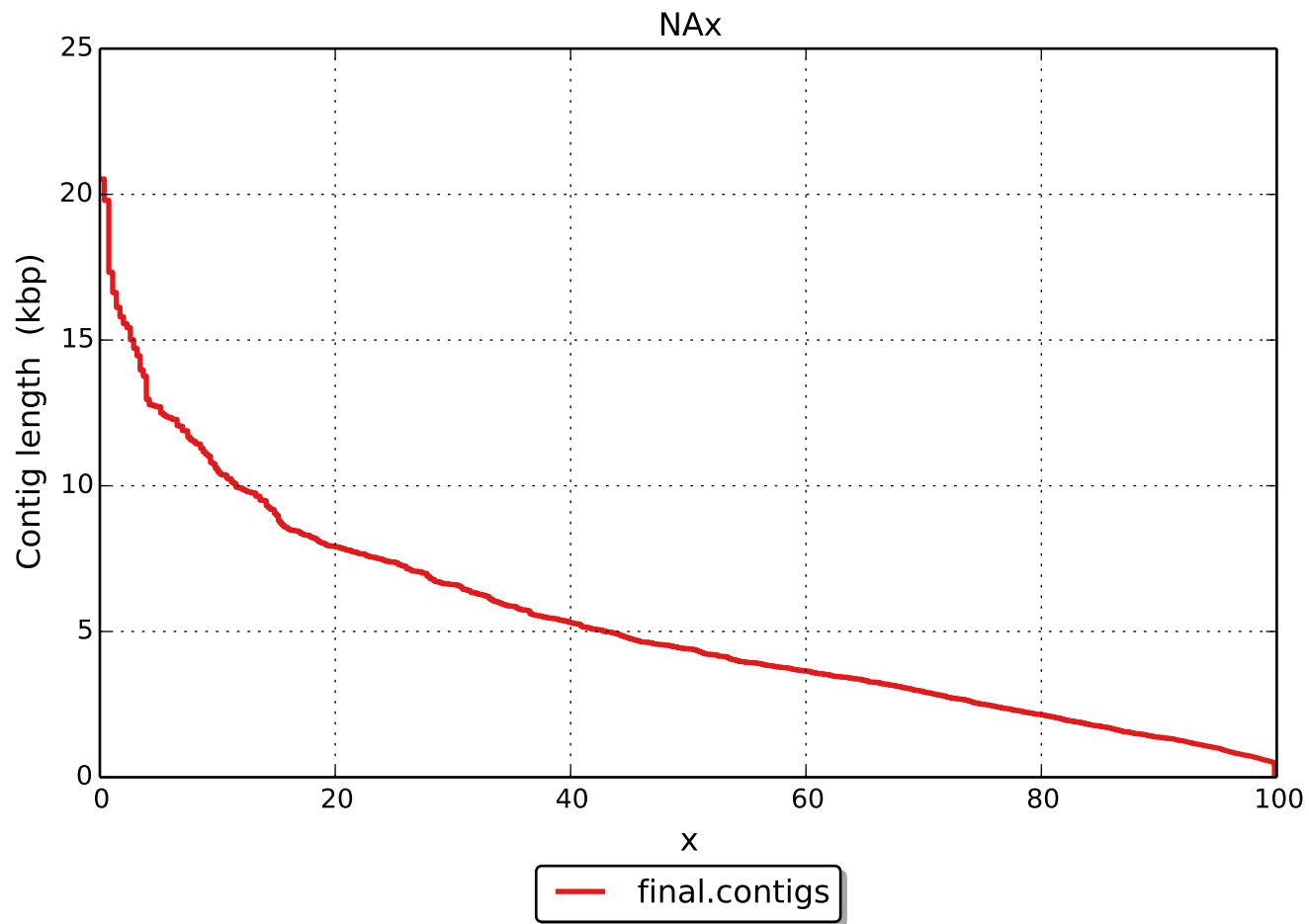












NGAx

