

**Table S1.** The top 50 of enriched GO terms with most significant *p* value in tangeretin-treated HepG2 cells

ID	Description	<i>p</i> value
GO:0015711	organic anion transport	0.000196631
GO:0006820	anion transport	0.000372626
GO:0038084	vascular endothelial growth factor signaling pathway	0.000460256
GO:0072330	monocarboxylic acid biosynthetic process	0.000538243
GO:0033554	cellular response to stress	0.000720838
GO:0033044	regulation of chromosome organization	0.000722807
GO:0042760	very long-chain fatty acid catabolic process	0.001045247
GO:0070482	response to oxygen levels	0.001135024
GO:0001666	response to hypoxia	0.001172772
GO:0071827	plasma lipoprotein particle organization	0.001263218
GO:0043687	post-translational protein modification	0.001533743
GO:0045861	negative regulation of proteolysis	0.001609589
GO:0043691	reverse cholesterol transport	0.001718139
GO:0006996	organelle organization	0.001743339
GO:0006629	lipid metabolic process	0.001883977
GO:0000725	recombinational repair	0.001942245
GO:0006260	DNA replication	0.0019534
GO:0002933	lipid hydroxylation	0.00201535
GO:0015838	amino-acid betaine transport	0.00201535
GO:0046942	carboxylic acid transport	0.002027223
GO:0006082	organic acid metabolic process	0.002275632
GO:0015910	peroxisomal long-chain fatty acid import	0.002333011
GO:0032902	nerve growth factor production	0.002333011
GO:0038190	VEGF-activated neuropilin signaling pathway	0.002333011
GO:0050722	regulation of interleukin-1 beta biosynthetic process	0.002333011
GO:0050725	positive regulation of interleukin-1 beta biosynthetic process	0.002333011
GO:1902336	positive regulation of retinal ganglion cell axon guidance	0.002333011
GO:0048519	negative regulation of biological process	0.002637618
GO:0006950	response to stress	0.002680827
GO:0035725	sodium ion transmembrane transport	0.002827659
GO:0003333	amino acid transmembrane transport	0.002864812
GO:0015849	organic acid transport	0.002908723
GO:0032787	monocarboxylic acid metabolic process	0.002997776
GO:0006633	fatty acid biosynthetic process	0.003089983

GO:0010876	lipid localization	0.003179142
GO:0019752	carboxylic acid metabolic process	0.003280088
GO:0035726	common myeloid progenitor cell proliferation	0.003400407
GO:0051004	regulation of lipoprotein lipase activity	0.003449952
GO:2000573	positive regulation of DNA biosynthetic process	0.003486182
GO:0050930	induction of positive chemotaxis	0.003674025
GO:0046394	carboxylic acid biosynthetic process	0.003766843
GO:0031638	zymogen activation	0.004223633
GO:0035924	cellular response to vascular endothelial growth factor stimulus	0.004817653
GO:0009611	response to wounding	0.004843104
GO:0010951	negative regulation of endopeptidase activity	0.004999759
GO:0000724	double-strand break repair via homologous recombination	0.005101266
GO:0021800	cerebral cortex tangential migration	0.00524607
GO:0071679	commissural neuron axon guidance	0.00524607
GO:0048048	embryonic eye morphogenesis	0.005272766
GO:0030071	regulation of mitotic metaphase/anaphase transition	0.005472417