## Report

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_	final.contigs
# contigs (>= 1000 bp)	941
# contigs (>= 5000 bp)	341
# contigs (>= 10000 bp)	81
# contigs (>= 25000 bp)	4
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4548620
Total length (>= 5000 bp)	2958366
Total length (>= 10000 bp)	1157119
Total length (>= 25000 bp)	125266
Total length (>= 50000 bp)	0
# contigs	1071
Largest contig	42421
Total length	4645604
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	6360
NG50	6372
N75	3776
NG75	3777
L50	230
LG50	229
L75	464
LG75	463
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	12535
# local misassemblies	11
# unaligned contigs	0 + 4 part
Unaligned length	325
Genome fraction (%)	97.627
Duplication ratio	1.025
# N's per 100 kbp	0.00
# mismatches per 100 kbp	193.14
# indels per 100 kbp	9.49
Largest alignment	42421
NA50	6340
NGA50	6357
NA75	3761
NGA75	3776
LA50	230
LGA50	229
LA75	465
LGA75	464

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	2
# relocations	2
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	12535
# local misassemblies	11
# mismatches	8752
# indels	430
# short indels	427
# long indels	3
Indels length	705

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	4
# with misassembly	0
# both parts are significant	0
Partially unaligned length	325
# 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).

















