Report

	final.contigs
# contigs (>= 1000 bp)	1789
# contigs (>= 5000 bp)	108
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4339143
Total length (>= 5000 bp)	666783
Total length (>= 10000 bp)	21815
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2567
Largest contig	11637
Total length	4911256
Reference length	4857432
GC (%)	52.23
Reference GC (%)	52.23
N50	2524
NG50	2554
N75	1496
NG75	1525
L50	623
LG50	612
L75	1253
LG75	1226
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 1 part
Unaligned length	11
Genome fraction (%)	97.315
Duplication ratio	1.039
# N's per 100 kbp	0.00
# mismatches per 100 kbp	46.39
# indels per 100 kbp	0.00
Largest alignment	11637
NA50	2524
NGA50	2554
NA75	1496
NGA75	1525
LA50	623
LGA50	612
LA75	1253
LGA75	1226

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	1
# mismatches	2193
# 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	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	11
# 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).















