

## Report

	final.contigs
# contigs (>= 0 bp)	1646
# contigs (>= 1000 bp)	1417
Total length (>= 0 bp)	5594891
Total length (>= 1000 bp)	5427385
# contigs	1646
Largest contig	24393
Total length	5594891
Reference length	5478683
GC (%)	50.51
Reference GC (%)	50.50
N50	4779
NG50	4896
N75	2900
NG75	3014
L50	362
LG50	350
L75	739
LG75	709
# misassemblies	4
# misassembled contigs	4
Misassembled contigs length	37200
# local misassemblies	0
# unaligned contigs	0 + 2 part
Unaligned length	13598
Genome fraction (%)	98.875
Duplication ratio	1.030
# N's per 100 kbp	0.00
# mismatches per 100 kbp	34.76
# indels per 100 kbp	0.04
Largest alignment	24393
NA50	4724
NGA50	4856
NA75	2859
NGA75	2980
LA50	364
LGA50	352
LA75	744
LGA75	714

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

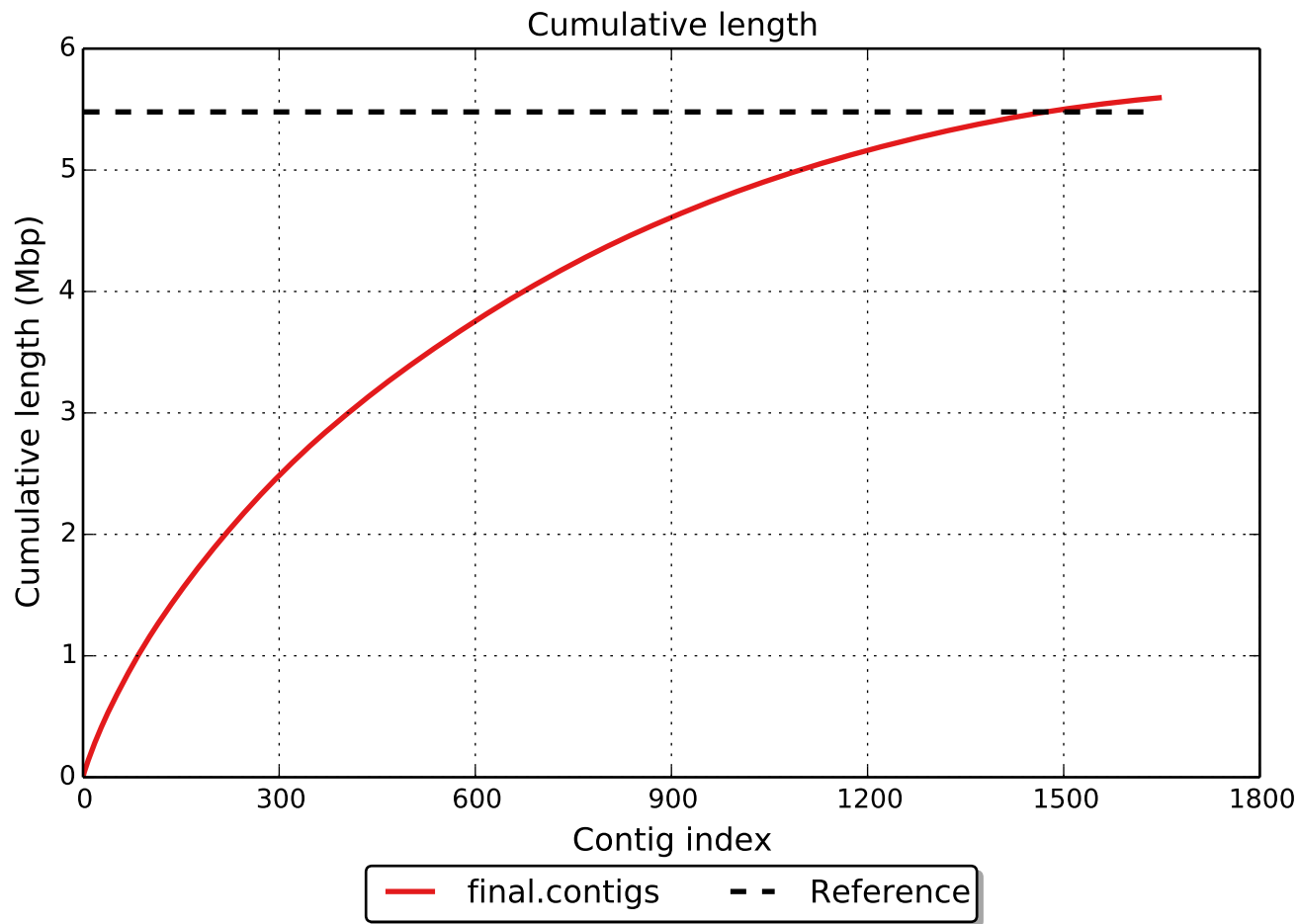
	final.contigs
# misassemblies	4
# relocations	4
# translocations	0
# inversions	0
# possibly misassembled contigs	3
# misassembled contigs	4
Misassembled contigs length	37200
# local misassemblies	0
# mismatches	1883
# indels	2
# short indels	2
# long indels	0
Indels length	2

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).

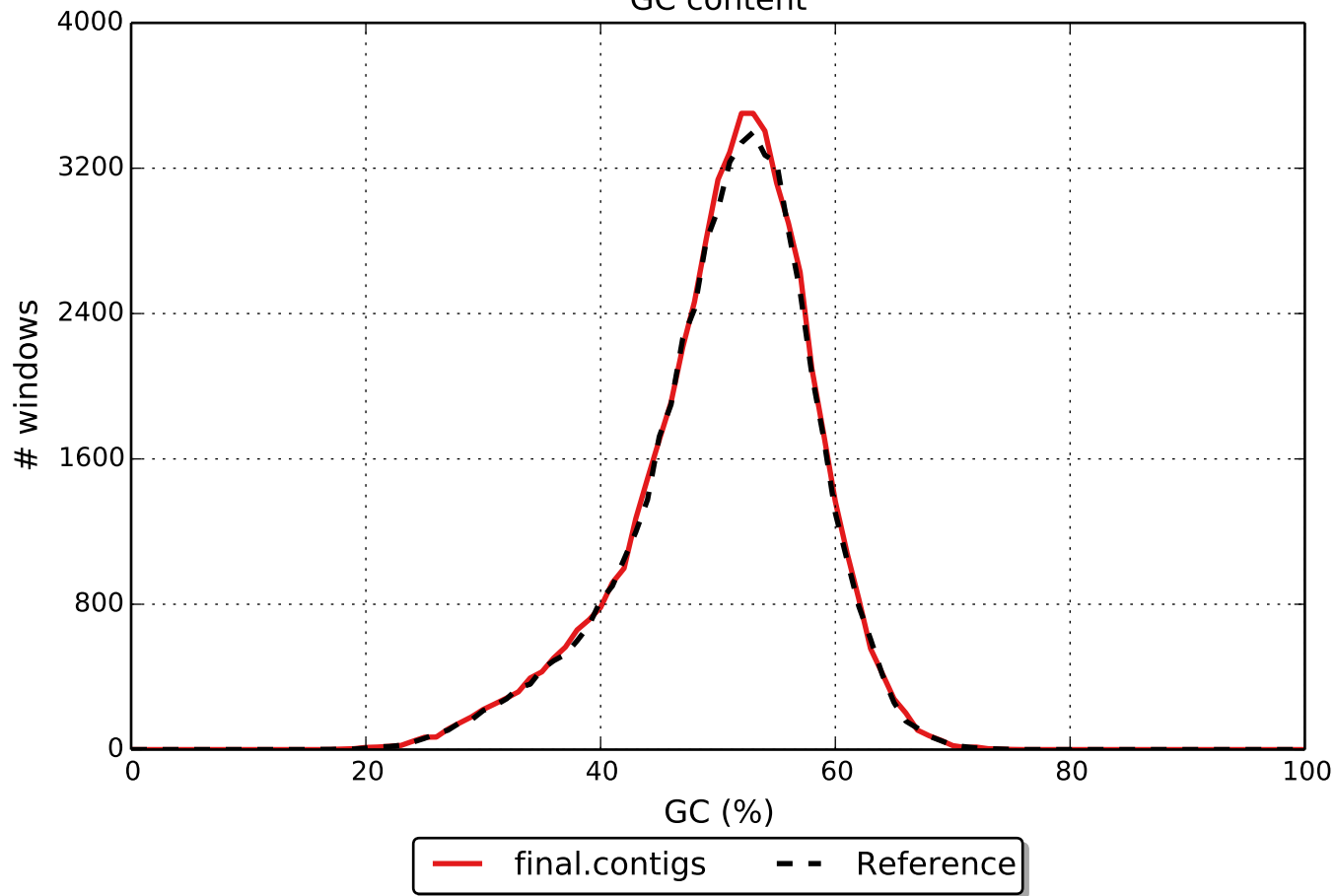
## Unaligned report

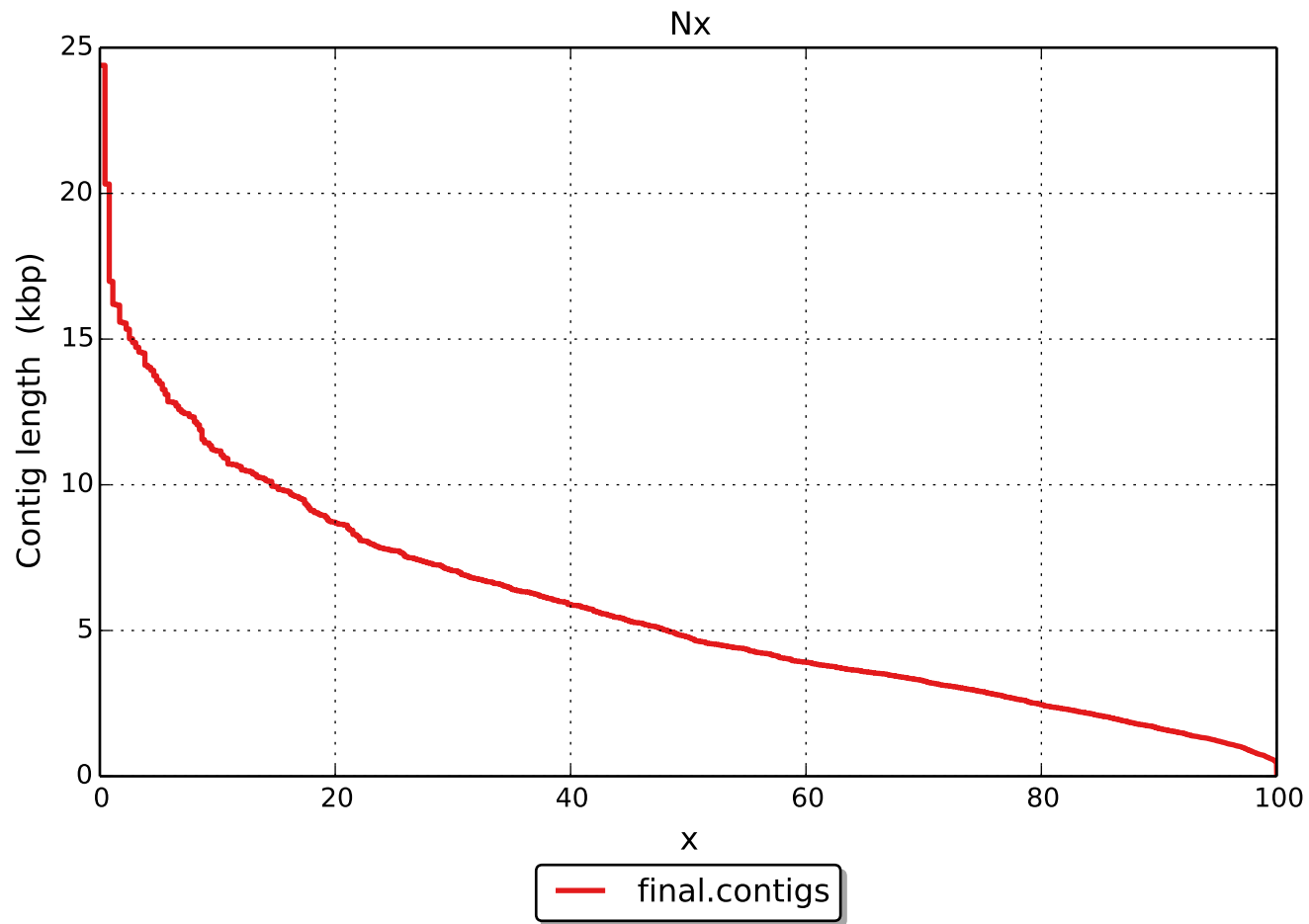
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	2
Partially unaligned length	13598
# N's	0

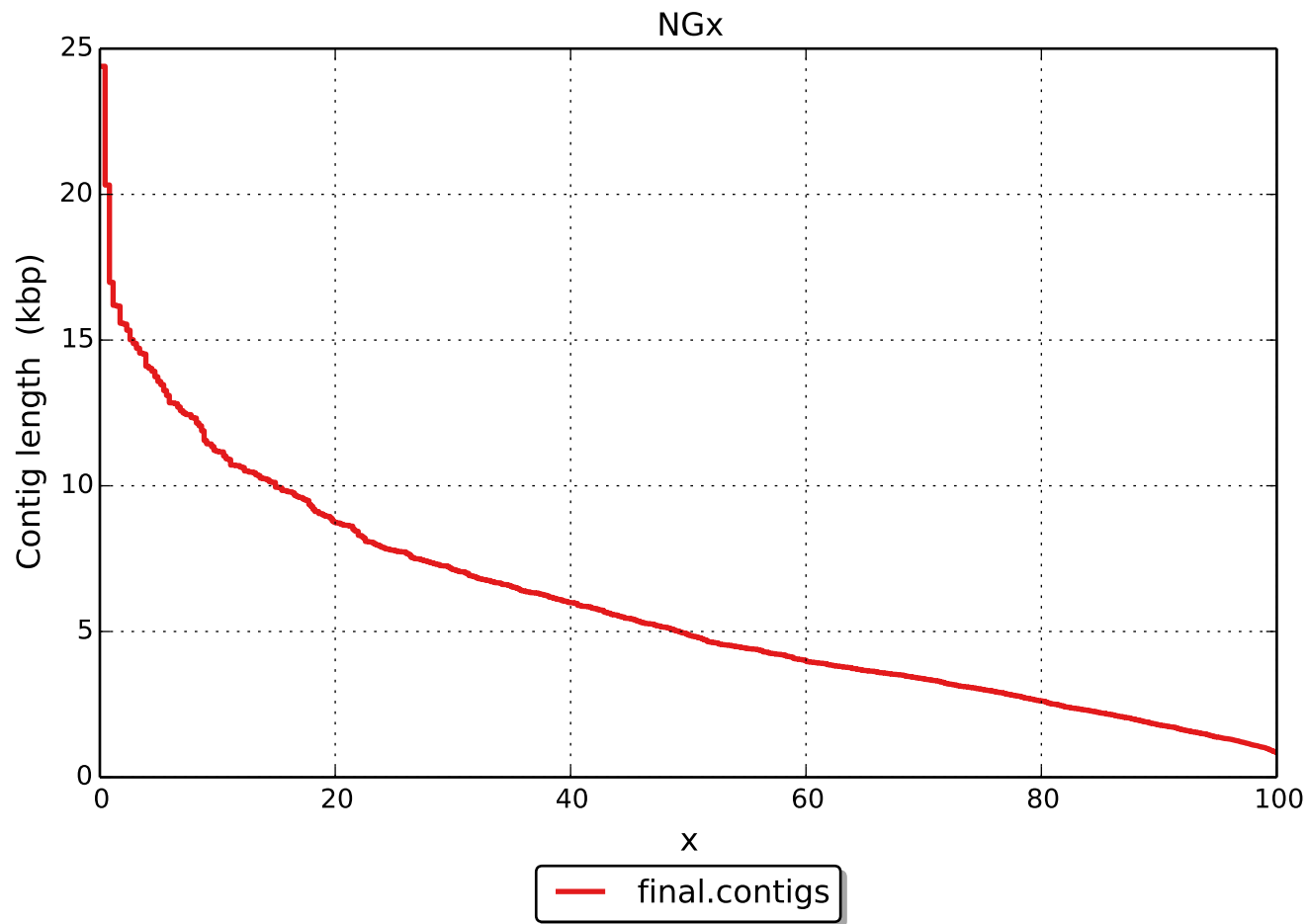
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

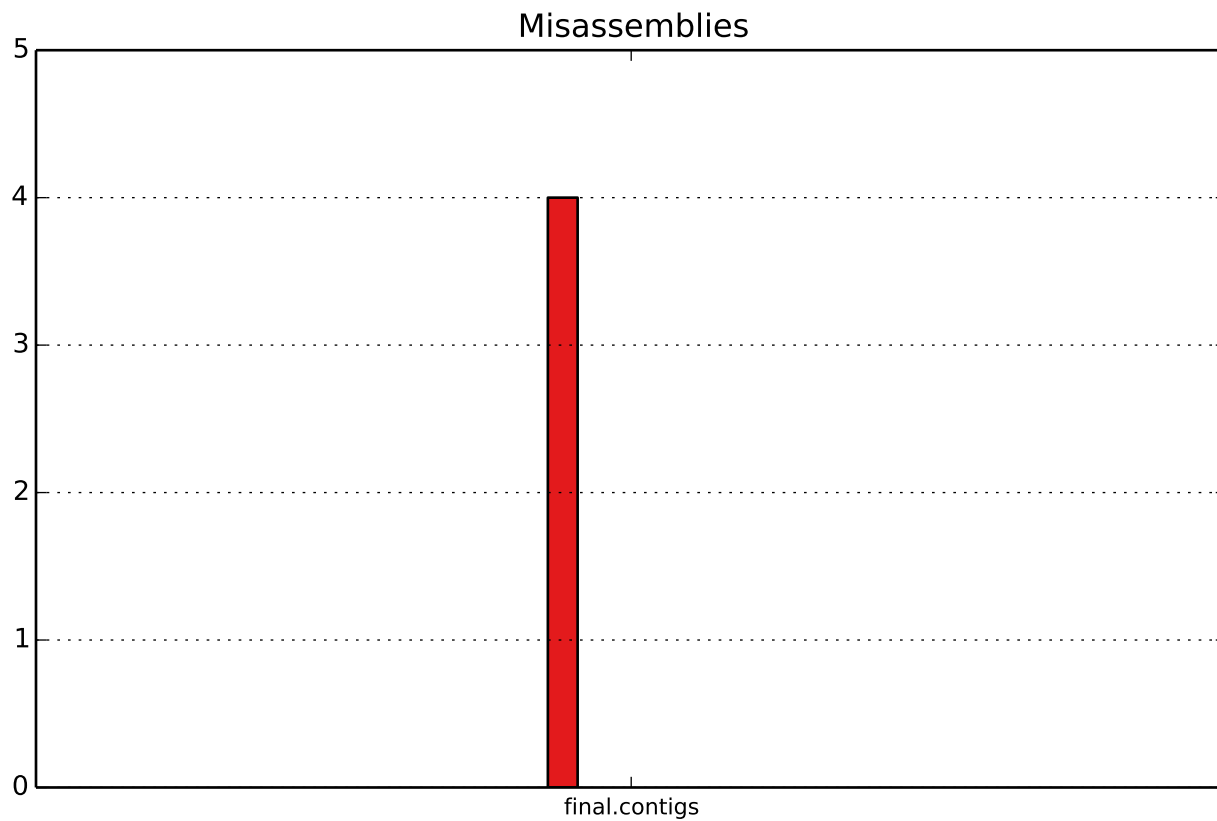


GC content

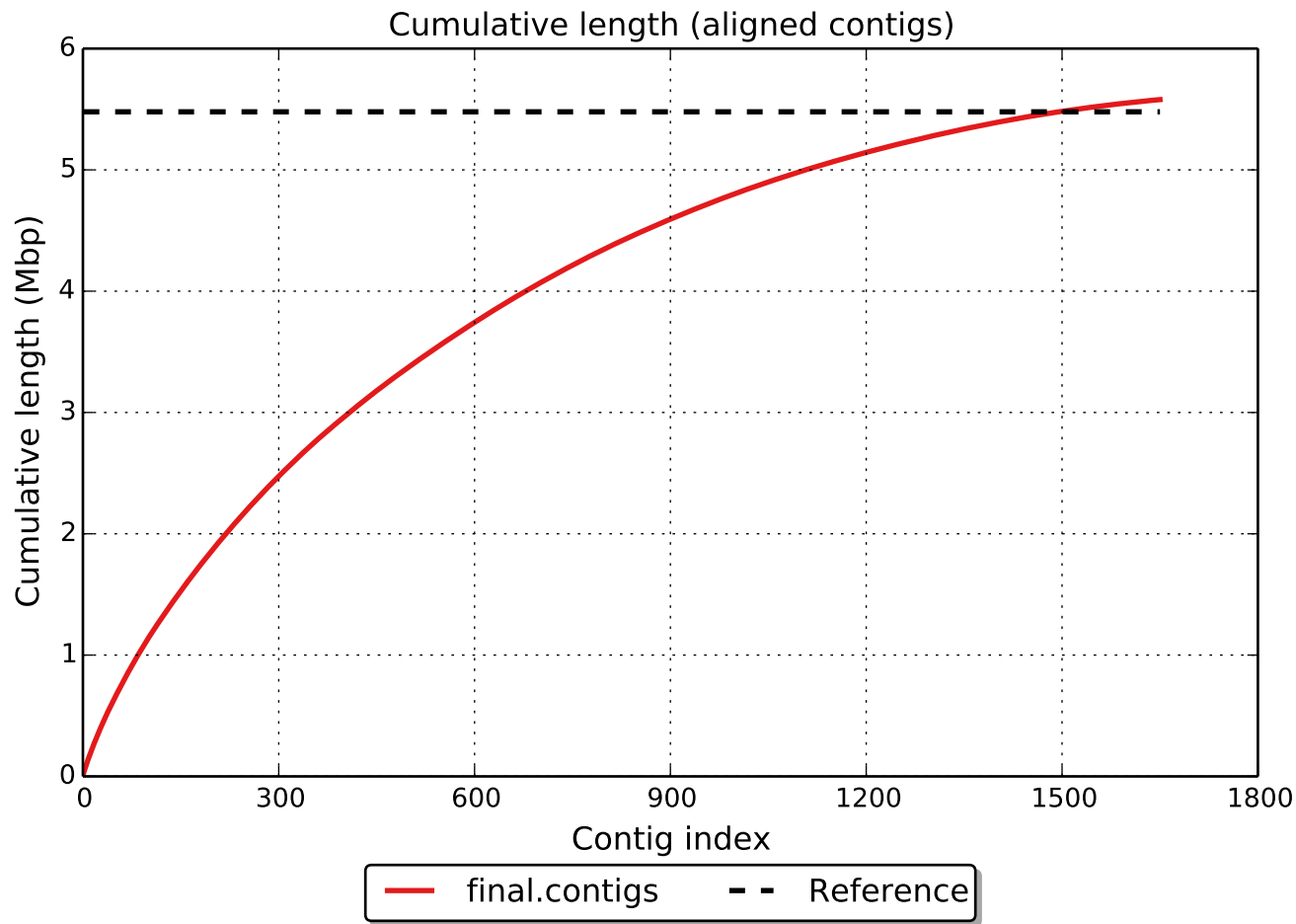


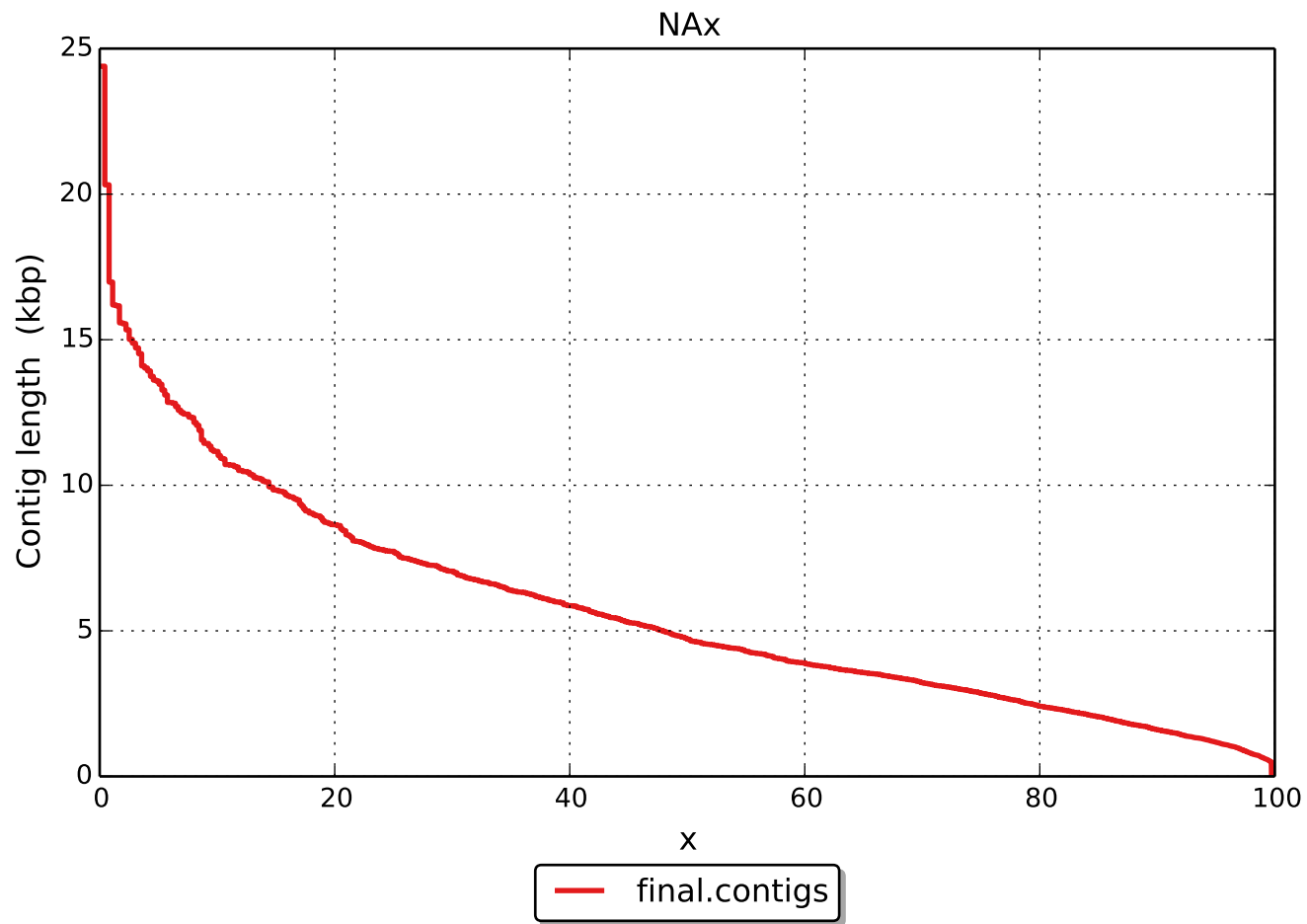












NGAx

