

Report

	meta_contigs_1	meta_contigs_2
# contigs (≥ 0 bp)	47	35
# contigs (≥ 1000 bp)	11	7
# contigs (≥ 5000 bp)	5	6
# contigs (≥ 10000 bp)	5	5
# contigs (≥ 25000 bp)	3	3
# contigs (≥ 50000 bp)	1	1
Total length (≥ 0 bp)	187773	179095
Total length (≥ 1000 bp)	173623	169301
Total length (≥ 5000 bp)	161370	165854
Total length (≥ 10000 bp)	161370	158866
Total length (≥ 25000 bp)	132733	132339
Total length (≥ 50000 bp)	55106	55421
# contigs	20	12
Largest contig	55106	55421
Total length	180875	173140
Reference length	179997	179997
N50	49658	49658
N75	17535	27260
L50	2	2
L75	4	3
# misassemblies	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	0	0
# unaligned contigs	2 + 0 part	1 + 0 part
Unaligned length	2730	885
Genome fraction (%)	96.042	96.000
Duplication ratio	1.030	1.002
# N's per 100 kbp	7.74	0.00
# mismatches per 100 kbp	32.97	27.20
# indels per 100 kbp	1.16	0.00
Largest alignment	55106	55421
NA50	49658	49658
NA75	17534	27260
LA50	2	2
LA75	4	3

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

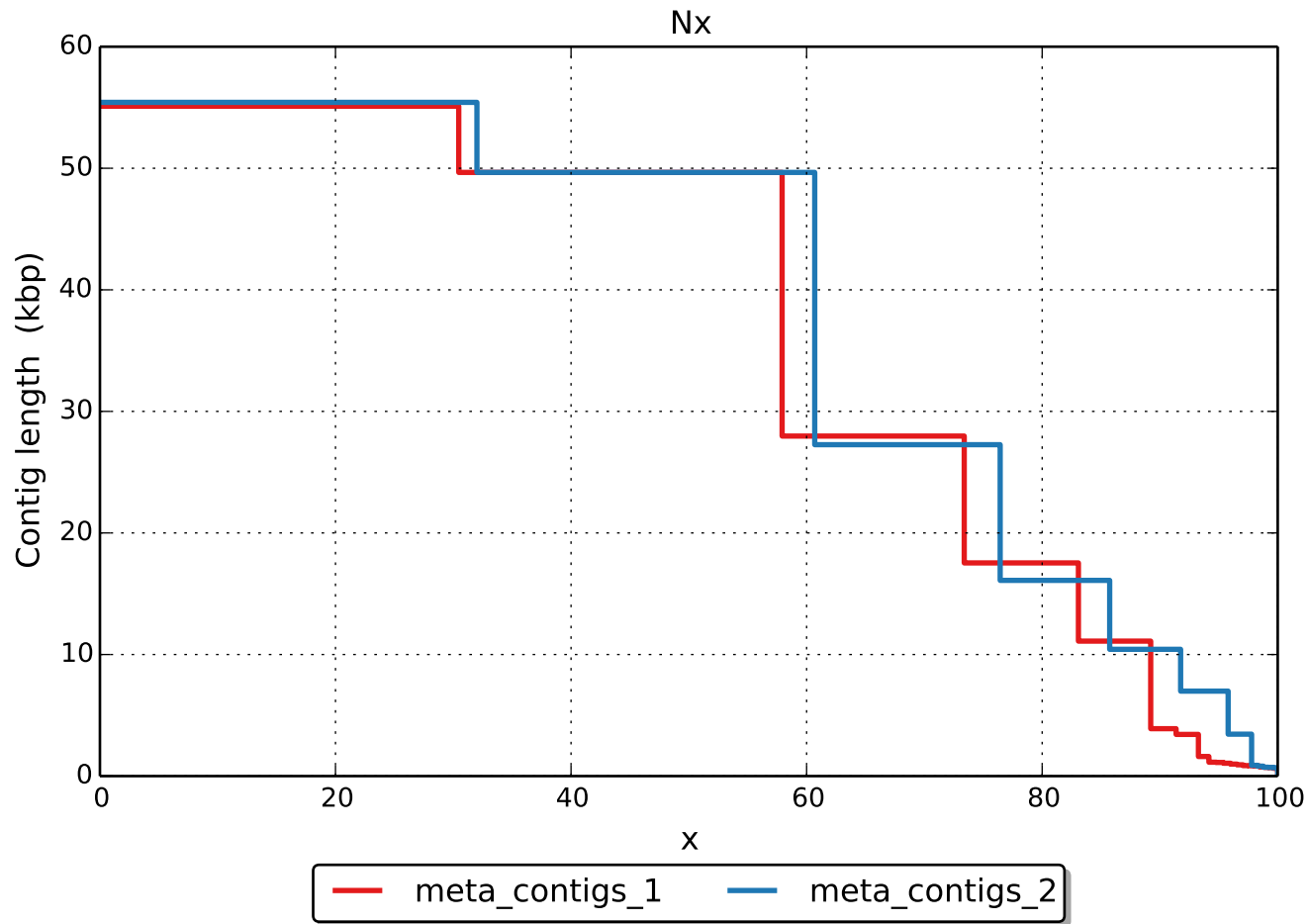
	meta_contigs_1	meta_contigs_2
# misassemblies	0	0
# relocations	0	0
# translocations	0	0
# inversions	0	0
# interspecies translocations	0	0
# possibly misassembled contigs	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	0	0
# mismatches	57	47
# indels	2	0
# short indels	2	0
# long indels	0	0
Indels length	2	0

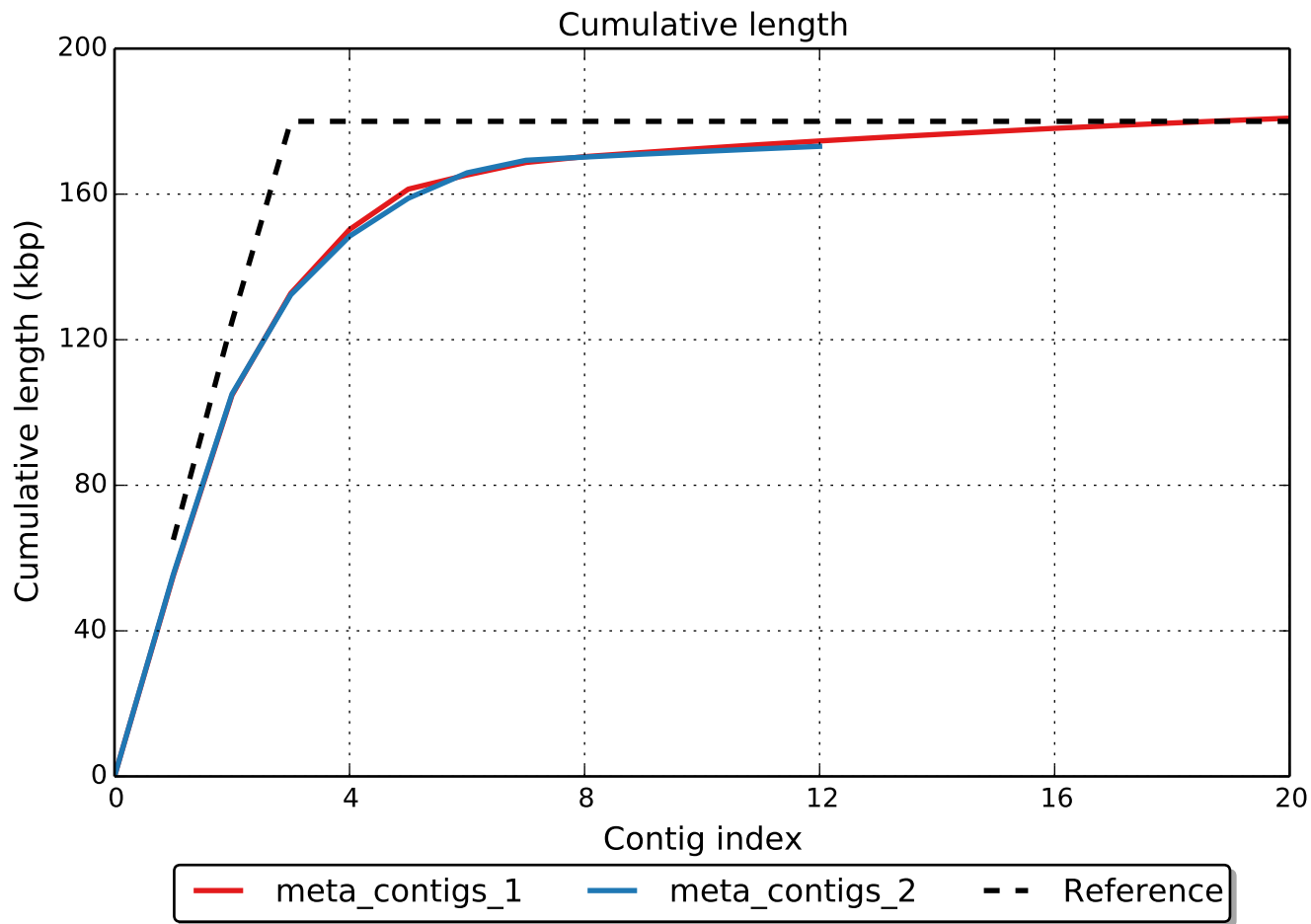
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Unaligned report

	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

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

