## Report

# contigs (>= 1000 bp) 33  # contigs (>= 5000 bp) 29  # contigs (>= 10000 bp) 26  # contigs (>= 25000 bp) 26  # contigs (>= 50000 bp) 26  # contigs (>= 50000 bp) 22  Total length (>= 1000 bp) 4848847  Total length (>= 5000 bp) 4832527  Total length (>= 25000 bp) 4805122  Total length (>= 25000 bp) 4643282  # contigs 45  Largest contig 472565  Total length 4857430  Reference length 4641652  GC (%) 50.70  Reference GC (%) 50.78  N50 305624  N75 201240  NG75 214400  L50 7  LG50 7  LG50 7  LG50 7  L75 12  LG75 11  # misassemblies 15  # misassembled contigs 2  Misassembled contigs length 401494  # local misassemblies 3  # unaligned length 222  Genome fraction (%) 98.834  Duplication ratio 1.059  # N's per 100 kbp 0.21
# contigs (>= 5000 bp) 29 # contigs (>= 10000 bp) 28 # contigs (>= 25000 bp) 26 # contigs (>= 50000 bp) 22 Total length (>= 1000 bp) 4848847 Total length (>= 5000 bp) 4841052 Total length (>= 10000 bp) 4832527 Total length (>= 25000 bp) 4805122 Total length (>= 50000 bp) 4643282 # contigs 45 Largest contig 472565 Total length 4857430 Reference length 4641652 GC (%) 50.70 Reference GC (%) 50.78 N50 305624 N75 201240 NG75 214400 L50 7 LG50 7 LG50 7 LG50 7 LG55 11 # misassemblies 15 # misassembled contigs 2 Misassembled contigs length 401494 # local misassemblies 3 # unaligned length 222 Genome fraction (%) 98.834 Duplication ratio 1.059 # N's per 100 kbp 0.21
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Total length (>= 1000 bp)
Total length (>= 10000 bp)
Total length (>= 25000 bp)         4805122           Total length (>= 50000 bp)         4643282           # contigs         45           Largest contig         472565           Total length         4857430           Reference length         4641652           GC (%)         50.70           Reference GC (%)         50.78           N50         305624           NG50         305624           NG75         201240           L50         7           L50         7           L75         12           LG75         11           # misassemblies         15           # misassembled contigs         2           Misassembled contigs length         401494           # local misassemblies         3           # unaligned contigs         0 + 1 part           Unaligned length         222           Genome fraction (%)         98.834           Duplication ratio         1.059           # N's per 100 kbp         0.21
# contigs 45 Largest contig 472565 Total length 4857430 Reference length 4641652 GC (%) 50.70 Reference GC (%) 50.78 N50 305624 NG50 305624 N75 201240 NG75 214400 L50 7 LG50 7 LG50 7 LG50 11 # misassemblies 15 # misassembled contigs 2 Misassembled contigs 2 Misassembled contigs 3 # unaligned contigs 0 + 1 part Unaligned length 222 Genome fraction (%) 98.834 Duplication ratio 1.059 # N's per 100 kbp 0.21
# contigs 45 Largest contig 472565 Total length 4857430 Reference length 4641652 GC (%) 50.70 Reference GC (%) 50.78 N50 305624 NG50 305624 N75 201240 NG75 214400 L50 7 LG50 7 LG50 7 LG50 12 # misassembles 15 # misassembled contigs 2 Misassembled contigs 2 Misassembled contigs 15 # unaligned contigs 0 + 1 part Unaligned length 222 Genome fraction (%) 98.834 Duplication ratio 1.059 # N's per 100 kbp 0.21
Largest contig         472565           Total length         4857430           Reference length         4641652           GC (%)         50.70           Reference GC (%)         50.78           N50         305624           NG50         305624           N75         201240           NG75         214400           L50         7           LG50         7           L75         12           LG75         11           # misassemblies         15           # misassembled contigs         2           Misassembled contigs length         401494           # local misassemblies         3           # unaligned contigs         0 + 1 part           Unaligned length         222           Genome fraction (%)         98.834           Duplication ratio         1.059           # N's per 100 kbp         0.21
Total length         4857430           Reference length         4641652           GC (%)         50.70           Reference GC (%)         50.78           N50         305624           NG50         305624           N75         201240           NG75         214400           L50         7           LG50         7           L75         12           LG75         11           # misassemblies         15           # misassembled contigs         2           Misassembled contigs length         401494           # local misassemblies         3           # unaligned contigs         0 + 1 part           Unaligned length         222           Genome fraction (%)         98.834           Duplication ratio         1.059           # N's per 100 kbp         0.21
Reference length         4641652           GC (%)         50.70           Reference GC (%)         50.78           N50         305624           NG50         305624           N75         201240           NG75         214400           L50         7           LG50         7           L75         12           LG75         11           # misassemblies         15           # misassembled contigs         2           Misassembled contigs length         401494           # local misassemblies         3           # unaligned contigs         0 + 1 part           Unaligned length         222           Genome fraction (%)         98.834           Duplication ratio         1.059           # N's per 100 kbp         0.21
GC (%)       50.70         Reference GC (%)       50.78         N50       305624         NG50       305624         N75       201240         NG75       214400         L50       7         LG50       7         L75       12         LG75       11         # misassemblies       15         # misassembled contigs       2         Misassembled contigs length       401494         # local misassemblies       3         # unaligned contigs       0 + 1 part         Unaligned length       222         Genome fraction (%)       98.834         Duplication ratio       1.059         # N's per 100 kbp       0.21
Reference GC (%)       50.78         N50       305624         NG50       305624         N75       201240         NG75       214400         L50       7         LG50       7         LG75       12         LG75       11         # misassemblies       15         # misassembled contigs       2         Misassembled contigs length       401494         # local misassemblies       3         # unaligned contigs       0 + 1 part         Unaligned length       222         Genome fraction (%)       98.834         Duplication ratio       1.059         # N's per 100 kbp       0.21
N50       305624         NG50       305624         N75       201240         NG75       214400         L50       7         LG50       7         L75       12         LG75       11         # misassemblies       15         # misassembled contigs       2         Misassembled contigs length       401494         # local misassemblies       3         # unaligned contigs       0 + 1 part         Unaligned length       222         Genome fraction (%)       98.834         Duplication ratio       1.059         # N's per 100 kbp       0.21
NG50       305624         N75       201240         NG75       214400         L50       7         LG50       7         L75       12         LG75       11         # misassemblies       15         # misassembled contigs       2         Misassembled contigs length       401494         # local misassemblies       3         # unaligned contigs       0 + 1 part         Unaligned length       222         Genome fraction (%)       98.834         Duplication ratio       1.059         # N's per 100 kbp       0.21
N75         201240           NG75         214400           L50         7           LG50         7           L75         12           LG75         11           # misassemblies         15           # misassembled contigs         2           Misassembled contigs length         401494           # local misassemblies         3           # unaligned contigs         0 + 1 part           Unaligned length         222           Genome fraction (%)         98.834           Duplication ratio         1.059           # N's per 100 kbp         0.21
NG75       214400         L50       7         LG50       7         L75       12         LG75       11         # misassemblies       15         # misassembled contigs       2         Misassembled contigs length       401494         # local misassemblies       3         # unaligned contigs       0 + 1 part         Unaligned length       222         Genome fraction (%)       98.834         Duplication ratio       1.059         # N's per 100 kbp       0.21
L50       7         LG50       7         L75       12         LG75       11         # misassemblies       15         # misassembled contigs       2         Misassembled contigs length       401494         # local misassemblies       3         # unaligned contigs       0 + 1 part         Unaligned length       222         Genome fraction (%)       98.834         Duplication ratio       1.059         # N's per 100 kbp       0.21
LG50       7         L75       12         LG75       11         # misassemblies       15         # misassembled contigs       2         Misassembled contigs length       401494         # local misassemblies       3         # unaligned contigs       0 + 1 part         Unaligned length       222         Genome fraction (%)       98.834         Duplication ratio       1.059         # N's per 100 kbp       0.21
L75       12         LG75       11         # misassemblies       15         # misassembled contigs       2         Misassembled contigs length       401494         # local misassemblies       3         # unaligned contigs       0 + 1 part         Unaligned length       222         Genome fraction (%)       98.834         Duplication ratio       1.059         # N's per 100 kbp       0.21
LG75       11         # misassemblies       15         # misassembled contigs       2         Misassembled contigs length       401494         # local misassemblies       3         # unaligned contigs       0 + 1 part         Unaligned length       222         Genome fraction (%)       98.834         Duplication ratio       1.059         # N's per 100 kbp       0.21
# misassemblies 15 # misassembled contigs 2 Misassembled contigs length 401494 # local misassemblies 3 # unaligned contigs 0 + 1 part Unaligned length 222 Genome fraction (%) 98.834 Duplication ratio 1.059 # N's per 100 kbp 0.21
# misassembled contigs 2  Misassembled contigs length 401494  # local misassemblies 3  # unaligned contigs 0 + 1 part  Unaligned length 222  Genome fraction (%) 98.834  Duplication ratio 1.059  # N's per 100 kbp 0.21
Misassembled contigs length 401494 # local misassemblies 3 # unaligned contigs 0 + 1 part Unaligned length 222 Genome fraction (%) 98.834 Duplication ratio 1.059 # N's per 100 kbp 0.21
# local misassemblies 3  # unaligned contigs 0 + 1 part  Unaligned length 222  Genome fraction (%) 98.834  Duplication ratio 1.059  # N's per 100 kbp 0.21
# unaligned contigs 0 + 1 part Unaligned length 222 Genome fraction (%) 98.834 Duplication ratio 1.059 # N's per 100 kbp 0.21
Unaligned length         222           Genome fraction (%)         98.834           Duplication ratio         1.059           # N's per 100 kbp         0.21
Genome fraction (%)         98.834           Duplication ratio         1.059           # N's per 100 kbp         0.21
Duplication ratio         1.059           # N's per 100 kbp         0.21
# N's per 100 kbp 0.21
' '
# mismatches per 100 kbp 526.65
# indels per 100 kbp 1.05
Largest alignment 472565
NA50 304586
NGA50 304586
NA75 156700
NGA75 183277
1 1450
LA50 7
LGA50 7

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

	scaffolds
# misassemblies	15
# relocations	15
# translocations	0
# inversions	0
# possibly misassembled contigs	2
# misassembled contigs	2
Misassembled contigs length	401494
# local misassemblies	3
# mismatches	24160
# indels	48
# short indels	48
# long indels	0
Indels length	50

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

	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	222
# N's	10

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).















