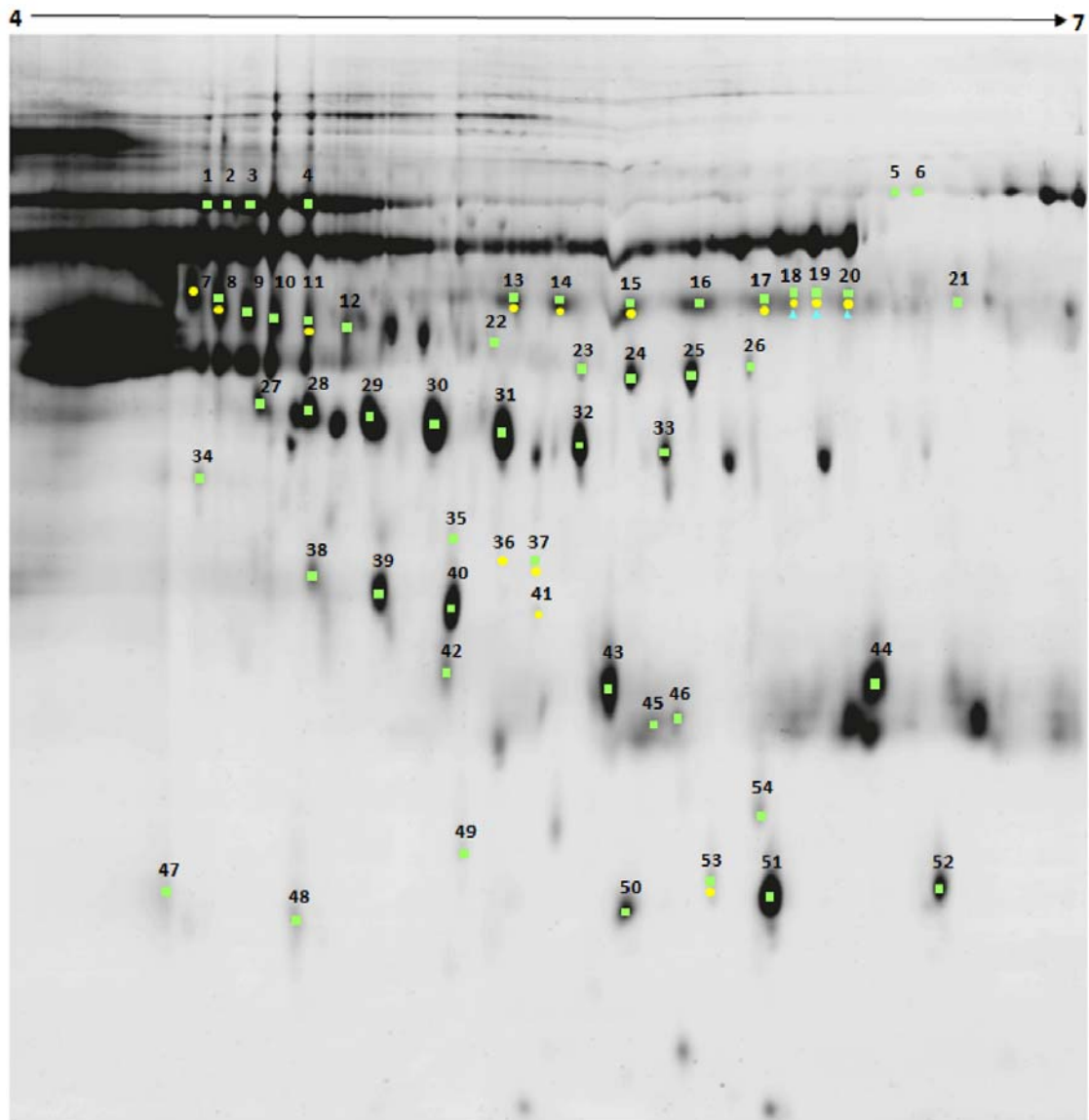


Supplementary document 1



Representative 2-D map of the urine proteome obtained by using IEF on pH 4–7 IPG strip and 2-D gel electrophoresis on 12.5% SDS-PAGE. Protein with differential abundance between studied groups are marked as follows: (●) PCa/BPH, (■) PCa/BC and (▲) PCa/RC. Details of spots identification by peptide mass fingerprinting using MALDI-TOF MS are given in Table 1.

The annotated MS spectra of selected spots representing each of the identified proteins with differential abundance in this study. The peaks submitted for Mascot search are annotated with orange lines and m/z values. The peaks specific for the identified protein are marked with green dots. Spectra annotated with orange star have significant number of peptide peaks in peptide mass fingerprinting not matching to the identified protein, indicating possible existence of more than one protein. The remaining (not annotated) peaks belong to matrix, trypsin autolysis products and other contaminants.

