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# contigs (>= 1000 bp) # contigs (>= 5000 bp) # contigs (>= 25000 bp) # contigs (>= 25000 bp) # contigs (>= 50000 bp) # contigs (>= 50000 bp) Total length (>= 0 bp) Total length (>= 1000 bp) Total length (>= 10000 bp) Total length (>= 5000 bp) Total length # contigs Largest contig  GC (%) Reference length Total length Reference GC (%) Reference GC	ab)         21           abp)         21           abp)         2           abp)         2           abp)         1557202           bp)         1556617           bp)         1550714           0 bp)         1550714           0 bp)         974342           25         920673           1556617         1521208           28.18         28.18           920673         920673           29922         29953           558251.9         571246.3           1         1           15         14           15         14           15         14           15         9           1ength         1145996           15         0           16         0           17         0           18         0           19         0           10         0           11         0           12         0           13         0           14         0           15         0           16         0           <	# contigs (>= 1000 bp)  # contigs (>= 5000 bp)  # contigs (>= 10000 bp)  # contigs (>= 25000 bp)  # contigs (>= 50000 bp)  Total length (>= 0 bp)  Total length (>= 1000 bp)  Total length (>= 5000 bp)  Total length (>= 1000 bp)
# contigs (>= 5000 bp) # contigs (>= 10000 bp) # contigs (>= 25000 bp) # contigs (>= 50000 bp) Total length (>= 0 bp) Total length (>= 1000 bp) Total length (>= 10000 bp) Total length (>= 5000 bp) Total length (>= 50000 bp) Total length (>= 50000 bp) Total length (>= 50000 bp) # contigs Largest contig Total length Reference length Total length Reference length Reference GC (%) Roso Roso Roso Roso Roso Roso Roso Ros	ab)         21           abp)         21           abp)         2           abp)         2           abp)         1557202           bp)         1556617           bp)         1550714           0 bp)         1550714           0 bp)         974342           25         920673           1556617         1521208           28.18         28.18           920673         920673           29922         29953           558251.9         571246.3           1         1           15         14           15         14           15         14           15         9           1ength         1145996           15         0           16         0           17         0           18         0           19         0           10         0           11         0           12         0           13         0           14         0           15         0           16         0           <	# contigs (>= 5000 bp)  # contigs (>= 10000 bp)  # contigs (>= 25000 bp)  # contigs (>= 50000 bp)  Total length (>= 0 bp)  Total length (>= 1000 bp)  Total length (>= 5000 bp)  Total length (>= 10000 bp)
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Total length (>= 0 bp)	bp) 1557202 bp) 1556617 bp) 1550714 0 bp) 1550714 0 bp) 1491460 0 bp) 974342 25 920673 1556617 1521208 28.18 28.18 920673 920673 29922 29953 558251.9 571246.3 1 1 1 1 1 1 5 9 1 14 15 9 19 10 11 5 0 10 10 10 10 10 10 10 10 10 10 10 10 1	Total length (>= 0 bp)  Total length (>= 1000 bp)  Total length (>= 5000 bp)  Total length (>= 10000 bp)
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Total length (>= 25000 bp) 14914  Total length (>= 50000 bp) 9743  # contigs  Largest contig 9206  Reference length 15522  GC (%) 28.  Reference GC (%) 28.  N50 9206  N50 9206  N90 299  NG50 9206  N90 299  auN 55825  auNG 57124  L50 LG50 L90  LG90 # misassembled contigs length 11459  # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned contigs length 332  Genome fraction (%) 96.5  Duplication ratio 1.0  # N's per 100 kbp 0.0  # mismatches per 100 kbp 225  # genomic features 1592 + 35 p	0 bp) 1491460 0 bp) 974342 25 920673 1556617 1521208 28.18 920673 920673 920673 29922 29953 558251.9 571246.3 1 1 1 15 95 91 elength 1145996 111 5. 0 95 0 + 5 part 33225 96.519 1.036	
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Largest contig         9206           Total length         15566           Reference length         15212           GC (%)         28           Reference GC (%)         28           N50         9206           NG50         9206           N90         299           auN         55825           auNG         57124           L50         LG50           L90         LG90           # misassemblies         # misassembled contigs           Misassembled contigs length         11459           # local misassemblies         # scaffold gap ext. mis.           # scaffold gap loc. mis.         # unaligned mis. contigs           # unaligned length         332           Genome fraction (%)         96.5           Duplication ratio         1.0           # N's per 100 kbp         0.           # mismatches per 100 kbp         216           # indels per 100 kbp         22           # genomic features         1592 + 35 p           Largest alignment         9106	920673 1556617 1521208 28.18 28.18 920673 920673 29922 29953 558251.9 571246.3 1 1 15 14 15 15 14 15 15 19 1145996 11 5. 0 16 10 10 10 11 11 11 11 11 11 11 11 11 11	
Total length 15566 Reference length 15212 GC (%) 28. Reference GC (%) 28. N50 9206 NG50 9206 NG50 9206 NG90 299 auN 55825 auNG 571246 L50 LG50 L90 LG90 # misassembled contigs # misassembled contigs length 11459 # local misassembles # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned length 332 Genome fraction (%) 96.5 Duplication ratio 1.00 # N's per 100 kbp 0.00 # mismatches per 100 kbp 226 # genomic features 1592 + 35 p Largest alignment 9106	1556617 1521208 28.18 28.18 920673 920673 920673 29922 29953 558251.9 571246.3 1 1 15 14 15 15 14 15 15 19 1145996 11 5. 0 15 0 19 0 + 5 part 33225 96.519 1.036	
Reference length 15212 GC (%) 28. Reference GC (%) 28. N50 9206 N50 9206 N90 299 NG90 299 auN 55825 auNG 57124 L50 LG50 L90 LG90 # misassembles # misassembled contigs length 11459 # local misassembles # scaffold gap ext. mis. # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned length 332 Genome fraction (%) 96.5 Duplication ratio 1.0 # N's per 100 kbp 0.0 # mismatches per 100 kbp 22. # genomic features 1592 + 35 p Largest alignment 9106	1521208 28.18 28.18 920673 920673 920673 29922 29953 558251.9 571246.3 1 1 1 15 15 14 15 15 19 1145996 11 10 10 10 11 11 11 11 11 11 11 11 11	
GC (%)         28.           Reference GC (%)         28.           N50         9206           NG50         9206           N90         299           NG90         299           auN         55825           auNG         57124           L50         L           LG50         L           L90         L           LG90         #           # misassemblies         #           # misassembled contigs         11459           # local misassemblies         #           # scaffold gap ext. mis.         #           # scaffold gap loc. mis.         #           # unaligned mis. contigs         0 + 5 p           Unaligned length         332           Genome fraction (%)         96.5           Duplication ratio         1.0           # N's per 100 kbp         0           # mismatches per 100 kbp         216           # indels per 100 kbp         22           # genomic features         1592 + 35 p           Largest alignment         9106	28.18 28.18 28.18 920673 920673 920673 29922 29953 558251.9 571246.3 1 1 1 15 15 14 15 15 19 1145996 11 5. 0 6. 0 19 10 15 10 15 10 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 10	
Reference GC (%)         28.           N50         9206           NG50         9206           N90         299           NG90         299           auN         55825           auNG         571246           L50         L50           LG50         L90           LG90         # misassemblies           # misassembled contigs         Misassembled contigs           # local misassemblies         # scaffold gap ext. mis.           # scaffold gap loc. mis.         # unaligned mis. contigs           # unaligned length         332           Genome fraction (%)         96.5           Duplication ratio         1.0           # N's per 100 kbp         0.           # mismatches per 100 kbp         216.           # indels per 100 kbp         22.           # genomic features         1592 + 35 p           Largest alignment         9106	28.18 920673 920673 920673 29922 29953 558251.9 571246.3 1 1 15 14 15 gs 9 length 1145996 11 5. 0 6. 0 195 0 + 5 part 33225 96.519 1.036	
N50         9206           NG50         9206           N90         299           NG90         299           auN         55825           auNG         57124           L50         L50           LG50         L90           LG90         # misassemblies           # misassembled contigs         # local misassembled           # local misassemblies         # scaffold gap ext. mis.           # scaffold gap loc. mis.         # unaligned mis. contigs           # unaligned length         332           Genome fraction (%)         96.5           Duplication ratio         1.0           # N's per 100 kbp         0.           # mismatches per 100 kbp         216.           # indels per 100 kbp         22.           # genomic features         1592 + 35 p           Largest alignment         9106	920673 920673 920673 29922 29953 558251.9 571246.3 1 1 15 14 15 15 14 15 15 16 1145996 11 5. 0 16 10 10 10 10 10 10 10 10 10 10 10 10 10	
NG50         9206           N90         299           NG90         299           auN         55825           auNG         57124           L50         LG50           L90         LG90           # misassemblies         # misassembled contigs           Misassembled contigs length         11459           # local misassemblies         # scaffold gap ext. mis.           # scaffold gap loc. mis.         # unaligned mis. contigs           # unaligned length         332           Genome fraction (%)         96.5           Duplication ratio         1.0           # N's per 100 kbp         0.           # mismatches per 100 kbp         216.           # indels per 100 kbp         22.           # genomic features         1592 + 35 p           Largest alignment         9106	920673 29922 29953 558251.9 571246.3 1 1 1 15 14 15 15 14 15 18 19 1145996 11 5. 0 6. 0 19 10 10 10 10 10 10 10 10 10 10 10 10 10	
N90         299           NG90         299           auN         55825           auNG         57124           L50         L50           LG50         L90           LG90         # misassemblies           # misassembled contigs         # 11459           # local misassemblies         # scaffold gap ext. mis.           # scaffold gap loc. mis.         # unaligned mis. contigs           # unaligned length         332           Genome fraction (%)         96.5           Duplication ratio         1.0           # N's per 100 kbp         0.           # mismatches per 100 kbp         216.           # indels per 100 kbp         22.           # genomic features         1592 + 35 p           Largest alignment         9106	29922 29953 558251.9 571246.3 1 1 1 15 14 15 15 14 15 18 195 10 10 11 10 11 11 11 11 11 11 11 11 11	
NG90         299           auN         55825           auNG         57124           L50         L50           L90         L90           LG90         # misassemblies           # misassembled contigs         # misassembled contigs           Misassembled contigs length         11459           # local misassemblies         # scaffold gap ext. mis.           # scaffold gap loc. mis.         # unaligned mis. contigs           # unaligned length         332           Genome fraction (%)         96.5           Duplication ratio         1.0           # N's per 100 kbp         0.           # mismatches per 100 kbp         216           # indels per 100 kbp         22           # genomic features         1592 + 35 p           Largest alignment         9106	29953 558251.9 571246.3 1 1 1 1 15 14 15 15 14 15 15 10 1145996 11 5. 0 6. 0 19 10 10 10 10 10 10 10 10 10 10 10 10 10	
auN 55825 auNG 57124 L50 LG50 LG90 # misassemblies # misassembled contigs Misassembled contigs length 11459 # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned length 332 Genome fraction (%) 96.5 Duplication ratio 1.0 # N's per 100 kbp 0.0 # mismatches per 100 kbp 22.0 # genomic features 1592 + 35 p Largest alignment 9106	558251.9 571246.3 1 1 1 15 14 15 15 14 15 15 16 17 18 19 10 10 10 11 10 10 10 10 10 10 10 10 10	N90
auNG 571246 L50 L50 LG50 L90 LG90 # misassemblies # misassembled contigs Misassembled contigs length 11459 # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned length 332 Genome fraction (%) 96.5 Duplication ratio 1.0 # N's per 100 kbp 0.0 # mismatches per 100 kbp 216. # indels per 100 kbp 22. # genomic features 1592 + 35 p Largest alignment 9106	571246.3  1  1  15  14  15  15  14  15  15  16  17  18  19  10  11  10  10  11  11  11  11  11	NG90
L50 LG50 LG90 LG90 # misassemblies # misassembled contigs Misassembled contigs length # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned length Genome fraction (%) Duplication ratio # N's per 100 kbp # mismatches per 100 kbp # indels per 100 kbp # genomic features Largest alignment  9106	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	auN
LG50 L90 LG90 # misassemblies # misassembled contigs Misassembled contigs length # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned length Genome fraction (%) Duplication ratio # N's per 100 kbp # mismatches per 100 kbp # indels per 100 kbp # genomic features Largest alignment 9106	1 15 14 15 15 19 19 1145996 11 15 10 10 11 11 11 11 11 11 11 11 11 11 11	auNG
L90 LG90 # misassemblies # misassembled contigs Misassembled contigs length 11459 # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned length 332 Genome fraction (%) 96.5 Duplication ratio 1.0 # N's per 100 kbp 0.0 # mismatches per 100 kbp 216. # indels per 100 kbp 22. # genomic features 1592 + 35 p Largest alignment 9106	15 14 15 15 17 18 19 19 10 11 11 11 11 11 11 11 11 11 11 11 11	L50
# misassemblies # misassembled contigs Misassembled contigs length # local misassembles # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned length  Genome fraction (%)  Duplication ratio # N's per 100 kbp # mismatches per 100 kbp # indels per 100 kbp # genomic features  Largest alignment  # 01459  1145	14 15 gs 9 length 1145996 11 s. 0 s. 0 igs 0 1 + 5 part 33225 96.519 1.036	LG50
# misassemblies # misassembled contigs Misassembled contigs length # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned contigs  Unaligned length 332 Genome fraction (%) 96.5 Duplication ratio # N's per 100 kbp 00 # mismatches per 100 kbp 216 # indels per 100 kbp 22. # genomic features 1592 + 35 p	15 gs 9 length 1145996 11 s. 0 s. 0 gs 0 1 + 5 part 33225 96.519 1.036	L90
# misassembled contigs Misassembled contigs length # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned contigs  Unaligned length 332 Genome fraction (%) 96.5 Duplication ratio # N's per 100 kbp 00 # mismatches per 100 kbp 216. # indels per 100 kbp 22. # genomic features 1592 + 35 p Largest alignment	gs 9 length 1145996 11 s. 0 s. 0 igs 0 1 + 5 part 33225 96.519 1.036	LG90
Misassembled contigs length # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned length Genome fraction (%) Duplication ratio # N's per 100 kbp # mismatches per 100 kbp # indels per 100 kbp # genomic features Largest alignment 11459  # 11459  # 11459  # 11459  # 259  # 11459  # 259  # 259  # 260  # 260  # 270  # 270  # 280  # 280  # 280  # 280  # 280  # 280  # 380	length 1145996 11 5. 0 6. 0 195 0 195 0 195 1 1036	# misassemblies
# local misassemblies  # scaffold gap ext. mis.  # scaffold gap loc. mis.  # unaligned mis. contigs  # unaligned length  Genome fraction (%)  Duplication ratio  # N's per 100 kbp  # mismatches per 100 kbp  # indels per 100 kbp  # genomic features  Largest alignment  100  # 1	11 s. 0 s. 0 ggs 0 + 5 part 33225 96.519	# misassembled contigs
# scaffold gap ext. mis.  # scaffold gap loc. mis.  # unaligned mis. contigs  # unaligned length  Genome fraction (%)  Duplication ratio  # N's per 100 kbp  # mismatches per 100 kbp  # indels per 100 kbp  # genomic features  Largest alignment  Dusis.  # Scaffold gap ext. mis.  # 0 + 5 p  96.5  0 + 5 p  96.5  1.0  22  # 1.0  1.0  1.0  1.0  1.0  1.0  1.0  1.0	s. 0 s. 0 gs 0 + 5 part 33225 96.519	Misassembled contigs length
# scaffold gap loc. mis.  # unaligned mis. contigs  # unaligned contigs  0 + 5 p  Unaligned length  332  Genome fraction (%)  Duplication ratio  1.0  # N's per 100 kbp  0 mismatches per 100 kbp  216.  # indels per 100 kbp  22.  # genomic features  1592 + 35 p  Largest alignment	s. 0 igs 0 + 5 part 33225 96.519	# local misassemblies
# unaligned mis. contigs  # unaligned contigs	96.519 0 + 5 part 33225 96.519	# scaffold gap ext. mis.
# unaligned contigs 0 + 5 p Unaligned length 332 Genome fraction (%) 96.5 Duplication ratio 1.0 # N's per 100 kbp 0.# mismatches per 100 kbp 216. # indels per 100 kbp 22.# genomic features 1592 + 35 p Largest alignment 9106	0 + 5 part 33225 96.519 1.036	# scaffold gap loc. mis.
Unaligned length       332         Genome fraction (%)       96.5         Duplication ratio       1.0         # N's per 100 kbp       0.         # mismatches per 100 kbp       216.         # indels per 100 kbp       22.         # genomic features       1592 + 35 p         Largest alignment       9106	33225 96.519 1.036	# unaligned mis. contigs
Genome fraction (%)       96.5         Duplication ratio       1.0         # N's per 100 kbp       0.         # mismatches per 100 kbp       216.         # indels per 100 kbp       22.         # genomic features       1592 + 35 p         Largest alignment       9106	96.519 1.036	# unaligned contigs
Duplication ratio       1.0         # N's per 100 kbp       0.         # mismatches per 100 kbp       216.         # indels per 100 kbp       22.         # genomic features       1592 + 35 p         Largest alignment       9106	1.036	Unaligned length
# N's per 100 kbp 0.  # mismatches per 100 kbp 216.  # indels per 100 kbp 22.  # genomic features 1592 + 35 p  Largest alignment 9106		Genome fraction (%)
# mismatches per 100 kbp 216. # indels per 100 kbp 22. # genomic features 1592 + 35 p Largest alignment 9106	0.00	Duplication ratio
# indels per 100 kbp 22.  # genomic features 1592 + 35 p  Largest alignment 9106		# N's per 100 kbp
# indels per 100 kbp 22.  # genomic features 1592 + 35 p  Largest alignment 9106	) kbp 216.20	# mismatches per 100 kbp
# genomic features 1592 + 35 p Largest alignment 9106	22.67	
Largest alignment 9106	1592 + 35 part	
3 3	910664	
3 3	1521753	
NA50 9106	910664	
	910664	
	17053	
	24180	
	544132.2	
	556797.9	
	1	
	1	LA50
LA90	17	LGA50

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

	URI39H
# misassemblies	15
# contig misassemblies	15
# c. relocations	5
# c. translocations	8
# c. inversions	2
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	9
Misassembled contigs length	1145996
# local misassemblies	11
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	3290
# indels	345
# indels (<= 5 bp)	294
# indels (> 5 bp)	51
Indels length	3178

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

	URI39H
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	5
Partially unaligned length	33225
# 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).

























