

Table S1. Sequences of primer pairs used in qPCR analyses of transcript expression levels in lumpfish (*Cyclopterus lumpus*) larvae.

Gene name (symbol) ^a	Trinity ID from NCBI SRA acc. no. SRP238224	Nucleotide sequence (5'-3')	Amplicon Size (bp)	Efficiency (%)
C-C motif chemokine-like 19 (<i>ccl19</i>)	DN10492_c0_g1_i4	F: GCTCAGGTACCAACGGACTG R: CGTGTCTCCGATCTGTCTC	94	94.33
cyclooxygenase-2 (<i>cox2</i>)	DN750_c1_g1_i1	F: GAATTCCTCACCTGGGTCAA R: ATGGCATCTCTGAGGAAGGA	122	99.18
hepcidin anti-microbial peptide (<i>hamp</i>)	DN2993_c0_g1_i4	F: GCTCGCCTTTATTTGCATTC R: ATATGCCGCAACTGGAGTGT	100	93.36
interleukin 8_a (<i>il8a</i>)	DN21169_c0_g1_i2	F: AAGTCATAGCCGGACTGTCG R: CCCTGCTGATGGAGTTGTCT	109	100.39
interleukin 8_b (<i>il8b</i>)	DN4613_c0_g1_i4	F: GTCTGAGAAGCCTGGGAGTG R: TCAGAGTGGCAATGATCTCG	138	98.15
interleukin 10 (<i>il10</i>)	DN41536_c0_g1_i1	F: AACCAGTGCTGTCGTTTCGT R: TGTCCAAGTCATCGTTTGCT	106	95.24
ATP-dependent RNA helicase lgp2 (<i>lgp2</i>)	DN49186_c0_g1_i1	F: GCAACCTGGTGGTACGCTAT R: CTCGGCGACCACTGAATACT	104	81.54
interferon-induced GTP-binding protein_a (<i>mxα</i>)	DN526_c0_g1_i6	F: TGCACAGACTCAAGCAGAGC R: CCACACTTGAGCTCCTCTCC	144	85.43
interferon-induced GTP-binding protein_b (<i>mxβ</i>)	DN526_c0_g1_i3	F: TTGCGGCTTGAAAAATATC R: TCCACGGTACCTTCGTTTCAT	95	92.78
interferon-induced GTP-binding protein_c (<i>mxγ</i>)	DN237_c1_g1_i1	F: GGAAGTGGCAGACATTGTGA R: CTGCTGCAATCTCCTTCTCC	131	90.70
signal transducer and activator of transcription 1 (<i>stat1</i>)	DN3250_c2_g1_i2	F: CTCAAGATGCTGGACTGCAA R: ATGCTCTCGATCCACTTGCT	104	84.99
toll-like receptor 3 (<i>tlr3</i>)	DN30532_c0_g1_i1	F: AGAGGGCAGGGAATTTGAGT R: TGCACGAGTCATTCTCCAAG	101	90.29

C-C motif chemokine-like 20 (<i>ccl20</i>)	DN9266_c0_g1_i3	F: ATGGGCTACACCATCCAGAC R: CCACTTGGATGAAGGGTCAG	102	80.07
immunoglobulin heavy chain variable region a (<i>igha</i>)	DN1665_c0_g3_i2	F: AGGACTGGAGTGGATTGGAA R: TGCATGGTCTGTCCGTTTAG	129	91.00
immunoglobulin heavy chain_b (<i>ighb</i>)	DN1665_c0_g4_i1	F: GAATGGAACAAGGGGACAAA R: CGGTCGTTGAGTCTCTCCTC	108	90.60
interferon regulatory factor 7 (<i>irf7</i>)	DN6933_c0_g1_i2	F: GGCTCATAGAGCAGGTGGAG R: CTGTCTTCGTCGTTGCAGTC	115	81.89
HLA class II histocompatibility antigen gamma chain (<i>cd74</i>)	DN13708_c0_g1_i6	F: ACGCCAAGACACCTCTGACT R: GGAAGGTCTCGTTGAACTGC	108	96.45
serum amyloid A 5 (<i>saa5</i>)	DN41536_c0_g1_i1	F: AGAGTGGGTGCAGGAAAGAA R: GAAGTCCTGGTGGCCTGTAA	116	95.9
T-cell surface glycoprotein CD4_a (<i>cd4a</i>) ^c	DN9678_c0_g2_i9	F: CGTTAAGGTGCTGCAGATCA R: GCGGAAACCATTTCAGTTGT	122	84.85
T-cell surface glycoprotein CD4_b (<i>cd4b</i>) ^c	DN24146_c0_g1_i7	F: TGTGGGGTTAGCTCCTTCAC R: TGTTTGCATCTCACCTTTG	138	94.24
interleukin 1 beta (<i>il1b</i>) ^c	DN22448_c0_g2_i1	F: ATTGTGTTTCGAGCTCGGTTTC R: CGAACTATGGTCCGCTTCTC	98	97.37
toll-like receptor 5_a (<i>tlr5a</i>) ^c	DN29432_c0_g1_i1	F: TGGACGAGTTTCAGCAGTTG R: AGACCCCTCACATGTCCAAG	129	95.58
toll-like receptor 5_b (<i>tlr5b</i>) ^c	DN55824_c0_g1_i5	F: CCATCATGCACCTTTGTACGG R: TGCTGTTGATCTCCCTGATG	127	88.57
tumour necrosis factor alpha (<i>tfa</i>) ^c	DN26791_c0_g1_i1	F: TTAGAAGGGAGCTGCGAAGA R: ATGACGATCCGGTTGTTCTC	119	90.06
lymphocyte antigen 6 complex locus protein G6f (<i>ly6g6f</i>) ^c	DN12606_c0_g1_i8	F: TCCATGTGGACGTGACTGTT R: AACGGTGTCTGAGCCTGAGT	100	88.17
T-cell surface glycoprotein CD8 alpha chain (<i>cd8a</i>) ^c	DN11791_c0_g1_i1	F: GCTTTGCTCTCTGGGCATAC R: TCCGGGTTCTTAAGTGGTTG	104	89.62
immunoglobulin mu heavy chain_a (<i>ighma</i>) ^c	DN121_c0_g3_i3	F: CAGCTTCTGGATTAGACTTTGA R: GATGTTGTTACTGTTGTGTTGG	107	90.17
immunoglobulin mu heavy chain_c (<i>ighmc</i>) ^c	DN121_c0_g3_i4	F: CAACATCCGGAATCACATTGAG R: GATTTTGAGGTCCCACTACCAT	112	87.68

interferon gamma (<i>ifg</i>) ^c	DN81754_c0_g1_i1	F: CTCTGGCTGGTTGTCTGTCA R: TCGCTCTCTCGATGGAATCT	105	90.75
immunoglobulin delta heavy chain (<i>ighd</i>) ^c	DN1665_c0_g2_i7	F: GGAGACAGTGTGTGCTGGA R: GGGCTTCAGGAAATCAACA	121	88.41
toll-like receptor 7 (<i>tlr7</i>) ^c	DN760_c1_g2_i1	F: GGCAAACCTGGAAGAATTGGA R: GAAGGGATTTGAGGGAGGAG	100	90.55
radical S-adenosyl methionine domain containing protein 2 / viperin (<i>rsad2</i>) ^c	DN16769_c0_g1_i1	F: AGGAGAGGGTGAAGGGAGAG R: ATCCAGAGGCAGGACAAATG	133	98.47
Normaliser^b				
eukaryotic translation initiation factor 3 subunit D (<i>etif3d</i>)	DN7623_c0_g1_i5	F: AGCCAGATCAACCTGAGCAT R: AGGCTGTACACCCGAATCAC	134	86.49
60S ribosomal protein L32 (<i>rpl32</i>)	DN3569_c0_g1_i2	F: GTAAGCCCAGGGGTATCGAC R: GGGCAGCATGTACTTGGTCT	107	80.08
elongation factor 1 alpha_a (<i>ef1a_a</i>)	DN12280_c0_g1_i3	F: CAAGGGATGGAAGATTGAGC R: TGTTCCGATACCTCCGATTT	151	83.81
elongation factor 1 alpha_c (<i>ef1a_c</i>)	DN12280_c0_g1_i4	F: AAGCGCTTTGAGGAAATCACC R: GCTCGACCTTCCAACCTTG	160	*95.60
polyadenylate-binding protein 1_a (<i>pabpc1_a</i>)	DN6565_c0_g2_i3, DN6565_c0_g2_i4	F: CAAGAACTTTGGGGAGGACA R: TGACAAAGCCAAATCCCTTC	125	84.76
polyadenylate-binding protein 1_b (<i>pabpc1_b</i>)	DN6565_c0_g2_i5	F: GACTCAGGAGGCAGCTGAAC R: TCGCGCTCTTTACGAGATTT	102	88.11

*4-pt standard curve

^aExpression levels of the transcripts of interest were normalized to expression levels of these two transcripts.

^bCandidate endogenous control transcripts

^cExpression levels of these transcripts were low in lumpfish larvae; efficiencies are those reported for lumpfish head kidney (Gnanagobal et al., submitted).