

Supplementary Material S2. List of differentially expressed transcripts with annotation found in digestive gland tissue showing an expression change greater than 100-fold ( $|\log\text{FC}| > 2$ ).

UPREGULATED

<b>description</b>	<b>logFC</b>
nose resistant to fluoxetine protein 6	8.95
autocrine motility factor receptor	8.80
c1q domain containing protein 1q3	8.77
hypothetical protein CGI_10026086 [Crassostrea gigas]	7.86
cathepsin d	7.55
nacre protein	6.74
bcl2 adenovirus e1b 19-kd protein-interacting	6.60
proteasome beta 4 subunit	6.58
mytimacin- partial	6.42
endo- -beta-xylanase	6.38
c1q domain containing protein 1q25	6.36
cathepsin b	5.83
mantle gene 8	5.32
collagen alpha-5 chain	5.11
interferon-inducible gtpase 5-like	5.10
acetylcholinesterase	4.96
hypothetical protein CGI_10012557 [Crassostrea gigas]	4.72
deleted in malignant brain tumors 1	4.64
atpase h <sup>+</sup> transporting lysosomal 21 kda v0 subunit	4.50
superoxide dismutase	4.42
vitelline membrane outer layer protein 1 homolog	4.38
col protein	4.37
uncharacterized protein loc102449188	4.24
hypothetical protein CGI_10015342 [Crassostrea gigas]	4.24
proteasome subunit beta type-4	4.09
developmentally-regulated vdg3	3.98
cell adhesion molecule-related down-regulated by oncogenes-like	3.92
vdg3 [Mytilus edulis]	3.87
neurogenic locus notch homolog protein 2-like	3.85
transitional endoplasmic reticulum atpase	3.85
peptidylglycine alpha-amidating monooxygenase precursor	3.79
collagen alpha-4 chain	3.78
fibrinogen c domain-containing protein 1	3.76
c-binding protein	3.75
fibrinogen-like protein a	3.71
ankyrin repeat domain-containing protein 50	3.68

mytimycin precursor	3.67
gtpase imap family member 7-like	3.65
hypothetical protein CGI_10011963 [Crassostrea gigas]	3.58
cytoplasmic partial	3.54
uncharacterized protein loc101862413	3.53
kazal-like serine protease inhibitor domain-containing protein	3.53
type-2 ice-structuring	3.51
nidogen and egf-like domain-containing protein 1	3.49
hypothetical protein [Paramecium tetraurelia strain d4-2]	3.49
gtpase imap family member 4-like	3.48
hypothetical protein [Acinetobacter sp. ANC 3789]	3.42
peptidylglycine alpha-amidating monooxygenase	3.35
sec1 family domain-containing protein 2	3.35
fimbrial protein pilin	3.34
hypothetical protein CGI_10003274 [Crassostrea gigas]	3.34
partial	3.31
synaptosomal-associated protein 25	3.25
proline iminopeptidase	3.19
heavy metal-binding protein hip	3.17
uncharacterized protein loc101850813	3.14
jagged protein	3.13
apical endosomal glyco	3.11
low-density lipoprotein receptor-related protein 6	3.02
nc domain-containing protein	3.02
component of the counting factor complex	3.00
hypothetical protein CGI_10020658 [Crassostrea gigas]	2.99
nfx1-type zinc finger-containing protein 1	2.99
apoptosis inhibitor iap	2.99
mammalian ependymin-related protein 1	2.98
si:ch211- protein	2.94
hypothetical protein BRAFLDRAFT_106560 [Branchiostoma floridae]	2.91
nattectin precursor	2.89
mytilin-1	2.88
hypothetical protein CGI_10012644 [Crassostrea gigas]	2.86
endo- -beta-d-glucanase	2.85
peroxisomal proliferator-activated receptor a-interacting complex 285 kda	2.83
fibrinogen-related protein	2.83
rab gdp dissociation inhibitor beta	2.79
nadh dehydrogenase subunit 6	2.79
pancreatic secretory granule membrane major glycoprotein gp2	2.78
peptidyl-glycine alpha-amidating monooxygenase-like	2.70
oncoprotein-induced transcript 3 protein	2.66
heat shock 70 kda protein 12b	2.66

daz interacting protein zinc finger-like	2.65
complement c1q tumor necrosis factor-related protein 3	2.60
neuronal nitric oxidse synthase protein	2.59
uncharacterized protein loc580197	2.59
hypothetical protein BRAFLDRAFT_79532 [Branchiostoma floridae]	2.59
predicted protein [Nematostella vectensis]	2.58
60 kda ss-a ro ribonucleoprotein	2.53
propionyl- carboxylase alpha mitochondrial	2.53
succinate dehydrogenase	2.51
hypothetical protein DAPPUDRAFT_255671 [Daphnia pulex]	2.50
elongation factor 2	2.47
sialic acid binding lectin	2.47
syringomycin biosynthesis enzyme	2.42
protocadherin fat 4-like	2.41
phenylalanine hydroxylase	2.40
PREDICTED: neuroglian-like [Acyrtosiphon pisum]	2.38
hypothetical protein CGI_10013901 [Crassostrea gigas]	2.36
low affinity immunoglobulin epsilon fc receptor	2.35
vitelline membrane outer layer protein 1	2.34
group xvi phospholipase a2	2.32
gtpase imap family member 4	2.28
hypothetical protein CGI_10014841 [Crassostrea gigas]	2.26
gtpase imap family member 8-like	2.26
uncharacterized protein loc585517 isoform 2	2.25
translational elongation factor-2	2.19
virion core protein (lumpy skin disease virus)	2.19
tartrate-resistant acid phosphatase type 5	2.17
complement c1q-like protein 4	2.12
endoglucanase [Mizuhopecten yessoensis]	2.11
interferon alpha-inducible protein 27-like protein 2-like	2.09
complement c1q tumor necrosis factor-related protein 8	2.09
microtubule-associated protein futsch	2.08
Titin [Crassostrea gigas]	2.05
ankyrin unc44	2.05
jagged 1-like	2.04
3-hydroxyisobutyrate mitochondrial-like	2.03
hypothetical protein CGI_10008425 [Crassostrea gigas]	2.01

DOWNREGULATED

description	logFC
sodium-dependent neutral amino acid transporter b at2-like	-2.01
alpha-tubulin	-2.04

ribonucleoside-diphosphate reductase subunit m2-like	-2.05
ribonucleotide reductase m2 polypeptide	-2.06
alpha- -mannosyl-glycoprotein 4-beta-n-acetylglucosaminyltransferase b	-2.10
kex2p	-2.13
gastrointestinal growth factor xp4-like	-2.14
vitelline envelope zona pellucida domain protein 14	-2.26
kif21a protein	-2.29
reticulon-like protein	-2.30
phosphatidylinositol-binding clathrin assembly	-2.31
low quality protein: solute carrier organic anion transporter family member 5a1	-2.39
zona pellucida domain-containing protein 1	-2.41
conserved protein	-2.47
cytokine induced apoptosis inhibitor 1	-2.62
hypothetical protein LOTGIDRAFT_155380 [Lottia gigantea]	-2.71
hypothetical protein [Vibrio anguillarum]	-2.78
schlafen family member 13	-2.88
hypothetical protein CGI_10008221 [Crassostrea gigas]	-3.04
microsomal glutathione s-transferase 3-like protein	-3.21
dna-directed rna polymerase	-3.46
starch-binding domain-containing protein 1	-3.48
hypothetical protein [Butyrivimonas synergistica]	-3.77
peroxisomal acyl-coenzyme a oxidase 2	-4.18
probable small nuclear ribonucleoprotein sm d2-like	-5.05
achain reduced peptidylglycine alpha-hydroxylating monooxygenase	-5.76