Report

	final.contigs
# contigs (>= 0 bp)	20580
# contigs (>= 1000 bp)	799
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	7832962
Total length (>= 1000 bp)	1091104
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2907
Largest contig	3029
Total length	2537847
Reference length	4641652
GC (%)	50.68
Reference GC (%)	50.79
N50	914
NG50	547
N75	669
L50	985
LG50	2492
L75	1804
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	4 + 1 part
Unaligned length	2341
Genome fraction (%)	53.845
Duplication ratio	1.014
# N's per 100 kbp	0.00
# mismatches per 100 kbp	25.01
# indels per 100 kbp	0.00
Largest alignment	3029
NA50	914
NGA50	547
NA75	669
LA50	985
LGA50	2492
LA75	1804

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
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	625
# 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	4
Fully unaligned length	2142
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	199
# 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).















