

Report

	contigs
# contigs (≥ 0 bp)	1019
# contigs (≥ 1000 bp)	349
# contigs (≥ 5000 bp)	238
# contigs (≥ 10000 bp)	157
# contigs (≥ 25000 bp)	54
# contigs (≥ 50000 bp)	12
Total length (≥ 0 bp)	4980951
Total length (≥ 1000 bp)	4750539
Total length (≥ 5000 bp)	4446394
Total length (≥ 10000 bp)	3855251
Total length (≥ 25000 bp)	2302653
Total length (≥ 50000 bp)	862603
# contigs	385
Largest contig	119434
Total length	4773660
Reference length	9283304
N50	23337
N75	11845
L50	58
L75	133
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	122783
# local misassemblies	4
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	85.247
Duplication ratio	1.031
# N's per 100 kbp	0.00
# mismatches per 100 kbp	903.88
# indels per 100 kbp	0.57
Largest alignment	119434
NA50	23315
NA75	11845
LA50	59
LA75	134

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

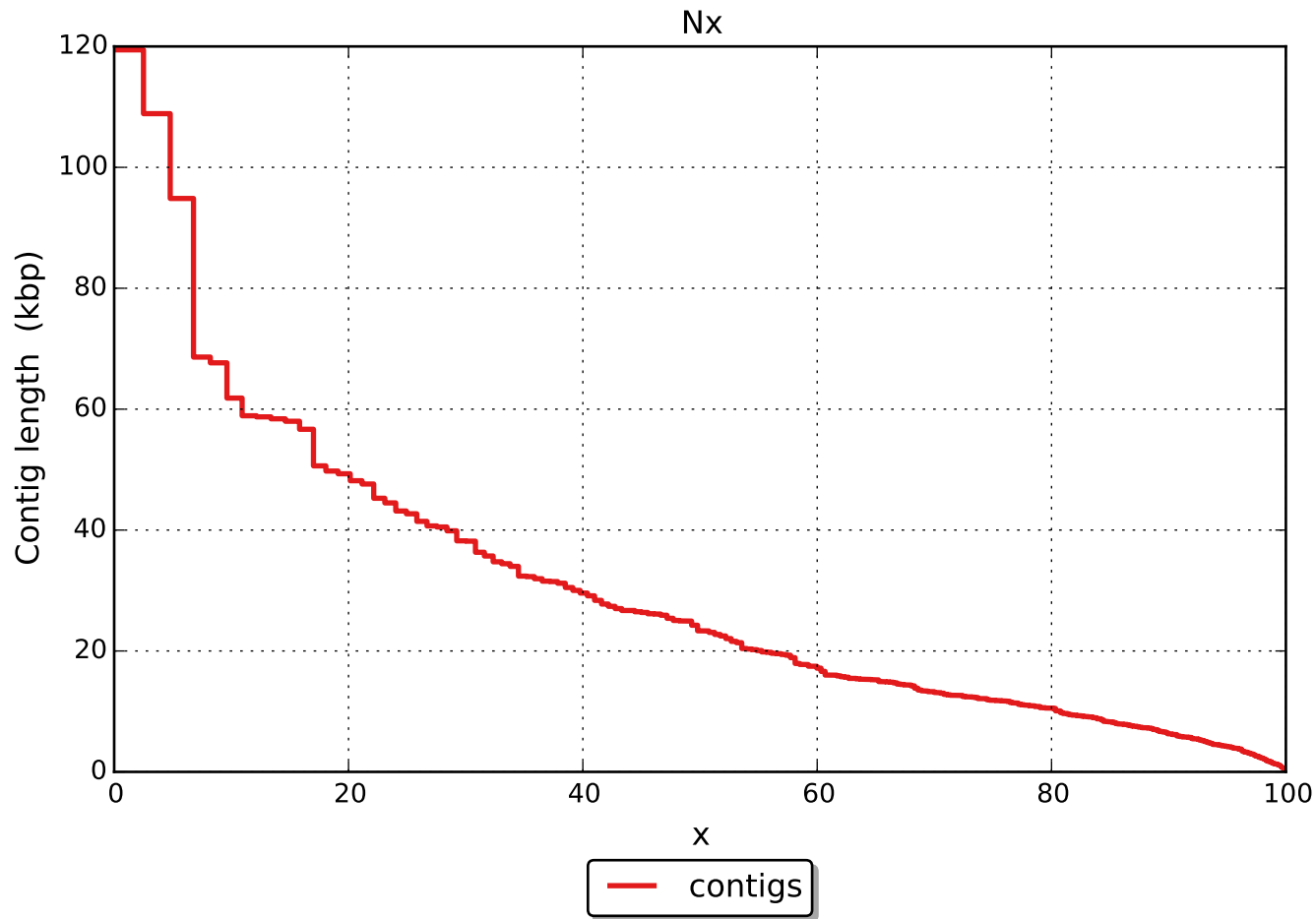
	contigs
# misassemblies	3
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	3
# possibly misassembled contigs	0
# misassembled contigs	3
Misassembled contigs length	122783
# local misassemblies	4
# mismatches	71531
# indels	45
# short indels	45
# long indels	0
Indels length	58

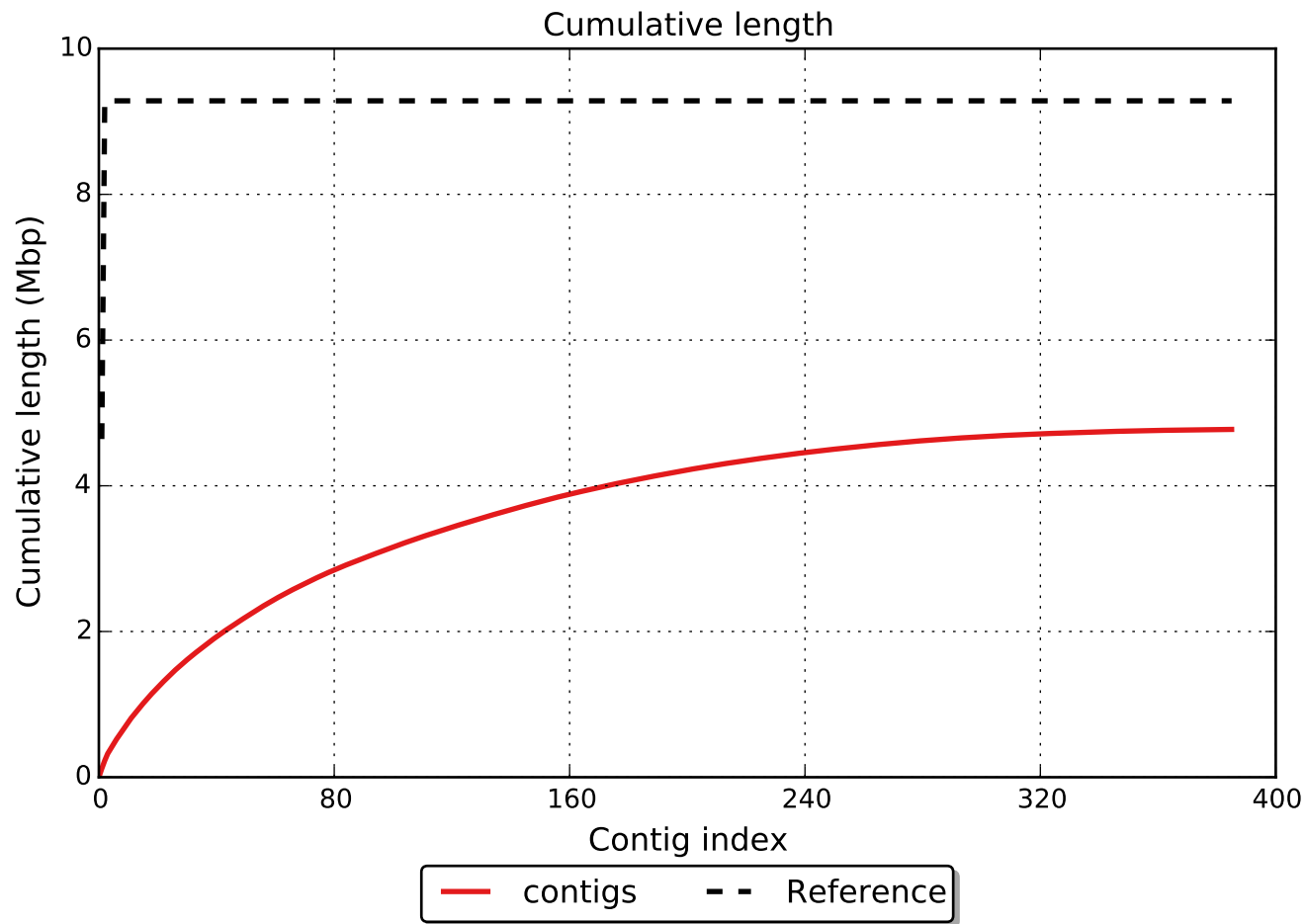
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

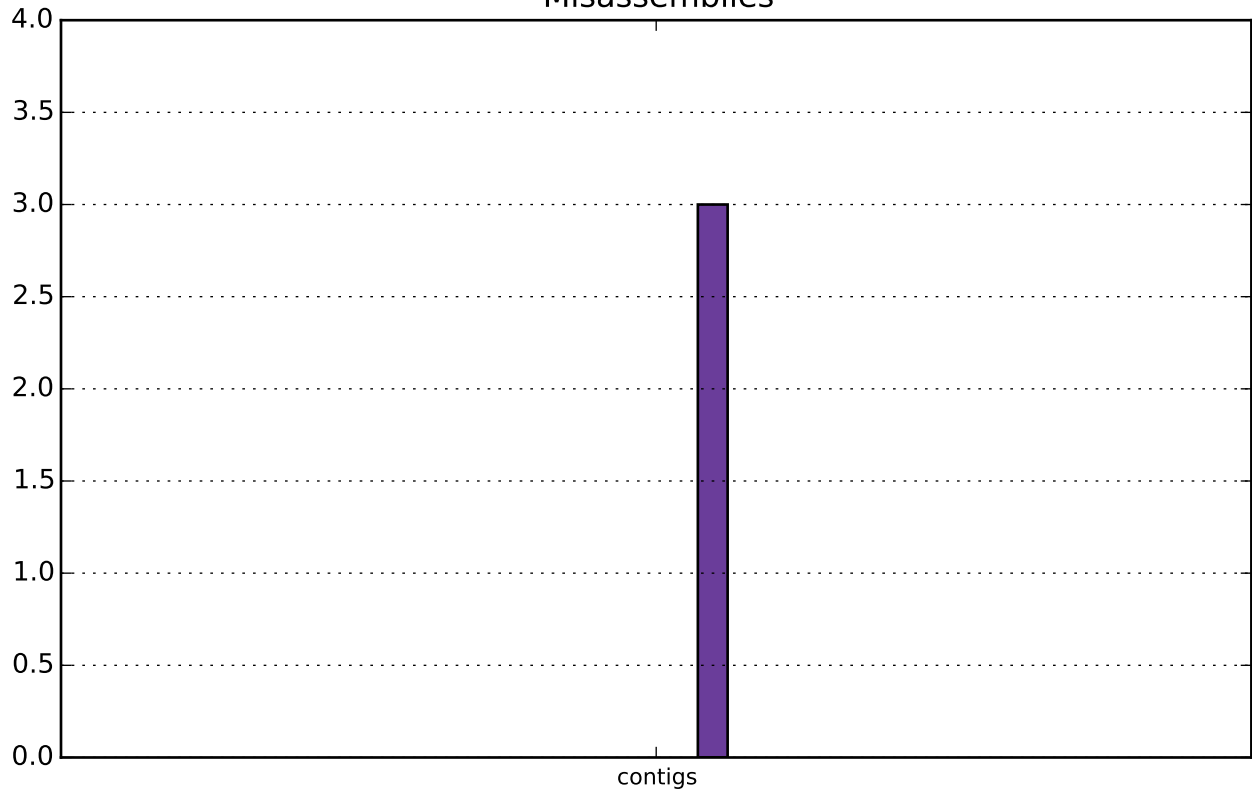
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0


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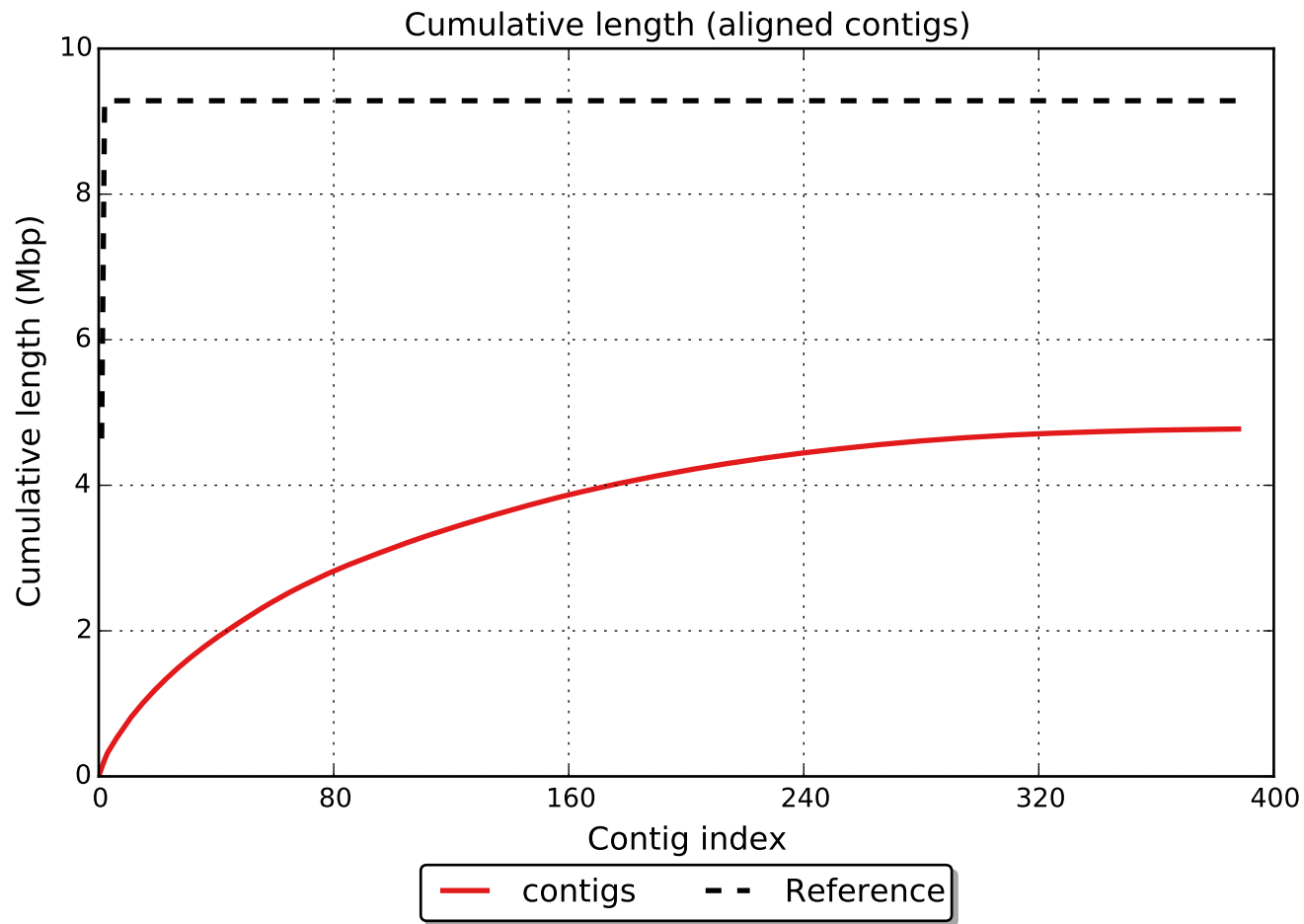




Misassemblies



 # interspecies translocations



NAx

