Report

# contigs (>= 1000 bp)		scaffolds
# contigs (>= 5000 bp) 122 # contigs (>= 10000 bp) 109 # contigs (>= 25000 bp) 81 # contigs (>= 50000 bp) 51 Total length (>= 10000 bp) 7922221 Total length (>= 10000 bp) 7825936 Total length (>= 10000 bp) 7825936 Total length (>= 50000 bp) 7352421 Total length (>= 50000 bp) 7352421 Total length (>= 50000 bp) 6316616 # contigs 221 Largest contig 333495 Total length 8085605 Reference length 4641652 GC (%) 50.79 Reference GC (%) 50.79 N50 97773 NG50 188986 N75 63382 NG75 125151 L50 22 LG50 9 L75 47 LG75 17 # misassemblies 178 # misassembled contigs 38 Misassembled contigs length 3564233 # local misassemblies 6 # unaligned length 1233 Genome fraction (%) 97.857 Duplication ratio 1.780 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.19 Largest alignment 317313 NA50 54877 NGA75 63382 LA50 39 LA50 39 LA50 39 LA50 14 LA75 99	# contigs (>= 1000 bp)	
# contigs (>= 10000 bp) 109 # contigs (>= 25000 bp) 81 # contigs (>= 50000 bp) 51 Total length (>= 1000 bp) 7922221 Total length (>= 10000 bp) 7825936 Total length (>= 25000 bp) 7352421 Total length (>= 50000 bp) 7352421 Total length (>= 50000 bp) 6316616 # contigs 221 Largest contig 333495 Total length 8085605 Reference length 4641652 GC (%) 50.79 Reference GC (%) 50.78 N50 97773 NG50 188986 N75 63382 NG75 125151 L50 22 LG50 9 L75 47 LG75 17 # misassemblies 178 # misassembled contigs 38 Misassembled contigs 178 # misassembled contigs 199 # local misassemblies 6 # unaligned length 1233 Genome fraction (%) 97.857 Duplication ratio 1.780 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.19 Largest alignment 317313 NA50 54877 NGA50 92158 NA75 63382 LA50 39 LGA50 14 LA75 99		122
# contigs (>= 25000 bp)		109
# contigs (>= 50000 bp) 51 Total length (>= 1000 bp) 8057406 Total length (>= 5000 bp) 7922221 Total length (>= 10000 bp) 7825936 Total length (>= 25000 bp) 7352421 Total length (>= 50000 bp) 6316616 # contigs 221 Largest contig 333495 Total length 8085605 Reference length 4641652 GC (%) 50.79 Reference GC (%) 50.78 N50 97773 NG50 188986 N75 63382 NG75 125151 L50 22 LG50 9 L75 47 LG75 17 # misassemblies 178 # misassembled contigs 38 Misassembled contigs 38 Misassembled contigs 6 # unaligned contigs 0 + 2 part Unaligned length 1233 Genome fraction (%) 97.857 Duplication ratio 1.780 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.19 Largest alignment 317313 NA50 54877 NGA50 92158 NA75 63382 LGA50 14 LA75 99		81
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Total length (>= 10000 bp) 7825936 Total length (>= 25000 bp) 7352421 Total length (>= 50000 bp) 6316616 # contigs 221 Largest contig 333495 Total length 8085605 Reference length 4641652 GC (%) 50.79 Reference GC (%) 50.78 N50 97773 NG50 188986 N75 63382 NG75 125151 L50 22 LG50 9 L75 47 LG75 17 # misassemblies 178 # misassembled contigs 38 Misassembled contigs 38 Misassembled contigs 178 # local misassemblies 6 # unaligned contigs 0 + 2 part Unaligned length 1233 Genome fraction (%) 97.857 Duplication ratio 1.780 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1322.01 # indels per 100 kbp 1.19 Largest alignment 317313 NA50 54877 NGA50 92158 NA75 24175 NGA75 63382 LA50 39 LA50 39 LA50 39 LA50 39	Total length (>= 1000 bp)	8057406
Total length (>= 25000 bp) 7352421 Total length (>= 50000 bp) 6316616 # contigs 221 Largest contig 333495 Total length 8085605 Reference length 4641652 GC (%) 50.79 Reference GC (%) 50.78 N50 97773 NG50 188986 N75 63382 NG75 125151 L50 22 LG50 9 L75 47 LG75 17 # misassemblies 178 # misassembled contigs 38 Misassembled contigs 38 Misassembled contigs 178 # local misassemblies 6 # unaligned contigs 0 + 2 part Unaligned length 1233 Genome fraction (%) 97.857 Duplication ratio 1.780 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1322.01 # indels per 100 kbp 1.19 Largest alignment 317313 NA50 54877 NGA50 92158 NA75 24175 NGA75 63382 LA50 39 LGA50 14 LA75 99	Total length (>= 5000 bp)	7922221
Total length (>= 50000 bp) 6316616 # contigs 221 Largest contig 333495 Total length 8085605 Reference length 4641652 GC (%) 50.79 Reference GC (%) 50.78 N50 97773 NG50 188986 N75 63382 NG75 125151 L50 22 LG50 9 L75 47 LG75 17 # misassemblies 178 # incal misassembled contigs 38 Misassembled contigs length 3564233 # local misassemblies 6 # unaligned contigs 0 + 2 part Unaligned length 1233 Genome fraction (%) 97.857 Duplication ratio 1.780 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1322.01 # indels per 100 kbp 1.19 Largest alignment 317313 NA50 92158 NA75 24175 NGA50 9	Total length (>= 10000 bp)	7825936
# contigs 221 Largest contig 333495 Total length 8085605 Reference length 4641652 GC (%) 50.79 Reference GC (%) 50.78 N50 97773 NG50 188986 N75 63382 NG75 125151 L50 22 LG50 9 L75 47 LG75 17 # misassemblies 178 # misassembled contigs 38 Misassembled contigs 38 Misassembled contigs 38 Misassembled contigs 0 + 2 part Unaligned length 1233 Genome fraction (%) 97.857 Duplication ratio 1.780 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1322.01 # indels per 100 kbp 1.19 Largest alignment 317313 NA50 54877 NGA50 92158 NA75 24175 NGA75 63382 LA50 39 LGA50 14 LA75 99	Total length (>= 25000 bp)	7352421
Largest contig 333495 Total length 8085605 Reference length 4641652 GC (%) 50.79 Reference GC (%) 50.78 N50 97773 NG50 188986 N75 63382 NG75 125151 L50 22 LG50 9 L75 47 LG75 17 # misassemblies 178 # misassembled contigs 38 Misassembled contigs length 3564233 # local misassemblies 6 # unaligned contigs 0 + 2 part Unaligned length 1233 Genome fraction (%) 97.857 Duplication ratio 1.780 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.322.01 # indels per 100 kbp 1.313 NA50 54877 NGA50 92158 NA75 24175 NGA50 92158 NA75 63382 LA50 39 LGA50 <td>Total length (>= 50000 bp)</td> <td>6316616</td>	Total length (>= 50000 bp)	6316616
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Reference length 4641652 GC (%) 50.79 Reference GC (%) 50.78 N50 97773 NG50 188986 N75 63382 NG75 125151 L50 22 LG50 9 L75 47 LG75 17 # misassemblies 178 # misassembled contigs 38 Misassembled contigs length 3564233 # local misassemblies 6 # unaligned contigs 0 + 2 part Unaligned length 1233 Genome fraction (%) 97.857 Duplication ratio 1.780 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1322.01 # indels per 100 kbp 1.19 Largest alignment 317313 NA50 54877 NGA50 92158 NA75 24175 NGA75 63382 LA50 39 LGA50 14 LA75 99	Largest contig	333495
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Reference GC (%) 50.78 N50 97773 NG50 188986 N75 63382 NG75 125151 L50 22 LG50 9 L75 47 LG75 17 # misassemblies 178 # misassembled contigs 38 Misassembled contigs length 3564233 # local misassemblies 6 # unaligned contigs 0 + 2 part Unaligned length 1233 Genome fraction (%) 97.857 Duplication ratio 1.780 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1322.01 # indels per 100 kbp 1.19 Largest alignment 317313 NA50 54877 NGA50 92158 NA75 24175 NGA75 63382 LA50 39 LGA50 14 LA75 99	Reference length	4641652
N50 97773 NG50 188986 N75 63382 NG75 125151 L50 22 LG50 9 L75 47 LG75 17 # misassemblies 178 # misassembled contigs 38 Misassembled contigs length 3564233 # local misassemblies 6 # unaligned contigs 0 + 2 part Unaligned length 1233 Genome fraction (%) 97.857 Duplication ratio 1.780 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1322.01 # indels per 100 kbp 1.19 Largest alignment 317313 NA50 54877 NGA50 92158 NA75 24175 NGA75 63382 LA50 39 LGA50 14 LA75 99	GC (%)	50.79
NG50 188986 N75 63382 NG75 125151 L50 22 LG50 9 L75 47 LG75 17 # misassemblies 178 # misassembled contigs 38 Misassembled contigs length 3564233 # local misassemblies 6 # unaligned contigs 0 + 2 part Unaligned length 1233 Genome fraction (%) 97.857 Duplication ratio 1.780 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1322.01 # indels per 100 kbp 1.19 Largest alignment 317313 NA50 54877 NGA50 92158 NA75 24175 NGA75 63382 LA50 39 LGA50 14 LA75 99	Reference GC (%)	50.78
N75 63382 NG75 125151 L50 22 LG50 9 L75 47 LG75 17 # misassemblies 178 # misassembled contigs 38 Misassembled contigs length 3564233 # local misassemblies 6 # unaligned contigs 0 + 2 part Unaligned length 1233 Genome fraction (%) 97.857 Duplication ratio 1.780 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1322.01 # indels per 100 kbp 1.19 Largest alignment 317313 NA50 54877 NGA50 92158 NA75 24175 NGA75 63382 LA50 39 LGA50 14 LA75 99	N50	97773
NG75 125151 L50 22 LG50 9 L75 47 LG75 17 # misassemblies 178 # misassembled contigs 38 Misassembled contigs length 3564233 # local misassemblies 6 # unaligned contigs 0 + 2 part Unaligned length 1233 Genome fraction (%) 97.857 Duplication ratio 1.780 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1322.01 # indels per 100 kbp 1.19 Largest alignment 317313 NA50 54877 NGA50 92158 NA75 24175 NGA75 63382 LA50 39 LGA50 14 LA75 99	NG50	188986
L50 22 LG50 9 L75 47 LG75 17 # misassemblies 178 # misassembled contigs 38 Misassembled contigs length 3564233 # local misassemblies 6 # unaligned contigs 0 + 2 part Unaligned length 1233 Genome fraction (%) 97.857 Duplication ratio 1.780 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1322.01 # indels per 100 kbp 1.19 Largest alignment 317313 NA50 54877 NGA50 92158 NA75 24175 NGA75 63382 LA50 39 LGA50 14 LA75 99	N75	63382
LG50 9 L75 47 LG75 17 # misassemblies 178 # misassembled contigs 38 Misassembled contigs length 3564233 # local misassemblies 6 # unaligned contigs 0 + 2 part Unaligned length 1233 Genome fraction (%) 97.857 Duplication ratio 1.780 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1322.01 # indels per 100 kbp 1.19 Largest alignment 317313 NA50 54877 NGA50 92158 NA75 24175 NGA75 63382 LA50 39 LGA50 14 LA75 99	NG75	125151
L75 47 LG75 17 # misassemblies 178 # misassembled contigs 38 Misassembled contigs length 3564233 # local misassemblies 6 # unaligned contigs 0 + 2 part Unaligned length 1233 Genome fraction (%) 97.857 Duplication ratio 1.780 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1322.01 # indels per 100 kbp 1.19 Largest alignment 317313 NA50 54877 NGA50 92158 NA75 24175 NGA75 63382 LA50 39 LGA50 14 LA75 99	L50	22
LG75 17 # misassemblies 178 # misassembled contigs 38 Misassembled contigs length 3564233 # local misassemblies 6 # unaligned contigs 0 + 2 part Unaligned length 1233 Genome fraction (%) 97.857 Duplication ratio 1.780 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1322.01 # indels per 100 kbp 1.19 Largest alignment 317313 NA50 54877 NGA50 92158 NA75 24175 NGA75 63382 LA50 39 LGA50 14 LA75 99	LG50	9
# misassemblies 178 # misassembled contigs 38 Misassembled contigs length 3564233 # local misassemblies 6 # unaligned contigs 0 + 2 part Unaligned length 1233 Genome fraction (%) 97.857 Duplication ratio 1.780 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1322.01 # indels per 100 kbp 1.19 Largest alignment 317313 NA50 54877 NGA50 92158 NA75 24175 NGA75 63382 LA50 39 LGA50 14	L75	47
# misassembled contigs 38 Misassembled contigs length 3564233 # local misassemblies 6 # unaligned contigs 0 + 2 part Unaligned length 1233 Genome fraction (%) 97.857 Duplication ratio 1.780 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1322.01 # indels per 100 kbp 1.19 Largest alignment 317313 NA50 54877 NGA50 92158 NA75 24175 NGA75 63382 LA50 39 LGA50 14 LA75 99	LG75	17
Misassembled contigs length 3564233 # local misassemblies 6 # unaligned contigs 0 + 2 part Unaligned length 1233 Genome fraction (%) 97.857 Duplication ratio 1.780 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1322.01 # indels per 100 kbp 1.19 Largest alignment 317313 NA50 54877 NGA50 92158 NA75 24175 NGA75 63382 LA50 39 LGA50 14 LA75 99	# misassemblies	178
# local misassemblies 6 # unaligned contigs 0 + 2 part Unaligned length 1233 Genome fraction (%) 97.857 Duplication ratio 1.780 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1322.01 # indels per 100 kbp 1.19 Largest alignment 317313 NA50 54877 NGA50 92158 NA75 24175 NGA75 63382 LA50 39 LGA50 14	# misassembled contigs	38
# unaligned contigs 0 + 2 part Unaligned length 1233 Genome fraction (%) 97.857 Duplication ratio 1.780 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1322.01 # indels per 100 kbp 1.19 Largest alignment 317313 NA50 54877 NGA50 92158 NA75 24175 NGA75 63382 LA50 39 LGA50 14 LA75 99	Misassembled contigs length	3564233
Unaligned length 1233 Genome fraction (%) 97.857 Duplication ratio 1.780 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1322.01 # indels per 100 kbp 1.19 Largest alignment 317313 NA50 54877 NGA50 92158 NA75 24175 NGA75 63382 LA50 39 LGA50 14 LA75 99	# local misassemblies	6
Genome fraction (%) 97.857 Duplication ratio 1.780 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1322.01 # indels per 100 kbp 1.19 Largest alignment 317313 NA50 54877 NGA50 92158 NA75 24175 NGA75 63382 LA50 39 LGA50 14 LA75 99		0 + 2 part
Duplication ratio 1.780 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1322.01 # indels per 100 kbp 1.19 Largest alignment 317313 NA50 54877 NGA50 92158 NA75 24175 NGA75 63382 LA50 39 LGA50 14 LA75 99	Unaligned length	1233
# N's per 100 kbp 0.00 # mismatches per 100 kbp 1322.01 # indels per 100 kbp 1.19 Largest alignment 317313 NA50 54877 NGA50 92158 NA75 24175 NGA75 63382 LA50 39 LGA50 14 LA75 99		97.857
# mismatches per 100 kbp 1322.01 # indels per 100 kbp 1.19 Largest alignment 317313 NA50 54877 NGA50 92158 NA75 24175 NGA75 63382 LA50 39 LGA50 14 LA75 99		
# indels per 100 kbp 1.19 Largest alignment 317313 NA50 54877 NGA50 92158 NA75 24175 NGA75 63382 LA50 39 LGA50 14 LA75 99		
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NGA75 63382 LA50 39 LGA50 14 LA75 99		92158
LA50 39 LGA50 14 LA75 99		
LGA50 14 LA75 99		
LA75 99		
LGA75 30		
	LGA75	30

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	178
# relocations	151
# translocations	0
# inversions	27
# possibly misassembled contigs	3
# misassembled contigs	38
Misassembled contigs length	3564233
# local misassemblies	6
# mismatches	60048
# indels	54
# short indels	54
# long indels	0
Indels length	62

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	2
# with misassembly	0
# both parts are significant	2
Partially unaligned length	1233
# 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).

















