Report

	scaffolds
# contigs (>= 0 bp)	2532
# contigs (>= 1000 bp)	539
# contigs (>= 5000 bp)	269
# contigs (>= 10000 bp)	149
# contigs (>= 25000 bp)	36
# contigs (>= 50000 bp)	1
Total length (>= 0 bp)	5279867
Total length (>= 1000 bp)	4490880
Total length (>= 5000 bp)	3899587
Total length (>= 10000 bp)	3011827
Total length (>= 25000 bp)	1258049
Total length (>= 50000 bp)	61819
# contigs	803
Largest contig	61819
Total length	4669416
Reference length	9283304
N50	14917
N75	7346
L50	94
L75	206
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	19577
# local misassemblies	4
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	63.826
Duplication ratio	1.036
# N's per 100 kbp	3250.24
# mismatches per 100 kbp	1017.72
# indels per 100 kbp	7.78
Largest alignment	59611
NA50	13558
NA75	6662
LA50	101
LA75	227

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).
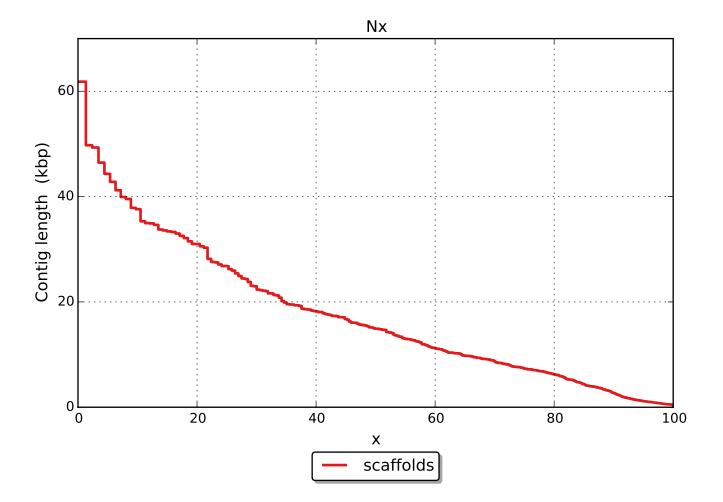
Misassemblies report

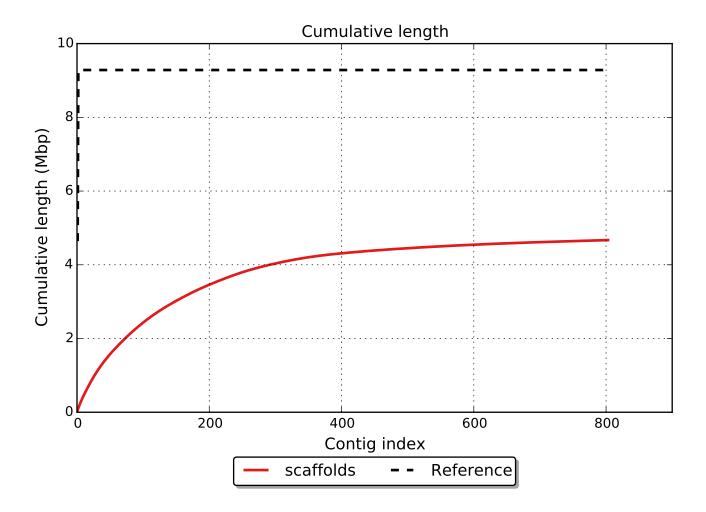|	scaffolds
# misassemblies	1
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	103
# misassembled contigs	1
Misassembled contigs length	19577
# local misassemblies	4
# mismatches	60302
# indels	461
# short indels	60
# long indels	401
Indels length	22109

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).
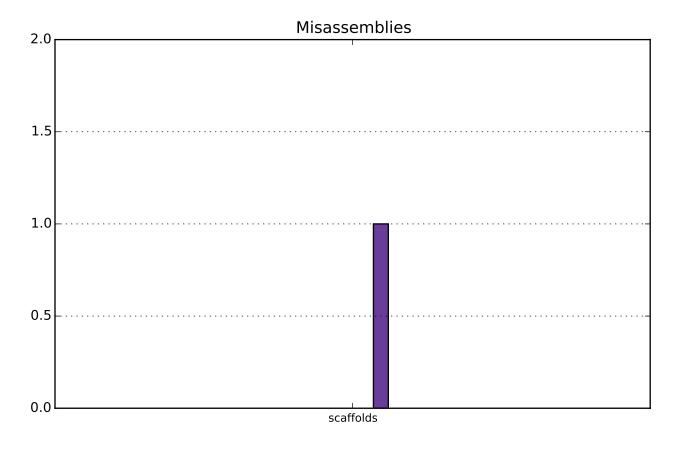
Unaligned report

	scaffolds
# 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	151767

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)