## Report

# contigs (>= 1000 bp) 671 # contigs (>= 5000 bp) 324 # contigs (>= 10000 bp) 137 # contigs (>= 25000 bp) 7 # contigs (>= 25000 bp) 7 # contigs (>= 50000 bp) 7 # contigs (>= 50000 bp) 7 Total length (>= 1000 bp) 4378994 Total length (>= 10000 bp) 3391793 Total length (>= 10000 bp) 2084597 Total length (>= 25000 bp) 198815 Total length (>= 50000 bp) 0 # contigs 813 Largest contig 35550 Total length 4472076 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.78 N50 9424 NG50 8865 N75 15167 NG75 1520 153 LG50 162 L75 317 LG75 343 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 1 # local misassemblies 0 # unaligned length 0 Genome fraction (%) 94.936 Duplication ratio 1.015 # N's per 100 kbp 0.00 # mismatches per 100 kbp 519.63 M 162 NG75 167 NG75 167 NG50 8865 NA50 9424 NGA50 8865 NA75 5167 NGA75 1567		final contine
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# contigs (>= 10000 bp)		
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Total length (>= 1000 bp)         4378994           Total length (>= 5000 bp)         3391793           Total length (>= 10000 bp)         2084597           Total length (>= 25000 bp)         198815           Total length (>= 50000 bp)         0           # contigs         813           Largest contig         35550           Total length         4472076           Reference length         4641652           GC (%)         50.74           Reference GC (%)         50.78           N50         9424           NG50         8865           N75         5167           NG75         4759           L50         153           LG50         162           L75         317           LG75         343           # misassemblies         1           # misassembled contigs         1           Misassembled contigs length         5468           # local misassemblies         0           # unaligned length         0           Genome fraction (%)         94.936           Duplication ratio         1.015           # N's per 100 kbp         0.00           # mismatches per 100 kbp	_	7
Total length (>= 5000 bp)         3391793           Total length (>= 10000 bp)         2084597           Total length (>= 25000 bp)         198815           Total length (>= 50000 bp)         0           # contigs         813           Largest contig         35550           Total length         4472076           Reference length         4641652           GC (%)         50.74           Reference GC (%)         50.78           N50         9424           NG50         8865           N75         5167           NG75         4759           L50         153           LG50         162           L75         317           LG75         343           # misassemblies         1           # misassembled contigs         1           Misassembled contigs         0           # unaligned length         0           Genome fraction (%)         94.936           Duplication ratio         1.015           # N's per 100 kbp         0.05           Largest alignment         35550           NA50         9424           NGA50         8865           NA75		
Total length (>= 10000 bp)         2084597           Total length (>= 25000 bp)         198815           Total length (>= 50000 bp)         0           # contigs         813           Largest contig         35550           Total length         4472076           Reference length         4641652           GC (%)         50.74           Reference GC (%)         50.78           N50         9424           NG50         8865           N75         5167           NG75         4759           L50         153           LG50         162           L75         317           LG75         343           # misassemblies         1           # misassembled contigs         1           Misassembled contigs length         5468           # local misassemblies         0           # unaligned length         0           Genome fraction (%)         94.936           Duplication ratio         1.015           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.05           Largest alignment         35550           NA50         9424		4378994
Total length (>= 25000 bp) 0  # contigs 813  Largest contig 35550  Total length (>= 50000 bp) 4472076  Reference length 4472076  Reference length 4641652  GC (%) 50.74  Reference GC (%) 50.78  N50 9424  NG50 8865  N75 5167  NG75 4759  L50 153  LG50 162  L75 317  LG75 343  # misassembled contigs 1  # misassembled contigs 1  # local misassemblies 0  # unaligned contigs 0 + 0 part  Unaligned length 0  Genome fraction (%) 94.936  Duplication ratio 1.015  # N's per 100 kbp 0.00  # mismatches per 100 kbp 1.05  Largest alignment 35550  NA50 9424  NGA50 8865  NA75 5167  NGA75 4759  LA50 153		3391793
Total length (>= 50000 bp)       0         # contigs       813         Largest contig       35550         Total length       4472076         Reference length       4641652         GC (%)       50.74         Reference GC (%)       50.78         N50       9424         NG50       8865         N75       5167         NG75       4759         L50       153         LG50       162         L75       317         LG75       343         # misassemblies       1         # nisassembled contigs       1         Misassembled contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       94.936         Duplication ratio       1.015         # N's per 100 kbp       0.00         # mismatches per 100 kbp       519.63         # indels per 100 kbp       0.05         Largest alignment       35550         NA50       9424         NGA50       8865         NA75       5167         NGA50       8865         NA75       4759	,	2084597
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Largest contig       35550         Total length       4472076         Reference length       4641652         GC (%)       50.74         Reference GC (%)       50.78         N50       9424         NG50       8865         N75       5167         NG75       4759         L50       153         LG50       162         L75       317         LG75       343         # misassemblies       1         # misassembled contigs       1         Misassembled contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       94.936         Duplication ratio       1.015         # N's per 100 kbp       0.00         # mismatches per 100 kbp       519.63         # indels per 100 kbp       0.05         Largest alignment       35550         NA50       9424         NGA50       8865         NA75       5167         NGA50       4759         LA50       153	Total length (>= 50000 bp)	0
Total length         4472076           Reference length         4641652           GC (%)         50.74           Reference GC (%)         50.78           N50         9424           NG50         8865           N75         5167           NG75         4759           L50         153           LG50         162           L75         317           LG75         343           # misassemblies         1           # local misassembled contigs         0 + 0 part           Unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         94.936           Duplication ratio         1.015           # N's per 100 kbp         0.00           # mismatches per 100 kbp         519.63           # indels per 100 kbp         0.05           Largest alignment         35550           NA50         9424           NGA50         8865           NA75         5167           NGA50         4759           LA50         153	# contigs	813
Reference length       4641652         GC (%)       50.74         Reference GC (%)       50.78         N50       9424         NG50       8865         N75       5167         NG75       4759         L50       153         LG50       162         L75       317         LG75       343         # misassemblies       1         # local misassembled contigs       1         # local misassembles       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       94.936         Duplication ratio       1.015         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.05         Largest alignment       35550         NA50       9424         NGA50       8865         NA75       5167         NGA75       4759         LA50       153	Largest contig	35550
GC (%)       50.74         Reference GC (%)       50.78         N50       9424         NG50       8865         N75       5167         NG75       4759         L50       153         LG50       162         L75       317         LG75       343         # misassemblies       1         # misassembled contigs       1         Misassembled contigs       0 + 0 part         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       94.936         Duplication ratio       1.015         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.05         Largest alignment       35550         NA50       9424         NGA50       8865         NA75       5167         NGA75       4759         LA50       153	Total length	4472076
Reference GC (%)       50.78         N50       9424         NG50       8865         N75       5167         NG75       4759         L50       153         LG50       162         L75       317         LG75       343         # misassemblies       1         # misassembled contigs       1         Misassembled contigs       0 + 0 part         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       94.936         Duplication ratio       1.015         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.05         Largest alignment       35550         NA50       9424         NGA50       8865         NA75       5167         NGA75       4759         LA50       153	Reference length	4641652
N50       9424         NG50       8865         N75       5167         NG75       4759         L50       153         LG50       162         L75       317         LG75       343         # misassemblies       1         # misassembled contigs       1         Misassembled contigs length       5468         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       94.936         Duplication ratio       1.015         # N's per 100 kbp       0.00         # mismatches per 100 kbp       519.63         # indels per 100 kbp       0.05         Largest alignment       35550         NA50       9424         NGA50       8865         NA75       5167         NGA75       4759         LA50       153	GC (%)	50.74
N50       9424         NG50       8865         N75       5167         NG75       4759         L50       153         LG50       162         L75       317         LG75       343         # misassemblies       1         # misassembled contigs       1         Misassembled contigs length       5468         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       94.936         Duplication ratio       1.015         # N's per 100 kbp       0.00         # mismatches per 100 kbp       519.63         # indels per 100 kbp       0.05         Largest alignment       35550         NA50       9424         NGA50       8865         NA75       5167         NGA75       4759         LA50       153	Reference GC (%)	50.78
N75       5167         NG75       4759         L50       153         LG50       162         L75       317         LG75       343         # misassemblies       1         # misassembled contigs       1         Misassembled contigs length       5468         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       94.936         Duplication ratio       1.015         # N's per 100 kbp       0.00         # mismatches per 100 kbp       519.63         # indels per 100 kbp       0.05         Largest alignment       35550         NA50       9424         NGA50       8865         NA75       5167         NGA75       4759         LA50       153	N50	9424
NG75 L50 L50 L50 L650 162 L75 L75 S17 LG75 S317 LG75 S43  # misassemblies # misassembled contigs Misassembled contigs Misassembled contigs length Focal misassemblies Unaligned contigs Unaligned length Genome fraction (♥) Supplication ratio Wisper 100 kbp Wisper 100 kbp Wisper 100 kbp Largest alignment NA50 NA50 NA50 NA75 NGA75 LA50 S167 NGA75 S167 NGA75 S167	NG50	8865
NG75 L50 L50 L50 L650 162 L75 L75 S17 LG75 S317 LG75 S43  # misassemblies # misassembled contigs Misassembled contigs Misassembled contigs length Focal misassemblies Unaligned contigs Unaligned length Genome fraction (♥) Supplication ratio Wisper 100 kbp Wisper 100 kbp Wisper 100 kbp Largest alignment NA50 NA50 NA50 NA75 NGA75 LA50 S167 NGA75 S167 NGA75 S167	N75	5167
L50       153         LG50       162         L75       317         LG75       343         # misassemblies       1         # misassembled contigs       1         Misassembled contigs length       5468         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       94.936         Duplication ratio       1.015         # N's per 100 kbp       0.00         # mismatches per 100 kbp       519.63         # indels per 100 kbp       0.05         Largest alignment       35550         NA50       9424         NGA50       8865         NA75       5167         NGA75       4759         LA50       153	NG75	
LG50 162  L75 317  LG75 343  # misassemblies 1  # misassembled contigs 1  Misassembled contigs 1  Misassembled contigs length 5468  # local misassemblies 0  # unaligned contigs 0 + 0 part  Unaligned length 0  Genome fraction (♥) 94.936  Duplication ratio 1.015  # N's per 100 kbp 0.00  # mismatches per 100 kbp 519.63  # indels per 100 kbp 0.05  Largest alignment 35550  NA50 9424  NGA50 8865  NA75 5167  NGA75 4759  LA50 153		
L75       317         LG75       343         # misassemblies       1         # misassembled contigs       1         Misassembled contigs length       5468         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       94.936         Duplication ratio       1.015         # N's per 100 kbp       0.00         # mismatches per 100 kbp       519.63         # indels per 100 kbp       0.05         Largest alignment       35550         NA50       9424         NGA50       8865         NA75       5167         NGA75       4759         LA50       153		162
# misassemblies		
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# misassembled contigs 1 Misassembled contigs length 5468 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 94.936 Duplication ratio 1.015 # N's per 100 kbp 0.00 # mismatches per 100 kbp 519.63 # indels per 100 kbp 0.05 Largest alignment 35550 NA50 9424 NGA50 8865 NA75 5167 NGA75 4759 LA50 153		
Misassembled contigs length       5468         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       94.936         Duplication ratio       1.015         # N's per 100 kbp       0.00         # mismatches per 100 kbp       519.63         # indels per 100 kbp       0.05         Largest alignment       35550         NA50       9424         NGA50       8865         NA75       5167         NGA75       4759         LA50       153		
# local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 94.936 Duplication ratio 1.015 # N's per 100 kbp 0.00 # mismatches per 100 kbp 519.63 # indels per 100 kbp 0.05 Largest alignment 35550 NA50 9424 NGA50 8865 NA75 5167 NGA75 4759 LA50 153		
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 94.936 Duplication ratio 1.015 # N's per 100 kbp 0.00 # mismatches per 100 kbp 519.63 # indels per 100 kbp 0.05 Largest alignment 35550 NA50 9424 NGA50 8865 NA75 5167 NGA75 4759 LA50 153		_
Unaligned length       0         Genome fraction (%)       94.936         Duplication ratio       1.015         # N's per 100 kbp       0.00         # mismatches per 100 kbp       519.63         # indels per 100 kbp       0.05         Largest alignment       35550         NA50       9424         NGA50       8865         NA75       5167         NGA75       4759         LA50       153		
Genome fraction (%)       94.936         Duplication ratio       1.015         # N's per 100 kbp       0.00         # mismatches per 100 kbp       519.63         # indels per 100 kbp       0.05         Largest alignment       35550         NA50       9424         NGA50       8865         NA75       5167         NGA75       4759         LA50       153		
Duplication ratio       1.015         # N's per 100 kbp       0.00         # mismatches per 100 kbp       519.63         # indels per 100 kbp       0.05         Largest alignment       35550         NA50       9424         NGA50       8865         NA75       5167         NGA75       4759         LA50       153		
# N's per 100 kbp 0.00 # mismatches per 100 kbp 519.63 # indels per 100 kbp 0.05 Largest alignment 35550 NA50 9424 NGA50 8865 NA75 5167 NGA75 4759 LA50 153		
# mismatches per 100 kbp 519.63 # indels per 100 kbp 0.05 Largest alignment 35550 NA50 9424 NGA50 8865 NA75 5167 NGA75 4759 LA50 153	·	
# indels per 100 kbp 0.05 Largest alignment 35550 NA50 9424 NGA50 8865 NA75 5167 NGA75 4759 LA50 153		
Largest alignment       35550         NA50       9424         NGA50       8865         NA75       5167         NGA75       4759         LA50       153		
NA50       9424         NGA50       8865         NA75       5167         NGA75       4759         LA50       153		
NGA50       8865         NA75       5167         NGA75       4759         LA50       153		
NA75       5167         NGA75       4759         LA50       153		
NGA75 4759 LA50 153		
LA50 153		
	LGA50	162
LA75 317		
LGA75 343	LGA75	343

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	1
# relocations	0
# translocations	0
# inversions	1
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	5468
# local misassemblies	0
# mismatches	22898
# indels	2
# short indels	2
# long indels	0
Indels length	2

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	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# 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).

















