Supplementary Figure 1. Correlation of SILAC ratios between replicates for the nucleus, cytoplasm and total (C&N) samples. Proteins with ≥ 3 ratio counts in both replicates are included. With the exception of a handful of outliers with low ratio counts and low recorded MS intensity, correlation between replicates is high.
Supplementary Figure 2. Analysis of the enrichment of the nuclear fraction. Plots of \( \log(f/f_n) \) as a function of the average number of SILAC ratio counts over the nucleus and total data sets for proteins with GO annotation to the indicated subcellular organelles. For each of the subcellular organelles, the set of proteins was divided into two groups: (a) those annotated to the location and the nucleus (red data points); and, (b) those annotated to the location, but not to the nucleus (blue data points). The number of proteins in each set is indicated in the legend at the top of each plot. For each organelle only a minority of proteins show appreciable changes in the fraction of the protein in the nucleus for oxidative stress (\( f_n \)) compared to control cells (\( f_0 \)). Both increases and decreases in nuclear fraction are seen for cells subjected to oxidative stress, but the average over all proteins is \( \log(f/f_n) \sim 0 \) for all organelles. There is no discernible difference between proteins that are/are not also annotated to the nucleus. The pattern for all organelles is consistent with appreciable nuclear redistribution for a small set of specific proteins from each organelle. The data also suggests that current GO annotations underestimate the number of different proteins in the nucleus of IMR90 cells.
Supplementary Figure 3. Confocal immunofluorescence imaging of ATP5A1 (top panels) and ALDH18A1 (bottom panels) for IMR90 cells with/without treatment with tert-butyl hydrogen peroxide. Nuclei were stained with DAPI and mitochondria with Mitotracker Deep red FM. The proteins were visualized with the same fluorescent secondary FITC antibody (see Materials and Methods).