

# Report

	meta_contigs_1	meta_contigs_2
# contigs ( $\geq 0$ bp)	47	35
# contigs ( $\geq 1000$ bp)	11	7
# contigs ( $\geq 5000$ bp)	5	6
# contigs ( $\geq 10000$ bp)	5	5
# contigs ( $\geq 25000$ bp)	3	3
# contigs ( $\geq 50000$ bp)	1	1
Total length ( $\geq 0$ bp)	187773	179095
Total length ( $\geq 1000$ bp)	173623	169301
Total length ( $\geq 5000$ bp)	161370	165854
Total length ( $\geq 10000$ bp)	161370	158866
Total length ( $\geq 25000$ bp)	132733	132339
Total length ( $\geq 50000$ bp)	55106	55421
# contigs	20	12
Largest contig	55106	55421
Total length	180875	173140
Reference length	21154421	21154421
N50	49658	49658
N75	17535	27260
L50	2	2
L75	4	3
# misassemblies	2	2
# misassembled contigs	1	1
Misassembled contigs length	55106	55421
# local misassemblies	1	1
# unaligned contigs	2 + 0 part	1 + 0 part
Unaligned length	2730	885
Genome fraction (%)	1.179	0.888
Duplication ratio	1.094	1.004
# N's per 100 kbp	7.74	0.00
# mismatches per 100 kbp	392.45	382.74
# indels per 100 kbp	38.48	31.41
Largest alignment	49639	49639
NA50	20813	20822
NA75	17534	16099
LA50	3	3
LA75	5	5

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

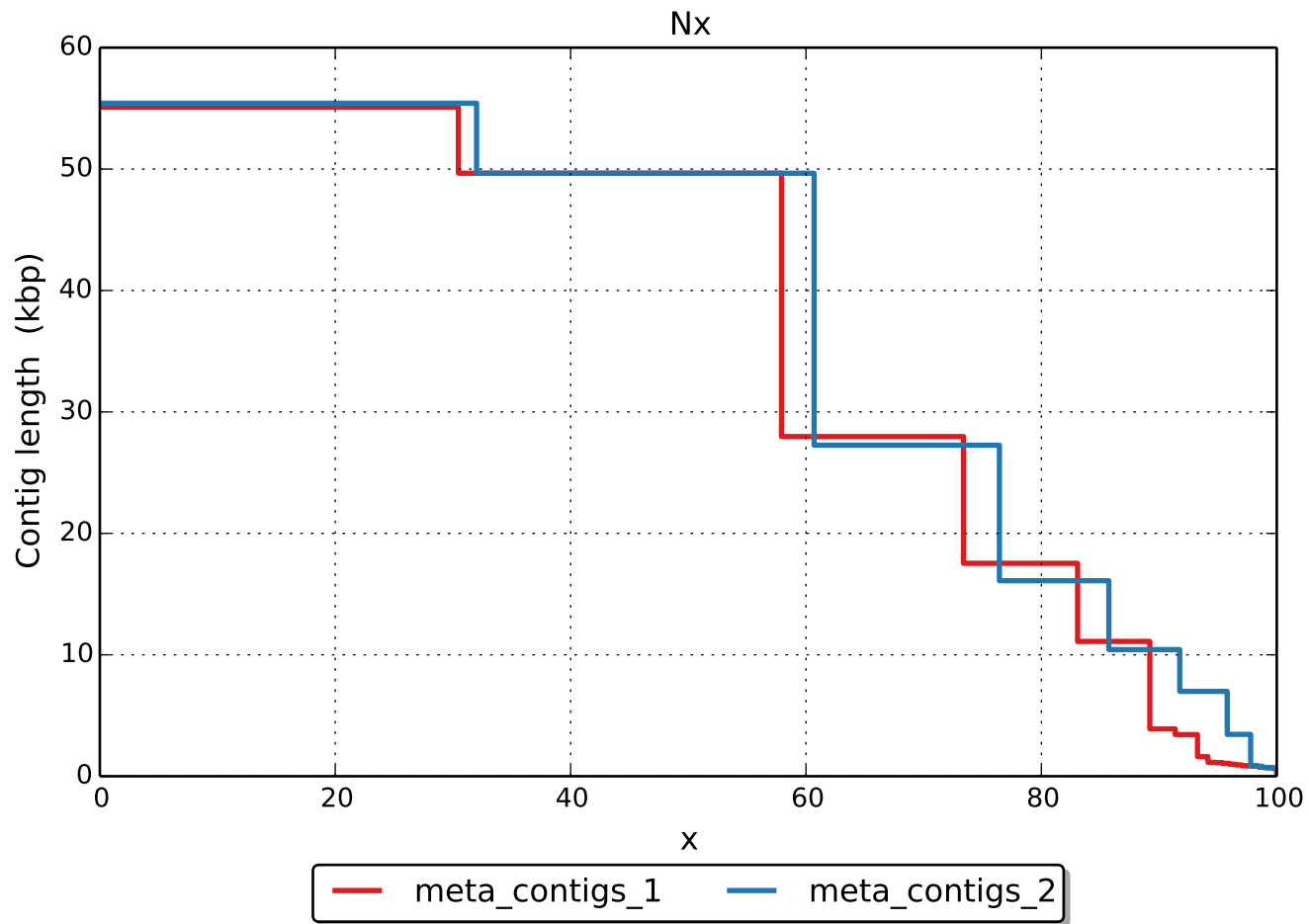
	meta_contigs_1	meta_contigs_2
# misassemblies	2	2
# relocations	1	1
# translocations	0	0
# inversions	0	0
# interspecies translocations	1	1
# possibly misassembled contigs	0	0
# misassembled contigs	1	1
Misassembled contigs length	55106	55421
# local misassemblies	1	1
# mismatches	979	719
# indels	96	59
# short indels	92	55
# long indels	4	4
Indels length	171	119

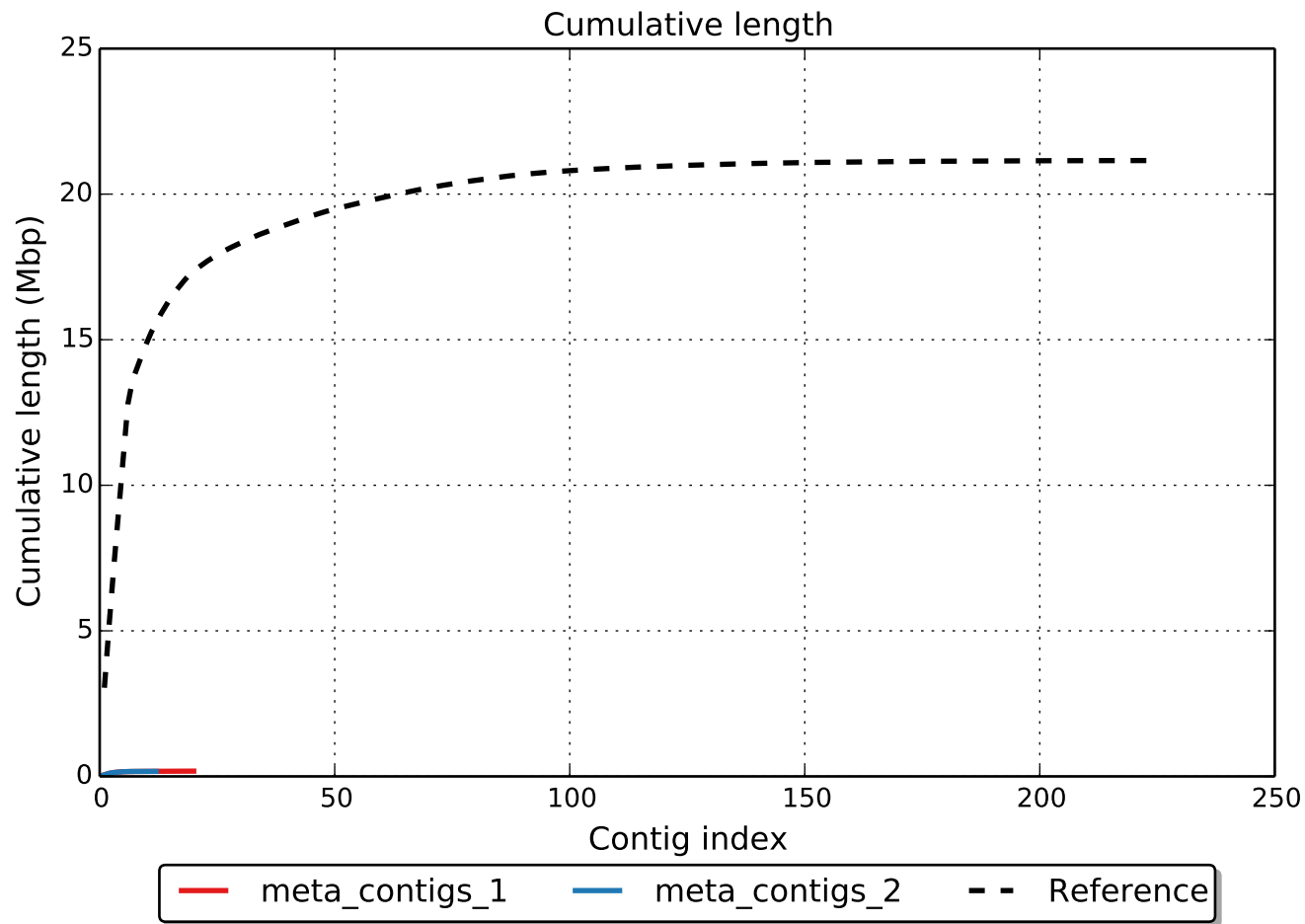
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## Unaligned report

	meta_contigs_1	meta_contigs_2
# fully unaligned contigs	2	1
Fully unaligned length	2730	885
# partially unaligned contigs	0	0
# with misassembly	0	0
# both parts are significant	0	0
Partially unaligned length	0	0
# N's	14	0

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# Misassemblies

