Report

# contigs (>= 1000 bp) 1529 # contigs (>= 5000 bp) 183 # contigs (>= 10000 bp) 16 # contigs (>= 25000 bp) 16 # contigs (>= 25000 bp) 0 # contigs (>= 50000 bp) 0 # contigs (>= 50000 bp) 0 Total length (>= 10000 bp) 1253261 Total length (>= 10000 bp) 196297 Total length (>= 25000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 1990 Largest contig 18483 Total length 4731551 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.78 Reference GC (%) 50.78 N50 3221 NG50 3290 N75 1917 NG75 1979 L50 462 LG50 4448 L75 936 LG75 901 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 1 # unaligned length 140 Genome fraction (%) 98.213 Duplication ratio 1.038 # N's per 100 kbp 0.00 # mismatches per 100 kbp 46.77 # indels per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA75 1917	# contigs (>= 1000 bp) 1529 # contigs (>= 5000 bp) 183 # contigs (>= 10000 bp) 16 # contigs (>= 25000 bp) 0 # contigs (>= 25000 bp) 0 Total length (>= 10000 bp) 1253261 Total length (>= 5000 bp) 196297 Total length (>= 10000 bp) 196297 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 1990 Largest contig 18483 Total length 4731551 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.78 Reference GC (%) 50.78 N50 3221 NG50 3290 N75 1917 NG75 1917 NG75 1917 NG75 1979 L50 462 LG50 448 L75 936 LG75 901 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 10 # local misassemblies 1 # unaligned length 0 # local misassembles 1 Unaligned length 140 Genome fraction (%) 98.213 Duplication ratio 1.038 # N's per 100 kbp 0.00 # mismatches per 100 kbp 46.77 # indels per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936		
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# contigs (>= 50000 bp)	# contigs (>= 50000 bp)		16
Total length (>= 1000 bp)	Total length (>= 1000 bp)		0
Total length (>= 5000 bp) 1253261 Total length (>= 10000 bp) 196297 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 1990 Largest contig 18483 Total length 4731551 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.78 N50 3221 NG50 3290 N75 1917 NG75 1979 L50 462 LG50 448 L75 936 LG75 901 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # unaligned length 140 Genome fraction (%) 98.213 Duplication ratio 1.038 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.11 Largest alignment 18483 NA50 3290	Total length (>= 5000 bp) 1253261 Total length (>= 10000 bp) 196297 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 1990 Largest contig 18483 Total length 4731551 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.78 N50 3221 NG50 3290 N75 1917 NG75 1979 L50 462 LG50 448 L75 936 LG75 901 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # unaligned length 140 Genome fraction (%) 98.213 Duplication ratio 1.038 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.11 Largest alignment 18483 NA50 3290	# contigs (>= 50000 bp)	0
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Total length (>= 50000 bp) 0 # contigs 1990 Largest contig 18483 Total length 4731551 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.78 N50 3221 NG50 3290 N75 1917 NG75 1979 L50 462 LG50 448 L75 936 LG75 901 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned length 0 Genome fraction (%) 98.213 Duplication ratio 1.038 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA50 3290	Total length (>= 50000 bp) 0 # contigs 1990 Largest contig 18483 Total length 4731551 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.78 N50 3221 NG50 3290 N75 1917 NG75 1979 L50 462 LG50 448 L75 936 LG75 901 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned length 0 # unaligned length 140 Genome fraction (%) 98.213 Duplication ratio 1.038 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA50 3290 NA75		196297
# contigs 1990 Largest contig 18483 Total length 4731551 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.78 N50 3221 NG50 3290 N75 1917 NG75 1979 L50 462 LG50 448 L75 936 LG75 901 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 1 # unaligned contigs 0 + 2 part Unaligned length 140 Genome fraction (%) 98.213 Duplication ratio 1.038 # N's per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	# contigs 1990 Largest contig 18483 Total length 4731551 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.78 N50 3221 NG50 3290 N75 1917 NG75 1979 L50 462 LG50 448 L75 936 LG75 901 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 1 # unaligned length 0 # local misassembles 1 # unaligned rottigs 0 Genome fraction (%) 98.213 Duplication ratio 1.038 # N's per 100 kbp 0.11 Largest alignment 18483 NA50 3290 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	Total length (>= 25000 bp)	0
Largest contig 18483 Total length 4731551 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.78 N50 3221 NG50 3290 N75 1917 NG75 1979 L50 462 LG50 448 L75 936 LG75 901 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Unaligned length 0 Unaligned length 140 Genome fraction (%) 98.213 Duplication ratio 1.038 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	Largest contig 18483 Total length 4731551 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.78 N50 3221 NG50 3290 N75 1917 NG75 1979 L50 462 LG50 448 L75 936 LG75 901 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 1 # unaligned length 0 Unaligned length 140 Genome fraction (%) 98.213 Duplication ratio 1.038 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA50 3290 NA75 1979 LA50 462 LGA50 448	Total length (>= 50000 bp)	0
Total length 4731551 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.78 N50 3221 NG50 3290 N75 1917 NG75 1979 L50 462 LG50 448 L75 936 LG75 901 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Unaligned length 0 Unaligned length 140 Genome fraction (%) 98.213 Duplication ratio 1.038 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA50 3290 NA75 1979 LA50 462 LGA50 448 LA75 936 </td <td>Total length 4731551 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.78 N50 3221 NG50 3290 N75 1917 NG75 1979 L50 462 LG50 448 L75 936 LG75 901 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned length 140 Genome fraction (%) 98.213 Duplication ratio 1.038 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA50 3290 NA75 1979 LA50 462 LGA50 448 LA75</td> <td># contigs</td> <td>1990</td>	Total length 4731551 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.78 N50 3221 NG50 3290 N75 1917 NG75 1979 L50 462 LG50 448 L75 936 LG75 901 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned length 140 Genome fraction (%) 98.213 Duplication ratio 1.038 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA50 3290 NA75 1979 LA50 462 LGA50 448 LA75	# contigs	1990
Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.78 N50 3221 NG50 3290 N75 1917 NG75 1979 L50 462 LG50 448 L75 936 LG75 901 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 + 2 part Unaligned length 140 Genome fraction (%) 98.213 Duplication ratio 1.038 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.78 N50 3221 NG50 3290 N75 1917 NG75 1979 L50 462 LG50 448 L75 936 LG75 901 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 + 2 part Unaligned length 140 Genome fraction (%) 98.213 Duplication ratio 1.038 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	Largest contig	18483
GC (%) 50.78 Reference GC (%) 50.78 N50 3221 NG50 3290 N75 1917 NG75 1979 L50 462 LG50 448 L75 936 LG75 901 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 + 2 part Unaligned length 140 Genome fraction (%) 98.213 Duplication ratio 1.038 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	GC (%) 50.78 Reference GC (%) 50.78 N50 3221 NG50 3290 N75 1917 NG75 1979 L50 462 LG50 448 L75 936 LG75 901 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 + 2 part Unaligned length 140 Genome fraction (%) 98.213 Duplication ratio 1.038 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	Total length	4731551
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N50 3221 NG50 3290 N75 1917 NG75 1979 L50 462 LG50 448 L75 936 LG75 901 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 1 # unaligned contigs 0 + 2 part Unaligned length 140 Genome fraction (%) 98.213 Duplication ratio 1.038 # N's per 100 kbp 0.00 # mismatches per 100 kbp 46.77 # indels per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	N50 3221 NG50 3290 N75 1917 NG75 1979 L50 462 LG50 448 L75 936 LG75 901 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 1 # unaligned contigs 0 + 2 part Unaligned length 140 Genome fraction (%) 98.213 Duplication ratio 1.038 # N's per 100 kbp 0.00 # mismatches per 100 kbp 46.77 # indels per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	GC (%)	50.78
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N75 1917 NG75 1979 L50 462 LG50 448 L75 936 LG75 901 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 2 part Unaligned length 140 Genome fraction (%) 98.213 Duplication ratio 1.038 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	N75 1917 NG75 1979 L50 462 LG50 448 L75 936 LG75 901 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 2 part Unaligned length 140 Genome fraction (%) 98.213 Duplication ratio 1.038 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	N50	3221
NG75 1979 L50 462 LG50 448 L75 936 LG75 901 # misassemblies 0 Misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 2 part Unaligned length 140 Genome fraction (%) 98.213 Duplication ratio 1.038 # N's per 100 kbp 0.00 # mismatches per 100 kbp 46.77 # indels per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	NG75 1979 L50 462 LG50 448 L75 936 LG75 901 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 2 part Unaligned length 140 Genome fraction (%) 98.213 Duplication ratio 1.038 # N's per 100 kbp 0.00 # mismatches per 100 kbp 46.77 # indels per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	NG50	3290
L50 462 LG50 448 L75 936 LG75 901 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 2 part Unaligned length 140 Genome fraction (%) 98.213 Duplication ratio 1.038 # N's per 100 kbp 0.00 # mismatches per 100 kbp 46.77 # indels per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA75 1979 LA50 462 LG50 448 LA75 936	L50 462 LG50 448 L75 936 LG75 901 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 2 part Unaligned length 140 Genome fraction (%) 98.213 Duplication ratio 1.038 # N's per 100 kbp 0.00 # mismatches per 100 kbp 46.77 # indels per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA75 1979 LA50 462 LG50 448 LA75 936	N75	1917
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L75 936 LG75 901 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 2 part Unaligned length 140 Genome fraction (%) 98.213 Duplication ratio 1.038 # N's per 100 kbp 0.00 # mismatches per 100 kbp 46.77 # indels per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	L75 936 LG75 901 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 2 part Unaligned length 140 Genome fraction (%) 98.213 Duplication ratio 1.038 # N's per 100 kbp 0.00 # mismatches per 100 kbp 46.77 # indels per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	L50	462
LG75 901 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 2 part Unaligned length 140 Genome fraction (%) 98.213 Duplication ratio 1.038 # N's per 100 kbp 0.00 # mismatches per 100 kbp 46.77 # indels per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	LG75 901 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 2 part Unaligned length 140 Genome fraction (%) 98.213 Duplication ratio 1.038 # N's per 100 kbp 0.00 # mismatches per 100 kbp 46.77 # indels per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	LG50	448
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 2 part Unaligned length 140 Genome fraction (%) 98.213 Duplication ratio 1.038 # N's per 100 kbp 0.00 # mismatches per 100 kbp 46.77 # indels per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3221 NGA50 3290 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	# misassembles 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassembles 1 # unaligned contigs 0 + 2 part Unaligned length 140 Genome fraction (%) 98.213 Duplication ratio 1.038 # N's per 100 kbp 0.00 # mismatches per 100 kbp 46.77 # indels per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3220 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	L75	936
# misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 2 part Unaligned length 140 Genome fraction (%) 98.213 Duplication ratio 1.038 # N's per 100 kbp 0.00 # mismatches per 100 kbp 46.77 # indels per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3220 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	# misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 2 part Unaligned length 140 Genome fraction (%) 98.213 Duplication ratio 1.038 # N's per 100 kbp 0.00 # mismatches per 100 kbp 46.77 # indels per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3220 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	LG75	901
Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 2 part Unaligned length 140 Genome fraction (%) 98.213 Duplication ratio 1.038 # N's per 100 kbp 0.00 # mismatches per 100 kbp 46.77 # indels per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 2 part Unaligned length 140 Genome fraction (%) 98.213 Duplication ratio 1.038 # N's per 100 kbp 0.00 # mismatches per 100 kbp 46.77 # indels per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	# misassemblies	0
# local misassemblies 1 # unaligned contigs 0 + 2 part Unaligned length 140 Genome fraction (%) 98.213 Duplication ratio 1.038 # N's per 100 kbp 0.00 # mismatches per 100 kbp 46.77 # indels per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3220 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	# local misassemblies 1 # unaligned contigs 0 + 2 part Unaligned length 140 Genome fraction (%) 98.213 Duplication ratio 1.038 # N's per 100 kbp 0.00 # mismatches per 100 kbp 46.77 # indels per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	# misassembled contigs	0
# unaligned contigs	# unaligned contigs	Misassembled contigs length	0
Unaligned length 140 Genome fraction (%) 98.213 Duplication ratio 1.038 # N's per 100 kbp 0.00 # mismatches per 100 kbp 46.77 # indels per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	Unaligned length 140 Genome fraction (%) 98.213 Duplication ratio 1.038 # N's per 100 kbp 0.00 # mismatches per 100 kbp 46.77 # indels per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	# local misassemblies	1
Genome fraction (%) 98.213 Duplication ratio 1.038 # N's per 100 kbp 0.00 # mismatches per 100 kbp 46.77 # indels per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	Genome fraction (%) 98.213 Duplication ratio 1.038 # N's per 100 kbp 0.00 # mismatches per 100 kbp 46.77 # indels per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	# unaligned contigs	0 + 2 part
Duplication ratio 1.038 # N's per 100 kbp 0.00 # mismatches per 100 kbp 46.77 # indels per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	Duplication ratio 1.038 # N's per 100 kbp 0.00 # mismatches per 100 kbp 46.77 # indels per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	Unaligned length	140
# N's per 100 kbp 0.00 # mismatches per 100 kbp 46.77 # indels per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	# N's per 100 kbp 0.00 # mismatches per 100 kbp 46.77 # indels per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	Genome fraction (%)	98.213
# mismatches per 100 kbp 46.77 # indels per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	# mismatches per 100 kbp 46.77 # indels per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	Duplication ratio	1.038
# indels per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	# indels per 100 kbp 0.11 Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	# N's per 100 kbp	0.00
Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	# mismatches per 100 kbp	46.77
Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	Largest alignment 18483 NA50 3221 NGA50 3290 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936		0.11
NGA50 3290 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	NGA50 3290 NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	Largest alignment	18483
NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	NA75 1917 NGA75 1979 LA50 462 LGA50 448 LA75 936	NA50	3221
NGA75 1979 LA50 462 LGA50 448 LA75 936	NGA75 1979 LA50 462 LGA50 448 LA75 936	NGA50	3290
LA50 462 LGA50 448 LA75 936	LA50 462 LGA50 448 LA75 936	NA75	1917
LGA50 448 LA75 936	LGA50 448 LA75 936	NGA75	1979
LA75 936	LA75 936	LA50	462
		LGA50	448
10475	· · · · · · · · · · · · · · · · · · ·	LA75	936
LGA/5 901	LGA75 901	1	+

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	1
# mismatches	2132
# indels	5
# short indels	5
# long indels	0
Indels length	5

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	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	140
# 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).















