Report

Report	
	contigs
# contigs (>= 0 bp)	149
# contigs (>= 1000 bp)	79
# contigs (>= 5000 bp)	60
# contigs (>= 10000 bp)	55
# contigs (>= 25000 bp)	46
# contigs (>= 50000 bp)	28
Total length (>= 0 bp)	4573251
Total length (>= 1000 bp)	4552893
Total length (>= 5000 bp)	4513463
Total length (>= 10000 bp)	4478710
Total length (>= 25000 bp)	4348045
Total length (>= 50000 bp)	3727937
# contigs	90
Largest contig	327173
Total length	4560905
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	132608
NG50	125468
N75	78649
NG75	67278
L50	12
LG50	13
L75	23
LG75	24
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	45368
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.226
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3.55
# indels per 100 kbp	0.11
Largest alignment	327173
NA50	132608
NGA50	125468
NA75	78649
NGA75	67278
LA50	12
LGA50	13
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

	contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# misassembled contigs	1
Misassembled contigs length	45368
# local misassemblies	3
# mismatches	162
# indels	5
# short indels	5
# long indels	0
Indels length	7

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	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).















