Report

	scaffolds
# contigs (>= 1000 bp)	148
# contigs (>= 5000 bp)	102
# contigs (>= 10000 bp)	74
# contigs (>= 25000 bp)	43
# contigs (>= 50000 bp)	22
Total length (>= 1000 bp)	3605021
Total length (>= 5000 bp)	3482122
Total length (>= 10000 bp)	3280169
Total length (>= 25000 bp)	2792769
Total length (>= 50000 bp)	2060403
# contigs	171
Largest contig	200996
Total length	3619149
Reference length	4641652
GC (%)	50.71
Reference GC (%)	50.78
N50	61078
NG50	39022
N75	26582
NG75	5237
L50	18
LG50	29
L75	40
LG75	102
# misassemblies	3
# misassembled contigs	2
Misassembled contigs length	127194
# local misassemblies	4
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	75.574
Duplication ratio	1.032
# N's per 100 kbp	0.00
# mismatches per 100 kbp	999.46
# indels per 100 kbp	0.60
Largest alignment	200996
NA50	57160
NGA50	38903
NA75	25852
NGA75	5237
LA50	18
LGA50	29
LA75	42
LGA75	105

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

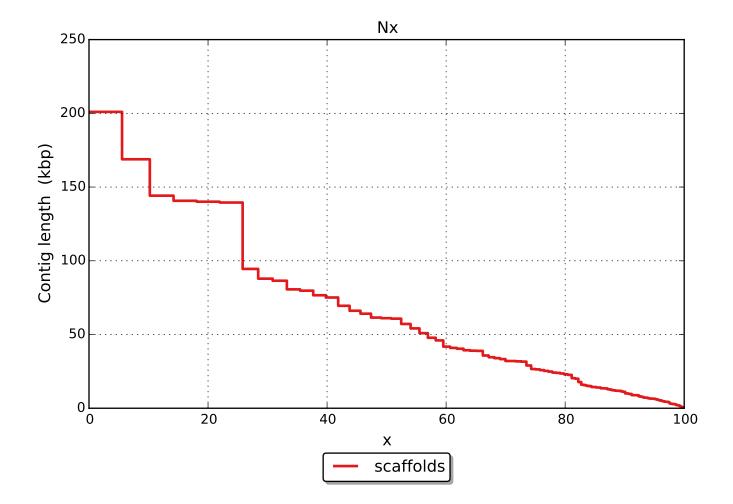
	scaffolds
# misassemblies	3
# relocations	3
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	127194
# local misassemblies	4
# mismatches	35060
# indels	21
# short indels	21
# long indels	0
Indels length	21

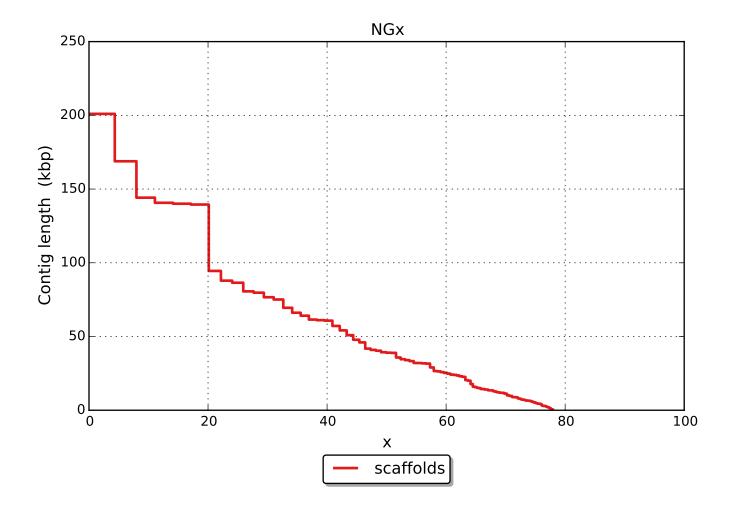
All statistics are based on contigs of size \geq 500 bp, unless otherwise noted (e.g., "# contigs (\geq 0 bp)" and "Total length (\geq 0 bp)" include all contigs).

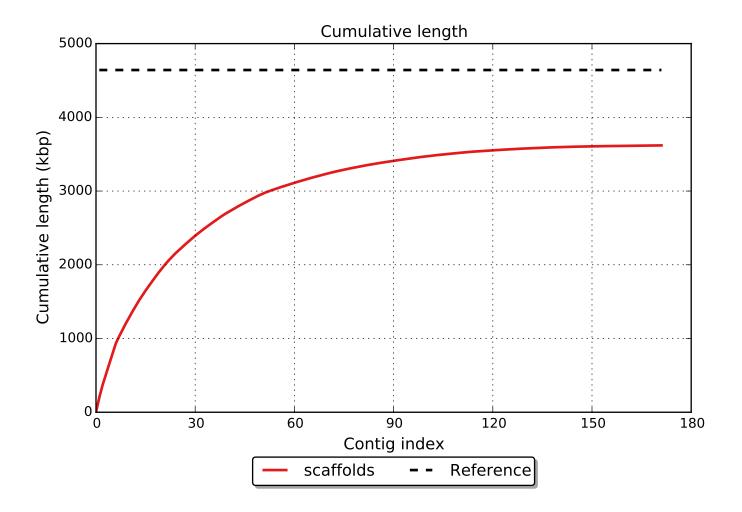
Unaligned report

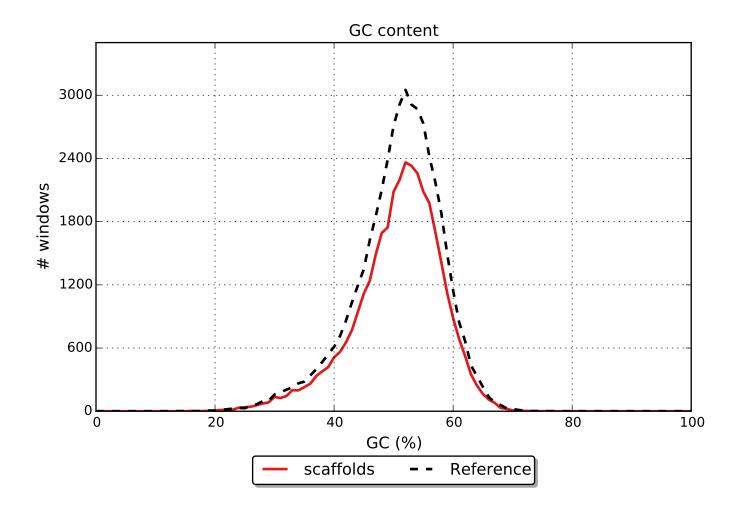
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

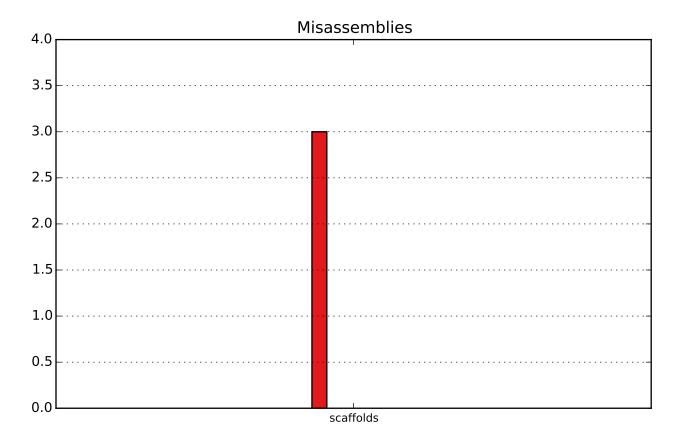
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).











relocations

