

Seasonal and spatial influences on gene expression in Antarctic krill *Euphausia superba*

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Supplement. Antarctic krill differential gene expression

Table S1. All transcripts up-regulated 2-fold or more ($p < 0.05$) in Antarctic Peninsula summer krill relative to Antarctic Peninsula winter krill that produced a BLASTX hit (E value $< 1 \times 10^{-6}$).

Accession number	Contig ID	Top informative BLASTX description	E value	Gene ontology	Fold	p-value
GW423837	443	AEG79569.1 sarcoplasmic calcium-binding protein variant c	1.12E-52	F:calcium ion binding	4.62	1.20E-05
GW423670	Singleton	Q00871.1 Chymotrypsin BI	5.92E-58	P:proteolysis	4.35	0.0263
JK623210	Singleton	ZP_08731733.1 hypothetical protein VINI7043_14910	2.49E-07		4.09	8.15E-05
GW422993	Singleton	EHB08916 Proteinase E	8.00E-09	P:proteolysis	4.02	4.82E-05
GW422086	166	BAF73806.1 calcification associated soluble matrix protein 2	1.16E-26	F:structural constituent of cuticle	3.98	1.38E-04
GW423611	87	ACQ45455.1 trypsin-like serine proteinase 2	6.86E-60	P:proteolysis	3.95	0.024
GW422555	87	ACQ45455.1 trypsin-like serine proteinase 2	3.26E-61	P:proteolysis	3.83	0.0354
GW422778	22	ACS44712.1 hemocyanin subunit 1	8.95E-47	P:metabolic process; P:oxygen transport	3.69	0.0458
GW423808	399	ZP_01872756.1 hypothetical protein LNTAR_17443	1.56E-11		3.56	1.78E-05
GW423017	167	ACE80257.1 trypsin	2.23E-36	P:proteolysis	3.55	0.027
GW421491	399	ZP_01872756.1 hypothetical protein LNTAR_17443	8.97E-12		3.50	3.08E-05
GW422506	471	ZP_01875437.1 hypothetical protein LNTAR_06159	1.21E-13	F:lyase activity	3.45	3.01E-06
GW422444	87	ACQ45455.1 trypsin-like serine proteinase 2	1.49E-07	P:proteolysis	3.32	0.0412
GW422924	Singleton	AEE25770.1 chymotrypsin	2.06E-55	P:proteolysis	3.21	0.0457
GW423105	Singleton	XP_003386083.1 PREDICTED: carboxypeptidase A1-like	3.62E-27	F:peptidase activity	3.15	0.0355
GW422616	414	XP_001662940 lumbrokinase-3(1) precursor, putative	2.00E-25	F:peptidase activity	3.13	0.0011
GW423687	22	ADE58571.1 hemocyanin HC2	2.86E-19	P:metabolic process; P:oxygen transport	3.10	0.0487
GW423138	22	AAO47336.1 hemocyanin 2	2.14E-21	P:metabolic process; P:oxygen transport	3.09	0.0455
GW423598	Singleton	P04069.1 Carboxypeptidase B	2.00E-38	P:vacuolar protein catabolic process	3.08	0.05
GW423756	Singleton	CAA75311.1 trypsin	4.56E-68	P:proteolysis	3.08	0.033
GW424041	Singleton	AEG78436.1 cathepsin K	2.65E-16	F:cysteine-type peptidase activity	3.06	0.0234

GW423896	Singleton	AAX39709.1 selenium-binding protein	4.62E-23	P:protein transport	3.02	0.0402
GW422781	414	EFN68636 Trypsin-1	2.00E-18	F:serine-type peptidase activity	2.97	7.55E-04
GW423327	22	ADE58571.1 hemocyanin HC2		P:metabolic process;	2.96	0.0477
GW422401	singleton	P05946.1 Sarcoplasmic calcium-binding protein 1	6.22E-32	P:oxygen transport		
GW422785	105	AAL67441.1 collagenolytic serine protease	8.25E-26	F:calcium ion binding	2.96	1.19E-04
JK623425	340	XP_002588050.1 hypothetical protein BRAFLDRAFT_83031	3.07E-30	P:macromolecule metabolic process	2.95	0.0354
GW422386	383	EGI69650 Insulin-like growth factor-binding protein 7	2.66E-08	P:cell adhesion	2.86	0.0253
GW423290	401	BAD38677.1 beta actin	3.00E-14	P:regulation of cell growth	2.84	3.76E-04
GW422511	Singleton	XP_002914034 PREDICTED: ribonuclease UK114-like	2.85E-75	F:ATP binding; P:vascular smooth muscle contraction	2.81	5.22E-04
JK623220	Singleton	XP_001976079.1 betaTrypsin	3.00E-32	P:regulation of translational termination	2.75	4.04E-06
GW421339	264	AEG79569.1 sarcoplasmic calcium-binding protein variant c	3.93E-13	P:proteolysis	2.74	9.25E-05
GW424052	Singleton	EFX79206.1 hypothetical protein DAPPUDRAFT_304918	1.01E-45	F:calcium ion binding	2.74	6.59E-04
GW424143	226	ACQ45455.1 trypsin-like serine proteinase 2	5.27E-18	F:carboxypeptidase activity	2.62	0.0253
GW424035	Singleton	EFN80497 Palmitoyl-protein thioesterase 1	1.12E-94	P:proteolysis	2.62	0.0432
GW423435	510	ACR54113.1 sarcoplasmic calcium-binding protein 1	9.00E-49	F:hydrolase activity	2.61	0.0319
GW421493	401	ABF72904.1 muscle-specific actin-like	4.38E-19	F:calcium ion binding	2.59	6.90E-05
JK623250	226	ACQ45455.1 trypsin-like serine proteinase 2	3.39E-87	F:ATP binding; P:vascular smooth muscle contraction	2.57	7.73E-04
GW422745	23	ACR54136.1 hemocyanin	6.59E-73	P:proteolysis	2.52	0.0476
GW423101	Singleton	P04069.1 Carboxypeptidase B	8.46E-19	P:metabolic process; P:oxygen transport	2.52	0.041
GW423413	22	ACR54136.1 hemocyanin	2.11E-46	F:carboxypeptidase activity	2.49	0.0328
GW423770	105	P00771.2 Collagenolytic protease	2.05E-16	P:metabolic process; P:oxygen transport	2.48	0.0325
GW422544	22	AAO47336.1 hemocyanin 2	8.15E-16	P:macromolecule metabolic process	2.48	0.0461
GW421571	22	ABM74404.1 hemocyanin subunit 1	1.32E-22	P:metabolic process; P:oxygen transport	2.43	0.0494
GW424191	105	P00771.2 Collagenolytic protease	2.95E-12	P:metabolic process; P:oxygen transport	2.42	0.0321
GW423607	Singleton	ACG60902.1 cathepsin C	4.60E-15	P:macromolecule metabolic process	2.39	0.0458
GW422543	342	ADD19839.1 hypothetical conserved protein	4.40E-58	P:immune response; P:proteolysis	2.39	0.0159
GW423943	655	XP_003229181.1 PREDICTED: carboxypeptidase A1-like	3.56E-38	F:serine-type peptidase activity	2.38	0.0459
GW421879	264	ACR54113.1 sarcoplasmic calcium-binding protein 1	2.03E-24	F:carboxypeptidase activity	2.37	0.0276
GW422926	Singleton	XP_003431282.1 glutathione peroxidase 1-like	1.14E-15	F:calcium ion binding	2.36	0.001
GW423733	154	ACG60902.1 cathepsin C	3.37E-11	P:glutathione metabolic process	2.31	0.0127
GW423794	653	XP_792420 PREDICTED: similar to alpha-amylase	5.58E-60	P:immune response; P:proteolysis	2.30	0.0495
GW422627	Singleton	XP_002732825.1 PREDICTED: all-trans-13,14-dihydroretinol saturase-like	2.00E-19	P:metabolic process	2.29	0.0162
JK623326	322	ABY85409.1 chitinase	6.62E-24	F:oxidoreductase activity	2.28	0.0113
GW423817	175	P04069.1 Carboxypeptidase B	1.06E-27	P:metabolic process; F:hydrolase activity	2.27	0.0280
GW423904	105	EFX79603.1 chymotrypsin-like protein	6.81E-50	P:proteolysis	2.26	0.0441
GW422906	Singleton	AAT66425.2 actin T2	1.10E-10	P:macromolecule metabolic process	2.23	0.0329
GW423584	340	ADG85659.1 lectin D	4.92E-43	F:ATP binding; P:vascular smooth muscle contraction	2.19	0.0044
GW424075	Singleton	ADB10837.1 lectin	9.47E-07	P:cell adhesion	2.19	0.0477
GW424043	479	ACG70181.1 cathepsin D-like protein	1.70E-07	P:cell adhesion	2.18	0.0303
JK623699	196	ACR43477.1 myosin light chain	1.91E-73	P:proteolysis; F:aspartic-type endopeptidase activity	2.17	0.0391
			6.76E-26	F:calcium ion binding	2.14	0.0254

GW423721	Singleton	AEA39652.1 cathepsin K	5.56E-12	P:proteolysis	2.14	0.0175
GW422118	196	ACR43477.1 myosin light chain	7.10E-29	F:calcium ion binding	2.09	0.0161
JK623665	714	ADB66713.1 trypsin 2	2.94E-43	P:digestion; P:proteolysis	2.07	0.0478
GW422898	510	P05946.1 Sarcoplasmic calcium-binding protein 1	7.40E-07	F:calcium ion binding	2.06	2.16E-05
GW424182	Singleton	ADN88091.1 arginine kinase 1	2.78E-73	F:kinase activity	2.05	5.74E-04
GW423271	113	AAX38505.1 beta-actin	4.52E-45	F:ATP binding; P:vascular smooth muscle contraction	2.05	0.0047
GW421502	Singleton	XP_971015.1 PREDICTED: similar to CG32155 CG32155-PA	3.94E-14	F:catalytic activity	2.04	0.0018

Table S2. All transcripts down-regulated 2-fold or more ($p < 0.05$) in Peninsula summer krill relative to Peninsula winter krill that produced a BLASTX hit (E value $< 1 \times 10^{-6}$).

Accession number	Contig ID	Top informative BLASTX description	E value	Gene ontology	Fold	p-value
JK623718	Singleton	EFX67953.1 putative neuroparsin	5.00E-18	P:neuropeptide signaling pathway	6.37	4.14E-09
JK623346	Singleton	EFX67953.1 putative neuroparsin	2.37E-12	P:neuropeptide signaling pathway	5.61	1.38E-07
GW422367	Singleton	BAF73806.1 calcification associated soluble matrix protein 2	3.83E-11	F:structural constituent of cuticle	3.24	0.0015
GW422235	Contig 490	ADI59753.1 early cuticle protein 5	2.36E-09	F:structural constituent of cuticle	3.01	0.0022
GW421925	Singleton	EFX68926.1 hypothetical protein DAPPUDRAFT_329602	6.48E-17		2.84	0.0167
GW421756	Singleton	XP_002428037 trypsin, putative	2.34E-24	F:peptidase activity	2.79	0.0014
GW422303	Singleton	EFX68928.1 hypothetical protein DAPPUDRAFT_259342	4.88E-15		2.49	0.0463
JK623517	Singleton	XP_001237083.2 AGAP007368-PA	1.84E-08	P:chitin metabolic process	2.41	0.0448
GW423134	Singleton	ACR78683.1 myosin S2 heavy chain	8.11E-46	F:actin binding	2.24	1.99E-04

Table S3. All transcripts up-regulated 2-fold or more ($p < 0.05$) in South Georgia winter krill relative to Peninsula winter krill that produced a BLASTX hit (E value $< 1 \times 10^{-6}$).

Accession number	Contig ID	Top informative BLASTX description	E value	Gene ontology	Fold	p-value
GW421651	Contig 565	XP_003225690 PREDICTED: tolloid-like protein 1-like	1.00E-06	F:calcium ion binding	5.27	5.07E-06
GW422894	Contig 479	ACG70181.1 cathepsin D-like protein	1.10E-55	P:proteolysis; F:aspartic-type endopeptidase activity	3.61	0.001144
GW422542	Singleton	XP_002416173.1 conserved hypothetical protein	8.94E-56	P:chitin binding domain	3.56	1.37E-04
GW423017	Contig 167	ACE80257.1 trypsin	2.24E-36	P:proteolysis	3.41	0.0012
GW422616	Contig 414	XP_001662940.1 lumbrokinase-3(1) precursor, putative	2.01E-25	F:peptidase activity	3.37	1.61E-04
GW423014	Contig 167	ACQ45455.1 trypsin-like serine proteinase 2	4.81E-67	P:proteolysis	3.28	9.96E-04
GW423731	Singleton	ADR30525.1 intracellular lipase	3.32E-30	P:lipid metabolic process	3.16	1.32E-04
GW422705	Contig 232	CAA75310.1 trypsin	2.32E-53	P:proteolysis	3.08	6.20E-04
GW423817	Contig 175	P04069.1 Carboxypeptidase B	6.84E-50	P:proteolysis	3.01	1.33E-05
GW422584	Contig 232	ABQ02514.1 trypsin	5.74E-77	P:proteolysis	2.92	0.0025
GW422781	Contig 414	EFN68636 Trypsin-1	8.00E-07	F:serine-type peptidase activity	2.89	5.45E-05
GW423244	Contig 175	P04069.1 Carboxypeptidase B	1.88E-59	P:proteolysis	2.87	2.99E-04
GW422787	Contig 226	ABQ02531.1 trypsin	3.27E-77	P:proteolysis	2.86	0.0015
GW423756	Singleton	CAA75311.1 trypsin	4.58E-68	P:proteolysis	2.84	5.34E-04
GW422555	Contig 87	ACQ45455.1 trypsin-like serine proteinase 2	3.28E-61	P:proteolysis	2.84	0.0019
JK623327	Singleton	ACO13952 Alcohol	8.00E-27	P:cellular aldehyde metabolic	2.81	0.004508

JK623207	Singleton	dehydrogenase CAB85963.1 alpha glucosidase	7.18E-21	process P:metabolic process	2.77	8.83E-04
GW422926	Singleton	XP_003431282.1 PREDICTED: glutathione peroxidase 1-like	3.38E-11	P:glutathione metabolic process	2.77	3.13E-05
GW423611	Contig 87	ACQ45455.1 trypsin-like serine proteinase 2	6.89E-60	P:proteolysis	2.70	0.0015
GW423735	Contig 175	P04069.1 Carboxypeptidase B	1.93E-49	P:proteolysis	2.67	1.95E-04
GW422596	Contig 167	ACE80257.1 trypsin	2.61E-50	P:proteolysis	2.66	0.0043
GW424255	Singleton	EFW46557.1 cathepsin L2	3.81E-41	F:peptidase activity	2.62	8.06E-04
JK623261	Contig 167	ACQ45455.1 trypsin-like serine proteinase 2	1.22E-81	P:proteolysis	2.62	0.0012
GW423168	Singleton	CAI11754 novel protein similar to vertebrate angiopoietin	2.00E-30	F:receptor binding; P:signal transduction	2.61	6.43E-04
JK623250	Contig 226	ACQ45455.1 trypsin-like serine proteinase 2	6.61E-73	P:proteolysis	2.59	4.33E-04
GW424074	Singleton	CAD20882 succinate semialdehyde dehydrogenase	9.00E-45	P:neurotransmitter catabolic process	2.59	6.85E-04
GW422444	Contig 87	ACQ45455.1 trypsin-like serine proteinase 2	1.50E-07	P:proteolysis	2.59	0.0013
GW424043	Contig 479	ACG70181.1 cathepsin D-like protein	1.91E-73	P:proteolysis; F:aspartic-type endopeptidase activity	2.58	1.56E-04
GW422713	Contig 582	ACE80257.1 trypsin	5.45E-40	P:proteolysis	2.55	0.0027
GW423598	Singleton	P04069.1 Carboxypeptidase B	2.00E-38	P:proteolysis	2.53	0.0027
GW422943	Contig 167	ACQ45457.1 trypsin-like serine proteinase 4	1.31E-78	P:proteolysis	2.50	0.0027
JK623639	Contig 531	EFX74668.1 hypothetical protein DAPPUDRAFT_307002	7.63E-13	F:binding	2.46	4.45E-05
GW424143	Contig 226	ACQ45455.1 trypsin-like serine proteinase 2	1.12E-94	P:proteolysis	2.45	0.0021
GW423101	Singleton	P04069.1 Carboxypeptidase B	2.12E-46	P:proteolysis	2.43	3.28E-04
GW423253	Contig 175	P04069.1 Carboxypeptidase B	1.49E-35	P:proteolysis	2.42	7.88E-04
GW423037	Singleton	AEE25770.1 chymotrypsin	1.08E-15	P:proteolysis	2.41	0.0028
GW423085	Singleton	ACR23316.1 beta-N- acetylglucosaminidase	4.77E-29	P:chitin catabolic process	2.38	9.22E-04
GW423206	Contig 531	EFX74668.1 hypothetical protein DAPPUDRAFT_307002	1.91E-17	F:binding	2.37	7.34E-05
GW423733	Contig 154	ACG60902.1 cathepsin C	5.60E-60	P:immune response; P:proteolysis	2.33	6.96E-04
GW423797	Contig 232	ACE80257.1 trypsin	1.01E-39	P:proteolysis	2.31	6.11E-04
GW422924	Singleton	AEE25770.1 chymotrypsin	2.07E-55	P:proteolysis	2.30	0.0017
GW423670	Singleton	CAA47046.1 preprochymotrypsin 1	5.95E-58	P:proteolysis	2.29	0.0022
GW422785	Contig 105	AAL67441.1 collagenolytic serine protease	3.08E-30	P:macromolecule metabolic process	2.27	1.95E-04
JK623324	Contig 430	ABE77153.1 intracellular fatty acid binding protein	5.12E-18	P:lipid metabolic process; P:transport	2.24	3.72E-04
GW421185	Singleton	XP_002738925.1 PREDICTED: PAPS-like	1.33E-52	F:adenylylsulfate kinase activity; P:blood coagulation	2.22	0.0025
GW423025	Contig 154	ACG60902.1 cathepsin C	7.61E-36	P:immune response; P:proteolysis	2.21	0.0011
GW424153	Contig 204	ACZ63471.1 i-type lysozyme-like protein 1	6.36E-21	F:lysozyme activity	2.20	0.0019
GW423035	Contig 87	ADB66711.1 trypsin 1a	5.14E-72	P:proteolysis	2.19	0.0012
GW422669	Singleton	ADN34745.1 putative cysteine peptidase	8.30E-17	P:metabolic process	2.17	7.53E-04
GW423794	Contig 653	XP_792420 PREDICTED: similar to alpha-amylase	2.00E-19	P:metabolic process	2.13	5.59E-05
GW422610	Contig 175	P04069.1 Carboxypeptidase B	1.30E-28	P:proteolysis	2.12	7.40E-04
JK623681	Contig 582	ABM65758 trypsin	7.00E-24	P:proteolysis	2.10	5.10E-04
GW422259	Contig 431	ABE77153.1 intracellular fatty acid binding protein	1.14E-49	P:lipid metabolic process; P:transport	2.10	0.0015
GW423212	Contig 154	ADO65979.1 cathepsin C	5.84E-54	P:response to organic substance; C:lysosome	2.08	0.006491
GW421989	Singleton	ACF57858.1 chymotrypsin inhibitor precursor	2.08E-12	P:negative regulation of peptidase activity	2.07	3.22E-04
GW423688	Contig 739	XP_002422744.1 zinc	1.02E-08	F:metallopeptidase activity	2.05	0.0011

GW424041	Singleton	metalloproteinase, putative AEG78436.1 cathepsin K	2.66E-16	F:cysteine-type peptidase activity	2.04	3.95E-04
GW423105	Singleton	XP_003386083.1 PREDICTED: carboxypeptidase A1-like	3.64E-27	F:peptidase activity	2.04	7.81E-04
GW424274	Contig 87	ADB66711.1 trypsin 1a	6.83E-96	P:proteolysis	2.03	0.0029
GW423164	Contig 154	ACG60902.1 cathepsin C	8.44E-51	P:immune response; P:proteolysis	2.03	0.0018
GW423450	Contig 618	ADD38111.1 Beta-crystallin A1	3.51E-10	P:visual perception	2.03	0.0051

Table S4. All transcripts down-regulated 2-fold or more ($p < 0.05$) in South Georgia winter krill relative to Peninsula winter krill that produced a BLASTX hit (E value $< 1 \times 10^{-6}$).

Accession number	Contig ID	Top informative BLASTX description	<i>E</i> value	Gene ontology	Fold	p-value
JK623498	Contig 122	AEL23055 CHK1 checkpoint-like protein	1.00E-11		3.12	7.18E-05
JK623403	Contig 122	ACY66592.1 hypothetical protein	1.88E-25		3.04	2.70E-05
JK623874	Singleton	XP_001895031.1 hypothetical protein Bm1_17870	1.20E-20		2.64	2.79E-05
GW422156	Singleton	EFN72287 Ankyrin repeat domain- containing protein 17	5.00E-07	F:RNA binding	2.25	3.59E-05