Report

	assembly.contigs
# contigs (>= 0 bp)	3
# contigs (>= 1000 bp)	3
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	3
# contigs (>= 25000 bp)	3
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	2658624
Total length (>= 1000 bp)	2658624
Total length (>= 5000 bp)	2658624
Total length (>= 10000 bp)	2658624
Total length (>= 25000 bp)	2658624
Total length (>= 50000 bp)	2623085
# contigs	3
Largest contig	2571483
Total length	2658624
Reference length	2610531
GC (%)	53.98
Reference GC (%)	54.14
N50	2571483
NG50	2571483
N75	2571483
NG75	2571483
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	2571483
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	2 + 0 part
Unaligned length	87141
Genome fraction (%)	97.566
Duplication ratio	1.010
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	8.60
Largest alignment	2291636
Total aligned length	2571483
NA50	2291636
NGA50	2291636
NA75	2291636
NGA75	2291636
LA50	1
LGA50	1
LA75	1
LGA75	1

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

	assembly.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# misassembled contigs	1
Misassembled contigs length	2571483
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	0
# indels	219
# indels (<= 5 bp)	219
# indels (> 5 bp)	0
Indels length	221

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

	assembly.contigs
# fully unaligned contigs	2
Fully unaligned length	87141
# partially unaligned contigs	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).





















