Report

# contigs (>= 1000 bp)		scaffolds
# contigs (>= 10000 bp) 28 # contigs (>= 25000 bp) 27 # contigs (>= 50000 bp) 24 Total length (>= 1000 bp) 6000633 Total length (>= 5000 bp) 5996107 Total length (>= 10000 bp) 5996107 Total length (>= 25000 bp) 5996107 Total length (>= 25000 bp) 5985304 Total length (>= 50000 bp) 5873027 # contigs 34 Largest contig 700824 Total length 6003325 Reference length 4641652 GC (%) 50.71 Reference GC (%) 50.78 N50 333124 NG50 373445 N75 184667 NG75 330294 L50 7 LG50 5 L75 12 LG75 8 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 1 # unaligned length 349059 # local misassemblies 1 # unaligned length 1194117 Genome fraction (%) 99.582 Duplication ratio 1.040 # N's per 100 kbp 0.00 # mismatches per 100 kbp 352.62 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 325448 NGA75 188536 LA50 7 LGA50 5 LA75 18	# contigs (>= 1000 bp)	31
# contigs (>= 25000 bp) 27 # contigs (>= 50000 bp) 24 Total length (>= 1000 bp) 6000633 Total length (>= 5000 bp) 5996107 Total length (>= 10000 bp) 5996107 Total length (>= 25000 bp) 5985304 Total length (>= 50000 bp) 5885304 Total length (>= 50000 bp) 58873027 # contigs 34 Largest contig 700824 Total length 6003325 Reference length 4641652 GC (%) 50.71 Reference GC (%) 50.78 N50 333124 NG50 373445 N75 184667 NG75 330294 L50 7 LG50 5 L75 12 LG75 8 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 0 + 8 part Unaligned length 1194117 Genome fraction (%) 99.582 Duplication ratio 1.040 # N's per 100 kbp 0.00 # mismatches per 100 kbp 352.62 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 325448 NGA50 373445 NA75 188536 LA50 7 LGA50 5 LA75 188536	# contigs (>= 5000 bp)	28
# contigs (>= 50000 bp) 24 Total length (>= 1000 bp) 6000633 Total length (>= 5000 bp) 5996107 Total length (>= 10000 bp) 5996107 Total length (>= 25000 bp) 5985304 Total length (>= 50000 bp) 5873027 # contigs 34 Largest contig 700824 Total length 6003325 Reference length 4641652 GC (%) 50.71 Reference GC (%) 50.78 N50 333124 NG50 373445 N75 184667 NG75 330294 L50 7 LG50 5 L75 12 LG75 8 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 0 + 8 part Unaligned length 1194117 Genome fraction (%) 99.582 Duplication ratio 1.040 # N's per 100 kbp 0.00 # mismatches per 100 kbp 352.62 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 325448 NGA50 373445 NA75 188536 LA50 7 LGA50 5 LA75 188536	# contigs (>= 10000 bp)	28
# contigs (>= 50000 bp) 24 Total length (>= 1000 bp) 6000633 Total length (>= 5000 bp) 5996107 Total length (>= 10000 bp) 5996107 Total length (>= 25000 bp) 5985304 Total length (>= 50000 bp) 5873027 # contigs 34 Largest contig 700824 Total length 6003325 Reference length 4641652 GC (%) 50.71 Reference GC (%) 50.78 N50 333124 NG50 373445 N75 184667 NG75 330294 L50 7 LG50 5 L75 12 LG75 8 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 0 + 8 part Unaligned length 1194117 Genome fraction (%) 99.582 Duplication ratio 1.040 # N's per 100 kbp 0.00 # mismatches per 100 kbp 352.62 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 325448 NGA50 373445 NA75 188536 LA50 7 LGA50 5 LA75 188536		27
Total length (>= 5000 bp) 5996107 Total length (>= 10000 bp) 5996107 Total length (>= 25000 bp) 5985304 Total length (>= 50000 bp) 5873027 # contigs 34 Largest contig 700824 Total length 6003325 Reference length 4641652 GC (%) 50.71 Reference GC (%) 50.78 N50 333124 NG50 373445 N75 184667 NG75 330294 L50 7 LG50 5 L75 12 LG75 8 # misassembles 1 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 1 # local misassemblies 1 # unaligned contigs 0 + 8 part 1 Unaligned length 1194117 Genome fraction (%) 99.582 Duplication ratio 1.040 # N's per 100 kbp 0.00 # mismatches per 100 kbp 352.62 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 325448 NGA50 7 NGA75 188536 LA50 7 LGA50 5 LA75 18	# contigs (>= 50000 bp)	24
Total length (>= 10000 bp) 5996107 Total length (>= 25000 bp) 5985304 Total length (>= 50000 bp) 5873027 # contigs 34 Largest contig 700824 Total length 6003325 Reference length 4641652 GC (%) 50.71 Reference GC (%) 50.78 N50 333124 NG50 373445 N75 184667 NG75 330294 L50 7 LG50 5 L75 12 LG75 8 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 1 # local misassemblies 1 # unaligned contigs 0 + 8 part 1 Unaligned length 1194117 Genome fraction (%) 99.582 Duplication ratio 1.040 # N's per 100 kbp 0.00 # mismatches per 100 kbp 352.62 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 325448 NGA50 7 LGA50 5 LA75 188536 LA50 7 LGA50 5 LA75 188536	Total length (>= 1000 bp)	6000633
Total length (>= 25000 bp) 5985304 Total length (>= 50000 bp) 5873027 # contigs 34 Largest contig 700824 Total length 6003325 Reference length 4641652 GC (%) 50.71 Reference GC (%) 50.78 N50 333124 NG50 373445 N75 184667 NG75 330294 L50 7 LG50 5 L75 12 LG75 8 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 1 # local misassemblies 1 # unaligned contigs 0 + 8 part Unaligned length 1194117 Genome fraction (%) 99.582 Duplication ratio 1.040 # N's per 100 kbp 0.00 # mismatches per 100 kbp 352.62 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 325448 NGA50 7 LGA50 5 LA75 188536 LA50 7 LGA50 5 LA75 188536	Total length (>= 5000 bp)	5996107
# contigs 34 Largest contig 700824 Total length 6003325 Reference length 4641652 GC (%) 50.71 Reference GC (%) 50.78 N50 333124 NG50 373445 N75 184667 NG75 330294 L50 7 LG50 5 L75 12 LG75 8 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 1 # local misassemblies 1 # unaligned contigs 0 + 8 part Unaligned length 1194117 Genome fraction (%) 99.582 Duplication ratio 1.040 # N's per 100 kbp 0.00 # mismatches per 100 kbp 352.62 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 325448 NGA50 373445 NA75 54773 NGA75 188536 LA50 7 LGA50 5 LA75 18	Total length (>= 10000 bp)	5996107
# contigs 34 Largest contig 700824 Total length 6003325 Reference length 4641652 GC (%) 50.71 Reference GC (%) 50.78 N50 333124 NG50 373445 N75 184667 NG75 330294 L50 7 LG50 5 L75 12 LG75 8 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 1 # local misassemblies 1 # unaligned length 349059 # local misassemblies 1 Unaligned length 1194117 Genome fraction (%) 99.582 Duplication ratio 1.040 # N's per 100 kbp 0.00 # mismatches per 100 kbp 352.62 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 325448 NGA50 373445 NA75 54773 NGA75 188536 LA50 7 LGA50 5 LA75 18	Total length (>= 25000 bp)	5985304
Largest contig 700824 Total length 6003325 Reference length 4641652 GC (%) 50.71 Reference GC (%) 50.78 N50 333124 NG50 373445 N75 184667 NG75 330294 L50 7 LG50 5 L75 12 LG75 8 # misassemblies 1 # misassembled contigs 1 # local misassemblies 1 # unaligned contigs 0 + 8 part Unaligned length 1194117 Genome fraction (%) 99.582 Duplication ratio 1.040 # N's per 100 kbp 0.00 # mismatches per 100 kbp 352.62 # indels per 100 kbp 352.62 # indels per 100 kbp 373445 NA50 325448 NGA50 373445 NA75 54773 NGA75 188536 LA50 7	Total length (>= 50000 bp)	5873027
Total length 6003325 Reference length 4641652 GC (%) 50.71 Reference GC (%) 50.78 N50 333124 NG50 373445 N75 184667 NG75 330294 L50 7 LG50 5 L75 12 LG75 8 # misassemblies 1 # local misassembled contigs 1 # local misassemblies 1 # unaligned contigs 0 + 8 part Unaligned length 1194117 Genome fraction (%) 99.582 Duplication ratio 1.040 # N's per 100 kbp 0.00 # mismatches per 100 kbp 352.62 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 325448 NGA50 373445 NA75 54773 NGA75 188536 LA50 7 LGA50 5	# contigs	34
Reference length 4641652 GC (%) 50.71 Reference GC (%) 50.78 N50 333124 NG50 373445 N75 184667 NG75 330294 L50 7 LG50 5 L75 12 LG75 8 # misassemblies 1 # local misassembled contigs 1 # local misassemblies 1 # unaligned contigs 0 + 8 part Unaligned length 1194117 Genome fraction (%) 99.582 Duplication ratio 1.040 # N's per 100 kbp 0.00 # mismatches per 100 kbp 352.62 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 325448 NGA50 373445 NA75 54773 NGA75 188536 LA50 7 LGA50 5 LA75 18	Largest contig	700824
GC (%) 50.71 Reference GC (%) 50.78 N50 333124 NG50 373445 N75 184667 NG75 330294 L50 7 LG50 5 L75 12 LG75 8 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 349059 # local misassemblies 1 # unaligned contigs 0 + 8 part Unaligned length 1194117 Genome fraction (%) 99.582 Duplication ratio 1.040 # N's per 100 kbp 0.00 # mismatches per 100 kbp 352.62 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 325448 NGA50 373445 NA75 54773 NGA75 188536 LA50 7 LGA50 5 LA75 18	Total length	6003325
Reference GC (%) 50.78 N50 333124 NG50 373445 N75 184667 NG75 330294 L50 7 LG50 5 L75 12 LG75 8 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 349059 # local misassemblies 1 # unaligned contigs 0 + 8 part Unaligned length 1194117 Genome fraction (%) 99.582 Duplication ratio 1.040 # N's per 100 kbp 0.00 # mismatches per 100 kbp 352.62 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 325448 NA75 54773 NGA75 188536 LA50 7 LGA50 5 LA75 18	Reference length	4641652
N50 333124 NG50 373445 N75 184667 NG75 330294 L50 7 LG50 5 L75 12 LG75 8 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 349059 # local misassemblies 1 # unaligned contigs 0 + 8 part Unaligned length 1194117 Genome fraction (%) 99.582 Duplication ratio 1.040 # N's per 100 kbp 0.00 # mismatches per 100 kbp 352.62 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 325448 NGA50 373445 NA75 54773 NGA75 188536 LA50 7 LGA50 5 LA75 18	GC (%)	50.71
NG50 373445 N75 184667 NG75 330294 L50 7 LG50 5 L75 12 LG75 8 # misassemblies 1 Misassembled contigs 1 Misassembled contigs length 349059 # local misassemblies 1 # unaligned contigs 0 + 8 part Unaligned length 1194117 Genome fraction (%) 99.582 Duplication ratio 1.040 # N's per 100 kbp 0.00 # mismatches per 100 kbp 352.62 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 325448 NGA50 373445 NA75 54773 NGA75 188536 LA50 7 LGA50 5 LA75 18	Reference GC (%)	50.78
N75 184667 NG75 330294 L50 7 LG50 5 L75 12 LG75 8 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 349059 # local misassemblies 1 # unaligned contigs 0 + 8 part Unaligned length 1194117 Genome fraction (%) 99.582 Duplication ratio 1.040 # N's per 100 kbp 0.00 # mismatches per 100 kbp 352.62 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 325448 NGA50 373445 NA75 54773 NGA75 188536 LA50 7 LGA50 5 LA75 18	N50	333124
NG75 330294 L50 7 LG50 5 L75 12 LG75 8 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 349059 # local misassemblies 1 # unaligned contigs 0 + 8 part Unaligned length 1194117 Genome fraction (%) 99.582 Duplication ratio 1.040 # N's per 100 kbp 0.00 # mismatches per 100 kbp 352.62 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 325448 NGA50 373445 NA75 54773 NGA75 188536 LA50 7 LGA50 5 LA75 18	NG50	373445
L50 7 LG50 5 L75 12 LG75 8 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 349059 # local misassemblies 1 # unaligned contigs 0 + 8 part Unaligned length 1194117 Genome fraction (%) 99.582 Duplication ratio 1.040 # N's per 100 kbp 0.00 # mismatches per 100 kbp 352.62 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 325448 NGA50 373445 NA75 54773 NGA75 188536 LA50 7 LGA50 5 LA75 18	N75	184667
LG50 5 L75 12 LG75 8 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 349059 # local misassemblies 1 # unaligned contigs 0 + 8 part Unaligned length 1194117 Genome fraction (%) 99.582 Duplication ratio 1.040 # N's per 100 kbp 0.00 # mismatches per 100 kbp 352.62 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 325448 NGA50 373445 NA75 54773 NGA75 188536 LA50 7 LGA50 5 LA75 18	NG75	330294
L75 12 LG75 8 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 349059 # local misassemblies 1 # unaligned contigs 0 + 8 part Unaligned length 1194117 Genome fraction (%) 99.582 Duplication ratio 1.040 # N's per 100 kbp 0.00 # mismatches per 100 kbp 352.62 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 325448 NGA50 373445 NA75 54773 NGA75 188536 LA50 7 LGA50 5 LA75 18	L50	7
# misassemblies 1 # misassembled contigs 1 Misassembled contigs length 349059 # local misassemblies 1 # unaligned contigs 0 + 8 part Unaligned length 1194117 Genome fraction (%) 99.582 Duplication ratio 1.040 # N's per 100 kbp 0.00 # mismatches per 100 kbp 352.62 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 325448 NGA50 373445 NA75 54773 NGA75 188536 LA50 7 LGA50 5 LA75 18	LG50	5
# misassemblies 1 # misassembled contigs 1 Misassembled contigs length 349059 # local misassemblies 1 # unaligned contigs 0 + 8 part Unaligned length 1194117 Genome fraction (%) 99.582 Duplication ratio 1.040 # N's per 100 kbp 0.00 # mismatches per 100 kbp 352.62 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 325448 NGA50 373445 NA75 54773 NGA75 188536 LA50 7 LGA50 5 LA75 18	L75	12
# misassembled contigs 1 Misassembled contigs length 349059 # local misassemblies 1 # unaligned contigs 0 + 8 part Unaligned length 1194117 Genome fraction (%) 99.582 Duplication ratio 1.040 # N's per 100 kbp 0.00 # mismatches per 100 kbp 352.62 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 325448 NGA50 373445 NA75 54773 NGA75 188536 LA50 7 LGA50 5 LA75 18	LG75	8
Misassembled contigs length 349059 # local misassemblies 1 # unaligned contigs 0 + 8 part Unaligned length 1194117 Genome fraction (%) 99.582 Duplication ratio 1.040 # N's per 100 kbp 0.00 # mismatches per 100 kbp 352.62 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 325448 NGA50 373445 NA75 54773 NGA75 188536 LA50 7 LGA50 5 LA75 18	# misassemblies	1
# local misassemblies 1 # unaligned contigs 0 + 8 part Unaligned length 1194117 Genome fraction (%) 99.582 Duplication ratio 1.040 # N's per 100 kbp 0.00 # mismatches per 100 kbp 352.62 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 325448 NGA50 373445 NA75 54773 NGA75 188536 LA50 7 LGA50 5 LA75 18	# misassembled contigs	1
# unaligned contigs 0 + 8 part Unaligned length 1194117 Genome fraction (%) 99.582 Duplication ratio 1.040 # N's per 100 kbp 0.00 # mismatches per 100 kbp 352.62 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 325448 NGA50 373445 NA75 54773 NGA75 188536 LA50 7 LGA50 5 LA75 18	Misassembled contigs length	349059
Unaligned length 1194117 Genome fraction (%) 99.582 Duplication ratio 1.040 # N's per 100 kbp 0.00 # mismatches per 100 kbp 352.62 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 325448 NGA50 373445 NA75 54773 NGA75 188536 LA50 7 LGA50 5 LA75 18	# local misassemblies	1
Genome fraction (%) 99.582 Duplication ratio 1.040 # N's per 100 kbp 0.00 # mismatches per 100 kbp 352.62 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 325448 NGA50 373445 NA75 54773 NGA75 188536 LA50 7 LGA50 5 LA75 18	# unaligned contigs	
Duplication ratio 1.040 # N's per 100 kbp 0.00 # mismatches per 100 kbp 352.62 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 325448 NGA50 373445 NA75 54773 NGA75 188536 LA50 7 LGA50 5 LA75 18	Unaligned length	1194117
# N's per 100 kbp 0.00 # mismatches per 100 kbp 352.62 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 325448 NGA50 373445 NA75 54773 NGA75 188536 LA50 7 LGA50 5 LA75 18	Genome fraction (%)	
# mismatches per 100 kbp 352.62 # indels per 100 kbp 1.10 Largest alignment 700544 NA50 325448 NGA50 373445 NA75 54773 NGA75 188536 LA50 7 LGA50 5 LA75 18	Duplication ratio	1.040
# indels per 100 kbp 1.10 Largest alignment 700544 NA50 325448 NGA50 373445 NA75 54773 NGA75 188536 LA50 7 LGA50 5 LA75 18		
Largest alignment 700544 NA50 325448 NGA50 373445 NA75 54773 NGA75 188536 LA50 7 LGA50 5 LA75 18		
NA50 325448 NGA50 373445 NA75 54773 NGA75 188536 LA50 7 LGA50 5 LA75 18		
NGA50 373445 NA75 54773 NGA75 188536 LA50 7 LGA50 5 LA75 18	Largest alignment	700544
NA75 54773 NGA75 188536 LA50 7 LGA50 5 LA75 18		
NGA75 188536 LA50 7 LGA50 5 LA75 18		
LA50 7 LGA50 5 LA75 18		
LGA50 5 LA75 18		188536
LA75 18		
LGA75 9		
	LGA75	9

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	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	8
# misassembled contigs	1
Misassembled contigs length	349059
# local misassemblies	1
# mismatches	16299
# indels	51
# short indels	51
# long indels	0
Indels length	51

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	8
# with misassembly	3
# both parts are significant	7
Partially unaligned length	1194117
# 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).















