Report

Report	
	contigs
# contigs (>= 0 bp)	120
# contigs (>= 1000 bp)	74
# contigs (>= 5000 bp)	55
# contigs (>= 10000 bp)	51
# contigs (>= 25000 bp)	43
# contigs (>= 50000 bp)	29
Total length (>= 0 bp)	4572959
Total length (>= 1000 bp)	4557661
Total length (>= 5000 bp)	4518930
Total length (>= 10000 bp)	4489662
Total length (>= 25000 bp)	4370418
Total length (>= 50000 bp)	3868080
# contigs	86
Largest contig	327173
Total length	4565978
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	133050
NG50	133050
N75	78649
NG75	67374
L50	12
LG50	12
L75	22
LG75	23
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.336
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.88
# indels per 100 kbp	0.07
Largest alignment	327173
NA50	133050
NGA50	133050
NA75	78649
NGA75	67374
LA50	12
LGA50	12
LA75	22
LGA75	23

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	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	40
# indels	3
# short indels	3
# long indels	0
Indels length	3

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).















