Report

# contigs (>= 1000 bp) 17 # contigs (>= 5000 bp) 3 # contigs (>= 10000 bp) 0 # contigs (>= 25000 bp) 0 # contigs (>= 25000 bp) 0 # contigs (>= 50000 bp) 0 Total length (>= 1000 bp) 49761 Total length (>= 5000 bp) 23066 Total length (>= 10000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 Total length (>= 50000 bp) 0 # contigs 37 Largest contig 8796 Total length 64491 Reference length 3576081 GC (%) 55.95 Reference GC (%) 51.82 N50 2823 N75 1085 L50 6 L75 16 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 10 # local misassemblies 1 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 3 # unaligned contigs 1 + 24 part 1 Unaligned length 50973 Genome fraction (%) 0.183 Duplication ratio 2.061 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3659.65 # indels per 100 kbp 137.24 Largest alignment 1743 Total aligned length 8319 NGA50		final.contigs
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Total length (>= 5000 bp) 23066 Total length (>= 10000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 37 Largest contig 8796 Total length 64491 Reference length 3576081 GC (%) 55.95 Reference GC (%) 51.82 N50 2823 N75 1085 L50 6 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 3 # unaligned length 50973 Genome fraction (%) 0.183 Duplication ratio 2.061 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3659.65 # indels per 100 kbp 137.24 Largest alignment 1743 <td></td> <td>49761</td>		49761
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Total length (>= 50000 bp) 0 # contigs 37 Largest contig 8796 Total length 64491 Reference length 3576081 GC (%) 55.95 Reference GC (%) 51.82 N50 2823 N75 1085 L50 6 L75 16 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 3 # unaligned length 50973 Genome fraction (%) 0.183 Duplication ratio 2.061 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3659.65 # indels per 100 kbp 137.24 Largest alignment 1743 Total aligned length 8319		0
# contigs 37 Largest contig 8796 Total length 64491 Reference length 3576081 GC (%) 55.95 Reference GC (%) 51.82 N50 2823 N75 1085 L50 6 L75 16 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 1 # local misassemblies 1 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 3 # unaligned contigs 1 + 24 part Unaligned length 50973 Genome fraction (%) 0.183 Duplication ratio 2.061 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3659.65 # indels per 100 kbp 137.24 Largest alignment 1743 Total aligned length 8319		0
Total length 64491 Reference length 3576081 GC (%) 55.95 Reference GC (%) 51.82 N50 2823 N75 1085 L50 6 L75 16 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 3 # unaligned length 50973 Genome fraction (%) 0.183 Duplication ratio 2.061 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3659.65 # indels per 100 kbp 137.24 Largest alignment 1743 Total aligned length 8319		37
Reference length 3576081 GC (%) 55.95 Reference GC (%) 51.82 N50 2823 N75 1085 L50 6 L75 16 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 3 # unaligned contigs 1 + 24 part Unaligned length 50973 Genome fraction (%) 0.183 Duplication ratio 2.061 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3659.65 # indels per 100 kbp 137.24 Largest alignment 1743 Total aligned length 8319	Largest contig	8796
GC (%) 55.95 Reference GC (%) 51.82 N50 2823 N75 1085 L50 6 L75 16 # misassemblies 0 Misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 3 # unaligned contigs 1 + 24 part Unaligned length 50973 Genome fraction (%) 0.183 Duplication ratio 2.061 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3659.65 # indels per 100 kbp 137.24 Largest alignment 1743 Total aligned length 8319	Total length	64491
Reference GC (%) 51.82 N50 2823 N75 1085 L50 6 L75 16 # misassemblies 0 Misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 3 # unaligned contigs 1 + 24 part Unaligned length 50973 Genome fraction (%) 0.183 Duplication ratio 2.061 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3659.65 # indels per 100 kbp 137.24 Largest alignment 1743 Total aligned length 8319	Reference length	3576081
N50 2823 N75 1085 L50 6 L75 16 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 3 # unaligned contigs 1 + 24 part Unaligned length 50973 Genome fraction (%) 0.183 Duplication ratio 2.061 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3659.65 # indels per 100 kbp 137.24 Largest alignment 1743 Total aligned length 8319	GC (%)	55.95
N75 1085 L50 6 L75 16 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 3 # unaligned contigs 1 + 24 part Unaligned length 50973 Genome fraction (%) 0.183 Duplication ratio 2.061 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3659.65 # indels per 100 kbp 137.24 Largest alignment 1743 Total aligned length 8319	Reference GC (%)	51.82
L50 6 L75 16 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 3 # unaligned contigs 1 + 24 part Unaligned length 50973 Genome fraction (%) 0.183 Duplication ratio 2.061 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3659.65 # indels per 100 kbp 137.24 Largest alignment 1743 Total aligned length 8319	N50	2823
L75 16 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 3 # unaligned contigs 1 + 24 part Unaligned length 50973 Genome fraction (%) 0.183 Duplication ratio 2.061 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3659.65 # indels per 100 kbp 137.24 Largest alignment 1743 Total aligned length 8319	N75	1085
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 3 # unaligned contigs 1 + 24 part Unaligned length 50973 Genome fraction (%) 0.183 Duplication ratio 2.061 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3659.65 # indels per 100 kbp 137.24 Largest alignment 1743 Total aligned length 8319	L50	6
# misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 3 # unaligned contigs 1 + 24 part Unaligned length 50973 Genome fraction (%) 0.183 Duplication ratio 2.061 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3659.65 # indels per 100 kbp 137.24 Largest alignment 1743 Total aligned length 8319	L75	16
Misassembled contigs length # local misassemblies 1 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 3 # unaligned contigs 1 + 24 part Unaligned length 50973 Genome fraction (%) 0.183 Duplication ratio 2.061 # N's per 100 kbp 0.00 # mismatches per 100 kbp 137.24 Largest alignment 1743 Total aligned length 8319	# misassemblies	0
# local misassemblies 1 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 3 # unaligned contigs 1 + 24 part Unaligned length 50973 Genome fraction (%) 0.183 Duplication ratio 2.061 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3659.65 # indels per 100 kbp 137.24 Largest alignment 1743 Total aligned length 8319	# misassembled contigs	0
# scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 3 # unaligned contigs 1 + 24 part Unaligned length 50973 Genome fraction (%) 0.183 Duplication ratio 2.061 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3659.65 # indels per 100 kbp 137.24 Largest alignment 1743 Total aligned length 8319	Misassembled contigs length	0
# scaffold gap loc. mis. 0 # unaligned mis. contigs 3 # unaligned contigs 1 + 24 part Unaligned length 50973 Genome fraction (%) 0.183 Duplication ratio 2.061 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3659.65 # indels per 100 kbp 137.24 Largest alignment 1743 Total aligned length 8319	# local misassemblies	1
# unaligned mis. contigs 3 # unaligned contigs 1 + 24 part Unaligned length 50973 Genome fraction (%) 0.183 Duplication ratio 2.061 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3659.65 # indels per 100 kbp 137.24 Largest alignment 1743 Total aligned length 8319	# scaffold gap ext. mis.	0
# unaligned contigs 1 + 24 part Unaligned length 50973 Genome fraction (%) 0.183 Duplication ratio 2.061 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3659.65 # indels per 100 kbp 137.24 Largest alignment 1743 Total aligned length 8319	# scaffold gap loc. mis.	0
Unaligned length 50973 Genome fraction (%) 0.183 Duplication ratio 2.061 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3659.65 # indels per 100 kbp 137.24 Largest alignment 1743 Total aligned length 8319	# unaligned mis. contigs	3
Genome fraction (%) 0.183 Duplication ratio 2.061 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3659.65 # indels per 100 kbp 137.24 Largest alignment 1743 Total aligned length 8319	# unaligned contigs	1 + 24 part
Duplication ratio 2.061 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3659.65 # indels per 100 kbp 137.24 Largest alignment 1743 Total aligned length 8319	Unaligned length	50973
# N's per 100 kbp 0.00 # mismatches per 100 kbp 3659.65 # indels per 100 kbp 137.24 Largest alignment 1743 Total aligned length 8319	Genome fraction (%)	0.183
# mismatches per 100 kbp 3659.65 # indels per 100 kbp 137.24 Largest alignment 1743 Total aligned length 8319	Duplication ratio	2.061
# indels per 100 kbp 137.24 Largest alignment 1743 Total aligned length 8319	# N's per 100 kbp	0.00
Largest alignment 1743 Total aligned length 8319	# mismatches per 100 kbp	3659.65
Total aligned length 8319	# indels per 100 kbp	137.24
, , , , , , , , , , , , , , , , , , ,	Largest alignment	1743
NGA50 -	Total aligned length	8319
	NGA50	-

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	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	20
# possible misassemblies	25
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	240
# indels	9
# indels (<= 5 bp)	9
# indels (> 5 bp)	0
Indels length	10

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	1
Fully unaligned length	901
# partially unaligned contigs	24
Partially unaligned length	50072
# 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).





















