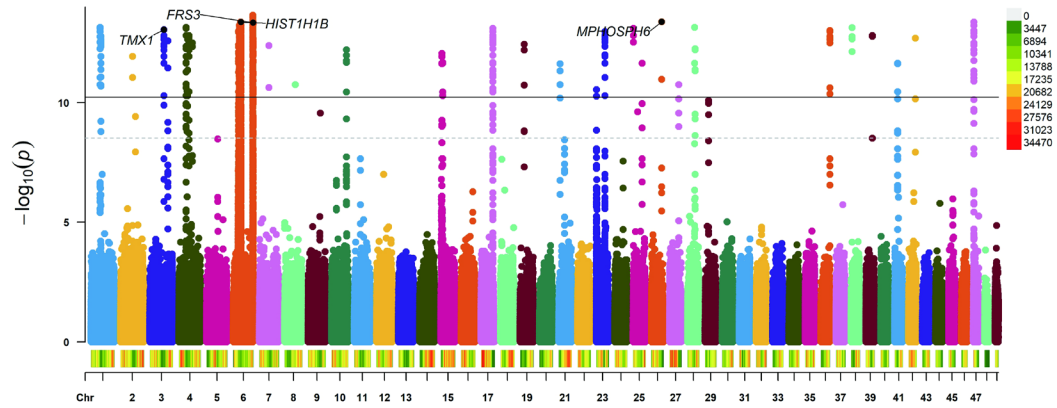
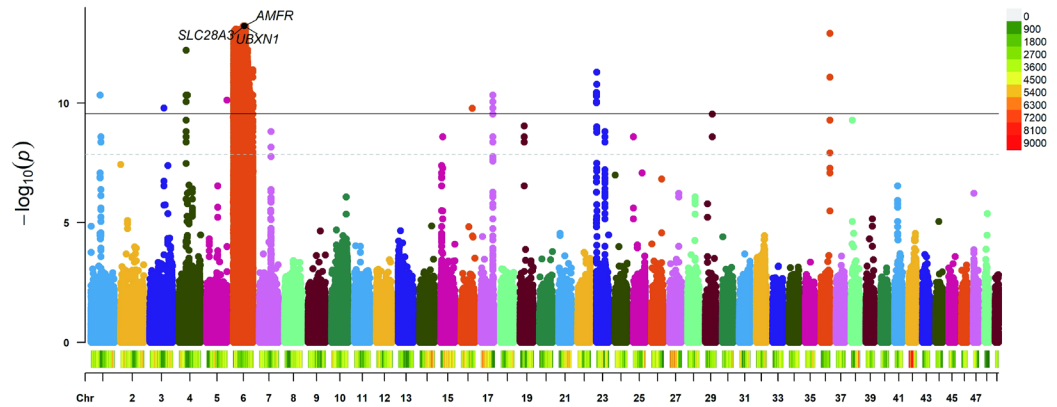


Supplementary Figures

A



B



C

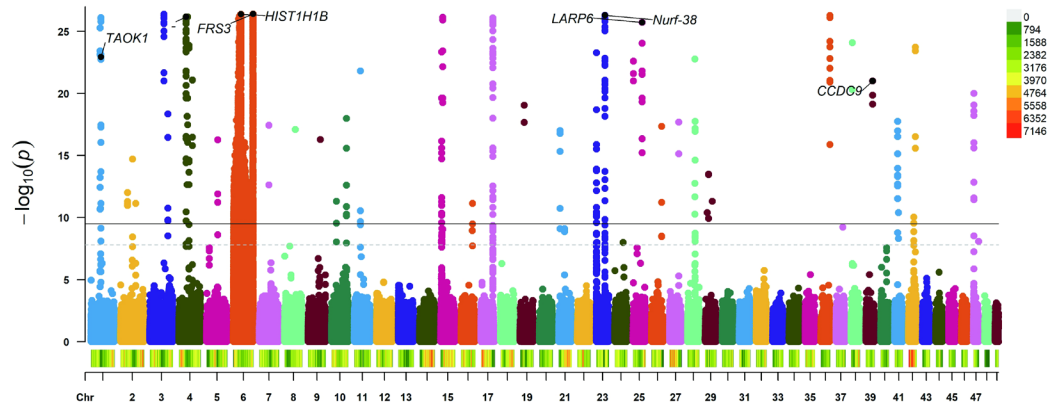


Fig. S1 Genome-wide association studies (GWAS) analysis of *Scylla paramamosain* genome using different generations of populations. **(A)** 146 individuals from wild. **(B)** 130 individuals from second generation of family group. **(C)** Complex of 146 individuals from wild and 130 individuals from second generation of family group.

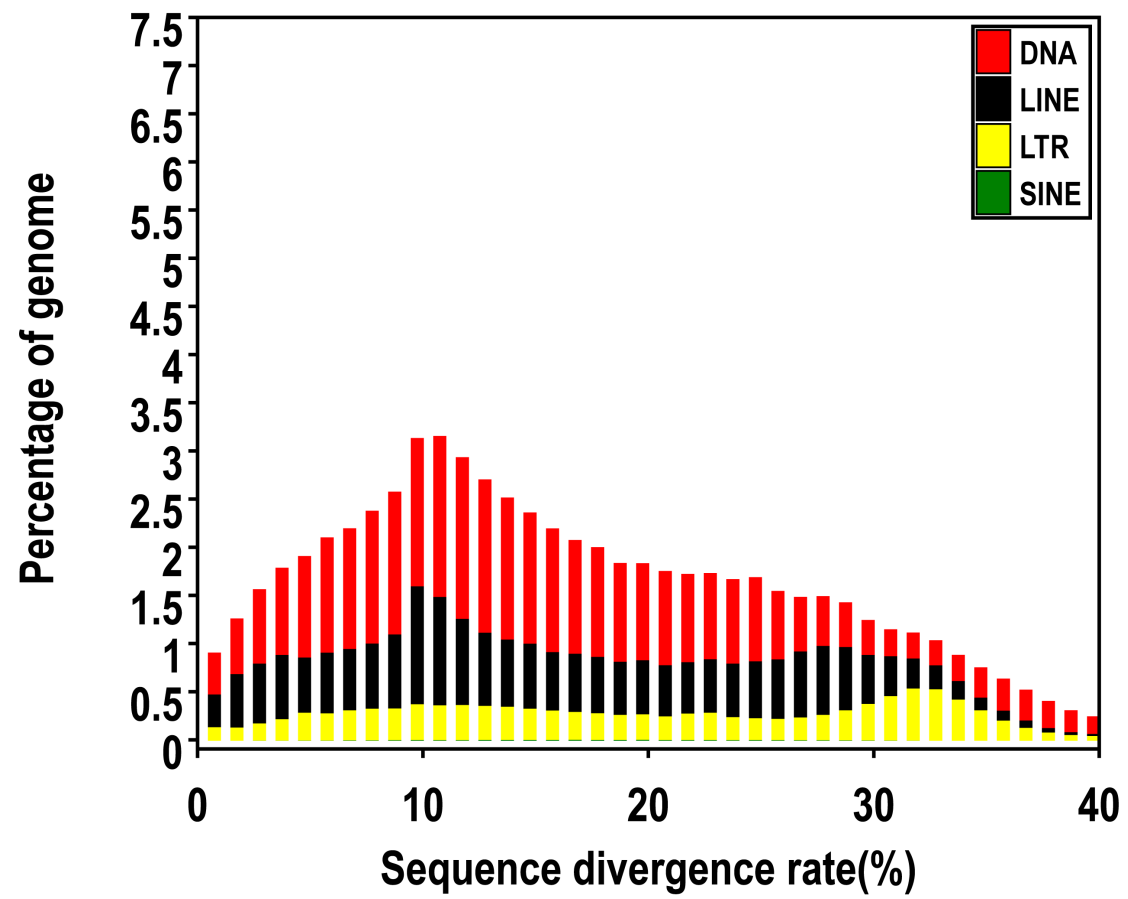


Fig. S2 Divergence rate of transposons in *Scylla paramamosain* genome

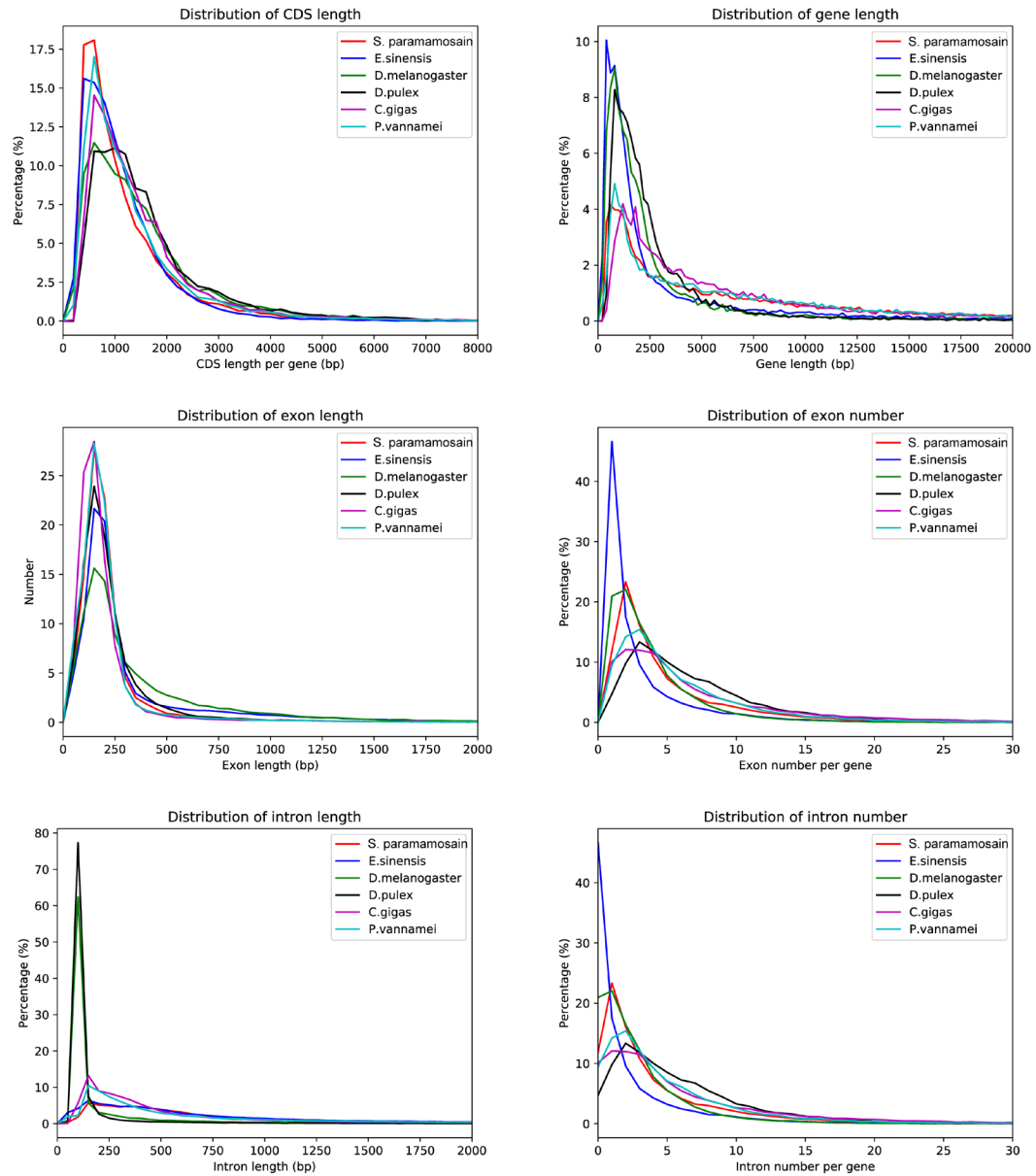


Fig. S3 Characterization of different genic regions in *Scylla paramamosain* and five other arthropods.

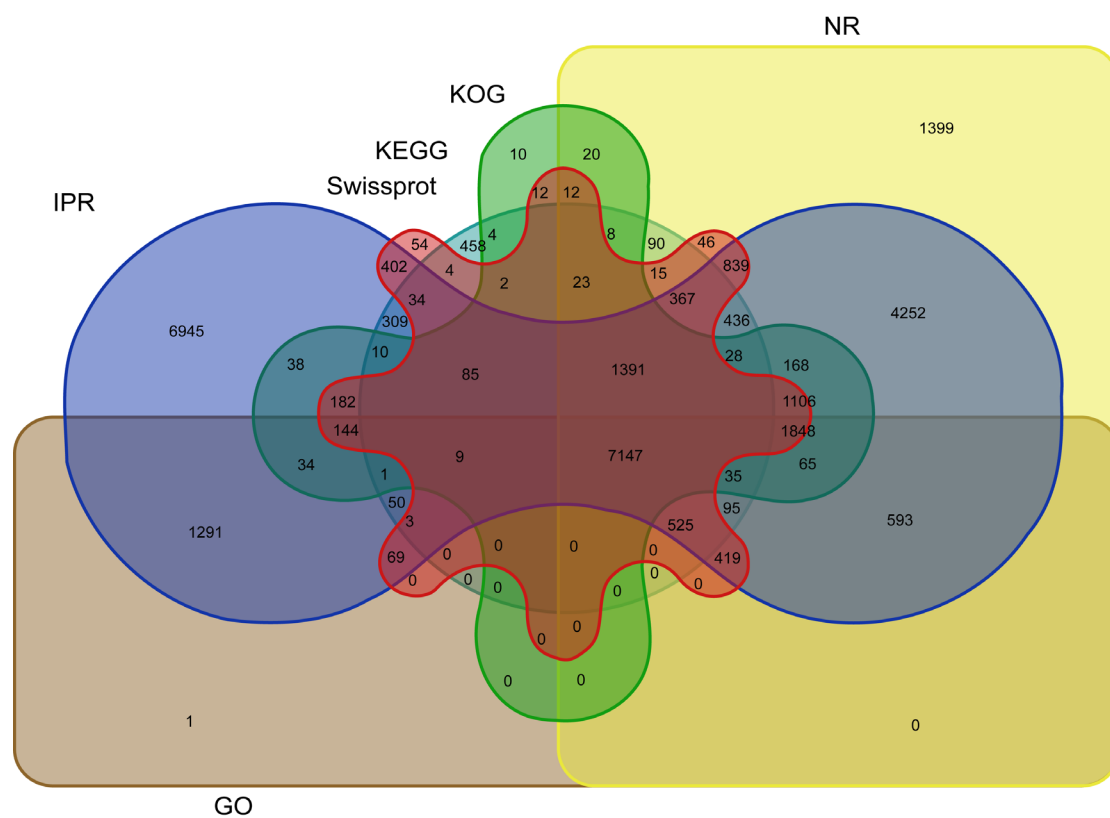


Fig. S4 Functional annotation of predicted genes in *Scylla paramamosain*

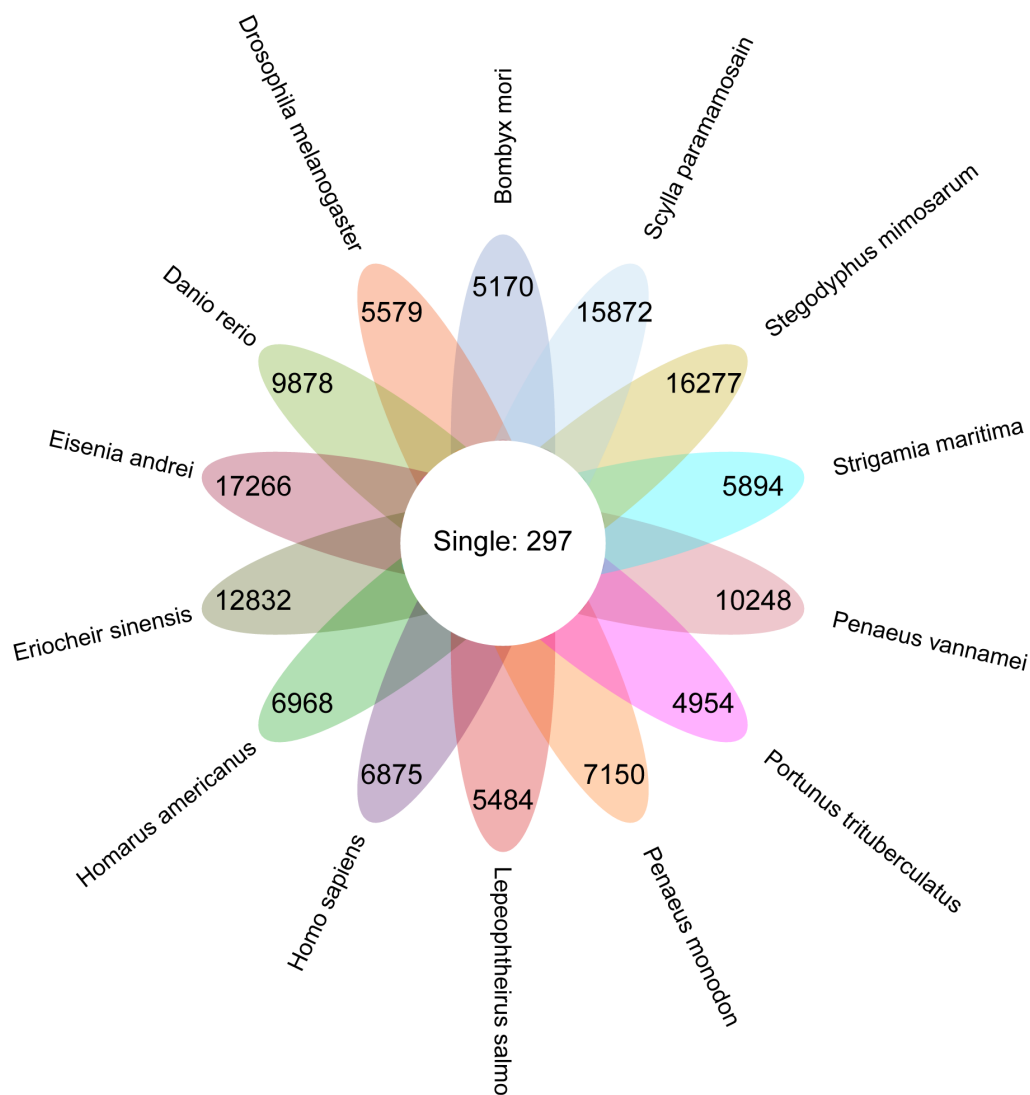


Fig. S5 Ortholog gene analysis and phylogenetic trees of 14 selected species

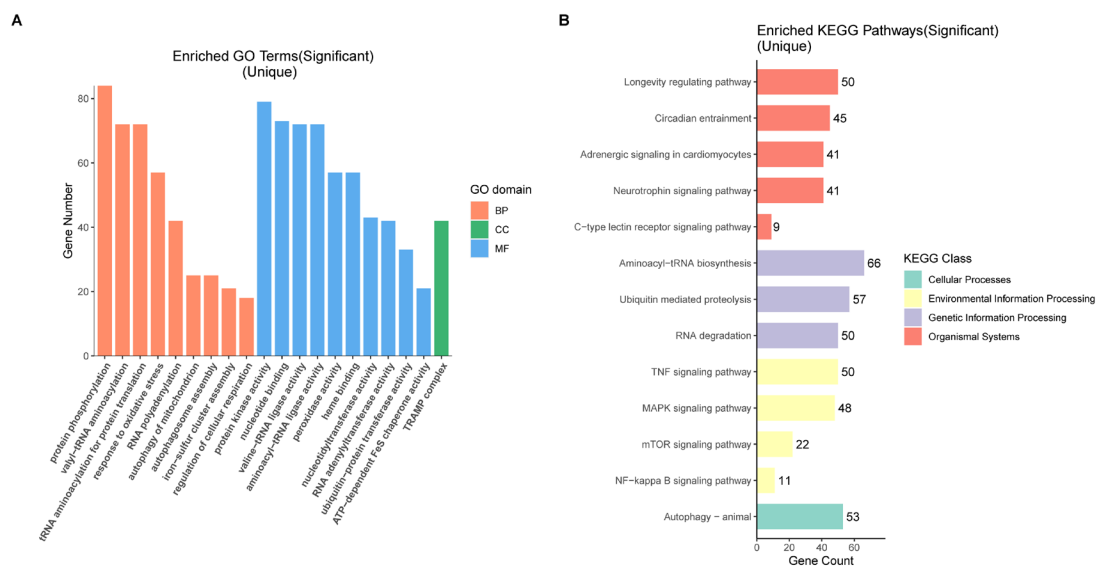


Fig. S6 GO (A) and KEGG (B) enrichment of unique genes in *Scylla paramamosain*

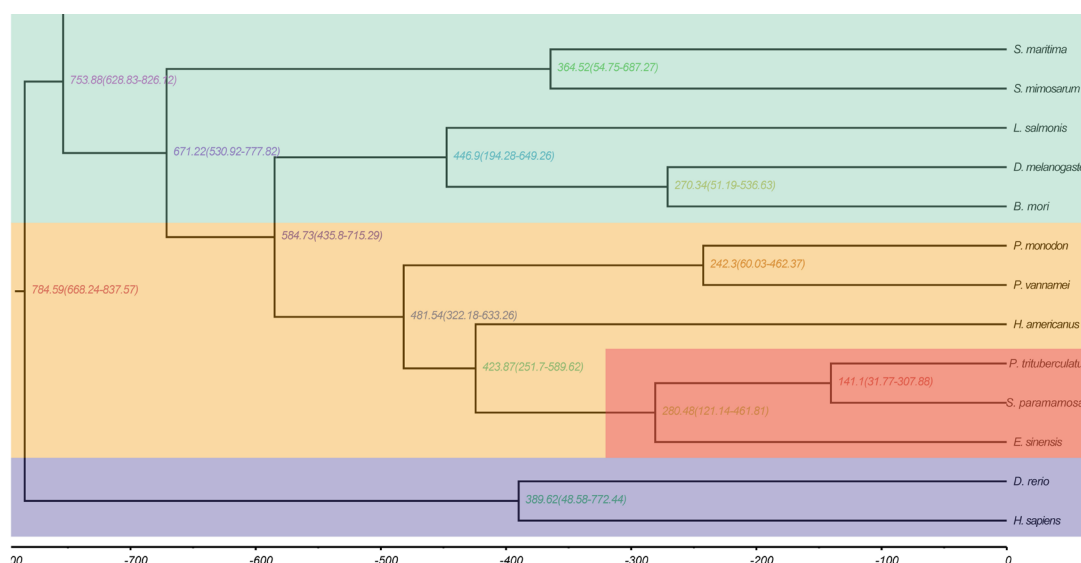


Fig. S7 Phylogenetic trees of 14 selected species including *Scylla paramamosain*, *Portunus trituberculatus*, *Eriocheir sinensis*, *Penaeus vannamei*, *Homarus americanus*, *Penaeus monodon*, *Drosophila melanogaster*, *Bombyx mori*, *Eisenia andrei*, *Lepeophtheirus salmonis*, *Stegodyphus mimosarum*, *Strigamia maritima*, *Danio rerio*, and *Homo sapiens*

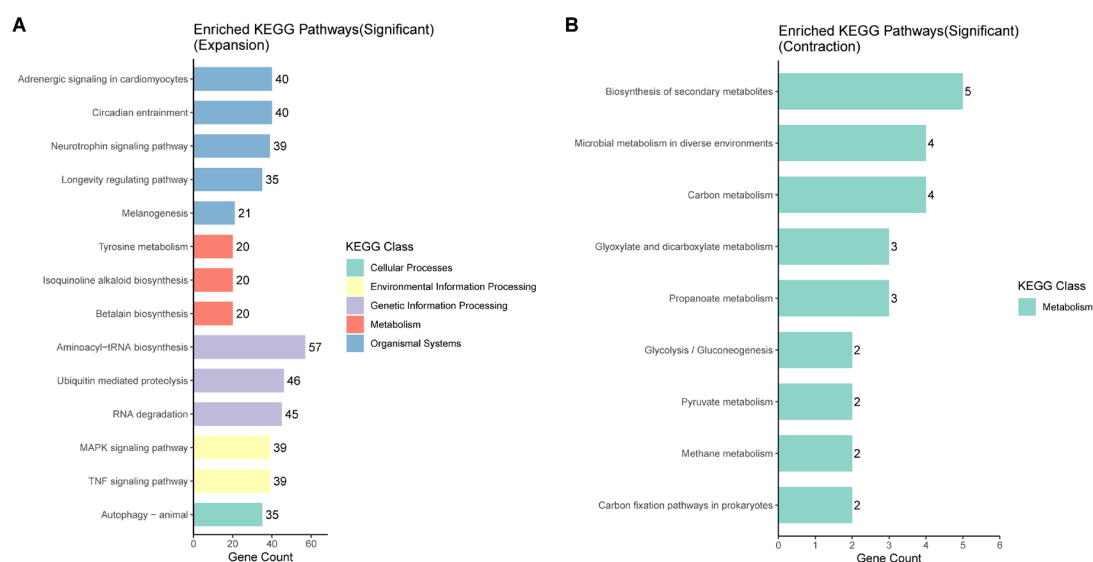


Fig. S8 KEGG enrichment of expansion (A) and contraction (B) genes in *Scylla paramamosain*

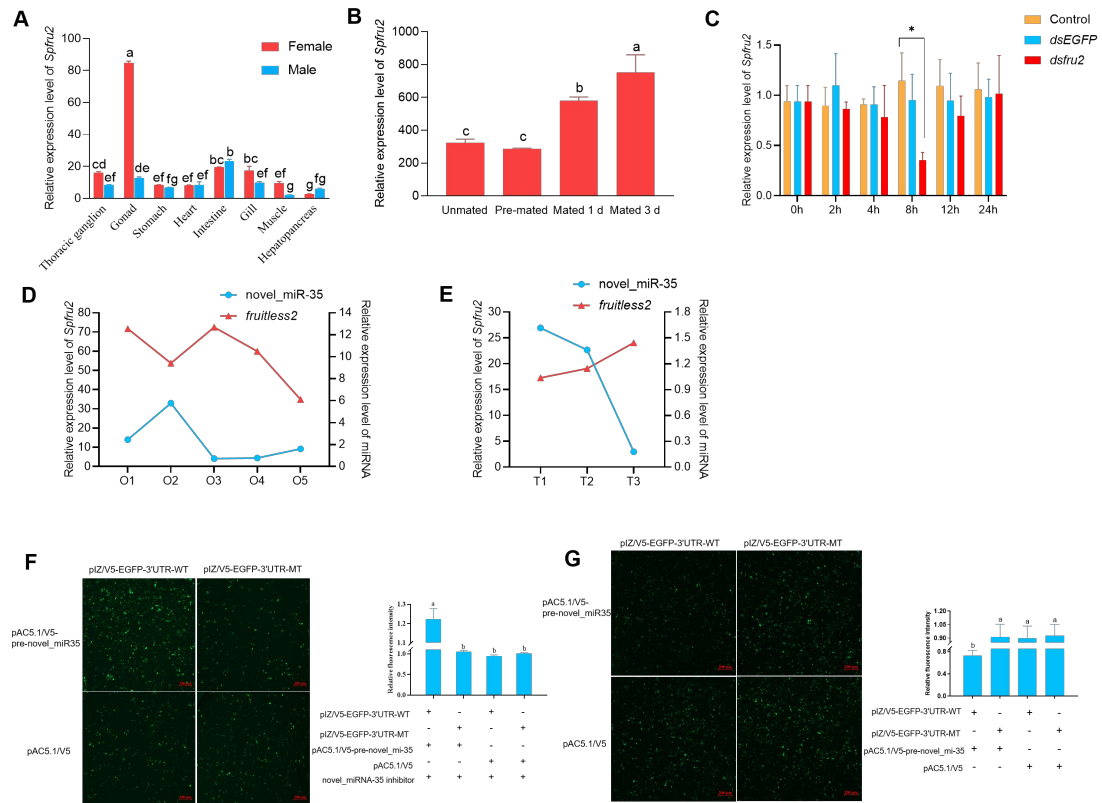


Fig. S9 The expression and regulation of *fru2* gene in gonads of *Scylla paramamosain*. **(A)** Relative expression of *Spfru2* in different tissues of *Scylla paramamosain*. Bars with different lowercase letters indicate significant difference ($p < 0.05$). **(B)** Relative expressions of *Spfru2* in different mating stages of *Scylla paramamosain* female. **(C)** Expression changes of *Spfru2* in ovary after the interference of *fru2* expression. **(D)** Relative expression of novel-miR35 and *Spfru2* in different developmental stages of ovary. O1-O5: stage OI to stage OV. **(E)** Relative expression of novel-miR35 and *Spfru2* in different developmental stages of testis. T1-T3: stage TI to stage TIII. Bars with different lowercase letters indicate significant difference ($p < 0.05$). **(F)** The S2 cells were co-transfected with WT *fru2* 3'-UTR, and the mutated-type of *fru2* 3'-UTR (MT), together with novel-miR35 inhibitor and pre-novel_miR-35 plasmid. The data were expressed as the relative fluorescence intensity. **(G)** pre-novel_miR-35 plasmid or control plasmid were co-transfected WT *fru2* 3'-UTR, and the mutated-type of *fru2* 3'-UTR (MT) for 48 h. The data were expressed as the relative fluorescence intensity. Bars with different lowercase letters indicate significant difference ($p < 0.05$).

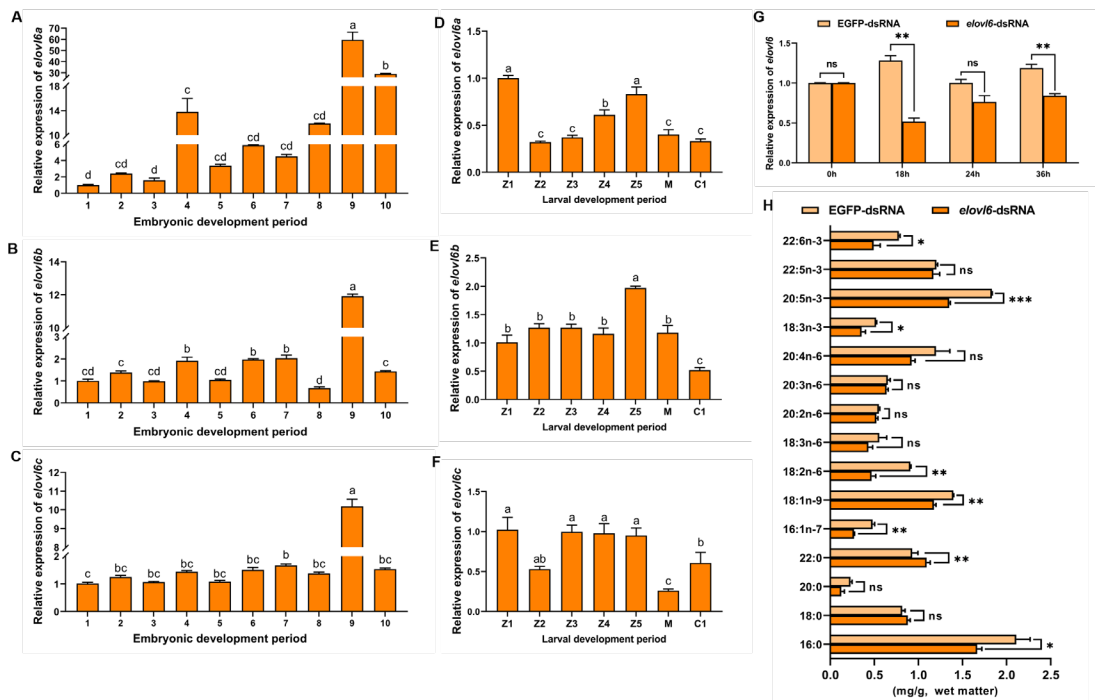


Fig. S10 Neo-functionalization of the *elovl6* gene in the LC-PUFA synthesis pathway in crustacean species. **(A)** Relative expressions of *elovl6a* in different developmental stages of embryo. 1: fertilized egg, 2: cleavage, 3: blastula, 4: gastrula, 5: nauplius, 6: five pairs of appendages, 7: seven pairs of appendages, 8: eye-pigment formation, 9: prehatching, 10: hatching. **(B)** Relative expressions of *elovl6b* in different developmental stages of embryo. **(C)** Relative expressions of *elovl6c* in different developmental stages of embryo. **(D)** Relative expressions of *elovl6a* in different developmental stages of larvae. **(E)** Relative expressions of *elovl6b* in different developmental stages of larvae. **(F)** Relative expressions of *elovl6c* in different developmental stages of larvae. **(G)** Expression levels of the *elovl6* gene after RNA interference in isolated hepatopancreas of *Scylla paramamosain*. **(H)** The contents of fatty acids in hepatopancreas after interfering the expression of *elovl6* gene.

Table S1 Comparison of published crustaceans genome

Species	Genome Size	Contig N50	Scaffold N50	Total number of genes	Average transcript length(bp)	Average CDS length(bp)	Average exons number per gene	Sequencing platform
<i>Scylla paramamosain</i>	1.21 Gb	11.45 Mb	23.61 Mb	33,662	22,869.83	1,187.71	6.06	Nanopore, HiFi, HiC
<i>Eriocheir sinensis</i>	1.57 Gb	26.05 kb	17.13 Mb	28,033	4,578.54	1,074.94	3.24	Pacbio, Illumina, HiC [31]
<i>Procambarus virginalis</i>	3.29 Gb	1.18 kb	39.28 kb	21,773	6,501.48	838.12	3.82	Illumina, Hiseq 2000 [26]
<i>Portunus trituberculatus</i>	1.01 Gb	4.12 Mb	21.79 Mb	16,796	11,195.08	1,465.56	6.6	Nanopore, BGISEQ, HiC [29]
<i>Litopenaeus vannamei</i>	1.66 Gb	57 kb	605 kb	25,596	10,464.60	1,305.76	6.16	Pacbio, Illumina, BAC [14]
<i>Penaeus monodon</i>	2.39 Gb	79 kb	44.86 Mb	30,038	1,428			Pacbio, Chicago, HiC [39]
<i>Homarus americanus</i>	2.29 Gb	133.3 kb	759.6 kb	25,284	9,560	1,171	5.79	Nanopore, Chicago, HiC [58]
<i>Scylla paramamosain</i>	1.55 Gb	191 kb	325 kb	17,821		1,527		Pacbio, Illumina, HiC [30]

Table S2 Details of repeat sequences in *Scylla paramamosain*

Class	Order	Super family	Number of elements	Length of sequence(bp)	Percentage of sequence(%)
Class I	LINE		2158996	311984072	25.77
			1164005	210695642	17.40
		Unknown	112579	25034486	2.07
		CR1	221126	63321706	5.23
		CR1-Zenon	115038	63628469	5.26
		L2	149069	10940876	0.90
		Penelope	143776	8079613	0.67
		L1-Tx1	86092	3991730	0.33
		L1	113353	5277990	0.44
		R2-NeSL	17665	1467079	0.12
		RTE-X	20908	3640916	0.30
		R1	19475	1326564	0.11
		Rex-Babar	22390	4570627	0.38
		RTE-BovB	26669	6252341	0.52
		I-Jockey	26536	2510007	0.21
		I	10844	2450867	0.20
		Jockey	3152	2132167	0.18
		Other	75333	6070204	0.50
	LTR		965998	99478958	8.22
		Gypsy	328359	52422981	4.33
		ERV1	214468	7323356	0.60
		Unknown	158516	23646993	1.95
		Pao	42247	5584457	0.46
		ERVK	132425	3968298	0.33
		Copia	48946	2513227	0.21
		DIRS	9729	2008485	0.17
		Other	31308	2011161	0.17
	SINE		28993	1809472	0.15

Class II			3006682	275205028	22.73	
	DNA		2881696	266918678	22.05	
		P	26684	1619787	0.13	
		Unknown	474614	86375737	7.13	
		hAT-Ac	321021	22462282	1.86	
		Maverick	220763	10879755	0.90	
		hAT-Tip100	52202	2404302	0.20	
		Ginger	146399	7828469	0.65	
		Kolobok-Hydra	117795	10636249	0.88	
		CMC-EnSpm	395444	45344214	3.75	
		PIF-Harbinger	109827	5212437	0.43	
		hAT-Blackjack	47799	2134384	0.18	
		Zisupton	113881	7930998	0.66	
		Kolobok-T2	46244	2426350	0.20	
		Sola-1	83332	6221745	0.51	
		PIF-Spy	44858	2769776	0.23	
		TcMar-Tc1	115337	4327601	0.36	
		hAT-Charlie	49113	2940755	0.24	
		Sola-3	31175	1844837	0.15	
		MULE-MuDR	86652	9113921	0.75	
		TcMar-Mariner	38700	13984044	1.15	
		TcMar-Fot1	42767	2510238	0.21	
		CMC-Transib	26917	2126293	0.18	
		TcMar-Tigger	10016	2460295	0.20	
		PiggyBac	10245	1235549	0.10	
		Other	269911	12128660	1.00	
		RC		111255	4050488	0.33
			Helitron	111255	4050488	0.33
		MITE		13731	4235862	0.35
	Unknown		13731	4235862	0.35	
	Total TEs			5165678	587189100	48.50

Table S3 Comparison of protein-coding genes between *Scylla paramamosain* and other species

Source	Number of gene	Average gene length(bp)	Average CDS length(bp)	Average exons per gene	Average exon length(bp)	Average intron per gene	Average intro length(bp)
<i>Scylla paramamosain</i>	33,662	12,535.06	1,208.52	5.36	225.29	4.36	2,595.33
<i>Eriocheir sinensis</i>	27,832	4,578.54	1,074.94	3.24	331.41	2.24	1,561.62
<i>Drosophila melanogaster</i>	13,955	4,593.23	1,558.47	3.89	400.27	2.89	1,048.79
<i>Daphnia pulex</i>	15,295	3,393.58	1,630.89	6.91	235.89	5.91	298.06
<i>Crassostrea gigas</i>	28,402	7,404.91	1,473.73	7.54	195.51	6.54	907.22
<i>Penaeus vannamei</i>	24,974	10,464.60	1,305.76	6.16	212.06	5.16	1,775.78

Table S4 Positive selection genes in *Scylla paramamosain*

Gene_ID	omega	P_value	FDR	Positive site number	Function
evm.model.Chr28.104	57.58545	1.93E-07	1.84E-05	11	Proteasome subunit alpha-type 7-like
evm.model.Chr37.191	20.5618	0.000803	0.028693	6	WD repeat-containing protein 82
evm.model.Chr01.2332	658.4223	8.28E-07	5.92E-05	3	ADP-ribosylation factor GTPase-activating protein 2
evm.model.Chr31.67	1	0.000214	0.010219	1	Ankyrin repeat domain-containing protein 13C
evm.model.Chr09.1832	120.0481	0	0	16	Probable ATP-dependent RNA helicase kurz
evm.model.Chr13.435	92.88146	0.000109	0.006239	6	Nucleolar protein 58
evm.model.Chr20.1414	999	0.000497	0.020311	4	Tetratricopeptide repeat protein 37
evm.model.Chr09.2036	82.29754	0	0	31	Acetyl-coenzyme A transporter 1

Table S5 Summary of non-coding genes in *Scylla paramamosain*

Type	Number	Average_length(bp)	Total_length(bp)	Percentage(%)
regulatory	361	47.94	17,307	0.0014
tRNA	3,153	73.85	232,845	0.0192
ncRNA	633	147.89	93,612	0.0077
rRNA	1,055	398.93	420,867	0.0348
rRNA_stat:				
18S	30	1,856.83	55,705	0.0046
28S	34	7,286.85	247,753	0.0205
5S	961	117.18	112,608	0.0093
5.8S	30	160.03	4,801	0.0004
ncRNA_stat:				
other	75	272.25	20,419	0.0017
snRNA	36	94.81	3,413	0.0003
miRNA	449	131.67	59,119	0.0049
spliceosomal	73	146.04	10,661	0.0009

Table S6 Functional characterization of *Eriocheir sinensis*, *Portunus trituberculatus*, and *Scylla paramamosain* Elovl6 via heterologous expression in yeast *Saccharomyces cerevisiae*

[illegible]

Table S7 Statistics of genome sequencing data of *Scylla paramamosain*.

	Nanopore	HiFi	Hi-C
Base number	86,478,669,383	48,787,892,247	34,339,251,309
Reads number	4,797,635	3,166,804	231,392,934
Mean length	18,025	15,406	
Max length	421,461	51,469	
N50	37,765	15,469	
Clean Q30 Bases Rate (%)			89.04
Valid Paired-end Reads			39,941,479

Table S8 RNA assemblies used in gene annotation of *Scylla paramamosain*.

Sample	Total reads	Total bases (bp)	Clean reads	Clean bases (bp)	Q20 rate(%)	Q30 rate(%)	GC(%)
SRR10493618	128,123,146	19,172,959,248	125,617,426	18,785,380,526	98.27	94.81	49.75
SRR10493619	128,971,638	19,282,087,696	127,050,738	18,983,967,546	98.49	95.42	50.24
SRR10493620	129,855,058	19,415,533,632	128,073,922	19,138,179,028	98.48	95.38	49.93
SRR12091740	54,198,790	7,863,446,770	54,187,692	7,855,660,947	98.64	95.82	46.33
SRR12091741	48,908,268	7,113,470,245	48,897,852	7,106,492,832	98.77	96.15	45.83
SRR12091742	51,237,134	7,429,856,855	51,226,858	7,422,105,729	98.7	96.01	45.57
SRR12091743	54,397,854	7,866,049,955	54,387,246	7,856,318,460	98.78	96.23	44.54
SRR12091744	52,572,856	7,611,407,371	52,565,402	7,604,340,620	98.59	95.68	45.7
SRR12091745	55,510,188	8,063,552,837	55,502,806	8,056,386,885	98.66	95.82	46.93
SRR12091746	47,955,458	6,972,528,373	47,945,908	6,965,778,562	98.78	96.19	45.76
SRR12091747	48,770,678	7,096,588,572	48,760,568	7,090,290,298	98.71	95.97	46.74
SRR13154296	61,136,612	6,113,661,200	60,484,294	6,042,955,794	97.91	94.3	45.24
SRR13154297	77,226,038	7,722,603,800	76,458,398	7,642,834,378	98.12	95.02	42.73
SRR13154298	73,940,440	7,394,044,000	73,214,822	7,317,780,906	98.04	94.62	44.64
SRR13154299	60,772,638	6,077,263,800	60,231,682	6,019,488,686	98.15	94.9	44.8
SRR13154300	70,715,990	7,071,599,000	70,101,978	7,006,188,434	98.1	94.92	45.68
SRR13154301	76,929,920	7,692,992,000	76,241,014	7,617,803,222	98.02	94.77	46
SRR13154302	71,230,606	7,123,060,600	70,545,904	7,051,619,964	98.05	94.67	42.69
SRR13154303	65,001,712	6,500,171,200	64,425,876	6,438,254,970	98.22	95.06	44.25
SRR13154304	72,685,614	7,268,561,400	71,930,056	7,188,107,628	97.97	94.63	45.82
SRR13154305	64,076,526	6,407,652,600	63,563,518	6,351,305,834	98.22	95.04	45.87
SRR13154306	62,467,070	6,246,707,000	62,012,386	6,197,235,712	98.26	95.16	44.52
SRR13154307	72,306,702	7,230,670,200	71,671,808	7,163,243,378	98.09	94.74	45.8
SRR13154308	71,301,500	7,130,150,000	70,688,866	7,065,509,776	98.17	94.91	43.11
SRR13154309	63,118,832	6,311,883,200	62,586,994	6,254,532,148	98.22	95.05	43.94
SRR13154310	93,889,328	9,388,932,800	92,959,698	9,292,840,018	98.28	95.31	40.61

SRR5814909	33,698,212	4,245,259,370	32,972,572	4,149,589,054	93.61	88.33	53.94
SRR5814910	31,254,718	3,937,273,175	30,614,842	3,853,261,200	93.85	88.69	54.27
SRR5814911	33,698,874	4,245,263,966	32,912,798	4,142,889,830	93.5	88.11	55.16
SRR5814912	37,275,230	4,695,854,468	36,426,072	4,582,282,851	93.64	88.51	52.66
SRR5814913	32,938,522	4,149,634,815	32,216,418	4,052,560,456	93.76	88.67	52.87
SRR5814914	36,968,102	4,656,967,106	36,220,468	4,558,554,477	93.98	88.99	53.96
SRR5814915	33,485,180	4,218,417,849	32,767,400	4,122,938,145	93.83	88.69	51.54
SRR5814916	34,702,562	4,371,802,474	33,918,590	4,268,936,144	93.56	88.24	54.39
SRR5814917	33,874,804	4,267,442,962	33,046,236	4,158,839,055	93.48	88.13	54.79
SRR8749191	89,994,540	13,499,181,000	86,403,350	12,900,193,564	96.7	92.29	48.15
SRR8749192	73,108,394	10,966,259,100	71,788,578	10,663,999,552	96.97	92.31	47.72
SRR8749197	64,650,158	9,697,523,700	63,559,074	9,468,409,800	97.19	92.64	47.93
SRR8749198	64,318,070	9,647,710,500	63,186,400	9,415,140,274	97.22	92.77	46.93
SRR8749199	64,622,632	9,693,394,800	63,371,054	9,422,600,704	97	92.38	47.3
SRR8749200	88,851,060	13,327,659,000	85,623,630	12,816,881,972	97.03	92.8	48.34
SRR8749201	77,561,448	11,634,217,200	72,876,038	10,805,035,592	96	90.55	49.14
SRR8749202	78,948,684	11,842,302,600	70,188,100	10,349,137,142	94.39	88.26	48.38
SRR8749203	65,454,782	9,818,217,300	61,726,938	9,135,353,294	96.1	90.67	48.44
SRR8749204	87,840,804	13,176,120,600	83,722,538	12,371,176,602	96.33	91.08	48.86
SRR8749205	80,737,948	12,110,692,200	76,878,776	11,390,572,144	96.33	91.08	48.18
SRR8749206	78,428,724	11,764,308,600	73,843,926	10,943,058,226	95.98	90.45	48.23
SRR5387739	79,854,234	10,061,633,484	78,808,632	9,198,519,120	96.45	92.86	51.77
SRR5387741	79,282,758	9,989,627,508	78,287,758	8,951,074,824	96.25	92.53	48.34

Table S9 Primers used for *Eselovl6*, *Ptelovl6*, and *Spelovl6* functional characterization

Transcript	Primer	Sequence
<i>Eselovl6</i>	<i>Eselovl6</i> -X1-F	GAATATTAAGCTTGGTACCGAGCTC <u>GGATCC</u> ATGACCGCAATGGACGCCTTGGCCAAGAGGTCCTTCTTCGAC AACACGA
	<i>Eselovl6</i> -X1-R	GCCGCCAGTGTGATGGATATCTGCAG <u>AATTCT</u> TATTCCAGTTTACCCTTGGTGCTCTTTCCTTCGTAGGCGAGA GACTCCTGG
	<i>Eselovl6</i> -X2-F	GAATATTAAGCTTGGTACCGAGCTC <u>GGATCC</u> ATGGAGAGCGAAAAGATGTTCTTCATCAATTTGACGAACGTG GAGGC
	<i>Eselovl6</i> -X2-R	GCCGCCAGTGTGATGGATATCTGCAG <u>AATTCT</u> TATTCCAGTTTACCCTTGGTGCTCTTTCCTTCGTAGGCGAGA GA
	<i>Eselovl6</i> -X3-F	GAATATTAAGCTTGGTACCGAGCTC <u>GGATCC</u> ATGGAGTCGGTCACCATGCCTAACTATTCTTACGTCTTC
	<i>Eselovl6</i> -X3-R	GCCGCCAGTGTGATGGATATCTGCAG <u>AATTCT</u> TATTCCAGTTTACCCTTGGTGCTCTTTCCTTCGTAGGCGAGA GA
<i>Ptelovl6</i>	<i>Ptelovl6</i> -X1-F	GAATATTAAGCTTGGTACCGAGCTC <u>GGATCC</u> ATGACAAGGAGCATGGAGACACTGCACAAATCTAGCTTCTTT GAAAACA
	<i>Ptelovl6</i> -X1-R	GCCGCCAGTGTGATGGATATCTGCAG <u>AATTCT</u> TATTCCAGTTTACCCTTGCTACCTTTTCCTTCATAAGCAATA GACTCCTT
	<i>Ptelovl6</i> -X2-F	GAATATTAAGCTTGGTACCGAGCTC <u>GGATCC</u> ATGAGTTTCTTCATCAATTTGACGAACGTGGAGGCAGCTG
	<i>Ptelovl6</i> -X2-R	GCCGCCAGTGTGATGGATATCTGCAG <u>AATTCT</u> TATTCCAGTTTACCCTTGCTACCTTTTCCTTCATAAGCAATA GACT
	<i>Ptelovl6</i> -X3-F	GAATATTAAGCTTGGTACCGAGCTC <u>GGATCC</u> ATGGAGTCGGTCACCATGCCAAATTATTCCTATGTCTTCAAGT TCGAGG
	<i>Ptelovl6</i> -X3-R	GCCGCCAGTGTGATGGATATCTGCAG <u>AATTCT</u> TATTCCAGTTTACCCTTGCTACCTTTTCCTTCATAAGCAATA GACTCCTTG
<i>Spelovl6</i>	<i>Spelovl6a</i> -F	GAATATTAAGCTTGGTACCGAGCTC <u>GGATCC</u> ATGGAGTCGGTCACCATGCCAAATTATTCCTATG
	<i>Spelovl6a</i> -R	CCGCCAGTGTGATGGATATCTGCAG <u>AATTCT</u> TATTCCAGTTTACCCTTGCTACCTTTCCCTTCATAA
	<i>Spelovl6b</i> -F	GAATATTAAGCTTGGTACCGAGCTC <u>GGATCC</u> ATGACAAGGAATATGGAGACACTGCATAAAT

<i>Spelovl6b</i> -R	CCGCCAGTGTGATGGATATCTGCAGA <u>ATTCTT</u> ATTCCAGTTTACCCTTGCTACCTTTCCCTTC
<i>Spelovl6c</i> -F	GAATATTAAGCTTGGTACCGAGCTC <u>GGATCC</u> ATGAGTTTCTTCATCAATTTGACGAACGTGGAGGC
<i>Spelovl6c</i> -R	CCGCCAGTGTGATGGATATCTGCAGA <u>ATTCTT</u> ATTCCAGTTTACCCTTGCTACCTTTCCCTT
