

## Report

	contigs1	contigs2	contigs3
# contigs ( $\geq 0$ bp)	128	1	305
# contigs ( $\geq 1000$ bp)	4	1	0
# contigs ( $\geq 5000$ bp)	0	1	0
# contigs ( $\geq 10000$ bp)	0	1	0
# contigs ( $\geq 25000$ bp)	0	1	0
# contigs ( $\geq 50000$ bp)	0	1	0
Total length ( $\geq 0$ bp)	49819	100000	56973
Total length ( $\geq 1000$ bp)	5313	100000	0
Total length ( $\geq 5000$ bp)	0	100000	0
Total length ( $\geq 10000$ bp)	0	100000	0
Total length ( $\geq 25000$ bp)	0	100000	0
Total length ( $\geq 50000$ bp)	0	100000	0
# contigs	20	1	11
Largest contig	1737	100000	998
Total length	15923	100000	7243
Reference length	4639675	4639675	4639675
GC (%)	51.21	52.59	50.71
Reference GC (%)	50.79	50.79	50.79
N50	718	100000	632
N75	635	100000	542
L50	8	1	5
L75	13	1	8
# misassemblies	1	0	0
# misassembled contigs	1	0	0
Misassembled contigs length	1084	0	0
# local misassemblies	0	0	0
# unaligned contigs	0 + 0 part	0 + 0 part	0 + 0 part
Unaligned length	0	0	0
Genome fraction (%)	0.343	2.155	0.156
Duplication ratio	1.000	1.000	1.000
# N's per 100 kbp	0.00	0.00	0.00
# mismatches per 100 kbp	31.40	0.00	0.00
# indels per 100 kbp	0.00	0.00	0.00
Largest alignment	1737	100000	998
Total aligned length	15923	100000	7243
NA50	715	100000	632
NGA50	-	-	-
NA75	587	100000	542
LA50	8	1	5
LA75	14	1	8

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

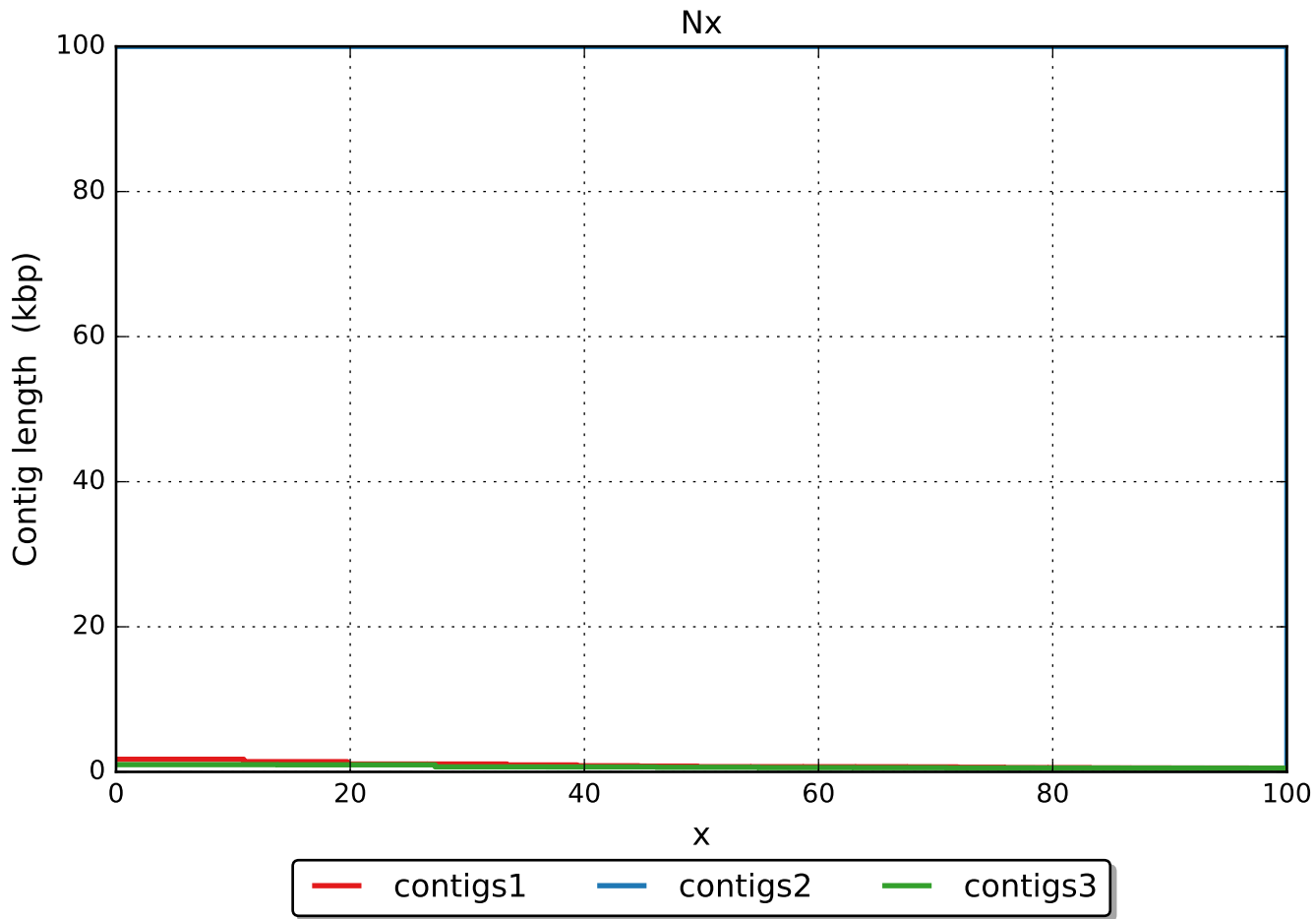
	contigs1	contigs2	contigs3
# misassemblies	1	0	0
# relocations	1	0	0
# translocations	0	0	0
# inversions	0	0	0
# misassembled contigs	1	0	0
Misassembled contigs length	1084	0	0
# local misassemblies	0	0	0
# mismatches	5	0	0
# indels	0	0	0
# short indels	0	0	0
# long indels	0	0	0
Indels length	0	0	0

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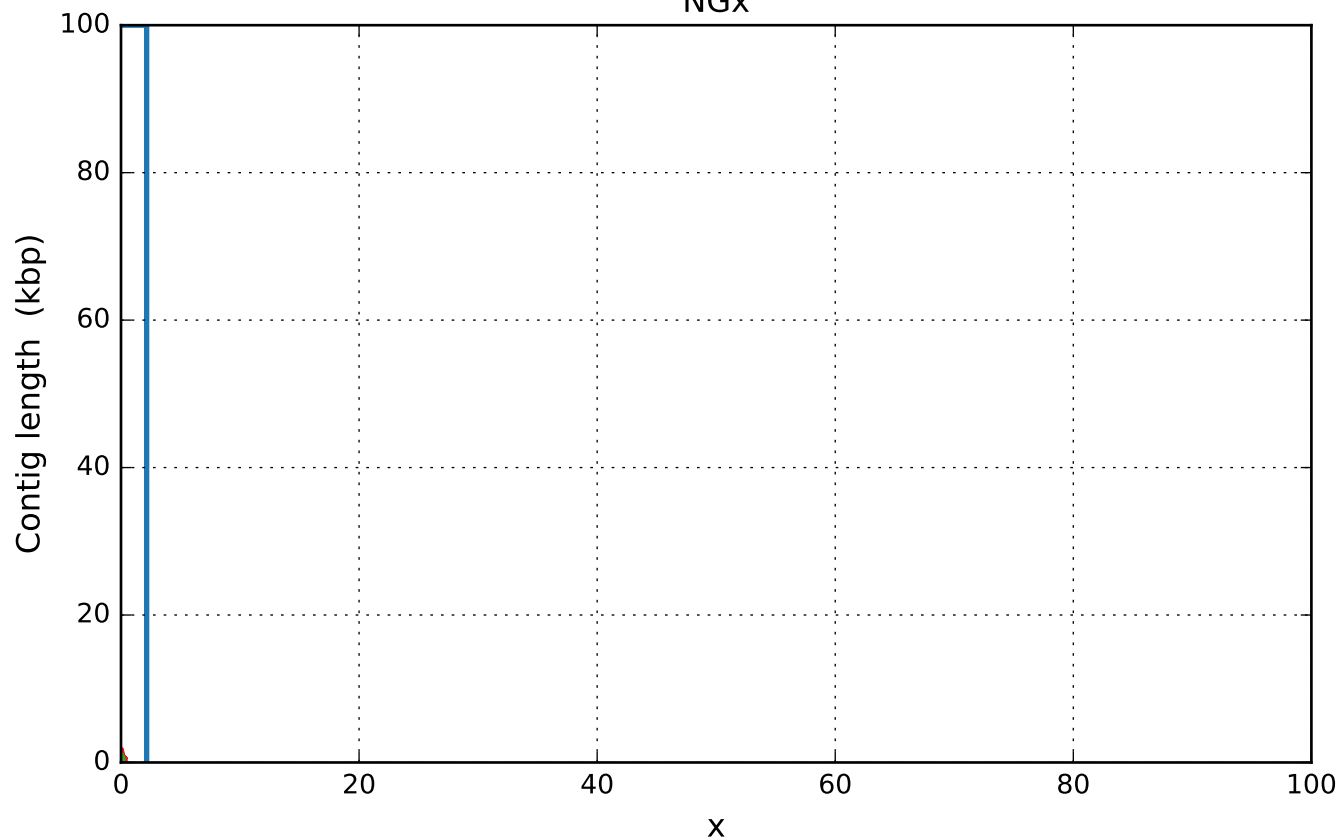
## Unaligned report

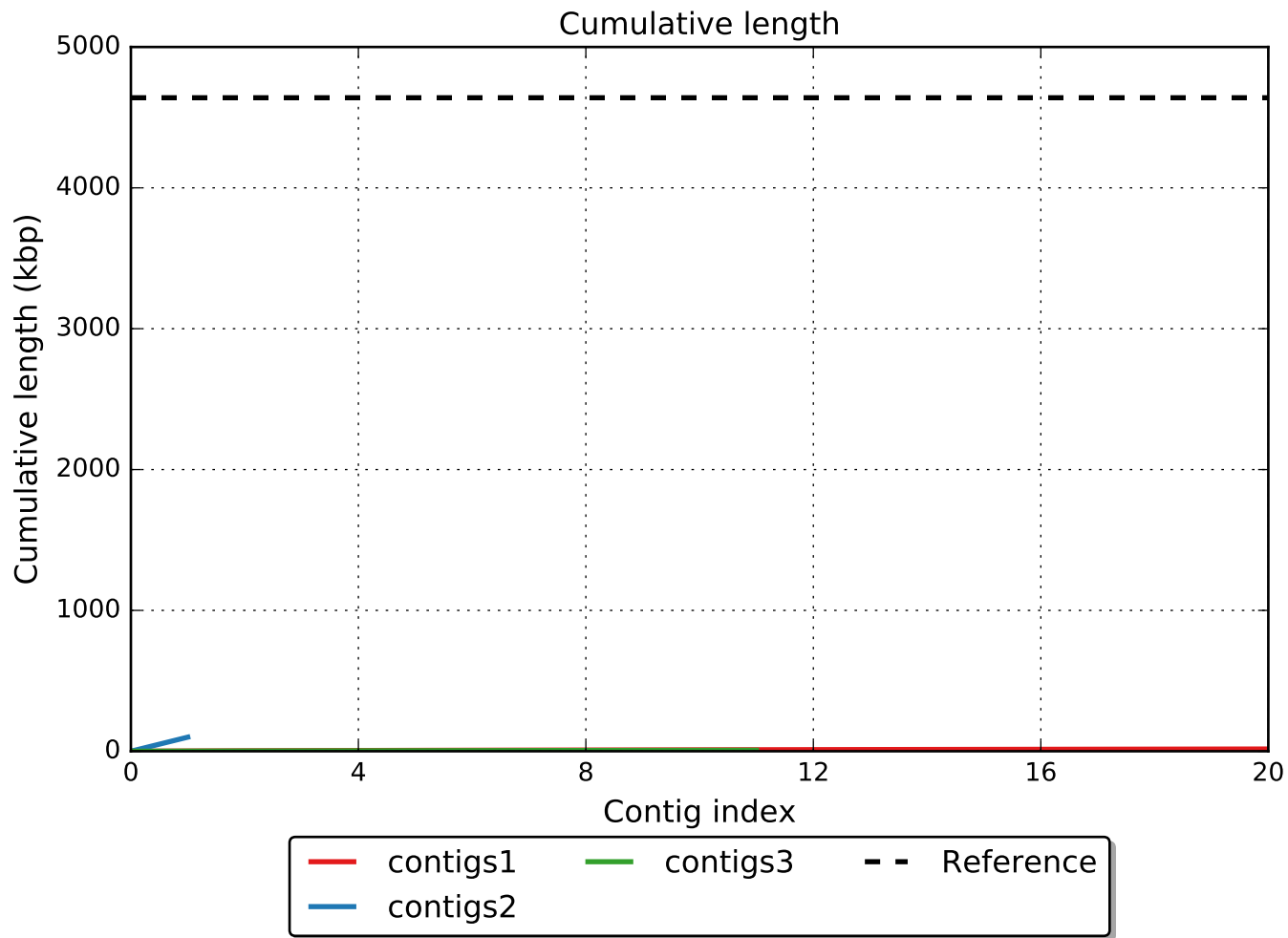
	contigs1	contigs2	contigs3
# fully unaligned contigs	0	0	0
Fully unaligned length	0	0	0
# partially unaligned contigs	0	0	0
# with misassembly	0	0	0
# both parts are significant	0	0	0
Partially unaligned length	0	0	0
# N's	0	0	0

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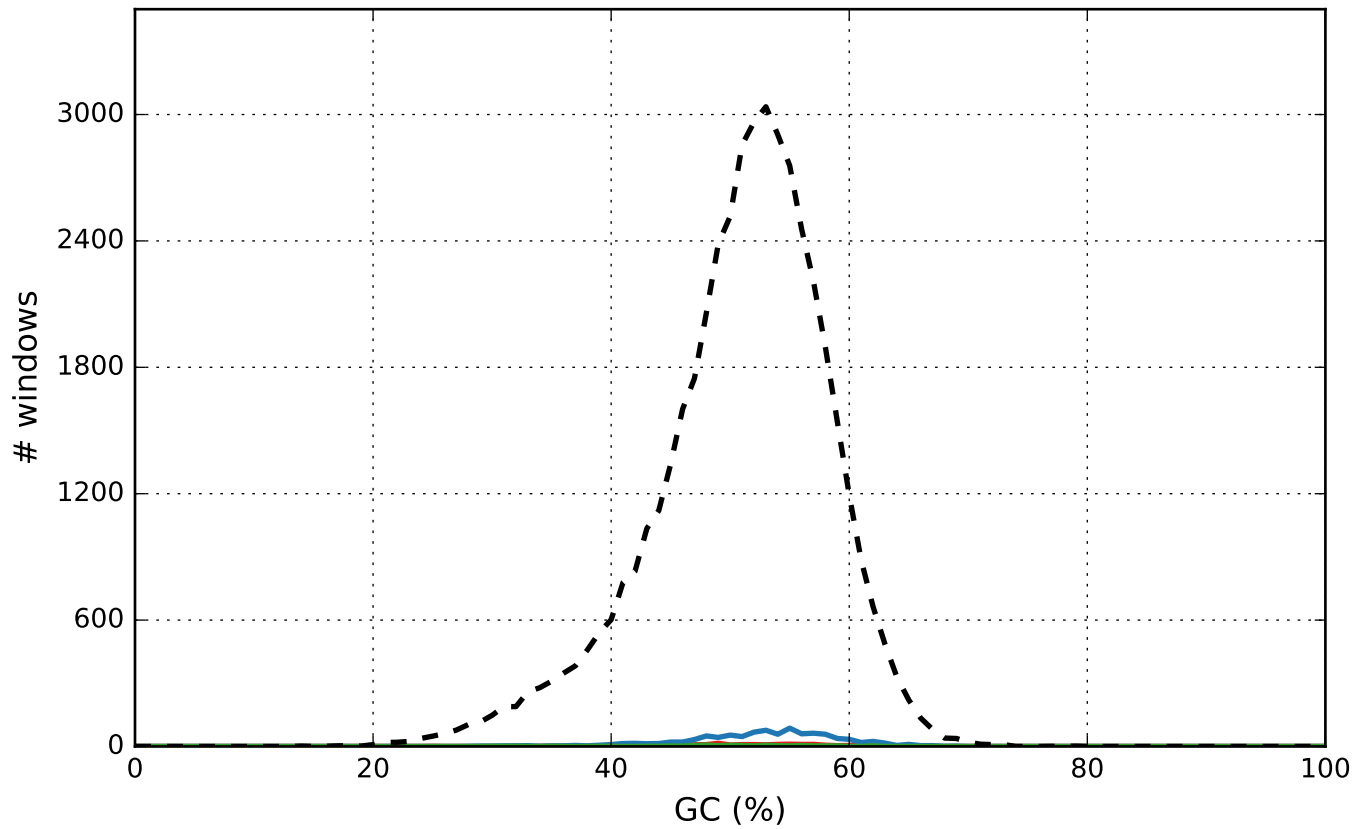


NGx

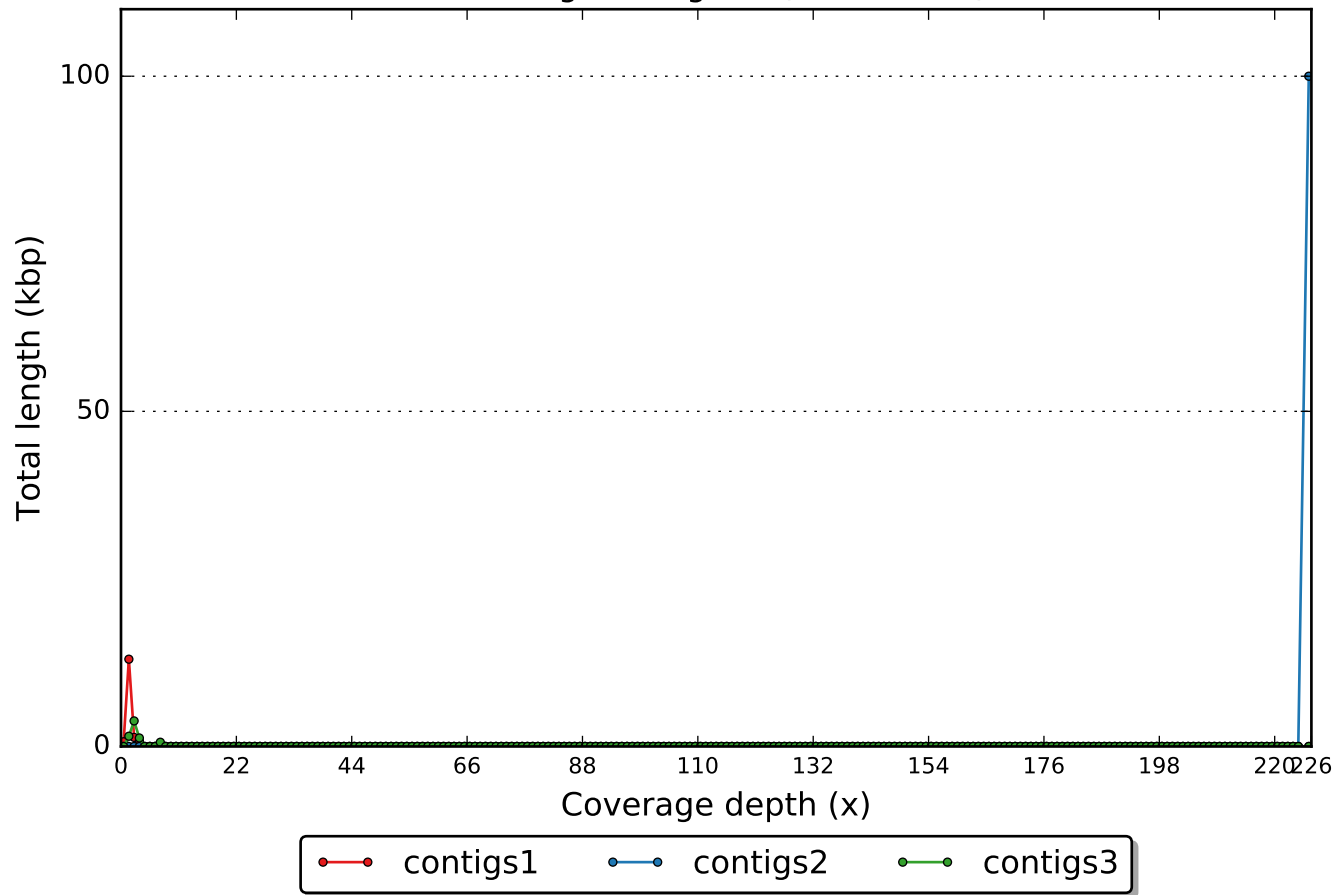




# GC content

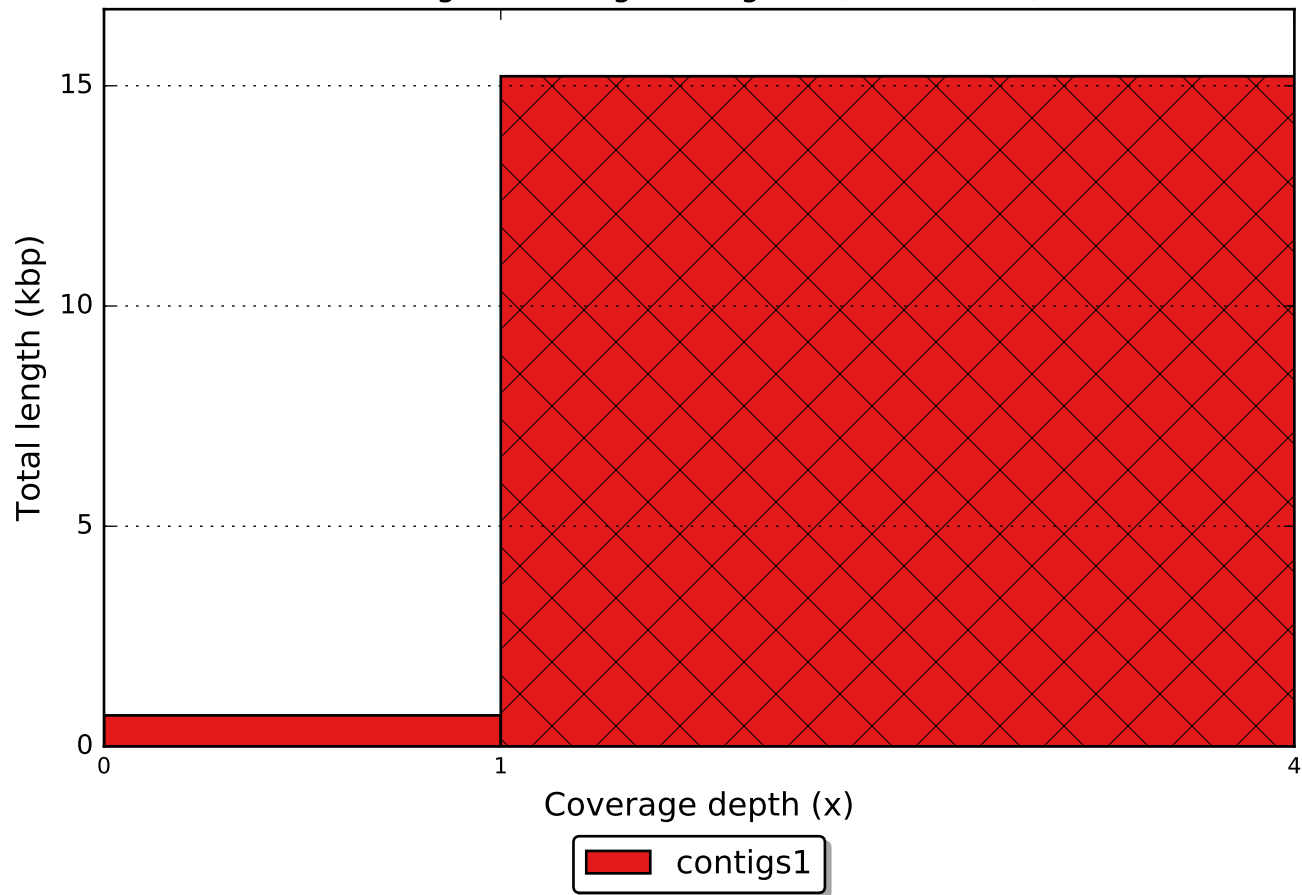


Coverage histogram (bin size: 1x)

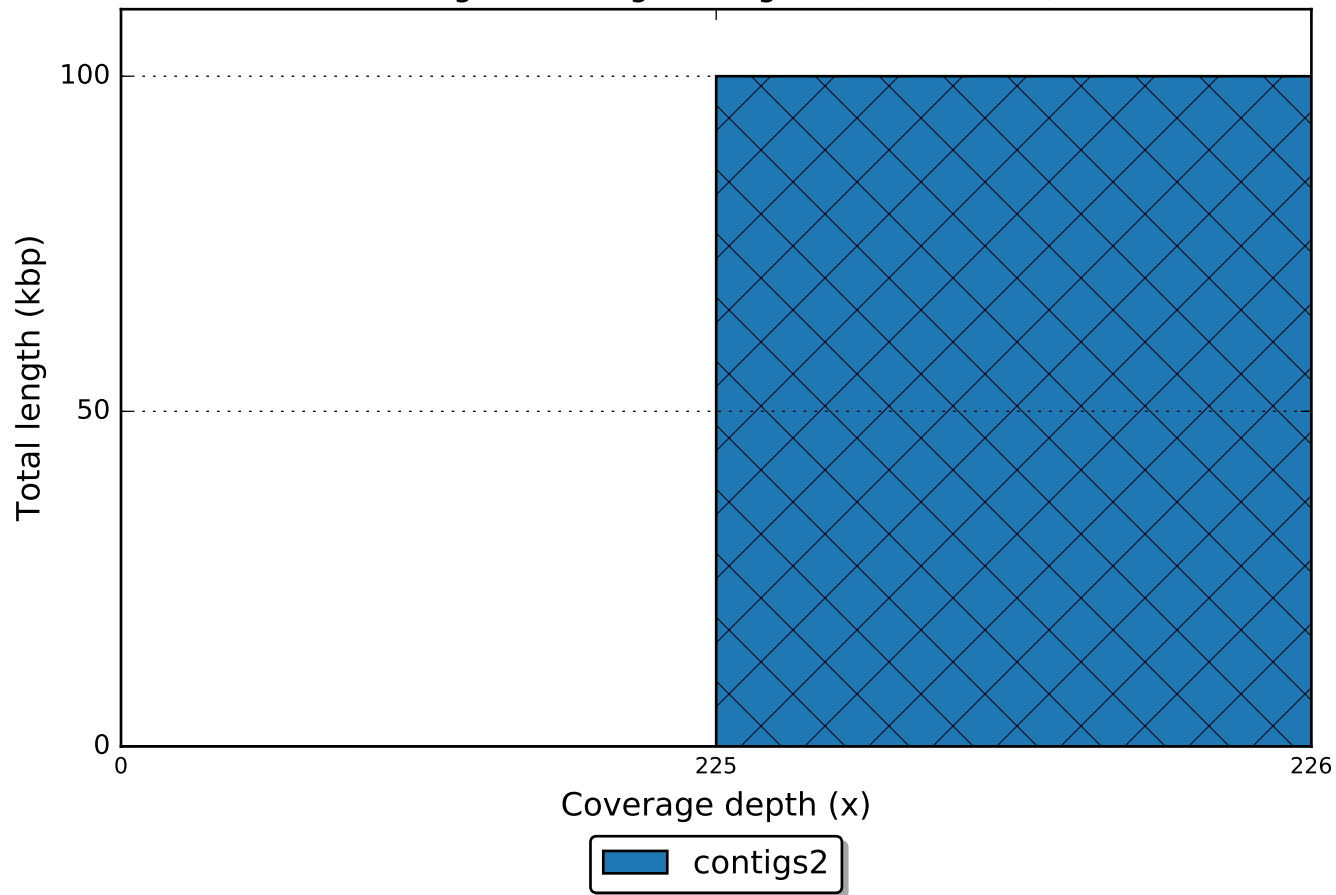




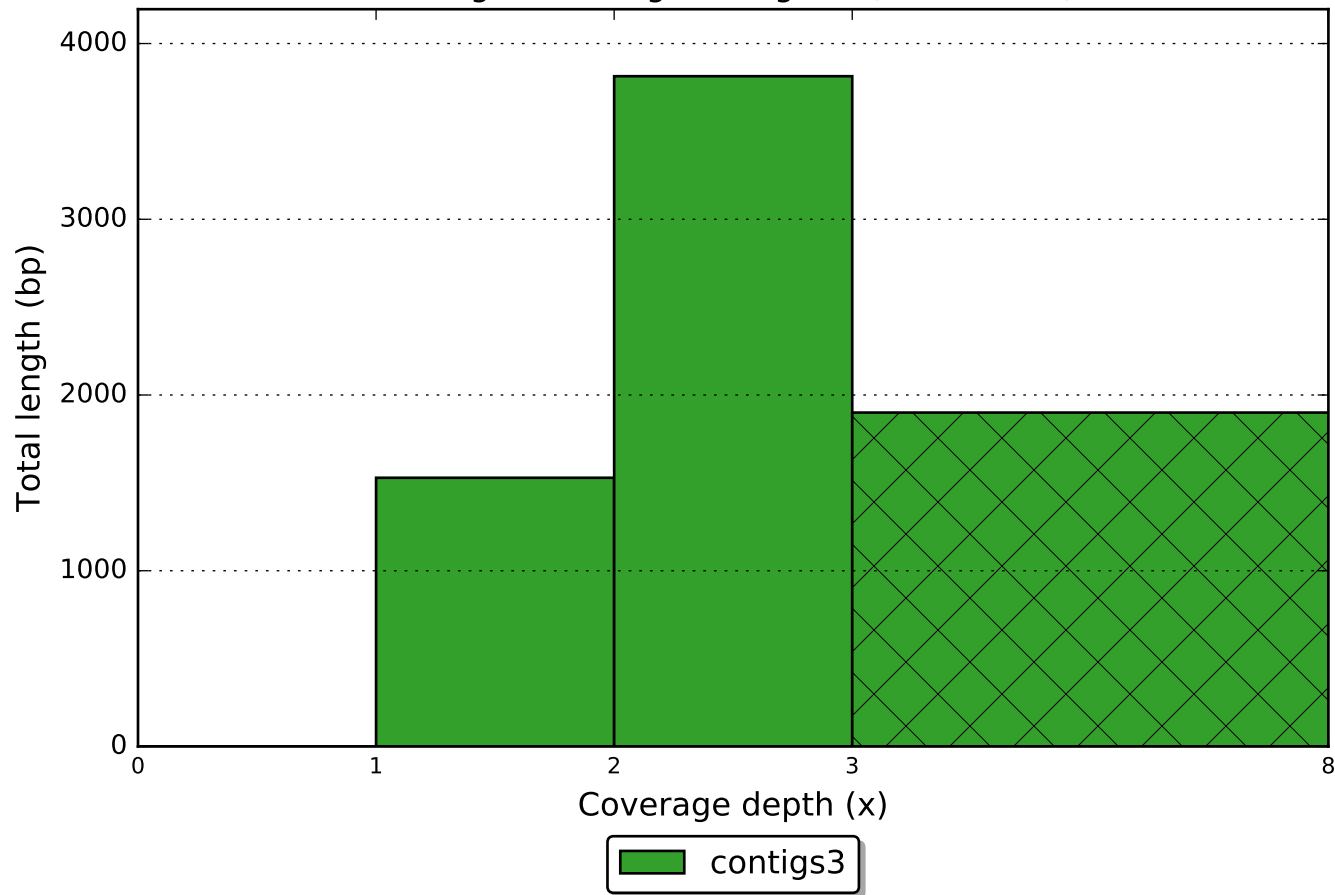
contigs1 coverage histogram (bin size: 1x)

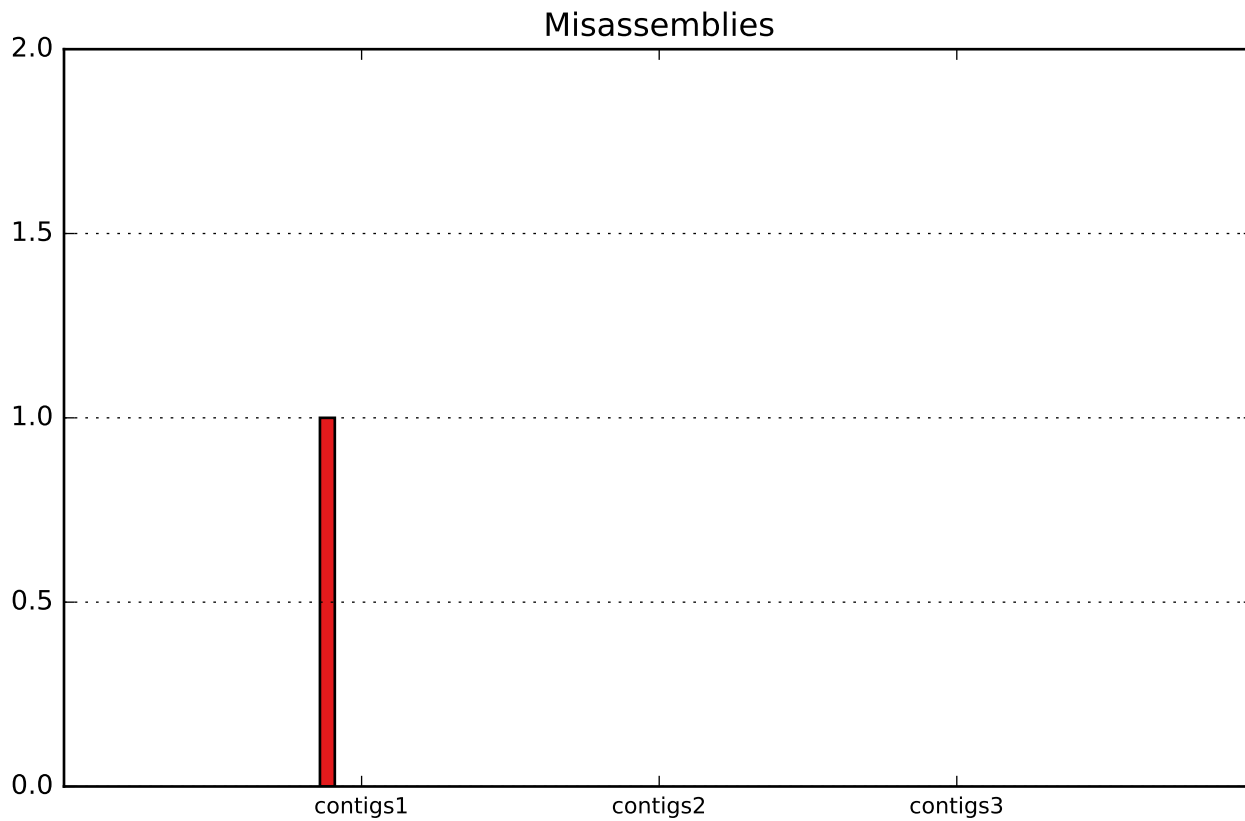


contigs2 coverage histogram (bin size: 1x)

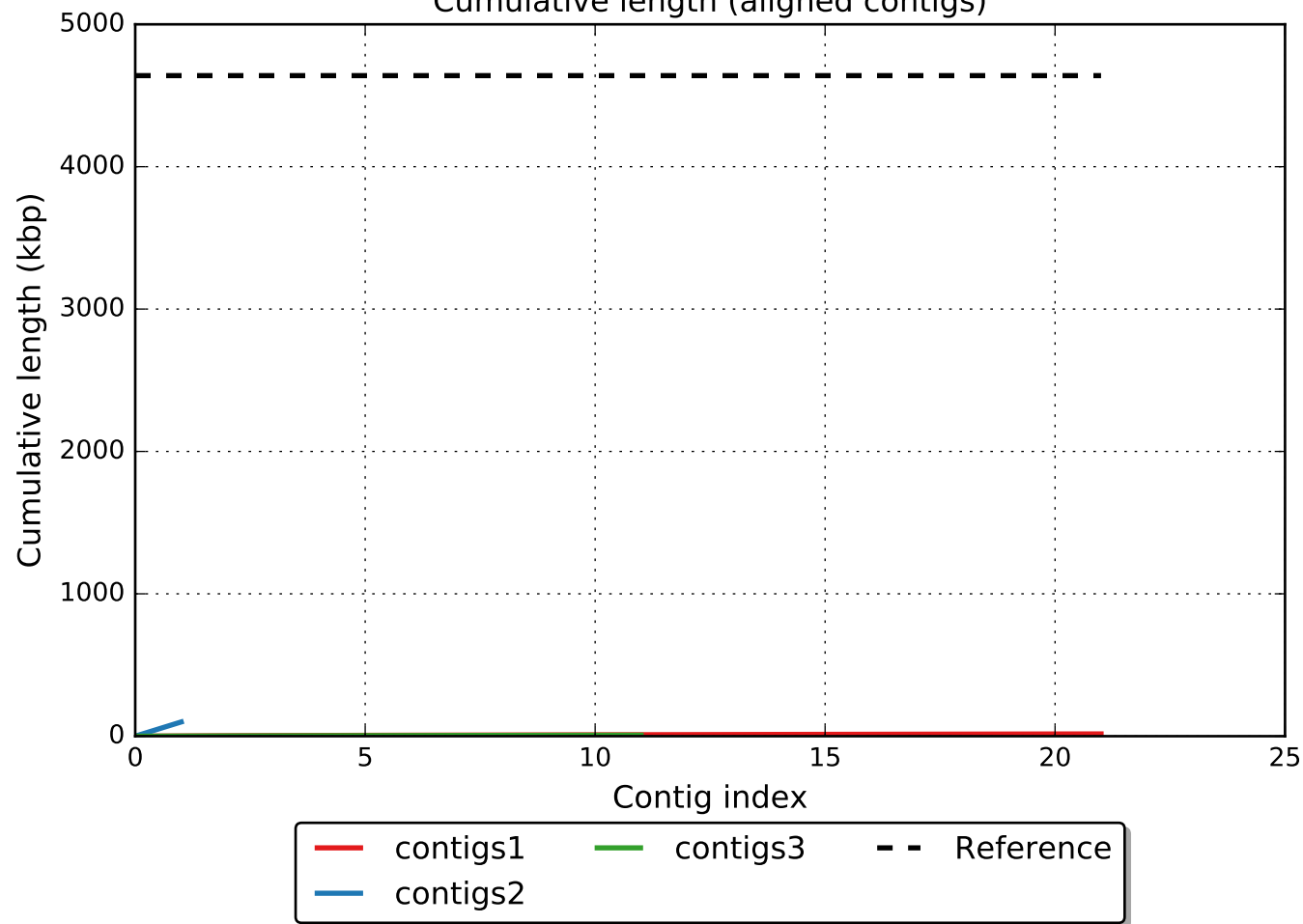


contigs3 coverage histogram (bin size: 1x)

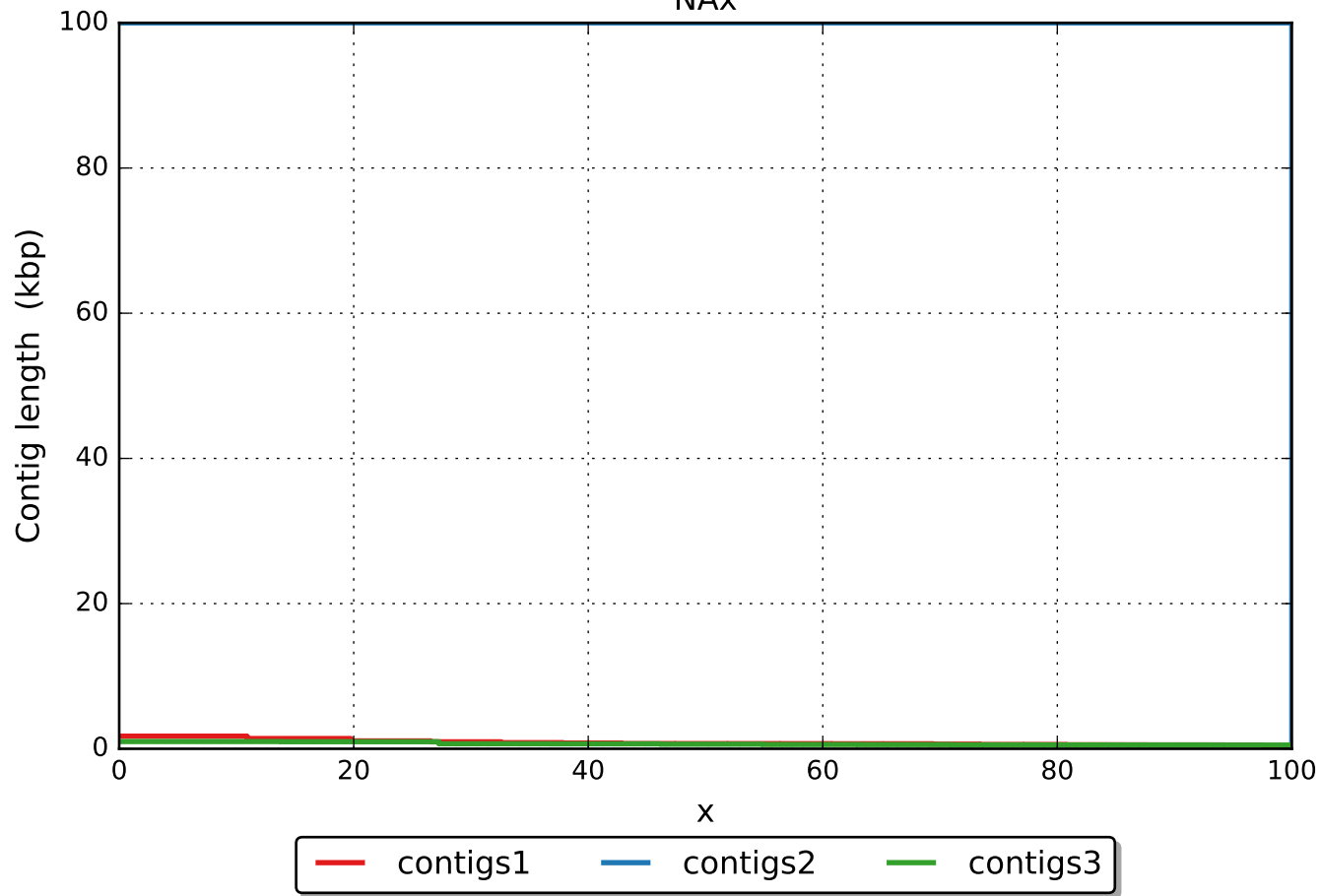




Cumulative length (aligned contigs)



NAx



NGAx

