CO2

HCO3−

Car8

Node types

−1 0 1

Carbamoyl phosp\
hate

Cps1

Arginine
biosynthesis

gene
(protein/enzyme)

NH3

Glutamine

Glul

group
(complex)

Glud1

compound
(metabolite/glycan)

Glutamic acid

Alanine,
aspartate and
glutamate
metabolism

map
(pathway)

Pathway name

Formic acid

Glyoxylate and
dicarboxylate
metabolism

−Data with KEGG pathway−
−Rendered by Pathview−

Graphviz 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 partioned 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.