Report

	66.11
Warating (c. Olan)	scaffolds
# contigs (>= 0 bp)	562
# contigs (>= 1000 bp)	7
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	172531
Total length (>= 1000 bp)	14460
Total length (>= 5000 bp)	5687
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	28
Largest contig	5687
Total length	26689
Reference length	4641652
N50	1268
N75	584
L50	6
L75	16
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	8583
# local misassemblies	0
# unaligned contigs	2 + 2 part
Unaligned length	1137
Genome fraction (%)	0.544
Duplication ratio	1.013
# N's per 100 kbp	1547.45
# mismatches per 100 kbp	435.99
# indels per 100 kbp	67.38
Largest alignment	5494
NA50	1039
NA75	544
LA50	7
LA75	17
, 5	<u> </u>

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

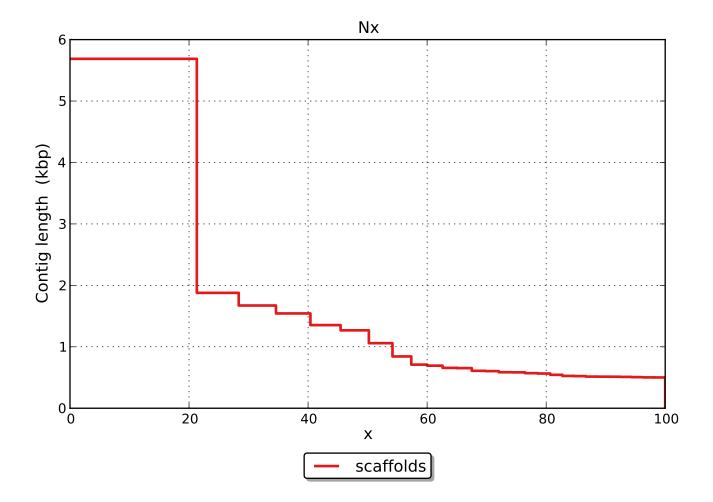
	scaffolds
# misassemblies	3
# relocations	3
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	3
Misassembled contigs length	8583
# local misassemblies	0
# mismatches	110
# indels	17
# short indels	12
# long indels	5
Indels length	104

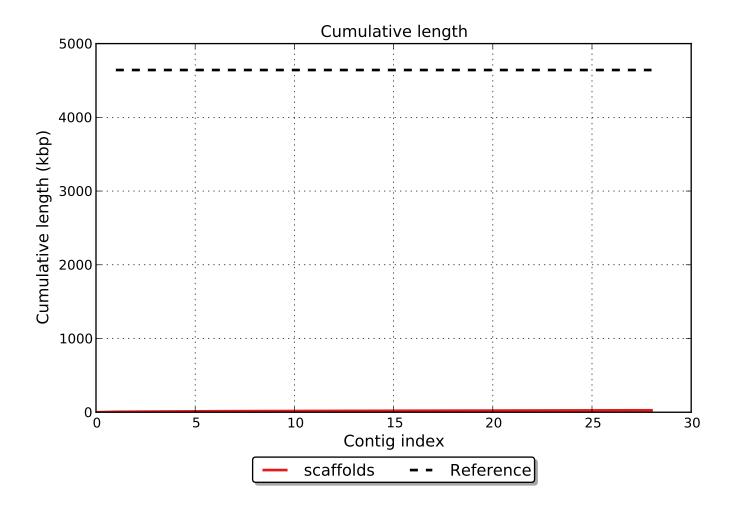
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

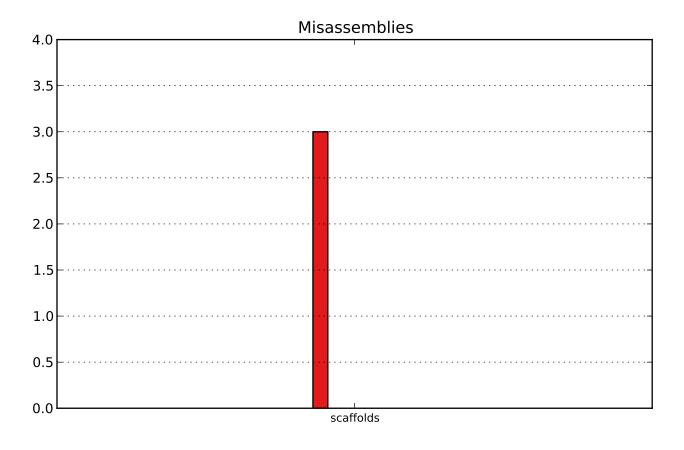
Unaligned report

	scaffolds
# fully unaligned contigs	2
Fully unaligned length	1097
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	40
# N's	413

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).







relocations

