Report

	scaffolds
# contigs (>= 1000 bp)	156
# contigs (>= 5000 bp)	102
# contigs (>= 10000 bp)	79
# contigs (>= 25000 bp)	49
# contigs (>= 50000 bp)	29
Total length (>= 1000 bp)	4657108
Total length (>= 5000 bp)	4521193
Total length (>= 10000 bp)	4354132
Total length (>= 25000 bp)	3829150
Total length (>= 50000 bp)	3135020
# contigs	194
Largest contig	276573
Total length	4681622
Reference length	4641652
GC (%)	50.86
Reference GC (%)	50.79
N50	85464
NG50	85464
N75	33296
NG75	33490
L50	16
LG50	16
L75	39
LG75	38
# misassemblies	3
# misassembled contigs	2
Misassembled contigs length	156398
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	89.952
Duplication ratio	1.121
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1112.48
# indels per 100 kbp	0.67
Largest alignment	276573
NA50	76984
NGA50	76984
NA75	33296
NGA75	33490
LA50	16
LGA50	16
LA75	40
LGA75	39

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

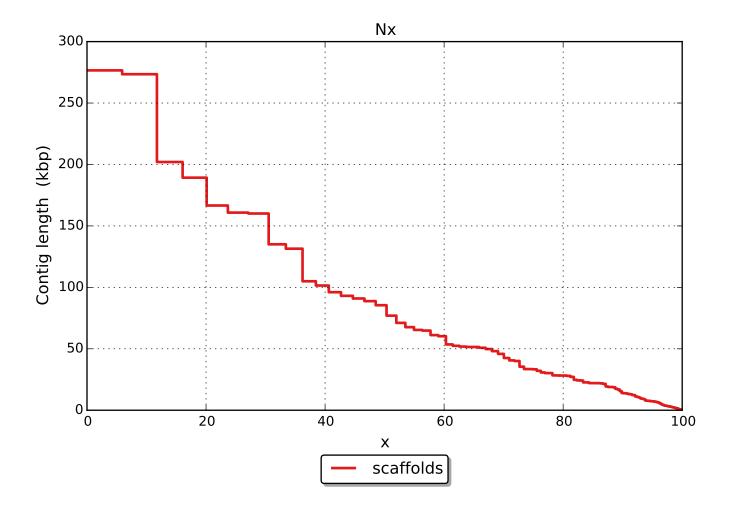
	scaffolds
# misassemblies	3
# relocations	3
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	156398
# local misassemblies	3
# mismatches	46449
# indels	28
# short indels	28
# long indels	0
Indels length	36

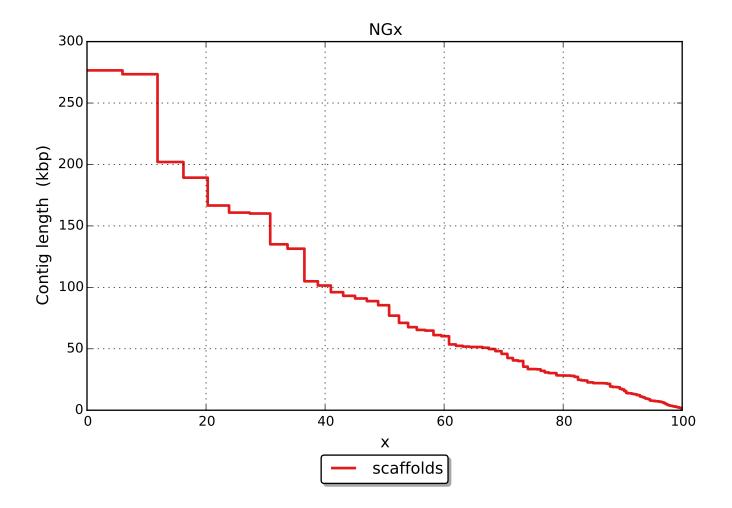
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

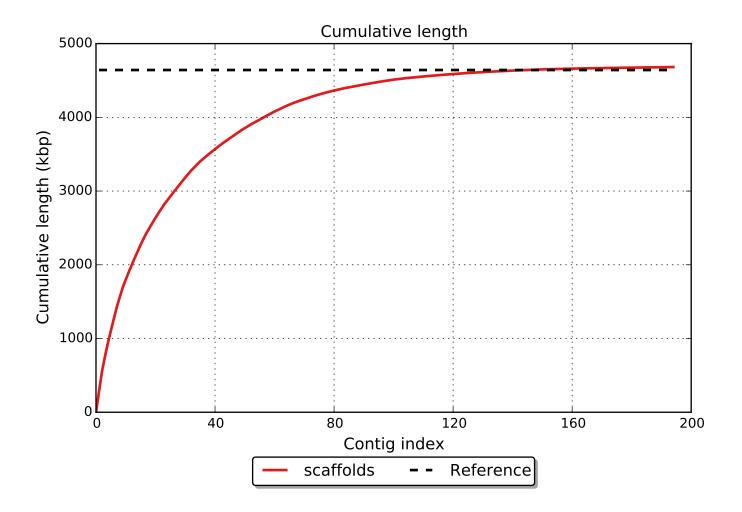
Unaligned report

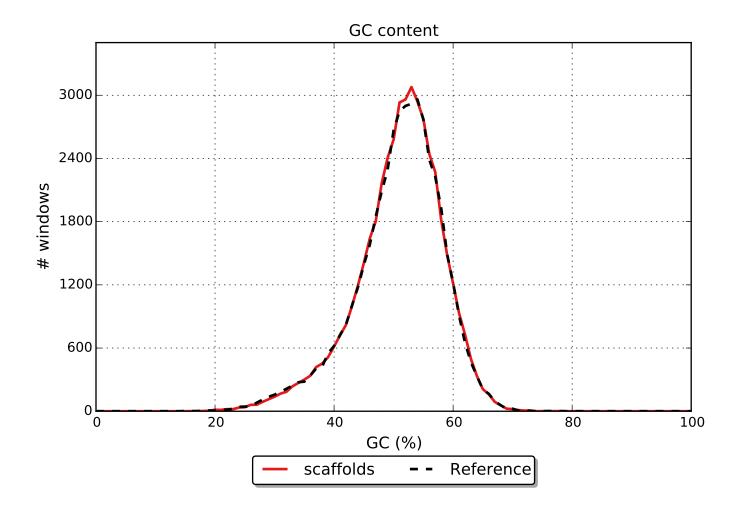
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

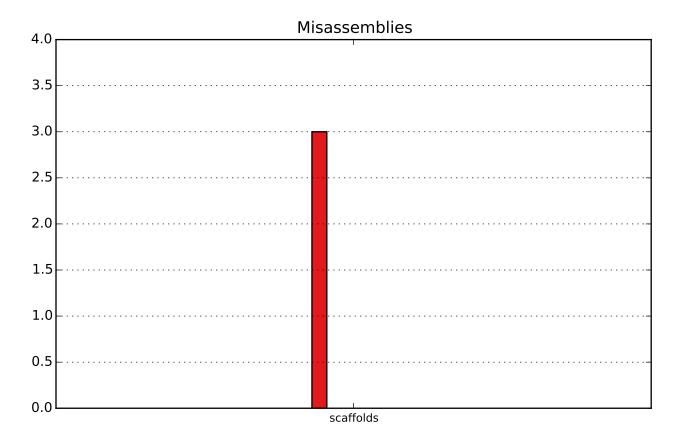
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).











relocations

