

1 Supplementary Table S3. The common up-regulated proteins shared in two batches (TR and AO) versus DW identified by label-free analysis.

Accession	Description	Organism	Coverage	Peptides	PSMs	Unique Peptides	AAs	MW [kDa]	calc. pI	emPAI	Score Sequest HT
G0ZJ10	2-phospho-D-glycerate hydrolase (Fragment)	<i>Cherax quadricarinatus</i>	31.08	4	66	2	222	24.3	5.07	1.955	76.91
O96658	Actin 2	<i>Penaeus monodon</i>	72.14	24	4967	1	377	41.8	5.24	1444.44	7004.08
H6CSY4	Actin 6 (Fragment)	<i>Pandalus platyceros</i>	50.43	10	1379	3	228	25.2	5.21	12.594	1103.45
Q962V5	Alpha actin	<i>Homarus americanus</i>	56.76	19	2670	1	377	41.9	5.31	35.308	2791.65
A0A2P1JJ58	Alpha-actinin, sarcomeric-like isoform X1 (Fragment)	<i>Procambarus clarkii</i>	60.33	53	774	12	890	102.7	5.35	27.23	1694.14
A0A0N7ZCJ7	ATP synthase subunit alpha	<i>Scylla olivacea</i>	33.45	14	71	2	550	59.3	9.1	1.33	169.1
A0T2V0	Beta-actin	<i>Penaeus monodon</i>	72.14	24	4730	3	377	42	5.14	574.44	5953.13
O17314	Calcium-transporting ATPase	<i>Procambarus clarkii</i>	24.21	23	388	2	1020	112.4	5.45	3.748	782.54
K9S0T9	Calmodulin	<i>Portunus trituberculatus</i>	46.97	6	23	6	149	16.8	4.22	4.623	52.25
O02449	Elongation factor 1-alpha (Fragment)	<i>Libinia emarginata</i>	42.85	10	63	1	364	40.1	8.18	1.471	88.84
E3T0W9	Elongation factor 1-alpha	<i>Litopenaeus vannamei</i>	42.95	13	85	1	461	50.8	8.95	1.818	170.72
R9YWA0	Enolase (Fragment)	<i>Kiwa sp. n. Southwest Indian Ridge</i>	36.28	3	32	1	113	12.4	5.1	1.848	87.32
A0A068FCL9	Fructose-bisphosphate aldolase	<i>Fenneropenaeus chinensis</i>	64.93	23	609	18	365	39.8	7.06	45.416	1039.47
A0A0P4WGN0	Glycerol-3-phosphate dehydrogenase [NAD(+)]	<i>Scylla olivacea</i>	24.28	9	37	9	420	46.2	7.31	1.336	111.66
G1AP69	Hemocyanin	<i>Penaeus monodon</i>	33.67	20	191	2	683	77.9	5.57	7.072	319.82

H9LFA4	Mitochondrial ATP synthase delta subunit	<i>Litopenaeus vannamei</i>	9.49	1	13	1	158	16.5	4.74	0.52	18.45
Q8T6G0	Myosin heavy chain (Fragment)	<i>Homarus gammarus</i>	51.21	1	4	1	41	4.6	5.11	3.642	3.61
K4Q111	Myosin heavy chain type 1	<i>Litopenaeus vannamei</i>	70.46	191	9279	53	1913	219.6	6.02	265.708	17224.86
K4Q2Y1	Myosin heavy chain type 2	<i>Penaeus monodon</i>	60.60	148	6644	8	1909	219	6.16	95.041	11270.86
D7F2L7	Paramyosin (Fragment)	<i>Palaemon varians</i>	33.82	2	26	2	68	8	8.15	4.179	55.51
A0A0P4VU A5	Phosphorylase b kinase regulatory subunit	<i>Scylla olivacea</i>	5.28	7	12	7	1212	136.1	6.65	0.216	28.42
Q86GD6	Projectin	<i>Procambarus clarkii</i>	10.55	80	389	77	8625	962	6.43	0.406	766.82
C4PL18	Ribosomal protein L3	<i>Penaeus monodon</i>	20.93	8	14	6	406	46.4	10.3	1.021	31.35
Q2I3E8	Ribosomal protein L8	<i>Litopenaeus vannamei</i>	24.90	5	18	5	257	28.2	11.05	0.957	30.16
D7F2L3	Sarcoplasmic calcium-binding protein 1 (Fragment)	<i>Palaemon varians</i>	32.35	3	379	1	68	7.7	4.84	2.162	129.08
C7A639	Sarcoplasmic calcium-binding protein	<i>Litopenaeus vannamei</i>	87.04	25	2938	5	193	22.1	4.89	706.946	3631.2
A0A0B5JEF 0	Sarcoplasmic calcium-binding protein variant a	<i>Eriocheir sinensis</i>	25.38	5	532	1	193	21.9	4.81	1.154	473.55
P02636	Sarcoplasmic calcium-binding protein, alpha-B and -A chains	<i>Penaeus sp.</i>	69.79	20	2169	4	192	22	4.81	49.119	2120.46
B6EAU4	Skeletal muscle actin 4	<i>Homarus americanus</i>	55.70	21	3194	5	377	41.9	5.31	189.546	3690
K4EG00	Skeletal muscle alpha actin (Fragment)	<i>Pandalus platyceros</i>	33.94	7	1508	1	218	24.2	5.29	7.483	1587.83
Q6XGZ8	Slow muscle myosin S1 heavy chain (Fragment)	<i>Homarus americanus</i>	36.88	23	906	3	507	58.5	5.27	5.19	846.45
A0A139Z42	Sodium/potassium-transporting	<i>Litopenaeus vannamei</i>	31.98	26	51	17	1038	115.3	5.48	1.31	130.01

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4	ATPase subunit alpha											
A0A0P0C4 Q7	Tetraspanin	<i>Litopenaeus vannamei</i>	29.28	3	14	3	239	25.7	4.65	2.162	43.35	
A1KYZ2	Tropomyosin	<i>Penaeus monodon</i>	77.46	37	1486	9	284	32.8	4.75	130.113	2038.73	
K7WFT8	Troponin I	<i>Litopenaeus vannamei</i>	48.61	15	294	3	216	24.8	9.51	19.153	601.98	
A0A2P0ND U9	Troponin T	<i>Palaemon carinicauda</i>	17.92	11	245	11	385	45.7	5.06	3.541	325.73	
Q94570	Tubulin alpha-2 chain	<i>Homarus americanus</i>	13.08	4	35	2	451	50.2	5.19	0.585	81.25	

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