Report

# conting (> 1000 hm)	contigs
# contigs (>= 1000 bp)	216
# contigs (>= 5000 bp)	159
# contigs (>= 10000 bp)	108
# contigs (>= 25000 bp)	54
# contigs (>= 50000 bp)	28
Total length (>= 1000 bp)	4314010
Total length (>= 5000 bp)	4152620
Total length (>= 10000 bp)	3764904
Total length (>= 25000 bp)	2973596
Total length (>= 50000 bp)	2052610
# contigs	231
Largest contig	130415
Total length	4324443
Reference length	4641652
GC (%)	50.73
Reference GC (%)	50.79
N50	41809
NG50	40191
N75	17470
NG75	13416
L50	31
LG50	35
L75	68
LG75	84
# misassemblies	4
# misassembled contigs	4
Misassembled contigs length	339551
# local misassemblies	1
# unaligned contigs	0 + 1 part
Unaligned length	55
Genome fraction (%)	92.009
Duplication ratio	1.013
# N's per 100 kbp	0.00
# mismatches per 100 kbp	735.14
# indels per 100 kbp	0.26
Largest alignment	122264
NA50	40191
NGA50	36001
NA75	17470
NGA75	13416
LA50	33
LGA50	37
LA75	72
LGA75	88

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

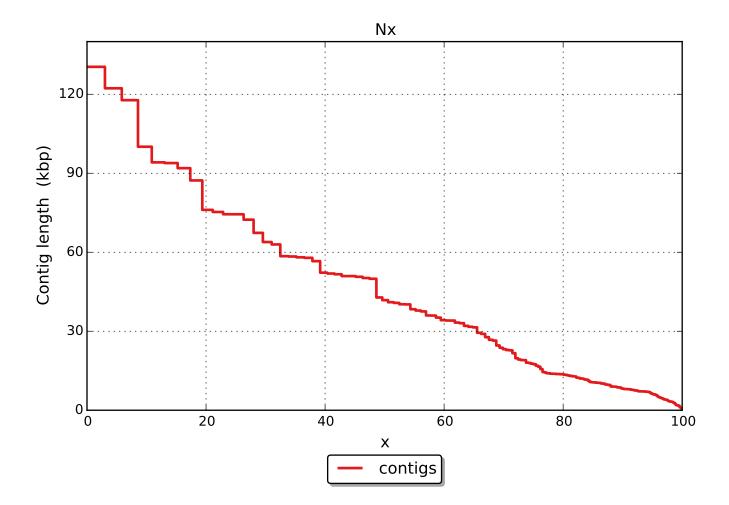
	contigs
# misassemblies	4
# relocations	4
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	4
Misassembled contigs length	339551
# local misassemblies	1
# mismatches	31396
# indels	11
# short indels	11
# long indels	0
Indels length	12

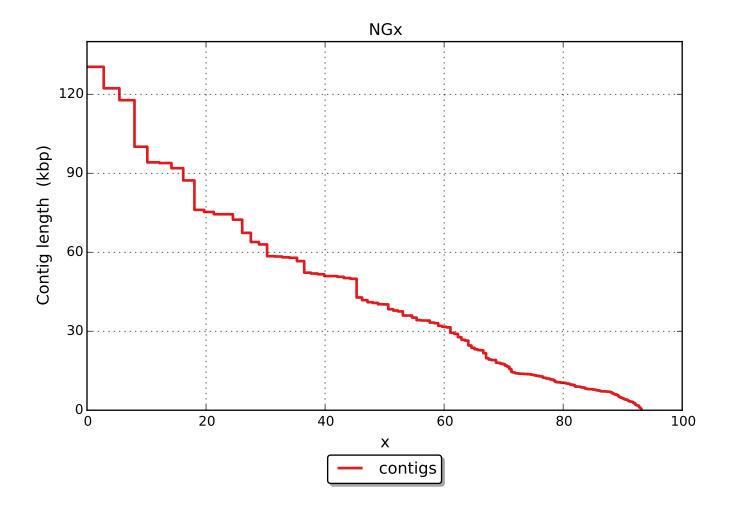
All statistics are based on contigs of size \geq 500 bp, unless otherwise noted (e.g., "# contigs (\geq 0 bp)" and "Total length (\geq 0 bp)" include all contigs).

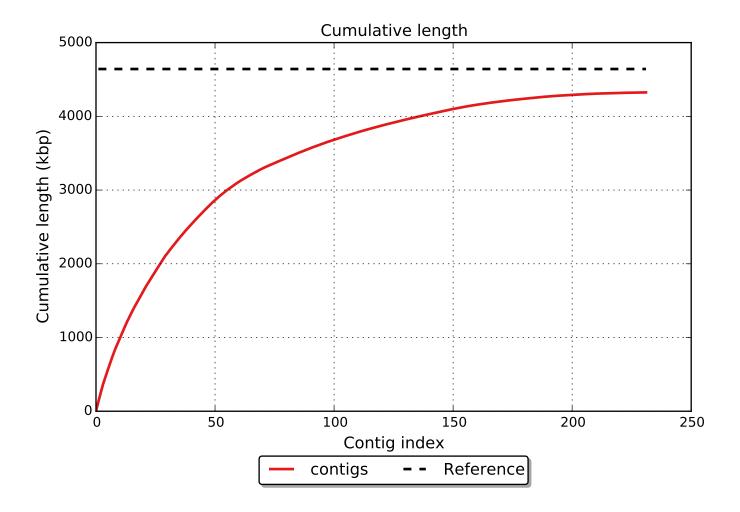
Unaligned report

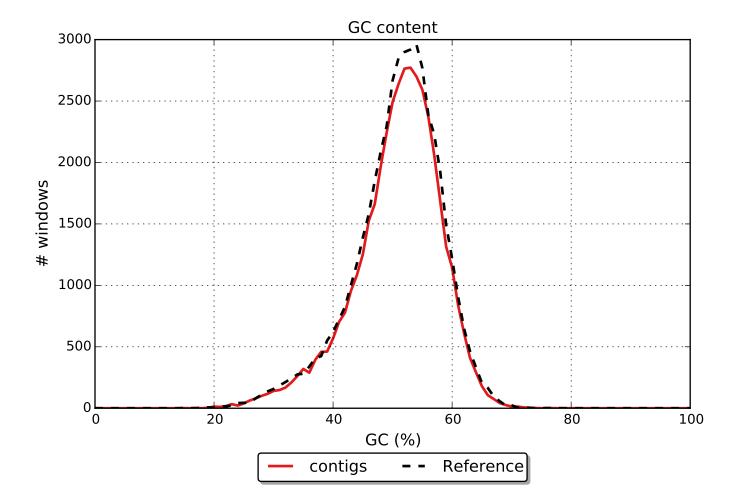
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	55
# N's	0

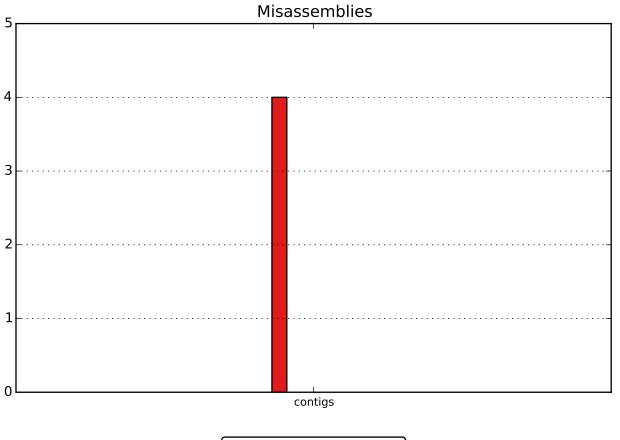
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).











relocations

