

**p38 MAPK regulates PKA α and CUB-serine protease in
Amphibalanus amphitrite cyprids**

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Supplementary information

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H. longicornis CUB  AGRD I R V T G L T S G I L V T P G F T G G Q P V P H N F Q G A V T I Q A P R 40
P. argus CUB       CGAR V T V T P G S S V T F Q S T N Y P S S Y P N R E - - N C F W R F Q A A D 38
A. amphitrite CUB1 C D S H V - I A E G S T V V I E S P N Y P S N Y P N Y E - - D C V Y T L T T D - 36
A. amphitrite CUB2 C G G S R - L A R G Q H T I T D G D - - - G D Y S N N V - - D C Y Y Q L Y A D Q 34
      ↑
H. longicornis CUB  G F S R I R L E F Q E F D L E T S P Q C S G D R L V V R E - - - G N M A P D I 76
P. argus CUB       P Q D T L T V E C S P F N V R G S N S C T R D R L I F G E K V V G R Y F Q S T R 78
A. amphitrite CUB1 T G K D L E L S C E A F D L E S H S Q C R Y D W L R V N G - - - - - I K 67
A. amphitrite CUB2 A G D Q L S V T C S Q F D V E S H S S C A Y D W L S V D G - - - - - N K 65
      ↑
H. longicornis CUB  F C S N Q R P K A Y L S Q S S L V N L L L V T D G L K R S R G F R I R F T A T 115
P. argus CUB       Y C G V G F Y E P Y I S F S S T L F V R F R T D R S S T A S G F S C E V T V T 117
A. amphitrite CUB1 Y C G S - S G P S T V A A P - Q L D I D F H S D Y S V V R S G Y R C T V T L V 104
A. amphitrite CUB2 F C G S - N G P S G V A A I D Q M A I H W H T D Y S V V R S G F V C A V T V G 103
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Figure S1. Amino acid sequence alignment of the CUB domain from *A. amphitrite*, *H. longicornis* and *P. argus*. Six conserved cysteine residues are labeled with red arrows.

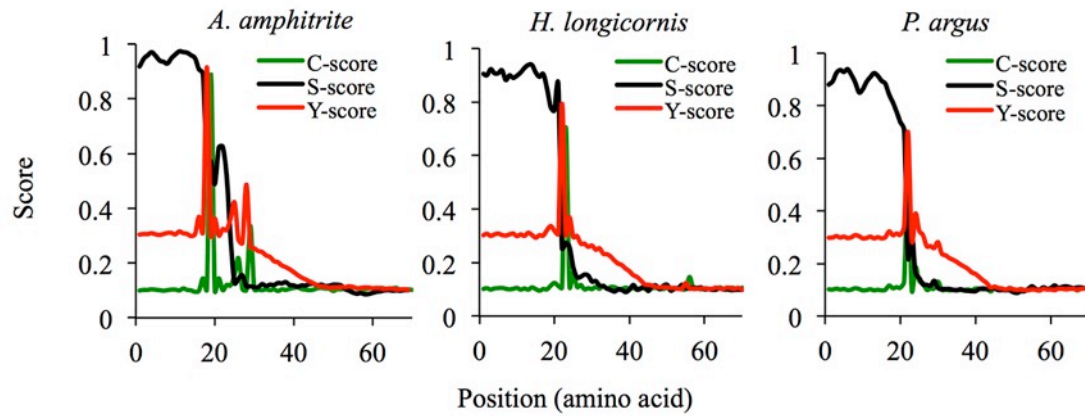


Figure S2. Signal peptide prediction of the CUB-serine protease from *A. amphitrite*, *H. longicornis* and *P. argus*. The C-score (raw cleavage site score), S-score (signal peptide score) and Y-score (combined cleavage site score) were calculated using SignalP 4.1 Server.

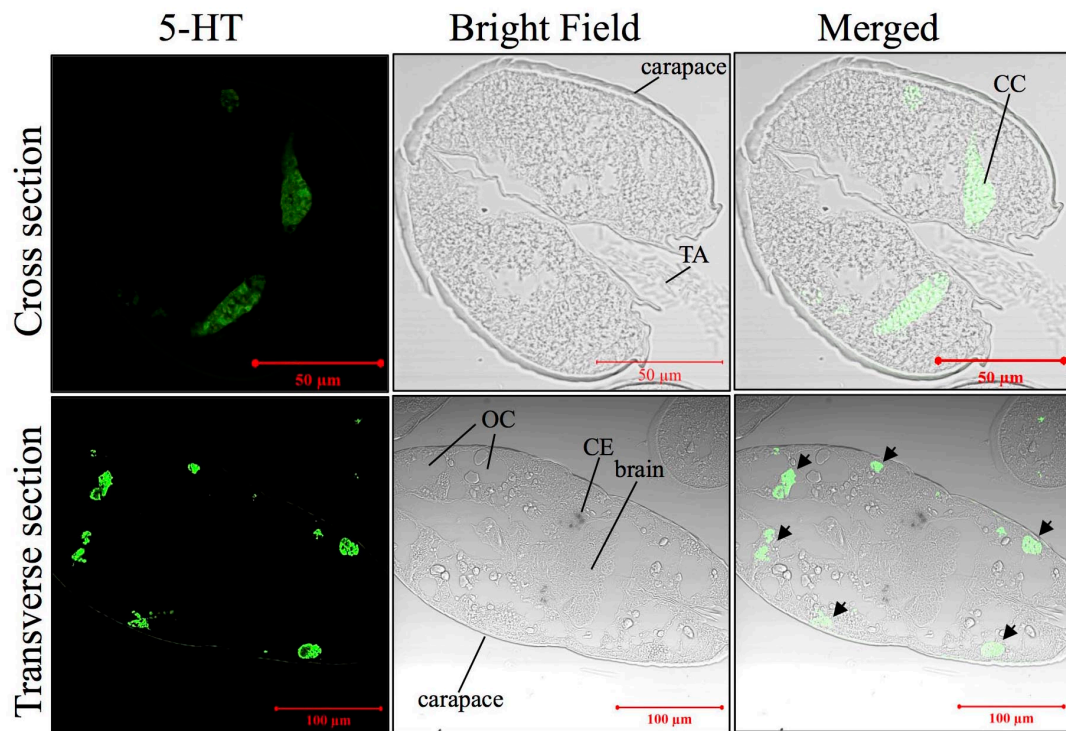


Figure S3. Immunostaining of serotonin in cyprid sections. Signals were revealed at the circumesophageal connectives in the cross sections. In the transverse sections, symmetrical singles were localized to nerve fibers nearby cyprid body wall (indicated with arrows). TA: thoracic appendage; CC: circumesophageal connective; OC: oil cell; CE: compound eye.

<i>A. amphitrite</i>	RRRGAISAEPVTEDDATSYVKKVVPKDYKTM E ALSKAIAKNVLF S HLDEN	50
<i>H. sapiens</i>	RRRGAISAEVYTEEDAASVYRKVI I PKDYKTMAALAKAIE E KNVLF S HLD D EN	50
<i>D. melanogaster</i>	RRRGGISAEPVTEEDATN N YVKKVVPKDYKTM N ALSKAIAKNVLF A HLD E S	50
<i>M. rotundata</i>	RRRGGISAEPVSEEDATSYVKKVVPKDYKTM A ALSKAIAKNVLF A HLDEN	50
<i>C. capitata</i>	RRRGGISAEPVTEEDATSYVKKVVPKDYKTM A ALSKAIAKNVLF S HLDEN	50
<i>A. mellifera</i>	RRRGGISAEPVSEEDATSYVKKVVPKDYKTM A ALSKAIAKNVLF A HLDEN	50
<i>C. capitata</i>	RRRGGISAEPVTEEDATSYVKKVVPKDYKTM A ALSKAIAKNVLF S HLDEN	50
<i>A. aegypti</i>	RRRGGISAEPVSEEDATSYVKKVVPKDYKTM A ALSKAIAKNVLF A HLDEN	50
<i>R. pedestris</i>	RRRGGISAEPVTEEDATSYVKKVVPKDYKTM A ALSKAIAKNVLF S HLDEN	50
<i>A. amphitrite</i>	ERSDIFDAMFSQTFLKGETI I KQGDEGDNFYVIDSGD V EVYVNDALVTTI	100
<i>H. sapiens</i>	ERSDIFDAMFSV S FIAGETVI I QQGDEGDNFYVIDQGETD V YVNN E WATS V	100
<i>D. melanogaster</i>	ERSDIFDAMFPVNHIA G ENI I QQGDEGDNFYVIDVGEV D VFNSELVTTI	100
<i>M. rotundata</i>	ERSDIFDAMFPVTF L PGEA I RQGDEGDNFYVIDQGEVE I FVNGELVTTI	100
<i>C. capitata</i>	ERSDIFDAMFPVTH L MGENI I QQGDEGDNFYVIDHGEVE V FVNS E LVTTI	100
<i>A. mellifera</i>	ERSDIFDAMFPVTF L PGEA I RQGDEGDNFYVIDQGEVE I FVNGEL A TTI	100
<i>C. capitata</i>	ERSDIFDAMFPVTH L MGENI I QQGDEGDNFYVIDHGEVE V FVNS E LVTTI	100
<i>A. aegypti</i>	ERSDIFDAMFP C TFLPGESI I QQGDEGDNFYVIDIGEVE V FVNN E LVTTI	100
<i>R. pedestris</i>	ERSDIFDAMFPV N FLPGETI I QQGDEGDNFYVIDQGEVE V YVNS E LVTTI	100
<i>A. amphitrite</i>	SEGGSGF E LAL I YGT P RAATV K AS S DV K LW A IDRDTYRRILMGSTIRK R K	150
<i>H. sapiens</i>	GEGGSFGELAL I YGT P RAATV K AKT N V K LWGIDRDSYRRILMGST L RK R K	150
<i>D. melanogaster</i>	SEGGSGF E LAL I YGT P RAATV R AKTDV K LWGIDRDSYRRILMGSTIRK R K	150
<i>M. rotundata</i>	GEGGSFGELAL I YGT P RAATV R AKTDV K LWGIDRDSYRRILMGSTIRK R K	150
<i>C. capitata</i>	GEGGSFGELAL I YGT P RAATV R AKTDV K LWGIDRDSYRRILMGSTIRK R K	150
<i>A. mellifera</i>	GEGGSFGELAL I YGT P RAATV R AKTDV K LWGIDRDSYRRILMGSTIRK R K	150
<i>C. capitata</i>	GEGGSFGELAL I YGT P RAATV R AKTDV K LWGIDRDSYRRILMGSTIRK R K	150
<i>A. aegypti</i>	SEGGSGF E LAL I YGT P RAATV R AKTDV K LWGIDRDSYRRILMGSTIRK R K	150
<i>R. pedestris</i>	GEG S SFGELAL I YGT P RAATV K AKT A V K LWGIDRDSYRRILMGSTIRK R K	150
<i>A. amphitrite</i>	MYEEFLSRVSI E SLDKWERLTVAD S LEPVSFA D GETIVRQGE P GDDFYI	200
<i>H. sapiens</i>	MYEEFLS K VSI E SLDKWERLTVADALEP V Q F EDGQ K IV V QGE P GDE F F I	200
<i>D. melanogaster</i>	MYEEFLSRVSI E SLDKWERLTVAD S LET C S F DDGETIV K QGA A GDDFYI	200
<i>M. rotundata</i>	MYEEFLSRVSI E SLDKWERLTVADALEP V A F DDGETIVRQGE P GEDFYI	200
<i>C. capitata</i>	MYEEFLSRVSI E SLDKWERLTVADALEPVS F EDGETIV K QGE P GDDFYI	200
<i>A. mellifera</i>	MYEEFLSRVSI E SLDKWERLTVADALEP V A F DDGETIVRQGE P GEDFYI	200
<i>C. capitata</i>	MYEEFLSRVSI E SLDKWERLTVADALEPVS F EDGETIV K QGE P GDDFYI	200
<i>A. aegypti</i>	MYEEFLSRVSI E SLDKWERLTVADALEPVS F EDGETIVRQGE P GNDFYI	200
<i>R. pedestris</i>	MYE G FLSRVSI E SLDKWERLTVADALEPVS F S D GETIVRQGE P GDDFYI	200
<i>A. amphitrite</i>	I V EGRAAVLQR R TEG- E QEQEVGQLG P SDYFGEIALM L DRPRAATVVARG	249
<i>H. sapiens</i>	I L EGSA A V L QR R SEN- E EFVEVGR L GPSDYFGEIALL M N R PRAATVVARG	249
<i>D. melanogaster</i>	I L EGCAV L QR R SEG- E EPAEVGR L GPSDYFGEIALL L DRPRAATVVARG	249
<i>M. rotundata</i>	I V EGTAV L QR R SEG- E EPAEVGR L GPSDYFGEIALL L DRPRAATVVARG	249
<i>C. capitata</i>	I L DGTAV L QR R AEG Q DEPAEVGR L GPSDYFGEIALL L DRPRAATVVARG	250
<i>A. mellifera</i>	I V EGTAV L QR R SEG- E EPAEVGR L GPSDYFGEIALL L DRPRAATVVARG	249
<i>C. capitata</i>	I L DGTAV L QR R AEG Q DEPAEVGR L GPSDYFGEIALL L DRPRAATVVARG	250
<i>A. aegypti</i>	I V EGCA T V R QKRDEN- E EPAEVGR L GPSDYFGEIALL L DRPRAATV I ARG	249
<i>R. pedestris</i>	I V EGTAL V LQCRGEG-DTAV E VGK L GPSDYFGEIALL L DRPRAATV V AKG	249
<i>A. amphitrite</i>	PLKCVKLD R GRFERVLG P CADILKRN I QQYNSFVSL T V	287
<i>H. sapiens</i>	PLKCVKLD R PRFERVLG P C S DILKRN I QQYNSFVSL S V	287
<i>D. melanogaster</i>	PLKCVKLD R ARFERVLG P CADILKRN I TQYNSFVSL S V	287
<i>M. rotundata</i>	PLKCVKLD R ARFERVLG P CADILKRN I TQYNSFVSL S V	287
<i>C. capitata</i>	PLKCVKLD R ARFERVLG T CADILKRN I TQYNSFVSL S V	288
<i>A. mellifera</i>	PLKCVKLD R ARFERVLG P CADILKRN I TQYNSFVSL S V	287
<i>C. capitata</i>	PLKCVKLD R ARFERVLG T CADILKRN I TQYNSFVSL S V	288
<i>A. aegypti</i>	PLKCVKLD R ARFERVLG T CADILKRN I TQYNSFVSL S V	287
<i>R. pedestris</i>	PLKCVKLD R ARFERVLG P CADILKRN I TQYNSFVSL S V	287

Figure S4. Amino acid alignment of deduced PKA α sequences. The sequences were obtained from *A. amphitrite*, *Homo sapiens* (NP002725.1), *Drosophila melanogaster* (NP524189.2), *Megachile rotundata* (XP003707654.1), *Ceratitidis capitata* (XP004520213.1), *Apis mellifera* (XP006561792.1), *Ceratitidis capitata* (XP004520214.1), *Aedes aegypti* (XP001661170.1) and *Riptortus pedestris* (BAN20503.1).

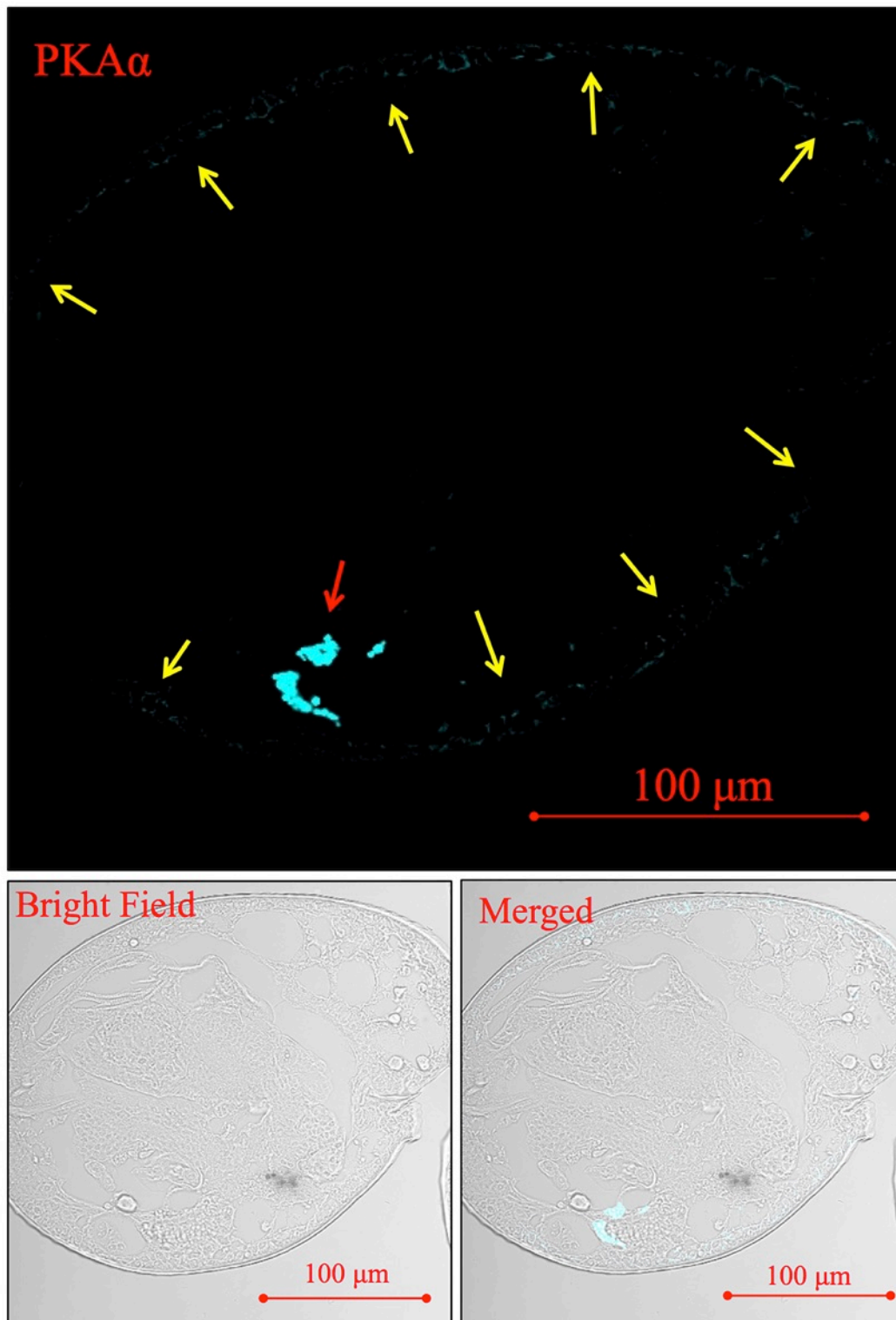


Figure S5. Immunohistology of PKA α revealed weak signals in the cells of the body wall. To better visualize the weak signal, the original red fluorescence (Alexa Fluor 594) is shown as light blue in the picture. The red arrow indicates the strong PKA α signal in the cement gland. Weak signals are shown by yellow arrows.

Table S1. Spectral counts of proteins that were significantly changed in response to SB203580 treatment. The spectral counts among three biological replicates are represented as the mean±SE.

No.	Contig	Protein name	Functional description	Control	SB203580	P value
Energy production and conversion						
1	Unigene23224	glycogen synthase	synthesize glycogen	9.3±3.1	24.7±3.1	0.0036
2	CL7578.Contig1	GG20479	NADH dehydrogenase (ubiquinone), produce ATP	5.0±1.0	8.7±1.2	0.0241
3	CL3129.Contig1	Mitochondrial 2-oxoglutarate/malate carrier protein (OGCP)	transport of 2-oxoglutarate across mitochondrial membrane	10.0±2.0	15.3±1.2	0.0161
4	CL6901.Contig1 Unigene11462	dihydrolipoyl dehydrogenase, mitochondrial-like	pyruvate decarboxylation	1.3±2.3	6.7±1.2	0.0232
5	CL1569.Contig1	V-type proton ATPase subunit B	pump protons across plasma membranes	79.3±6.1	62.0±7.2	0.0337
6	CL791.Contig1	Vacuolar ATP synthase catalytic subunit A	pump protons across plasma membranes	93.3±7.0	65.3±9.5	0.0146
7	CL593.Contig1 CL593.Contig2	AGAP006099-PA isoform 2	Ubiquinol-Cytochrome C Reductase, generation of ATP	36.0±6.0	54.7±5.0	0.0145
8	CL1.Contig245	Arginine kinase	maintenance of ATP level	150.0±21.4	102.0±7.8	0.0010
9	Unigene11511	Mitochondrial ATP synthase subunit g	Mitochondrial ATP synthase	5.3±2.3	0.7±1.2	0.0352
Secondary metabolites biosynthesis, transport and catabolism						
10	CL15192.Contig1	cytochrome P450 15A1	drug metabolism	14.0±5.3	2.7±1.2	0.0223
11	Unigene30671	cytochrome P450 2P3	drug metabolism	8.0±3.5	0.7±1.2	0.0254
12	CL7151.Contig1	cytochrome p450	drug metabolism	92.7±8.1	73.3±8.1	0.0428
Cell cycle control, cell division, chromosome partitioning						
13	CL9561.Contig1	GL10641	form the nuclear lamina	8.7±1.2	4.7±1.2	0.0132
14	CL2695.Contig1	Lamin-C	form the nuclear lamina	18.7±4.6	10.0±2.0	0.0406
Amino acid transport and metabolism						
15	CL15271.Contig1 Unigene5261	serine proteinase-like 2a	protease	16.7±2.3	5.3±3.1	0.0069
16	Unigene10435	saccharopine dehydrogenase	metabolism of the amino acid lysine	1.3±2.3	6.7±2.3	0.0474
17	CL11184.Contig1	sluggish A CG1417-PE isoform 2	conversion of proline to glutamate	1.3±1.2	8.7±3.1	0.0177
18	CL16496.Contig1	spermine synthase-like	convert spermidine into spermine	2.0±3.5	11.3±4.2	0.0405
19	CL374.Contig1	GI17616	serine-type endopeptidase activity	16.7±1.2	0.0±0.0	0.0000
20	CL6481.Contig1	GH20777	serine-type endopeptidase activity	10.0±4.0	0.0±0.0	0.0123
21	CL7.Contig19	CUB-serine protease	signal transduction	101.3±9.5	72.7±11.4	0.0284
22	CL1088.Contig2	serine protease	protease	14.0±5.3	2.7±3.1	0.0325
23	CL3.Contig27	GA26108	peptidease inhibitor	29.3±1.2	0.0±0.0	0.0000
24	CL3.Contig24 CL3.Contig30	GA26108	peptidease inhibitor	26.0±2.0	0.0±0.0	0.0000
Nucleotide transport and metabolism						
25	CL6274.Contig1	s-methyl-5'-thioadenosine phosphorylase-like	methionine metabolism	6.7±3.1	0.7±1.2	0.0335
Carbohydrate transport and metabolism						
26	CL17624.Contig1	glucose-6-phosphate 1-epimerase-like	isomerases	17.3±2.3	22.7±2.3	0.0474
27	CL11285.Contig1	Probable methylmalonate-semialdehyde dehydrogenase	generate acetyl-CoA	11.3±9.2	30.7±6.4	0.0409
28	CL4410.Contig1	Phosphotriesterase-related protein	hydrolase activity on ester bonds	8.7±2.3	0.7±1.2	0.0058
29	CL992.Contig1	beta-N-acetylglucosaminidase	degradation of glucuronic acid-containing glycosaminoglycans	75.3±4.2	9.3±9.0	0.0003
30	CL304.Contig4 CL304.Contig5	epidermal retinol dehydrogenase 2	retinoic acid biosynthesis	7.3±1.2	16.0±3.5	0.0147
Lipid transport and metabolism						
31	CL17009.Contig1	methylmalonyl-CoA epimerase, mitochondrial	degradation of branched chain amino acids, odd chain-length fatty acids, and other metabolites	1.3±1.2	7.3±2.3	0.0158
32	CL4572.Contig1	propionyl CoA carboxylase, alpha polypeptide	fatty acid beta-oxidation	16.7±2.3	27.3±4.2	0.0178
Translation, ribosomal structure and biogenesis						
33	CL6243.Contig1	advillin-like	regenerative sensory axon growth	11.0±1.4	6.0±2.0	0.0249
34	CL6482.Contig1	transmembrane protein 2	multicellular organismal development	35.3±6.4	20.0±5.3	0.0332
35	CL11.Contig4	Polyadenylate-binding protein 1	cytoplasmic regulatory processes of mRNA metabolism	17.3±1.2	14.0±0.0	0.0075
36	CL14024.Contig1	60S ribosomal protein L34	ribosomal protein	2.7±3.1	11.3±3.1	0.0255
37	CL15766.Contig1 Unigene36236	S10e ribosomal protein	ribosomal protein	42.7±5.0	64.0±2.0	0.0024
Cell wall/membrane/envelope biogenesis						
38	CL4543.Contig1	peroxiredoxin 6 protein	regulation of phospholipid turnover	6.0±2.0	0.0±0.0	0.0065
39	CL2680.Contig1	Transmembrane protein 69	integral component of membrane	2.0±2.0	7.3±2.3	0.0390
Cell motility						
40	CL14396.Contig1 CL9899.Contig1 Unigene5067	neither inactivation nor afterpotential protein C	encode photoreceptors	15.3±2.3	4.0±3.5	0.0092

Table S1. Continued

No.	Contig	Protein name	Functional description	Control	SB203580	P value
Posttranslational modification, protein turnover, chaperones						
41	CL888.Contig1	Gasp protein	control of myostatin activity;preventing myostatin proteolysis	18.0±7.2	35.3±4.2	0.0226
42	CL6240.Contig1	60 kDa heat shock protein, mitochondrial-like	protein import and macromolecular assembly	6.7±3.1	22.0±3.5	0.0045
43	Unigene11234	AGAP009694-PA	protein folding	5.3±6.1	16.0±2.0	0.0453
44	CL2410.Contig1	14-3-3 protein epsilon-like	Adapter protein affecting various pathways	5.3±1.2	2.0±0.0	0.0075
45	CL8957.Contig1	thioredoxin-dependent peroxide reductase	protects radical-sensitive enzymes from oxidative damage	5.3±1.2	16.7±1.2	0.0003
46	CL2356.Contig1 CL4955.Contig1	glutathione S-transferase	detoxification	0.0±0.0	20.7±7.6	0.0091
47	CL4041.Contig1	glutamine:fructose-6-phosphate aminotransferase 1	regulating the availability of precursors for N- and O-linked glycosylation of proteins	0.0±0.0	5.3±3.1	0.0390
48	CL14928.Contig1 CL16649.Contig1	cathepsin D-1	lysosomal aspartyl protease	48.0±8.7	27.3±1.2	0.0152
49	CL1199.Contig2	glutathione reductase	resisting oxidative stress	26.0±3.5	10.7±7.0	0.0275
Signal transduction mechanisms						
50	CL3558.Contig1	cAMP-dependent protein kinase	regulation of glycogen, sugar, and lipid metabolism	14.7±1.2	10.0±2.0	0.0249
Extracellular structures						
51	CL3.Contig8 CL3.Contig20 CL3.Contig33	dummy	gigantic extracellular protein	16.7±3.1	0.0±0.0	0.0007
52	CL3.Contig21	dummy	gigantic extracellular protein	19.3±8.3	0.0±0.0	0.0158
53	CL336.Contig1 CL336.Contig5	cuticular protein	cuticular protein	30.0±3.5	11.3±1.2	0.0009
54	CL1239.Contig2 Unigene4984	CG42749, isoform C	cuticular protein	5.3±1.2	0.0±0.0	0.0013
55	CL888.Contig2	cuticular protein analogous to peritrophins 3-C5 isoform 1	cuticular protein	18.0±7.2	35.3±4.2	0.0226
56	CL21.Contig3	chitin binding protein	bind chitins	0.0±0.0	7.3±3.1	0.0142
57	CL14958.Contig1	AGAP011936-PA	chitin binding	0.0±0.0	10.7±2.3	0.0013
58	CL8680.Contig1	chorion peroxidase	shell formation	14.0±7.2	0.0±0.0	0.0282
Cytoskeleton						
59	Unigene25886	Myosin heavy chain CG17927-PF isoform 3	Moysin component	22.7±4.2	8.7±2.3	0.0070
60	Unigene15759	Plectin-1	link cytoskeletons and different cells	5.3±1.2	1.3±1.2	0.0132
61	CL7850.Contig1	f-actin-capping protein subunit alpha-like isoform 2	protect the growing ends of actin filaments	6.7±1.2	12.7±1.2	0.0031
62	CL2450.Contig1	CBN-CYK-1 protein	actin filament organization	18.7±5.0	4.0±4.0	0.0168
Function unknown						
63	CL2677.Contig1	HyTSRp1 protein	unknown	22.0±2.0	12.0±4.0	0.0179
64	CL2236.Contig1	CG15449-PA	unknown	6.7±2.3	1.3±1.2	0.0232
65	CL7397.Contig1 Unigene5246	GL15817	unknown	12.0±2.0	20.0±3.5	0.0257
66	CL9979.Contig1	AGAP005990-PA	unknown	12.0±0.0	8.7±1.2	0.0075
67	CL7745.Contig1	MGC147117 protein	unknown	6.7±3.1	15.3±2.3	0.0173
68	CL2357.Contig1	GA20276-PA	unknown	9.3±4.2	0.7±1.2	0.0255
69	CL2646.Contig1	Putative oxidoreductase yrbE	unknown	19.3±3.1	38.0±5.3	0.0061
70	Unigene34863	C9orf68 homolog	unknown	10.0±3.5	20.0±2.0	0.0123
71	CL74.Contig3 CL74.Contig5 CL74.Contig6	AGAP004418-PA	unknown	31.3±2.3	23.3±2.3	0.0132
72	CL14828.Contig1	AGAP006918-PA	unknown	3.3±3.1	9.3±1.2	0.0335
73	Unigene9033	unknown	unknown	0.0±0.0	9.3±1.2	0.0002
74	CL46.Contig1 Unigene11352	unknown	unknown	18.0±2.0	1.3±1.2	0.0002
75	CL1824.Contig3	unknown	unknown	27.3±5.0	4.0±4.0	0.0033
76	CL2298.Contig1	unknown	unknown	60.0±2.0	16.7±14.7	0.0073
77	CL1824.Contig2	unknown	unknown	18.0±4.0	5.3±3.1	0.0121
78	Unigene5401	unknown	unknown	184.7±16.2	144.0±5.3	0.0144
79	CL166.Contig1	unknown	unknown	109.3±16.0	76.7±7.6	0.0332
80	CL4124.Contig1	unknown	unknown	2.7±4.6	12.0±3.5	0.0488

Appendix I: Protein sequences of the contigs involved in the present study.

>Unigene23224_Ba_mix

GRWLVDGNPQIILFDVGSASWKMNEMKDELWNLGIGIPNPDVECNDAVVFGYMVA
EFLQQFRNRLPEFTDGPFRMVAHFHEWLAGVGLILARLRKIDLATVFTTHATLLGRFL
CAGNTDFYNNLPYFNIDEEAGKRQIYHRYCMERASTHLCHTFTTVSEITGLEAEHLLK
RKPDIIVTPNGLNVKKSALHEFQNLHALSKAKINDFVRGHFYGFDFNLDKTLTYFFIA
GRYEFGNKGADIFIESLSRLNHLYKSSGSDVTVVAFMIFPTKTNNFNVESLRGHAVTKT
LKDSIEDIQKKIGSRMFEICMTGRLPESTELLTREDNVRLKRCIYSMQRSCLPPITTHNV
VNDGEDPVLRLRCHLFNDKSDRVKVVVFHPEFLSHTNPLLGM DYEEFVVRGCHMGVF
PSYYEPWGYTPAECTVMGIPSMTTNLSGFGCFMSEHIADPMSYGIYIVDRRSIGLEDSIR
ELAKYMYDFTRLNRRQRIIQNRNTERLSDLLDWRNLGIYYRRARQLALHAVYPEMAV
SEEHGGRMSYPRPLSEPPSP TTSRSTTPAPSEIGSDDEVDDEEELLELAIKD

>CL7578.Contig1_Ba_mix

ISPQEKRLIEERNHRMKAQWQKLVSDPHSHKHGGYVFD PAMQRFMSMRVTQY
ESFRPTLGNFFRGIGITAIPILLFAQLMHWRTRKEKEFSTGQVAYKDRLWK

>CL3129.Contig1_Ba_mix

QETSIPNYVKFIFGGSAGMAATMFVQPLDLLKNRMQMSGMGAAREHKTSFHFARAI
VMKEGVRGMYSGLSAGLLRQATYTTTTLRGIYTELFERASKDGKPPFPFTKAAIAMVAG
LVGSFIGTPAELCLIRMTSDGRLPEAERRNYKHAFDALFRVAREEGVTALWRGAVPT
MGRAVVVNAAQVSYQAKQSLMSTGYFSDNIFLHFCSSMISGLVTTAASMPVDIAKT
RIQNMKVVNGVPEYRGGLDVLAKVVRNEG VFALWKGFTPYARIGPHTVLT FIFLEQ
MNKAYKKFVLHDT SAGG

>CL6901.Contig1_Ba_mix

DGSKEVIKTKNILIATGSEVTPFPGIEIDEDTIVSSTGALS LKQVPK KLV LIGAGVIGLELG
SVWSRLGAEVTAVEFLGHVGGVGIDAEVSKNFQRILGKQGIKFKLGHKVTGAERSGDN
ISVSVENVKDSSK KETLDCDALLVCVGRRPYTDRLGLEKMGIERDEKGRIPVNSRFQTV
IPNIHAIGDCIHGPMLAHKAED EGIVCV EGIAGGPVHIDYNCVPSVIYTFPEVAWVGKT
EEDLKADGVEYKVGKFPFSANSRAKTNQETDGFVKVLGDSATDRMLGVHIIGPGAGE
MINEAVLAMEYGASCEDLARVCHAHPTCSEALREANLAAYCGKAIN

>Unigene11462_Ba_mix

DLVVIGSGPGGYVAAIKAAQLGLKTVCEKNETLGGTCLNVGCIPSKALLHNSHLYHEA
VHEFKNRGIDVEGVKLNLEQMMNTKKKAVSGLTSGVAYLFKNNKVTHVKGHGTITGT
NEVTATAADGSKEVIKTKNILIATGSEVTPFPGIEIDEDTIVSSTGALS LKQVPK KLV LIG
AGVIGLELGSVWSRLGAEVTAVEFLGHVGGVGIDAEVSKNFQRILGKQGIKFKLGHKVT
GAERSGDNISVSVENVKDSSK KETLDCDALLVCVGRRPYTDRLGLEKMGIERDEKGRIP
VNSRFQTVIPNIHAIGDCIHGPMLAHKAED EGIVCV EGIAGGPVHIDYNCVPSVIYTFPE
VAWVGKTEEDLKADGVEYKVGKFPFSANSRAKTNQETDGFVKVLGDSATDRMLGVH
IIGPGAGEMINEAVLAMEYGASCEDLARVCHAHPTCSEALREANLAAYCGKAIN

>CL1569.Contig1_Ba_mix

MPTTLTPHQARTEHTMAITRDYISQPRITYKTVSGVNGPLVILEGVKFPKFGEIVNLTL
GDGTDQRQGVLEVSGSKAIVQVFEGTSGIDAKNTICEFTGDILRTPVSEDMLGRVFNCS
GKPIDKGPPVLAEDFLDIQGGPINPWSRIYPEEMIQTGISAIDVMNSIARGQKIPIFSAAG
LPHNEIAAQICRQGGVLKLPKSVMDHSDNFAIVFAAMGVNMEAARFFKQDFEENG
SMENVCLFLNLANPTIERIITPRLALTTAEFLAYQCEKHVLVILTDMTSYAEALREVS
AAREEVPGRRGFPGYMYTDLATYERAGRVEGRNGSITQIPILTMPNDDITHPIPDLTG
YITEGQIYVDRQLHNRQIYPPINVLPSLSRLMKS AIGEGMTRKDHADVSNQLYACYAIG
KDVQAMKAVVGEEALTADDLLYLEFLTKEFKHFITQGNYENRSVFESLDIGWQLLRIF
PKEMLKRIPASTIAEFYPRENK

>CL791.Contig1_Ba_mix

CGGERGNEMSEVLRDFPELTVEIGGQTESIMKRTALVANTSNNMPVAAREASIYTGITLS
EYFRDMGYNVSMADSTSRWAEALREISGRLEMPADSGYPAYLGARLASFYERAGR
VNCLGNPNREGSVSIVGAVSPPGGDFSDPVTSATLGIVQVFWGLDKKLAQRKHFPSIN
WLISYSKYIRALDDFYEKNFQEFTALRTKVKEILQEEEDLSEIVQLVGKASLAETDKITL
EVAKLLKDDFLQQNGYTPYDRFCPFYKTVGMLKNMIAFYELARHAVESTAQADNKIT
WNVIRETMSQTMYLSSMKFKDPVKDGEAKIKADFEALHEEMQQAFRNLED

>CL593.Contig1_Ba_mix

MASKLMKSNILRSLPARRFAAQAATKSSDYGVLPREPLKTTTLPNGVVVASIENQSPLS
RVAIAVRGGSRYETPDNRGATHLLRIVAGLTNAENTAFGLTRELQQLGASLACSADRE
VLIYSADATRNHMDVVMELLANAATRQVFKPWEITDIKPHLKLVDVETTPAEVSLIEDL
HLAAFRQSDLGNSVVPAPHLIGQLGPDQLASHLSRTLLAGRTAVCGTGIDHETLVEYA
QGLQLPQGEPPAPAARYGGGELRTEIGGGVALVAVAAEGAGRSSATAAQQAVLQAVLG
AGAVVKYAGRGVVGAAAAQAGGAAAALNAVYSDTGLVGYTVAAEADKAGQVIEAVN
KAFKTTSLTAEDVNRGKALAKAAVLRADDNSGSCVETMGVQASLGKVS AVSDALAA
IDAVKLSDVQTLHKRLVGGKLSMAARGNLRTVPYLDQL

>CL593.Contig2_Ba_mix

MASKLMKSNILRSLPARRFAAQAATKSSDYGVLPREPLKTTTLPNGVVVASIENQSPLS
RVAIAVRGGSRYETPDNRGATHLLRIVAGLTNAENTAFGLTRELQQLGASLACSADRE
VLIYSADATRNHMDVVMELLANAATRQVFKPWEITDIKPHLKLVDVETTPAEVSLIEDL
HLAAFRQSDLGNSVVPAPHLIGQLGPDQLASHLSRTLLAGRTAVCGTGIDHETLVEYA
QGLQLPQGEPPAPAARYGGGELRTEIGGGVALVAVAAEGAGRSSATAAQQAVLQAVLG
AGAVVKYAGRGVVGAAAAQAGGAAAALNAVYSDTGLVGYTVAAEADKAGQVIEAVN
KAFKTTSLTAEDVNRGKALAKAAVLRADDNSGSCVETMGVQASLGKVS AVSDALAA
IDAVKLSDVQTLHKRLVGGKLSMAARGNLRTVPYLDQL

>CL1.Contig245_Ba_mix

SQPKDSKPAKSSNMVDAATMQKLDAGFQKLQAATDCKSLLKKYLTKEVYDSLKNKK
TSFGSTLLDVIQSGVENLDSGVGVYAPDDEAYRVFADLFDPIIEDYHGGFKKTDKHPNK
DFGDVSTVGNVDPEGQFVISTRVRCGRSMKGYFPNCLTEAQYKEMEDKVSSTLSGLD
GELKGTfyPLTGMAKDVQQLIDDHFLFKEGDRFLQAANACRFWPTGRGIYHNNDKT

FLVWCNEEDHLRIISMQMGGDLGQVYRRLVNAATDIEKRIPFSHHDRLGFLTFCPTNL
GTTIRASVHIKVPKLAADKKKLEEVAAKYNLQVRGTRGEHTEAEGGIYDISNKRRMGL
TEYEAVKEMHDGILELIKIEKSL

>Unigene11511_Ba_mix

MAGVVAKLPAMGTNLVNAARPLATFLKYARVELTPPSPADVPAIQGLSNLVKSAR
TGAWKNLTVKEATVNALVGAEVVFWFFIGECIGKGS�VGYQV

>CL15192.Contig1_Ba_mix

RPTNYPPGPPMFLIFGNLFETFRSLKGDPEVMVKEHRKKYGDIMAYIMPGNFKIVHLL
NYDLIKESCARQEFSGRPSNFIVLYRSFQKKLGVILNDGPAWQEHRRFTLRHLRDLGFG
TNSMETIILEEFEHLAKEMEQDMHSPMKVNQRFNLTVLNVLWRLVASKRLDRSEPEA
KQRVKEVNDFTITGSPNPLSMFPFLRFISPNSFGLKELKNNRDNSLAMFQELMKEHR
QTLDRAAPRDFIDRFLIEMESPDAARSFTDENLSIVCMDLFLAGMETTSTSLTWALL
LLVMHPDVQTRVQQEIDAVLGVGADRRLPSYTDNANMPYTEATLQEVSRRTVVPRA
VGHSAQDAPLGGYTVAKGSLVLMHLDVHMDPAYWGPDPDFRPERFINADGTV

>Unigene30671_Ba_mix

FGIGRRFCLGESLARMEMFVLFCLLQRFSAAPGQTLSESRVAAVRQPNEF

>CL7151.Contig1_Ba_mix

VVFFVLLVTYLWVTRPKRPPNFPPGPPTFLIFGNVIDLVRTASNDFQKHLNRLRSEH
KSDIIGMVDVFGQPLVYVFGGELVKEAGNITELTGRPELFTVMYLSEMKRAGIFFNEGP
LWQEQRRFALKHLRDLGMGKSVLNTMIADYALFAEHLKVVGVQEVKANNLFTVVL
NIIWKMVASRRFDYDDPERQLQDIVTEFTQITGPQNILFLFPSARFVAPESSGFNKIK
VYHSAMQGLFGPCIAEHRATLDP SHPRDFIDAFLIESQRPDAEKRGFDENLR TLCLD
FFIAGSETTSLSMTWALLMVLYPDVQAKVQAELEVVGEGRLPSYEDRPRLPYTEAV
MTEIWRYTSFVPLAVPHRSSVGAQLGGYTLPKDTTVMIHLSAHHDRGHWDPDV
FRPERFIGEDGKFRKDDYFVPFGLGKRACLGESMARTEFFTLSCMLHQFHVRLPKGA
KKPS

>CL9561.Contig1_Ba_mix

RTTMSTSSGSAATSPVRARSPHSPTRTSRLQEKEQLAGLNDRLAAYIEKVRNLELEN
SRLTHQVRSSQEVVTREVSNIKSLYESELADARRLLDETAKEKAKLQIDLGNLKTERTD
DLQSRLIRRELDNAEKKISMQDMQIRDQLGRLHQALQDKKKAQEELEEVQLENMK
LKKQLDEVKQLESEALGRVDMENRCQSLKEELEFKTNVYEGQLTETRAKKTETTEL
DGRLQEQEYVRLRESLQDLRDQYEAQMKANREEIEAIYNLKMDELRSQARNQLSTA
TTLKELREMRRIEGLTGKI

>CL2695.Contig1_Ba_mix

SARMFKKTSTMSVSSGSAASPARSRSPSSPARTTRLEEKQQLAGLNDRLAAYIEK
VRSLEAENNRSLQVRTSQEVVTREVSNIKSLYESELADARRLLDETARERAKLQIDLG
NLKTERDDLAAKLVRRELEGAEKQVSLQEAQVRDLQGRLNQLADKKKAQDDLK
DAQLENMKLKKQLDEVKQLESEALARVDMENRCQSLKEELEFKTNVYEEQLTETRS

KKTEEITELDGQLQSEYEARLRESLHELREQYEMQMRVNREEIETIYESKLEDLRAAQS
RNQSSTATTRELRRETKARIDDLGKISDLEGTNTTLLARVRDLERQLDDERTSSASM
LVAKNEEIERLQELMQQQLQEYQDLMDIKVALDVEIAAYRKLESEEARLNLSPGGRH
VVEVSASSSARGSRATPSAGRAGKRKRMVLESEEAESTSGFAVANTCHGDVEIVDECAD
GKFVKLRNKSNEVSLGGMQLVRKADGNETDYKFHRAIKLGAGEETTVWASEAGAV
HDAPHSVMKGTWFVADKMTTTLYDMEGEEIAQRVSQRENRSASFTTSRQQVIAT
GSEE

>CL15271.Contig1_Ba_mix

GACVPYYLCKDGDIVTDGAGLIDMRFGGDEDESKSNSQCPNFLDVFCRVPLTEPDPDI
LGELTEYEYQPSCGHRNPEGVSIILDGFKEGESQFGEFPWMGILLEDELDDYDQVIQRY
VCGCSLIHPQVIMTGAHCINGKDKPAKLTVRLGDWDTQNDKEIFPHEHHRVVDMEIHE
RFNSANLRYDVGLLFLEKPVVLQQHIDTICLPAANEDFDLASC VATGFGKDQFHGGRF
QNIMKQVDLPVPHRTCQNRLRETRLGRWFRHLHRTFTCAGGEAGVDTCRGGGSPLA
CPSKEDPSKYVQVGIVAWGIGCGEDGVPGVYASVPKLVGWVNEKMAEHGIYTDLQV

>Unigene5261_Ba_mix

GACVPYYLCKDGDIVTDGAGLIDMRFGGDEDESKSNSQCPNFLDVFCRVPLTEPDPDI
LGELTEYEYQPSCGHRNPEGVSIILDGFKEGESQFGEFPWMGILLEDELDDYDQVIQRY
VCGCSLIHPQVIMTGAHCINGKDKPAKLTVRLGDWDTQNDKEIFPHEHHRVVDMEIHE
RFNSANLRYDVGLLFLEKPVVLQQHIDTICLPAANEDFDLASC VATGFGKDQFHGGRF
QNIMKQVDLPVPHRTCQNRLRETRLGRWFRHLHRTFTCAGGEAGVDTCRGGGSPLA
CPSKEDPSKYVQVGIVAWGINCHQAGVPGVYADVVALMPWIRS

>Unigene10435_Ba_mix

RAYPMQAYINAGAQIKEDIGEASVIMGVKQVPIDALIPNKTYCFFSHTIKAQEANMPLL
DAILEKNIRLLDYERMCDERGRVVAFGKYAGVAGMINIMHGMGLRLLALGHHTPFM
HIGPAHNYRNSEMARQAVRDAGYEIALGMLPRSLGALTFVFTG

>CL11184.Contig1_Ba_mix

ADAAKLGPRDQLDLTFTDTRAAFQSKTTWEVFRGVLVYTLCTSRYLVEHNATLMKL
FRKLLGQKLFHTVMRATFYGQFVAGADQASIRPQIENMRSFGVKSILDYSVEEDISTEE
AEQAEMRSCSTPGEQEQLTVQKDPMARYHAHREFADRRVKVQSARTYFYMNEAQC
EKNMETFLKSIEAVSGSTQCTGLAAIKMTALGRPQLLMQLSEVIMRTRRYLAELAGSE
RATDVISQDVSVEQIQSRLKETS GPGVEQWLKGLTYDQDGLIHLFSWSGLIDTKTLM
DLFRVPLTTGRMEPLITSLTKDEEEMFKNMMRRLHTIFSARECDVRVMVDAEQTY
FQPAISRLTMELMRKYNREKAIVFNTYQCYLKEAYHNLSVDLDQADRQHFYFGAKLV
RGAYMEQERYRAASLGYEDPINPTFEATSEMYERCLLETLRRIQHYKKGQPRKLAIM
VASHNEDTVRFTVQKMDDELDIKREDKVVCFGQLLGMCDHVSFPLGQAGYSVYKYVPY
GPIDEVLPYLSRRAQENKGI LTKVAKERKMLRSELLRRLVSGQLFYKPVGNYPV

>CL16496.Contig1_Ba_mix

MSFNNTLLDFSVAPEIITNPVASATLHQVVEEVGAVVPGLTRLIEDLLPSGGFHMTYT
AENETFVTFRGRHSLVSVQIENYGETFLMENRAVVELEKRIRAKIGAHRGKAILPLKR

GRDIDSYFYTSDERLLEYGVLETIFDEVTPYQHVVVRRTRDFGKILVLDGFHNMSEKDF
IYTETLMGGENYEGKTALILGGGDGLLCELLKQNPKFVTMVEIDEVVIRECRKHLRAI
CGDCLDKFDGDNYKIIVGDAFQYLKDSVQEGRTFDYIFYDLSVVPVSPRHDRDLWNM
VKDVLQDSMSLLPAGGKYMSHVMGVNCPAEEFERLVDELPAKTSRTSSSAYVPSF
METWVVFYQVT

>CL374.Contig1_Ba_mix

GSTCDTPDGRSGVCLARSSCRWTRESSEDDFNSLVRTLGACVSTDSFSPRGEPVSRGVC
CPGQGAASAPATTTARPPGGTQWWQTTWSPPPSATTTTTTTRRPATVPWWQQQP
AASSQRTEPAGTTLHPPYITHAWQATRSTSRPPAAPHTPWQKPPGSTTVQSPTTTA
WWATTTTTTRGTTTTTRRPTTTAWWATTATTKKPTTTAWWATTATTKGTTTTKRPT
TTAWWATTTKSTTAAAPPASGGGGPYSCGTRDPEGSDRIVGGKQAVQGEFPWLAGIF
KNGRQFCGGLIDEKHILTAHCVAHMSSYDVSQLLIRLGDYDVSTPFEAKHETYKVA
RVVRHKGFFSEKTLHTDIALITLSKPVKYKSNIRPICLDSGVSARGAAGQTVTVAGWGLR
EGGRQASIMQKVS LKVVWDNSKCRSTYGPSAPGGIISMLCAGRQKDCSCGDSGGPLM
HISGVVYQVGVVSWGIGCGKAQYPGVYTRVSEMRDWIDRN

>CL6481.Contig1_Ba_mix

CGKTKFSTRIVGGTEPPAHAFWLVALQTRKRKKQFCGGTIINERFILTAHCVDRRK
PTGLAIAVAKHKRRDDPTEKIFNVKNIKIHEKYNRATQDRDIAIHELTRSLRSMIADER
GWVRPICLPRKTCRSENNCYTARSAILAGWGLLDSTFFEGPATVQYVKVPVLSNNQCQ
ENYAKDRIGITRRMVCAGYPDGGKDCSCQGDSSGPMVVSADEVYTLAGVVVSGKGC
LPGYPGVYVRVSEFTDWIRDNTR

>CL7.Contig19_Ba_mix

TDGDGDYSNNVDCYYQLYADQAGDQLSVTCSQFDVESHSSCAYDWLSVDGNKFCGSN
GPSGVAIDQMAIHWHTDYSVVRSGFVCAVTVGEAPPPTTTAAPPPSDNCACGNVN
RASRIVGGVQTEANEYPWQAGLVSTGGRTWCGGTVINSRYVLTAAHCTAGSSASRIQ
VLLREHLINQDDGEIRFNIAQIKNHPNYNSGTYANDFLLKLATAITFPADNKIAPACL
PTASNDFVGADAIVTGFGTTASGGSQATALREVTVPVISNSACQSAYSGYSITSSMVC
GLLGTGGKDCSCQGDSSGPLVSLNRYSLIGVVSWGISCADPSYPGVYARVTDALTWIS
TNAAD

>CL1088.Contig2_Ba_mix

RPDPPSTSREVTQCASQECVRPDLCDENGRITDGSGLLNARFNNREFCRTPGGGKGR
CCLPADPEPQLVCGQSLDIRILGVTDPDSTEANFGELPWQAIISYTNITFCGGSLVGRQ
HVVTAAHCVQSLQPGAIQVRLGEYRVNAEDEPLPHQDQGVSEIHIHPQYERGPLFYDL
AVLRLSSPVQLDSHIQPICLPTPGQQTGRCVASGWGKDAFEGRFSTILKKVRLPMVS
HEQCQENMRNTRLGSFFVLNKSFCAGGEEVDACKGDGGGPLACPSNGRYTLAGVT
SWGIGCGARDVPGIYASAEAGLDFIRQHADS

>CL3.Contig27_Ba_mix

CPAGQECVQTRSGRVCRRDDSCRPKMSPGGCPGGSYCGQEGRCTPLLDVDAPCWSG
VQCLHHVCRGHVCKLDACPQLDSDQDCPEGQFCSSSQRGNICINRRADGEACSSDAQC

QSYRCDGRRCSRDTCKTLLSRDGCPCDGHICQGGQHGNLCVPLLARGASCSSDRSCRSD
SCRAGRCYEDLCPTPLDTAGCDFSLLCVHTLIGNECMTKLTIGADCTADLQCLSNFCDN
NQCRRLAKNGDSCRFDNDCFSRNCFKGICRPSLASNGERCQFDDECFSGNCFRGRVA
HREQ

>CL3.Contig24_Ba_mix

PGECQTPYSQSGCPYDQVCTADYRCVPLKPTGSRCRSEFECLSGKCRESRCVHDECLGE
GFNSGCPAGQECVQTRSGLVCRPRDNNSCRPAMSAGSCPSGNYCGQEGRCTALLDVNAP
CWNDVQCLHHVCRGHVCKMDACPQLDSDQDCPEGQFCSSSQRGNICIDRRPDGEACS
SDAQCQSYRCDGRRCSRDTCKTLLSRDGCPCDGHICQGGQHGNLCVPLLARGASCSSGR
SCLSDSCRAGRCYEDLCP

>CL3.Contig30_Ba_mix

PGECQTPYSQSGCPYDQVCTADYRCVPLKPTGSRCRSEFECLSGKCRESRCVHDECLGE
GFNSGCPAGQECVQTRSGLVCRPRDNNSCRPAMSAGSCPSGNYCGQEGRCTALLDVNAP
CWNDVQCLHHVCRGHVCKMDACPQLDSDQDCPEGQFCSSSQRGNICIDRRPDGEACS
SDAQCQSYRCDGRRCSRDTCKTLLSRDGCPCDGHICQGGQHGNLCVPLLARGASCSSGR
SCLSDSCRAGRCYEDLCP

>CL6274.Contig1_Ba_mix

IGIIGSGFSDPSALGVEDAKDVEYDTPFGKPSPLLTGTLGVPVAVLARHGRRHTILP
SAVNYRANVYALRRHGCTHVLVSTACGLREEYRPGQLVLLDQFIDRTTKRPLTFFDG
SCDEFVIGICHLPMADPFCGETRGVLGEAAKELGITMHDKGTIVTIEGSRFSTRAESHMF
RSWGCDVINMTTVPEVTLGQGGG

>CL17624.Contig1_Ba_mix

MAAPTAVVVLDGRNNTTCTVNLHGATVVSWRVNNQEQLFVSKQAVFDGKKAIRGGI
PIVFPHPGWSLGPQHGFARTSRWHLEKAPERLPSGDIEAIFVLMSEYTHQFWKHSL
RLTYRLILREKELHFNIGVYNPLGSQDTFSFTLLLHTYFKCPDVRKCQVTGMHGCTFID
KTRDGAVYQEGRDVVMINEWTDRIYQNTPEHIITNVVSGRKMRIQKFNLPDTPVW
NPWEHKAKEIADFGDEEFPNICVEAGNVSTGIILPPNTVFEASQILQVM

>CL11285.Contig1_Ba_mix

LRLGQRFASVDTTKLFINGKFVESASSDWIDLHNPATNEVITRVPKSTPGEMQAAVDA
AKTAFPTWSRSTVLTRQQIMFNFQNLIKKNMKVLAANITSEQGKTLADAEGDVLRLGL
QVVEHCCSITSLQLGETMSDVSRDMDTLSFRIPLGVTAGITPFNFPAMIPLWMFPTAV
VCGNTSVIKPSERDPGACMLLVQLLQEAGLPDGVVNVHGEHEAVNFICDSPDIRAISF
VGSQAGKHIYERGSRNGKRVQCNMGAKNHGVIMPDANKENMLNQLVGAAGAAG
QRCMALSTAVLVGEAKHWLPELVERSSRLRVSAGTEPDADLGPVISPKAKERIIQLVES
GIREGAKCLLDGRAVKVPGYEHGNFVGPTILADV KPEMECYREEIFGPVLCVLTVDTL
DAIELINNNPYGNGTAIFTTSGATARRFTHDIDVGQVGVNVPIPVPLPMFSFTGSRGSF
LGDANFYGKAGINFYTQLKTVTQLWRADDVTHSKAATTMPVMR

>CL4410.Contig1_Ba_mix

MATTKGKVQTVLGLVEPSSLGVTMMHEHMHLDFNVAFIPPEGKYAHKADCDFTLEN
SGWIRQNPYASRQNVTFCDAAVDAAMRDELRTYRENGGGAVVEVTNYGIGRDAALLA
AYSRTAVTIVTGTGFYQHMFQLESDLALTVEEMHDRALKDITDGCPEAPLVKAGVIG
EVGSGWPIHDFERRAIQAAALGQQATGCPVNFHPGRDPAAAPEVLRIFQEAGGDVSN
IMSHLDRSIQTAEGLSEFAKIGSYLEFDLFGIETSHYTLAPHVDMPSDAQRIQRIKHLVE
DGYEDRVVISHDIHTKHRLTKFGGHGFSHILENVVPMMKVRGLTEETINKILSTNPQA
AMTFK

>CL992.Contig1_Ba_mix

LTFPWMWECREGACL RTPVSEATNGMTLGGCKLTCGKGLTLWPKPTGTFTLGKTPV
SFKYSQVIVIVDAPQDVRGHVEKAGNRLKETLRDMRPPGGSCLELSSASDANLATRQL
TIRVTVEQSDASLTLKTDESYKLNITHTDADQLEAHIEAKTFFGARHGMETLSQLVAY
DDANDALMTVTADVRDAPVYPVRALTLDTSRNFISVAGLRRTIGAMAMNKLN TLHW
HITDTHSFPIEITGEPRLAQYGAYSPREVVYTRAEVEELVQFALERGVRLPELDMPAHV
GYGWQWGEKAGMGNLTVCLGKEPWQQFCVEPPCGQMNIINENLYKVLKTLVEYND
VFQPDFLHIGGDEINLNCWKTTPEIAAFVKEKGGDPTDDEEYMKLWIQFQERVYDM
WTSIAGEQKTLWTSHLTQRPAEESRLDPSKYHIQIWTGKDQQIGDLLKQGYELILSN
YDAWYLDCCGSAWVGKGNWCSPIKSWQTVYENS PRKIAQSFQSNDAASQPASQ
SDFSAQILGGSAAWTEQADDANLDNKLWPRGAALAEERLWAEPETDSLAAQWRLVH
HRRRMVARGVHAETMQPKYCHQYDGTCTYI

>CL304.Contig4_Ba_mix

METVLNGLLCVAQALFLWLQSVVLFVPAKYREKSVSGDVALITGAGSGIGRLLALRLA
KRGARIVTWDVNAEGNEETVRQIRAAGGEAHAYTCDLSNREVIYKTAERVKREVGKV
TILVNNAGMVTGKPLLDIPDNLIEKTFEVNTLAHFWTCKAFLPDMMIAKKGHVVNIA
LAGLQGMGRLLTDYCASKFAAVGFHESLTVELKVGHEGVKTTVICPFFINTGMFDGAK
SNIIPFLEPEYVAERIEQAILLNEEQVLIPGYLAALFYLLKAMPWRAYWTLGLAFKVER
AMDTFTGRTKQ

>CL304.Contig5_Ba_mix

METVLNGLLCVAQALFLWLQSVVLFVPAKYREKSVSGDVALITGAGSGIGRLLALRLA
KRGARIVTWDVNAEGNEETVRQIRAAGGEAHAYTCDLSNREVIYKTAERVKREVGKV
TILVNNAGMVTGKPLLDIPDNLIEKTFEVNTLAHFWTCKAFLPDMMIAKKGHVVNIA
LAGLQGMGRLLTDYCASKFAAVGFHESLTVELKVGHEGVKTTVICPFFINTGMFDGAK
SNIIPFLEPEYVAERIEQAILLNEEQVLIPGYLAALFYLLKAMPWRAYWTLGLAFKVER
AMDTFTGRTKQ

>CL17009.Contig1_Ba_mix

DSGVPKALWKLGRNLHVAIATPDLKKSTALFRDVLGADVSEPEALPEHGVRTVFINLG
NTKLELLHPLGPDSPITNFLDKNPSGGMHHICIEVDNIAEAVASLQQKQIRCLNEPRPG
AHGKPVVFLHPKDCAGVLVELEEA

>CL4572.Contig1_Ba_mix

DKIQSKLAIDAGVNTIPGFEGEIRDVDHCVAVSREIGYPVMIKASAGGGGKGMRIARN

DDEAREGFRLSQQEAAASSFGDDRILVEKFVDCPRHIEIQVLADQHNNNAVYLNERECSIQ
RRNQKVIEEAPSVFLDEETRRAMGQQAVALARRINYSSAGTVEFLVDSARNFYFLEMN
TRLQVEHPITECITGVDLVQQMIRVAKGHKCLKQEDIPIRGWAIESRVYAEDPFKNFG
LPSVGRLSKYIEPNHLPGVRCDSGVAEGSDISIYYDPMICKLVAYGNSRQEAIARSLDAL
DSYVIQGVTHNIPLLRDILTEPRFVSGDITTNYLPEVYPDGFQGHRLEGESLLRLAALSA
VIHVKHTQRSSLVSGHHALQPVATKWDLVV

>CL6243.Contig1_Ba_mix

GDVFLDAREAVYVWTGKEANHMEKIQAAKTAQSIKDDHGGADIIVVESGKENEMSK
NEKALFNKLLPLSDRSVRPASAAPSDDKQERRVAEDIRLYRCSDEDGALKVTEVKGGP
LLQSDLDKNDTFIIDNGEQIWWVVGRRATHKERAEAMRNAQGFIKKKNYSQATPVT
RVIDGGEPDFKSLFQSWRDKDATTGLGKKATIGQVAKTIQTSFDASTLHEHPDLAAH
TQMVDGDTGKKEIWRVEFDLKPVPDVKYKFFSGDCYVILYTYHARGREEQIIYYWL
GSHSAQDEQGTAAALKTVELDDSLGGRPVQVRVVQGKEPPHFLAMFGGRMVVYSGGVS
SAFESAEGVNGGHNATVGDYLLQVRGTTNYNTHAVQVDCRAGSLNSNDCFVLRHGG
EVFVWCGKGATGDEREMAKTIAAEMHSEPQIIYEGQERDDFWAKLGGLEPYASSPRL
AEADQMOPARLFQCSNASGRFLVEEIPDFIQDDLVPDVMMLLDWNTIFIWIGSGSNK
TERERAEKTAIEYLRTPAGRGVGTPIVRVKQGCEPPTFTGFFGVWDDGLWESQPDW
EAVRRDVSAGNKGISEVTVAAAKAVELPVYELETLRQHDPPELLPEDVDPSIKERYLAPE
VFEELFGMSRDAFSALPTWKQQQLKKKVDLF

>CL6482.Contig1_Ba_mix

CPHEGTLKSWSDAASWASGTVPAEGEAVVSEPMMLDTATPDLLSVTVEAGGRLVFD
PAADLAKLAAEWIKVAGELHVGAEPCPFTGQAEIELLGKKNVTVGQVHEHGAEFKA
LVVVDGGRLEVHGQPRQAWTRLQTTLPTTRELVVGDALFNHRETEVAHWYRGF
MGYQFNSTGQPVRMRLRRSCDFSDLVTMQGSVLLVVQRKVELDRDQQLEHAADA
FEQVCYGGGQRSHLRDLSLGETVAWAAICHVGHPEPENTIEELGHPEGDNSVTSRLVKQV
GDVEYLAQSVTRLTSDWPYEIDMLTYTAGNVPDAHIVLDVSSNVSDWRAGDTVAITS
TDYDWRQAEFTLLDCPDCSATQIMIGWPVRWTHWGETTDGVNMGAEVGLLNRNV
RIHGRMEDACYGDNHCGRFNFDTFGGQIKVFANFASVRIVNAEIFHMGQNSVLGAYPI
HFHMCGDVTTRELRAYVRSNAIHHTFARCVTVHGTSGLLVEGNMAYDHFHGCFFLE
DGSEKRTVFRNNLGFSTRRTTLTPSDHGRASTFWITNPLTTMEGNVAGGSEGWGIWY
TFPRKPIGSAALDVMENHNEAMKTPLDPFIDNVAHSNNEYGLHFDGVLRSNGHIHG
FNYDPREDPLNATSPTVVVTLTGFTAFAKKNYKSVWLRMSRVVAKRFNIAESVEGVVFA
WSGAGEKRLEDVSLVGETANKGRPEGWIRLTNGTSIWWDRQIRMNGADNALPIIGVIF
HDTIMSLNRVTFDRFESNIVRPSGGIGMRRKIRHYTSPVNSVSGLVFRYADPLEGNRAF
DASEGRGFADLAGNIQNVIRDLGSLTTYANSTVVKPYDIHLNARCAPVPQWNLYVCP
TMFTKLLFMWWDRSVGNLNTFLTRNDGSATFTYGVNFQNSYALNSQEGYIVHFNTS
VPRYFKIRLAGVEAGVVQTVGLCIGKGVTPLTVMNSVPVPSFDSLDDQGADVHWYL
DTEAGVLFFRFSSPYHRTADTVDECPGQDGKPAAGCEVLVVLPSNTDGDSCGRAYPA
YS

>CL11.Contig4_Ba_mix

MNSAGPNYPMASLYVGDLPDVTTEAMLFKFKSTAGPVLSIRVCRDMITRRSLGYAYV

NFQQSADAERALDTMNFVVKGRPIRIMWSQRDPSLRRSGVGNIFIKSLDKSIDNKAM
YDTFSAFGNIMSCR VATDENGVS KGYGFVHFETEKAANDAIEKVNGMLLNDKKVFG
KFVPRKEREKELGEKAKRFTNVYVKNFGEDLDDTKLLEMFEPFGTISSHKVASGEDGK
AKGFGFVSFEDPEAAEKAVNEMNGKEINGKTIYVGRAQKKAERQHELKRKFEQIKLER
MNRYQGVNLYVKNLDDGIDDERLRREFAQFGTITSARVMMEDGRSRGFGFVCFSSPE
EATKAVTEMNGRIVSSKPLYVALAQRKEDRKAHLASQYMQRMTSMRMPGVNPMFQ
AGAGGYFVPTMPQAAQRFYPPAQMAHQMRPGPRWQQPAGGQMRLLGGQAAGGMPA
PFRGQAQRAAGGQAPAGGMQAGQTRPMAQQALLPAGMQPRPMPAQGAAGQ
QPRPAYKYTANMRNLQQLSAAGVSGQAPLMPGAAQALAMQQPAVRVQGGQEPLTAS
MLAAAPEQEQQMLGERLYPMIQRMYPELAGKVTGMLLEIDNSELVHMLEHHESLK
GKVDEAVAVLQAHQAKATPA

>CL14024.Contig1_Ba_mix

MVQRLTYRRRLSYNTRS NRVKVVKTPGGRLVYHYRKKPRRVPRCADTGKKLTGIRSA
RPQEKKRMKRKHKT VNR TYGGVLCHSAVRERIIRAFLVEEQKIVRKVLKAQQASAKA
K

>CL15766.Contig1_Ba_mix

MLMPKKDRVKIYEYLFKEGVMVAQKNPHRPRHPNVPVPLYVMKALQSLKSRGYVS
EQFAWRHYYWTLTNEGITYLRDFLHLPSEIVPATLKRPTRAETARPRAAAPRPDGGK
MEGDRAAYRRVGE GGPDKKGEAGAGAGQMEFRGGFGRGRGMPQ

>Unigene36236_Ba_mix

MLMPKKDRVKIYEYLFKEGVMVAQKNPHRPRHPNVPVPLYVMKALQSLKSRGYVS
EQFAWRHYYWTLTNEGITYLRDFLHLPSEIVPATLKRPTRAETARPRAAAPRPDGAK
TEGDRAAYRRAGE GGPDKKGEAGAGAGQMEFRGGFGRGRGMPQ

>CL4543.Contig1_Ba_mix

MVVLGEVFPNFEAESTEGHIRFHDFIRGSWCILLAHPSDFTPVCTTEMGAAKMAPAL
LRRGVKMACISCDPVSSHKTWIEDIRAYNGLSGPFPFPIISDEERQLAKKLG MIDPDE
PRFDNKPATARAVFIIGPDLRLKLSMLYPGTTGRNF AEIQRIMESLLVTAKHKVVTPEQ
WQVGEKCFVVPFLSMEEAKDMFPAGVQVHPVPSGKQYLRTTPMP

>CL2680.Contig1_Ba_mix

KCFYLPQVLURSL SLLGRMSALS VLRCLAAAGRPPALCSPRLLPPAGRTVWRGPAAHS
RALVVLDDLRLQPQSPRALLLGAAGLLPFAAAPVLMMLRTGHFSAELLHAQLAYGACI
LSFLGGVRWGVTL PDGAPQRPDWANLTRSVTPSLLAWAGLLAPPSAGGLMLIGGLL
AGYWDMVMYGYPAWFKALRFCLSVGAILSLWTAL

>CL14396.Contig1_Ba_mix

EGLLALLDESTLSEKASDQYFVENCKETIESRHHFFPEKDGFAIAHYAGKVSYSNKDIVA
KNKDYLDPEVFDTLRQSENPFIA PMFLLPLTKTGNLTM DREQAQREAGGKARPVKLN
DDVGNKRFDTRS RGRLSQTSLVLLTQASCYRYSAMEVMHKLINSTAHFVRCVRSNSEG
AADTWD TGLVAHQKCMQIANTIAIRKDGYSQRIDFAEFLRRYQFLAFDFDETVEVTR

ENCRLLMVRLKLDGYRMGRQKIFLKYFNEEYMSRLYEHEVKKIAKVQAMIRAFLVRR
R

>CL9899.Contig1_Ba_mix

EGLLALLDESTLSEKASDQYFVENCKETIESRHFFPEKDGFAIAHYAGKVSYSNKDIVA
KNKDYLDPEVFDTLRQSENPFIAMFLLPLTKTGNLTMREQAQREAGGKARPVKLN
DDVGNKRFDTRSRGRSLQTSVLVLLTQASCYRYSAMEVMHKLINSTAHFVRCVRSNSEG
AADTWDGTGLVAHQKCMQIANTIAIRKDGYSQRIDFAEFLRRYQFLAFDFDETVEVTR
ENCRLLMVRLKLDGYRMGRQKIFLKYFNEEYMSRLYEHEVKKIAKVQAMIRAFLVRR
R

>Unigene5067_Ba_mix

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KNKDYLDPEVFDTLRQSENPFIAMFLLPLTKTGNLTMREQAQREAGGKARPVKLN
DDVGNKRFDTRSRGRSLQTSVLVLLTQASCYRYSAMEVMHKLINSTAHFVRCVRSNSEG
AADTWDGTGLVAHQKCMQIANTIAIRKDGYSQRIDFAEFLRRYQFLAFDFDETVEVTR
ENCRLLMVRLKLDGYRMGRQKIFLKYFNEEYMSRLYEHEVKKIAKVQAMIRAFLVRR
R

>CL888.Contig1_Ba_mix

ALGVPALGQAGFECPDQLPGFFPHDVSCDKYWACEEGVATLKTGNGLAFDDTDPNY
EKENDYLHNVQCGQRTELEPPISSPNCPRQYGFIDEANCNTFWSCWAGEANKYEC
PPGLAYDSEQRVCVWADQVAACKSEKEGDFQCPAEGNGLGTYSLYAHQEDCRLYYV
CMGGAPREYGCPLGTVFKIGDLGSGQCADPADVPGCEEYYGDVDIRALRALGF

>CL6240.Contig1_Ba_mix

MYRIPGLLRGPAARQLTRCFAKDVRFGDVRASMLQGVDVLADAVAVTMGPKGRNVI
LEQSWGSPKITKDGVTVAKAIKELKDKFQNIQAKLVQDVANNTNDEAGDTTTTATVLA
RAIAKEGFEEKISGANPTEVRKGVMLAVQAVVANLKNMSKAVTTPEEIAQVASISANG
DKTIGDLISSAMKKVGRDGVITVKDGKTLHDELEVIEMKFDGRGYISPYFINSSKGAQV
EYQDALVLLCEKKISNIQQIIPTELEANTARKPLVIAEDVDGEALTTLVVNRLKIGLQV
VAVKAPGFGDNRKNTLQDMAIATGSIVFGDEASTIKLEDVQLSDLGQIGEVQITKDDTL
MLKGRGNKTDIEQRCVQLKDKIEETNSEYEKEKLQERLARLASGVGVKLVGGSSEVEV
NEKKDRVTDALNATRAAVEEGIVPGGVALLRSATALSALQPANEDQKTGVEIVRRAL
RMPLQTIAANAGVDAAVVVARVQDAQPEIGYDALNDEMVMNMMERGIIDPTKVVRTA
LTDAAGVASLLTTAEAVVCELPKEDKADAMGGGMGGMGGMGGMGGMGGMGGMGGM

>Unigene11234_Ba_mix

MASLNPVHVLRRGAAEEKAEIARLSSFVGAIAIGDLVKSTLGPKGMDKILISVGRSEGKV
EVTNDGATILKNIGVDNPAKVLVNMSCVQDDEVGDGTTSVTVLASELLKEAEKLVG
MKLHPQNIAGWRRATDIARKALAGSTVNHGSDPKFRNDLMNIARTTLGSKILAQH
KDFFAELAVNAVLRKSSGNLQAIQVLKVQGKTLRDSFLDEGFILNKKIGVHQPKRME
NAQILIANTPMDTDKIKVFGSRVKADSTARVAELEVAAEKEKMKDKVEKIVKHGINVFI
NRQLIYNYPEQLFADAGVMAIEHADFDGIERLALVTGGEIVSTFDHPELVKLGSKVIE

EVFIGEEKMIKFSGVPLGEACTVVLRGATQQILDEAERSLHDALCVLTSTIKETRTRTVFGG
GCSETLMAVAVLEEAARTPGKEAVAMEAYARALLQLPTIADNGGYDSALLVSQLRAG
HTQGQNRLGINMLDGTVGNMEELGITESFMVKQQMVASASEAAEMILRVDDIIKAAP
RRRVDDRGC

>CL2410.Contig1_Ba_mix

EREDSVYKAKLAEQAERYEEMVEAMQTLACLDVELTVEERNLLSVAYKNVIGARRAS
WRIISSIEQKEETKSAEEKLEMIRSYRIKVEKELKDKCGEILQLLDHSHVIPSATTEESKVF
FHKMKGDYHRYLAEFATGNERKDAEAENSLAYKAATDIAMTELPPHPHRLGLALNF
SVFYEILNSPDRACRLAKAAFDDAITELDRLSEENYKDSTLIMQLLRDNLTLWTSDM
QTDGKEGEAGTGEEAPAVQDVVEEQDVA

>CL8957.Contig1_Ba_mix

AIPFRMLASSASRLLRGLSASVRPVRLSRTAPALAPRVQQPAPDFKQAVVDGEFRT
VQLSDFKQYLVLFYPLDFTFVCPTeltaFSDRMDEFRALNTAVVGVSTDSQFSLA
WIDTPRRSGGLGGLSYPLSDFSKAIAREYGVLEDEGVALRGLFLIDPSGVLRQMSVN
DLPVGRSVDETLRLVRAFQFVEEHGEVCPANWQPGGATIKPSPAESKEYFEKV

>CL2356.Contig1_Ba_mix

MGIDIYAIKPSPPCRAAFLVAKAIDLKIVSLEKGENRTPEFLKMNPAHTVPVMTD
GELSIGDSKAIITYMMNQYAPANLQSLYPRDPAARALVDQRLYFDSQLFASLRGIVFPL
VFMKDLKQSQANMPRVNENMALLETLTRSTYLAGEHLTIADLATLANVSSVEAGGL
DMSRWPHVQAWLAKLKAELPYEQANGEGAQMMGAMYKNALKE

>CL4955.Contig1_Ba_mix

MGIDIYAIKPSPPCRAVFLVAKAIGLDYNLKIVDMEKGENRTPEFLKMNPAHTVPVMT
DGELSIGDSKAIITYMMNQYAPANLQSLYPRDPAARALVDQRLYFDSQLFASLRGIVFP
LVFMKDLKQSQANMPRVNENMALLETLTRSTYLAGEHLTIADLAMLSNVSSVETGG
LDMSRWPHVQAWLAKLKAELPYEQANGEGAQMMGAMYKNALKE

>CL4041.Contig1_Ba_mix

MCGIFAYLNHLTPKDRKEVFQILIQGLQRLEYRGYDSAGVGVGDKDGSIEIYRAKGKVK
NLEDLIMSEDNKQDMSEILKTHVGISHTRWATHGVPAPVNAHPQPSDASKQFICVHN
GIITNYKDIKQFLIAKNHVFESSETDEIISKLTLMYRDHPNHTFQQIVELVIQQLGAF
ALCFKSVHFPNQVVAARRGSPLLVAIKTKEHLATDHIPIIMYSKEDFKGENTKSRKISPA
DARHVPAGTHGGNVPLIPRTESTAEFLPTGDSQEIEYFLASDASAVIEHTNRVIYLED
DVAWIRDGMLSIHRLKRESMDECSTREVHTLMEIQEIMKGSFSSFMQKEIFEQPEV
VNTMRGRINFEDETIVLGGIKDYLPKRCRRLILACGTSFHSAIATRQLLEELTELPV
MIDLASDFLDRKTPIFRDDVCFISQSGETADTLMALRYCKSRGALIVGITNTVGSICR
ESHCGVHINAGPEIGVASTKAYTSQFISLVMFALVVSEDRLSMLPRRREIIQGLKVLPEL
IKEVLALDSKIEELATGLKGARSMVMGRGYNATCLEGALKVKEITYMHSEGILAGEL
KHGPLALVDPGMPVILICTRDPTYVKCMNALQQVTAREGRPILICSKGDTEPARFSNAL
LEIPHAVDCLQGLLTVIPLQLLSYHLAVLRGCNVDCPRNLAKSVTVE

>CL14928.Contig1_Ba_mix

LLVACLGAIQAKMHITLKTCKDAPEQNPNTPKEDAPSFHVQLLKNIAKAGVQTFVGE
ISLGTTPQLMSVSVETSSALSYPFVSRVEDQFCKTRRQYNSSASSTYEALGTPFELPPGI
NASGVLKDSISFAGITVEGVVFGAEESMWNKWLSILPPDGVGLGLQGMPEGVPRPIL
DVMAEQGVISERVFGMWLGRDPQGGELTLGGLNDQLYRGELTWANLTPPDGQWWT
APADSIVLDGLTQLDLCPGGHCVVLPASNSPYFIVSEAQAAINEALGGLDIGQPGAAGL
DCTTLYRLPNLTITVGGGRAMVGLPLEYTFLLRFEGGLQMCVSGFLGFPVDDHTMLLG
TLFMQKYYIAFDRENNRLGFADSA

>CL16649.Contig1_Ba_mix

LLAACLGAIQAKMHITLKTCKDAPEQNPNTPKEDAPSFHVQLLKNIAKAGVQTFVGE
ISLGTTPQLMSVSVETSSALSYPFVSRVEDQFCKSRRQYNSSASSTYEALGTPFELPPGI
NASGVLKDSISFAGITVEGVVFGAEESMWNKWLSILPPDGVGLGLQGMPEGVPRPIL
DVMAEQGVISERVFGMWLGRDPQGGELTLGGLNDQLYRGELTWANLTPPDGQWWT
APADSIVLDGLTQLDLCPGGRCVVLPASNSPYFIVSEAQAAINEALGGLDIGQPGAAGL
DCTTLYRLPNLTITVGGGRAMVGLPLEYTFLLRFEGGLQMCVSGFLGFPVDDHTMLLG
TLFMQKYYIAFDRENNRLGFADSA

>CL1199.Contig2_Ba_mix

ISGVDCLLFAIGRDPNVELDLDKTGVTLEKGHKIVDAFQNTSAPGVYALGDVCGRALLT
PVAIAAGRRLAHLRFDGKTDLKLKDYNNIPSVVFSHPSPGSGVGLTEREARDKFGDAAVR
VYRSSFAPLYYALSERKVKTHMKLVCAGDEQRVVGLHMVGQAVDEMLQGFVAVKM
GATKAQFDDCVAIHPTSAEELVTMR

>CL3558.Contig1_Ba_mix

EVPPQLEDLLEFTVNVLVNQPDNLVAYAVEYFTRLNESGNKYSGANSKLAPADTNN
VQDGGVSDQDDSMSEDEGPPQNCNYRRKSVFAEAYNPEEDDDEGQKAVFPKSDEQ
RARLSDAVQGILLFRALDPHQMQEVIDAMFERKVTAGENVIQGDDGDNFYVIESGRY
SIYVKMDDSAEPKKVGSYDNKGSFGELALMYNMPRAATITADEEGSLWAMDRQTFR
RIVLKNAFKRRKMYESLLETVPMLKALEPYERMNLADALVPRTFTDGEIIEQGDEA

>CL3.Contig8_Ba_mix

GSGRVCRRDDSCRPA MSAGNCPSGSYCGQQGRCTPLLDVNAPCWNDVQCLHHVCR
GHVCKMDACPQLDSDQDCPEGQFCSSSQRGNICIDRRPDGEACSSDAQCSYRCDGRR
CSRDTCKTLLSRDGC PDGHICQQGQHGNLCVPLLARGASCSSDRSCLSDSCRAGRC

>CL3.Contig20_Ba_mix

GSGRVCRRDDSCRPA MSAGNCPSGSYCGQQGRCTPLLDVNAPCWNDVQCLHHVCR
GHVCKMDACPQLDSDQDCPEGQFCSSSQRGNICIDRRPDGEACSSDAQCSYRCDGRR
CSRDTCKTLLSRDGC PDGHICQQGQHGNLCVPLLARGASCSSDRSCLSDSCRAGRC

>CL3.Contig33_Ba_mix

GSGRVCRRDDSCRPA MSAGNCPSGSYCGQQGRCTPLLDVNAPCWNDVQCLHHVCR
GHVCKMDACPQLDSDQDCPEGQFCSSSQRGNICIDRRPDGEACSSDAQCSYRCDGRR

CSRDTCKTLLSRDGC PDGHICQQGQHGNLCVPLLARGASCSSDRSCLSDSCRAGRC

>CL3.Contig21_Ba_mix

CGKSQICVHTLIGNECMTRLPLGAQCTSNLQCLTNICRDNHCRRPLAQNGDRCRADND
CLSRNCRRTGTCRPPPAQDGDRCRSNKDCLSRNCFKGTCSPPGTGGGSRCSNEDCLL
GFVCSQGICSQLGGDGDGFCRGNRECQLDLVCLDGICGPPRTADNDGRFCQFNNDCLL
LVCISGICSETGGEGGICQLNSDCLLGFSCLDGLCVGDGDGGGGDGGTVDVDTLLGIG
EQCFAAIECFSGRCAGGQCAEPLLGIGDDCSTAESMPSNALCR

>CL336.Contig1_Ba_mix

GVTDNQYRYIDAEGTVRTVKYWADTPSLRSSGAHTPHSPQLRMAAPAPAPVQDTPEV
AAAKAQFMATFRMAQQGVIPAPVQDTPEVAAAKAEFMAKFRAAQRAQRKRRSVTVG
LSHTPASTALLP

>CL336.Contig5_Ba_mix

GVTDNQYRYIDAEGTVRTVKYWADTPSLRSSGAHTPHSPQLRMAAPAPAPVQDTPEV
AAAKAQFMATFRMAQQGVIPAPVQDTPEVAAAKAEFMAKFRAAQRAQRKRRSVTVG
LSHTPASTALLPGAYWKWSPLY

>CL1239.Contig2_Ba_mix

GAMIPVLLLVLVGHVAGHGRLMDPPARNAMWRFNFSNPVNYNDNELFCGGFVVQY
QQNDGKCGVCGDNYALDEPRPHEAGGEFAKGLIGKRYSPGQLIDIEVELTANHMGNFV
IRLCPHNDRKTVTQECLNKHVLRVAGTNSIRYVIPEDSGKAGIFRWKVELPPYLTCT
QCVMQWTTYAGNTWGTCSGDGEQAVGCGPQETFINCADIAIVSNTPYFGPVHNSLDRT
LPLTKSEVARVVQEDLDNEPRAPAFRPQICLPHGEFKQEEGADRFLRCMVNPEACPT
DRCMCVTECEAQGEFAKRPQADLFCHECLGFP SHCPEDKCRCF

>Unigene4984_Ba_mix

LVRHAAGHGRLMDPPARNALWRFKGPVNYNDNELYCGGFVVQYEQNGGKCGVCG
DNYASETPRPHEAGGEFANGVITRRYAPGQIIDVEAELTANHKGNFVIRLCPNNPNE
TVTQECLNKHVLRLAGSKAIRFVIPEDSKKSETFRWKVELPPYLTCTQCVMQWTTYA
GNTWGTCSGDGEQAVGCGPQETFINCADIAIVSNTPYFGPVHNSLDRTLPLTKSEVARV
VQEDLDNEPRAPAFRPQICLPHGEFKQEEGADRFLRCMVNPEACPTDRCMCVTECE
AQGEFAKRPQADLFCHECLGFP SHCPEDKCRCF

>CL888.Contig2_Ba_mix

ALGVPALGQAGFECPDQLPGFFPHDVSCDKYWACEEGVATLKTGNGLAFDDTDPNY
EKENDYLHNVQCGQRTELEPPISSPNCPRQYGFIDEANCNTFWSCWAGEANKYEC
PPGLAYDSEQRVCVWADQVAACKKSEKEGDFQCPAEGNGLGTYSLYAHQEDCRLYYV
CMGGAPREYGCPLGTVFKIGDLGSGQCADPADVPGCEEYGDLDVKELAMRALGGG
SGTSG

>CL21.Contig3_Ba_mix

RRFLCVVALAVVVADASSVRERRQALRKKDSAKLEELCRDRGDEYFRLEDENDCKVV

YRCTRGGLKRIQCPDGLAFDIRQQTCLWKRHVKNCDLLSKERKVLPLLKTDEPLCPVD
QLACGSGDCIDSFLFCDGQPCADKSDENACEVGVDPNGSFLCDTSQCLLPSCFCSSDG
TQIPENLEPAQTPQMITMTFTGAVNVDNINLYQEIFRDERQNPNGCTAKGTFVSHKY
TNYSAVQELHRKGHEIGVFSITTNDDPSYWSDSYEIWRDEMAGARDIENFANITDG
TVAGVRAPQLRVGGNNQFAMMIDQQFVYDSSITAPYGRVPIWPYTLDYQMPHKCLGT
SQNCPSQSHPVWEMVINELDLRENPEETERLPGCHLLSSCASINNPEQFAKILRNNFE
HHYSTNRAPFGLHLTADWLQNNKGFINELIKFIDEMQAKNDVYFVTESQVISWMQAP
KETNAIRDFDDWKLKCEVKGLPECSIPNACLTTRELPGDNFYLNTCMECPKNYPWI
KDYTGNGFA

>CL14958.Contig1_Ba_mix

MQLAAALVVLLAVSANGLRVQRQDAEATEDEAVQAICLGKGPGEWFRLNAGSASCNV
VVQCTSAGLQKIKCPHGLAFDLNKQACDWKDTVSDCDQTRPKLVLPRINTDEPLCA
TQDELACGDSTCIARSLFCDGKPCADSSDENICDAESDPNRAPPCDPAQCQLPSCFCS
ETGNQIPGGLAPEQVPQMIMITFNGAINNNNIDLFDDLFSRSLNPNNGCPMKGTFVVS
HKYTNHTAVQDLHNRGHEIGVFSITQNDTANYWTNASTEWAREMAGQRYIIEQFAG
IADNSVVMRTPYLVRVGGNNQFSMMDDQTFLYDSTITAPLGDLPYWPYTLNKMPPH
CHGNAQKCPTRAFPVWEMVMNELDRREDPRIDNLPGCAQVDSNINLNGEQFYNF
LNHNFRHYLTNRAPLSLNFHSAWLKKGDFLDYLLRWIEDIQISVTDVYFVTMTQVIE
WMQEPLDVQQTKFASWLTKCDESTGFECTKPGGSNCALHTDGVAGTFNMQTCRC
PPNFPWLNDPSGKGYF

>CL8680.Contig1_Ba_mix

LDRIPGCTLPEQPACQPREKFRRMNGECNSDAEPRLGRAQTAFSRFFPAEYEDGIWQP
RSKALSGDPLPSARLVSERVVRTTPVMDPWSSLSVMQLGQILNHDIISTAAFTLENGG
GLFCCNRDNTMPAEPLHPLGCNPIVPADDPWYAQFGRTCMNQVRSLPAPFENCIAG
PTGQLNQVTHFLDLSTVYGSSDTDMRRLRLNAGGLFKMSEGNLLPQSGGRFISGEGRL
SENPGLAFMHTVWVWTRHNRVANTLSRLHRHWSDEQLFQEARRIVIGEYQHIIYNEYL
PVILGFKYTREHGLDPEFGHSFSYTNVIDPRVTAEFSTAAFRFGHAQIPDVFLMTQNG
MNLTAIAMEDSFFREDMLKLPNFMNTLATTLTRQKQRMVDNTFSPAVHEKLFASGQ
PSGLDLIALNINRGRDHGLPGYATVLENCLERTLSGGWDEMSEFFEPDVLRLRAVYQ
SVFDIDLYIGGVSEKKVPGALVGPFAFQCIIGEQQFATRYGDRYFYDNGDMPHSLTFTQV
REIQKASWARILCDNVEDVNMQLAFFAPNPLFNAVRHCRSFAIPTVDLRAF

>Unigene25886_Ba_mix

GAVKGLKDKLLLSGSRDYHFVSQGKTTIPGVDDKEEMEATDEAFDILGFTQQEKENI
YRIVAAMHLGTMKFKQRGREGAEADGAEEGERVAKL

>Unigene15759_Ba_mix

VSQHHPAGSTVEAYLAAMQTQWSWILQLTLCLETHLKHAQLSHKLFKDVEDMTRVI
NQQDDRLNSEFSRSEFTLDDGEQLLRDMQLLRDAMAQQAEIERLERRAQQATPLRQ
RRHPDTGVRLTTICNYK

>CL7850.Contig1_Ba_mix

ISDQEKVRIVSDFILHSPPGFNEVFNDVRHLINNDNLLKEGASGAFVQYNKDQLTPVR
LPGSDYPAFITDFNDLGGSRFFDPRTKQSFRFDHLKKEASDLKPHEGDSTAEPWRRAL
EAEMTAYTADHYKNGACAVFGHSNDGDVTLVACIEDHQFQPKNFWNGRWRSQWTV
TIPSSGTAQLKGVLVQVHYEDGNVQLVSSKDAADGAVVASESQTAKEVRLIETSE
NDYQTAICENYQTMSETTFKALRRQLPVTRCKIDWKGKIIQYGIGRELKQQ

>CL2450.Contig1_Ba_mix

PPTTEAPPTTAAPTAAPEGGSRSSPVAGGPPPLGGSRSSPVAGGPPPPGSRSTPMAGG
PPPPMPGSRSTPMMSGPPALPESPKTPTVGIADPDFVIPDDIDLPLDLPPYDPNFFF
DYPPEPLPDTYLIDLILPPEQPDWPPP

>CL2677.Contig1_Ba_mix

REQGGKHQDGVYWFTGMPVPVYCDFSHDGGGWTLTLLTAVSADGWDALSALGRSRRS
PTLTDNYSILAHADAIRDLGHSARFAYRIEAQVETGRQRWGGVWLAPRHYSFIHESPS
QTDVTIVRKFDWEYKDIGIEKRMPWLSTDSAHDVLTTSASVSVEWWGTLVSHKT
HTYYKHSPWLNGE

>CL2236.Contig1_Ba_mix

LKLLQIALCLTCLGLIRNYGLAFGGSSGDALNRQLVGHACGGMVLVTAPLLIALVAGEI
AIEKSFLETLYNVVGFIMMITAGIMAVEFYNSFGSSETRDAGLAMGSLAINAIYLVDAF
VAFR

>CL7397.Contig1_Ba_mix

LRLSTSPSCGSESDGWLSKLLVRKIEPTKESHSRMLSDKEVIYELQTHNVRGEMDK
VPSTTTAATTARWPSGRPPASWPRSWSAAGRSPWATRTSASTCGSTTADTRPVDDA
RNAHIDDKSLAALVKERGTLRLRARHSQYLLAFSFWPAPAPRSGKHLYEIRSYLLKPGT
MIEWGNNWARAIHFRREGDEAFAGFFSQVGRLYNVHHLWCYDSMAHRKEIRETAW
RKPGWDECVAYTVPLITNFQSRIIVPTPFSPTR

>Unigene5246_Ba_mix

RLVSSLGLRLLSTSPSCGSESDGWLSKLLVRKIEPTKESHSRMLSDKEVIYELQTHNVR
CGEMDKYIDNYGRYHGEVAERTAAGQLAQELVGSWEVTVGDQDQCIHLWKYNGGYK
AVDDARNAHIDDKSLAALVKERGTLRLRARHSQYLLAFSFWPAPAPRSGKHLYEIRSYL
LKPGTMIEWGNNWARAIHFRREGDEAFAGFFSQVGRLYNVHHLWCYNDLQHRKET
RESAWLRPGWDECVAHTVPLIGGMQSRIMWANPFSPTQ

>CL9979.Contig1_Ba_mix

DSKFDIGLVLASFKKCGEDTGGSLTMDDYIAGYVELNKFFGLLGTVFGFVGSVDVHQLV
QLECLRKGGASDSYVTVERMILYEKQNGVFESDKAGNGCRTLLRLHRALAFIADFLRE
LHRSDEQKMGVCQASYKRTLAVHHPWLQVQGGALLAMHMLGTRGDIVEKAVGGDS
SDKEKHKDTLLECIDVMQAVYADTQKLYEQH

>CL7745.Contig1_Ba_mix

VVTGCSRGIGLAMVSELVKNFVKVFATCRNPASASQLSGLLTSLEQPAVALDVTDEA

SIQAAYGTVKEAAGRVDLLINNAGISVKTHPVDPCETAQLSELNRLLETNVGGLVRVTQ
VFLPLLRRASPRRVVNISLLGSIGVCKER GALAPDHFFSYRISKAAGNMATVAMSTAIT
EVEFLAVHPGWVATDMGNSSGRTADITVEESAEGVVREALRPQRRTGEFVDWRGNP
VPW

>CL2357.Contig1_Ba_mix

LKYAVGLAPSDPDSQPVMILGQIRHLARVSWDTIKVKLEPQVSEAVWQRAVSELPSP
TDSLHLYLNQATLAALPGKCSRHNTPSRAHSVTRLVRSLLTGADQTVVLCERADML
ATGCAVARALPLFTRKSGPQPEPTITVEVLVVDGEQASAEVQLMQDAARGIRLTARL
VDT PANEMHTDAFVEEVKKVGEELGVSLTLIRGEDLKARGFGGIYGVGKAAVHPPALA
ILSHTPAGATQSIWVGKIVYDTGGLSMKTKTTPMGMKRDLGGAAAILGAFLVTVKA
GFTQNLHAVFCLAENAVGPIATKPDDIHTLYSGRTVEINNTDAEGRLVLADGVAYANK
DLKCTTILDMATLTGAQGTATGKYHGALLTNEDTWEVLGAAAGRASGDLLFPVYTP
ELHFSEFASSVADMKNSAADRSNALVSCAGLFIAANLGFDFPGSWIHV

>CL2646.Contig1_Ba_mix

FSRPSPYLDGARTQHVSDFKYTRYQNQINGSVPTGAAGATDSVKVERRTKIVDKKTIGI
ALYGLGRAGVIHLGNLMINPRVSLVYTLSDQARYDAMKERWGD RMPPNVLPADSGT
VLADPRVDAVMVATPTHTHFDIIQQALLADKLVFSEKPIGENEQQARRCYQLAEQRGL
SVFCAFNRFRDPALQTVRSGVRRGDVGVVHTIKTVARDSPLPSIDFLRQSGGIFHDCAV
HDIDLICWILGQFPLRVLASASAHVPEIAALGDHDTAAIVMEFEGGTIGSIDLSRNAVY
YDQRTEVFGPGLLTAGNERPVNVHHLTSGGETAVPFYFSFPSRYSESYANELDSFLDY
VQGKIPLPIRPEDSLRVSQIASACEESLRTRAFVELDY

>Unigene34863_Ba_mix

RSQKVEILLDIQSVRSPDAWVPCNGAIYLSICLLGQYIRTKDKAPIFPINFNETFVVEKVF
GHVFRLADLDDMLDAEVVYLELIQRPPAGPDTVLASFETSARELLFP

>CL74.Contig3_Ba_mix

DADKQSGDVTCMRFHNGKLYTGAEGGKLIVYNPDLTIYKTMQAQFNTINAICFFQGDL
VTTGNDGLIKVWDSSSLELKKTLEGHENEVRVLKARDDKLFSGDMNGKVKIWDKNY
TMLFTLSVVEEVWSMDMARDIYTARCNDVTCTQIGFKEMSVPGETKFIILDTFEGRG
PMCIAGEHIIYTNREGTVLLVKENKPGHKHVNNMTGHEKIINALIYTDNLVYSAGYDG
MVKIWDGTTYKPVASGTTVGPNPVFSLGVGDNGEVYAGLNDGSI

>CL74.Contig5_Ba_mix

DADKQSGDVTCMRFHNGKLYTGAEGGKLIVYNPDLTIYKTMQAQFNTINAICFFQGDL
VTTGNDGLIKVWDSSSLELKKTLEGHENEVRVLKARDDKLFSGDMNGKVKIWDKNY
TMLFTLSVVEEVWSMDMARDIYTARCNDVTCTQIGFKEMSVPGETKFIILDTFEGRG
PMCIAGEHIIYTNREGTVLLVKENKPGHKHVNNMTGHEKIINALIYTDNLVYSAGYDG
MVKIWDGTTYKPVASGTTVGPNPVFSLGVGDNGEVYAGLNDGSI

>CL74.Contig6_Ba_mix

DADKQSGDVTCMRFHNGKLYTGAEGGKLIVYNPDLTIYKTMQAQFNTINAICFFQGDL

VTGNDGLIKVWDSSSLELKKTLEGHENEVRVLKARDDKLFSGDMNGKVKIWDKNY
TMLFTLSVVEEVWSMDMARDIYTARCNDVTCTQIGFKEMSVPGETKFIILDTFEGRG
PMCIAGEHIIYTNREGTVLLVKENKPGHKHVNNMTGHEKIINALIYTDNLVYSAGYDG
MVKIWDGTTYKPVASGTTVGNPVFSLGVGDNGEVYAGLNDGSI

>CL14828.Contig1_Ba_mix

MPVTLDTYLPSEQELTVEELNIGYPALKAGSFHLGKYCEAQRDEFMLCRQEEKDPRKC
LAEGRAVTSCELEFFRKVKSTCLDEFNQYANCLDRGSPDLKFRMCRNTQSVFDKCVQ
DNMGMERPYGYFCAPKVIRTNRPRPAPEPPLEFPNTPDELPTMPRKPAPY

>Unigene9033_Ba_mix

XGLVQQISNQAMYQYGAEAAACYSGQRLYEESCGELLRSPGFENWSYENRIIDGSVVPQ
HRDIQTD

>CL46.Contig1_Ba_mix

TQKNALEVHSPHCKYKADESRLILLSDPQRKKRSAPEAPAEDQQADAAMFYRSYR
YPAFGYTYPGVRILKKRAADPEKEEEDEKKKVVYINAMPYSSLGYPFYSYAPYIYKK

>Unigene11352_Ba_mix

XNHNSSQLTMKCVLLFAVWSCASAYYFVTPSAYYGGVSPYIWRKKRSAPEAPAEDQQ
ADAAMFYRSYRPAFGYTYPGVRILKKRAADPEKEEEDEKKKVVYINAMPYSSLGYPF
YSYAPYIYKK

>CL1824.Contig3_Ba_mix

XSMPQPASTGGLSYAVQNLGGYVIVNNEAVPVGFSATQPSGDWKS LGQMSVSACL
GTCYHGDGLFMMVQTVDGVTSWSSSSVDMGQLSQTVPSPAGAYEVFDISSMRIGSQ
MAVSHSSGFVVKSTAANKGYTDFDVTMPDKEESSELTIIYTSAPSSLQLFPMSEGHP
AECVASAMGMMCDVAIWNPSDPEKPCQCGQLINGGPLGLTDTSPDVAGYMEVIQLR
AMQPPADFEGLSYTMYDLFAGYFRLIVNYKALAVRFSGSEPAGNWKNLGHLSVSECL
DACYQGDGLFMMVQTMNDVTSCWSASLVDMSLLSREYPSGPGEYEILDISP MKIGSEN
TVTHSNGLVVTSTGIQNGYRAFTVTMPGTSFPELTVYYTSAPSSLRLLPVSSAQPAK
CVSSATLMLCDVAVWDPNNSDMPCQCCEIVEGETLGLTDTSPD TVGFVEVIQLIPMP
PPDVEPGHASFQSFWMTPVEYRLILNGEIIPASFARSAAVQAAAGVNLDR AIVKEACAT
TCFGLHYNGAALSHQTCRCLEDPSSVSSQQYVAGDDLVS LINFAKYQPKPDGSSSTIT
LQVPGTRYGRFLFGNAVLPCGFTPQNVDPSTGPPGSWKDAGERTGLRDCASECSKLQL
NFGAMLPLGKNIFKCWCAESVDMSAFSTAMPEVGGRAQILDFTDVIRGISSRLQIRHV

>CL2298.Contig1_Ba_mix

XLQSQAWRRLPAVPPLFCLQMCALRGYTYAAVGNSEDPTCDCSKRSPNEADLFRTAK
TDSDRQVFFLKGLPRIGKMSLVYVTENSFLQFIFSGTSAARPIVLYLRSAPPAGWTFRL
PSGGDSFPQKYRLLAYCPLMCRAQGFYAAVRFQPAGECCLGPAEVD AVRSDTSSSPD
GASPDSTIQIIQLGSLQGSAFPKE LLVLDRTSSGDQWSFSPRWITISIRLGAGLQGSLELE
GQTRS SVSLASGIPIKTPPVFIDASMAAIPKGFNIRGRLRISR DAGFFTS DLSQLSGQWQ
TVDAERNAECPQKCLEAGFSYAAMQTQTKRGWCKCALQLQNIDKYARRDSVKTGDIQ

VISLRRIGEKQLQVARLAELHRQAAIKAYKMIMQNPKWYRQVTVVSVPRTYGQNIGIA
SNPASCFCGCATSNFNAYFYTVYGCLCSNDKSDVKVVRPRYRSLKYFAAGRTSLFYIGR
VNRLKPSGTA AVIKGRKGYLILRSPNGRVQTGRFMAASLLQSQA WRRLPAVPPFLCLQ
MCALRGYTYAAVGN SKTQH VTAQELHQILLFRVWRS DSKQVFMLSGLPKAGKMT
SVTVMRGSFLQFTFSGT SAARPIVLYLRSAPPAGWTFRLPSGGDSFPQKYRLLAYCPLM
CRAQGF PYAAVRFQPAGCSCLGPAEVD AVRSDTSSSPDGASPDSTIQIIQLGSLQGA AIP
KELLVLDRTASGDQWSFX

>CL1824.Contig2_Ba_mix

XLINDGPLELTDTSVPRERGSLEVIQLRAMPP LAGELTAISYSVFEFIASYYRVIVNNDIV
PAGFSVSQPAGAWTSLGQMTISECIDTCSRES DFLMVRTVDNVTSCWSAPLVDMSLL
RQQFPSVSGEYQVLDLSVMKIGTKITVTHSAGFNVSSTGIKNGYRGYAVKMPDESE PSE
LTVYYTKSAPSSLQLFFMTEHYPGNCVASAMGMMCDVAIWNPSESEKPCQCGQLING
GPLGLTDTSVPDVAGYMEVIQLRAMQPPADFEGLSYTMYDLFAGYFRLIVNYKALAVR
FSGSEPAGNWKNLGHL SVSECLDAC

>Unigene5401_Ba_mix

PDQYAALIDDQSSNLTDPTVSAALDKSRQAQSMSTSSISSIRDGLYEGQSKLLVEIRDAL
GGSPSGKNLDDVITTMNALHNDLMH SVGTLVTAMSDTNAALQTIISKMDGGSKQDPF
REIGLLATDRPLHSGDPDTGAMYDCTFD DAAAYENLNRAIGIIRSTRTDPDDVVVIRF
SGVGLSIYMGDTAPPHSPDIWLTPVDRAATIGADSQMMIMLSTYTKQLGHDSL YKFI
VWGGGFMSLLRAVATNPNVAARVSIQKLGHLIANXACVNDCFFENLCTLFSNCRLSGC
SACLRVIVPAMVKRGRRGGSPSRGRGRVSTIVIPLDREDHATDGAGNAILPANNTVYAA
VTGEHILSAAPT VNGVRPSYARIRKITLDTTTGAALTTAGMGYYQAWRQYTVDPKTD
DIGGSIINAANKRPIPGSAGRFNYRNFPRFLGLSLMGVERQDVTINDKEPIYFAGVVYPD
ATPKPAVMLHIRAEFGGVA FVDSREPEVHSTTPHFDTNYGPDFLTRDFLASAMLALG
MTLGVL RDGVIMCERV

>CL166.Contig1_Ba_mix

XSHRFGGNSAYRSDEAHAYAAINPVVSNVRRAVGVSYSQGAPIVRSVSVEGPAPIAYSA
AAPITYSGLGYAGYHL

>CL4124.Contig1_Ba_mix

PLTALLAVLLLLALVYWYGTKDFGSLEKLGVPVIKPYPFISILKPWESFCVSDDLQNA
RKYGRLWGLYEGPWAQLFVADVDM AKHIMIKDFDHFQDRPVLFDFEYGRDQMDMM
PADRWKVLRSLLAPALTTSGRLKAMTPTMQQCLDDACRRMETKLRDSPVIDAQADL
FGPLTLDVMAQFSFGMKVPDVADKNSV FVKHASAFGVPTDATPNPLITYILTSFPSLG
NRVAGRQLIPAFRYFLEMIRRSIKQRR AEGVHRPDLVGVIMDAIDNKVPTAEYRQLRL
TEEILLLQGAEMLMAAYDTVGSALNKSAYFLATEPEAAEEVAQEAQELDELTYESVAQ
LPKLEAFI KEVLRMAPLLVRHFRVCTR DWEYQGLRVPAGTSVTIPMSV FHMDEQLFP
EARQFRPARWLEEDAHRSHQYSWMPFGLGPHACL GARLAMVECKFFLAGFLRRYRF
LACDQTKFEYLP GSGLFAT