

**Supplemental Figure 1. The StrataClean approach is a very efficient method of capturing protein from dilute proteomes.** A serial dilution experiment was performed to confirm the linearity of capture of proteins from secretome samples using StrataClean. StrataClean was used to capture secreted protein from mixtures of 'cell-conditioned' (cc) media and 'virgin' (v) media in the ratios 100:0, 80:20, 50:50, 20:80 and 0:100. Each was then proteolytically digested on-bead as described in the experimental procedures section, prior to LC-MS/MS and analysis using MaxQuant. For 622 proteins across all samples (except 0:100), the total signal intensity was measured and linear regression performed to investigate the relationship between it and protein input (conditioned:virgin media ratio, denoted cc:v mix). The  $R^2$  of all 622 correlations are plotted as a distribution curve using kernel density estimation confirming the approach to be very efficient at capturing dilute proteomes (see subsequent pages for protein-by-protein linear regression plots).





















































































































