# contigs (>= 0 bp) # contigs (>= 1000 bp) # contigs (>= 1000 bp) # contigs (>= 5000 bp) # contigs (>= 5000 bp) # contigs (>= 50000 bp) # contigs (>= 50000 bp) # contigs (>= 50000 bp) Total sength (>= 0 bp) Total length (>= 1000 bp) Total length (>= 10000 bp) Total length (>= 50000 bp) # contigs Largest contig Total length GC (%) Reference length GC (%) S1.1 Reference GC (%) N50 93 NG50 93 NG90 13 auN 833. auNG 856. L50 LG50 LG90 # misassemblies # misassembled contigs Misassembled contigs Misassembled contigs # unaligned mis. contigs # unaligned length Genome fraction (%) Duplication ratio # N°s per 100 kbp # mismatches per 100 kb	Report	assymbly_35
# contigs (>= 1000 bp) # contigs (>= 5000 bp) # contigs (>= 10000 bp) # contigs (>= 50000 bp) # contigs (>= 50000 bp) # contigs (>= 50000 bp) Total length (>= 0 bp) Total length (>= 10000 bp) Total length (>= 5000 bp) Total length (>= 5000 bp) Total length (>= 50000 bp) # contigs Largest contig # contigs Largest contig # contigs Largest contig # contigs  Largest contig # contigs  Largest contig # contigs  Largest contig # contigs  Largest contig # contigs  Largest contig # contigs # misassemblies # misassemblies # misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned contigs # unaligned contigs # unaligned length # Genome fraction (%) # no particular contigs # unaligned length # contigs contigs # unaligned length # contigs contigs # unaligned length # contigs # conti	# contigs (>= 0 bp)	2 2
# contigs (>= 5000 bp) # contigs (>= 10000 bp) # contigs (>= 25000 bp) # contigs (>= 50000 bp) # contigs (>= 50000 bp) Total length (>= 0 bp) Total length (>= 1000 bp) Total length (>= 5000 bp) Total length (>= 50000 bp) Total length (>= 50000 bp) Total length (>= 50000 bp) # contigs Largest contig 93 Total length 104 GC (%) 51.1 Reference length 104 GC (%) 850 93 NG50 93 NG50 93 NG90 13 auN 833. auNG 856. L50 LG90 # misassembles # misassembled contigs # misassembled contigs Misassembled contigs # misassembled contigs # misassembled contigs # unaligned mis. contigs # unaligned length Genome fraction (%) Duplication ratio 1.02 # N's per 100 kbp 0.0 # mismatches per 100 kbp 0.0 # mismatches per 100 kbp 0.0 # mismatches per 100 kbp 0.0 Largest alignment 93 Total aligned length 106 NA50 93 NA90 13 NA90 14 NA90 18 NA9		(
# contigs (>= 10000 bp) # contigs (>= 25000 bp) # contigs (>= 25000 bp) # contigs (>= 50000 bp) Total length (>= 0 bp)		(
# contigs (>= 25000 bp) # contigs (>= 50000 bp) Total length (>= 0 bp) Total length (>= 1000 bp) Total length (>= 50000 bp) # contigs Largest contig		(
# contigs (>= 50000 bp) Total length (>= 0 bp) Total length (>= 1000 bp) Total length (>= 50000 bp) # contigs Largest contig 93 Total length 106 Reference length 107 Reference length 108 Reference GC (%) 109 Rogo 13 Rogo 13 Rogo 13 Rogo 13 Rogo 14 Rogo 15 Rogo 16 Rogo 17 Rogo 18 Rogo 18 Rogo 19 Rogo 19 Rogo 19 Rogo 19 Rogo 19 Rogo 10 Rogo 10 Rogo 10 Rogo 11 Rogo 12 Rogo 13 Rogo 14 Rogo 15 Rogo 16 Rogo 17 Rogo 18 Rogo 18 Rogo 19 Rogo 10 Rogo		(
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Total length (>= 1000 bp) Total length (>= 5000 bp) Total length (>= 5000 bp) Total length (>= 25000 bp) Total length (>= 25000 bp) Total length (>= 50000 bp) # contigs Largest contig 93 Total length 106 Reference length 104 GC (%) 51.1 Reference GC (%) 51.2 N50 93 NG50 93 NG90 13 auN 833. auNG 856. L50 LG90 # misassemblies # misassembled contigs length # local misassembles # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned length Genome fraction (%) 100.00 Duplication ratio 1.02 # N's per 100 kbp 0.0 # mismatches per 100 kbp 0.0 # Angon 13 NGA90 13 NA90 13		1068
Total length (>= 5000 bp) Total length (>= 10000 bp) Total length (>= 25000 bp) Total length (>= 50000 bp) # contigs Largest contig Page 1		(
Total length (>= 10000 bp) Total length (>= 25000 bp) Total length (>= 50000 bp) # contigs Largest contig Total length 106 Reference length 104 GC (%) 51.1 Reference GC (%) 51.2 N50 93 NG50 93 NG50 93 NG90 13 auN 833. auNG 856. L50 LG50 L90 LG90 # misassemblies # misassemblies # misassembled contigs Misassembled contigs Misassembled contigs # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned length Genome fraction (%) 100.00 Duplication ratio 1.02 # N's per 100 kbp 0.0 # mismatches per 100 kbp 0.0 # nodes per 100 kbp		(
Total length (>= 25000 bp)  # contigs  Largest contig 93  Total length 106  Reference length 104  GC (%) 51.1  Reference GC (%) 93  NG50 93  NG90 13  auN 833.  auNG 856.  L50  LG50  L90  # misassembled contigs # misassemblies # misassembled contigs length # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned length Genome fraction (%) 100.00  Duplication ratio 1.02  # N's per 100 kbp 0.0  # mismatches per 100 kbp 0.0  # mismatoh 106  NA50 93  NA90 13		(
Total length (>= 50000 bp)  # contigs  Largest contig  93  Total length  106  Reference length  GC (%)  51.1  Reference GC (%)  NS50  93  NG50  93  NG90  13  auN  833.  auNG  L50  LG50  LG90  # misassembled contigs  Misassembled contigs  Misassembled contigs length  # local misassemblies  # scaffold gap ext. mis.  # scaffold gap loc. mis.  # unaligned mis. contigs  # unaligned length  Genome fraction (%)  Duplication ratio  1.02  # N's per 100 kbp  0.0  # mismatches per 100 kbp  0.0  Largest alignment  93  Total aligned length  106  NA50  93  NA90  13  NA90  13  NA90  13  AUNA  833.  auNA  833.  auNA  833.  auNA  833.  auNA  833.  auNA  833.  auNA  834.  AUNGA  856.  LGA50		(
# contigs Largest contig Total length Reference length GC (%) S1.1 Reference GC (%) N50 93 NG50 93 NG90 13 auN auNG L50 LG90 # misassembled contigs # misassembled contigs length # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned length Genome fraction (%) Duplication ratio 1.02 # N's per 100 kbp 1.04 Largest alignment 93 NA90 13 NA90 13 NA90 13 NA90 13 NA90 13 NA90 13 AUNA 1833. auNA 1833. auNA 18433. auNA 18433. auNA 18433. auNA 18433. auNA 1856. LA50 LCA50		(
Largest contig 93 Total length 106 Reference length 104 GC (%) 51.1 Reference GC (%) 51.2 N50 93 NG50 93 NG90 13 auN 833. auNG 856. L50 LG90 # misassembled contigs # misassembled contigs length # local misassembled series # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned length Genome fraction (%) 100.00 Duplication ratio 1.02 # N's per 100 kbp 0.0 # mismatches per 100 kbp 0.0 Largest alignment 93 NA90 13 NA90 14		1 2
Total length 104 Reference length 104 GC (%) 51.1 Reference GC (%) 51.2 N50 93 NG50 93 NG50 93 NG90 13 auN 833. auNG 856. L50 LG50 L90 LG90 # misassemblies # misassembled contigs length # local misassembles # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned contigs Unaligned length Genome fraction (%) 100.00 Duplication ratio 1.02 # N's per 100 kbp 0.0 # mismatches per 100 kbp 0.0 # mismatches per 100 kbp 0.0 Raigned length 106 NA50 93 NA90 13 NA90 13 NA90 13 NA90 13 NA90 13 AuNA 833. auNGA 856. LGA50		
Reference length 104 GC (%) 51.1 Reference GC (%) 51.2 N50 93 NG50 93 NG50 93 NG90 13 AuuN 833. auuNG 856. L50 LG50 LG90 # misassemblies # misassembled contigs length # local misassembled contigs length # unaligned mis. contigs # unaligned length Genome fraction (%) 100.00 Duplication ratio 1.02 # N's per 100 kbp 0.0 # mismatches per 100 kbp 0.0 # mismatches per 100 kbp 0.0 Rafo50 93 NA90 13 NA90 13 AuuNA 833. AuuNGA 856. LGA50		<del> </del>
GC (%) 51.1 Reference GC (%) 51.2 N50 93 NG50 93 N90 13 NG90 13 auN 833. auNG 856. L50 LG50 L90 LG90 # misassemblies # misassembled contigs   Misassembled contigs   Misassembled contigs   Misassembled contigs   Wisassembled conti		1040
Reference GC (%) 51.2  N50 93  NG50 93  N90 13  NG90 13  auN 833.  auNG 856.  L50  LG50 L90  LG90 # misassemblies # misassembled contigs   Misassembled contigs length # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned contigs   Unaligned length   Genome fraction (%) 100.00  Duplication ratio 1.02  # N's per 100 kbp 0.0  # mismatches per 100 kbp 0.0  # mismatches per 100 kbp 0.0  Largest alignment 93  Total aligned length 106  NA50 93  NA90 13  NA90 13  NA90 13  AUNA 833.  auNA 833.  auNGA 856.  LGA50	-	
N50 93 NG50 93 NG50 93 NG90 13 NG90 13 auN 833. auNG 856. L50 LG50 LG90 # misassemblies # misassembled contigs   Misassembled contigs length # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned contigs 0 + 0 par Unaligned length Genome fraction (%) 100.00 Duplication ratio 1.02 # N's per 100 kbp 0.0 # mismatches per 100 kbp 0.0 # mismatches per 100 kbp 0.0 Largest alignment 93 Total aligned length 106 NA50 93 NA90 13 NA90 13 NA90 13 NA90 13 AuNA 833. auNA 833. auNGA 856. LGA50		51.25
NG50 93 N90 13 NG90 13 auN 833. auNG 856. L50 LG50 LG50 LG90 # misassemblies # misassembled contigs   # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs   # unaligned contigs   Unaligned length   Genome fraction (%) 100.00 Duplication ratio 1.02 # N's per 100 kbp 0.0 # mismatches per 100 kbp 0.0 # mismatches per 100 kbp 0.0 Largest alignment 93 Total aligned length 106 NA50 93 NA90 13 NA90 13 NA90 13 NA90 13 AUNA 833. auNA 833. auNA 856. LA50 LGA50		
N90 13 NG90 13 NG90 13 NG90 13 AuN 833. auNG 856. L50 LG50 LG50 LG90		
NG90 13 auN 833. auNG 856. L50 LG50 LG50 L90 LG90 # misassemblies # misassembled contigs Misassembled contigs length # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned contigs 0 + 0 par Unaligned length Genome fraction (%) 100.00 Duplication ratio 1.02 # N's per 100 kbp 0.0 # mismatches per 100 kbp 0.0 # mismatches per 100 kbp 0.0 Largest alignment 93 Total aligned length 106 NA50 93 NA90 13 NA90 13 NA90 13 ABUNA 833. auNA 833. auNGA 856. LA50 LGA50		
auN 833. auNG 856. L50 LG50 LG90 # misassemblies # misassembled contigs Misassembled contigs length # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned length Genome fraction (%) 100.00 Duplication ratio 1.02 # N's per 100 kbp 0.0 # mismatches per 100 kbp 0.0 # mismatches per 100 kbp 0.0 Largest alignment 93 Total aligned length 106 NA50 93 NA90 13 NA90 13 NA90 13 AuNA 833. auNA 856. LA50 LGA50		
auNG 856.  L50  L50  L50  L90  LG90  # misassemblies  # misassembled contigs  Misassembled contigs length  # local misassemblies  # scaffold gap ext. mis.  # scaffold gap loc. mis.  # unaligned mis. contigs  # unaligned rength  Genome fraction (%) 100.00  Duplication ratio 1.02  # N's per 100 kbp 0.0  # mismatches per 100 kbp 0.0  # mismatches per 100 kbp 0.0  Largest alignment 93  Total aligned length 106  NA50 93  NA90 13  NA90 13  NA90 13  NA90 13  AUNA 833.  auNA 835.  LA50  LGA50		
L50  LG50  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  Largest alignment  93  Total aligned length  106  NA50  93  NA90  13  NA90  13  NA90  13  NA90  13  NA90  13  AB40  AB56  LA50  LGA50		
LG50 LG90 # misassemblies # misassembled contigs Misassembled contigs length # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned length Genome fraction (%) 100.00 Duplication ratio 1.02 # N's per 100 kbp 0.0 # mismatches per 100 kbp 0.0 # mismatches per 100 kbp 0.0 Largest alignment 93 Total aligned length 106 NA50 93 NA90 13 NA90 13 NA90 13 ABUNA 833. BUNA 856. LA50 LGA50		050.
L90 LG90 # misassemblies # misassembled contigs Misassembled contigs length # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned contigs  Unaligned length Genome fraction (%) Duplication ratio # N's per 100 kbp 0.0 # mismatches per 100 kbp 0.0 # arigned length Cargest alignment 93 Total aligned length 106 NA50 93 NA90 13 NA90 13 NA90 13 NA90 13 ABUNA 833. auNA 833. auNA 856. LA50 LGA50		
# misassemblies # misassembled contigs  # misassembled contigs length # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned length  Genome fraction (%) 100.00  Duplication ratio 1.02 # N's per 100 kbp 0.0 # mismatches per 100 kbp 0.0 # mismatches per 100 kbp 0.0 Largest alignment 93 Total aligned length 106 NA50 93 NA90 13 NA90 13 NA90 13 ABJORASO 856 LA50  LA50 LA50		2
# misassemblies # misassembled contigs Misassembled contigs length # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned contigs  Unaligned length Genome fraction (%) Duplication ratio  # N's per 100 kbp 0.0 # mismatches per 100 kbp 0.0 Largest alignment Total aligned length 106 NA50 93 NA90 13 NGA90 13 auNA 833. auNGA 856. LA50 LGA50		2
# misassembled contigs  Misassembled contigs length  # local misassemblies  # scaffold gap ext. mis.  # scaffold gap loc. mis.  # unaligned mis. contigs  # unaligned length  Genome fraction (%) 100.00  Duplication ratio 1.02  # N's per 100 kbp 0.0  # mismatches per 100 kbp 0.0  Largest alignment 93  Total aligned length 106  NA50 93  NA90 13  NA90 13  NA90 13  ABUNA 833.  BUNA 856.  LA50  LCA50		(
Misassembled contigs length # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned contigs O + 0 par Unaligned length Genome fraction (%) Duplication ratio 1.02 # N's per 100 kbp 0.0 # mismatches per 100 kbp 0.0 Largest alignment 93 Total aligned length 106 NA50 93 NA90 13 NA90 13 NA90 13 NA90 13 AUNA 833. auNA 856. LA50 LGA50		,
# local misassemblies  # scaffold gap ext. mis.  # scaffold gap loc. mis.  # unaligned mis. contigs  # unaligned contigs  0 + 0 par  Unaligned length  Genome fraction (%)  Duplication ratio  1.02  # N's per 100 kbp  0.0  # mismatches per 100 kbp  1.06  Largest alignment  7 total aligned length  NA50  93  NGA50  93  NA90  13  NA90  14  15  NA50  15  NA50  16  NA50  17  NA50  18  NA50  18  NA50  19  NA50  18  NA50		,
# scaffold gap ext. mis.  # scaffold gap loc. mis.  # unaligned mis. contigs  # unaligned contigs  0 + 0 par  Unaligned length  Genome fraction (%) 100.00  Duplication ratio 1.02  # N's per 100 kbp 0.0  # mismatches per 100 kbp 0.0  Largest alignment 93  Total aligned length 106  NA50 93  NGA50 93  NA90 13  NGA90 13  auNA 833.  auNGA 856.  LA50  LGA50		,
# scaffold gap loc. mis.  # unaligned mis. contigs  # unaligned contigs  0 + 0 par  Unaligned length  Genome fraction (%)  1.02  # N's per 100 kbp  0.0  # mismatches per 100 kbp  1.02  # indels per 100 kbp  1.03  Largest alignment  7 total aligned length  NA50  93  NGA50  93  NGA90  13  auNA  833.  auNGA  856.  LA50  LAGA50		,
# unaligned mis. contigs  # unaligned contigs  0 + 0 par  Unaligned length  Genome fraction (%)  Duplication ratio  1.02  # N's per 100 kbp  0.0  # mismatches per 100 kbp  100.00  Clargest alignment  Total aligned length  NA50  NA50  NA90  13  NGA90  13  auNA  333.  auNA  856.  LA50  LA50  LA50		,
# unaligned contigs 0 + 0 par Unaligned length  Genome fraction (%) 100.00 Duplication ratio 1.02 # N's per 100 kbp 0.0 # mismatches per 100 kbp 0.0 Largest alignment 93 Total aligned length 106 NA50 93 NGA50 93 NA90 13 NGA90 13 auNA 833. auNGA 856. LA50 LGA50		,
Unaligned length  Genome fraction (%) 100.00  Duplication ratio 1.02  # N's per 100 kbp 0.0  # mismatches per 100 kbp 0.0  Largest alignment 93  Total aligned length 106  NA50 93  NGA50 93  NA90 13  NGA90 13  auNA 833.  auNGA 856.  LA50  LGA50		
Genome fraction (%) 100.00 Duplication ratio 1.02 # N's per 100 kbp 0.0 # mismatches per 100 kbp 0.0 Largest alignment 93 Total aligned length 106 NA50 93 NGA50 93 NA90 13 NGA90 13 auNA 833. auNGA 856. LA50 LGA50		0 + 0 pai
Duplication ratio 1.02 # N's per 100 kbp 0.0 # mismatches per 100 kbp 0.0 # indels per 100 kbp 0.0 Largest alignment 93 Total aligned length 106 NA50 93 NGA50 93 NA90 13 NGA90 13 auNA 833. auNGA 856. LA50		
# N's per 100 kbp 0.0 # mismatches per 100 kbp 0.0 # indels per 100 kbp 0.0 Largest alignment 93 Total aligned length 106 NA50 93 NGA50 93 NA90 13 NGA90 13 auNA 833. auNGA 856. LA50		
# mismatches per 100 kbp 0.0  # indels per 100 kbp 0.0  Largest alignment 93  Total aligned length 106  NA50 93  NGA50 93  NGA90 13  auNA 833.  auNGA 856.  LA50  LGA50	<u> </u>	
# indels per 100 kbp 0.0 Largest alignment 93 Total aligned length 106 NA50 93 NGA50 93 NA90 13 NGA90 13 auNA 833. auNGA 856. LA50		
Largest alignment     93       Total aligned length     106       NA50     93       NGA50     93       NA90     13       NGA90     13       auNA     833.       auNGA     856.       LA50     LGA50		
Total aligned length 106 NA50 93 NGA50 93 NA90 13 NGA90 13 auNA 833. auNGA 856. LA50		
NA50 93 NGA50 93 NA90 13 NGA90 13 auNA 833. auNGA 856. LA50		
NGA50 93 NA90 13 NGA90 13 auNA 833. auNGA 856. LA50		
NA90 13 NGA90 13 auNA 833. auNGA 856. LA50		
NGA90 13 auNA 833. auNGA 856. LA50 LGA50		
auNA 833. auNGA 856. LASO LGA50		
auNGA 856. LA50 LGA50		
LA50 LGA50		
LGA50		
LA90		
LGA90		2

All statistics are based on contigs of size >= 100 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

## Misassemblies report

	assymbly_35
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	0
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

All statistics are based on contigs of size >= 100 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

## Unaligned report

	assymbly_35
# 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 >= 100 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).



















