






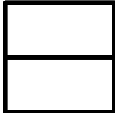





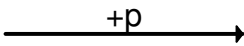
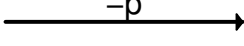
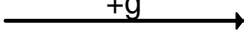
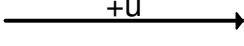
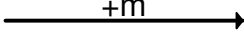
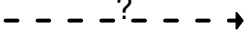


Graphviz representation of Regulation of lipolysis in adipocytes (mmu04923). Box of expressed genes are colored according to the scaled log₂FC between epi and ing expression levels. Each box is partitioned into six parts, each representing one time point (-2,0,2,4,6,8), so that the whole time course for the gene is shown. The log₂FC is scaled between -1 to 1. When the gene is higher expressed in ing the color is in a shade of green, while it is red, when the gene is higher expressed in epi. Grey color indicates a similar expression intensity in both adipose tissues, and no filling means no expression was measured.

KEGG diagram legend

Edge Types

Node Types

compound			
hidden compound			
activation		gene (protein/enzyme)	
inhibition			
expression			
repression		group (complex)	
indirect effect			
state change			
binding/association		compound (metabolite/glycan)	
dissociation			
phosphorylation			
dephosphorylation			
glycosylation			
ubiquitination			
methylation			
others/unknown			
		map (pathway)	Pathway name