# contigs (>= 1000 bp)  # contigs (>= 5000 bp)  # contigs (>= 5000 bp)  # contigs (>= 10000 bp)  # contigs (>= 25000 bp)  # contigs (>= 25000 bp)  # contigs (>= 25000 bp)  # contigs (>= 50000 bp)  # contigs (>= 25000 bp)  # contigs (>= 25000 bp)  # contigs  # conti	Repor	URI87H
# contigs (>= 1000 bp)	# contigs (>= 0 bp)	66
# contigs (>= 5000 bp) # contigs (>= 10000 bp) # contigs (>= 10000 bp) # contigs (>= 25000 bp) # contigs (>= 50000 bp) Total length (>= 1000 bp) Total length (>= 1000 bp) Total length (>= 5000 bp) Total length (>= 50000 bp) Total length (>= 50000 bp) # contigs # contigs # contigs  Largest contig # contigs  GC (%) Reference length # 1521208 # Co (%) Reference GC (%) Roso # 10570 Roso Roso Roso # 10570 Roso Roso Roso Roso Roso Roso Roso Ros		24
# contigs (>= 10000 bp) # contigs (>= 25000 bp) # contigs (>= 25000 bp) # contigs (>= 50000 bp) # contigs (>= 50000 bp) # contigs (>= 50000 bp) Total length (>= 10000 bp) Total length (>= 10000 bp) Total length (>= 50000 bp) # contigs # contigs  Largest contig # contigs  GC (%) Reference length # 1521208 # Co (%) Reference GC (%) Roso # 1050  Roso # 10570  Roso # 10570  Roso # 10570  Roso # 10570  R		19
# contigs (>= 25000 bp) # contigs (>= 50000 bp) # contigs (>= 50000 bp) Total length (>= 0 bp) Total length (>= 1000 bp) Total length (>= 1000 bp) Total length (>= 10000 bp) Total length (>= 10000 bp) Total length (>= 10000 bp) Total length (>= 25000 bp) Total length (>= 50000 bp) Total length (>= 50000 bp) Total length (>= 50000 bp) # contigs # contigs # contigs # contigs # contig  Reference length # 1521206 # Reference length # 1521206 # Reference GC (%) Roso Roso Roso Roso Roso Roso Roso Ros		19
# contigs (>= 50000 bp) Total length (>= 0 bp) Total length (>= 1000 bp) Total length (>= 10000 bp) Total length (>= 50000 bp) Total length (>= 50000 bp) Total length (>= 10000 bp) Total length (>= 50000 bp) # contigs Largest contig Total length Reference length GC (%) Reference length Reference GC (%) Roso Roso Roso Roso Roso Roso Roso Ros		18
Total length (>= 0 bp) Total length (>= 1000 bp) Total length (>= 1000 bp) Total length (>= 5000 bp) Total length (>= 5000 bp) Total length (>= 5000 bp) Total length (>= 50000 bp) Total length (>= 50000 bp) Total length (>= 50000 bp) # contigs Largest contig Total length Reference length GC (%) Reference length GC (%) Reference GC (%) Referenc		2
Total length (>= 1000 bp) 1491333 Total length (>= 5000 bp) 1482048 Total length (>= 10000 bp) 1482048 Total length (>= 25000 bp) 1460107 Total length (>= 50000 bp) 1460107 Total length (>= 50000 bp) 964183 # contigs 34 Largest contig 910576 Total length 1498567 Reference length 1521208 GC (%) 28.22 Reference GC (%) 28.18 NSO 910576 N9O 29801 NG9O 29801 NG9O 29802 LG9O 15 LG9O 16 LG9O 16 # misassemblies 12 # misassembled contigs 16 # local misassemblies 12 # scaffold gap ext. mis. 16 # scaffold gap loc. mis. 17 # unaligned length 14744 Genome fraction (%) 93.766 Duplication ratio 1.046 # N's per 100 kbp 0.06 # mismatches per 100 kbp 152.86 # indels per 100 kbp 152.86 NGASO 910576 NASO 910576		
Total length (>= 5000 bp)		
Total length (>= 10000 bp)		
Total length (>= 25000 bp)		
Total length (>= 50000 bp) 964183 # contigs 34 Largest contig 910570 Total length 1498567 Reference length 1521208 GC (%) 28.22 Reference GC (%) 28.18 N50 910570 NG50 910570 NG90 29801 NG90 28162 auN 565982.2 auNG 557558.3 L50 1 L650 1 L90 14 LG90 15 # misassemblies 12 # misassembled contigs 12 # misassembled contigs 12 # local misassemblies 13 # scaffold gap ext. mis. 10 # unaligned mis. contigs 10 # unaligned length 14744 Genome fraction (%) 93.766 Duplication ratio 1.040 # N's per 100 kbp 152.86 # genomic features 1547 + 38 part Largest alignment 910570 NGA50 910570 NA90 16800 NA90 14682 auNA 563861.9 auNA 5		
# contigs		
Largest contig         910570           Total length         1498567           Reference length         1521208           GC (%)         28.18           N50         910570           NG50         910570           NG90         29801           NG90         29802           auN         565982.2           auNG         557558.3           L50         1           LG50         1           LG90         15           # misassemblies         12           # misassembled contigs         2           Misassembled contigs length         246397           # local misassemblies         1           # scaffold gap loc. mis.         0           # unaligned mis. contigs         0           # unaligned length         14744           Genome fraction (%)         93.766           Duplication ratio         1.040           # N's per 100 kbp         15.37           # genomic features         1547 + 38 part           Largest alignment         910570           NA50         910570           NA90         16800           NA90         16800           NA90		
Total length Reference length GC (%) Reference GC (%) Reference GC (%) Reference GC (%) Reference GC (%) ROSO ROSO ROSO ROSO ROSO ROSO ROSO ROS		
Reference length GC (%) Reference GC (%) Reference GC (%) R50 R910570 R90 R90 R90 R90 R90 R90 R90 R90 R90 R9		
Reference GC (%)  Reference GC (%)  Reference GC (%)  RS50  P10570  R950  P10570  R990  R990  R990  R990  R090  R0	Total length	
Reference GC (%)  N50  910576  N650  910576  N90  28816  auN  565982.2  auNG  L50  L50  L90  L40  L690  # misassembled contigs  # local misassemblies  # scaffold gap ext. mis.  # scaffold gap ext. mis.  # unaligned mis. contigs  # unaligned length  Unaligned length  Cenome fraction (%)  Duplication ratio  # N's per 100 kbp  # mismatches per 100 kbp  # indels per 100 kbp  # genomic features  Largest alignment  Total aligned length  NA50  NA90  NA90  NA90  NA90  NA90  LA50	Reference length	1521208
N50         910570           NG50         910570           N90         29801           NG90         28162           auN         565982.2           auNG         557558.3           L50         1           LG50         1           LG90         1           # misassemblies         1           # misassembled contigs         9           Misassembled contigs         9           Misassembled contigs         9           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         0           # unaligned length         14744           Genome fraction (%)         93.766           Duplication ratio         1.040           # N's per 100 kbp         152.86           # indels per 100 kbp         152.86           # genomic features         1547 + 38 part           Largest alignment         910570           NA50         910570           NA50         910570           NA90         16800           NA90         16800           NA90         16800           NA90         16800	GC (%)	28.22
NG50         910570           N90         29801           NG90         28162           auN         565982.2           auNG         557558.3           L50         1           LG50         1           L90         1.4           LG90         1.5           # misassemblies         1.2           # misassembled contigs         2           Misassembled contigs length         246397           # local misassemblies         1           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         0 + 4 part           Unaligned length         14744           Genome fraction (%)         93.766           Duplication ratio         1.040           # N's per 100 kbp         152.86           # indels per 100 kbp         152.86           # genomic features         1547 + 38 part           Largest alignment         910570           NA50         910570           NA90         16800           NA90         16800           NGA90         14632           auNA         563861.9           auNGA <td>Reference GC (%)</td> <td>28.18</td>	Reference GC (%)	28.18
N90         29801           NG90         28162           auN         565982.2           auNG         557558.3           L50         1           LG50         1           L90         14           LG90         15           # misassemblies         12           # misassembled contigs         9           Misassembled contigs length         246397           # local misassemblies         1           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         0 + 4 part           Unaligned length         14744           Genome fraction (%)         93.766           Duplication ratio         1.040           # N's per 100 kbp         152.86           # indels per 100 kbp         152.86           # indels per 100 kbp         153.70           # genomic features         1547 + 38 part           Largest alignment         910570           NA50         910570           NA90         16800           NA90         16800           NA90         16800           NGA90         14632 <td< td=""><td>N50</td><td>910570</td></td<>	N50	910570
NG90       28162         auN       565982.2         auNG       557558.3         L50       1         LG50       1         L90       14         LG90       15         # misassemblies       12         # misassembled contigs       9         Misassembled contigs length       246397         # local misassemblies       1         # scaffold gap ext. mis.       0         # scaffold gap loc. mis.       0         # unaligned mis. contigs       0         # unaligned length       14744         Genome fraction (%)       93.766         Duplication ratio       1.040         # mismatches per 100 kbp       152.86         # indels per 100 kbp       152.86         # indels per 100 kbp       152.86         # genomic features       1547 + 38 part         Largest alignment       910570         NA50       910570         NA90       16800         NA90       16800         NA90       16800         NA90       16800         NA90       16800         NGA90       14682         auNA       563861.9 <td>NG50</td> <td>910570</td>	NG50	910570
auN 565982.2 auNG 557558.3 L50 1 LG50 1 LG90 12 LG90 15 # misassemblies 12 # misassembled contigs 12 # local misassembled contigs 14 # local misassembles 15 # scaffold gap ext. mis. 16 # unaligned mis. contigs 17 # unaligned contigs 17 # unaligned length 17 Genome fraction (%) 17 Duplication ratio 10 # N's per 100 kbp 152.86 # indels per 100 kbp 153.76 # genomic features 1547 + 38 part 1547 +	N90	29801
auNG 557558.3 L50 1 L50 1 L50 1 L650 1 L90 14 L690 15 # misassemblies 12 # misassembled contigs 1 # local misassembled contigs 2 # scaffold gap ext. mis. 1 # scaffold gap loc. mis. 1 # unaligned mis. contigs 1 # unaligned length 1 Genome fraction (%) 1 Duplication ratio 1 # N's per 100 kbp 1 # indels per 100 kbp 1 # genomic features 1 Largest alignment 1 Total aligned length 1 NA50 1 NA50 1 NA90 1	NG90	28162
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  Unaligned length Genome fraction (%) Duplication ratio # N's per 100 kbp # mismatches per 100 kbp # indels per 100 kbp # genomic features Largest alignment Total aligned length NA50 NGA50 NGA90 16800 NGA90 14682 auNA 563861.9 auNGA LA50 LGA50 LGA5	auN	565982.2
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 Total aligned length NA50 NGA50 NA90 NGA90 auNA S63861.9 auNGA LA50 LGA50 LGA5	auNG	557558.3
L90 LG90 15 # misassemblies 12 # misassembled contigs Misassembled contigs length 246397 # local misassemblies 15 # scaffold gap ext. mis. 16 # scaffold gap loc. mis. 17 # unaligned mis. contigs 18 # unaligned length 14744 Genome fraction (%) 10 10 10 10 11 11 12 13 14 14 15 15 16 16 16 16 16 16 16 16 16 16 16 16 16	L50	1
# misassemblies	LG50	1
# misassemblies 12 # misassembled contigs Misassembled contigs length 246397 # local misassemblies 13 # scaffold gap ext. mis. 15 # unaligned mis. contigs 16 # unaligned contigs 17 # unaligned length 17 # unaligned length 17 # Genome fraction (%) 17 # Duplication ratio 17 # N's per 100 kbp 152.86 # indels per 100 kbp 153.77 # genomic features 1547 + 38 part 17 # Largest alignment 17 # Total aligned length 17 # NA50 17 # NA50 17 # NASO 18 # NA	L90	14
# 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  Total aligned length  NA50  NA90  NGA50  NA90  NGA90  auNA  auNA  563861.5  auNGA  LA50  LA90  LA630  LA90  1 16806  1 246397	LG90	15
# 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  # agenomic features  Largest alignment  Total aligned length  NA50  NA90  NGA50  NA90  NGA90  auNA  auNA  563861.9  auNGA  LA50  LA90  LA630  LA90  16800	# misassemblies	12
Misassembled contigs length		9
# local misassemblies  # scaffold gap ext. mis.  # scaffold gap loc. mis.  # unaligned mis. contigs  # unaligned contigs  O + 4 part  Unaligned length  Duplication ratio  # N's per 100 kbp  # mismatches per 100 kbp  # genomic features  Largest alignment  Total aligned length  NA50  NA50  NA90  NGA90  auNA  auNGA  LA50  LGA50  LGA50  LGA50  LGA50  LGA50  LGA50  LGA50  LGA50  LGA50  LA90  # scaffold gap ext. mis.  O 4  4 part  1474  0 93.766  9 1.040  1.0		
# scaffold gap ext. mis.  # scaffold gap loc. mis.  # unaligned mis. contigs  # unaligned contigs  O + 4 part  Unaligned length  Genome fraction (%)  Duplication ratio  # N's per 100 kbp  # mismatches per 100 kbp  # indels per 100 kbp  # genomic features  Largest alignment  Total aligned length  NA50  NGA50  NGA90  14682  auNA  563861.9  auNGA  LA50  LA90  16800  LA90  16800  1		1
# scaffold gap loc. mis.  # unaligned mis. contigs  # unaligned contigs  0 + 4 part  Unaligned length  Genome fraction (%)  Duplication ratio  1.040  # N's per 100 kbp  findels per 100 kbp  152.86  # indels per 100 kbp  1547 + 38 part  Largest alignment  Total aligned length  NA50  NGA50  NGA50  NGA90  14682  auNA  563861.9  auNA  563861.9  LGA50  LGA50  LGA50  LGA50  LGA50  LGA50  LA90  16800  168		0
# unaligned mis. contigs  # unaligned contigs  0 + 4 part  14744  Genome fraction (%)  Duplication ratio  1.040  # nismatches per 100 kbp  152.86  # indels per 100 kbp  153.77  Total aligned length  NASO  NGASO  NGASO  NGA9O  14682  auNA  563861.9  auNA  563861.9  LGASO  LGASO  LAGO  16800  LGASO  LAGO  16800		
# unaligned contigs 0 + 4 part Unaligned length 14744 Genome fraction (%) 93.766 Duplication ratio 1.040 # N's per 100 kbp 0.00 # mismatches per 100 kbp 152.86 # indels per 100 kbp 15.37 # genomic features 1547 + 38 part Largest alignment 910570 Total aligned length 1483054 NA50 910570 NA90 16800 NGA90 14662 auNA 563861.9 auNA 563861.9 LASO 1 LGA50 1 LGA50 1		
Unaligned length 14744  Genome fraction (%) 93.766  Duplication ratio 1.040  # N's per 100 kbp 0.00  # mismatches per 100 kbp 152.86  # indels per 100 kbp 1547 + 38 part  Largest alignment 910570  Total aligned length 1483054  NA50 910570  NGA50 910570  NA90 16800  NGA90 14682  auNA 563861.9  auNA 555469.6  LAS0 1  LGA50 1  L		
Genome fraction (%) 93.766  Duplication ratio 1.040 # N's per 100 kbp 0.00 # mismatches per 100 kbp 152.86 # indels per 100 kbp 15.37 # genomic features 1547 + 38 part Largest alignment 910570  Total aligned length 1483054  NA50 910570  NGA50 910570  NA90 16800  NA90 16800  NGA90 14682  auNA 563861.9  auNGA 555469.6  LA50 1  LGA50 1		<u> </u>
Duplication ratio 1.040 # N's per 100 kbp 0.00 # mismatches per 100 kbp 152.86 # indels per 100 kbp 15.37 # genomic features 1547 + 38 part Largest alignment 910570 Total aligned length 1483054 NA50 910570 NGA50 910570 NA90 16800 NGA90 14682 auNA 563861.9 auNA 555469.6 LA50 1 LGA50 16		ļ
# N's per 100 kbp		
# mismatches per 100 kbp 152.86 # indels per 100 kbp 15.37 # genomic features 1547 + 38 part Largest alignment 910570 NA50 910570 NA90 16800 NGA90 14682 auNA 563861.9 auNA 555469.6 LA90 16	· · · · · · · · · · · · · · · · · · ·	
# indels per 100 kbp 15.37 # genomic features 1547 + 38 part Largest alignment 910570 Total aligned length 1483054 NA50 910570 NGA50 910570 NA90 16800 NGA90 14682 auNA 563861.9 auNGA 555469.6 LA50 1 LGA50 1		
# genomic features 1547 + 38 part Largest alignment 910570 Total aligned length 1483054 NA50 910570 NGA50 910570 NA90 16800 NGA90 14682 auNA 563861.9 auNGA 555469.6 LA50 1 LGA50 1	# mismatches per 100 kbp	152.86
Largest alignment 910570 Total aligned length 1483054 NA50 910570 NGA50 910570 NA90 16800 NGA90 14682 auNA 563861.9 auNGA 555469.6 LA50 1 LGA50 1	# indels per 100 kbp	15.37
Total aligned length 1483054 NA50 910570 NGA50 910570 NA90 16800 NGA90 14682 auNA 563861.9 auNGA 555469.6 LA50 1 LGA50 1	# genomic features	1547 + 38 part
NA50     910570       NGA50     910570       NA90     16800       NGA90     14682       auNA     563861.9       auNGA     555469.6       LA50     1       LGA50     1       LA90     16	Largest alignment	910570
NGA50     910570       NA90     16800       NGA90     14682       auNA     563861.9       auNGA     555469.6       LA50     1       LGA50     1       LA90     16	Total aligned length	1483054
NA90 16800 NGA90 14682 auNA 563861.9 auNGA 555469.6 LA50 1 LGA50 1	NA50	910570
NGA90 14682 auNA 563861.9 auNGA 555469.6 LA50 1 LGA50 1	NGA50	910570
auNA 563861.9 auNGA 555469.6 LA50 1 LGA50 1 LA90 16	NA90	16800
auNGA 555469.6  LA50 1  LGA50 1  LA90 16	NGA90	14682
LA50 1 LGA50 1 LA90 16	auNA	563861.9
LGA50 1 LA90 16	auNGA	555469.6
LGA50 1 LA90 16	LA50	1
LA90 16	LGA50	1
		16
LGA90 17		

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

# misassemblies 12 # contig misassemblies 12 # c. relocations 6 # c. translocations 0 # scaffold misassemblies 0 # s. relocations 0 # s. relocations 0 # s. inversions 0 # sinversions 0 # sinversions 0 # misassembled contigs 9 Misassembled contigs 19 # local misassemblies 1 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 0 # mismatches 2267 # indels (<= 5 bp) 203		
# contig misassemblies 12  # c. relocations 6  # c. translocations 0  # scaffold misassemblies 0  # s. relocations 0  # s. inversions 0  # s. inversions 0  # s. inversions 0  # sinversions 0  # sinversions 0  # misassembled contigs 9  Misassembled contigs length 246397  # local misassemblies 1  # scaffold gap ext. mis. 0  # scaffold gap loc. mis. 0  # unaligned mis. contigs 0  # mismatches 2267  # indels 228		URI87H
# c. relocations 6  # c. translocations 6  # c. inversions 0  # scaffold misassemblies 0  # s. relocations 0  # s. translocations 0  # s. inversions 0  # misassembled contigs 9  Misassembled contigs length 246397  # local misassemblies 1  # scaffold gap ext. mis. 0  # scaffold gap loc. mis. 0  # unaligned mis. contigs 0  # mismatches 2267  # indels 228	# misassemblies	12
# c. translocations 6  # c. inversions 0  # scaffold misassemblies 0  # s. relocations 0  # s. translocations 0  # s. inversions 0  # misassembled contigs 9  Misassembled contigs length 246397  # local misassemblies 1  # scaffold gap ext. mis. 0  # scaffold gap loc. mis. 0  # unaligned mis. contigs 0  # mismatches 2267  # indels 228	# contig misassemblies	12
# c. inversions 0  # scaffold misassemblies 0  # s. relocations 0  # s. translocations 0  # s. inversions 0  # misassembled contigs 9  Misassembled contigs length 246397  # local misassemblies 1  # scaffold gap ext. mis. 0  # scaffold gap loc. mis. 0  # unaligned mis. contigs 0  # mismatches 2267  # indels 228	# c. relocations	6
# scaffold misassemblies 0  # s. relocations 0  # s. translocations 0  # s. inversions 0  # misassembled contigs 9  Misassembled contigs length 246397  # local misassemblies 1  # scaffold gap ext. mis. 0  # scaffold gap loc. mis. 0  # unaligned mis. contigs 0  # mismatches 2267  # indels 228	# c. translocations	6
# s. relocations 0  # s. translocations 0  # s. inversions 0  # misassembled contigs 9  Misassembled contigs length 246397  # local misassemblies 1  # scaffold gap ext. mis. 0  # scaffold gap loc. mis. 0  # unaligned mis. contigs 0  # mismatches 2267  # indels 228	# c. inversions	0
# s. translocations 0 # s. inversions 0 # misassembled contigs 9 Misassembled contigs length 246397 # local misassemblies 1 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 0 # mismatches 2267 # indels 228	# scaffold misassemblies	0
# s. inversions 0  # misassembled contigs 9  Misassembled contigs length 246397  # local misassemblies 1  # scaffold gap ext. mis. 0  # scaffold gap loc. mis. 0  # unaligned mis. contigs 0  # mismatches 2267  # indels 228	# s. relocations	0
# misassembled contigs 9 Misassembled contigs length 246397 # local misassemblies 1 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 0 # mismatches 2267 # indels 228	# s. translocations	0
Misassembled contigs length         246397           # local misassemblies         1           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         0           # mismatches         2267           # indels         228	# s. inversions	0
# local misassemblies 1  # scaffold gap ext. mis. 0  # scaffold gap loc. mis. 0  # unaligned mis. contigs 0  # mismatches 2267  # indels 228	# misassembled contigs	9
# scaffold gap ext. mis. 0  # scaffold gap loc. mis. 0  # unaligned mis. contigs 0  # mismatches 2267  # indels 228	Misassembled contigs length	246397
# scaffold gap loc. mis. 0 # unaligned mis. contigs 0 # mismatches 2267 # indels 228	# local misassemblies	1
# unaligned mis. contigs 0 # mismatches 2267 # indels 228	# scaffold gap ext. mis.	0
# mismatches 2267 # indels 228	# scaffold gap loc. mis.	0
# indels 228	# unaligned mis. contigs	0
	# mismatches	2267
# indels (<= 5 bp) 203	# indels	228
	# indels (<= 5 bp)	203
# indels (> 5 bp) 25	# indels (> 5 bp)	25
Indels length 1331	Indels length	1331

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

	URI87H
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	4
Partially unaligned length	14744
# 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).























