

Table S1 Formulation and proximate composition of experimental diets

Ingredient/%	6% (Con)	12% (HFD)	Nutritional value (% dry matter)	6% (Con)	12% (HFD)
Fish meal	55	55	Dry matter, DM	87.001	88.216
Vital wheat gluten	4	4	Crude protein, CP	45.131	45.131
Soybean protein concentrate	6	6	Ether extract, EE	6.07	12.048
$\alpha$ -Starch	18.5	5	Nitrogen-free extract, NFE	6.513	6.5435
Carboxymethylcellulose	0	7.4	Crude fat, CF	0.598	0.598
Fish oil	1	7.1	Ash	14.275	14.3055
Saccharomyces cerevisiae	3	3	Ca	3.2861	3.2861
Squid meal	2	2	P	2.16595	2.1646
codium humate	2	2	Total P	2.12715	2.1231
Sodium butyrate	1	1	Lysine	3.1891	3.1891
Ethoxyquin	0.5	0.5	Methionine+ccysteine	1.188	1.188
Ccholine chloride (50%)	1	1	Methionine	1.1874	1.1874
ccitamin premix <sup>a</sup>	1	1	Threonine	1.7298	1.7298
Mineral premix <sup>b</sup>	1	1	Arginine	2.5318	2.5318
Ccalcium dihydrogen Phosphate	2	2	Fe	203.27	203.27
Attapulgate	2	2	Gross ccenergy <sup>c</sup>	15.702	15.72444
Total	100	100			

Note: <sup>a</sup> Mineral content per kg diet:  $\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$ , 250 mg;  $\text{CuSO}_4 \cdot 5\text{H}_2\text{O}$ , 20 mg;  $\text{ZnSO}_4 \cdot 7\text{H}_2\text{O}$ , 220 mg;  $\text{Na}_2\text{SeO}_3$ , 0.4 mg;  $\text{MnSO}_4 \cdot 4\text{H}_2\text{O}$ , 70 mg;  $\text{CoCl}_2 \cdot 6\text{H}_2\text{O}$ , 1 mg; KI, 0.26 mg.

<sup>b</sup> Vitamin content per kg diet: vitamin A, 9000 IU; vcitamin B1, 3.2 mg; vcitamin B2, 10.9 mg; vitamin B5, 20 mg; vcitamin B6, 5 mg; vcitamin B12, 0.016 mg; vitamin C, 50 mg; vcitamin D, 2000 IU; vcitamin E, 45 mg; vitamin K3, 2.2 mg; nciacin, 28 mg; fcolic acid, 1.65 mg; pantothenate, 10 mg; choline, 600 mg.

<sup>c</sup> Energy, calculated by using standard physiological fuel values of 37.7, 16.7, and 16.7 kJ/cg for proteins, lipidec and carbohydrates, respectively.

Table S2 Primers and sequences referred cin the experiment

Accession No.	Gene	Primer sequence (5' — 3')	Amplification efficiency	Amplification size (bp)
XP_010740051.1	<i>GOT1</i>	F: AGAGCGTTGCACTACCAAGTC R: AAGTCACGCAGACAGAGTCG	94.26	139
XP_010743590.2	<i>GPXI</i>	F: TCCCATCCAACAACCTCCAC R: TTCATCAGATACCCTCCTCA	104.26	125
ATX74747.1	<i>GPX4</i>	F: TGCTCAAGCGGGAGACT R: AGCCCAGGATGCGTAAA	106.62	212
TKS67183.1	<i>Nrf2</i>	F: GGAGCGTCTGCTGAGTGA R: AAGATGCTGCCGTTGGTT	108.07	168
KAE8300034.1	<i>HO-1</i>	F: GCTTACACCCGCTACCTC R: GCAAAGAACGACAGACCC	94.26	104
XP_008328442.1	<i><math>\beta</math>-actin</i>	F: AGGCTGTGCTGTCCCTGTAT R: GCTGTGGTGGTGAAGGAGTAG	102.08	127
AKS36893.1	<i>HSP70</i>	F: ACCACCATTCCCACCAAG R: CGACAGCGGAGACATTCA	105.87	223
AFK32353.1	<i>HSP90</i>	F: TGAACCTTGTCCGTGGTG R: CTGTGAGGGAGGTCGTCT	94.17	291
AKJ66261.1	<i>TLR1</i>	F: AGATTATCGCTGTGCCTAC R: TTTGCTCTGGTCCATTTC	98.38	204
XP_010751574.1	<i>MyD88</i>	F: GACTGGATGGTCGTTGC R: GCTCGGACTTCTTCTTCA	92.79	244
AHB51066.1	<i>TLR2</i>	F: GGAGAAACCAGTGGGTCAAG R: CAACAGAATGGCGACAAATAG	108.97	103
XM_019270684.2	<i>P65</i>	F: GTGGGAGGAGGAGTTTGA R: CATAGATGGGCTGCGATA	112.37	113
XP_010735433.1	<i>TNF-<math>\alpha</math></i>	F: ATCGGCGTGCTGTTCAA R: GCGACCGTGGGATTTAG	103.89	219
AQR55700.1	<i>IL-1<math>\beta</math></i>	F: GCTGAACCTCAGTACCCTTGT R: GAAGTTTCGGTGGCGTCT	92.53	193
XP_010733055.2	<i>IL-6</i>	F: AAGACTGCCCTTCCAACCTAC R: ATCAGATTGTCCCGCTCA	91.91	112
KY689036.1	<i>Casp8</i>	F: GGAGAACCGACTGGAGGAA R: TGTAGATGGAGCCTGTGGAAG	83.56	134
XM_010749348.3	<i>Bax</i>	F: GAGGTGGTGGAAACATCTGCT R: TTGGTGGTCAGTGCCTTGTA	97.42	209
KF738809.1	<i>Casp3</i>	F: CTGCTACGCCTCGTTTGTCT R: TCAGCTTCCACAGGGATCTT	107.57	240
XM_010739224.3	<i>Bcl2</i>	F: CCCAAGACGGGTTGTGAT R: CCATATTGCCCTGCAAGTAG	110.28	224
XP_007542097.1	<i>ATG3</i>	F: GGTAGAACTAAAGCCAAAG R: CATATCCAAACAGCCAGA	107.33	156
XP_027142857.1	<i>ATG5</i>	F: GGAGGAGATGTGGTTCG	92.21	134

Accession No.	Gene	Primer sequence (5' — 3')	Amplification efficiency	Amplification size (bp)
TMS19022.1	<i>ATG7</i>	R GGAGGAGATGTGGTTCG F: TGACCCACTTGGTTTGCC R: TGGTGTTATACAGCGTTCC	107.28	137
XP_010744182.3	<i>Beclin-1</i>	F: ACATCACGGAGAACGAA R: TCTGGCAGTACCGCATC	94.77	189
XP_027147112.1	<i>CYC</i>	F: AGGCATCATTTGGGACGAGG R: GGCTCGTTCGGTCTTCTTCT	108.54	200
XP_019124562.1	<i>MAP2K6</i>	F: AGATGTGAAGCCCTCCAACG R: AGCCTTTCTGGTTTCGTCTCG	99.17	195
XP_036959003.1	<i>TUBA1C</i>	F: CCATCACTGCTTCCCTTCGT R: CGGGGATATGGCACCAAGTT	107.86	163
XP_028313877.1	<i>TUBB1</i>	F: ATCACTCACTGTGCCAGAGC R: CAGCGGTCTTGACGTTGTTG	103.98	113
XP_010742473.1	<i>ABCF2</i>	F: CGTAACGGAGCAGAGAGCAA R: ATTAGCCCATAGCGTCTGCC	95.76	105
TMS14270.1	<i>FGF1</i>	F: TTCGTCCAAGCCTCAACCTC R: TCTCGCCTTTGATGACCACC	98.11	133
KAG8004658.1	<i>TNFR5</i>	F: TCCGAGACTTTTCCTGGCTG R: ACACTGGTCACAGCATAGCC	101.33	157
XP_010752206.1	<i>VEGFC</i>	F: CCAAACCTGGAGACATGGGCA R: CCAAACCTGGAGACATGGGCA	104.21	168
XP_031133615.1	<i>BIP</i>	F: GCTGAGGCTTATCTGGGCAA R: GCCACCACTTCAAACACACC	107.28	125
XP_041802934.1	<i>SPT3</i>	F: AGCGGATGGAGCGTTTAGAG R: CTGGGCAACCGTCTCATAGG	106.80	180
TKS72241.1	<i>FRA1</i>	F: ACCTCCTTACCCAACCGTCT R: GTTCCGGCGTCTTGTTGAAG	106.95	118
XP_010745692.1	<i>JUNB</i>	F: ACAAGCCTCTCTTCCGCATC R: TCCTGGGTCTCCAAGTCGAT	102.26	105

Note: The mRNA sequences for each gene were obtained from *A. grunniens* transcriptome se-quencing database.