Supplemental figure 1: Expression fold-change in 2h Pointer-treated cells vs. control cells. Proteins are indicated with the name of their genes and with the number reported in Figure 1 and Table 2 of the manuscript. The fold-change values were calculated by the ratio of average of % relative abundance of protein spots in the P-treated cells vs. the control (indicated with the sign +, over-expressed proteins) or viceversa (indicated with the sign –, under-expressed proteins). With p the presence of proteins is indicated. * $P<0.05$; ** $P<0.01$ vs. the control.
Supplemental figure 2: Expression fold-change in 2h Silglif-treated cells vs. control cells. Proteins are indicated with the name of their genes and with the number reported in Figure 1 and Table 2 of the manuscript. The fold-change values were calculated by the ratio of average of % relative abundance of protein spots in the S-treated cells vs. the control (indicated with the sign +, over-expressed proteins) or viceversa (indicated with the sign –, under-expressed proteins). With a the absence of proteins is indicated. * P <0.05; ** P <0.01 vs. the control.
Supplemental figure 3: Expression fold-change in 2h Proper Energy-treated cells vs. control cells. Proteins are indicated with the name of their genes and with the number reported in Figure 1 and Table 2 of the manuscript. The fold-change values were calculated by the ratio of average of % relative abundance of protein spots in the PE-treated cells vs. the control (indicated with the sign +, over-expressed proteins) or vice versa (indicated with the sign −, under-expressed proteins). With p the presence of proteins is indicated. * P <0.05; ** P <0.01 vs. the control.