Supplementary Figure legends

Supplementary Figure 1 (PART1-3).

Annotated CID tandem mass spectra of all sites of lysine acetylation reported in primary murine astrocyte cultures. Spectra correspond to peptides provided in Supplemental Table 3. The spectra were filtered to retain the top 8 product ions per 100 m/z and were annotated in MaxQuant. The gene name, precursor ion m/z, Andromeda score, and observed fragment ions are indicated. Tandem mass spectra with multiple unassigned intense peaks that did not correspond to neutral losses from the precursor were removed (195 spectra). The statistical analysis was performed after removing these peptides. Annotated spectra can be accessed in an interactive format in MS-Viewer at http://prospector2.ucsf.edu/prospector/cgi-bin/msform.cgi?form=msviewer using the search key: nhh2vn348o.

Supplementary Figure 2.

A) Distribution of the normalized Log2 SILAC ratios for the acetylated peptides identified in the indicated experimental replicates (Exp. 1-3). Experiment 2 corresponds to the experiment in which the SILAC label swap was introduced. B) Multi-scatterplots showing the Pearson's correlation coefficients of Log2 GCLM(-/-)/GCLM(+/+) ratios determined in the different biological replicates.

Supplementary Figure 3.

(A-D) Annotated tandem mass spectra of peptides that were differentially lysine-acetylated in GCLM(-/-) astrocytes. Spectra are in order by gene name and the

corresponding peptides are provided in Supplemental Table 4. In addition to the MaxQuant annotated spectra, the raw spectra with fragment ions predicted by ProteinProspector are indicated.