Report

	contigs
# contigs (>= 0 bp)	148
# contigs (>= 1000 bp)	73
# contigs (>= 5000 bp)	55
# contigs (>= 10000 bp)	49
# contigs (>= 25000 bp)	43
# contigs (>= 50000 bp)	28
Total length (>= 0 bp)	4581403
Total length (>= 1000 bp)	4557850
Total length (>= 5000 bp)	4516322
Total length (>= 10000 bp)	4473681
Total length (>= 25000 bp)	4383496
Total length (>= 50000 bp)	3869336
# contigs	86
Largest contig	327173
Total length	4566921
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	133063
NG50	133063
N75	86908
NG75	78649
L50	11
LG50	11
L75	21
LG75	22
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	10
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.313
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2.08
# indels per 100 kbp	0.26
Largest alignment	327173
NA50	133063
NGA50	133063
NA75	86908
NGA75	78649
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	10
# mismatches	95
# indels	12
# short indels	11
# long indels	1
Indels length	98

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).















