Report

Report	
	contigs
# contigs (>= 0 bp)	135
# contigs (>= 1000 bp)	75
# contigs (>= 5000 bp)	54
# contigs (>= 10000 bp)	50
# contigs (>= 25000 bp)	42
# contigs (>= 50000 bp)	28
Total length (>= 0 bp)	4574269
Total length (>= 1000 bp)	4556301
Total length (>= 5000 bp)	4511382
Total length (>= 10000 bp)	4481722
Total length (>= 25000 bp)	4362915
Total length (>= 50000 bp)	3865478
# contigs	85
Largest contig	327173
Total length	4563178
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	133059
NG50	133059
N75	87059
NG75	78649
L50	11
LG50	11
L75	21
LG75	22
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.281
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.55
# indels per 100 kbp	0.04
Largest alignment	327173
NA50	133059
NGA50	133059
NA75	87059
NGA75	78649
LA50	11
LGA50	11
LA75	21
LGA75	22

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	25
# indels	2
# short indels	2
# 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).















