Supplementary Table Legend

Table S1 Lists of proteins identified and quantified in the three senescence secretome analyses

The table contains the lists of proteins identified and quantified in the secretome proteomic analysis of senescent cells induced by Ras (RAS), etoposide (ETO), or replicative telomere exhaustion (REP). Also included is the list of SASP/SMS factors identified in these analyses (SASP). These datasets contain proteins with ProteinProphet probability score ≥ 0.5. Protein abundance ratios were calculated using the ASAPRatio software tool. Abundance ratio of 999 or 0 denotes that the protein displayed obvious increase or decrease, respectively, but was difficult to quantify. Abundance ratio indicated as '?' denotes that the protein was identified, but was not quantifiable.

The description of each column in these datasets is as follows:
A: ProteinProphet probability score
B: Protein abundance ratio (senescent cells/non-senescent cells)
C: Number of peptides identified
D: Gene name
E: Description
F: Y denotes previously reported SASP/SMS factor.