Report

	final.contigs
# contigs (>= 0 bp)	5222
# contigs (>= 1000 bp)	1126
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	3995685
Total length (>= 1000 bp)	1659247
Total length (>= 5000 bp)	5490
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3425
Largest contig	5490
Total length	3278442
Reference length	4641652
GC (%)	50.73
Reference GC (%)	50.79
N50	1006
NG50	770
N75	731
L50	1107
LG50	1884
L75	2068
# misassemblies	12
# misassembled contigs	12
Misassembled contigs length	20015
# local misassemblies	5
# unaligned contigs	1 + 4 part
Unaligned length	1018
Genome fraction (%)	68.923
Duplication ratio	1.024
# N's per 100 kbp	0.00
# mismatches per 100 kbp	785.74
# indels per 100 kbp	0.41
Largest alignment	5093
NA50	1004
NGA50	769
NA75	729
LA50	1109
LGA50	1888
LA75	2073

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	12
# relocations	12
# translocations	0
# inversions	0
# misassembled contigs	12
Misassembled contigs length	20015
# local misassemblies	5
# mismatches	25137
# indels	13
# short indels	12
# long indels	1
Indels length	97

All statistics are based on contigs of size \geq 500 bp, unless otherwise noted (e.g., "# contigs (\geq 0 bp)" and "Total length (\geq 0 bp)" include all contigs).

Unaligned report

	final.contigs
# fully unaligned contigs	1
Fully unaligned length	570
# partially unaligned contigs	4
# with misassembly	0
# both parts are significant	0
Partially unaligned length	448
# 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).

















