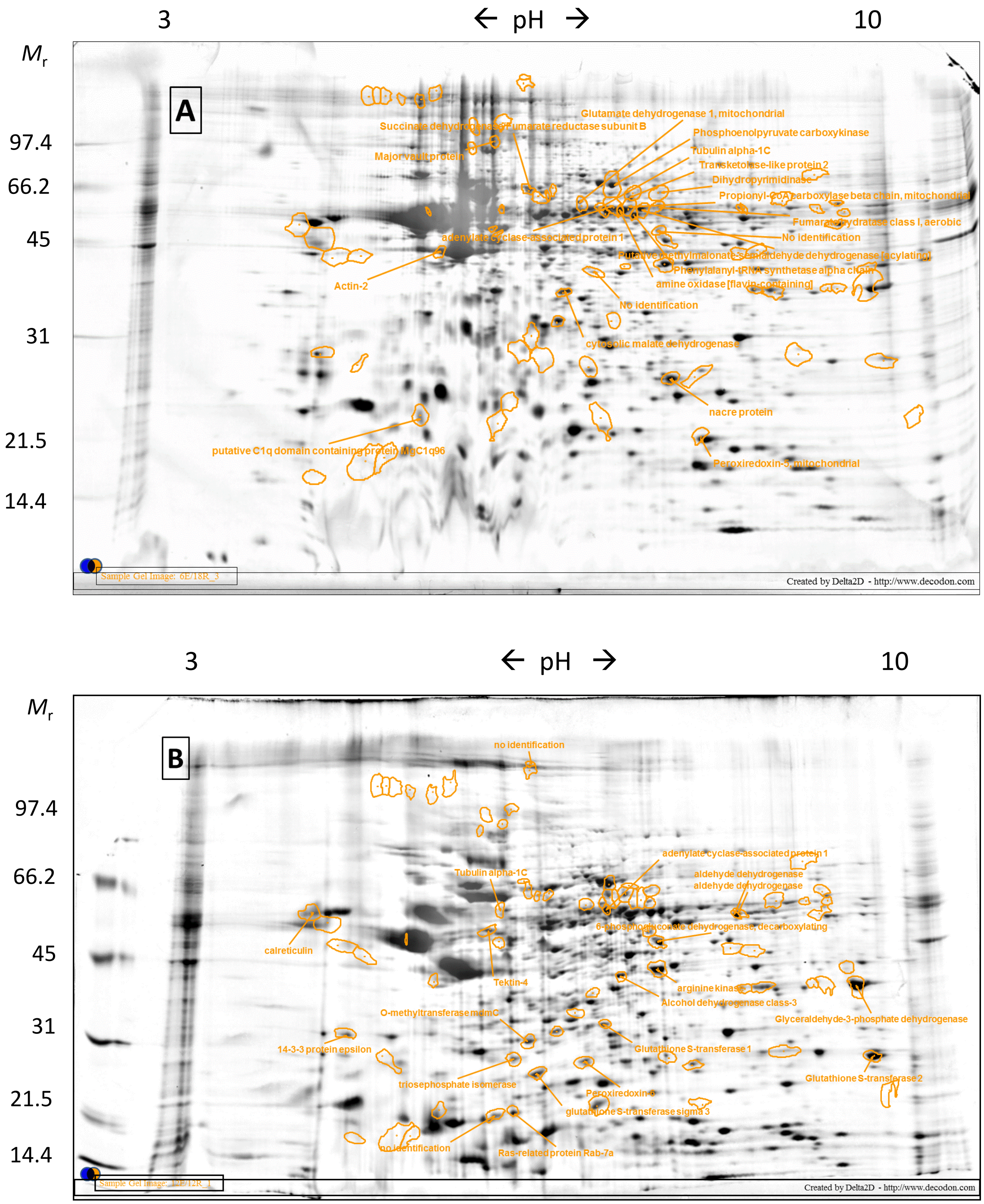
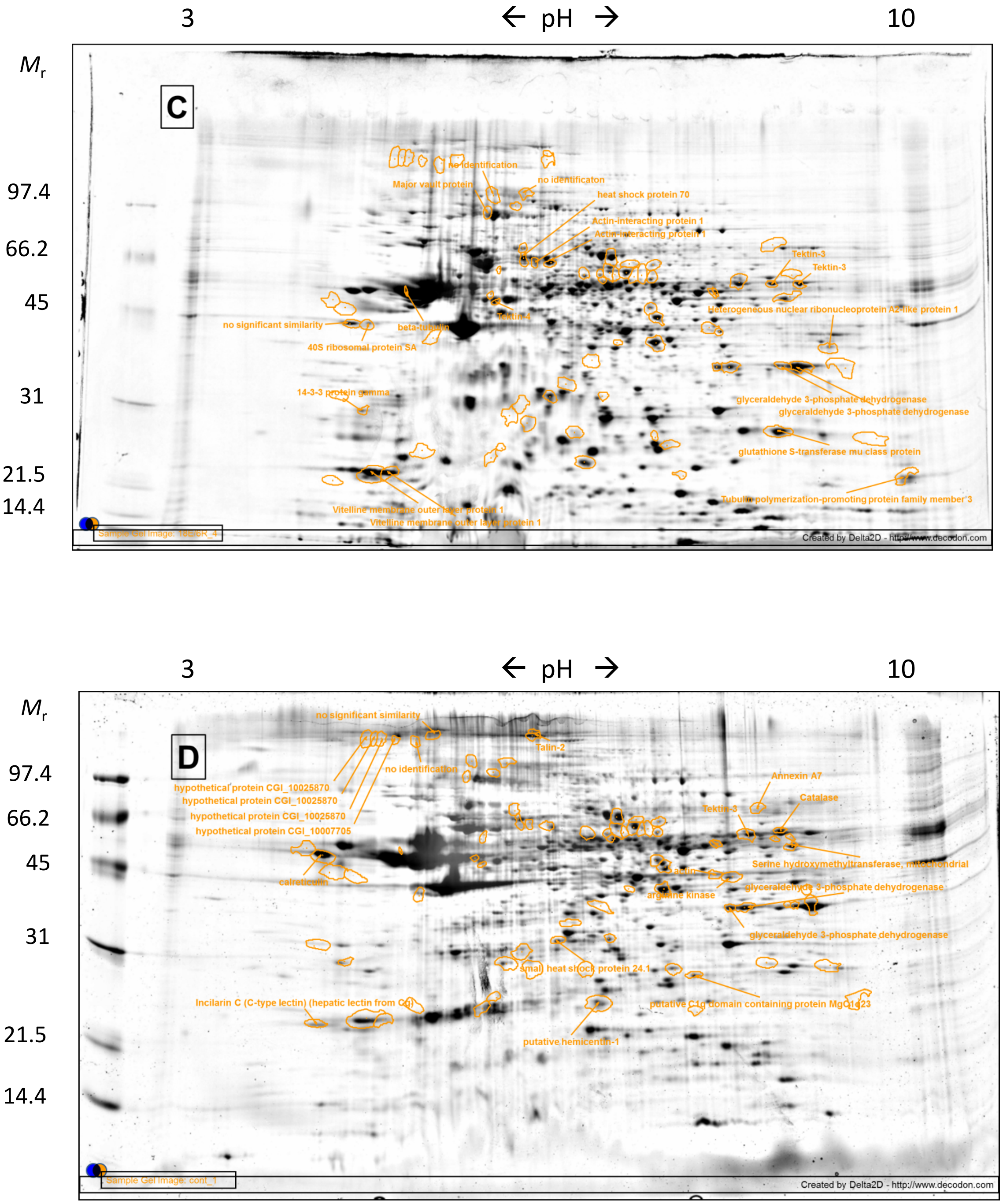
SUPPLEMENTAL FIGURES:

Supplemental Figure 1. Representative two-dimensional SDS-PAGE gel images from each of the four treatment groups: 6E/18R **(A)**, 12E/12R **(B)**, 18E/6R **(C)** and control **(D)**. Proteins are separated by isoelectric point (pI) (pH range 3 – 10) along the horizontal dimension and by relative molecular mass (M_r; x 10^3) along the vertical dimension. Biorad low range molecular weight standards were used for the ladder. The eighty spots selected for identification are outlined on each gel, and those proteins with the highest loading factors for the respective group are labeled. See Table 1 and Supplemental Table 1 for further information about identified proteins.



Supplemental Figure 1



Supplemental Figure 1

Supplemental Table 1A. Protein identifications (using MS/MS) of spots with high positive component loading values along PC1 (Figure 1), corresponding to treatment 6E/18R. A Mascot score > 45 indicates a significant match, with P < 0.05.

Delta2D spot ID	Loading (PC1)	# of EST matches	Mascot score	# of peptide matches	Genbank accession #	E value	Species providing match	Protein ID
37	2.33036	3	113	2	gi|405969875	2.00E-127	*Crassostrea gigas*	Succinate dehydrogenase / Fumarate reductase subunit B
85	2.2822	2	457	12	gi|405976463	0	*C. gigas*	Transketolase-like protein 2
49	2.20716	2	193	6	gi|405953047	0	*C. gigas*	Phenylalanyl-tRNA synthetase alpha chain
181	2.17435	2	265	5	gi|405970294	0	*C. gigas*	Putative methylmalonate-semialdehyde dehydrogenase [acylating]
65	2.11392	2	472	13	gi|405974984	0	*C. gigas*	Glutamate dehydrogenase 1, mitochondrial
253	2.0961	3	375	7	gi|405978690	5.00E-129	*C. gigas*	Propionyl-CoA carboxylase beta chain, mitochondrial
269	2.06661	1	64	2	gi|405963253	9.00E-24	*C. gigas*	Fumarate hydratase class I, aerobic
343	1.94754	3	816	23	gi|405961263	0.00E+00	*C. gigas*	Phosphoenolpyruvate carboxykinase [GTP]
188	1.92459	1	411	10	gi|73656362	0.00E+00	*C. gigas*	cytosolic malate dehydrogenase
155	1.89351	2	337	10	gi|342330738	1.00E-25	*Pinctada fucata*	nacre protein
357	1.88715	5	234	7	gi|297341134	6.00E-50	*C. gigas*	adenylate cyclase-associated protein 1
131	1.88668	6	289	12	gi|405966729	6.00E-09	*C. gigas*	amine oxidase [flavin-containing]
95	1.84696	7	138	4	gi|405965638	0	*C. gigas*	tubulin alpha-1C
187	1.83939	0	NA	NA	NA	NA	NA	NA
145	1.83145	1	248	7	gi|405974897	2.00E-81	*C. gigas*	Peroxiredoxin-5, mitochondrial
75	1.78633	1	189	7	gi|405974681	0	*C. gigas*	Major vault protein
156	1.76051	1	50	1	gi|405953142	3.00E-37	*C. gigas*	Dihydropyrimidinase
117	1.7508	0	NA	NA	NA	NA	NA	NA
31	1.7502	5	855	38	gi|405973339	0.00E+00	*C. gigas*	Actin-2
169	1.71706	1	173	3	gi|325504491	2.00E-51	*Mytilus galloprovincialis*	putative C1q domain containing protein MgC1q96

Supplemental Table 1B. Protein identifications (using MS/MS) of spots with high positive component loading values along PC2 (Figure 1), corresponding to treatment 12E/12R. A Mascot score > 45 indicates a significant match, with $P < 0.05$.

Delta2D spot ID	Loading (PC2)	# of EST matches	Mascot score	# of peptide matches	Genbank accession #	E value	Species providing match	Protein ID
190	2.1966	4	313	11	gi|297341134	5.00E-87	*C. gigas*	adenylate cyclase-associated protein 1
90	2.19315	1	218	6	gi|405971996	1.00E-39	*C. gigas*	Glutathione S-transferase 2
229	2.17843	3	474	10	gi|8131883	0	*Placopecten magellanicus*	aldehyde dehydrogenase
25	2.08739	2	429	10	gi|405972460	2.00E-110	*C. gigas*	Alcohol dehydrogenase class-3
150	2.08357	3	209	5	gi|405976318	3e-137	*C. gigas*	6-phosphogluconate dehydrogenase, decarboxylating
128	2.07798	3	267	9	gi|148717307	3E-175	*C. gigas*	calreticulin
171	2.06763	2	166	4	gi|193878315	1.00E-70	*Chlamys farreri*	Glutathione S-transferase 1
88	2.05665	2	173	6	gi|405954307	6.00E-128	*C. gigas*	Ras-related protein Rab-7a
142	2.03273	1	329	7	gi|405963584	1.00E-134	*C. gigas*	14-3-3 protein epsilon
215	1.98457	3	767	22	gi|405957058	0.00E+00	*C. gigas*	Glyceraldehyde-3-phosphate dehydrogenase
77	1.92374	0	NA	NA	NA	NA	NA	NA
72	1.81408	0	NA	NA	NA	NA	NA	NA
231	1.79468	2	288	8	gi|405965638	0	*C. gigas*	Tubulin alpha-1C
257	1.76302	3	192	6	gi|402227995	4.00E-49	*M. galloprovincialis*	glutathione S-transferase sigma 3
68	1.71781	6	679	17	gi|405967050	8E-146	*Saccostrea kegaki*	Tektin-4
28	1.69084	3	606	14	gi|8131883	0	*P. magellanicus*	aldehyde dehydrogenase
96	1.687	2	189	3	gi|333449422	6.00E-90	*C. ariakensis*	triosephosphate isomerase
306	1.68581	3	64	2	gi|126697314	7e-100	*Haliotis discus*	peroxiredoxin 6**
305	1.68184	2	1208	36	gi|301341836	2.00E-177	*Conus novaehollandiae*	arginine kinase
106	1.62479	3	454	15	gi|405953767	6.00E-50	*C. gigas*	O-methyltransferase mdmC

Supplemental Table 1C. Protein identifications (using MS/MS) of spots with high negative component loading values along PC2 (Figure 1), corresponding to treatment 18E/6R. A Mascot score > 45 indicates a significant match, with P < 0.05.

Delta2D spot ID	Loading (PC2)	# of EST matches	Mascot score	# of peptide matches	Genbank accession #	E value	Species providing match	Protein ID
51	-2.45667	1	131	3	gi|124264151	2.00E-90	*Leptochiton sp.*	glyceraldehyde 3-phosphate dehydrogenase
313	-2.25346	2	426	9	gi|405975469	3.00E-82	*C. gigas*	Tektin-3
352	-2.184	2	649	14	gi|405975469	3.00E-82	*C. gigas*	Tektin-3
308	-2.17835	1	131	3	gi|124264151	2.00E-90	*Leptochiton sp.*	glyceraldehyde 3-phosphate dehydrogenase
193	-2.07508	7	1001	31	gi|194068375	0.00E+00	*Saccostrea kegaki*	beta-tubulin
105	-2.07046	2	102	3	NA	NA	NA	no significant similarity
261	-2.03477	1	56	2	gi|405947583	5.00E-30	*C. gigas*	Tubulin polymerization-promoting protein family member 3
336	-2.0237	1	84	2	gi|405959466	6.00E-55	*C. gigas*	Vitelline membrane outer layer protein 1
247	-1.98668	1	130	3	gi|229891605	5.00E-137	*P. fucata*	40S ribosomal protein SA
54	-1.91326	2	71	2	gi|405966870	0.00E+00	*C. gigas*	Actin-interacting protein 1
184	-1.90996	8	485	15	gi|405967050	8.00E-146	*C. gigas*	Tektin-4
196	-1.88737	1	60	2	gi|405959466	6.00E-55	*C. gigas*	Vitelline membrane outer layer protein 1
162	-1.83526	3	1062	23	gi|405966870	0.00E+00	*C. gigas*	Actin-interacting protein 1
281	-1.81784	3	360	12	gi|210076789	3e-120	*C. ariakensis*	glutathione S-transferase mu class protein
10	-1.76586	4	457	17	gi|405974681	0.00E+00	*C. gigas*	Major vault protein
124	-1.74853	1	128	3	gi|405977263	5.00E-26	*C. gigas*	Heterogeneous nuclear ribonucleoprotein A2-like protein 1
309	-1.73295	0	NA	NA	NA	NA	NA	NA
314	-1.70076	0	NA	NA	NA	NA	NA	NA
134	-1.69759	3	341	7	gi|405950430	4.00E-82	*C. gigas*	14-3-3 protein gamma
275	-1.69718	5	193	4	gi|305689813	7E-79	*Cristaria plicata*	heat shock protein 70

Supplemental Table 1D. Protein identifications (using MS/MS) of spots with high negative component loading values along PC3 (Figure 1), corresponding to control. A Mascot score > 45 indicates a significant match, with $P < 0.05$.

Delta2D spot ID	Loading (PC3)	# of EST matches	Mascot score	# of peptide matches	Genebank accession #	E value	Species providing match	Protein ID
347	-2.91148	2	414	10	gi|405968267	2.00E-99	*C. gigas*	hypothetical protein CGI_10025870
346	-2.87454	2	414	10	gi|405968267	2.00E-99	*C. gigas*	hypothetical protein CGI_10025870
39	-2.77464	3	260	6	gi|46909311	3.00E-151	*Modiolus americanus*	Catalase
195	-2.66832	2	58	3	gi|301341836	1.00E-173	*Conus novahollandiae*	arginine kinase
212	-2.65056	1	82	3	gi|405976099	8.00E-143	*C. gigas*	Annexin A7
113	-2.63658	1	49	3	NA	NA	NA	no significant similarity
11	-2.57958	2	530	12	gi|405968267	2.00E-99	*C. gigas*	hypothetical protein CGI_10025870
2	-2.35992	1	415	12	gi|156571893	7.00E-52	*C. virginica*	glyceraldehyde 3-phosphate dehydrogenase
358	-2.2624	2	249	9	gi|148717307	6.00E-172	*C. gigas*	calreticulin
219	-2.24851	2	827	24	gi|405975469	7.00E-80	*C. gigas*	Tektin-3
225	-2.22598	0	NA	NA	NA	NA	NA	no identification
127	-2.14443	3	25	5	gi|405951868	5.00E-47	*C. gigas*	hypothetical protein CGI_10007705
35	-1.96663	1	340	8	gi|325504345	4.00E-35	*M. galloprovincialis*	putative C1q domain containing protein MgC1q23
15	-1.93665	1	134	4	gi|405946057	1.00E-68	*C. gigas*	Talin-2
94	-1.92085	2	481	13	gi|28475277	6.00E-155	*C. gigas*	glyceraldehyde 3-phosphate dehydrogenase
363	-1.91151	4	364	11	gi|405960692	2.00E-22	*C. gigas*	Putative hemicentin-1
154	-1.90472	1	270	7	gi|32816054	0.00E+00	*Chlamys farreri*	actin
126	-1.84329	1	325	8	gi|347545633	6.00E-109	*M. galloprovincialis*	small heat shock protein 24.1
38	-1.80212	1	87	3	gi|405951471	6.00E-41	*C. gigas*	Serine hydroxymethy-ltransferase, mitochondrial
32	-1.72586	1	254	5	gi|2073146	1.00E-10	*Incilaria fruhstorferi*	Incilarin C (C-type lectin)