

Supplementary material

Supplementary Table 1a-b. RT-qPCR-Primers

a. Primer sequences for real-time q-PCR assays for transcripts expressed differentially in response to broodstock nutritional history (COM - VEG)

<i>Gene</i>	<i>Primer 5'-3' (FW)</i>	<i>Primer 5'-3' (RV)</i>	<i>Annealing temperature, C°</i>
Muscle growth/contraction			
ACTA1	AAAACAGGCCAGGGACAACA	CCTGGTATTGCTGCCCCTAT	60
CKM	TGCGTTGGTCTGAAAAGGATTGA	TCTCCTCAAACCTGGGGTGTGT	60
MYBPC1	CCAGCATCCAGAACCATCCT	TACACTGGGGAAGGTCGACA	60
MYBPC2	GTGAGTGTCCGTTTGTGTC	CTGCCAAGTGAGACTGACGT	60
Carbohydrate/energy metabolism			
PYGM	TGCAATGTGTGTCGGTGTG	AAGTTCCTGGAGACCACGA	60
PYGL	AACCGACACCTCCACTTCACC	CCTGCATCTTCCTCCATCTC	60
6PFKM	GAGGGCGAAGATGAAGCTTG	GGGACCTCGAGATGAACGTA	60
SDHA	TGGTGTGTTGGACGTGCCTGC	AACACAGCGGCGTGGTTCTG	60
GPD1	CTTCGCCCCGATATTCTGCA	GACCCTGGAGCTTCTGCCCA	60
PGK1	TTCGGCACAGCACACAGAGC	AAAGGGCCTGGCTGGTTTCTCC	60
Reference gene			
<i>EF1-α</i>	TCCTCTTGGTCGTTTCGCTG	ACCCGAGGGACATCCTGTG	59

ACTA1, actin-alpha 1; CKM, creatin kinase muscle; MYBPC1, myosin binding protein-C slow type; MYBPC2, myosin binding protein-C fast type; PYGM, phosphorylase glycogen muscle; PYGL, phosphorylase glycogen liver; 6PFKM, 6-phosphofructokinase muscle; SDHA, succinate dehydrogenase complex, subunit A, flavoprotein; GPD1, glycerol-3-phosphate dehydrogenase 1; PGK1, phosphoglycerate kinase 1; EF1-α, α-elongation factor-1

b. Primer sequences for real-time q-PCR assays for transcripts expressed differentially in response to first feeding diets (M-C-V)

<i>Gene</i>	<i>Primer 5'-3' (FW)</i>	<i>Primer 5'-3' (RV)</i>	<i>Annealing temperature, C°</i>
Carbohydrate metabolism			
GCK	GCACGGCTGAGATGCTCTTTG	GCCTTGAACCCTTTGGTCCAG	60
HK2	CGCCGTGGTCGATAAGAT	TGATGAGAGCCGCCCTTT	60
LDHA	ATGCGTGCTGGGCAACAGTG	GCTGATAAATTAACCCTCCGC	60
Lipid/cholesterol metabolism			
HMGCR	GAACGGTGAATGTGCTGTGT	GACCATTTGGGAGCTTGTGT	60
HMGCS1	AGTGGCAAAGAGAGGGTGTG	TTCTGGTTGGAGACGAGGAG	60
Amino acids/protein metabolism			
DARS	GACCTGGCGGACATTGTGAA	GAGAGGGCCATTCACCACAA	60
EPRS	GTCGTCTGATGCCCTCTTGA	TGAAGCAGGGTCAGTGTGTG	60
IARS	ACATCGTGACTCGCTTCGCC	CTACAACCGTCAGATACGCGG	60
LARS	CGGCAGTGACATGAATGCAG	CCACTGGCCACAATGCTTTC	60
Reference gene			
<i>EF1-α</i>	TCCTCTTGGTCGTTTCGCTG	ACCCGAGGGACATCCTGTG	59

GCK, glucokinase; HK2, hexokinase-2; LDHA, lactate dehydrogenase-A; HMGCR, 3-hydroxy-3-methylglutaryl-CoA reductase; HMGCS1, 3-hydroxy-3-methylglutaryl-CoA synthetase ; DARS, aspartyl-

tRNA synthetase ; EPRS, glutamyl-tRNA synthetase ; IARS, isoleucyl-tRNA synthetase ; LARS, leucyl-tRNA synthetase; EF1- α , α -elongation factor-1

Supplementary Table 2. Global effects of different first feeding diets on whole body transcriptome of alevins after three weeks of feeding.

Probe Name	Gene Symbol	Description	Fold change (FC)				p-value
			COM-C/COM-M	COM-V/COM-M	VEG-C/VEG-M	VEG-V/VEG-M	
<u>Biological Process</u>							
<i>Amino acids/protein metabolism</i>							
TC105786	AARS	alanyl-tRNA synthetase	+ 1.1	+ 1.4	+ 1.0	+ 1.3	0.046
CUST_8078_PI425536763	EPRS	glutamyl-prolyl-tRNA synthetase	+ 1.0	+ 1.4	+ 1.1	+ 1.4	0.002
CUST_5873_PI425536763	DARS	aspartyl-tRNA synthetase	+ 1.1	+ 1.5	+ 1.0	+ 1.2	0.001
CUST_11065_PI425536763	HARS	histidyl-tRNA synthetase	+ 1.1	+ 1.6	+ 1.0	+ 1.9	0.001
CUST_9823_PI425536763	IARS	isoleucyl-tRNA synthetase	+ 1.6	+ 1.6	+ 1.3	+ 3.1	0.037
TC99236	LARS	leucyl-tRNA synthetase	+ 1.1	+ 1.3	+ 1.1	+ 1.2	0.017
CUST_2969_PI425536763	NARS	asparaginyl-tRNA synthetase	+ 1.2	+ 1.7	+ 1.1	+ 1.3	0.001
TC113600	QARS	glutaminyl-tRNA synthetase	+ 1.2	+ 1.5	+ 1.1	+ 1.3	0.007
CUST_1945_PI425536763	SARS	seryl-tRNA synthetase	+ 1.1	+ 1.6	+ 1.0	+ 1.5	0.001
CUST_27479_PI425536763	TARS	threonyl-tRNA synthetase	+ 1.2	+ 1.6	+ 1.1	+ 1.3	0.025
CUST_6009_PI425536763	WARS	tryptophanyl-tRNA synthetase	+ 1.2	+ 1.6	+ 1.1	+ 1.2	0.016
TC108527	PHGDH	dehydrogenase	+ 1.3	+ 4.3	- 1.1	+ 2.2	<0.001
CUST_5305_PI425536763	EEF1E1	eukaryotic translation elongation factor 1 epsilon 1	+ 1.1	+ 1.5	+ 1.1	+ 1.3	0.007
TC97482	EIF2B1	eukaryotic translation initiation factor 2B, subunit 1 alpha	+ 1.1	+ 1.6	+ 1.2	+ 1.2	0.005
CUST_14068_PI425536763	EIF2B3	eukaryotic translation initiation factor 2B, subunit 3 gamma	+ 1.0	+ 1.6	+ 1.1	+ 1.4	0.015
TC95289	EIF2S2	eukaryotic translation initiation factor 2, subunit 2 beta	- 1.1	+ 2.8	+ 1.0	+ 1.9	<0.001

Probe Name	Gene Symbol	Description	Fold change (FC)				p-value
			COM-C/COM-M	COM-V/COM-M	VEG-C/VEG-M	VEG-V/VEG-M	
<i>Cholesterol/ Lipid metabolism</i>							
<i>CUST_16218_PI425536763</i>	HMGCR	3-hydroxy-3-methylglutaryl-CoA reductase	+ 1.5	+ 1.7	+ 1.4	+ 1.4	0.035
<i>TC114256</i>	HMGCS1	3-hydroxy-3-methylglutaryl-CoA synthase 1 (soluble)	+ 1.7	+ 2.1	+ 1.2	+ 1.3	0.004
<i>CUST_8711_PI425536763</i>	SQLE	squalene epoxidase	+ 1.6	+ 1.7	+ 1.5	+ 1.6	<i>0.009</i>
<i>TC121390</i>	CYB5R2	cytochrome b5 reductase 2	+ 1.4	+ 1.5	+ 1.3	+ 1.4	<i>0.011</i>
<i>CUST_2668_PI425536763</i>	CYP2F1	cytochrome P450, family 2, subfamily F, polypeptide 1	- 1.0	- 2.3	- 1.5	- 2.3	<i>0.003</i>
<i>TC121294</i>	CYP51A1	cytochrome P450, family 51, subfamily A, polypeptide 1	+ 1.5	+ 1.9	+ 1.5	+ 1.6	<i>0.001</i>
<i>TC112425</i>	CYP46A1	cytochrome P450, family 46, subfamily A, polypeptide 1	+ 1.0	- 1.3	+ 1.3	- 1.5	<i>0.005</i>
<i>TC107840</i>	IDI1	isopentenyl-diphosphate delta isomerase 1	+ 1.6	+ 1.7	+ 1.2	+ 1.4	<i>0.006</i>
<i>TC130899</i>	INSIG1	insulin induced gene 1	+ 1.3	+ 1.7	+ 1.0	+ 1.3	<i>0.003</i>
<i>CUST_12877_PI425536763</i>	INSIG2	insulin induced gene 2	+ 1.5	+ 1.7	+ 1.2	+ 1.2	<i>0.029</i>
<i>CUST_5335_PI425536763</i>	MVD	mevalonate (diphospho) decarboxylase	+ 1.6	+ 1.9	+ 1.1	+ 1.3	<i>0.026</i>
<i>CUST_28240_PI425536763</i>	LSS	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	+ 1.6	+ 1.9	+ 1.3	+ 1.0	<i>0.007</i>
<i>CUST_16670_PI425536763</i>	HSD17B7	hydroxysteroid (17-beta) dehydrogenase 7	+ 1.3	+ 1.7	+ 1.2	+ 1.4	<i>0.011</i>

Probe Name	Gene Symbol	Description	Fold change (FC)				p-value
			COM-C/COM-M	COM-V/COM-M	VEG-C/VEG-M	VEG-V/VEG-M	
Carbohydrate/ Energy metabolism							
CUST_8779_PI425536763	ENO1	enolase 1, (alpha)	- 1.0	- 1.5	- 1.3	- 1.7	0.004
CUST_21534_PI425536763	ENO2	enolase 2 (gamma, neuronal)	+ 1.0	+ 1.5	+ 1.5	+ 1.4	0.012
CUST_21688_PI425536763	ENO3	enolase 3, beta muscle	- 1.0	- 1.5	- 1.3	- 1.7	0.046
CUST_6475_PI425536763	GCK	glucokinase (hexokinase 4)	- 1.5	- 2.1	- 1.4	- 1.6	0.031
CUST_2361_PI425536763	HK2	hexokinase 2	+ 1.1	+ 1.3	+ 1.2	+ 1.2	0.017
CUST_21617_PI425536763	LDHA	lactate dehydrogenase A	- 1.1	- 1.7	- 1.3	- 1.9	0.043
CUST_21434_PI425536763	LDHB	lactate dehydrogenase B	- 1.0	- 1.9	- 1.3	- 1.7	0.030
TC95453	G6PC	glucose-6-phosphatase, catalytic subunit	- 1.4	- 2.7	- 1.2	- 1.7	0.012
CUST_11963_PI425536763	GSK3A	glycogen synthase kinase 3 alpha	+ 1.1	+ 1.3	+ 1.3	+ 1.4	0.012
CUST_8266_PI425536763	ATP5C1	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, gamma polypeptide 1	+ 1.1	- 1.2	+ 1.1	- 1.3	0.011
CUST_5461_PI425536763	ATP5J	ATP synthase, H ⁺ transporting, mitochondrial Fo complex, subunit F6	- 1.1	- 1.2	- 1.2	- 1.3	0.047
Muscle contraction							
CUST_8882_PI425536763	ACTA1	actin, alpha 1, skeletal muscle	- 1.1	- 1.4	-1.0	- 1.3	0.017
CUST_7817_PI425536763	ACTN2	actinin, alpha 2	- 1.1	- 1.3	- 1.2	- 1.3	0.025
CUST_18923_PI425536763	GAMT	guanidinoacetate N- methyltransferase	+ 1.1	- 1.7	+ 1.0	- 2.0	0.027
TC102031	TCAP	titin-cap	- 1.2	+ 1.9	+ 1.0	+ 1.7	0.017
TC96295	TNNI2	troponin I type 2 (skeletal, fast)	- 1.2	- 1.6	- 1.1	- 1.5	0.027
CUST_20992_PI425536763	TNNT2	troponin T type 2 (cardiac)	- 1.2	- 1.5	- 1.3	- 1.7	0.002

Probe Name	Gene Symbol	Description	Fold change (FC)				p-value
			COM-C/COM-M	COM-V/COM-M	VEG-C/VEG-M	VEG-V/VEG-M	
<i>CUST_8764_PI425536763</i>	TNNT3	troponin T type 3 (skeletal, fast)	- 1.1	- 1.5	- 1.3	- 1.6	<i>0.001</i>
<i>Transport and Catabolism</i>							
<i>CUST_23987_PI425536763</i>	SLC3A2	solute carrier family 3 (amino acid transporter heavy chain), member 2	+ 1.0	+ 1.9	+ 1.3	+ 2.6	<i><0.001</i>
<i>TC120357</i>	SLC15A1	solute carrier family 15 (oligopeptide transporter), member 1		- 2.4	- 1.6	- 2.5	<i>< 0.001</i>
<i>CUST_27328_PI425536763</i>	SLC1A4		+ 1.0	+ 4.0	+ 1.2	+ 3.2	<i>< 0.001</i>
<i>TC119001</i>	NXT2	nuclear transport factor 2-like export factor 2	+ 1.3	+ 1.9	+ 1.1	+ 1.2	<i>0.005</i>
<i>TC98320</i>	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10,	+ 1.0	+ 1.4	+ 1.0	+ 1.8	<i>0.045</i>
<i>CUST_8732_PI425536763</i>	CAPN3	calpain 3	+ 1.1	- 1.2	+ 1.1	- 1.3	<i>0.048</i>
<i>TC128968</i>	CASP8	caspase 8, apoptosis-related cysteine peptidase	+ 1.0	+ 1.5	+ 1.5	+ 1.8	<i>0.036</i>
<i>TC103006</i>	CHIA	chitinase, acidic	- 1.3	- 1.9	- 1.3	- 1.7	<i>0.035</i>
<i>TC118835</i>	ACR	Acrosin	- 1.1	+ 1.9	+ 1.1	+ 1.5	<i><0.001</i>
<i>Oxidation-reduction process</i>							
<i>CUST_8851_PI425536763</i>	MTHFD2	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase	- 1.2	+ 2.2	+ 1.4	+ 2.1	<i><0.001</i>

Probe Name	Gene Symbol	Description	Fold change (FC)				p-value
			COM-C/COM-M	COM-V/COM-M	VEG-C/VEG-M	VEG-V/VEG-M	
<i>CUST_9084_PI425536763</i>	DHODH	dihydroorotate dehydrogenase (quinone)	+ 1.4	+ 1.5	+ 1.1	+ 1.4	0.002
<i>CUST_7365_PI425536763</i>	COX15	cytochrome c oxidase assembly homologue 15 (yeast)	+ 1.0	+ 1.8	- 1.1	+ 1.1	0.026
<i>CUST_4068_PI425536763</i>	NDUFS7	NADH dehydrogenase (ubiquinone) Fe-S protein 7, 20kDa (NADH-coenzyme Q reductase)	- 1.1	- 1.2	- 1.1	- 1.2	0.047
<i>CUST_9914_PI425536763</i>	TM7SF2	transmembrane 7 superfamily member 2	+ 2.0	+ 2.2	+ 1.5	+ 1.6	0.001
<i>CUST_3410_PI425536763</i>	MDH1	malate dehydrogenase 1, NAD (soluble)	- 1.1	- 1.3	- 1.3	- 1.4	0.023
Transcription/Translation							
<i>CUST_7617_PI425536763</i>	ATF3	activating transcription factor 3	- 1.1	+ 2.4	+ 1.2	+ 2.8	<0.001
<i>TC117725</i>	ATF4	activating transcription factor 4	+ 1.0	+ 2.2	+ 1.3	+ 2.8	<0.001
<i>CUST_28448_PI425536763</i>	ATF5	activating transcription factor 5	+ 1.2	+ 2.4	+ 1.3	+ 2.5	0.011
<i>CUST_13247_PI425536763</i>	CEBPB	CCAAT/enhancer binding protein (C/EBP), beta	+ 1.4	+ 2.1	- 1.0	+ 1.6	<0.001
<i>CUST_20799_PI425536763</i>	MEF2C	myocyte enhancer factor 2C	+ 1.2	+ 1.4	+ 1.0	+ 1.4	0.035
<i>TC127379</i>	MAP2K6	mitogen-activated protein kinase kinase 6	- 1.2	- 1.3	- 1.1	-1.4	0.025
Apoptotic process							
<i>TC119464</i>	GADD45G	growth arrest and DNA-damage-inducible, gamma	+ 1.0	+ 1.7	+ 1.1	+ 1.4	0.035
<i>TC113845</i>	NMT1	N-myristoyltransferase 1	+ 1.1	+ 3.4	+ 1.2	+ 2.7	<0.001

Probe Name	Gene Symbol	Description	Fold change (FC)				p-value
			COM-C/COM-M	COM-V/COM-M	VEG-C/VEG-M	VEG-V/VEG-M	
Trans-sulfuration pathways							
TC129723	CBS	cystathionine-beta-synthase	+ 1.7	+ 2.9	+ 1.2	+ 1.7	0.020
CUST_5923_PI425536763	CTH	cystathionase (cystathionine gamma-lyase)	+ 1.2	+ 1.7	+ 1.2	+ 1.2	0.035
Others							
CUST_5617_PI425536763	FBLN2	fibulin 2	+ 1.1	+ 1.4	+ 1.0	+ 1.2	0.021
TC111317	LCT	Lactase	- 1.5	- 4.7	- 2.6	- 4.8	<0.001
CUST_3595_PI425536763	ADK	adenylate kinase	+ 1.1	- 1.2	+ 1.0	- 1.3	0.030
CUST_28134_PI425536763	FBXO25	F-box protein 25	- 2.3	- 2.3	- 1.7	- 1.6	0.041
TC104210	MEP1A	meprin 1 alpha	- 1.5	- 6.1	+ 1.0	- 2.5	<0.001
CUST_2492_PI425536763	CCRN4L	CCR4 carbon catabolite repression 4-like (<i>S. cerevisiae</i>)	+ 1.0	+ 1.3	+ 1.0	+ 1.3	0.011
TC95024	HAGH	hydroxyacylglutathione hydrolase	+ 1.0	+ 1.4	+ 1.0	+ 1.5	0.043
TC95784	HMGB3	high mobility group box 3	+ 1.1	+ 1.9	+ 1.0	+ 1.4	<0.001
CUST_5459_PI425536763	RAB15	RAB15, member RAS oncogene family	- 1.2	+ 1.9	+ 1.2	+ 2.4	0.036
TC112850	RGN	regucalcin (senescence marker protein-30)	- 1.2	+ 1.3	+ 1.3	+ 4.3	0.002
CUST_577_PI425536763	SMYD1	SET and MYND domain containing 1	- 1.1	- 1.3	- 1.2	- 1.5	0.021
TC108261	TP53BP1	tumor protein p53 binding protein 1	+ 1.0	+ 1.4	- 1.0	+ 1.2	0.047
TC119917	XBP1	X-box binding protein 1	+ 1.0	+ 1.7	+ 1.0	+ 1.4	0.005
TC110767	PISD	phosphatidylserine decarboxylase	+ 1.4	+ 1.8	+ 1.4	+ 1.7	0.009

Probe Name	Gene Symbol	Description	Fold change (FC)				<i>p</i> -value
			<i>COM-C/COM-M</i>	<i>COM-V/COM-M</i>	<i>VEG-C/VEG-M</i>	<i>VEG-V/VEG-M</i>	
<i>TC95665</i>	EBP	emopamil binding protein	+ 1.5	+ 1.6	+ 1.4	+ 1.3	<i>0.018</i>
<i>CUST_8110_PI425536763</i>	TPI	triose phosphate isomerase apolipoprotein B mRNA	- 1.1	- 1.6	- 1.1	+ 1.3	<i>0.046</i>
<i>TC118127</i>	APOBEC2	editing enzyme, catalytic polypeptide-like 2	+ 1.3	+ 1.3	+ 1.2	+ 1.1	<i>0.027</i>
<i>TC108960</i>	GLA	galactosidase, alpha	+ 1.0	+ 1.7	+ 1.1	+ 1.9	<i>0.009</i>
<i>TC109455</i>	FDPS	farnesyl diphosphate synthase	+ 1.6	+ 2.5	+ 1.3	+ 1.5	<i>0.010</i>
<i>CUST_27735_PI425536763</i>	FN1	fibronectin 1	- 1.0	+ 1.7	+ 1.3	+ 2.7	<i>0.015</i>

Genes tested by RT-qPCR are in bold. Fold changes refer to progeny fed C or V-diet compared to fish fed the M diet.