Report

	contigs
# contigs (>= 0 bp)	90
# contigs (>= 1000 bp)	69
# contigs (>= 5000 bp)	52
# contigs (>= 10000 bp)	47
# contigs (>= 25000 bp)	40
# contigs (>= 50000 bp)	27
Total length (>= 0 bp)	4571365
Total length (>= 1000 bp)	4566128
Total length (>= 5000 bp)	4527934
Total length (>= 10000 bp)	4488081
Total length (>= 25000 bp)	4386670
Total length (>= 50000 bp)	3929662
# contigs	71
Largest contig	327130
Total length	4567356
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	173982
NG50	173982
N75	80764
NG75	80764
L50	10
LG50	10
L75	20
LG75	20
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	40209
# local misassemblies	5
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.373
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	7.73
# indels per 100 kbp	0.48
Largest alignment	327130
NA50	173982
NGA50	173982
NA75	80764
NGA75	80764
LA50	10
LGA50	10
LA75	20
LGA75	20

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
1
1
0
0
1
40209
5
353
22
22
0
29

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).















