Report

	contigs
# contigs (>= 0 bp)	666
# contigs (>= 1000 bp)	107
# contigs (>= 5000 bp)	80
# contigs (>= 10000 bp)	68
# contigs (>= 25000 bp)	51
# contigs (>= 50000 bp)	30
Total length (>= 0 bp)	4663272
Total length (>= 1000 bp)	4545865
	4484332
Total length (>= 5000 bp)	
Total length (>= 10000 bp)	4393936
Total length (>= 25000 bp)	4130454
Total length (>= 50000 bp)	3342343
# contigs	122
Largest contig	270058
Total length	4556258
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	95119
NG50	88492
N75	45385
NG75	45329
L50	15
LG50	16
L75	32
LG75	33
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# unaligned contigs	0 + 1 part
Unaligned length	25
Genome fraction (%)	98.088
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	12.28
# indels per 100 kbp	0.46
Largest alignment	269883
NA50	95116
NGA50	88492
NA75	45385
NGA75	45329
LA50	15
LGA50	16
LA75	32
LGA75	33
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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	4
# mismatches	559
# indels	21
# short indels	20
# long indels	1
Indels length	39

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	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	25
# 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).















