## Report

	contigs
# contigs (>= 0 bp)	93
# contigs (>= 1000 bp)	70
# contigs (>= 5000 bp)	53
# contigs (>= 10000 bp)	50
# contigs (>= 25000 bp)	43
# contigs (>= 50000 bp)	27
Total length (>= 0 bp)	4569505
Total length (>= 1000 bp)	4562930
	4524825
Total length (>= 5000 bp)	
Total length (>= 10000 bp)	4500857
Total length (>= 25000 bp)	4396881
Total length (>= 50000 bp)	3851252
# contigs	74
Largest contig	327064
Total length	4565990
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	175735
NG50	133022
N75	78626
NG75	78626
L50	10
LG50	11
L75	21
LG75	21
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.310
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4.87
# indels per 100 kbp	0.39
Largest alignment	327064
NA50	175735
NGA50	133022
NA75	78626
NGA75	78626
LA50	10
LGA50	11
LA75	21
LGA75	21

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	222
# indels	18
# short indels	18
# long indels	0
Indels length	25

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).

## 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).















