



KEGG view representation of Nitrogen metabolism (mmu00910). 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.