

Supplementary Information for

Phylogenomics of crabs provides insights into their origin and evolution

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Supplementary Table S1: Statistics of the long reads generated for genome assembly of all sampled species

Species	Average length(bp)	N50 lengt(bp)	Read number	Total base (bp)
<i>A. integerrimus</i>	10,540	22,599	14,782,343	155,809,900,657
<i>P. platypus</i>	9,248	15,502	24,804,609	229,398,714,670
<i>P. trituberculatus</i>	10,620	20,950	5,977,353	63,479,561,229
<i>D. horrida</i>	6,973	12,150	25,578,949	178,351,798,956
<i>C. philargius</i>	7,259	15,910	14,719,692	106,849,810,063
<i>L. dehaani</i>	10,167	18,977	17,163,793	174,504,766,276
<i>R. ranina</i>	10,188	21,309	54,920,655	559,527,971,790
<i>S. planum</i>	17,674	24,475	59,278,746	1,047,707,879,007
<i>C. carnifex</i>	10,674	17,178	25,436,195	271,501,842,180
<i>C. brevimanus</i>	18,290	24,359	16,411,019	300,151,098,858

Supplementary Table S2: Statistics of the long reads generated for genome assembly of *A. integerrimus*

Sequencing ID	Average length (bp)	N50 length(bp)	Read number	Total base (bp)
20181004-NPL0321-P2-E7-H7	9,668	16,370	2,171,127	20,989,714,925
20181123-NPL0321-P1-E7-H7	5,562	17,217	2,566,862	14,277,970,498
20181125-NPL0321-P1-A7-D7	10,242	18,736	2,494,875	25,553,025,725
20181125-NPL0321-P2-E7-H7	11,452	21,392	577,338	6,611,891,207
20181201-NPL0321-P2-A3-D3	9,609	18,219	2,073,825	19,927,128,845
20181205-NPL0321-P1-E1-H1	11,287	19,391	1,959,400	22,114,730,049
20181218-NPL0321-P1-E3-H3	14,012	35,973	948,074	13,284,209,693
20181219-NPL0321-P2-E1-H1	21,430	36,343	783,209	16,784,204,704
20190113-NPL0321-P1-A3-D3	12,391	34,181	311,823	3,863,685,609
20190113-NPL0321-P1-E7-H7	13,846	35,793	895,810	12,403,339,402
Total	10,540	22,599	14,782,343	155,809,900,657

Supplementary Table S3: Statistics of the long reads generated for genome assembly of *P. platypus*

Sequencing ID	Average length (bp)	N50 length (bp)	Read number	Total base (bp)
m54136_180731_085011	8,614	14,920	837,653	7,215,890,808
m54136_180801_103725	8,630	14,719	802,334	6,923,734,749
m54136_180801_205028	7,783	13,551	812,785	6,325,844,885
m54136_180802_070641	9,048	15,420	794,395	7,187,764,561
m54136_180804_101006	9,760	15,835	836,727	8,166,183,035
m54136_180807_191740	9,423	15,774	958,808	9,034,994,012
m54136_180808_052954	8,510	14,653	851,476	7,246,135,591
m54136_180814_100433	9,750	15,853	818,118	7,976,894,721
m54136_180815_200030	9,446	15,441	757,189	7,152,387,817
m54136_180816_061553	10,450	16,299	730,707	7,635,904,322
m54136_180816_163214	9,680	15,685	780,127	7,551,686,722
m54136_180818_055946	9,968	16,037	758,658	7,562,554,564
m54136_180818_161654	9,487	15,386	743,718	7,055,601,298
m54136_180819_090957	9,422	15,361	665,972	6,274,592,303
m54136_180820_155845	10,443	16,464	674,592	7,044,794,035
m54136_180821_172628	9,820	15,804	677,130	6,649,671,718
m54136_180822_034246	9,879	15,884	655,501	6,475,811,091
m54136_180822_135839	9,156	15,116	720,608	6,598,025,122
m54136_180823_041748	9,496	15,595	777,593	7,383,815,965
m54136_180823_143219	9,584	15,630	751,968	7,206,652,103
m54136_180824_005016	9,042	14,868	714,113	6,456,625,732
m54139_180728_091624	8,913	15,134	834,394	7,436,998,696
m54139_180803_073931	9,261	15,647	890,674	8,248,116,889
m54139_180803_175352	9,132	15,522	869,799	7,942,776,712
m54139_180804_083645	9,038	15,680	908,269	8,209,337,685
m54139_180805_051556	7,750	13,914	511,734	3,965,752,042
m54139_180805_153114	8,508	14,855	885,797	7,535,961,946
m54139_180806_072743	8,503	14,804	853,423	7,256,703,337
m54139_180806_174331	8,701	14,998	877,321	7,633,414,848
m54139_180818_122743	9,137	15,301	686,418	6,271,792,166
m54139_180820_085407	9,973	15,975	695,918	6,940,662,827
m54139_180820_190623	10,186	16,180	670,690	6,831,632,368
Total	9,248	15,502	24,804,609	229,398,714,670

Supplementary Table S4: Statistics of the long reads generated for genome assembly of *C. brevimanus*

Sequencing ID	Average Length (bp)	N50 length (bp)	Read number	Total base (bp)
PAF24291_4cd67e90	21,949	26,862	2,390,016	52,459,404,693
PAF28131_9f0c130c	19,990	26,349	2,182,308	43,623,175,133
PAF28114_f0ae1f2d	19,863	25,762	412,445	8,192,503,913
PAF28221_2bce4b34	15,260	21,842	1,584,000	24,172,087,351
PAG02582_f4d654cc	19,827	23,564	1,566,772	31,064,449,474
PAG01652_c43cdce2	13,169	20,811	3,838,803	50,553,285,680
PAG04178_f021c957	20,701	24,080	2,312,047	47,861,884,122
PAG04132_8f0b53d7	19,874	24,222	2,124,628	42,224,308,492
Total	18,290	24,359	16,411,019	300,151,098,858

Supplementary Table S5: Statistics of the long reads generated for genome assembly of *D.****horrida***

Sequencing ID	Average length (bp)	N50 length(bp)	Read number	Total base (bp)
20181008-NPL0322-P1-E9-H9	7,605	13,557	2,776,763	21,117,974,454
20181123-NPL0322-P1-A9-D9	7,051	13,646	4,587,173	32,343,846,397
20181201-NPL0322-P1-E1-H1	6,955	11,483	2,849,060	19,816,122,756
20181205-NPL0322-P1-A7-D7	6,872	11,551	5,750,402	39,517,636,131
20181218-NPL0322-P1-A9-D9	7,048	12,608	4,797,571	33,815,372,540
20181219-NPL0322-P1-E7-H7	6,588	11,446	4,817,980	31,740,846,678
Total	6,973	12,150	25,578,949	178,351,798,956

Supplementary Table S6: Statistics of the long reads generated for genome assembly of *C. philargius*

Sequencing ID	Average length (bp)	N50 length (bp)	Read number	Total base (bp)
20190113-NPL0445-P2-A7-D7	9,197	18,162	710,880	6,538,113,556
20190127-NPL0445-P1-A9-D9	6,782	16,006	2,292,804	15,549,301,740
20190127-NPL0445-P1-E9-H9	8,560	17,025	1,709,771	14,634,804,203
20190127-NPL0445-P2-E9-H9	8,914	16,634	1,736,118	15,475,365,436
20190128-NPL0445-P1-A7-D7	6,257	14,183	2,582,336	16,156,396,768
20190128-NPL0445-P1-E1-H1	10,053	16,138	615,217	6,184,886,452
20190128-NPL0445-P1-E7-H7	10,796	17,088	1,287,574	13,900,695,251
20190128-NPL0445-P2-A1-D1	4,864	12,825	3,784,992	18,410,246,657
Total	7,259	15,910	14,719,692	106,849,810,063

Supplementary Table S7: Statistics of the long reads generated for genome assembly of *L. dehaani*

Sequencing ID	Average length (bp)	N50 length (bp)	Read number	Total base (bp)
20190115-NPL0552-P1-E3-H3	10,638	19,571	738,246	7,853,320,471
20190115-NPL0552-P2-E9-H9	10,625	18,369	1,401,277	14,888,482,227
20190117-NPL0552-P1-E7-H7	11,799	17,360	1,197,635	14,130,968,721
20190117-NPL0552-P2-E3-H3	9,495	18,028	2,380,809	22,604,580,162
20190120-NPL0552-P1-A11-D11	3,201	8,387	85,545	273,788,375
20190120-NPL0552-P2-A7-D7	11,078	19,861	2,295,831	25,432,579,091
20190120-NPL0552-P2-E1-H1	10,012	19,505	1,494,178	14,959,953,743
20190120-NPL0552-P2-E7-H7	10,736	19,362	2,028,906	21,782,053,427
20190121-NPL0552-P2-A7-D7	10,548	20,424	1,307,156	13,788,058,889
20190121-NPL0552-P2-E7-H7	9,705	21,261	1,467,145	14,238,064,310
20190128-NPL0552-P2-E1-H1	8,873	16,999	2,767,065	24,552,916,860
Total	10,167	18,977	17,163,793	174,504,766,276

Supplementary Table S8: Statistics of the long reads generated for genome assembly of *P. trituberculatus*

Sequencing ID	Average length (bp)	N50 length (bp)	Read number	Total base (bp)
20181001-NPL0319-P1-A9-D9	11,034	19,156	1,194,900	13,184,967,611
20181121-NPL0319-P1-A9-D9	10,460	21,706	1,852,374	19,375,978,706
20181125-NPL0319-P1-E7-H7	10,182	20,915	1,713,133	17,443,725,196
20181126-NPL0319-P2-A7-D7	11,073	21,390	1,216,946	13,474,889,716
Total	10,620	20,950	5,977,353	63,479,561,229

Supplementary Table S9: Statistics of the long reads generated for genome assembly of *R. ranina*

Sequencing ID	Average length (bp)	N50 length (bp)	Read number	Total base (bp)
20190115-NPL0585-P2-A11-D11	13,217	27,890	2,481,894	32,801,857,311
20190122-NPL0585-P1-A9-D9	12,150	26,133	2,476,955	30,094,406,775
20190122-NPL0585-P1-E3-H3	11,796	26,527	2,631,662	31,041,849,713
20190123-NPL0585-P1-A11-D11	11,781	24,607	1,664,442	19,608,896,064
20190123-NPL0585-P1-E11-H11	8,516	24,398	2,192,420	18,671,225,440
20190124-NPL0585-P1-E3-H3	7,997	16,798	2,521,153	20,160,369,932
20190124-NPL0585-P2-A3-D3	8,819	16,814	3,720,982	32,815,647,728
20190124-NPL0585-P2-A7-D7	8,671	17,034	4,203,033	36,446,306,924
20190124-NPL0585-P2-E1-H1	7,673	16,747	3,450,210	26,473,063,341
20190124-NPL0585-P2-E7-H7	14,064	23,539	217,958	3,065,353,976
20190125-NPL0585-P1-A11-D11	9,754	19,726	3,640,846	35,514,133,868
20190125-NPL0585-P1-E11-H11	9,335	20,298	2,823,126	26,354,881,268
20190125-NPL0585-P2-A11-D11	10,164	19,909	2,301,399	23,392,307,448
20190125-NPL0585-P2-A5-D5	7,438	17,542	4,244,520	31,571,643,187
20190125-NPL0585-P2-A9-D9	10,790	23,740	2,669,779	28,806,616,537
20190126-NPL0585-P1-A7-D7	10,003	20,125	2,978,741	29,796,154,823
20190126-NPL0585-P1-E1-H1	11,573	20,504	2,852,900	33,015,508,784
20190126-NPL0585-P1-E7-H7	12,606	23,609	2,219,142	27,973,753,114
20190126-NPL0585-P2-A1-D1	11,390	20,172	1,368,476	15,586,219,109
20190126-NPL0585-P2-E1-H1	12,544	21,550	2,164,161	27,147,651,560
20190126-NPL0585-P2-E7-H7	13,921	21,829	2,096,856	29,190,124,888
Total	10,188	21,309	54,920,655	559,527,971,790

Supplementary Table S10: Statistics of the long reads generated for genome assembly of *S. planum*

Sequencing ID	Average length (bp)	N50 length (bp)	Read number	Total base (bp)
20190327-NPL0820-P2-E1-H1	22,706	30,821	663,223	15,058,966,198
20190328-NPL0820-P2-E11-H11	22,026	29,793	517,800	11,404,810,627
20190328-NPL0820-P2-E5-H5	21,627	29,471	460,602	9,961,544,780
20190329-NPL0820-P2-A7-D7	19,146	24,508	428,663	8,207,371,765
20190329-NPL0820-P2-A9-D9	17,978	23,365	374,172	6,726,819,346
20190329-NPL0820-P2-E1-H1	18,981	24,016	762,923	14,480,667,414
20190330-NPL0820-P1-A7-D7	24,710	33,937	555,181	13,718,478,069
20190330-NPL0820-P1-E3-H3	15,815	26,421	13,353	211,181,895
20190330-NPL0820-P2-A3-D3	20,643	29,580	54,336	1,121,674,421
20190330-NPL0820-P2-E11-H11	18,378	23,582	268,034	4,925,943,721
20190330-NPL0820-P2-E5-H5	20,636	26,939	689,099	14,220,314,864
20190331-NPL0820-P1-E3-H3	24,203	33,152	551,486	13,347,403,083
20190331-NPL0820-P1-E9-H9	24,645	33,858	494,099	12,177,046,643
20190331-NPL0820-P2-A3-D3	23,510	32,371	366,040	8,605,571,826
20190401-NPL0820-P1-A7-D7	24,561	33,676	570,667	14,016,226,983
20190401-NPL0820-P1-E1-H1	23,823	33,202	388,541	9,256,137,646
20190401-NPL0820-P1-E7-H7	25,088	34,598	511,035	12,820,885,722
20190402-NPL0820-P1-A1-D1	24,364	33,551	311,886	7,598,639,869
20190402-NPL0820-P2-A9-D9	20,204	31,782	76,426	1,544,077,552
20190402-NPL0820-P2-E1-H1	22,048	32,129	33,567	740,086,910
20190403-NPL0820-P1-E7-H7	6,932	9,208	11,380	78,885,444
20190403-NPL0820-P2-A9-D9	23,218	31,759	646,940	15,020,657,190
20190403-NPL0820-P2-E3-H3	21,184	30,787	183,166	3,880,146,051
20190404-NPL0820-P1-E7-H7	19,799	27,203	956,106	18,929,430,996
20190404-NPL0820-P2-E1-H1	21,730	29,779	415,979	9,039,383,747
20190404-NPL0820-P2-E9-H9	22,256	30,706	267,550	5,954,578,664
20190405-NPL0820-P1-E11-H11	22,828	31,189	586,815	13,395,612,829
20190405-NPL0820-P2-A9-D9	22,935	31,138	672,943	15,433,708,407
20190405-NPL0820-P2-E7-H7	23,580	32,531	408,628	9,635,523,219
20190406-NPL0820-P2-A3-D3	19,376	25,349	932,987	18,077,263,487
20190406-NPL0820-P2-E3-H3	20,127	25,864	430,092	8,656,499,886
20190407-NPL0820-P1-A1-D1	18,499	25,395	451,333	8,349,113,601
20190407-NPL0820-P1-A7-D7	21,479	30,569	116,138	2,494,519,421
20190407-NPL0820-P1-E1-H1	18,862	25,941	480,030	9,054,292,966
20190407-NPL0820-P1-E7-H7	23,769	33,201	109,397	2,600,238,805
20190408-NPL0820-P2-A9-D9	24,210	33,604	109,651	2,654,689,998
20190408-NPL0820-P2-E11-H11	24,965	33,802	481,522	12,021,097,405
20190408-NPL0820-P2-E3-H3	25,343	34,366	306,594	7,769,975,436
20190408-NPL0820-P2-E9-H9	24,419	32,518	176,967	4,321,284,350
20190409-NPL0820-P1-E7-H7	25,342	34,094	227,063	5,754,231,929

20190409-NPL0820-P2-A1-D1	25,683	34,386	253,316	6,505,839,974
20190409-NPL0820-P2-A7-D7	25,994	34,851	207,695	5,398,764,552
20190409-NPL0820-P2-E1-H1	24,053	34,445	99,980	2,404,857,950
20190410-NPL0820-P2-E9-H9	24,188	33,394	477,356	11,546,026,537
20190420-NPL0820-P1-A3-D3	20,275	27,172	981,917	19,907,942,326
20190420-NPL0820-P1-A5-D5	20,358	27,360	1,178,471	23,991,274,604
20190421-NPL0820-P1-A9-D9	20,719	27,878	921,171	19,086,155,992
20190421-NPL0820-P1-E3-H3	19,577	26,158	1,031,571	20,194,978,404
20190421-NPL0820-P1-E9-H9	20,054	27,273	1,011,132	20,277,394,631
20190505-NPL0820-P1-A1-D1	19,333	24,148	720,727	13,933,477,602
20190505-NPL0820-P1-A7-D7	19,177	24,046	796,407	15,272,811,827
20190505-NPL0820-P1-E1-H1	18,586	23,241	655,807	12,188,702,268
20190506-NPL0820-P1-A9-D9-1	19,298	24,226	768,329	14,827,215,197
20190506-NPL0820-P1-A9-D9-2	17,729	22,361	60,000	1,063,718,710
20190506-NPL0820-P1-E3-H3	18,906	23,750	709,157	13,407,496,197
20190506-NPL0820-P1-E9-H9	18,793	23,527	891,062	16,745,683,788
20190506-NPL0820-P2-A3-D3	18,654	23,235	837,641	15,624,938,264
20190506-NPL0820-P2-E3-H3	18,582	23,261	551,346	10,245,085,087
20190513-NPL0820-P1-2-A3-D3	20,336	26,650	134,830	2,741,909,121
20190514-NPL0820-P1-1-A1-D1	20,638	26,122	352,536	7,275,595,503
20190514-NPL0820-P1-1-A7-D7	19,408	24,144	101,159	1,963,317,612
20190514-NPL0820-P1-1-E1-H1	20,551	25,655	605,766	12,449,352,176
20190520-NPL0820-P1-PAD42703	14,214	24,928	493,495	7,014,635,068
20190520-NPL0820-P1-PAD42745	20,441	25,895	905,703	18,513,817,501
20190520-NPL0820-P1-PAD43139	20,554	26,558	415,362	8,537,442,580
20190521-NPL0820-P1-PAD56257	19,951	25,202	618,920	12,348,189,611
PAG23645	11,718	18,849	2,437,984	28,567,716,711
PAG24471	11,000	20,432	4,998,741	54,987,283,153
PAG25176	18,811	21,976	1,458,655	27,438,236,629
PAG25181	8,488	18,603	4,785,516	40,617,238,499
PAG25198	15,522	21,701	2,873,651	44,603,464,908
PAG25326	18,427	24,580	929,161	17,121,676,513
PAG25402	18,659	24,947	2,284,780	42,631,335,257
PAG96071	16,497	19,999	2,808,415	46,329,804,847
PAG96678	15,738	19,614	3,553,299	55,923,358,742
PAH48924	17,434	24,729	1,305,274	22,756,157,501
Total	17,674	24,475	59,278,746	1,047,707,879,007

Supplementary Table S11: Statistics of the long reads generated for genome assembly of *C. carnifex*

Sequencing ID	Average length (bp)	N50 length (bp)	Read number	Total base (bp)
20180927-NPL0318-P2-E5-H5	9,435	19,031	883,146	8,332,765,207
20181201-NPL0318-P1-E9-H9	8,488	18,944	940,116	7,979,300,368
20190113-NPL0318-P1-A7-D7	9,642	18,523	2,271,484	21,902,143,655
20190116-NPL0318-P1-E1-H1	7,964	19,738	1,013,325	8,070,034,087
20190120-NPL0318-P1-A7-D7	8,025	14,974	2,417,386	19,398,961,543
20190120-NPL0318-P1-E1-H1	9,524	17,262	2,138,714	20,368,985,504
20190120-NPL0318-P1-E7-H7	7,867	14,952	1,661,967	13,073,830,596
20190120-NPL0318-P2-A1-D1	10,445	16,036	3,160,843	33,014,730,931
20190121-NPL0318-P2-E11-H11	8,003	15,697	2,701,314	21,618,202,227
20190522-NPL0942-P1-PAD58355	14,033	17,465	2,134,758	29,956,889,932
20190522-NPL0942-P1-PAD58553	15,040	18,300	835,937	12,572,364,931
20190522-NPL0942-P1-PAD59223	13,680	16,789	1,738,779	23,785,615,198
20190524-NPL0942-P5-PAD54197	14,711	17,939	701,780	10,324,023,846
20190524-NPL0942-P5-PAD58558	14,590	18,048	1,720,941	25,108,161,429
20190524-NPL0942-P5-PAD59121	14,337	17,864	1,115,705	15,995,832,726
Total	10,674	17,178	25,436,195	271,501,842,180

Supplementary Table S12: Statistics of the genomic short reads generated for 10 species

Species	Read pairs	Total bases (bp)	Sequencing strategy
<i>A. integerrimus</i>	1,060,135,828	210,562,224,872	PE100
<i>P. platypus</i>	2,239,017,674	447,803,534,800	PE100
<i>P. trituberculatus</i>	1,027,526,394	205,505,278,800	PE100
<i>D. horrida</i>	1,138,902,469	227,780,493,800	PE100
<i>C. philargius</i>	1,053,499,078	209,822,562,610	PE100
<i>L. dehaani</i>	885,566,402	177,113,280,400	PE100
<i>R. ranina</i>	3,132,800,688	581,279,939,320	PE100
<i>S. planum</i>	7,588,932,354	1,409,230,840,320	PE100
<i>C. carnifex</i>	1,027,724,277	204,533,078,536	PE100
<i>C. brevimanus</i>	1,651,002,716	495,300,814,800	PE150

Supplementary Table S13: Statistics of the genomic short reads generated for *A. integerrimus*

Sequencing ID	Read pairs	Total bases (bp)	Sequencing strategy
V100007616_L3_ANIlmkRAAAG-578	14,603,469	2,920,693,800	PE100
V100007616_L3_ANIlmkRAAAG-579	23,456,808	4,691,361,600	PE100
V100007616_L3_ANIlmkRAAAG-580	25,569,687	5,113,937,400	PE100
V100007616_L3_ANIlmkRAAAG-581	23,088,742	4,617,748,400	PE100
V100007616_L3_ANIlmkRAAAG-582	28,991,597	5,798,319,400	PE100
V100007616_L3_ANIlmkRAAAG-583	22,182,990	4,436,598,000	PE100
V100007616_L3_ANIlmkRAAAG-584	10,997,653	2,199,530,600	PE100
V100007616_L3_ANIlmkRAAAG-585	20,922,421	4,184,484,200	PE100
V100007616_L3_ANIlmkRAAAH-588	25,864,217	5,172,843,400	PE100
V100007616_L3_ANIlmkRAAAH-589	27,891,062	5,578,212,400	PE100
V100007616_L3_ANIlmkRAAAH-590	31,173,904	6,234,780,800	PE100
V100007616_L3_ANIlmkRAAAH-591	16,381,748	3,276,349,600	PE100
V100007616_L3_ANIlmkRAAAH-592	20,874,887	4,174,977,400	PE100
V100007616_L3_ANIlmkRAAAH-593	12,977,671	2,595,534,200	PE100
V100007616_L3_ANIlmkRAAAH-594	22,594,193	4,518,838,600	PE100
V100007616_L3_ANIlmkRAAAH-595	13,945,955	2,789,191,000	PE100
V100007616_L4_ANIlmkRAAAG-578	14,670,286	2,934,057,200	PE100
V100007616_L4_ANIlmkRAAAG-579	21,580,442	4,316,088,400	PE100
V100007616_L4_ANIlmkRAAAG-580	25,267,509	5,053,501,800	PE100
V100007616_L4_ANIlmkRAAAG-581	21,543,246	2,843,708,472	PE100
V100007616_L4_ANIlmkRAAAG-582	28,602,675	5,720,535,000	PE100
V100007616_L4_ANIlmkRAAAG-583	20,035,090	4,007,018,000	PE100
V100007616_L4_ANIlmkRAAAG-584	10,674,888	2,134,977,600	PE100
V100007616_L4_ANIlmkRAAAG-585	20,606,905	4,121,381,000	PE100
V100007616_L4_ANIlmkRAAAH-588	24,934,130	4,986,826,000	PE100
V100007616_L4_ANIlmkRAAAH-589	26,785,433	5,357,086,600	PE100
V100007616_L4_ANIlmkRAAAH-590	30,115,734	6,023,146,800	PE100
V100007616_L4_ANIlmkRAAAH-591	16,757,431	3,351,486,200	PE100
V100007616_L4_ANIlmkRAAAH-592	20,979,756	4,195,951,200	PE100
V100007616_L4_ANIlmkRAAAH-593	12,586,784	2,517,356,800	PE100
V100007616_L4_ANIlmkRAAAH-594	22,074,116	4,414,823,200	PE100
V100007616_L4_ANIlmkRAAAH-595	13,500,791	2,700,158,200	PE100
V100007736_L2_ANIlmkRAAAG-578	24,975,379	4,995,075,800	PE100
V100007736_L2_ANIlmkRAAAG-579	25,194,851	5,038,970,200	PE100
V100007736_L2_ANIlmkRAAAG-580	26,214,930	5,242,986,000	PE100
V100007736_L2_ANIlmkRAAAG-581	26,581,251	5,316,250,200	PE100
V100007736_L2_ANIlmkRAAAG-582	29,838,339	5,967,667,800	PE100
V100007736_L2_ANIlmkRAAAG-583	25,013,839	5,002,767,800	PE100
V100007736_L2_ANIlmkRAAAG-584	11,419,708	2,283,941,600	PE100
V100007736_L2_ANIlmkRAAAG-585	21,343,257	4,268,651,400	PE100
V100007736_L2_ANIlmkRAAAH-588	26,581,741	5,316,348,200	PE100
V100007736_L2_ANIlmkRAAAH-589	29,514,680	5,902,936,000	PE100

V100007736_L2_ANIlmkRAAAH-590	32,109,465	6,421,893,000	PE100
V100007736_L2_ANIlmkRAAAH-591	24,664,102	4,932,820,400	PE100
V100007736_L2_ANIlmkRAAAH-592	23,114,804	4,622,960,800	PE100
V100007736_L2_ANIlmkRAAAH-593	16,946,194	3,389,238,800	PE100
V100007736_L2_ANIlmkRAAAH-594	23,640,960	4,728,192,000	PE100
V100007736_L2_ANIlmkRAAAH-595	20,750,108	4,150,021,600	PE100
Total	1,060,135,828	210,562,224,872	PE100

Supplementary Table S14: Statistics of the genomic short reads generated for *P. platypus*

Sequencing ID	Read pairs	Total bases (bp)	Sequencing strategy
NGS1	728,811,972	145,762,394,400	PE100
NGS2	756,810,576	151,362,115,200	PE100
NGS3	753,395,126	150,679,025,200	PE100
Total	2,239,017,674	447,803,534,800	PE100

Supplementary Table S15: Statistics of the genomic short reads generated for *C. brevimanus*

Sequencing ID	Read pairs	Total bases (bp)	Sequencing strategy
FDSW202264228-1r_L2	457,804,133	137,341,239,900	PE150
FDSW202264228-1r_L3	478,411,784	143,523,535,200	PE150
jiace1-FDSW202264228-1r_L4	84,210,045	25,263,013,500	PE150
jiace2-FDSW202264228-1r_L1	314,219,447	94,265,834,100	PE150
jiace2-FDSW202264228-1r_L2	316,357,307	94,907,192,100	PE150
Total	1,651,002,716	495,300,814,800	PE150

Supplementary Table S16: Statistics of the genomic short reads generated for *D. horrida*

Sequencing ID	Read pairs	Total bases (bp)	Sequencing strategy
V100007736_L3_ANIlmkRAAAI-501	13,795,872	2,759,174,400	PE100
V100007736_L3_ANIlmkRAAAI-502	19,686,174	3,937,234,800	PE100
V100007736_L3_ANIlmkRAAAI-503	20,734,089	4,146,817,800	PE100
V100007736_L3_ANIlmkRAAAI-504	19,960,628	3,992,125,600	PE100
V100007736_L3_ANIlmkRAAAI-505	18,850,438	3,770,087,600	PE100
V100007736_L3_ANIlmkRAAAI-506	19,111,812	3,822,362,400	PE100
V100007736_L3_ANIlmkRAAAI-507	22,581,892	4,516,378,400	PE100
V100007736_L3_ANIlmkRAAAI-508	24,165,791	4,833,158,200	PE100
V100007736_L3_ANIlmkRAAAJ-509	31,477,866	6,295,573,200	PE100
V100007736_L3_ANIlmkRAAAJ-510	30,910,134	6,182,026,800	PE100
V100007736_L3_ANIlmkRAAAJ-511	29,557,740	5,911,548,000	PE100
V100007736_L3_ANIlmkRAAAJ-512	28,384,096	5,676,819,200	PE100
V100007736_L3_ANIlmkRAAAJ-513	27,340,772	5,468,154,400	PE100
V100007736_L3_ANIlmkRAAAJ-514	19,701,968	3,940,393,600	PE100
V100007736_L3_ANIlmkRAAAJ-515	25,239,832	5,047,966,400	PE100
V100007736_L3_ANIlmkRAAAJ-516	33,299,100	6,659,820,000	PE100
V100007779_L1_ANIlmkRAAAI-501	13,518,971	2,703,794,200	PE100
V100007779_L1_ANIlmkRAAAI-502	19,926,162	3,985,232,400	PE100
V100007779_L1_ANIlmkRAAAI-503	20,210,688	4,042,137,600	PE100
V100007779_L1_ANIlmkRAAAI-504	19,502,633	3,900,526,600	PE100
V100007779_L1_ANIlmkRAAAI-505	18,388,120	3,677,624,000	PE100
V100007779_L1_ANIlmkRAAAI-506	18,611,621	3,722,324,200	PE100
V100007779_L1_ANIlmkRAAAI-507	22,019,188	4,403,837,600	PE100
V100007779_L1_ANIlmkRAAAI-508	23,614,903	4,722,980,600	PE100
V100007779_L1_ANIlmkRAAAJ-509	31,091,633	6,218,326,600	PE100
V100007779_L1_ANIlmkRAAAJ-510	30,408,175	6,081,635,000	PE100
V100007779_L1_ANIlmkRAAAJ-511	29,107,717	5,821,543,400	PE100
V100007779_L1_ANIlmkRAAAJ-512	27,649,933	5,529,986,600	PE100
V100007779_L1_ANIlmkRAAAJ-513	26,924,321	5,384,864,200	PE100
V100007779_L1_ANIlmkRAAAJ-514	19,461,300	3,892,260,000	PE100
V100007779_L1_ANIlmkRAAAJ-515	24,790,501	4,958,100,200	PE100
V100007779_L1_ANIlmkRAAAJ-516	32,791,663	6,558,332,600	PE100
V100007779_L2_ANIlmkRAAAI-501	13,456,832	2,691,366,400	PE100
V100007779_L2_ANIlmkRAAAI-502	19,826,997	3,965,399,400	PE100
V100007779_L2_ANIlmkRAAAI-503	20,147,828	4,029,565,600	PE100
V100007779_L2_ANIlmkRAAAI-504	19,438,014	3,887,602,800	PE100
V100007779_L2_ANIlmkRAAAI-505	18,319,956	3,663,991,200	PE100
V100007779_L2_ANIlmkRAAAI-506	18,508,312	3,701,662,400	PE100
V100007779_L2_ANIlmkRAAAI-507	21,913,817	4,382,763,400	PE100
V100007779_L2_ANIlmkRAAAI-508	23,480,117	4,696,023,400	PE100
V100007779_L2_ANIlmkRAAAJ-509	30,975,183	6,195,036,600	PE100
V100007779_L2_ANIlmkRAAAJ-510	30,252,647	6,050,529,400	PE100

V100007779_L2_ANIlmkRAAAJ-511	28,945,475	5,789,095,000	PE100
V100007779_L2_ANIlmkRAAAJ-512	27,454,892	5,490,978,400	PE100
V100007779_L2_ANIlmkRAAAJ-513	26,755,380	5,351,076,000	PE100
V100007779_L2_ANIlmkRAAAJ-514	19,342,394	3,868,478,800	PE100
V100007779_L2_ANIlmkRAAAJ-515	24,650,998	4,930,199,600	PE100
V100007779_L2_ANIlmkRAAAJ-516	32,617,894	6,523,578,800	PE100
Total	1,138,902,469	227,780,493,800	PE100

Supplementary Table S17: Statistics of the genomic short reads generated for *C. philargius*

Sequencing ID	Read pairs	Total bases (bp)	Sequencing strategy
V100007736_L4_ANIlmkRAAAK-517	31,780,441	6,356,088,200	PE100
V100007736_L4_ANIlmkRAAAK-518	27,231,238	5,446,247,600	PE100
V100007736_L4_ANIlmkRAAAK-519	26,885,763	5,377,152,600	PE100
V100007736_L4_ANIlmkRAAAK-520	23,626,027	4,725,205,400	PE100
V100007736_L4_ANIlmkRAAAK-521	23,988,871	4,797,774,200	PE100
V100007736_L4_ANIlmkRAAAK-522	26,768,338	5,353,667,600	PE100
V100007736_L4_ANIlmkRAAAK-523	27,173,854	5,434,770,800	PE100
V100007736_L4_ANIlmkRAAAK-524	28,719,263	5,743,852,600	PE100
V100007736_L4_ANIlmkRAAAL-525	16,348,173	3,269,634,600	PE100
V100007736_L4_ANIlmkRAAAL-526	16,097,770	3,219,554,000	PE100
V100007736_L4_ANIlmkRAAAL-527	18,204,532	3,640,906,400	PE100
V100007736_L4_ANIlmkRAAAL-528	13,339,772	2,667,954,400	PE100
V100007736_L4_ANIlmkRAAAL-529	23,592,523	4,718,504,600	PE100
V100007736_L4_ANIlmkRAAAL-530	13,209,920	2,641,984,000	PE100
V100007736_L4_ANIlmkRAAAL-531	20,444,851	4,088,970,200	PE100
V100007736_L4_ANIlmkRAAAL-532	22,166,951	4,433,390,200	PE100
V100007779_L3_ANIlmkRAAAK-517	30,643,467	6,128,693,400	PE100
V100007779_L3_ANIlmkRAAAK-518	26,519,218	5,303,843,600	PE100
V100007779_L3_ANIlmkRAAAK-519	25,949,404	5,189,880,800	PE100
V100007779_L3_ANIlmkRAAAK-520	22,843,631	4,568,726,200	PE100
V100007779_L3_ANIlmkRAAAK-521	23,155,029	4,631,005,800	PE100
V100007779_L3_ANIlmkRAAAK-522	25,915,860	5,183,172,000	PE100
V100007779_L3_ANIlmkRAAAK-523	26,265,280	5,253,056,000	PE100
V100007779_L3_ANIlmkRAAAK-524	27,752,269	5,550,453,800	PE100
V100007779_L3_ANIlmkRAAAL-525	15,771,567	3,154,313,400	PE100
V100007779_L3_ANIlmkRAAAL-526	15,479,188	3,095,837,600	PE100
V100007779_L3_ANIlmkRAAAL-527	17,685,475	3,537,095,000	PE100
V100007779_L3_ANIlmkRAAAL-528	12,947,329	2,589,465,800	PE100
V100007779_L3_ANIlmkRAAAL-529	22,662,811	4,532,562,200	PE100
V100007779_L3_ANIlmkRAAAL-530	12,741,225	2,548,245,000	PE100
V100007779_L3_ANIlmkRAAAL-531	19,652,024	3,930,404,800	PE100
V100007779_L3_ANIlmkRAAAL-532	21,314,805	4,262,961,000	PE100
V100007779_L4_ANIlmkRAAAK-517	30,610,622	6,122,124,400	PE100
V100007779_L4_ANIlmkRAAAK-518	26,449,661	5,289,932,200	PE100
V100007779_L4_ANIlmkRAAAK-519	25,871,834	5,174,366,800	PE100
V100007779_L4_ANIlmkRAAAK-520	22,802,009	4,560,401,800	PE100
V100007779_L4_ANIlmkRAAAK-521	23,085,605	3,739,868,010	PE100
V100007779_L4_ANIlmkRAAAK-522	25,811,671	5,162,334,200	PE100
V100007779_L4_ANIlmkRAAAK-523	26,262,966	5,252,593,200	PE100
V100007779_L4_ANIlmkRAAAK-524	27,686,871	5,537,374,200	PE100
V100007779_L4_ANIlmkRAAAL-525	15,748,364	3,149,672,800	PE100
V100007779_L4_ANIlmkRAAAL-526	15,425,023	3,085,004,600	PE100

V100007779_L4_ANIlmkRAAAL-527	17,694,628	3,538,925,600	PE100
V100007779_L4_ANIlmkRAAAL-528	12,926,371	2,585,274,200	PE100
V100007779_L4_ANIlmkRAAAL-529	22,642,053	4,528,410,600	PE100
V100007779_L4_ANIlmkRAAAL-530	12,745,717	2,549,143,400	PE100
V100007779_L4_ANIlmkRAAAL-531	19,615,550	3,923,110,000	PE100
V100007779_L4_ANIlmkRAAAL-532	21,243,264	4,248,652,800	PE100
Total	1,053,499,078	209,822,562,610	PE100

Supplementary Table S18: Statistics of the genomic short reads generated for *L. dehaani*

Sequencing ID	Read pairs	Total bases (bp)	Sequencing strategy
V300010932_L1_ANIngyRAAAA-509	62,258,214	12,451,642,800	PE100
V300010932_L1_ANIngyRAAAA-510	62,082,771	12,416,554,200	PE100
V300010932_L1_ANIngyRAAAA-511	58,392,540	11,678,508,000	PE100
V300010932_L1_ANIngyRAAAA-512	53,748,658	10,749,731,600	PE100
V300010932_L1_ANIngyRAAAA-513	58,787,512	11,757,502,400	PE100
V300010932_L1_ANIngyRAAAA-514	38,089,205	7,617,841,000	PE100
V300010932_L1_ANIngyRAAAA-515	52,511,045	10,502,209,000	PE100
V300010932_L1_ANIngyRAAAA-516	65,733,447	13,146,689,400	PE100
V300010932_L2_ANIngyRAAAB-517	63,295,239	12,659,047,800	PE100
V300010932_L2_ANIngyRAAAB-518	52,621,407	10,524,281,400	PE100
V300010932_L2_ANIngyRAAAB-519	53,268,420	10,653,684,000	PE100
V300010932_L2_ANIngyRAAAB-520	50,770,294	10,154,058,800	PE100
V300010932_L2_ANIngyRAAAB-521	49,046,885	9,809,377,000	PE100
V300010932_L2_ANIngyRAAAB-522	51,309,086	10,261,817,200	PE100
V300010932_L2_ANIngyRAAAB-523	55,470,319	11,094,063,800	PE100
V300010932_L2_ANIngyRAAAB-524	58,181,360	11,636,272,000	PE100
Total	885,566,402	177,113,280,400	PE100

Supplementary Table S19: Statistics of the genomic short reads generated for *P. trituberculatus*

Sequencing ID	Read pairs	Total bases (bp)	Sequencing strategy
V100007441_L4_ANIImkRAAAC-517	27,653,685	5,530,737,000	PE100
V100007441_L4_ANIImkRAAAC-518	17,421,357	3,484,271,400	PE100
V100007441_L4_ANIImkRAAAC-519	23,771,266	4,754,253,200	PE100
V100007441_L4_ANIImkRAAAC-520	15,588,649	3,117,729,800	PE100
V100007441_L4_ANIImkRAAAC-521	20,743,106	4,148,621,200	PE100
V100007441_L4_ANIImkRAAAC-522	20,627,773	4,125,554,600	PE100
V100007441_L4_ANIImkRAAAC-523	23,747,742	4,749,548,400	PE100
V100007441_L4_ANIImkRAAAC-524	21,051,291	4,210,258,200	PE100
V100007441_L4_ANIImkRAAAD-525	11,913,263	2,382,652,600	PE100
V100007441_L4_ANIImkRAAAD-526	15,733,915	3,146,783,000	PE100
V100007441_L4_ANIImkRAAAD-527	15,561,291	3,112,258,200	PE100
V100007441_L4_ANIImkRAAAD-528	14,110,767	2,822,153,400	PE100
V100007441_L4_ANIImkRAAAD-529	27,996,396	5,599,279,200	PE100
V100007441_L4_ANIImkRAAAD-530	13,760,163	2,752,032,600	PE100
V100007441_L4_ANIImkRAAAD-531	24,252,291	4,850,458,200	PE100
V100007441_L4_ANIImkRAAAD-532	26,373,028	5,274,605,600	PE100
V100007748_L3_ANIImkRAAAC-517	27,258,485	5,451,697,000	PE100
V100007748_L3_ANIImkRAAAC-518	22,806,238	4,561,247,600	PE100
V100007748_L3_ANIImkRAAAC-519	23,494,744	4,698,948,800	PE100
V100007748_L3_ANIImkRAAAC-520	20,700,523	4,140,104,600	PE100
V100007748_L3_ANIImkRAAAC-521	20,734,704	4,146,940,800	PE100
V100007748_L3_ANIImkRAAAC-522	23,274,288	4,654,857,600	PE100
V100007748_L3_ANIImkRAAAC-523	23,398,073	4,679,614,600	PE100
V100007748_L3_ANIImkRAAAC-524	24,593,849	4,918,769,800	PE100
V100007748_L3_ANIImkRAAAD-525	18,264,214	3,652,842,800	PE100
V100007748_L3_ANIImkRAAAD-526	18,983,986	3,796,797,200	PE100
V100007748_L3_ANIImkRAAAD-527	19,553,174	3,910,634,800	PE100
V100007748_L3_ANIImkRAAAD-528	17,726,308	3,545,261,600	PE100
V100007748_L3_ANIImkRAAAD-529	27,709,047	5,541,809,400	PE100
V100007748_L3_ANIImkRAAAD-530	15,906,204	3,181,240,800	PE100
V100007748_L3_ANIImkRAAAD-531	24,164,119	4,832,823,800	PE100
V100007748_L3_ANIImkRAAAD-532	26,818,622	5,363,724,400	PE100
V100007748_L4_ANIImkRAAAC-517	27,225,129	5,445,025,800	PE100
V100007748_L4_ANIImkRAAAC-518	22,350,018	4,470,003,600	PE100
V100007748_L4_ANIImkRAAAC-519	23,409,881	4,681,976,200	PE100
V100007748_L4_ANIImkRAAAC-520	20,577,035	4,115,407,000	PE100
V100007748_L4_ANIImkRAAAC-521	20,664,406	4,132,881,200	PE100
V100007748_L4_ANIImkRAAAC-522	23,033,222	4,606,644,400	PE100
V100007748_L4_ANIImkRAAAC-523	23,421,674	4,684,334,800	PE100
V100007748_L4_ANIImkRAAAC-524	24,323,672	4,864,734,400	PE100
V100007748_L4_ANIImkRAAAD-525	17,321,870	3,464,374,000	PE100
V100007748_L4_ANIImkRAAAD-526	18,835,711	3,767,142,200	PE100

V100007748_L4_ANIlmkRAAAD-527	18,980,537	3,796,107,400	PE100
V100007748_L4_ANIlmkRAAAD-528	17,329,500	3,465,900,000	PE100
V100007748_L4_ANIlmkRAAAD-529	27,661,058	5,532,211,600	PE100
V100007748_L4_ANIlmkRAAAD-530	15,912,690	3,182,538,000	PE100
V100007748_L4_ANIlmkRAAAD-531	24,070,524	4,814,104,800	PE100
V100007748_L4_ANIlmkRAAAD-532	26,716,906	5,343,381,200	PE100
Total	1,027,526,394	205,505,278,800	PE100

Supplementary Table S20: Statistics of the genomic short reads generated for *R. ranina*

Sequencing ID	Read pairs	Total bases (bp)	Sequencing strategy
209023057D1_HUM_C_GD1A_5370_Z_0_A	2,264,009,914	407,521,784,520	PE100
V300010932_L3_ANIngyRAAAC-525	53,469,324	10,693,864,800	PE100
V300010932_L3_ANIngyRAAAC-526	47,478,508	9,495,701,600	PE100
V300010932_L3_ANIngyRAAAC-527	58,283,978	11,656,795,600	PE100
V300010932_L3_ANIngyRAAAC-528	45,417,141	9,083,428,200	PE100
V300010932_L3_ANIngyRAAAC-529	64,585,172	12,917,034,400	PE100
V300010932_L3_ANIngyRAAAC-530	44,740,967	8,948,193,400	PE100
V300010932_L3_ANIngyRAAAC-531	55,749,662	11,149,932,400	PE100
V300010932_L3_ANIngyRAAAC-532	64,212,747	12,842,549,400	PE100
V300010932_L4_ANIngyRAAAD-550	54,501,059	10,900,211,800	PE100
V300010932_L4_ANIngyRAAAD-551	49,980,168	9,996,033,600	PE100
V300010932_L4_ANIngyRAAAD-552	60,482,827	12,096,565,400	PE100
V300010932_L4_ANIngyRAAAD-553	53,585,658	10,717,131,600	PE100
V300010932_L4_ANIngyRAAAD-554	53,854,235	10,770,847,000	PE100
V300010932_L4_ANIngyRAAAD-555	58,912,517	11,782,503,400	PE100
V300010932_L4_ANIngyRAAAD-556	56,167,102	11,233,420,400	PE100
V300010932_L4_ANIngyRAAAD-557	47,369,709	9,473,941,800	PE100
Total	3,132,800,688	581,279,939,320	PE100

Supplementary Table S21: Statistics of the genomic short reads generated for *S. planum*

Sequencing ID	Read pairs	Total bases (bp)	Sequencing strategy
219001208D1_HUM_C_GD1A_5004_Z_0_A	1,131,484,231	203,667,161,580	PE100
219001209D1_HUM_C_GD1A_5003_Z_0_A	2,091,111,618	376,400,091,240	PE100
219001213D1_HUM_C_GD1A_5002_Z_0_A	1,212,242,433	218,203,637,940	PE100
219001214D1_HUM_C_GD1A_5001_Z_0_A	992,943,242	178,729,783,560	PE100
V100007616_L1_ANIImkRAAAE-550	8,582,189	1,716,437,800	PE100
V100007616_L1_ANIImkRAAAE-551	21,775,048	4,355,009,600	PE100
V100007616_L1_ANIImkRAAAE-552	15,251,144	3,050,228,800	PE100
V100007616_L1_ANIImkRAAAE-553	16,369,646	3,273,929,200	PE100
V100007616_L1_ANIImkRAAAE-554	20,677,798	4,135,559,600	PE100
V100007616_L1_ANIImkRAAAE-555	22,649,194	4,529,838,800	PE100
V100007616_L1_ANIImkRAAAE-556	11,091,463	2,218,292,600	PE100
V100007616_L1_ANIImkRAAAE-557	10,579,277	2,115,855,400	PE100
V100007616_L1_ANIImkRAAAF-558	13,130,228	2,626,045,600	PE100
V100007616_L1_ANIImkRAAAF-559	19,899,388	3,979,877,600	PE100
V100007616_L1_ANIImkRAAAF-560	21,428,781	4,285,756,200	PE100
V100007616_L1_ANIImkRAAAF-561	20,304,508	4,060,901,600	PE100
V100007616_L1_ANIImkRAAAF-562	8,806,038	1,761,207,600	PE100
V100007616_L1_ANIImkRAAAF-563	7,988,247	1,597,649,400	PE100
V100007616_L1_ANIImkRAAAF-564	16,473,919	3,294,783,800	PE100
V100007616_L1_ANIImkRAAAF-565	24,293,353	4,858,670,600	PE100
V100007616_L2_ANIImkRAAAE-550	8,468,648	1,693,729,600	PE100
V100007616_L2_ANIImkRAAAE-551	21,482,528	4,296,505,600	PE100
V100007616_L2_ANIImkRAAAE-552	14,634,830	2,926,966,000	PE100
V100007616_L2_ANIImkRAAAE-553	15,937,123	3,187,424,600	PE100
V100007616_L2_ANIImkRAAAE-554	20,413,346	4,082,669,200	PE100
V100007616_L2_ANIImkRAAAE-555	22,486,671	4,497,334,200	PE100
V100007616_L2_ANIImkRAAAE-556	10,965,237	2,193,047,400	PE100
V100007616_L2_ANIImkRAAAE-557	10,309,373	2,061,874,600	PE100
V100007616_L2_ANIImkRAAAF-558	12,900,974	2,580,194,800	PE100
V100007616_L2_ANIImkRAAAF-559	19,402,485	3,880,497,000	PE100
V100007616_L2_ANIImkRAAAF-560	21,059,113	4,211,822,600	PE100
V100007616_L2_ANIImkRAAAF-561	19,991,691	3,998,338,200	PE100
V100007616_L2_ANIImkRAAAF-562	8,625,498	1,725,099,600	PE100
V100007616_L2_ANIImkRAAAF-563	7,907,493	1,581,498,600	PE100
V100007616_L2_ANIImkRAAAF-564	16,230,718	3,246,143,600	PE100
V100007616_L2_ANIImkRAAAF-565	24,114,378	4,822,875,600	PE100
V100007736_L1_ANIImkRAAAE-550	19,563,924	3,912,784,800	PE100
V100007736_L1_ANIImkRAAAE-551	22,214,168	4,442,833,600	PE100
V100007736_L1_ANIImkRAAAE-552	25,795,078	5,159,015,600	PE100
V100007736_L1_ANIImkRAAAE-553	22,402,528	4,480,505,600	PE100
V100007736_L1_ANIImkRAAAE-554	21,555,097	4,311,019,400	PE100

V100007736_L1_ANIlmkRAAAE-555	22,875,982	4,575,196,400	PE100
V100007736_L1_ANIlmkRAAAE-556	22,479,944	4,495,988,800	PE100
V100007736_L1_ANIlmkRAAAE-557	20,175,216	4,035,043,200	PE100
V100007736_L1_ANIlmkRAAAF-558	13,825,217	2,765,043,400	PE100
V100007736_L1_ANIlmkRAAAF-559	21,787,305	4,357,461,000	PE100
V100007736_L1_ANIlmkRAAAF-560	21,976,343	4,395,268,600	PE100
V100007736_L1_ANIlmkRAAAF-561	21,020,878	4,204,175,600	PE100
V100007736_L1_ANIlmkRAAAF-562	22,025,599	4,405,119,800	PE100
V100007736_L1_ANIlmkRAAAF-563	17,957,927	3,591,585,400	PE100
V100007736_L1_ANIlmkRAAAF-564	16,619,713	3,323,942,600	PE100
V100007736_L1_ANIlmkRAAAF-565	24,599,610	4,919,922,000	PE100
V300028144_L2_ANIndxRAAAA-573	50,813,083	10,162,616,600	PE100
V300028144_L2_ANIndxRAAAA-574	56,684,999	11,336,999,800	PE100
V300028144_L2_ANIndxRAAAA-575	53,117,834	10,623,566,800	PE100
V300028144_L2_ANIndxRAAAA-576	45,652,666	9,130,533,200	PE100
V300028144_L2_ANIndxRAAAA-577	55,348,256	11,069,651,200	PE100
V300028144_L2_ANIndxRAAAA-578	55,651,620	11,130,324,000	PE100
V300028144_L2_ANIndxRAAAA-579	60,445,448	12,089,089,600	PE100
V300028144_L2_ANIndxRAAAA-580	52,317,107	10,463,421,400	PE100
V300028144_L3_ANIndxRAAAA-573	51,688,800	10,337,760,000	PE100
V300028144_L3_ANIndxRAAAA-574	57,784,871	11,556,974,200	PE100
V300028144_L3_ANIndxRAAAA-575	54,521,008	10,904,201,600	PE100
V300028144_L3_ANIndxRAAAA-576	46,590,923	9,318,184,600	PE100
V300028144_L3_ANIndxRAAAA-577	56,412,846	11,282,569,200	PE100
V300028144_L3_ANIndxRAAAA-578	56,845,339	11,369,067,800	PE100
V300028144_L3_ANIndxRAAAA-579	61,982,321	12,396,464,200	PE100
V300028144_L3_ANIndxRAAAA-580	53,388,274	10,677,654,800	PE100
V300028144_L4_ANIndxRAAAA-573	51,733,873	10,346,774,600	PE100
V300028144_L4_ANIndxRAAAA-574	58,023,922	11,604,784,400	PE100
V300028144_L4_ANIndxRAAAA-575	54,537,252	10,907,450,400	PE100
V300028144_L4_ANIndxRAAAA-576	46,832,469	9,366,493,800	PE100
V300028144_L4_ANIndxRAAAA-577	56,805,529	11,361,105,800	PE100
V300028144_L4_ANIndxRAAAA-578	56,995,866	11,399,173,200	PE100
V300028144_L4_ANIndxRAAAA-579	62,170,946	12,434,189,200	PE100
V300028144_L4_ANIndxRAAAA-580	53,700,722	10,740,144,400	PE100
Total	7,588,932,354	1,409,230,840,320	PE100

Supplementary Table S22: Statistics of the genomic short reads generated for *C. carnifex*

Sequencing ID	Read pairs	Total bases (bp)	Sequencing strategy
V100007441_L3_ANIlmkRAAAA-501	20,782,290	4,156,458,000	PE100
V100007441_L3_ANIlmkRAAAA-502	7,077,843	1,415,568,600	PE100
V100007441_L3_ANIlmkRAAAA-503	11,039,053	2,207,810,600	PE100
V100007441_L3_ANIlmkRAAAA-504	17,450,354	3,490,070,800	PE100
V100007441_L3_ANIlmkRAAAA-505	20,298,548	4,059,709,600	PE100
V100007441_L3_ANIlmkRAAAA-506	19,728,266	3,945,653,200	PE100
V100007441_L3_ANIlmkRAAAA-507	23,515,448	4,703,089,600	PE100
V100007441_L3_ANIlmkRAAAA-508	24,389,141	4,877,828,200	PE100
V100007441_L3_ANIlmkRAAAB-509	13,572,400	2,714,480,000	PE100
V100007441_L3_ANIlmkRAAAB-510	26,529,287	5,305,857,400	PE100
V100007441_L3_ANIlmkRAAAB-511	20,215,598	4,043,119,600	PE100
V100007441_L3_ANIlmkRAAAB-512	23,989,934	4,797,986,800	PE100
V100007441_L3_ANIlmkRAAAB-513	21,957,163	4,391,432,600	PE100
V100007441_L3_ANIlmkRAAAB-514	22,462,683	4,492,536,600	PE100
V100007441_L3_ANIlmkRAAAB-515	22,148,414	4,429,682,800	PE100
V100007441_L3_ANIlmkRAAAB-516	28,664,967	5,732,993,400	PE100
V100007748_L1_ANIlmkRAAAA-501	21,493,362	4,298,672,400	PE100
V100007748_L1_ANIlmkRAAAA-502	13,185,319	2,637,063,800	PE100
V100007748_L1_ANIlmkRAAAA-503	18,126,413	3,625,282,600	PE100
V100007748_L1_ANIlmkRAAAA-504	20,654,887	4,130,977,400	PE100
V100007748_L1_ANIlmkRAAAA-505	19,906,112	3,981,222,400	PE100
V100007748_L1_ANIlmkRAAAA-506	19,301,881	3,860,376,200	PE100
V100007748_L1_ANIlmkRAAAA-507	22,982,228	4,596,445,600	PE100
V100007748_L1_ANIlmkRAAAA-508	23,877,935	4,775,587,000	PE100
V100007748_L1_ANIlmkRAAAB-509	22,885,564	4,577,112,800	PE100
V100007748_L1_ANIlmkRAAAB-510	26,604,522	5,320,904,400	PE100
V100007748_L1_ANIlmkRAAAB-511	25,218,596	5,043,719,200	PE100
V100007748_L1_ANIlmkRAAAB-512	24,092,752	4,818,550,400	PE100
V100007748_L1_ANIlmkRAAAB-513	24,069,752	4,813,950,400	PE100
V100007748_L1_ANIlmkRAAAB-514	22,129,222	4,425,844,400	PE100
V100007748_L1_ANIlmkRAAAB-515	21,813,269	4,362,653,800	PE100
V100007748_L1_ANIlmkRAAAB-516	28,052,658	5,610,531,600	PE100
V100007748_L2_ANIlmkRAAAA-501	21,130,668	4,226,133,600	PE100
V100007748_L2_ANIlmkRAAAA-502	13,691,502	2,738,300,400	PE100
V100007748_L2_ANIlmkRAAAA-503	18,067,444	2,601,711,936	PE100
V100007748_L2_ANIlmkRAAAA-504	20,379,298	4,075,859,600	PE100
V100007748_L2_ANIlmkRAAAA-505	19,577,431	3,915,486,200	PE100
V100007748_L2_ANIlmkRAAAA-506	18,927,753	3,785,550,600	PE100
V100007748_L2_ANIlmkRAAAA-507	22,615,493	4,523,098,600	PE100
V100007748_L2_ANIlmkRAAAA-508	23,458,825	4,691,765,000	PE100
V100007748_L2_ANIlmkRAAAB-509	22,818,373	4,563,674,600	PE100
V100007748_L2_ANIlmkRAAAB-510	26,162,903	5,232,580,600	PE100

V100007748_L2_ANIlmkRAAAB-511	24,745,253	4,949,050,600	PE100
V100007748_L2_ANIlmkRAAAB-512	23,481,115	4,696,223,000	PE100
V100007748_L2_ANIlmkRAAAB-513	23,669,505	4,733,901,000	PE100
V100007748_L2_ANIlmkRAAAB-514	21,820,232	4,364,046,400	PE100
V100007748_L2_ANIlmkRAAAB-515	21,386,445	4,277,289,000	PE100
V100007748_L2_ANIlmkRAAAB-516	27,576,176	5,515,235,200	PE100
Total	1,027,724,277	204,533,078,536	PE100

Supplementary Table S23. Statistics of the Hi-C reads for *C. brevimanus*

Sequencing ID	Read pairs	Total bases (bp)	Sequencing strategy
BDHC200000561-1A_L2	6,547,794	1,964,338,200	PE150
BDHC200000561-1A_L3	342,895,358	102,868,607,400	PE150
BDHC200000561-1A_L4	377,913,665	113,374,099,500	PE150
BDHC200000562-1A_L1	284,239,937	85,271,981,100	PE150
BDHC200000562-1A_L2	324,853,648	97,456,094,400	PE150
BDHC200000562-1A_L3	134,551,915	40,365,574,500	PE150
BDHC200000563-1A_L1	267,852,082	80,355,624,600	PE150
BDHC200000563-1A_L2	308,066,378	92,419,913,400	PE150
BDHC200000563-1A_L4	209,957,288	62,987,186,400	PE150
BDHC200000576-1A_L1	261,975,649	78,592,694,700	PE150
BDHC200000576-1A_L2	5,236,886	1,571,065,800	PE150
BDHC200000576-1A_L3	236,681,185	71,004,355,500	PE150
BDHC200000576-1A_L4	183,819,262	55,145,778,600	PE150
Total	2,944,591,047	883,377,314,100	PE150

Supplementary Table S24. Statistics of the Hi-C reads for *P. platypus*

Sequencing ID	Read pairs	Total bases (bp)	Sequencing strategy
L1	610,171,560	122,034,312,000	PE100
L2	576,326,352	115,265,270,400	PE100
L3	422,180,255	84,436,051,000	PE100
Total	1,608,678,167	321,735,633,400	PE100

Supplementary Table S25. Statistics of the Hi-C reads for *P. trituberculatus*

Sequencing ID	Read pairs	Total bases (bp)	Sequencing strategy
FRHC190047931-1a_L2_1_clean	319,848,853	95,954,655,900	PE150
Total	319,848,853	95,954,655,900	PE150

Supplementary Table S26. Statistics of the transcript reads for 10 species

Species	Read pairs	Total bases (bp)	Sequencing strategy
<i>A. integerrimus</i>	56,316,167	16,894,850,100	PE150
<i>P. platypus</i>	125,602,883	25,120,576,600	PE100
<i>P. trituberculatus</i>	25,044,513	7,513,353,900	PE150
<i>D. horrida</i>	83,490,101	25,047,030,300	PE150
<i>C. philargius</i>	84,956,076	25,486,822,800	PE150
<i>L. dehaani</i>	84,488,014	25,346,404,200	PE150
<i>R. ranina</i>	111,494,234	33,448,270,200	PE150
<i>S. planum</i>	136,876,294	41,062,888,200	PE150
<i>C. carnifex</i>	141,597,065	42,479,119,500	PE150
<i>C. brevimanus</i>	156,029,316	46,808,794,800	PE150

Supplementary Table S27. Statistics of the transcript reads for *A. integerrimus*

Sequencing ID	Read pairs	Total bases (bp)	Sequencing strategy
AJXjingA	28,330,021	8,499,006,300	PE150
AJXxinA	27,986,146	8,395,843,800	PE150
Total	56,316,167	16,894,850,100	PE150

Supplementary Table S28. Statistics of the transcript reads for *P. platypus*

Sequencing ID	Read pairs	Total bases (bp)	Sequencing strategy
Gill	31,288,152	6,257,630,400	PE100
Heart	33,116,506	6,623,301,200	PE100
Liver	30,668,756	6,133,751,200	PE100
Stomach	30,529,469	6,105,893,800	PE100
Total	125,602,883	25,120,576,600	PE100

Supplementary Table S29. Statistics of the transcript reads for *C. brevimanus*

Sequencing ID	Read pairs	Total bases (bp)	Sequencing strategy
JJX_batch1	31,418,750	9,425,625,000	PE150
JJX_batch2	86,586,353	25,975,905,900	PE150
JJX_batch3	38,024,213	11,407,263,900	PE150
Total	156,029,316	46,808,794,800	PE150

Supplementary Table S30. Statistics of the transcript reads for *D. horrida*

Sequencing ID	Read pairs	Total bases (bp)	Sequencing strategy
LXganA	28,126,493	8,437,947,900	PE150
LXjingA	27,652,463	8,295,738,900	PE150
LXxinA	27,711,145	8,313,343,500	PE150
Total	83,490,101	25,047,030,300	PE150

Supplementary Table S31. Statistics of the transcript reads for *C. philargius*

Sequencing ID	Read pairs	Total bases (bp)	Sequencing strategy
MTXganA	28,166,565	8,449,969,500	PE150
MTXjingA	28,213,724	8,464,117,200	PE150
MTXxinA	28,575,787	8,572,736,100	PE150
Total	84,956,076	25,486,822,800	PE150

Supplementary Table S32. Statistics of the transcript reads for *L. dehaani*

Sequencing ID	Read pairs	Total bases (bp)	Sequencing strategy
MXganA	28,282,465	8,484,739,500	PE150
MXjingchaoA	28,457,048	8,537,114,400	PE150
MXxinA	27,748,501	8,324,550,300	PE150
Total	84,488,014	25,346,404,200	PE150

Supplementary Table S33. Statistics of the transcript reads for *P. trituberculatus*

Sequencing ID	Read pairs	Total bases (bp)	Sequencing strategy
SZX_Lp	25,044,513	7,513,353,900	PE150
Total	25,044,513	7,513,353,900	PE150

Supplementary Table S34. Statistics of the transcript reads for *R. ranina*

Sequencing ID	Read pairs	Total bases (bp)	Sequencing strategy
WXganA	28,126,670	8,438,001,000	PE150
WXjingchaoA	27,813,062	8,343,918,600	PE150
WXshengzhixianA	28,052,740	8,415,822,000	PE150
WXxinA	27,501,762	8,250,528,600	PE150
Total	111,494,234	33,448,270,200	PE150

Supplementary Table S35. Statistics of the transcript reads for *S. planum*

Sequencing ID	Read pairs	Total bases (bp)	Sequencing strategy
19082201-ganyixianA	34,650,289	10,395,086,700	PE150
19082201-jingchaoA	33,506,043	10,051,812,900	PE150
19082201-jirouA	34,517,690	10,355,307,000	PE150
19082201-xinzangA	34,202,272	10,260,681,600	PE150
Total	136,876,294	41,062,888,200	PE150

Supplementary Table S36. Statistics of the transcript reads for *C. carnifex*

Sequencing ID	Read pairs	Total bases (bp)	Sequencing strategy
18080701-ganyixianA	35,907,176	10,772,152,800	PE150
18080701-jiedizuzhiA	35,980,735	10,794,220,500	PE150
18080701-jirouA	33,560,563	10,068,168,900	PE150
18080701-luanchaoA	36,148,591	10,844,577,300	PE150
Total	141,597,065	42,479,119,500	PE150

Supplementary Table S37. Statistics of the genome survey results

species	heterozygosity	genome size	software
<i>A. integerrimus</i>	1.91%	2,432,560,725	kmerfreq
<i>P. platypus</i>	-	5,491,400,507	jellyfish
<i>P. trituberculatus</i>	0.99%	926,181,981	kmerfreq
<i>D. horrida</i>	1.91%	2,643,904,376	kmerfreq
<i>C. philargius</i>	-	640,001,073	jellyfish
<i>L. dehaani</i>	1.04%	2,643,818,683	kmerfreq
<i>R. ranina</i>	0.91%	7,881,984,894	kmerfreq
<i>S. planum</i>	2.46%	16,044,227,866	kmerfreq
<i>C. carnifex</i>	-	1,416,988,930	jellyfish
<i>C. brevimanus</i>	1.46%	4,926,944,088	kmerfrep

Supplementary Table S38. Statistics of the polished contig level genome assembly results

species	Total length(bp)	Total number	N50 (bp)
<i>A. integerrimus</i>	2,613,035,345	3,056	2,181,172
<i>P. platypus</i>	5,041,403,153	20,066	400,250
<i>C. brevimanus</i>	4,734,685,508	6,556	2,024,488
<i>D. horrida</i>	2,577,612,728	5,819	991,837
<i>C. philargius</i>	707,342,361	607	5,540,472
<i>L. dehaani</i>	2,147,180,685	1,982	3,046,074
<i>E. j. sinensis</i>	1,163,278,087	2,909	897,864
<i>P. trituberculatus</i>	1,022,012,505	1,040	3,335,278
<i>R. ranina</i>	7,478,065,989	17,325	639,209
<i>S. planum</i>	17,711,448,170	558,657	51,520
<i>C. carnifex</i>	1,503,958,490	2,412	3,187,901

Supplementary Table S39. Statistics of the polished contig level genome assembly of *A. integerrimus*

Term	Size (bp)	Number
N90	320,224	1,645
N80	563,841	1,027
N70	966,470	668
N60	1,492,101	449
N50	2,181,172	306
Max length (bp)	15,481,825	-
Total size (bp)	2,613,035,345	3,056
Total number (>500 bp)	-	3,056
Total number (>5kb)	-	3,056

Supplementary Table S40. Statistics of the polished contig level genome assembly of *P. platypus*

Term	Size (bp)	Number
N90	107,734	13,018
N80	165,798	9,267
N70	231,694	6,698
N60	305,392	4,796
N50	400,250	3,345
Max length (bp)	3,824,894	-
Total size (bp)	5,041,403,153	20,066
Total number (>500 bp)	-	20,066
Total number (>5kb)	-	20,066

Supplementary Table S41. Statistics of the polished contig level genome assembly of *C.****brevimanus***

Term	Size (bp)	Number
N90	276,773	3,311
N80	499,678	2,026
N70	843,683	1,289
N60	1,352,583	844
N50	2,024,488	554
Max length (bp)	27,512,322	-
Total size (bp)	4,734,685,508	6,556
Total number (>500 bp)	-	6,556
Total number (>5kb)	-	6,556

Supplementary Table S42. Statistics of the polished contig level genome assembly of *D. horrida*

Term	Size (bp)	Number
N90	176,521	3,131
N80	310,638	2,032
N70	518,780	1,392
N60	738,330	975
N50	991,837	672
Max length (bp)	6,675,626	-
Total size (bp)	2,577,612,728	5,819
Total number (>500 bp)	-	5,819
Total number (>5kb)	-	5,819

Supplementary Table S43. Statistics of the polished contig level genome assembly of *C. philargius*

Term	Size (bp)	Number
N90	374,690	201
N80	1,692,279	106
N70	3,122,554	77
N60	4,577,093	58
N50	5,540,472	45
Max length (bp)	16,062,582	-
Total size (bp)	707,342,361	607
Total number (>500 bp)	-	607
Total number (>5kb)	-	607

Supplementary Table S44. Statistics of the polished contig level genome assembly of *L. dehaani*

Term	Size (bp)	Number
N90	443,766	883
N80	983,498	560
N70	1,640,736	392
N60	2,303,627	281
N50	3,046,074	201
Max length (bp)	16,349,844	-
Total size (bp)	2,147,180,685	1,982
Total number (>500 bp)	-	1,982
Total number (>5kb)	-	1,982

Supplementary Table S45. Statistics of the polished contig level genome assembly of *P.****trituberculatus***

Term	Size (bp)	Number
N90	366,928	429
N80	924,089	253
N70	1,670,565	172
N60	2,576,397	122
N50	3,335,278	87
Max length (bp)	15,486,717	-
Total size (bp)	1,022,012,505	1,040
Total number (>500 bp)	-	1,040
Total number (>5kb)	-	1,040

Supplementary Table S46. Statistics of the polished contig level genome assembly of *R. ranina*

Term	Size (bp)	Number
N90	190,870	11,731
N80	272,889	8,458
N70	368,731	6,099
N60	482,558	4,325
N50	639,209	2,965
Max length (bp)	6,704,943	-
Total size (bp)	7,478,065,989	17,325
Total number (>500 bp)	-	17,325
Total number (>5kb)	-	17,325

Supplementary Table S47. Statistics of the polished contig level genome assembly of *S. planum*

Term	Size (bp)	Number
N90	15,258	339,518
N80	24,003	248,170
N70	32,615	184,979
N60	41,138	136,568
N50	51,520	98,041
Max length (bp)	858,247	-
Total size (bp)	17,711,448,170	558,657
Total number (>500 bp)	-	558,657
Total number (>5kb)	-	498,106

Supplementary Table S48. Statistics of the polished contig level genome assembly of *C. carnifex*

Term	Size (bp)	Number
N90	197,529	1,207
N80	362,409	630
N70	720,005	327
N60	1,546,542	177
N50	3,187,901	108
Max length (bp)	21,469,221	-
Total size (bp)	1,503,958,490	2,412
Total number (>500 bp)	-	2,412
Total number (>5kb)	-	2,412

Supplementary Table S49. Statistics of the chromosome level genome assembly results of *P. platypus*

Term	Chromosome-level genome		Contig-level genome	
	Size (bp)	Number	Size (bp)	Number
N90	29,998,146	84	100,123	14,793
N80	36,444,511	69	148,779	10,673
N70	44,103,325	57	204,227	7,777
N60	51,087,984	46	266,454	5,616
N50	55,470,530	37	344,241	3,946
Max length (bp)	148,438,538	-	3,415,958	-
Total size (bp)	5,043,581,053	2,434	5,041,403,153	24,213
Total number (>500 bp)	-	2,434	-	24,213
Total number (>5kb)	-	662	-	22,435
chromosome number	103		-	
chromosome mounting ratio	97.91%		-	

Supplementary Table S50. Statistics of the chromosome level genome assembly results of *C. brevimanus*

Term	Chromosome-level genome		Contig-level genome	
	Size (bp)	Number	Size (bp)	Number
N90	22,895,174	99	230,046	3,847
N80	32,153,061	82	420,795	2,335
N70	36,926,850	68	706,679	1,466
N60	40,036,666	56	1,164,633	940
N50	42,958,566	44	1,754,762	609
Max length (bp)	75,339,048	-	18,206,006	-
Total size (bp)	4,735,323,108	3,720	4,734,685,508	10,096
Total number (>500 bp)	-	3,720	-	10,096
Total number (>5kb)	-	2,236	-	8,600
chromosome number	117		-	
chromosome mounting ratio	96.54%		-	

Supplementary Table S51. Statistics of the chromosome level genome assembly results of *P. trituberculatus*

Term	Chromosome-level genome		Contig-level genome	
	Size (bp)	Number	Size (bp)	Number
N90	10,725,976	42	192,035	736
N80	14,447,815	34	502,893	406
N70	17,180,601	28	964,717	263
N60	18,717,106	22	1,488,138	177
N50	21,677,145	17	2,146,809	120
Max length (bp)	43,752,247	-	14,543,453	-
Total size (bp)	1,022,190,805	1,628	1,022,012,505	3,411
Total number (>500 bp)	-	1,628	-	3,407
Total number (>5kb)	-	1,152	-	2,901
chromosome number	49		-	
chromosome mounting ratio	95.89%		-	

Supplementary Table S52. Statistics of the mapping ratio of the genomic short reads to the genome assembly.

Term	Total Mapped reads		Properly paired reads		Single mapped reads	
	Number	Percent	Number	Percent	Number	Percent
<i>A. integerrimus</i>	2,100,155,556	99.65	2,040,649,964	97.04	2,595,904	0.12
<i>P. platypus</i>	4,236,372,723	97.15	3,925,841,052	90.58	49,620,281	1.14
<i>C. brevimanus</i>	2,910,833,887	99.48	2,735,893,678	94.62	9,761,423	0.34
<i>D. horrida</i>	2,251,402,874	99.37	2,177,394,142	96.35	3,742,984	0.17
<i>C. philargius</i>	2,070,591,467	99.72	2,010,917,574	97.09	2,799,885	0.14
<i>L. dehaani</i>	1,725,896,412	99.47	1,673,432,844	96.63	2,765,338	0.16
<i>P. trituberculatus</i>	2,013,194,818	98.85	1,954,608,328	96.21	4,164,622	0.20
<i>R. ranina</i>	5,944,217,062	99.03	5,747,871,724	96.00	8,819,410	0.15
<i>S. planum</i>	4,337,052,284	99.55	3,774,205,294	87.32	5,834,013	0.13
<i>C. carnifex</i>	2,023,778,193	99.28	1,969,515,382	96.89	3,821,254	0.19

Supplementary Table S53. Merquery evaluation of genome assembly using Illumina reads.

genome	QV	Completeness	Duplication
<i>A. integerrimus</i>	32.56	83.63	4.00
<i>P. platypus</i>	32.02	73.99	4.33
<i>C. brevimanus</i>	35.88	80.83	4.22
<i>D. horrida</i>	32.63	85.26	3.68
<i>C. philargius</i>	32.79	89.21	2.96
<i>L. dehaani</i>	31.76	88.73	2.31
<i>P. trituberculatus</i>	34.28	88.57	2.67
<i>R. ranina</i>	30.56	81.11	5.35
<i>S. planum</i>	14.11	75.63	28.34
<i>C. carnifex</i>	26.97	81.83	3.19
Average	30.36	82.88	6.10

Supplementary Table S54. Statistics on the presence of conserved BUSCO orthologs of genome assembly.

species	Complete BUSCOs (C)	Fragmented BUSCOs (F)	Missing BUSCOs (M)	Total BUSCOs	Summar ize
<i>A. integerrimus</i>	967	28	18	1,013	95.50%
<i>P. platypus</i>	896	60	57	1,013	88.50%
<i>C. brevimanus</i>	965	28	20	1,013	95.30%
<i>D. horrida</i>	951	33	29	1,013	93.90%
<i>C. philargius</i>	964	30	19	1,013	95.20%
<i>L. dehaani</i>	965	23	25	1,013	95.30%
<i>P. trituberculatus</i>	950	35	28	1,013	93.80%
<i>R. ranina</i>	699	187	127	1,013	69.00%
<i>S. planum</i>	615	242	156	1,013	60.70%
<i>C. carnifex</i>	959	30	24	1,013	94.70%

Supplementary Table S55. Statistics on the presence of conserved BUSCO orthologs of protein-coding genes.

species	gene number	Complete BUSCOs	Fragmented BUSCOs	Missing BUSCOs	Total BUSCOs	Summarize
<i>A. integerrimus</i>	28,007	997	5	11	1,013	98.40%
<i>P. platypus</i>	27,109	937	19	57	1,013	92.50%
<i>C. brevimanus</i>	27,556	994	8	11	1,013	98.10%
<i>D. horrida</i>	28,521	987	8	18	1,013	97.50%
<i>C. philargius</i>	26,168	1,002	5	6	1,013	98.90%
<i>L. dehaani</i>	27,967	999	6	8	1,013	98.60%
<i>P. trituberculatus</i>	26,953	985	10	18	1,013	97.20%
<i>R. ranina</i>	27,839	726	104	183	1,013	71.60%
<i>S. planum</i>	27,214	640	104	269	1,013	63.20%
<i>C. carnifex</i>	27,043	995	6	12	1,013	98.20%

Supplementary Table S56. Different software and parameters used in genome assembly of *S. planum*

Version	Software	Data	Parameters
V1	wtdbg2.1	corrected reads	-p 21 -k 0 -AS 2 -E 1 -K 0.05 -s 0.5
V2	wtdbg_huge	corrected reads	-p 21 -k 0 -AS 4 -K 0.05 -s 0.5 -L 10000
V3	wtdbg_huge	corrected reads	-p 19 -k 0 -AS 2 -K 0.05 -s 0.5 -E 1 -L 15000
V4	wtdbg2.5	corrected reads	-p 21 -k 0 -AS 4 -K 0.05 -s 0.5
V5	wtdbg2.5	corrected reads	-p 19 -k 0 -AS 4 -K 0.05 -s 0.5
V6	wtdbg2.1	raw reads	-p 21 -k 0 -AS 4 -K 0.05 -s 0.5
V7	wtdbg2.5	raw reads	-p 21 -k 0 -AS 4 -K 0.05 -s 0.5
V8	shasta	corrected reads	default
V9	shasta	corrected reads	--memoryBacking 2M --memoryMode filesystem
V10	wtdbg2.5	raw reads	-g 16g --keep-isolated-nodes --no-read-clip --ctg-min-length 1000 -p 21 -k 0 -AS 2 -K 0.05 -s 0.05

Supplementary Table S57. Statistics of published crustacean assemblies with big genome size (>3Gb)

Organism Scientific Name	Assembly Accession	Contig N50 (bp)	Total length(bp)	Complete busco (Arthropoda)
<i>Bathynomus jamesi</i>	GCA_023014485.1	586,500	5,894,292,451	92.10%
<i>Euphausia superba</i>	CNGB-CNP0001930	178,989	47,969,258,292	61.60%
<i>Paralithodes platypus</i>	GCA_013283005.1	147,786	4,805,175,703	71.77%
<i>Cherax quadricarinatus</i>	GCA_026875155.2	146,379	5,247,605,071	81.15%
<i>Cherax destructor</i>	GCA_009830355.1	80,900	3,336,744,225	81.64%
<i>Trachelipus rathkii</i>	GCA_015478945.1	39,690	5,161,626,233	41.36%
<i>Procambarus virginalis</i>	GCA_020271785.1	12,232	3,700,845,369	67.03%
<i>Paralithodes camtschaticus</i>	GCA_018397895.1	5,760	3,809,538,835	44.42%
<i>Gammarus roeselii</i>	GCA_016164225.1	4,736	3,239,433,295	35.14%
<i>Cherax quadricarinatus</i>	GCA_009761615.1	3,285	3,236,648,033	69.99%
<i>Procambarus virginalis</i>	GCA_002838885.1	1,187	3,290,406,880	84.80%
<i>Palaemon carinicauda</i>	GCA_004011675.1	696	6,699,723,695	12.64%

Supplementary Table S58. Functional annotation statistics of coding genes

species	Total	Annotated	InterPro	GO	KEGG	Swissprot	TrEMBL	Cog
<i>A. integerrimus</i>	28,007	22,761	17,769	10,463	14,823	16,284	21,829	6,855
<i>P. platypus</i>	27,109	24,661	20,280	11,057	18,045	18,637	24,307	8,480
<i>C. brevimanus</i>	27,556	23,498	19,325	12,388	16,853	19,035	22,730	8,990
<i>D. horrida</i>	28,521	22,230	16,797	9,890	13,900	15,122	21,618	6,838
<i>C. philargius</i>	26,168	17,658	13,730	8,794	11,569	13,319	17,207	5,695
<i>L. dehaani</i>	27,967	23,575	16,194	10,604	15,721	17,278	22,865	7,098
<i>P. trituberculatus</i>	26,953	18,205	14,237	8,879	11,979	12,977	17,044	5,706
<i>R. ranina</i>	27,839	24,537	17,633	8,915	16,302	17,070	24,119	6,536
<i>S. planum</i>	27,214	19,295	13,214	6,744	12,059	12,270	18,442	5,009
<i>C. carnifex</i>	27,043	20,416	15,646	9,470	13,647	15,257	19,674	6,079

Supplementary Table S59. The length and proportion of repeated sequences annotated by different annotation methods for all species in this project

Species	Trf	Repeatmasker	Proteinmask	<i>de novo</i>	Total
<i>A. integerrimus</i>	447,032,189 (17.11%)	96,212,722 (3.68%)	490,820,700 (18.78%)	1,678,598,431 (64.24%)	1,813,771,201 (69.41%)
<i>P. platypus</i>	571,062,278 (11.32%)	314,854,470 (6.24%)	1,238,527,085 (24.56%)	3,870,687,491 (76.74%)	4,205,198,005 (83.38%)
<i>C. brevimanus</i>	501,204,503 (10.58%)	1,246,267,061 (26.32%)	1,130,487,460 (23.87%)	3,205,522,688 (67.69%)	3,531,207,807 (74.57%)
<i>D. horrida</i>	297,353,776 (11.54%)	114,429,899 (4.44%)	656,625,785 (25.47%)	1,805,703,304 (70.05%)	1,900,751,609 (73.74%)
<i>C. philargius</i>	162,896,664 (23.03%)	22,475,169 (3.18%)	27,099,687 (3.83%)	333,039,753 (47.08%)	356,802,162 (50.44%)
<i>L. dehaani</i>	333,875,808 (15.55%)	72,673,874 (3.38%)	380,923,315 (17.74%)	1,255,423,465 (58.47%)	1,412,719,546 (65.79%)
<i>P. trituberculatus</i>	204,927,259 (20.05%)	154,775,820 (15.14%)	102,263,944 (10.00%)	508,180,604 (49.71%)	566,946,170 (55.46%)
<i>R. ranina</i>	1,318,790,050 (17.64%)	1,100,504,297 (14.72%)	3,686,946,421 (49.30%)	6,081,532,602 (81.32%)	6,781,991,132 (90.69%)
<i>S. planum</i>	2,216,121,384 (12.51%)	1,046,439,115 (5.91%)	2,155,880,189 (12.17%)	13,804,597,630 (77.94%)	16,967,111,973 (95.80%)
<i>C. carnifex</i>	282,301,790 (18.77%)	58,481,546 (3.89%)	235,387,173 (15.65%)	839,941,673 (55.85%)	922,542,683 (61.34%)

Supplementary Table S60. For all *de novo* annotated repeats of all species used in this study, the first percentage value in parentheses represents the ratio of the length of the type sequence to the *de novo* annotated repeats, and the second percentage value represents the ratio of the length of the type sequence to the genome size of the corresponding species

Species	DNA	LINE	LTR	SINE	Unknown
<i>A. integerrimus</i>	246,236,242 (17.45%/9.42%)	558,534,914 (39.58%/21.37%)	90,812,817 (6.44%/3.48%)	44,625,784 (3.16%/1.71%)	470,944,293 (33.37%/18.02%)
<i>P. platypus</i>	328,934,902 (8.89%/6.52%)	1,162,672,783 (31.41%/23.05%)	573,871,567 (15.50%/11.38%)	61,728,710 (1.67%/1.22%)	1,574,845,990 (42.54%/31.22%)
<i>H. azteca</i>	18,098,619 (14.02%/3.29%)	21,390,266 (16.57%/3.88%)	2,562,001 (1.98%/0.47%)	362,347 (0.28%/0.07%)	86,702,269 (67.15%/15.74%)
<i>P. monodon</i>	50,737,562 (6.86%/2.12%)	366,493,492 (49.58%/15.31%)	81,941,708 (11.09%/3.42%)	35,587,721 (4.81%/1.49%)	204,399,270 (27.65%/8.54%)
<i>C. brevimanus</i>	250,404,913 (8.67%/5.29%)	1,081,263,432 (37.46%/22.83%)	338,341,645 (11.72%/7.15%)	28,436,877 (0.99%/0.60%)	1,188,076,270 (41.16%/25.09%)
<i>C. sapidus</i>	20,538,334 (8.76%/2.06%)	60,623,283 (25.87%/6.07%)	18,453,131 (7.87%/1.85%)	3,298,462 (1.41%/0.33%)	131,431,168 (56.08%/13.17%)
<i>D. horrida</i>	268,664,323 (16.97%/10.42%)	659,166,044 (41.64%/25.57%)	174,201,575 (11.00%/6.76%)	46,692,962 (2.95%/1.81%)	434,471,067 (27.44%/16.86%)
<i>C. philargius</i>	19,960,398 (10.60%/2.82%)	44,665,568 (23.71%/6.31%)	7,824,379 (4.15%/1.11%)	2,131,103 (1.13%/0.30%)	113,762,536 (60.40%/16.08%)
<i>H. americanus</i>	153,189,862 (13.88%/6.68%)	259,438,961 (23.50%/11.32%)	97,685,983 (8.85%/4.26%)	7,856,292 (0.71%/0.34%)	585,791,910 (53.06%/25.56%)
<i>L. dehaani</i>	73,207,315 (6.83%/3.41%)	509,123,994 (47.50%/23.71%)	37,613,224 (3.51%/1.75%)	11,310,852 (1.06%/0.53%)	440,648,687 (41.11%/20.52%)
<i>S. paramamosain</i>	91,779,138 (13.04%/5.94%)	282,411,625 (40.13%/18.27%)	62,963,258 (8.95%/4.07%)	4,474,427 (0.64%/0.29%)	262,123,651 (37.25%/16.95%)
<i>P. japonicus</i>	17,477,905 (5.14%/1.03%)	93,112,455 (27.37%/5.46%)	5,099,428 (1.50%/0.30%)	4,216,931 (1.24%/0.25%)	220,276,251 (64.75%/12.92%)
<i>E. j. sinensis_SA</i>	54,154,837 (7.17%/3.07%)	236,416,237 (31.29%/13.39%)	37,399,672 (4.95%/2.12%)	11,985,027 (1.59%/0.68%)	415,712,151 (55.01%/23.54%)
<i>P. trituberculatus</i>	27,643,959 (8.38%/2.70%)	131,302,973 (39.80%/12.85%)	17,827,847 (5.40%/1.74%)	17,740,831 (5.38%/1.74%)	135,374,652 (41.04%/13.24%)
<i>R. ranina</i>	455,707,764 (8.03%/6.09%)	3,838,615,968 (67.63%/51.33%)	438,609,501 (7.73%/5.87%)	250,743,398 (4.42%/3.35%)	691,952,227 (12.19%/9.25%)

<i>P. clarkii</i>	99,287,808 (5.99%/3.63%)	686,560,272 (41.42%/25.10%)	203,339,371 (12.27%/7.43%)	56,081,060 (3.38%/2.05%)	612,108,745 (36.93%/22.38%)
<i>S. planum</i>	528,631,212 (4.09%/2.98%)	6,419,872,105 (49.71%/36.25%)	1,553,709,438 (12.03%/8.77%)	93,540,379 (0.72%/0.53%)	4,320,064,087 (33.45%/24.39%)
<i>C. opilio</i>	167,514,550 (15.73%/8.36%)	280,375,369 (26.33%/14.00%)	56,651,101 (5.32%/2.83%)	18,126,787 (1.70%/0.91%)	542,153,605 (50.91%/27.07%)
<i>C. carnifex</i>	58,983,677 (9.46%/3.92%)	265,815,076 (42.63%/17.67%)	34,908,612 (5.60%/2.32%)	23,256,098 (3.73%/1.55%)	240,582,139 (38.58%/16.00%)
<i>P. chinensis</i>	36,548,809 (7.58%/2.31%)	184,981,794 (38.38%/11.70%)	16,673,401 (3.46%/1.05%)	35,551,294 (7.38%/2.25%)	208,189,208 (43.20%/13.17%)

Supplementary Table S61. Statistical significance of relative usage frequency of synonymous codons of crab and non-crab RSCU

Amino_acid	Codon	<i>p-value</i>
Ala	GCC	0.034066
	GCA	0.722818
	GCU	0.0316
	GCG	0.869492
Arg	AGG	0.017645
	CGC	0.926757
	AGA	0.059072
	CGG	0.001146
	CGU	0.168428
Asn	CGA	1.08E-07
	AAC	0.003886
	AAU	0.003886
Asp	GAC	0.133929
	GAU	0.133929
Cys	UGU	0.658375
	UGC	0.658375
Gln	CAG	0.030866
	CAA	0.030866
Glu	GAG	9.21E-08
	GAA	9.21E-08
Gly	GGC	0.776105
	GGA	0.046683
	GGG	6.77E-05
	GGU	0.67738
His	CAC	0.000215
	CAU	0.000215
Ile	AUC	0.092795
	AUU	0.003279
	AUA	0.860998
Leu	CUG	0.002304
	CUC	0.461704
	CUU	0.023932
	UUG	0.016999
	CUA	0.988142
Lys	UUA	0.011675
	AAG	0.004057
	AAA	0.004057

Supplementary Table S62. CNet top 15 results of gene family expansion enrichment

Type	Top-level	Term
Brachyura	1	RAVE complex
	2	proton-transporting V-type ATPase complex assembly
	3	vacuolar proton-transporting V-type ATPase complex assembly
	4	proton-transporting two-sector ATPase complex assembly
	5	vacuolar acidification
	6	lumen formation, open tracheal system
	7	intracellular pH reduction
	8	pH reduction
	9	regulation of intracellular pH
	10	regulation of cellular pH
	11	GO:0030004
	12	regulation of pH
	13	synaptic vesicle membrane
	14	exocytic vesicle membrane
	15	GO:0055067
<i>L. dehaani</i>	1	extracellular ligand-gated monoatomic ion channel activity
	2	ligand-gated monoatomic ion channel activity
	3	ligand-gated channel activity
	4	transmitter-gated channel activity
	5	transmitter-gated monoatomic ion channel activity
	6	glutamate receptor activity
	7	neurotransmitter receptor activity
	8	ionotropic glutamate receptor activity
	9	glutamate receptor signaling pathway
	10	ionotropic glutamate receptor signaling pathway
	11	organic anion transmembrane transporter activity
	12	excitatory extracellular ligand-gated monoatomic ion channel activity
	13	chemical synaptic transmission, postsynaptic
	14	regulation of postsynaptic membrane potential
	15	excitatory postsynaptic potential
Decapoda	1	ligand-gated monoatomic ion channel activity
	2	ligand-gated channel activity
	3	extracellular ligand-gated monoatomic ion channel activity
	4	transmitter-gated monoatomic ion channel activity
	5	transmitter-gated channel activity
	6	neurotransmitter receptor activity
	7	ionotropic glutamate receptor activity
	8	monoatomic anion transmembrane transporter activity
	9	glutamate receptor activity
	10	ionotropic glutamate receptor signaling pathway

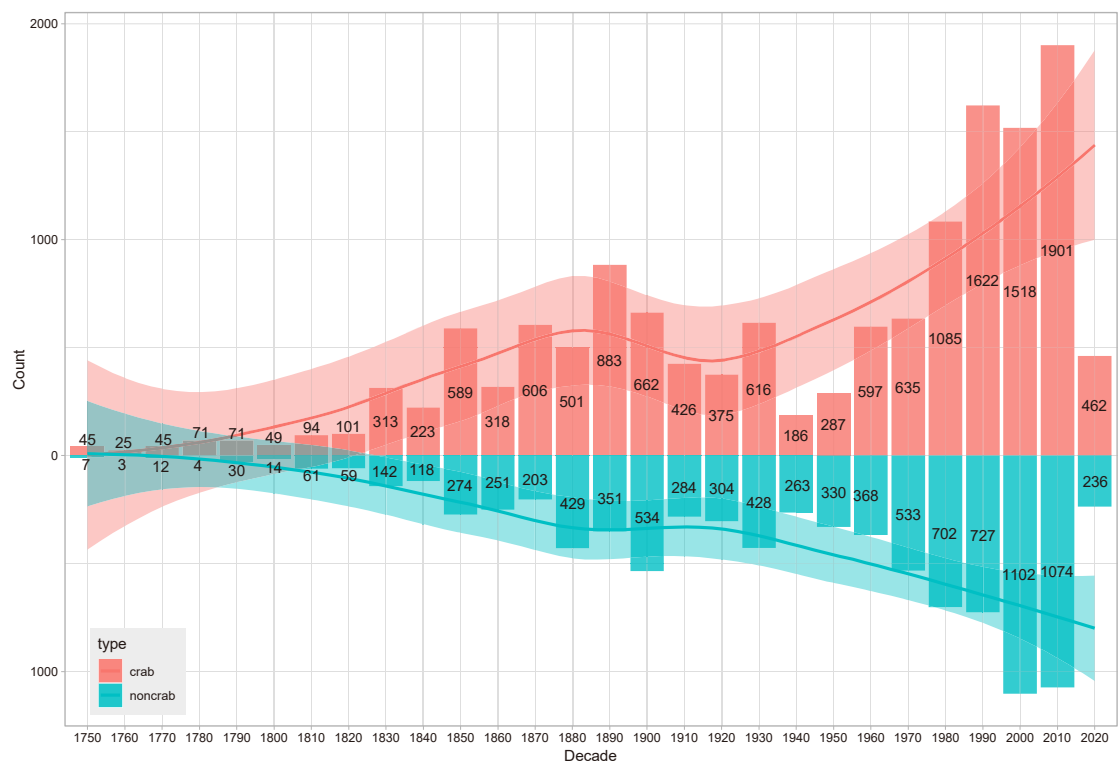
	11	glutamate receptor signaling pathway
	12	minus-end-directed microtubule motor activity
	13	dynein light intermediate chain binding
	14	dynein intermediate chain binding
	15	dynein light chain binding
<i>R. ranina</i>	1	microtubule motor activity
	2	thigmotaxis
	3	cytoskeletal motor activity
	4	kinesin complex
	5	central nervous system projection neuron axonogenesis
	6	central nervous system neuron axonogenesis
	7	retrograde vesicle-mediated transport, Golgi to endoplasmic reticulum
	8	microtubule associated complex
	9	antigen processing and presentation of exogenous peptide antigen via MHC class II
	10	sister chromatid cohesion
	11	mitotic metaphase chromosome alignment
	12	antigen processing and presentation of peptide antigen via MHC class II
	13	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II
	14	metaphase chromosome alignment
	15	antigen processing and presentation of peptide antigen
<i>Meiura</i>	1	glutamate receptor activity
	2	glutamate receptor signaling pathway
	3	ionotropic glutamate receptor activity
	4	ionotropic glutamate receptor signaling pathway
	5	transmitter-gated monoatomic ion channel activity
	6	extracellular ligand-gated monoatomic ion channel activity
	7	transmitter-gated channel activity
	8	ligand-gated monoatomic ion channel activity
	9	ligand-gated channel activity
	10	neurotransmitter receptor activity
	11	detection of chemical stimulus
	12	organic anion transmembrane transporter activity
	13	R8 cell development
	14	extracellularly glutamate-gated ion channel activity
	15	excitatory extracellular ligand-gated monoatomic ion channel activity
<i>S. planum</i>	1	GO:0042623
	2	ATP hydrolysis activity
	3	microtubule motor activity

	4	cytoskeletal motor activity
	5	GO:1990939
	6	minus-end-directed microtubule motor activity
	7	dynein intermediate chain binding
	8	regulation of cytoskeleton organization
	9	dynein light intermediate chain binding
	10	DNA helicase activity
	11	dynein complex
	12	polytene chromosome puff
	13	GO:0044447
	14	DNA duplex unwinding
	15	dynein light chain binding
Anomyura	1	glutamate receptor activity
	2	extracellular ligand-gated monoatomic ion channel activity
	3	ligand-gated monoatomic ion channel activity
	4	ligand-gated channel activity
	5	glutamate receptor signaling pathway
	6	ionotropic glutamate receptor activity
	7	transmitter-gated monoatomic ion channel activity
	8	transmitter-gated channel activity
	9	ionotropic glutamate receptor signaling pathway
	10	neurotransmitter receptor activity
	11	sensory perception of chemical stimulus
	12	extracellularly glutamate-gated ion channel activity
	13	excitatory extracellular ligand-gated monoatomic ion channel activity
	14	chemical synaptic transmission, postsynaptic
	15	regulation of postsynaptic membrane potential
Eubrachyura	1	vascular endothelial growth factor receptor activity
	2	hemocyte proliferation
	3	humoral immune response
	4	anterior Malpighian tubule development
	5	hemocyte migration
	6	imaginal disc-derived male genitalia morphogenesis
	7	hemocyte development
	8	vascular endothelial growth factor signaling pathway
	9	post-embryonic genitalia morphogenesis
	10	imaginal disc-derived genitalia morphogenesis
	11	TORC1 signaling
	12	genital disc morphogenesis
	13	hemocyte differentiation
	14	cellular response to vascular endothelial growth factor stimulus
	15	regulation of hemocyte differentiation

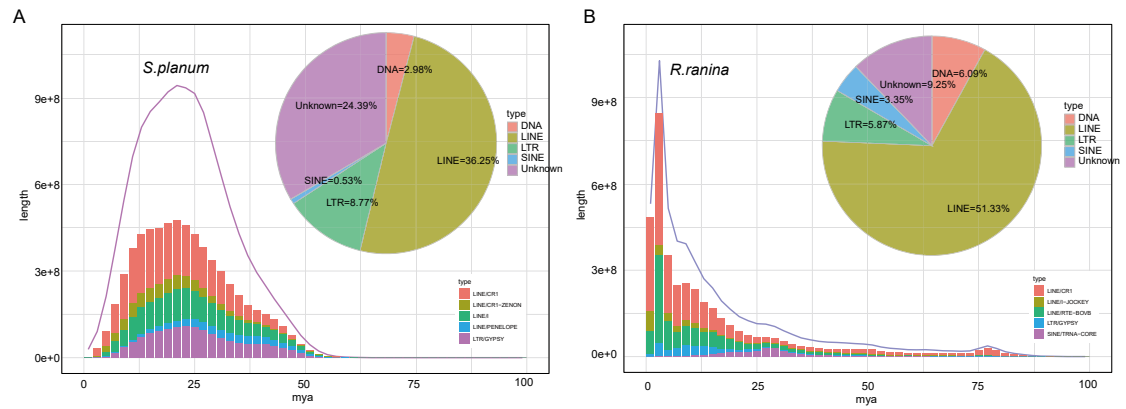
Supplementary Table S67. Homologous sequence copies identified across genomes of all species

Species	BRD9	GHRA	PAPD7	PFD1	SHLB2	SMG1	SOSB2	TCB2	TYSD1
<i>P. monodon</i>	0	0	0	0	0	0	0	4	0
<i>H. americanus</i>	0	0	0	0	0	0	0	5	0
<i>P. japonicus</i>	0	0	0	0	0	0	0	0	0
<i>P. clarkii</i>	0	0	0	0	0	0	0	0	0
<i>P. chinensis</i>	0	0	0	0	0	0	0	1	0
<i>H. azteca</i>	0	0	0	0	0	0	0	0	0
<i>P. platypus</i>	1	1	10	0	0	0	1	7	0
<i>C. brevimanus</i>	1	0	0	1	1	0	0	9	0
<i>C. sapidus</i>	1	4	1	1	1	1	1	16	1
<i>S. paramamosain</i>	2	2	28	2	1	1	1	15	1
<i>E. j. sinensis</i>	1	7	8	1	1	1	1	12	1
<i>C. opilio</i>	1	2	14	1	1	1	1	6	1
<i>A. integerrimus</i>	1	8	6	1	1	1	1	11	1
<i>D. horrida</i>	1	7	15	1	1	1	2	13	1
<i>C. philargius</i>	1	5	24	1	1	1	1	9	1
<i>L. dehaani</i>	1	6	8	1	1	1	1	8	1
<i>P. trituberculatus</i>	1	5	2	1	1	1	1	9	1
<i>R. ranina</i>	1	9	1	1	1	2	1	24	1
<i>S. planum</i>	1	4	8	1	2	1	1	16	1
<i>C. carnifex</i>	1	2	21	1	1	1	1	8	1

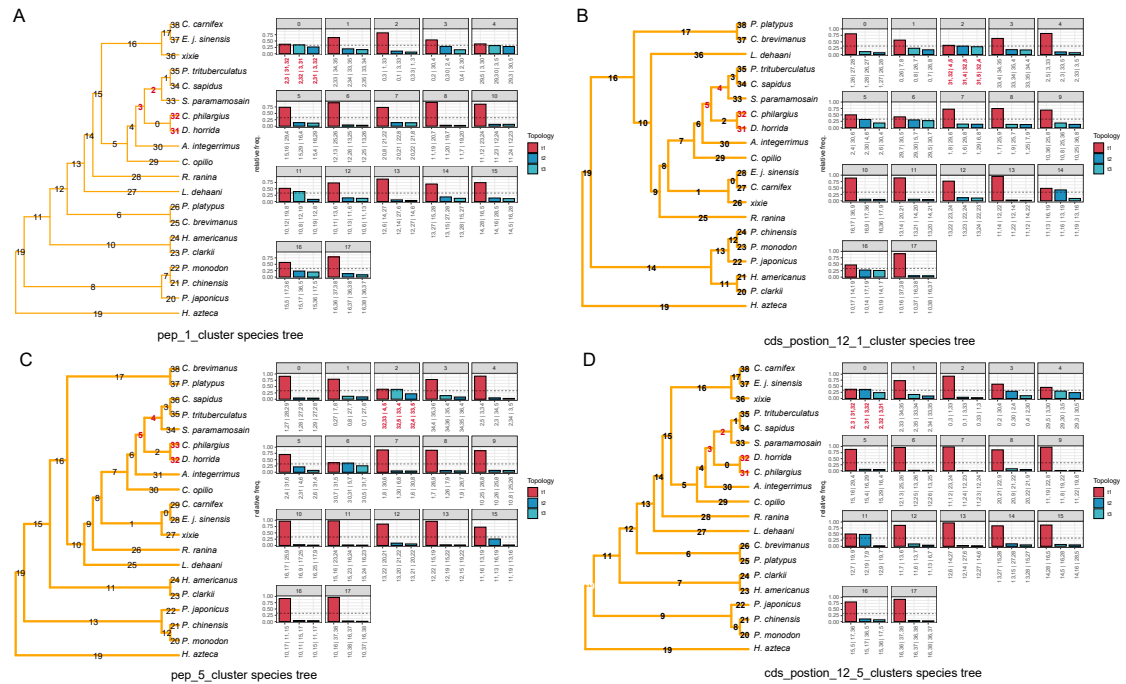
Supplementary Figure



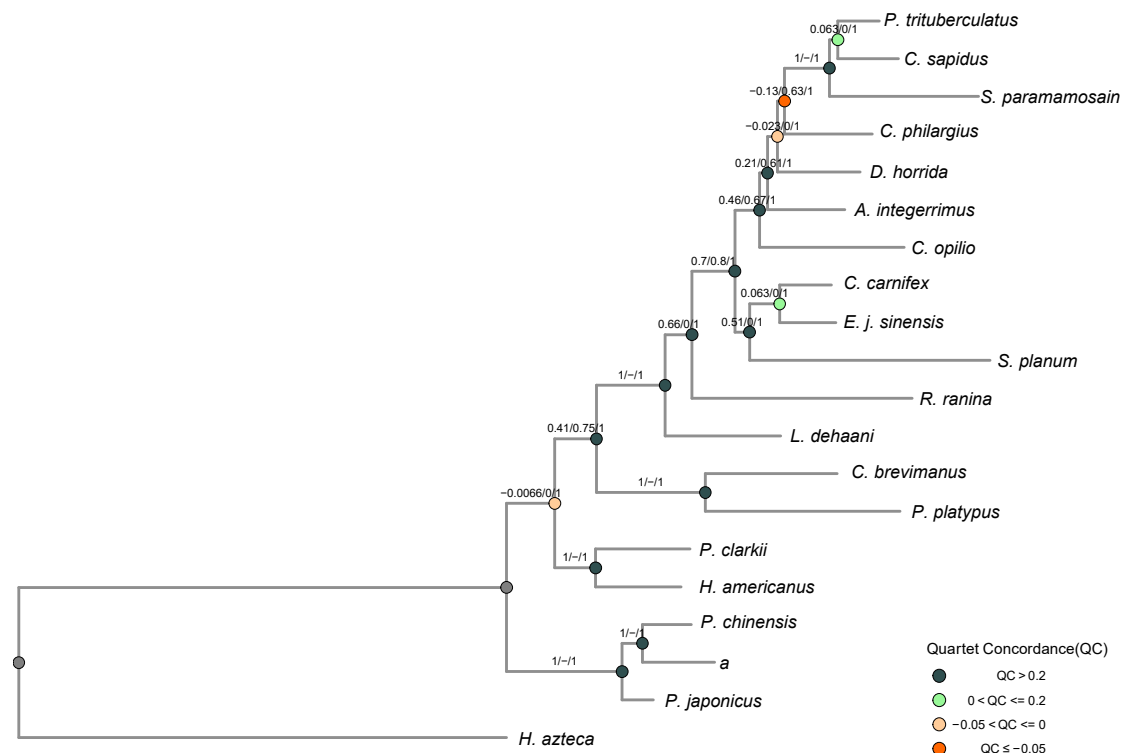
Supplementary Figure S1. Published Decapoda species number according to GBIF and Crab Database are shown, with red bars representing crab species and green bars indicating non-crab species. The results reveal that the past decade has witnessed an explosive increase in crab species discovery.



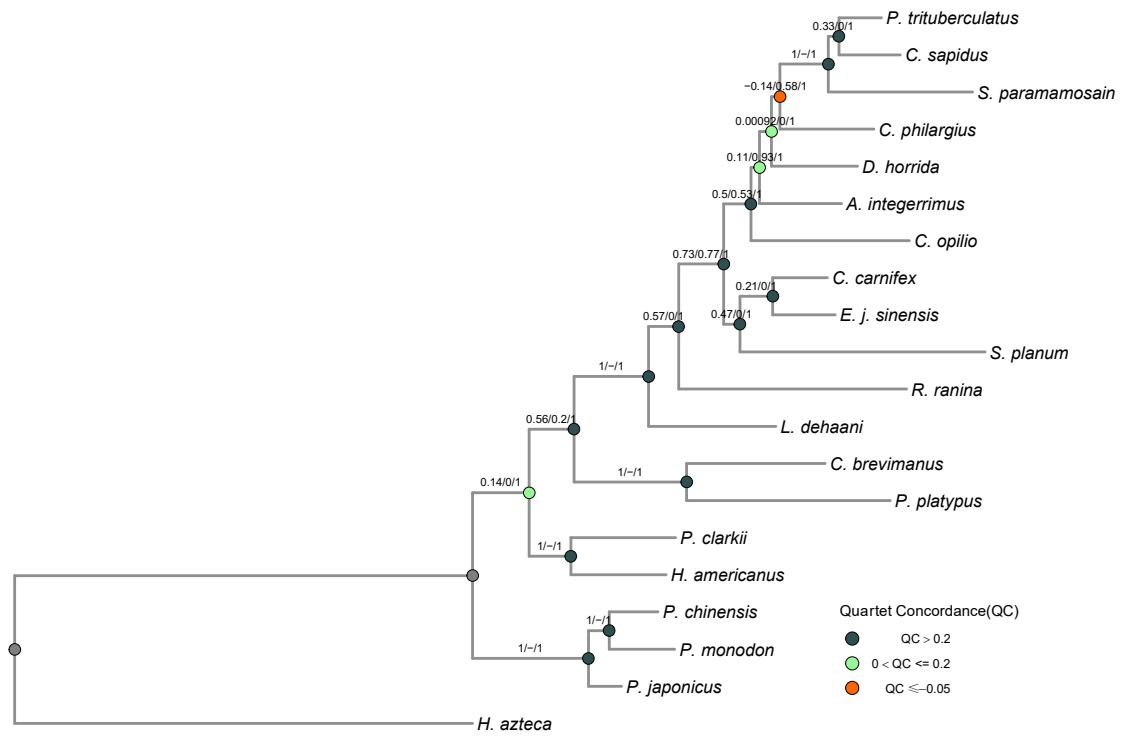
Supplementary Figure S2. Insertion histories of transposable elements (TEs) for *S. planum* (A) and *R. ranina* (B). The line graph depicts the overall distribution of TEs, while the stacked bar chart illustrates the distribution of the top five TE families. The pie charts show the proportions of different TE types present in each species



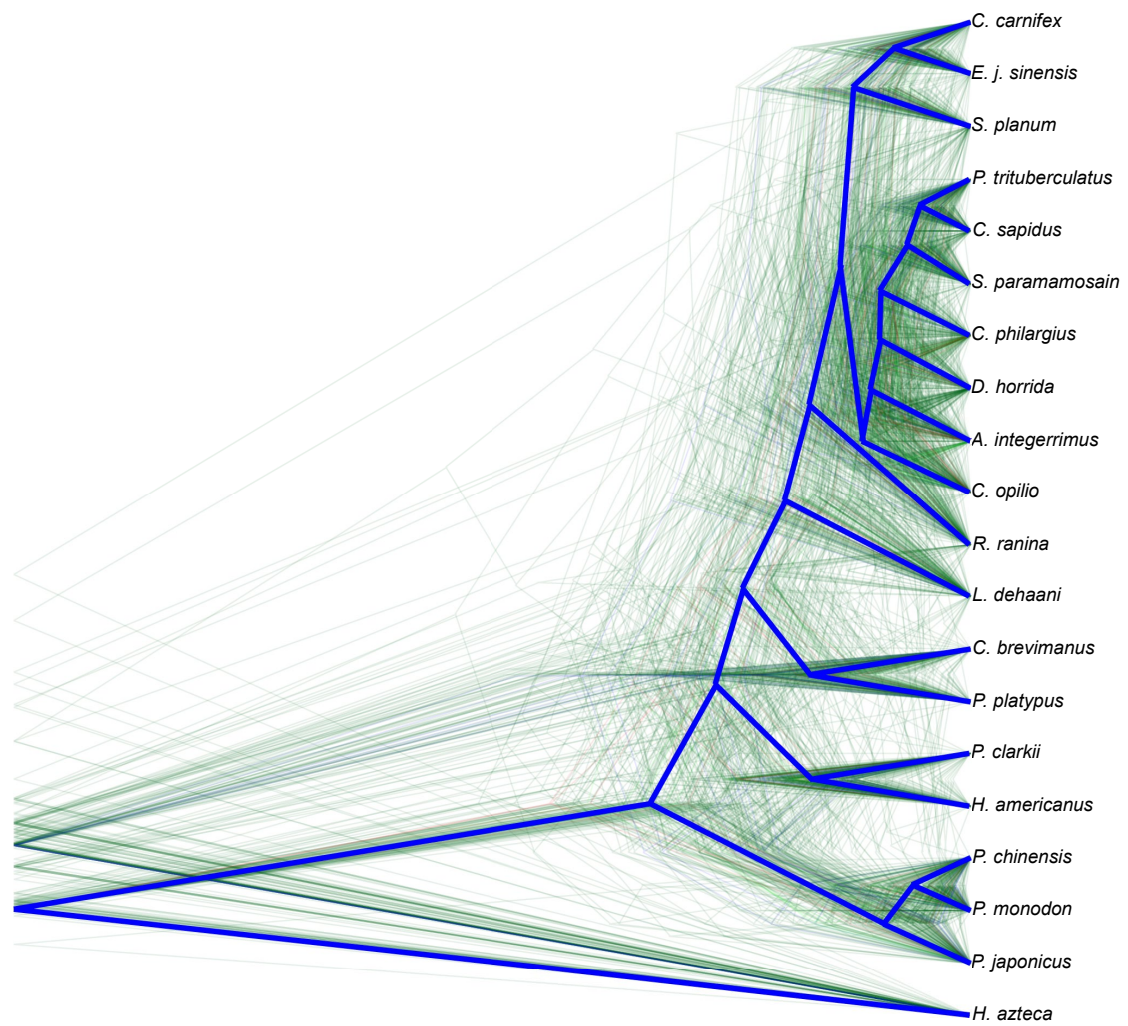
Supplementary Figure S3. Results of the species tree analysis using the Discovista homology-based phylogenetic approach. A. Visualization of the species tree constructed from a single protein cluster. B. Visualization of the species tree constructed from a cluster based on the first and second codon positions of the coding sequences (CDS). C. Visualization of the species tree constructed from concatenated five protein clusters. D. Visualization of the species tree constructed from concatenated five clusters based on the first and second codon positions of the CDS.



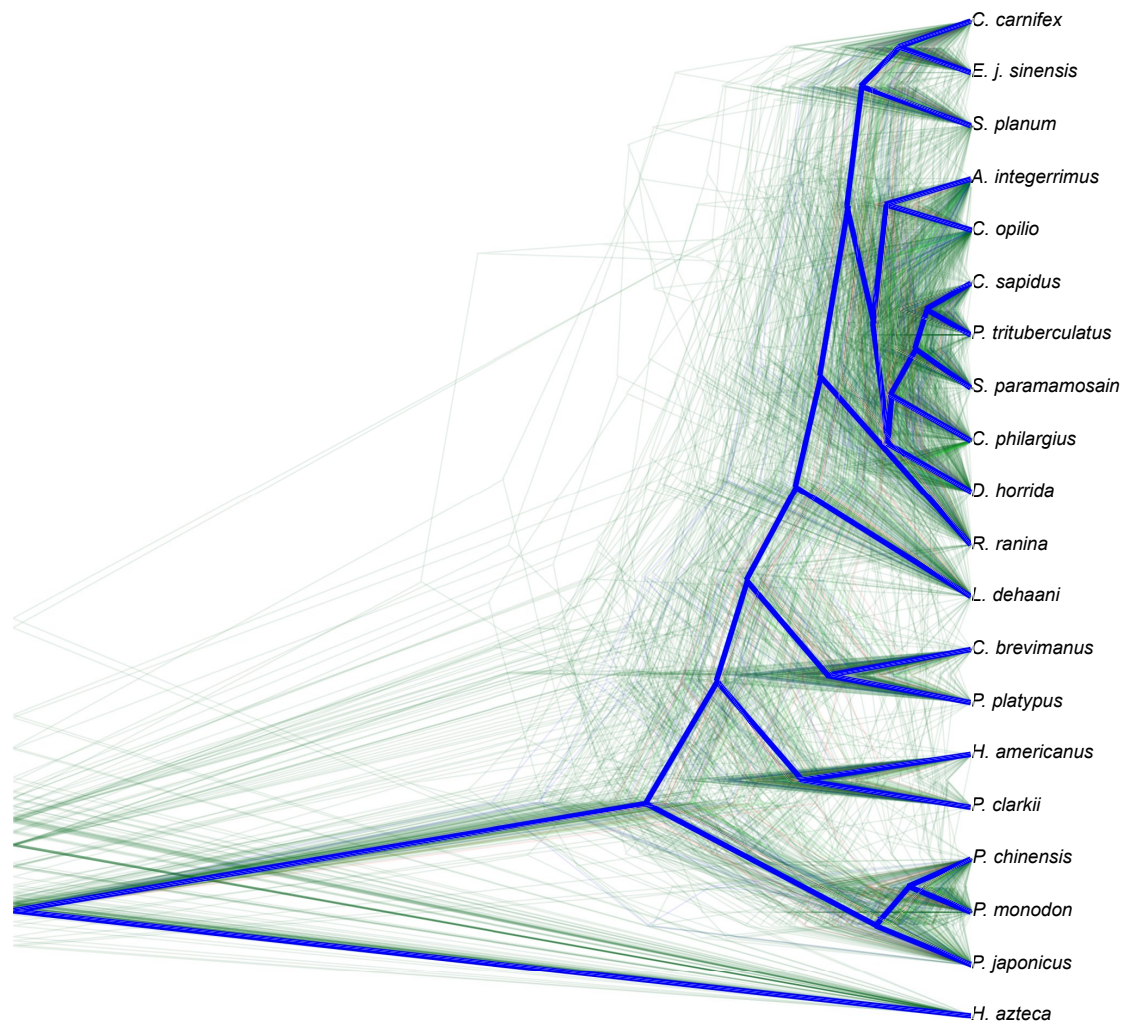
Supplementary Figure S4. Visualization of the quartet sampling results of the first and second codon positions of CDS.



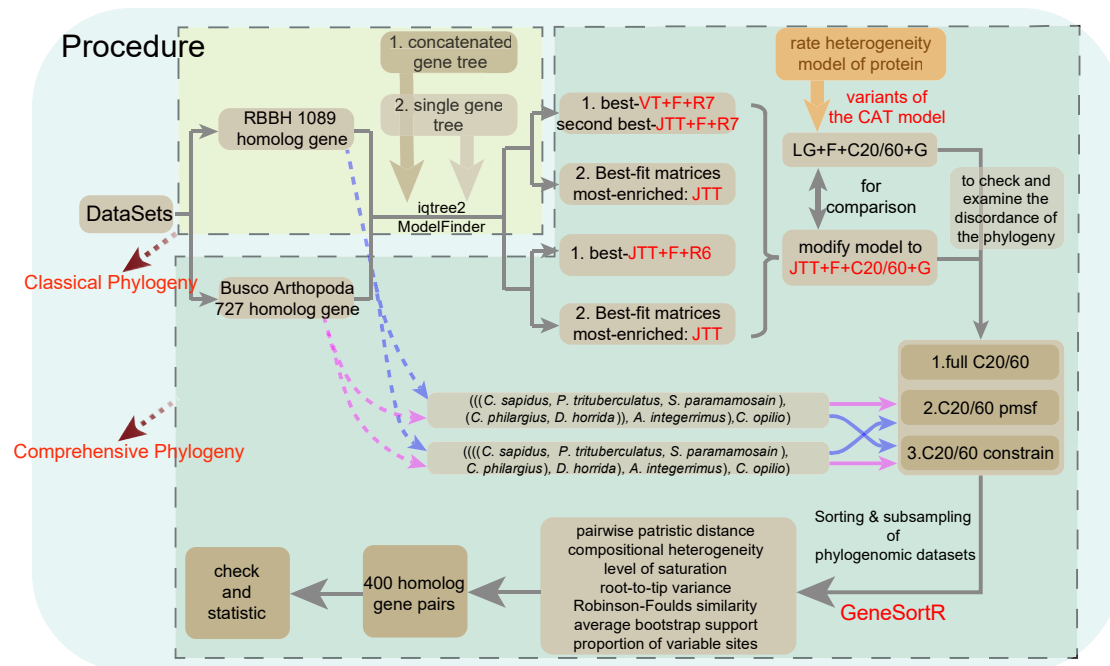
Supplementary Figure S5. Visualization of the quartet sampling results of concatenated protein sequences.



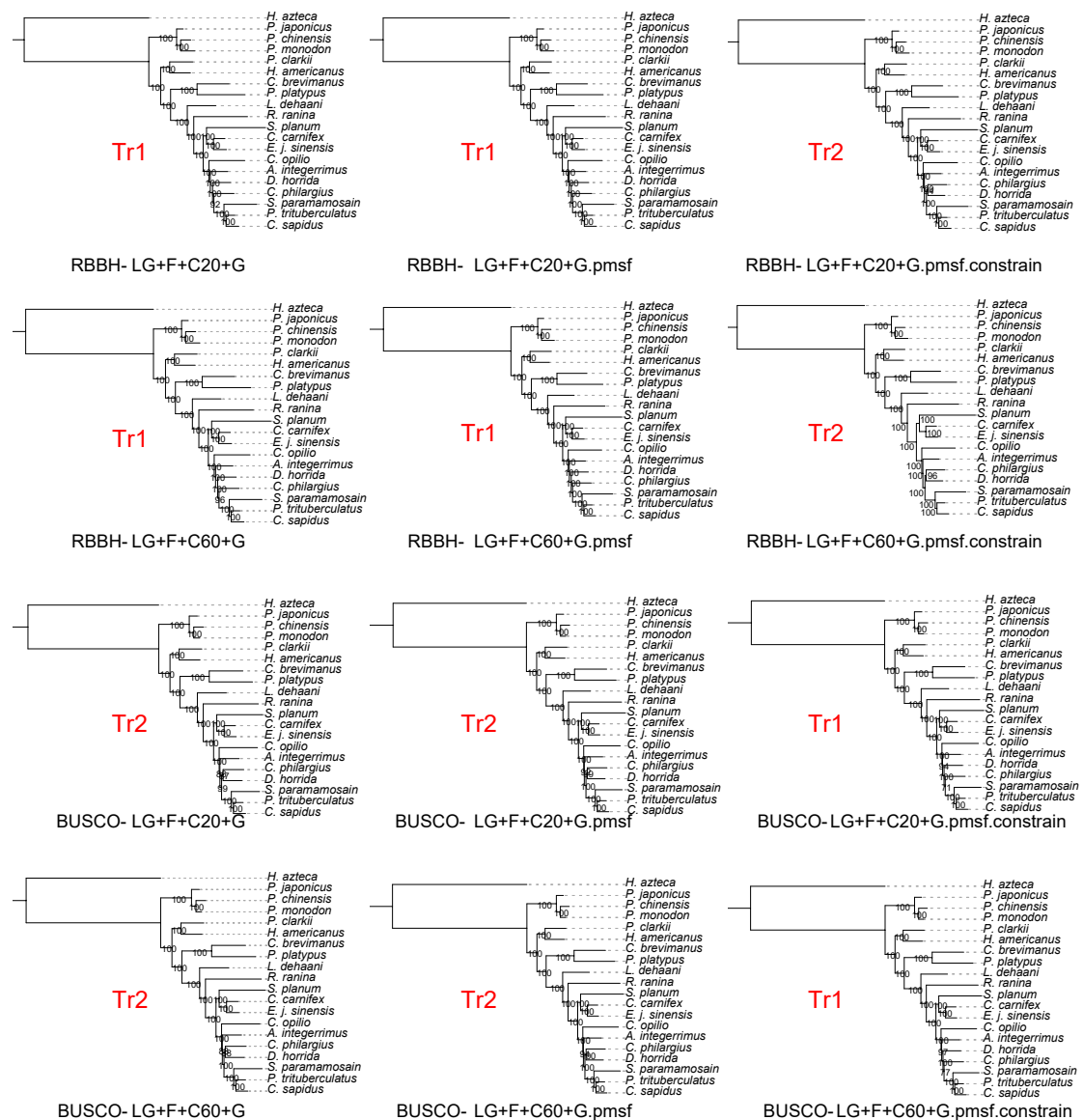
Supplementary Figure S6. Densitree visualization of the species tree generated from concatenated five RBBH clusters based on the first and second codon positions of CDS.



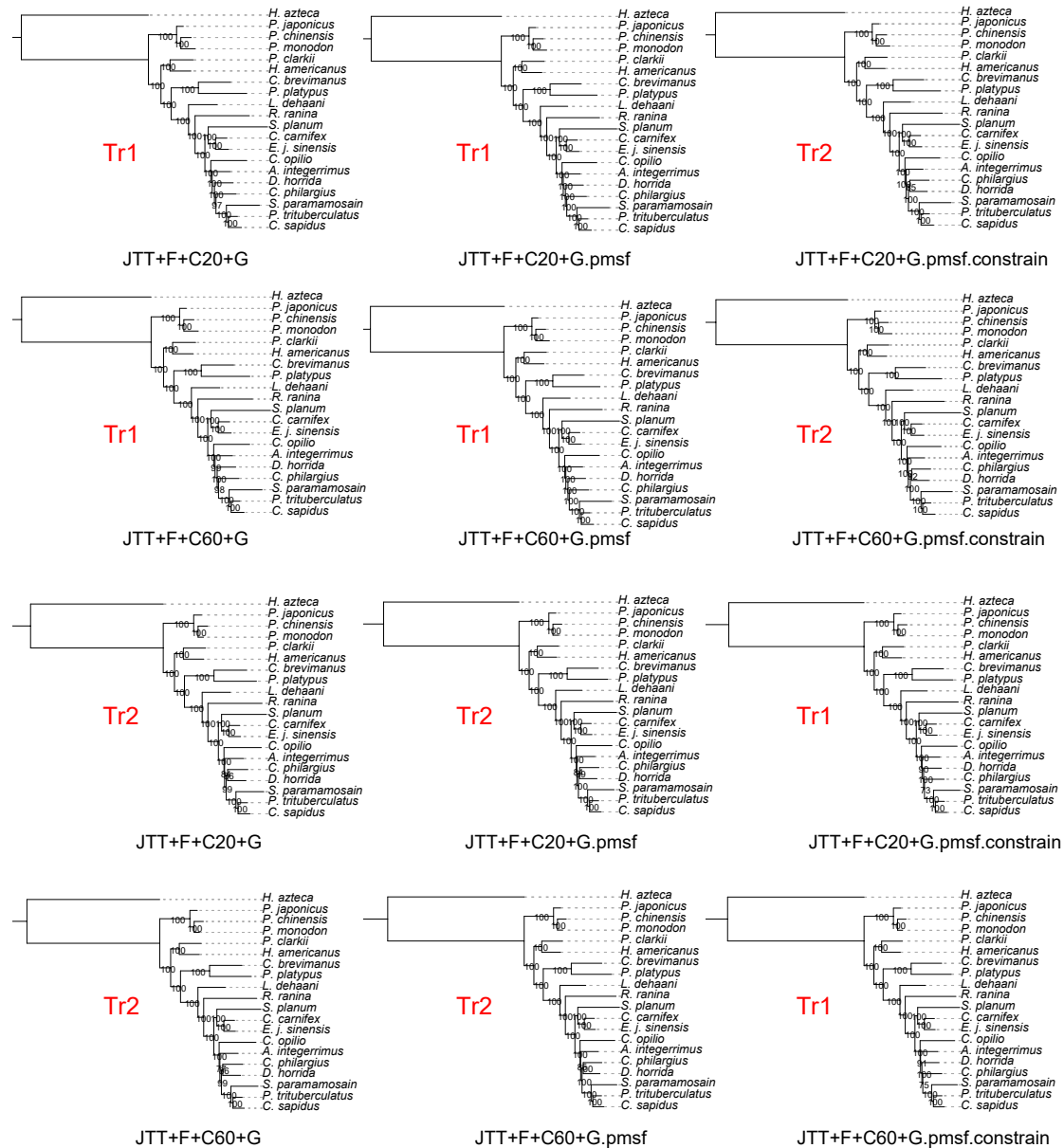
Supplementary Figure S7. Densitree visualization of the species tree generated from concatenated five RBBH clusters based on protein sequences.



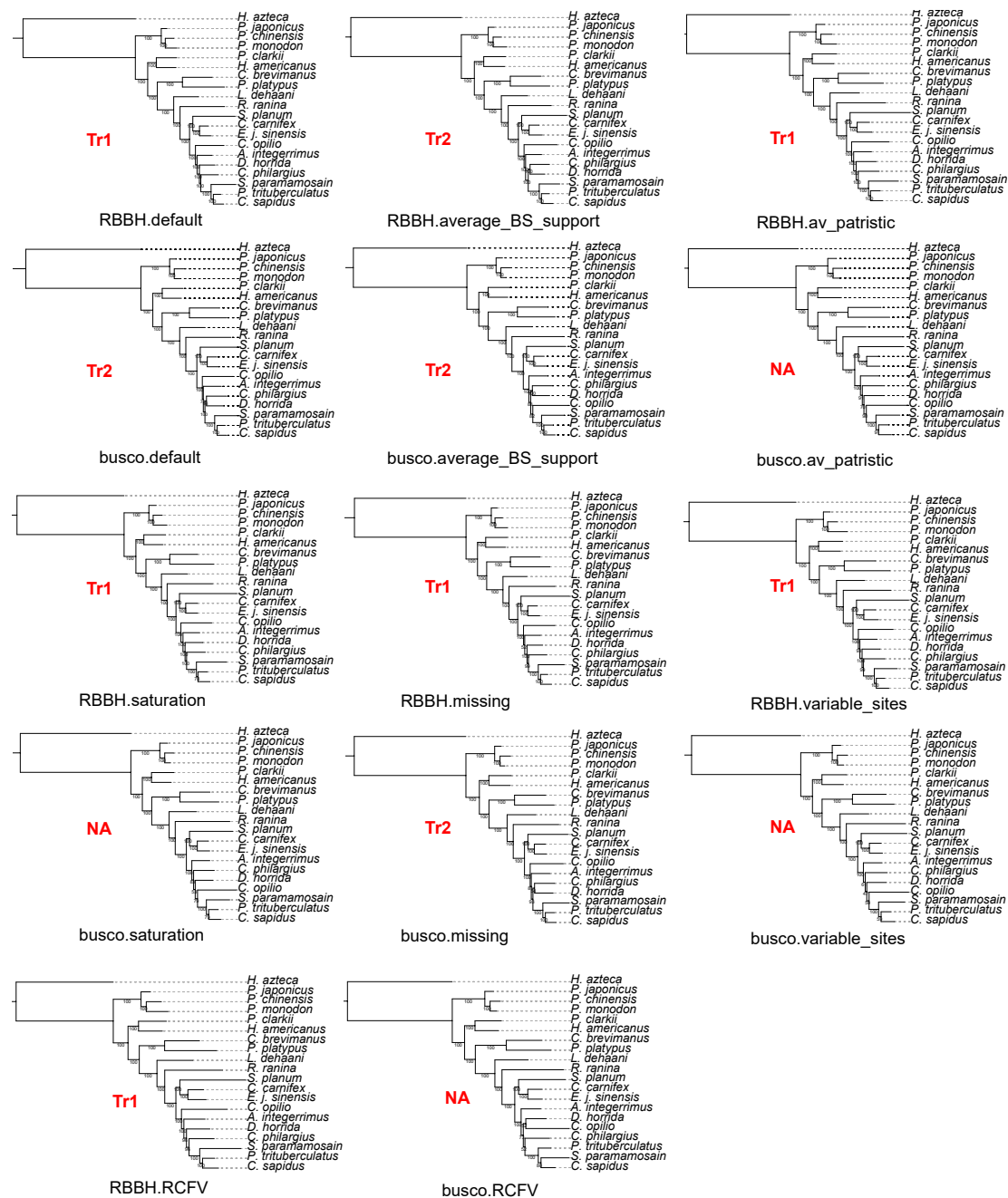
Supplementary Figure S8. The procedure of deep phylogeny reconstruction. The light-yellow dashed box represents the classical phylogenetic methods (simple), while the light green dashed box depicts the comprehensive phylogenetic construction method adopted in this study.



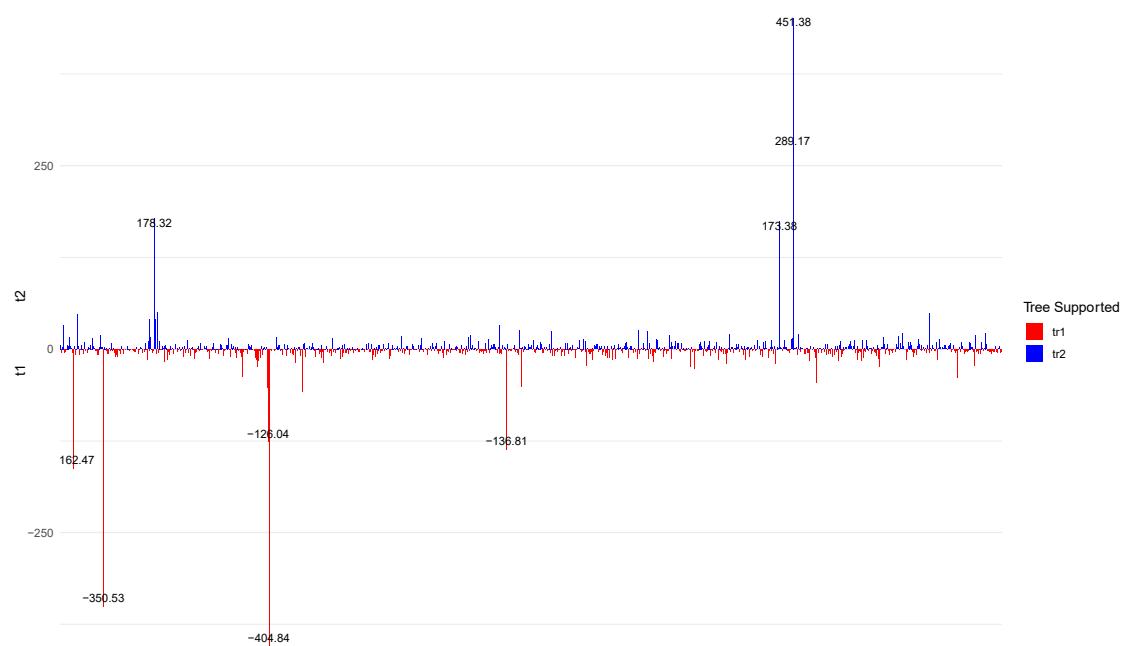
Supplementary Figure S9. Heterogeneous phylogenetic tree reconstruction results based on the LG+F+G model. The top two rows and bottom two rows utilized the RBBH and BUSCO datasets, respectively. The first and third row employed the C20 heterogeneous model, while the second and fourth row utilized the C60 heterogeneous model. The red text indicates the supported tree topologies in Figure 3B.



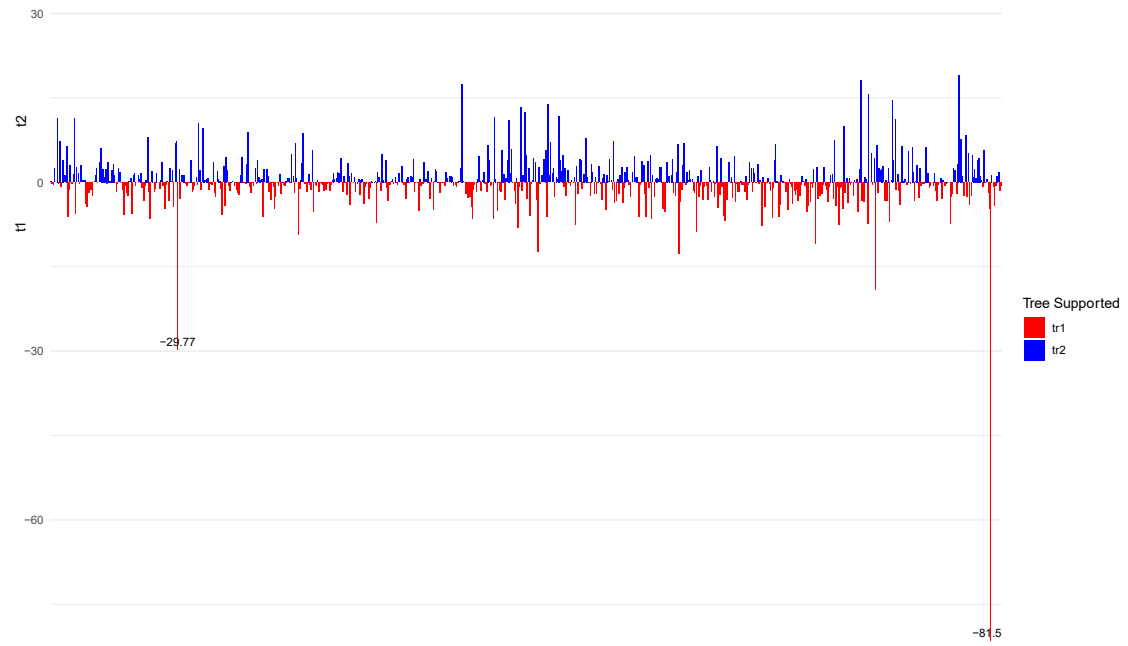
Supplementary Figure S10. Heterogeneous phylogenetic tree reconstruction results based on the JTT+F+G model. The top two rows and bottom two rows utilized the RBBH and BUSCO datasets, respectively. The first and third row employed the C20 heterogeneous model, while the second and fourth row utilized the C60 heterogeneous model. The red text indicates the supported tree topologies in Figure 3B.



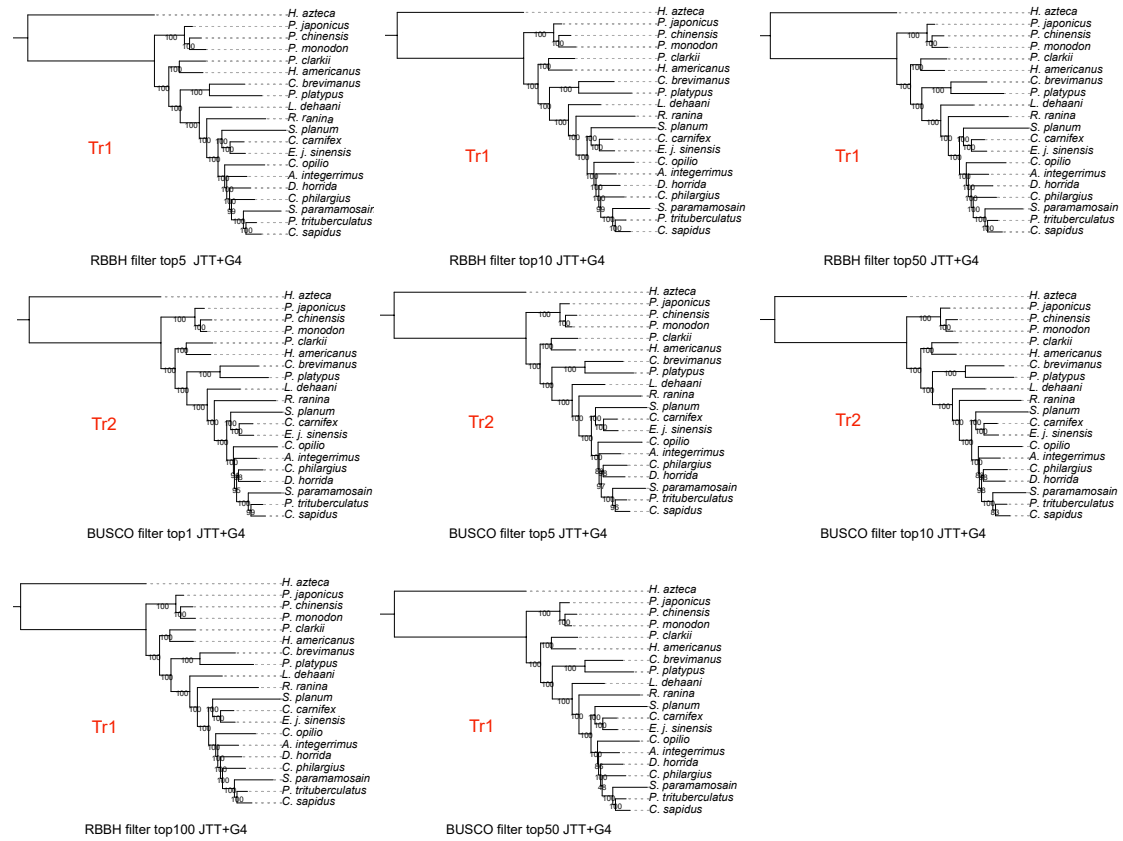
Supplementary Figure S11. GenesortR. Phylogenetic trees constructed using the GenesortR tool, which performs data sorting and filtering based on different aspects, including "default", "average BS_support", "av patristic", "missing", "RCFV", "robinson sim", "saturation", and "variable sites". The red text indicates the supported tree topologies in Figure 3B.



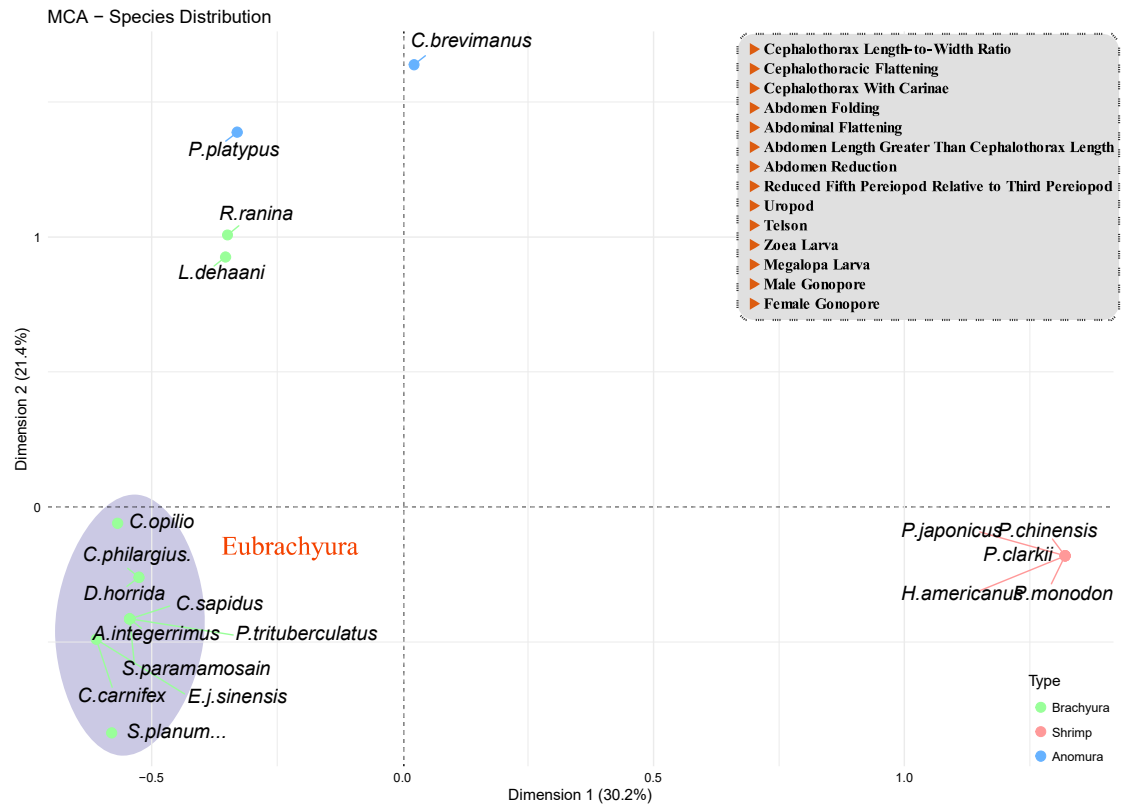
Supplementary Figure S12. The difference in likelihood support (signal) for different tree topologies for each cluster in the RBBH dataset.



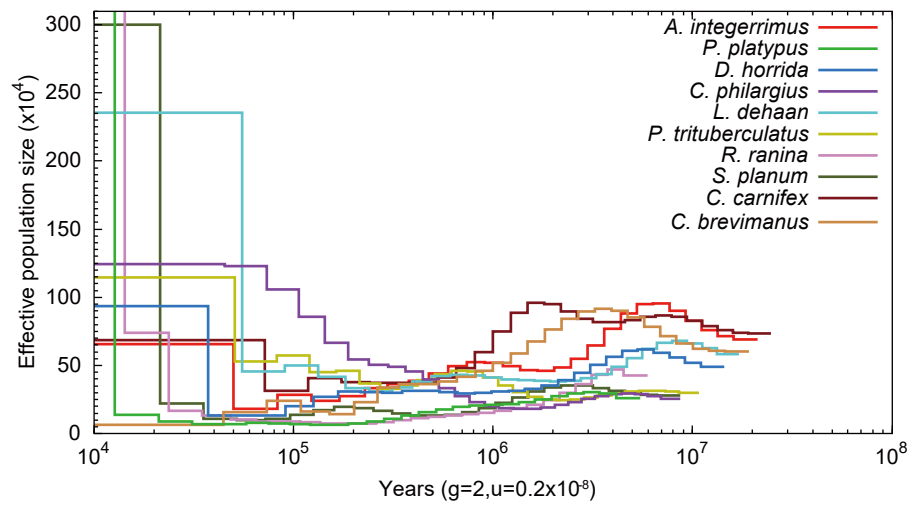
Supplementary Figure S13. The difference in likelihood support (signal) for different tree topologies for each cluster in the BUSCO dataset.



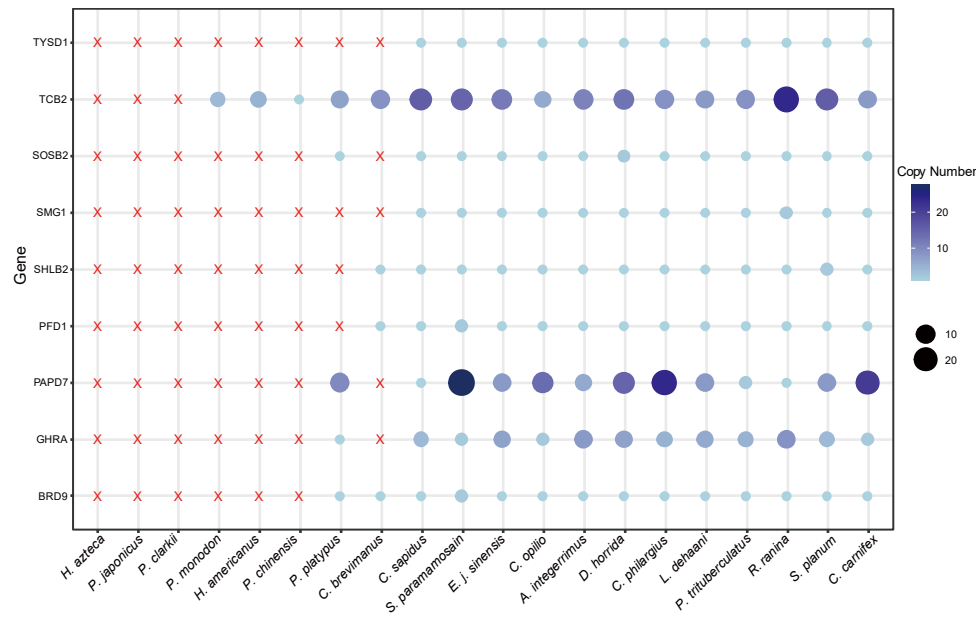
Supplementary Figure S14. Phylogenetic tree reconstruction results based on the JTT+G4 model after data filtering based on the signal results from the RBBH and BUSCO datasets.



Supplementary Figure S15. MCA dimensionality reduction clustering diagram for phenotypic characterization statistics of different taxonomic groups within the order Decapoda.



Supplementary Figure S16. Effective population size of the sampled species. Parameter “g” represents generation time, and “u” represents mutation rate per generation per year calculated by r8s



Supplementary Figure S17. Genome-wide examination of copy number variations. The red symbols indicate species where no homologous sequences were detected.