

## Supplemental Experimental Procedures

**Exoprotein sample preparation and LC-MS analysis.** Reconstituted exoprotein isolates were reduced with 0.02 M dithiothreitol and alkylated with 0.05 M iodoacetamide. To remove detergent and other non-MS compatible components from the sample the sample was run approximately 2 cm into a NuPAGE gel (Life Technologies) so that the entire sample was concentrated into a single gel band. The gel was stained with GelCode Blue Stain Reagent (Thermo). The gel bands ('plugs') for each strain were excised and destained for 15 minutes in a 1:1 (v/v) solution of methanol and 100mM ammonium bicarbonate. The buffer was exchanged and the samples were destained for another 15 minutes. This was repeated for another 4 cycles. The gel plugs were dehydrated by washing with acetonitrile, and then further dried by placing them in a SpeedVac for 20 minutes. 500ng of sequencing grade modified trypsin (Promega) was added directly to the dried gel plugs followed by enough 100mM ammonium bicarbonate to cover the gel plugs. The digestion was allowed to proceed overnight with gentle agitation at room temperature. Peptides were extracted and desalted as previously described (42).

**LC-MS method detail.** The peptides were gradient eluted into a Lumos Fusion (Thermo Scientific) mass spectrometer using a 120min gradient from 5% to 23% solvent B (90% acetonitrile, 0.5% acetic acid), followed by 20 minutes from 23% to 45% solvent B. Solvent B was then ramped up to 100% and was held at 100% for 20minutes for column wash. High resolution full MS spectra were acquired with a resolution of 120,000, an AGC target of  $4e5$ , a maximum ion time of 60 ms, and scan range of 400 to 1500 m/z. Following each full MS scan as many data-dependent HCD MS/MS spectra were

acquired in the ion trap with rapid scan rate as possible in a 3 second cycle time.

Monoisotopic precursor selection (MIPS) was on and set to peptide, precursors with a charge state of 2 – 7 and minimum intensity of  $5e3$  were selected for MS/MS. Dynamic exclusion was set to 30 seconds exclusion time after a single selection. All MS/MS spectra were collected using the following instrument parameters: AGC target of  $1e4$ , maximum ion time of 60 ms, one microscan, 2.0 m/z isolation window, and Normalized Collision Energy (NCE) of 32.