SUPPORTING INFORMATION

SAFER, an analysis method of quantitative proteomic data, reveals new interactors of the *C. elegans* autophagic protein LGG-1

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List of Supporting Information.

Legends:

Figure S-1: Gel slicing illustration

Visualization of a representative silver-stained (left) and a representative comassie-stained (right) gel. Left lane of the silver stained gel corresponds to the molecular weight standards and right lane to the immunoprecipitated protein sample. Immunoglobulins light and heavy chains (arrows), around 25kDa and 60kDa respectively, are intense and were excluded from the gel fractions used for further protein identification. Sub-slices of the gel lane into four gel fractions made prior to trypsin digestion and MS analysis are indicated by brackets. Each line was sliced in four fragments, avoiding the Ig chains. MS analysis were realized on coomassie stained gels, as described in the experimental procedures.

Table S-1: List of LGG-1 interactors identified only by SAFER

This table contains the Mass spectrometry raw data, the GO terms for all these proteins and the Fold Change calculated by SAFER (FCs) for the 56 interactors of LGG-1 identified only by SAFER. The "NC" indicates that the FCs has bot not been calculated when the protein is absent in at least three control replicates.

Table S-2: Comparison of MiSt, SAINT t-test and SAFER on interactors for ASH2L, RBBP5 et WDR82.

The * indicates that the prey was independently identified as an interactor of the protein ASH2L or RBBP5 or WDR82. The + indicates that the prey is selected, the - that the prey is removed.