## Report

# contigs (>= 1000 bp) 217 # contigs (>= 5000 bp) 172 # contigs (>= 5000 bp) 173 # contigs (>= 10000 bp) 143 # contigs (>= 25000 bp) 66 # contigs (>= 50000 bp) 20 Total length (>= 10000 bp) 4549760 Total length (>= 10000 bp) 4445537 Total length (>= 10000 bp) 4223740 Total length (>= 25000 bp) 2959535 Total length (>= 25000 bp) 1358550 # contigs 235 Largest contig 105740 Total length (>= 50000 bp) 1358550 # contigs 235 Largest contig 105740 Total length (>= 50000 bp) 3959535  Got (%) 50.74 Reference length 4641652 GC (%) 50.79 N50 33685 NG50 33314 N75 19315 NG75 18542 L50 43 LG50 45 L75 88 LG75 91 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 # unaligned length 53 Genome fraction (%) 98.209 Duplication ratio 1.001 # N's per 100 kbp 9.59 Largest alignment 105740 NA50 33685 NGA50 33314 NA75 19315 NGA75 19315 NGA75 18542 LA50 43 LGA50 43 LGA50 43 LGA55 88 LGA55 89		
# contigs (>= 5000 bp) 172 # contigs (>= 10000 bp) 66 # contigs (>= 25000 bp) 66 # contigs (>= 50000 bp) 20 Total length (>= 10000 bp) 4549760 Total length (>= 10000 bp) 444537 Total length (>= 10000 bp) 4223740 Total length (>= 50000 bp) 2959535 Total length (>= 50000 bp) 1358550 # contigs 235 Largest contig 105740 Total length (>= 50000 bp) 1358550 # contigs 235 Largest contig 105740 Total length (>= 50000 bp) 36234 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 33685 NG50 33314 N75 19315 NG75 18542 L50 43 LG50 45 L75 88 LG75 91 # misassemblies 0 # misassembled contigs length 0 # local misassembles 7 # unaligned contigs length 53 Genome fraction (%) 98.209 Duplication ratio 1.001 # N's per 100 kbp 9.59 Largest alignment 105740 NA50 33685 NGA50 43 LGA50 43		final.contigs
# contigs (>= 10000 bp)	# contigs (>= 1000 bp)	217
# contigs (>= 25000 bp)	# contigs (>= 5000 bp)	172
# contigs (>= 50000 bp)		143
Total length (>= 1000 bp)         4549760           Total length (>= 5000 bp)         4445537           Total length (>= 10000 bp)         4223740           Total length (>= 25000 bp)         2959535           Total length (>= 50000 bp)         1358550           # contigs         235           Largest contig         105740           Total length         4562347           Reference length         4641652           GC (%)         50.74           Reference GC (%)         50.79           N50         33685           NG50         33314           N75         19315           NG75         18542           L50         43           LG50         45           L75         88           LG75         91           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         7           # unaligned length         53           Genome fraction (%)         98.209           Duplication ratio         1.001           # mismatches per 100 kbp         50.5           # indels per 100 kbp	# contigs (>= 25000 bp)	66
Total length (>= 5000 bp)         4445537           Total length (>= 10000 bp)         4223740           Total length (>= 25000 bp)         2959535           Total length (>= 50000 bp)         1358550           # contigs         235           Largest contig         105740           Total length         4562347           Reference length         4641652           GC (%)         50.74           Reference GC (%)         50.79           N50         33685           NG50         33314           N75         19315           NG75         18542           L50         43           LG50         45           L75         88           LG75         91           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         7           # unaligned length         53           Genome fraction (%)         98.209           Duplication ratio         1.001           # N's per 100 kbp         50.5           # indels per 100 kbp         50.5           # indels per 100 kbp         9.59<	# contigs (>= 50000 bp)	20
Total length (>= 10000 bp)         4223740           Total length (>= 25000 bp)         2959535           Total length (>= 50000 bp)         1358550           # contigs         235           Largest contig         105740           Total length         4562347           Reference length         4641652           GC (%)         50.74           Reference GC (%)         50.79           N50         33685           NG50         33314           N75         19315           NG75         18542           L50         43           L650         45           L75         88           LG75         91           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         7           # unaligned length         53           Genome fraction (%)         98.209           Duplication ratio         1.001           # N's per 100 kbp         57.65           # indels per 100 kbp         57.65           # indels per 100 kbp         9.59           Largest alignment         105740	1	4549760
Total length (>= 25000 bp)         2959535           Total length (>= 50000 bp)         1358550           # contigs         235           Largest contig         105740           Total length         4562347           Reference length         4641652           GC (%)         50.74           Reference GC (%)         50.79           N50         33685           NG50         33314           N75         19315           NG75         18542           L50         43           LG50         45           L75         88           LG75         91           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         7           # unaligned length         53           Genome fraction (%)         98.209           Duplication ratio         1.001           # N's per 100 kbp         0.00           # mismatches per 100 kbp         9.59           Largest alignment         105740           NA50         33685           NGA50         33314           NA75 <td>1</td> <td>4445537</td>	1	4445537
# contigs 235 Largest contig 105740 Total length (>= 50000 bp) 4562347 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 33685 NG50 33314 N75 19315 NG75 18542 L50 43 LG50 45 L75 88 LG75 91 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 7 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.209 Duplication ratio 1.001 # N's per 100 kbp 9.59 Largest alignment 105740 NA50 33685 NGA75 18542 LA50 43 LGA50 445 LA75 88		4223740
# contigs       235         Largest contig       105740         Total length       4562347         Reference length       4641652         GC (%)       50.74         Reference GC (%)       50.79         N50       33685         NG50       33314         N75       19315         NG75       18542         L50       43         LG50       45         L75       88         LG75       91         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       7         # unaligned contigs       0 + 1 part         Unaligned length       53         Genome fraction (%)       98.209         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       57.65         # indels per 100 kbp       95.9         Largest alignment       105740         NA50       33685         NGA50       33314         NA75       19315         NGA75       18542         LA50<	Total length (>= 25000 bp)	2959535
Largest contig       105740         Total length       4562347         Reference length       4641652         GC (%)       50.74         Reference GC (%)       50.79         N50       33685         NG50       33314         N75       19315         NG75       18542         L50       43         LG50       45         L75       88         LG75       91         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       7         # unaligned length       53         Genome fraction (%)       98.209         Duplication ratio       1.001         # N's per 100 kbp       57.65         # indels per 100 kbp       9.59         Largest alignment       105740         NA50       33685         NGA50       33314         NA75       19315         NGA75       18542         LA50       43         LA50       45         LA75       88	Total length (>= 50000 bp)	1358550
Total length         4562347           Reference length         4641652           GC (%)         50.74           Reference GC (%)         50.79           N50         33685           NG50         33314           N75         19315           NG75         18542           L50         43           LG50         45           L75         88           LG75         91           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         7           # unaligned contigs         0 + 1 part           Unaligned length         53           Genome fraction (%)         98.209           Duplication ratio         1.001           # N's per 100 kbp         0.00           # mismatches per 100 kbp         57.65           # indels per 100 kbp         9.59           Largest alignment         105740           NA50         33685           NGA50         33314           NA75         19315           NGA75         18542           LA50         43     <	# contigs	235
Reference length       4641652         GC (%)       50.74         Reference GC (%)       50.79         N50       33685         NG50       33114         N75       19315         NG75       18542         L50       43         LG50       45         L75       88         LG75       91         # misassemblies       0         # misassembled contigs       0         Misassembled contigs       0         # local misassemblies       7         # unaligned contigs       0 + 1 part         Unaligned length       53         Genome fraction (%)       98.209         Duplication ratio       1.001         # Ni's per 100 kbp       57.65         # indels per 100 kbp       9.59         Largest alignment       105740         NA50       33685         NGA50       33314         NA75       19315         NGA75       18542         LA50       43         LA50       45         LA75       88	Largest contig	105740
GC (%)       50.74         Reference GC (%)       50.79         N50       33685         NG50       33314         N75       19315         NG75       18542         L50       43         LG50       45         L75       88         LG75       91         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       7         # unaligned contigs       0 + 1 part         Unaligned length       53         Genome fraction (%)       98.209         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       57.65         # indels per 100 kbp       9.59         Largest alignment       105740         NA50       33685         NGA50       33314         NA75       19315         NGA75       18542         LA50       43         LA50       45         LA75       88	Total length	4562347
Reference GC (%)       50.79         N50       33685         NG50       33314         N75       19315         NG75       18542         L50       43         LG50       45         L75       88         LG75       91         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       7         # unaligned contigs       0 + 1 part         Unaligned length       53         Genome fraction (%)       98.209         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       57.65         # indels per 100 kbp       9.59         Largest alignment       105740         NA50       33685         NGA50       33314         NA75       19315         NGA75       18542         LA50       43         LA50       45         LA75       88	Reference length	4641652
N50       33685         NG50       33314         N75       19315         NG75       18542         L50       43         LG50       45         L75       88         LG75       91         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       7         # unaligned contigs       0 + 1 part         Unaligned length       53         Genome fraction (%)       98.209         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       57.65         # indels per 100 kbp       9.59         Largest alignment       105740         NA50       33685         NGA50       33314         NA75       19315         NGA75       18542         LA50       43         LGA50       45         LA75       88	GC (%)	50.74
NG50       33314         N75       19315         NG75       18542         L50       43         LG50       45         L75       88         LG75       91         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       7         # unaligned contigs       0 + 1 part         Unaligned length       53         Genome fraction (%)       98.209         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       57.65         # indels per 100 kbp       9.59         Largest alignment       105740         NA50       33685         NGA50       33314         NA75       19315         NGA75       18542         LA50       43         LGA50       45         LA75       88	Reference GC (%)	50.79
N75       19315         NG75       18542         L50       43         LG50       45         L75       88         LG75       91         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       7         # unaligned contigs       0 + 1 part         Unaligned length       53         Genome fraction (%)       98.209         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       57.65         # indels per 100 kbp       9.59         Largest alignment       105740         NA50       33685         NGA50       33314         NA75       19315         NGA75       18542         LA50       43         LGA50       45         LA75       88	N50	33685
NG75       18542         L50       43         LG50       45         L75       88         LG75       91         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       7         # unaligned contigs       0 + 1 part         Unaligned length       53         Genome fraction (%)       98.209         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       57.65         # indels per 100 kbp       9.59         Largest alignment       105740         NA50       33685         NGA50       33314         NA75       19315         NGA75       18542         LA50       43         LGA50       45         LA75       88	NG50	33314
L50       43         LG50       45         L75       88         LG75       91         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       7         # unaligned contigs       0 + 1 part         Unaligned length       53         Genome fraction (%)       98.209         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       57.65         # indels per 100 kbp       9.59         Largest alignment       105740         NA50       33685         NGA50       33314         NA75       19315         NGA75       18542         LA50       43         LGA50       45         LA75       88	N75	19315
LG50       45         L75       88         LG75       91         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       7         # unaligned contigs       0 + 1 part         Unaligned length       53         Genome fraction (%)       98.209         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       57.65         # indels per 100 kbp       9.59         Largest alignment       105740         NA50       33685         NGA50       33314         NA75       19315         NGA75       18542         LA50       43         LGA50       45         LA75       88	NG75	18542
L75       88         LG75       91         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       7         # unaligned contigs       0 + 1 part         Unaligned length       53         Genome fraction (%)       98.209         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       57.65         # indels per 100 kbp       9.59         Largest alignment       105740         NA50       33685         NGA50       33314         NA75       19315         NGA75       18542         LA50       43         LGA50       45         LA75       88	L50	43
LG75       91         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       7         # unaligned contigs       0 + 1 part         Unaligned length       53         Genome fraction (%)       98.209         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       57.65         # indels per 100 kbp       9.59         Largest alignment       105740         NA50       33685         NGA50       33314         NA75       19315         NGA75       18542         LA50       43         LGA50       45         LA75       88	LG50	45
# misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       7         # unaligned contigs       0 + 1 part         Unaligned length       53         Genome fraction (%)       98.209         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       57.65         # indels per 100 kbp       9.59         Largest alignment       105740         NA50       33685         NGA50       33314         NA75       19315         NGA75       18542         LA50       43         LGA50       45         LA75       88	L75	88
# misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       7         # unaligned contigs       0 + 1 part         Unaligned length       53         Genome fraction (%)       98.209         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       57.65         # indels per 100 kbp       9.59         Largest alignment       105740         NA50       33685         NGA50       33314         NA75       19315         NGA75       18542         LA50       43         LGA50       45         LA75       88	LG75	91
Misassembled contigs length       0         # local misassemblies       7         # unaligned contigs       0 + 1 part         Unaligned length       53         Genome fraction (%)       98.209         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       57.65         # indels per 100 kbp       9.59         Largest alignment       105740         NA50       33685         NGA50       33314         NA75       19315         NGA75       18542         LA50       43         LGA50       45         LA75       88	# misassemblies	0
# local misassemblies 7 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.209 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 57.65 # indels per 100 kbp 9.59 Largest alignment 105740 NA50 33685 NGA50 33314 NA75 19315 NGA75 18542 LA50 43 LGA50 45 LA75 88	# misassembled contigs	0
# unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.209 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 57.65 # indels per 100 kbp 9.59 Largest alignment 105740 NA50 33685 NGA50 33314 NA75 19315 NGA75 18542 LA50 43 LGA50 45 LA75 88	Misassembled contigs length	0
Unaligned length       53         Genome fraction (%)       98.209         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       57.65         # indels per 100 kbp       9.59         Largest alignment       105740         NA50       33685         NGA50       33314         NA75       19315         NGA75       18542         LA50       43         LGA50       45         LA75       88	# local misassemblies	7
Genome fraction (%)       98.209         Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       57.65         # indels per 100 kbp       9.59         Largest alignment       105740         NA50       33685         NGA50       33314         NA75       19315         NGA75       18542         LA50       43         LGA50       45         LA75       88	# unaligned contigs	0 + 1 part
Duplication ratio       1.001         # N's per 100 kbp       0.00         # mismatches per 100 kbp       57.65         # indels per 100 kbp       9.59         Largest alignment       105740         NA50       33685         NGA50       33314         NA75       19315         NGA75       18542         LA50       43         LGA50       45         LA75       88	Unaligned length	53
# N's per 100 kbp 0.00 # mismatches per 100 kbp 57.65 # indels per 100 kbp 9.59 Largest alignment 105740 NA50 33685 NGA50 33314 NA75 19315 NGA75 18542 LA50 43 LGA50 45 LA75 88	Genome fraction (%)	98.209
# mismatches per 100 kbp 57.65 # indels per 100 kbp 9.59 Largest alignment 105740 NA50 33685 NGA50 33314 NA75 19315 NGA75 18542 LA50 43 LGA50 45 LA75 88	Duplication ratio	1.001
# indels per 100 kbp 9.59 Largest alignment 105740 NA50 33685 NGA50 33314 NA75 19315 NGA75 18542 LA50 43 LGA50 45 LA75 88	# N's per 100 kbp	0.00
Largest alignment       105740         NA50       33685         NGA50       33314         NA75       19315         NGA75       18542         LA50       43         LGA50       45         LA75       88	# mismatches per 100 kbp	57.65
NA50       33685         NGA50       33314         NA75       19315         NGA75       18542         LA50       43         LGA50       45         LA75       88	# indels per 100 kbp	9.59
NGA50       33314         NA75       19315         NGA75       18542         LA50       43         LGA50       45         LA75       88	Largest alignment	105740
NA75       19315         NGA75       18542         LA50       43         LGA50       45         LA75       88	NA50	33685
NGA75     18542       LA50     43       LGA50     45       LA75     88	NGA50	33314
LA50       43         LGA50       45         LA75       88	NA75	19315
LGA50 45 LA75 88	NGA75	18542
LA75 88	LA50	43
	LGA50	45
	LA75	88
LUM/3   91	LGA75	91

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	7
# mismatches	2628
# indels	437
# short indels	431
# long indels	6
Indels length	757

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	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	53
# 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).















