Additional file 1

LTP recording

After delivery, Mice were housed in standard ventilated cages (IVC, Sealsafe, Techniplast, Marcoussis, France) coupled to an air-handling unit (TouchSLIMline, Exhaust, Techniplast, Marcoussis, France), equipped with solid floors and a layer of bedding. The cages were cleaned at regular intervals to maintain hygiene. Environmental parameters were as follows: temperature: ~22°C, relative humidity: ~55%. Mice had *ad libitum* access to standard rodent chow. The food was stored under dry and cool conditions in a well-ventilated storage room. Mice had *ad libitum* access to pre-filtered and sterile water. The amounts of food and water were checked daily, supplied when necessary and refreshed once a week. Mice were kept on a 12-h light/dark cycle. Experimenters were blinded to genotype and treatment for all experiments. Data were analyzed by measuring the slope of individual fEPSPs at 0-1.5 ms from the top of the signal by linear fitting using Clampfit (Molecular Devices, Union City, CA). LTP was quantified by comparing the mean fEPSP slope over the post- high frequency stimulation (HFS) period with the mean fEPSP slope during the baseline period. Group effects was assessed by changes in fEPSP slope, expressed as the percentage of the baseline value. For figure 5, only one hippocampal slide was used per animals.

For the first experiment (**Table 1**), intracellular metabolites were analyzed as described in [17] Briefly, analysis was performed by high performance anion exchange chromatography (Dionex ICS 2000 system, Sunnyvale, USA) coupled to a triple quadrupole QTrap 4000 (AB Sciex, CA USA) mass spectrometer. This analytical technology allows the separation and analysis of numerous highly polar metabolites belonging to several chemical families in the same analytical run. All samples were analyzed in the negative mode by multiple reaction monitoring. The amounts of metabolites of glycolysis, pentose phosphate pathways, tricarboxylic acid cycle as

well as nucleotides were determined. To ensure highly accurate quantification, the isotope dilution mass spectrometry (IDMS) method was used. For quantification the addition of full ^{13}C *E. coli* extract which contains a majority of the target metabolites was used, the internal standard. The quantification for each metabolite was first expressed as $^{13}C/^{12}C$ ratio or as ^{12}C area if the internal ^{13}C standard was not available. For metabolites for which a chemical standard was available, the absolute quantification was calculated from the corresponding calibration curve. For the second and the third experiment (**Table 1 and Supplementary Fig. 6a**), we used a LTQ Orbitrap Velos™ / Liquid anion exchange chromatography Dionex™ ICS-5000+ Reagent-Free™ HPIC™ equipment. The analyses were carried out on an IC-MS platform of a liquid anion exchange chromatography Dionex™ ICS-5000+ Reagent-Free™ HPIC™ (Thermo Fisher Scientific™, Sunnyvale, CA, USA) system, coupled to a Thermo Scientific™ LTQ Orbitrap Velos™ mass spectrometer (Thermo Fisher Scientific, San Jose, CA, USA) equipped with a heated electrospray ionization probe. Liquid anion exchange chromatography was performed with the Thermo Scientific Dionex ICS-5000+ Reagent-Free HPIC system (Thermo Fisher Scientific, Sunnyvale, CA, USA) equipped with an eluent generator system (ICS-5000+EG, Dionex) for automatic base generation (KOH). Analytes were separated within 50 min, using a linear KOH gradient elution applied to an IonPac AS11 column (250 x 2 mm, Dionex) equipped with an AG11 guard column (50 x 2 mm, Dionex) at a flow rate of 0.35 ml/min. The gradient program was following: 0 min: 0.5 mM, 1 min: 0.5 mM, 9.5 min: 4.1 mM, 14.6 min: 4.1 mM, 24 min: 9.65 mM, 31.1 min: 90 mM and 43 min: 90 mM, then 43 to 48 min vat 0.5 mM. The column and autosampler temperatures were thermostated at 25°C and 4°C, respectively. The injected sample volume was 15 µl. Measures were performed in triplicates from separate specimens. Mass detection was carried out in a negative electrospray ionization (ESI) mode at a resolution of 60 000 (at 400 m/z) in full-scan mode, with the following source parameters: the capillary temperature was 350°C, the source heater

temperature, 300°C, the sheath gas flow rate, 50 arbitrary units (a.u.), the auxiliary gas flow rate, 5 arbitrary units (a.u.), the S-Lens RF level, 60%, and the source voltage, 2.75 kV. Data acquisition was performed using Thermo Scientific Xcalibur software. Metabolites were determined by extracting the exact mass with a tolerance of 5-10 ppm. For quantification the addition of full ^{13}C *E. coli* extract which contains a majority of the target metabolites was used, and quantified as above. Data were processed using TraceFinder 4.1 software. For the third experiment (**Supplementary Fig. 6a**), the gradient was modified as follows equilibration with 7 mM KOH during 1.0 min; then KOH ramp from 7 to 15 mM, 1–9.5 min; constant concentration 10.5 min; ramp to 45 mM in 10 min; ramp to 70 mM in 3 min; ramp to 100 mM in 0.1 min; constant concentration 8.9 min; drop to 7 mM in 0.5 min; and equilibration at 7 mM KOH for 7.5 min.