

Differentially expressed genes involved in the metabolic pathways in normally hatched and helped ducklings.

Unigenes Locus	Gene name	Helped_Expression value	Normal_Expression value	Log ₂ Ratio(Helped/Norma	FDR
Norm_comp221_c0_seq7	Glucose-6-phosphatase	204.609	87.7132	1.222	0.045876
Norm_comp171_c0_seq4	ATP synthase subunit alpha	74.6398	26.2309	1.50868	0.001884
Help_comp33382_c0_seq1	Inositol oxygenase	3.75044	0.698638	2.42444	0.006602
Help_comp15352_c1_seq1	Sodium/myo-inositol cotransporter	3.47908	1.22972	1.50037	0.003237
Norm_comp14068_c0_seq1	Neuropeptide Y receptor 4	2.21758	0.797231	1.47591	0.040749
Norm_comp685_c0_seq3	Hyaluronidase-1	49.3671	20.2078	1.28864	0.023467
Norm_comp9226_c0_seq1	All-trans-retinol 13,14-reductase	3.1277	0.187764	4.05811	0.029544
Norm_comp4988_c0_seq1	Aquaporin-1	11.1005	3.97338	1.48218	0.01881
Norm_comp973_c0_seq5	Sulfotransferase family cytosolic 2B member 1	59.8945	19.8305	1.5947	0.00226
Help_comp11371_c0_seq1	Elongation of very long chain fatty acids family member protein 2	10.1844	1.41012	2.85248	0
Norm_comp13976_c0_seq1	Intestinal-type alkaline phosphatase	3.0879	0.063036	5.61431	0.000106
Norm_comp1658_c0_seq1	Low-density lipoprotein receptor-related protein 1	8.66838	3.87403	1.16193	0.03711
Help_comp15933_c0_seq2	cytochrome P450 2C45	6.41979	1.84481	1.79905	0.0069833
Norm_comp1621_c0_seq1	N-acetylgalactosamine-6-sulfatase	11.8727	3.84753	1.62564	0.0004957
Help_comp1780_c0_seq4	galactokinase	1.45E+00	1.06E+01	-2.86E+00	4.84E-09
Help_comp1197_c3_seq1	Xanthine dehydrogenase/oxidase	8.06485	17.8975	-1.15004	0.042085
Help_comp19286_c0_seq1	Septin-4	0.231552	1.12764	-2.2839	0.017205
Help_comp2563_c0_seq1	Rho-related GTP-binding protein RhoC	7.14251	17.2506	-1.27215	0.02548
Help_comp3856_c0_seq1	Oligoadenylate synthetase-like 2	0.919919	11.6429	-3.66179	4.49E-11
Help_comp476_c0_seq249	Cytosolic purine 5'-nucleotidase	0.419083	1.70154	-2.02153	0.013445
Help_comp6680_c0_seq4	Ephrin-A1	1.77044	8.43337	-2.252	0.001117
Help_comp707_c2_seq2	Bifunctional coenzyme A synthase	4.29691	10.2518	-1.25451	0.019976
Help_comp7075_c0_seq1	Galactose-1-phosphate uridylyltransferase	0.921413	2.8304	-1.61909	0.012216
Help_comp8232_c0_seq1	Elongation factor 1-alpha	0	3.02535		0.006327
Norm_comp10156_c0_seq3	UMP-CMP kinase 2	1.09273	3.63923	-1.73569	0.008128
Help_comp1671_c0_seq1	Phosphatidate phosphatase	8.66133	19.649	-1.18179	0.0363
Help_comp6076_c0_seq1	Insulin-induced gene 1	2.72723	6.11561	-1.16506	0.049106
Help_comp833_c0_seq1	Apolipoprotein AIV	33.8998	88.0706	-1.37738	0.004379
Norm_comp3973_c0_seq1	Phosphoenolpyruvate carboxykinase	3.31411	13.4821	-2.02435	2.81E-06
Help_comp675_c0_seq2	Cytochrome P450 1A5	10.254	32.9315	-1.68328	9.49E-05
Help_comp9412_c0_seq3	DNA-directed RNA polymerase	1.23401	5.79832	-2.23228	0.011598
Help_comp9249_c0_seq2	Argininosuccinate synthase	0.424901	2.66004	-2.64625	0.006633
Help_comp8021_c0_seq13	Proline dehydrogenase 1	0.46345	1.62117	-1.80655	0.019567
Help_comp1125_c0_seq1	Glycine dehydrogenase	18.9211	45.6986	-1.27215	0.019743
Norm_comp408_c0_seq1	Phosphoserine aminotransferase	175.142	526.476	-1.58784	0.049025
Help_comp3970_c0_seq1	Cyclin-dependent kinase inhibitor 1	0.525997	2.06208	-1.97097	0.000274
Help_comp13964_c0_seq1	Carnitine O-acetyltransferase b	0.64084	3.36148	-2.39106	0.039983
Help_comp283_c0_seq2	D-dopachrome decarboxylase	4.13703	9.51741	-1.20197	0.037217
Help_comp1651_c0_seq9	acyl-coenzyme A thioesterase 8 isoform 2	0.893905	5.42971	-2.60268	0.0040784
Help_comp16256_c0_seq1	gamma-glutamyl transpeptidase 4	0.301961	1.35712	-2.16812	0.0028576
Help_comp12087_c0_seq1	hydroxymethylglutaryl-CoA lyase, mitochondrial isoform 1	0.995497	3.42279	-1.78168	0.0322201
Help_comp22677_c0_seq1	stearoyl-CoA desaturase	0.195097	1.09521	-2.48895	0.048467
Help_comp2399_c0_seq33	mitochondrial GTPase 1 homolog	1.16885	13.817	-3.56329	0.0005322
Help_comp2841_c0_seq3	zinc transporter 10	5.71497	16.0306	-1.48801	0.0297753
Help_comp3315_c0_seq2	inositol oxygenase	4.7091	13.5864	-1.52864	0.0027061
Help_comp10288_c0_seq1	ATP-binding cassette sub-family A member 12	0.436308	3.03592	-2.79871	0.0025599
Help_comp11283_c0_seq1	adipose differentiation-related protein	1.25367	5.29827	-2.07937	0.0135286
Help_comp12660_c0_seq1	cytochrome P450 1A4	0.222969	2.52975	-3.50408	0.0250334
Help_comp2399_c0_seq33	mitochondrial GTPase 1 homolog	1.16885	13.817	-3.56329	0.0005322
Help_comp39814_c1_seq1	fatty acid synthase	6.125	18.334	-1.58174	0.0007343
Help_comp4110_c0_seq1	deoxyhypusine synthase-like	3.67614	9.71265	-1.40167	0.0158005
Help_comp564_c0_seq13	uridine phosphorylase 2	1.65427	5.98313	-1.8547	9.59E-05
Help_comp6198_c0_seq1	insulin-like growth factor-binding protein 3	1.82705	4.73386	-1.3735	0.0160568
Help_comp7003_c0_seq1	galactose-1-phosphate uridylyltransferase	1.45757	6.27895	-2.10696	0.0302042
Norm_comp249_c3_seq5	glutathione S-transferase 1	19.3586	60.4215	-1.64209	0.000181
Help_comp9739_c0_seq1	dihydropyrimidinase-related protein 3	2.00848	5.97706	-1.57334	0.034616
Norm_comp12383_c0_seq1	myosin-11	2.69159	10.1288	-1.91193	0.0115919
Norm_comp1997_c0_seq12	uridine phosphorylase 2	1.93795	7.9388	-2.03439	0.0152395
Norm_comp4303_c0_seq3	corticosteroid 11-beta-dehydrogenase isozyme 1	1.24823	4.46252	-1.83798	0.0415636
Norm_comp4542_c0_seq1	ornithine decarboxylase 1	12.7809	38.768	-1.60087	0.0002816
Norm_comp6361_c0_seq2	fumarylacetoacetase	4.18884	20.7687	-2.30979	0.0005119

Differentially expressed genes involved in the immune defense pathways between normally hatched and helped ducklings.

Locus	Gene name	Helped_Expression value	Normal_Expression value	Log ₂ Ratio(Helped/Norma	FDR
Help_comp12196_c0_seq4	Alpha-2-macroglobulin-like protein 1	1.14625	0.376249	1.60716	0.025902
Help_comp5926_c1_seq1	C-C motif chemokine 4 homolog	29.8608	7.64233	1.96617	0.00012
Norm_comp934_c0_seq1	Complement receptor type 2	48.6709	20.0917	1.27646	0.019601
Norm_comp9683_c0_seq5	Tripartite motif protein 39	7.77346	0.373288	4.3802	0.0000178
Norm_comp16674_c0_seq1	immunoresponsive 1 homolog	2.00805	0	1.79769e+308	0.0001318
Help_comp237_c1_seq1	MHC class I antigen alpha chain	26.8458	137.259	-2.35414	3.93E-06
Help_comp2155_c0_seq2	Major histocompatibility complex class II beta chain BLB1	1.56305	8.77694	-2.48935	0.0002
Help_comp7965_c0_seq1	interferon-induced guanylate-binding protein 1	1.49212	5.07832	-1.76698	0.0056822
Help_comp11426_c0_seq1	interferon alpha-inducible protein 6	0.283368	1.30658	-2.20504	0.0394725
Help_comp20926_c0_seq1	beta-defensin 9	0	1.55888	-1.79769e+308	0.0364704
Help_comp1124_c0_seq1	Chemokine	17.8396	60.4402	-1.76043	0.000208
Help_comp8674_c0_seq2	Intercellular adhesion molecule 1	0.417914	4.46346	-3.41689	0.033469
Help_comp1410_c0_seq4	C4b-binding protein alpha chain	3.42917	11.0794	-1.69194	0.0168318
Help_comp18064_c0_seq1	tumor necrosis factor receptor superfamily member 27	0.185702	1.46661	-2.98142	0.0042059
Help_comp16136_c0_seq1	Ubiquitin carboxyl-terminal hydrolase	0.434828	1.59959	-1.87919	0.01453
Help_comp1602_c1_seq17	Fibroblast growth factor receptor 1	4.12311	10.155	-1.30039	0.019288
Help_comp1602_c1_seq22	Fibroblast growth factor receptor 4	7.7469	18.5225	-1.25759	0.022833
Help_comp1790_c0_seq1	DNA-binding protein inhibitor ID-2	39.404	120.676	-1.61472	0.006053
Help_comp4639_c0_seq1	Ras-like without CAAX 1	2.18977	5.00889	-1.19371	0.035438
Help_comp3728_c1_seq1	Macrophage colony-stimulating factor 1	0.319688	1.51881	-2.24821	0.000882
Help_comp4419_c0_seq9	Hepatocyte cell adhesion molecule	0.481206	3.83589	-2.99484	0.037629

Help_comp25610_c0_seq1	ras homolog gene family, member C	0.042223	0.971676	-4.52438	0.0082717
Help_comp10168_c0_seq4	similar to butyrophilin, subfamily 1	0.0942799	4.06144	-5.4289	0.041373
Help_comp36533_c0_seq1	radical S-adenosyl methionine domain-containing protein 2	0	0.727092	-1.79769e+308	0.0196517