Report

# contigs (>= 1000 bp) 1033 # contigs (>= 5000 bp) 1 # contigs (>= 10000 bp) 0 # contigs (>= 25000 bp) 0 # contigs (>= 50000 bp) 0 # contigs (>= 50000 bp) 0 # contigs (>= 50000 bp) 0 Total length (>= 10000 bp) 1559808 Total length (>= 10000 bp) 6977 Total length (>= 10000 bp) 6977 Total length (>= 50000 bp) 0 # contigs 3367 Largest contig 6977 Total length 3194862 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 978 NG50 732 N75 712 L50 1072 LG50 1072 LG50 1072 LG50 1072 LG50 1930 L75 2034 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassembles 0 # unaligned length 0 Genome fraction (%) 65.544 Duplication ratio 1.050 # N's per 100 kbp 0.00 # mismatches per 100 kbp 185.75 # indels per 100 kbp 0.07 Largest alignment 6977 NA50 978 NGA50 732 NA75 122 LA50 1072 LGA50 1072 LGA50 1072 LGA50 1072 LGA50 1072 LGA50 1072 LA50 1072 LA75 2034		
# contigs (>= 5000 bp)		final.contigs
# contigs (>= 10000 bp)	-	1033
# contigs (>= 25000 bp) 0 # contigs (>= 50000 bp) 1559808 Total length (>= 1000 bp) 6977 Total length (>= 10000 bp) 6977 Total length (>= 10000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 Total length (>= 50000 bp) 0 # contigs 3367 Largest contig 6977 Total length 3194862 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 978 NG50 732 N75 712 L50 1072 LG50 1072 LG50 1930 L75 2034 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 # unaligned length 0 Genome fraction (%) 65.544 Duplication ratio 1.050 # N's per 100 kbp 0.00 # mismatches per 100 kbp 185.75 # indels per 100 kbp 0.77 Largest alignment 6977 NA50 978 NGA50 732 NA75 712 LA50 1072 LA50 1072 LA50 1072 LA50 1072 LA50 1072		1
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# contigs 3367 Largest contig 6977 Total length 3194862 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 978 NG50 732 N75 712 L50 1072 LG50 1930 L75 2034 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 65.544 Duplication ratio 1.050 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.07 Largest alignment 6977 NA50 978 NGA50 732 NA75 712 LA50 1072 LGA50 1930	,	0
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Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 978 NG50 732 N75 712 L50 1072 LG50 1930 L75 2034 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 65.544 Duplication ratio 1.050 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.07 Largest alignment 6977 NA50 978 NGA50 732 NA75 712 LA50 1072 LGA50 1930	Largest contig	6977
GC (%) 50.74 Reference GC (%) 50.79 N50 978 NG50 732 N75 712 L50 1072 LG50 1930 L75 2034 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 65.544 Duplication ratio 1.050 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.07 Largest alignment 6977 NA50 978 NGA50 732 NA75 712 LA50 1072 LGA50 1930	Total length	3194862
Reference GC (%) 50.79 N50 978 NG50 732 N75 712 L50 1072 LG50 1930 L75 2034 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 65.544 Duplication ratio 1.050 # N's per 100 kbp 0.00 # mismatches per 100 kbp 185.75 # indels per 100 kbp 0.07 Largest alignment 6977 NA50 978 NGA50 732 NA75 712 LA50 1072 LGA50 1930	Reference length	4641652
N50 978 NG50 732 N75 712 L50 1072 LG50 1930 L75 2034 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 65.544 Duplication ratio 1.050 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.07 Largest alignment 6977 NA50 978 NGA50 732 NA75 712 LA50 1072 LGA50 1930	GC (%)	50.74
NG50 732 N75 712 L50 1072 LG50 1930 L75 2034 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 65.544 Duplication ratio 1.050 # N's per 100 kbp 0.00 # mismatches per 100 kbp 185.75 # indels per 100 kbp 0.07 Largest alignment 6977 NA50 978 NGA50 732 NA75 712 LA50 1072 LGA50 1930	Reference GC (%)	50.79
N75 712 L50 1072 LG50 1930 L75 2034 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 65.544 Duplication ratio 1.050 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.07 Largest alignment 6977 NA50 978 NGA50 732 NA75 712 LA50 1072 LGA50 1930	N50	978
L50 1072 LG50 1930 L75 2034 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 65.544 Duplication ratio 1.050 # N's per 100 kbp 0.00 # mismatches per 100 kbp 185.75 # indels per 100 kbp 0.07 Largest alignment 6977 NA50 978 NGA50 732 NA75 712 LA50 1072 LGA50 1930	NG50	732
LG50 1930 L75 2034 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 65.544 Duplication ratio 1.050 # N's per 100 kbp 0.00 # mismatches per 100 kbp 185.75 # indels per 100 kbp 0.07 Largest alignment 6977 NA50 978 NGA50 732 NA75 712 LA50 1072 LGA50 1930	N75	712
L75 2034 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 65.544 Duplication ratio 1.050 # N's per 100 kbp 0.00 # mismatches per 100 kbp 185.75 # indels per 100 kbp 0.07 Largest alignment 6977 NA50 978 NGA50 732 NA75 712 LA50 1072 LGA50 1930	L50	1072
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 65.544 Duplication ratio 1.050 # N's per 100 kbp 0.00 # mismatches per 100 kbp 185.75 # indels per 100 kbp 0.07 Largest alignment 6977 NA50 978 NGA50 732 NA75 712 LA50 1072 LGA50 1930	LG50	1930
# misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 65.544 Duplication ratio 1.050 # N's per 100 kbp 0.00 # mismatches per 100 kbp 185.75 # indels per 100 kbp 0.07 Largest alignment 6977 NA50 978 NGA50 732 NA75 712 LA50 1072 LGA50 1930	L75	2034
Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 65.544 Duplication ratio 1.050 # N's per 100 kbp 0.00 # mismatches per 100 kbp 185.75 # indels per 100 kbp 0.07 Largest alignment 6977 NA50 978 NGA50 732 NA75 712 LA50 1072 LGA50 1930		0
# local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 65.544 Duplication ratio 1.050 # N's per 100 kbp 0.00 # mismatches per 100 kbp 185.75 # indels per 100 kbp 0.07 Largest alignment 6977 NA50 978 NGA50 732 NA75 712 LA50 1072 LGA50 1930)	0
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 65.544 Duplication ratio 1.050 # N's per 100 kbp 0.00 # mismatches per 100 kbp 185.75 # indels per 100 kbp 0.07 Largest alignment 6977 NA50 978 NGA50 732 NA75 712 LA50 1072 LGA50 1930	Misassembled contigs length	0
Unaligned length 0 Genome fraction (%) 65.544 Duplication ratio 1.050 # N's per 100 kbp 0.00 # mismatches per 100 kbp 185.75 # indels per 100 kbp 0.07 Largest alignment 6977 NA50 978 NGA50 732 NA75 712 LA50 1072 LGA50 1930	# local misassemblies	0
Genome fraction (%) 65.544 Duplication ratio 1.050 # N's per 100 kbp 0.00 # mismatches per 100 kbp 185.75 # indels per 100 kbp 0.07 Largest alignment 6977 NA50 978 NGA50 732 NA75 712 LA50 1072 LGA50 1930)	0 + 0 part
Duplication ratio 1.050 # N's per 100 kbp 0.00 # mismatches per 100 kbp 185.75 # indels per 100 kbp 0.07 Largest alignment 6977 NA50 978 NGA50 732 NA75 712 LA50 1072 LGA50 1930	Unaligned length	0
# N's per 100 kbp 0.00 # mismatches per 100 kbp 185.75 # indels per 100 kbp 0.07 Largest alignment 6977 NA50 978 NGA50 732 NA75 712 LA50 1072 LGA50 1930	Genome fraction (%)	65.544
# mismatches per 100 kbp 185.75 # indels per 100 kbp 0.07 Largest alignment 6977 NA50 978 NGA50 732 NA75 712 LA50 1072 LGA50 1930	Duplication ratio	1.050
# indels per 100 kbp 0.07 Largest alignment 6977 NA50 978 NGA50 732 NA75 712 LA50 1072 LGA50 1930	# N's per 100 kbp	0.00
Largest alignment 6977 NA50 978 NGA50 732 NA75 712 LA50 1072 LGA50 1930	# mismatches per 100 kbp	185.75
NA50 978 NGA50 732 NA75 712 LA50 1072 LGA50 1930	# indels per 100 kbp	0.07
NGA50 732 NA75 712 LA50 1072 LGA50 1930	Largest alignment	6977
NA75 712 LA50 1072 LGA50 1930	NA50	978
LA50 1072 LGA50 1930	NGA50	732
LGA50 1930	NA75	712
	LA50	1072
LA75 2034	LGA50	1930
	LA75	2034

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
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	5651
# indels	2
# short indels	2
# long indels	0
Indels length	2

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	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).















