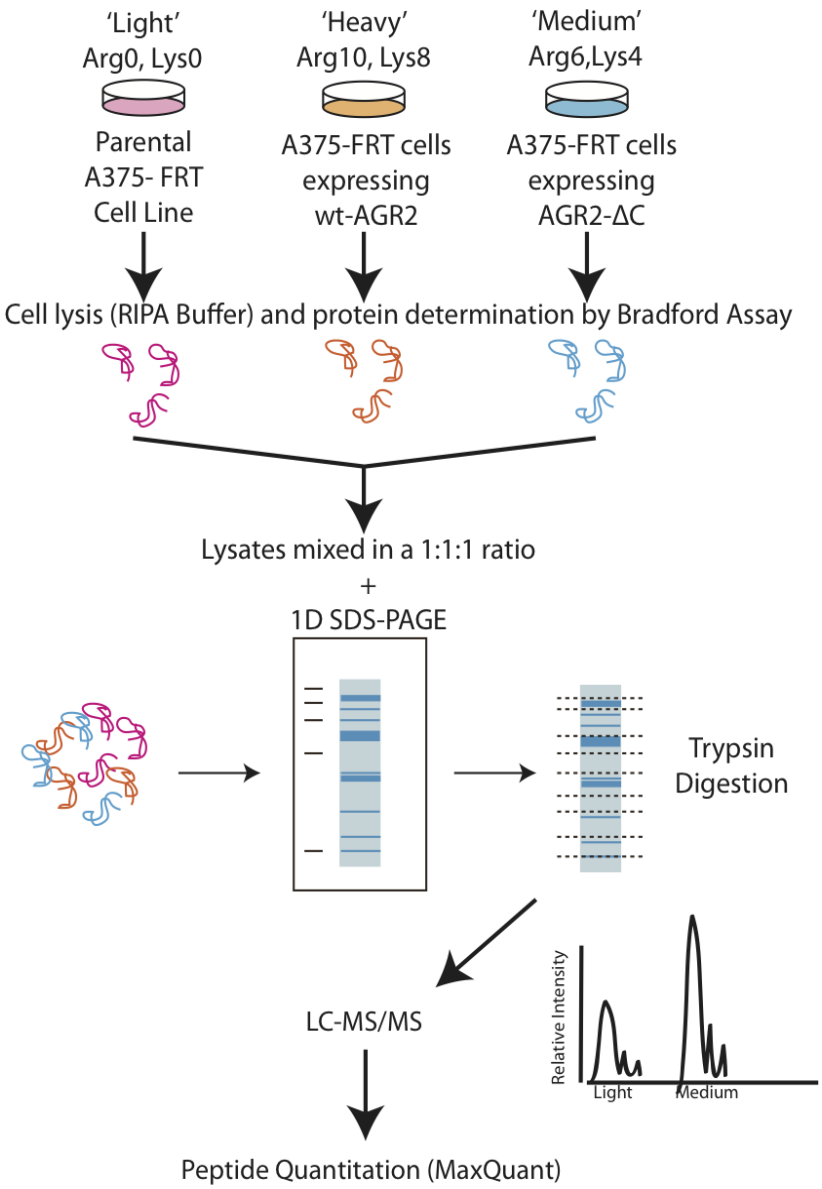

Supplementary Figure 1. Schematic of SILAC experimental protocol. Isogenic cells were in media containing stable isotope labelled amino acids for 6 division cycles to allow incorporation of labelled amino acid residues into newly synthesised proteins[50]. Cells were then lysed in RIPA buffer before protein concentration was determined by Bradford assay. Labelled proteins were then mixed in a 1:1:1 ratio before reduction with DTT and alkylation (iodoacetamide) prior to being separated by 1D SDS-PAGE and visualised by Coomassie staining. The gel lane was then excised and cut into 10 sections. Each section was subjected to in-gel trypsinization before the tryptic peptides were extracted by 1% formic acid and processes as indicated in the Methods.

Supplementary Table 1. Identification of proteins differentially expressed through AGR2 expression. Summary of the fold changes in the expression (normalized and log2 ratios) of the indicated proteins in indicated AGR2 expressing cell line, relative to FRT-AGR2 negative control cell line.