# contigs (>= 0 bp) # contigs (>= 1000 bp) # contigs (>= 1000 bp) # contigs (>= 5000 bp) # contigs (>= 5000 bp) # contigs (>= 50000 bp) Total length (>= 0 bp) Total length (>= 1000 bp) Total length (>= 10000 bp) Total length (>= 50000 bp) Total l	Re	port CFL_ICFL_R_35_COMB_50
# contigs (>= 1000 bp) # contigs (>= 5000 bp) # contigs (>= 5000 bp) # contigs (>= 10000 bp) # contigs (>= 25000 bp) # contigs (>= 50000 bp) # contigs (>= 50000 bp) # contigs (>= 50000 bp) Total length (>= 0 bp) Total length (>= 10000 bp) Total length (>= 5000 bp) Total length (>= 5000 bp) Total length (>= 50000 bp)	# contigs (>= 0 bp)	5
# contigs (>= 5000 bp) # contigs (>= 10000 bp) # contigs (>= 10000 bp) # contigs (>= 25000 bp) # contigs (>= 50000 bp) Total length (>= 0 bp) Total length (>= 1000 bp) Total length (>= 5000 bp) Total length (>= 50000 bp) Total length # contigs Largest contig Total length # Contigs Largest contig Total length # Contigs Reference length # Contigs Reference length # GC (%) # So.7: Reference GC (%) # So.7: Ro50 # So.9: Ro50 # Wisassembled # Wisassembles # wisassemblies # misassemblies # misassembled contigs # misassembled contigs # unaligned mis. contigs # unaligned length # Unaligned length # Contigs length # Unaligned length # One # Wis per 100 kbp # Wis per 100 kbp # Misassemble length # Total aligned length # Total aligned length # Na50 # So.9: Ro50 # Ro50		5
# contigs (>= 10000 bp) # contigs (>= 25000 bp) # contigs (>= 25000 bp) # contigs (>= 50000 bp) Total length (>= 0 bp) Total length (>= 1000 bp) Total length (>= 5000 bp) Total length (>= 25000 bp) Total length (>= 50000 bp) Total length (>= 50000 bp) Total length (>= 50000 bp) # contigs Largest contig Total length # Contigs Reference length # Contigs Reference length # Contigs Reference GC (%) # So.77 Reference GC (%) Ref		5
# contigs (>= 25000 bp) # contigs (>= 50000 bp) Total length (>= 0 bp)		5
# contigs (>= 50000 bp) Total length (>= 0 bp)		5
Total length (>= 0 bp) 473598: Total length (>= 1000 bp) 473598: Total length (>= 10000 bp) 473598: Total length (>= 5000 bp) 473598: Total length (>= 25000 bp) 473598: Total length (>= 25000 bp) 473598: Total length (>= 50000 bp) 473598: # contigs Largest contig 394478: Total length 468613 GC (%) 50.77 Reference length 468613 GC (%) 50.77 Reference GC (%) 50.77 NSO 394478: N90 513470 Aunu 3347216. Aunu 3		5
Total length (>= 1000 bp) 473598. Total length (>= 5000 bp) 473598. Total length (>= 5000 bp) 473598. Total length (>= 10000 bp) 473598. Total length (>= 25000 bp) 473598. Total length (>= 50000 bp) 473598. Total length 473598. Reference length 468613 GC (%) 50.73 Reference GC (%) 50.73 NS0 394478. NS0 394478. NS0 394478. NS0 394478. S382819. LS0 LG50 L90 LG90 # misassembles # misassembled contigs Misassembled contigs Misassembled contigs # misassembled contigs # will coal misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned length Genome fraction (%) 98.49. Duplication ratio 1.022 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # and and an analysis of the state of		4735982
Total length (>= 5000 bp) 473598. Total length (>= 10000 bp) 473598. Total length (>= 25000 bp) 473598. Total length (>= 50000 bp) 473598. Total length (>= 50000 bp) 473598. # contigs Largest contig 394478. Total length 473598. Reference length 468613. GC (%) 50.7. Reference GC (%) 50.7. N50 394478. N90 51347. N990 51347. auN 3347216. auN 3347216. LG50 L90 LG90 # misassembled contigs # misassembled contigs length # local misassembles # scaffold gap loc. mis. # unaligned mis. contigs # unaligned length Genome fraction (%) 98.49. Duplication ratio 1.02. # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # most and mismatches per 100 kbp 0.00 # mismatches pe		4735982
Total length (>= 10000 bp) 473598. Total length (>= 25000 bp) 473598. Total length (>= 50000 bp) 473598. # contigs Largest contig 394478. Total length 473598. Reference length 468613. GC (%) 50.7. Reference GC (%) 50.7. N50 394478. N650 394478. N690 51347. Largest contig 394478. # inclaim sassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned length Genome fraction (%) 98.49. Duplication ratio 1.02. # mismatches per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # indels per 100 kbp 0.00 # indels per 100 kbp 0.00 # NA50 394478. NA50 394478. NA90 51347.		4735982
Total length (>= 25000 bp) 473598: Total length (>= 50000 bp) 473598: # contigs Largest contig 394478: Total length 468613: GC (%) 50.7: Reference length 468613: GC (%) 50.7: N50 394478: N90 394478: N90 51347: auN 3347216. auNG 3382819. L50 LG50 L90 LG90 # misassemblies # misassembled contigs length # local misassembles # unaligned mis. contigs # unaligned length Genome fraction (%) 98.49: Duplication ratio 1.02: # N's per 100 kbp 0.0: # mismatches per 100 kbp 0.0: # MA50 394478: NA90 51347: NA90 51347: AuNG 3382656. LA90 LG50 LA90		4735982
Total length (>= 50000 bp)		4735982
# contigs Largest contig Total length Reference length GC (%) SO.7: Reference GC (%) NSO S94478: S980 S1347: auN S347216. auNG S382819. LSO LG50 LG50 L90 LG90 # misassembles # misassembles # misassembled contigs Misassembled contigs Misassembled contigs Misassembled contigs # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned length Genome fraction (%) Duplication ratio # N's per 100 kbp Cond # mismatches per 100 kbp S94478: NASO S944		4735982
Largest contig 394478 Total length 473598 Reference length 468613 GC (%) 50.7 Reference GC (%) 50.7 NSO 394478 NGSO 394478 N90 51347 auN 3347216 auNG 3382819 L50 L50 LG50 L90 LG90 # # misassemblies # # scaffold gap ext. mis. # # scaffold gap loc. mis. # # unaligned mis. contigs 0 + 0 par Unaligned length 0 Genome fraction (%) 98.49 Duplication ratio 1.02 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # argest alignment 394478 NA50 394478 NA50 394478 NA50 394478 NA90 51347 auNA 3347054 auNA 3347054 auNGA<		5
Total length 473598: Reference length 468613: GC (%) 50.7: Reference GC (%) 50.7: N50 394478: N50 394478: N90 51347: N690 51347: auNG 3382819. L50 L650 L90 L690		3944785
GC (%) 50.7: Reference GC (%) 50.7: N50 394478. NG50 394478. N90 51347. NG90 51347. auN 3347216. auNG 3382819. L50 LG50 LG90 LG90 # misassemblies # misassembled contigs Misassembled contigs length 12587. # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned contigs 0 + 0 par Unaligned length 0 Genome fraction (%) 98.49. Duplication ratio 1.02. # N's per 100 kbp 0.0 # mismatches per 100 kbp 0.0 # argest alignment 394478. NA50 394478. NA50 394478. NA90 51347. NA90 51347. auNA 3347054. auNA 3347054. auNA 3347054. auNA 3347054. auNA	Total length	4735982
GC (%) 50.7: Reference GC (%) 50.7: N50 394478. NG50 394478. N90 51347. NG90 51347. auN 3347216. auNG 3382819. L50 LG50 LG90 LG90 # misassemblies # misassembled contigs Misassembled contigs length 12587. # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned contigs 0 + 0 par Unaligned length 0 Genome fraction (%) 98.49. Duplication ratio 1.02. # N's per 100 kbp 0.0 # mismatches per 100 kbp 0.0 # argest alignment 394478. NA50 394478. NA50 394478. NA90 51347. NA90 51347. auNA 3347054. auNA 3347054. auNA 3347054. auNA 3347054. auNA	<u>_</u>	4686137
Reference GC (%) 50.7: N50 394478: NG50 394478: N90 51347: auN 3347216. auNG 3382819. L50 L50 LG50 L90 LG90 # LG90 # Misassemblies # # incal misassemblies # # scaffold gap ext. mis. # # scaffold gap loc. mis. # # unaligned mis. contigs 0 + 0 par Unaligned length 0 Genome fraction (%) 98.49: Duplication ratio 1.02: # N's per 100 kbp 0.0: # mismatches per 100 kbp 0.0: # augest alignment 394478: Total aligned length 473598: NA50 394478: NA50 394478: NA90 51347: auNA 3347054. auNA 3347054. auNA 3347054. auNA 3347054. <td></td> <td>50.75</td>		50.75
N50 394478 NG50 394478 N90 51347 auN 3347216 auNG 3382819 L50 L50 LG50 L90 LG90 # misassemblies # misassembled contigs # scaffold gap text. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned length 0 + 0 par Unaligned length 0 + 0 par Unaligned length 0.00 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # nodels per 100 kbp 0.00		50.78
N90 51347 NG90 51347 auN 3347216. auNG 3382819. L50 L50 LG90 L90 LG90 # # misassemblies # # misassembled contigs # Misassembled contigs length 12587 # local misassemblies # # scaffold gap ext. mis. # # scaffold gap loc. mis. # # unaligned mis. contigs 0 + 0 par Unaligned length 98.49 Genome fraction (%) 98.49 Duplication ratio 1.02 # N's per 100 kbp 0.0 # mismatches per 100 kbp 0.0 Largest alignment 394478 NA50 394478 NA50 394478 NA90 51347 auNA 3347054 auNA 3347054 auNGA 3382656 LA50 LA90		3944785
N90 51347 NG90 51347 auN 3347216. auNG 3382819. L50 L50 LG90 L90 LG90 # # misassemblies # # misassembled contigs # Misassembled contigs length 12587 # local misassemblies # # scaffold gap ext. mis. # # scaffold gap loc. mis. # # unaligned mis. contigs 0 + 0 par Unaligned length 98.49 Genome fraction (%) 98.49 Duplication ratio 1.02 # N's per 100 kbp 0.0 # mismatches per 100 kbp 0.0 Largest alignment 394478 NA50 394478 NA50 394478 NA90 51347 auNA 3347054 auNA 3347054 auNGA 3382656 LA50 LA90		
NG90 51347 auN 3347216. auNG 3382819. L50 L50 LG50 L90 LG90 # misassemblies # misassembled contigs # misassembled contigs Misassembled contigs length 12587 # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned length 0 + 0 par Unaligned length 98.49 Genome fraction (%) 98.49 Duplication ratio 1.02 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 394478 NA50 394478 NA50 394478 NA50 394478 NA90 51347 auNA 3347054 auNA 3347054 auNGA 3382656 LA50 LA90		513470
auN 3347216. auNG 3382819. L50 L50 LG50 L90 LG90 # misassemblies # misassembled contigs Misassembled contigs length 12587: # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned length Genome fraction (%) 98.49: Duplication ratio 1.02: # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 394478: Total aligned length 473598: NA50 394478: NA90 51347: NA90 51347: NA90 51347: AuNA 3347054. auNA 3347054. auNA 3382656. LA50 LGA50 LA90		
auNG 3382819. 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 # mismatches per 100 kbp Largest alignment Total aligned length NA50 394478: NA90 51347: NA90 51347: NA90 51347: AuNA 3347054. auNA 3382656. LA50 LGA50 LA90		
L50 LG50 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 51347 NA90 51347 NA90 51347 AuNA 3347054. auNA 3347054. auNGA LA50 LGA50 LA90		
LG50 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 S13470 NA90 S13470 S1470 S1		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 Largest alignment Total aligned length NA50 NA90 S13470 NA90 LGA50 LGA50 LGA50 LGA50 LA90		1
# misassembles # misassembled contigs Misassembled contigs length # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned contigs O + 0 par Unaligned length Genome fraction (%) Puplication ratio N's per 100 kbp mismatches per 100 kbp findels per 100 kbp Largest alignment 394478 NA50 NA50 NA90 S13470 NA90 S13470 NA90 LGA50 LGA50 LGA50 LGA50 LGA50 LGA50 LA90	L90	2
# misassembles # misassembled contigs Misassembled contigs length # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned contigs O + 0 par Unaligned length Genome fraction (%) Puplication ratio N's per 100 kbp mismatches per 100 kbp findels per 100 kbp Largest alignment 394478 NA50 NA50 NA90 S13470 NA90 S13470 NA90 LGA50 LGA50 LGA50 LGA50 LGA50 LGA50 LA90		2
Misassembled contigs length 12587 # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned length 0 + 0 par Genome fraction (%) 98.49 Duplication ratio 1.02 # N's per 100 kbp 0.0 # mismatches per 100 kbp 0.0 # indels per 100 kbp 394478 Total aligned length 473598 NA50 394478 NAS0 394478 NA90 51347 NA90 51347 auNA 3347054 auNGA 3382656 LA50 LA50 LA90 LA90	# misassemblies	1
Misassembled contigs length 12587 # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned length 0 + 0 par Genome fraction (%) 98.49 Duplication ratio 1.02 # N's per 100 kbp 0.0 # mismatches per 100 kbp 0.0 # indels per 100 kbp 394478 Total aligned length 473598 NA50 394478 NAS0 394478 NA90 51347 NA90 51347 auNA 3347054 auNGA 3382656 LA50 LA50 LA90 LA90	# misassembled contigs	1
# 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 Cargest alignment Total aligned length NA50 NA90 NA90 S1347 NA90 S1347 NA90 S1347 S1347		125872
# 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 0.00 # mismatches per 100 kbp 1.02e # nindels per 100 kbp 1.01 1.02e		C
# scaffold gap loc. mis. # unaligned mis. contigs # unaligned contigs O + 0 par Unaligned length Genome fraction (%) Duplication ratio # N's per 100 kbp o.ou # mismatches per 100 kbp largest alignment Total aligned length NA50 NA50 NGA50 NA90 513470 NA90 513470 auNA 3347054. auNGA LA50 LGA50 LGA50 LA90		C
# unaligned mis. contigs # unaligned contigs 0 + 0 par Unaligned length Genome fraction (%) Puplication ratio 1.02 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.01 1.02 1.02 1.02 1.03 1.04 1.05 1		C
# unaligned contigs 0 + 0 par Unaligned length Genome fraction (%) 98.49 Duplication ratio 1.02 # N's per 100 kbp 0.00 # indels per 100 kbp 0.00 Largest alignment 394478 Total aligned length 473598 NA50 394478 NA50 394478 NA90 513470 NA90 513470 auNA 3347054. auNGA 3382656. LA50 LGA50 LA90		C
Unaligned length Genome fraction (%) Duplication ratio # N's per 100 kbp # mismatches per 100 kbp 1.02 # nidels per 100 kbp Largest alignment Total aligned length NA50 S94478: NA50 NA90 S1347: NA90 S1347: NA90 S1347: NA90 S1347: NA90 S1347: AuNA 3347054. auNA 3382656. LA50 LA90		
Genome fraction (%) 98.49 Duplication ratio 1.02 # N's per 100 kbp 0.0 # mismatches per 100 kbp 0.0 # indels per 100 kbp 0.0 Largest alignment 394478 Total aligned length 473598 NA50 394478 NGA50 394478 NA90 51347 auNA 3347054 auNGA 3382656 LA50 LA50 LA90 LA90		0
Duplication ratio 1.02 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # indels per 100 kbp 0.00 Largest alignment 394478 Total aligned length 473598 NA50 394478 NA90 513470 NGA90 513470 auNA 3347054 auNGA 3382656 LA50 LA90		98.492
# N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # indels per 100 kbp 0.00 Largest alignment 394478: Total aligned length 473598: NA50 394478: NGA50 394478: NA90 513470 NA90 513470 auNA 3347054. auNGA 3382656. LA50 LGA50		1.026
# mismatches per 100 kbp		0.00
# indels per 100 kbp 0.00 Largest alignment 394478: Total aligned length 473598: NA50 394478: NGA50 394478: NGA90 513470 AUNA 3347054. AUNGA 3382656.: LGA50 LGA50		0.00
Largest alignment 394478 Total aligned length 473598 NA50 394478 NGA50 394478 NA90 51347 NGA90 51347 auNA 3347054 auNGA 3382656 LA50 LGA50 LA90		0.00
Total aligned length 473598: NA50 394478: NGA50 394478: NA90 51347: NGA90 51347: auNA 3347054. auNGA 3382656. LA50 LGA50 LA90 LA90	· · · · · · · · · · · · · · · · · · ·	
NA50 394478 NGA50 394478 NA90 51347 NGA90 51347 auNA 3347054. auNGA 3382656. LA50 LGA50 LA90		
NGA50 394478. NA90 513470 NGA90 513470 auNA 3347054. auNGA 3382656.: LA50 LGA50 LA90		
NA90 513470 NGA90 513470 auNA 3347054. auNGA 3382656. LA50 LGA50 LA90		
NGA90 513470 auNA 3347054. auNGA 3382656. LA50 LGA50 LA90		
auNA 3347054. auNGA 3382656. LA50 LGA50 LA90		
auNGA 3382656 LA50 LGA50 LA90		J134/U
LA50 LGA50 LA90	NGA90	22/705/4
LGA50 LA90	NGA90 auNA	3347054.6
LA90 :	NGA90 auNA auNGA	3382656.2
	NGA90 auNA auNGA LA50	3382656.2 1
LGA90	NGA90 auNA auNGA LA50 LGA50	

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

	CFL_ICFL_R_35_COMB_50
# misassemblies	1
# contig misassemblies	1
# c. relocations	1
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	125872
# 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

	CFL_ICFL_R_35_COMB_50
# 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).





















