Electronic Supplementary Material (ESI) for Molecular Omics.

Supplemental UPLC file: HILIC-UPLC (hydrophilic interaction ultra-performance liquid chromatography) glycan analysis of 2-AB labelled *N*-glycans digested with exoglycosidases. To determine the *N*-glycan structures of each peak: WCLs, Cytoplasm, Membrane and EVs of control and PTX induced TIS Cal51 cells were of digested with exoglycosidase arrays: ABS, ABS+BTG, ABS+SPG, ABS+BTG+GUH, ABS+BTG+AMF, ABS+BTG+BKF, JBM and NAN1. The digestions and reference dextran were run on the Waters ACQUITY® UPLC system, integrated using the Empower software and *N*-linked glycan structures were determined via data analysis of the shifts in peak areas. A table of summary of the peak areas of the different glycan structures is present for each sample type. Features like sialylation, galactosylation and others were calculated from the percentages of areas of glycans containing this feature. Samples were pooled for the digestions from the three replicates.

Supplemental MS file: Liquid chromatography mass spectrometry (LC/MS) confirmation of the UPLC results. To confirm the HILIC-UPLC data WCLs, Cytoplasm, Membrane and EVs were run on the Acquity® UPLC-FLD-QTof LC/MS system. Data analysis using MassLynx V4.1 and GlycoWorkbench 2 ensured that all *N*-linked glycans determined using HILIC-UPLC were also present in the LC/MS data. The experimental mass (m/z), theoretical mass (m/z), Error (ppm), ion, assignment, monosaccharide composition and monoisotopic mass were described for each glycan assignment. Samples were pooled for the MS from the three replicates.