Report

	final.contigs
# contigs (>= 1000 bp)	1775
# contigs (>= 5000 bp)	51
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	3728308
Total length (>= 5000 bp)	313285
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2858
Largest contig	9722
Total length	4519000
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	1966
NG50	1924
N75	1214
NG75	1157
L50	740
LG50	771
L75	1469
LG75	1546
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	93.434
Duplication ratio	1.042
# N's per 100 kbp	0.00
# mismatches per 100 kbp	55.66
# indels per 100 kbp	0.00
Largest alignment	9722
NA50	1966
NGA50	1922
NA75	1214
NGA75	1157
LA50	740
LGA50	772
LA75	1469
LGA75	1546

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	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# mismatches	2414
# indels	0
# short indels	0
# long indels	0
Indels length	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).

Unaligned report

	final.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).















