Figure S1. Proteomic analysis flowchart. Left panel shows the steps at which proteins identified by LC-MS/MS were discarded according to the quality criteria defined in the present study, and the final number of proteins used for overrepresentation analysis. Right panel shows how the spots were discarded and the number that were retained for identification. PCA, principal component analysis; 2DE, 2D electrophoresis; MALDI-TOF, matrix-assisted laser desorption/ionization-time of flight; LC-MS/MS, liquid chromatography coupled to tandem mass spectrometry; PPI, protein-protein interaction.

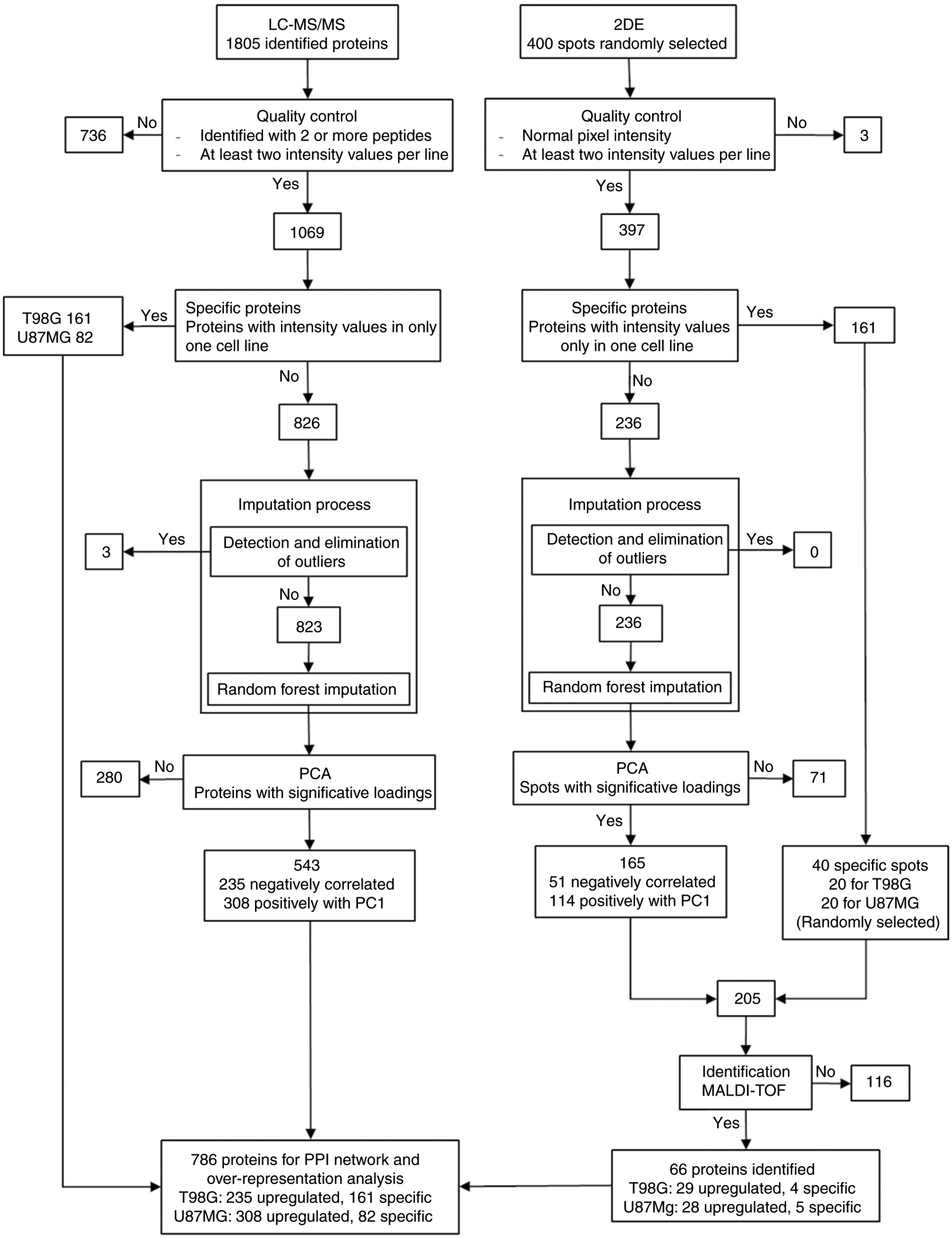
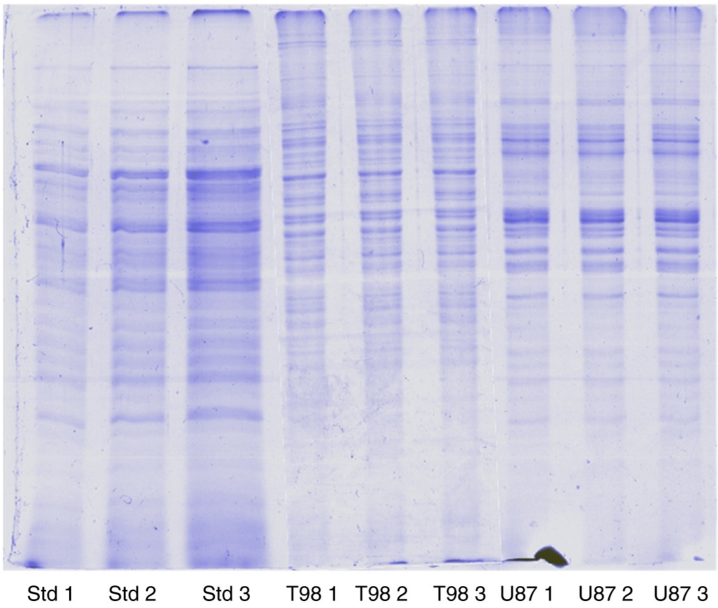


Figure S2. Loading control for oxidative phosphorylation and bioenergetic signature. Left panel shows the SDS-PAGE for Std1, 2 and 3 with 3, 5 and 10 μg of protein, respectively, and three biological replicates each for T98G and U87MG cells. Right panel shows the densitometry analysis using the Quantity One software v4.1 from Bio-Rad Laboratories, Inc. Std, standard.



Name	Concentration	Area mm^2
Std 1	3.00	201.61
Std 2	5.00	201.61
Std 3	10.00	201.61
T98 1	4.51	201.61
T98 2	4.53	201.61
T98 3	4.96	201.61
U87 1	4.84	201.61
U87 2	4.58	201.61
U87 3	4.99	201.61