Report

	scaffolds
# contigs (>= 0 bp)	125
# contigs (>= 1000 bp)	77
# contigs (>= 5000 bp)	64
# contigs (>= 10000 bp)	61
# contigs (>= 25000 bp)	54
# contigs (>= 50000 bp)	41
Total length (>= 0 bp)	9146130
Total length (>= 1000 bp)	9129851
Total length (>= 5000 bp)	9102772
Total length (>= 10000 bp)	9077538
Total length (>= 25000 bp)	8967925
Total length (>= 50000 bp)	8536857
# contigs	86
Largest contig	663492
Total length	9137424
Reference length	9283304
N50	263950
N75	151678
L50	12
L75	24
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	478751
# local misassemblies	0
# unaligned contigs	54 + 9 part
Unaligned length	4348582
Genome fraction (%)	49.802
Duplication ratio	1.036
# N's per 100 kbp	0.51
# mismatches per 100 kbp	221.49
# indels per 100 kbp	0.65
Largest alignment	663492
NA50	27851
LA50	17

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

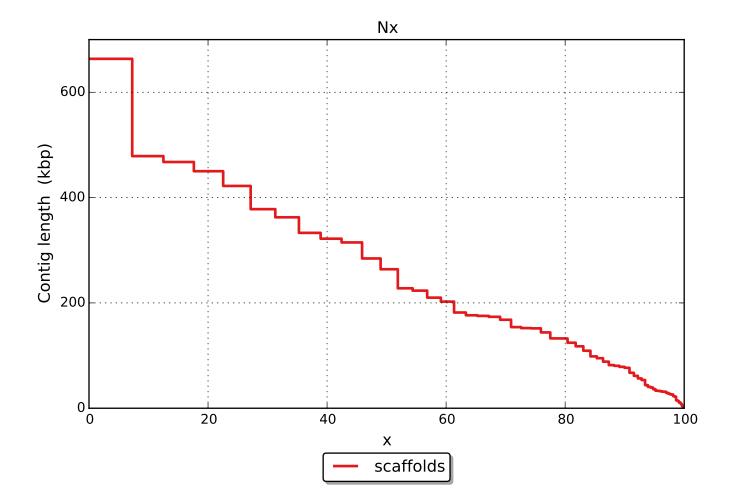
	scaffolds
# misassemblies	1
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	7
# misassembled contigs	1
Misassembled contigs length	478751
# local misassemblies	0
# mismatches	10240
# indels	30
# short indels	28
# long indels	2
Indels length	94

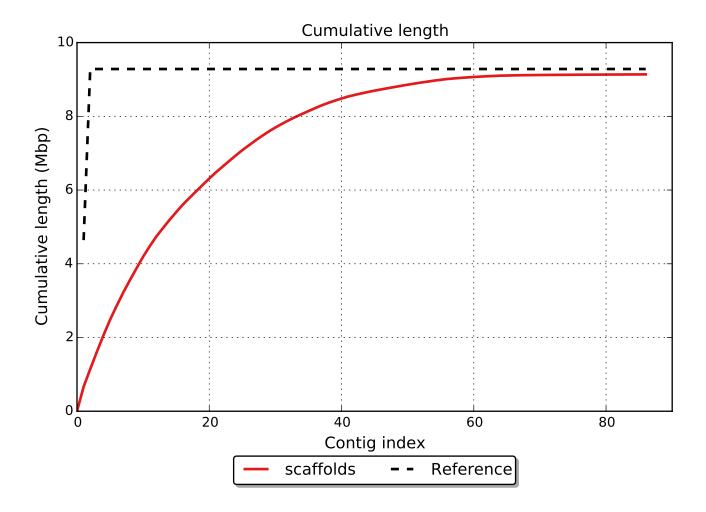
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

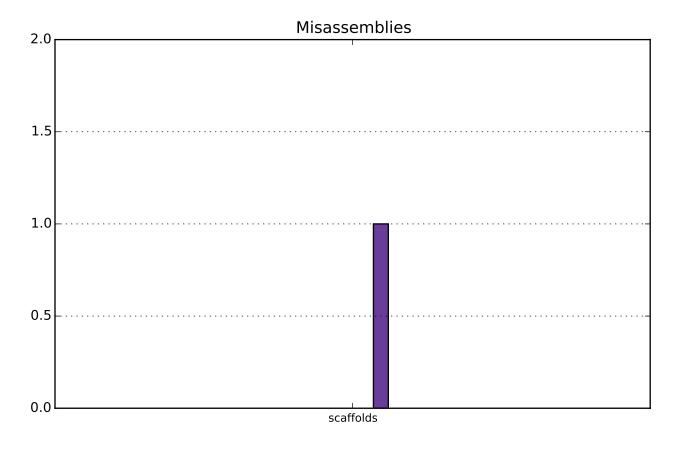
Unaligned report

	scaffolds
# fully unaligned contigs	54
Fully unaligned length	3304638
# partially unaligned contigs	9
# with misassembly	2
# both parts are significant	6
Partially unaligned length	1043944
# N's	47

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).







interspecies translocations

