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 (%)	75.292
Duplication ratio	1.024
# N's per 100 kbp	0.00
# mismatches per 100 kbp	992.20
# indels per 100 kbp	0.66
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).
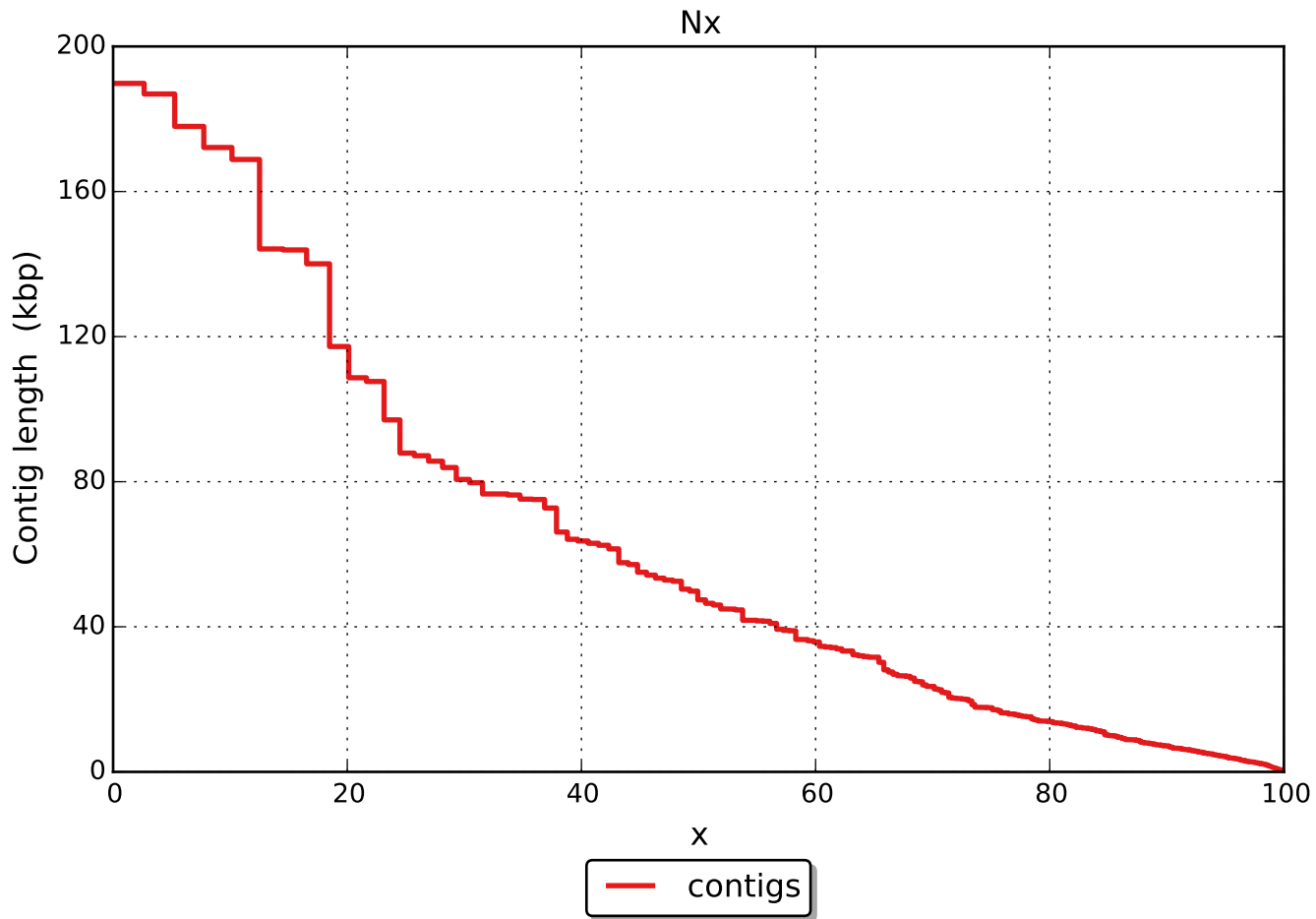
Misassemblies report

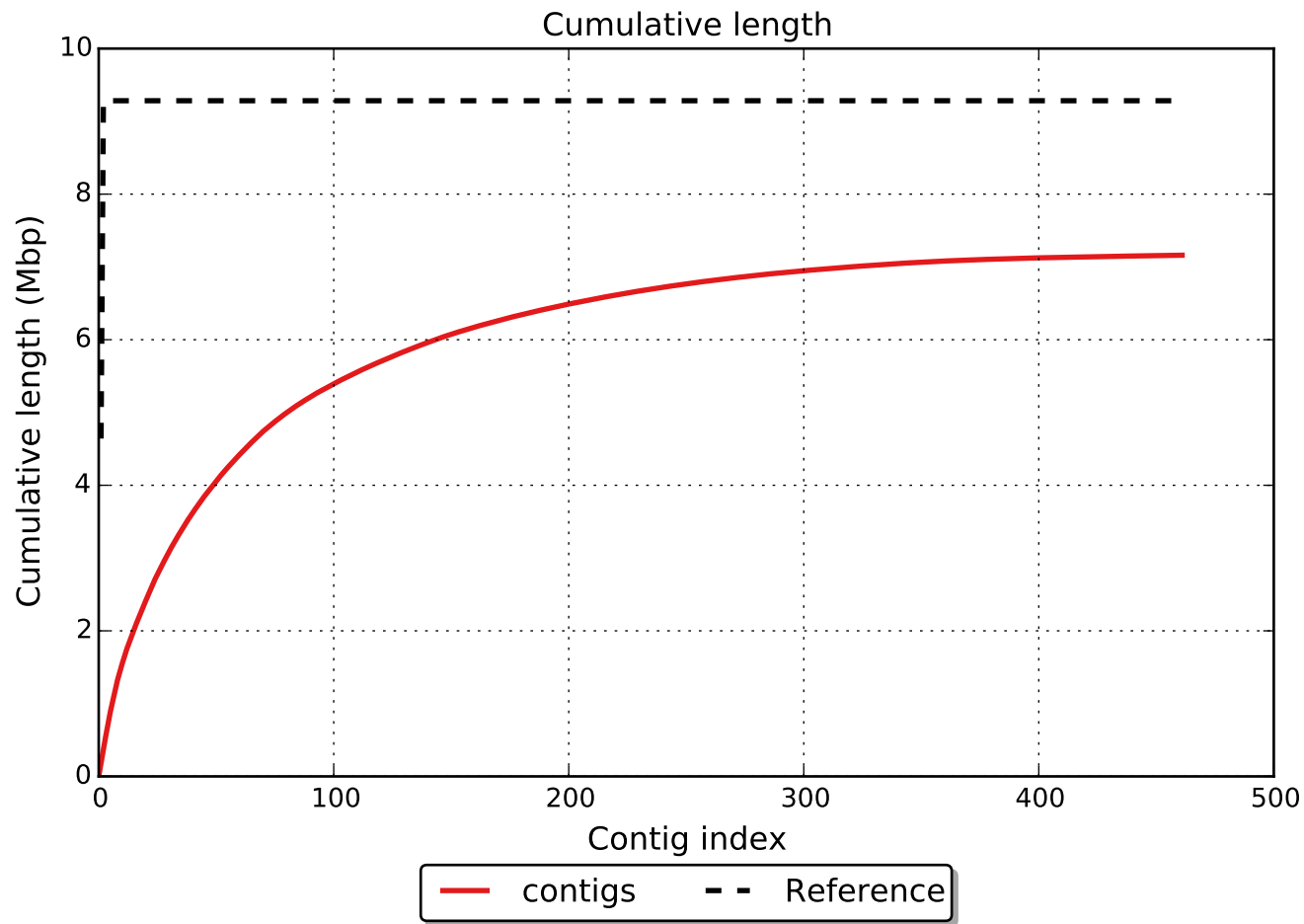|	contigs
# misassemblies	2
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	129141
# local misassemblies	4
# mismatches	69351
# indels	46
# short indels	46
# long indels	0
Indels length	52

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).
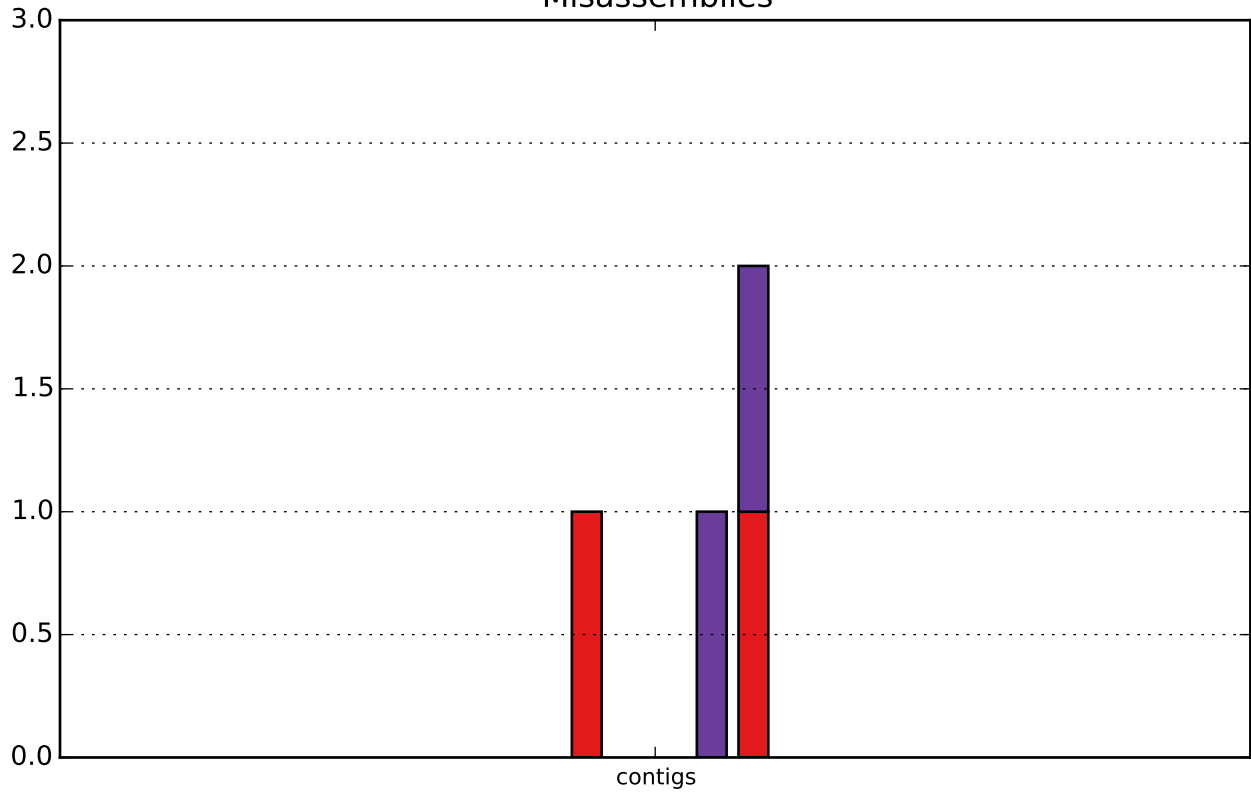
Unaligned report

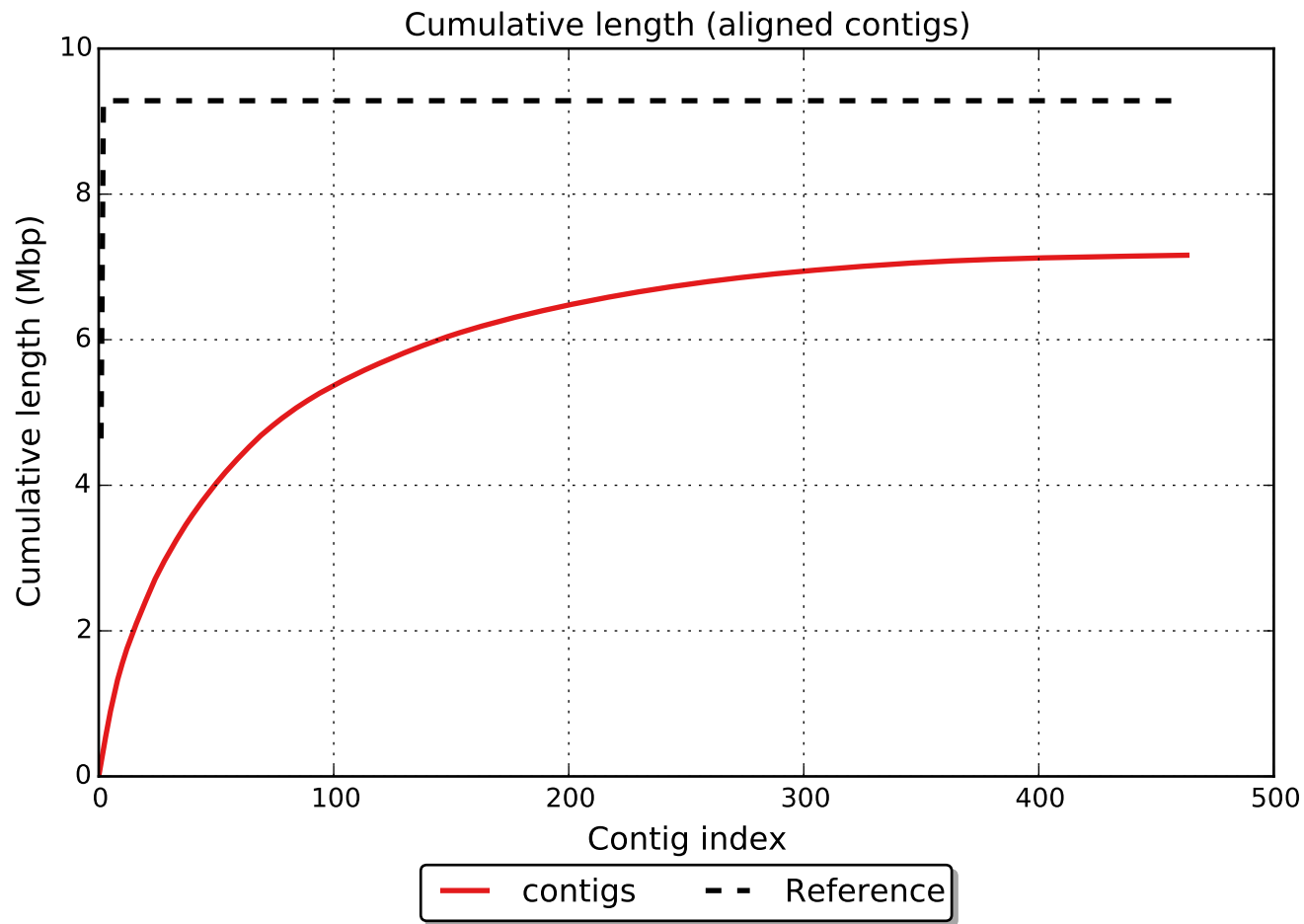|	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

Cumulative length

Misassemblies

relocations
interspecies translocations

Cumulative length (aligned contigs)