Report

# contigs (>= 1000 bp)		scaffolds
# contigs (>= 10000 bp) 47 # contigs (>= 25000 bp) 41 # contigs (>= 50000 bp) 28 Total length (>= 10000 bp) 4415110 Total length (>= 50000 bp) 4368531 Total length (>= 10000 bp) 4354332 Total length (>= 25000 bp) 4245246 Total length (>= 50000 bp) 3796503 # contigs 112 Largest contig 330825 Total length 4442118 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.79 N50 149239 NG50 132163 N75 79547 NG75 75686 L50 11 LG50 12 L75 22 LG75 24 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned length 0 Genome fraction (%) 95.368 Duplication ratio 1.003 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.95 Largest alignment 330825 NA50 149239 NGA50 132163 NA75 79547 NGA75 75686 LA50 11 LGA50 12 LA75 22	# contigs (>= 1000 bp)	
# contigs (>= 25000 bp)		49
# contigs (>= 25000 bp)	# contigs (>= 10000 bp)	47
# contigs (>= 50000 bp) 28 Total length (>= 1000 bp) 4415110 Total length (>= 5000 bp) 4368531 Total length (>= 10000 bp) 4354332 Total length (>= 25000 bp) 4245246 Total length (>= 50000 bp) 3796503 # contigs 112 Largest contig 330825 Total length 4442118 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.79 N50 149239 NG50 132163 N75 79547 NG75 75686 L50 11 LG50 11 LG50 12 L75 22 LG75 24 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 10 # local misassemblies 1 # unaligned length 0 Genome fraction (%) 95.368 Duplication ratio 1.003 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.95 Largest alignment 330825 NA50 132163 NA75 79547 NGA75 75686 LAGO 112 LAGSO 132163 NA75 79547 NGA75 75686 LAGO 132163 NA75 79547 NGA75 75686 LAGO 132163 NA75 79547 NGA75 75686		41
Total length (>= 5000 bp)		28
Total length (>= 10000 bp)	Total length (>= 1000 bp)	4415110
Total length (>= 25000 bp)	Total length (>= 5000 bp)	4368531
# contigs 112 Largest contig 330825 Total length (>= 50000 bp) 4442118 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.79 N50 149239 NG50 132163 N75 79547 NG75 75686 L50 11 LG50 12 L75 22 LG75 24 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 95.368 Duplication ratio 1.003 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.95 Largest alignment 330825 NA50 132163 NA75 79547 NGA75 75686 LA50 11 LGA50 12 LA75 22	Total length (>= 10000 bp)	4354332
# contigs 112 Largest contig 330825 Total length 4442118 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.79 N50 149239 NG50 132163 N75 79547 NG75 75686 L50 11 LG50 11 LG50 12 L75 22 LG75 24 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 10 # local misassemblies 1 # unaligned length 0 Genome fraction (%) 95.368 Duplication ratio 1.003 # N's per 100 kbp 0.00 # mismatches per 100 kbp 10.95 Largest alignment 330825 NA50 149239 NGA50 132163 NA75 79547 NGA75 75686 LA50 11 LGA50 12 LA75 22	Total length (>= 25000 bp)	4245246
Largest contig 330825 Total length 4442118 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.79 N50 149239 NG50 132163 N75 79547 NG75 75686 L50 11 LG50 12 L75 22 LG75 24 # misassemblies 0 Misassembled contigs 0 Misassembled contigs 0 Unaligned length 0 Genome fraction (%) 95.368 Duplication ratio 1.003 # N's per 100 kbp 0.00 # mismatches per 100 kbp 810.86 # indels per 100 kbp 0.95 Largest alignment 330825 NA50 149239 NGA50 132163 NA75 79547 NGA75 75686 LA50 11 LGA50 12 LA7	Total length (>= 50000 bp)	3796503
Total length 4442118 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.79 N50 149239 NG50 132163 N75 79547 NG75 75686 L50 11 LG50 12 L75 22 LG75 24 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 95.368 Duplication ratio 1.003 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.95 Largest alignment 330825 NA50 149239 NGA50 132163 NA75 79547 NGA75 75686 LA50 11 LGA50 12	# contigs	112
Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.79 N50 149239 NG50 132163 N75 79547 NG75 75686 L50 11 LG50 12 L75 22 LG75 24 # misassemblies 0 # local misassembled contigs 0 Misassembled contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 95.368 Duplication ratio 1.003 # N's per 100 kbp 0.00 # mismatches per 100 kbp 810.86 # indels per 100 kbp 0.95 Largest alignment 330825 NA50 149239 NGA50 132163 NA75 79547 NGA75 75686 LA50 11 LGA50 12 LA75 22	Largest contig	330825
GC (%) 50.78 Reference GC (%) 50.79 N50 149239 NG50 132163 N75 79547 NG75 75686 L50 11 LG50 12 L75 22 LG75 24 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 95.368 Duplication ratio 1.003 # N's per 100 kbp 0.00 # mismatches per 100 kbp 810.86 # indels per 100 kbp 0.95 Largest alignment 330825 NA50 149239 NGA50 132163 NA75 79547 NGA75 75686 LA50 11 LGA50 12 LA75 22	Total length	4442118
Reference GC (%) 50.79 N50 149239 NG50 132163 N75 79547 NG75 75686 L50 11 LG50 12 L75 22 LG75 24 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 95.368 Duplication ratio 1.003 # N's per 100 kbp 0.00 # mismatches per 100 kbp 810.86 # indels per 100 kbp 0.95 Largest alignment 330825 NA50 149239 NGA50 132163 NA75 79547 NGA75 75686 LA50 11 LGA50 12 LA75 22	Reference length	4641652
N50 149239 NG50 132163 N75 79547 NG75 75686 L50 11 LG50 12 L75 22 LG75 24 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 95.368 Duplication ratio 1.003 # N's per 100 kbp 0.00 # mismatches per 100 kbp 810.86 # indels per 100 kbp 0.95 Largest alignment 330825 NA50 149239 NGA50 132163 NA75 79547 NGA75 75686 LA50 11 LGA50 12 LA75 22	GC (%)	50.78
NG50 132163 N75 79547 NG75 75686 L50 11 LG50 12 L75 22 LG75 24 # misassemblies 0 Misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 95.368 Duplication ratio 1.003 # N's per 100 kbp 0.00 # mismatches per 100 kbp 810.86 # indels per 100 kbp 0.95 Largest alignment 330825 NA50 149239 NGA50 132163 NA75 79547 NGA75 75686 LA50 11 LGA50 12 LA75 22	Reference GC (%)	50.79
N75 79547 NG75 75686 L50 11 LG50 12 L75 22 LG75 24 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 95.368 Duplication ratio 1.003 # N's per 100 kbp 0.00 # mismatches per 100 kbp 810.86 # indels per 100 kbp 0.95 Largest alignment 330825 NA50 149239 NGA50 132163 NA75 79547 NGA75 75686 LA50 11 LGA50 12 LA75 22	N50	149239
NG75 75686 L50 11 LG50 12 L75 22 LG75 24 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 95.368 Duplication ratio 1.003 # N's per 100 kbp 0.00 # mismatches per 100 kbp 810.86 # indels per 100 kbp 0.95 Largest alignment 330825 NA50 149239 NGA50 132163 NA75 79547 NGA75 75686 LA50 11 LGA50 12 LA75 22	NG50	132163
L50 11 LG50 12 L75 22 LG75 24 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 95.368 Duplication ratio 1.003 # N's per 100 kbp 0.00 # mismatches per 100 kbp 810.86 # indels per 100 kbp 0.95 Largest alignment 330825 NA50 149239 NGA50 132163 NA75 79547 NGA75 75686 LA50 11 LGA50 12 LA75 22	N75	79547
LG50 12 L75 22 LG75 24 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 95.368 Duplication ratio 1.003 # N's per 100 kbp 0.00 # mismatches per 100 kbp 810.86 # indels per 100 kbp 0.95 Largest alignment 330825 NA50 149239 NGA50 132163 NA75 79547 NGA75 75686 LA50 11 LGA50 12 LA75 22	NG75	75686
L75 22 LG75 24 # misassemblies 0 Misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 95.368 Duplication ratio 1.003 # N's per 100 kbp 0.00 # mismatches per 100 kbp 810.86 # indels per 100 kbp 0.95 Largest alignment 330825 NA50 149239 NGA50 132163 NA75 79547 NGA75 75686 LA50 11 LGA50 12 LA75 22	L50	11
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 95.368 Duplication ratio 1.003 # N's per 100 kbp 0.00 # mismatches per 100 kbp 810.86 # indels per 100 kbp 0.95 Largest alignment 330825 NA50 149239 NGA50 132163 NA75 79547 NGA75 75686 LA50 11 LGA50 122	LG50	12
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 95.368 Duplication ratio 1.003 # N's per 100 kbp 0.00 # mismatches per 100 kbp 810.86 # indels per 100 kbp 0.95 Largest alignment 330825 NA50 149239 NGA50 132163 NA75 79547 NGA75 75686 LA50 11 LGA50 12	L75	22
# misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 95.368 Duplication ratio 1.003 # N's per 100 kbp 0.00 # mismatches per 100 kbp 810.86 # indels per 100 kbp 0.95 Largest alignment 330825 NA50 149239 NGA50 132163 NA75 79547 NGA75 75686 LA50 11 LGA50 12	LG75	24
Misassembled contigs length 0 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 95.368 Duplication ratio 1.003 # N's per 100 kbp 0.00 # mismatches per 100 kbp 810.86 # indels per 100 kbp 0.95 Largest alignment 330825 NA50 149239 NGA50 132163 NA75 79547 NGA75 75686 LA50 11 LGA50 12 LA75 22	# misassemblies	0
# local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 95.368 Duplication ratio 1.003 # N's per 100 kbp 0.00 # mismatches per 100 kbp 810.86 # indels per 100 kbp 0.95 Largest alignment 330825 NA50 149239 NGA50 132163 NA75 79547 NGA75 75686 LA50 11 LGA50 122	# misassembled contigs	0
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 95.368 Duplication ratio 1.003 # N's per 100 kbp 0.00 # mismatches per 100 kbp 810.86 # indels per 100 kbp 0.95 Largest alignment 330825 NA50 149239 NGA50 132163 NA75 79547 NGA75 75686 LA50 11 LGA50 12	Misassembled contigs length	0
Unaligned length 0 Genome fraction (%) 95.368 Duplication ratio 1.003 # N's per 100 kbp 0.00 # mismatches per 100 kbp 810.86 # indels per 100 kbp 0.95 Largest alignment 330825 NA50 149239 NGA50 132163 NA75 79547 NGA75 75686 LA50 11 LGA50 12 LA75 22	# local misassemblies	1
Genome fraction (%) 95.368 Duplication ratio 1.003 # N's per 100 kbp 0.00 # mismatches per 100 kbp 810.86 # indels per 100 kbp 0.95 Largest alignment 330825 NA50 149239 NGA50 132163 NA75 79547 NGA75 75686 LA50 11 LGA50 12 LA75 22	# unaligned contigs	0 + 0 part
Duplication ratio 1.003 # N's per 100 kbp 0.00 # mismatches per 100 kbp 810.86 # indels per 100 kbp 0.95 Largest alignment 330825 NA50 149239 NGA50 132163 NA75 79547 NGA75 75686 LA50 11 LGA50 12 LA75 22	Unaligned length	0
# N's per 100 kbp 0.00 # mismatches per 100 kbp 810.86 # indels per 100 kbp 0.95 Largest alignment 330825 NA50 149239 NGA50 132163 NA75 79547 NGA75 75686 LA50 11 LGA50 12 LA75 22	Genome fraction (%)	95.368
# mismatches per 100 kbp 810.86 # indels per 100 kbp 0.95 Largest alignment 330825 NA50 149239 NGA50 132163 NA75 79547 NGA75 75686 LA50 11 LGA50 12 LA75 22	Duplication ratio	1.003
# indels per 100 kbp 0.95 Largest alignment 330825 NA50 149239 NGA50 132163 NA75 79547 NGA75 75686 LA50 11 LGA50 12 LA75 22	# N's per 100 kbp	
Largest alignment 330825 NA50 149239 NGA50 132163 NA75 79547 NGA75 75686 LA50 11 LGA50 12 LA75 22	# mismatches per 100 kbp	810.86
NA50 149239 NGA50 132163 NA75 79547 NGA75 75686 LA50 11 LGA50 12 LA75 22	# indels per 100 kbp	
NGA50 132163 NA75 79547 NGA75 75686 LA50 11 LGA50 12 LA75 22	Largest alignment	330825
NA75 79547 NGA75 75686 LA50 11 LGA50 12 LA75 22	NA50	149239
NGA75 75686 LA50 11 LGA50 12 LA75 22		
LA50 11 LGA50 12 LA75 22		
LGA50 12 LA75 22		75686
LA75 22		
LGA75 24		
	LGA75	24

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	1
# mismatches	35894
# indels	42
# short indels	42
# long indels	0
Indels length	48

All statistics are based on contigs of size \geq 500 bp, unless otherwise noted (e.g., "# contigs (\geq 0 bp)" and "Total length (\geq 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	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).















