**Analysis of protein by reverse phase nanospray-spray liquid chromatography with tandem mass spectrometry (RP nano-LC-MS/MS).** Protein bands were individually excised from the gel and cut into small (~1 x 1 mm2 pieces using a scalpel. The gel pieces were destained, disulfide bonds were reduced, unmodified thiol groups were alkylated, and proteins were digested with trypsin overnight using the In-Gel Tryptic Digestion Kit (Pierce, Rockford, IL) according to the manufacturer’s instructions. After digestion, the liquid containing the peptides were transferred to a 1.5 ml tube. The peptides were further extracted from the gel pieces by covering gel pieces with extraction buffer consisting of formic acid/acetonitrile/water (5:50:45, v/v/v) for 10 min then collecting the liquid and adding it to the appropriate tube. The peptides in the vial inserts were completely dried using a DNA Speed Vac Concentrator (Thermo Fisher Scientific, Asheville, N.C.). Peptides were rehydrated with 0.1% formic acid and further purified using zip tips (ZipTipU-C18, Millipore Corp., Billerica, MA) according to manufacturer’s instructions. Peptides eluted from zip tips were transferred to vial inserts. The peptides in the vial inserts were completely dried using the Speed Vac Concentrator and then rehydrated in a volume of 6 μl of formic acid/acetonitrile/water (0.1:20:79.9, v/v/v). A volume of 2 μl was injected into a C18 picofrit column (New Objective, Inc., Woburn, MA). The column was first equilibrated in solvent A (0.1% formic acid in water/acetonitrile (98:2, v/v)) and then eluted with a gradient of 2 – 40% of solvent B containing 0.1% formic acid in acetonitrile over 60 min at a flow rate of 200 nL/min. Eluted peptides were analyzed by electrospray ionization LTQ-XL ion trap mass spectrometer (Thermo Scientific, Waltham. MA). Mass spectrometry data were acquired using data-dependent acquisition with a series of one full scan followed by a zoom scan and then a MS/MS scan of the ions. The dynamic exclusion duration was 30 ms. Proteins were identified from each mass spectrometry raw data file using Thermo Proteome Discoverer 1.2 (Thermo Fisher) with a signal to noise threshold of 1.5, precursor mass tolerance of 1400 mmu, and fragment mass tolerance of 0.8 Da.