

Report

	contigs
# contigs (≥ 0 bp)	607
# contigs (≥ 1000 bp)	230
# contigs (≥ 5000 bp)	168
# contigs (≥ 10000 bp)	115
# contigs (≥ 25000 bp)	59
# contigs (≥ 50000 bp)	31
Total length (≥ 0 bp)	4724465
Total length (≥ 1000 bp)	4611108
Total length (≥ 5000 bp)	4437305
Total length (≥ 10000 bp)	4036697
Total length (≥ 25000 bp)	3222986
Total length (≥ 50000 bp)	2241364
# contigs	249
Largest contig	130415
Total length	4623710
Reference length	9283304
N50	42832
N75	17945
L50	33
L75	71
# misassemblies	4
# misassembled contigs	4
Misassembled contigs length	339551
# local misassemblies	4
# unaligned contigs	0 + 1 part
Unaligned length	55
Genome fraction (%)	49.721
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	702.64
# indels per 100 kbp	0.39
Largest alignment	122264
NA50	40767
NA75	17675
LA50	35
LA75	74

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	4
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	4
# possibly misassembled contigs	0
# misassembled contigs	4
Misassembled contigs length	339551
# local misassemblies	4
# mismatches	32432
# indels	18
# short indels	18
# long indels	0
Indels length	25

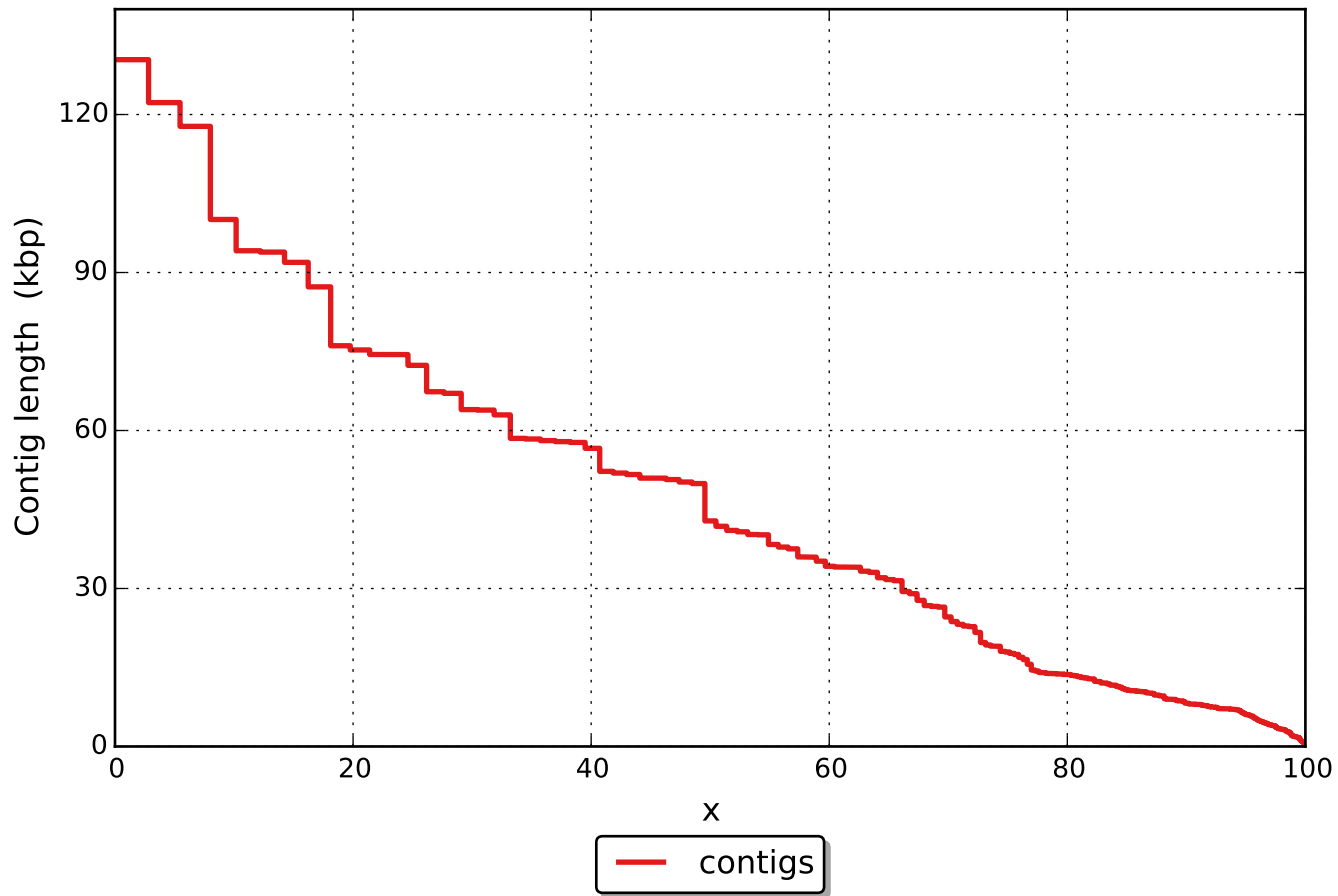
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

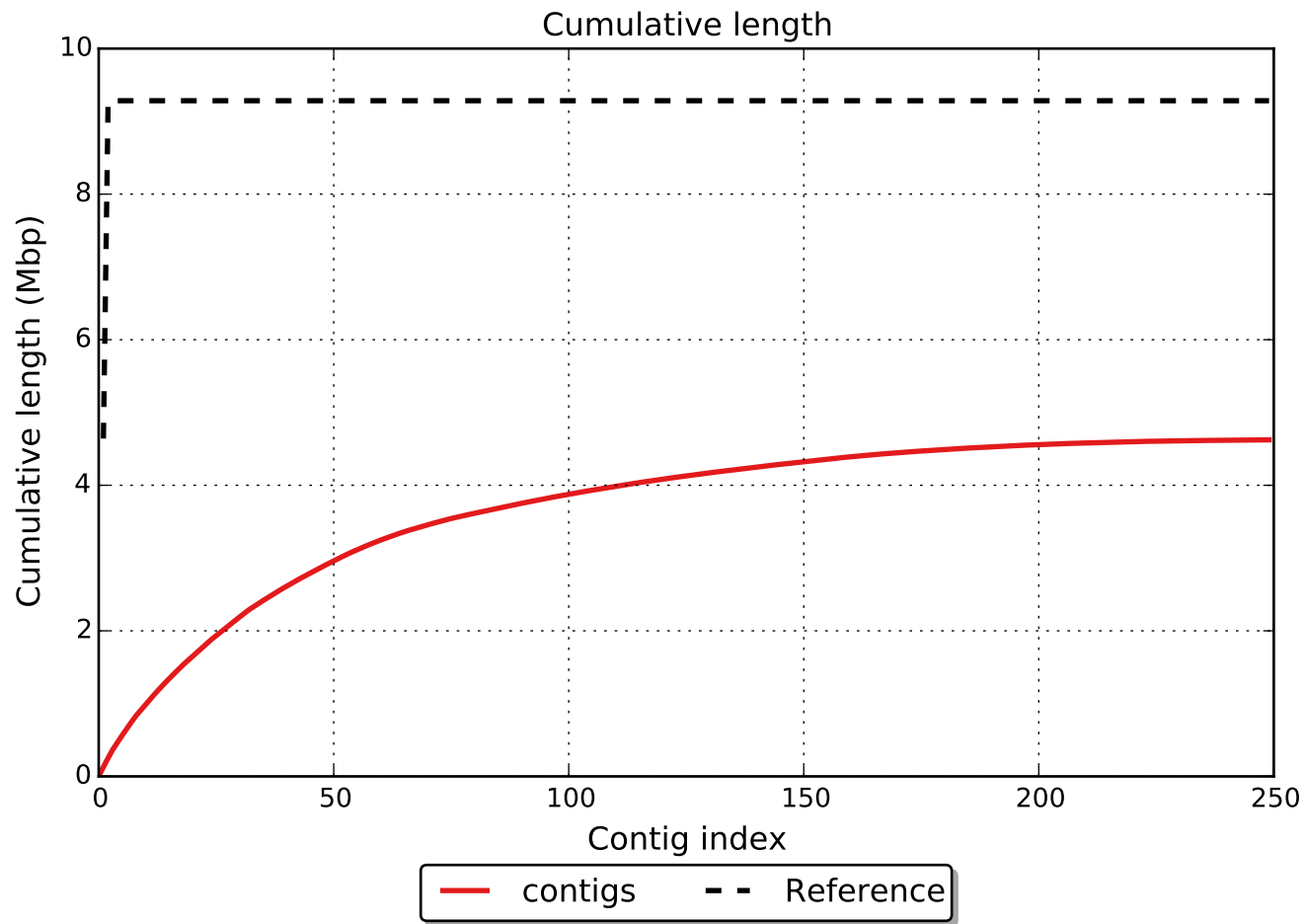
Unaligned report

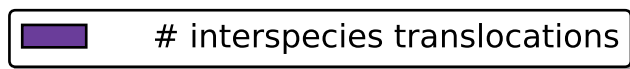
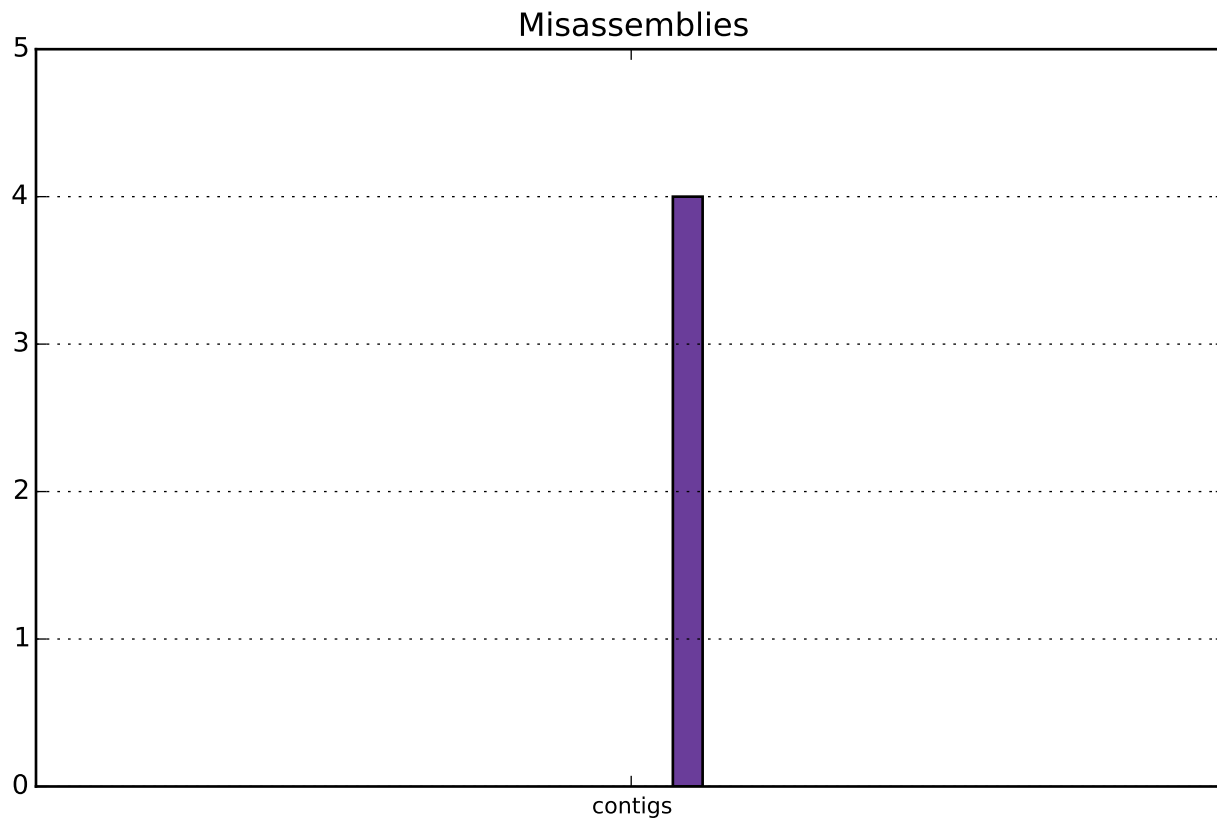
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	55
# N's	0

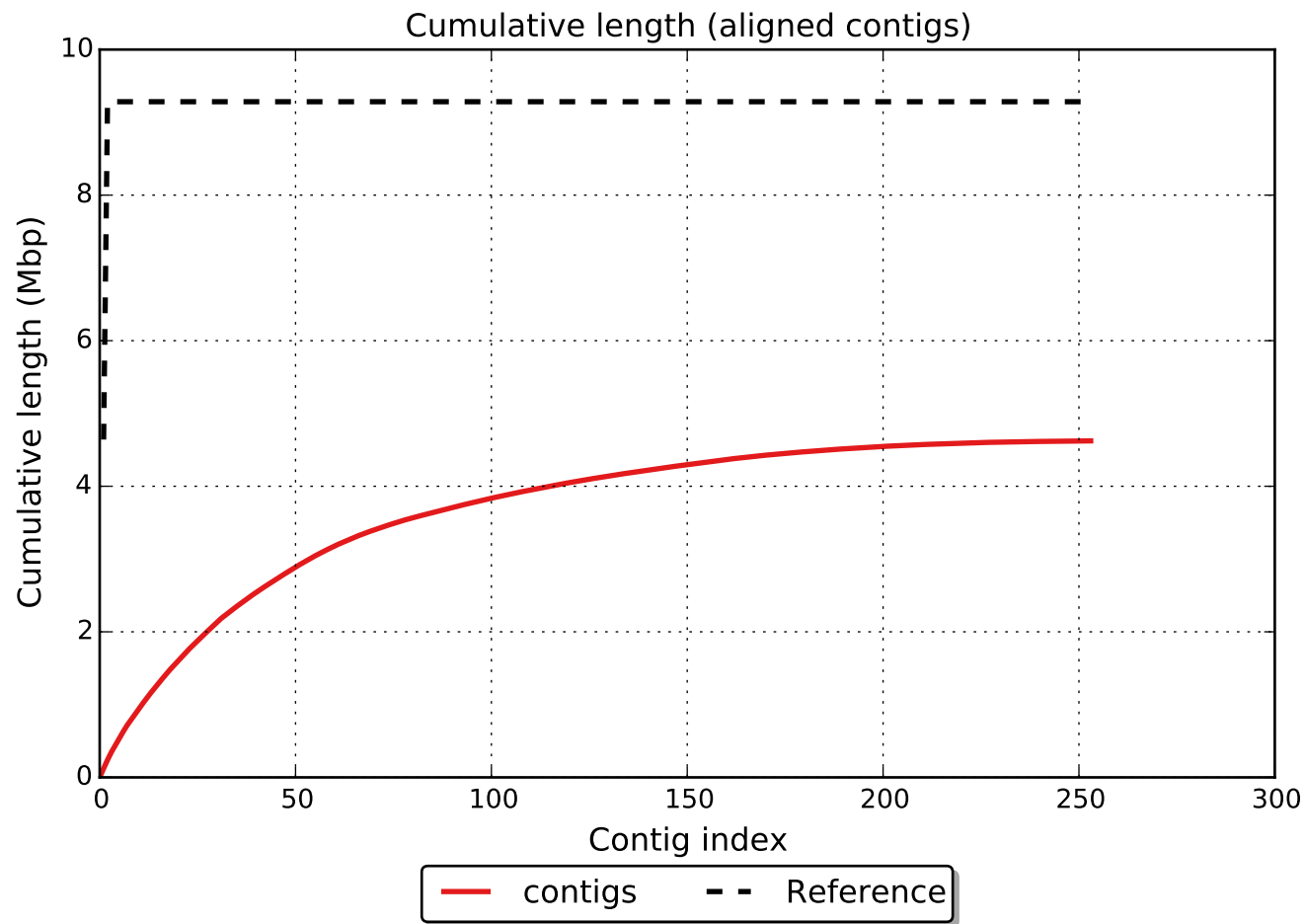
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx









NAx

