

Supplementary Figures and Tables

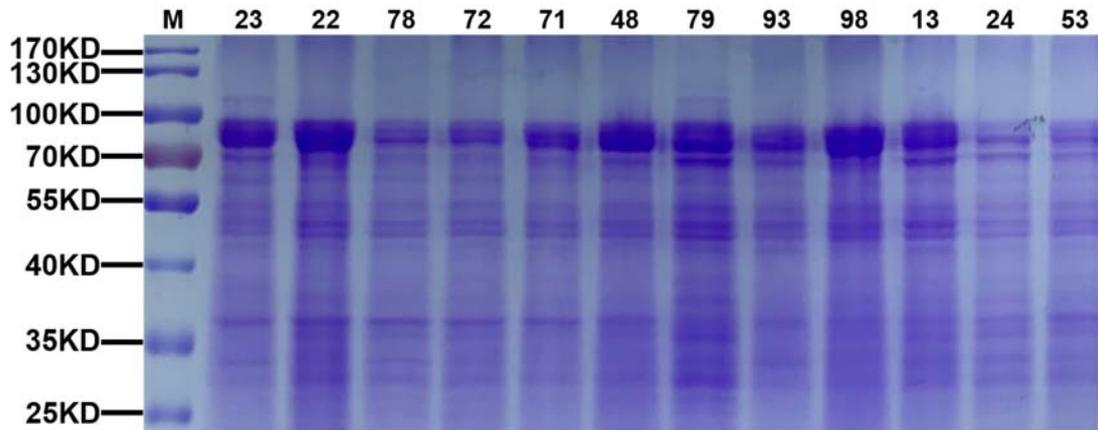


Figure S1. The quality control by SDS-PAGE.

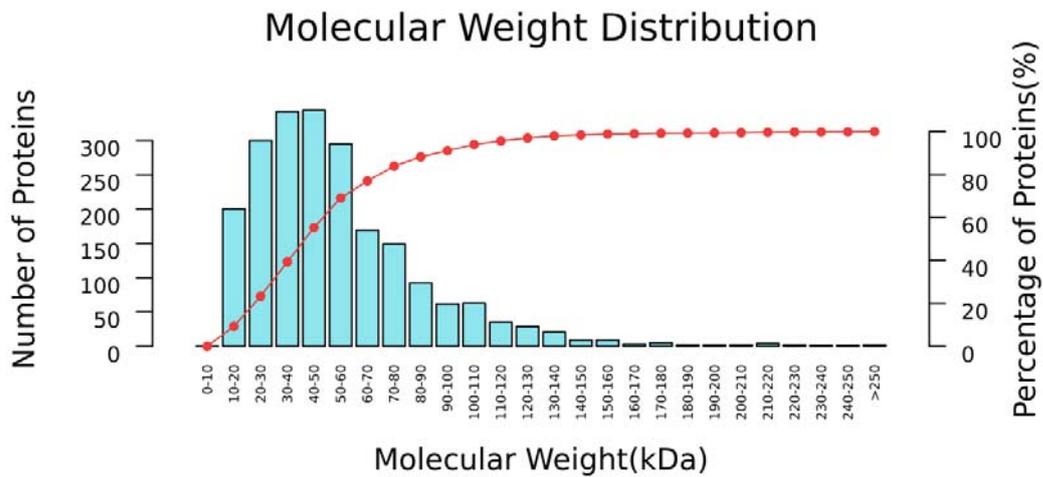


Figure S2. The molecular weight distribution for identified proteins.

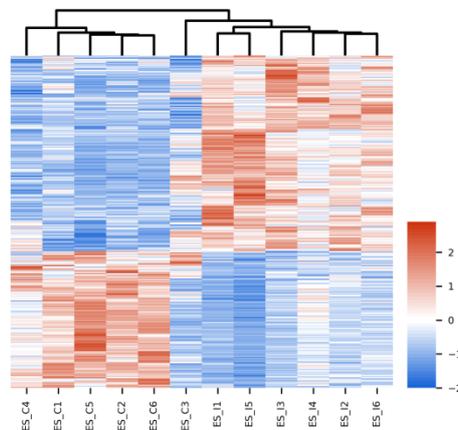


Figure S3. The heatmap image analysis between parasitized and non-parasitized crabs.

Table S1 The concentration of proteins detected in Chinese mitten crab hepatopancreas.

ID	30223	30222	30178	30172	30171	30148	30079	30093	30098	30113	30124	30153
hepatopancreas (μg/μl)	17.3	30.1	23.1	26.9	25	18.5	23.1	23.3	27.4	22.4	20.1	23.6
volume(μl)	400	400	400	400	400	400	400	400	400	400	400	400
Total(μg)	6920	12040	9240	10760	10000	7400	9240	9320	10960	8960	8040	9440

Table S2 Significant enrichment of GO terms (p<0.05) in Chinese mitten crab infected with *P. gregaria*.

GO-ID	GO-Term	Category	P-Value	Diff
GO:0043202	lysosomal lumen	C	0.00033	10
GO:0005886	plasma membrane	C	0.00034	81
GO:0003677	DNA binding	F	0.00052	1
GO:0005790	smooth endoplasmic reticulum	C	0.00086	10
GO:0035577	azurophil granule membrane	C	0.00091	8
GO:0005615	extracellular space	C	0.0012	40
GO:0030246	carbohydrate binding	F	0.00135	12
GO:0005525	GTP binding	F	0.00157	36
GO:0019882	antigen processing and presentation	P	0.00167	5
GO:0098993	anchored component of synaptic vesicle membrane	C	0.00167	5
GO:0003924	GTPase activity	F	0.0024	31
GO:0035099	hemocyte migration	P	0.00247	6
GO:0000184	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	P	0.00274	13
GO:0008305	integrin complex	C	0.00389	10
GO:0048471	perinuclear region of cytoplasm	C	0.00414	50
GO:0005764	lysosome	C	0.00521	19
GO:0051489	regulation of filopodium assembly	P	0.00602	4
GO:0051593	response to folic acid	P	0.00602	4
GO:0045298	tubulin complex	C	0.00658	7
GO:0007476	imaginal disc-derived wing morphogenesis	P	0.00674	7
GO:0006012	galactose metabolic process	P	0.00674	7
GO:0016282	eukaryotic 43S preinitiation complex	C	0.00756	6
GO:0000045	autophagosome assembly	P	0.00756	6
GO:0030521	androgen receptor signaling pathway	P	0.00756	6
GO:0034446	substrate adhesion-dependent cell spreading	P	0.00756	6
GO:0034663	endoplasmic reticulum chaperone complex	C	0.00756	6
GO:0050905	neuromuscular process	P	0.00771	5
GO:0001731	formation of translation preinitiation complex	P	0.00771	5
GO:0000082	G1/S transition of mitotic cell cycle	P	0.0108	11
GO:0055114	oxidation-reduction process	P	0.01336	18
GO:0005198	structural molecule activity	F	0.01366	1
GO:0008285	negative regulation of cell population proliferation	P	0.01366	1

GO:0032482	Rab protein signal transduction	P	0.01412	7
GO:0005788	endoplasmic reticulum lumen	C	0.01728	14
GO:0031625	ubiquitin protein ligase binding	F	0.02048	26
GO:0031430	M band	C	0.02078	9
GO:0022627	cytosolic small ribosomal subunit	C	0.02078	9
GO:0001732	formation of cytoplasmic translation initiation complex	P	0.0208	5
GO:0051721	protein phosphatase 2A binding	F	0.0208	5
GO:0007349	cellularization	P	0.0208	5
GO:0051787	misfolded protein binding	F	0.0208	5
GO:0010469	regulation of signaling receptor activity	P	0.02165	3
GO:0007424	open tracheal system development	P	0.02165	3
GO:0042623	ATPase activity, coupled	F	0.02165	3
GO:0035253	ciliary rootlet	C	0.02165	3
GO:0030317	flagellated sperm motility	P	0.02165	3
GO:0007494	midgut development	P	0.02165	3
GO:0071796	K6-linked polyubiquitin modification-dependent protein binding	F	0.02165	3
GO:0010888	negative regulation of lipid storage	P	0.02165	3
GO:0004560	alpha-L-fucosidase activity	F	0.02165	3
GO:0017177	glucosidase II complex	C	0.02165	3
GO:0006360	transcription by RNA polymerase I	P	0.02165	3
GO:0042340	keratan sulfate catabolic process	P	0.02165	3
GO:0016125	sterol metabolic process	P	0.02165	3
GO:0006650	glycerophospholipid metabolic process	P	0.02165	3
GO:0019377	glycolipid catabolic process	P	0.02165	3
GO:0006004	fucose metabolic process	P	0.02165	3
GO:0016139	glycoside catabolic process	P	0.02165	3
GO:1902416	positive regulation of mRNA binding	P	0.02165	3
GO:0071006	U2-type catalytic step 1 spliceosome	C	0.02165	3
GO:0046809	replication compartment	C	0.02165	3
GO:0003688	DNA replication origin binding	F	0.02165	3
GO:0008094	DNA-dependent ATPase activity	F	0.02165	3
GO:0070181	small ribosomal subunit rRNA binding	F	0.02165	3
GO:2000767	positive regulation of cytoplasmic translation	P	0.02165	3
GO:0005850	eukaryotic translation initiation factor 2 complex	C	0.02165	3
GO:0008199	ferric iron binding	F	0.02165	3
GO:0016235	aggresome	C	0.02165	3
GO:0044437	vacuolar part	C	0.02165	3
GO:0097452	GAIT complex	C	0.02165	3
GO:2000535	regulation of entry of bacterium into host cell	P	0.02165	3
GO:0030904	retromer complex	C	0.02165	3
GO:0034067	protein localization to Golgi apparatus	P	0.02165	3
GO:0004553	hydrolase activity, hydrolyzing O-glycosyl compounds	F	0.02341	4

GO:0000028	ribosomal small subunit assembly	P	0.02341	4
GO:0007628	adult walking behavior	P	0.02341	4
GO:0016197	endosomal transport	P	0.02341	4
GO:0007040	lysosome organization	P	0.02341	4
GO:0043614	multi-eIF complex	C	0.02341	4
GO:0033290	eukaryotic 48S preinitiation complex	C	0.02341	4
GO:0003735	structural constituent of ribosome	F	0.02412	19
GO:0005777	peroxisome	C	0.02467	3
GO:0006886	intracellular protein transport	P	0.02719	19
GO:0031252	cell leading edge	C	0.03013	8
GO:0071346	cellular response to interferon-gamma	P	0.03013	8
GO:0005178	integrin binding	F	0.03013	8
GO:0045169	fusome	C	0.03013	8
GO:0043687	post-translational protein modification	P	0.03165	23
GO:0008209	androgen metabolic process	P	0.03331	6
GO:0042026	protein refolding	P	0.03331	6
GO:0005815	microtubule organizing center	C	0.03331	6
GO:0070125	mitochondrial translational elongation	P	0.03331	6
GO:0042769	DNA damage response, detection of DNA damage	P	0.03331	6
GO:0006119	oxidative phosphorylation	P	0.03376	1
GO:0007030	Golgi organization	P	0.03765	14
GO:0070374	positive regulation of ERK1 and ERK2 cascade	P	0.03993	8
GO:0005802	trans-Golgi network	C	0.0402	12
GO:0098793	presynapse	C	0.04144	10
GO:0045121	membrane raft	C	0.04216	16
GO:0048646	anatomical structure formation involved in morphogenesis	P	0.04287	5
GO:0070126	mitochondrial translational termination	P	0.04287	5
GO:0016485	protein processing	P	0.04287	5
GO:0032781	positive regulation of ATPase activity	P	0.04287	5
GO:0016477	cell migration	P	0.04533	7

Diff: The number of different expression proteins corresponding the GO term.