

Supplementary Tables and Figures

Supplementary Table S1 Scaffold statistics of *C. quinquecirrha*

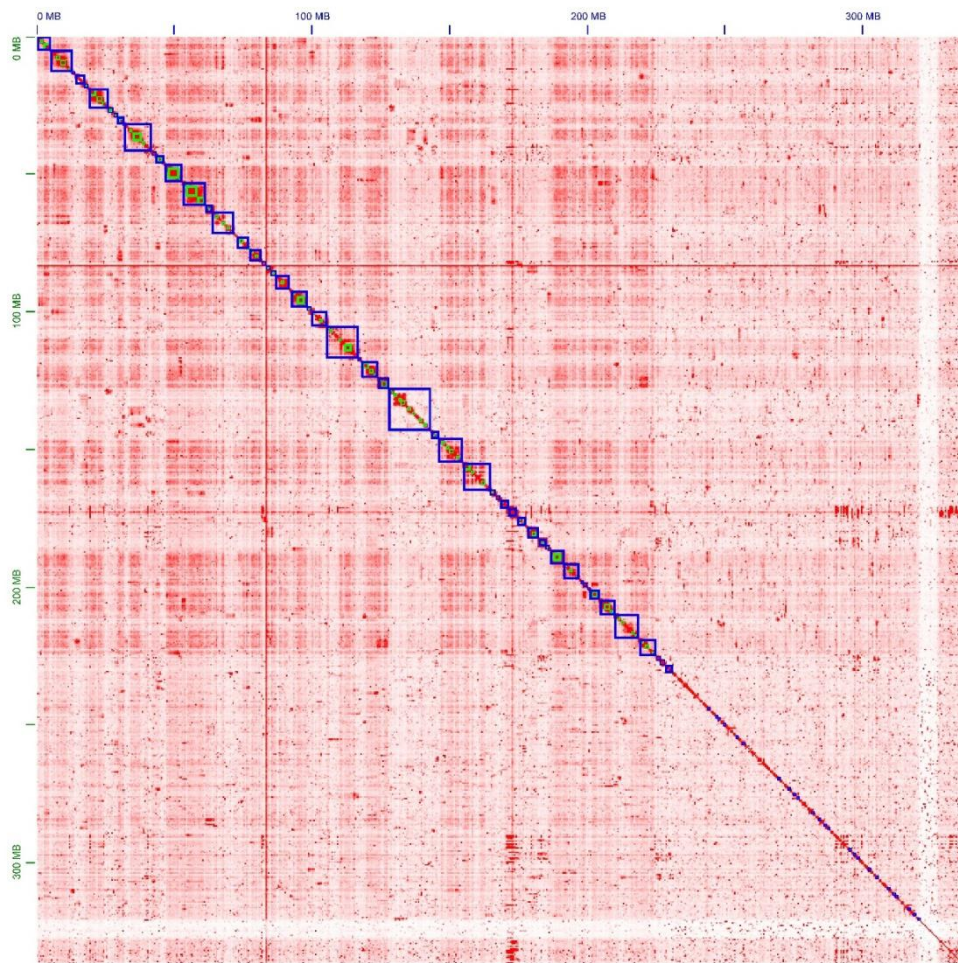
Scaffold ID	Length (bp)	Scaffold ID	Length (bp)
Scaf1	5 149 220	Scaf27	5 598 669
Scaf2	7 906 628	Scaf28	4 391 500
Scaf3	1 085 000	Scaf29	15 257 941
Scaf4	3 825 607	Scaf30	2 805 058
Scaf5	1 519 393	Scaf31	8 698 500
Scaf6	7 036 558	Scaf32	10 155 000
Scaf7	1 985 107	Scaf33	1 828 394
Scaf8	1 547 226	Scaf34	1 710 361
Scaf9	2 312 428	Scaf35	2 941 639
Scaf10	9 889 076	Scaf36	3 049 000
Scaf11	1 379 500	Scaf37	2 870 879
Scaf12	3 004 805	Scaf38	3 810 444
Scaf13	6 503 500	Scaf39	2 897 894
Scaf14	8 499 568	Scaf40	1 295 083
Scaf15	2 729 391	Scaf41	4 840 932
Scaf16	7 844 609	Scaf42	5 879 406
Scaf17	4 613 000	Scaf43	1 090 000
Scaf18	4 418 028	Scaf44	1 579 293
Scaf19	1 462 328	Scaf45	3 446 000
Scaf20	1 160 172	Scaf46	5 709 418
Scaf21	2 355 614	Scaf47	9 020 731
Scaf22	5 017 578	Scaf48	5 888 604
Scaf23	6 294 754	Scaf49	1 293 500
Scaf24	1 377 740	Scaf50	2 412 000
Scaf25	5 640 661	Scaf51	2 133 000
Scaf26	11 530 542		
Total length of long scaffolds (bp)		226 691 279	
Total genome size (bp)		337 419 359	
Ratio of long scaffolds in whole genome (%)		67.18%	

Supplementary Table S2 Genome QC results of two genome versions

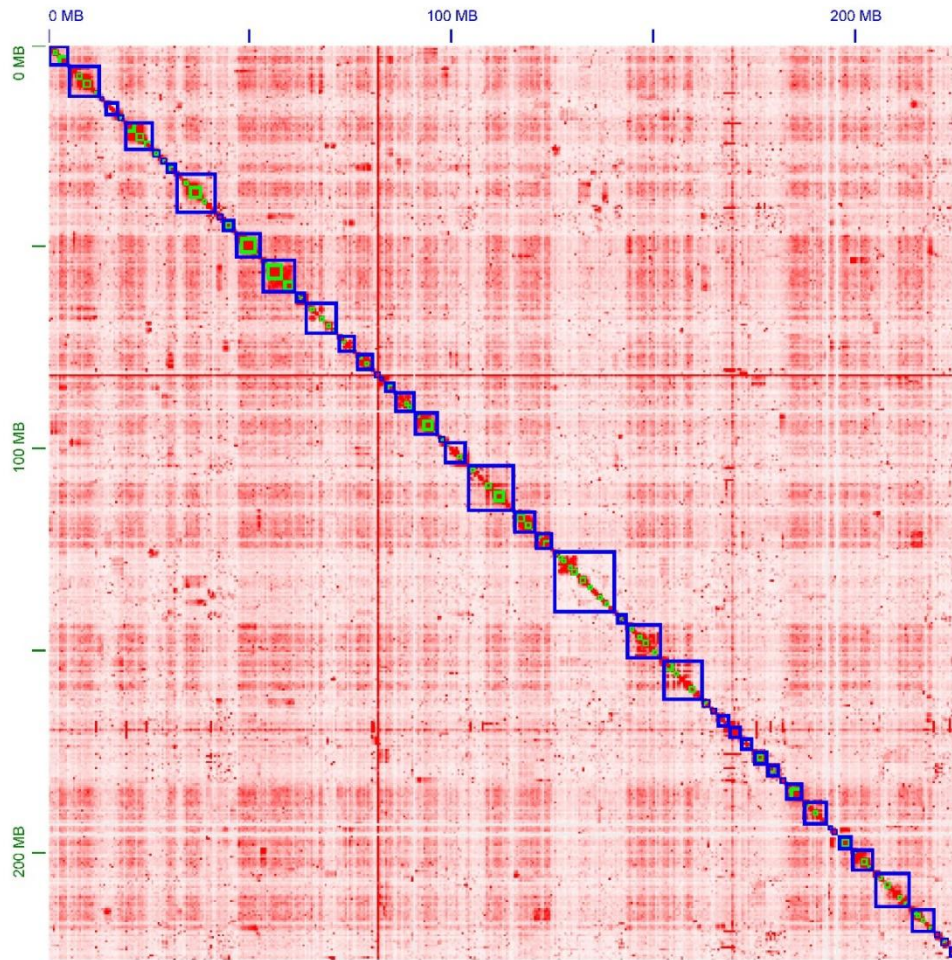
Term	Hi-C version	Contig-version
	(this study)	(Xia et al., 2020)
Number of scaffolds	1 882	2 496
Total size of scaffolds	337 419 359	336 819 409
Total scaffold length as percentage of assumed genome size	104.789	104.602
useful amount of scaffold sequences (≥ 25 K nt)	325 818 692	322 354 749
% of estimated genome that is useful	101.186	100.110
Longest scaffold	15 257 941	4 015 784
Shortest scaffold	527	1 873
Number of scaffolds > 1K nt	1 857	2 496
Number of scaffolds > 10K nt	822	1 691
Number of scaffolds > 100K nt	278	516
Number of scaffolds > 1M nt	51	76
Number of scaffolds > 10M nt	3	0
N50	3 825 607	733 647
L50	24	125
NG50	4 418 028	770 816
LG50	22	115
%A	29.628	29.635
%C	17.786	17.791
%G	17.843	17.901
%T	29.678	29.776
Total Number of Ns	17 091 689	16 491 739
%N	5.065	4.896

Supplementary Table S3 Statistics of BUSCO scores of two genome versions

Term	Contig-version		Hi-C version	
	(Xia et al., 2020)		(this study)	
Library	Eukaryota	Metazoa	Eukaryota	Metazoa
Complete BUSCOs (C)	226	701	240	718
Complete and single-copy BUSCOs (S)	195	585	210	605
Complete and duplicated BUSCOs (D)	31	116	30	113
Fragmented BUSCOs (F)	32	73	26	70
Missing BUSCOs (M)	45	204	37	190
Total BUSCO groups searched	303	978	303	978
Summarize	74.60%	71.70%	79.20%	73.50%



Supplementary Figure S1 Heatmap of interactions of all scaffolds



Supplementary Figure S2 Heatmap of interactions of 51 super-scaffolds