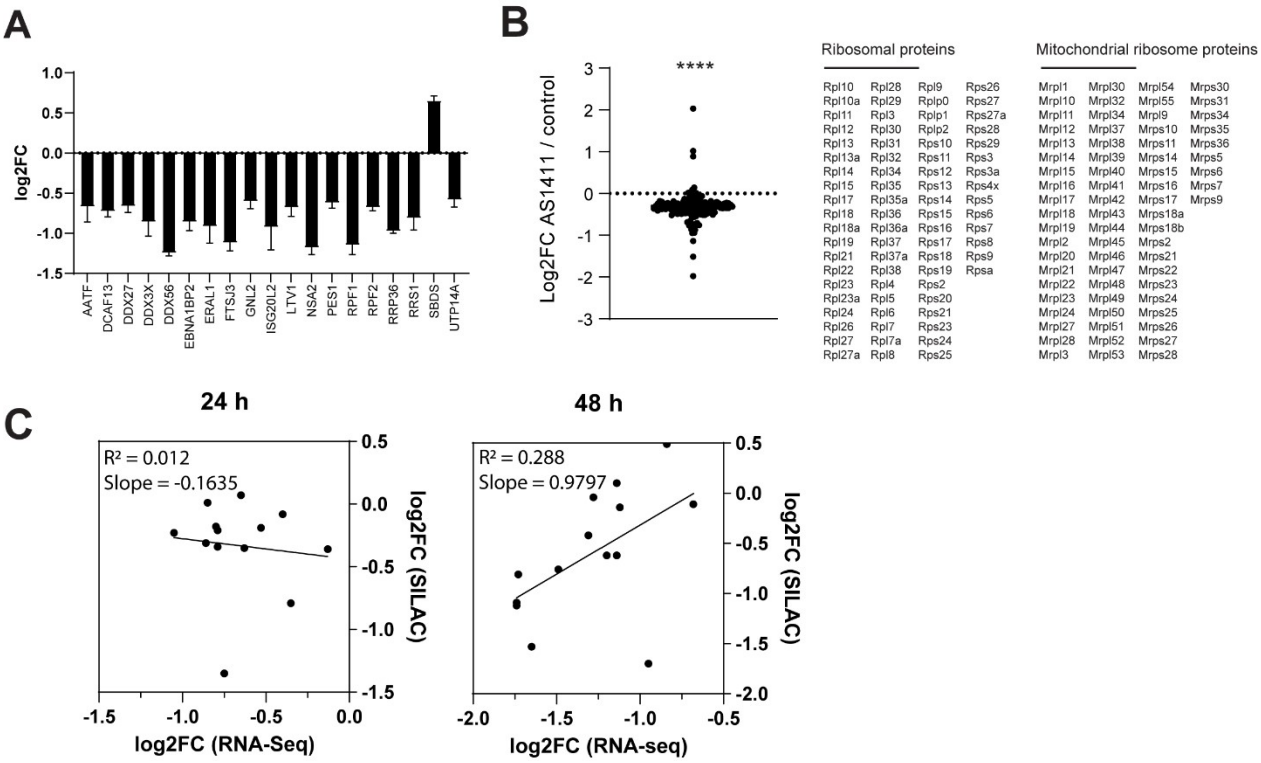
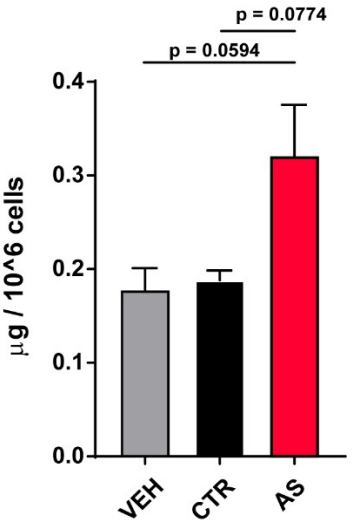
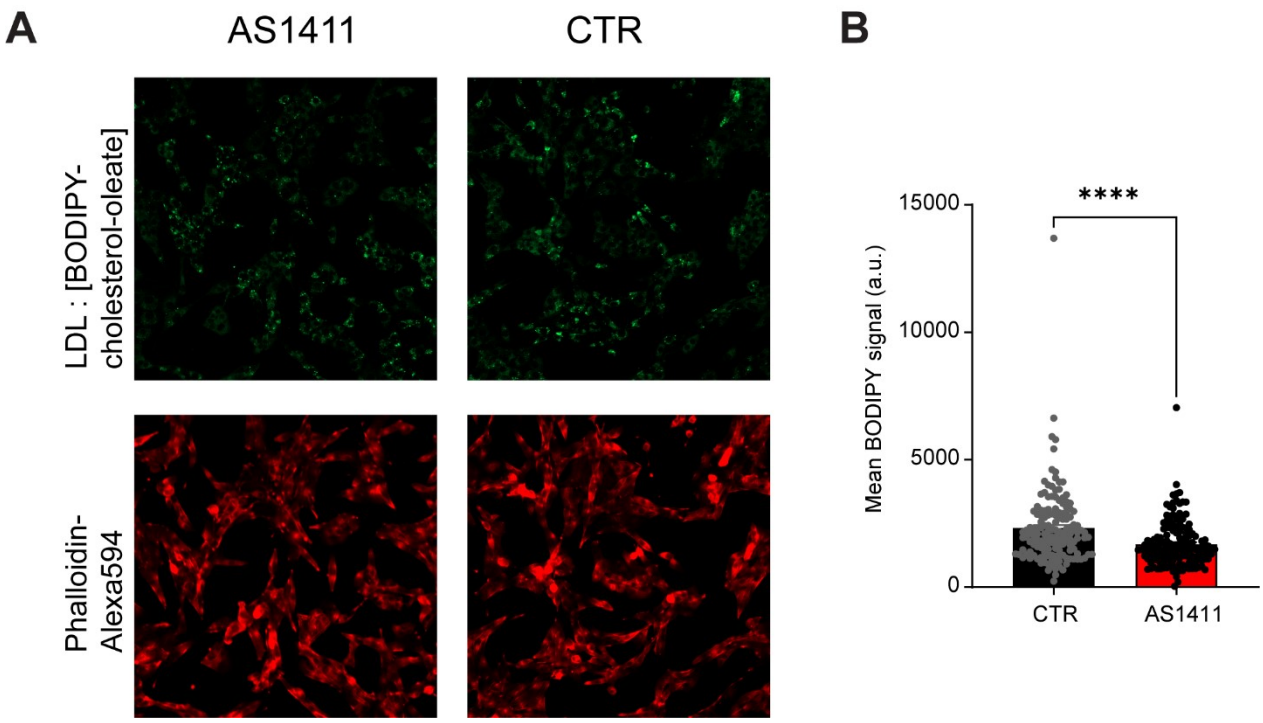
Supplementary Figures



Supplementary Figure 1. SILAC supporting data (related to Figure 2*).* (**A**) AS1411-induced changes in proteins of the "Ribosome biogenesis" GO term in Fig2.C (right panel); mean log2 fold changes (AS1411/control) ± SEM are shown (n = 2-3). (**B**) AS1411/control log2 fold changes of all cytosolic and mitochondrial ribosomal proteins identified in the SILAC proteomics experiment (indicated on the right). The group median -0.3149 is significantly different from the reference median of 0 indicating downregulation (*** $p < 0.0001$, one sample Wilcoxon test). (**C**) Correlation plots of log2FC values in RNA-seq and SILAC analyses of cholesterol pathway members (shown in Fig. 2F).



Supplementary Figure 2 (related to Figure 4). 48h treatment of NIH-3T3 cells increases protein content per cell. After AS1411 treatment, cells were trypsinized, counted using a hemocytometer, lysed in RIPA buffer and protein content was measured by BCA assay. Shown is protein content per one million cells (means ± SEM from three independent biological repeats; statistics: one-way ANOVA with Tukey's post-hoc test.



Supplementary Figure 3 (related to Figure 5). (A) Uptake of LDL:BODIPY-cholesterol oleate into NIH-3T3 cells, measured 24h after incubating cells with 50 µg/mL of LDL complexed with BODIPY-cholesterol oleate and AS1411 or control aptamer (both 10 µM) in serum-free DMEM. BODIPY fluorescence was quantified in fixed and phalloidin-counterstained cells by confocal microscopy. (**B**) Quantification of cholesterol uptake per cell 150 cells per condition, pooled from from two independent experiments. Mean integrated density (total fluorescence per cell) values ± SEM are shown.