

Supplementary Table 2. Functional annotation analysis based on GO terms in zebrafish embryos 4 hpi

GO Term	Name	Genes	<i>p</i> value
Biological process			
GO:0006457	protein folding	29	<0.001
GO:0000038	very long-chain fatty acid metabolic process	6	<0.01
GO:0055085	transmembrane transport	53	<0.05
GO:0007423	sensory organ development	25	<0.05
GO:0022600	digestive system process	7	<0.05
GO:0048706	embryonic skeletal system development	11	<0.05
GO:0035556	intracellular signal transduction	179	<0.001
GO:0009725	response to hormone	67	<0.001
GO:0035556	protein kinase cascade	64	<0.001
GO:0016310	phosphorylation	113	<0.001
GO:0032496	response to lipopolysaccharide	22	<0.001
GO:0032868	response to insulin stimulus	25	<0.001
GO:0042981	regulation of apoptosis	107	<0.001
GO:0046326	positive regulation of glucose import	10	<0.001
GO:0009611	response to wounding	74	<0.001
GO:0001817	regulation of cytokine production	33	<0.001
GO:0031667	response to nutrient levels	34	<0.001
GO:0045089	up-regulation of innate immune response	13	<0.001
GO:0046626	regulation of insulin receptor signaling pathway	8	<0.001
GO:0050920	regulation of chemotaxis	10	<0.01
GO:0043122	regulation of I-kappaB kinase/NF-kappaB signaling	20	<0.01
GO:0007623	circadian rhythm	11	<0.01
Cellular component			
GO:0031974	membrane-enclosed lumen	209	<0.001
GO:0005667	transcription factor complex	22	<0.01
GO:0045177	apical part of cell	22	<0.01
GO:0044459	plasma membrane part	301	<0.001
GO:0034702	ion channel complex	39	<0.001
GO:0043235	receptor complex	20	<0.01
GO:0005899	insulin receptor complex	3	<0.05
GO:0033256	I-kappaB/NF-kappaB complex	3	<0.05
Molecular function			
GO:0003723	RNA binding	85	<0.001
GO:0020037	heme binding	18	<0.01
GO:0008395	steroid hydroxylase activity	5	<0.05
GO:0004672	protein kinase activity	97	<0.001
GO:0022843	voltage-gated cation channel activity	35	<0.001
GO:0022803	passive transmembrane transporter activity	66	<0.001
GO:0003700	transcription factor activity	124	<0.001
GO:0008289	lipid binding	62	<0.001
GO:0043560	insulin receptor substrate binding	5	<0.05

The table indicates the number of genes in each list that are associated with the indicated GO term resulting from applying the significance cutoff of *p*-value (*p*) <0.05 and fold change >|1.5|. Yellow indicates up regulated terms and blue indicates down regulated terms.