## Report

# contigs (>= 0 bp)		
# contigs (>= 1000 bp) 522 # contigs (>= 5000 bp) 518 # contigs (>= 10000 bp) 456 # contigs (>= 25000 bp) 125 # contigs (>= 50000 bp) 62 Total length (>= 0 bp) 33628515 Total length (>= 1000 bp) 33628515 Total length (>= 1000 bp) 33628515 Total length (>= 5000 bp) 33628515 Total length (>= 10000 bp) 33094350 Total length (>= 25000 bp) 27736641 Total length (>= 50000 bp) 25778906 # contigs 522 Largest contig 2322263 Total length 33628515 Reference length 33643051 GC (%) 31.15 Reference GC (%) 31.13 N50 446274 N75 84359 NG75 84359 L50 19 LG50 19 LG50 19 LG50 19 L75 54 # misassembles 7 # misassembled contigs 6 Misassembled contigs 6 Misassembled contigs 90 # unaligned mis. contigs 0 # unaligned length 0 Genome fraction (%) 99.924 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 236.12 # indels per 100 kbp 102.66 Largest alignment 2322168 Total aligned length 33626778 NA50 407732 NA50 407732 NA50 407732 NA50 407732 NA50 23 LA50 23 LA50 23 LA55 60		corrected_DNA
# contigs (>= 5000 bp)		
# contigs (>= 10000 bp)		
# contigs (>= 25000 bp)		
# contigs (>= 50000 bp) 62  Total length (>= 0 bp) 33628515  Total length (>= 1000 bp) 33628515  Total length (>= 5000 bp) 33617261  Total length (>= 10000 bp) 33094350  Total length (>= 25000 bp) 27736641  Total length (>= 50000 bp) 25778906  # contigs 522  Largest contig 2322263  Total length 33628515  Reference length 33643051  GC (%) 31.15  Reference GC (%) 31.15  Reference GC (%) 31.13  N50 446274  N75 84359  NG75 84359  L50 19  L650 19  L75 54  LG75 54  # misassembled contigs 6  Misassembled contigs 6  Misassembled contigs 16  Misassembled contigs 10  # unaligned mis. contigs 0  # unaligned length 0  Genome fraction (%) 99.924  Duplication ratio 1.000  # N's per 100 kbp 0.00  # mismatches per 100 kbp 102.66  Largest alignment 2322168  Total aligned length 33626778  NA50 407732  NA50 407732  NA75 84359  LA50 23  LA50 23  LA75 660		
Total length (>= 0 bp)         33628515           Total length (>= 1000 bp)         33628515           Total length (>= 5000 bp)         33617261           Total length (>= 10000 bp)         33094350           Total length (>= 25000 bp)         27736641           Total length (>= 50000 bp)         25778906           # contigs         522           Largest contig         2322263           Total length         33628515           Reference length         33643051           GC (%)         31.13           N50         446274           NG50         446274           N75         84359           L50         19           L650         19           L75         54           LG75         54           # misassemblies         7           # misassembled contigs         6           Misassembled contigs length         5953694           # local misassemblies         33           # unaligned length         0           Genome fraction (%)         99.924           Duplication ratio         1.000           # N's per 100 kbp         0.00           # indels per 100 kbp         102.66		
Total length (>= 1000 bp)         33628515           Total length (>= 5000 bp)         33617261           Total length (>= 10000 bp)         33094350           Total length (>= 25000 bp)         27736641           Total length (>= 50000 bp)         25778906           # contigs         522           Largest contig         2322263           Total length         33628515           Reference length         33643051           GC (%)         31.13           NS0         446274           NG50         446274           N75         84359           L50         19           L50         19           L50         19           L75         54           LG75         54           # misassemblies         7           # misassembled contigs length         5953694           # local misassemblies         33           # unaligned length         0           Genome fraction (%)         99.924           Duplication ratio         1.000           # N's per 100 kbp         0.00           # mismatches per 100 kbp         236.12           # indels per 100 kbp         102.66           Largest al		
Total length (>= 5000 bp)         33617261           Total length (>= 10000 bp)         33094350           Total length (>= 25000 bp)         27736641           Total length (>= 50000 bp)         25778906           # contigs         522           Largest contig         2322263           Total length         33628515           Reference length         33643051           GC (%)         31.15           Reference GC (%)         31.13           N50         446274           NG50         446274           N75         84359           L50         19           L50         19           L75         54           # misassemblies         7           # misassembled contigs         6           Misassembled contigs length         5953694           # local misassemblies         33           # unaligned mis. contigs         0           # unaligned length         0           Genome fraction (%)         99.924           Duplication ratio         1.000           # N's per 100 kbp         0.00           # mismatches per 100 kbp         236.12           # indels per 100 kbp         236.12		
Total length (>= 10000 bp) 33094350  Total length (>= 25000 bp) 27736641  Total length (>= 50000 bp) 25778906  # contigs 522  Largest contig 2322263  Total length 33628515  Reference length 33643051  GC (%) 31.15  Reference GC (%) 31.13  N50 446274  N75 84359  NG75 84359  L50 19  LG50 19  L75 54  # misassembles 7  # misassembled contigs 6  Misassembled contigs 6  Misassembled contigs 19  # local misassemblies 33  # unaligned mis. contigs 0  # unaligned length 0  Genome fraction (%) 99.924  Duplication ratio 1.000  # N's per 100 kbp 0.00  # mismatches per 100 kbp 236.12  # indels per 100 kbp 102.66  Largest alignment 2322168  Total aligned length 33626778  NA50 407732  NGA50 23  LA50 23  LA75 60		
Total length (>= 25000 bp) 27736641  Total length (>= 50000 bp) 25778906  # contigs 522  Largest contig 2322263  Total length 33628515  Reference length 33643051  GC (%) 31.15  Reference GC (%) 31.13  N50 446274  N75 84359  N675 84359  L50 19  LG50 19  LG50 19  LG75 54  # misassembled contigs 6  Misassembled contigs 6  Misassembled contigs 7  # local misassemblies 33  # unaligned mis. contigs 0  # unaligned length 0  Genome fraction (%) 99.924  Duplication ratio 1.000  # N's per 100 kbp 0.00  # mismatches per 100 kbp 236.12  # indels per 100 kbp 102.66  Largest alignment 2322168  Total aligned length 33626778  NA50 407732  NGA50 407732  NGA50 23  LA50 23  LA50 23  LA75 60		<b>.</b>
Total length (>= 50000 bp)         25778906           # contigs         522           Largest contig         2322263           Total length         33628515           Reference length         33643051           GC (%)         31.15           Reference GC (%)         31.13           N50         446274           NG50         446274           N75         84359           L50         19           L50         19           LG50         19           L75         54           LG75         54           # misassemblies         7           # misassembled contigs         6           Misassembled contigs length         5953694           # local misassemblies         33           # unaligned length         0           Genome fraction (%)         99.924           Unaligned length         0           Genome fraction (%)         99.924           Duplication ratio         1.000           # N's per 100 kbp         0.00           # mismatches per 100 kbp         236.12           # indels per 100 kbp         102.66           Largest alignment         2322168		
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Largest contig         2322263           Total length         33628515           Reference length         33643051           GC (%)         31.15           Reference GC (%)         31.13           N50         446274           NG50         446274           N75         84359           NG75         84359           L50         19           LG50         19           L75         54           LG75         54           # misassemblies         7           # misassembled contigs         6           Misassembled contigs length         5953694           # local misassemblies         33           # unaligned mis. contigs         0           # unaligned length         0           Genome fraction (%)         99.924           Duplication ratio         1.000           # N's per 100 kbp         0.00           # mismatches per 100 kbp         236.12           # indels per 100 kbp         102.66           Largest alignment         2322168           Total aligned length         33626778           NA50         407732           NGA50         407732		
Total length         33628515           Reference length         33643051           GC (%)         31.15           Reference GC (%)         31.13           N50         446274           NG50         446274           N75         84359           NG75         84359           L50         19           L50         19           L75         54           LG75         54           # misassemblies         7           # misassembled contigs         6           Misassembled contigs length         5953694           # local misassemblies         33           # unaligned mis. contigs         0           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         99.924           Duplication ratio         1.000           # N's per 100 kbp         0.00           # mismatches per 100 kbp         236.12           # indels per 100 kbp         102.66           Largest alignment         2322168           Total aligned length         33626778           NA50         407732           NGA50         407732 <tr< td=""><td></td><td></td></tr<>		
Reference length         33643051           GC (%)         31.15           Reference GC (%)         31.13           N50         446274           NG50         446274           N75         84359           NG75         84359           L50         19           LG50         19           L75         54           LG75         54           # misassemblies         7           # misassembled contigs         6           Misassembled contigs length         5953694           # local misassemblies         33           # unaligned mis. contigs         0           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         99.924           Duplication ratio         1.000           # N's per 100 kbp         0.00           # mismatches per 100 kbp         102.66           Largest alignment         232.168           Total aligned length         33626778           NA50         407732           NGA50         407732           NGA50         407732           NGA50         407732           NGA50 <td></td> <td></td>		
GC (%)         31.15           Reference GC (%)         31.13           N50         446274           NG50         446274           N75         84359           NG75         84359           L50         19           LG50         19           L75         54           LG75         54           # misassemblies         7           # misassembled contigs         6           Misassembled contigs length         5953694           # local misassemblies         33           # unaligned mis. contigs         0           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         99.924           Duplication ratio         1.000           # N's per 100 kbp         0.00           # mismatches per 100 kbp         236.12           # indels per 100 kbp         102.66           Largest alignment         2322168           Total aligned length         33626778           NA50         407732           NGA50         407732           NGA50         407732           NGA50         407732           NGA75 </td <td></td> <td><b>.</b></td>		<b>.</b>
Reference GC (%)       31.13         N50       446274         NG50       446274         N75       84359         NG75       84359         L50       19         LG50       19         L75       54         LG75       54         # misassemblies       7         # misassembled contigs       6         Misassembled contigs length       5953694         # local misassemblies       33         # unaligned mis. contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.924         Duplication ratio       1.000         # N's per 100 kbp       0.00         # mismatches per 100 kbp       236.12         # indels per 100 kbp       102.66         Largest alignment       2322168         Total aligned length       33626778         NA50       407732         NGA50       407732         NA75       84359         LA50       23         LA50       23         LA50       23         LA75       60		
N50       446274         NG50       446274         N75       84359         NG75       84359         L50       19         LG50       19         L75       54         LG75       54         # misassemblies       7         # misassembled contigs       6         Misassembled contigs length       5953694         # local misassemblies       33         # unaligned mis. contigs       0         # unaligned length       0         Genome fraction (%)       99.924         Duplication ratio       1.000         # N's per 100 kbp       0.00         # mismatches per 100 kbp       236.12         # indels per 100 kbp       102.66         Largest alignment       2322168         Total aligned length       33626778         NA50       407732         NGA50       407732         NA75       84359         LA50       23         LA50       23         LA75       60		
NG50         446274           N75         84359           NG75         84359           L50         19           LG50         19           L75         54           LG75         54           # misassemblies         7           # misassembled contigs         6           Misassembled contigs length         5953694           # local misassemblies         33           # unaligned mis. contigs         0           # unaligned length         0           Genome fraction (%)         99.924           Duplication ratio         1.000           # N's per 100 kbp         0.00           # mismatches per 100 kbp         236.12           # indels per 100 kbp         102.66           Largest alignment         2322168           Total aligned length         33626778           NA50         407732           NGA50         407732           NA75         84359           LA50         23           LA50         23           LA75         60	Reference GC (%)	31.13
N75       84359         NG75       84359         L50       19         LG50       19         L75       54         LG75       54         # misassemblies       7         # misassembled contigs       6         Misassembled contigs length       5953694         # local misassemblies       33         # unaligned mis. contigs       0         # unaligned length       0         Genome fraction (%)       99.924         Duplication ratio       1.000         # N's per 100 kbp       0.00         # mismatches per 100 kbp       236.12         # indels per 100 kbp       102.66         Largest alignment       2322168         Total aligned length       33626778         NA50       407732         NGA50       407732         NA75       84359         LA50       23         LA50       23         LA75       60	N50	446274
NG75       84359         L50       19         LG50       19         L75       54         LG75       54         # misassemblies       7         # misassembled contigs       6         Misassembled contigs length       5953694         # local misassemblies       33         # unaligned mis. contigs       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.924         Duplication ratio       1.000         # N's per 100 kbp       0.00         # mismatches per 100 kbp       236.12         # indels per 100 kbp       102.66         Largest alignment       2322168         Total aligned length       33626778         NA50       407732         NGA50       407732         NA75       84359         NGA75       84359         LA50       23         LA75       60	NG50	446274
L50       19         LG50       19         L75       54         LG75       54         # misassemblies       7         # misassembled contigs       6         Misassembled contigs length       5953694         # local misassemblies       33         # unaligned mis. contigs       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.924         Duplication ratio       1.000         # N's per 100 kbp       0.00         # mismatches per 100 kbp       236.12         # indels per 100 kbp       102.66         Largest alignment       2322168         Total aligned length       33626778         NA50       407732         NGA50       407732         NA75       84359         NGA75       84359         LA50       23         LA75       60	N75	84359
LG50       19         L75       54         LG75       54         # misassemblies       7         # misassembled contigs       6         Misassembled contigs length       5953694         # local misassemblies       33         # unaligned mis. contigs       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.924         Duplication ratio       1.000         # N's per 100 kbp       0.00         # mismatches per 100 kbp       236.12         # indels per 100 kbp       102.66         Largest alignment       2322168         Total aligned length       33626778         NA50       407732         NGA50       407732         NA75       84359         LA50       23         LA50       23         LA75       60	NG75	84359
L75       54         LG75       54         # misassemblies       7         # misassembled contigs       6         Misassembled contigs length       5953694         # local misassemblies       33         # unaligned mis. contigs       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.924         Duplication ratio       1.000         # N's per 100 kbp       0.00         # mismatches per 100 kbp       236.12         # indels per 100 kbp       102.66         Largest alignment       2322168         Total aligned length       33626778         NA50       407732         NGA50       407732         NA75       84359         LA50       23         LA50       23         LA75       60	L50	19
# misassemblies 7  # misassembled contigs 6  Misassembled contigs length 5953694  # local misassemblies 33  # unaligned mis. contigs 0  # unaligned length 0  Genome fraction (%) 99.924  Duplication ratio 1.000  # N's per 100 kbp 0.00  # mismatches per 100 kbp 236.12  # indels per 100 kbp 102.66  Largest alignment 2322168  Total aligned length 33626778  NA50 407732  NGA50 407732  NGA50 407732  NGA75 84359  LA50 23  LGA50 23  LGA50 23	LG50	19
# misassemblies 7  # misassembled contigs 6  Misassembled contigs length 5953694  # local misassemblies 33  # unaligned mis. contigs 0  # unaligned length 0  Genome fraction (%) 99.924  Duplication ratio 1.000  # N's per 100 kbp 0.00  # mismatches per 100 kbp 236.12  # indels per 100 kbp 102.66  Largest alignment 2322168  Total aligned length 33626778  NA50 407732  NGA50 407732  NA75 84359  NGA75 84359  LA50 23  LGA50 23  LA75 60	L75	54
# misassembled contigs 6 Misassembled contigs length 5953694 # local misassemblies 33 # unaligned mis. contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.924 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 236.12 # indels per 100 kbp 102.66 Largest alignment 2322168 Total aligned length 33626778 NA50 407732 NGA50 407732 NA75 84359 NGA75 84359 LA50 23 LGA50 23 LGA50 23	LG75	54
Misassembled contigs length         5953694           # local misassemblies         33           # unaligned mis. contigs         0           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         99.924           Duplication ratio         1.000           # N's per 100 kbp         0.00           # mismatches per 100 kbp         236.12           # indels per 100 kbp         102.66           Largest alignment         2322168           Total aligned length         33626778           NA50         407732           NGA50         407732           NA75         84359           NGA75         84359           LA50         23           LA75         60	# misassemblies	7
# local misassemblies 33  # unaligned mis. contigs 0  # unaligned contigs 0 + 0 part  Unaligned length 0  Genome fraction (%) 99.924  Duplication ratio 1.000  # N's per 100 kbp 0.00  # mismatches per 100 kbp 102.66  Largest alignment 2322168  Total aligned length 33626778  NA50 407732  NGA50 407732  NA75 84359  NGA75 84359  LA50 23  LGA50 23  LA75 60	# misassembled contigs	6
# unaligned mis. contigs  # unaligned contigs  0 + 0 part  Unaligned length  Genome fraction (%)  99.924  Duplication ratio  1.000  # N's per 100 kbp  0.00  # mismatches per 100 kbp  102.66  Largest alignment  2322168  Total aligned length  33626778  NA50  407732  NGA50  NA75  84359  NGA75  84359  LA50  23  LGA50  23  LGA50  60	Misassembled contigs length	5953694
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.924 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 236.12 # indels per 100 kbp 102.66 Largest alignment 2322168 Total aligned length 33626778 NA50 407732 NGA50 407732 NGA50 407732 NGA75 84359 LA50 23 LGA50 23 LGA50 23	# local misassemblies	33
Unaligned length       0         Genome fraction (%)       99.924         Duplication ratio       1.000         # N's per 100 kbp       0.00         # mismatches per 100 kbp       236.12         # indels per 100 kbp       102.66         Largest alignment       2322168         Total aligned length       33626778         NA50       407732         NGA50       407732         NA75       84359         NGA75       84359         LA50       23         LA75       60	# unaligned mis. contigs	0
Genome fraction (%)       99.924         Duplication ratio       1.000         # N's per 100 kbp       0.00         # mismatches per 100 kbp       236.12         # indels per 100 kbp       102.66         Largest alignment       2322168         Total aligned length       33626778         NA50       407732         NGA50       407732         NA75       84359         NGA75       84359         LA50       23         LA75       60	# unaligned contigs	0 + 0 part
Duplication ratio         1.000           # N's per 100 kbp         0.00           # mismatches per 100 kbp         236.12           # indels per 100 kbp         102.66           Largest alignment         2322168           Total aligned length         33626778           NA50         407732           NGA50         407732           NA75         84359           NGA75         84359           LA50         23           LGA50         23           LA75         60	Unaligned length	0
# N's per 100 kbp 0.00 # mismatches per 100 kbp 236.12 # indels per 100 kbp 102.66 Largest alignment 2322168 Total aligned length 33626778 NA50 407732 NGA50 407732 NA75 84359 NGA75 84359 LA50 23 LGA50 23 LA75 60	Genome fraction (%)	99.924
# mismatches per 100 kbp 236.12 # indels per 100 kbp 102.66 Largest alignment 2322168 Total aligned length 33626778 NA50 407732 NGA50 407732 NA75 84359 NGA75 84359 LA50 23 LGA50 23 LA75 60	Duplication ratio	1.000
# indels per 100 kbp 102.66 Largest alignment 2322168 Total aligned length 33626778 NA50 407732 NGA50 407732 NA75 84359 NGA75 84359 LA50 23 LGA50 23 LA75 60	# N's per 100 kbp	0.00
Largest alignment       2322168         Total aligned length       33626778         NA50       407732         NGA50       407732         NA75       84359         NGA75       84359         LA50       23         LGA50       23         LA75       60	# mismatches per 100 kbp	236.12
Total aligned length         33626778           NA50         407732           NGA50         407732           NA75         84359           NGA75         84359           LA50         23           LGA50         23           LA75         60	# indels per 100 kbp	102.66
NA50     407732       NGA50     407732       NA75     84359       NGA75     84359       LA50     23       LGA50     23       LA75     60	Largest alignment	2322168
NGA50     407732       NA75     84359       NGA75     84359       LA50     23       LGA50     23       LA75     60	Total aligned length	33626778
NA75     84359       NGA75     84359       LA50     23       LGA50     23       LA75     60	NA50	407732
NGA75     84359       LA50     23       LGA50     23       LA75     60	NGA50	407732
LA50     23       LGA50     23       LA75     60	NA75	84359
LGA50 23 LA75 60	NGA75	84359
LA75 60	LA50	23
	LGA50	23
LGA75 60	LA75	60
I	LGA75	60

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

	corrected_DNA
# misassemblies	7
# relocations	7
# translocations	0
# inversions	0
# misassembled contigs	6
Misassembled contigs length	5953694
# local misassemblies	33
# unaligned mis. contigs	0
# mismatches	79377
# indels	34512
# indels (<= 5 bp)	32449
# indels (> 5 bp)	2063
Indels length	69935

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

	corrected_DNA
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	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).





















