# contigs (>= 0 bp) # contigs (>= 1000 bp) # contigs (>= 1000 bp) # contigs (>= 10000 bp) # contigs (>= 25000 bp) # contigs (>= 25000 bp) # contigs (>= 25000 bp) # contigs (>= 50000 bp) # contigs (>= 50000 bp) Total length (>= 0 bp) Total length (>= 10000 bp) Total length (>= 50000 bp) Total length (>= 50000 bp) Total length (>= 50000 bp) Total length (>= 25000 bp) Total length (>= 50000 bp) Total length (>= 50000 bp) Total length (>= 50000 bp) # contigs Largest contig Total length # contigs Understand # contigs  # massembled contigs # misassembled contigs # unaligned length # coal misassemblies # coal misassemblies # coal misassemblies # unaligned length # coal misassembles # unaligned contigs Unaligned length # coal misassembles # # coal misassemble	F	Report
# contigs (>= 1000 bp) # contigs (>= 5000 bp) # contigs (>= 5000 bp) # contigs (>= 25000 bp) # contigs (>= 25000 bp) # contigs (>= 25000 bp) # contigs (>= 50000 bp)  # contigs (>= 50000 bp)  # contigs (>= 50000 bp)  Total length (>= 1000 bp)  Total length (>= 1000 bp)  Total length (>= 10000 bp)  # contigs  Largest contig  Total length (>= 50000 bp) # contigs  Largest contig  Total length # contigs  NSO		min5_CFL_ICFL_30_COMB_100
# contigs (>= 5000 bp) # contigs (>= 10000 bp) # contigs (>= 10000 bp) # contigs (>= 25000 bp) # contigs (>= 25000 bp) # contigs (>= 50000 bp) # contigs (>= 50000 bp) # contigs (>= 5000 bp) # contigs (>= 5000 bp) # contigs (>= 5000 bp) # contigs (>= 1000 bp) # contigs (>= 1000 bp) # contigs (>= 1000 bp) # contigs (>= 10000 bp) # contigs (>= 25000 bp) # contigs (>= 25000 bp) # contigs (>= 25000 bp) # contigs (==	# contigs (>= 0 bp)	3
# contigs (>= 10000 bp) # contigs (>= 25000 bp) # contigs (>= 25000 bp) # contigs (>= 50000 bp) Total length (>= 0 bp) Total length (>= 10000 bp) Total length (>= 10000 bp) Total length (>= 5000 bp) Total length (>= 5000 bp) Total length (>= 5000 bp) Total length (>= 50000 bp) Total length (>= 25000 bp) Total length (>= 25000 bp) Total length (>= 50000 bp) Total length	# contigs (>= 1000 bp)	3
# contigs (>= 25000 bp) # contigs (>= 50000 bp) # contigs (>= 50000 bp) Total length (>= 0 bp) # contigs (>= 50000 bp) Total length (>= 10000 bp) # contigs (>= 50000 bp) # contigs (>= 50000 bp) # contigs (>= 50000 bp) # contigs (>= 25000 bp) # contigs (>= 25000 bp) # contigs (>= 50000 bp) # contigs (>= 50000 bp) # contigs (>= 50000 bp) # contigs (>= 3980818 total length (>= 6000 bp) # contigs (>= 3980818 total length (>= 6000 bp) # contigs (>= 3980818 total length (>= 6000 bp) # contigs (>= 3980818 total length (>= 6000 bp) # contigs (>= 3980818 total length (>= 6000 bp) # contigs (>= 3980818 total length (>= 6000 bp) # contigs (>= 3980818 total length (>= 6000 bp) # contigs (>= 3980818 total length (>= 6000 bp) # contigs (>= 3980818 total length (>= 6000 bp) # contigs (>= 3980818 total length (>= 6000 bp) # contigs (>= 3980818 total length (>= 6000 bp) # contigs (>= 6000 bp) # conti	# contigs (>= 5000 bp)	3
# contigs (>= 50000 bp) Total length (>= 0 bp) Total length (>= 1000 bp) Total length (>= 1000 bp) Total length (>= 1000 bp) Total length (>= 50000 bp) Total length (>= 25000 bp) Total length (>= 25000 bp) Total length (>= 50000 bp) Total lingned length (>= 50000 bp) Total length (>= 50000 bp) Total lingned length (>= 50000 bp) Total le	# contigs (>= 10000 bp)	3
Total length (>= 0 bp)	# contigs (>= 25000 bp)	3
Total length (>= 1000 bp) 4699144 Total length (>= 5000 bp) 4699144 Total length (>= 5000 bp) 4699144 Total length (>= 25000 bp) 4699144 Total length (>= 50000 bp) 4699144 Total length (>= 50000 bp) 4699144 Total length (>= 50000 bp) 4699144 Reference length 4686133 GC (%) 50.77 Reference GC (%) 5	# contigs (>= 50000 bp)	3
Total length (>= 5000 bp)	Total length (>= 0 bp)	4699144
Total length (>= 10000 bp) 4699144 Total length (>= 25000 bp) 4699144 Total length (>= 50000 bp) 4699144 # contigs 3980818 Total length 4699144 Reference length 4686137 GC (%) 50.77 Reference GC (%) 50.78 Reference GC (%) 50.78 Reference GC (%) 3980818 ROSO 3980818	Total length (>= 1000 bp)	4699144
Total length (>= 25000 bp) 4699144 Total length (>= 50000 bp) 4699144 # contigs Largest contig 3980818 Total length 4699144 Reference length 4686133 GC (%) 50.77 Reference GC (%) 50.78 Reference GC (%) 50.7	Total length (>= 5000 bp)	4699144
Total length (>= 50000 bp)	Total length (>= 10000 bp)	4699144
# contigs Largest contig 13980818 Total length 14699144 Reference length 150.77 Reference GC (%) 150.7	Total length (>= 25000 bp)	4699144
Largest contig         3980818           Total length         4699144           Reference length         468613           GC (%)         50.77           Reference GC (%)         50.78           NSO         3980818           NSO         3444643.0           3454204.3         3454204.3           4         4650           LESO         3           LESO         3           LESO         3           LESO         3           LESO         3           Misassembled contigs         3           Misassembled contigs length         3           Misassembled contigs         3           Misassembled contigs         3           Unaligned length         3	Total length (>= 50000 bp)	4699144
Total length         4699144           Reference length         4686133           GC (%)         50.77           Reference GC (%)         3980818           NS0         3980818           NS90         561609           NG90         561609           auN         3444643.0           auNG         3454204.3           L50         3           LG50         3           LG90         2           # misassemblies         3           # misassembled contigs         3           Misassembled contigs length         3           # local misassemblies         3           # scaffold gap loc. mis.         3           # unaligned mis. contigs         3           # unaligned length         3           Genome fraction (%)         99.215           Unplication ratio         1.011           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.00           # aligned length         4699002           NA50         3980818           NA50         3980818           NA90         561602           NA90         561603           NA90         <	# contigs	3
Reference length       4686137         GC (%)       50.77         Reference GC (%)       50.77         N50       3980818         N90       561609         NG90       561609         auN       3444643.0         auNG       3454204.1         L50       1         LG50       2         LG90       2         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # scaffold gap ext. mis.       0         # scaffold gap loc. mis.       0         # unaligned mis. contigs       0         # unaligned length       0         Genome fraction (%)       99.215         Unaligned length       0         Genome fraction (%)       99.215         Undigned length       0         Majon       3980818         NA50       3980818         NA50       3980818         NA90       561609         NA90       561609         NA90       561609         auNA       3444633.6         auNGA <t< td=""><td>Largest contig</td><td>3980818</td></t<>	Largest contig	3980818
GC (%) 50.77  Reference GC (%) 50.78  N50 3980818  N50 3980818  N90 561609  NG90 561609  auN 3444643.0  auNG 3454204.1  L50 10  LG50 10  LG90 20  # misassemblies (contigs (misassembled contigs (misa	Total length	4699144
Reference GC (%)       50.76         N50       3980818         NG50       3980818         N90       561609         NG90       561609         auN       3444643.0         auNG       3454204.3         L50       1         LG50       1         L90       2         LG90       2         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # scaffold gap ext. mis.       0         # scaffold gap loc. mis.       0         # unaligned mis. contigs       0         # unaligned length       0         Genome fraction (%)       99.215         Duplication ratio       1.013         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         # indels per 100 kbp       0.00         # argest alignment       3980818         Total aligned length       4699002         NA50       3980818         NA90       561605         NA90       561605         NA90       561605         auNA       3444633.6	Reference length	4686137
N50       3980818         NG50       3980818         N90       561609         NG90       361609         auN       3444643.0         auNG       3454204.3         L50       3         LG50       3         L90       2         LG90       3         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # scaffold gap ext. mis.       0         # scaffold gap loc. mis.       0         # unaligned mis. contigs       0         # unaligned length       0         Genome fraction (%)       99.215         Duplication ratio       1.011         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         # indels per 100 kbp       0.00         Largest alignment       3980818         Total aligned length       4699002         NA50       3980818         NA90       561605         auNA       3444633.6         auNA       3444633.6         auNA       3454194.6 <tr< td=""><td>GC (%)</td><td>50.77</td></tr<>	GC (%)	50.77
N50       3980818         NG50       3980818         N90       561609         NG90       361609         auN       3444643.0         auNG       3454204.3         L50       3         LG50       3         L90       2         LG90       3         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # scaffold gap ext. mis.       0         # scaffold gap loc. mis.       0         # unaligned mis. contigs       0         # unaligned length       0         Genome fraction (%)       99.215         Duplication ratio       1.011         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         # indels per 100 kbp       0.00         Largest alignment       3980818         Total aligned length       4699002         NA50       3980818         NA90       561605         auNA       3444633.6         auNA       3444633.6         auNA       3454194.6 <tr< td=""><td>Reference GC (%)</td><td>50.78</td></tr<>	Reference GC (%)	50.78
N90         561605           NG90         561605           auN         3444643.0           auNG         3454204.1           L50         1           LG50         2           L90         2           LG90         3           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         0           # unaligned length         0           Genome fraction (%)         99.215           Duplication ratio         1.011           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.00           #	N50	3980818
N90         561605           NG90         561605           auN         3444643.0           auNG         3454204.1           L50         1           LG50         2           L90         2           LG90         3           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         0           # unaligned length         0           Genome fraction (%)         99.215           Duplication ratio         1.011           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.00           #		3980818
NG90       561605         auN       3444643.6         auNG       3454204.1         L50       1         LG50       2         L90       2         LG90       3         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # scaffold gap ext. mis.       0         # scaffold gap loc. mis.       0         # unaligned mis. contigs       0         # unaligned length       0         Genome fraction (%)       99.215         Duplication ratio       1.011         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         # indels per 100 kbp       0.00         # aligned length       4699002         NA50       3980818         NA90       561605         NA90       561605         auNA       3444633.6         auNA       3444633.6         auNA       3454194.6         LA50       1         LA90       2	N90	561605
auN 3444643.0 auNG 3454204.1 L50	NG90	
auNG L50 L50 LG50 L90 LG90 # misassemblies # misassembled contigs Misassembled contigs length # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned length Genome fraction (%) Duplication ratio # N's per 100 kbp # mismatches per 100 kbp # indels per 100 kbp Largest alignment Total aligned length NA50 NA50 NA90 S61605 NA90 S61605 auNA 3444633.6 auNGA LA50 LGA50 LA90  2  2  2  3  3  4  3  454194.6 2  3  4  46900 2  4  46900 3  4  46900 3  4  46900 3  4  46900 4600 46	auN	
L50 LG50 LG90 # misassemblies # misassembled contigs Misassembled contigs length # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned contigs Unaligned length Genome fraction (%) Duplication ratio # N's per 100 kbp # mismatches per 100 kbp # indels per 100 kbp Largest alignment Total aligned length NA50 NA50 NA90 S61605 NA90 auNA 3444633.6 auNGA LA50 LGA50 LA90  2   # misassemblies  (		
LG50 L90 LG90 # misassemblies # misassembled contigs Misassembled contigs length # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned contigs Unaligned length Genome fraction (%) Duplication ratio # N's per 100 kbp # mismatches per 100 kbp # indels per 100 kbp Largest alignment Total aligned length NA50 NA90 NGA90 Solon		1
L90 LG90 # misassemblies # misassembled contigs Misassembled contigs length # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned length Genome fraction (%) Duplication ratio # N's per 100 kbp # mismatches per 100 kbp # indels per 100 kbp Largest alignment Total aligned length NA50 NA90 NGA90 Solida Additional States Solida Additional Stat		1
# misassemblies		2
# misassemblies  # misassembled contigs Misassembled contigs length # local misassemblies  # scaffold gap ext. mis.  # scaffold gap loc. mis.  # unaligned mis. contigs  # unaligned contigs  Unaligned length  Genome fraction (%)  Duplication ratio  # N's per 100 kbp  # mismatches per 100 kbp  1.010  # mismatches per 100 kbp  Largest alignment  Total aligned length  NA50  NA90  NGA50  NA90  Solidon  Solidon		2
# misassembled contigs Misassembled contigs length # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned length Genome fraction (%) # by per 100 kbp # mismatches per 100 kbp # mismatches per 100 kbp # contigs and an analyse an		0
Misassembled contigs length         (0)           # local misassemblies         (0)           # scaffold gap ext. mis.         (0)           # scaffold gap loc. mis.         (0)           # unaligned mis. contigs         (0)           # unaligned contigs         (0)           Unaligned length         (0)           Genome fraction (%)         99.215           Duplication ratio         1.013           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.00           # indels per 100 kbp         0.00           Largest alignment         3980818           NA50         3980818           NA50         3980818           NA90         561605           NA90         561605           auNA         3444633.6           auNA         3454194.6           LA50         1           LA90         2		0
# local misassemblies (1) # scaffold gap ext. mis. (2) # scaffold gap loc. mis. (3) # unaligned mis. contigs (3) # unaligned contigs (4) # unaligned length (5) Genome fraction (%) (6) # N's per 100 kbp (7) # nismatches per 100 kbp (7) # nismatches per 100 kbp (7) # nidels per 100 kbp (7) # notal aligned length (4699002) # NA50 (7) # NA50 (7) # NA90 (		0
# scaffold gap ext. mis.  # scaffold gap loc. mis.  # unaligned mis. contigs  # unaligned contigs  O + 0 par  Unaligned length  Genome fraction (%)  Duplication ratio  # N's per 100 kbp  mismatches per 100 kbp  0.00  # mismatches per 100 kbp  1.013  1.01		0
# scaffold gap loc. mis.  # unaligned mis. contigs  # unaligned contigs  O + 0 par  Unaligned length  Genome fraction (%)  Duplication ratio  # N's per 100 kbp  # mismatches per 100 kbp  1.000  # mismatches per 100 kbp  Largest alignment  Total aligned length  NA50  NA50  NA90  Safe of the saf		
# unaligned mis. contigs  # unaligned contigs  0 + 0 par  Unaligned length  Genome fraction (%)  99.215  Duplication ratio  1.013  # N's per 100 kbp  0.00  # mismatches per 100 kbp  0.00  Largest alignment  3980818  Total aligned length  NA50  NA50  NA90  NGA50  NA90  Solidation  NA90  Solidation  NA90  Solidation  S		
# unaligned contigs		
Unaligned length (Common fraction (%) 99.215  Duplication ratio 1.011  # N's per 100 kbp 0.00  # mismatches per 100 kbp 0.00  # indels per 100 kbp 0.00  Largest alignment 3980818  Total aligned length 4699002  NA50 3980818  NA90 561605  NA90 561605  auNA 3444633.6  auNA 3454194.6  LA50 1  LA50 2  LA90 2		
Genome fraction (%)       99.215         Duplication ratio       1.011         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         # indels per 100 kbp       0.00         Largest alignment       3980818         Total aligned length       4699002         NA50       3980818         NA90       561605         NGA90       561605         auNA       3444633.6         auNGA       3454194.6         LA50       1         LA90       2		· ·
Duplication ratio       1.013         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         # indels per 100 kbp       0.00         Largest alignment       3980818         Total aligned length       4699002         NA50       3980818         NA90       561605         NGA90       561605         auNA       3444633.6         auNGA       3454194.6         LA50       1         LA90       2		
# N's per 100 kbp		
# mismatches per 100 kbp	· · · · · · · · · · · · · · · · · · ·	
# indels per 100 kbp 0.00 Largest alignment 3980818 Total aligned length 4699002 NA50 3980818 NGA50 3980818 NA90 561605 NGA90 561605 auNA 3444633.6 auNGA 3454194.6 LA50 1 LGA50 2		
Largest alignment       3980818         Total aligned length       4699002         NA50       3980818         NGA50       3980818         NA90       561605         NGA90       561605         auNA       3444633.6         auNGA       3454194.6         LA50       3         LGA50       3         LA90       2		
Total aligned length     4699002       NA50     3980818       NGA50     3980818       NA90     561605       NGA90     561605       auNA     3444633.6       auNGA     3454194.6       LA50     3       LGA50     3       LA90     2		
NA50     3980818       NGA50     3980818       NA90     561605       NGA90     561605       auNA     3444633.6       auNGA     3454194.6       LA50     1       LGA50     1       LA90     2		
NGA50 3980818 NA90 561605 NGA90 561605 auNA 3444633.6 auNGA 3454194.6 LA50 1 LGA50 1 LA90 2		
NA90     561605       NGA90     561605       auNA     3444633.6       auNGA     3454194.6       LA50     3       LGA50     3       LA90     2		
NGA90 561605 auNA 3444633.6 auNGA 3454194.6 LA50 5 LGA50 5 LA90 5		
auNA 3444633.6 auNGA 3454194.6 LA50 1 LGA50 1 LA90 2		
auNGA 3454194.6 LA50 1 LGA50 2 LA90 2		561605
LA50 3 LGA50 3 LA90 2		3444633.6
LGA50 1 LA90 2		3454194.6
LA90 2	LA50	1
		1
LGA90 2	LA90	2
	LGA90	2

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

	min5_CFL_ICFL_30_COMB_100
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	0
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	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).

## Unaligned report

	min5_CFL_ICFL_30_COMB_100
# 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).



















