

Figure S2.

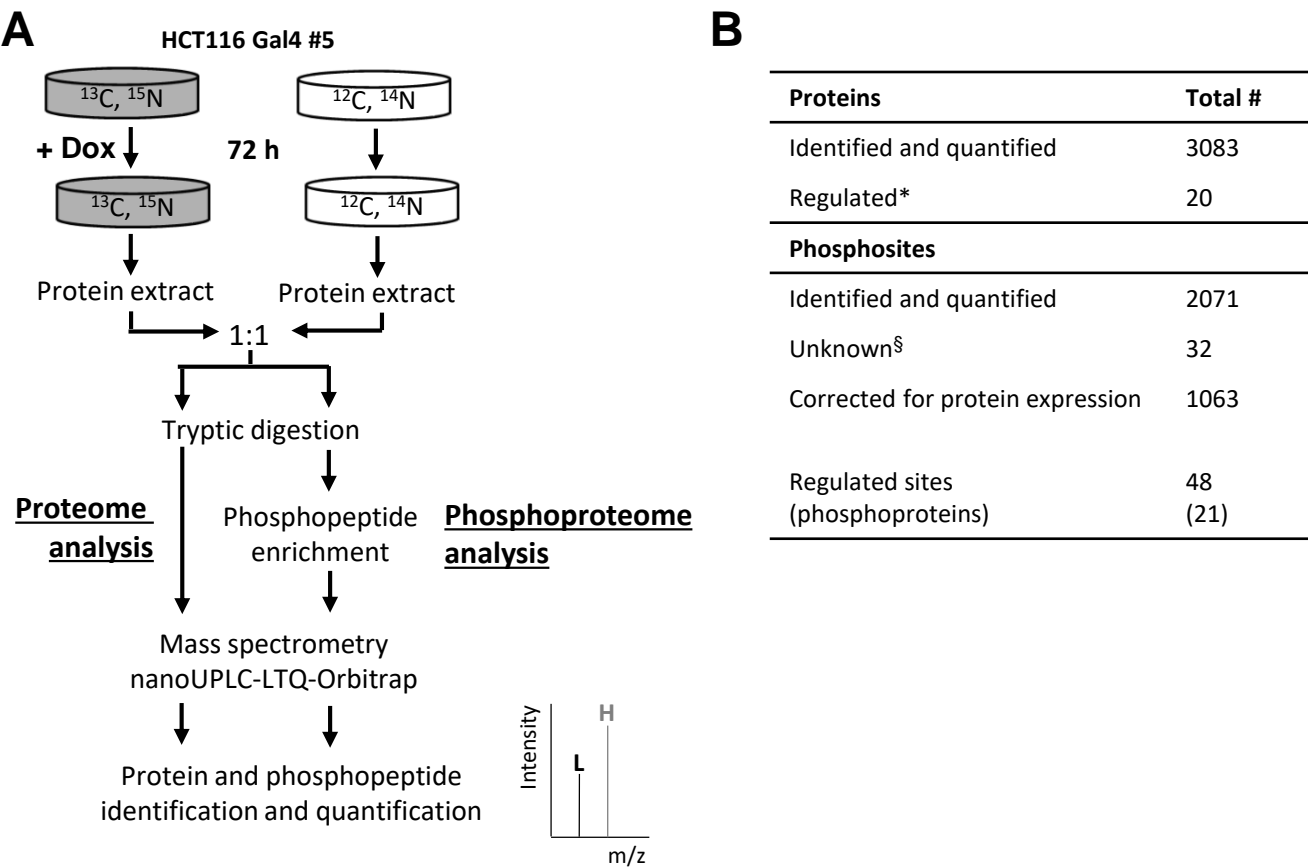


Figure S2. SILAC-based proteomic and phosphoproteomic analysis: (A) Workflow: SILAC labeling with Arg-10 and Lys-8 was applied to HCT116 Gal4 #5 cells followed by treatment with doxycycline (0.5 $\mu\text{g}/\text{ml}$) and mass spectrometric analysis leading to protein and phosphopeptide identification and quantification. (B) Summary of the proteome and phosphoproteome profiling upon Gal4 expression (*more than 1.5-fold in at least 2 biological replicates; [§]according to PhosphoSitePlus).