Report

	contigs
# contigs (>= 1000 bp)	181
# contigs (>= 5000 bp)	120
# contigs (>= 10000 bp)	81
# contigs (>= 25000 bp)	32
# contigs (>= 50000 bp)	5
Total length (>= 1000 bp)	2484381
Total length (>= 5000 bp)	2318144
Total length (>= 10000 bp)	2036683
Total length (>= 25000 bp)	1318799
Total length (>= 50000 bp)	382034
# contigs	205
Largest contig	119434
Total length	2500405
Reference length	4641652
GC (%)	50.79
Reference GC (%)	50.79
N50	26371
NG50	4993
N75	12301
L50	30
LG50	121
L75	67
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	122783
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	52.688
Duplication ratio	1.022
# N's per 100 kbp	0.00
# mismatches per 100 kbp	831.41
# indels per 100 kbp	0.16
Largest alignment	119434
NA50	26371
NGA50	4839
NA75	11935
LA50	30
LGA50	123
LA75	68

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

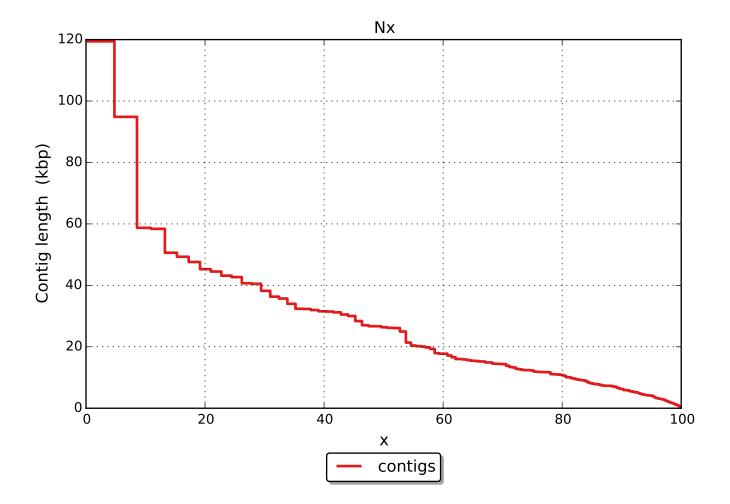
	contigs
# misassemblies	3
# relocations	3
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	3
Misassembled contigs length	122783
# local misassemblies	2
# mismatches	20333
# indels	4
# short indels	4
# long indels	0
Indels length	6

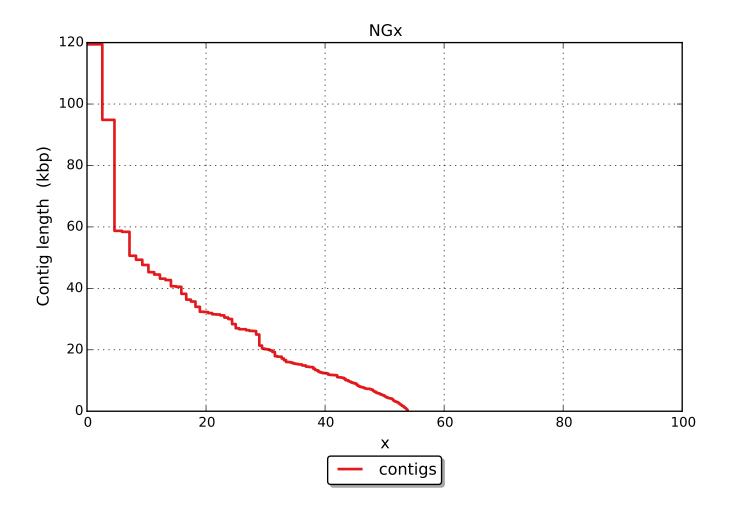
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

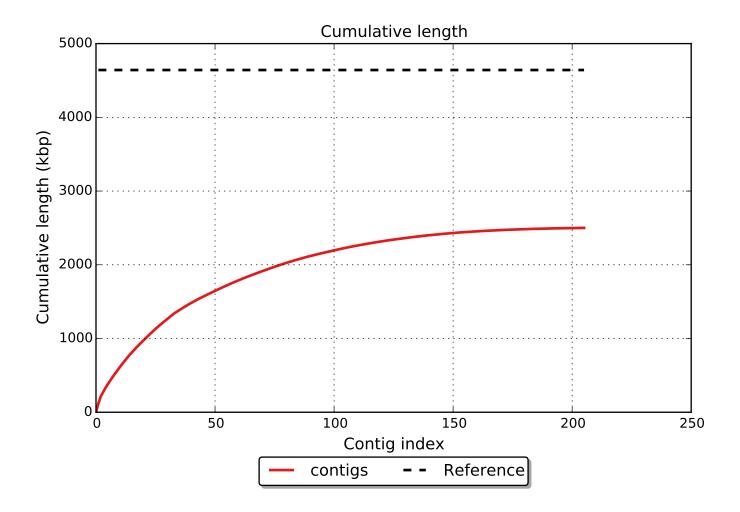
Unaligned report

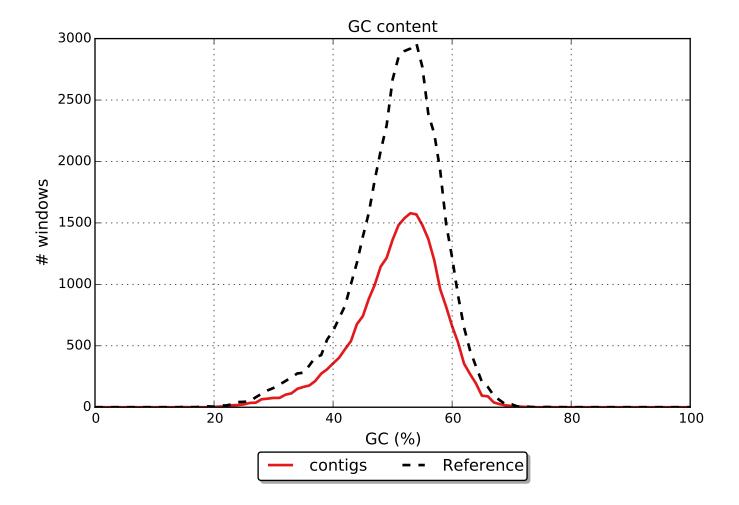
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

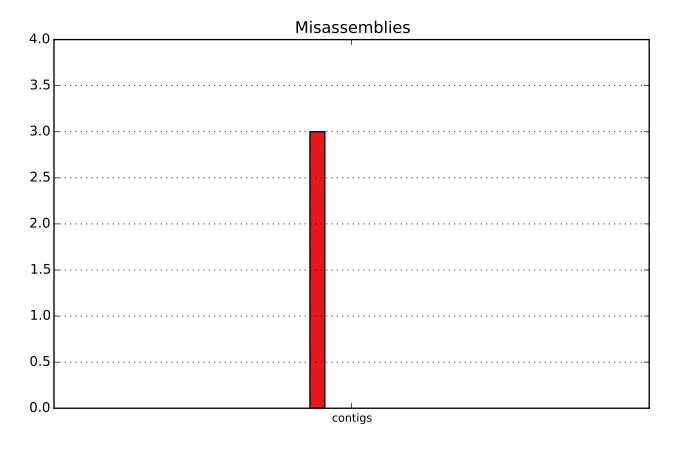
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).











relocations

