Report

contigs (>= 1000 bp) 52 # contigs (>= 5000 bp) 45 # contigs (>= 10000 bp) 42 # contigs (>= 25000 bp) 39 # contigs (>= 50000 bp) 26 Total length (>= 10000 bp) 4690269 Total length (>= 50000 bp) 4667324 Total length (>= 25000 bp) 4620809 Total length (>= 25000 bp) 4620809 Total length (>= 50000 bp) 4177287 # contigs 58 Largest contig 349059 Total length 4708824 Reference length 4641652 GC (%) 50.72 Reference GC (%) 50.79 N50 177303 N75 99302 NG75 99302 L50 9 L50 9 L75 18 LG75 18 # misassemblies 4 # misassembled contigs 3 Misassembled contigs 3 Misassembled contigs 18 # unaligned length 0 Genome fraction (%) 97.533 Duplication ratio 1.040 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.44 Largest alignment 333124
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L75 18 LG75 18 # misassemblies 4 # misassembled contigs 3 Misassembled contigs length 711322 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.533 Duplication ratio 1.040 # N's per 100 kbp 0.00 # mismatches per 100 kbp 246.65 # indels per 100 kbp 0.44
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Misassembled contigs length 711322 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.533 Duplication ratio 1.040 # N's per 100 kbp 0.00 # mismatches per 100 kbp 246.65 # indels per 100 kbp 0.44
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Largest alignment 333124
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NA50 173841
NGA50 173841
NA75 87711
NGA75 94467
LA50 10
LGA50 10
LGA50 10 LA75 20 LGA75 19

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

	scaffolds
# misassemblies	4
# relocations	4
# translocations	0
# inversions	0
# possibly misassembled contigs	1
# misassembled contigs	3
Misassembled contigs length	711322
# local misassemblies	1
# mismatches	11166
# indels	20
# short indels	20
# long indels	0
Indels length	20

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

	scaffolds
# 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).

















