Report

	contigs
# contigs (>= 0 bp)	149
# contigs (>= 1000 bp)	89
# contigs (>= 5000 bp)	67
# contigs (>= 10000 bp)	60
# contigs (>= 25000 bp)	49
# contigs (>= 50000 bp)	30
Total length (>= 0 bp)	4568976
Total length (>= 1000 bp)	4552548
Total length (>= 5000 bp)	4501174
Total length (>= 10000 bp)	4444161
Total length (>= 25000 bp)	4272903
Total length (>= 50000 bp)	3577539
# contigs	96
Largest contig	218665
Total length	4557157
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	125834
NG50	111959
N75	56662
NG75	56395
L50	14
LG50	15
L75	28
LG75	29
# misassemblies	7
# misassembled contigs	6
Misassembled contigs length	551437
# local misassemblies	15
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.119
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	14.84
# indels per 100 kbp	0.37
Largest alignment	203215
NA50	97563
NGA50	97563
NA75	54905
NGA75	46804
LA50	15
LGA50	15
LA75	30
LGA75	31
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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

	contigs
# misassemblies	7
# relocations	7
# translocations	0
# inversions	0
# misassembled contigs	6
Misassembled contigs length	551437
# local misassemblies	15
# mismatches	676
# indels	17
# short indels	17
# long indels	0
Indels length	18

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

	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

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