Report

# contigs (>= 1000 bp) 91 # contigs (>= 5000 bp) 91 # contigs (>= 10000 bp) 73 # contigs (>= 25000 bp) 48 # contigs (>= 50000 bp) 31 Total length (>= 10000 bp) 3847604 Total length (>= 50000 bp) 3784308 Total length (>= 10000 bp) 3656982 Total length (>= 25000 bp) 3267331 Total length (>= 50000 bp) 3267331 Total length (>= 50000 bp) 2692246 # contigs 124 Largest contig 161420 Total length 3853478 Reference length 4641652 GC (%) 50.76 Reference GC (%) 50.78 N50 73015 NG50 73015 NG50 73015 NG50 15441 L50 19 LG50 25 L75 36 LG75 39 # misassemblies 5 # misassembled contigs 5 # misassembled contigs 5 Misassembled contigs 1000 # N's per 100 kbp 15.93 # mismatches per 100 kbp 0.42 Largest alignment 142244 NA50 72917 NGA50 19 LGA50 25 LA75 3351 LA50 19 LGA50 25 LA75 338 LGA75 338 LGA75 338 LGA75 338 LGA75 338 LGA75 338		scaffolds
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# contigs (>= 50000 bp) 31 Total length (>= 1000 bp) 3847604 Total length (>= 5000 bp) 3784308 Total length (>= 10000 bp) 3656982 Total length (>= 25000 bp) 3267331 Total length (>= 50000 bp) 2692246 # contigs 124 Largest contig 161420 Total length 3853478 Reference length 4641652 GC (%) 50.76 Reference GC (%) 50.78 N50 73015 NG50 73015 NG50 59673 N75 35258 NG75 15441 L50 19 LG50 25 L75 36 LG75 59 # misassemblies 5 # misassembled contigs 5 Misassembled contigs 10368 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 82.879 Duplication ratio 1.002 # N's per 100 kbp 15.93 # mismatches per 100 kbp 556.28 # indels per 100 kbp 0.42 Largest alignment 142244 NA50 72917 NGA50 59359 NA75 33561 NGA75 15351 LGA50 25 LA75 38		48
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Total length (>= 50000 bp) 2692246 # contigs 124 Largest contig 161420 Total length 3853478 Reference length 4641652 GC (%) 50.76 Reference GC (%) 50.78 N50 73015 NG50 59673 N75 35258 NG75 15441 L50 19 LG50 25 L75 36 LG75 59 # misassemblies 5 # misassembled contigs 5 Misassembled contigs length 310368 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 82.879 Duplication ratio 1.002 # N's per 100 kbp 15.93 # mismatches per 100 kbp 556.28 # indels per 100 kbp 0.42 Largest alignment 142244 NA50 59359	Total length (>= 10000 bp)	3656982
# contigs 124 Largest contig 161420 Total length 3853478 Reference length 4641652 GC (%) 50.76 Reference GC (%) 50.78 N50 73015 NG50 59673 N75 35258 NG75 15441 L50 19 LG50 25 L75 36 LG75 59 # misassemblies 5 # misassembled contigs 5 Misassembled contigs 5 Misassembled contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 82.879 Duplication ratio 1.002 # N's per 100 kbp 15.93 # mismatches per 100 kbp 556.28 # indels per 100 kbp 0.42 Largest alignment 142244 NA50 72917 NGA50 59359 NA75 33561 NGA75 15351 LA50 19 LGA50 25 LA75 38	Total length (>= 25000 bp)	3267331
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Reference GC (%) 50.78 N50 73015 NG50 59673 N75 35258 NG75 15441 L50 19 LG50 25 L75 36 LG75 59 # misassemblies 5 # misassembled contigs 5 Misassembled contigs length 310368 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 82.879 Duplication ratio 1.002 # N's per 100 kbp 15.93 # mismatches per 100 kbp 556.28 # indels per 100 kbp 0.42 Largest alignment 142244 NA50 72917 NGA50 59359 NA75 33561 NGA75 15351 LA50 19 LGA50 25 LA75 38	Reference length	4641652
N50 73015 NG50 59673 N75 35258 NG75 15441 L50 19 LG50 25 L75 36 LG75 59 # misassemblies 5 # misassembled contigs 5 Misassembled contigs length 310368 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 82.879 Duplication ratio 1.002 # N's per 100 kbp 15.93 # mismatches per 100 kbp 556.28 # indels per 100 kbp 0.42 Largest alignment 142244 NA50 72917 NGA50 59359 NA75 33561 NGA75 15351 LA50 19 LGA50 25 LA75 38	GC (%)	50.76
NG50 59673 N75 35258 NG75 15441 L50 19 LG50 25 L75 36 LG75 59 # misassemblies 5 Misassembled contigs 5 Misassembled contigs length 310368 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 82.879 Duplication ratio 1.002 # N's per 100 kbp 15.93 # mismatches per 100 kbp 556.28 # indels per 100 kbp 0.42 Largest alignment 142244 NA50 72917 NGA50 59359 NA75 33561 NGA75 15351 LA50 19 LGA50 25 LA75 38	Reference GC (%)	50.78
N75 35258 NG75 15441 L50 19 LG50 25 L75 36 LG75 59 # misassemblies 5 # misassembled contigs 5 Misassembled contigs length 310368 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 82.879 Duplication ratio 1.002 # N's per 100 kbp 15.93 # mismatches per 100 kbp 556.28 # indels per 100 kbp 0.42 Largest alignment 142244 NA50 72917 NGA50 59359 NA75 33561 NGA75 15351 LA50 19 LGA50 25 LA75 38	N50	73015
NG75 15441 L50 19 LG50 25 L75 36 LG75 59 # misassemblies 5 # misassembled contigs 5 Misassembled contigs length 310368 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 82.879 Duplication ratio 1.002 # N's per 100 kbp 15.93 # mismatches per 100 kbp 556.28 # indels per 100 kbp 0.42 Largest alignment 142244 NA50 72917 NGA50 59359 NA75 33561 NGA75 15351 LA50 19 LGA50 25 LA75 38	NG50	59673
L50 19 LG50 25 L75 36 LG75 59 # misassemblies 5 # misassembled contigs 5 Misassembled contigs length 310368 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 82.879 Duplication ratio 1.002 # N's per 100 kbp 15.93 # mismatches per 100 kbp 556.28 # indels per 100 kbp 0.42 Largest alignment 142244 NA50 72917 NGA50 59359 NA75 33561 NGA75 15351 LA50 19 LGA50 25 LA75 38	N75	35258
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L75 36 LG75 59 # misassemblies 5 # misassembled contigs 5 Misassembled contigs length 310368 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 82.879 Duplication ratio 1.002 # N's per 100 kbp 15.93 # mismatches per 100 kbp 556.28 # indels per 100 kbp 0.42 Largest alignment 142244 NA50 72917 NGA50 59359 NA75 33561 NGA75 15351 LA50 19 LGA50 25 LA75 38	L50	19
LG75 59 # misassemblies 5 # misassembled contigs 5 Misassembled contigs length 310368 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 82.879 Duplication ratio 1.002 # N's per 100 kbp 15.93 # mismatches per 100 kbp 556.28 # indels per 100 kbp 0.42 Largest alignment 142244 NA50 72917 NGA50 59359 NA75 33561 NGA75 15351 LA50 19 LGA50 25 LA75 38	LG50	25
# misassemblies 5 # misassembled contigs 5 Misassembled contigs length 310368 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 82.879 Duplication ratio 1.002 # N's per 100 kbp 15.93 # mismatches per 100 kbp 556.28 # indels per 100 kbp 0.42 Largest alignment 142244 NA50 72917 NGA50 59359 NA75 33561 NGA75 15351 LA50 19 LGA50 25 LA75 38	L75	36
# misassembled contigs 5 Misassembled contigs length 310368 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 82.879 Duplication ratio 1.002 # N's per 100 kbp 15.93 # mismatches per 100 kbp 556.28 # indels per 100 kbp 0.42 Largest alignment 142244 NA50 72917 NGA50 59359 NA75 33561 NGA75 15351 LA50 19 LGA50 25 LA75 38	LG75	59
Misassembled contigs length 310368 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 82.879 Duplication ratio 1.002 # N's per 100 kbp 15.93 # mismatches per 100 kbp 556.28 # indels per 100 kbp 0.42 Largest alignment 142244 NA50 72917 NGA50 59359 NA75 33561 NGA75 15351 LA50 19 LGA50 25 LA75 38	# misassemblies	5
# local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 82.879 Duplication ratio 1.002 # N's per 100 kbp 15.93 # mismatches per 100 kbp 556.28 # indels per 100 kbp 0.42 Largest alignment 142244 NA50 72917 NGA50 59359 NA75 33561 NGA75 15351 LA50 19 LGA50 25 LA75 38	# misassembled contigs	5
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 82.879 Duplication ratio 1.002 # N's per 100 kbp 15.93 # mismatches per 100 kbp 556.28 # indels per 100 kbp 0.42 Largest alignment 142244 NA50 72917 NGA50 59359 NA75 33561 NGA75 15351 LA50 19 LGA50 25 LA75 38	Misassembled contigs length	310368
Unaligned length 0 Genome fraction (%) 82.879 Duplication ratio 1.002 # N's per 100 kbp 15.93 # mismatches per 100 kbp 556.28 # indels per 100 kbp 0.42 Largest alignment 142244 NA50 72917 NGA50 59359 NA75 33561 NGA75 15351 LA50 19 LGA50 25 LA75 38	# local misassemblies	2
Genome fraction (%) 82.879 Duplication ratio 1.002 # N's per 100 kbp 15.93 # mismatches per 100 kbp 556.28 # indels per 100 kbp 0.42 Largest alignment 142244 NA50 72917 NGA50 59359 NA75 33561 NGA75 15351 LA50 19 LGA50 25 LA75 38	# unaligned contigs	0 + 0 part
Duplication ratio 1.002 # N's per 100 kbp 15.93 # mismatches per 100 kbp 556.28 # indels per 100 kbp 0.42 Largest alignment 142244 NA50 72917 NGA50 59359 NA75 33561 NGA75 15351 LA50 19 LGA50 25 LA75 38	Unaligned length	0
# N's per 100 kbp 15.93 # mismatches per 100 kbp 556.28 # indels per 100 kbp 0.42 Largest alignment 142244 NA50 72917 NGA50 59359 NA75 33561 NGA75 15351 LA50 19 LGA50 25 LA75 38	Genome fraction (%)	82.879
# mismatches per 100 kbp 556.28 # indels per 100 kbp 0.42 Largest alignment 142244 NA50 72917 NGA50 59359 NA75 33561 NGA75 15351 LA50 19 LGA50 25 LA75 38	Duplication ratio	1.002
# indels per 100 kbp 0.42 Largest alignment 142244 NA50 72917 NGA50 59359 NA75 33561 NGA75 15351 LA50 19 LGA50 25 LA75 38		
Largest alignment 142244 NA50 72917 NGA50 59359 NA75 33561 NGA75 15351 LA50 19 LGA50 25 LA75 38	# mismatches per 100 kbp	556.28
NA50 72917 NGA50 59359 NA75 33561 NGA75 15351 LA50 19 LGA50 25 LA75 38	# indels per 100 kbp	<u> </u>
NGA50 59359 NA75 33561 NGA75 15351 LA50 19 LGA50 25 LA75 38	Largest alignment	142244
NA75 33561 NGA75 15351 LA50 19 LGA50 25 LA75 38		72917
NGA75 15351 LA50 19 LGA50 25 LA75 38		59359
LA50 19 LGA50 25 LA75 38		ļ
LGA50 25 LA75 38		
LA75 38		
LGA75 63		
-	LGA75	63

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	5
# relocations	4
# translocations	0
# inversions	1
# possibly misassembled contigs	0
# misassembled contigs	5
Misassembled contigs length	310368
# local misassemblies	2
# mismatches	21400
# indels	16
# short indels	14
# long indels	2
Indels length	130

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

	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	614

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).

















