Report

# contigs (>= 1000 bp) 19 # contigs (>= 5000 bp) 0 # contigs (>= 10000 bp) 0 # contigs (>= 25000 bp) 0 # contigs (>= 25000 bp) 0 # contigs (>= 50000 bp) 0 # contigs (>= 50000 bp) 0 Total length (>= 1000 bp) 27737 Total length (>= 5000 bp) 0 Total length (>= 10000 bp) 0 Total length (>= 5000 bp) 0 Total length (>= 50000 bp) 0 Total length (>= 50000 bp) 0 Total length (>= 50000 bp) 0 # contigs 503 Largest contig 3642 Total length 332733 Reference length 4641652 GC (%) 51.10 Reference GC (%) 50.79 N50 631 N75 556 L50 204 L75 345 # misassemblies 3 # misassembled contigs 3 Misassembled contigs 193 # local misassemblies 1 # unaligned length 326 Genome fraction (%) 7.150 Duplication ratio 1.002 # N's per 100 kbp 834.31 # indels per 100 kbp 834.31 # indels per 100 kbp 834.31 # largest alignment 3642 NA50 630 NGA50 NA75 555 LA50 206 LA75 346		[c: .:
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L75 345 # misassemblies 3 # misassembled contigs 3 Misassembled contigs length 4593 # local misassemblies 1 # unaligned contigs 0 + 6 part Unaligned length 326 Genome fraction (%) 7.150 Duplication ratio 1.002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 834.31 # indels per 100 kbp 8.14 Largest alignment 3642 NA50 630 NGA50 - NA75 555 LA50 206	N75	556
# misassemblies 3 # misassembled contigs 3 Misassembled contigs length 4593 # local misassemblies 1 # unaligned contigs 0 + 6 part Unaligned length 326 Genome fraction (%) 7.150 Duplication ratio 1.002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 834.31 # indels per 100 kbp 8.14 Largest alignment 3642 NA50 630 NGA50 - NA75 555 LA50 206	L50	
# misassembled contigs 3 Misassembled contigs length 4593 # local misassemblies 1 # unaligned contigs 0 + 6 part Unaligned length 326 Genome fraction (%) 7.150 Duplication ratio 1.002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 834.31 # indels per 100 kbp 8.14 Largest alignment 3642 NA50 630 NGA50 - NA75 555 LA50 206	L75	345
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# local misassemblies # unaligned contigs Unaligned length Genome fraction (%) Duplication ratio # N's per 100 kbp mismatches per 100 kbp # indels per 100 kbp Largest alignment NA50 NGA50 NA75 LA50 # unaligned contigs 0 + 6 part 0 - 7 - 7 - 7 - 7 - 7 - 7 - 7 - 7 - 7 -	# misassembled contigs	3
# unaligned contigs 0 + 6 part Unaligned length 326 Genome fraction (%) 7.150 Duplication ratio 1.002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 834.31 # indels per 100 kbp 8.14 Largest alignment 3642 NA50 630 NGA50 - NA75 555 LA50 206	Misassembled contigs length	4593
Unaligned length 326 Genome fraction (%) 7.150 Duplication ratio 1.002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 834.31 # indels per 100 kbp 8.14 Largest alignment 3642 NA50 630 NGA50 - NA75 555 LA50 206	# local misassemblies	1
Genome fraction (%) 7.150 Duplication ratio 1.002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 834.31 # indels per 100 kbp 8.14 Largest alignment 3642 NA50 630 NGA50 - NA75 555 LA50 206	# unaligned contigs	0 + 6 part
Duplication ratio 1.002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 834.31 # indels per 100 kbp 8.14 Largest alignment 3642 NA50 630 NGA50 - NA75 555 LA50 206	Unaligned length	326
# N's per 100 kbp 0.00 # mismatches per 100 kbp 834.31 # indels per 100 kbp 8.14 Largest alignment 3642 NA50 630 NGA50 - NA75 555 LA50 206	Genome fraction (%)	7.150
# mismatches per 100 kbp 834.31 # indels per 100 kbp 8.14 Largest alignment 3642 NA50 630 NGA50 - NA75 555 LA50 206	Duplication ratio	1.002
# indels per 100 kbp 8.14 Largest alignment 3642 NA50 630 NGA50 - NA75 555 LA50 206	# N's per 100 kbp	0.00
Largest alignment 3642 NA50 630 NGA50 - NA75 555 LA50 206		834.31
NA50 630 NGA50 - NA75 555 LA50 206	,	8.14
NGA50 - NA75 555 LA50 206	Largest alignment	3642
NA75 555 LA50 206	NA50	630
LA50 206	NGA50	-
	NA75	555
LA75 346	LA50	206
	LA75	346

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

	final.contigs
# misassemblies	3
# relocations	3
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	3
Misassembled contigs length	4593
# local misassemblies	1
# mismatches	2769
# indels	27
# short indels	27
# long indels	0
Indels length	35

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

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	6
# with misassembly	0
# both parts are significant	0
Partially unaligned length	326
# 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).

















