## Report

# contigs (>= 1000 bp)		
# contigs (>= 5000 bp) 137 # contigs (>= 10000 bp) 114 # contigs (>= 25000 bp) 71 # contigs (>= 50000 bp) 35 Total length (>= 10000 bp) 4867173 Total length (>= 10000 bp) 4869988 Total length (>= 50000 bp) 4655025 Total length (>= 25000 bp) 3991755 Total length (>= 50000 bp) 3991755 Total length (>= 50000 bp) 2826197 # contigs 162 Largest contig 197199 Total length 4870605 Reference length 4857432 GC (%) 52.23 Reference GC (%) 52.23 Reference GC (%) 52.23 N50 56927 N75 27696 NG75 28009 L50 28 LG50 28 LG50 28 LG75 59 LG75 58 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.989 Duplication ratio 1.003 # N's per 100 kbp 0.00 Largest alignment 197199 NA50 56927 NA50 288 LGA50 28		final.contigs
# contigs (>= 10000 bp)	# contigs (>= 1000 bp)	157
# contigs (>= 25000 bp)	# contigs (>= 5000 bp)	137
# contigs (>= 50000 bp)		114
Total length (>= 1000 bp)         4867173           Total length (>= 5000 bp)         4809988           Total length (>= 10000 bp)         4655025           Total length (>= 25000 bp)         3991755           Total length (>= 50000 bp)         2826197           # contigs         162           Largest contig         197199           Total length         4870605           Reference length         4857432           GC (%)         52.23           Reference GC (%)         52.23           N50         56927           NG50         56927           N75         27696           NG75         28009           L50         28           LG50         28           L75         59           LG75         58           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # unaligned length         0           Genome fraction (%)         99.989           Duplication ratio         1.003           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.00           Largest alignment	# contigs (>= 25000 bp)	71
Total length (>= 5000 bp)         4809988           Total length (>= 10000 bp)         4655025           Total length (>= 25000 bp)         3991755           Total length (>= 50000 bp)         2826197           # contigs         162           Largest contig         197199           Total length         4870605           Reference length         4857432           GC (%)         52.23           Reference GC (%)         52.23           N50         56927           NG50         56927           N75         27696           NG75         28009           L50         28           LG50         28           L75         59           LG75         58           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # unaligned length         0           Genome fraction (%)         99.989           Duplication ratio         1.003           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.00           # mismatches per 100 kbp <t< td=""><td># contigs (&gt;= 50000 bp)</td><td>35</td></t<>	# contigs (>= 50000 bp)	35
Total length (>= 10000 bp)         4655025           Total length (>= 25000 bp)         3991755           Total length (>= 50000 bp)         2826197           # contigs         162           Largest contig         197199           Total length         4870605           Reference length         4857432           GC (%)         52.23           Reference GC (%)         52.23           N50         56927           NG50         56927           N75         27696           NG75         28009           L50         28           LG50         28           LG75         58           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # unaligned length         0           Genome fraction (%)         99.989           Duplication ratio         1.003           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.00           # mismatches per 100 kbp         0.00           Largest alignment         197199           NA50         5692	1	4867173
Total length (>= 25000 bp)         3991755           Total length (>= 50000 bp)         2826197           # contigs         162           Largest contig         197199           Total length         4870605           Reference length         4857432           GC (%)         52.23           Reference GC (%)         52.23           N50         56927           NG50         56927           N75         27696           NG75         28009           L50         28           LG50         28           L75         59           LG75         58           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # unaligned length         0           Genome fraction (%)         99.989           Duplication ratio         1.003           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.00           Largest alignment         197199           NA50         56927           NA75         27696           NGA75 <td>1</td> <td>4809988</td>	1	4809988
# contigs 162 Largest contig 197199 Total length (>= 50000 bp) 4870605 Reference length 4870605 Reference length 4857432 GC (%) 52.23 Reference GC (%) 52.23 N50 56927 NG50 56927 N75 27696 NG75 28009 L50 28 LG50 28 LG50 28 L75 59 LG75 58 # misassemblies 0 # misassembled contigs 0 # local misassemblies 0 # unaligned contigs length 0 # local misassemblies 0 # unaligned length 0 Genome fraction (%) 99.989 Duplication ratio 1.003 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 197199 NA50 56927 NGA50 56927 NGA75 28009 LA50 28 LGA50 28 LGA50 28 LGA50 28 LGA50 28 LGA50 28 LGA50 28		4655025
# contigs       162         Largest contig       197199         Total length       4870605         Reference length       4857432         GC (%)       52.23         Reference GC (%)       52.23         N50       56927         NG50       56927         NG75       27696         NG75       28009         L50       28         LG50       28         L75       59         LG75       58         # misassemblies       0         # wisassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.989         Duplication ratio       1.003         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         # rindels per 100 kbp       0.00         Largest alignment       197199         NA50       56927         NGA50       56927         NGA75       28009         LA50       28         LA50 <td></td> <td>3991755</td>		3991755
Largest contig         197199           Total length         4870605           Reference length         4857432           GC (%)         52.23           Reference GC (%)         52.23           N50         56927           NG50         56927           NG75         28009           L50         28           L550         28           L75         59           LG75         58           # misassemblies         0           # sassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # unaligned length         0           Genome fraction (%)         99.989           Duplication ratio         1.003           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.00           # midels per 100 kbp         0.00           Largest alignment         197199           NA50         56927           NGA50         56927           NGA50         56927           NGA75         28009           LA50         28           LA50         28 <tr< td=""><td>Total length (&gt;= 50000 bp)</td><td>2826197</td></tr<>	Total length (>= 50000 bp)	2826197
Total length         4870605           Reference length         4857432           GC (%)         52.23           Reference GC (%)         52.23           N50         56927           NG50         56927           N75         27696           NG75         28009           L50         28           L575         59           LG75         58           # misassemblies         0           # local misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         99.989           Duplication ratio         1.003           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.00           # indels per 100 kbp         0.00           Largest alignment         197199           NA50         56927           NGA50         56927           NGA50         56927           NGA75         28009           LA50         28           LA50         28	# contigs	162
Reference length       4857432         GC (%)       52.23         Reference GC (%)       52.23         N50       56927         NG50       56927         N75       27696         NG75       28009         L50       28         LG50       28         LG75       59         LG75       58         # misassemblies       0         # local misassembled contigs       0         Misassembled contigs       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.989         Duplication ratio       1.003         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         # indels per 100 kbp       0.00         Largest alignment       197199         NA50       56927         NGA50       56927         NGA75       28009         LA50       28         LA50       28         LA50       28	Largest contig	197199
GC (%)       52.23         Reference GC (%)       52.23         N50       56927         NG50       56927         N75       27696         NG75       28009         L50       28         LG50       28         L75       59         LG75       58         # misassemblies       0         # local misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.989         Duplication ratio       1.003         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         # indels per 100 kbp       0.00         Largest alignment       197199         NA50       56927         NGA50       56927         NA75       27696         NGA75       28009         LA50       28         LA51       28         LA52       28	Total length	4870605
Reference GC (%)       52.23         N50       56927         NG50       56927         N75       27696         NG75       28009         L50       28         LG50       28         L75       59         LG75       58         # misassemblies       0         # inisassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.989         Duplication ratio       1.003         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         # indels per 100 kbp       0.00         Largest alignment       197199         NA50       56927         NGA50       56927         NGA75       28009         LA50       28         LA50       28         LA75       59	Reference length	4857432
N50       56927         NG50       56927         N75       27696         NG75       28009         L50       28         LG50       28         L75       59         LG75       58         # misassemblies       0         # inisassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.989         Duplication ratio       1.003         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         # indels per 100 kbp       0.00         Largest alignment       197199         NA50       56927         NA75       27696         NGA75       28009         LA50       28         LA55       59	GC (%)	52.23
NG50       56927         N75       27696         NG75       28009         L50       28         LG50       28         L75       59         LG75       58         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.989         Duplication ratio       1.003         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         # indels per 100 kbp       0.00         Largest alignment       197199         NA50       56927         NGA50       56927         NA75       27696         NGA75       28009         LA50       28         LA55       59	Reference GC (%)	52.23
N75       27696         NG75       28009         L50       28         L650       28         L75       59         LG75       58         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.989         Duplication ratio       1.003         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         # indels per 100 kbp       0.00         Largest alignment       197199         NA50       56927         NGA50       56927         NA75       27696         NGA75       28009         LA50       28         LA50       28         LA75       59	N50	56927
NG75       28009         L50       28         LG50       28         L75       59         LG75       58         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.989         Duplication ratio       1.003         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         # indels per 100 kbp       0.00         Largest alignment       197199         NA50       56927         NGA50       56927         NGA75       27696         NGA75       28009         LA50       28         LA55       59	NG50	56927
L50       28         LG50       28         L75       59         LG75       58         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.989         Duplication ratio       1.003         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         # indels per 100 kbp       0.00         Largest alignment       197199         NA50       56927         NGA50       56927         NA75       27696         NGA75       28009         LA50       28         LGA50       28         LA75       59	N75	27696
LG50       28         L75       59         LG75       58         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.989         Duplication ratio       1.003         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         # indels per 100 kbp       0.00         Largest alignment       197199         NA50       56927         NGA50       56927         NA75       27696         NGA75       28009         LA50       28         LGA50       28         LA75       59	NG75	28009
L75       59         LG75       58         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.989         Duplication ratio       1.003         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         # indels per 100 kbp       0.00         Largest alignment       197199         NA50       56927         NGA50       56927         NA75       27696         NGA75       28009         LA50       28         LGA50       28         LA75       59	L50	28
LG75       58         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.989         Duplication ratio       1.003         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         Largest alignment       197199         NA50       56927         NA75       27696         NGA75       28009         LA50       28         LGA50       28         LA75       59		
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.989 Duplication ratio 1.003 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # indels per 100 kbp 0.00 Largest alignment 197199 NA50 56927 NGA50 56927 NGA50 56927 NGA75 27696 NGA75 28009 LA50 28 LGA50 28 LA75 59	L75	59
# misassembled contigs	LG75	58
Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.989         Duplication ratio       1.003         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         # indels per 100 kbp       0.00         Largest alignment       197199         NA50       56927         NGA50       56927         NA75       27696         NGA75       28009         LA50       28         LGA50       28         LA75       59	# misassemblies	0
# local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.989 Duplication ratio 1.003 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 197199 NA50 56927 NGA50 56927 NGA50 56927 NA75 27696 NGA75 28009 LA50 28 LGA50 28 LA75 59		0
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.989 Duplication ratio 1.003 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 197199 NA50 56927 NGA50 56927 NA75 27696 NGA75 28009 LA50 28 LGA50 28 LGA50 28	Misassembled contigs length	0
Unaligned length       0         Genome fraction (%)       99.989         Duplication ratio       1.003         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         # indels per 100 kbp       0.00         Largest alignment       197199         NA50       56927         NGA50       56927         NA75       27696         NGA75       28009         LA50       28         LGA50       28         LA75       59	# local misassemblies	0
Genome fraction (%)       99.989         Duplication ratio       1.003         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         # indels per 100 kbp       0.00         Largest alignment       197199         NA50       56927         NGA50       56927         NA75       27696         NGA75       28009         LA50       28         LGA50       28         LA75       59	# unaligned contigs	0 + 0 part
Duplication ratio       1.003         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         # indels per 100 kbp       0.00         Largest alignment       197199         NA50       56927         NGA50       56927         NA75       27696         NGA75       28009         LA50       28         LGA50       28         LA75       59	Unaligned length	0
# N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # indels per 100 kbp 0.00 Largest alignment 197199 NA50 56927 NGA50 56927 NA75 27696 NGA75 28009 LA50 28 LGA50 28 LA75 59		99.989
# mismatches per 100 kbp 0.00 # indels per 100 kbp 0.00 Largest alignment 197199 NA50 56927 NGA50 56927 NA75 27696 NGA75 28009 LA50 28 LGA50 28 LA75 59	Duplication ratio	1.003
# indels per 100 kbp 0.00 Largest alignment 197199 NA50 56927 NGA50 56927 NA75 27696 NGA75 28009 LA50 28 LGA50 28 LA75 59	# N's per 100 kbp	0.00
Largest alignment       197199         NA50       56927         NGA50       56927         NA75       27696         NGA75       28009         LA50       28         LGA50       28         LA75       59		0.00
NA50       56927         NGA50       56927         NA75       27696         NGA75       28009         LA50       28         LGA50       28         LA75       59	# indels per 100 kbp	0.00
NGA50       56927         NA75       27696         NGA75       28009         LA50       28         LGA50       28         LA75       59	Largest alignment	197199
NA75     27696       NGA75     28009       LA50     28       LGA50     28       LA75     59	NA50	56927
NGA75     28009       LA50     28       LGA50     28       LA75     59	NGA50	56927
LA50     28       LGA50     28       LA75     59	NA75	27696
LGA50 28 LA75 59	NGA75	28009
LA75 59	LA50	28
	LGA50	28
LGA75 58		59
<u> </u>	LGA75	58

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	0
# mismatches	0
# indels	0
# short indels	0
# long indels	0
Indels length	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).

## 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).















