Report

	contigs
# contigs (>= 0 bp)	656
# contigs (>= 1000 bp)	116
# contigs (>= 5000 bp)	84
# contigs (>= 10000 bp)	65
# contigs (>= 25000 bp)	46
# contigs (>= 50000 bp)	27
Total length (>= 0 bp)	4615950
Total length (>= 1000 bp)	4551391
Total length (>= 5000 bp)	4478070
Total length (>= 10000 bp)	4337092
Total length (>= 25000 bp)	4018067
Total length (>= 50000 bp)	3322011
# contigs	126
Largest contig	442003
Total length	4559173
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	103408
NG50	103408
N75	47849
NG75	45031
L50	13
LG50	13
L75	29
LG75	31
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	751189
# local misassemblies	731103
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# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.108
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	21.54
# indels per 100 kbp	1.03
Largest alignment	327778
NA50	103372
NGA50	95452
NA75	45031
NGA75	43809
LA50	14
LGA50	15
LA75	32
LGA75	33
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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

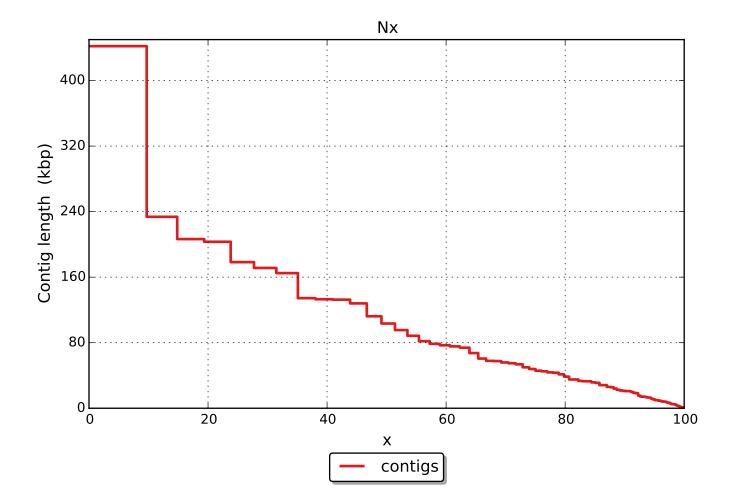
	contigs
# misassemblies	3
# relocations	3
# translocations	0
# inversions	0
# misassembled contigs	3
Misassembled contigs length	751189
# local misassemblies	4
# mismatches	981
# indels	47
# short indels	46
# long indels	1
Indels length	66

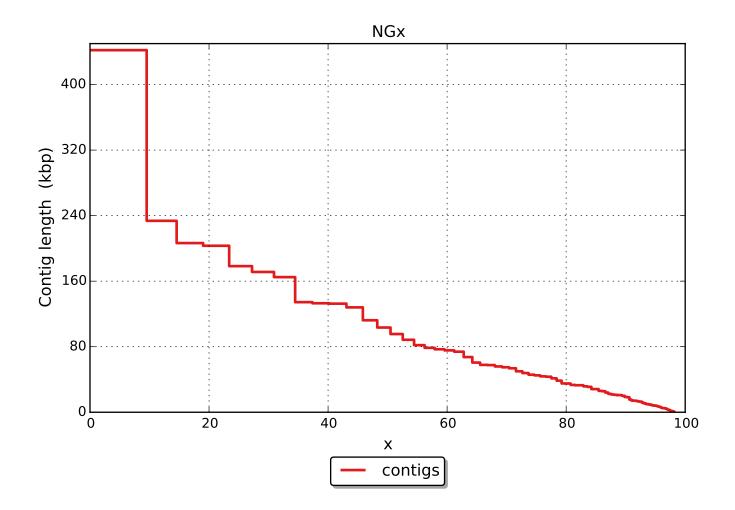
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

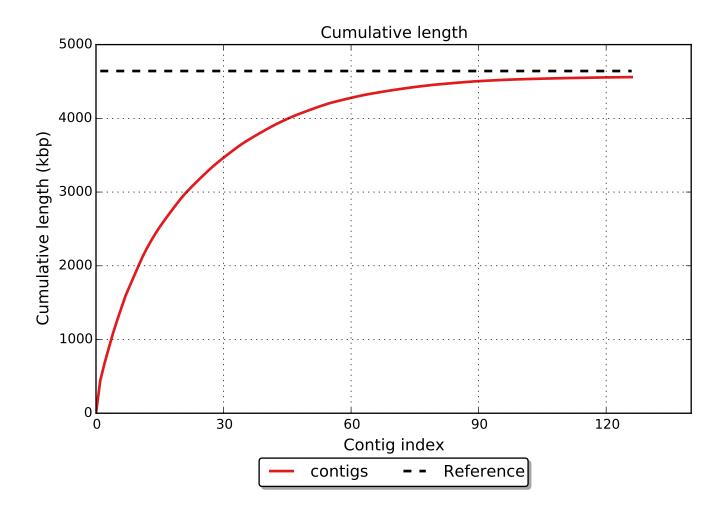
Unaligned report

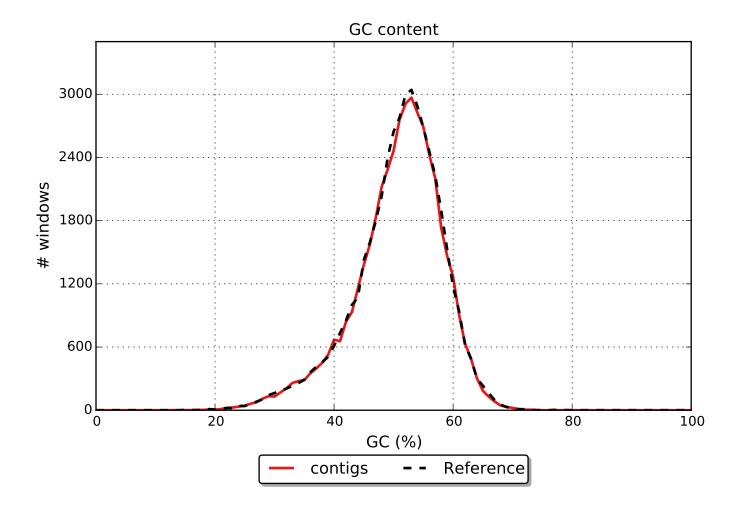
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

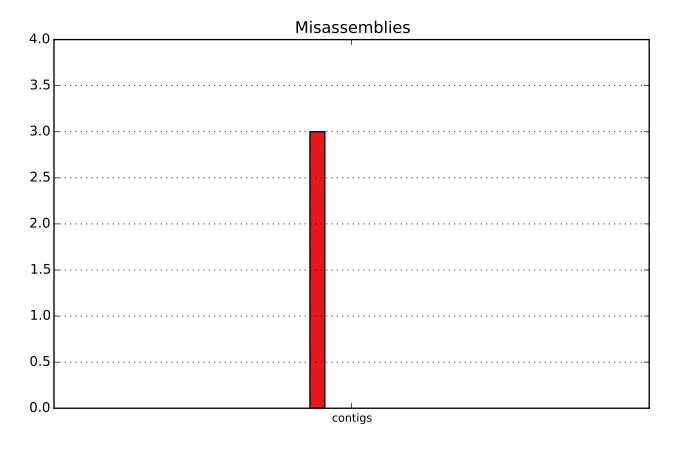
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).











relocations

