

SUPPLEMENTARY FIGURES AND TABLES

Figure S1

Quality control of SILAC experiments. A, Incorporation rate of heavy amino acids after 5 passages. B, Fold change- (Log₂ ratio) distribution of peptides derived from total extracts of untreated cells grown with light or heavy isotopes.

Figure S2

A, Quantitative analysis of LMB effect on whole cell proteome. Scatterplot of quantified proteins after LMB treatment on whole cell extract. Proteins are coloured according to significance B, where grey donates > 0.01 , blue < 0.01 , yellow < 0.001 and red $< 1e-11$. B, Protein interaction network (STRING) of up- and down-regulated proteins in total cell extract (TCE) after LMB-treatment. Only high-confidence interactions (score > 0.7) were represented in the network. Red circles indicate down-regulated proteins, blue circles indicate up-regulated proteins.

Figure S3

Protein identification summary and comparison of different SILAC-experiments. The Venn-diagrams depict the numbers of A, cytosolic and nuclear proteins, B, of proteins significantly depleted in the cytosol and the total cell extract (TCE; AAMP, DDX3X, eIF6, GRWD1, PTPN23, RPL22L1, RRM2 and SQSTM1), C, of proteins significantly enriched in the nucleus and in the TCE, D, of proteins significantly enriched in the cytosol and depleted in the nucleus (BCCIP; POLR2G; SNRPD1; SNRPD2; SNRPD3).

Table S1

List of all identified proteins from three SILAC experiments.

Table S2

List of all identified peptides from three SILAC experiments.

Table S3A

List of 60S ribosomal complex proteins identified either as depleted from cytosol or enriched in nucleus or both, in HeLa cells in response to LMB-treatment.

Table S3B

List of COP9 signalosome complex proteins identified as depleted from cytosol of HeLa cells in response to LMB-treatment.