Report

Report	
	contigs
# contigs (>= 0 bp)	132
# contigs (>= 1000 bp)	76
# contigs (>= 5000 bp)	56
# contigs (>= 10000 bp)	52
# contigs (>= 25000 bp)	44
# contigs (>= 50000 bp)	30
Total length (>= 0 bp)	4571954
Total length (>= 1000 bp)	4555574
Total length (>= 5000 bp)	4511972
Total length (>= 10000 bp)	4482704
Total length (>= 25000 bp)	4363458
Total length (>= 50000 bp)	3865590
# contigs	87
Largest contig	327173
Total length	4563047
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	129098
NG50	129098
N75	78649
NG75	67374
L50	12
LG50	12
L75	23
LG75	24
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.278
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.69
# indels per 100 kbp	0.18
Largest alignment	327173
NA50	129098
NGA50	129098
NA75	78649
NGA75	67374
LA50	12
LGA50	12
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	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# mismatches	77
# indels	8
# short indels	7
# long indels	1
Indels length	95

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).















