

Report

	contigs
# contigs (≥ 0 bp)	141
# contigs (≥ 1000 bp)	83
# contigs (≥ 5000 bp)	65
# contigs (≥ 10000 bp)	62
# contigs (≥ 25000 bp)	55
# contigs (≥ 50000 bp)	42
Total length (≥ 0 bp)	9160811
Total length (≥ 1000 bp)	9137739
Total length (≥ 5000 bp)	9098010
Total length (≥ 10000 bp)	9072776
Total length (≥ 25000 bp)	8963163
Total length (≥ 50000 bp)	8532095
# contigs	100
Largest contig	663492
Total length	9151282
Reference length	9283304
N50	263950
N75	149242
L50	12
L75	24
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	478751
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.502
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	160.16
# indels per 100 kbp	0.51
Largest alignment	663492
NA50	227737
NA75	149242
LA50	13
LA75	25

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	1
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	478751
# local misassemblies	2
# mismatches	14645
# indels	47
# short indels	46
# long indels	1
Indels length	58

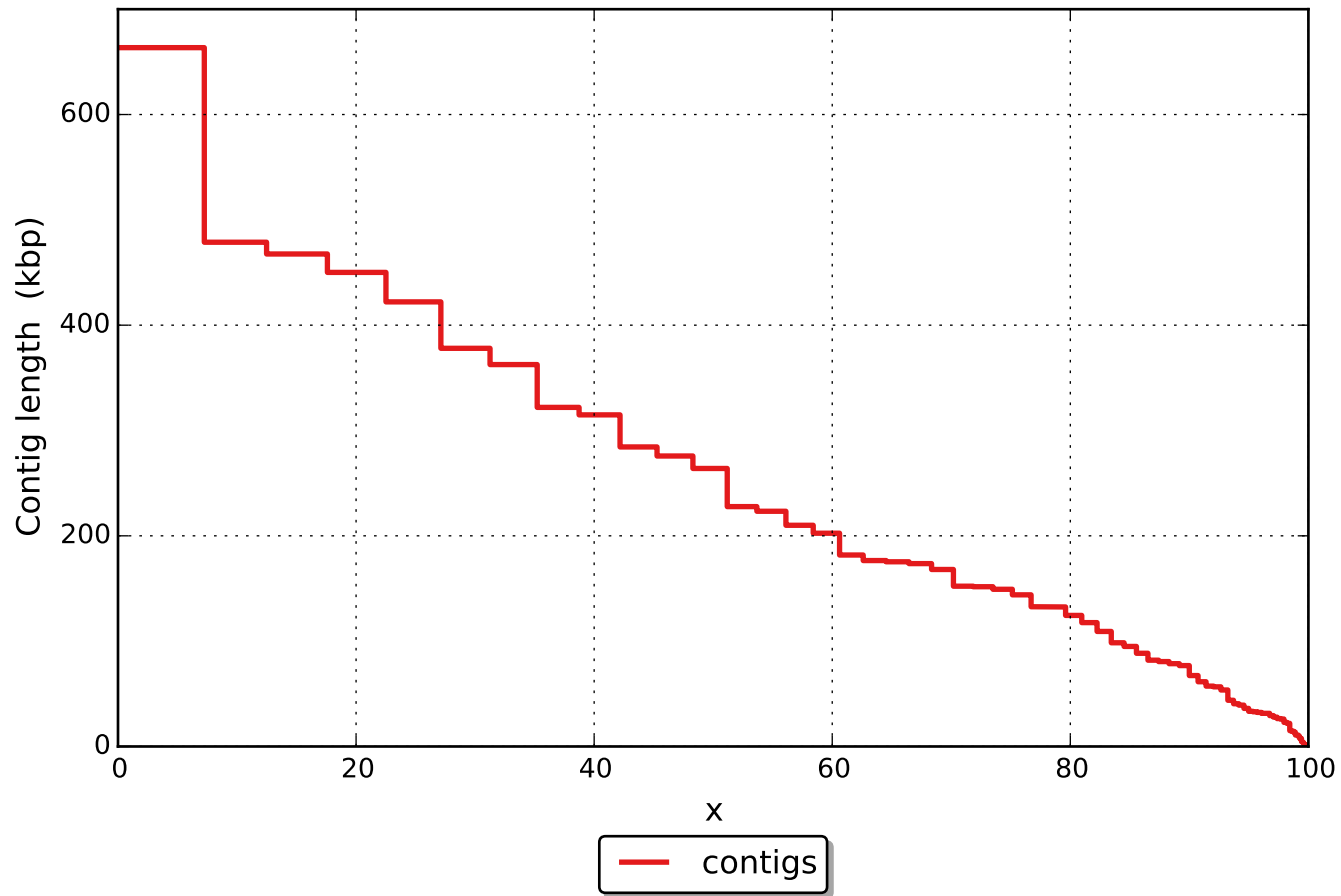
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

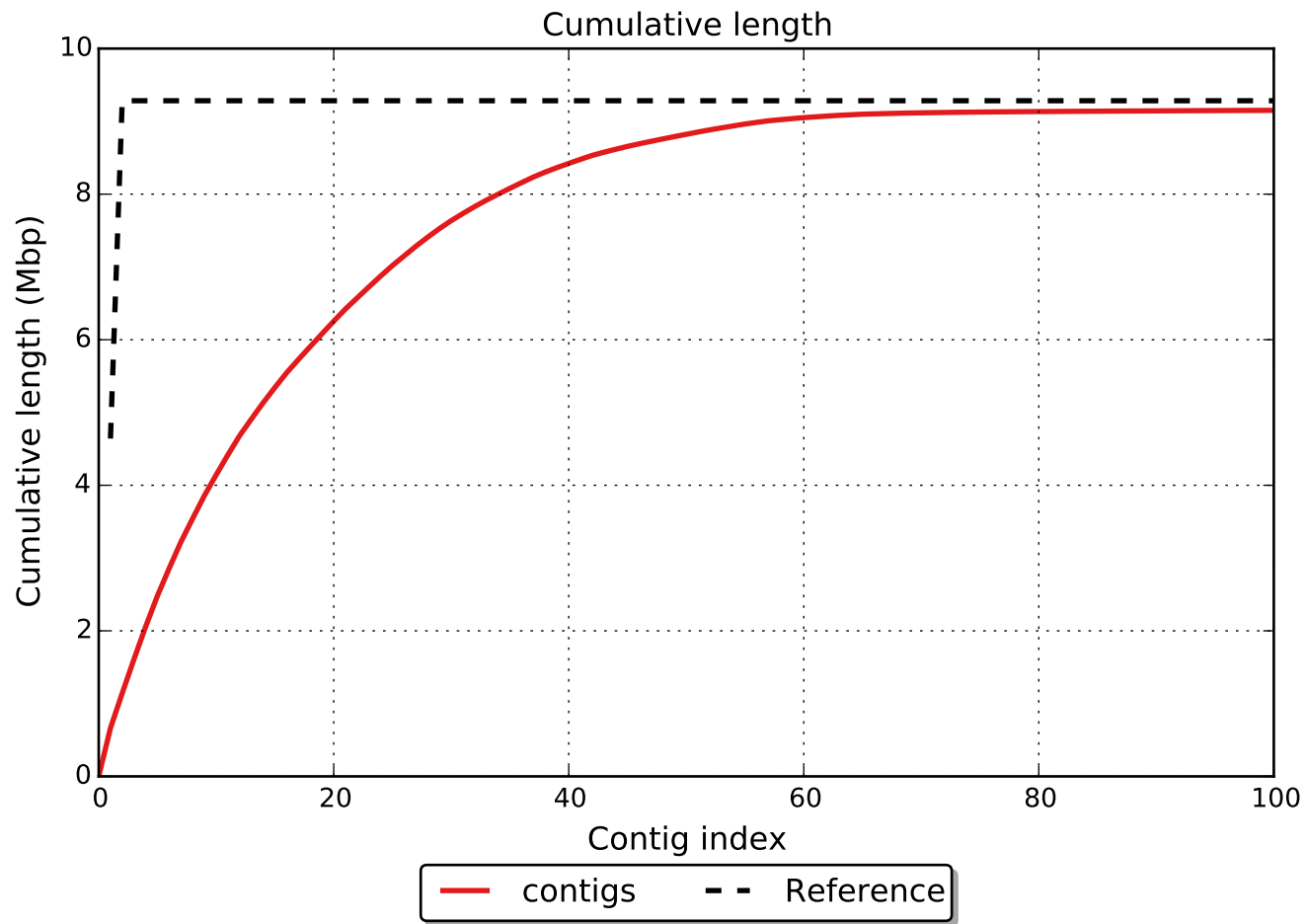
Unaligned report

	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

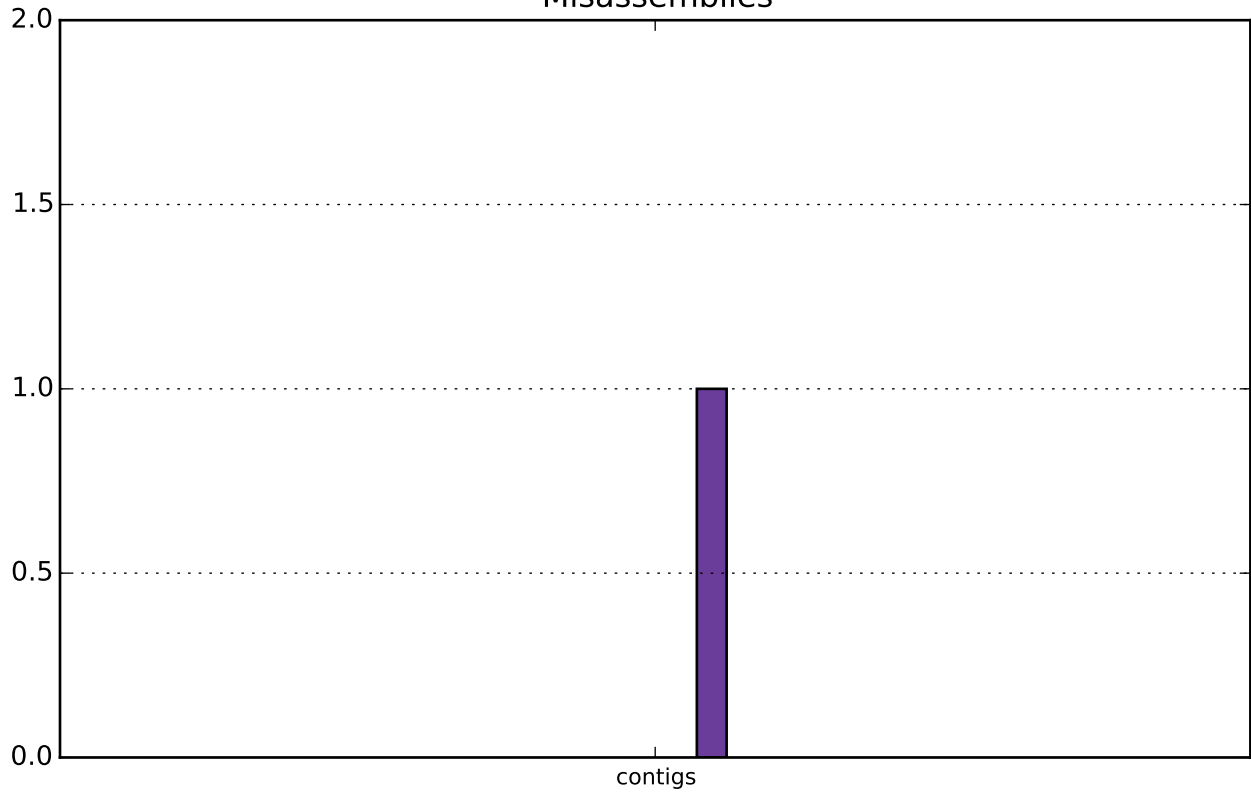
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).


Nx

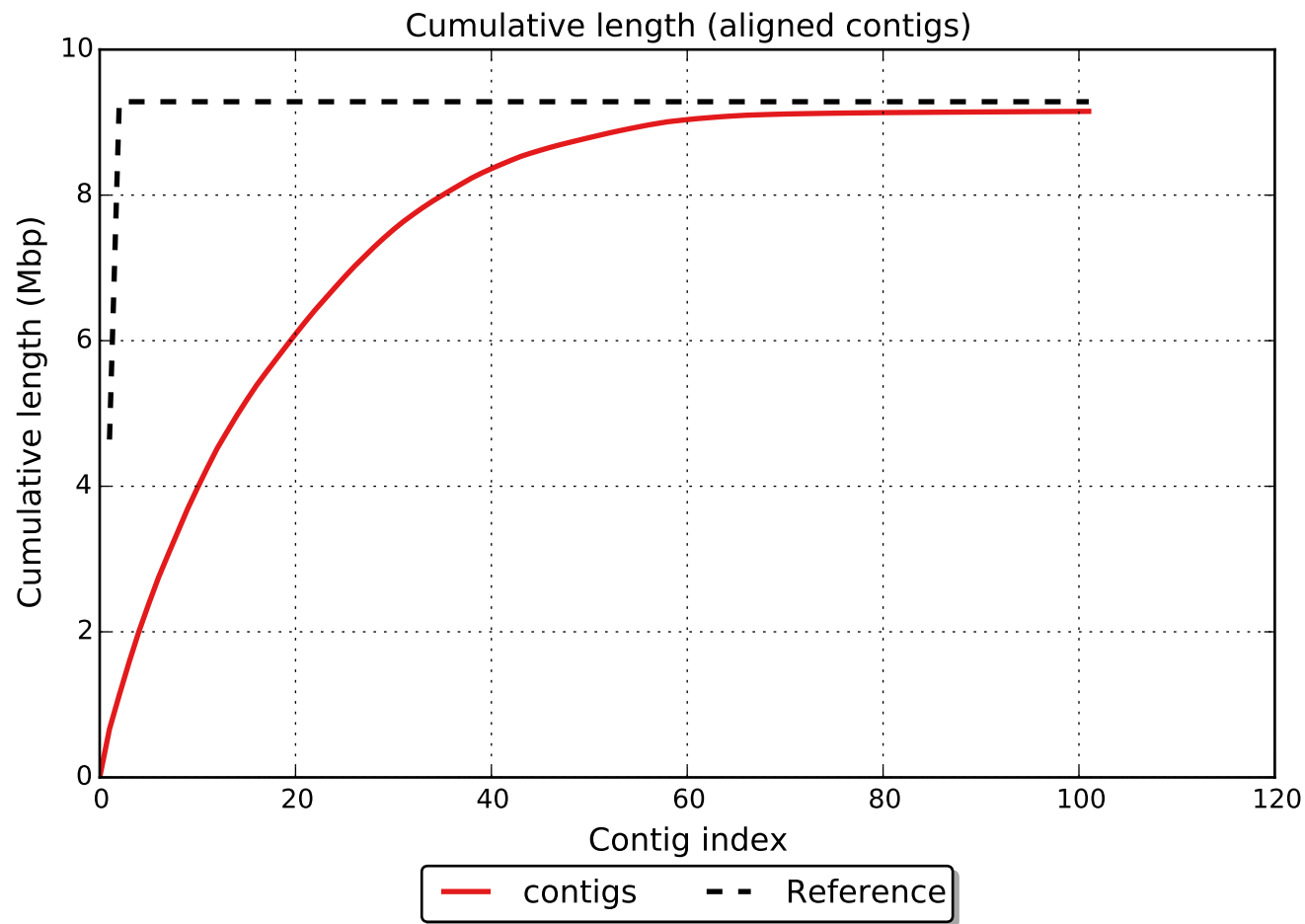




Misassemblies



 # interspecies translocations



NAx

