Report

|	contigs
# contigs (>= 0 bp)	451
# contigs (>= 1000 bp)	164
# contigs (>= 5000 bp)	107
# contigs (>= 10000 bp)	98
# contigs (>= 25000 bp)	86
# contigs (>= 50000 bp)	63
Total length (>= 0 bp)	8961052
Total length (>= 1000 bp)	8844614
Total length (>= 5000 bp)	8723933
Total length (>= 10000 bp)	8656530
Total length (>= 25000 bp)	8443368
Total length (>= 50000 bp)	7666345
# contigs	221
Largest contig	431470
Total length	8882335
Reference length	9283304
N50	105688
N75	69219
L50	22
L75	47
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	198850
# local misassemblies	8
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	95.514
Duplication ratio	1.015
# N's per 100 kbp	0.00
# mismatches per 100 kbp	941.04
# indels per 100 kbp	1.26
Largest alignment	431470
NA50	105224
NA75	66896
LA50	22
LA75	48

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	0
# translocations	0
# inversions	0
# interspecies translocations	2
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	198850
# local misassemblies	8
# mismatches	83440
# indels	112
# short indels	111
# long indels	1
Indels length	130

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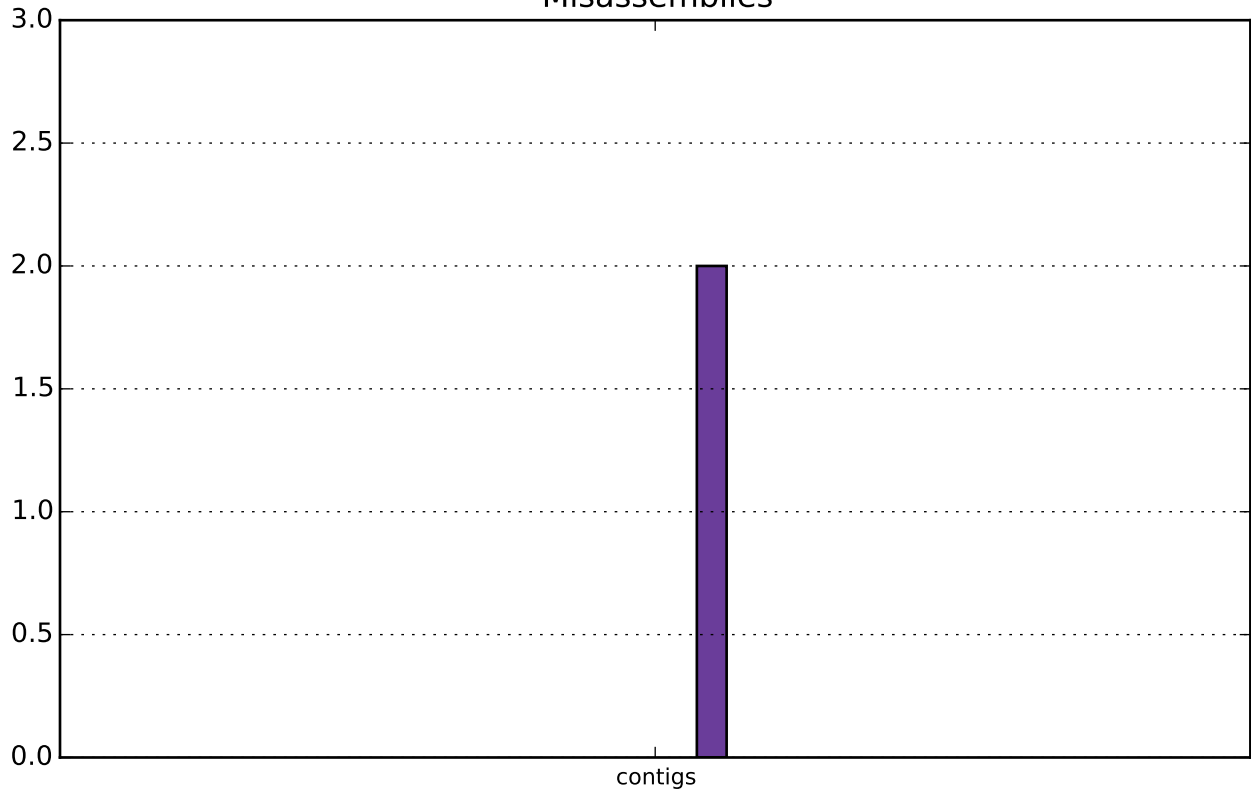(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

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).
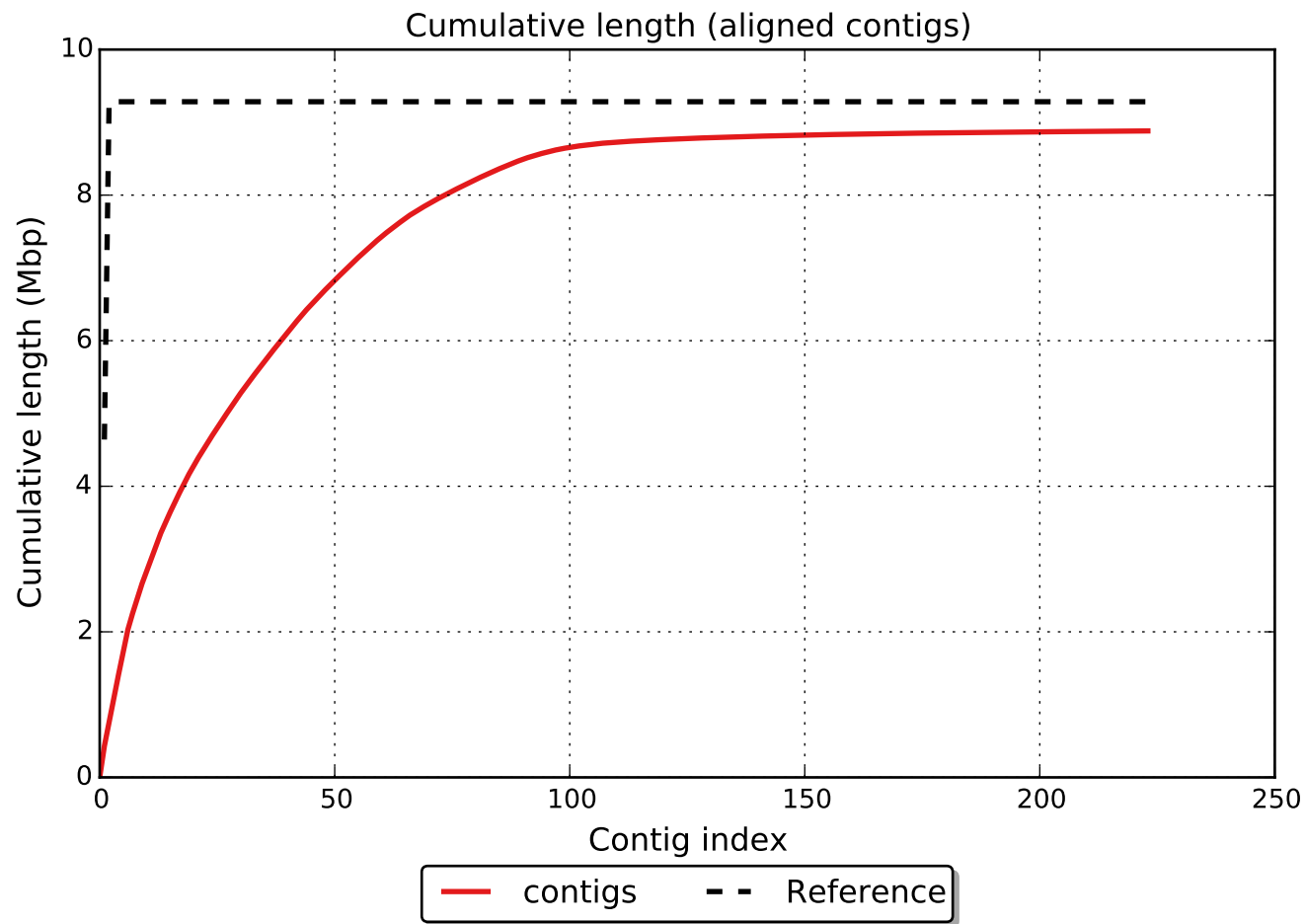
Nx

Cumulative length
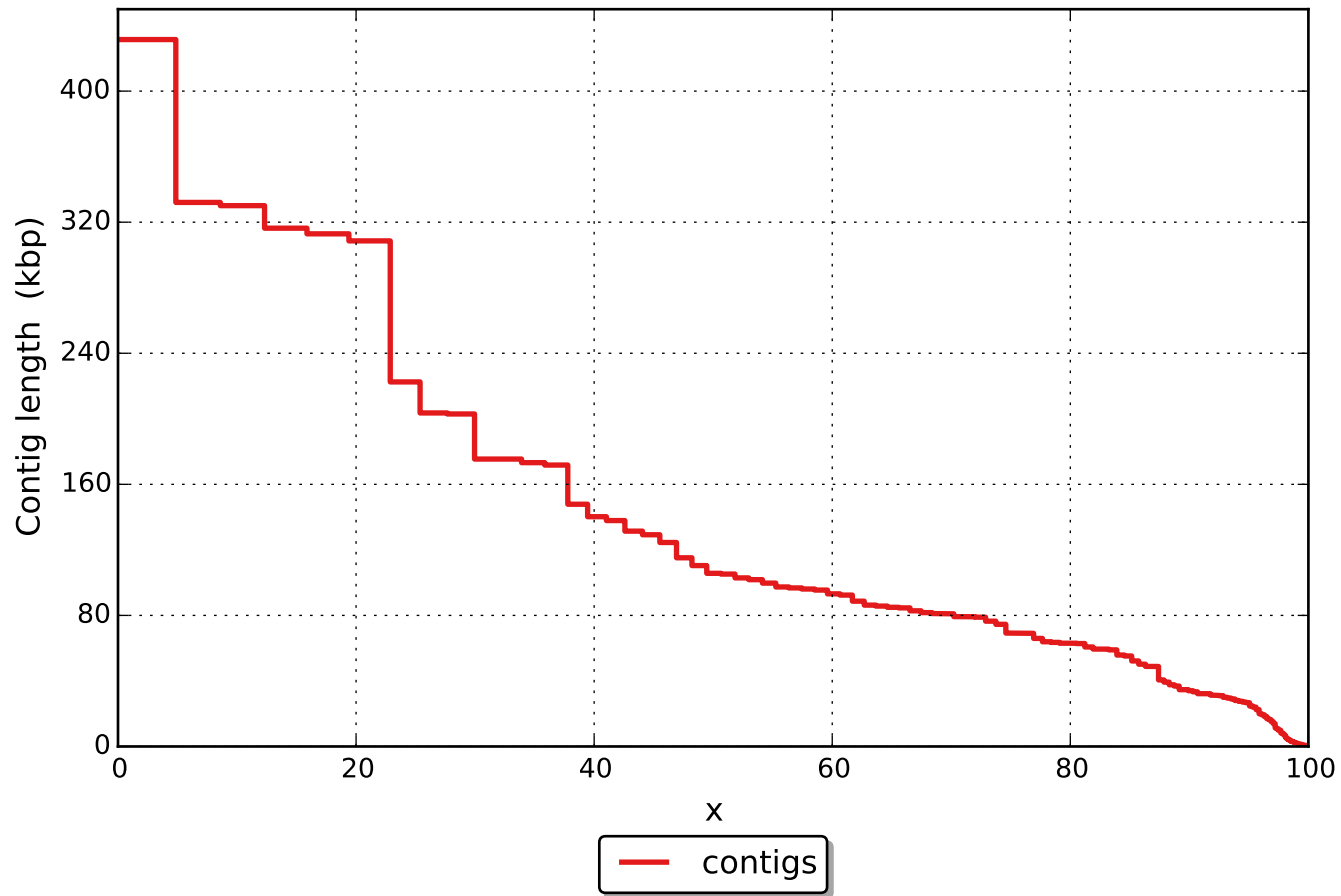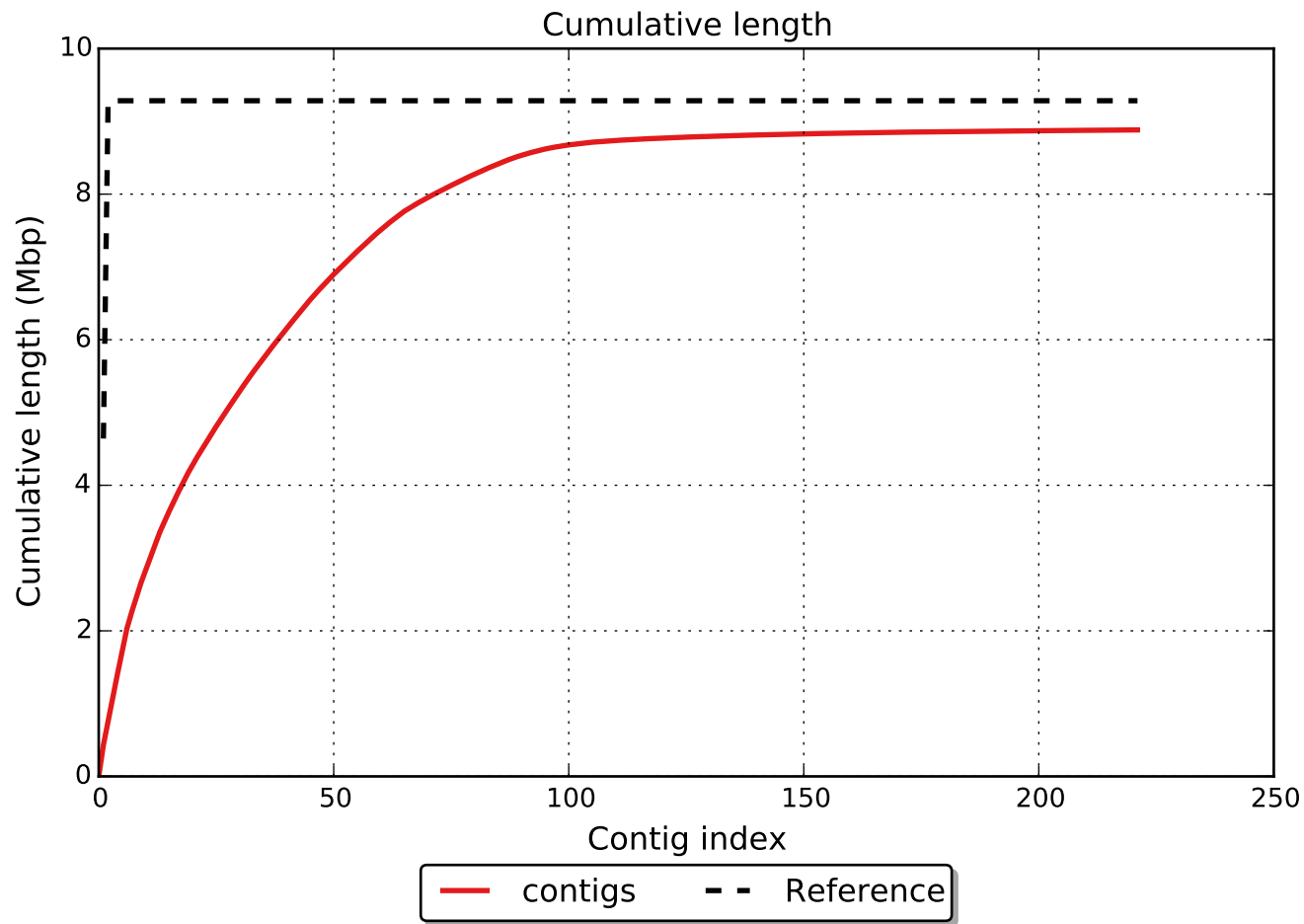
Misassemblies

interspecies translocations

Cumulative length (aligned contigs)