## Report

# contigs (>= 1000 bp)		scaffolds
# contigs (>= 5000 bp) 19 # contigs (>= 10000 bp) 17 # contigs (>= 25000 bp) 17 # contigs (>= 50000 bp) 16 Total length (>= 10000 bp) 4609155 Total length (>= 50000 bp) 4602598 Total length (>= 10000 bp) 4602598 Total length (>= 25000 bp) 4568433 Total length (>= 50000 bp) 4529848 # contigs 23 Largest contig 1053360 Total length 4609731 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.79 N50 451601 N75 178093 NG75 178093 L50 4 LG50 4 L75 7 LG75 7 # misassemblies 0 # misassembled contigs length 0 # local misassemblies 0 # unaligned length 0 Genome fraction (%) 99.309 Duplication ratio 1.000 # N's per 100 kbp 0.22 # mismatches per 100 kbp 181.32 # indels per 100 kbp 0.72 Largest alignment 1053360 NA75 178093 NGA75 178093	# contigs (>= 1000 bp)	
# contigs (>= 10000 bp) 19 # contigs (>= 25000 bp) 17 # contigs (>= 50000 bp) 16 Total length (>= 1000 bp) 4609155 Total length (>= 5000 bp) 4602598 Total length (>= 10000 bp) 4602598 Total length (>= 25000 bp) 4568433 Total length (>= 50000 bp) 4529848 # contigs 23 Largest contig 1053360 Total length 4609731 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.79 N50 451601 N75 178093 NG75 178093 L50 4 LG50 4 L75 7 LG75 7 # misassemblies 0 # misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.309 Duplication ratio 1.000 # N's per 100 kbp 0.22 # mismatches per 100 kbp 181.32 # indels per 100 kbp 0.72 Largest alignment 1053360 NA75 178093 NGA75 178093		19
# contigs (>= 25000 bp) 17 # contigs (>= 50000 bp) 16 Total length (>= 1000 bp) 4609155 Total length (>= 5000 bp) 4602598 Total length (>= 10000 bp) 4602598 Total length (>= 25000 bp) 4508433 Total length (>= 50000 bp) 4568433 Total length (>= 50000 bp) 4529848 # contigs 23 Largest contig 1053360 Total length 4609731 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.79 N50 451601 NG50 451601 N75 178093 NG75 178093 L50 4 LG50 4 L75 7 LG75 7 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 # unaligned length 0 Genome fraction (%) 99.309 Duplication ratio 1.000 # N's per 100 kbp 0.22 # mismatches per 100 kbp 181.32 # indels per 100 kbp 0.72 Largest alignment 1053360 NA50 451601 NA75 178093 NGA75 178093		19
# contigs (>= 50000 bp) 16  Total length (>= 1000 bp) 4609155  Total length (>= 5000 bp) 4602598  Total length (>= 10000 bp) 4602598  Total length (>= 25000 bp) 4568433  Total length (>= 50000 bp) 4529848  # contigs 23  Largest contig 1053360  Total length 4609731  Reference length 4641652  GC (%) 50.78  Reference GC (%) 50.79  N50 451601  N75 178093  NG75 178093  L50 4  LG50 4  LG50 4  LG50 4  L75 7  LG75 7  # misassemblies 0  # misassembled contigs 0  Misassembled contigs 0  Misassembled contigs 0  # unaligned length 0  Genome fraction (%) 99.309  Duplication ratio 1.000  # N's per 100 kbp 0.22  # mismatches per 100 kbp 181.32  # indels per 100 kbp 0.72  Largest alignment 1053360  NA50 451601  NA50 451601  NA50 451601  NA75 178093  NGA75 178093		17
Total length (>= 5000 bp)		16
Total length (>= 10000 bp)	Total length (>= 1000 bp)	4609155
Total length (>= 25000 bp)	Total length (>= 5000 bp)	4602598
Total length (>= 50000 bp)         4529848           # contigs         23           Largest contig         1053360           Total length         4609731           Reference length         4641652           GC (%)         50.78           Reference GC (%)         50.79           N50         451601           NG50         451601           N75         178093           NG75         178093           L50         4           LG50         4           L75         7           # misassemblies         0           # misassembled contigs         0           Misassembled contigs         0           # local misassemblies         0           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         99.309           Duplication ratio         1.000           # N's per 100 kbp         0.22           # mismatches per 100 kbp         181.32           # indels per 100 kbp         0.72           Largest alignment         1053360           NA50         451601           NA75         178093 <t< td=""><td>Total length (&gt;= 10000 bp)</td><td>4602598</td></t<>	Total length (>= 10000 bp)	4602598
# contigs 23 Largest contig 1053360 Total length 4609731 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.79 N50 451601 NG50 451601 N75 178093 L50 4 LG50 4 L75 7 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned length 0 Genome fraction (%) 99.309 Duplication ratio 1.000 # N's per 100 kbp 0.22 # mismatches per 100 kbp 181.32 # indels per 100 kbp 0.72 Largest alignment 1053360 NA50 451601 NA75 178093 NGA75 178093 NGA75 178093 NGA75 178093 NGA75 178093 NGA75 178093 LA50 4 LGA50 4 LGA50 4 LGA50 4 LGA50 4	Total length (>= 25000 bp)	4568433
Largest contig         1053360           Total length         4609731           Reference length         4641652           GC (%)         50.78           Reference GC (%)         50.79           N50         451601           NG50         451601           N75         178093           NG75         178093           L50         4           L75         7           LG75         7           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         99.309           Duplication ratio         1.000           # N's per 100 kbp         0.22           # mismatches per 100 kbp         0.72           Largest alignment         1053360           NA50         451601           NA75         178093           NGA75         178093           LA50         4           LA50         4           LA75         7 </td <td>Total length (&gt;= 50000 bp)</td> <td>4529848</td>	Total length (>= 50000 bp)	4529848
Total length         4609731           Reference length         4641652           GC (%)         50.78           Reference GC (%)         50.79           N50         451601           NG50         451601           N75         178093           NG75         178093           L50         4           LG50         4           L75         7           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         99.309           Duplication ratio         1.000           # N's per 100 kbp         0.22           # mismatches per 100 kbp         181.32           # indels per 100 kbp         0.72           Largest alignment         1053360           NA50         451601           NA75         178093           NGA75         178093           LA50         4           LGA50         4           LA75         7 </td <td># contigs</td> <td>23</td>	# contigs	23
Reference length       4641652         GC (%)       50.78         Reference GC (%)       50.79         N50       451601         NG50       451601         N75       178093         NG75       178093         L50       4         LG50       4         L75       7         LG75       7         # misassemblies       0         # local misassembled contigs       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.309         Duplication ratio       1.000         # N's per 100 kbp       0.22         # mismatches per 100 kbp       181.32         # indels per 100 kbp       0.72         Largest alignment       1053360         NA50       451601         NA75       178093         NGA75       178093         LA50       4         LGA50       4         LA75       7	Largest contig	1053360
GC (%)       50.78         Reference GC (%)       50.79         N50       451601         NG50       451601         N75       178093         NG75       178093         L50       4         LG50       4         L75       7         LG75       7         # misassemblies       0         # local misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.309         Duplication ratio       1.000         # N's per 100 kbp       0.22         # mismatches per 100 kbp       181.32         # indels per 100 kbp       0.72         Largest alignment       1053360         NA50       451601         NA75       178093         NGA75       178093         LA50       4         LGA50       4         LA75       7	Total length	4609731
Reference GC (%)       50.79         N50       451601         NG50       451601         N75       178093         NG75       178093         L50       4         LG50       4         L75       7         LG75       7         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.309         Duplication ratio       1.000         # N's per 100 kbp       0.22         # mismatches per 100 kbp       181.32         # indels per 100 kbp       0.72         Largest alignment       1053360         NA50       451601         NA75       178093         NGA75       178093         LA50       4         LGA50       4         LA75       7	Reference length	4641652
N50       451601         NG50       451601         N75       178093         L50       4         L50       4         L75       7         LG75       7         # misassemblies       0         # misassembled contigs       0         Misassembled contigs       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.309         Duplication ratio       1.000         # N's per 100 kbp       0.22         # mismatches per 100 kbp       181.32         # indels per 100 kbp       0.72         Largest alignment       1053360         NA50       451601         NA75       178093         NGA75       178093         LA50       4         LGA50       4         LA75       7	GC (%)	50.78
NG50       451601         N75       178093         NG75       178093         L50       4         LG50       4         L75       7         LG75       7         # misassemblies       0         Misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.309         Duplication ratio       1.000         # N's per 100 kbp       0.22         # mismatches per 100 kbp       181.32         # indels per 100 kbp       0.72         Largest alignment       1053360         NA50       451601         NA75       178093         NGA75       178093         LA50       4         LGA50       4         LA75       7	Reference GC (%)	50.79
N75       178093         NG75       178093         L50       4         LG50       4         L75       7         LG75       7         # misassemblies       0         Misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.309         Duplication ratio       1.000         # N's per 100 kbp       0.22         # mismatches per 100 kbp       181.32         # indels per 100 kbp       0.72         Largest alignment       1053360         NA50       451601         NA75       178093         NGA75       178093         LA50       4         LGA50       4         LA75       7	N50	451601
NG75       178093         L50       4         LG50       4         L75       7         LG75       7         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.309         Duplication ratio       1.000         # N's per 100 kbp       0.22         # mismatches per 100 kbp       181.32         # indels per 100 kbp       0.72         Largest alignment       1053360         NA50       451601         NA75       178093         NGA75       178093         LA50       4         LGA50       4         LA75       7	NG50	451601
L50       4         LG50       4         L75       7         LG75       7         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.309         Duplication ratio       1.000         # N's per 100 kbp       0.22         # mismatches per 100 kbp       181.32         # indels per 100 kbp       0.72         Largest alignment       1053360         NA50       451601         NA75       178093         NGA75       178093         LA50       4         LGA50       4         LA75       7	N75	178093
LG50       4         L75       7         LG75       7         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.309         Duplication ratio       1.000         # N's per 100 kbp       0.22         # mismatches per 100 kbp       181.32         # indels per 100 kbp       0.72         Largest alignment       1053360         NA50       451601         NA75       178093         NGA75       178093         LA50       4         LGA50       4         LA75       7	NG75	178093
L75       7         LG75       7         # misassemblies       0         Misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.309         Duplication ratio       1.000         # N's per 100 kbp       0.22         # mismatches per 100 kbp       181.32         # indels per 100 kbp       0.72         Largest alignment       1053360         NA50       451601         NA75       178093         NGA75       178093         LA50       4         LGA50       4         LA75       7	L50	4
LG75       7         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.309         Duplication ratio       1.000         # N's per 100 kbp       0.22         # mismatches per 100 kbp       181.32         # indels per 100 kbp       0.72         Largest alignment       1053360         NA50       451601         NA75       178093         NGA75       178093         LA50       4         LGA50       4         LA75       7	LG50	4
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.309 Duplication ratio 1.000 # N's per 100 kbp 0.22 # mismatches per 100 kbp 181.32 # indels per 100 kbp 10.72 Largest alignment 1053360 NA50 451601 NA75 178093 NGA75 178093 LA50 4 LGA50 4 LGA50 4 LA75 7	L75	7
# misassembled contigs 0  Misassembled contigs length 0  # local misassemblies 0  # unaligned contigs 0 + 0 part  Unaligned length 0  Genome fraction (%) 99.309  Duplication ratio 1.000  # N's per 100 kbp 0.22  # mismatches per 100 kbp 181.32  # indels per 100 kbp 0.72  Largest alignment 1053360  NA50 451601  NGA50 451601  NA75 178093  NGA75 178093  LA50 4  LGA50 4  LGA50 4  LA75 7	LG75	7
Misassembled contigs length         0           # local misassemblies         0           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         99.309           Duplication ratio         1.000           # N's per 100 kbp         0.22           # mismatches per 100 kbp         181.32           # indels per 100 kbp         0.72           Largest alignment         1053360           NA50         451601           NGA50         451601           NA75         178093           NGA75         178093           LA50         4           LGA50         4           LA75         7	# misassemblies	0
# local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.309 Duplication ratio 1.000 # N's per 100 kbp 0.22 # mismatches per 100 kbp 181.32 # indels per 100 kbp 0.72 Largest alignment 1053360 NA50 451601 NGA50 451601 NA75 178093 NGA75 178093 LA50 4 LGA50 4 LA75 7	# misassembled contigs	0
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.309 Duplication ratio 1.000 # N's per 100 kbp 0.22 # mismatches per 100 kbp 181.32 # indels per 100 kbp 0.72 Largest alignment 1053360 NA50 451601 NGA50 451601 NA75 178093 NGA75 178093 LA50 4 LGA50 4 LA75 7	Misassembled contigs length	0
Unaligned length 0 Genome fraction (%) 99.309 Duplication ratio 1.000 # N's per 100 kbp 0.22 # mismatches per 100 kbp 181.32 # indels per 100 kbp 0.72 Largest alignment 1053360 NA50 451601 NGA50 451601 NA75 178093 NGA75 178093 LA50 4 LGA50 4 LA75 7	# local misassemblies	0
Genome fraction (%)       99.309         Duplication ratio       1.000         # N's per 100 kbp       0.22         # mismatches per 100 kbp       181.32         # indels per 100 kbp       0.72         Largest alignment       1053360         NA50       451601         NGA50       451601         NA75       178093         NGA75       178093         LA50       4         LGA50       4         LA75       7	# unaligned contigs	0 + 0 part
Duplication ratio       1.000         # N's per 100 kbp       0.22         # mismatches per 100 kbp       181.32         # indels per 100 kbp       0.72         Largest alignment       1053360         NA50       451601         NGA50       451601         NA75       178093         NGA75       178093         LA50       4         LGA50       4         LA75       7	Unaligned length	0
# N's per 100 kbp 0.22  # mismatches per 100 kbp 181.32  # indels per 100 kbp 0.72  Largest alignment 1053360  NA50 451601  NGA50 451601  NA75 178093  NGA75 178093  LA50 4  LGA50 4  LA75 7	Genome fraction (%)	
# mismatches per 100 kbp	Duplication ratio	1.000
# indels per 100 kbp 0.72 Largest alignment 1053360 NA50 451601 NGA50 451601 NA75 178093 NGA75 178093 LA50 4 LGA50 4 LA75 7	· '	<u> </u>
Largest alignment       1053360         NA50       451601         NGA50       451601         NA75       178093         NGA75       178093         LA50       4         LGA50       4         LA75       7		181.32
NA50       451601         NGA50       451601         NA75       178093         NGA75       178093         LA50       4         LGA50       4         LA75       7		<b></b>
NGA50       451601         NA75       178093         NGA75       178093         LA50       4         LGA50       4         LA75       7	Largest alignment	1053360
NA75     178093       NGA75     178093       LA50     4       LGA50     4       LA75     7		<b></b>
NGA75     178093       LA50     4       LGA50     4       LA75     7		
LA50 4 LGA50 4 LA75 7		
LGA50 4 LA75 7		
LA75 7		
LGA75 7		
· · · · · · · · · · · · · · · · · · ·	LGA75	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	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	8358
# indels	33
# short indels	31
# long indels	2
Indels length	109

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















