## Report

# contigs (>= 1000 bp)		scaffolds
# contigs (>= 5000 bp)	# contigs (>= 1000 bp)	
# contigs (>= 10000 bp)		81
# contigs (>= 25000 bp) 49 # contigs (>= 50000 bp) 30 Total length (>= 1000 bp) 4546459 Total length (>= 5000 bp) 4504936 Total length (>= 10000 bp) 4403489 Total length (>= 25000 bp) 4111791 Total length (>= 50000 bp) 3453079 # contigs 103 Largest contig 327367 Total length 4548491 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 105658 NG50 105658 NG50 105658 N75 53520 NG75 48989 L50 14 LG50 14 LG50 14 L75 30 LG75 31 # misassemblies 10 # misassembled contigs 10 Misassembled contigs 10 Misassembled contigs 10 Misassembled contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.962 Duplication ratio 1.000 # N's per 100 kbp 9.65 Largest alignment 327367 NGA50 82766 NA75 43798 NGA75 43798 NGA75 42166 LA50 15 LA75 32		67
# contigs (>= 50000 bp) 30  Total length (>= 1000 bp) 4546459  Total length (>= 5000 bp) 4504936  Total length (>= 10000 bp) 4403489  Total length (>= 25000 bp) 4111791  Total length (>= 50000 bp) 3453079  # contigs 103  Largest contig 327367  Total length 4548491  Reference length 4641652  GC (%) 50.74  Reference GC (%) 50.79  N50 105658  N75 53520  NG75 48989  L50 14  LG50 14  L75 30  LG75 31  # misassemblies 10  # misassembled contigs 10  Misassembled contigs 10  Misassembled contigs 10  Misassembled contigs 10  Misassembled contigs 0 + 0 part  Unaligned length 0  Genome fraction (%) 97.962  Duplication ratio 1.000  # N's per 100 kbp 9.65  Largest alignment 327367  NA50 95467  NA50 95467  NA50 10568  NA75 43798  NGA75 42166  LA50 14  LGA50 15  LA75 32		49
Total length (>= 5000 bp)		30
Total length (>= 10000 bp)	Total length (>= 1000 bp)	4546459
Total length (>= 25000 bp)  4111791  Total length (>= 50000 bp)  3453079  # contigs	Total length (>= 5000 bp)	4504936
# contigs 103 Largest contig 327367 Total length 4548491 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 105658 NG50 105658 N75 53520 NG75 48989 L50 14 LG50 14 L75 30 LG75 31 # misassemblies 10 # misassembled contigs 10 Misassembled contigs 10 Misassembled contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.962 Duplication ratio 1.000 # N's per 100 kbp 9.65 Largest alignment 327367 NA50 95467 NGA50 82766 NA75 43798 NGA75 42166 LA50 14 LGA50 15	Total length (>= 10000 bp)	4403489
# contigs 103 Largest contig 327367 Total length 4548491 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 105658 NG50 105658 N75 53520 NG75 48989 L50 14 LG50 14 LG50 14 LG50 14 L75 30 LG75 31 # misassemblies 10 # misassembled contigs 10 Misassembled contigs 10 Misassembled contigs 8 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.962 Duplication ratio 1.000 # N's per 100 kbp 9.65 Largest alignment 327367 NA50 95467 NGA50 82766 NA75 43798 NGA75 42166 LA50 14 LGA50 15 LA75 30	Total length (>= 25000 bp)	4111791
Largest contig       327367         Total length       4548491         Reference length       4641652         GC (%)       50.74         Reference GC (%)       50.79         N50       105658         NG50       105658         N75       53520         NG75       48989         L50       14         LG50       14         L75       30         LG75       31         # misassemblies       10         Misassembled contigs       10         Misassembled contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       97.962         Duplication ratio       1.000         # N's per 100 kbp       27.77         # mismatches per 100 kbp       64.86         # indels per 100 kbp       9.65         Largest alignment       327367         NA50       95467         NGA50       82766         NA75       43798         NGA75       42166         LA50       14         LGA50       15         LA75       32	Total length (>= 50000 bp)	3453079
Total length Reference length Reference length GC (%) S0.74 Reference GC (%) N50 N50 N50 N650 N650 N675 N675 L50 L50 L75 S30 L675 # misassembled contigs # misassembled contigs length # local misassemblies # unaligned contigs Unaligned length Genome fraction (%) Duplication ratio Wis per 100 kbp # mismatches per 100 kbp Largest alignment N450 N675 N675 N676 N6775 N676 N6775 N6	# contigs	103
Reference length       4641652         GC (%)       50.74         Reference GC (%)       50.79         N50       105658         NG50       105658         N75       53520         NG75       48989         L50       14         LG50       14         L75       30         LG75       31         # misassemblies       10         # misassembled contigs       10         Misassembled contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       97.962         Duplication ratio       1.000         # N's per 100 kbp       27.77         # mismatches per 100 kbp       64.86         # indels per 100 kbp       9.65         Largest alignment       327367         NA50       95467         NGA50       82766         NA75       43798         NGA75       42166         LA50       14         LGA50       15         LA75       32	Largest contig	327367
GC (%)       50.74         Reference GC (%)       50.79         N50       105658         NG50       105658         N75       53520         NG75       48989         L50       14         LG50       14         L75       30         LG75       31         # misassemblies       10         # misassembled contigs       10         Misassembled contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       97.962         Duplication ratio       1.000         # N's per 100 kbp       27.77         # mismatches per 100 kbp       64.86         # indels per 100 kbp       9.65         Largest alignment       327367         NA50       95467         NGA50       82766         NA75       43798         NGA75       42166         LA50       14         LGA50       15         LA75       32	Total length	4548491
Reference GC (%)       50.79         N50       105658         NG50       105658         N75       53520         NG75       48989         L50       14         LG50       14         L75       30         LG75       31         # misassemblies       10         # misassembled contigs       10         Misassembled contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       97.962         Duplication ratio       1.000         # N's per 100 kbp       27.77         # mismatches per 100 kbp       64.86         # indels per 100 kbp       9.65         Largest alignment       327367         NA50       95467         NGA50       82766         NA75       43798         NGA75       42166         LA50       14         LGA50       15         LA75       32	Reference length	4641652
N50       105658         NG50       105658         N75       53520         NG75       48989         L50       14         LG50       14         L75       30         LG75       31         # misassemblies       10         # misassembled contigs       10         Misassembled contigs       0 + 0 part         # local misassemblies       8         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       97.962         Duplication ratio       1.000         # N's per 100 kbp       27.77         # mismatches per 100 kbp       64.86         # indels per 100 kbp       9.65         Largest alignment       327367         NA50       95467         NGA50       82766         NA75       43798         NGA75       42166         LA50       14         LGA50       15         LA75       32	GC (%)	50.74
NG50       105658         N75       53520         NG75       48989         L50       14         LG50       14         L75       30         LG75       31         # misassemblies       10         Misassembled contigs       10         Misassembled contigs       624215         # local misassemblies       8         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       97.962         Duplication ratio       1.000         # N's per 100 kbp       27.77         # mismatches per 100 kbp       64.86         # indels per 100 kbp       9.65         Largest alignment       327367         NA50       95467         NGA50       82766         NA75       43798         NGA75       42166         LA50       14         LGA50       15         LA75       32	Reference GC (%)	50.79
N75       53520         NG75       48989         L50       14         LG50       14         L75       30         LG75       31         # misassemblies       10         # misassembled contigs       10         Misassembled contigs       624215         # local misassemblies       8         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       97.962         Duplication ratio       1.000         # N's per 100 kbp       27.77         # mismatches per 100 kbp       64.86         # indels per 100 kbp       9.65         Largest alignment       327367         NA50       95467         NGA50       82766         NA75       43798         NGA75       42166         LA50       14         LGA50       15         LA75       32	N50	105658
NG75       48989         L50       14         LG50       14         L75       30         LG75       31         # misassemblies       10         # misassembled contigs       10         Misassembled contigs       624215         # local misassemblies       8         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       97.962         Duplication ratio       1.000         # N's per 100 kbp       27.77         # mismatches per 100 kbp       64.86         # indels per 100 kbp       9.65         Largest alignment       327367         NA50       95467         NGA50       82766         NA75       43798         NGA75       42166         LA50       14         LGA50       15         LA75       32	NG50	105658
L50 14  LG50 14  LG50 14  L75 30  LG75 31  # misassemblies 10  # misassembled contigs 10  Misassembled contigs length 624215  # local misassemblies 8  # unaligned contigs 0 + 0 part  Unaligned length 0  Genome fraction (%) 97.962  Duplication ratio 1.000  # N's per 100 kbp 27.77  # mismatches per 100 kbp 64.86  # indels per 100 kbp 9.65  Largest alignment 327367  NA50 95467  NGA50 82766  NA75 43798  NGA75 42166  LA50 14  LGA50 15	N75	53520
LG50       14         L75       30         LG75       31         # misassemblies       10         # misassembled contigs       10         Misassembled contigs       10         Misassembled contigs       624215         # local misassemblies       8         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       97.962         Duplication ratio       1.000         # N's per 100 kbp       27.77         # mismatches per 100 kbp       64.86         # indels per 100 kbp       9.65         Largest alignment       327367         NA50       95467         NGA50       82766         NA75       43798         NGA75       42166         LA50       14         LGA50       15         LA75       32	NG75	48989
L75       30         LG75       31         # misassemblies       10         # misassembled contigs       10         Misassembled contigs length       624215         # local misassemblies       8         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       97.962         Duplication ratio       1.000         # N's per 100 kbp       27.77         # mismatches per 100 kbp       64.86         # indels per 100 kbp       9.65         Largest alignment       327367         NA50       95467         NGA50       82766         NA75       43798         NGA75       42166         LA50       14         LGA50       15         LA75       32	L50	14
LG75       31         # misassemblies       10         # misassembled contigs       10         Misassembled contigs length       624215         # local misassemblies       8         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       97.962         Duplication ratio       1.000         # N's per 100 kbp       27.77         # mismatches per 100 kbp       64.86         # indels per 100 kbp       9.65         Largest alignment       327367         NA50       95467         NGA50       82766         NA75       43798         NGA75       42166         LA50       14         LGA50       15         LA75       32	LG50	14
# misassemblies 10 # misassembled contigs 10 Misassembled contigs length 624215 # local misassemblies 8 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.962 Duplication ratio 1.000 # N's per 100 kbp 27.77 # mismatches per 100 kbp 64.86 # indels per 100 kbp 9.65 Largest alignment 327367 NA50 95467 NGA50 82766 NA75 43798 NGA75 42166 LA50 14 LGA50 15	L75	30
# misassembled contigs 10  Misassembled contigs length 624215  # local misassemblies 8  # unaligned contigs 0 + 0 part  Unaligned length 0  Genome fraction (%) 97.962  Duplication ratio 1.000  # N's per 100 kbp 27.77  # mismatches per 100 kbp 64.86  # indels per 100 kbp 9.65  Largest alignment 327367  NA50 95467  NGA50 82766  NA75 43798  NGA75 42166  LA50 14  LGA50 15  LA75 32	LG75	31
Misassembled contigs length         624215           # local misassemblies         8           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         97.962           Duplication ratio         1.000           # N's per 100 kbp         27.77           # mismatches per 100 kbp         64.86           # indels per 100 kbp         9.65           Largest alignment         327367           NA50         95467           NGA50         82766           NA75         43798           NGA75         42166           LA50         14           LGA50         15           LA75         32	# misassemblies	10
# local misassemblies 8 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.962 Duplication ratio 1.000 # N's per 100 kbp 27.77 # mismatches per 100 kbp 64.86 # indels per 100 kbp 9.65 Largest alignment 327367 NA50 95467 NGA50 82766 NA75 43798 NGA75 42166 LA50 14 LGA50 15	# misassembled contigs	10
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.962 Duplication ratio 1.000 # N's per 100 kbp 27.77 # mismatches per 100 kbp 64.86 # indels per 100 kbp 9.65 Largest alignment 327367 NA50 95467 NGA50 82766 NA75 43798 NGA75 42166 LA50 14 LGA50 15 LA75 32	Misassembled contigs length	624215
Unaligned length       0         Genome fraction (%)       97.962         Duplication ratio       1.000         # N's per 100 kbp       27.77         # mismatches per 100 kbp       64.86         # indels per 100 kbp       9.65         Largest alignment       327367         NA50       95467         NGA50       82766         NA75       43798         NGA75       42166         LA50       14         LGA50       15         LA75       32	# local misassemblies	8
Genome fraction (%)       97.962         Duplication ratio       1.000         # N's per 100 kbp       27.77         # mismatches per 100 kbp       64.86         # indels per 100 kbp       9.65         Largest alignment       327367         NA50       95467         NGA50       82766         NA75       43798         NGA75       42166         LA50       14         LGA50       15         LA75       32	# unaligned contigs	0 + 0 part
Duplication ratio       1.000         # N's per 100 kbp       27.77         # mismatches per 100 kbp       64.86         # indels per 100 kbp       9.65         Largest alignment       327367         NA50       95467         NGA50       82766         NA75       43798         NGA75       42166         LA50       14         LGA50       15         LA75       32	Unaligned length	0
# N's per 100 kbp 27.77  # mismatches per 100 kbp 64.86  # indels per 100 kbp 9.65  Largest alignment 327367  NA50 95467  NGA50 82766  NA75 43798  NGA75 42166  LA50 14  LGA50 15  LA75 32	Genome fraction (%)	97.962
# mismatches per 100 kbp 64.86 # indels per 100 kbp 9.65 Largest alignment 327367 NA50 95467 NGA50 82766 NA75 43798 NGA75 42166 LA50 14 LGA50 15 LA75 32	Duplication ratio	1.000
# indels per 100 kbp 9.65 Largest alignment 327367 NA50 95467 NGA50 82766 NA75 43798 NGA75 42166 LA50 14 LGA50 15 LA75 32	# N's per 100 kbp	27.77
Largest alignment       327367         NA50       95467         NGA50       82766         NA75       43798         NGA75       42166         LA50       14         LGA50       15         LA75       32		
NA50     95467       NGA50     82766       NA75     43798       NGA75     42166       LA50     14       LGA50     15       LA75     32	# indels per 100 kbp	
NGA50       82766         NA75       43798         NGA75       42166         LA50       14         LGA50       15         LA75       32	Largest alignment	327367
NA75     43798       NGA75     42166       LA50     14       LGA50     15       LA75     32	NA50	95467
NGA75       42166         LA50       14         LGA50       15         LA75       32		82766
LA50     14       LGA50     15       LA75     32		
LGA50 15 LA75 32	NGA75	42166
LA75 32		
		15
LGA75 34		
	LGA75	34

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	10
# relocations	10
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	10
Misassembled contigs length	624215
# local misassemblies	8
# mismatches	2949
# indels	439
# short indels	409
# long indels	30
Indels length	1107

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	1263

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).















