Report

	final.contigs
# contigs (>= 1000 bp)	1574
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	2377918
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	4416
Largest contig	4818
Total length	4384923
Reference length	4857432
GC (%)	52.21
Reference GC (%)	52.22
N50	1061
NG50	984
N75	750
NG75	662
L50	1394
LG50	1626
L75	2623
LG75	3127
# misassemblies	5
# misassembled contigs	4
Misassembled contigs length	3459
# local misassemblies	0
# unaligned contigs	0 + 2 part
Unaligned length	112
Genome fraction (%)	84.485
Duplication ratio	1.068
# N's per 100 kbp	0.00
# mismatches per 100 kbp	182.39
# indels per 100 kbp	0.37
Largest alignment	4818
NA50	1061
NGA50	983
NA75	749
NGA75	662
LA50	1394
LGA50	1626
LA75	2624
LGA75	3129

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

	final.contigs
# misassemblies	5
# relocations	3
# translocations	0
# inversions	2
# possibly misassembled contigs	0
# misassembled contigs	4
Misassembled contigs length	3459
# local misassemblies	0
# mismatches	7485
# indels	15
# short indels	15
# long indels	0
Indels length	15

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

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	112
# 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).

















