

## Report

	final.contigs
# contigs (>= 0 bp)	4166
# contigs (>= 1000 bp)	2809
Total length (>= 0 bp)	11044432
Total length (>= 1000 bp)	10369505
# contigs	3390
Largest contig	24393
Total length	10791536
Reference length	10957366
GC (%)	50.39
Reference GC (%)	50.49
N50	4540
NG50	4489
N75	2705
NG75	2618
L50	729
LG50	747
L75	1489
LG75	1536
# misassemblies	6
# misassembled contigs	6
Misassembled contigs length	52677
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	96.657
Duplication ratio	1.028
# N's per 100 kbp	0.00
# mismatches per 100 kbp	37.59
# indels per 100 kbp	0.13
Largest alignment	24393
NA50	4534
NGA50	4481
NA75	2689
NGA75	2609
LA50	730
LGA50	749
LA75	1492
LGA75	1539

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

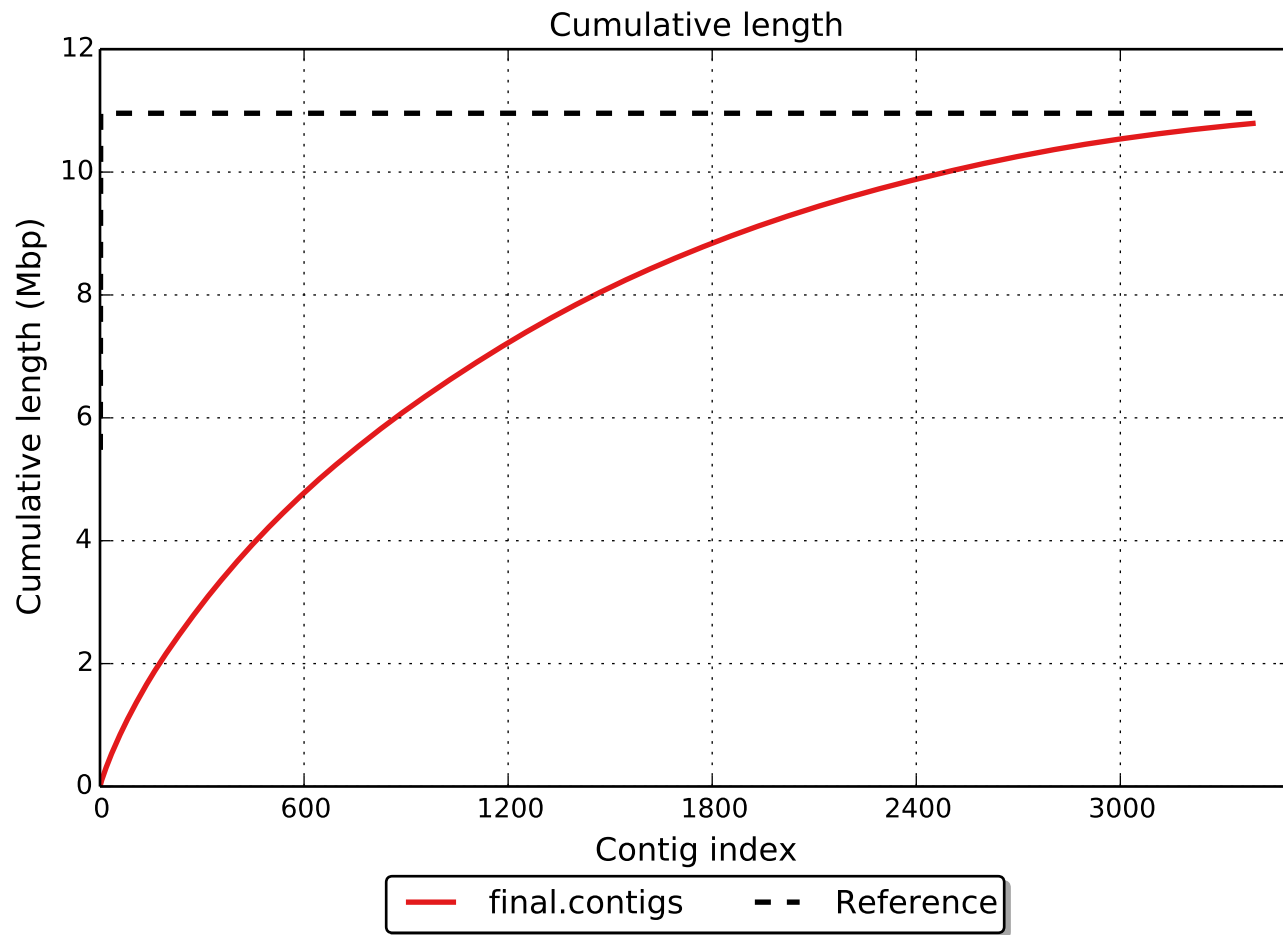
	final.contigs
# misassemblies	6
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	6
# possibly misassembled contigs	0
# misassembled contigs	6
Misassembled contigs length	52677
# local misassemblies	1
# mismatches	3981
# indels	14
# short indels	13
# long indels	1
Indels length	25

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).

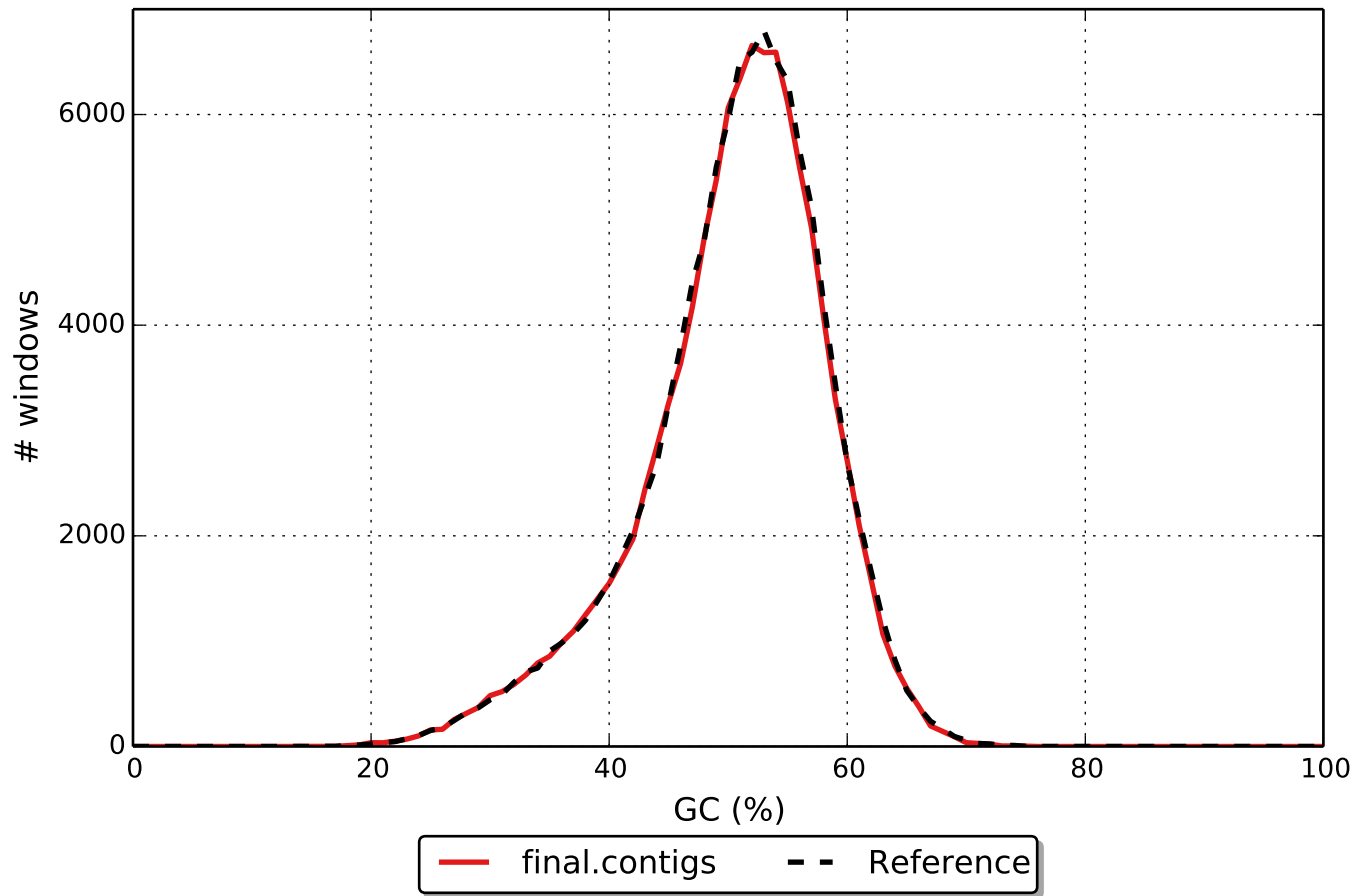
## Unaligned report

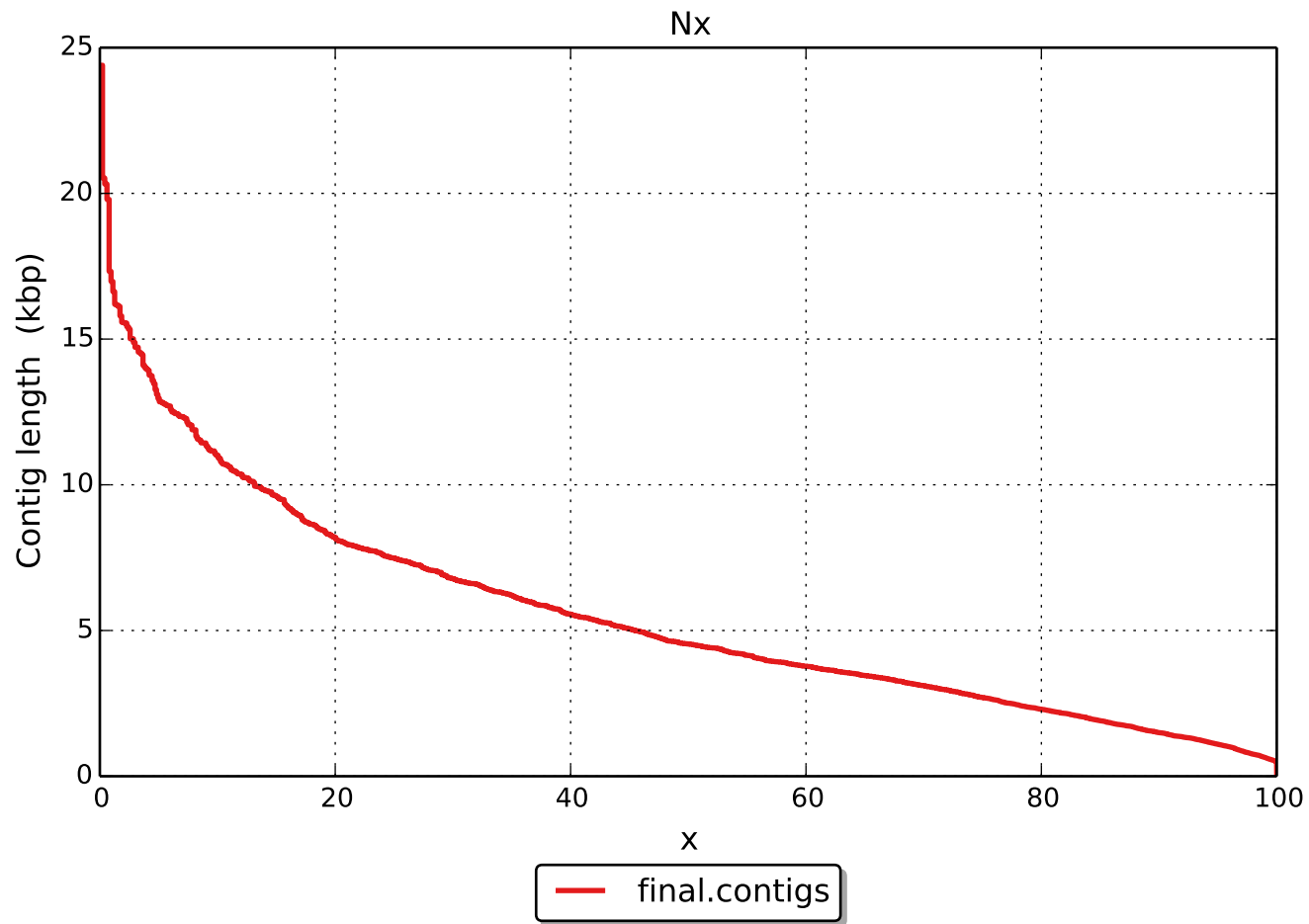
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

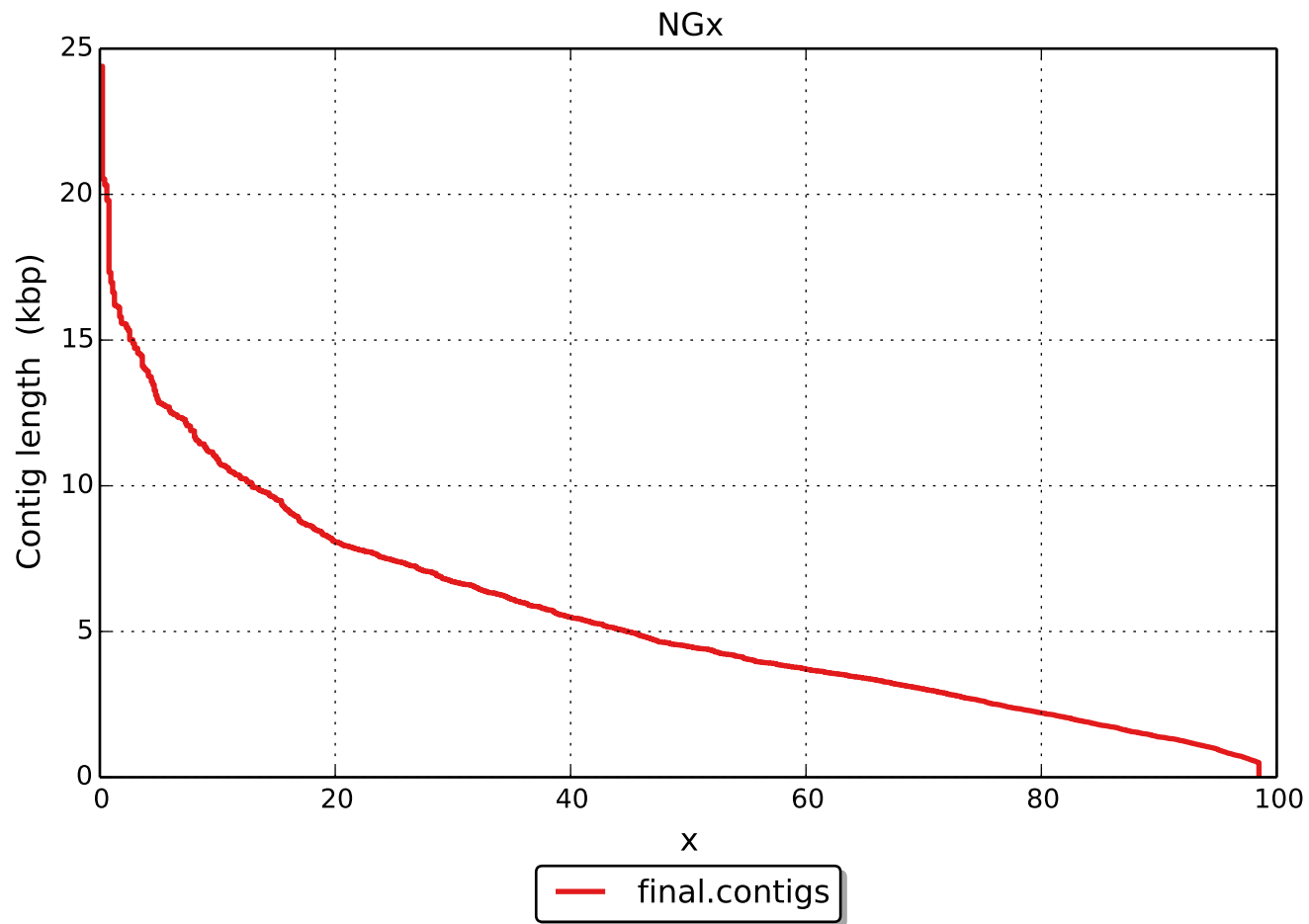
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

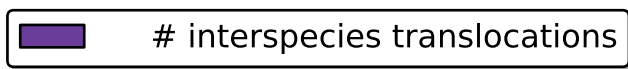
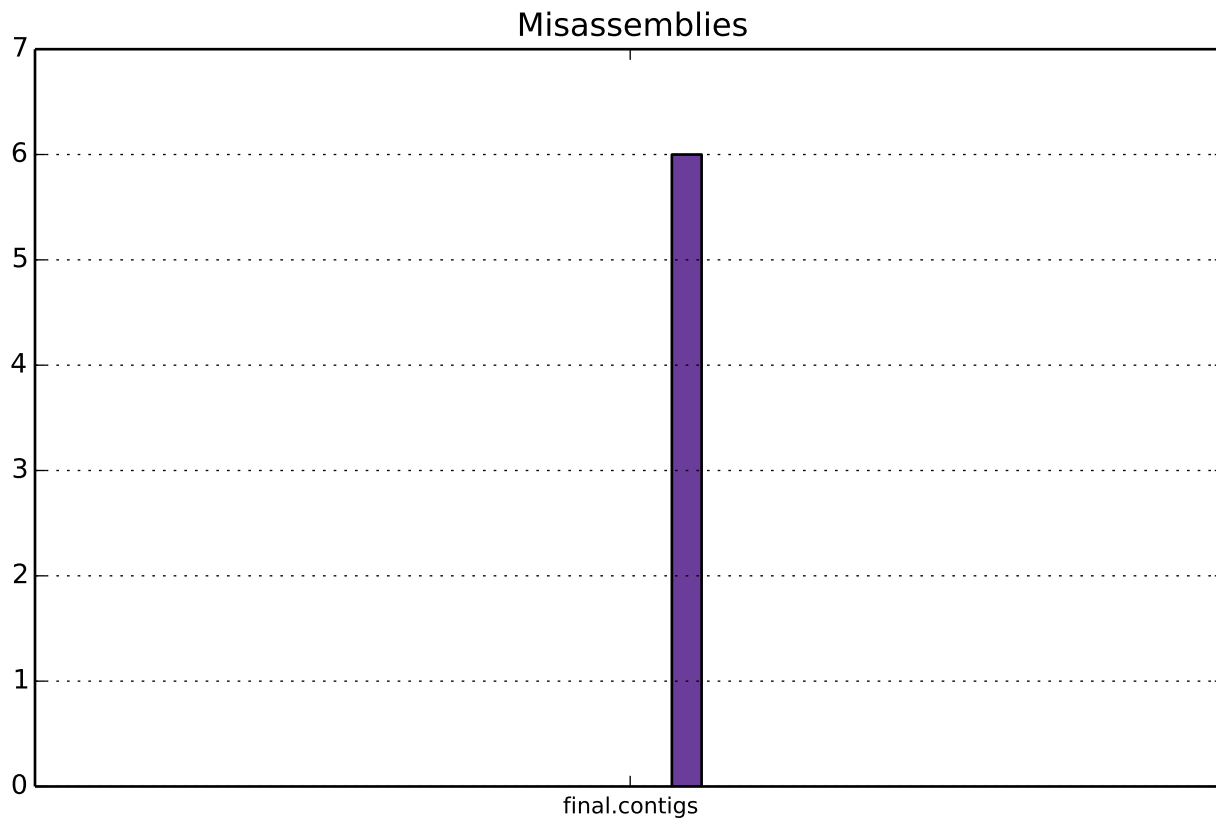


GC content

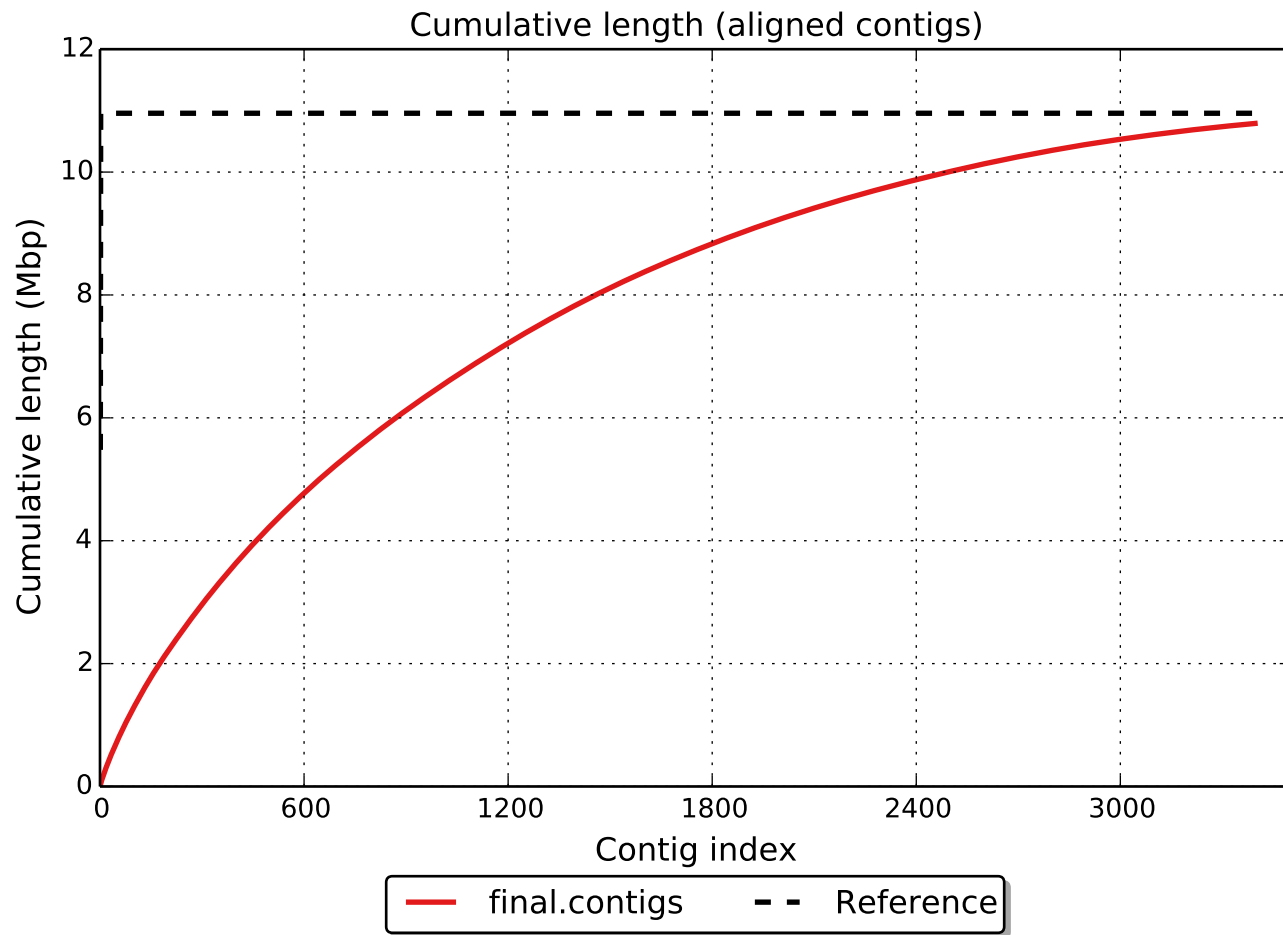


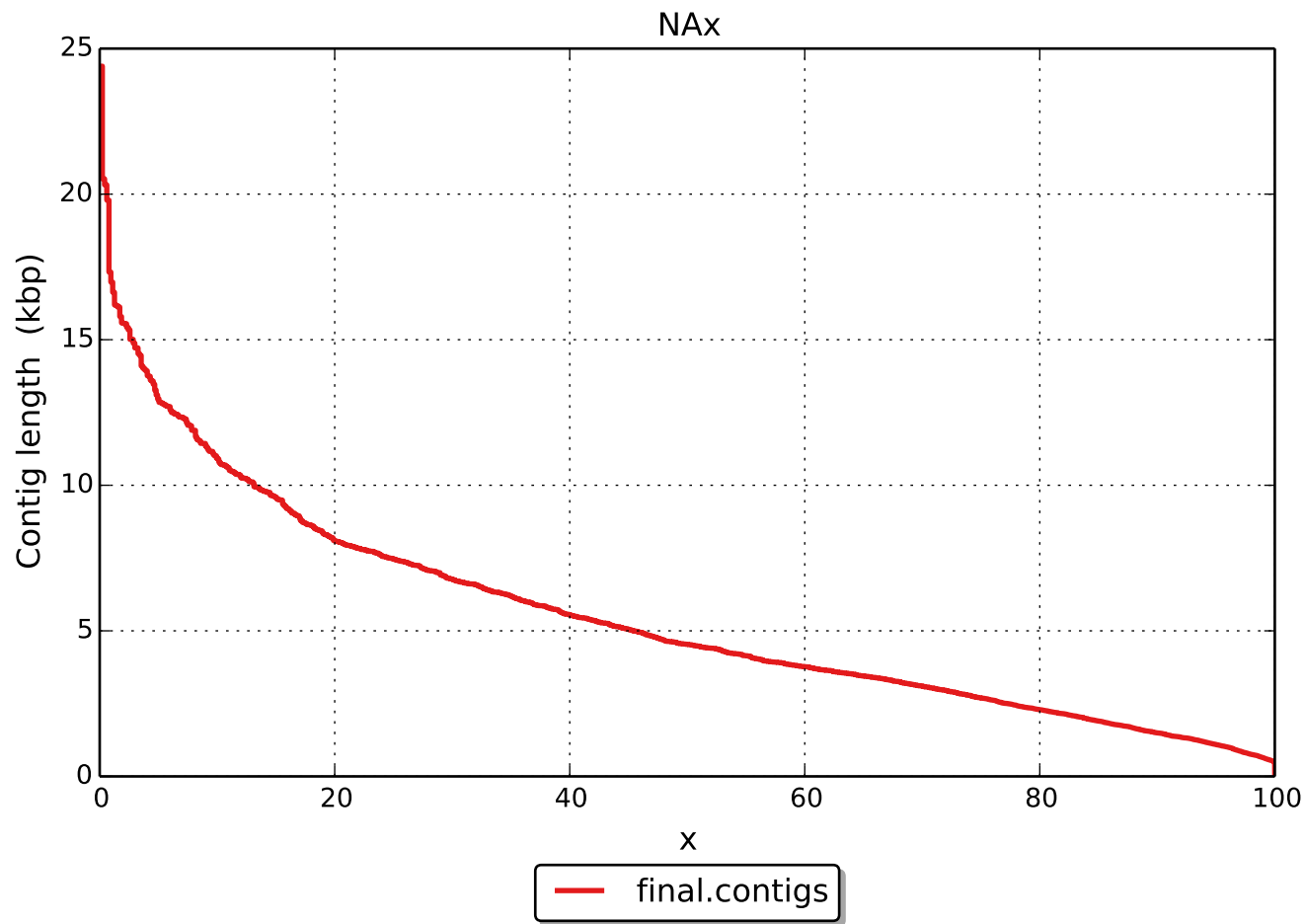












NGAx

