Report

	final.contigs
# contigs (>= 1000 bp)	1521
# contigs (>= 5000 bp)	11
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	2675318
Total length (>= 5000 bp)	63112
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3762
Largest contig	6821
Total length	4222475
Reference length	4857432
GC (%)	52.24
Reference GC (%)	52.22
N50	1285
NG50	1121
N75	796
NG75	644
L50	1023
LG50	1288
L75	2073
LG75	2740
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	11
Genome fraction (%)	80.145
Duplication ratio	1.085
# N's per 100 kbp	0.00
# mismatches per 100 kbp	551.53
# indels per 100 kbp	0.13
Largest alignment	6821
NA50	1285
NGA50	1121
NA75	796
NGA75	644
LA50	1023
LGA50	1288
LA75	2073
LGA75	2740

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	0
# mismatches	21471
# indels	5
# short indels	4
# long indels	1
Indels length	49

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).















