## Report

# contigs (>= 1000 bp)
# contigs (>= 10000 bp)  # contigs (>= 25000 bp)  # contigs (>= 50000 bp)  Total length (>= 1000 bp)  Total length (>= 5000 bp)  Total length (>= 10000 bp)  Total length (>= 25000 bp)  Total length (>= 25000 bp)  Total length (>= 50000 bp)  Total length (>= 50000 bp)  Total length (>= 50000 bp)  # contigs  4111  Largest contig  4559  Total length  8896849  Reference length  4641652  GC (%)  50.73  Reference GC (%)  N50  989  NG50  N75  709  NG75  583  L50  1304  LG50  1707  L75  2473  LG75  4 misassemblies  # misassembled contigs  Misassembled contigs  Misassembled contigs length  # local misassemblies  # unaligned contigs  Unaligned length  255  Genome fraction (%)  77.241  Duplication ratio  # N's per 100 kbp  00
# contigs (>= 25000 bp)  # contigs (>= 50000 bp)  Total length (>= 1000 bp)  Total length (>= 5000 bp)  Total length (>= 10000 bp)  Total length (>= 25000 bp)  Total length (>= 25000 bp)  Total length (>= 50000 bp)  Total length (>= 50000 bp)  # contigs  4111  Largest contig  Total length  Reference length  GC (%)  N50  Reference GC (%)  N75  N75  N70  N75  N70  N75  N75  N70  N75  S83  L50  LG50  1707  L75  LG75  473  LG75  # misassemblies  # misassembled contigs  Misassembled contigs length  # local misassemblies  # unaligned length  Unaligned length  255  Genome fraction (%)  # N's per 100 kbp  # nisassembled contigs  # nisassembled contigs  # N's per 100 kbp  # Noon  # nisassembled contigs  # nisassembled contigs  # N's per 100 kbp  # 0.00  # mismatches per 100 kbp  410.43
# contigs (>= 50000 bp)  Total length (>= 1000 bp)  Total length (>= 5000 bp)  Total length (>= 10000 bp)  Total length (>= 25000 bp)  Total length (>= 25000 bp)  Total length (>= 50000 bp)  Total length (>= 50000 bp)  # contigs  4111  Largest contig  Total length  Reference length  4641652  GC (%)  S0.73  Reference GC (%)  N50  989  NG50  N75  N75  N70  NG75  L50  1304  LG50  1707  L75  2473  LG75  # misassemblies  # misassembled contigs  Misassembled contigs length  # local misassemblies  # unaligned contigs  Genome fraction (%)  T7.241  Duplication ratio  # N's per 100 kbp  # noon bp  10  10  10  10  10  10  10  10  10  1
Total length (>= 1000 bp)         1916020           Total length (>= 5000 bp)         0           Total length (>= 10000 bp)         0           Total length (>= 25000 bp)         0           Total length (>= 50000 bp)         0           # contigs         4111           Largest contig         4559           Total length         3896849           Reference length         4641652           GC (%)         50.73           Reference GC (%)         50.79           N50         989           NG50         870           N75         709           NG75         583           L50         1304           LG50         1707           L75         2473           LG75         3340           # misassemblies         0           # misassembled contigs         0           Misassembled contigs         0           Unaligned length         255           Genome fraction (%)         77.241           Duplication ratio         1.087           # N's per 100 kbp         0.00           # mismatches per 100 kbp         410.43
Total length (>= 1000 bp)         1916020           Total length (>= 5000 bp)         0           Total length (>= 10000 bp)         0           Total length (>= 25000 bp)         0           Total length (>= 50000 bp)         0           # contigs         4111           Largest contig         4559           Total length         3896849           Reference length         4641652           GC (%)         50.73           Reference GC (%)         50.79           N50         989           NG50         870           N75         709           NG75         583           L50         1304           LG50         1707           L75         2473           LG75         3340           # misassemblies         0           # misassembled contigs         0           Misassembled contigs         0           Unaligned length         255           Genome fraction (%)         77.241           Duplication ratio         1.087           # N's per 100 kbp         0.00           # mismatches per 100 kbp         410.43
Total length (>= 10000 bp)  Total length (>= 25000 bp)  Total length (>= 50000 bp)  # contigs  4111  Largest contig  Total length  Reference length  Reference length  GC (%)  N50  N850  NG50  N75  N75  N75  N675  L50  1304  LG50  1707  L75  LG75  # misassemblies  # misassembled contigs  Misassembled contigs length  # local misassemblies  # unaligned length  Unaligned length  Cenome fraction (%)  Total length (>= 25000 bp)  0  # mismatches per 100 kbp  0  100  100  100  100  100  100  100
Total length (>= 10000 bp)  Total length (>= 25000 bp)  Total length (>= 50000 bp)  # contigs  4111  Largest contig  Total length  Reference length  Reference length  GC (%)  N50  N850  NG50  N75  N75  N75  N675  L50  1304  LG50  1707  L75  LG75  # misassemblies  # misassembled contigs  Misassembled contigs length  # local misassemblies  # unaligned length  Unaligned length  Cenome fraction (%)  Total length (>= 25000 bp)  0  # mismatches per 100 kbp  0  100  100  100  100  100  100  100
Total length (>= 50000 bp)         0           # contigs         4111           Largest contig         4559           Total length         3896849           Reference length         4641652           GC (%)         50.73           Reference GC (%)         50.79           N50         989           NG50         870           N75         709           NG75         583           L50         1304           LG50         1707           L75         2473           LG75         3340           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         1           # unaligned length         255           Genome fraction (%)         77.241           Duplication ratio         1.087           # N's per 100 kbp         0.00           # mismatches per 100 kbp         410.43
# contigs 4111 Largest contig 4559 Total length 3896849 Reference length 4641652 GC (%) 50.73 Reference GC (%) 50.79 N50 989 NG50 870 N75 709 NG75 583 L50 1304 LG50 1707 L75 2473 LG75 3340 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 1 # local misassemblies 1 # unaligned contigs 0 + 4 part Unaligned length 255 Genome fraction (%) 77.241 Duplication ratio 1.087 # N's per 100 kbp 0.00 # mismatches per 100 kbp 410.43
Largest contig         4559           Total length         3896849           Reference length         4641652           GC (%)         50.73           Reference GC (%)         50.79           N50         989           NG50         870           N75         709           NG75         583           L50         1304           LG50         1707           L75         2473           LG75         3340           # misassemblies         0           # misassembled contigs         0           Misassembled contigs         0           Unaligned length         0           Unaligned length         255           Genome fraction (%)         77.241           Duplication ratio         1.087           # N's per 100 kbp         0.00           # mismatches per 100 kbp         410.43
Total length         3896849           Reference length         4641652           GC (%)         50.73           Reference GC (%)         50.79           N50         989           NG50         870           N75         709           NG75         583           L50         1304           LG50         1707           L75         2473           LG75         3340           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         1           # unaligned length         255           Genome fraction (%)         77.241           Duplication ratio         1.087           # N's per 100 kbp         0.00           # mismatches per 100 kbp         410.43
Reference length         4641652           GC (%)         50.73           Reference GC (%)         50.79           N50         989           NG50         870           N75         709           NG75         583           L50         1304           LG50         1707           L75         2473           LG75         3340           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         1           # unaligned contigs         0 + 4 part           Unaligned length         255           Genome fraction (%)         77.241           Duplication ratio         1.087           # N's per 100 kbp         0.00           # mismatches per 100 kbp         410.43
GC (%)       50.73         Reference GC (%)       50.79         N50       989         NG50       870         N75       709         NG75       583         L50       1304         LG50       1707         L75       2473         LG75       3340         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       1         # unaligned contigs       0 + 4 part         Unaligned length       255         Genome fraction (%)       77.241         Duplication ratio       1.087         # N's per 100 kbp       0.00         # mismatches per 100 kbp       410.43
Reference GC (%)       50.79         N50       989         NG50       870         N75       709         NG75       583         L50       1304         LG50       1707         L75       2473         LG75       3340         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       1         # unaligned contigs       0 + 4 part         Unaligned length       255         Genome fraction (%)       77.241         Duplication ratio       1.087         # N's per 100 kbp       0.00         # mismatches per 100 kbp       410.43
N50       989         NG50       870         N75       709         NG75       583         L50       1304         LG50       1707         L75       2473         LG75       3340         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       1         # unaligned contigs       0 + 4 part         Unaligned length       255         Genome fraction (%)       77.241         Duplication ratio       1.087         # N's per 100 kbp       0.00         # mismatches per 100 kbp       410.43
NG50       870         N75       709         NG75       583         L50       1304         LG50       1707         L75       2473         LG75       3340         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       1         # unaligned contigs       0 + 4 part         Unaligned length       255         Genome fraction (%)       77.241         Duplication ratio       1.087         # N's per 100 kbp       0.00         # mismatches per 100 kbp       410.43
N75       709         NG75       583         L50       1304         LG50       1707         L75       2473         LG75       3340         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       1         # unaligned contigs       0 + 4 part         Unaligned length       255         Genome fraction (%)       77.241         Duplication ratio       1.087         # N's per 100 kbp       0.00         # mismatches per 100 kbp       410.43
NG75       583         L50       1304         LG50       1707         L75       2473         LG75       3340         # misassemblies       0         Misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       1         # unaligned contigs       0 + 4 part         Unaligned length       255         Genome fraction (%)       77.241         Duplication ratio       1.087         # N's per 100 kbp       0.00         # mismatches per 100 kbp       410.43
L50       1304         LG50       1707         L75       2473         LG75       3340         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       1         # unaligned contigs       0 + 4 part         Unaligned length       255         Genome fraction (%)       77.241         Duplication ratio       1.087         # N's per 100 kbp       0.00         # mismatches per 100 kbp       410.43
LG50       1707         L75       2473         LG75       3340         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       1         # unaligned contigs       0 + 4 part         Unaligned length       255         Genome fraction (%)       77.241         Duplication ratio       1.087         # N's per 100 kbp       0.00         # mismatches per 100 kbp       410.43
L75       2473         LG75       3340         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       1         # unaligned contigs       0 + 4 part         Unaligned length       255         Genome fraction (%)       77.241         Duplication ratio       1.087         # N's per 100 kbp       0.00         # mismatches per 100 kbp       410.43
LG75 # misassemblies # misassembled contigs O Misassembled contigs length # local misassemblies # unaligned contigs Unaligned length Cenome fraction (%) Duplication ratio # N's per 100 kbp # mismatches per 100 kbp  3340 0 # mismatches 340 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 4 part Unaligned length 255 Genome fraction (%) 77.241 Duplication ratio 1.087 # N's per 100 kbp 0.00 # mismatches per 100 kbp 410.43
# misassembled contigs 0  Misassembled contigs length 0  # local misassemblies 1  # unaligned contigs 0 + 4 part  Unaligned length 255  Genome fraction (%) 77.241  Duplication ratio 1.087  # N's per 100 kbp 0.00  # mismatches per 100 kbp 410.43
Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 4 part Unaligned length 255 Genome fraction (%) 77.241 Duplication ratio 1.087 # N's per 100 kbp 0.00 # mismatches per 100 kbp 410.43
# local misassemblies 1  # unaligned contigs 0 + 4 part  Unaligned length 255  Genome fraction (%) 77.241  Duplication ratio 1.087  # N's per 100 kbp 0.00  # mismatches per 100 kbp 410.43
# unaligned contigs 0 + 4 part Unaligned length 255 Genome fraction (%) 77.241 Duplication ratio 1.087 # N's per 100 kbp 0.00 # mismatches per 100 kbp 410.43
Unaligned length         255           Genome fraction (%)         77.241           Duplication ratio         1.087           # N's per 100 kbp         0.00           # mismatches per 100 kbp         410.43
Genome fraction (%)       77.241         Duplication ratio       1.087         # N's per 100 kbp       0.00         # mismatches per 100 kbp       410.43
Duplication ratio         1.087           # N's per 100 kbp         0.00           # mismatches per 100 kbp         410.43
# N's per 100 kbp 0.00 # mismatches per 100 kbp 410.43
# mismatches per 100 kbp 410.43
# indole per 100 kbp
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Largest alignment 4559
NA50 988
NGA50 869
NA75 709
NGA75 583
LA50 1304
LGA50 1707
LA75 2473
LGA75 3341

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

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	14715
# indels	11
# short indels	11
# long indels	0
Indels length	11

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

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	4
# with misassembly	0
# both parts are significant	0
Partially unaligned length	255
# 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).















