# contigs (>= 1000 bp)		Report canu	flye	shasta
# contigs (>= 5000 bp)	# contigs (>= 0 bp)	41	16	16
# contigs (>= 10000 bp)	# contigs (>= 1000 bp)	41	16	16
# contigs (>= 25000 bp)	# contigs (>= 5000 bp)	41	15	15
# contigs (>= 50000 bp)	# contigs (>= 10000 bp)	41	15	13
Total length (>= 0 bp) 35577586 34532450 33046224 Total length (>= 1000 bp) 35577586 34532450 33046224 Total length (>= 5000 bp) 35577586 34528293 33041364 Total length (>= 10000 bp) 35577586 34528293 33020887 Total length (>= 25000 bp) 35559156 34528293 33030303 # contigs 41 16 16 Largest contig 5884780 12078680 1106286 Total length 35577586 34532450 33046224 Reference length 34204973 34204973 34204973 GC (%) 23.04 22.95 22.91 Reference GC (%) 22.44 22.44 22.44 N50 3312350 3363344 6899527 N50 3312350 3363344 6899527 N90 1236530 1717044 1177246 auN 3299140.5 6181024.9 6398498.1 auN 3299140.5 6181024.9 6398498.1 LG90	# contigs (>= 25000 bp)	40	15	11
Total length (>= 1000 bp) 35577586 34532450 33046224 Total length (>= 5000 bp) 35577586 34528293 33041364 Total length (>= 10000 bp) 35577586 34528293 3300303 Total length (>= 25000 bp) 35559156 34528293 3300303 Total length (>= 50000 bp) 35559156 34528293 3300303 # contigs 41 16 1162866 Largest contig 5884780 12078680 11062865 Total length 35577586 34532450 33046224 Reference length 34204973 34204973 34204973 GC (%) 23.04 22.95 22.91 Reference GC (%) 22.44 22.44 22.44 NSO 3312350 3363344 6899527 NG50 3312350 3363344 6899527 NG90 1756805 1717044 1199308 NG90 1756805 1717044 117244 LG9 17 68181024.9 639498.1 LG9	# contigs (>= 50000 bp)	26	13	11
Total length (>= 5000 bp) 35577586 34528293 33041364 Total length (>= 10000 bp) 35577586 34528293 33026887 Total length (>= 25000 bp) 35559156 34528293 3300303 # contigs 41 16 16 Largest contig 5884780 12078680 11062865 Total length 35577586 34532450 33046224 Reference length 34204973 34204973 34204973 GC (%) 23.04 22.95 22.91 Reference GC (%) 22.44 22.44 22.44 N50 3312350 3363344 6899527 NG50 3312350 3363344 6899527 NG90 1756805 1717044 1197326 auN 3299140.5 6181024.9 6398498.1 auNG 34315319 6240201.8 6181738.2 L50 4 3 2 L690 10 8 8 H misassembled contigs 38 14 11	Total length (>= 0 bp)	35577586	34532450	33046224
Total length (>= 5000 bp) 35577586 34528293 33041364 Total length (>= 10000 bp) 35577586 34528293 33026887 Total length (>= 25000 bp) 35559156 34528293 3300303 # contigs 41 16 16 Largest contig 5884780 12078680 11062865 Total length 35577586 34532450 33046224 Reference length 34204973 34204973 34204973 GC (%) 23.04 22.95 22.91 Reference GC (%) 22.44 22.44 22.44 N50 3312350 3363344 6899527 NG50 3312350 3363344 6899527 NG90 1756805 1717044 1197326 auN 3299140.5 6181024.9 6398498.1 auNG 34315319 6240201.8 6181738.2 L50 4 3 2 L690 10 8 8 H misassembled contigs 38 14 11	Total length (>= 1000 bp)	35577586	34532450	33046224
Total length (>= 10000 bp) 35577586 34528293 33026887 Total length (>= 25000 bp) 35559156 34528293 3300303 Total length (>= 50000 bp) 35019221 34449109 3300303 # contigs 41 16 16 Largest contig 5884780 12078680 11062863 Total length 35577586 34532450 33046224 Reference length 34204973 34204973 34204973 GC (%) 23.04 22.95 22.91 Reference GC (%) 22.44 22.44 22.44 N50 3312350 3363344 6899527 NG50 3312350 3363344 6899527 NG90 1756805 1717044 1199305 NG90 1756805 1717044 1199305 LG50 4 3 2 LG50 4 3 2 LG50 4 3 2 LG50 4 3 2 LG50 <t< td=""><td></td><td>35577586</td><td>34528293</td><td>33041364</td></t<>		35577586	34528293	33041364
Total length (>= 25000 bp) 35559156 34528293 3300303 Total length (>= 50000 bp) 35019221 34449109 3300303 # contigs 41 16 16 Largest contig 5884780 12078680 11062868 Total length 35577586 34532450 33046224 Reference length 34204973 34204973 34204973 GC (%) 23.04 22.95 22.91 Reference GC (%) 22.44 22.44 22.44 NSO 3312350 3363344 6899527 NG50 3312350 3363344 6899527 NG90 1756805 1717044 1199305 NG90 1756805 1717044 1197246 auN 3299140.5 6181024.9 6398498.1 LG50 4 3 2 LG90 11 8 7 LG90 11 8 7 LG90 11 8 1 # misassembled contigs length			34528293	33026887
Total length (>= 50000 bp) 35019221 34449109 3300303 # contigs 41 16 16 Largest contig 5884780 12078680 11062869 Total length 35577586 34532450 33046224 Reference length 34204973 34204973 34204973 GC (%) 23.04 22.95 22.91 Reference GC (%) 22.44 22.44 22.44 N50 3312350 3363344 6899527 NG50 3312350 3363344 6899527 NG90 1236530 1717044 1199305 NG90 1756805 1717044 1199305 auN 3299140.5 6181024.9 6398498.1 LS0 4 3 2 LG50 4 3 2 LG90 11 8 6 H misassemblies 721 663 638 # misassembled contigs length 35454535 34472865 3300303 # scaffold gap ext. m			34528293	33003033
# contigs 41 16 16 Largest contig 5884780 12078680 11062868 Total length 35577586 34532450 33046224 Reference length 34204973 34204973 34204973 GC (%) 23.04 22.95 22.91 Reference GC (%) 22.44 22.44 22.44 NSO 3312350 3363344 6899527 NG50 3123530 376344 6899527 N90 1236530 1717044 1199305 NG90 1756805 1717044 1197246 auN 3299140.5 6181024.9 6398498.1 L50 4 3 2 L50 4 3 2 L50 4 3 2 L650 4 3 2 L90 11 8 7 L690 10 8 8 # misassemblies 721 663 636 # misassembled				
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Total length 35577586 34532450 33046224 Reference length 34204973 34204973 34204973 GC (%) 23.04 22.95 22.91 Reference GC (%) 22.44 22.44 22.44 N50 3312350 3363344 6899527 NG50 3312350 3363344 6899527 N90 1236530 1717044 1199305 NG90 1756805 1717044 1199305 auN 3299140.5 6181024.9 6398498.1 auNG 3431531.9 6240201.8 6181738.5 L50 4 3 2 LG50 4 3 2 LG90 11 8 7 Hisassemblies 721 663 636 # misassembled contigs 38 14 11 Misassembled contigs 38 14 15 # scaffold gap ext. mis. 0 0 0 # caffold gap loc. mis. 0 0 <td></td> <td></td> <td></td> <td></td>				
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# misassembled contigs 38				
Misassembled contigs length 35454535 34472865 33003033 # local misassemblies 164 157 136 # scaffold gap ext. mis. 0 0 0 # scaffold gap loc. mis. 0 0 0 # unaligned mis. contigs 0 0 0 # unaligned contigs 0 + 20 part 0 + 14 part 0 + 8 part Unaligned length 554700 426867 354940 Genome fraction (%) 97.060 97.163 93.504 Duplication ratio 1.054 1.024 1.020 # N's per 100 kbp 0.00 0.00 0.00 # mismatches per 100 kbp 125.02 127.02 131.07 # indels per 100 kbp 419.22 395.63 374.06 Largest alignment 1435619 1440049 1442157 Total aligned length 34961051 34002985 32597422 NA50 396866 400706 401295 NA90 33921 77988 78116 NGA90				
# local misassemblies				
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# N's per 100 kbp				93.504
# mismatches per 100 kbp 125.02 127.02 131.07 # indels per 100 kbp 419.22 395.63 374.06 Largest alignment 1435619 1440049 1442157 Total aligned length 34961051 34002985 32597422 NA50 396866 400706 401295 NGA50 399719 401037 398753 NA90 33921 77988 78116 NGA90 77740 82801 30838 auNA 455858.8 471592.5 476557.5 auNGA 474152.0 476107.5 460413.4 LA50 28 27 25 LGA50 26 26 26 LA90 1117 94 92	· ·	1.054	1.024	1.020
# indels per 100 kbp				
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NGA90 77740 82801 30838 auNA 455858.8 471592.5 476557.5 auNGA 474152.0 476107.5 460413.4 LA50 28 27 25 LGA50 26 26 26 LA90 117 94 92	# mismatches per 100 kbp # indels per 100 kbp Largest alignment Total aligned length	125.02 419.22 1435619 34961051	127.02 395.63 1440049 34002985	131.07 374.06 1442157 32597422
auNA 455858.8 471592.5 476557.5 auNGA 474152.0 476107.5 460413.4 LA50 28 27 25 LGA50 26 26 26 LA90 117 94 92	# mismatches per 100 kbp # indels per 100 kbp Largest alignment Total aligned length NA50	125.02 419.22 1435619 34961051 396866	127.02 395.63 1440049 34002985 400706	131.07 374.06 1442157 32597422 401295
auNGA 474152.0 476107.5 460413.4 LA50 28 27 25 LGA50 26 26 26 LA90 117 94 92	# mismatches per 100 kbp # indels per 100 kbp Largest alignment Total aligned length NA50 NGA50	125.02 419.22 1435619 34961051 396866 399719	127.02 395.63 1440049 34002985 400706 401037	131.07 374.06 1442157 32597422 401295 398753
LA50 28 27 25 LGA50 26 26 26 LA90 117 94 92	# mismatches per 100 kbp # indels per 100 kbp Largest alignment Total aligned length NA50 NGA50 NA90	125.02 419.22 1435619 34961051 396866 399719 33921	127.02 395.63 1440049 34002985 400706 401037 77988	131.07 374.06 1442157 32597422 401295 398753 78116
LGA50 26 26 26 LA90 117 94 92	# mismatches per 100 kbp # indels per 100 kbp Largest alignment Total aligned length NA50 NGA50 NA90 NGA90	125.02 419.22 1435619 34961051 396866 399719 33921 77740	127.02 395.63 1440049 34002985 400706 401037 77988 82801	131.07 374.06 1442157 32597422 401295 398753 78116 30838
LA90 117 94 92	# mismatches per 100 kbp # indels per 100 kbp Largest alignment Total aligned length NA50 NGA50 NA90 NGA90 auNA	125.02 419.22 1435619 34961051 396866 399719 33921 77740 455858.8	127.02 395.63 1440049 34002985 400706 401037 77988 82801 471592.5	131.07 374.06 1442157 32597422 401295 398753 78116 30838 476557.5
	# mismatches per 100 kbp # indels per 100 kbp Largest alignment Total aligned length NA50 NGA50 NA90 NGA90 auNA auNGA	125.02 419.22 1435619 34961051 396866 399719 33921 77740 455858.8 474152.0	127.02 395.63 1440049 34002985 400706 401037 77988 82801 471592.5 476107.5	131.07 374.06 1442157 32597422 401295 398753 78116 30838 476557.5
LGA90 93 91 112	# mismatches per 100 kbp # indels per 100 kbp Largest alignment Total aligned length NA50 NGA50 NA90 NGA90 auNA auNGA LA50	125.02 419.22 1435619 34961051 396866 399719 33921 77740 455858.8 474152.0	127.02 395.63 1440049 34002985 400706 401037 77988 82801 471592.5 476107.5	131.07 374.06 1442157 32597422 401295 398753 78116 30838 476557.5 460413.4
	# mismatches per 100 kbp # indels per 100 kbp Largest alignment Total aligned length NA50 NGA50 NA90 NGA90 auNA auNGA LA50 LGA50	125.02 419.22 1435619 34961051 396866 399719 33921 77740 455858.8 474152.0 28	127.02 395.63 1440049 34002985 400706 401037 77988 82801 471592.5 476107.5 27	0.00 131.07 374.06 1442157 32597422 401295 398753 78116 30838 476557.5 460413.4 25 26

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

	canu	flye	shasta
# misassemblies	721	663	636
# contig misassemblies	721	663	636
# c. relocations	288	267	259
# c. translocations	421	386	365
# c. inversions	12	10	12
# scaffold misassemblies	0	0	0
# s. relocations	0	0	0
# s. translocations	0	0	0
# s. inversions	0	0	0
# misassembled contigs	38	14	11
Misassembled contigs length	35454535	34472865	33003033
# local misassemblies	164	157	136
# scaffold gap ext. mis.	0	0	0
# scaffold gap loc. mis.	0	0	0
# unaligned mis. contigs	0	0	0
# mismatches	43709	43189	42725
# indels	146564	134525	121935
# indels (<= 5 bp)	122855	120385	111855
# indels (> 5 bp)	23709	14140	10080
Indels length	529209	415684	372359

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

	canu	flye	shasta
# fully unaligned contigs	0	0	0
Fully unaligned length	0	0	0
# partially unaligned contigs	20	14	8
Partially unaligned length	554700	426867	354940
# N's	0	0	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).



























