

## Report

	meta_contigs_1	meta_contigs_2
# contigs ( $\geq 1000$ bp)	2	2
# contigs ( $\geq 5000$ bp)	1	1
# contigs ( $\geq 10000$ bp)	1	1
# contigs ( $\geq 25000$ bp)	1	1
# contigs ( $\geq 50000$ bp)	1	1
Total length ( $\geq 1000$ bp)	56247	58868
Total length ( $\geq 5000$ bp)	55106	55421
Total length ( $\geq 10000$ bp)	55106	55421
Total length ( $\geq 25000$ bp)	55106	55421
Total length ( $\geq 50000$ bp)	55106	55421
# contigs	5	2
Largest contig	55106	55421
Total length	58663	58868
Reference length	1872918	1872918
GC (%)	50.17	50.19
Reference GC (%)	49.68	49.68
N50	55106	55421
N75	55106	55421
L50	1	1
L75	1	1
# misassemblies	2	2
# misassembled contigs	1	1
Misassembled contigs length	55106	55421
# local misassemblies	0	0
# unaligned contigs	0 + 0 part	0 + 0 part
Unaligned length	0	0
Genome fraction (%)	2.798	2.812
Duplication ratio	1.120	1.118
# N's per 100 kbp	1.70	0.00
# mismatches per 100 kbp	746.15	750.05
# indels per 100 kbp	87.78	89.25
Largest alignment	20813	20822
NA50	19894	20200
NGA50	-	-
NA75	8193	8193
LA50	2	2
LA75	3	3

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

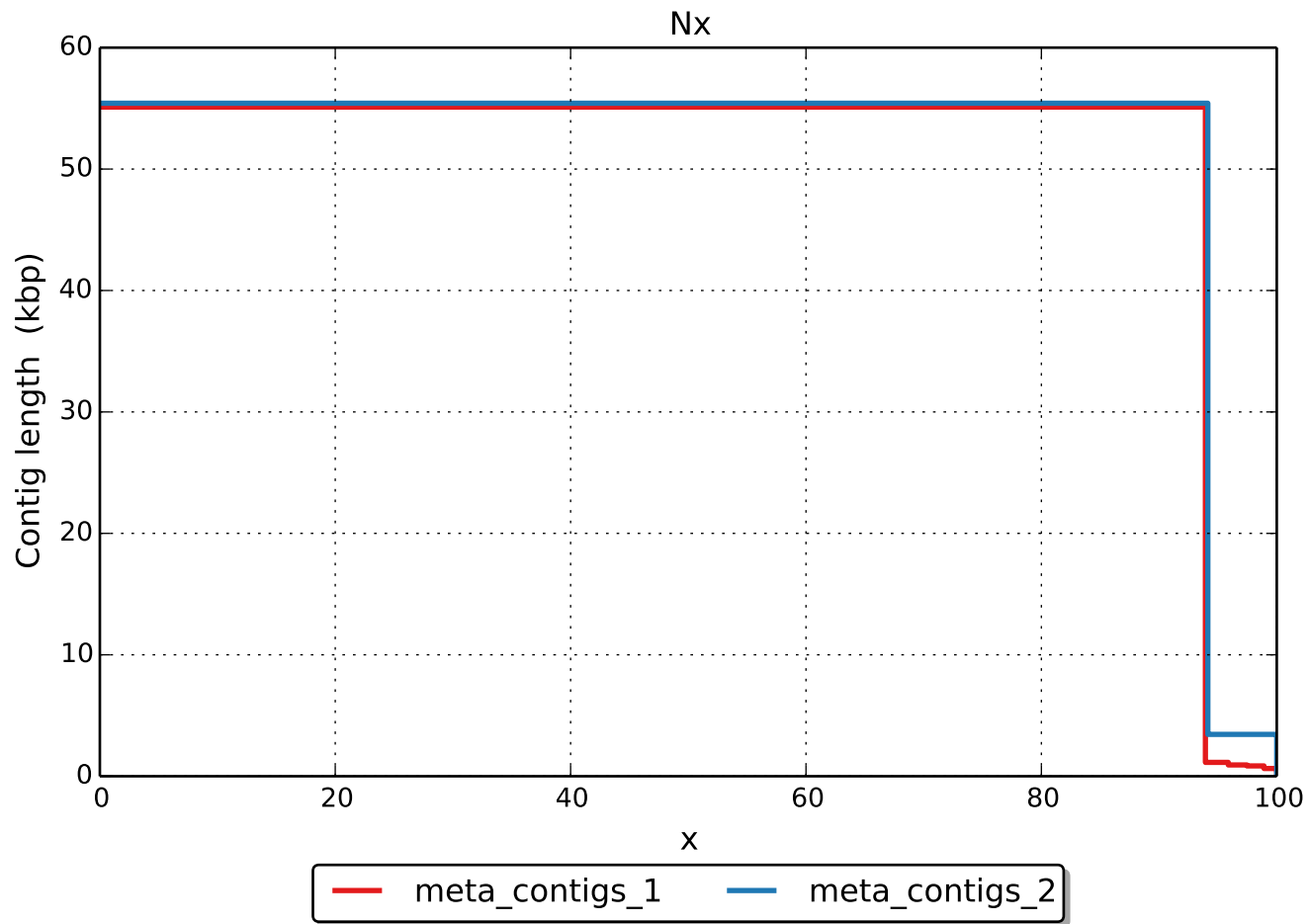
	meta_contigs_1	meta_contigs_2
# misassemblies	2	2
# relocations	2	2
# translocations	0	0
# inversions	0	0
# possibly misassembled contigs	1	1
# misassembled contigs	1	1
Misassembled contigs length	55106	55421
# local misassemblies	0	0
# mismatches	391	395
# indels	46	47
# short indels	44	45
# long indels	2	2
Indels length	87	88

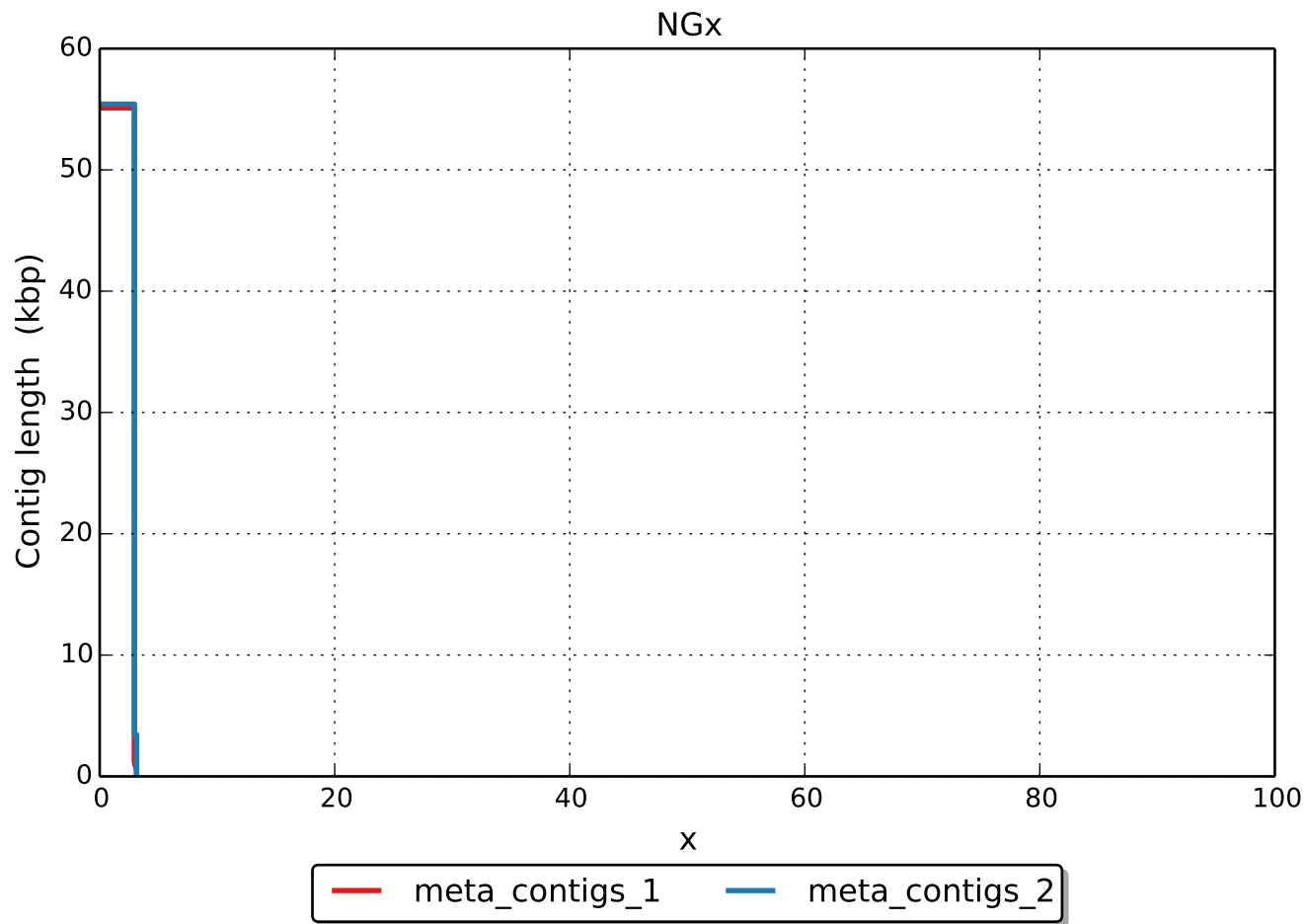
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

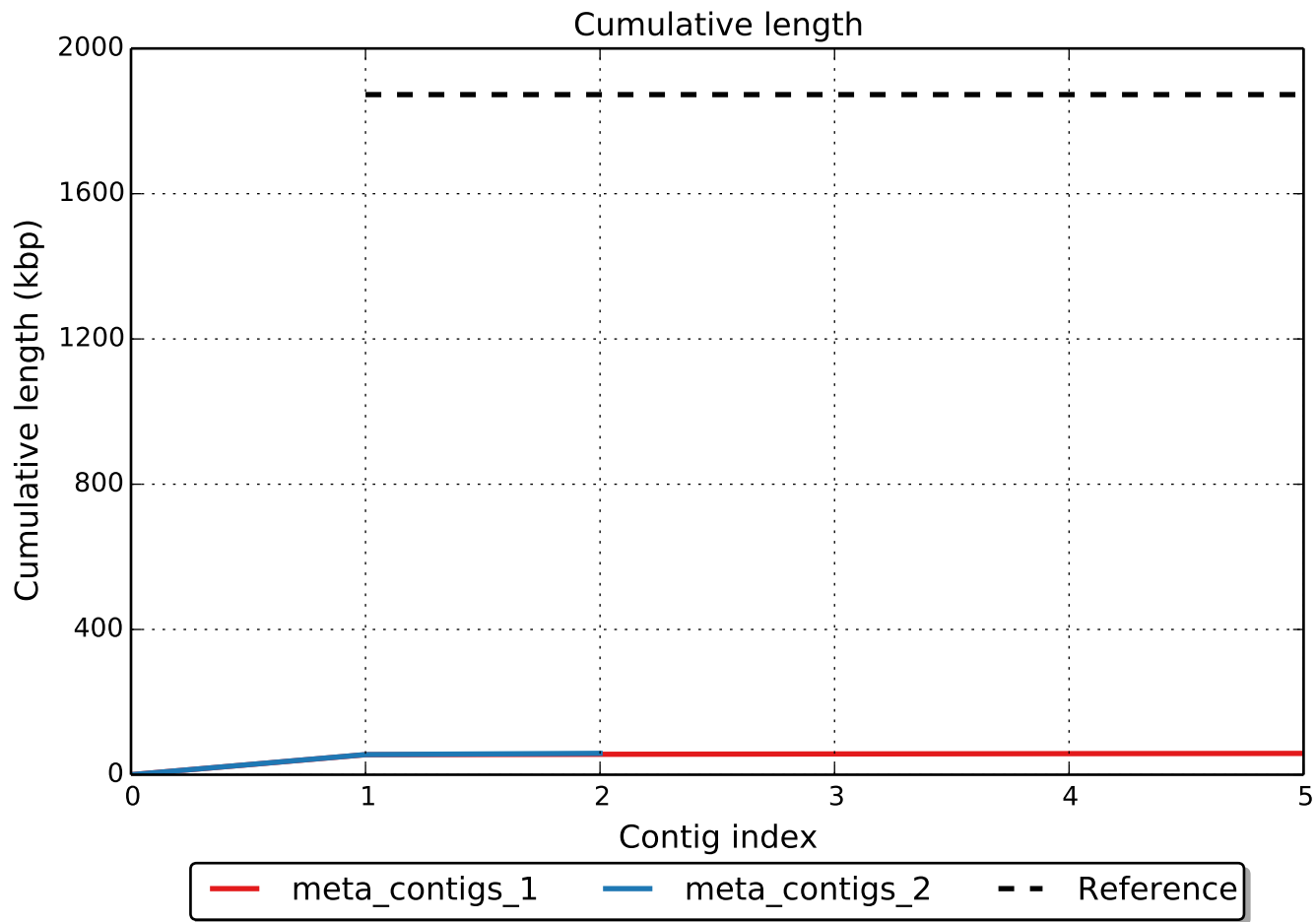
## Unaligned report

	meta_contigs_1	meta_contigs_2
# fully unaligned contigs	0	0
Fully unaligned length	0	0
# partially unaligned contigs	0	0
# with misassembly	0	0
# both parts are significant	0	0
Partially unaligned length	0	0
# N's	1	0

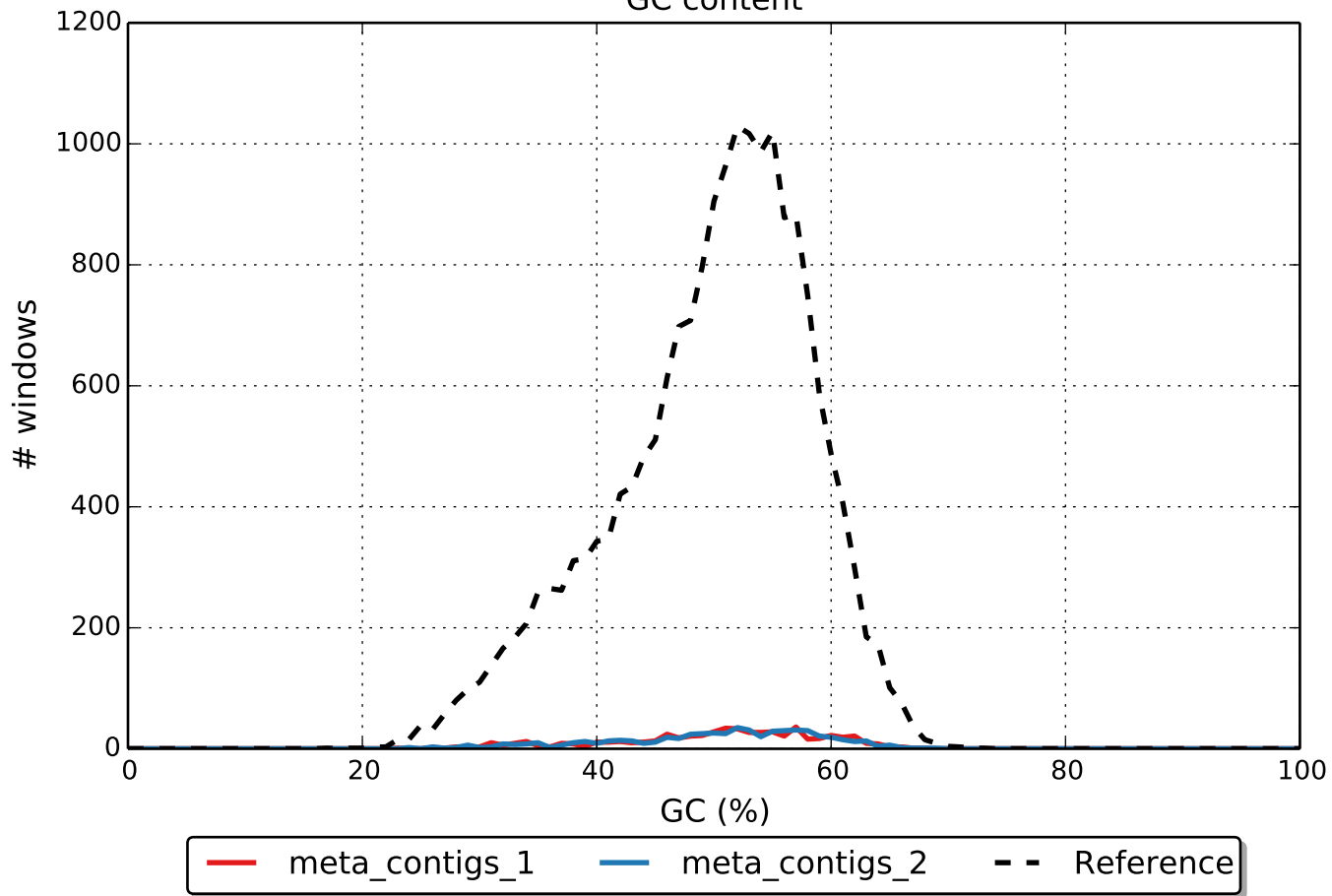
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

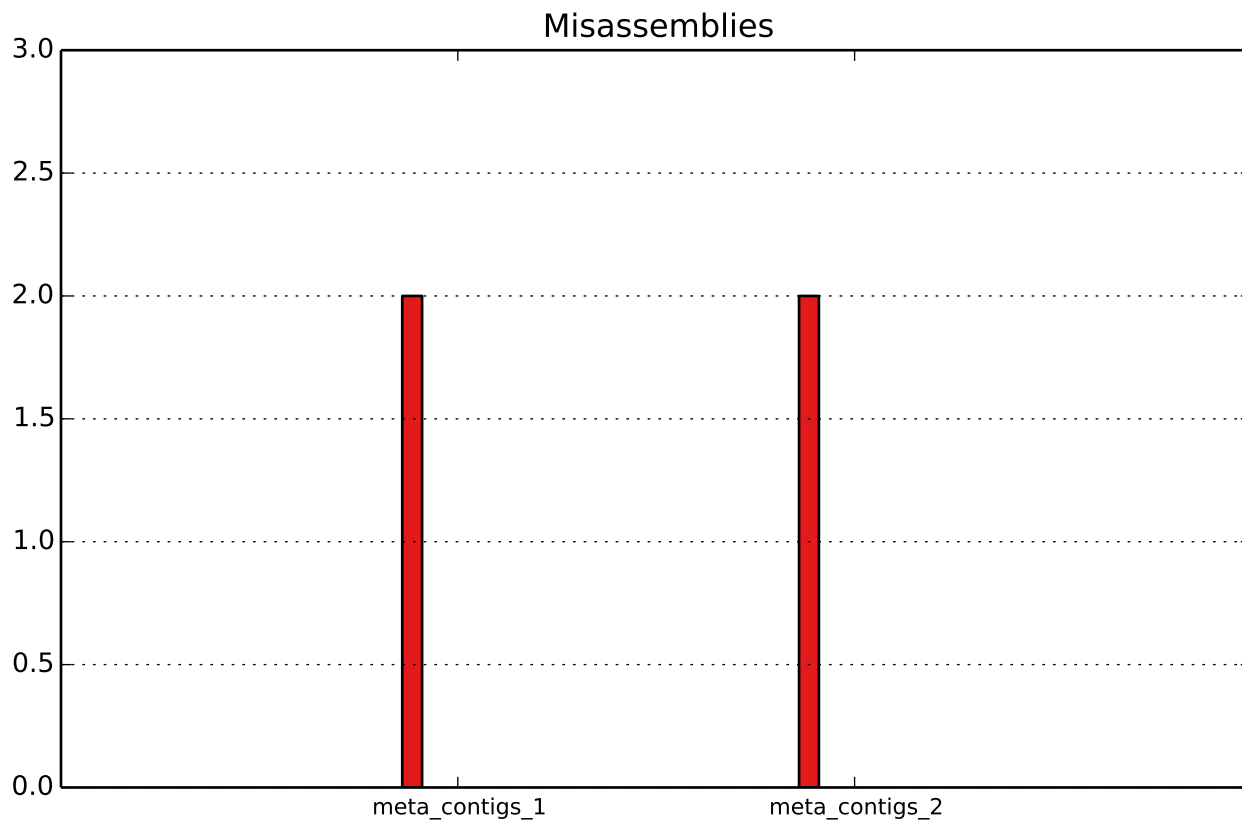






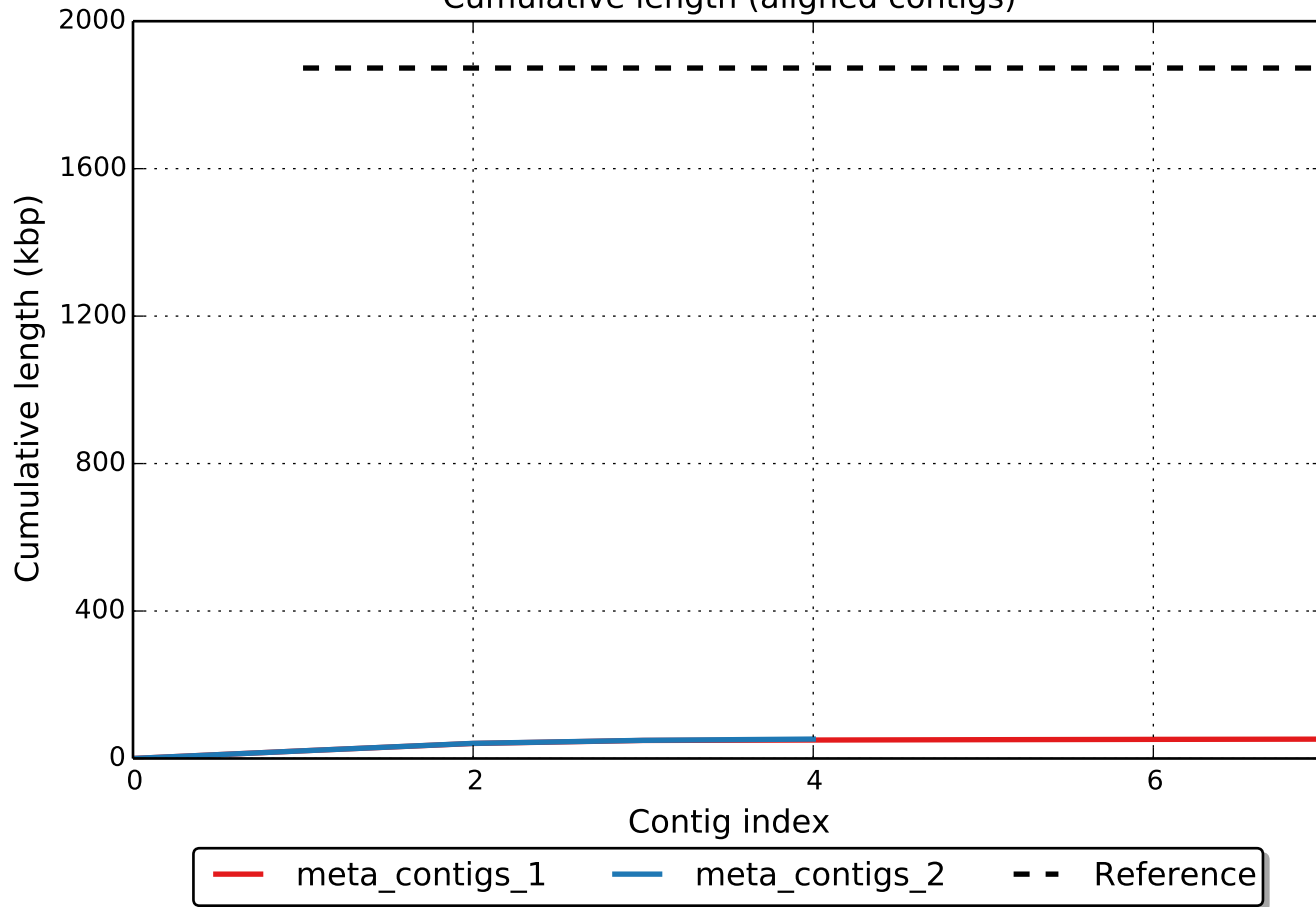
# GC content

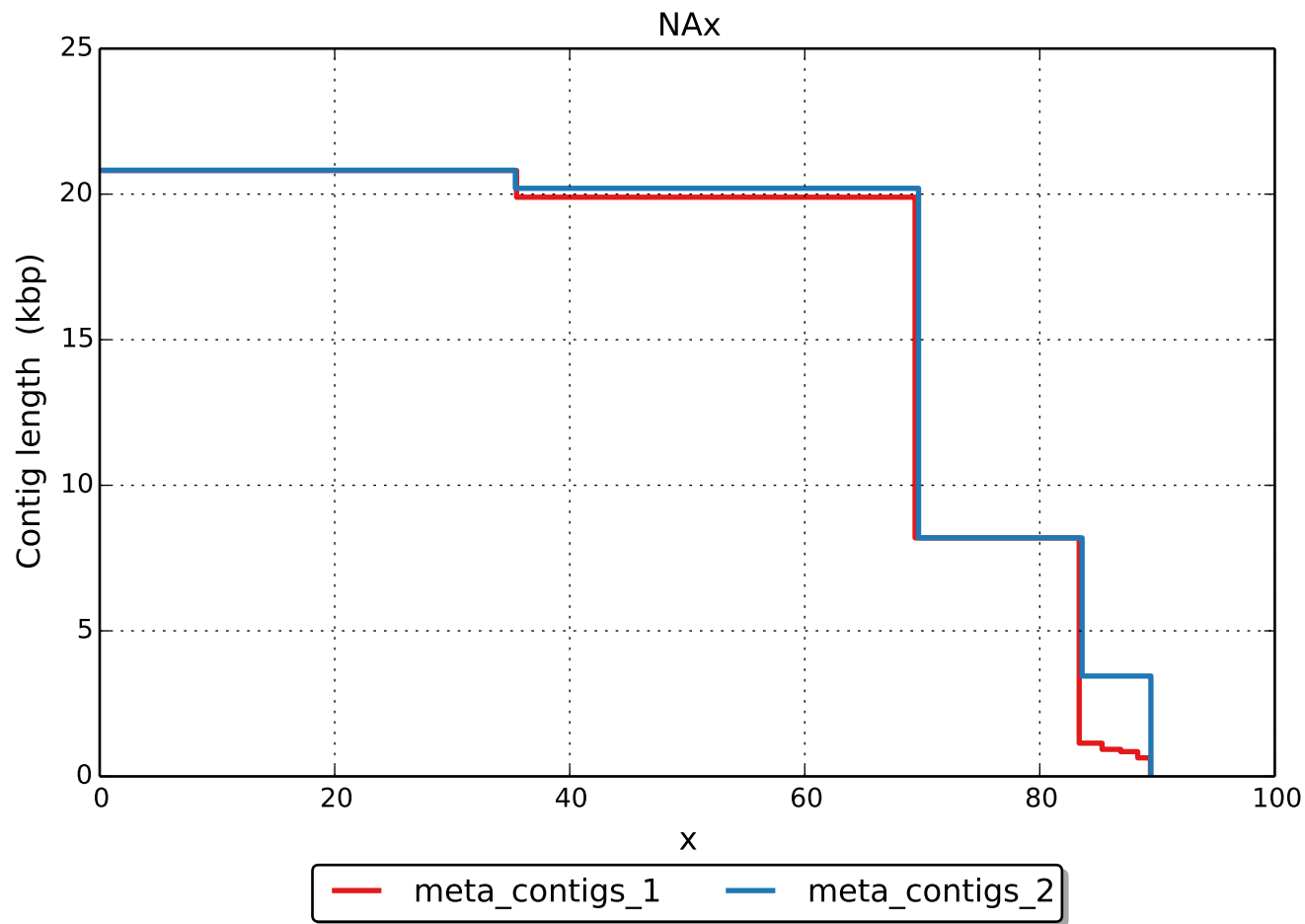






Cumulative length (aligned contigs)





# NGAx

