Electronic Supplementary Material (ESI) for Molecular Omics.

Supplemental Figures legend.

Supplemental figure S1: HILIC-UPLC (hydrophilic interaction ultra-performance liquid chromatography) analysis of 2-AB labelled *N*-glycans demonstrates significant differential profiles in the cytoplasm, the membrane and in the EV progeny from TIS and non-senescent TNBC cells. Cal51 cells were treated with 75 nM PTX for 7 days to induce senescence. **A.** Whole cell lysates (WCLs), **B.** Cytoplasm, **C.** Membrane and **D.** Extracellular vesicles (EVs) were isolated. *N*-linked glycans were released using the *in-gel-block* high throughput (IGB-HT) method and PNGase F treatment. Samples were labelled with 2AB and analysed using the Waters ACQUITY® UPLC. All the samples were then integrated and quantitated using dextran as the glucose unit (GU) ladder. The data were transformed using the following formula: log(peak/(100-peak)) and checked for normality using the Kolmogorov Smirnov test. Normally distributed data were then analysed using the multivariate analysis of variance (MANOVA) test. The post hoc and Tukey tests were utilised to test for significance between the groups. Levene's test was carried out to test for homogeneity of variance. Significant differences are defined as $p \leq 0.05$ *, $p \leq 0.01$ **, $p \leq 0.001$ ***. Significant differences in peaks are represented as red (increase) and green (decrease) arrows. This figure represents n=3 biological replicates.

Supplemental figure S2: Three biological replicates of 2-AB labelled *N*-glycans from control and TIS WCL, cytoplasm, membrane and EVs ran on HILIC-UPLC (hydrophilic interaction ultra-performance liquid chromatography). Cal51 cells were treated with 75 nM PTX for 7 days to induce senescence. Three biological replicates of *N*-linked glycans from **A.** Whole cell lysates (WCLs), **B.** Cytoplasm, **C.** Membrane and **D.** Extracellular vesicles (EVs) were isolated using the *in-gel-block* high throughput (IGB-HT) method and PNGase F treatment. Samples were labelled with 2AB and analysed using the Waters ACQUITY® UPLC. All the samples were then integrated and quantitated using dextran as the glucose unit (GU) ladder. This figure represents n=3 biological replicates.

Supplemental figure S3: HILIC-UPLC (hydrophilic interaction ultra-performance liquid chromatography) glycan analysis of 2-AB labelled *N*-glycans digested with exoglycosidases and liquid chromatography mass spectrometry (LC/MS) confirmation of the UPLC results. To determine the *N*-glycan structures of each peak **A.** WCLs, **C.** Cytoplasm, **E.** Membrane and **G.** EVs of control and PTX induced TIS Cal51 cells were of digested with exoglycosidase arrays: ABS, ABS+SPG, ABS+BTG, ABS+BTG+BKF, ABS+BTG+GUH, ABS+BTG+AMF, JBM and NAN1. The digestions were run on the Waters ACQUITY® UPLC system, integrated and *N*-linked glycan structures were determined via data analysis. To confirm the HILIC-UPLC data **B.** WCLs, **D.** Cytoplasm, **F.** Membrane and **H.** EVs were run on the Acquity® UPLC-FLD-QTof LC/MS system. Data analysis ensured that all *N*-linked glycans determined using HILIC-UPLC were also present in the LC/MS data. Samples were pooled for the digestions and MS from the three replicates.