Report

	final.contigs
# contigs (>= 1000 bp)	1083
# contigs (>= 5000 bp)	312
# contigs (>= 10000 bp)	53
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4482026
Total length (>= 5000 bp)	2474976
Total length (>= 10000 bp)	713597
Total length (>= 25000 bp)	713337
Total length (>= 50000 bp)	0
# contigs	1282
Largest contig	20716
Total length	4628058
Reference length	4641652
GC (%)	50.73
Reference GC (%)	50.79
N50	5312
NG50	5266
N75	3140
NG75	3121
L50	281
LG50	283
L75	564
LG75	567
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.377
Duplication ratio	1.024
# N's per 100 kbp	0.00
# mismatches per 100 kbp	23.85
# indels per 100 kbp	0.11
Largest alignment	20716
NA50	5312
NGA50	5266
NA75	3140
NGA75	3121
LA50	281
LGA50	283
LA75	564
LGA75	567

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	2
# mismatches	1078
# indels	5
# short indels	5
# long indels	0
Indels length	5

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).















