Report

	final.contigs
# contigs (>= 1000 bp)	1779
# contigs (>= 5000 bp)	20
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	3264161
Total length (>= 5000 bp)	121456
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3374
Largest contig	8916
Total length	4416820
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	1531
NG50	1468
N75	981
NG75	914
L50	930
LG50	1005
L75	1828
LG75	2007
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	90.688
Duplication ratio	1.049
# N's per 100 kbp	0.00
# mismatches per 100 kbp	71.46
# indels per 100 kbp	0.17
Largest alignment	8916
NA50	1531
NGA50	1468
NA75	981
NGA75	914
LA50	930
LGA50	1005
LA75	1829
LGA75	2007

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	3008
# indels	7
# short indels	7
# long indels	0
Indels length	7

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).















