

**Supplementary Table 3. Functional annotation analysis based on GO terms**

GO Term	Name	Genes	<i>p</i> value
<b>Biological process</b>			
GO:0035556	protein kinase cascade	39	<0.001
GO:0006796	phosphate metabolism	75	<0.001
GO:0048667	cell morphogenesis involved in neuron differentiation	27	<0.001
GO:0001889	liver development	11	<0.001
GO:0007259	JAK-STAT cascade	8	<0.01
GO:0001822	kidney development	11	<0.05
GO:0007507	heart development	18	<0.05
GO:0051148	negative regulation of muscle cell differentiation	4	<0.05
GO:0055085	transmembrane transport	36	<0.05
GO:0007398	ectoderm development	10	<0.001
GO:0010033	response to organic substance	18	<0.001
GO:0030239	myofibril assembly	4	<0.001
GO:0008202	steroid metabolic process	8	<0.01
GO:0055001	muscle cell development	4	<0.05
GO:0042445	hormone metabolic process	5	<0.05
GO:0048739	cardiac muscle fiber development	2	<0.05
<b>Celullar component</b>			
GO:0031226	intrinsic component of plasma membrane	94	<0.001
GO:0043005	Neuron projection	40	<0.001
GO:0005856	cytoskeleton	81	<0.05
GO:0045177	apical part of cell	7	<0.01
GO:0044449	contractile fibre component	5	<0.05
GO:0005578	proteinaceous extracellular matrix	6	<0.05
<b>Mollecular function</b>			
GO:0030695	GTPase regulator activity	46	<0.001
GO:0004674	protein serine/threonine kinase activity	41	<0.001
GO:0008092	cytoskeletal protein binding	38	<0.05
GO:0004857	enzyme inhibitor activity	14	<0.001
GO:0004175	endopeptidase activity	14	<0.001
GO:0008289	lipid binding	12	<0.01

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.