

Report

	contigs
# contigs (≥ 0 bp)	1231
# contigs (≥ 1000 bp)	388
# contigs (≥ 5000 bp)	238
# contigs (≥ 10000 bp)	153
# contigs (≥ 25000 bp)	76
# contigs (≥ 50000 bp)	38
Total length (≥ 0 bp)	7429549
Total length (≥ 1000 bp)	7114291
Total length (≥ 5000 bp)	6710161
Total length (≥ 10000 bp)	6105724
Total length (≥ 25000 bp)	4901192
Total length (≥ 50000 bp)	3526081
# contigs	461
Largest contig	189810
Total length	7160822
Reference length	9283304
N50	47425
N75	17671
L50	40
L75	99
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	129141
# local misassemblies	4
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	89.271
Duplication ratio	1.182
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1104.90
# indels per 100 kbp	0.92
Largest alignment	189810
NA50	46469
NA75	17671
LA50	40
LA75	100

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

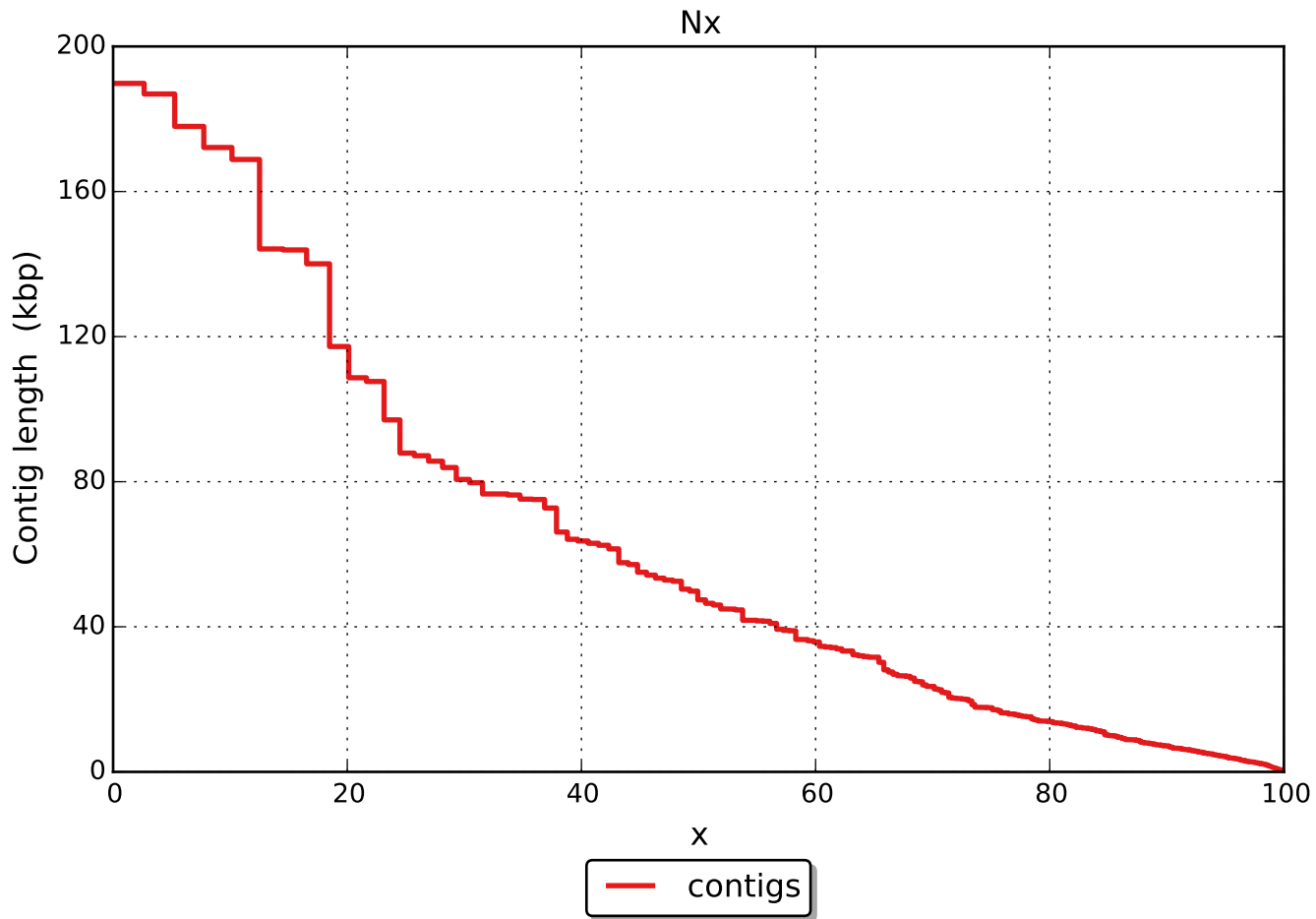
	contigs
# misassemblies	2
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	129141
# local misassemblies	4
# mismatches	91567
# indels	76
# short indels	76
# long indels	0
Indels length	94

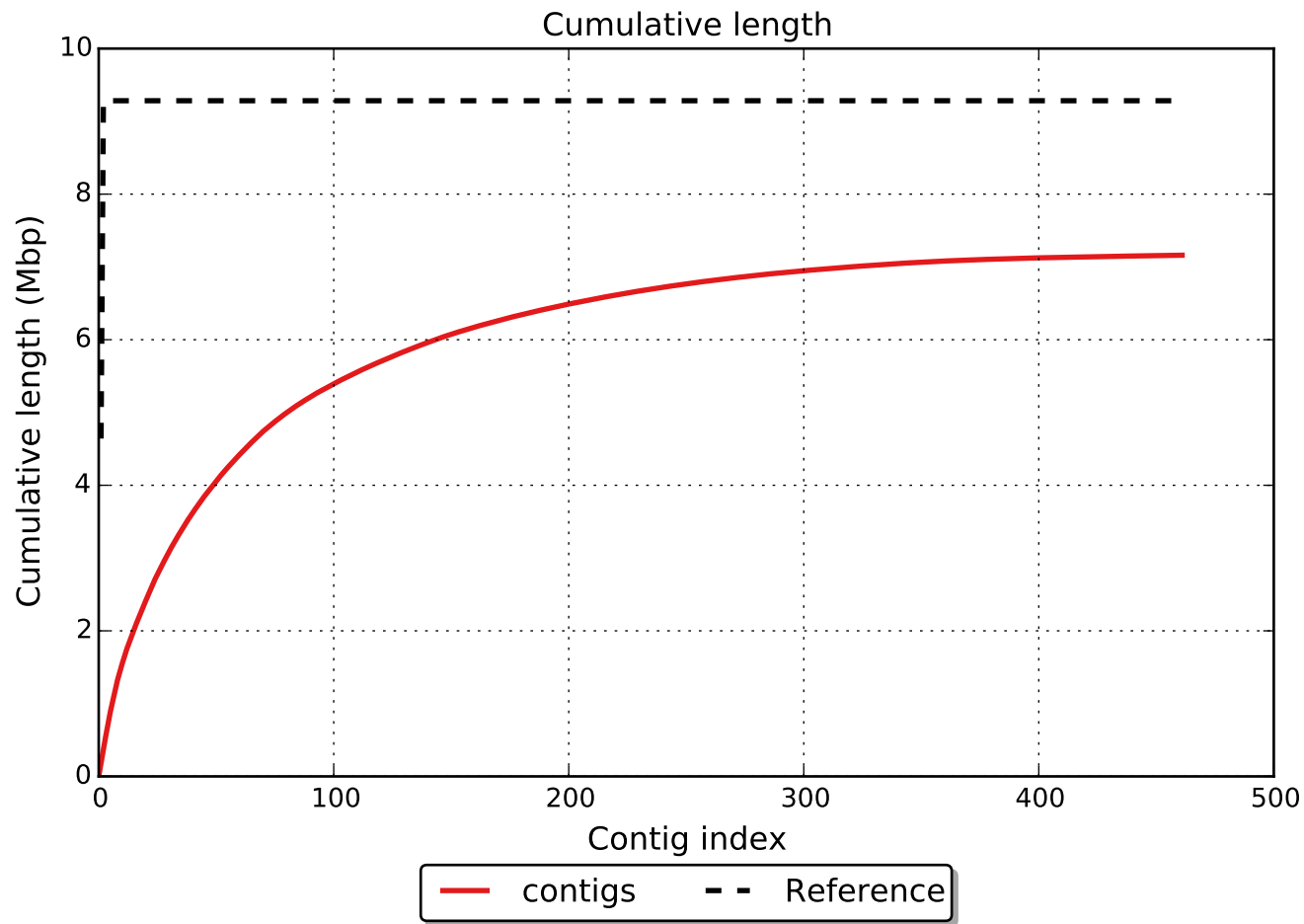
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

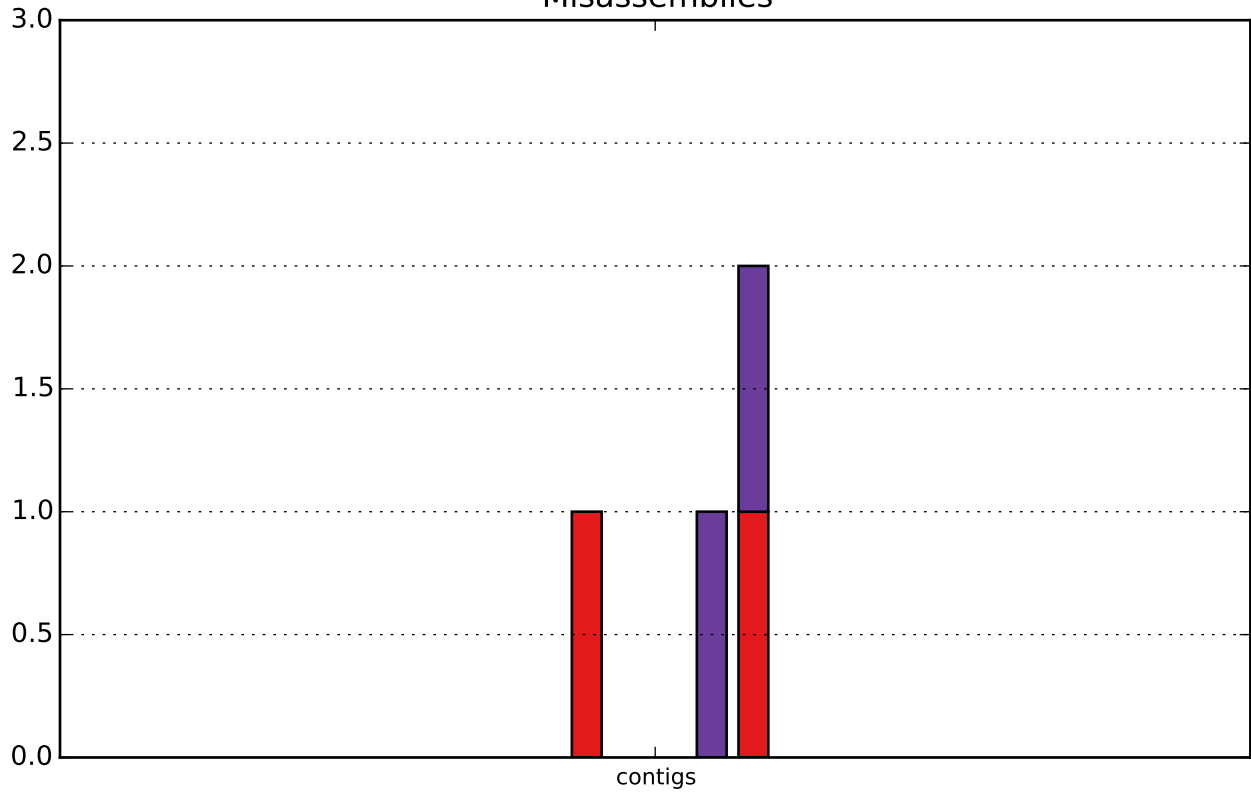
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

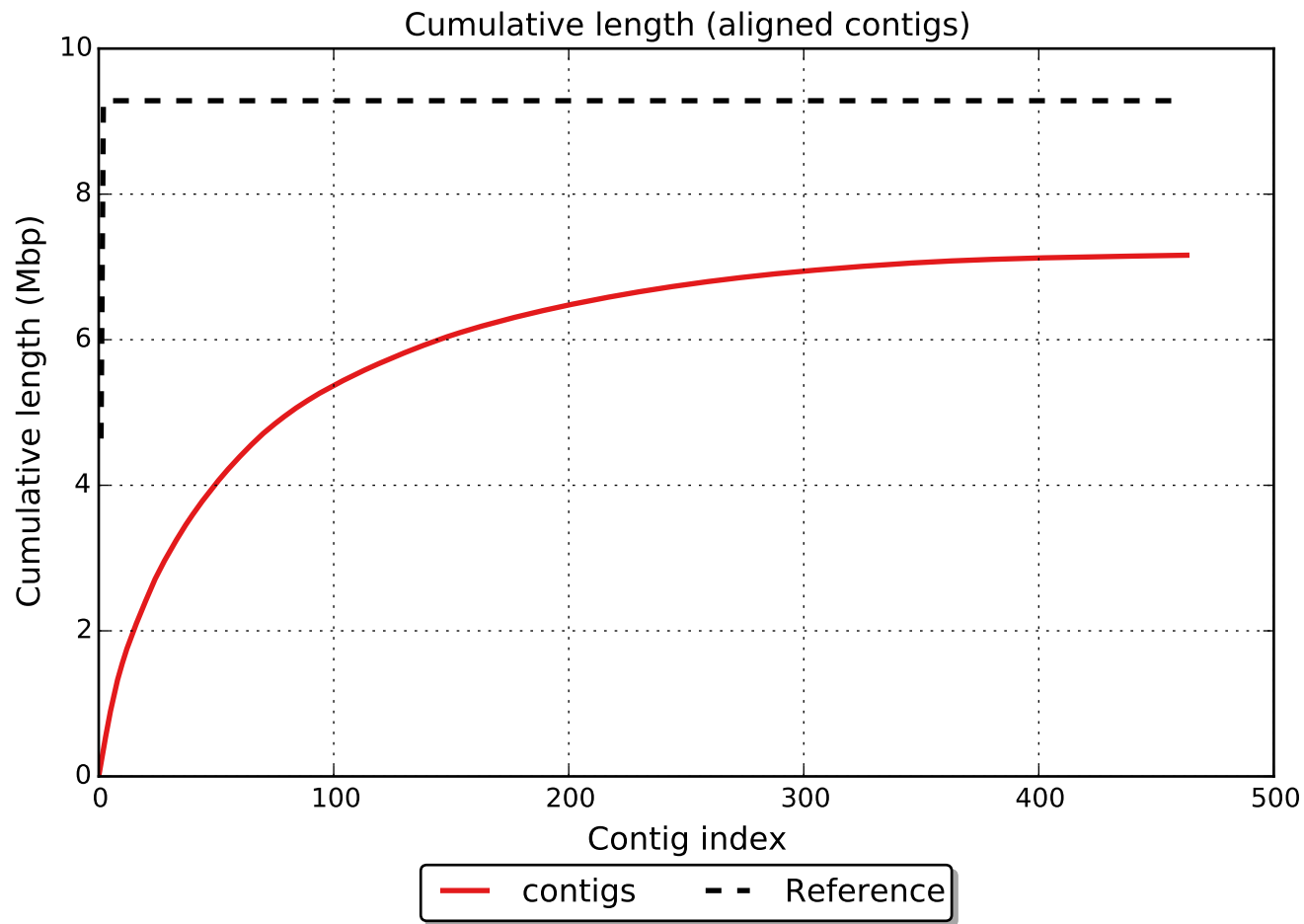
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).





Misassemblies





NAx

