Report

# contigs (>= 0 bp)	Report	
# contigs (>= 1000 bp) 35 # contigs (>= 5000 bp) 35 # contigs (>= 10000 bp) 33 # contigs (>= 25000 bp) 24 # contigs (>= 50000 bp) 19 Total length (>= 50000 bp) 4920161 Total length (>= 10000 bp) 4920161 Total length (>= 10000 bp) 4920161 Total length (>= 50000 bp) 4920161 Total length (>= 50000 bp) 496506 Total length (>= 25000 bp) 4753145 Total length (>= 50000 bp) 4544034 # contigs 35 Largest contig 663575 Total length 4920161 Reference length 5000040 GC (%) 35.80 Reference GC (%) 35.80 Reference GC (%) 35.81 NSO 297761 N75 186935 NG75 182381 L50 6 LG50 6 L75 11 LG75 12 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # unaligned mis. contigs 0 # unaligned length 0 Genome fraction (%) 96.454 Duplication ratio 1.020 # N's per 100 kbp 9.54 Largest alignment 663575 Total aligned length 4920160 NA50 297761 NA50 297761 NG50 304040 NA50 297761 NG50 305040 NG50 305040 NG50 305040 NG50 30505 NG75 12 NG761 NGA50 297761		sim5M.CanuL
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# contigs (>= 10000 bp) 24 # contigs (>= 25000 bp) 24 # contigs (>= 50000 bp) 19 Total length (>= 0 bp) 4920161 Total length (>= 10000 bp) 4920161 Total length (>= 50000 bp) 4920161 Total length (>= 50000 bp) 496506 Total length (>= 25000 bp) 4753145 Total length (>= 50000 bp) 4753145 Total length (>= 50000 bp) 4544034 # contigs 33 Largest contig 663575 Total length 4920161 Reference length 5000040 GC (%) 35.80 Reference GC (%) 35.84 N50 297761 N75 186935 NG75 182381 L50 6 LG50 6 L75 11 LG75 12 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned mis. contigs 0 # unaligned length 0 Genome fraction (%) 96.454 Duplication ratio 1.020 # N's per 100 kbp 9.54 Largest alignment 663575 Total aligned length 4920160 NA50 297761 NA50 297761 NA50 297761 NA50 297761 NA50 297761 NA50 396.454 Duplication ratio 1.020 # N's per 100 kbp 9.54 Largest alignment 663575 Total aligned length 4920160 NA50 297761 NA75 186935 NGA75 182381 LA50 6 LA50 6 LA50 6 LA75 11	# contigs (>= 1000 bp)	35
# contigs (>= 25000 bp) 19 # contigs (>= 50000 bp) 19 Total length (>= 0 bp) 4920161 Total length (>= 1000 bp) 4920161 Total length (>= 50000 bp) 4920161 Total length (>= 50000 bp) 4920161 Total length (>= 50000 bp) 496506 Total length (>= 25000 bp) 4753145 Total length (>= 50000 bp) 4544034 # contigs 35 Largest contig 663575 Total length 4920161 Reference length 5000040 GC (%) 35.80 Reference GC (%) 35.84 N50 297761 N75 186935 NG75 182381 L50 6 LG50 6 L75 11 LG75 12 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 10 # local misassemblies 0 # unaligned mis. contigs 0 # unaligned length 0 Genome fraction (%) 96.454 Duplication ratio 1.020 # N's per 100 kbp 9.54 Largest alignment 663575 Total aligned length 4920160 NA50 297761 NA50 66 LA50 66 LA75 111	# contigs (>= 5000 bp)	35
# contigs (>= 50000 bp) 19 Total length (>= 0 bp) 4920161 Total length (>= 1000 bp) 4920161 Total length (>= 5000 bp) 4920161 Total length (>= 5000 bp) 4906506 Total length (>= 25000 bp) 4753145 Total length (>= 50000 bp) 4544034 # contigs 35 Largest contig 663575 Total length 4920161 Reference length 5000040 GC (%) 35.80 Reference GC (%) 35.84 N50 297761 N75 186935 NG75 182381 L50 6 LG50 6 L75 11 LG75 12 # misassembles 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned mis. contigs 0 # unaligned length 0 Genome fraction (%) 96.454 Duplication ratio 1.020 # N's per 100 kbp 9.54 Largest alignment 663575 Total aligned length 4920160 NA50 297761 NA50 297761 NA50 36.454 Duplication ratio 1.020 # N's per 100 kbp 9.54 Largest alignment 663575 Total aligned length 4920160 NA50 297761 NA75 186935 NGA75 182381 LASO 6 LA75 182381 LASO 6 LASO 6 LA75 182381	# contigs (>= 10000 bp)	33
Total length (>= 0 bp) 4920161 Total length (>= 1000 bp) 4920161 Total length (>= 5000 bp) 4920161 Total length (>= 10000 bp) 4906506 Total length (>= 25000 bp) 4753145 Total length (>= 50000 bp) 4544034 # contigs 35 Largest contig 663575 Total length 4920161 Reference length 5000040 GC (%) 35.80 Reference GC (%) 35.84 N50 297761 NG50 297761 N75 186935 NG75 182381 L50 6 LG50 6 L75 11 LG75 12 # misassembles 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 # unaligned mis. contigs 0 # unaligned length 0 Genome fraction (%) 96.454 Duplication ratio 1.020 # N's per 100 kbp 9.54 Largest alignment 663575 Total aligned length 4920160 NA50 297761 NA50 297761 NG50 30 40 4966 H 10cal misassemble 90 4.966 NA50 297761 NG50 30 4.966 NA50 297761 NA50 297761 NA75 186935 NGA75 182381 LA50 6 LA50 6 LA50 6 LA75 111	# contigs (>= 25000 bp)	24
Total length (>= 1000 bp) 4920161 Total length (>= 5000 bp) 4920161 Total length (>= 10000 bp) 4906506 Total length (>= 25000 bp) 4753145 Total length (>= 50000 bp) 4544034 # contigs 35 Largest contig 663575 Total length 4920161 Reference length 5000040 GC (%) 35.80 Reference GC (%) 35.84 N50 297761 NG50 297761 N75 186935 NG75 182381 L50 6 LG50 6 L75 11 LG75 12 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # unaligned length 0 # unaligned length 0 Genome fraction (%) 96.454 Duplication ratio 1.020 # N's per 100 kbp 9.54 Largest alignment 6635	# contigs (>= 50000 bp)	19
Total length (>= 5000 bp) 4920161 Total length (>= 10000 bp) 4906506 Total length (>= 25000 bp) 4753145 Total length (>= 50000 bp) 4544034 # contigs 35 Largest contig 663575 Total length 4920161 Reference length 5000040 GC (%) 35.80 Reference GC (%) 35.84 N50 297761 NG50 297761 N75 186935 NG75 182381 L50 6 LG50 6 L75 11 LG75 12 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # unaligned mis. contigs 0 # unaligned length 0 Genome fraction (%) 96.454 Duplication ratio 1.020 # N's per 100 kbp 9.54 Largest alignment 663575 Total aligned length 4920	Total length (>= 0 bp)	4920161
Total length (>= 10000 bp) 4906506 Total length (>= 25000 bp) 4753145 Total length (>= 50000 bp) 4544034 # contigs 35 Largest contig 663575 Total length 4920161 Reference length 5000040 GC (%) 35.80 Reference GC (%) 35.84 N50 297761 NG50 297761 N75 186935 NG75 182381 L50 6 LG50 6 L75 11 LG75 12 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # unaligned mis. contigs 0 # unaligned length 0 Genome fraction (%) 96.454 Duplication ratio 1.020 # N's per 100 kbp 9.54 Largest alignment 663575 Total aligned length 4920160 NA50 297761	Total length (>= 1000 bp)	4920161
Total length (>= 25000 bp) 4753145 Total length (>= 50000 bp) 4544034 # contigs 35 Largest contig 663575 Total length 4920161 Reference length 5000040 GC (%) 35.80 Reference GC (%) 35.84 N50 297761 NG50 297761 N75 186935 NG75 182381 L50 6 LG50 6 L75 11 LG75 12 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # unaligned mis. contigs 0 # unaligned length 0 Genome fraction (%) 96.454 Duplication ratio 1.020 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4.96 # indels per 100 kbp 4.96 # indels per 100 kbp 4.96 # indels per 100 kbp 4.96 </td <td>Total length (>= 5000 bp)</td> <td>4920161</td>	Total length (>= 5000 bp)	4920161
# contigs 35 Largest contig 663575 Total length 4920161 Reference length 5000040 GC (%) 35.80 Reference GC (%) 35.84 N50 297761 N75 186935 NG75 182381 L50 6 LG50 6 L75 11 LG75 12 # misassembled contigs 0 # misassembled contigs 10 # local misassemblies 0 # unaligned length 0 Genome fraction (%) 96.454 Duplication ratio 1.020 # N's per 100 kbp 4.96 # indels per 100 kbp 9.54 Largest alignment 663575 Total aligned length 4920160 NA50 297761 NA75 186935 NGA75 182381 L50 6 LG50 6 L75 12 # misassembled contigs 0 # unaligned mis. contigs 0 # unaligned length 0 Genome fraction (%) 96.454 Duplication ratio 1.020 # N's per 100 kbp 9.54 Largest alignment 663575 Total aligned length 4920160 NA50 297761 NGA50 297761 NGA50 6 LGA50 6 LGA50 6 LGA50 6	Total length (>= 10000 bp)	4906506
# contigs 35 Largest contig 663575 Total length 4920161 Reference length 5000040 GC (%) 35.80 Reference GC (%) 35.84 N50 297761 NG50 297761 N75 186935 NG75 182381 L50 6 LG50 6 L75 11 LG75 12 # misassembled contigs 0 # misassembled contigs 0 # local misassemblies 0 # unaligned contigs 0 # unaligned length 0 Genome fraction (%) 96.454 Duplication ratio 1.020 # N's per 100 kbp 4.96 # indels per 100 kbp 9.54 Largest alignment 663575 Total aligned length 4920160 NA50 297761 NGA50 297761 NGA50 297761 NGA50 6 LGA50 6	Total length (>= 25000 bp)	4753145
Largest contig 663575 Total length 4920161 Reference length 5000040 GC (%) 35.80 Reference GC (%) 35.84 N50 297761 NG50 297761 N75 186935 NG75 182381 L50 6 LG50 6 L75 11 LG75 12 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # unaligned misassemblies 0 # unaligned misassemblies 0 # unaligned length 0 Genome fraction (%) 96.454 Duplication ratio 1.020 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4.96 # indels per 100 kbp 9.54 Largest alignment 663575 Total aligned length 4920160 NA50 297761 NA50 297761 NA75	Total length (>= 50000 bp)	4544034
Total length 4920161 Reference length 5000040 GC (%) 35.80 Reference GC (%) 35.84 N50 297761 NG50 297761 N75 186935 NG75 182381 L50 6 LG50 6 L75 11 LG75 12 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned mis. contigs 0 # unaligned length 0 Genome fraction (%) 96.454 Duplication ratio 1.020 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4.96 # indels per 100 kbp 9.54 Largest alignment 663575 Total aligned length 4920160 NA50 297761 NA50 297761 NA75 186935 NGA75	# contigs	35
Reference length 5000040 GC (%) 35.80 Reference GC (%) 35.84 N50 297761 NG50 297761 N75 186935 NG75 182381 L50 6 LG50 6 L75 11 LG75 12 # misassemblies 0 Misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned mis. contigs 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 96.454 Duplication ratio 1.020 # N's per 100 kbp 0.00 # mismatches per 100 kbp 9.54 Largest alignment 663575 Total aligned length 4920160 NA50 297761 NA50 297761 NA75 186935 NGA75 182381 LA50 6 </td <td>Largest contig</td> <td>663575</td>	Largest contig	663575
GC (%) 35.80 Reference GC (%) 35.84 N50 297761 NG50 297761 N75 186935 NG75 182381 L50 6 LG50 6 L75 11 LG75 12 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned mis. contigs 0 # unaligned length 0 Genome fraction (%) 96.454 Duplication ratio 1.020 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4.96 # indels per 100 kbp 9.54 Largest alignment 663575 Total aligned length 4920160 NA50 297761 NA50 297761 NA75 186935 NGA75 182381 LA50 6 LA50 6 <	Total length	4920161
Reference GC (%) 35.84 N50 297761 NG50 297761 N75 186935 NG75 182381 L50 6 LG50 6 L75 11 LG75 12 # misassemblies 0 Misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned mis. contigs 0 # unaligned length 0 Genome fraction (%) 96.454 Duplication ratio 1.020 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4.96 # indels per 100 kbp 9.54 Largest alignment 663575 Total aligned length 4920160 NA50 297761 NA75 186935 NGA75 182381 LA50 6 LGA50 6 LA75 11	Reference length	5000040
N50 297761 NG50 297761 N75 186935 NG75 182381 L50 6 LG50 6 L75 11 LG75 12 # misassemblies 0 Misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned mis. contigs 0 # unaligned length 0 Genome fraction (%) 96.454 Duplication ratio 1.020 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4.96 # indels per 100 kbp 9.54 Largest alignment 663575 Total aligned length 4920160 NA50 297761 NGA50 297761 NA75 186935 NGA75 182381 LA50 6 LA75 11	GC (%)	35.80
NG50 297761 N75 186935 NG75 182381 L50 6 LG50 6 L75 11 LG75 12 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned mis. contigs 0 # unaligned length 0 Genome fraction (%) 96.454 Duplication ratio 1.020 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4.96 # indels per 100 kbp 9.54 Largest alignment 663575 Total aligned length 4920160 NA50 297761 NGA50 297761 NA75 186935 NGA75 182381 LA50 6 LA75 11	Reference GC (%)	35.84
N75 186935 NG75 182381 L50 6 LG50 6 L75 11 LG75 12 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned mis. contigs 0 # unaligned length 0 Genome fraction (%) 96.454 Duplication ratio 1.020 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4.96 # indels per 100 kbp 9.54 Largest alignment 663575 Total aligned length 4920160 NA50 297761 NGA50 297761 NA75 186935 NGA75 182381 LA50 6 LA75 11	N50	297761
NG75 182381 L50 6 LG50 6 L75 11 LG75 12 # misassemblies 0 # misassembles 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned mis. contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 96.454 Duplication ratio 1.020 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4.96 # indels per 100 kbp 9.54 Largest alignment 663575 Total aligned length 4920160 NA50 297761 NGA50 297761 NA75 186935 NGA75 182381 LA50 6 LA75 11	NG50	297761
L50 6 LG50 6 L75 11 LG75 12 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned mis. contigs 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 96.454 Duplication ratio 1.020 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4.96 # indels per 100 kbp 9.54 Largest alignment 663575 Total aligned length 4920160 NA50 297761 NA75 186935 NGA75 182381 LA50 6 LA75 11	N75	186935
LG50 6 L75 11 LG75 12 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned mis. contigs 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 96.454 Duplication ratio 1.020 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4.96 # indels per 100 kbp 9.54 Largest alignment 663575 Total aligned length 4920160 NA50 297761 NA75 186935 NGA75 182381 LA50 6 LA75 11	NG75	182381
L75 11 LG75 12 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned mis. contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 96.454 Duplication ratio 1.020 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4.96 # indels per 100 kbp 9.54 Largest alignment 663575 Total aligned length 4920160 NA50 297761 NGA50 297761 NA75 186935 NGA75 182381 LA50 6 LGA50 6 LA75 11	L50	6
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassembles 0 # unaligned mis. contigs 0 # unaligned length 0 Genome fraction (%) 96.454 Duplication ratio 1.020 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4.96 # indels per 100 kbp 9.54 Largest alignment 663575 Total aligned length 4920160 NA50 297761 NGA50 297761 NGA50 297761 NGA50 6 LGA50 6 LGA50 6 LGA50 6	LG50	6
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned mis. contigs 0 + 0 part 0 Unaligned length 0 Genome fraction (%) 96.454 0 Duplication ratio 1.020 1.02	L75	11
# misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned mis. contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 96.454 Duplication ratio 1.020 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4.96 # indels per 100 kbp 9.54 Largest alignment 663575 Total aligned length 4920160 NA50 297761 NGA50 297761 NGA50 186935 NGA75 186935 NGA75 182381 LA50 6 LGA50 6 LA75 11	LG75	12
Misassembled contigs length 0 # local misassemblies 0 # unaligned mis. contigs 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 96.454 Duplication ratio 1.020 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4.96 # indels per 100 kbp 9.54 Largest alignment 663575 Total aligned length 4920160 NA50 297761 NGA50 297761 NA75 186935 NGA75 182381 LA50 6 LGA50 6 LA75 11	# misassemblies	0
# local misassemblies 0 # unaligned mis. contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 96.454 Duplication ratio 1.020 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4.96 # indels per 100 kbp 9.54 Largest alignment 663575 Total aligned length 4920160 NA50 297761 NGA50 297761 NA75 186935 NGA75 182381 LA50 6 LGA50 6 LA75 11	# misassembled contigs	0
# unaligned mis. contigs 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 96.454 Duplication ratio 1.020 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4.96 # indels per 100 kbp 9.54 Largest alignment 663575 Total aligned length 4920160 NA50 297761 NGA50 297761 NA75 186935 NGA75 182381 LA50 6 LGA50 6 LA75 11	Misassembled contigs length	0
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 96.454 Duplication ratio 1.020 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4.96 # indels per 100 kbp 9.54 Largest alignment 663575 Total aligned length 4920160 NA50 297761 NGA50 297761 NA75 186935 NGA75 182381 LA50 6 LGA50 6 LA75 11	# local misassemblies	0
Unaligned length 0 Genome fraction (%) 96.454 Duplication ratio 1.020 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4.96 # indels per 100 kbp 9.54 Largest alignment 663575 Total aligned length 4920160 NA50 297761 NGA50 297761 NA75 186935 NGA75 182381 LA50 6 LGA50 6 LA75 11	# unaligned mis. contigs	0
Genome fraction (%) 96.454 Duplication ratio 1.020 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4.96 # indels per 100 kbp 9.54 Largest alignment 663575 Total aligned length 4920160 NA50 297761 NGA50 297761 NA75 186935 NGA75 182381 LA50 6 LGA50 6 LA75 11	# unaligned contigs	0 + 0 part
Duplication ratio 1.020 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4.96 # indels per 100 kbp 9.54 Largest alignment 663575 Total aligned length 4920160 NA50 297761 NGA50 297761 NA75 186935 NGA75 182381 LA50 6 LGA50 6 LA75 11	Unaligned length	0
# N's per 100 kbp 0.00 # mismatches per 100 kbp 4.96 # indels per 100 kbp 9.54 Largest alignment 663575 Total aligned length 4920160 NA50 297761 NGA50 297761 NA75 186935 NGA75 182381 LA50 6 LGA50 6 LA75 11	Genome fraction (%)	96.454
# mismatches per 100 kbp 4.96 # indels per 100 kbp 9.54 Largest alignment 663575 Total aligned length 4920160 NA50 297761 NGA50 297761 NA75 186935 NGA75 182381 LA50 6 LGA50 6 LA75 11	Duplication ratio	1.020
# mismatches per 100 kbp 4.96 # indels per 100 kbp 9.54 Largest alignment 663575 Total aligned length 4920160 NA50 297761 NGA50 297761 NA75 186935 NGA75 182381 LA50 6 LGA50 6 LA75 11	# N's per 100 kbp	0.00
Largest alignment 663575 Total aligned length 4920160 NA50 297761 NGA50 297761 NA75 186935 NGA75 182381 LA50 6 LGA50 6 LA75 11		4.96
Total aligned length 4920160 NA50 297761 NGA50 297761 NA75 186935 NGA75 182381 LA50 6 LGA50 6 LA75 11	# indels per 100 kbp	9.54
NA50 297761 NGA50 297761 NA75 186935 NGA75 182381 LA50 6 LGA50 6 LA75 11	Largest alignment	663575
NGA50 297761 NA75 186935 NGA75 182381 LA50 6 LGA50 6 LA75 11	Total aligned length	4920160
NA75 186935 NGA75 182381 LA50 6 LGA50 6 LA75 11	NA50	297761
NGA75 182381 LA50 6 LGA50 6 LA75 11	NGA50	297761
LA50 6 LGA50 6 LA75 11	NA75	186935
LGA50 6 LA75 11	NGA75	182381
LA75 11	LA50	6
	LGA50	6
LGA75 12	LA75	11
	LGA75	12

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

	sim5M.CanuL
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	239
# indels	460
# indels (<= 5 bp)	460
# indels (> 5 bp)	0
Indels length	506

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

	sim5M.CanuL
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	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).



















