Supplementary figure legends

Supplementary Figure 1. Metabolic pathways affected by Mg deficiency.

Metabolic pathways detected by Enrichment Analysis of MetaboAnalyst, i.e., taurine/hypotaurine metabolism, methionine metabolism, and glycine/serine/threonine metabolism are shown. Detected metabolites are shown in red. Metabolites whose cellular content is significantly lower or higher in the Mg-deficient group than in the control group are underlined and boxed, respectively. Enzyme, which was determined its expression level, is shown in blue. 2-KBA: 2-ketobutyric acid, ACSP: N1-acetylspermine, AOBA: 2-amino-3-oxobutanoic acid, CSA: cysteine sulfinic acid, Cys: cysteine, CYSTA: cystathionine, Gly: glycine, HCYS: homocysteine, HYP: hypotaurine, Met: methionine, MTAD: 5'-methylthioadenosine, NMG: *N*-methylglycine, PUT: putrescine, PYR: pyruvic acid, SAH: *S*-adenosylhomocysteine, SAM: *S*-adenosylmethionine, SAMA: *S*-adenosylmethioninamine, Ser: serine, SPM: spermidine, SucCoA: succinyl CoA, TAU: taurine, Thr: threonine, Amd1: adenosylmethionine decarboxylase, Cdo1: cysteine dioxygennase type 1, Csad: cysteine sulfinic acid decarboxylase, Gnmt: glycine *N*-methyltransferase, Mat1a: methionine adenosyltransferase IMat2a: methionine adenosyltransferase IIMat2b: methionine adenosyltransferase II Sardh: sarcosine dehydrogenase, Sat1: spermidine/spermine N1-acetyl transferase 1, Sds: serine dehydratase, Srm: spermidine synthase.

Supplementary Figure 2. Expression level of enzymes in the liver of rats fed the control diet or Mg-deficient diet.

Gene transcript levels of hepatic enzymes shown in Fig. 2B and 3B were normalised against Hprt1 expression, and the expression level in the control group is set to 100. Cdo1: cysteine dioxygenase type 1, Csad: cysteine sulfinic acid decarboxylase, Mat1a: methionine adenosyltransferase IMat2a: methionine adenosyltransferase IIMat2b: methionine adenosyltransferase II Gnmt: glycine *N*-methyltransferase, Sardh: sarcosine dehydrogenase, Amd1: adenosylmethionine decarboxylase, Srm: spermidine synthase, Sat1: spermidine/spermine N1-acetyl transferase 1, Sds: serine dehydratase, Gck: glucokinase, G6p: glucose 6-phosphatase, G6pd: glucose-6-phosphate dehydrogenase, Pck1: phosphoenolpyruvate carboxykinase 1. Mean ± SE. \*: *P* < 0.05, *vs.* control group.

Supplementary Figure 3. Relative content of the other metabolites, which were significantly different in the liver of rats fed the control diet or Mg-deficient diet.

Rats were fed the control diet (n = 5) or the Mg-deficient diet (n = 6) for ~~12~~ 8 weeks. Metabolites in the liver were analysed by metabolomic analysis. The peak area of the metabolite was divided by that of 2-isopropylmalic acid, an internal control, and DNA content. Metabolite content in the control group was set to 100. Relative content of 22 additional metabolites, in which hepatic content is significantly different between the groups and is not shown in Fig. 2 and 3, is shown. Mean ± SE. \* and \*\*: *P* < 0.05 and *P* < 0.01, respectively, *vs.* control group.

Supplementary Figure 4. Relative content of the other metabolites, which were not significantly different in the liver of rats, fed the control diet or Mg-deficient diet.

Rats were fed the control diet (n = 5) or the Mg-deficient diet (n = 6) for ~~12~~ 8 weeks. Metabolites in the liver were analysed by metabolomic analysis. The peak area of the metabolite was divided by that of 2-isopropylmalic acid, an internal control, and DNA content. Metabolite content in the control group was set to 100. Relative content of 48 metabolites, in which hepatic content is not significantly different between the groups and is not shown in Figs. 2 and 3, is shown. Mean ± SE. (A–C) Metabolites are ordered in descending order based on the cellular content in the Mg-deficient group; because of space limitation, the metabolites were divided into three parts.