Report

	contigs
# contigs (>= 0 bp)	104
# contigs (>= 1000 bp)	71
# contigs (>= 5000 bp)	53
# contigs (>= 10000 bp)	48
# contigs (>= 25000 bp)	42
# contigs (>= 50000 bp)	28
Total length (>= 0 bp)	4576278
Total length (>= 1000 bp)	4563195
Total length (>= 5000 bp)	4524242
Total length (>= 10000 bp)	4486972
Total length (>= 25000 bp)	4396655
Total length (>= 50000 bp)	3920790
# contigs	83
Largest contig	327173
Total length	4571621
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	133063
NG50	133063
N75	87186
NG75	78670
L50	11
LG50	11
L75	21
LG75	22
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.414
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.34
# indels per 100 kbp	0.18
Largest alignment	327173
NA50	133063
NGA50	133063
NA75	87186
NGA75	78670
LA50	11
LGA50	11
LA75	21
LGA75	22
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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	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	61
# indels	8
# short indels	7
# long indels	1
Indels length	93

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

	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

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).















