## Report

	scaffolds
# contigs (>= 1000 bp)	79
# contigs (>= 5000 bp)	60
# contigs (>= 10000 bp)	52
# contigs (>= 25000 bp)	44
# contigs (>= 50000 bp)	29
Total length (>= 1000 bp)	4558446
Total length (>= 5000 bp)	4511261
Total length (>= 10000 bp)	4449976
Total length (>= 25000 bp)	4332798
Total length (>= 50000 bp)	3835290
# contigs	84
Largest contig	327053
Total length	4562233
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	120066
NG50	117666
N75	67343
NG75	66312
L50	11
LG50	12
L75	23
LG75	24
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	140539
# local misassemblies	7
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.210
Duplication ratio	1.001
# N's per 100 kbp	2.37
# mismatches per 100 kbp	63.37
# indels per 100 kbp	8.75
Largest alignment	327053
NA50	120066
NGA50	117666
NA75	66312
NGA75	64689
LA50	11
LGA50	12
LA75	23
LGA75	24

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

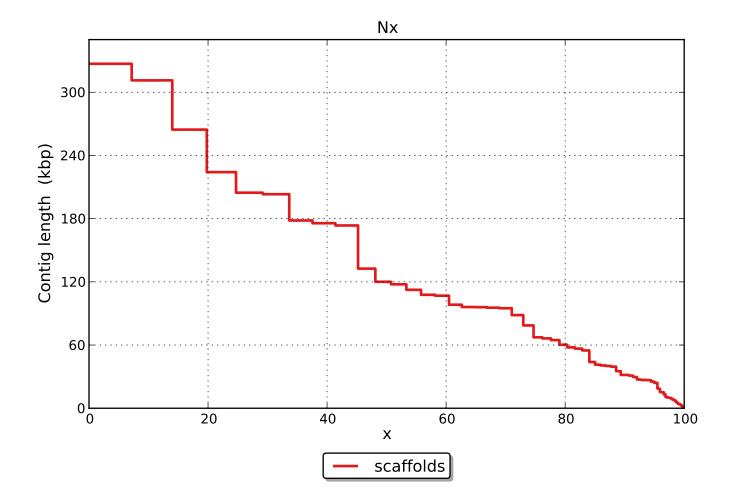
	scaffolds
# misassemblies	3
# relocations	3
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	3
Misassembled contigs length	140539
# local misassemblies	7
# mismatches	2889
# indels	399
# short indels	397
# long indels	2
Indels length	670

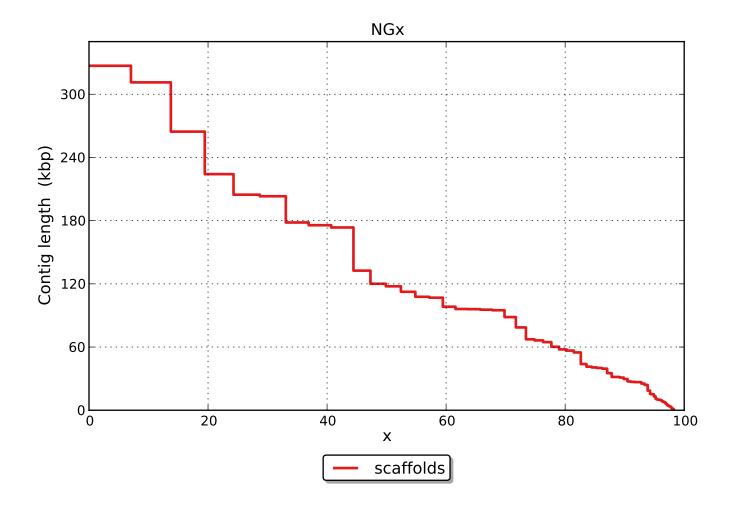
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

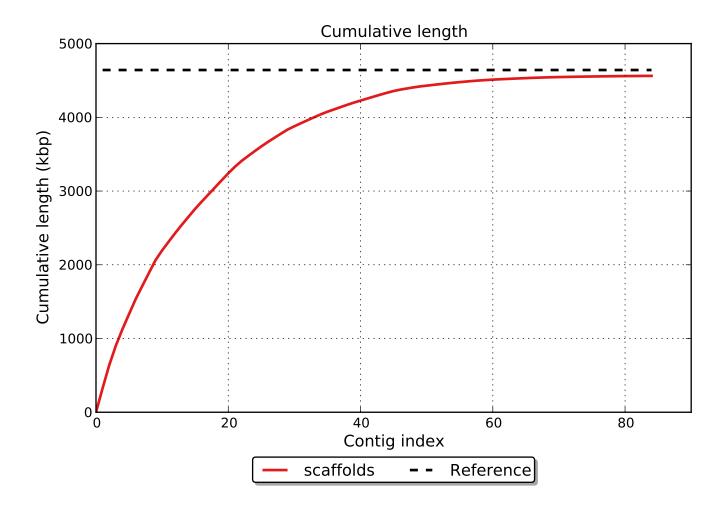
## Unaligned report

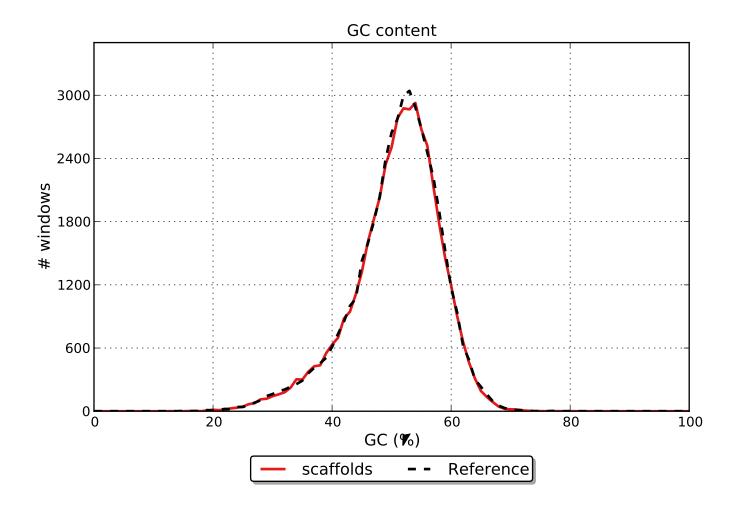
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	108

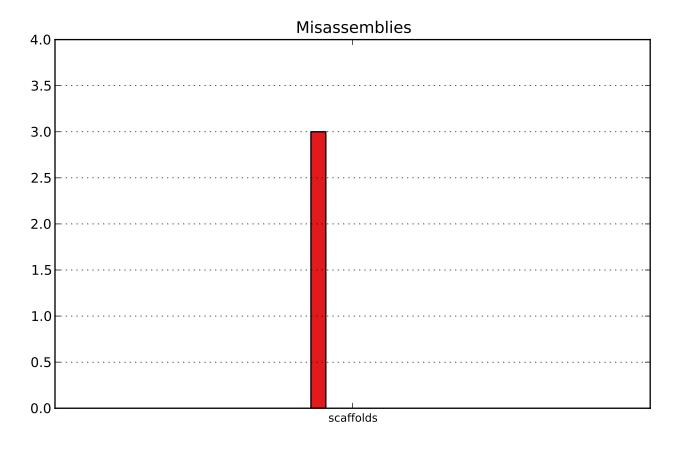
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).











# relocations

