Report

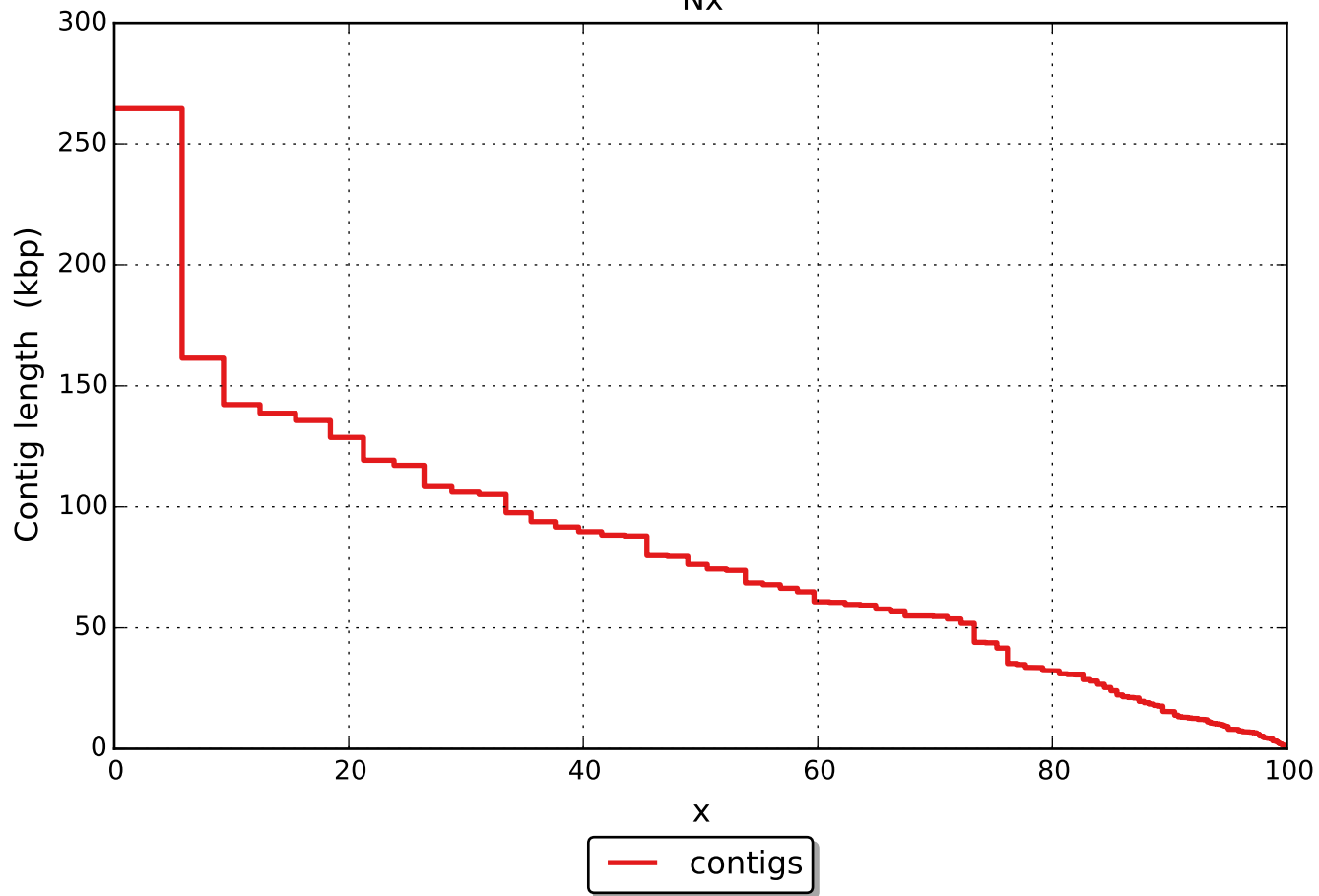|	contigs
# contigs (>= 0 bp)	319
# contigs (>= 1000 bp)	136
# contigs (>= 5000 bp)	104
# contigs (>= 10000 bp)	81
# contigs (>= 25000 bp)	53
# contigs (>= 50000 bp)	37
Total length (>= 0 bp)	4606247
Total length (>= 1000 bp)	4564721
Total length (>= 5000 bp)	4480098
Total length (>= 10000 bp)	4313499
Total length (>= 25000 bp)	3884378
Total length (>= 50000 bp)	3352307
# contigs	144
Largest contig	264572
Total length	4570595
Reference length	9283304
N50	76208
N75	43808
L50	20
L75	39
# misassemblies	5
# misassembled contigs	5
Misassembled contigs length	310368
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	78.025
Duplication ratio	0.998
# N's per 100 kbp	0.00
# mismatches per 100 kbp	561.31
# indels per 100 kbp	0.57
Largest alignment	264572
NA50	76208
NA75	34830
LA50	20
LA75	41

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	5
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	4
# possibly misassembled contigs	0
# misassembled contigs	5
Misassembled contigs length	310368
# local misassemblies	3
# mismatches	40657
# indels	41
# short indels	41
# long indels	0
Indels length	53

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).
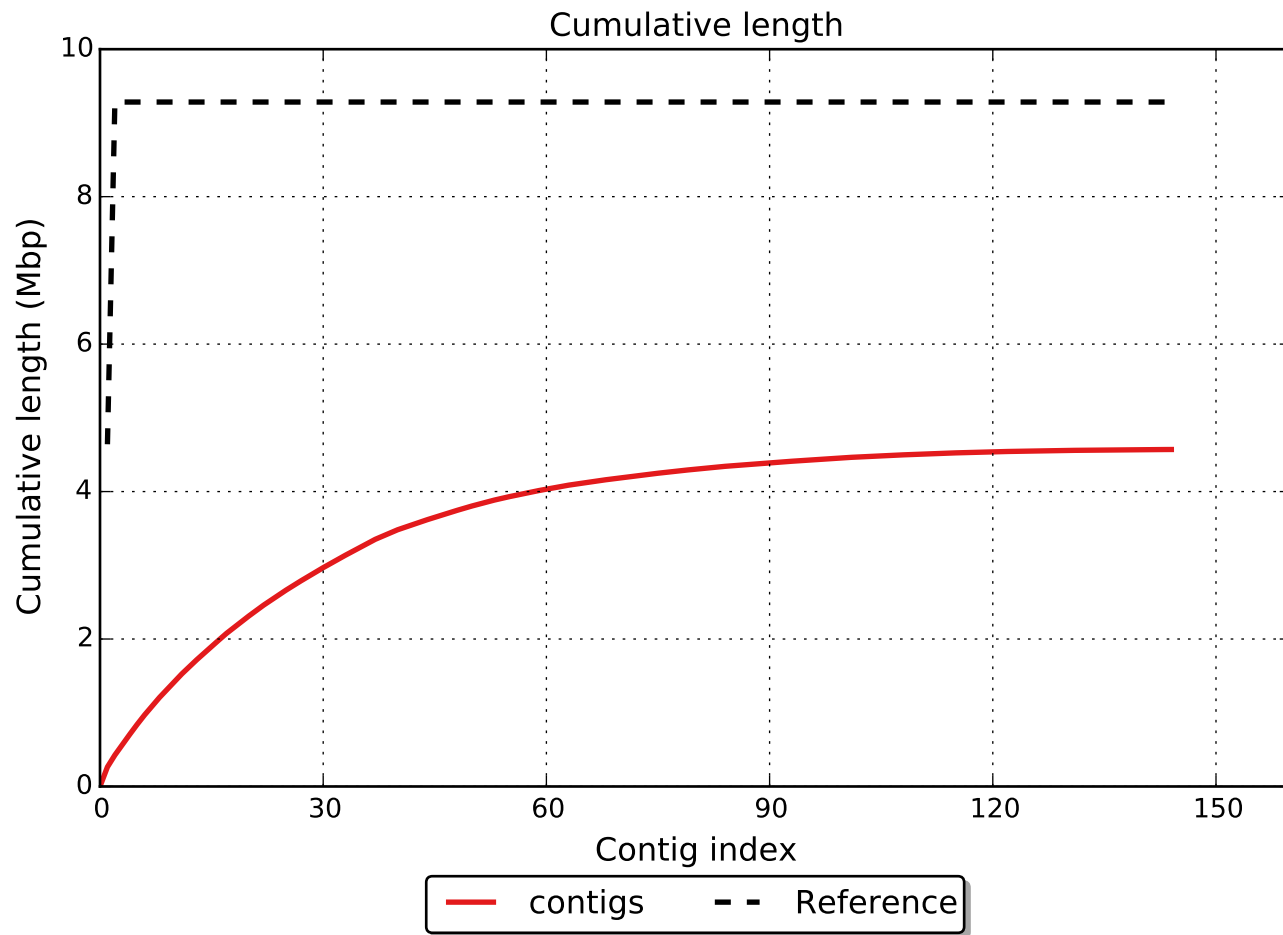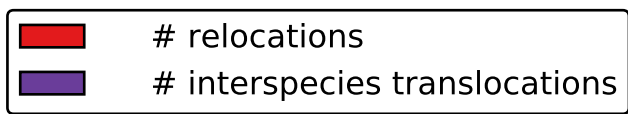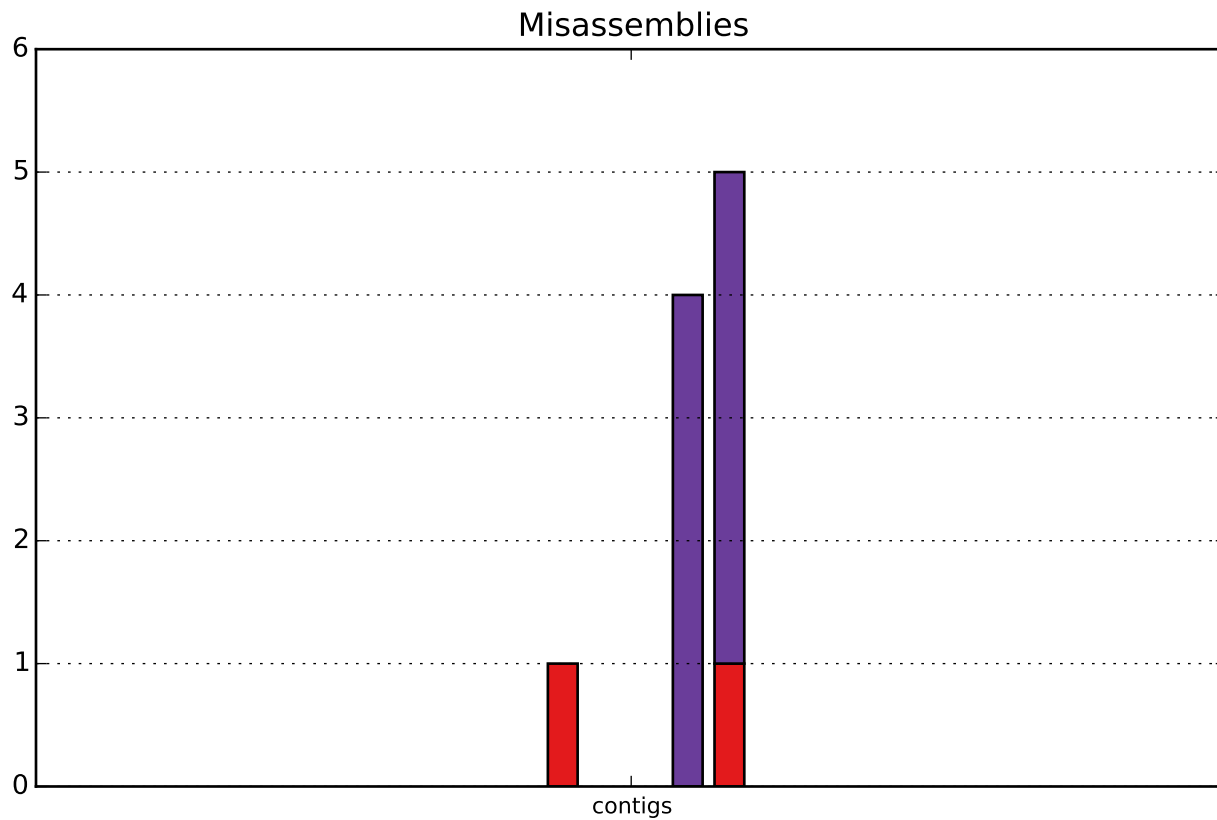
Unaligned report

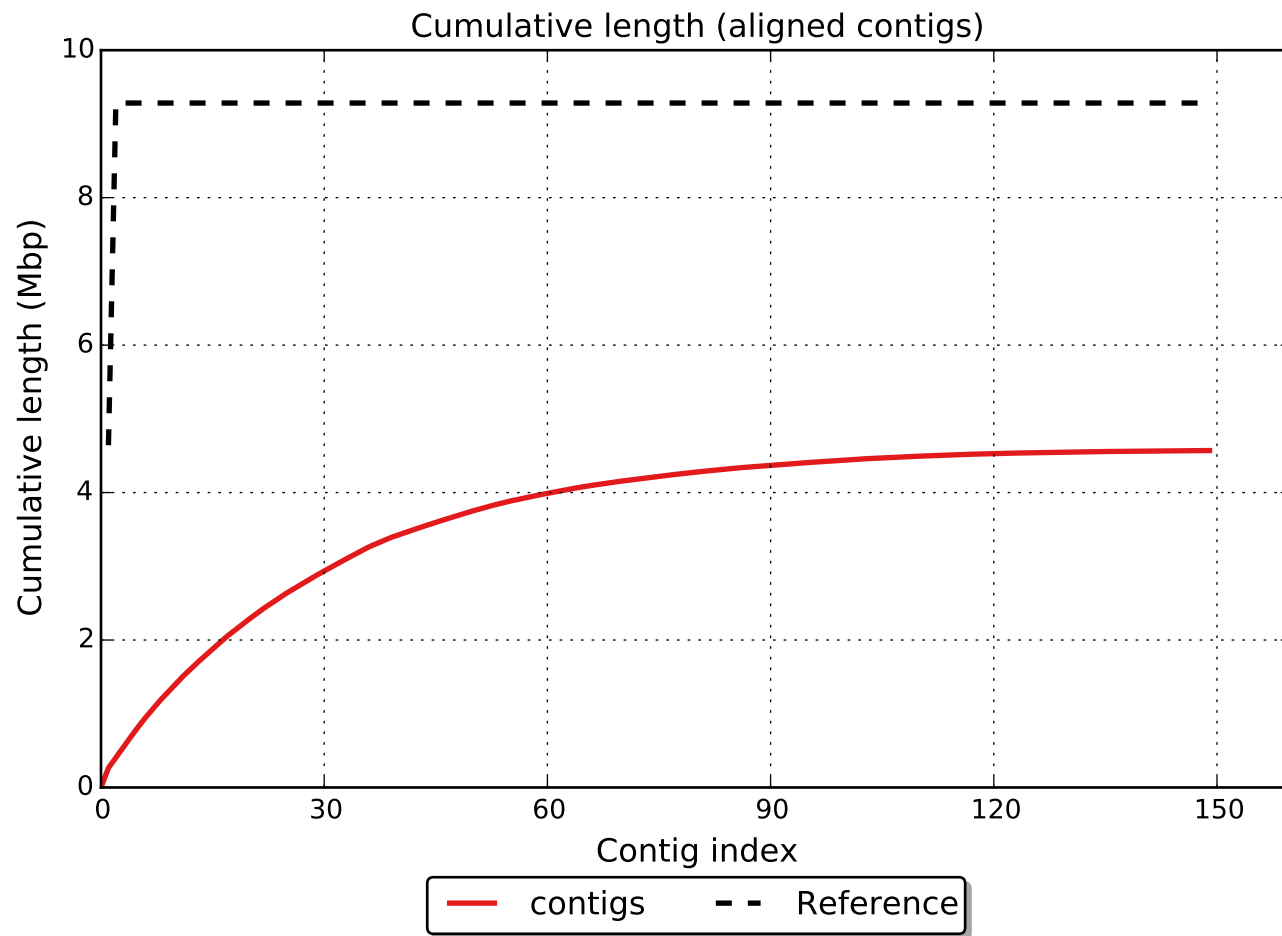|	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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

Cumulative length (aligned contigs)